

# What shapes genome-wide diversity?

A case study in *Drosophila melanogaster*

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## 1 Drosophila-like neutral simulations of 2L (True Landscapes)

Second batch of 10 replicate datasets simulated using parameters as inferred from real Drosophila data.

Here we present results using true (simulated) genomic landscapes.

### 1.1 50 kb scale

```
r2.sim.50kb <- as.data.frame(matrix(ncol = nreps, nrow = 5))
row.names(r2.sim.50kb) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
colnames(r2.sim.50kb) <- reps

sim.rho.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/dm.sim.rho.50000.txt", header = T)
sim.theta.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/dm.sim.theta.50000.txt", header = T)
```

#### 1.1.1 Replicate 1

```
rep_1.pi.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_1/rep_1.pi.50kb.bedgraph", header = F)
rep_1.tmrca.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_1/sim.tmrca.50k.map", header = F)

sim.lands.50kb <- as.data.frame(cbind(rep_1.pi.50kb$pi, sim.theta.50kb$sim, sim.rho.50kb$sim, rep_1.tmrca.50kb$tmrca))
names(sim.lands.50kb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 36665911, p-value = 0.6511
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.01850036

cor.test(~theta+rho, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
```

```

## data: theta and rho
## S = 37660747, p-value = 0.2592
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##          rho
## -0.04613476

cor.test(~rho+tmrca, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 35649572, p-value = 0.8119
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##          rho
## 0.00973136

# centering
sim.lands.50kb$thetaC <- sim.lands.50kb$theta - mean(sim.lands.50kb$theta)
sim.lands.50kb$tmrcaC <- sim.lands.50kb$tmrca - mean(sim.lands.50kb$tmrca)
sim.lands.50kb$rhoC <- sim.lands.50kb$rho - mean(sim.lands.50kb$rho)

sim.lands.50kb$bin <- 1:nrow(sim.lands.50kb)

# for merging:
sim.lands.50kb.rep5 <- sim.lands.50kb
sim.lands.50kb.rep5$Replicate <- 1

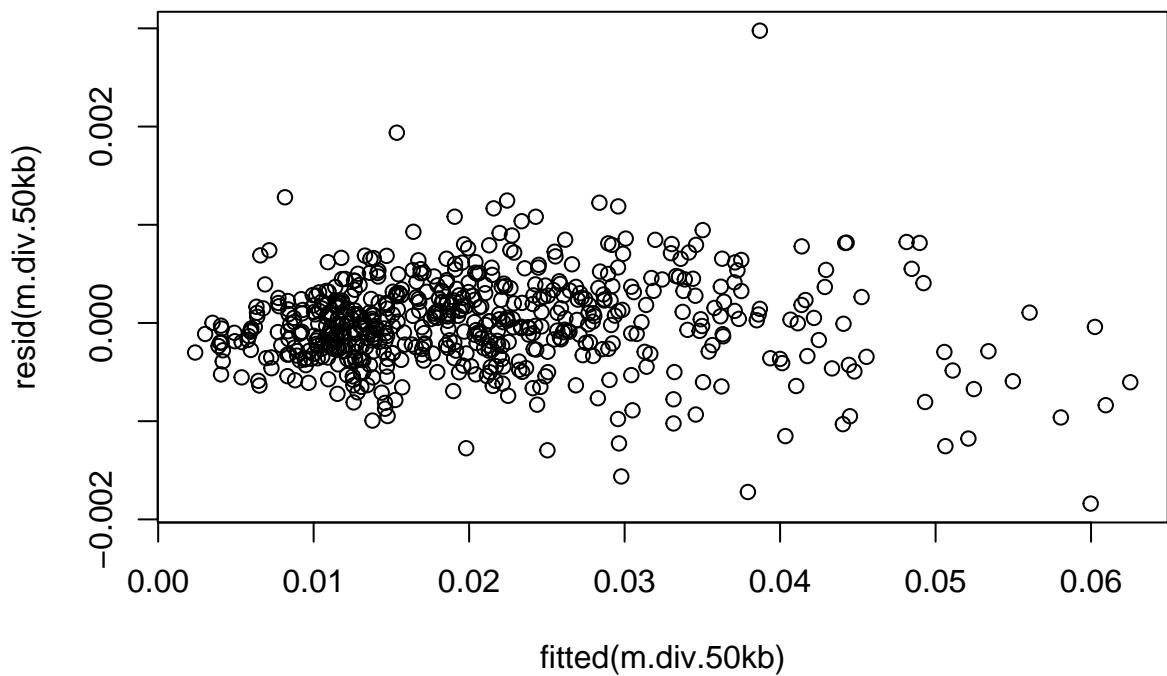
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.50kb)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = sim.lands.50kb)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = sim.lands.50kb)

AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

##           df      AIC
## m.div.50kb    6 -7492.648
## m.div.50kb.2   7 -7491.365
## m.div.50kb.3   8 -7491.767

plot(resid(m.div.50kb)~fitted(m.div.50kb))

```

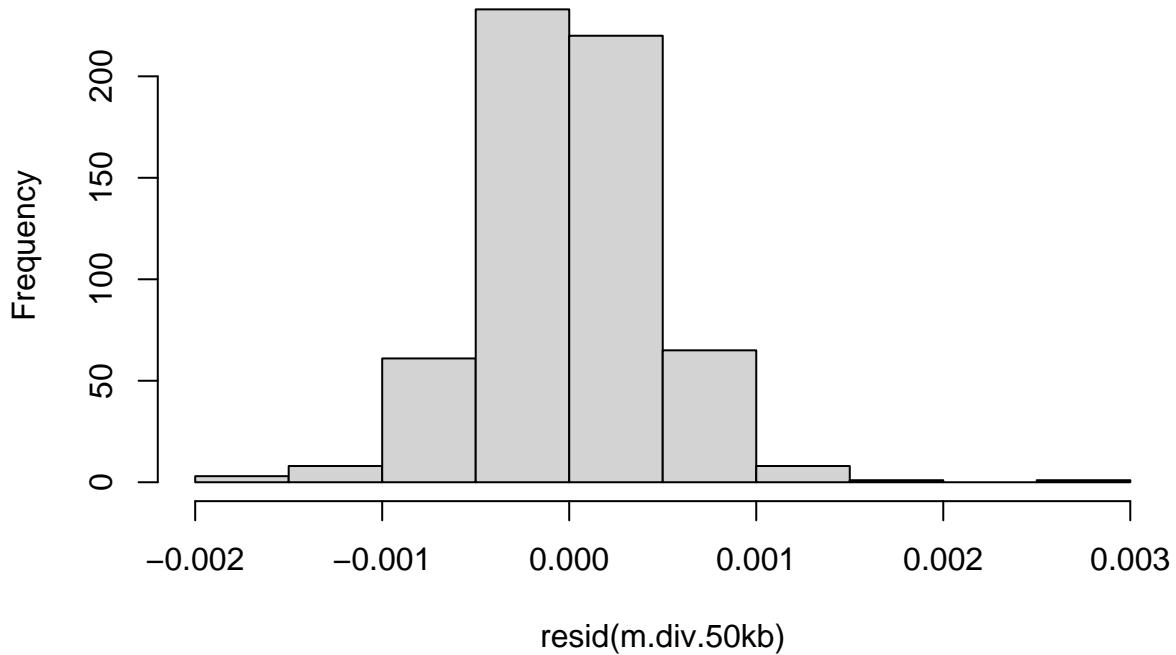


```
dwtest(m.div.50kb)
```

```
##
## Durbin-Watson test
##
## data: m.div.50kb
## DW = 2.1111, p-value = 0.9056
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)
```

```
##
## Harrison-McCabe test
##
## data: m.div.50kb
## HMC = 0.39214, p-value < 2.2e-16
hist(resid(m.div.50kb))
```

## Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,  
##      data = sim.lands.50kb)  
##  
## Residuals:  
##      Min       1Q   Median       3Q      Max  
## -1.839e-03 -2.676e-04 -1.006e-05  2.647e-04  2.976e-03  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 2.069e-02 1.908e-05 1084.381 <2e-16 ***  
## thetaC      1.309e+00 2.283e-03  573.279 <2e-16 ***  
## rhoC        1.435e-02 6.455e-03   2.223  0.0266 *  
## tmrcaC      2.342e-02 2.686e-04   87.195 <2e-16 ***  
## thetaC:tmrcaC 1.483e+00 3.029e-02   48.983 <2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0004673 on 595 degrees of freedom  
## Multiple R-squared:  0.9982, Adjusted R-squared:  0.9982  
## F-statistic: 8.37e+04 on 4 and 595 DF,  p-value: < 2.2e-16
```

```
anova.diversity <- Anova(m.div.50kb)  
apiss <- anova.diversity$"Sum Sq"  
anova.diversity$VarExp <- apiss / sum(apiss)
```

```
r2.sim.50kb[1, 1] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.sim.50kb[2, 1] <- anova.diversity$VarExp[1] * 100
r2.sim.50kb[3, 1] <- anova.diversity$VarExp[2] * 100
r2.sim.50kb[4, 1] <- anova.diversity$VarExp[3] * 100
r2.sim.50kb[5, 1] <- anova.diversity$VarExp[4] * 100

g.div.50kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = sim.lands.50kb, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method =
                      "ML")

g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = sim.lands.50kb, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method =
                      "ML")

g.div.50kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = sim.lands.50kb, weights = varPower(0, ~theta), method = "ML")

g.div.50kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = sim.lands.50kb, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.50kb.1, g.div.50kb.2, g.div.50kb.3, g.div.50kb.4)

##             df      AIC
## g.div.50kb.1 8 -7490.623
## g.div.50kb.2 8 -7570.956
## g.div.50kb.3 7 -7572.341
## g.div.50kb.4 7 -7490.654

summary(g.div.50kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: sim.lands.50kb
##       AIC      BIC  logLik
##   -7572.341 -7541.562 3793.17
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##       power
## 0.4774622
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0206901 0.00001905 1086.3241 0.0000
## thetaC       1.3155987 0.00236880  555.3850 0.0000
## rhoC        0.0087173 0.00554727    1.5715 0.1166
## tmrcaC      0.0234411 0.00026760    87.5965 0.0000
## thetaC:tmrcaC 1.4652196 0.03311231    44.2500 0.0000
##
## Correlation:
##              (Intr) thetaC rhoC   tmrcaC
## thetaC      0.497
## rhoC        0.001  0.052
## tmrcaC     0.013  0.026 -0.004
## thetaC:tmrcaC 0.026  0.025  0.036  0.494

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -2.955335880 -0.608690299  0.006577071  0.610719662  4.719725050
## 
## Residual standard error: 0.003393872
## Degrees of freedom: 600 total; 595 residual
vif(g.div.50kb.3)

##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
##     1.003575    1.004633    1.323896    1.325415

```

### 1.1.2 Replicate 2

```

rep_2.pi.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_2/rep_2.pi.50kb.bedgraph", header = FALSE)
rep_2.tmrca.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_2/sim.tmrca.50k.map", header = FALSE)

sim.lands.50kb <- as.data.frame(cbind(rep_2.pi.50kb$pi, sim.theta.50kb$sim, sim.rho.50kb$sim, rep_2.tmrca.50kb))
names(sim.lands.50kb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.50kb, method = "spearman")

## 
## Spearman's rank correlation rho
## 
## data: theta and tmrca
## S = 36499595, p-value = 0.7344
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.01388046

cor.test(~theta+rho, data = sim.lands.50kb, method = "spearman")

## 
## Spearman's rank correlation rho
## 
## data: theta and rho
## S = 37660747, p-value = 0.2592
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.04613476

cor.test(~rho+tmrca, data = sim.lands.50kb, method = "spearman")

## 
## Spearman's rank correlation rho
## 
## data: rho and tmrca
## S = 33177308, p-value = 0.05494
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.07840555

```

```

# centering
sim.lands.50kb$thetaC <- sim.lands.50kb$theta - mean(sim.lands.50kb$theta)
sim.lands.50kb$tmrcaC <- sim.lands.50kb$tmrca - mean(sim.lands.50kb$tmrca)
sim.lands.50kb$rhoC <- sim.lands.50kb$rho - mean(sim.lands.50kb$rho)

sim.lands.50kb$bin <- 1:nrow(sim.lands.50kb)

# for merging:
sim.lands.50kb.rep2 <- sim.lands.50kb
sim.lands.50kb.rep2$Replicate <- 2

m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.50kb)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = sim.lands.50kb)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = sim.lands.50kb)

AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

##          df      AIC
## m.div.50kb     6 -7408.739
## m.div.50kb.2   7 -7409.225
## m.div.50kb.3   8 -7407.388

plot(resid(m.div.50kb)~fitted(m.div.50kb))




dwtest(m.div.50kb)



```

##
##  Durbin-Watson test
##
##  data:  m.div.50kb
##  DW = 1.9715, p-value = 0.3445
##  alternative hypothesis: true autocorrelation is greater than 0

```


```

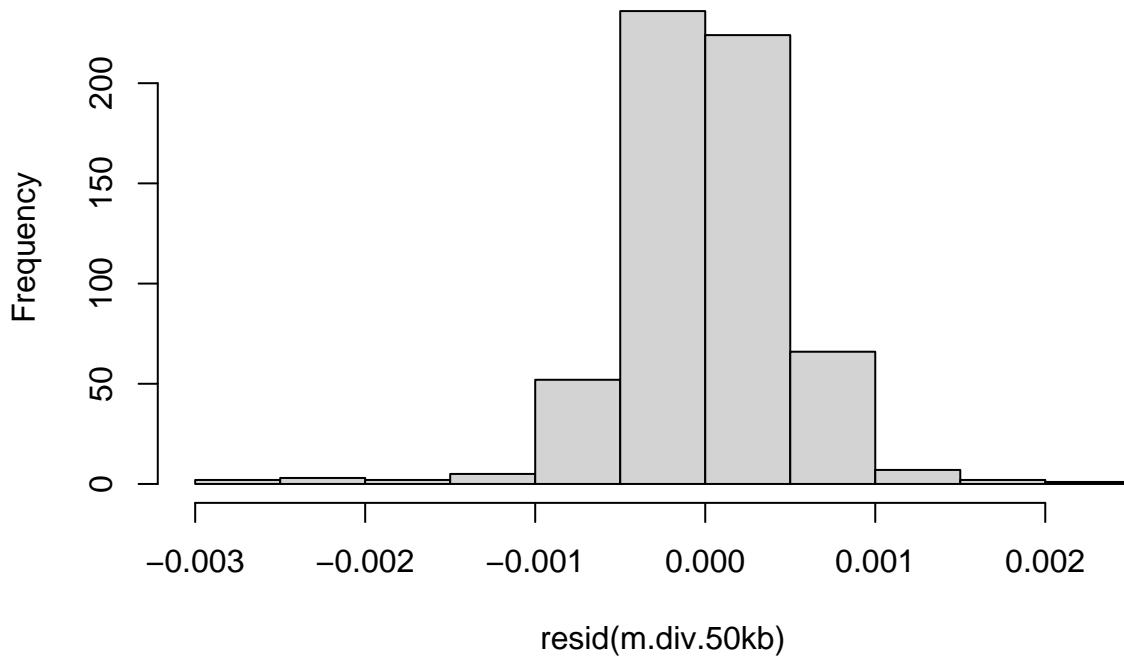
```

hmctest(m.div.50kb)

##
##  Harrison-McCabe test
##
## data: m.div.50kb
## HMC = 0.51438, p-value = 0.697
hist(resid(m.div.50kb))

```

**Histogram of resid(m.div.50kb)**



```

summary(m.div.50kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.50kb)
##
## Residuals:
##       Min         1Q     Median         3Q        Max
## -2.857e-03 -2.640e-04  1.830e-06  2.990e-04  2.087e-03
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.057e-02 2.047e-05 1005.301 <2e-16 ***
## thetaC       1.299e+00 2.448e-03  530.815 <2e-16 ***
## rhoC        -1.009e-02 6.919e-03   -1.459   0.145
## tmrcaC       2.385e-02 2.831e-04    84.273 <2e-16 ***
## thetaC:tmrcaC 1.515e+00 3.222e-02    47.015 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

## 
## Residual standard error: 0.0005011 on 595 degrees of freedom
## Multiple R-squared:  0.9979, Adjusted R-squared:  0.9979
## F-statistic: 7.16e+04 on 4 and 595 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$`Sum Sq`
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.50kb[1, 2] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]
r2.sim.50kb[2, 2] <- anova.diversity$VarExp[1] * 100
r2.sim.50kb[3, 2] <- anova.diversity$VarExp[2] * 100
r2.sim.50kb[4, 2] <- anova.diversity$VarExp[3] * 100
r2.sim.50kb[5, 2] <- anova.diversity$VarExp[4] * 100

```

### 1.1.3 Replicate 3

```

rep_3.pi.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_3/rep_3.pi.50kb.bedgraph", header = FALSE)
rep_3.tmrca.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_3/sim.tmrca.50k.map", header = FALSE)

sim.lands.50kb <- as.data.frame(cbind(rep_3.pi.50kb$pi, sim.theta.50kb$sim, sim.rho.50kb$sim, rep_3.tmrca.50kb))
names(sim.lands.50kb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.50kb, method = "spearman")

## 
## Spearman's rank correlation rho
## 
## data: theta and tmrca
## S = 37873663, p-value = 0.203
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##          rho
## -0.05204912

cor.test(~theta+rho, data = sim.lands.50kb, method = "spearman")

## 
## Spearman's rank correlation rho
## 
## data: theta and rho
## S = 37660747, p-value = 0.2592
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##          rho
## -0.04613476

cor.test(~rho+tmrca, data = sim.lands.50kb, method = "spearman")

## 
## Spearman's rank correlation rho
## 
## data: rho and tmrca
## S = 35383984, p-value = 0.6757
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##          rho
## -0.04613476

```

```

##          rho
## 0.01710883

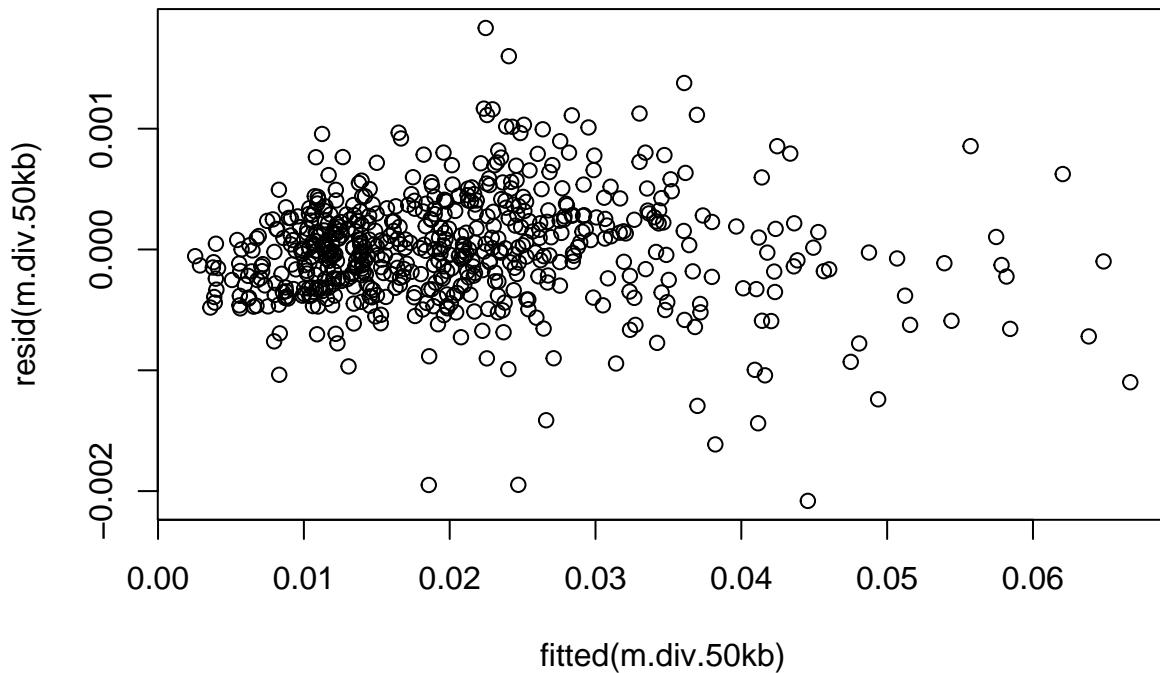
# centering
sim.lands.50kb$thetaC <- sim.lands.50kb$theta - mean(sim.lands.50kb$theta)
sim.lands.50kb$tmrcaC <- sim.lands.50kb$tmrca - mean(sim.lands.50kb$tmrca)
sim.lands.50kb$rhoC <- sim.lands.50kb$rho - mean(sim.lands.50kb$rho)

sim.lands.50kb$bin <- 1:nrow(sim.lands.50kb)

# for merging:
sim.lands.50kb.rep3 <- sim.lands.50kb
sim.lands.50kb.rep3$Replicate <- 3

m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.50kb)
plot(resid(m.div.50kb)~fitted(m.div.50kb))

```



```

dwtest(m.div.50kb)

##
##  Durbin-Watson test
##
## data: m.div.50kb
## DW = 1.9214, p-value = 0.1563
## alternative hypothesis: true autocorrelation is greater than 0

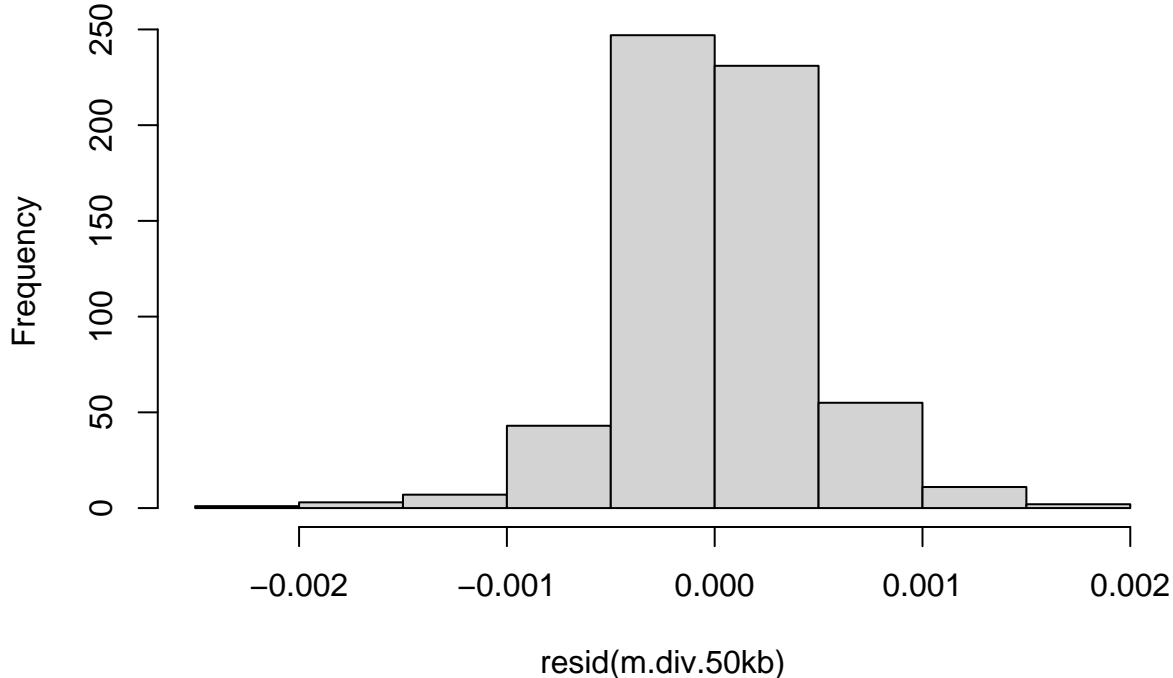
hmctest(m.div.50kb)

##
##  Harrison-McCabe test
##
## data: m.div.50kb
## HMC = 0.50434, p-value = 0.579

```

```
hist(resid(m.div.50kb))
```

Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,  
##      data = sim.lands.50kb)  
##  
## Residuals:  
##       Min        1Q     Median        3Q       Max  
## -2.081e-03 -2.636e-04 -7.680e-06  2.600e-04  1.833e-03  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 0.0206720  0.0000187 1105.47 <2e-16 ***  
## thetaC       1.3103632  0.0022312  587.29 <2e-16 ***  
## rhoC         0.0064418  0.0063164    1.02   0.308  
## tmrcaC       0.0236099  0.0002297  102.80 <2e-16 ***  
## thetaC:tmrcaC 1.5012872  0.0254605   58.97 <2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0004578 on 595 degrees of freedom  
## Multiple R-squared:  0.9983, Adjusted R-squared:  0.9983  
## F-statistic: 8.857e+04 on 4 and 595 DF,  p-value: < 2.2e-16  
anova.diversity <- Anova(m.div.50kb)  
apiss <- anova.diversity$"Sum Sq"  
anova.diversity$VarExp <- apiss / sum(apiss)
```

```
r2.sim.50kb[1, 3] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.sim.50kb[2, 3] <- anova.diversity$VarExp[1] * 100
r2.sim.50kb[3, 3] <- anova.diversity$VarExp[2] * 100
r2.sim.50kb[4, 3] <- anova.diversity$VarExp[3] * 100
r2.sim.50kb[5, 3] <- anova.diversity$VarExp[4] * 100
```

#### 1.1.4 Replicate 4

```
rep_4.pi.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_4/rep_4.pi.50kb.bedgraph", header = TRUE)
rep_4.tmrca.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_4/sim.tmrca.50k.map", header = TRUE)

sim.lands.50kb <- as.data.frame(cbind(rep_4.pi.50kb$pi, sim.theta.50kb$sim, sim.rho.50kb$sim, rep_4.tmrca.50kb))
names(sim.lands.50kb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 36135074, p-value = 0.9269
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##          rho
## -0.003754843

cor.test(~theta+rho, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 37660747, p-value = 0.2592
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##          rho
## -0.04613476

cor.test(~rho+tmrca, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 37039432, p-value = 0.4801
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##          rho
## -0.02887597

# centering
sim.lands.50kb$thetaC <- sim.lands.50kb$theta - mean(sim.lands.50kb$theta)
sim.lands.50kb$tmrcaC <- sim.lands.50kb$tmrca - mean(sim.lands.50kb$tmrca)
sim.lands.50kb$rhoC <- sim.lands.50kb$rho - mean(sim.lands.50kb$rho)
```

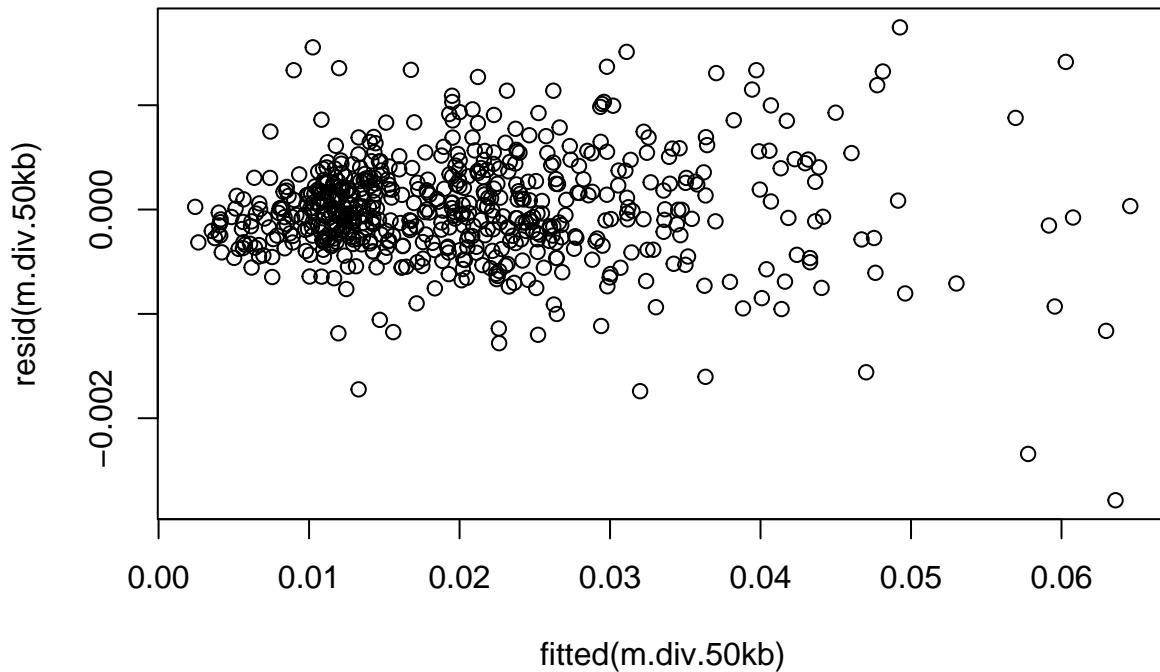
```

sim.lands.50kb$bin <- 1:nrow(sim.lands.50kb)

# for merging:
sim.lands.50kb.rep4 <- sim.lands.50kb
sim.lands.50kb.rep4$Replicate <- 4

m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.50kb)
plot(resid(m.div.50kb)~fitted(m.div.50kb))

```



```

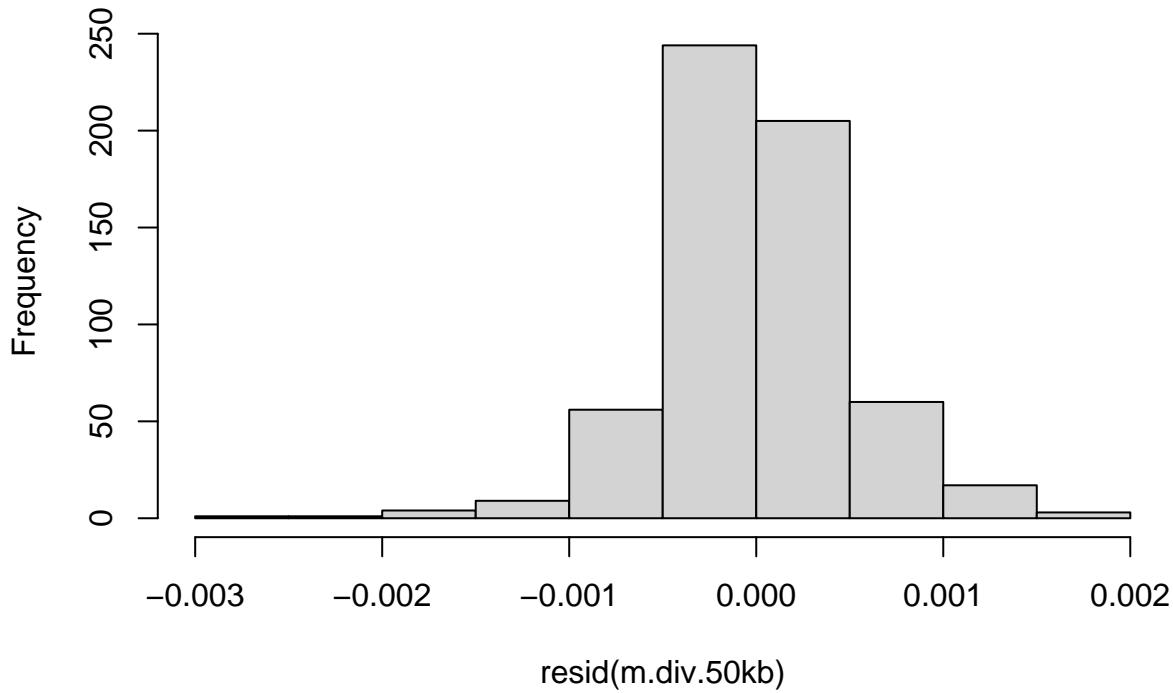
dwtest(m.div.50kb)

##
##  Durbin-Watson test
##
##  data: m.div.50kb
##  DW = 2.0985, p-value = 0.8779
##  alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)

##
##  Harrison-McCabe test
##
##  data: m.div.50kb
##  HMC = 0.53836, p-value = 0.925
hist(resid(m.div.50kb))

```

## Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.50kb)
##
## Residuals:
##       Min         1Q     Median         3Q        Max
## -2.787e-03 -2.851e-04 -3.163e-05  2.685e-04  1.746e-03
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.050e-02 2.077e-05 987.094 <2e-16 ***
## thetaC      1.300e+00 2.476e-03 525.118 <2e-16 ***
## rhoC        1.386e-02 7.016e-03  1.976  0.0486 *
## tmrcaC     2.349e-02 2.643e-04  88.857 <2e-16 ***
## thetaC:tmrcaC 1.493e+00 3.134e-02  47.634 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0005088 on 595 degrees of freedom
## Multiple R-squared:  0.9979, Adjusted R-squared:  0.9979
## F-statistic: 7.205e+04 on 4 and 595 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.50kb[1, 4] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```
r2.sim.50kb[2, 4] <- anova.diversity$VarExp[1] * 100
r2.sim.50kb[3, 4] <- anova.diversity$VarExp[2] * 100
r2.sim.50kb[4, 4] <- anova.diversity$VarExp[3] * 100
r2.sim.50kb[5, 4] <- anova.diversity$VarExp[4] * 100
```

### 1.1.5 Replicate 5

```
rep_5.pi.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_5/rep_5.pi.50kb.bedgraph", header = FALSE)
rep_5.tmrca.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_5/sim.tmrca.50k.map", header = FALSE)

sim.lands.50kb <- as.data.frame(cbind(rep_5.pi.50kb$pi, sim.theta.50kb$sim, sim.rho.50kb$sim, rep_5.tmrca.50kb))
names(sim.lands.50kb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 35425520, p-value = 0.6965
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.01595505

cor.test(~theta+rho, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 37660747, p-value = 0.2592
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.04613476

cor.test(~rho+tmrca, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 37018948, p-value = 0.4888
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.02830697

# centering
sim.lands.50kb$thetaC <- sim.lands.50kb$theta - mean(sim.lands.50kb$theta)
sim.lands.50kb$tmrcaC <- sim.lands.50kb$tmrca - mean(sim.lands.50kb$tmrca)
sim.lands.50kb$rhoC <- sim.lands.50kb$rho - mean(sim.lands.50kb$rho)

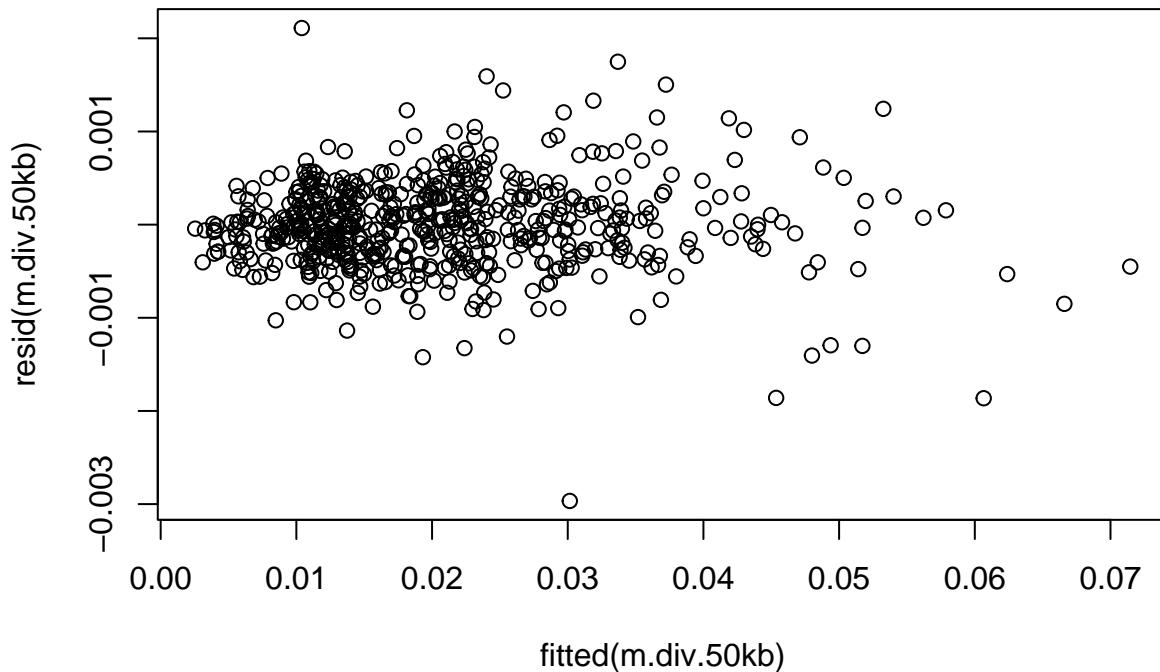
sim.lands.50kb$bin <- 1:nrow(sim.lands.50kb)
```

```

# for merging:
sim.lands.50kb.rep5 <- sim.lands.50kb
sim.lands.50kb.rep5$Replicate <- 5

m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.50kb)
plot(resid(m.div.50kb)~fitted(m.div.50kb))

```



```
dwtest(m.div.50kb)
```

```

##
## Durbin-Watson test
##
## data: m.div.50kb
## DW = 2.0931, p-value = 0.864
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)

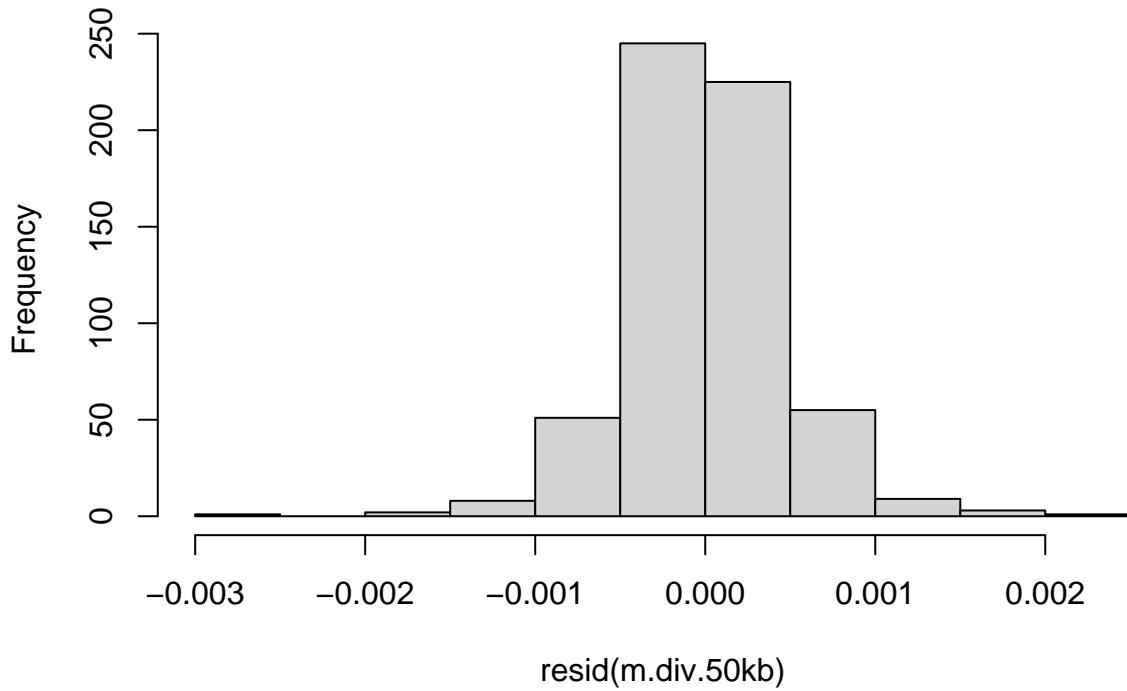
```

```

##
## Harrison-McCabe test
##
## data: m.div.50kb
## HMC = 0.45962, p-value = 0.084
hist(resid(m.div.50kb))

```

## Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.50kb)
##
## Residuals:
##       Min         1Q     Median         3Q        Max
## -2.966e-03 -2.902e-04 -1.674e-05  2.879e-04  2.110e-03
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.062e-02 1.967e-05 1048.31 <2e-16 ***
## thetaC      1.308e+00 2.348e-03  557.06 <2e-16 ***
## rhoC        1.528e-03 6.645e-03   0.23  0.818
## tmrcaC     2.374e-02 2.674e-04   88.80 <2e-16 ***
## thetaC:tmrcaC 1.471e+00 3.126e-02   47.05 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0004816 on 595 degrees of freedom
## Multiple R-squared:  0.9981, Adjusted R-squared:  0.9981
## F-statistic: 7.932e+04 on 4 and 595 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.50kb[1, 5] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```
r2.sim.50kb[2, 5] <- anova.diversity$VarExp[1] * 100
r2.sim.50kb[3, 5] <- anova.diversity$VarExp[2] * 100
r2.sim.50kb[4, 5] <- anova.diversity$VarExp[3] * 100
r2.sim.50kb[5, 5] <- anova.diversity$VarExp[4] * 100
```

### 1.1.6 Replicate 6

```
rep_6.pi.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_6/rep_6.pi.50kb.bedgraph", header = FALSE)
rep_6.tmrca.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_6/sim.tmrca.50k.map", header = FALSE)

sim.lands.50kb <- as.data.frame(cbind(rep_6.pi.50kb$pi, sim.theta.50kb$sim, sim.rho.50kb$sim, rep_6.tmrca.50kb))
names(sim.lands.50kb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 36901608, p-value = 0.5403
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.0250475

cor.test(~theta+rho, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 37660747, p-value = 0.2592
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.04613476

cor.test(~rho+tmrca, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 37734896, p-value = 0.2384
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.04819447

# centering
sim.lands.50kb$thetaC <- sim.lands.50kb$theta - mean(sim.lands.50kb$theta)
sim.lands.50kb$tmrcaC <- sim.lands.50kb$tmrca - mean(sim.lands.50kb$tmrca)
sim.lands.50kb$rhoC <- sim.lands.50kb$rho - mean(sim.lands.50kb$rho)

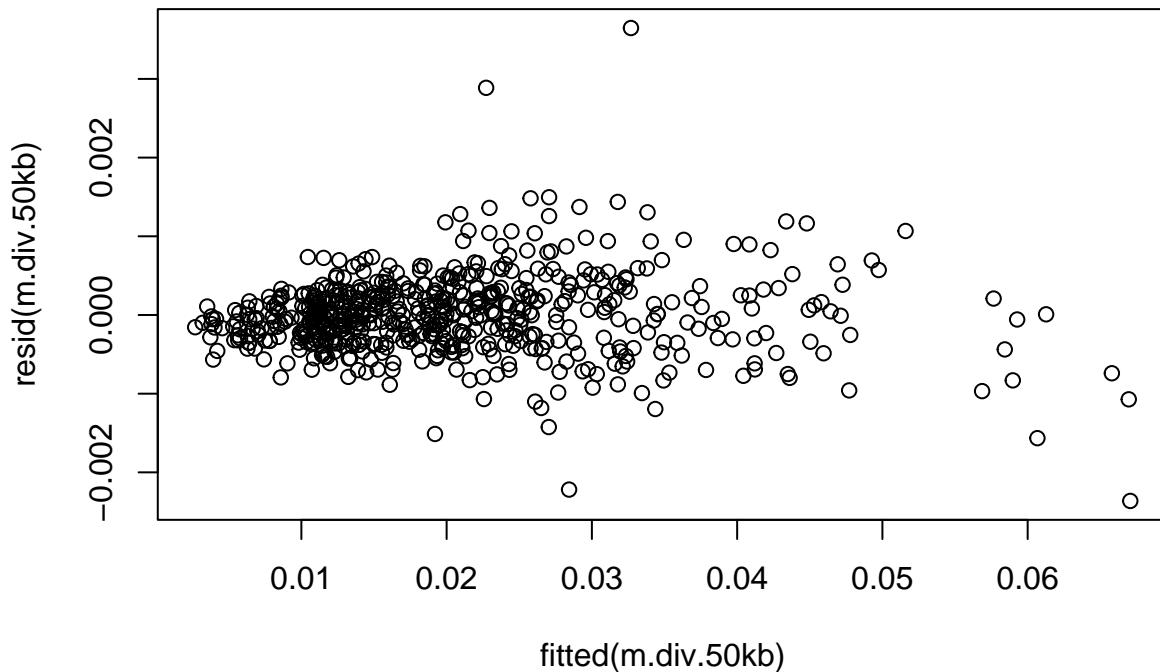
sim.lands.50kb$bin <- 1:nrow(sim.lands.50kb)
```

```

# for merging:
sim.lands.50kb.rep6 <- sim.lands.50kb
sim.lands.50kb.rep6$Replicate <- 6

m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.50kb)
plot(resid(m.div.50kb)~fitted(m.div.50kb))

```



```

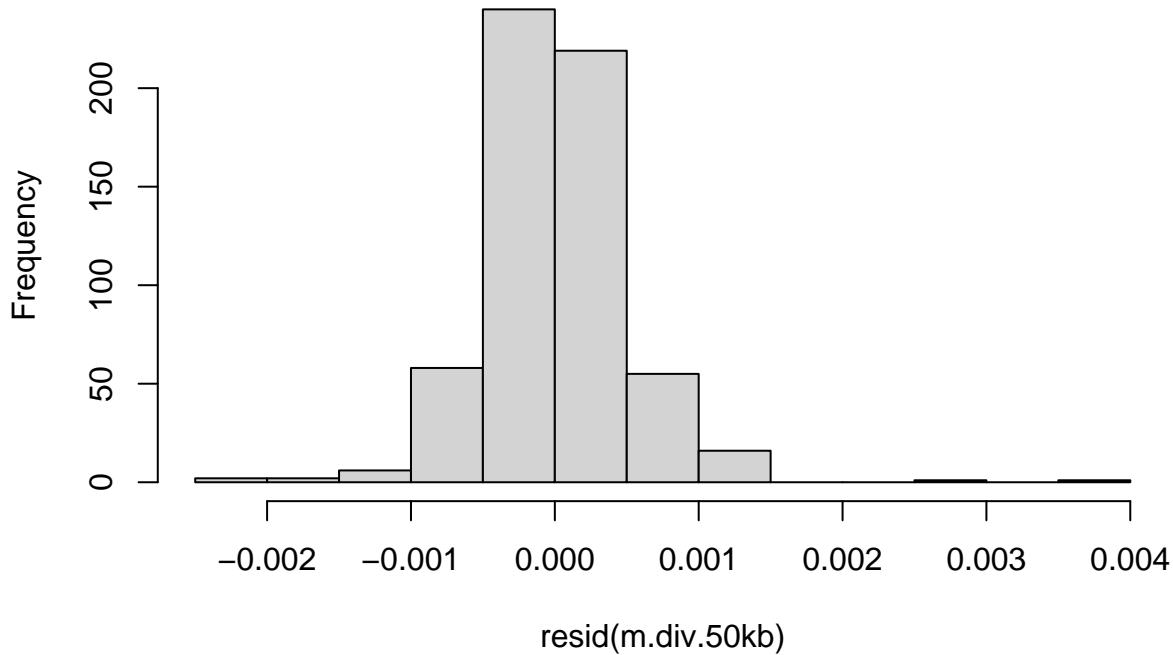
dwtest(m.div.50kb)

##
## Durbin-Watson test
##
## data: m.div.50kb
## DW = 2.1478, p-value = 0.9618
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)

##
## Harrison-McCabe test
##
## data: m.div.50kb
## HMC = 0.46094, p-value = 0.095
hist(resid(m.div.50kb))

```

## Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.50kb)
##
## Residuals:
##       Min         1Q     Median        3Q       Max
## -0.0023630 -0.0002937 -0.0000107  0.0002498  0.0036466
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.058e-02 2.073e-05 993.114 <2e-16 ***
## thetaC      1.304e+00 2.479e-03 526.030 <2e-16 ***
## rhoC       -1.179e-02 7.005e-03 -1.683 0.0929 .
## tmrcaC     2.363e-02 2.752e-04  85.861 <2e-16 ***
## thetaC:tmrcaC 1.439e+00 3.174e-02  45.345 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0005077 on 595 degrees of freedom
## Multiple R-squared:  0.998, Adjusted R-squared:  0.9979
## F-statistic: 7.29e+04 on 4 and 595 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.50kb[1, 6] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```
r2.sim.50kb[2, 6] <- anova.diversity$VarExp[1] * 100
r2.sim.50kb[3, 6] <- anova.diversity$VarExp[2] * 100
r2.sim.50kb[4, 6] <- anova.diversity$VarExp[3] * 100
r2.sim.50kb[5, 6] <- anova.diversity$VarExp[4] * 100
```

### 1.1.7 Replicate 7

```
rep_7.pi.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_7/rep_7.pi.50kb.bedgraph", header = FALSE)
rep_7.tmrca.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_7/sim.tmrca.50k.map", header = FALSE)

sim.lands.50kb <- as.data.frame(cbind(rep_7.pi.50kb$pi, sim.theta.50kb$sim, sim.rho.50kb$sim, rep_7.tmrca.50kb$tmrca))
names(sim.lands.50kb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 38638560, p-value = 0.0728
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.0732963

cor.test(~theta+rho, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 37660747, p-value = 0.2592
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.04613476

cor.test(~rho+tmrca, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 36196758, p-value = 0.8936
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.005468293

# centering
sim.lands.50kb$thetaC <- sim.lands.50kb$theta - mean(sim.lands.50kb$theta)
sim.lands.50kb$tmrcaC <- sim.lands.50kb$tmrca - mean(sim.lands.50kb$tmrca)
sim.lands.50kb$rhoC <- sim.lands.50kb$rho - mean(sim.lands.50kb$rho)

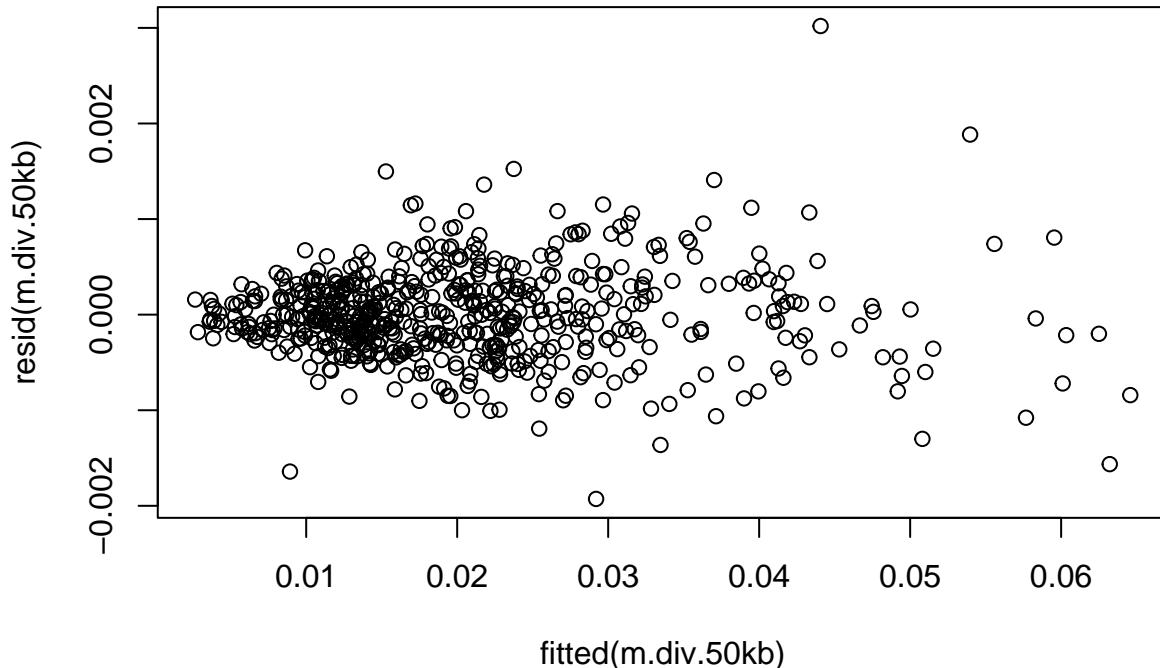
sim.lands.50kb$bin <- 1:nrow(sim.lands.50kb)
```

```

# for merging:
sim.lands.50kb.rep7 <- sim.lands.50kb
sim.lands.50kb.rep7$Replicate <- 7

m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.50kb)
plot(resid(m.div.50kb)~fitted(m.div.50kb))

```



```
dwtest(m.div.50kb)
```

```

##
## Durbin-Watson test
##
## data: m.div.50kb
## DW = 1.959, p-value = 0.2918
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)

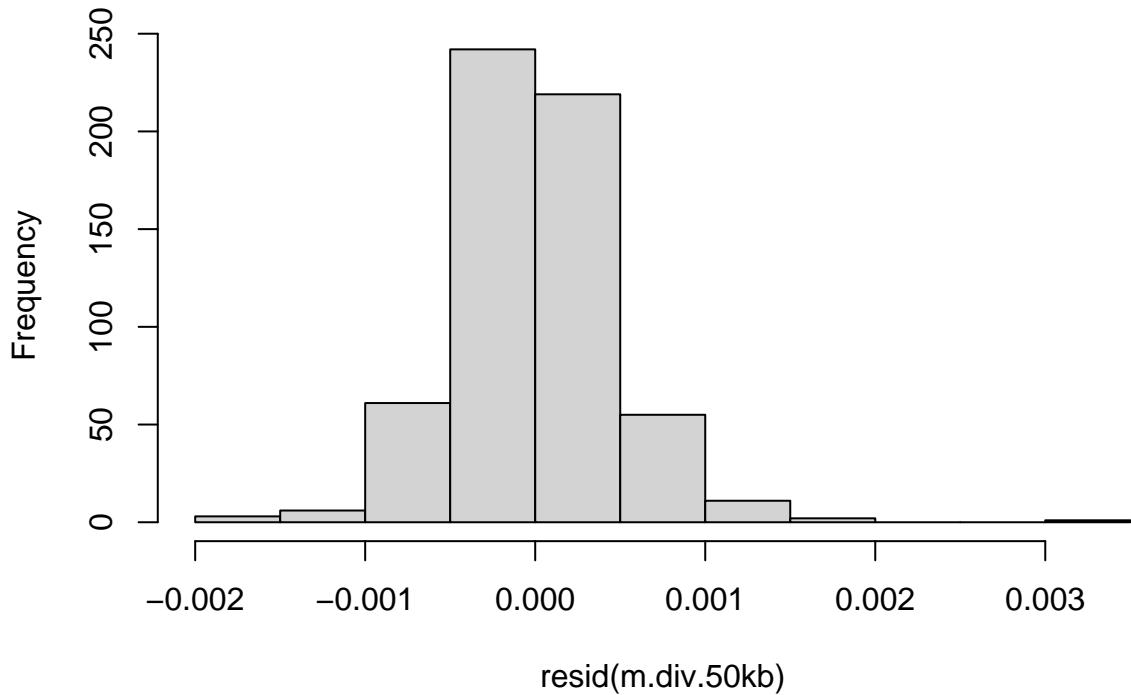
```

```

##
## Harrison-McCabe test
##
## data: m.div.50kb
## HMC = 0.47957, p-value = 0.252
hist(resid(m.div.50kb))

```

## Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.50kb)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -1.928e-03 -2.610e-04 -1.731e-05  2.569e-04  3.020e-03
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 2.061e-02 1.945e-05 1059.614 <2e-16 ***
## thetaC      1.313e+00 2.320e-03  565.892 <2e-16 ***
## rhoC       -5.753e-03 6.560e-03  -0.877  0.381  
## tmrcaC      2.389e-02 2.547e-04   93.801 <2e-16 ***
## thetaC:tmrcaC 1.491e+00 3.019e-02   49.398 <2e-16 ***
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0004759 on 595 degrees of freedom
## Multiple R-squared:  0.9982, Adjusted R-squared:  0.9982 
## F-statistic: 8.263e+04 on 4 and 595 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.50kb[1, 7] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```
r2.sim.50kb[2, 7] <- anova.diversity$VarExp[1] * 100
r2.sim.50kb[3, 7] <- anova.diversity$VarExp[2] * 100
r2.sim.50kb[4, 7] <- anova.diversity$VarExp[3] * 100
r2.sim.50kb[5, 7] <- anova.diversity$VarExp[4] * 100
```

### 1.1.8 Replicate 8

```
rep_8.pi.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_8/rep_8.pi.50kb.bedgraph", header = FALSE)
rep_8.tmrca.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_8/sim.tmrca.50k.map", header = FALSE)

sim.lands.50kb <- as.data.frame(cbind(rep_8.pi.50kb$pi, sim.theta.50kb$sim, sim.rho.50kb$sim, rep_8.tmrca.50kb))
names(sim.lands.50kb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.50kb, method = "spearman")

## Warning in cor.test.default(x = mf[[1L]], y = mf[[2L]], ...): Cannot compute
## exact p-value with ties

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 37183069, p-value = 0.4216
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.03286589

cor.test(~theta+rho, data = sim.lands.50kb, method = "spearman")

## Warning in cor.test.default(x = mf[[1L]], y = mf[[2L]], ...): Cannot compute
## exact p-value with ties

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 37660747, p-value = 0.2592
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.04613476

cor.test(~rho+tmrca, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 37073930, p-value = 0.4656
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.02983425
```

```

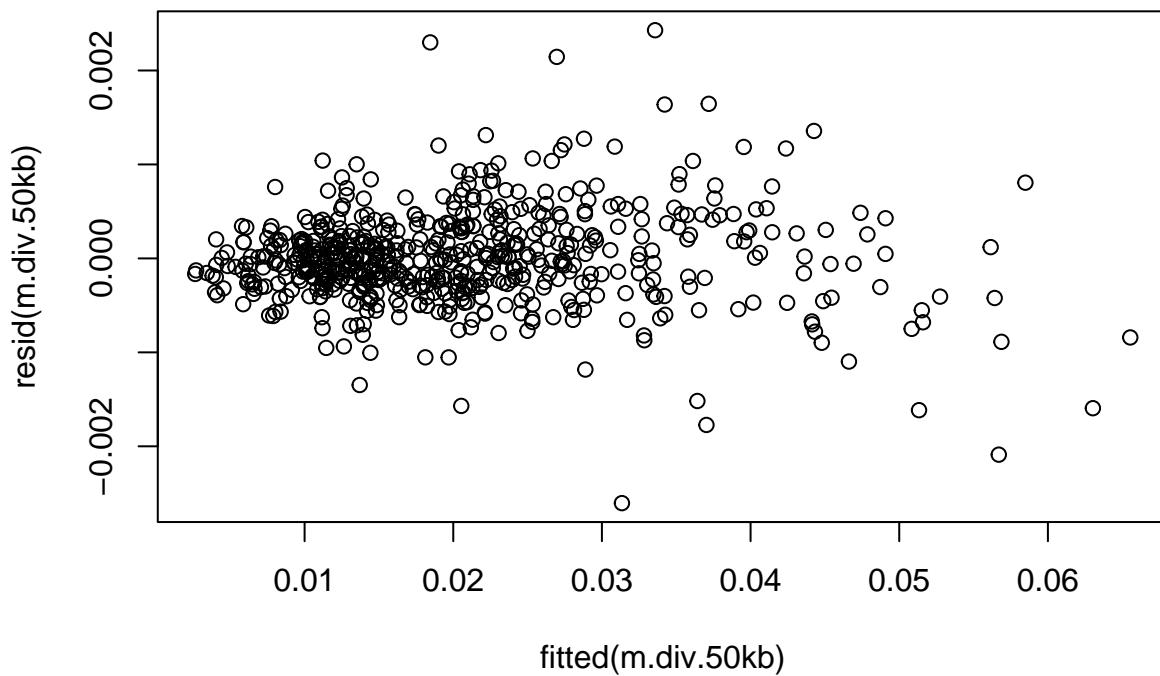
# centering
sim.lands.50kb$thetaC <- sim.lands.50kb$theta - mean(sim.lands.50kb$theta)
sim.lands.50kb$tmrcaC <- sim.lands.50kb$tmrca - mean(sim.lands.50kb$tmrca)
sim.lands.50kb$rhoC <- sim.lands.50kb$rho - mean(sim.lands.50kb$rho)

sim.lands.50kb$bin <- 1:nrow(sim.lands.50kb)

# for merging:
sim.lands.50kb.rep8 <- sim.lands.50kb
sim.lands.50kb.rep8$Replicate <- 8

m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.50kb)
plot(resid(m.div.50kb)~fitted(m.div.50kb))

```



```

dwtest(m.div.50kb)

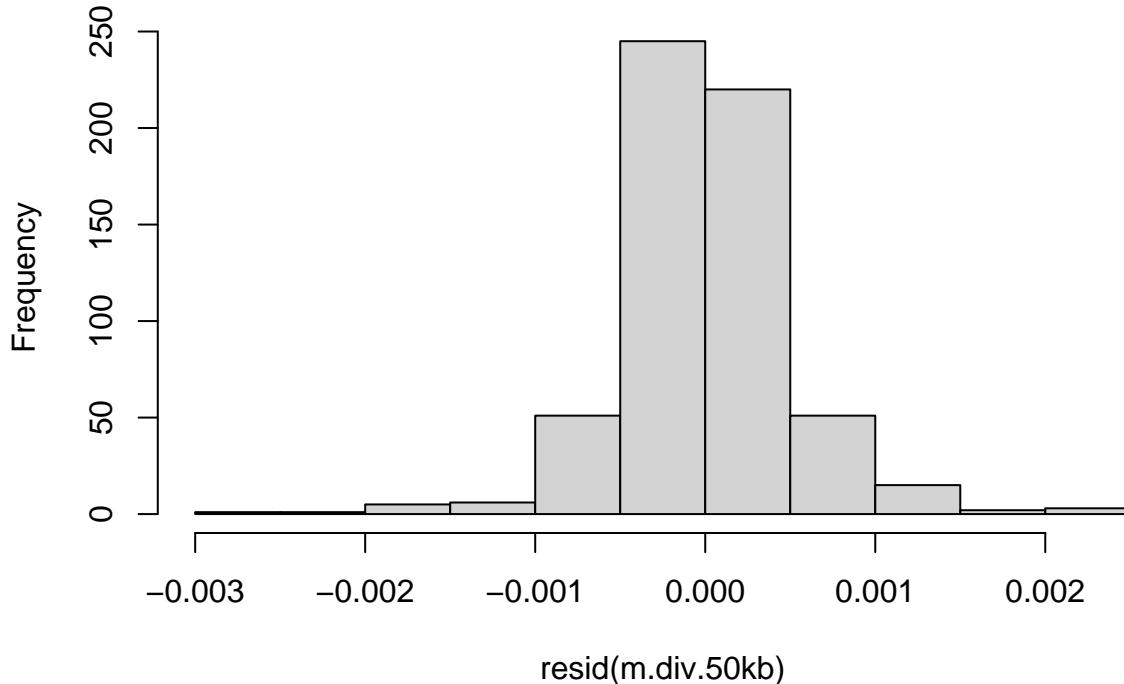
##
##  Durbin-Watson test
##
##  data: m.div.50kb
##  DW = 2.0323, p-value = 0.6384
##  alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)

##
##  Harrison-McCabe test
##
##  data: m.div.50kb
##  HMC = 0.48525, p-value = 0.291

```

```
hist(resid(m.div.50kb))
```

Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,  
##      data = sim.lands.50kb)  
##  
## Residuals:  
##      Min       1Q   Median       3Q      Max  
## -2.605e-03 -2.691e-04 -1.686e-05  2.620e-04  2.428e-03  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 2.057e-02 2.065e-05 996.284 <2e-16 ***  
## thetaC       1.303e+00 2.468e-03 527.803 <2e-16 ***  
## rhoC        -8.730e-04 6.970e-03 -0.125     0.9  
## tmrcaC       2.380e-02 2.848e-04  83.583 <2e-16 ***  
## thetaC:tmrcaC 1.383e+00 3.162e-02  43.722 <2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0005051 on 595 degrees of freedom  
## Multiple R-squared:  0.9979, Adjusted R-squared:  0.9979  
## F-statistic: 7.078e+04 on 4 and 595 DF,  p-value: < 2.2e-16  
anova.diversity <- Anova(m.div.50kb)  
apiss <- anova.diversity$"Sum Sq"  
anova.diversity$VarExp <- apiss / sum(apiss)
```

```
r2.sim.50kb[1, 8] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.sim.50kb[2, 8] <- anova.diversity$VarExp[1] * 100
r2.sim.50kb[3, 8] <- anova.diversity$VarExp[2] * 100
r2.sim.50kb[4, 8] <- anova.diversity$VarExp[3] * 100
r2.sim.50kb[5, 8] <- anova.diversity$VarExp[4] * 100
```

### 1.1.9 Replicate 9

```
rep_9.pi.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_9/rep_9.pi.50kb.bedgraph", header = FALSE)
rep_9.tmrca.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_9/sim.tmrca.50k.map", header = FALSE)

sim.lands.50kb <- as.data.frame(cbind(rep_9.pi.50kb$pi, sim.theta.50kb$sim, sim.rho.50kb$sim, rep_9.tmrca.50kb))
names(sim.lands.50kb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 35536739, p-value = 0.7531
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.01286561

cor.test(~theta+rho, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 37660747, p-value = 0.2592
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.04613476

cor.test(~rho+tmrca, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 37091756, p-value = 0.4583
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.03032942

# centering
sim.lands.50kb$thetaC <- sim.lands.50kb$theta - mean(sim.lands.50kb$theta)
sim.lands.50kb$tmrcaC <- sim.lands.50kb$tmrca - mean(sim.lands.50kb$tmrca)
sim.lands.50kb$rhoC <- sim.lands.50kb$rho - mean(sim.lands.50kb$rho)
```

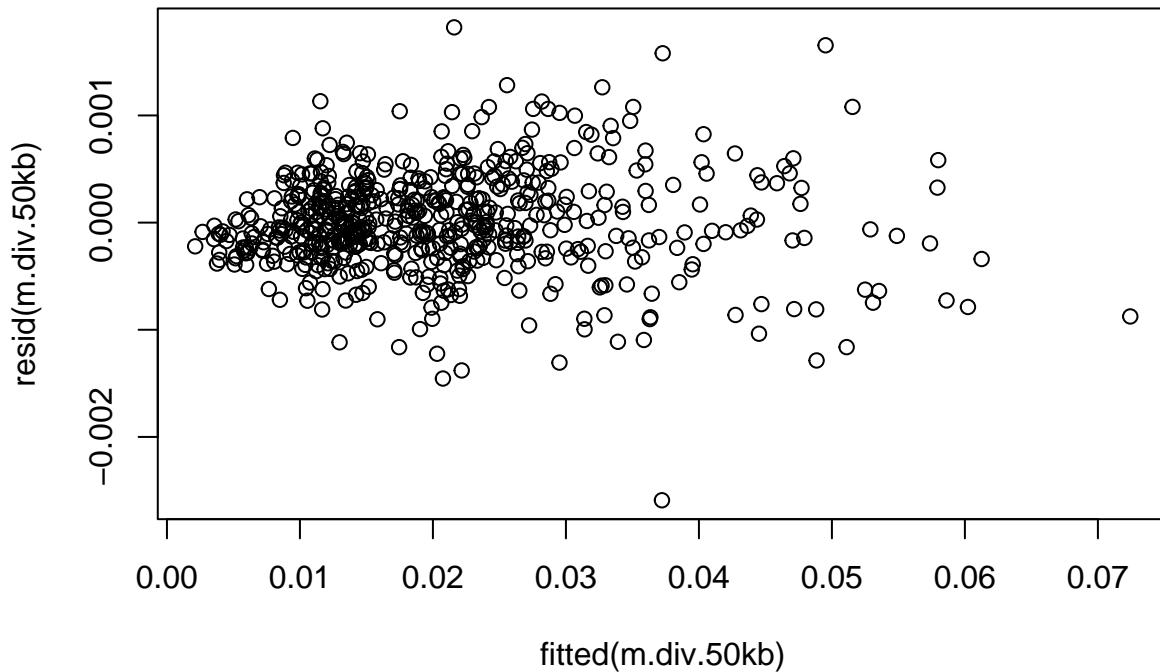
```

sim.lands.50kb$bin <- 1:nrow(sim.lands.50kb)

# for merging:
sim.lands.50kb.rep9 <- sim.lands.50kb
sim.lands.50kb.rep9 $Replicate <- 9

m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.50kb)
plot(resid(m.div.50kb)~fitted(m.div.50kb))

```



```

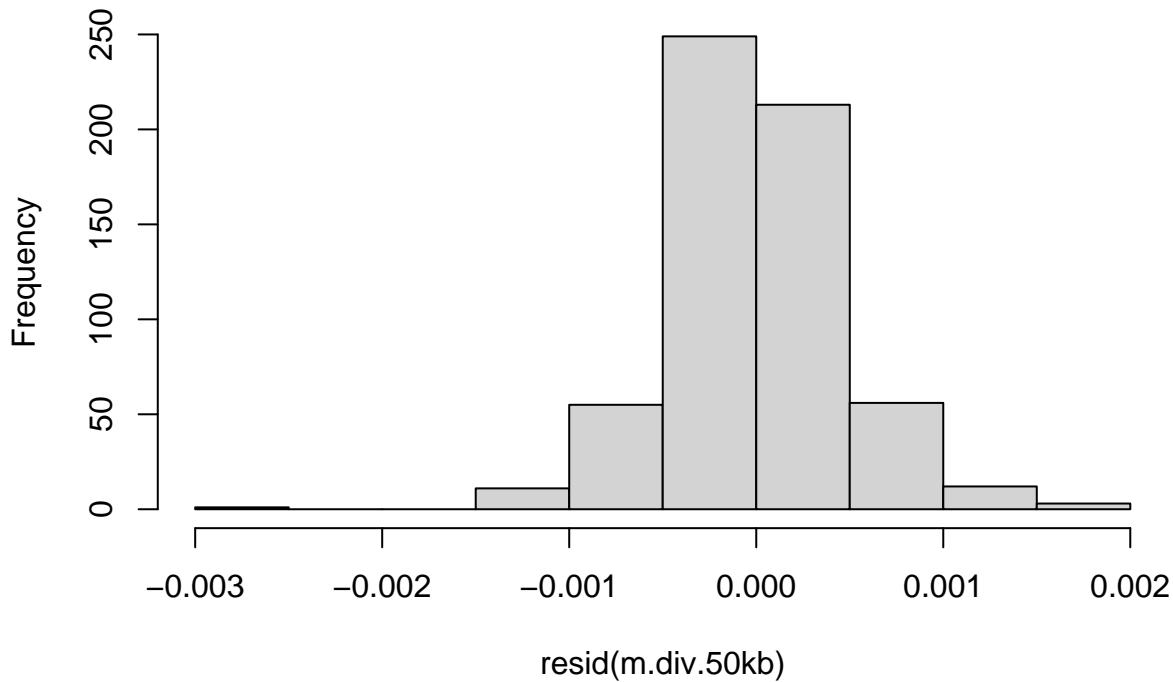
dwtest(m.div.50kb)

##
##  Durbin-Watson test
##
##  data: m.div.50kb
##  DW = 1.9547, p-value = 0.2758
##  alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)

##
##  Harrison-McCabe test
##
##  data: m.div.50kb
##  HMC = 0.55455, p-value = 0.967
hist(resid(m.div.50kb))

```

## Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.50kb)
##
## Residuals:
##       Min         1Q     Median         3Q        Max
## -2.591e-03 -2.409e-04 -2.982e-05  2.668e-04  1.822e-03
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.065e-02 1.899e-05 1087.271 <2e-16 ***
## thetaC      1.308e+00 2.265e-03  577.567 <2e-16 ***
## rhoC       -7.769e-03 6.412e-03  -1.212   0.226
## tmrcaC     2.404e-02 2.565e-04   93.731 <2e-16 ***
## thetaC:tmrcaC 1.508e+00 2.888e-02   52.235 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.000465 on 595 degrees of freedom
## Multiple R-squared:  0.9983, Adjusted R-squared:  0.9983
## F-statistic: 8.777e+04 on 4 and 595 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.50kb[1, 9] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```
r2.sim.50kb[2, 9] <- anova.diversity$VarExp[1] * 100
r2.sim.50kb[3, 9] <- anova.diversity$VarExp[2] * 100
r2.sim.50kb[4, 9] <- anova.diversity$VarExp[3] * 100
r2.sim.50kb[5, 9] <- anova.diversity$VarExp[4] * 100
```

### 1.1.10 Replicate 10

```
rep_10.pi.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_10/rep_10.pi.50kb.bedgraph", header = TRUE)
rep_10.tmrca.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_10/sim.tmrca.50k.map", header = TRUE)

sim.lands.50kb <- as.data.frame(cbind(rep_10.pi.50kb$pi, sim.theta.50kb$sim, sim.rho.50kb$sim, rep_10.tmrca.50kb$tmrca))
names(sim.lands.50kb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 37655834, p-value = 0.2606
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.0459983

cor.test(~theta+rho, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 37660747, p-value = 0.2592
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.04613476

cor.test(~rho+tmrca, data = sim.lands.50kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 36687846, p-value = 0.6403
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.01910966

# centering
sim.lands.50kb$thetaC <- sim.lands.50kb$theta - mean(sim.lands.50kb$theta)
sim.lands.50kb$tmrcaC <- sim.lands.50kb$tmrca - mean(sim.lands.50kb$tmrca)
sim.lands.50kb$rhoC <- sim.lands.50kb$rho - mean(sim.lands.50kb$rho)

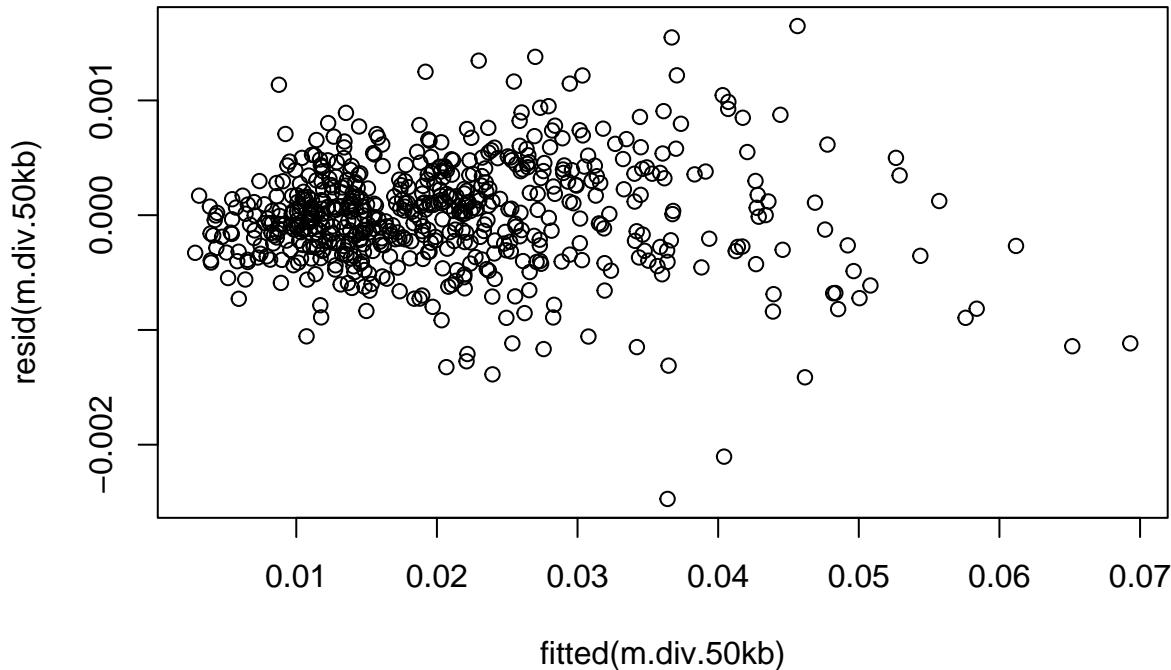
sim.lands.50kb$bin <- 1:nrow(sim.lands.50kb)
```

```

# for merging:
sim.lands.50kb.rep50 <- sim.lands.50kb
sim.lands.50kb.rep50$Replicate <- 10

m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.50kb)
plot(resid(m.div.50kb)~fitted(m.div.50kb))

```



```
dwtest(m.div.50kb)
```

```

##
## Durbin-Watson test
##
## data: m.div.50kb
## DW = 1.9775, p-value = 0.3738
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)

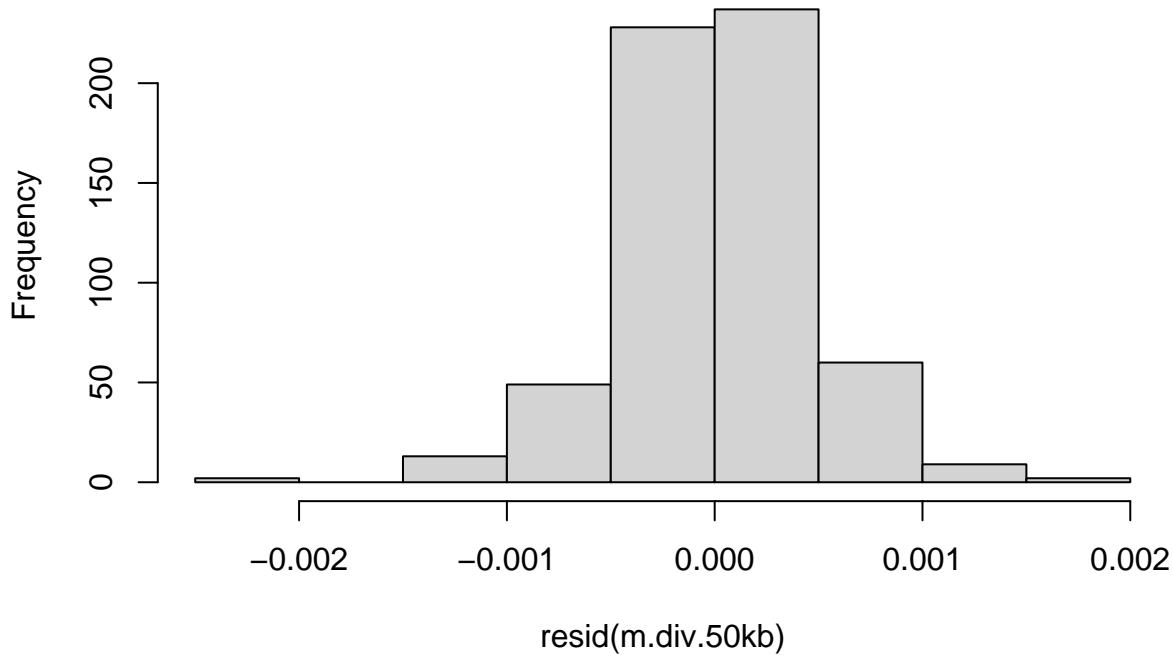
```

```

##
## Harrison-McCabe test
##
## data: m.div.50kb
## HMC = 0.43153, p-value = 0.014
hist(resid(m.div.50kb))

```

## Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.50kb)
##
## Residuals:
##       Min         1Q     Median         3Q        Max
## -2.473e-03 -2.632e-04  1.203e-05  2.861e-04  1.648e-03
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.070e-02 1.924e-05 1075.884 <2e-16 ***
## thetaC      1.311e+00 2.304e-03  568.969 <2e-16 ***
## rhoC        7.558e-03 6.493e-03   1.164   0.245
## tmrcaC     2.376e-02 2.376e-04  100.018 <2e-16 ***
## thetaC:tmrcaC 1.554e+00 2.642e-02   58.816 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0004703 on 595 degrees of freedom
## Multiple R-squared:  0.9982, Adjusted R-squared:  0.9982
## F-statistic: 8.211e+04 on 4 and 595 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.50kb[1, 10] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.sim.50kb[2, 10] <- anova.diversity$VarExp[1] * 100
r2.sim.50kb[3, 10] <- anova.diversity$VarExp[2] * 100
r2.sim.50kb[4, 10] <- anova.diversity$VarExp[3] * 100
r2.sim.50kb[5, 10] <- anova.diversity$VarExp[4] * 100

r2.sim.50kb$average <- rowMeans(r2.sim.50kb)
r2.sim.50kb <- transform(r2.sim.50kb, sd=apply(r2.sim.50kb, 1, sd, na.rm = TRUE))

```

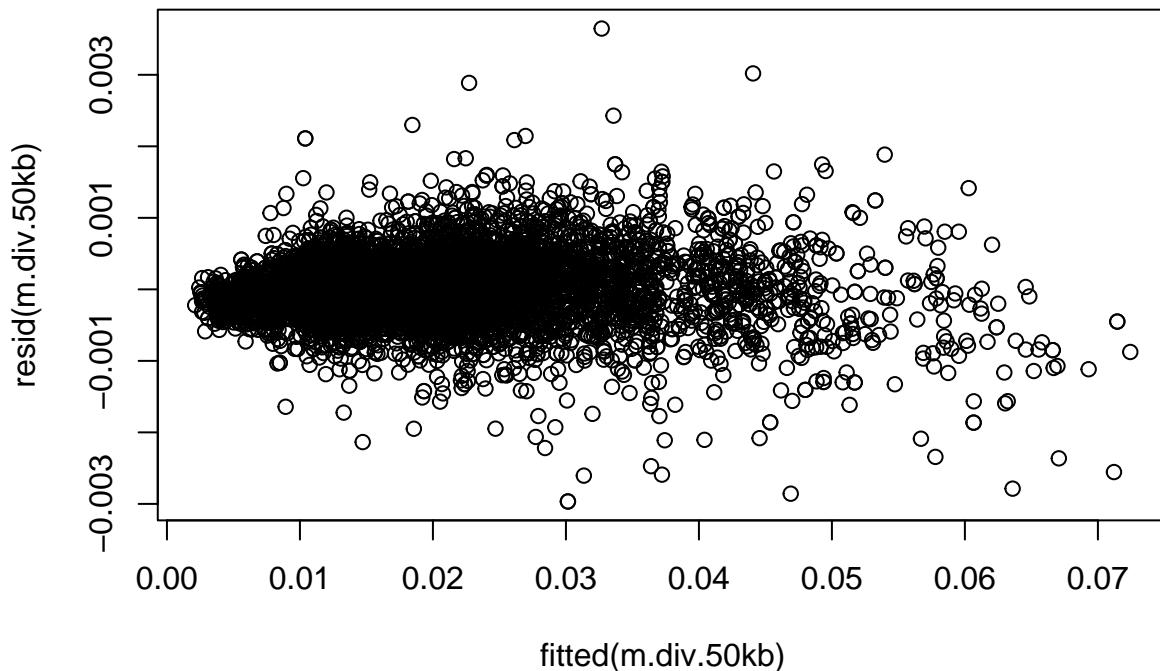
### 1.1.11 all replicates:

```

sim.lands.50kb.all <- rbind(sim.lands.50kb.rep5, sim.lands.50kb.rep2, sim.lands.50kb.rep3, sim.lands.50kb.rep4)

m.div.50kb <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC)*as.factor(Replicate), data = sim.lands.50kb.all)
plot(resid(m.div.50kb)~fitted(m.div.50kb))

```



```

dwtest(m.div.50kb)

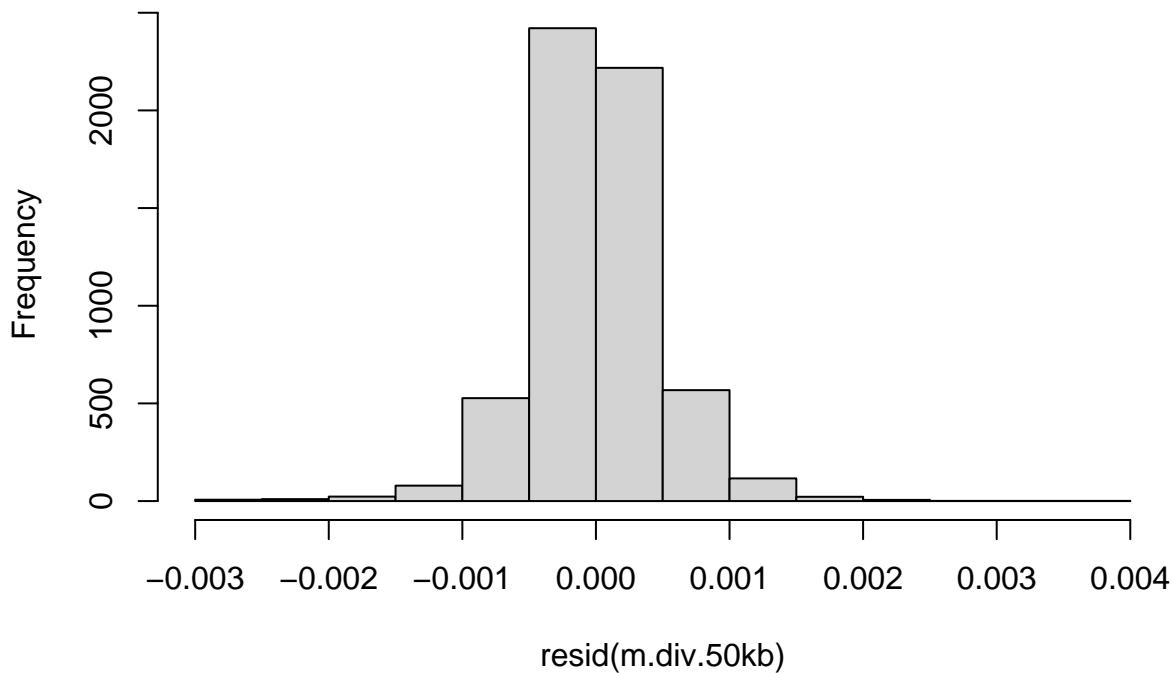
##
##  Durbin-Watson test
##
## data: m.div.50kb
## DW = 2.0313, p-value = 0.8378
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)

##
##  Harrison-McCabe test
##
## data: m.div.50kb
## HMC = 0.50138, p-value = 0.569

```

```
hist(resid(m.div.50kb))
```

Histogram of resid(m.div.50kb)



```
m.div.50kb.2 <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC + thetaC:rhoC)*as.factor(Replicate), data = sim.lands.50kb.all)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC + thetaC:rhoC + rhoC:tmrcaC)*as.factor(Replicate), data = sim.lands.50kb.all)
```

```
AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)
```

```
##          df      AIC
## m.div.50kb   46 -74487.09
## m.div.50kb.2 55 -74476.67
## m.div.50kb.3 64 -74469.15
```

```
summary(m.div.50kb)
```

```
##
## Call:
## lm(formula = diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC) *
##       as.factor(Replicate), data = sim.lands.50kb.all)
##
## Residuals:
##      Min        1Q    Median        3Q        Max
## -0.0029659 -0.0002718 -0.0000139  0.0002767  0.0036466
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.057e-02 1.983e-05 1037.362 < 2e-16
## thetaC      1.299e+00 2.372e-03  547.744 < 2e-16
## rhoC       -1.009e-02 6.706e-03  -1.505 0.132298
## tmrcaC     2.385e-02 2.743e-04   86.961 < 2e-16
## as.factor(Replicate)3 9.708e-05 2.805e-05   3.461 0.000543
```

```

## as.factor(Replicate)4      -6.998e-05  2.804e-05  -2.495  0.012614
## as.factor(Replicate)5      4.112e-05  2.429e-05  1.693  0.090555
## as.factor(Replicate)6      8.307e-06  2.804e-05  0.296  0.767075
## as.factor(Replicate)7      3.621e-05  2.806e-05  1.290  0.197011
## as.factor(Replicate)8      -2.113e-06 2.806e-05  -0.075  0.939967
## as.factor(Replicate)9      7.290e-05  2.805e-05  2.599  0.009365
## as.factor(Replicate)10     1.253e-04  2.807e-05  4.465  8.14e-06
## thetaC:tmrcaC             1.515e+00  3.122e-02  48.515 < 2e-16
## thetaC:as.factor(Replicate)3 1.091e-02  3.351e-03  3.254  0.001143
## thetaC:as.factor(Replicate)4 9.175e-04  3.349e-03  0.274  0.784112
## thetaC:as.factor(Replicate)5 8.367e-03  2.904e-03  2.882  0.003971
## thetaC:as.factor(Replicate)6 4.459e-03  3.354e-03  1.329  0.183796
## thetaC:as.factor(Replicate)7 1.356e-02  3.352e-03  4.045  5.29e-05
## thetaC:as.factor(Replicate)8 3.160e-03  3.355e-03  0.942  0.346264
## thetaC:as.factor(Replicate)9 8.544e-03  3.350e-03  2.551  0.010780
## thetaC:as.factor(Replicate)10 1.150e-02  3.360e-03  3.422  0.000626
## rhoC:as.factor(Replicate)3  1.654e-02  9.480e-03  1.744  0.081155
## rhoC:as.factor(Replicate)4  2.396e-02  9.476e-03  2.528  0.011491
## rhoC:as.factor(Replicate)5  1.162e-02  8.210e-03  1.415  0.156986
## rhoC:as.factor(Replicate)6  -1.695e-03 9.479e-03  -0.179  0.858054
## rhoC:as.factor(Replicate)7  4.341e-03  9.475e-03  0.458  0.646844
## rhoC:as.factor(Replicate)8  9.221e-03  9.479e-03  0.973  0.330721
## rhoC:as.factor(Replicate)9  2.325e-03  9.476e-03  0.245  0.806184
## rhoC:as.factor(Replicate)10 1.765e-02  9.482e-03  1.862  0.062717
## tmrcaC:as.factor(Replicate)3 -2.443e-04 3.669e-04  -0.666  0.505586
## tmrcaC:as.factor(Replicate)4 -3.682e-04 3.727e-04  -0.988  0.323169
## tmrcaC:as.factor(Replicate)5 -1.113e-04 3.340e-04  -0.333  0.738997
## tmrcaC:as.factor(Replicate)6 -2.224e-04 3.802e-04  -0.585  0.558571
## tmrcaC:as.factor(Replicate)7  3.626e-05  3.779e-04  0.096  0.923556
## tmrcaC:as.factor(Replicate)8 -5.299e-05 3.875e-04  -0.137  0.891250
## tmrcaC:as.factor(Replicate)9  1.871e-04  3.834e-04  0.488  0.625634
## tmrcaC:as.factor(Replicate)10 -9.171e-05 3.680e-04  -0.249  0.803197
## thetaC:tmrcaC:as.factor(Replicate)3 -1.346e-02 4.128e-02  -0.326  0.744413
## thetaC:tmrcaC:as.factor(Replicate)4 -2.192e-02 4.324e-02  -0.507  0.612153
## thetaC:tmrcaC:as.factor(Replicate)5 -4.384e-02 3.836e-02  -1.143  0.253171
## thetaC:tmrcaC:as.factor(Replicate)6 -7.532e-02 4.355e-02  -1.729  0.083798
## thetaC:tmrcaC:as.factor(Replicate)7 -2.354e-02 4.386e-02  -0.537  0.591443
## thetaC:tmrcaC:as.factor(Replicate)8 -1.321e-01 4.358e-02  -3.032  0.002438
## thetaC:tmrcaC:as.factor(Replicate)9 -6.256e-03 4.341e-02  -0.144  0.885413
## thetaC:tmrcaC:as.factor(Replicate)10 3.941e-02 4.146e-02  0.950  0.341925
##
## (Intercept)                      ***
## thetaC                                ***
## rhoC                                 ***
## tmrcaC                               ***
## as.factor(Replicate)3                  ***
## as.factor(Replicate)4                  *
## as.factor(Replicate)5                  .
## as.factor(Replicate)6
## as.factor(Replicate)7
## as.factor(Replicate)8
## as.factor(Replicate)9                  **
## as.factor(Replicate)10                 ***
## thetaC:tmrcaC                         ***

```

```

## thetaC:as.factor(Replicate)3      **
## thetaC:as.factor(Replicate)4      **
## thetaC:as.factor(Replicate)5      **
## thetaC:as.factor(Replicate)6      **
## thetaC:as.factor(Replicate)7      ***
## thetaC:as.factor(Replicate)8      *
## thetaC:as.factor(Replicate)9      *
## thetaC:as.factor(Replicate)10     ***
## rhoC:as.factor(Replicate)3       .
## rhoC:as.factor(Replicate)4       *
## rhoC:as.factor(Replicate)5       .
## rhoC:as.factor(Replicate)6       .
## rhoC:as.factor(Replicate)7       .
## rhoC:as.factor(Replicate)8       .
## rhoC:as.factor(Replicate)9       .
## rhoC:as.factor(Replicate)10      .
## tmrcaC:as.factor(Replicate)3     .
## tmrcaC:as.factor(Replicate)4     .
## tmrcaC:as.factor(Replicate)5     .
## tmrcaC:as.factor(Replicate)6     .
## tmrcaC:as.factor(Replicate)7     .
## tmrcaC:as.factor(Replicate)8     .
## tmrcaC:as.factor(Replicate)9     .
## tmrcaC:as.factor(Replicate)10    .
## thetaC:tmrcaC:as.factor(Replicate)3
## thetaC:tmrcaC:as.factor(Replicate)4
## thetaC:tmrcaC:as.factor(Replicate)5
## thetaC:tmrcaC:as.factor(Replicate)6   .
## thetaC:tmrcaC:as.factor(Replicate)7
## thetaC:tmrcaC:as.factor(Replicate)8 ** 
## thetaC:tmrcaC:as.factor(Replicate)9
## thetaC:tmrcaC:as.factor(Replicate)10
## --- 
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0004856 on 5955 degrees of freedom
## Multiple R-squared:  0.9981, Adjusted R-squared:  0.9981
## F-statistic: 7.12e+04 on 44 and 5955 DF,  p-value: < 2.2e-16

```

## 1.2 200 kb scale

```

r2.sim.200kb <- as.data.frame(matrix(ncol = nreps, nrow = 5))
row.names(r2.sim.200kb) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
colnames(r2.sim.200kb) <- reps

sim.rho.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/dm.sim.rho.2e+05.txt", header = T)
sim.theta.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/dm.sim.theta.2e+05.txt", header = T)

```

### 1.2.1 Replicate 1

```

rep_1.pi.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_1/rep_1.pi.200kb.bedgraph", header = T)
rep_1.tmrca.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_1/sim.tmrca.200k.map", header = T)

```

```

sim.lands.200kb <- as.data.frame(cbind(rep_1.pi.200kb$pi, sim.theta.200kb$sim, sim.rho.200kb$sim, rep_1
names(sim.lands.200kb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 569023, p-value = 0.8876
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.01164184

cor.test(~theta+rho, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 593676, p-value = 0.5002
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.0554712

cor.test(~rho+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 570624, p-value = 0.8602
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.01448776

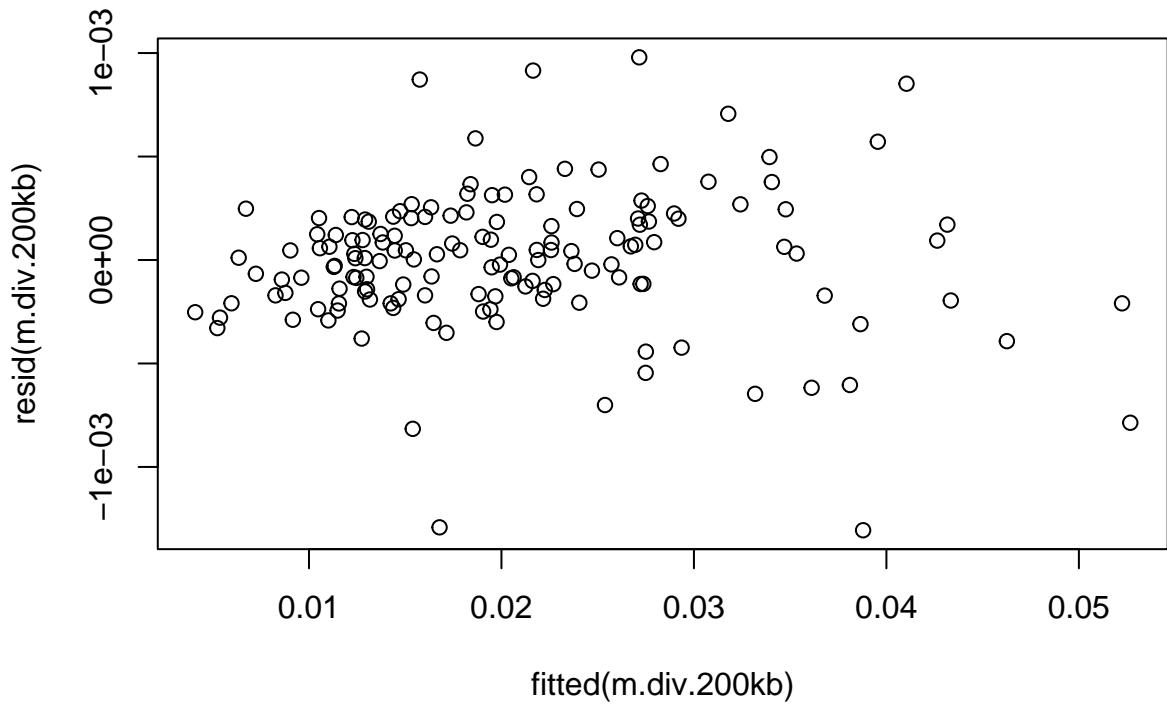
# centering
sim.lands.200kb$thetaC <- sim.lands.200kb$theta - mean(sim.lands.200kb$theta)
sim.lands.200kb$tmrcaC <- sim.lands.200kb$tmrca - mean(sim.lands.200kb$tmrca)
sim.lands.200kb$rhoC <- sim.lands.200kb$rho - mean(sim.lands.200kb$rho)

sim.lands.200kb$bin <- 1:nrow(sim.lands.200kb)

# for merging:
sim.lands.200kb.rep5 <- sim.lands.200kb
sim.lands.200kb.rep5$Replicate <- 1

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.200kb)
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```

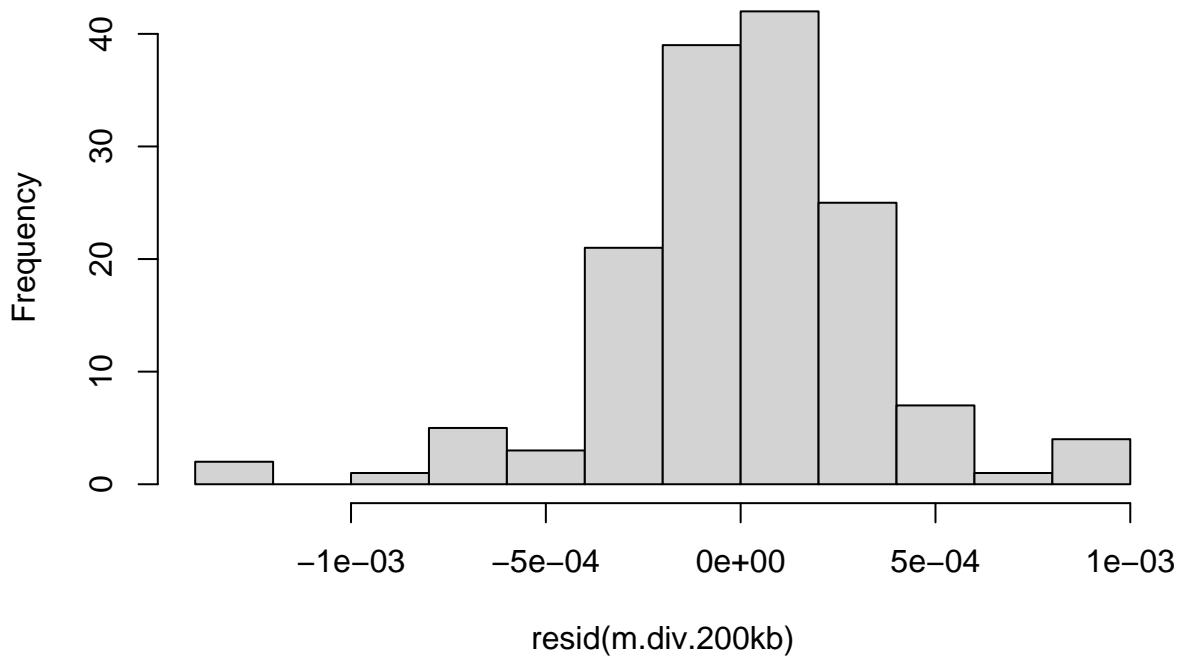


```
dwtest(m.div.200kb)
```

```
##
##  Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.9751, p-value = 0.4234
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.49982, p-value = 0.503
hist(resid(m.div.200kb))
```

## Histogram of resid(m.div.200kb)



```
summary(m.div.200kb)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.200kb)
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -1.306e-03 -1.718e-04  1.801e-05  1.985e-04  9.793e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 2.067e-02 2.788e-05 741.370 <2e-16 ***
## thetaC      1.306e+00 3.769e-03 346.532 <2e-16 ***
## rhoC        3.201e-02 1.870e-02  1.712   0.089 .  
## tmrcaC     2.526e-02 7.654e-04 32.997 <2e-16 ***
## thetaC:tmrcaC 1.536e+00 1.072e-01 14.325 <2e-16 ***
## ---      
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0003415 on 145 degrees of freedom
## Multiple R-squared:  0.9988, Adjusted R-squared:  0.9988 
## F-statistic: 3.049e+04 on 4 and 145 DF,  p-value: < 2.2e-16
anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
```

```
r2.sim.200kb[1, 1] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```
r2.sim.200kb[2, 1] <- anova.diversity$VarExp[1] * 100
r2.sim.200kb[3, 1] <- anova.diversity$VarExp[2] * 100
r2.sim.200kb[4, 1] <- anova.diversity$VarExp[3] * 100
r2.sim.200kb[5, 1] <- anova.diversity$VarExp[4] * 100
```

### 1.2.2 Replicate 2

```
rep_2.pi.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_2/rep_2.pi.200kb.bedgraph", header=TRUE)
rep_2.tmrca.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_2/sim.tmrca.200k.map", header=TRUE)

sim.lands.200kb <- as.data.frame(cbind(rep_2.pi.200kb$pi, sim.theta.200kb$sim, sim.rho.200kb$sim, rep_2.tmrca.200kb))
names(sim.lands.200kb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 551432, p-value = 0.8115
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.01963361

cor.test(~theta+rho, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 593676, p-value = 0.5002
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.0554712

cor.test(~rho+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 533372, p-value = 0.529
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.05174097

# centering
sim.lands.200kb$thetaC <- sim.lands.200kb$theta - mean(sim.lands.200kb$theta)
sim.lands.200kb$tmrcaC <- sim.lands.200kb$tmrca - mean(sim.lands.200kb$tmrca)
sim.lands.200kb$rhoC <- sim.lands.200kb$rho - mean(sim.lands.200kb$rho)

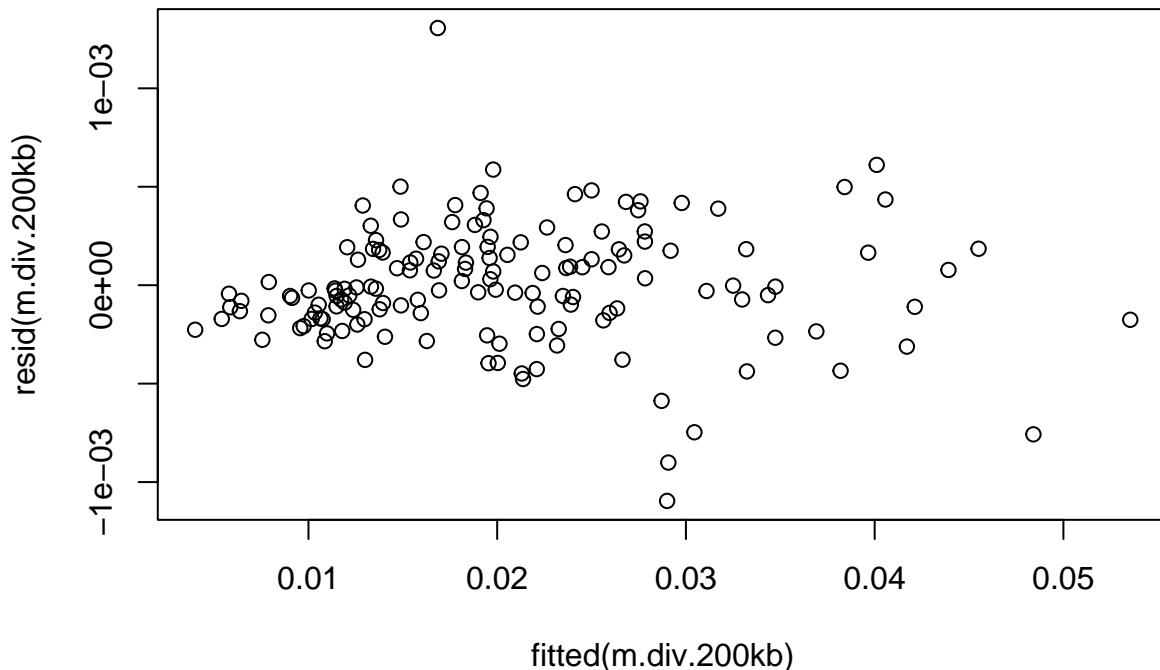
sim.lands.200kb$bin <- 1:nrow(sim.lands.200kb)
```

```

# for merging:
sim.lands.200kb.rep2 <- sim.lands.200kb
sim.lands.200kb.rep2$Replicate <- 2

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.200kb)
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```



```
dwtest(m.div.200kb)
```

```

##
## Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.5928, p-value = 0.005174
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb)

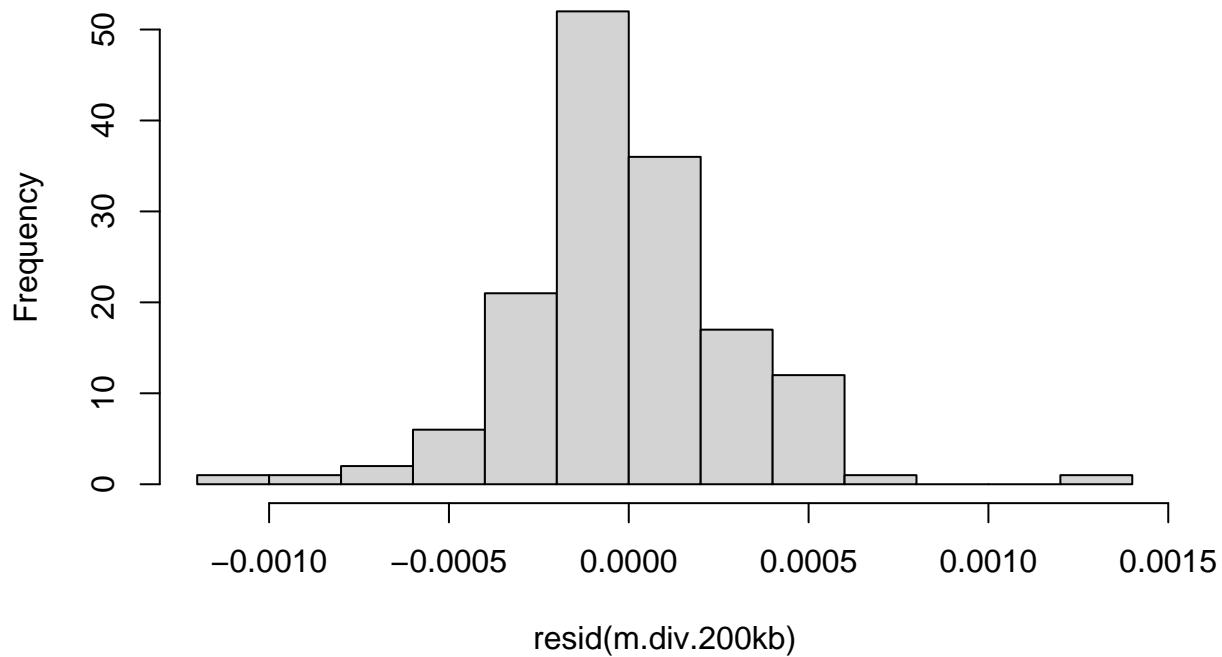
```

```

##
## Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.59119, p-value = 0.959
hist(resid(m.div.200kb))

```

## Histogram of resid(m.div.200kb)



```
summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.200kb)
##
## Residuals:
##       Min         1Q     Median        3Q       Max
## -1.096e-03 -1.706e-04 -2.456e-05  1.813e-04  1.306e-03
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.056e-02 2.494e-05 824.14 <2e-16 ***
## thetaC      1.297e+00 3.394e-03 382.15 <2e-16 ***
## rhoC       -3.118e-02 1.667e-02  -1.87  0.0635 .
## tmrcaC     2.455e-02 6.157e-04  39.88 <2e-16 ***
## thetaC:tmrcaC 1.643e+00 8.199e-02  20.04 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0003054 on 145 degrees of freedom
## Multiple R-squared:  0.999, Adjusted R-squared:  0.999
## F-statistic: 3.71e+04 on 4 and 145 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.200kb[1, 2] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```
r2.sim.200kb[2, 2] <- anova.diversity$VarExp[1] * 100
r2.sim.200kb[3, 2] <- anova.diversity$VarExp[2] * 100
r2.sim.200kb[4, 2] <- anova.diversity$VarExp[3] * 100
r2.sim.200kb[5, 2] <- anova.diversity$VarExp[4] * 100
```

### 1.2.3 Replicate 3

```
rep_3.pi.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_3/rep_3.pi.200kb.bedgraph", header=TRUE)
rep_3.tmrca.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_3/sim.tmrca.200k.map", header=TRUE)

sim.lands.200kb <- as.data.frame(cbind(rep_3.pi.200kb$pi, sim.theta.200kb$sim, sim.rho.200kb$sim, rep_3.tmrca.200kb))
names(sim.lands.200kb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 592174, p-value = 0.5211
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.05280076

cor.test(~theta+rho, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 593676, p-value = 0.5002
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.0554712

cor.test(~rho+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 594376, p-value = 0.4902
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.05671541

# centering
sim.lands.200kb$thetaC <- sim.lands.200kb$theta - mean(sim.lands.200kb$theta)
sim.lands.200kb$tmrcaC <- sim.lands.200kb$tmrca - mean(sim.lands.200kb$tmrca)
sim.lands.200kb$rhoC <- sim.lands.200kb$rho - mean(sim.lands.200kb$rho)

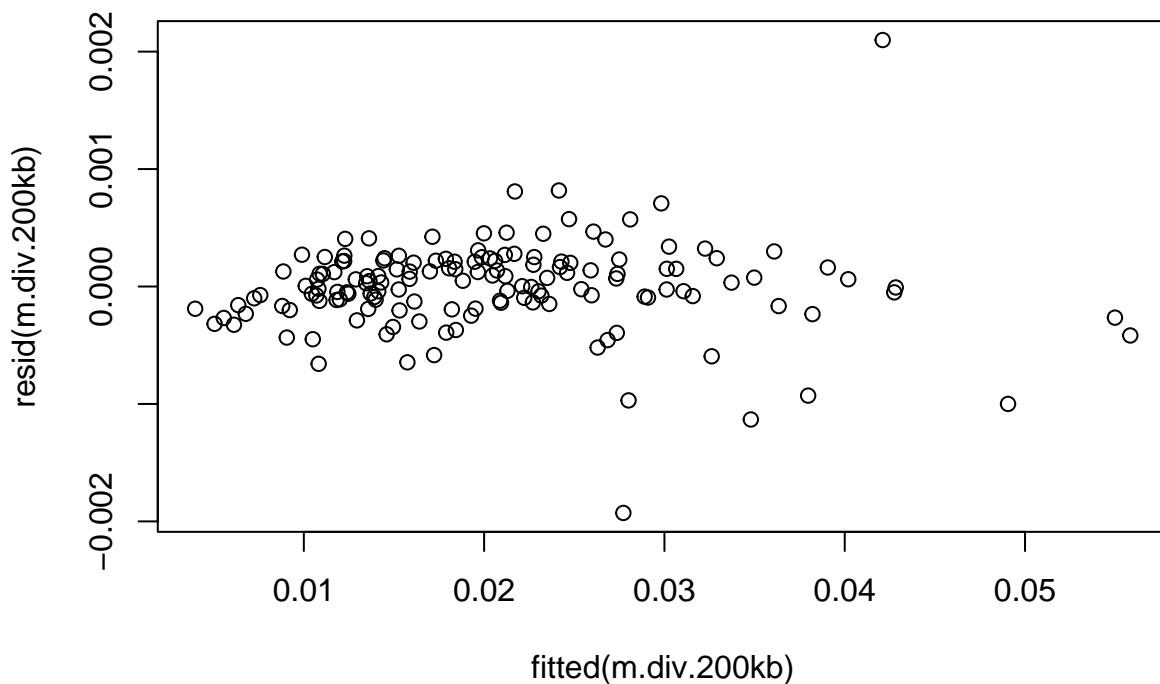
sim.lands.200kb$bin <- 1:nrow(sim.lands.200kb)
```

```

# for merging:
sim.lands.200kb.rep3 <- sim.lands.200kb
sim.lands.200kb.rep3$Replicate <- 3

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.200kb)
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```



```

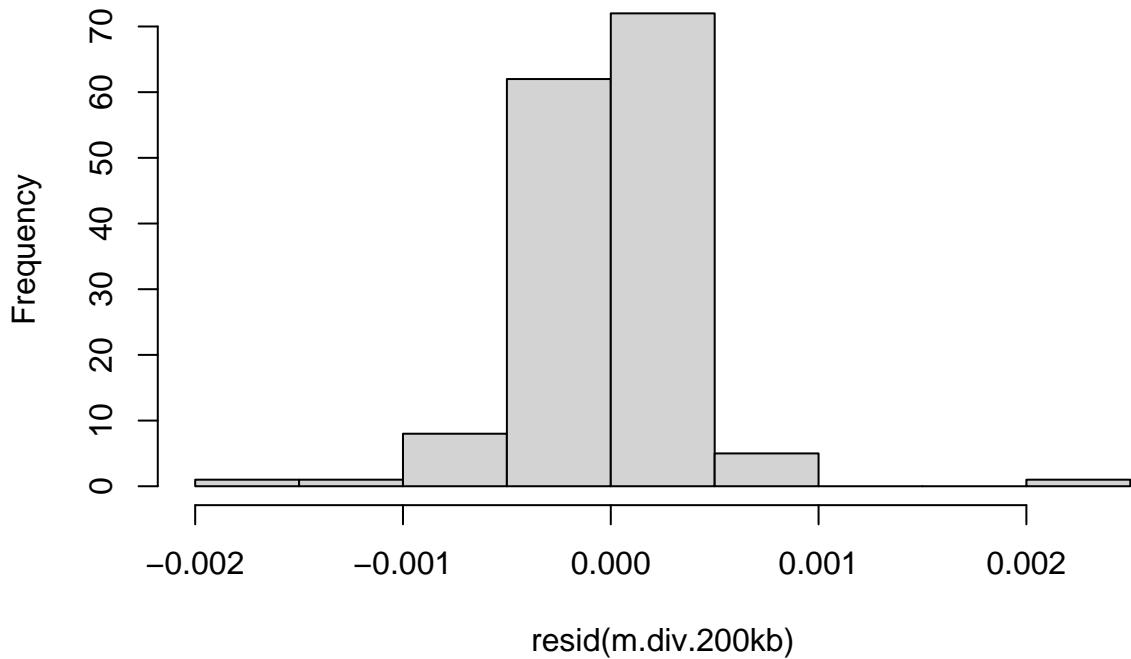
dwtest(m.div.200kb)

##
## Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.9205, p-value = 0.2965
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb)

##
## Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.45845, p-value = 0.249
hist(resid(m.div.200kb))

```

## Histogram of resid(m.div.200kb)



```
summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.200kb)
##
## Residuals:
##       Min         1Q     Median        3Q       Max
## -1.928e-03 -1.460e-04  3.044e-05  2.110e-04  2.099e-03
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.064e-02 3.245e-05 636.263 <2e-16 ***
## thetaC      1.309e+00 4.394e-03 297.825 <2e-16 ***
## rhoC        3.167e-02 2.173e-02   1.458   0.147
## tmrcaC     2.488e-02 7.859e-04  31.662 <2e-16 ***
## thetaC:tmrcaC 1.472e+00 1.097e-01 13.422 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0003972 on 145 degrees of freedom
## Multiple R-squared:  0.9984, Adjusted R-squared:  0.9984
## F-statistic: 2.269e+04 on 4 and 145 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.200kb[1, 3] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```
r2.sim.200kb[2, 3] <- anova.diversity$VarExp[1] * 100
r2.sim.200kb[3, 3] <- anova.diversity$VarExp[2] * 100
r2.sim.200kb[4, 3] <- anova.diversity$VarExp[3] * 100
r2.sim.200kb[5, 3] <- anova.diversity$VarExp[4] * 100
```

#### 1.2.4 Replicate 4

```
rep_4.pi.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_4/rep_4.pi.200kb.bedgraph", head=TRUE)
rep_4.tmrca.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_4/sim.tmrca.200k.map", head=TRUE)

sim.lands.200kb <- as.data.frame(cbind(rep_4.pi.200kb$pi, sim.theta.200kb$sim, sim.rho.200kb$sim, rep_4.tmrca.200kb))
names(sim.lands.200kb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 554491, p-value = 0.8631
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.01419494

cor.test(~theta+rho, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 593676, p-value = 0.5002
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.0554712

cor.test(~rho+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 559798, p-value = 0.9539
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.004759323

# centering
sim.lands.200kb$thetaC <- sim.lands.200kb$theta - mean(sim.lands.200kb$theta)
sim.lands.200kb$tmrcaC <- sim.lands.200kb$tmrca - mean(sim.lands.200kb$tmrca)
sim.lands.200kb$rhoC <- sim.lands.200kb$rho - mean(sim.lands.200kb$rho)

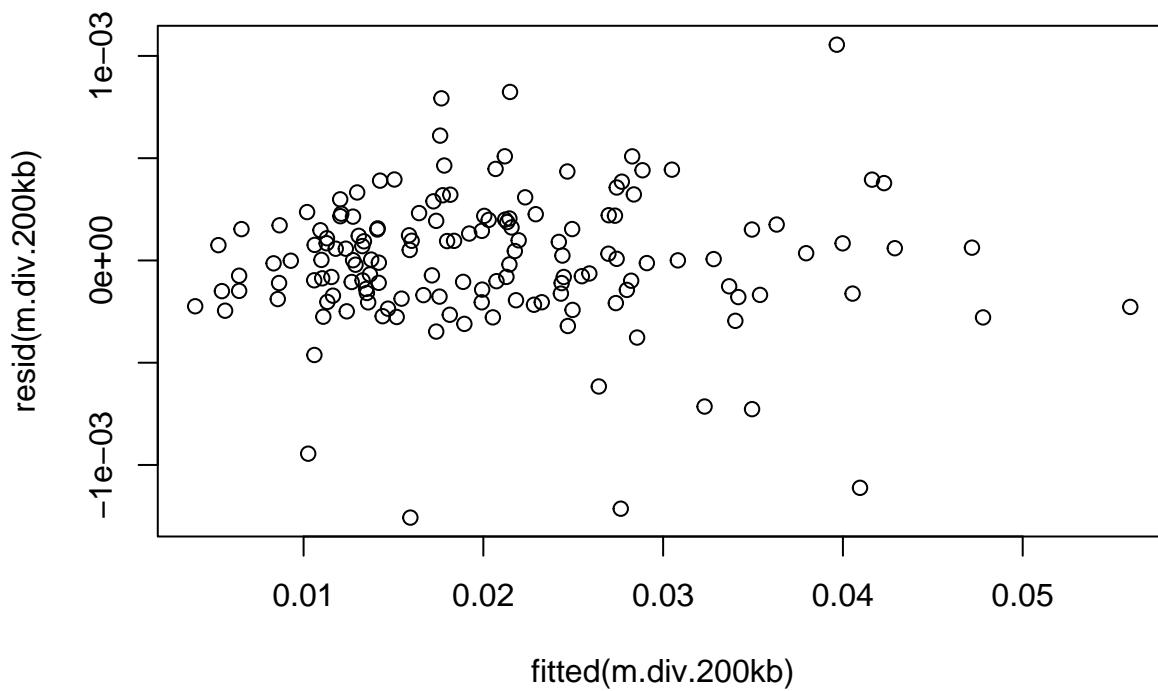
sim.lands.200kb$bin <- 1:nrow(sim.lands.200kb)
```

```

# for merging:
sim.lands.200kb.rep4 <- sim.lands.200kb
sim.lands.200kb.rep4$Replicate <- 4

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.200kb)
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```



```

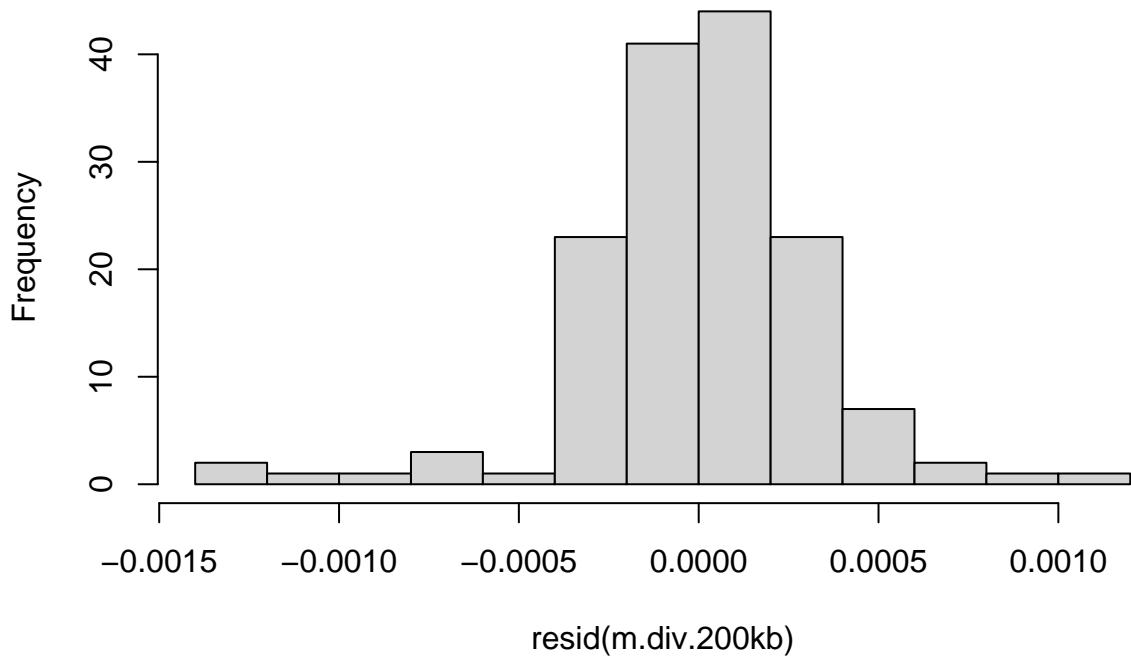
dwtest(m.div.200kb)

##
##  Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.9887, p-value = 0.4477
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb)

##
##  Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.4058, p-value = 0.053
hist(resid(m.div.200kb))

```

## Histogram of resid(m.div.200kb)



```
summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.200kb)
##
## Residuals:
##       Min         1Q     Median         3Q        Max
## -1.257e-03 -1.693e-04  3.530e-06  1.847e-04  1.055e-03
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.0205018  0.0000271 756.559 <2e-16 ***
## thetaC      1.3010756  0.0036626 355.236 <2e-16 ***
## rhoC        0.0087841  0.0181026  0.485   0.628
## tmrcaC      0.02444436 0.0006814  35.873 <2e-16 ***
## thetaC:tmrcaC 1.4688735  0.0873643 16.813 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0003317 on 145 degrees of freedom
## Multiple R-squared:  0.9989, Adjusted R-squared:  0.9989
## F-statistic: 3.248e+04 on 4 and 145 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.200kb[1, 4] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```
r2.sim.200kb[2, 4] <- anova.diversity$VarExp[1] * 100
r2.sim.200kb[3, 4] <- anova.diversity$VarExp[2] * 100
r2.sim.200kb[4, 4] <- anova.diversity$VarExp[3] * 100
r2.sim.200kb[5, 4] <- anova.diversity$VarExp[4] * 100
```

### 1.2.5 Replicate 5

```
rep_5.pi.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_5/rep_5.pi.200kb.bedgraph", header=TRUE)
rep_5.tmrca.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_5/sim.tmrca.200k.map", header=TRUE)

sim.lands.200kb <- as.data.frame(cbind(rep_5.pi.200kb$pi, sim.theta.200kb$sim, sim.rho.200kb$sim, rep_5.tmrca.200kb))
names(sim.lands.200kb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 570758, p-value = 0.858
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.01472654

cor.test(~theta+rho, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 593676, p-value = 0.5002
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.0554712

cor.test(~rho+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 582370, p-value = 0.6671
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.03537046

# centering
sim.lands.200kb$thetaC <- sim.lands.200kb$theta - mean(sim.lands.200kb$theta)
sim.lands.200kb$tmrcaC <- sim.lands.200kb$tmrca - mean(sim.lands.200kb$tmrca)
sim.lands.200kb$rhoC <- sim.lands.200kb$rho - mean(sim.lands.200kb$rho)

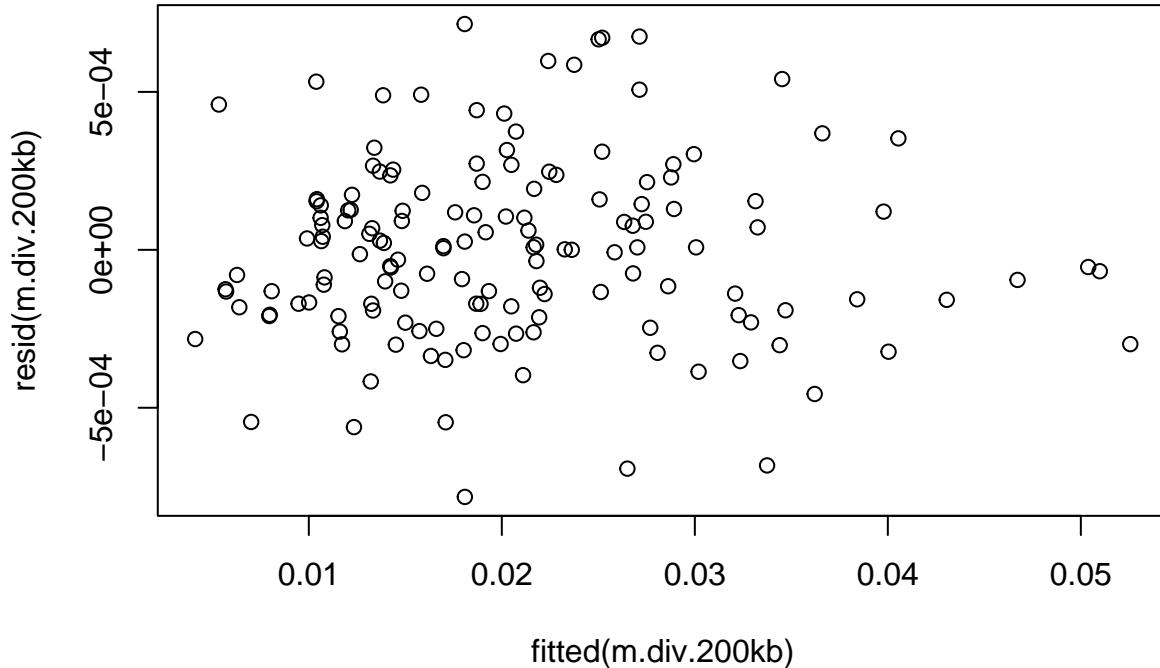
sim.lands.200kb$bin <- 1:nrow(sim.lands.200kb)
```

```

# for merging:
sim.lands.200kb.rep5 <- sim.lands.200kb
sim.lands.200kb.rep5$Replicate <- 5

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.200kb)
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```



```

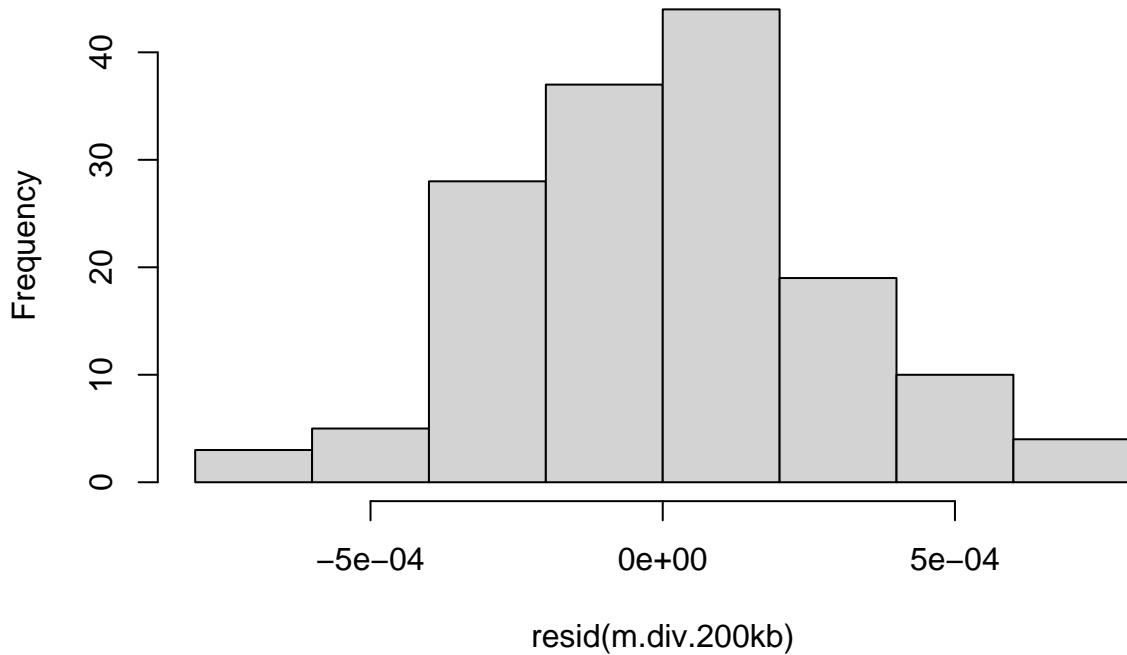
dwtest(m.div.200kb)

##
## Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.9065, p-value = 0.2691
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb)

##
## Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.42468, p-value = 0.087
hist(resid(m.div.200kb))

```

## Histogram of resid(m.div.200kb)



```

summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.200kb)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -7.823e-04 -1.890e-04  3.370e-06  1.582e-04  7.148e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 2.061e-02 2.367e-05 870.811 <2e-16 ***
## thetaC      1.306e+00 3.205e-03 407.532 <2e-16 ***
## rhoC        8.924e-03 1.586e-02  0.563  0.575  
## tmrcaC      2.402e-02 6.327e-04 37.957 <2e-16 ***
## thetaC:tmrcaC 1.380e+00 7.367e-02 18.728 <2e-16 ***
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0002897 on 145 degrees of freedom
## Multiple R-squared:  0.9991, Adjusted R-squared:  0.9991 
## F-statistic: 4.197e+04 on 4 and 145 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.200kb[1, 5] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])

```

```
r2.sim.200kb[2, 5] <- anova.diversity$VarExp[1] * 100
r2.sim.200kb[3, 5] <- anova.diversity$VarExp[2] * 100
r2.sim.200kb[4, 5] <- anova.diversity$VarExp[3] * 100
r2.sim.200kb[5, 5] <- anova.diversity$VarExp[4] * 100
```

### 1.2.6 Replicate 6

```
rep_6.pi.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_6/rep_6.pi.200kb.bedgraph", header=TRUE)
rep_6.tmrca.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_6/sim.tmrca.200k.map", header=TRUE)

sim.lands.200kb <- as.data.frame(cbind(rep_6.pi.200kb$pi, sim.theta.200kb$sim, sim.rho.200kb$sim, rep_6.tmrca.200kb))
names(sim.lands.200kb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 577585, p-value = 0.7442
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##          rho
## -0.02686264

cor.test(~theta+rho, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 593676, p-value = 0.5002
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##          rho
## -0.0554712

cor.test(~rho+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 606554, p-value = 0.3401
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##          rho
## -0.07836615

# centering
sim.lands.200kb$thetaC <- sim.lands.200kb$theta - mean(sim.lands.200kb$theta)
sim.lands.200kb$tmrcaC <- sim.lands.200kb$tmrca - mean(sim.lands.200kb$tmrca)
sim.lands.200kb$rhoC <- sim.lands.200kb$rho - mean(sim.lands.200kb$rho)

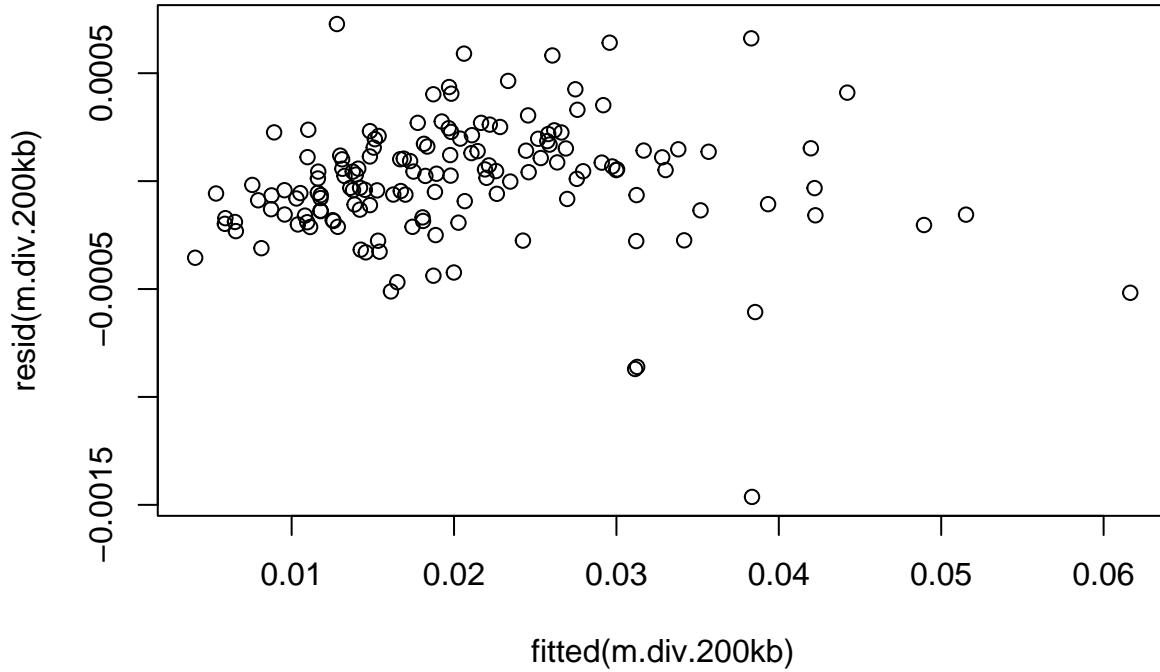
sim.lands.200kb$bin <- 1:nrow(sim.lands.200kb)
```

```

# for merging:
sim.lands.200kb.rep6 <- sim.lands.200kb
sim.lands.200kb.rep6$Replicate <- 6

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.200kb)
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```



```
dwtest(m.div.200kb)
```

```

##
## Durbin-Watson test
##
## data: m.div.200kb
## DW = 2.0877, p-value = 0.6996
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb)

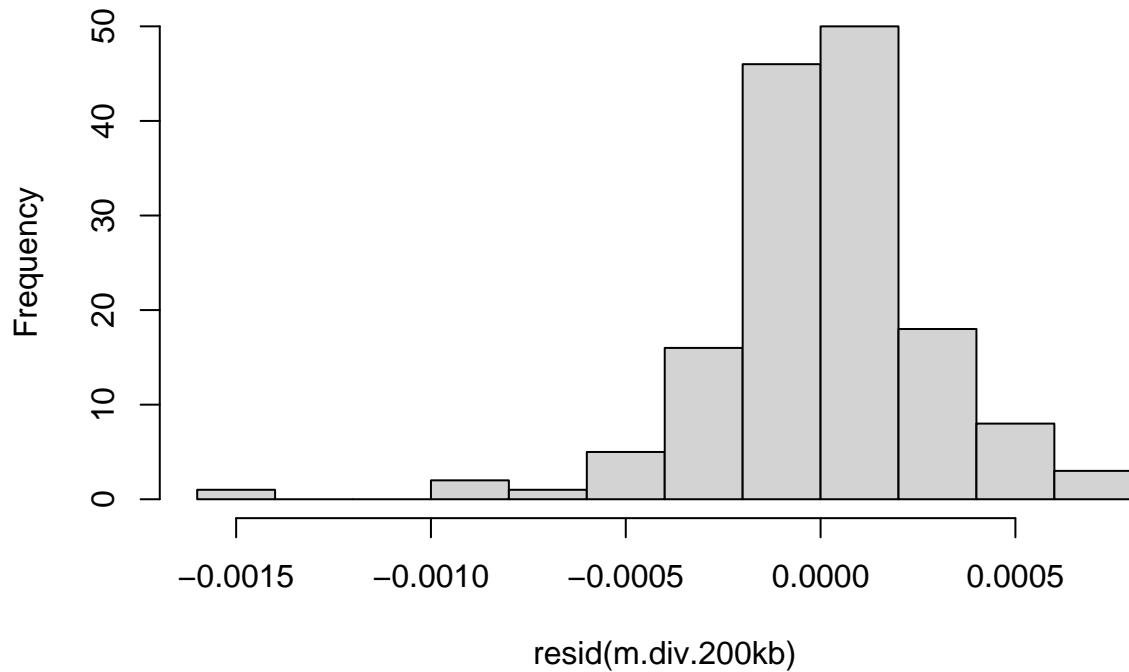
```

```

##
## Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.59616, p-value = 0.951
hist(resid(m.div.200kb))

```

## Histogram of resid(m.div.200kb)



```
summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.200kb)
##
## Residuals:
##       Min         1Q     Median         3Q        Max
## -1.463e-03 -1.507e-04  2.405e-05  1.519e-04  7.279e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.055e-02 2.337e-05 879.460 <2e-16 ***
## thetaC      1.299e+00 3.288e-03 395.145 <2e-16 ***
## rhoC        3.569e-03 1.559e-02   0.229   0.819
## tmrcaC     2.392e-02 6.333e-04  37.771 <2e-16 ***
## thetaC:tmrcaC 1.533e+00 6.794e-02  22.563 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.000286 on 145 degrees of freedom
## Multiple R-squared:  0.9992, Adjusted R-squared:  0.9992
## F-statistic: 4.499e+04 on 4 and 145 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.200kb[1, 6] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```
r2.sim.200kb[2, 6] <- anova.diversity$VarExp[1] * 100
r2.sim.200kb[3, 6] <- anova.diversity$VarExp[2] * 100
r2.sim.200kb[4, 6] <- anova.diversity$VarExp[3] * 100
r2.sim.200kb[5, 6] <- anova.diversity$VarExp[4] * 100
```

### 1.2.7 Replicate 7

```
rep_7.pi.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_7/rep_7.pi.200kb.bedgraph", header=TRUE)
rep_7.tmrca.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_7/sim.tmrca.200k.map", header=TRUE)

sim.lands.200kb <- as.data.frame(cbind(rep_7.pi.200kb$pi, sim.theta.200kb$sim, sim.rho.200kb$sim, rep_7.tmrca.200kb))
names(sim.lands.200kb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 647408, p-value = 0.06511
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.150999

cor.test(~theta+rho, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 593676, p-value = 0.5002
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.0554712

cor.test(~rho+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 523746, p-value = 0.402
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.06885462

# centering
sim.lands.200kb$thetaC <- sim.lands.200kb$theta - mean(sim.lands.200kb$theta)
sim.lands.200kb$tmrcaC <- sim.lands.200kb$tmrca - mean(sim.lands.200kb$tmrca)
sim.lands.200kb$rhoC <- sim.lands.200kb$rho - mean(sim.lands.200kb$rho)

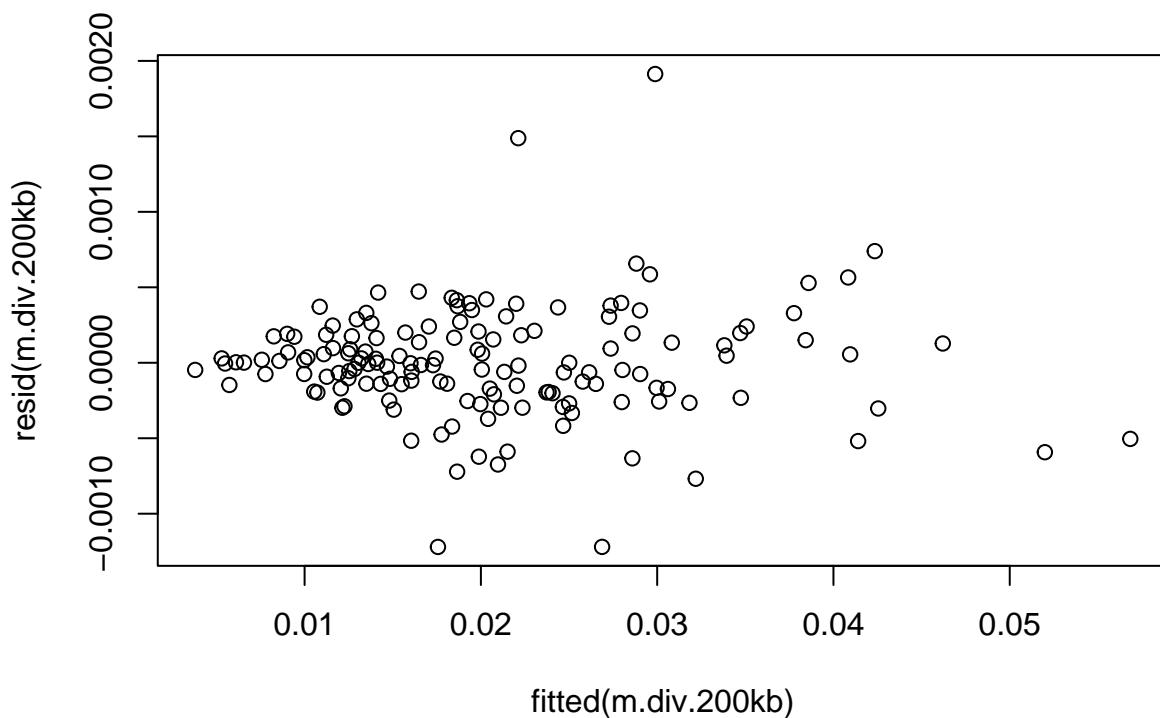
sim.lands.200kb$bin <- 1:nrow(sim.lands.200kb)
```

```

# for merging:
sim.lands.200kb.rep7 <- sim.lands.200kb
sim.lands.200kb.rep7$Replicate <- 7

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.200kb)
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```



```

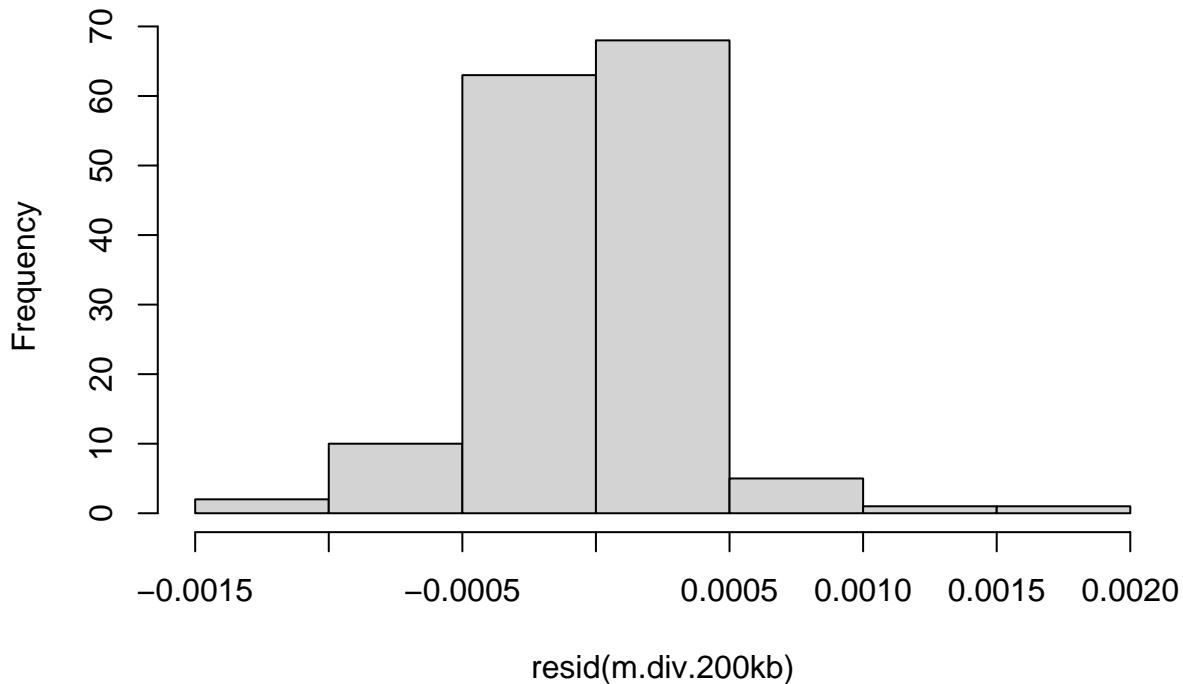
dwtest(m.div.200kb)

##
##  Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.9801, p-value = 0.4361
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb)

##
##  Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.40495, p-value = 0.056
hist(resid(m.div.200kb))

```

## Histogram of resid(m.div.200kb)



```

summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##     data = sim.lands.200kb)
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -1.220e-03 -1.868e-04 -1.610e-06  1.848e-04  1.913e-03
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 2.062e-02 3.141e-05 656.642 <2e-16 ***
## thetaC      1.315e+00 4.235e-03 310.525 <2e-16 ***
## rhoC       -1.620e-02 2.076e-02 -0.781  0.436    
## tmrcaC      2.369e-02 8.316e-04 28.486 <2e-16 ***
## thetaC:tmrcaC 1.422e+00 1.203e-01 11.823 <2e-16 ***
## ---      
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0003796 on 145 degrees of freedom
## Multiple R-squared:  0.9985, Adjusted R-squared:  0.9985 
## F-statistic: 2.432e+04 on 4 and 145 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.200kb[1, 7] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])

```

```
r2.sim.200kb[2, 7] <- anova.diversity$VarExp[1] * 100
r2.sim.200kb[3, 7] <- anova.diversity$VarExp[2] * 100
r2.sim.200kb[4, 7] <- anova.diversity$VarExp[3] * 100
r2.sim.200kb[5, 7] <- anova.diversity$VarExp[4] * 100
```

### 1.2.8 Replicate 8

```
rep_8.pi.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_8/rep_8.pi.200kb.bedgraph", header=TRUE)
rep_8.tmrca.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_8/sim.tmrca.200k.map", header=TRUE)

sim.lands.200kb <- as.data.frame(cbind(rep_8.pi.200kb$pi, sim.theta.200kb$sim, sim.rho.200kb$sim, rep_8.tmrca.200kb))
names(sim.lands.200kb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 588671, p-value = 0.5714
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.0465727

cor.test(~theta+rho, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 593676, p-value = 0.5002
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.0554712

cor.test(~rho+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 624456, p-value = 0.1793
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.1101933

# centering
sim.lands.200kb$thetaC <- sim.lands.200kb$theta - mean(sim.lands.200kb$theta)
sim.lands.200kb$tmrcaC <- sim.lands.200kb$tmrca - mean(sim.lands.200kb$tmrca)
sim.lands.200kb$rhoC <- sim.lands.200kb$rho - mean(sim.lands.200kb$rho)

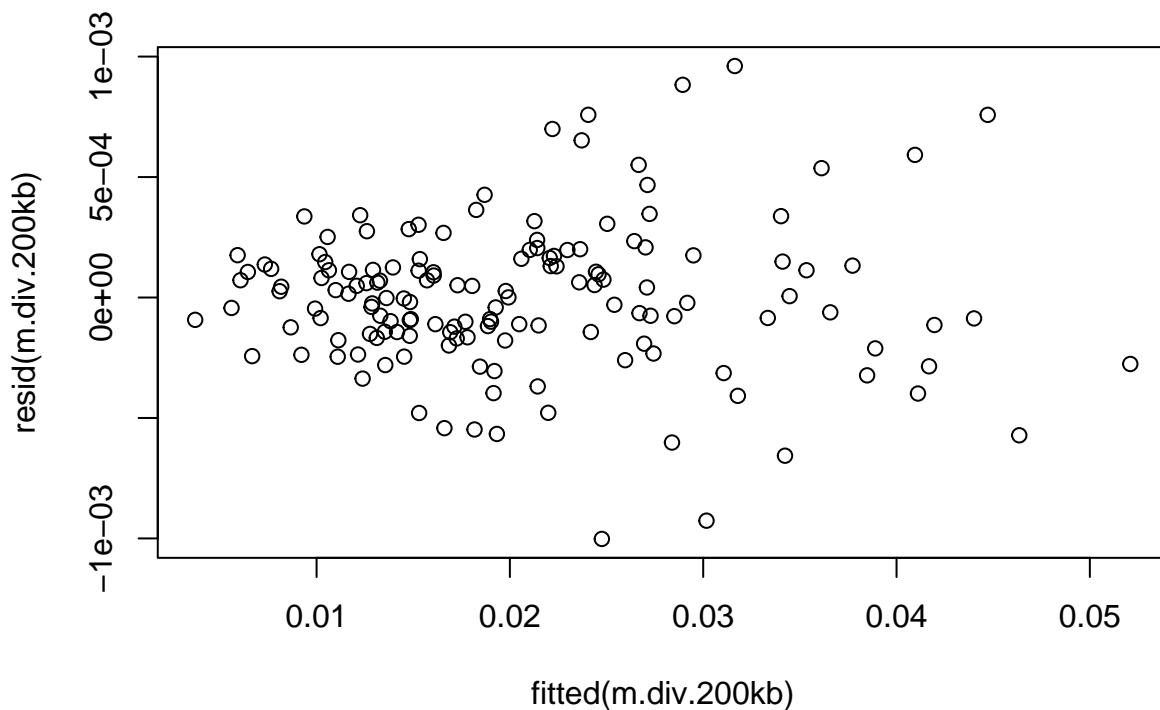
sim.lands.200kb$bin <- 1:nrow(sim.lands.200kb)
```

```

# for merging:
sim.lands.200kb.rep8 <- sim.lands.200kb
sim.lands.200kb.rep8$Replicate <- 8

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.200kb)
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```



```

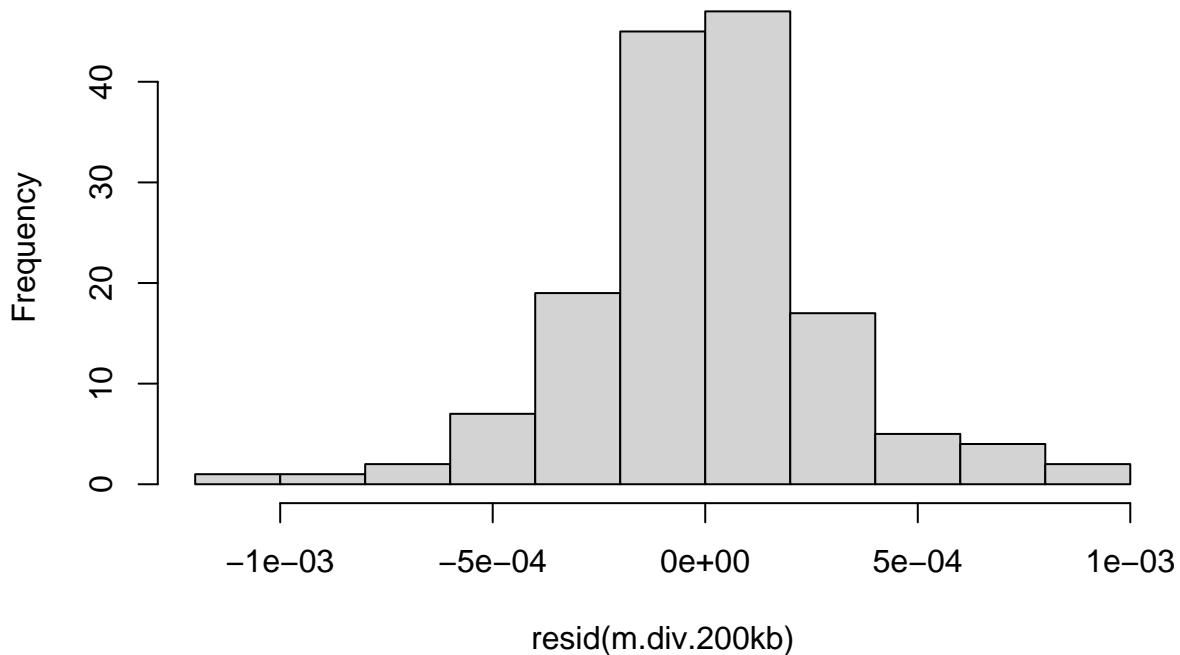
dwtest(m.div.200kb)

##
## Durbin-Watson test
##
## data: m.div.200kb
## DW = 2.036, p-value = 0.577
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb)

##
## Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.54355, p-value = 0.792
hist(resid(m.div.200kb))

```

## Histogram of resid(m.div.200kb)



```
summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.200kb)
##
## Residuals:
##       Min         1Q     Median         3Q        Max
## -0.0010021 -0.0001570 -0.0000008  0.0001486  0.0009608
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.057e-02 2.534e-05 811.819 <2e-16 ***
## thetaC      1.309e+00 3.478e-03 376.496 <2e-16 ***
## rhoC       -9.189e-03 1.709e-02 -0.538  0.592
## tmrcaC      2.531e-02 6.716e-04 37.681 <2e-16 ***
## thetaC:tmrcaC 1.518e+00 7.926e-02 19.154 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.000309 on 145 degrees of freedom
## Multiple R-squared:  0.999, Adjusted R-squared:  0.999
## F-statistic: 3.616e+04 on 4 and 145 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.200kb[1, 8] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```
r2.sim.200kb[2, 8] <- anova.diversity$VarExp[1] * 100
r2.sim.200kb[3, 8] <- anova.diversity$VarExp[2] * 100
r2.sim.200kb[4, 8] <- anova.diversity$VarExp[3] * 100
r2.sim.200kb[5, 8] <- anova.diversity$VarExp[4] * 100
```

### 1.2.9 Replicate 9

```
rep_9.pi.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_9/rep_9.pi.200kb.bedgraph", head=TRUE)
rep_9.tmrca.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_9/sim.tmrca.200k.map", head=TRUE)

sim.lands.200kb <- as.data.frame(cbind(rep_9.pi.200kb$pi, sim.theta.200kb$sim, sim.rho.200kb$sim, rep_9.tmrca.200kb))
names(sim.lands.200kb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 493800, p-value = 0.1366
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.1220935

cor.test(~theta+rho, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 593676, p-value = 0.5002
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.0554712

cor.test(~rho+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 597682, p-value = 0.4463
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.062593

# centering
sim.lands.200kb$thetaC <- sim.lands.200kb$theta - mean(sim.lands.200kb$theta)
sim.lands.200kb$tmrcaC <- sim.lands.200kb$tmrca - mean(sim.lands.200kb$tmrca)
sim.lands.200kb$rhoC <- sim.lands.200kb$rho - mean(sim.lands.200kb$rho)

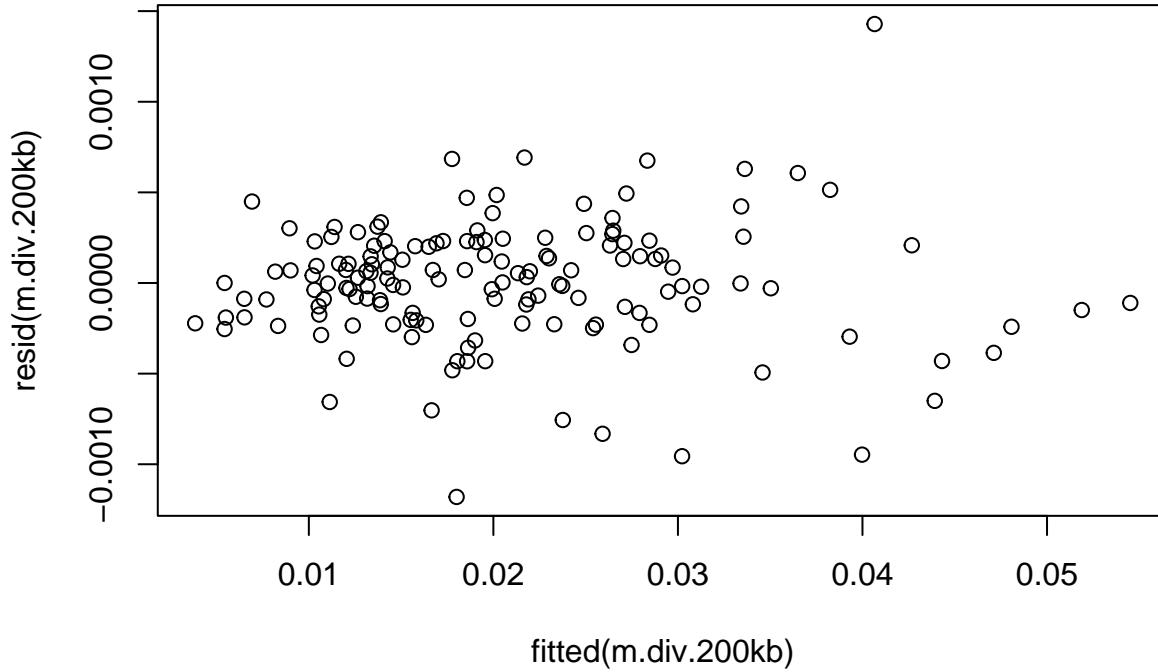
sim.lands.200kb$bin <- 1:nrow(sim.lands.200kb)
```

```

# for merging:
sim.lands.200kb.rep9 <- sim.lands.200kb
sim.lands.200kb.rep9$Replicate <- 9

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.200kb)
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```



```

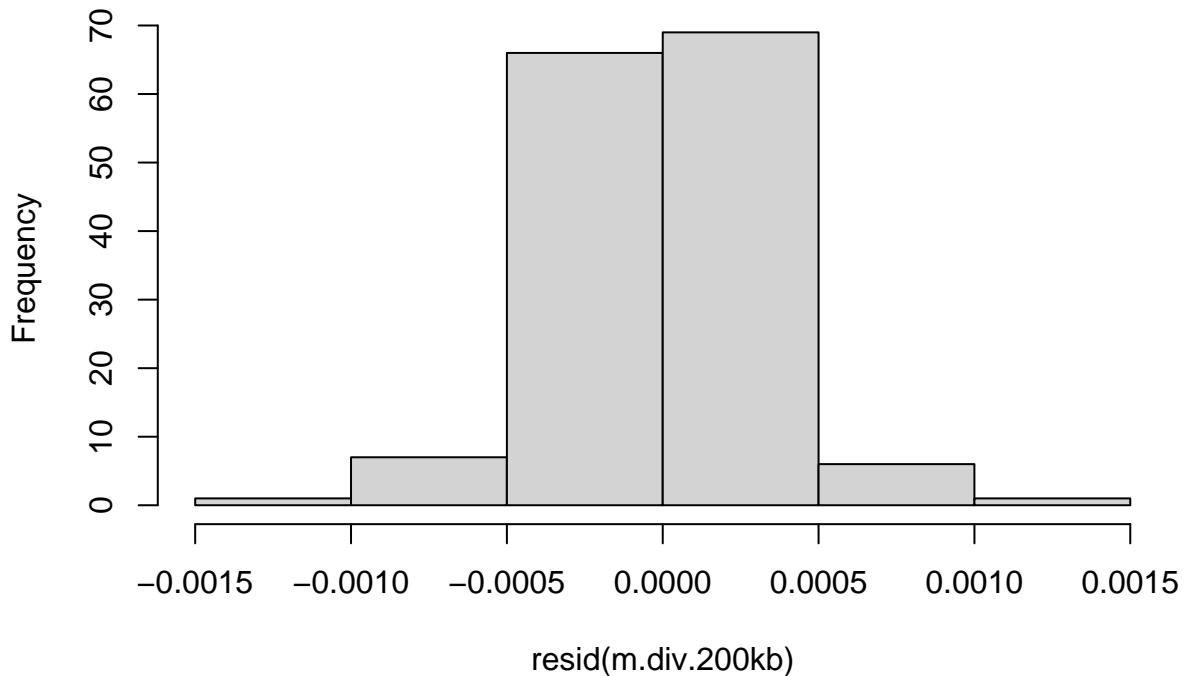
dwtest(m.div.200kb)

##
## Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.6818, p-value = 0.022
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb)

##
## Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.42403, p-value = 0.077
hist(resid(m.div.200kb))

```

## Histogram of resid(m.div.200kb)



```
summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##     data = sim.lands.200kb)
##
## Residuals:
##      Min        1Q    Median        3Q       Max
## -1.180e-03 -1.904e-04  1.650e-06  2.078e-04  1.429e-03
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.061e-02 2.834e-05 727.360 <2e-16 ***
## thetaC      1.308e+00 3.854e-03 339.390 <2e-16 ***
## rhoC        6.075e-03 1.879e-02   0.323   0.747
## tmrcaC      2.558e-02 8.061e-04  31.733 <2e-16 ***
## thetaC:tmrcaC 1.713e+00 1.105e-01  15.505 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0003441 on 145 degrees of freedom
## Multiple R-squared:  0.9988, Adjusted R-squared:  0.9988
## F-statistic: 3.126e+04 on 4 and 145 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.200kb[1, 9] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```
r2.sim.200kb[2, 9] <- anova.diversity$VarExp[1] * 100
r2.sim.200kb[3, 9] <- anova.diversity$VarExp[2] * 100
r2.sim.200kb[4, 9] <- anova.diversity$VarExp[3] * 100
r2.sim.200kb[5, 9] <- anova.diversity$VarExp[4] * 100
```

### 1.2.10 Replicate 10

```
rep_10.pi.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_10/rep_10.pi.200kb.bedgraph", header = TRUE)
rep_10.tmrca.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_10/sim.tmrca.200k.map", header = TRUE)

sim.lands.200kb <- as.data.frame(cbind(rep_10.pi.200kb$pi, sim.theta.200kb$sim, sim.rho.200kb$sim, rep_10.tmrca.200kb))
names(sim.lands.200kb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 605678, p-value = 0.3502
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.07680806

cor.test(~theta+rho, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 593676, p-value = 0.5002
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.0554712

cor.test(~rho+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 612862, p-value = 0.2753
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.08958087

# centering
sim.lands.200kb$thetaC <- sim.lands.200kb$theta - mean(sim.lands.200kb$theta)
sim.lands.200kb$tmrcaC <- sim.lands.200kb$tmrca - mean(sim.lands.200kb$tmrca)
sim.lands.200kb$rhoC <- sim.lands.200kb$rho - mean(sim.lands.200kb$rho)

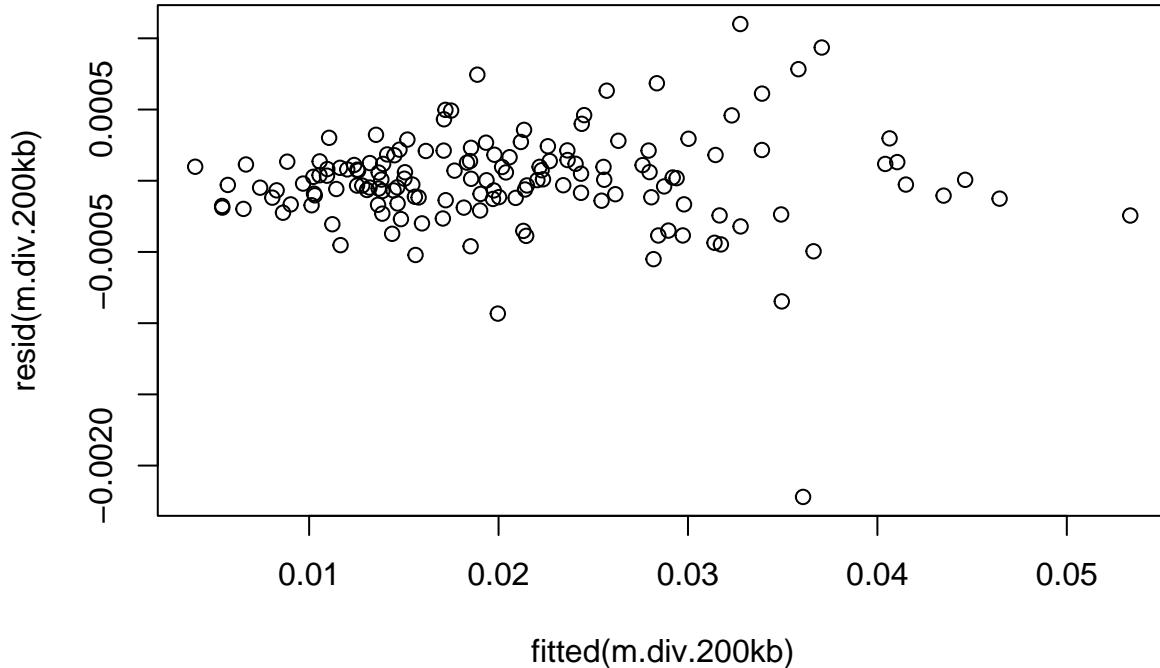
sim.lands.200kb$bin <- 1:nrow(sim.lands.200kb)
```

```

# for merging:
sim.lands.200kb.rep50 <- sim.lands.200kb
sim.lands.200kb.rep50$Replicate <- 10

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.200kb)
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```



```
dwtest(m.div.200kb)
```

```

##
## Durbin-Watson test
##
## data: m.div.200kb
## DW = 2.1646, p-value = 0.8354
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb)

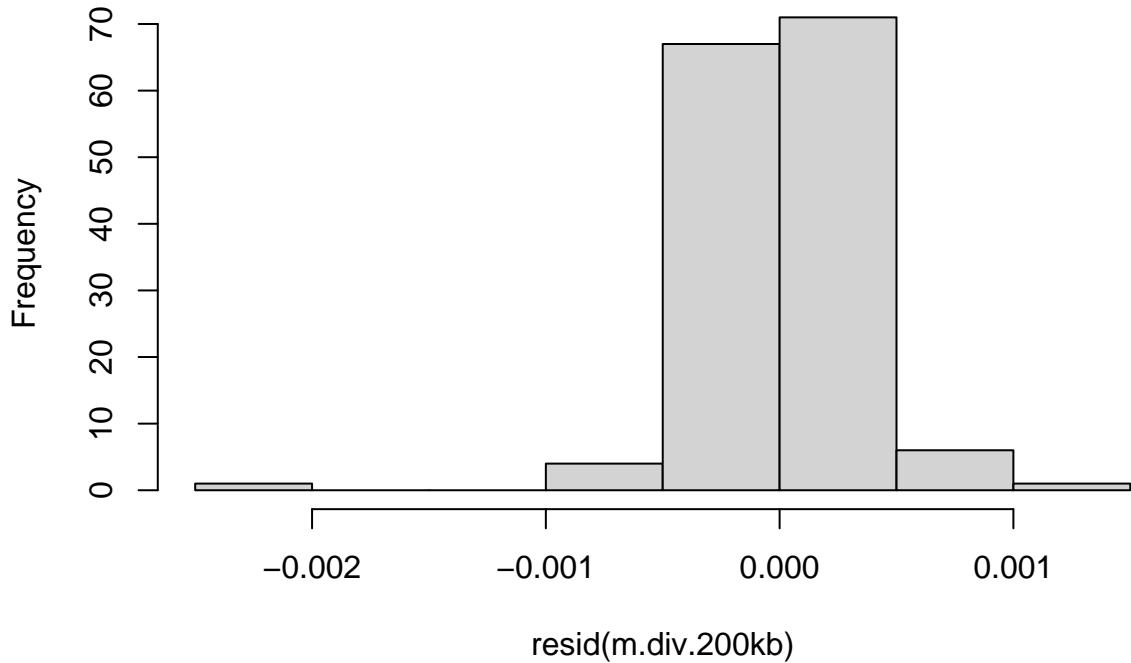
```

```

##
## Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.41358, p-value = 0.078
hist(resid(m.div.200kb))

```

## Histogram of resid(m.div.200kb)



```
summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.200kb)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -2.220e-03 -1.345e-04  6.710e-06  1.375e-04  1.100e-03
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 2.071e-02 2.877e-05 720.015 <2e-16 ***
## thetaC      1.317e+00 4.037e-03 326.195 <2e-16 ***
## rhoC        4.763e-03 1.928e-02  0.247   0.805    
## tmrcaC      2.484e-02 6.682e-04  37.182 <2e-16 ***
## thetaC:tmrcaC 1.796e+00 7.919e-02 22.681 <2e-16 ***
## ---      
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0003493 on 145 degrees of freedom
## Multiple R-squared:  0.9987, Adjusted R-squared:  0.9987 
## F-statistic: 2.783e+04 on 4 and 145 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.200kb[1, 10] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) / 3
```

```

r2.sim.200kb[2, 10] <- anova.diversity$VarExp[1] * 100
r2.sim.200kb[3, 10] <- anova.diversity$VarExp[2] * 100
r2.sim.200kb[4, 10] <- anova.diversity$VarExp[3] * 100
r2.sim.200kb[5, 10] <- anova.diversity$VarExp[4] * 100

r2.sim.200kb$average <- rowMeans(r2.sim.200kb)
r2.sim.200kb <- transform(r2.sim.200kb, sd=apply(r2.sim.200kb, 1, sd, na.rm = TRUE))

```

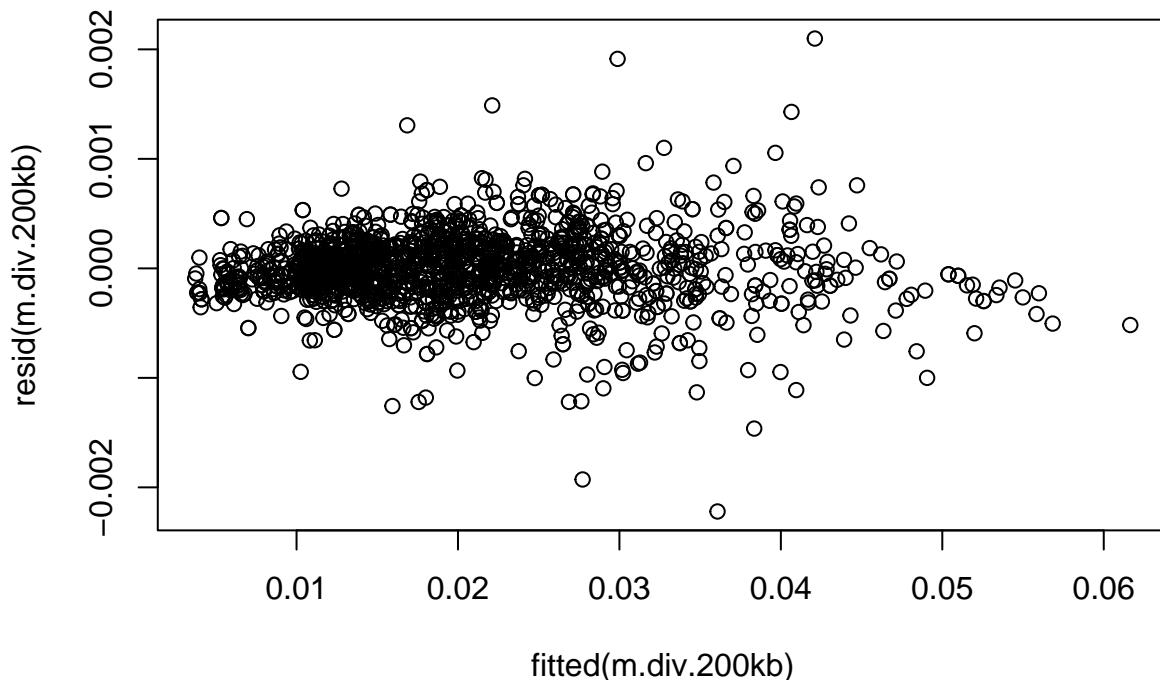
### 1.2.11 all replicates:

```

sim.lands.200kb.all <- rbind(sim.lands.200kb.rep5, sim.lands.200kb.rep2, sim.lands.200kb.rep3, sim.lands.200kb.rep1)

m.div.200kb <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC)*as.factor(Replicate), data = sim.lands.200kb.all)
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```



```

dwtest(m.div.200kb)

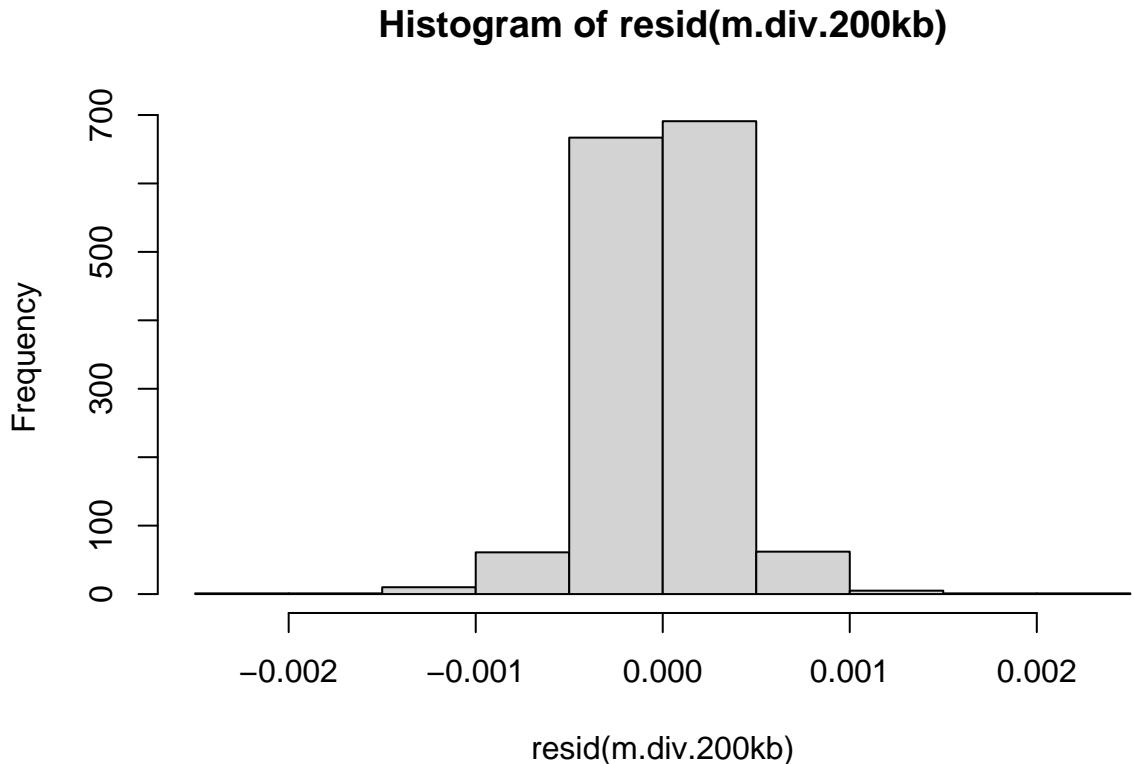
##
##  Durbin-Watson test
##
##  data:  m.div.200kb
##  DW = 1.9357, p-value = 0.05828
##  alternative hypothesis: true autocorrelation is greater than 0

hmctest(m.div.200kb)

##
##  Harrison-McCabe test
##
##  data:  m.div.200kb
##  HMC = 0.48495, p-value = 0.199

```

```
hist(resid(m.div.200kb))
```



```
m.div.200kb.2 <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC + thetaC:rhoC)*as.factor(Replicate), data = sim.lands.200kb.all)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC + thetaC:rhoC + rhoC:tmrcaC)*as.factor(Replicate), data = sim.lands.200kb.all)
```

```
AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)
```

```
##                df      AIC
## m.div.200kb    46 -19748.95
## m.div.200kb.2  55 -19741.46
## m.div.200kb.3  64 -19728.72
```

```
summary(m.div.200kb)
```

```
##
## Call:
## lm(formula = diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC) *
##       as.factor(Replicate), data = sim.lands.200kb.all)
##
## Residuals:
##      Min        1Q     Median        3Q       Max
## -2.220e-03 -1.705e-04  1.390e-06  1.741e-04  2.099e-03
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.056e-02 2.693e-05 763.480 < 2e-16 ***
## thetaC      1.297e+00 3.664e-03 354.022 < 2e-16 ***
## rhoC       -3.118e-02 1.800e-02 -1.733 0.083394 .
## tmrcaC     2.455e-02 6.646e-04 36.941 < 2e-16 ***
## as.factor(Replicate)3 8.648e-05 3.808e-05   2.271 0.023308 *
```

```

## as.factor(Replicate)4      -5.611e-05  3.808e-05 -1.473 0.140907
## as.factor(Replicate)5      5.158e-05  3.298e-05  1.564 0.118060
## as.factor(Replicate)6     -3.139e-06  3.809e-05 -0.082 0.934334
## as.factor(Replicate)7      6.595e-05  3.833e-05  1.721 0.085525 .
## as.factor(Replicate)8      1.320e-05  3.816e-05  0.346 0.729361
## as.factor(Replicate)9      5.572e-05  3.824e-05  1.457 0.145329
## as.factor(Replicate)10     1.554e-04  3.824e-05  4.064 5.09e-05 ***
## thetaC:tmrcaC              1.643e+00  8.851e-02 18.565 < 2e-16 ***
## thetaC:as.factor(Replicate)3 1.170e-02  5.170e-03  2.263 0.023812 *
## thetaC:as.factor(Replicate)4 4.031e-03  5.165e-03  0.780 0.435225
## thetaC:as.factor(Replicate)5 9.218e-03  4.481e-03  2.057 0.039834 *
## thetaC:as.factor(Replicate)6 2.241e-03  5.272e-03  0.425 0.670855
## thetaC:as.factor(Replicate)7 1.818e-02  5.192e-03  3.502 0.000476 ***
## thetaC:as.factor(Replicate)8 1.225e-02  5.214e-03  2.349 0.018958 *
## thetaC:as.factor(Replicate)9 1.109e-02  5.202e-03  2.131 0.033240 *
## thetaC:as.factor(Replicate)10 1.971e-02  5.286e-03  3.728 0.000200 ***
## rhoC:as.factor(Replicate)3   6.285e-02  2.548e-02  2.467 0.013739 *
## rhoC:as.factor(Replicate)4   3.996e-02  2.545e-02  1.570 0.116550
## rhoC:as.factor(Replicate)5   4.010e-02  2.206e-02  1.818 0.069319 .
## rhoC:as.factor(Replicate)6   3.475e-02  2.543e-02  1.366 0.172044
## rhoC:as.factor(Replicate)7   1.498e-02  2.547e-02  0.588 0.556651
## rhoC:as.factor(Replicate)8   2.199e-02  2.562e-02  0.858 0.390926
## rhoC:as.factor(Replicate)9   3.725e-02  2.546e-02  1.463 0.143599
## rhoC:as.factor(Replicate)10  3.594e-02  2.559e-02  1.404 0.160426
## tmrcaC:as.factor(Replicate)3 3.319e-04  9.312e-04  0.356 0.721606
## tmrcaC:as.factor(Replicate)4 -1.072e-04 9.489e-04 -0.113 0.910045
## tmrcaC:as.factor(Replicate)5 -5.334e-04 8.373e-04 -0.637 0.524142
## tmrcaC:as.factor(Replicate)6 -6.326e-04 9.872e-04 -0.641 0.521738
## tmrcaC:as.factor(Replicate)7 -8.605e-04 9.816e-04 -0.877 0.380793
## tmrcaC:as.factor(Replicate)8  7.566e-04 9.773e-04  0.774 0.438985
## tmrcaC:as.factor(Replicate)9  1.030e-03 1.019e-03  1.011 0.312387
## tmrcaC:as.factor(Replicate)10 2.934e-04 9.162e-04  0.320 0.748831
## thetaC:tmrcaC:as.factor(Replicate)3 -1.709e-01 1.270e-01 -1.346 0.178522
## thetaC:tmrcaC:as.factor(Replicate)4 -1.743e-01 1.240e-01 -1.406 0.160029
## thetaC:tmrcaC:as.factor(Replicate)5 -2.634e-01 1.065e-01 -2.473 0.013515 *
## thetaC:tmrcaC:as.factor(Replicate)6 -1.102e-01 1.182e-01 -0.933 0.351213
## thetaC:tmrcaC:as.factor(Replicate)7 -2.207e-01 1.369e-01 -1.612 0.107174
## thetaC:tmrcaC:as.factor(Replicate)8 -1.250e-01 1.224e-01 -1.021 0.307456
## thetaC:tmrcaC:as.factor(Replicate)9  6.939e-02 1.380e-01  0.503 0.615071
## thetaC:tmrcaC:as.factor(Replicate)10 1.530e-01 1.158e-01  1.321 0.186722
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0003297 on 1455 degrees of freedom
## Multiple R-squared:  0.9989, Adjusted R-squared:  0.9989
## F-statistic: 2.96e+04 on 44 and 1455 DF,  p-value: < 2.2e-16

```

### 1.3 1 Mb scale

```

r2.sim.1Mb <- as.data.frame(matrix(ncol = nreps, nrow = 5))
row.names(r2.sim.1Mb) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
colnames(r2.sim.1Mb) <- reps

```

```

sim.rho.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/dm.sim.rho.1e+06.txt", header = T)
sim.theta.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/dm.sim.theta.1e+06.txt", header = T)

1.3.1 Replicate 1

rep_1.pi.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_1/rep_1.pi.1Mb.bedgraph", header = T)
rep_1.tmrca.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_1/sim.tmrca.1M.map", header = T)

sim.lands.1Mb <- as.data.frame(cbind(rep_1.pi.1Mb$pi, sim.theta.1Mb$sim, sim.rho.1Mb$sim, rep_1.tmrca.1Mb$tmrca))
names(sim.lands.1Mb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 5134, p-value = 0.452
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.142158

cor.test(~theta+rho, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 5654, p-value = 0.1684
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.257842

cor.test(~rho+tmrca, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 4576, p-value = 0.9251
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.01802002

# centering
sim.lands.1Mb$thetaC <- sim.lands.1Mb$theta - mean(sim.lands.1Mb$theta)
sim.lands.1Mb$tmrcaC <- sim.lands.1Mb$tmrca - mean(sim.lands.1Mb$tmrca)
sim.lands.1Mb$rhoC <- sim.lands.1Mb$rho - mean(sim.lands.1Mb$rho)

sim.lands.1Mb$bin <- 1:nrow(sim.lands.1Mb)

# for merging:

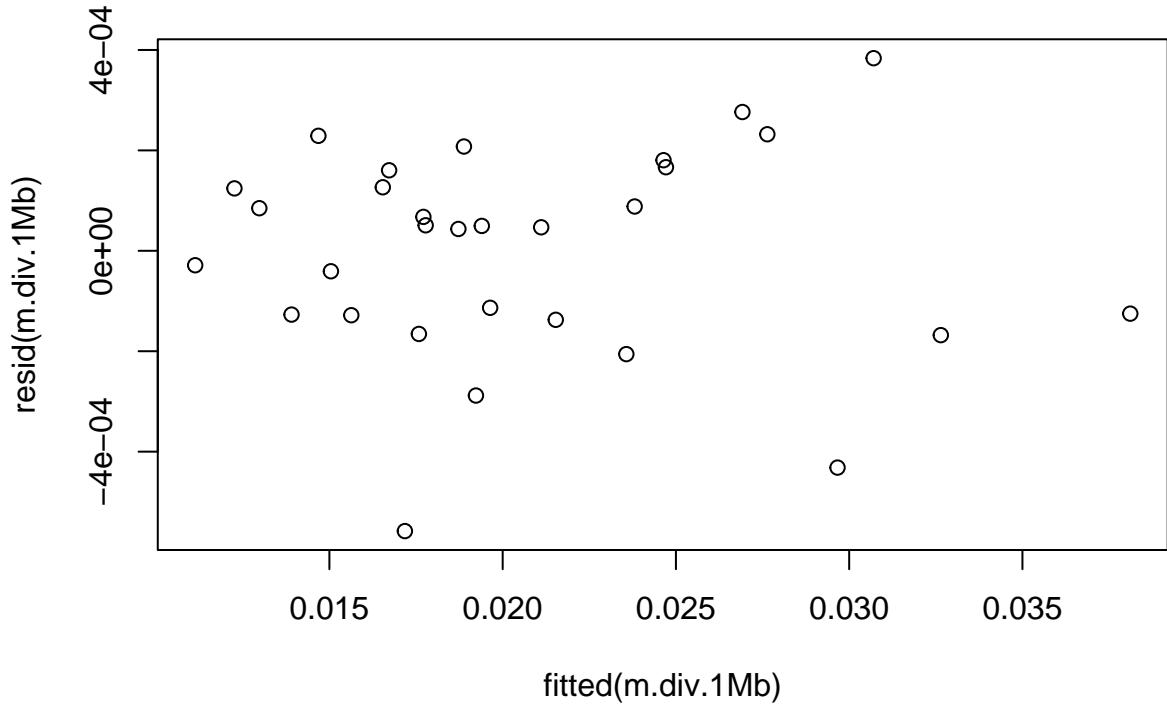
```

```

sim.lands.1Mb.rep5 <- sim.lands.1Mb
sim.lands.1Mb.rep5$Replicate <- 1

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.1Mb)
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```



```

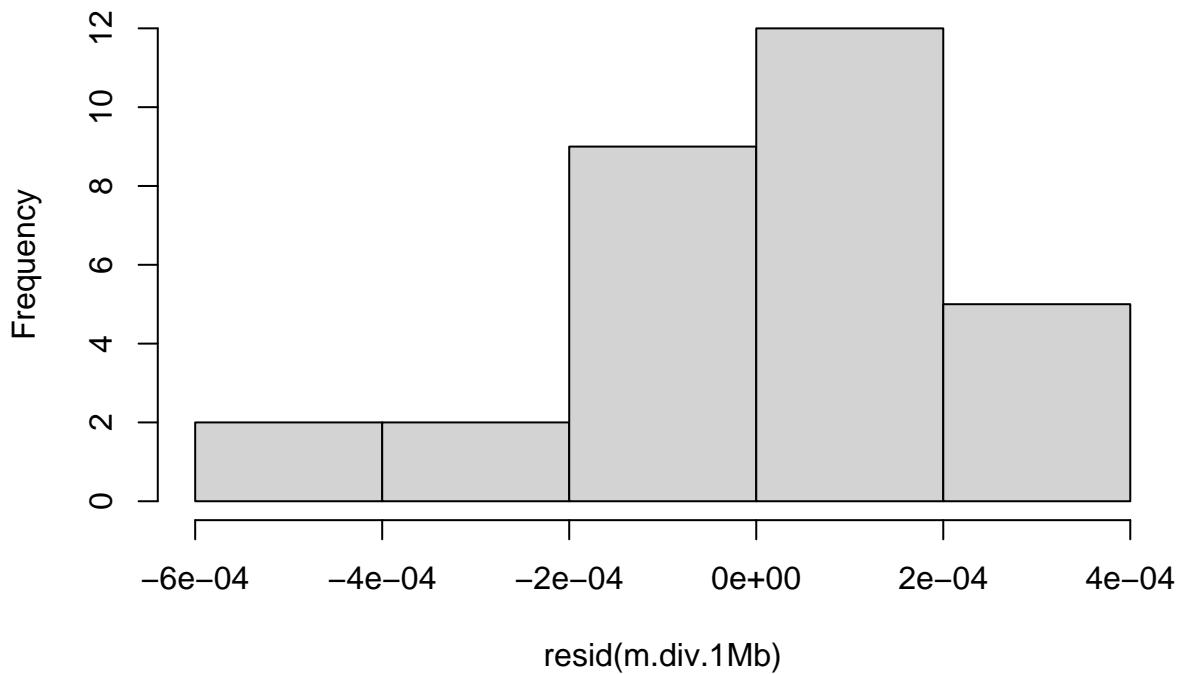
dwtest(m.div.1Mb)

##
##  Durbin-Watson test
##
## data: m.div.1Mb
## DW = 1.5295, p-value = 0.09374
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.1Mb)

##
##  Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.59412, p-value = 0.74
hist(resid(m.div.1Mb))

```

## Histogram of resid(m.div.1Mb)



```
summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.1Mb)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -0.0005582 -0.0001279  0.0000482  0.0001519  0.0003836
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 2.067e-02 4.132e-05 500.181 < 2e-16 ***
## thetaC      1.313e+00 9.626e-03 136.418 < 2e-16 ***
## rhoC        -2.472e-03 6.889e-02 -0.036  0.9717    
## tmrcaC      2.602e-02 2.881e-03  9.031 2.41e-09 ***
## thetaC:tmrcaC 1.182e+00 6.258e-01  1.889  0.0706 .  
## ---      
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0002263 on 25 degrees of freedom
## Multiple R-squared:  0.9989, Adjusted R-squared:  0.9988 
## F-statistic:  5910 on 4 and 25 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.1Mb[1, 1] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
```

```
r2.sim.1Mb[2, 1] <- anova.diversity$VarExp[1] * 100
r2.sim.1Mb[3, 1] <- anova.diversity$VarExp[2] * 100
r2.sim.1Mb[4, 1] <- anova.diversity$VarExp[3] * 100
r2.sim.1Mb[5, 1] <- anova.diversity$VarExp[4] * 100
```

### 1.3.2 Replicate 2

```
rep_2.pi.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_2/rep_2.pi.1Mb.bedgraph", header = TRUE)
rep_2.tmrca.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_2/sim.tmrca.1M.map", header = TRUE)

sim.lands.1Mb <- as.data.frame(cbind(rep_2.pi.1Mb$pi, sim.theta.1Mb$sim, sim.rho.1Mb$sim, rep_2.tmrca.1Mb$tmrca))
names(sim.lands.1Mb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 3982, p-value = 0.5467
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.1141268

cor.test(~theta+rho, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 5654, p-value = 0.1684
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.257842

cor.test(~rho+tmrca, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 3726, p-value = 0.3645
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.171079

cor.test(~diversity+theta, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: diversity and theta
```

```

## S = 4053.2, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9927941
cor.test(~diversity+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: diversity and tmrca
## S = 552924, p-value = 0.8364
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.01698031
cor.test(~diversity+rho, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: diversity and rho
## S = 596694, p-value = 0.4591
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.06083648

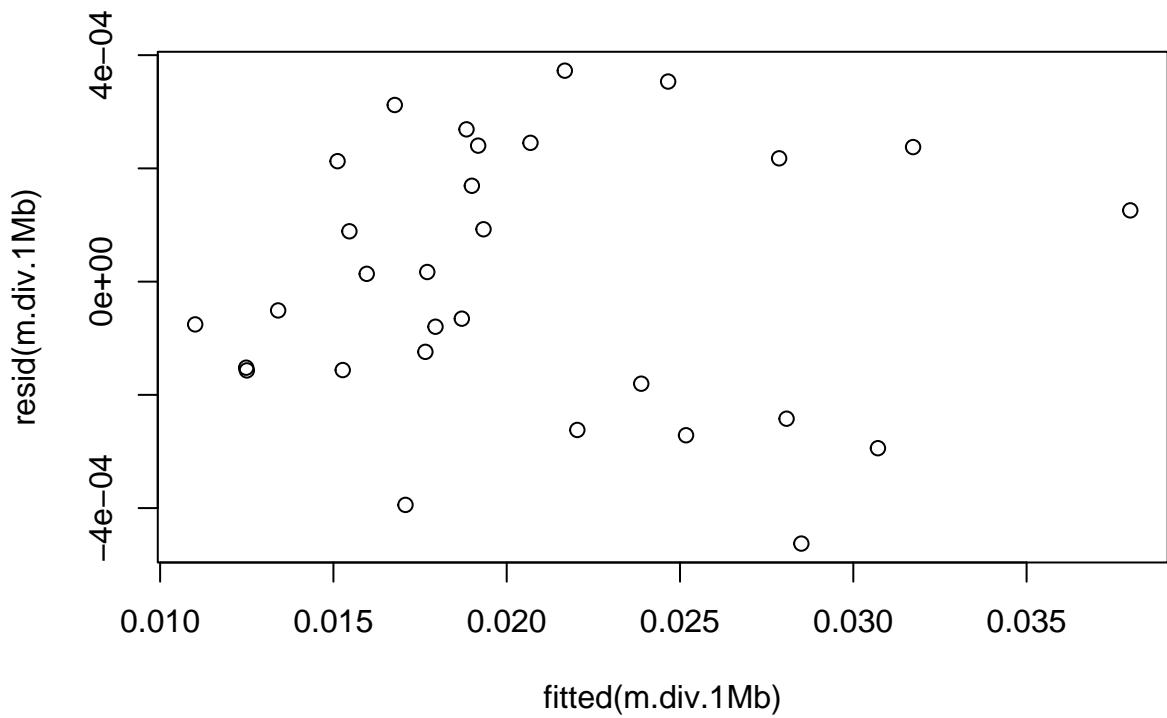
# centering
sim.lands.1Mb$thetaC <- sim.lands.1Mb$theta - mean(sim.lands.1Mb$theta)
sim.lands.1Mb$tmrcaC <- sim.lands.1Mb$tmrca - mean(sim.lands.1Mb$tmrca)
sim.lands.1Mb$rhoC <- sim.lands.1Mb$rho - mean(sim.lands.1Mb$rho)

sim.lands.1Mb$bin <- 1:nrow(sim.lands.1Mb)

# for merging:
sim.lands.1Mb.rep2 <- sim.lands.1Mb
sim.lands.1Mb.rep2$Replicate <- 2

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.1Mb)
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```



```

dwtest(m.div.1Mb)

##
##  Durbin-Watson test
##
##  data:  m.div.1Mb
##  DW = 2.6531, p-value = 0.9631
##  alternative hypothesis: true autocorrelation is greater than 0

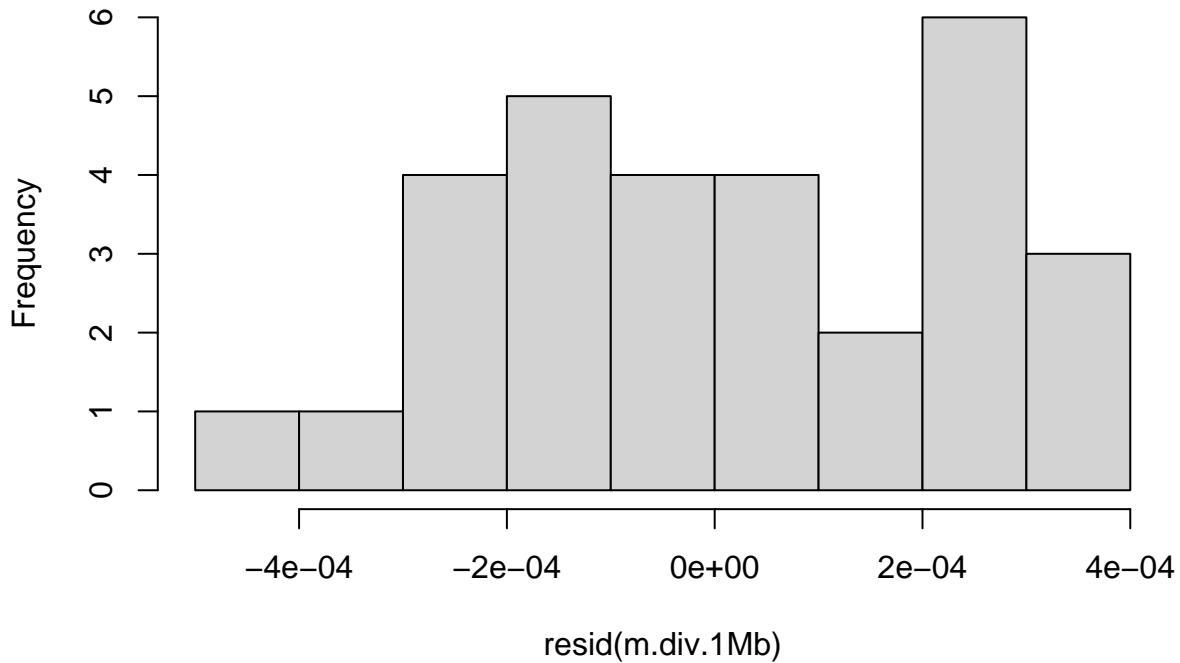
hmctest(m.div.1Mb)

##
##  Harrison-McCabe test
##
##  data:  m.div.1Mb
##  HMC = 0.51119, p-value = 0.558

hist(resid(m.div.1Mb))

```

## Histogram of resid(m.div.1Mb)



```
summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.1Mb)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -4.627e-04 -1.567e-04 -1.856e-05  2.165e-04  3.726e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 2.052e-02 4.606e-05 445.437 < 2e-16 ***
## thetaC      1.285e+00 1.013e-02 126.882 < 2e-16 ***
## rhoC        -4.630e-02 7.505e-02 -0.617 0.542900  
## tmrcaC      2.480e-02 2.820e-03  8.796 3.99e-09 ***
## thetaC:tmrcaC 2.351e+00 5.373e-01   4.376 0.000188 ***
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0002496 on 25 degrees of freedom
## Multiple R-squared:  0.9987, Adjusted R-squared:  0.9985 
## F-statistic: 4800 on 4 and 25 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.1Mb[1, 2] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```
r2.sim.1Mb[2, 2] <- anova.diversity$VarExp[1] * 100
r2.sim.1Mb[3, 2] <- anova.diversity$VarExp[2] * 100
r2.sim.1Mb[4, 2] <- anova.diversity$VarExp[3] * 100
r2.sim.1Mb[5, 2] <- anova.diversity$VarExp[4] * 100
```

### 1.3.3 Replicate 3

```
rep_3.pi.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_3/rep_3.pi.1Mb.bedgraph", header = TRUE)
rep_3.tmrca.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_3/sim.tmrca.1M.map", header = TRUE)

sim.lands.1Mb <- as.data.frame(cbind(rep_3.pi.1Mb$pi, sim.theta.1Mb$sim, sim.rho.1Mb$sim, rep_3.tmrca.1Mb$tmrca))
names(sim.lands.1Mb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 6456, p-value = 0.01674
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.4362625

cor.test(~theta+rho, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 5654, p-value = 0.1684
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.257842

cor.test(~rho+tmrca, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 4500, p-value = 0.9963
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.001112347

cor.test(~diversity+theta, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: diversity and theta
```

```

## S = 4053.2, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9927941
cor.test(~diversity+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: diversity and tmrca
## S = 552924, p-value = 0.8364
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.01698031
cor.test(~diversity+rho, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: diversity and rho
## S = 596694, p-value = 0.4591
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.06083648

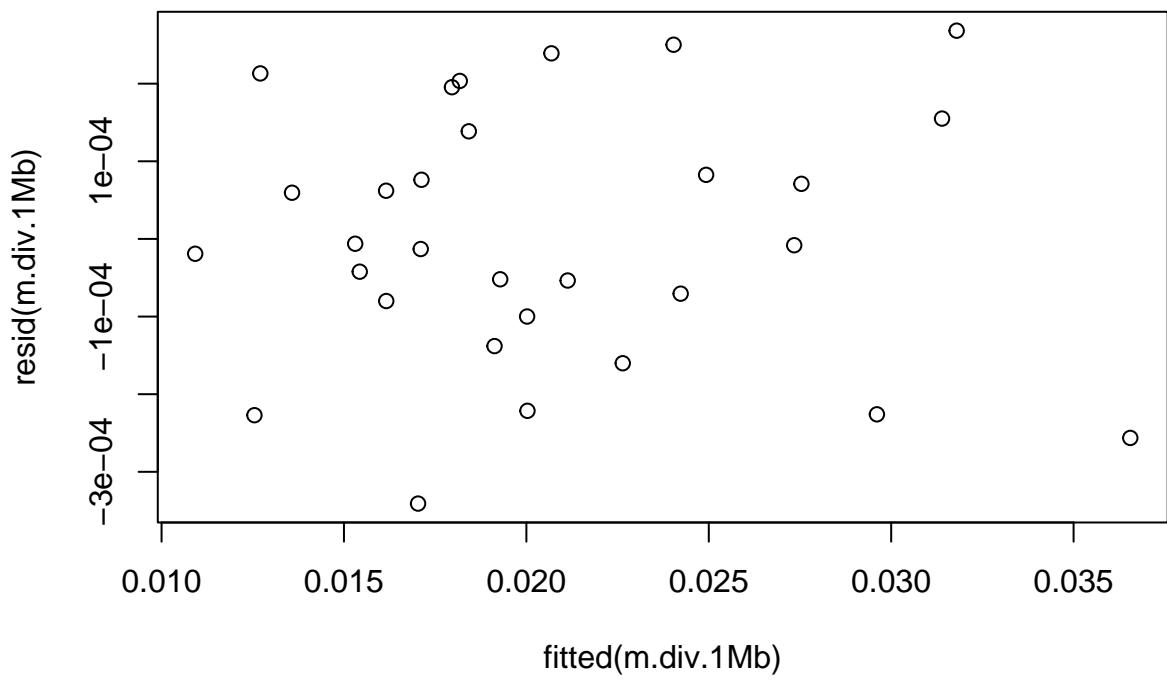
# centering
sim.lands.1Mb$thetaC <- sim.lands.1Mb$theta - mean(sim.lands.1Mb$theta)
sim.lands.1Mb$tmrcaC <- sim.lands.1Mb$tmrca - mean(sim.lands.1Mb$tmrca)
sim.lands.1Mb$rhoC <- sim.lands.1Mb$rho - mean(sim.lands.1Mb$rho)

sim.lands.1Mb$bin <- 1:nrow(sim.lands.1Mb)

# for merging:
sim.lands.1Mb.rep3 <- sim.lands.1Mb
sim.lands.1Mb.rep3$Replicate <- 3

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.1Mb)
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```

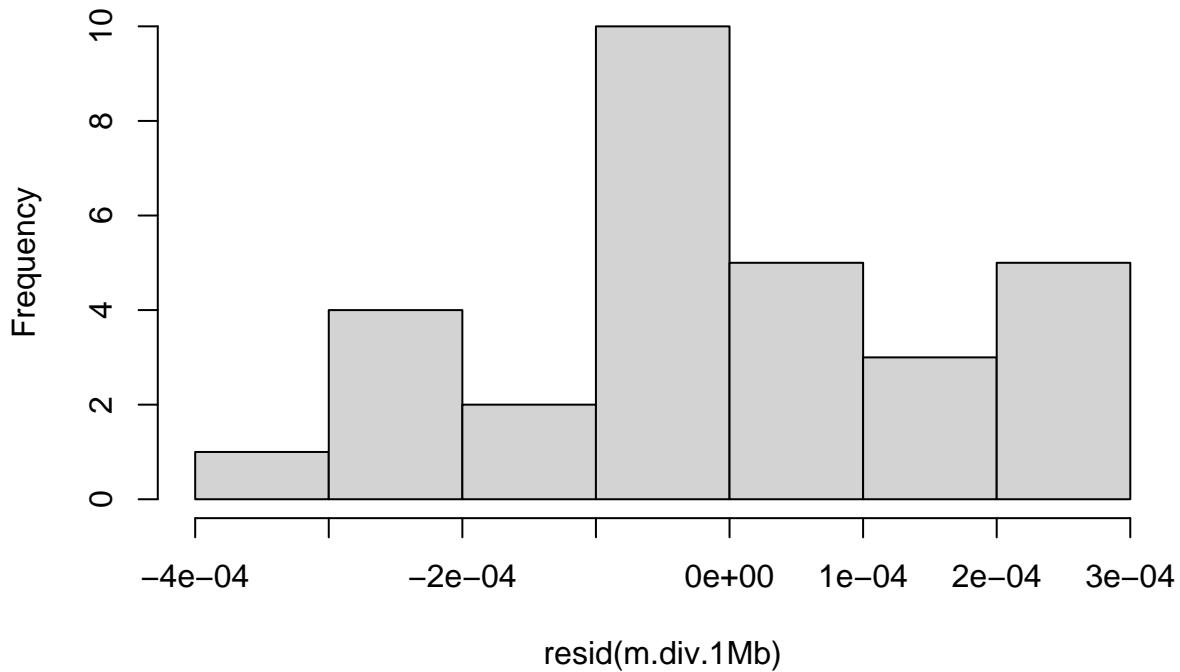


```
dwtest(m.div.1Mb)
```

```
##
##  Durbin-Watson test
##
## data: m.div.1Mb
## DW = 2.3611, p-value = 0.8304
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.1Mb)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.69982, p-value = 0.949
hist(resid(m.div.1Mb))
```

## Histogram of resid(m.div.1Mb)



```
summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.1Mb)
##
## Residuals:
##       Min         1Q     Median         3Q        Max
## -3.409e-04 -9.496e-05 -1.057e-05  1.246e-04  2.682e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.070e-02 3.559e-05 581.752 < 2e-16 ***
## thetaC      1.326e+00 7.629e-03 173.822 < 2e-16 ***
## rhoC        6.225e-02 5.347e-02   1.164   0.255
## tmrcaC     3.071e-02 2.054e-03  14.949 5.67e-14 ***
## thetaC:tmrcaC 2.593e+00 5.197e-01    4.990 3.83e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0001781 on 25 degrees of freedom
## Multiple R-squared:  0.9993, Adjusted R-squared:  0.9992
## F-statistic:  9011 on 4 and 25 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.1Mb[1, 3] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```
r2.sim.1Mb[2, 3] <- anova.diversity$VarExp[1] * 100
r2.sim.1Mb[3, 3] <- anova.diversity$VarExp[2] * 100
r2.sim.1Mb[4, 3] <- anova.diversity$VarExp[3] * 100
r2.sim.1Mb[5, 3] <- anova.diversity$VarExp[4] * 100
```

### 1.3.4 Replicate 4

```
rep_4.pi.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_4/rep_4.pi.1Mb.bedgraph", header = TRUE)
rep_4.tmrca.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_4/sim.tmrca.1M.map", header = TRUE)

sim.lands.1Mb <- as.data.frame(cbind(rep_4.pi.1Mb$pi, sim.theta.1Mb$sim, sim.rho.1Mb$sim, rep_4.tmrca.1Mb$tmrca))
names(sim.lands.1Mb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 4678, p-value = 0.8307
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.0407119

cor.test(~theta+rho, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 5654, p-value = 0.1684
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.257842

cor.test(~rho+tmrca, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 3482, p-value = 0.2302
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.2253615

cor.test(~diversity+theta, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: diversity and theta
```

```

## S = 4053.2, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9927941
cor.test(~diversity+tmrca, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: diversity and tmrca
## S = 552924, p-value = 0.8364
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.01698031
cor.test(~diversity+rho, data = sim.lands.200kb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: diversity and rho
## S = 596694, p-value = 0.4591
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.06083648

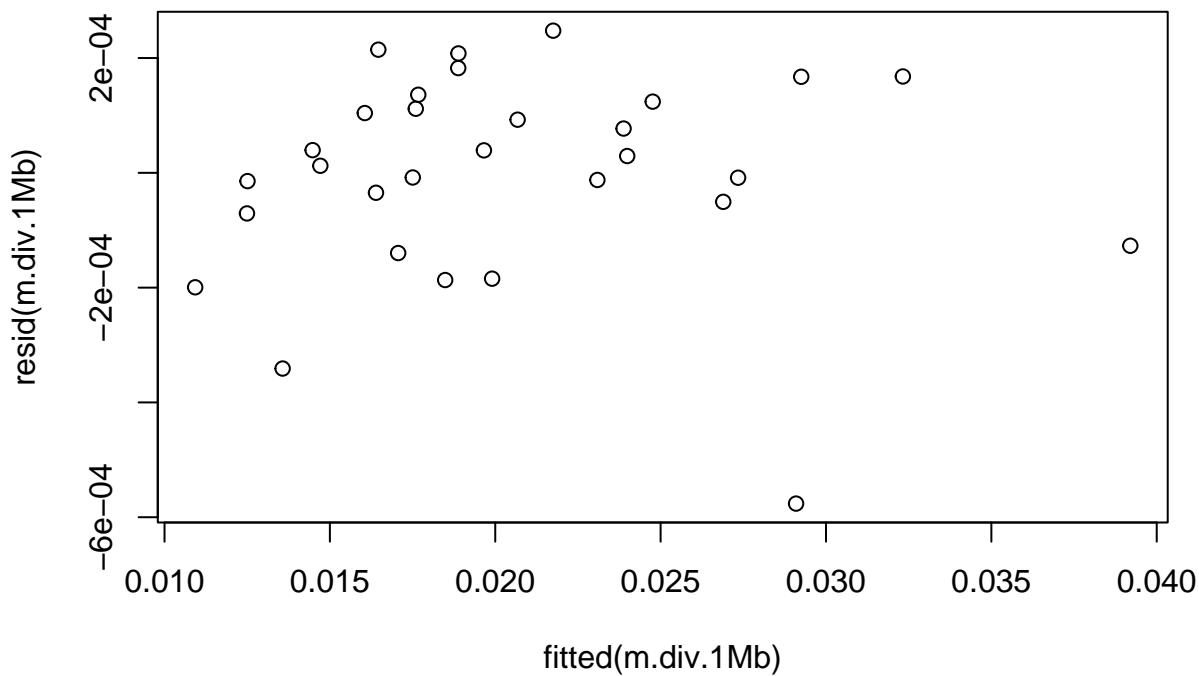
# centering
sim.lands.1Mb$thetaC <- sim.lands.1Mb$theta - mean(sim.lands.1Mb$theta)
sim.lands.1Mb$tmrcaC <- sim.lands.1Mb$tmrca - mean(sim.lands.1Mb$tmrca)
sim.lands.1Mb$rhoC <- sim.lands.1Mb$rho - mean(sim.lands.1Mb$rho)

sim.lands.1Mb$bin <- 1:nrow(sim.lands.1Mb)

# for merging:
sim.lands.1Mb.rep4 <- sim.lands.1Mb
sim.lands.1Mb.rep4$Replicate <- 4

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.1Mb)
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```

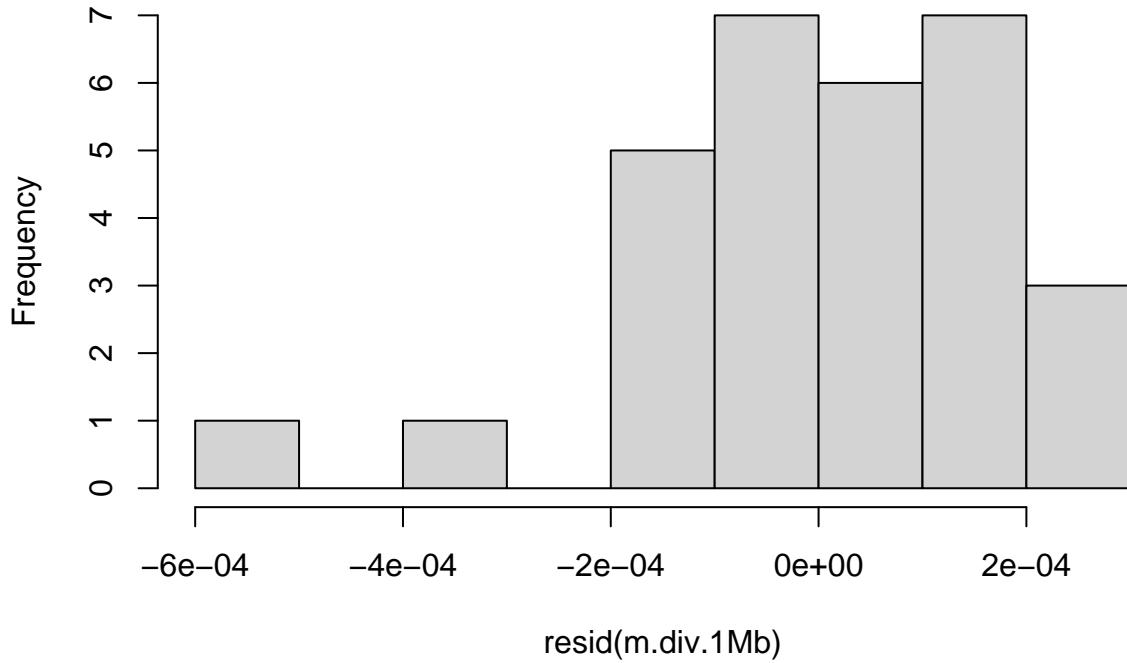


```
dwtest(m.div.1Mb)
```

```
##
##  Durbin-Watson test
##
## data: m.div.1Mb
## DW = 2.4044, p-value = 0.8773
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.1Mb)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.39065, p-value = 0.18
hist(resid(m.div.1Mb))
```

## Histogram of resid(m.div.1Mb)



```
summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##     data = sim.lands.1Mb)
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -5.763e-04 -6.567e-05  2.077e-05  1.210e-04  2.477e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 2.049e-02 3.521e-05 582.000 < 2e-16 ***
## thetaC      1.290e+00 7.811e-03 165.192 < 2e-16 ***
## rhoC        1.009e-02 5.807e-02  0.174   0.863  
## tmrcaC      2.364e-02 1.989e-03 11.884 8.84e-12 ***
## thetaC:tmrcaC 2.028e+00 3.007e-01  6.744 4.55e-07 ***
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0001916 on 25 degrees of freedom
## Multiple R-squared:  0.9992, Adjusted R-squared:  0.9991 
## F-statistic: 8277 on 4 and 25 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.1Mb[1, 4] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
```

```
r2.sim.1Mb[2, 4] <- anova.diversity$VarExp[1] * 100
r2.sim.1Mb[3, 4] <- anova.diversity$VarExp[2] * 100
r2.sim.1Mb[4, 4] <- anova.diversity$VarExp[3] * 100
r2.sim.1Mb[5, 4] <- anova.diversity$VarExp[4] * 100
```

### 1.3.5 Replicate 5

```
rep_5.pi.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_5/rep_5.pi.1Mb.bedgraph", header = TRUE)
rep_5.tmrca.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_5/sim.tmrca.1M.map", header = TRUE)

sim.lands.1Mb <- as.data.frame(cbind(rep_5.pi.1Mb$pi, sim.theta.1Mb$sim, sim.rho.1Mb$sim, rep_5.tmrca.1Mb$tmrca))
names(sim.lands.1Mb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 4438, p-value = 0.9476
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.01268076

cor.test(~theta+rho, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 5654, p-value = 0.1684
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.257842

cor.test(~rho+tmrca, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 4306, p-value = 0.8252
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.04204672

# centering
sim.lands.1Mb$thetaC <- sim.lands.1Mb$theta - mean(sim.lands.1Mb$theta)
sim.lands.1Mb$tmrcaC <- sim.lands.1Mb$tmrca - mean(sim.lands.1Mb$tmrca)
sim.lands.1Mb$rhoC <- sim.lands.1Mb$rho - mean(sim.lands.1Mb$rho)

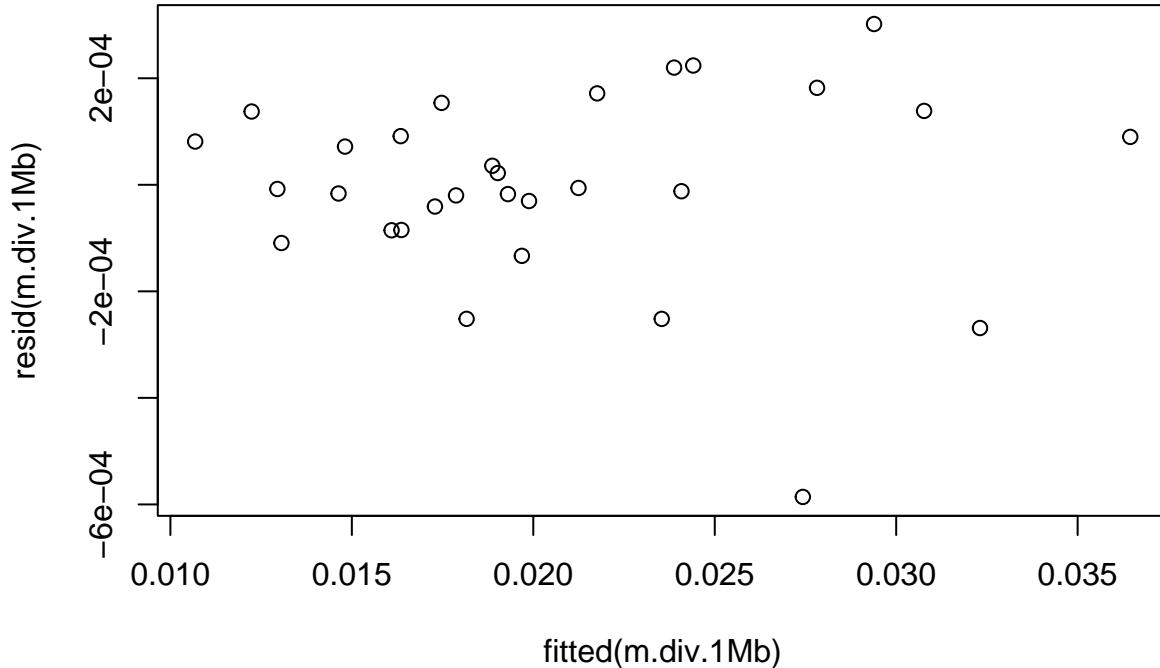
sim.lands.1Mb$bin <- 1:nrow(sim.lands.1Mb)
```

```

# for merging:
sim.lands.1Mb.rep5 <- sim.lands.1Mb
sim.lands.1Mb.rep5$Replicate <- 5

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.1Mb)
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```



```
dwtest(m.div.1Mb)
```

```

##
## Durbin-Watson test
##
## data: m.div.1Mb
## DW = 1.9571, p-value = 0.43
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.1Mb)

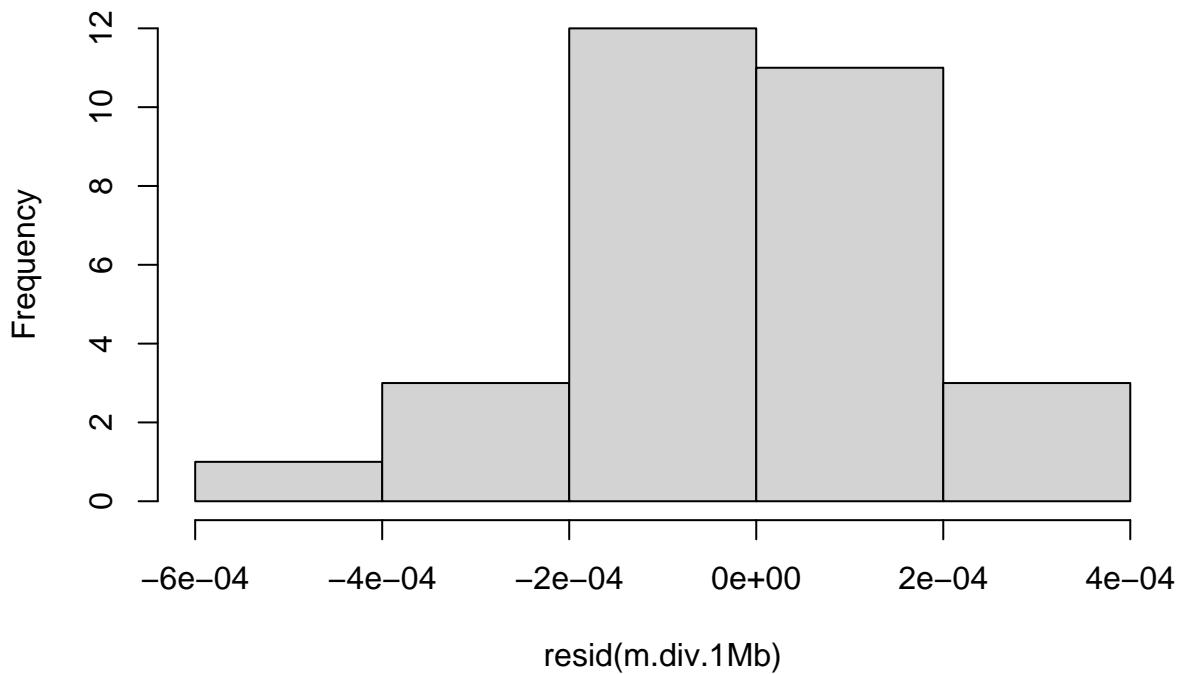
```

```

##
## Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.35533, p-value = 0.128
hist(resid(m.div.1Mb))

```

## Histogram of resid(m.div.1Mb)



```
summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.1Mb)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -5.859e-04 -7.379e-05 -6.890e-06  1.260e-04  3.018e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 2.060e-02 3.534e-05 582.791 < 2e-16 ***
## thetaC      1.306e+00 7.849e-03 166.389 < 2e-16 ***
## rhoC        -3.495e-02 5.720e-02 -0.611  0.5467  
## tmrcaC      2.514e-02 2.157e-03 11.655 1.34e-11 ***
## thetaC:tmrcaC 1.135e+00 5.053e-01  2.246  0.0338 *  
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0001933 on 25 degrees of freedom
## Multiple R-squared:  0.9992, Adjusted R-squared:  0.9991 
## F-statistic: 7809 on 4 and 25 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.1Mb[1, 5] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
```

```
r2.sim.1Mb[2, 5] <- anova.diversity$VarExp[1] * 100
r2.sim.1Mb[3, 5] <- anova.diversity$VarExp[2] * 100
r2.sim.1Mb[4, 5] <- anova.diversity$VarExp[3] * 100
r2.sim.1Mb[5, 5] <- anova.diversity$VarExp[4] * 100
```

### 1.3.6 Replicate 6

```
rep_6.pi.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_6/rep_6.pi.1Mb.bedgraph", header = TRUE)
rep_6.tmrca.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_6/sim.tmrca.1M.map", header = TRUE)

sim.lands.1Mb <- as.data.frame(cbind(rep_6.pi.1Mb$pi, sim.theta.1Mb$sim, sim.rho.1Mb$sim, rep_6.tmrca.1Mb$tmrca))
names(sim.lands.1Mb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 3592, p-value = 0.2858
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.2008899

cor.test(~theta+rho, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 5654, p-value = 0.1684
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.257842

cor.test(~rho+tmrca, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 4268, p-value = 0.7906
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.05050056

# centering
sim.lands.1Mb$thetaC <- sim.lands.1Mb$theta - mean(sim.lands.1Mb$theta)
sim.lands.1Mb$tmrcaC <- sim.lands.1Mb$tmrca - mean(sim.lands.1Mb$tmrca)
sim.lands.1Mb$rhoC <- sim.lands.1Mb$rho - mean(sim.lands.1Mb$rho)

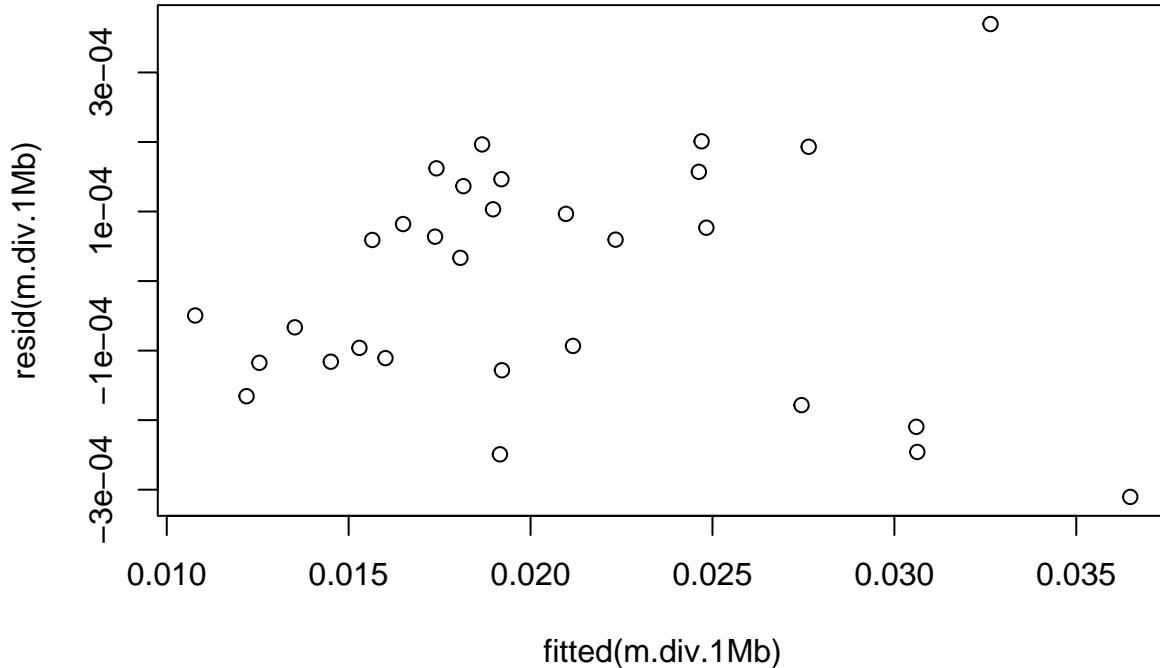
sim.lands.1Mb$bin <- 1:nrow(sim.lands.1Mb)
```

```

# for merging:
sim.lands.1Mb.rep6 <- sim.lands.1Mb
sim.lands.1Mb.rep6$Replicate <- 6

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.1Mb)
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```



```

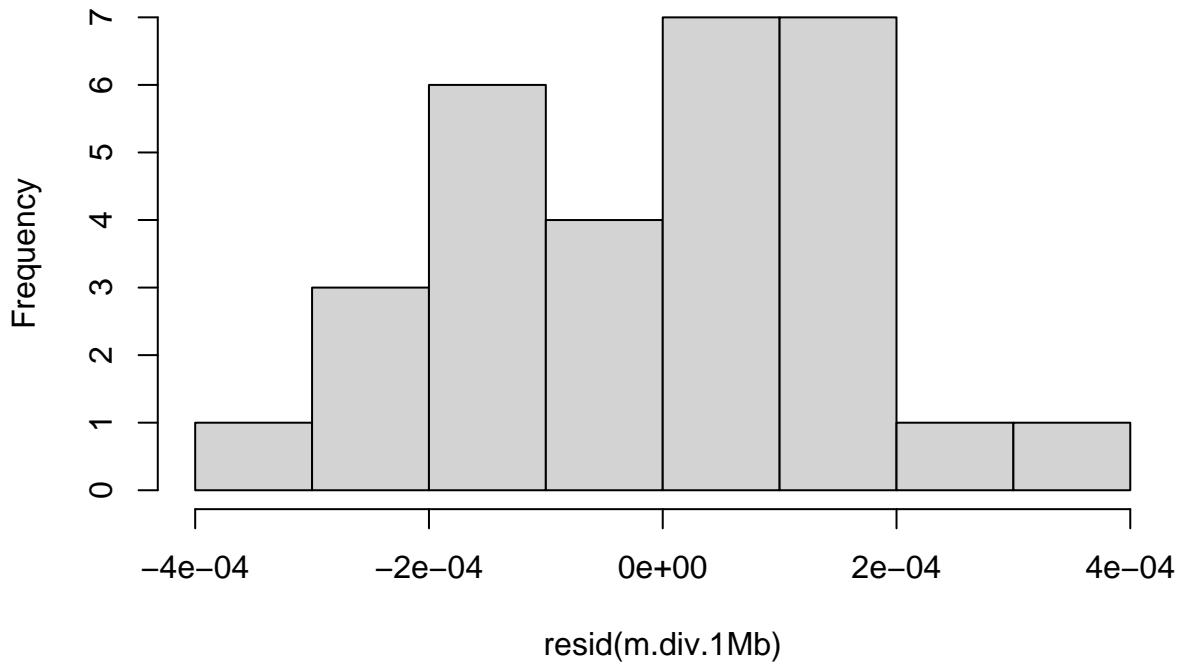
dwtest(m.div.1Mb)

##
## Durbin-Watson test
##
## data: m.div.1Mb
## DW = 1.956, p-value = 0.4515
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.1Mb)

##
## Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.62113, p-value = 0.832
hist(resid(m.div.1Mb))

```

## Histogram of resid(m.div.1Mb)



```

summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.1Mb)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -3.104e-04 -1.172e-04  4.625e-05  1.282e-04  3.696e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 2.055e-02 3.357e-05 612.052 < 2e-16 ***
## thetaC      1.305e+00 7.159e-03 182.260 < 2e-16 ***
## rhoC        6.955e-02 5.357e-02  1.298  0.20607  
## tmrcaC      2.808e-02 2.754e-03 10.193 2.18e-10 ***
## thetaC:tmrcaC 2.260e+00 6.739e-01   3.353  0.00255 ** 
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.000178 on 25 degrees of freedom
## Multiple R-squared:  0.9993, Adjusted R-squared:  0.9992 
## F-statistic:  9504 on 4 and 25 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.1Mb[1, 6] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +

```

```
r2.sim.1Mb[2, 6] <- anova.diversity$VarExp[1] * 100
r2.sim.1Mb[3, 6] <- anova.diversity$VarExp[2] * 100
r2.sim.1Mb[4, 6] <- anova.diversity$VarExp[3] * 100
r2.sim.1Mb[5, 6] <- anova.diversity$VarExp[4] * 100
```

### 1.3.7 Replicate 7

```
rep_7.pi.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_7/rep_7.pi.1Mb.bedgraph", header = TRUE)
rep_7.tmrca.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_7/sim.tmrca.1M.map", header = TRUE)

sim.lands.1Mb <- as.data.frame(cbind(rep_7.pi.1Mb$pi, sim.theta.1Mb$sim, sim.rho.1Mb$sim, rep_7.tmrca.1Mb$tmrca))
names(sim.lands.1Mb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 5750, p-value = 0.135
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.2791991

cor.test(~theta+rho, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 5654, p-value = 0.1684
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.257842

cor.test(~rho+tmrca, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 3620, p-value = 0.3013
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.1946607

# centering
sim.lands.1Mb$thetaC <- sim.lands.1Mb$theta - mean(sim.lands.1Mb$theta)
sim.lands.1Mb$tmrcaC <- sim.lands.1Mb$tmrca - mean(sim.lands.1Mb$tmrca)
sim.lands.1Mb$rhoC <- sim.lands.1Mb$rho - mean(sim.lands.1Mb$rho)

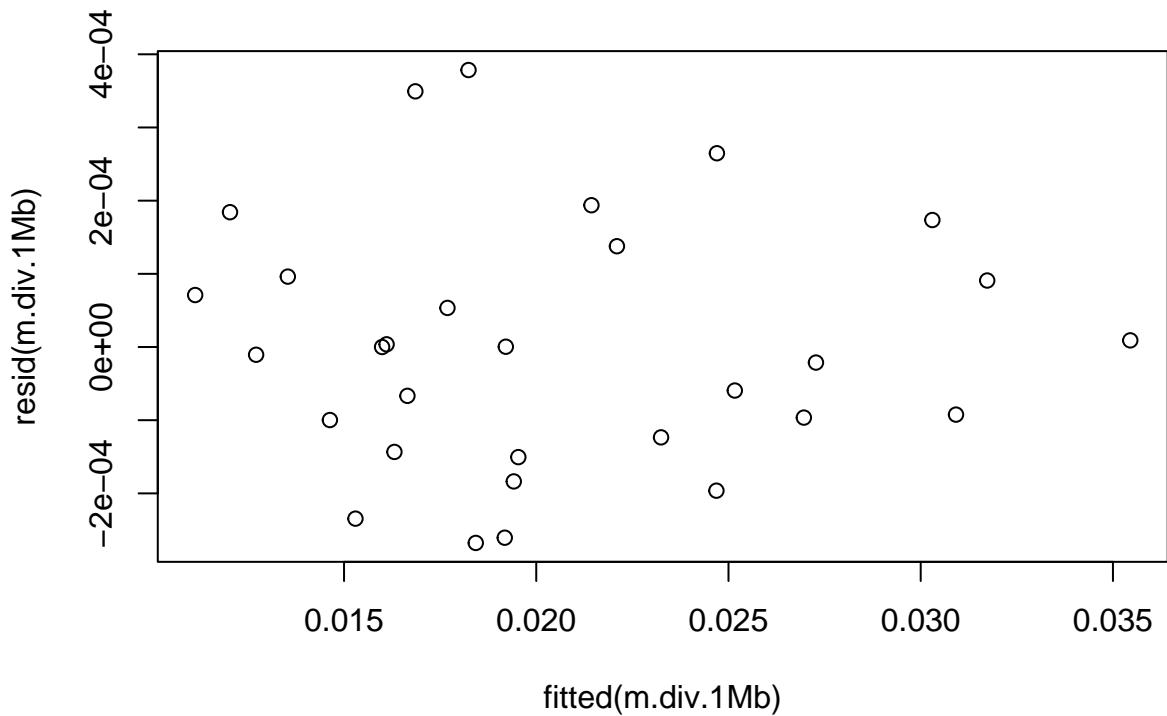
sim.lands.1Mb$bin <- 1:nrow(sim.lands.1Mb)
```

```

# for merging:
sim.lands.1Mb.rep7 <- sim.lands.1Mb
sim.lands.1Mb.rep7$Replicate <- 7

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.1Mb)
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```



```

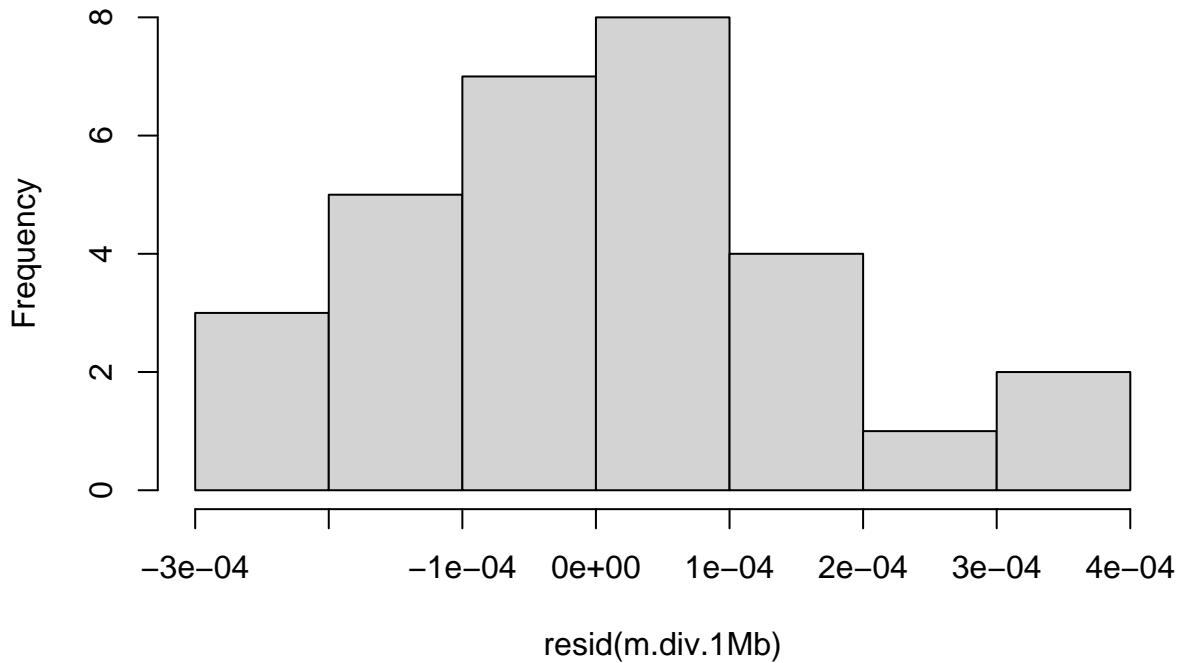
dwtest(m.div.1Mb)

##
##  Durbin-Watson test
##
## data: m.div.1Mb
## DW = 1.9852, p-value = 0.4718
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.1Mb)

##
##  Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.65923, p-value = 0.9
hist(resid(m.div.1Mb))

```

## Histogram of resid(m.div.1Mb)



```
summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.1Mb)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -2.677e-04 -1.175e-04 -5.270e-06  9.488e-05  3.785e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 2.060e-02 3.433e-05 599.990 < 2e-16 ***
## thetaC      1.322e+00 7.722e-03 171.218 < 2e-16 ***
## rhoC        -5.037e-02 5.447e-02 -0.925 0.363900  
## tmrcaC      2.856e-02 1.841e-03 15.507 2.47e-14 ***
## thetaC:tmrcaC 1.507e+00 3.301e-01  4.565 0.000115 *** 
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0001836 on 25 degrees of freedom
## Multiple R-squared:  0.9993, Adjusted R-squared:  0.9991 
## F-statistic:  8510 on 4 and 25 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.1Mb[1, 7] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
```

```
r2.sim.1Mb[2, 7] <- anova.diversity$VarExp[1] * 100
r2.sim.1Mb[3, 7] <- anova.diversity$VarExp[2] * 100
r2.sim.1Mb[4, 7] <- anova.diversity$VarExp[3] * 100
r2.sim.1Mb[5, 7] <- anova.diversity$VarExp[4] * 100
```

### 1.3.8 Replicate 8

```
rep_8.pi.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_8/rep_8.pi.1Mb.bedgraph", header = TRUE)
rep_8.tmrca.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_8/sim.tmrca.1M.map", header = TRUE)

sim.lands.1Mb <- as.data.frame(cbind(rep_8.pi.1Mb$pi, sim.theta.1Mb$sim, sim.rho.1Mb$sim, rep_8.tmrca.1Mb$tmrca))
names(sim.lands.1Mb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 4082, p-value = 0.628
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.09187987

cor.test(~theta+rho, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 5654, p-value = 0.1684
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.257842

cor.test(~rho+tmrca, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 4888, p-value = 0.6448
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.08743048

# centering
sim.lands.1Mb$thetaC <- sim.lands.1Mb$theta - mean(sim.lands.1Mb$theta)
sim.lands.1Mb$tmrcaC <- sim.lands.1Mb$tmrca - mean(sim.lands.1Mb$tmrca)
sim.lands.1Mb$rhoC <- sim.lands.1Mb$rho - mean(sim.lands.1Mb$rho)

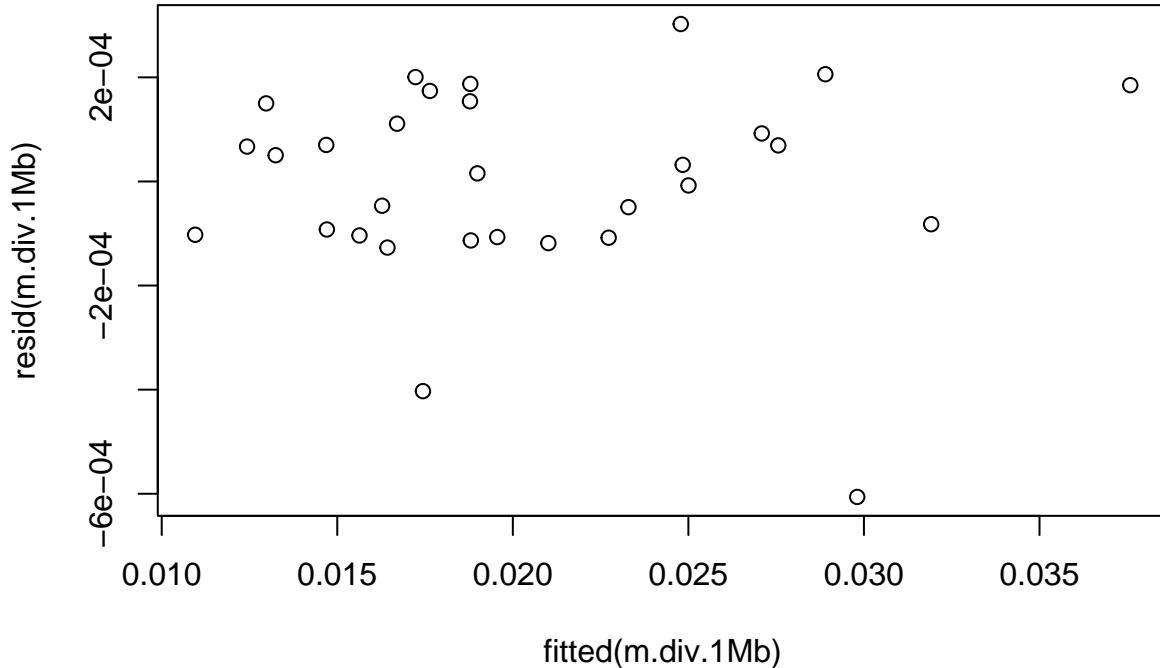
sim.lands.1Mb$bin <- 1:nrow(sim.lands.1Mb)
```

```

# for merging:
sim.lands.1Mb.rep8 <- sim.lands.1Mb
sim.lands.1Mb.rep8$Replicate <- 8

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.1Mb)
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```



```

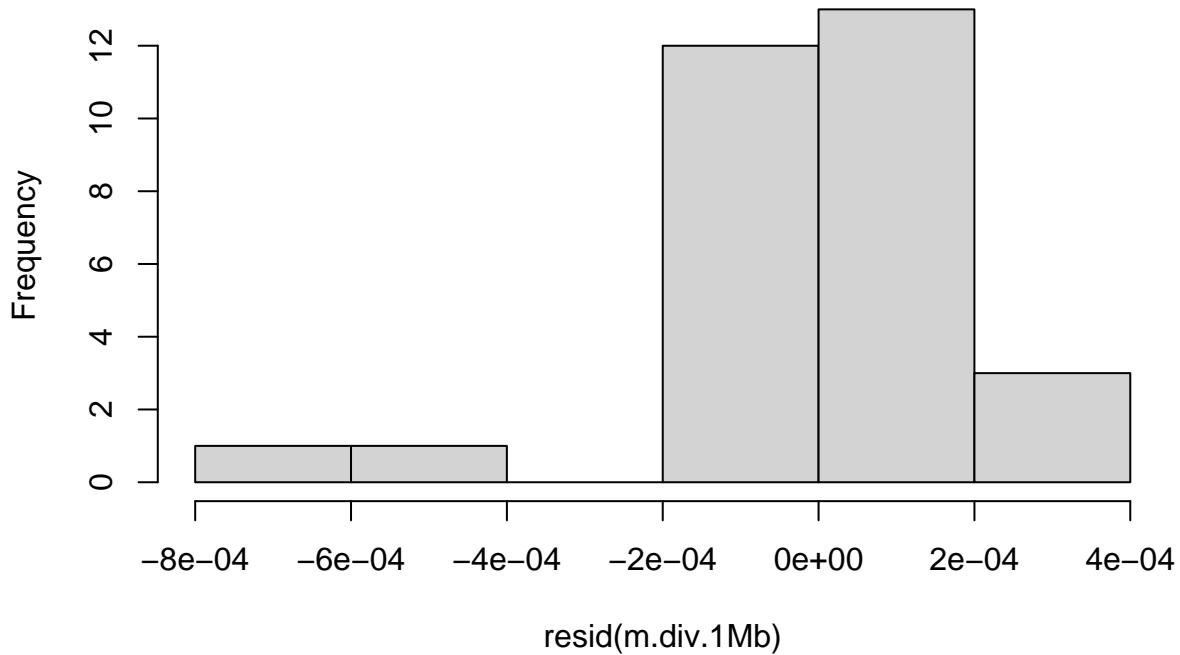
dwtest(m.div.1Mb)

##
## Durbin-Watson test
##
## data: m.div.1Mb
## DW = 2.4886, p-value = 0.9089
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.1Mb)

##
## Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.6984, p-value = 0.948
hist(resid(m.div.1Mb))

```

## Histogram of resid(m.div.1Mb)



```
summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.1Mb)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -6.061e-04 -1.034e-04  2.376e-05  1.402e-04  3.024e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 2.051e-02 3.685e-05 556.403 < 2e-16 ***
## thetaC      1.294e+00 7.915e-03 163.527 < 2e-16 ***
## rhoC        2.309e-02 5.876e-02  0.393  0.69767  
## tmrcaC      2.659e-02 2.276e-03 11.682 1.27e-11 ***
## thetaC:tmrcaC 2.000e+00 5.608e-01   3.567  0.00149 ** 
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0001996 on 25 degrees of freedom
## Multiple R-squared:  0.9992, Adjusted R-squared:  0.999 
## F-statistic: 7462 on 4 and 25 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.1Mb[1, 8] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
```

```
r2.sim.1Mb[2, 8] <- anova.diversity$VarExp[1] * 100
r2.sim.1Mb[3, 8] <- anova.diversity$VarExp[2] * 100
r2.sim.1Mb[4, 8] <- anova.diversity$VarExp[3] * 100
r2.sim.1Mb[5, 8] <- anova.diversity$VarExp[4] * 100
```

### 1.3.9 Replicate 9

```
rep_9.pi.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_9/rep_9.pi.1Mb.bedgraph", header = TRUE)
rep_9.tmrca.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_9/sim.tmrca.1M.map", header = TRUE)

sim.lands.1Mb <- as.data.frame(cbind(rep_9.pi.1Mb$pi, sim.theta.1Mb$sim, sim.rho.1Mb$sim, rep_9.tmrca.1Mb$tmrca))
names(sim.lands.1Mb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 3806, p-value = 0.4171
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.1532814

cor.test(~theta+rho, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 5654, p-value = 0.1684
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.257842

cor.test(~rho+tmrca, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 4996, p-value = 0.5562
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.1114572

# centering
sim.lands.1Mb$thetaC <- sim.lands.1Mb$theta - mean(sim.lands.1Mb$theta)
sim.lands.1Mb$tmrcaC <- sim.lands.1Mb$tmrca - mean(sim.lands.1Mb$tmrca)
sim.lands.1Mb$rhoC <- sim.lands.1Mb$rho - mean(sim.lands.1Mb$rho)

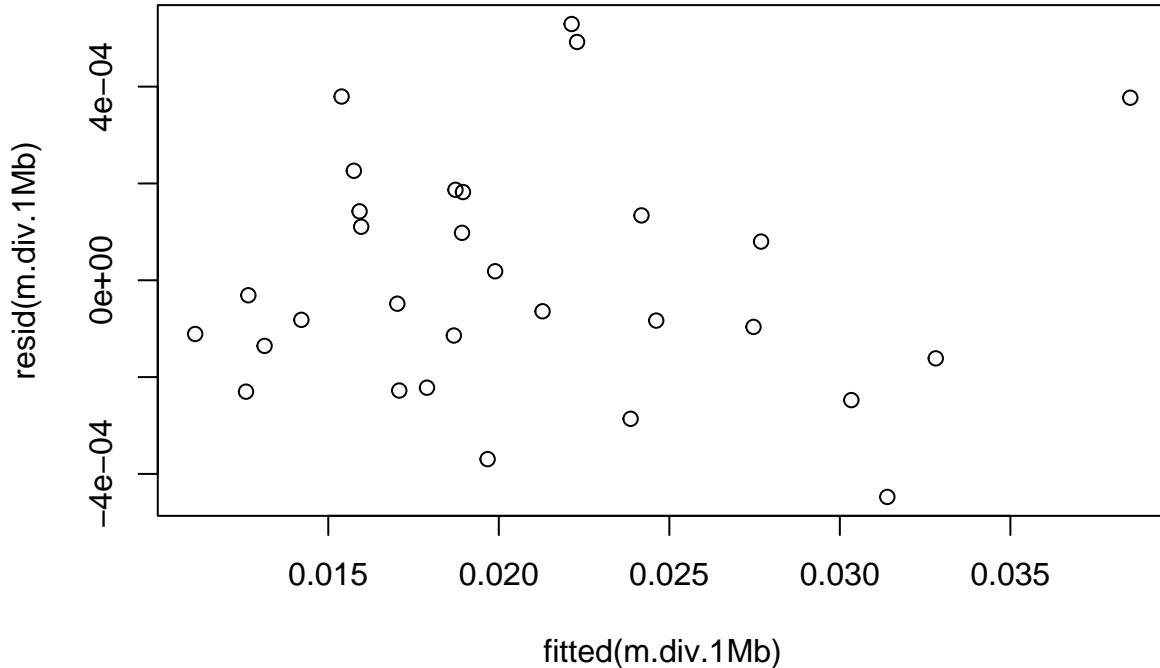
sim.lands.1Mb$bin <- 1:nrow(sim.lands.1Mb)
```

```

# for merging:
sim.lands.1Mb.rep9 <- sim.lands.1Mb
sim.lands.1Mb.rep9$Replicate <- 9

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.1Mb)
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```



```

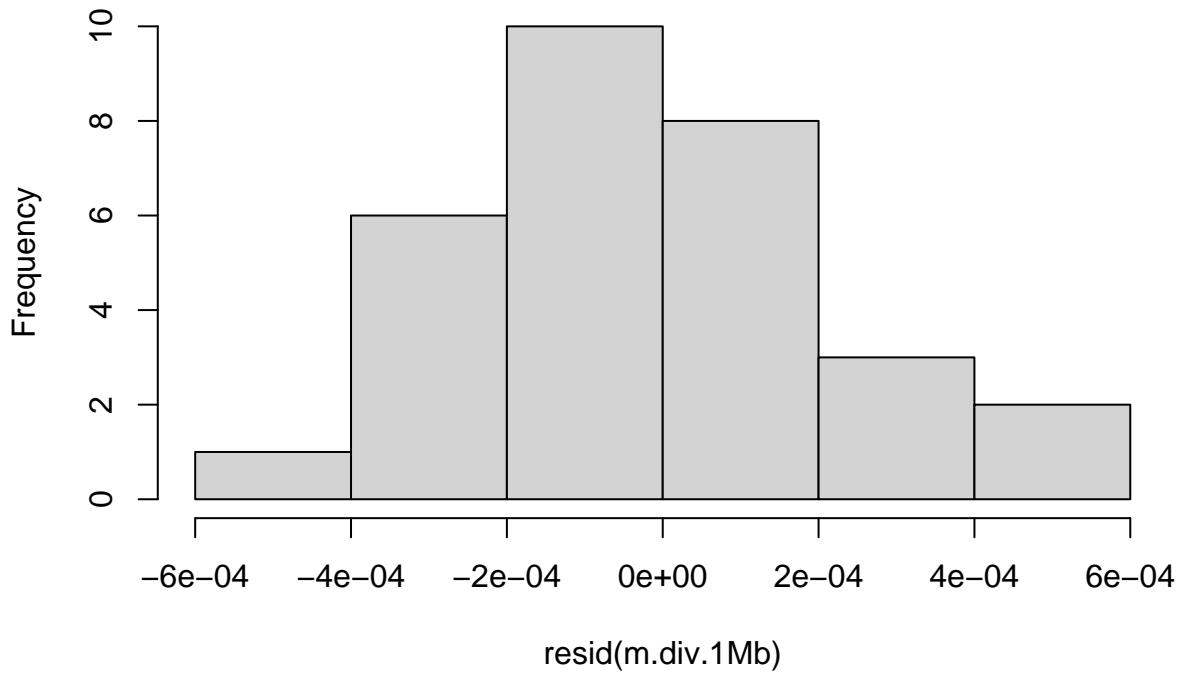
dwtest(m.div.1Mb)

##
## Durbin-Watson test
##
## data: m.div.1Mb
## DW = 2.2409, p-value = 0.7322
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.1Mb)

##
## Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.5612, p-value = 0.691
hist(resid(m.div.1Mb))

```

## Histogram of resid(m.div.1Mb)



```
summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.1Mb)
##
## Residuals:
##       Min         1Q     Median        3Q       Max
## -0.0004475 -0.0001548 -0.0000562  0.0001403  0.0005293
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.064e-02 5.033e-05 410.041 < 2e-16 ***
## thetaC      1.316e+00 1.246e-02 105.593 < 2e-16 ***
## rhoC        3.532e-02 8.105e-02   0.436   0.6667
## tmrcaC      2.428e-02 2.655e-03   9.145 1.89e-09 ***
## thetaC:tmrcaC 1.211e+00 5.581e-01    2.171   0.0396 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.000263 on 25 degrees of freedom
## Multiple R-squared:  0.9986, Adjusted R-squared:  0.9984
## F-statistic:  4623 on 4 and 25 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.1Mb[1, 9] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```
r2.sim.1Mb[2, 9] <- anova.diversity$VarExp[1] * 100
r2.sim.1Mb[3, 9] <- anova.diversity$VarExp[2] * 100
r2.sim.1Mb[4, 9] <- anova.diversity$VarExp[3] * 100
r2.sim.1Mb[5, 9] <- anova.diversity$VarExp[4] * 100
```

### 1.3.10 Replicate 10

```
rep_10.pi.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_10/rep_10.pi.1Mb.bedgraph", header = FALSE)
rep_10.tmrca.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_10/sim.tmrca.1M.map", header = FALSE)

sim.lands.1Mb <- as.data.frame(cbind(rep_10.pi.1Mb$pi, sim.theta.1Mb$sim, sim.rho.1Mb$sim, rep_10.tmrca.1Mb))
names(sim.lands.1Mb) <- c("diversity", "theta", "rho", "tmrca")

cor.test(~theta+tmrca, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 4496, p-value = 1
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##          rho
## -0.0002224694

cor.test(~theta+rho, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 5654, p-value = 0.1684
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##          rho
## -0.257842

cor.test(~rho+tmrca, data = sim.lands.1Mb, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 5530, p-value = 0.22
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##          rho
## -0.2302558

# centering
sim.lands.1Mb$thetaC <- sim.lands.1Mb$theta - mean(sim.lands.1Mb$theta)
sim.lands.1Mb$tmrcaC <- sim.lands.1Mb$tmrca - mean(sim.lands.1Mb$tmrca)
sim.lands.1Mb$rhoC <- sim.lands.1Mb$rho - mean(sim.lands.1Mb$rho)

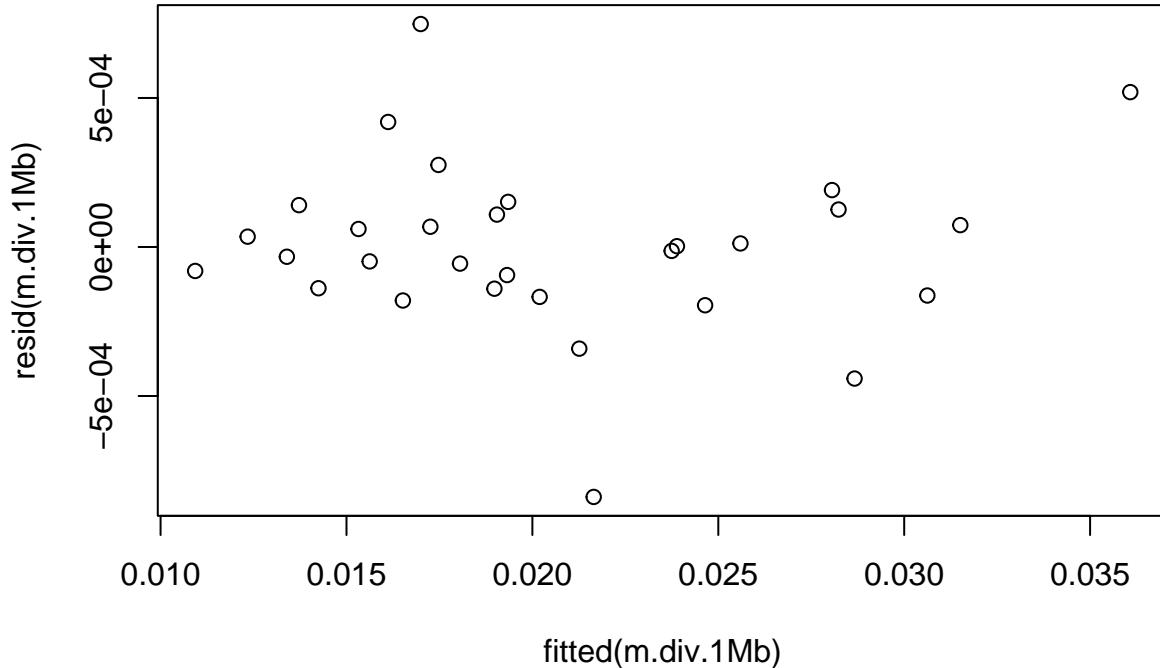
sim.lands.1Mb$bin <- 1:nrow(sim.lands.1Mb)
```

```

# for merging:
sim.lands.1Mb.rep50 <- sim.lands.1Mb
sim.lands.1Mb.rep50$Replicate <- 10

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.1Mb)
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```



```
dwtest(m.div.1Mb)
```

```

##
## Durbin-Watson test
##
## data: m.div.1Mb
## DW = 2.2351, p-value = 0.7114
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.1Mb)

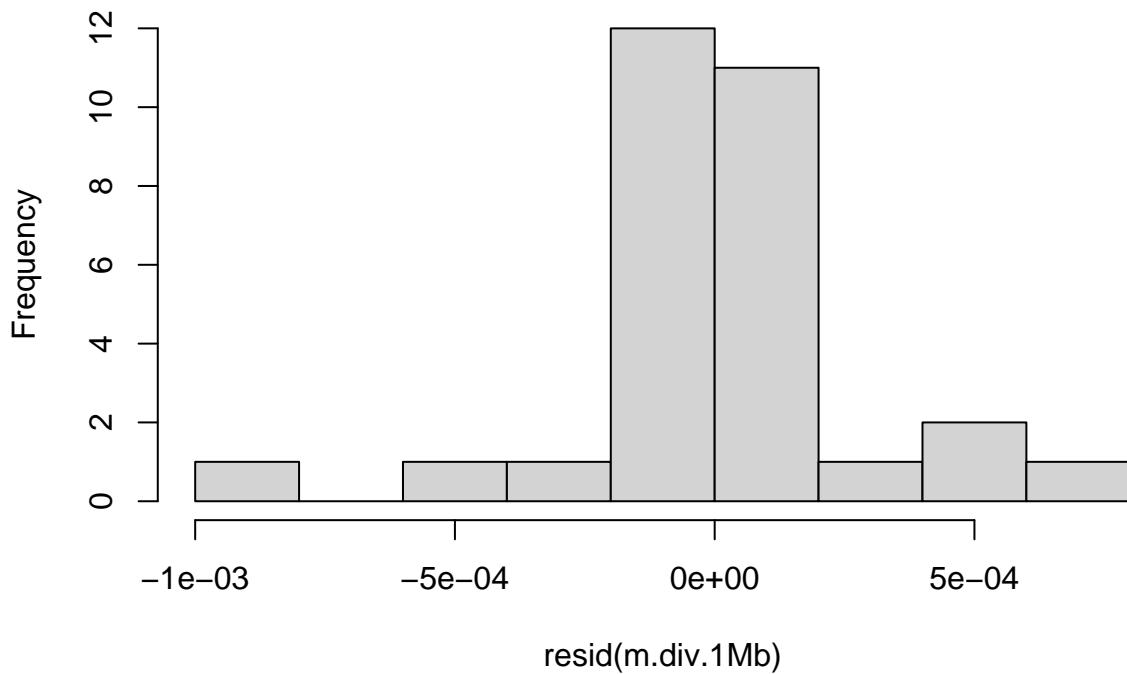
```

```

##
## Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.50343, p-value = 0.533
hist(resid(m.div.1Mb))

```

## Histogram of resid(m.div.1Mb)



```
summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = sim.lands.1Mb)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -8.386e-04 -1.396e-04 -5.280e-06  1.214e-04  7.480e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 2.066e-02 5.729e-05 360.639 < 2e-16 ***
## thetaC      1.308e+00 1.273e-02 102.725 < 2e-16 ***
## rhoC        -9.102e-02 9.370e-02 -0.971  0.34066  
## tmrcaC      2.340e-02 3.129e-03  7.479  7.84e-08 ***
## thetaC:tmrcaC 1.965e+00 5.383e-01   3.651  0.00121 ** 
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0003101 on 25 degrees of freedom
## Multiple R-squared:  0.9979, Adjusted R-squared:  0.9976 
## F-statistic: 2967 on 4 and 25 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.sim.1Mb[1, 10] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

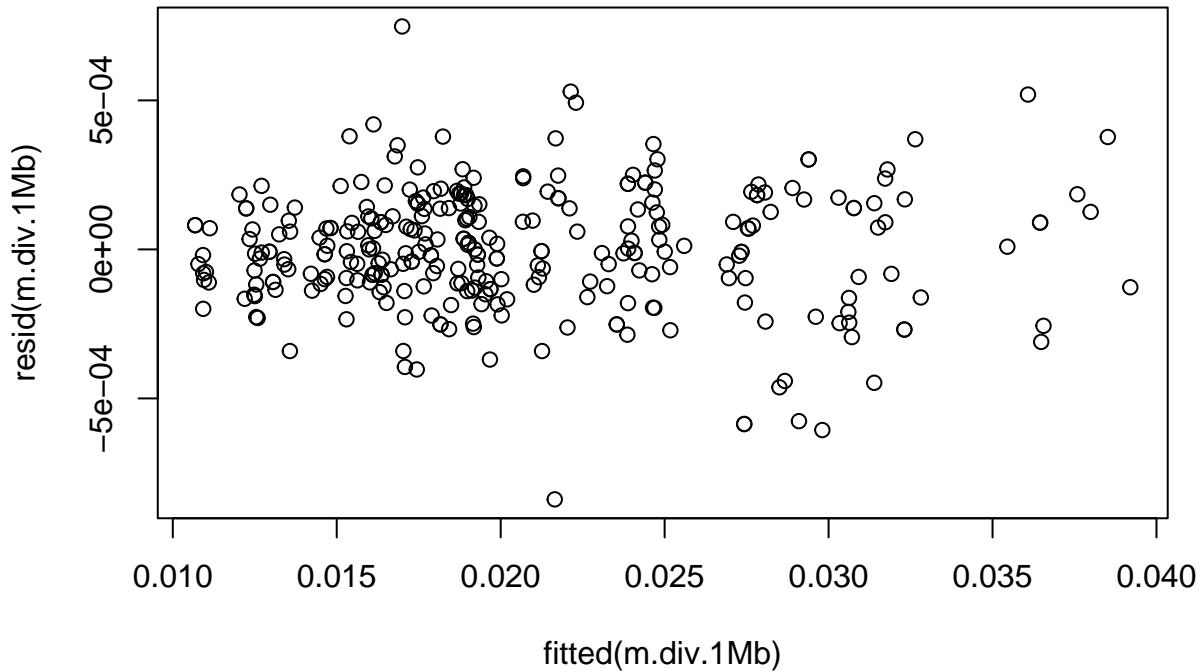
```
r2.sim.1Mb[2, 10] <- anova.diversity$VarExp[1] * 100
r2.sim.1Mb[3, 10] <- anova.diversity$VarExp[2] * 100
r2.sim.1Mb[4, 10] <- anova.diversity$VarExp[3] * 100
r2.sim.1Mb[5, 10] <- anova.diversity$VarExp[4] * 100
```

```
r2.sim.1Mb$average <- rowMeans(r2.sim.1Mb)
r2.sim.1Mb <- transform(r2.sim.1Mb, sd=apply(r2.sim.1Mb, 1, sd, na.rm = TRUE))
```

### 1.3.11 all replicates:

```
sim.lands.1Mb.all <- rbind(sim.lands.1Mb.rep5, sim.lands.1Mb.rep2, sim.lands.1Mb.rep3, sim.lands.1Mb.rep4)

m.div.1Mb <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC)*as.factor(Replicate), data = sim.lands.1Mb.all)
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))
```



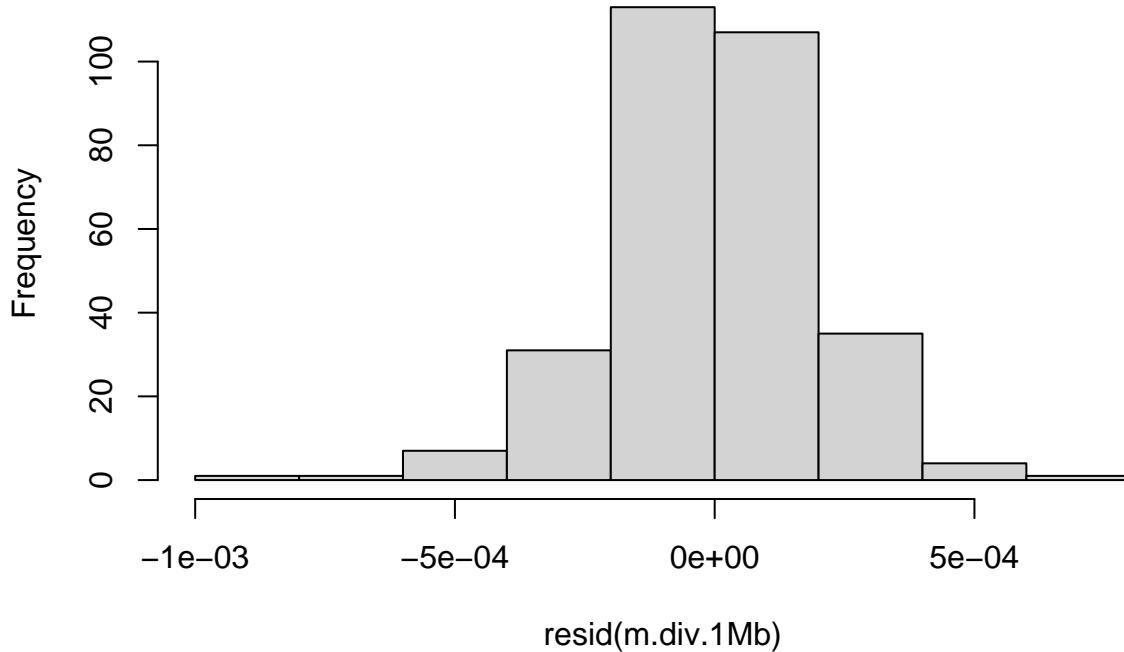
```
dwtest(m.div.1Mb)
```

```
##
##  Durbin-Watson test
##
##  data:  m.div.1Mb
##  DW = 2.2764, p-value = 0.9657
##  alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.1Mb)
```

```
##
##  Harrison-McCabe test
##
##  data:  m.div.1Mb
##  HMC = 0.43169, p-value = 0.052
```

```
hist(resid(m.div.1Mb))
```

**Histogram of resid(m.div.1Mb)**



```
m.div.1Mb.2 <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC + thetaC:rhoC)*as.factor(Replicate)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC + thetaC:rhoC + rhoC:tmrcaC)*as.factor(Replicate)
```

```
AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)
```

```
##          df      AIC
## m.div.1Mb 46 -4169.467
## m.div.1Mb.2 55 -4178.038
## m.div.1Mb.3 64 -4167.214
```

```
summary(m.div.1Mb)
```

```
##
## Call:
## lm(formula = diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC) *
##     as.factor(Replicate), data = sim.lands.1Mb.all)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -8.386e-04 -1.136e-04 -6.930e-06  1.376e-04  7.480e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.052e-02 3.986e-05 514.704 < 2e-16 ***
## thetaC      1.285e+00 8.766e-03 146.613 < 2e-16 ***
## rhoC       -4.630e-02 6.495e-02 -0.713  0.47663
## tmrcaC     2.480e-02 2.440e-03 10.164 < 2e-16 ***
## as.factor(Replicate)3 1.876e-04 5.876e-05  3.192  0.00159 **
```

```

## as.factor(Replicate)4      -2.641e-05  5.625e-05 -0.469  0.63918
## as.factor(Replicate)5      8.122e-05  4.867e-05  1.669  0.09640 .
## as.factor(Replicate)6      3.169e-05  5.701e-05  0.556  0.57872
## as.factor(Replicate)7      8.047e-05  5.674e-05  1.418  0.15738
## as.factor(Replicate)8      -1.073e-05 5.640e-05 -0.190  0.84927
## as.factor(Replicate)9      1.217e-04  5.743e-05  2.119  0.03508 *
## as.factor(Replicate)10     1.433e-04  5.641e-05  2.540  0.01167 *
## thetaC:tmrcaC              2.351e+00  4.650e-01  5.057  8.14e-07 ***
## thetaC:as.factor(Replicate)3 4.083e-02  1.275e-02  3.203  0.00153 **
## thetaC:as.factor(Replicate)4 5.115e-03  1.243e-02  0.412  0.68094
## thetaC:as.factor(Replicate)5 2.072e-02  1.074e-02  1.929  0.05483 .
## thetaC:as.factor(Replicate)6 1.952e-02  1.234e-02  1.581  0.11512
## thetaC:as.factor(Replicate)7 3.691e-02  1.262e-02  2.924  0.00377 **
## thetaC:as.factor(Replicate)8 9.043e-03  1.226e-02  0.738  0.46136
## thetaC:as.factor(Replicate)9 3.056e-02  1.348e-02  2.268  0.02419 *
## thetaC:as.factor(Replicate)10 2.246e-02  1.247e-02  1.801  0.07285 .
## rhoC:as.factor(Replicate)3   1.085e-01  9.179e-02  1.183  0.23810
## rhoC:as.factor(Replicate)4   5.639e-02  9.222e-02  0.611  0.54146
## rhoC:as.factor(Replicate)5   1.134e-02  7.913e-02  0.143  0.88611
## rhoC:as.factor(Replicate)6   1.158e-01  9.191e-02  1.260  0.20868
## rhoC:as.factor(Replicate)7   -4.076e-03 9.123e-02 -0.045  0.96440
## rhoC:as.factor(Replicate)8   6.939e-02  9.091e-02  0.763  0.44600
## rhoC:as.factor(Replicate)9   8.161e-02  9.301e-02  0.877  0.38106
## rhoC:as.factor(Replicate)10  -4.473e-02 9.209e-02 -0.486  0.62761
## tmrcaC:as.factor(Replicate)3 5.904e-03  3.488e-03  1.693  0.09173 .
## tmrcaC:as.factor(Replicate)4 -1.165e-03 3.314e-03 -0.352  0.72538
## tmrcaC:as.factor(Replicate)5  3.357e-04  2.977e-03  0.113  0.91029
## tmrcaC:as.factor(Replicate)6  3.272e-03  4.139e-03  0.790  0.43002
## tmrcaC:as.factor(Replicate)7  3.752e-03  3.263e-03  1.150  0.25125
## tmrcaC:as.factor(Replicate)8  1.784e-03  3.468e-03  0.514  0.60735
## tmrcaC:as.factor(Replicate)9  -5.270e-04 3.273e-03 -0.161  0.87221
## tmrcaC:as.factor(Replicate)10 -1.399e-03 3.272e-03 -0.428  0.66933
## thetaC:tmrcaC:as.factor(Replicate)3 2.416e-01  7.833e-01  0.308  0.75800
## thetaC:tmrcaC:as.factor(Replicate)4 -3.235e-01  5.754e-01 -0.562  0.57447
## thetaC:tmrcaC:as.factor(Replicate)5 -1.217e+00  6.129e-01 -1.985  0.04820 *
## thetaC:tmrcaC:as.factor(Replicate)6 -9.153e-02  9.410e-01 -0.097  0.92259
## thetaC:tmrcaC:as.factor(Replicate)7 -8.443e-01  6.058e-01 -1.394  0.16463
## thetaC:tmrcaC:as.factor(Replicate)8 -3.510e-01  7.646e-01 -0.459  0.64659
## thetaC:tmrcaC:as.factor(Replicate)9 -1.140e+00  6.530e-01 -1.746  0.08206 .
## thetaC:tmrcaC:as.factor(Replicate)10 -3.859e-01  5.974e-01 -0.646  0.51885
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.000216 on 255 degrees of freedom
## Multiple R-squared:  0.999, Adjusted R-squared:  0.9988
## F-statistic:  5772 on 44 and 255 DF,  p-value: < 2.2e-16

```

## 2 Drosophila-like neutral simulations of chr 2L (Inferred Landscapes)

First batch of 10 replicate datasets simulated using parameters as inferred from real Drosophila data.

Here we present results using genomic landscapes are inferred by iSMC

## 2.1 50 kb scale

```
r2.inf.50kb <- as.data.frame(matrix(ncol = nreps, nrow = 5))
row.names(r2.inf.50kb) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
colnames(r2.inf.50kb) <- reps

# sim landscapes
sim.rho.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims/dm.sim.rho.50000.txt")
sim.theta.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims/dm.sim.theta.50000.txt")
sim.lands.50kb <- as.data.frame(cbind(sim.theta.50kb$sim, sim.rho.50kb$sim))
names(sim.lands.50kb) <- c("theta", "rho")
```

### 2.1.1 Replicate 1

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_1/rs.pair_1.", sep = "")
pi.50kb <- read.table(paste(p, "diversity.50kb.bedgraph", sep = ""), header = T)
pi.50kb$avg <- apply(pi.50kb[4:ncol(pi.50kb)], 1, mean)
tmrca.50kb <- read.table(paste(p, "TMRCA.50kb.bedgraph", sep = ""), header = T)
tmrca.50kb$avg <- apply(tmrca.50kb[4:ncol(tmrca.50kb)], 1, mean)
rho.50kb <- read.table(paste(p, "rho.50kb.bedgraph", sep = ""), header = T)
theta.50kb <- read.table(paste(p, "theta.50kb.bedgraph", sep = ""), header = T)

inf.lands.50kb.rep_1 <- as.data.frame(cbind(pi.50kb$avg, theta.50kb$sample_mean, rho.50kb$sample_mean,
names(inf.lands.50kb.rep_1) <- c("diversity", "theta", "rho", "tmrca")

cor.test(sim.theta.50kb$sim, theta.50kb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.50kb$sim and theta.50kb$sample_mean
## S = 781576, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9782895

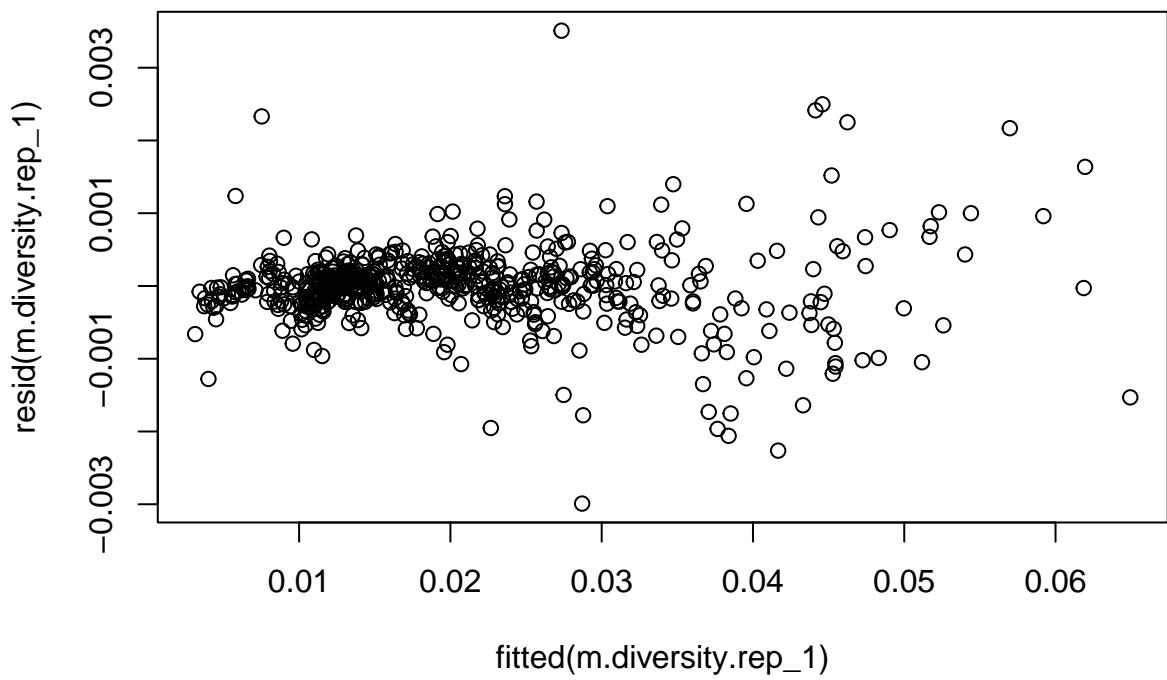
# centering
inf.lands.50kb.rep_1$thetaC <- inf.lands.50kb.rep_1$theta - mean(inf.lands.50kb.rep_1$theta)
inf.lands.50kb.rep_1$tmrcaC <- inf.lands.50kb.rep_1$tmrca - mean(inf.lands.50kb.rep_1$tmrca)
inf.lands.50kb.rep_1$rhoC <- inf.lands.50kb.rep_1$rho - mean(inf.lands.50kb.rep_1$rho)

inf.lands.50kb.rep_1$bin <- 1:nrow(inf.lands.50kb.rep_1)

# for merging:
inf.lands.50kb.rep_1$Replicate <- 1

m.diversity.rep_1 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.50kb.rep_1)

plot(resid(m.diversity.rep_1)~fitted(m.diversity.rep_1))
```

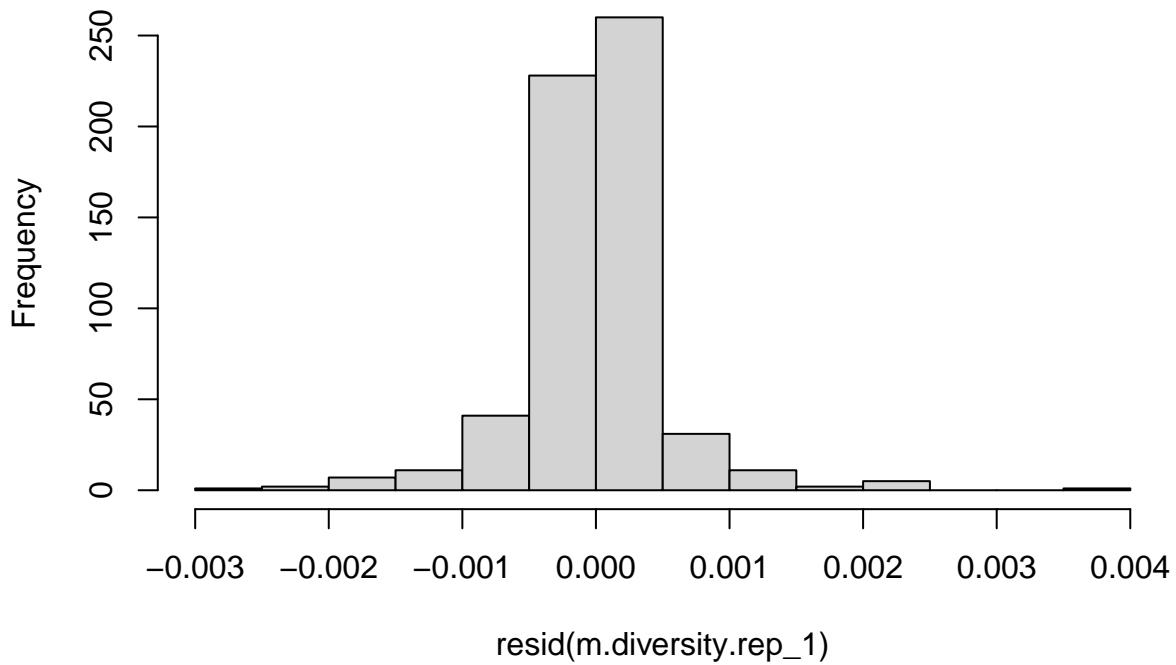


```
dwtest(m.diversity.rep_1)
```

```
##
##  Durbin-Watson test
##
## data: m.diversity.rep_1
## DW = 1.4157, p-value = 2.024e-13
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_1)
```

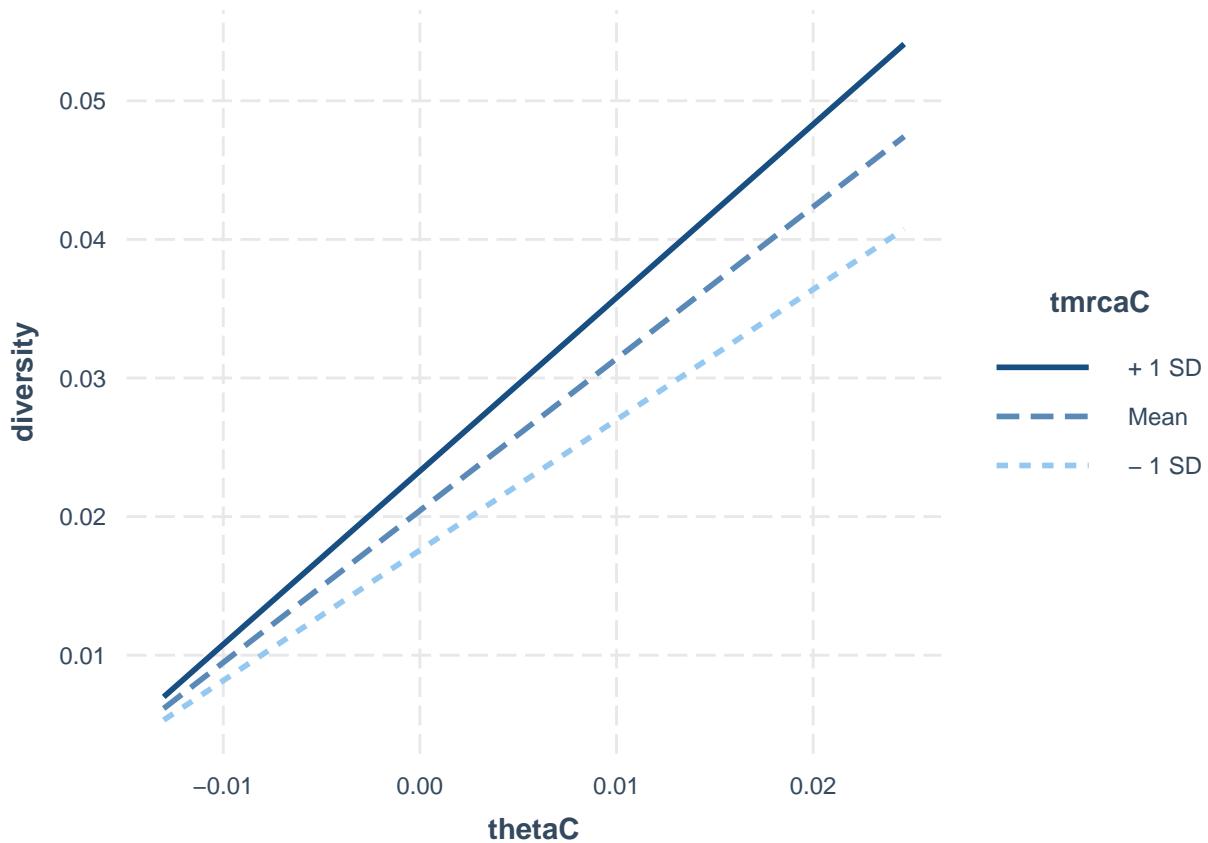
```
##
##  Harrison-McCabe test
##
## data: m.diversity.rep_1
## HMC = 0.61568, p-value = 1
hist(resid(m.diversity.rep_1))
```

## Histogram of resid(m.diversity.rep\_1)



```
summary(m.diversity.rep_1)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.50kb.rep_1)
##
## Residuals:
##      Min        1Q    Median        3Q       Max
## -0.0029908 -0.0002117  0.0000130  0.0001979  0.0035089
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.043e-02 2.236e-05 913.668 <2e-16 ***
## thetaC      1.096e+00 2.364e-03 463.564 <2e-16 ***
## rhoC       -4.461e-03 1.756e-02 -0.254     0.8
## tmrcaC      2.026e-02 1.640e-04 123.483 <2e-16 ***
## thetaC:tmrcaC 1.100e+00 1.587e-02  69.290 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0005436 on 595 degrees of freedom
## Multiple R-squared:  0.9977, Adjusted R-squared:  0.9977
## F-statistic: 6.386e+04 on 4 and 595 DF,  p-value: < 2.2e-16
interact_plot(m.diversity.rep_1, pred = thetaC, modx= tmrcaC)
```



```
g.rep_1 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
                 data = inf.lands.50kb.rep_1, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_1)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep_1
##          AIC      BIC    logLik
##     -7367.645 -7336.866 3690.822
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.3212747
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0204388 0.000031255 653.9355 0.0000
## thetaC      1.0980191 0.002985790 367.7482 0.0000
## tmrcaC      0.0199958 0.000176128 113.5300 0.0000
## rhoC        0.0035408 0.017040672  0.2078 0.8355
## thetaC:tmrcaC 1.0653107 0.017126226  62.2035 0.0000
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC      0.010
## tmrcaC     -0.018 -0.155
## rhoC       -0.003  0.009  0.012
## thetaC:tmrcaC -0.096 -0.101  0.181  0.042
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -5.45341396 -0.37367657  0.05022105  0.36056906  6.43069153
##
## Residual standard error: 0.000544344
## Degrees of freedom: 600 total; 595 residual
vif(g.rep_1)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##      1.030576     1.054551    1.001941     1.041465

g.rep_1.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.50kb.rep_1, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_1.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.50kb.rep_1
##          AIC      BIC   logLik
## -5449.253 -5427.268 2729.626
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.5079669
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0206321 0.00021240 97.13730 0.0000
## thetaC      1.1816867 0.01703572 69.36522 0.0000
## rhoC       0.0057369 0.08137302  0.07050 0.9438
##
## Correlation:
##      (Intr) thetaC
## thetaC 0.000
## rhoC   0.001  0.003
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -4.88116216 -0.45332037  0.04478515  0.48762545  4.98107994
##
## Residual standard error: 0.002969561
## Degrees of freedom: 600 total; 597 residual
anova.diversity <- Anova(m.diversity.rep_1)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.50kb[1, 1] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.inf.50kb[2, 1] <- anova.diversity$VarExp[1] * 100
r2.inf.50kb[3, 1] <- anova.diversity$VarExp[2] * 100
r2.inf.50kb[4, 1] <- anova.diversity$VarExp[3] * 100
r2.inf.50kb[5, 1] <- anova.diversity$VarExp[4] * 100
```

## 2.1.2 Replicate 2

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_2/rs.pair_2.", sep = "")
pi.50kb <- read.table(paste(p, "diversity.50kb.bedgraph", sep = ""), header = T)
pi.50kb$avg <- apply(pi.50kb[4:ncol(pi.50kb)], 1, mean)
tmrca.50kb <- read.table(paste(p, "TMRCAs.50kb.bedgraph", sep = ""), header = T)
tmrca.50kb$avg <- apply(tmrca.50kb[4:ncol(tmrca.50kb)], 1, mean)
rho.50kb <- read.table(paste(p, "rho.50kb.bedgraph", sep = ""), header = T)
theta.50kb <- read.table(paste(p, "theta.50kb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.50kb$sim, theta.50kb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.50kb$sim and theta.50kb$sample_mean
## S = 557174, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9845229

inf.lands.50kb.rep_2 <- as.data.frame(cbind(pi.50kb$avg, theta.50kb$sample_mean, rho.50kb$sample_mean,
names(inf.lands.50kb.rep_2) <- c("diversity", "theta", "rho", "tmrca")

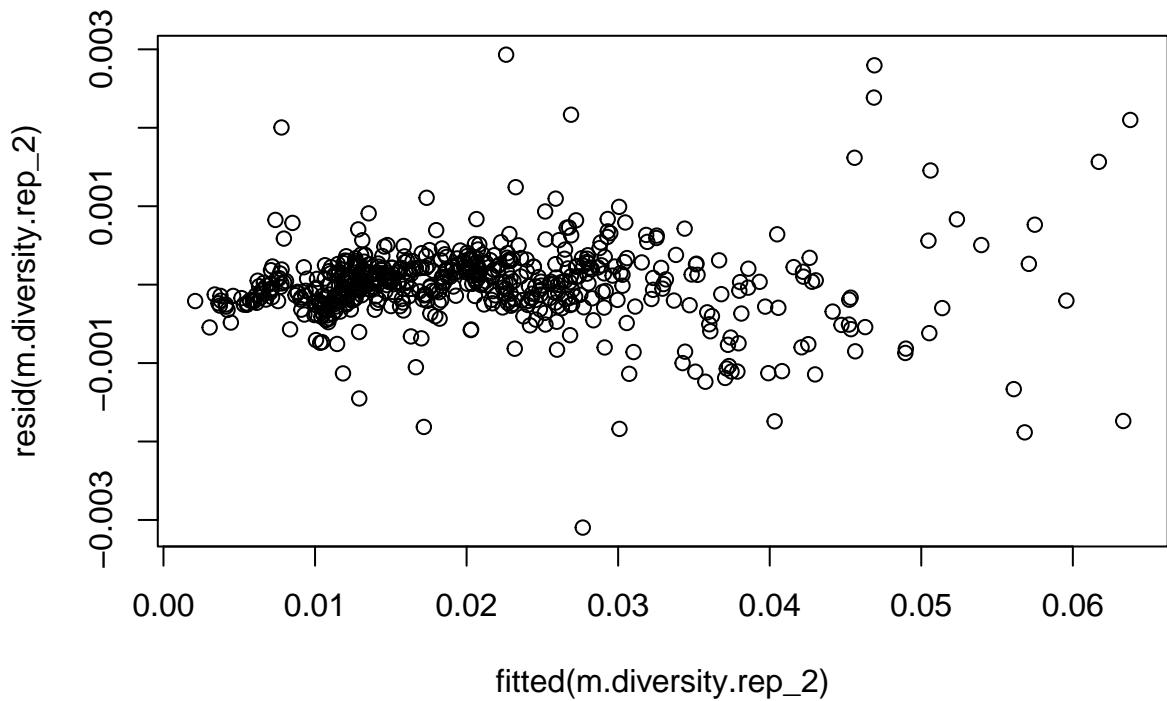
# centering
inf.lands.50kb.rep_2$thetaC <- inf.lands.50kb.rep_2$theta - mean(inf.lands.50kb.rep_2$theta)
inf.lands.50kb.rep_2$tmrcaC <- inf.lands.50kb.rep_2$tmrca - mean(inf.lands.50kb.rep_2$tmrca)
inf.lands.50kb.rep_2$rhoC <- inf.lands.50kb.rep_2$rho - mean(inf.lands.50kb.rep_2$rho)

inf.lands.50kb.rep_2$bin <- 1:nrow(inf.lands.50kb.rep_2)

# for merging:
inf.lands.50kb.rep_2$Replicate <- 2

m.diversity.rep_2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.50kb.rep_2)

plot(resid(m.diversity.rep_2)~fitted(m.diversity.rep_2))
```

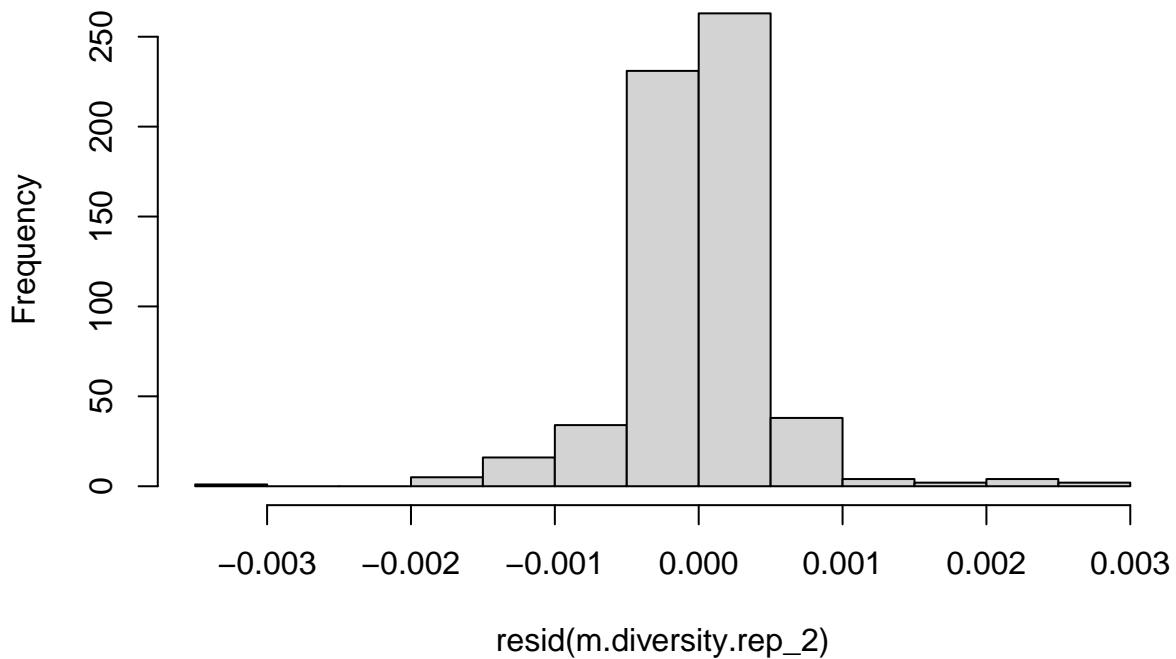


```
dwtest(m.diversity.rep_2)
```

```
##
## Durbin-Watson test
##
## data: m.diversity.rep_2
## DW = 1.3609, p-value = 1.173e-15
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_2)
```

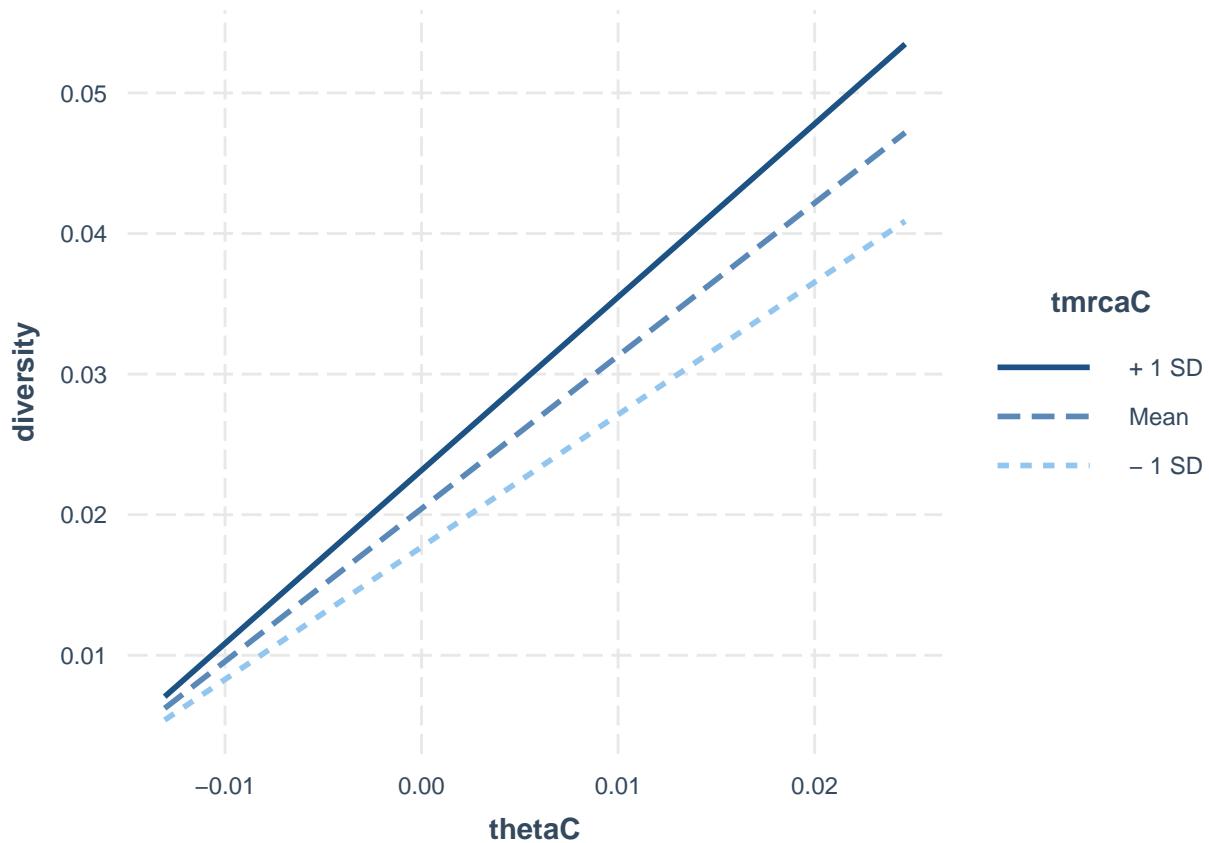
```
##
## Harrison-McCabe test
##
## data: m.diversity.rep_2
## HMC = 0.61478, p-value = 1
hist(resid(m.diversity.rep_2))
```

## Histogram of resid(m.diversity.rep\_2)



```
summary(m.diversity.rep_2)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,  
##      data = inf.lands.50kb.rep_2)  
##  
## Residuals:  
##       Min        1Q     Median        3Q       Max  
## -3.097e-03 -2.018e-04  1.307e-05  2.192e-04  2.932e-03  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 2.043e-02 2.069e-05 987.265 <2e-16 ***  
## thetaC      1.087e+00 2.167e-03 501.668 <2e-16 ***  
## rhoC       -1.167e-02 1.648e-02 -0.708  0.479  
## tmrcaC      1.999e-02 1.568e-04 127.438 <2e-16 ***  
## thetaC:tmrcaC 1.063e+00 1.365e-02 77.841 <2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0005043 on 595 degrees of freedom  
## Multiple R-squared:  0.998, Adjusted R-squared:  0.9979  
## F-statistic: 7.242e+04 on 4 and 595 DF,  p-value: < 2.2e-16  
interact_plot(m.diversity.rep_2, pred = thetaC, modx= tmrcaC)
```



```
g.rep_2 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
                 data = inf.lands.50kb.rep_2, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_2)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep_2
##          AIC      BIC    logLik
## -7474.789 -7444.011 3744.395
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##     Phi
## 0.3693417
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept) 0.0204377 0.000030697 665.7833 0.0000
## thetaC       1.0884205 0.002800847 388.6041 0.0000
## tmrcaC       0.0196845 0.000163272 120.5625 0.0000
## rhoC        -0.0167357 0.015485360  -1.0807 0.2802
## thetaC:tmrcaC 1.0175254 0.014295984  71.1756 0.0000
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC      0.001
## tmrcaC     -0.004 -0.116
## rhoC       -0.002  0.001  0.001
## thetaC:tmrcaC -0.073 -0.014  0.052  0.045
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -5.967387960 -0.392529054  0.008556582  0.424116285  5.938323518
##
## Residual standard error: 0.0005073101
## Degrees of freedom: 600 total; 595 residual
vif(g.rep_2)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
## 1.013673   1.016230   1.002036   1.004808

g.rep_2.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.50kb.rep_2, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_2.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.50kb.rep_2
##          AIC      BIC    logLik
## -5390.022 -5368.037 2700.011
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.3415288
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0205980 0.00016691 123.40674 0.0000
## thetaC       1.1278261 0.01545460  72.97670 0.0000
## rhoC        -0.0736804 0.08844426  -0.83307 0.4051
##
## Correlation:
## (Intr) thetaC
## thetaC 0.000
## rhoC   0.001  0.003
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -3.532949546 -0.502347038  0.001576082  0.522732374  6.220744946
##
## Residual standard error: 0.002859674
## Degrees of freedom: 600 total; 597 residual
anova.diversity <- Anova(m.diversity.rep_2)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.50kb[1, 2] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.inf.50kb[2, 2] <- anova.diversity$VarExp[1] * 100
r2.inf.50kb[3, 2] <- anova.diversity$VarExp[2] * 100
r2.inf.50kb[4, 2] <- anova.diversity$VarExp[3] * 100
r2.inf.50kb[5, 2] <- anova.diversity$VarExp[4] * 100
```

### 2.1.3 Replicate 3

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_3/rs.pair_3.", sep = "")
pi.50kb <- read.table(paste(p, "diversity.50kb.bedgraph", sep = ""), header = T)
pi.50kb$avg <- apply(pi.50kb[4:ncol(pi.50kb)], 1, mean)
tmrca.50kb <- read.table(paste(p, "TMRCAs.50kb.bedgraph", sep = ""), header = T)
tmrca.50kb$avg <- apply(tmrca.50kb[4:ncol(tmrca.50kb)], 1, mean)
rho.50kb <- read.table(paste(p, "rho.50kb.bedgraph", sep = ""), header = T)
theta.50kb <- read.table(paste(p, "theta.50kb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.50kb$sim, theta.50kb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.50kb$sim and theta.50kb$sample_mean
## S = 789617, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## 0.9780661

inf.lands.50kb.rep_3 <- as.data.frame(cbind(pi.50kb$avg, theta.50kb$sample_mean, rho.50kb$sample_mean,
names(inf.lands.50kb.rep_3) <- c("diversity", "theta", "rho", "tmrca")

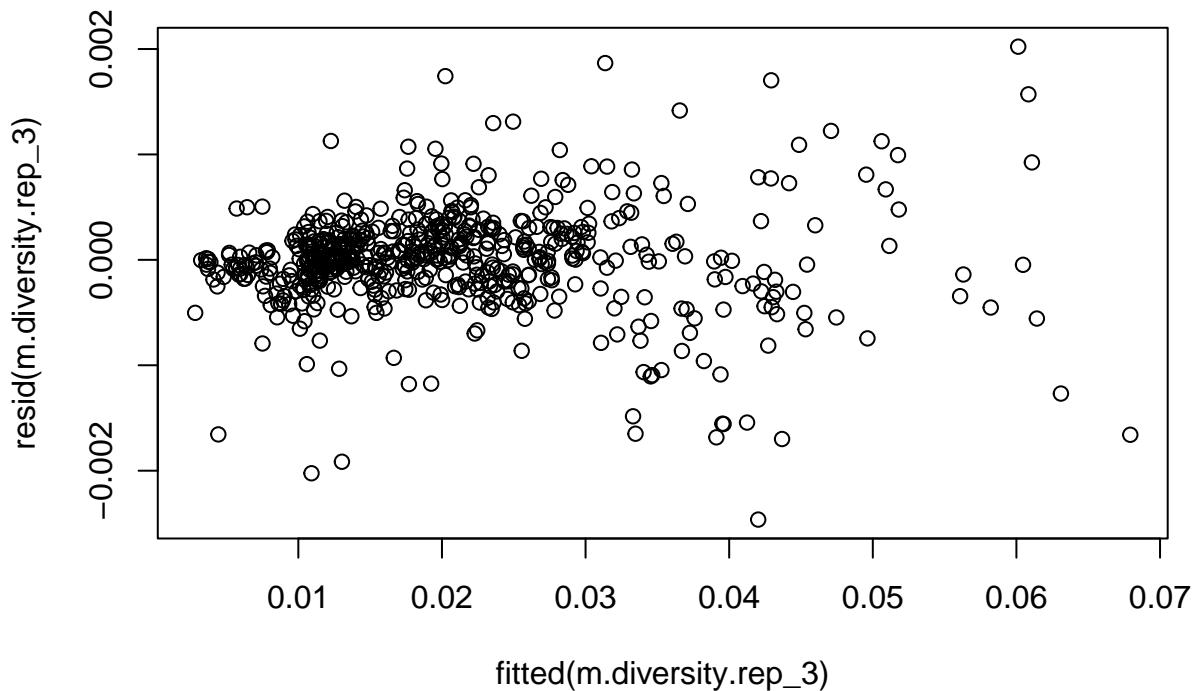
# centering
inf.lands.50kb.rep_3$thetaC <- inf.lands.50kb.rep_3$theta - mean(inf.lands.50kb.rep_3$theta)
inf.lands.50kb.rep_3$tmrcaC <- inf.lands.50kb.rep_3$tmrca - mean(inf.lands.50kb.rep_3$tmrca)
inf.lands.50kb.rep_3$rhoC <- inf.lands.50kb.rep_3$rho - mean(inf.lands.50kb.rep_3$rho)

inf.lands.50kb.rep_3$bin <- 1:nrow(inf.lands.50kb.rep_3)

# for merging:
inf.lands.50kb.rep_3$Replicate <- 3

m.diversity.rep_3 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.50kb.rep_3)

plot(resid(m.diversity.rep_3)~fitted(m.diversity.rep_3))
```

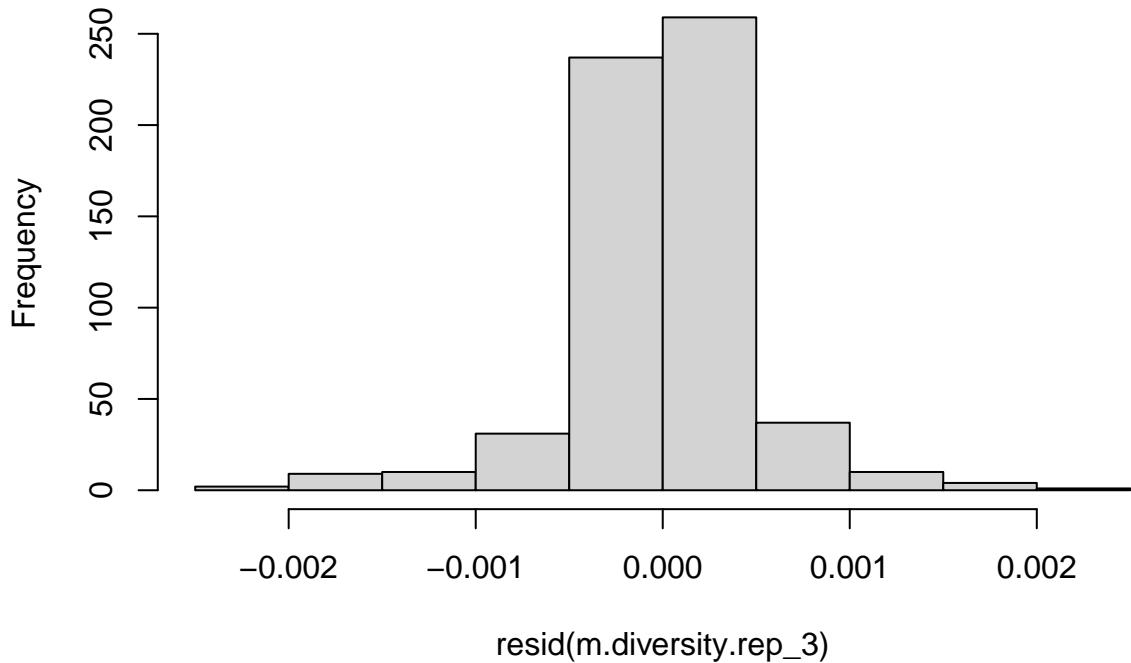


```
dwtest(m.diversity.rep_3)
```

```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_3  
## DW = 1.4619, p-value = 1.133e-11  
## alternative hypothesis: true autocorrelation is greater than 0  
hmctest(m.diversity.rep_3)
```

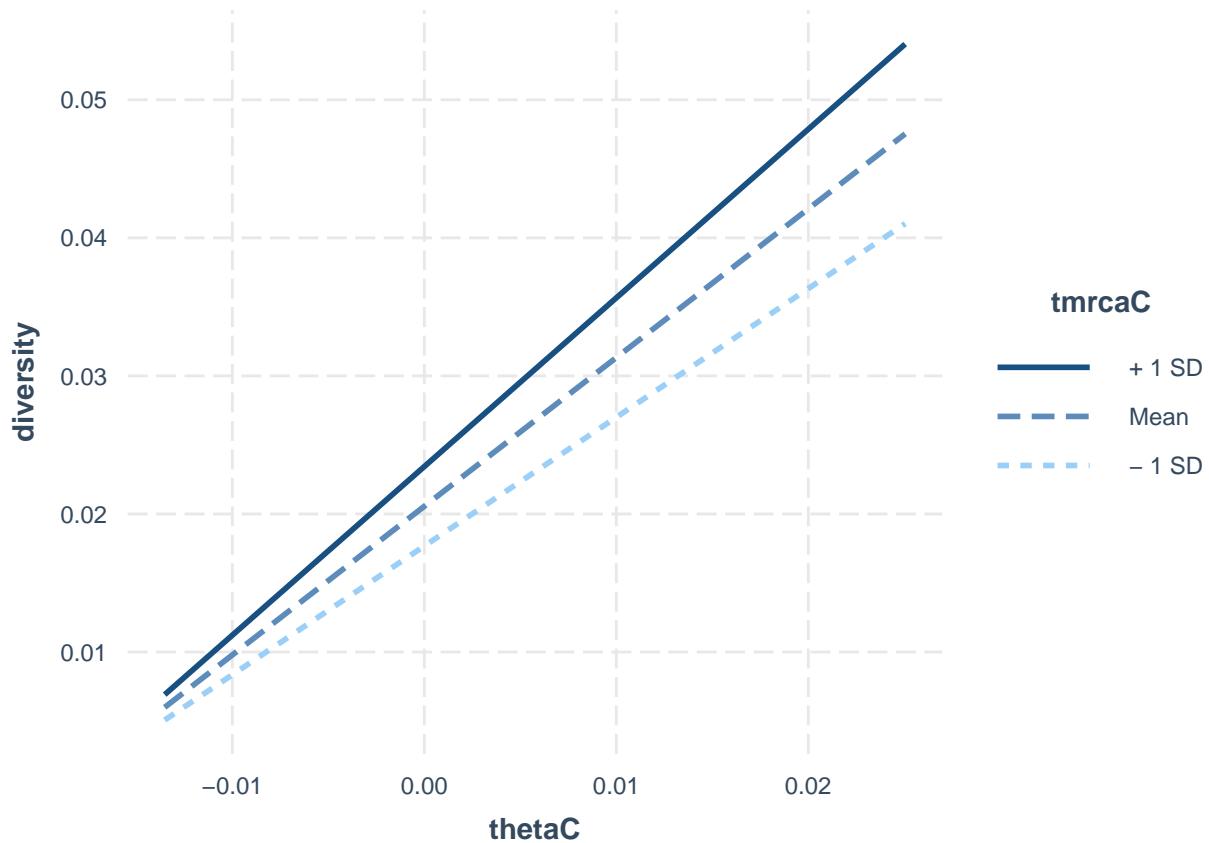
```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_3  
## HMC = 0.52153, p-value = 0.757  
hist(resid(m.diversity.rep_3))
```

## Histogram of resid(m.diversity.rep\_3)



```
summary(m.diversity.rep_3)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.50kb.rep_3)
##
## Residuals:
##      Min        1Q    Median        3Q       Max 
## -2.464e-03 -1.891e-04  1.021e-05  2.163e-04  2.022e-03 
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 0.0205593  0.0000198 1038.471 <2e-16 ***
## thetaC       1.0769710  0.0020324  529.902 <2e-16 ***
## rhoC        -0.0138881  0.0157297  -0.883   0.378    
## tmrcaC       0.0202409  0.0001408  143.768 <2e-16 ***
## thetaC:tmrcaC 1.0174596  0.0120993   84.092 <2e-16 ***
## ---      
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0004822 on 595 degrees of freedom
## Multiple R-squared:  0.9982, Adjusted R-squared:  0.9982 
## F-statistic: 8.432e+04 on 4 and 595 DF,  p-value: < 2.2e-16
interact_plot(m.diversity.rep_3, pred = thetaC, modx= tmrcaC)
```



```
g.rep_3 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
  data = inf.lands.50kb.rep_3, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_3)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep_3
##       AIC     BIC   logLik
##   -7500.229 -7469.45 3757.114
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.2838818
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept) 0.0205629 0.000026507 775.7537 0.0000
## thetaC      1.0781251 0.002506188 430.1853 0.0000
## tmrcaC      0.0201223 0.000150857 133.3870 0.0000
## rhoC        -0.0178210 0.015324110 -1.1629 0.2453
## thetaC:tmrcaC 0.9985038 0.013270574 75.2419 0.0000
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC      0.007
## tmrcaC     -0.006 -0.122
## rhoC       -0.004  0.009  0.029
## thetaC:tmrcaC -0.087 -0.075  0.058  0.056
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -5.02048902 -0.38805559  0.03745702  0.44738982  4.48985459
##
## Residual standard error: 0.0004813794
## Degrees of freedom: 600 total; 595 residual
vif(g.rep_3)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##      1.020199     1.018281    1.004142     1.011269

g.rep_3.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.50kb.rep_3, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_3.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.50kb.rep_3
##          AIC      BIC   logLik
## -5335.691 -5313.707 2672.846
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.4625776
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0207420 0.00021384 96.99954 0.0000
## thetaC       1.1398975 0.01768070 64.47130 0.0000
## rhoC        -0.1017491 0.09007408 -1.12962 0.2591
##
## Correlation:
##      (Intr) thetaC
## thetaC 0.000
## rhoC   0.001  0.011
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -4.53093269 -0.44179911 -0.01021147  0.44918244  5.33441211
##
## Residual standard error: 0.003171671
## Degrees of freedom: 600 total; 597 residual
anova.diversity <- Anova(m.diversity.rep_3)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```

r2.inf.50kb[1, 3] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.inf.50kb[2, 3] <- anova.diversity$VarExp[1] * 100
r2.inf.50kb[3, 3] <- anova.diversity$VarExp[2] * 100
r2.inf.50kb[4, 3] <- anova.diversity$VarExp[3] * 100
r2.inf.50kb[5, 3] <- anova.diversity$VarExp[4] * 100

```

## 2.1.4 Replicate 4

```

p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_4/rs.pair_4.", sep = "")
pi.50kb <- read.table(paste(p, "diversity.50kb.bedgraph", sep = ""), header = T)
pi.50kb$avg <- apply(pi.50kb[4:ncol(pi.50kb)], 1, mean)
tmrca.50kb <- read.table(paste(p, "TMRCAs.50kb.bedgraph", sep = ""), header = T)
tmrca.50kb$avg <- apply(tmrca.50kb[4:ncol(tmrca.50kb)], 1, mean)
rho.50kb <- read.table(paste(p, "rho.50kb.bedgraph", sep = ""), header = T)
theta.50kb <- read.table(paste(p, "theta.50kb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.50kb$sim, theta.50kb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.50kb$sim and theta.50kb$sample_mean
## S = 807402, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9775721

inf.lands.50kb.rep_4 <- as.data.frame(cbind(pi.50kb$avg, theta.50kb$sample_mean, rho.50kb$sample_mean,
names(inf.lands.50kb.rep_4) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.50kb.rep_4$thetaC <- inf.lands.50kb.rep_4$theta - mean(inf.lands.50kb.rep_4$theta)
inf.lands.50kb.rep_4$tmrcaC <- inf.lands.50kb.rep_4$tmrca - mean(inf.lands.50kb.rep_4$tmrca)
inf.lands.50kb.rep_4$rhoC <- inf.lands.50kb.rep_4$rho - mean(inf.lands.50kb.rep_4$rho)

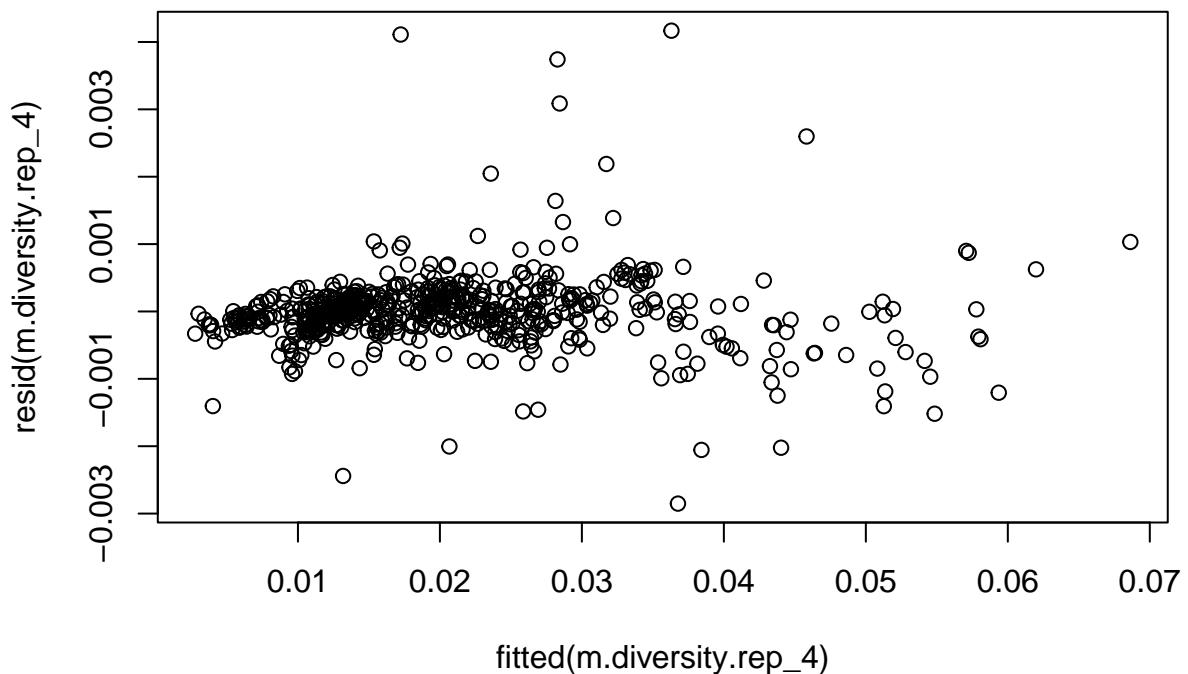
inf.lands.50kb.rep_4$bin <- 1:nrow(inf.lands.50kb.rep_4)

# for merging:
inf.lands.50kb.rep_4$Replicate <- 4

m.diversity.rep_4 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.50kb.rep_4)

plot(resid(m.diversity.rep_4)~fitted(m.diversity.rep_4))

```

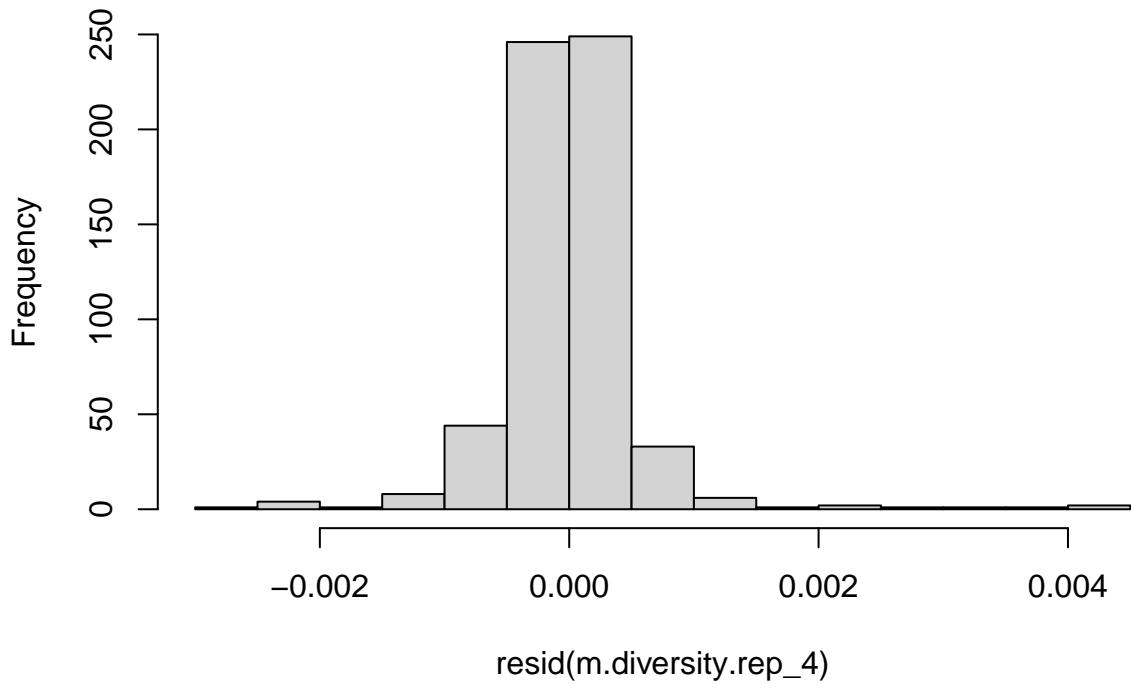


```
dwtest(m.diversity.rep_4)
```

```
##
## Durbin-Watson test
##
## data: m.diversity.rep_4
## DW = 0.96213, p-value < 2.2e-16
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_4)
```

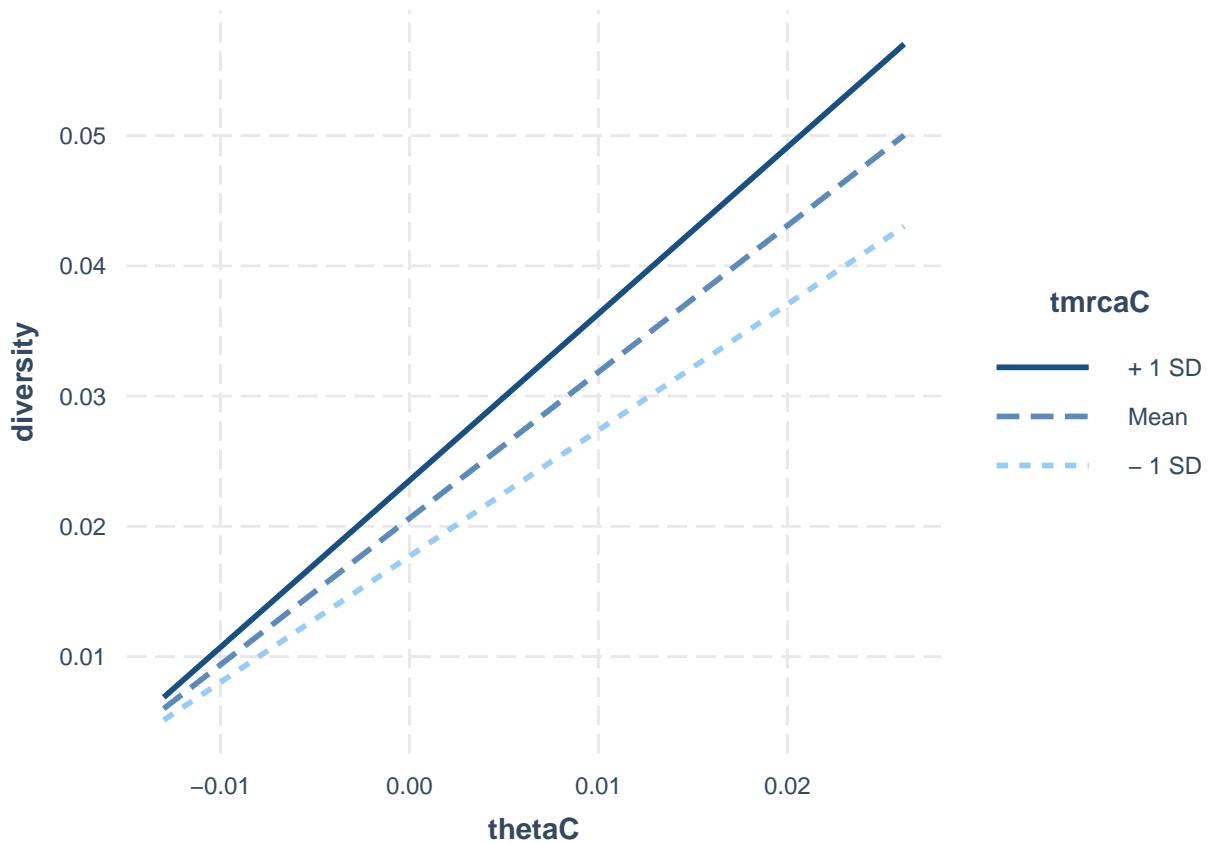
```
##
## Harrison-McCabe test
##
## data: m.diversity.rep_4
## HMC = 0.70321, p-value = 1
hist(resid(m.diversity.rep_4))
```

## Histogram of resid(m.diversity.rep\_4)



```
summary(m.diversity.rep_4)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,  
##      data = inf.lands.50kb.rep_4)  
##  
## Residuals:  
##       Min         1Q     Median        3Q       Max  
## -0.0028517 -0.0002016 -0.0000049  0.0001933  0.0041675  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 2.061e-02 2.304e-05 894.744 <2e-16 ***  
## thetaC      1.124e+00 2.418e-03 464.707 <2e-16 ***  
## rhoC      -1.112e-02 1.845e-02 -0.603  0.547  
## tmrcaC     1.960e-02 1.576e-04 124.378 <2e-16 ***  
## thetaC:tmrcaC 1.055e+00 1.499e-02 70.356 <2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0005637 on 595 degrees of freedom  
## Multiple R-squared:  0.9975, Adjusted R-squared:  0.9975  
## F-statistic: 5.993e+04 on 4 and 595 DF,  p-value: < 2.2e-16  
interact_plot(m.diversity.rep_4, pred = thetaC, modx= tmrcaC)
```



```
g.rep_4 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
  data = inf.lands.50kb.rep_4, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_4)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep_4
##          AIC      BIC    logLik
##     -7464.493 -7433.715 3739.247
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.5423451
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept) 0.0206153 0.000042516 484.8841 0.0000
## thetaC      1.1223093 0.003267770 343.4480 0.0000
## tmrcaC      0.0195383 0.000157223 124.2717 0.0000
## rhoC        -0.0073321 0.015064681  -0.4867 0.6266
## thetaC:tmrcaC 1.0070650 0.014339665  70.2293 0.0000
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC      0.001
## tmrcaC     -0.001 -0.069
## rhoC        0.000 -0.009  0.081
## thetaC:tmrcaC -0.024 -0.065 -0.008  0.006
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -5.20520625 -0.37375535 -0.02131367  0.35668752  7.22457562
##
## Residual standard error: 0.0005658744
## Degrees of freedom: 600 total; 595 residual
vif(g.rep_4)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##      1.009184     1.011566     1.006630     1.004416

g.rep_4.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.50kb.rep_4, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_4.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.50kb.rep_4
##      AIC      BIC    logLik
## -5330.615 -5308.631 2670.308
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.4710929
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0206892 0.00021819 94.82308 0.0000
## thetaC       1.1585830 0.01825400 63.47010 0.0000
## rhoC       -0.1715986 0.09086145 -1.88857 0.0594
##
## Correlation:
##      (Intr) thetaC
## thetaC 0.000
## rhoC   0.000  0.003
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -5.45522216 -0.42729625  0.05682276  0.47857205  5.82296892
##
## Residual standard error: 0.00320132
## Degrees of freedom: 600 total; 597 residual
anova.diversity <- Anova(m.diversity.rep_4)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.50kb[1, 4] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.inf.50kb[2, 4] <- anova.diversity$VarExp[1] * 100
r2.inf.50kb[3, 4] <- anova.diversity$VarExp[2] * 100
r2.inf.50kb[4, 4] <- anova.diversity$VarExp[3] * 100
r2.inf.50kb[5, 4] <- anova.diversity$VarExp[4] * 100
```

## 2.1.5 Replicate 5

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_5/rs.pair_5.", sep = "")
pi.50kb <- read.table(paste(p, "diversity.50kb.bedgraph", sep = ""), header = T)
pi.50kb$avg <- apply(pi.50kb[4:ncol(pi.50kb)], 1, mean)
tmrca.50kb <- read.table(paste(p, "TMRCAs.50kb.bedgraph", sep = ""), header = T)
tmrca.50kb$avg <- apply(tmrca.50kb[4:ncol(tmrca.50kb)], 1, mean)
rho.50kb <- read.table(paste(p, "rho.50kb.bedgraph", sep = ""), header = T)
theta.50kb <- read.table(paste(p, "theta.50kb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.50kb$sim, theta.50kb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.50kb$sim and theta.50kb$sample_mean
## S = 655949, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9817791

inf.lands.50kb.rep_5 <- as.data.frame(cbind(pi.50kb$avg, theta.50kb$sample_mean, rho.50kb$sample_mean,
names(inf.lands.50kb.rep_5) <- c("diversity", "theta", "rho", "tmrca")

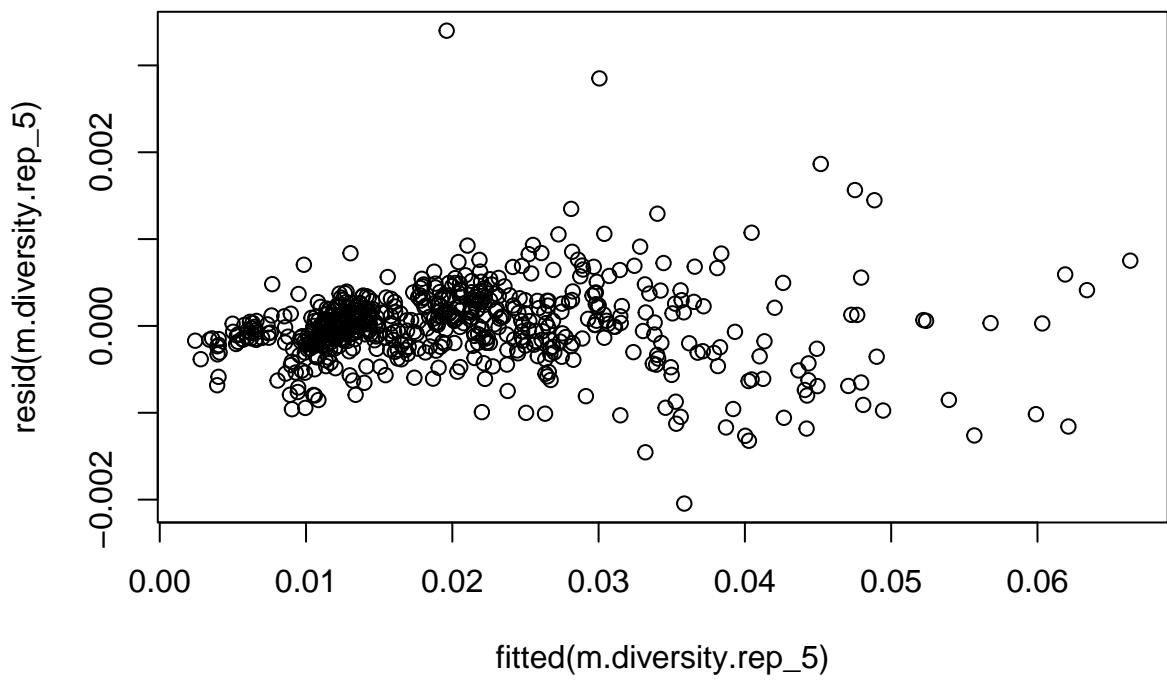
# centering
inf.lands.50kb.rep_5$thetaC <- inf.lands.50kb.rep_5$theta - mean(inf.lands.50kb.rep_5$theta)
inf.lands.50kb.rep_5$tmrcaC <- inf.lands.50kb.rep_5$tmrca - mean(inf.lands.50kb.rep_5$tmrca)
inf.lands.50kb.rep_5$rhoC <- inf.lands.50kb.rep_5$rho - mean(inf.lands.50kb.rep_5$rho)

inf.lands.50kb.rep_5$bin <- 1:nrow(inf.lands.50kb.rep_5)

# for merging:
inf.lands.50kb.rep_5$Replicate <- 5

m.diversity.rep_5 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.50kb.rep_5)

plot(resid(m.diversity.rep_5)~fitted(m.diversity.rep_5))
```

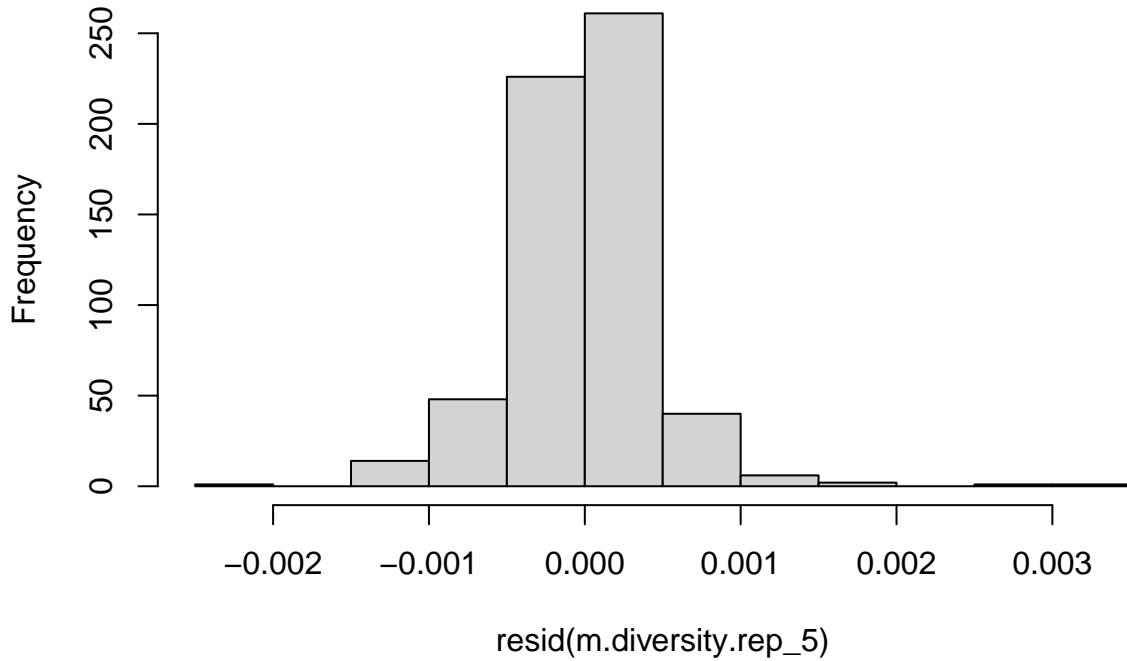


```
dwtest(m.diversity.rep_5)
```

```
##
##  Durbin-Watson test
##
## data: m.diversity.rep_5
## DW = 1.4275, p-value = 5.886e-13
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_5)
```

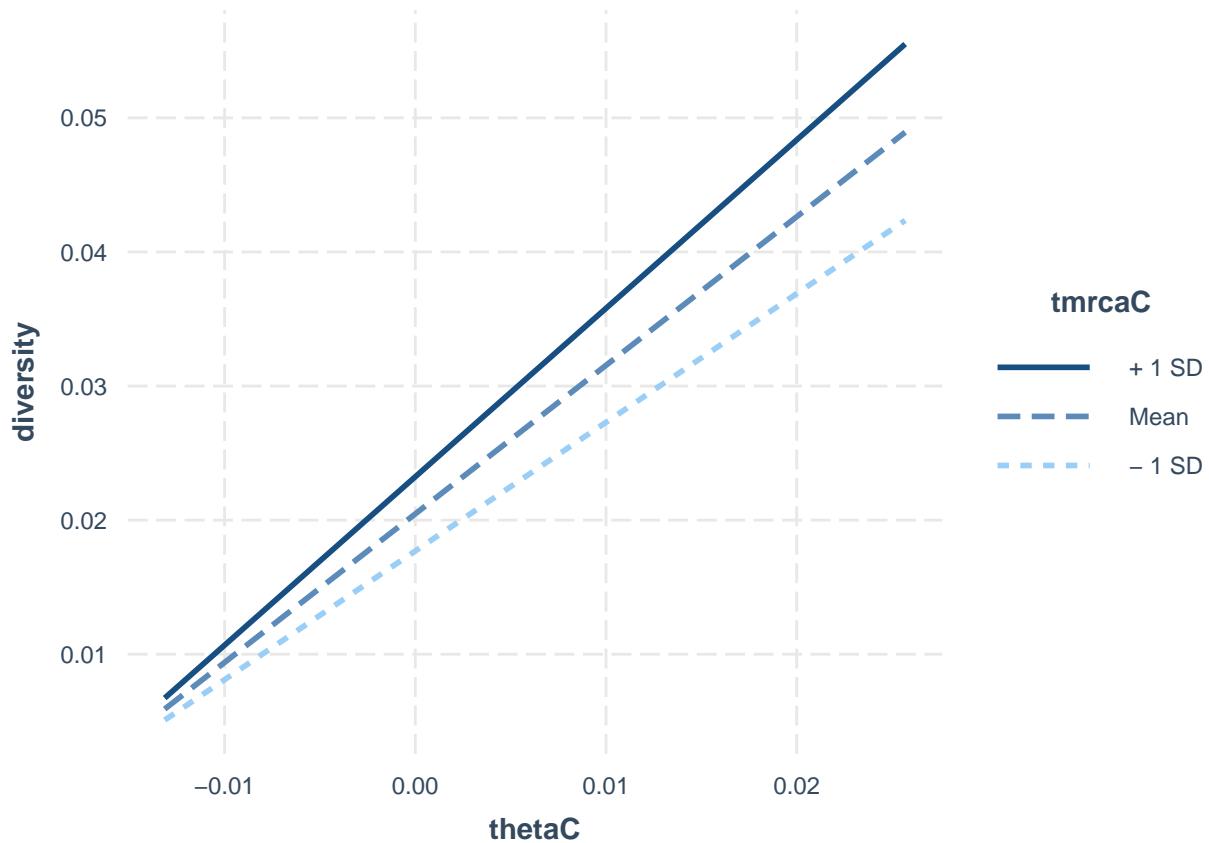
```
##
##  Harrison-McCabe test
##
## data: m.diversity.rep_5
## HMC = 0.55418, p-value = 0.967
hist(resid(m.diversity.rep_5))
```

## Histogram of resid(m.diversity.rep\_5)



```
summary(m.diversity.rep_5)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.50kb.rep_5)
##
## Residuals:
##       Min         1Q      Median         3Q        Max
## -0.0020455 -0.0002004  0.0000140  0.0002247  0.0033998
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.0204679  0.0000189 1082.787 <2e-16 ***
## thetaC      1.1078321  0.0019892  556.934 <2e-16 ***
## rhoC      -0.0069343  0.0156805   -0.442  0.658
## tmrcaC     0.0198380  0.0001375  144.318 <2e-16 ***
## thetaC:tmrcaC 1.0621447  0.0118730   89.459 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0004621 on 595 degrees of freedom
## Multiple R-squared:  0.9983, Adjusted R-squared:  0.9983
## F-statistic: 8.634e+04 on 4 and 595 DF,  p-value: < 2.2e-16
interact_plot(m.diversity.rep_5, pred = thetaC, modx= tmrcaC)
```



```
g.rep_5 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
                 data = inf.lands.50kb.rep_5, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_5)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep_5
##       AIC     BIC   logLik
##   -7570.892 -7540.114 3792.446
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.3687999
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0204733 0.000028264 724.3584 0.0000
## thetaC      1.1067703 0.002603042 425.1835 0.0000
## tmrcaC      0.0195333 0.000148186 131.8159 0.0000
## rhoC        -0.0117411 0.014941182 -0.7858 0.4323
## thetaC:tmrcaC 1.0119684 0.012760307 79.3060 0.0000
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC      -0.002
## tmrcaC      0.002 -0.094
## rhoC       -0.001  0.002  0.058
## thetaC:tmrcaC -0.045  0.037 -0.040  0.028
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -4.3488500199 -0.4439991675  0.0002670608  0.4775851241  7.1344633188
##
## Residual standard error: 0.0004681579
## Degrees of freedom: 600 total; 595 residual
vif(g.rep_5)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
## 1.010139    1.013921    1.004356    1.003709

g.rep_5.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.50kb.rep_5, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_5.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.50kb.rep_5
##      AIC      BIC logLik
## -5329.279 -5307.294 2669.64
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.4006009
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0205709 0.00019283 106.68153 0.0000
## thetaC       1.1335447 0.01727411  65.62102 0.0000
## rhoC       -0.1554325 0.09617437  -1.61615 0.1066
##
## Correlation:
##      (Intr) thetaC
## thetaC 0.000
## rhoC   0.001  0.007
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -4.31295794 -0.44285975  0.05270967  0.47530087  5.66926609
##
## Residual standard error: 0.003085565
## Degrees of freedom: 600 total; 597 residual
anova.diversity <- Anova(m.diversity.rep_5)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.50kb[1, 5] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.inf.50kb[2, 5] <- anova.diversity$VarExp[1] * 100
r2.inf.50kb[3, 5] <- anova.diversity$VarExp[2] * 100
r2.inf.50kb[4, 5] <- anova.diversity$VarExp[3] * 100
r2.inf.50kb[5, 5] <- anova.diversity$VarExp[4] * 100
```

## 2.1.6 Replicate 6

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_6/rs.pair_6.", sep = "")
pi.50kb <- read.table(paste(p, "diversity.50kb.bedgraph", sep = ""), header = T)
pi.50kb$avg <- apply(pi.50kb[4:ncol(pi.50kb)], 1, mean)
tmrca.50kb <- read.table(paste(p, "TMRCAs.50kb.bedgraph", sep = ""), header = T)
tmrca.50kb$avg <- apply(tmrca.50kb[4:ncol(tmrca.50kb)], 1, mean)
rho.50kb <- read.table(paste(p, "rho.50kb.bedgraph", sep = ""), header = T)
theta.50kb <- read.table(paste(p, "theta.50kb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.50kb$sim, theta.50kb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.50kb$sim and theta.50kb$sample_mean
## S = 576502, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.983986

inf.lands.50kb.rep_6 <- as.data.frame(cbind(pi.50kb$avg, theta.50kb$sample_mean, rho.50kb$sample_mean,
names(inf.lands.50kb.rep_6) <- c("diversity", "theta", "rho", "tmrca")

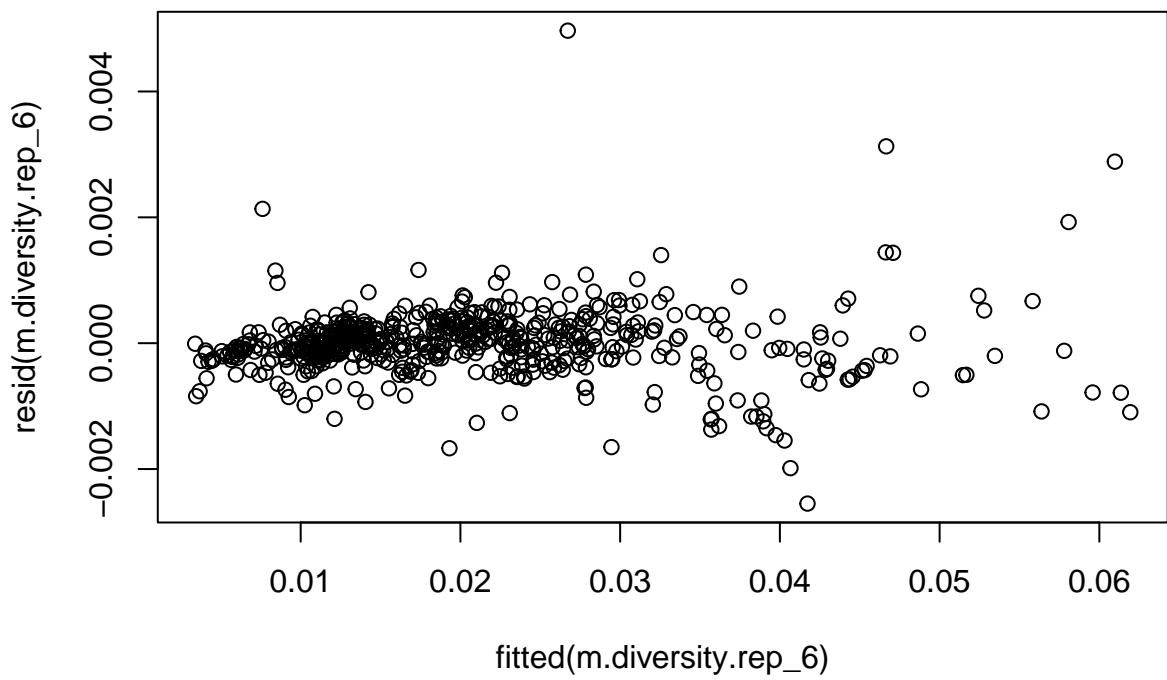
# centering
inf.lands.50kb.rep_6$thetaC <- inf.lands.50kb.rep_6$theta - mean(inf.lands.50kb.rep_6$theta)
inf.lands.50kb.rep_6$tmrcaC <- inf.lands.50kb.rep_6$tmrca - mean(inf.lands.50kb.rep_6$tmrca)
inf.lands.50kb.rep_6$rhoC <- inf.lands.50kb.rep_6$rho - mean(inf.lands.50kb.rep_6$rho)

inf.lands.50kb.rep_6$bin <- 1:nrow(inf.lands.50kb.rep_6)

# for merging:
inf.lands.50kb.rep_6$Replicate <- 6

m.diversity.rep_6 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.50kb.rep_6)

plot(resid(m.diversity.rep_6)~fitted(m.diversity.rep_6))
```

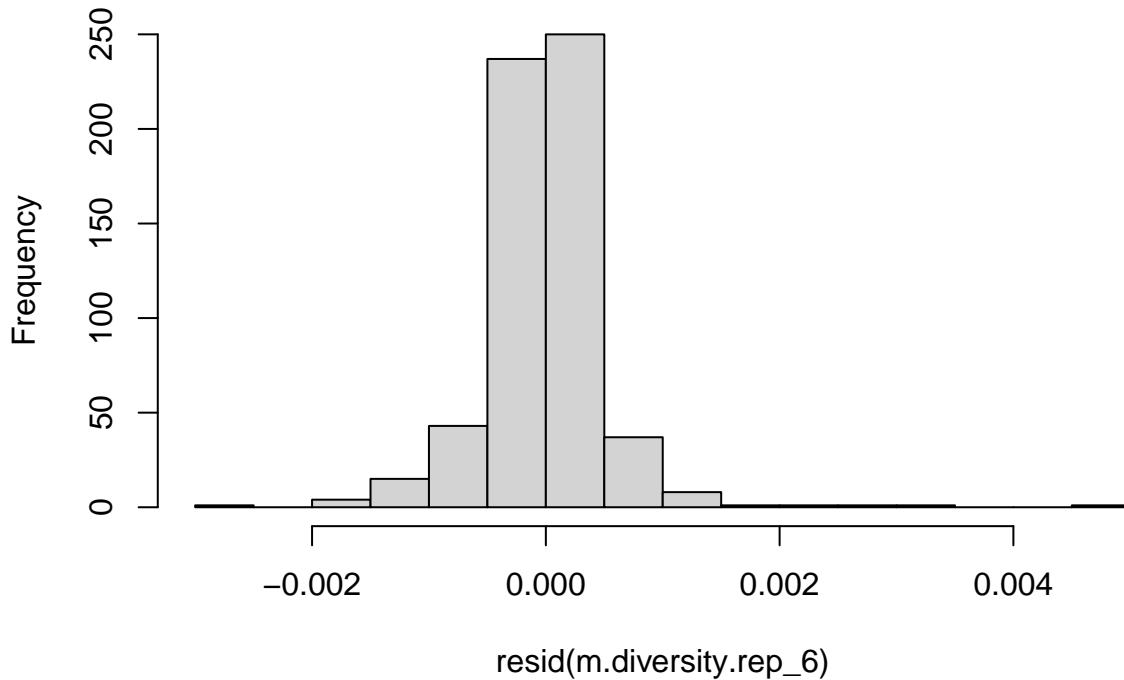


```
dwtest(m.diversity.rep_6)
```

```
##
## Durbin-Watson test
##
## data: m.diversity.rep_6
## DW = 1.4152, p-value = 1.956e-13
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_6)
```

```
##
## Harrison-McCabe test
##
## data: m.diversity.rep_6
## HMC = 0.5501, p-value = 0.964
hist(resid(m.diversity.rep_6))
```

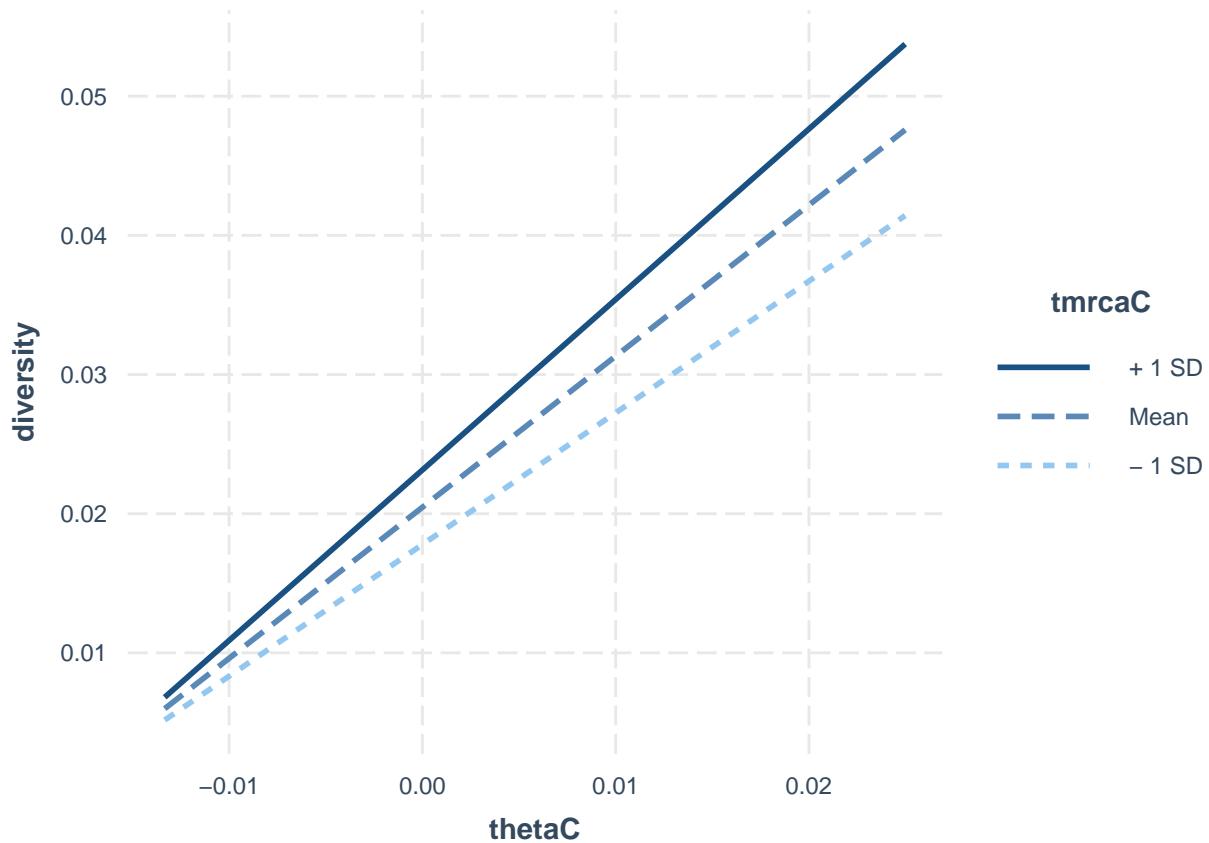
## Histogram of resid(m.diversity.rep\_6)



```
summary(m.diversity.rep_6)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,  
##      data = inf.lands.50kb.rep_6)  
##  
## Residuals:  
##       Min        1Q     Median        3Q       Max  
## -0.0025487 -0.0002073 -0.0000008  0.0002258  0.0049661  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 2.046e-02 2.183e-05 937.468 <2e-16 ***  
## thetaC      1.086e+00 2.249e-03 482.709 <2e-16 ***  
## rhoC       9.344e-03 1.682e-02   0.555   0.579  
## tmrcaC     2.016e-02 1.691e-04 119.259 <2e-16 ***  
## thetaC:tmrcaC 1.050e+00 1.470e-02  71.423 <2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0005333 on 595 degrees of freedom  
## Multiple R-squared:  0.9977, Adjusted R-squared:  0.9977  
## F-statistic: 6.529e+04 on 4 and 595 DF,  p-value: < 2.2e-16
```

```
interact_plot(m.diversity.rep_6, pred = thetaC, modx= tmrcaC)
```



```
g.rep_6 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
                  data = inf.lands.50kb.rep_6, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_6)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep_6
##          AIC      BIC logLik
## -7391.16 -7360.382 3702.58
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##     Phi
## 0.3219522
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept) 0.0204681 0.000030586 669.1903 0.0000
## thetaC       1.0858244 0.002832026 383.4091 0.0000
## tmrcaC       0.0199376 0.000176983 112.6524 0.0000
## rhoC         0.0002293 0.016283078   0.0141 0.9888
## thetaC:tmrcaC 1.0151180 0.015909552  63.8056 0.0000
##
## Correlation:
##   (Intr) thetaC tmrcaC rhoC
##
```

```

## thetaC      0.000
## tmrcaC     -0.006 -0.082
## rhoC        0.000  0.014  0.075
## thetaC:tmrcaC -0.056  0.002  0.082  0.013
##
## Standardized residuals:
##            Min         Q1         Med         Q3         Max
## -4.664990405 -0.377078774 -0.001461415  0.411936942  9.302435018
##
## Residual standard error: 0.0005339103
## Degrees of freedom: 600 total; 595 residual
vif(g.rep_6)

##          thetaC          tmrcaC          rhoC  thetaC:tmrcaC
##       1.007216       1.019473       1.006158       1.006869

g.rep_6.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.50kb.rep_6, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_6.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.50kb.rep_6
##      AIC      BIC   logLik
## -5414.912 -5392.927 2712.456
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##          Phi
## 0.4107098
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0205846 0.00018261 112.72153 0.0000
## thetaC       1.1129166 0.01585204  70.20654 0.0000
## rhoC       -0.1062152 0.08342243  -1.27322 0.2034
##
## Correlation:
## (Intr) thetaC
## thetaC 0.000
## rhoC   0.001  0.014
##
## Standardized residuals:
##            Min         Q1         Med         Q3         Max
## -4.246615321 -0.484784795 -0.004012756  0.502253352  5.520109924
##
## Residual standard error: 0.002887164
## Degrees of freedom: 600 total; 597 residual
anova.diversity <- Anova(m.diversity.rep_6)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.50kb[1, 6] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.inf.50kb[2, 6] <- anova.diversity$VarExp[1] * 100
r2.inf.50kb[3, 6] <- anova.diversity$VarExp[2] * 100
r2.inf.50kb[4, 6] <- anova.diversity$VarExp[3] * 100
r2.inf.50kb[5, 6] <- anova.diversity$VarExp[4] * 100
```

## 2.1.7 Replicate 7

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_7/rs.pair_7.", sep = "")
pi.50kb <- read.table(paste(p, "diversity.50kb.bedgraph", sep = ""), header = T)
pi.50kb$avg <- apply(pi.50kb[4:ncol(pi.50kb)], 1, mean)
tmrca.50kb <- read.table(paste(p, "TMRCAs.50kb.bedgraph", sep = ""), header = T)
tmrca.50kb$avg <- apply(tmrca.50kb[4:ncol(tmrca.50kb)], 1, mean)
rho.50kb <- read.table(paste(p, "rho.50kb.bedgraph", sep = ""), header = T)
theta.50kb <- read.table(paste(p, "theta.50kb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.50kb$sim, theta.50kb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.50kb$sim and theta.50kb$sample_mean
## S = 715696, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9801195

inf.lands.50kb.rep_7 <- as.data.frame(cbind(pi.50kb$avg, theta.50kb$sample_mean, rho.50kb$sample_mean,
names(inf.lands.50kb.rep_7) <- c("diversity", "theta", "rho", "tmrca")

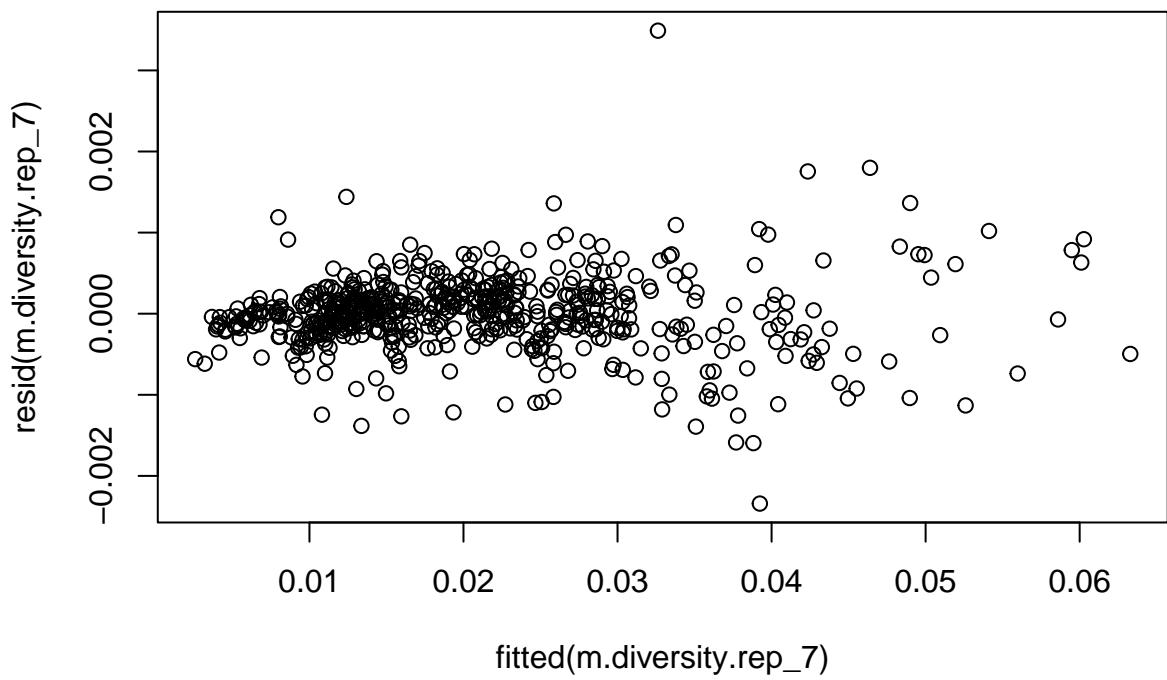
# centering
inf.lands.50kb.rep_7$thetaC <- inf.lands.50kb.rep_7$theta - mean(inf.lands.50kb.rep_7$theta)
inf.lands.50kb.rep_7$tmrcaC <- inf.lands.50kb.rep_7$tmrca - mean(inf.lands.50kb.rep_7$tmrca)
inf.lands.50kb.rep_7$rhoC <- inf.lands.50kb.rep_7$rho - mean(inf.lands.50kb.rep_7$rho)

inf.lands.50kb.rep_7$bin <- 1:nrow(inf.lands.50kb.rep_7)

# for merging:
inf.lands.50kb.rep_7$Replicate <- 7

m.diversity.rep_7 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.50kb.rep_7)

plot(resid(m.diversity.rep_7)~fitted(m.diversity.rep_7))
```

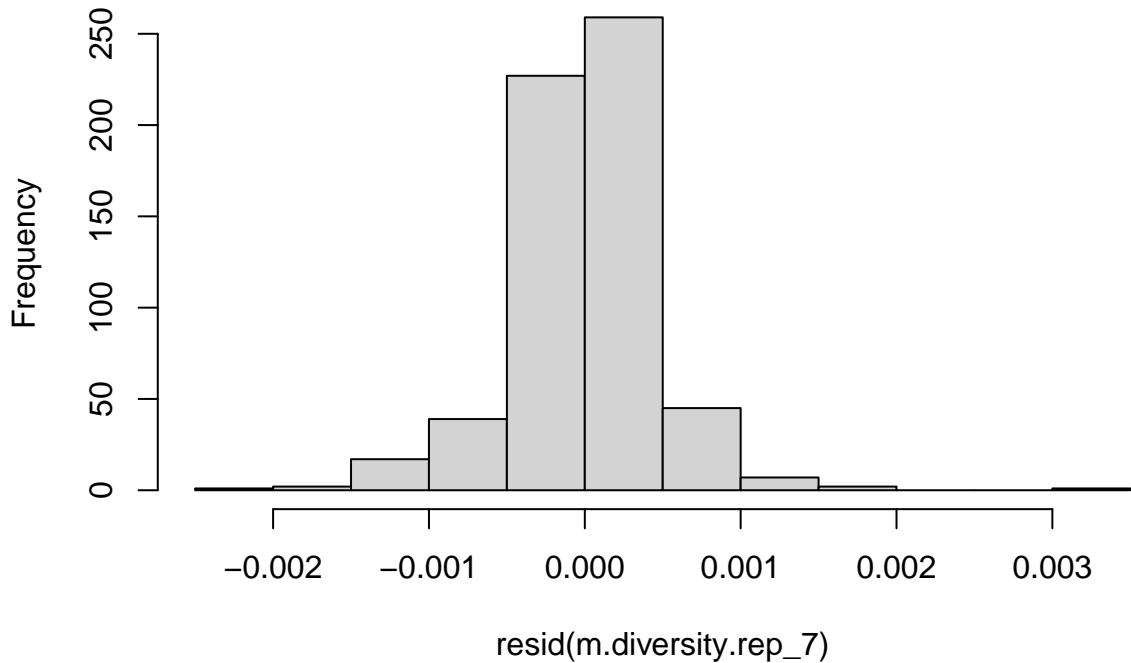


```
dwtest(m.diversity.rep_7)
```

```
##
## Durbin-Watson test
##
## data: m.diversity.rep_7
## DW = 1.2084, p-value < 2.2e-16
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_7)
```

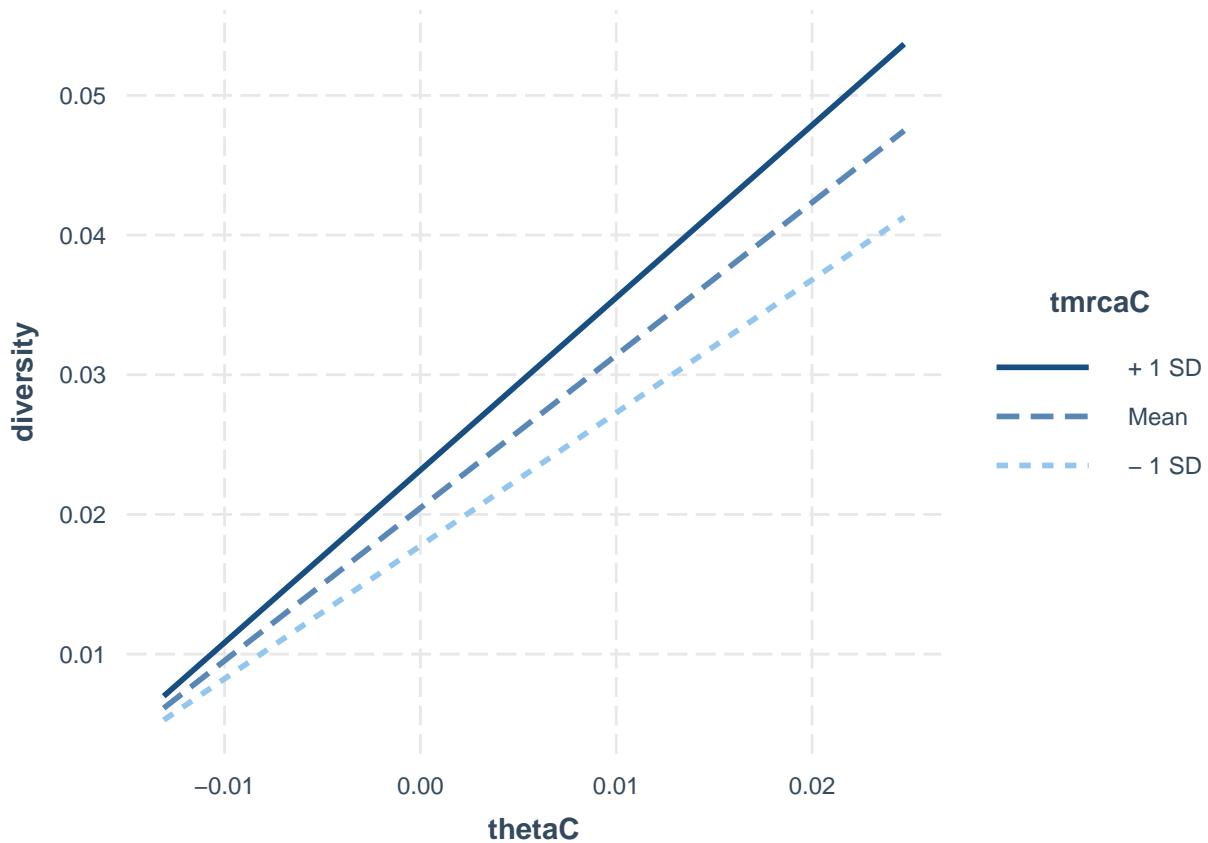
```
##
## Harrison-McCabe test
##
## data: m.diversity.rep_7
## HMC = 0.58586, p-value = 0.998
hist(resid(m.diversity.rep_7))
```

## Histogram of resid(m.diversity.rep\_7)



```
summary(m.diversity.rep_7)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,  
##      data = inf.lands.50kb.rep_7)  
##  
## Residuals:  
##       Min        1Q     Median        3Q       Max  
## -0.0023413 -0.0001931  0.0000183  0.0002113  0.0034898  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 2.046e-02 1.906e-05 1073.378 < 2e-16 ***  
## thetaC      1.093e+00 1.994e-03  548.323 < 2e-16 ***  
## rhoC       -3.984e-02 1.517e-02   -2.627  0.00885 **  
## tmrcaC      2.021e-02 1.462e-04   138.265 < 2e-16 ***  
## thetaC:tmrcaC 1.056e+00 1.344e-02    78.551 < 2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0004657 on 595 degrees of freedom  
## Multiple R-squared:  0.9982, Adjusted R-squared:  0.9982  
## F-statistic: 8.313e+04 on 4 and 595 DF,  p-value: < 2.2e-16  
interact_plot(m.diversity.rep_7, pred = thetaC, modx= tmrcaC)
```



```
g.rep_7 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
  data = inf.lands.50kb.rep_7, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_7)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep_7
##       AIC     BIC   logLik
##   -7617.29 -7586.512 3815.645
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.4690905
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0204701 0.000032313 633.4967 0.0000
## thetaC      1.0964625 0.002720215 403.0793 0.0000
## tmrcaC      0.0197764 0.000149360 132.4076 0.0000
## rhoC        -0.0310546 0.013470566  -2.3054 0.0215
## thetaC:tmrcaC 0.9959236 0.014228586 69.9946 0.0000
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC      -0.001
## tmrcaC     -0.006 -0.099
## rhoC        0.002  0.005 -0.022
## thetaC:tmrcaC -0.047  0.014  0.100 -0.014
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -4.79375373 -0.41801231  0.05547631  0.45600293  7.65648237
##
## Residual standard error: 0.0004740043
## Degrees of freedom: 600 total; 595 residual
vif(g.rep_7)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##      1.010511     1.020984    1.000614     1.010927

g.rep_7.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.50kb.rep_7, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_7.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.50kb.rep_7
##          AIC      BIC   logLik
## -5472.449 -5450.464 2741.224
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.469828
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0205801 0.00019340 106.41030 0.0000
## thetaC       1.1283864 0.01620181  69.64571 0.0000
## rhoC        0.0166423 0.08056264   0.20658 0.8364
##
## Correlation:
##      (Intr) thetaC
## thetaC 0.000
## rhoC   0.001  0.003
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -4.47464746 -0.42695326  0.04565358  0.50179301  5.14163869
##
## Residual standard error: 0.002842278
## Degrees of freedom: 600 total; 597 residual
anova.diversity <- Anova(m.diversity.rep_7)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.50kb[1, 7] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.inf.50kb[2, 7] <- anova.diversity$VarExp[1] * 100
r2.inf.50kb[3, 7] <- anova.diversity$VarExp[2] * 100
r2.inf.50kb[4, 7] <- anova.diversity$VarExp[3] * 100
r2.inf.50kb[5, 7] <- anova.diversity$VarExp[4] * 100
```

## 2.1.8 Replicate 8

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_8/rs.pair_8.", sep = "")
pi.50kb <- read.table(paste(p, "diversity.50kb.bedgraph", sep = ""), header = T)
pi.50kb$avg <- apply(pi.50kb[4:ncol(pi.50kb)], 1, mean)
tmrca.50kb <- read.table(paste(p, "TMRCAs.50kb.bedgraph", sep = ""), header = T)
tmrca.50kb$avg <- apply(tmrca.50kb[4:ncol(tmrca.50kb)], 1, mean)
rho.50kb <- read.table(paste(p, "rho.50kb.bedgraph", sep = ""), header = T)
theta.50kb <- read.table(paste(p, "theta.50kb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.50kb$sim, theta.50kb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.50kb$sim and theta.50kb$sample_mean
## S = 682855, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9810318

inf.lands.50kb.rep_8 <- as.data.frame(cbind(pi.50kb$avg, theta.50kb$sample_mean, rho.50kb$sample_mean,
names(inf.lands.50kb.rep_8) <- c("diversity", "theta", "rho", "tmrca")

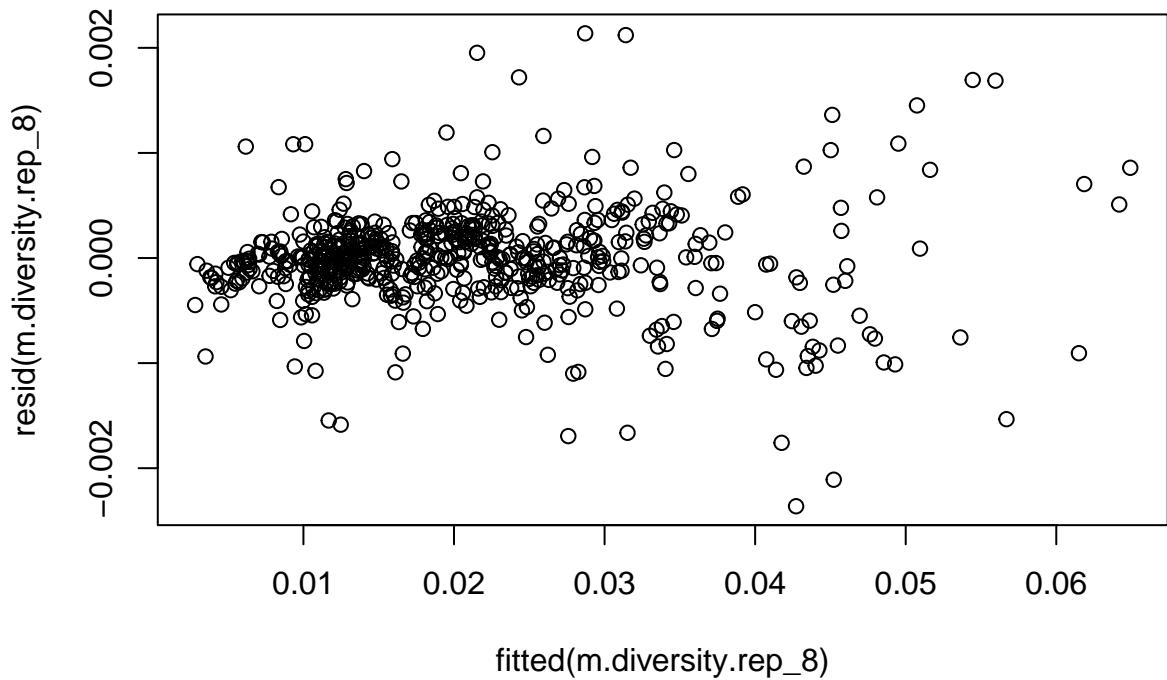
# centering
inf.lands.50kb.rep_8$thetaC <- inf.lands.50kb.rep_8$theta - mean(inf.lands.50kb.rep_8$theta)
inf.lands.50kb.rep_8$tmrcaC <- inf.lands.50kb.rep_8$tmrca - mean(inf.lands.50kb.rep_8$tmrca)
inf.lands.50kb.rep_8$rhoC <- inf.lands.50kb.rep_8$rho - mean(inf.lands.50kb.rep_8$rho)

inf.lands.50kb.rep_8$bin <- 1:nrow(inf.lands.50kb.rep_8)

# for merging:
inf.lands.50kb.rep_8$Replicate <- 8

m.diversity.rep_8 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.50kb.rep_8)

plot(resid(m.diversity.rep_8)~fitted(m.diversity.rep_8))
```

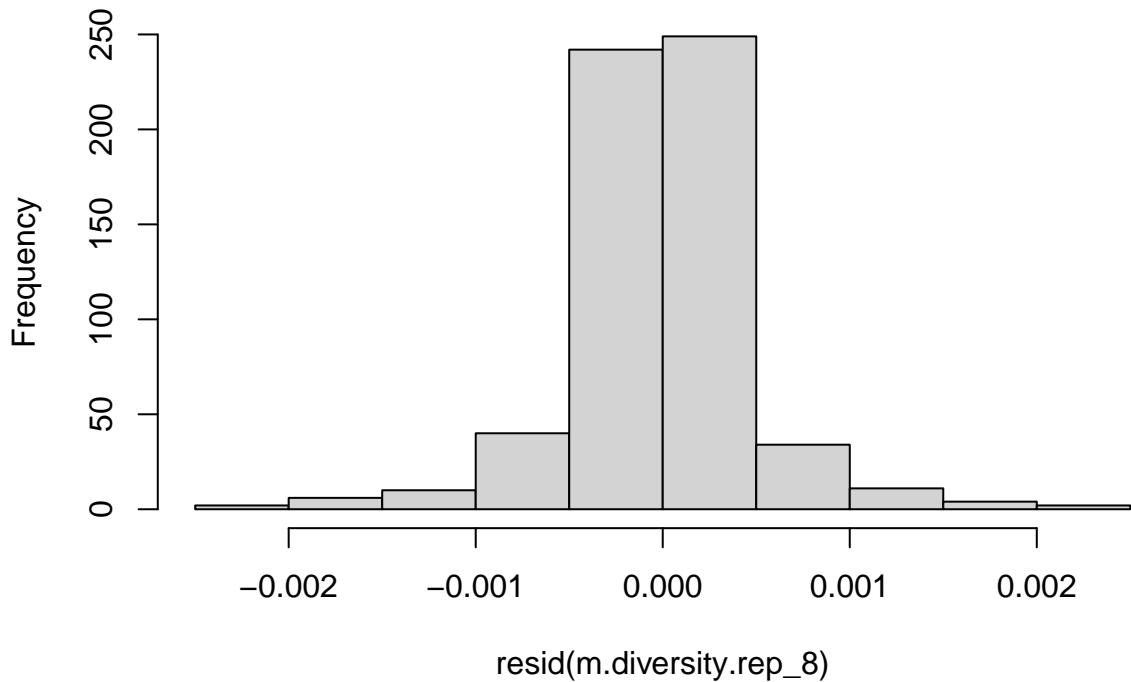


```
dwtest(m.diversity.rep_8)
```

```
##
## Durbin-Watson test
##
## data: m.diversity.rep_8
## DW = 1.3796, p-value = 6.877e-15
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_8)
```

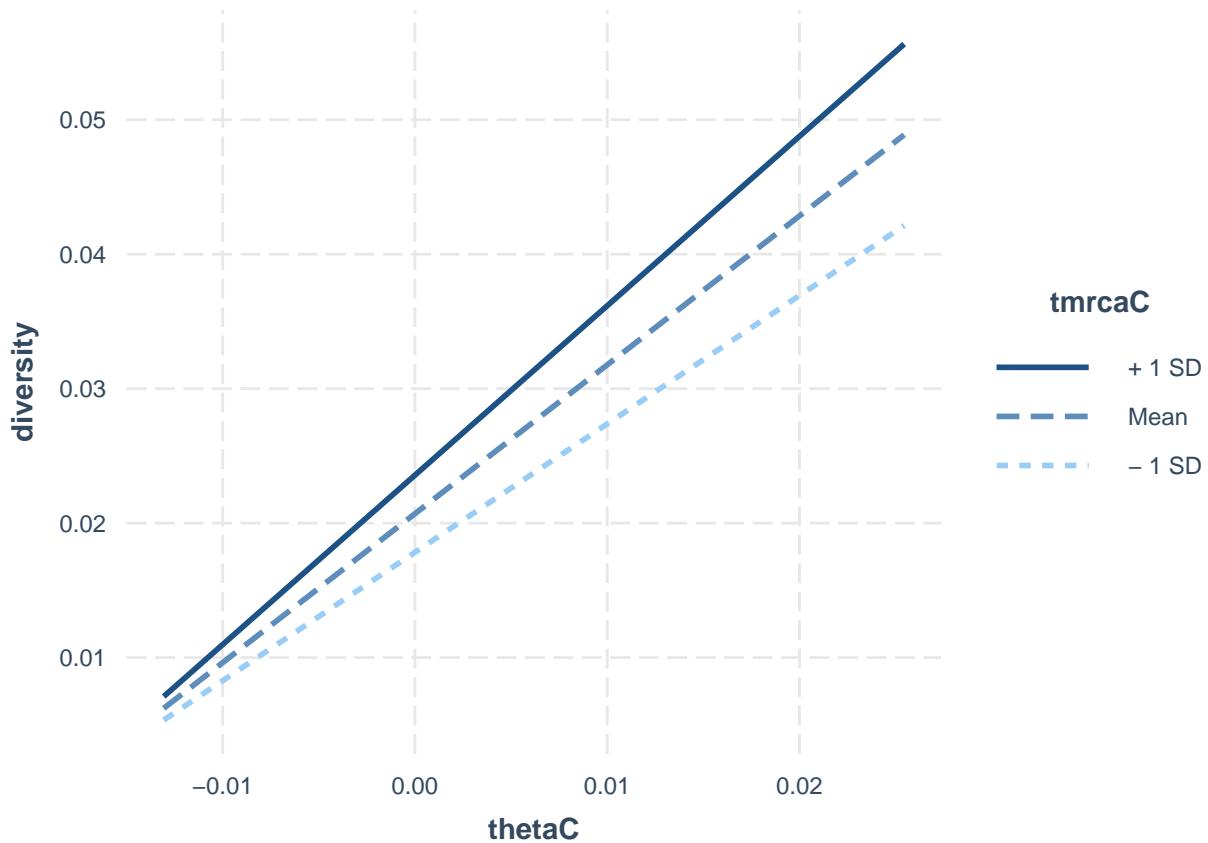
```
##
## Harrison-McCabe test
##
## data: m.diversity.rep_8
## HMC = 0.62278, p-value = 1
hist(resid(m.diversity.rep_8))
```

## Histogram of resid(m.diversity.rep\_8)



```
summary(m.diversity.rep_8)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.50kb.rep_8)
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -2.362e-03 -1.893e-04  3.500e-07  2.086e-04  2.138e-03
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 2.070e-02 1.938e-05 1067.98 <2e-16 ***
## thetaC      1.107e+00 2.023e-03  547.27 <2e-16 ***
## rhoC       -6.776e-03 1.539e-02   -0.44    0.66    
## tmrcaC      2.013e-02 1.393e-04  144.50 <2e-16 ***
## thetaC:tmrcaC 1.071e+00 1.222e-02    87.61 <2e-16 ***
## ---      
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0004737 on 595 degrees of freedom
## Multiple R-squared:  0.9982, Adjusted R-squared:  0.9982 
## F-statistic: 8.292e+04 on 4 and 595 DF,  p-value: < 2.2e-16
interact_plot(m.diversity.rep_8, pred = thetaC, modx= tmrcaC)
```



```
g.rep_8 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
  data = inf.lands.50kb.rep_8, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_8)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep_8
##          AIC      BIC    logLik
##     -7548.618 -7517.839 3781.309
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.3796214
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0207031 0.000029299 706.6176 0.0000
## thetaC      1.1082548 0.002641688 419.5253 0.0000
## tmrcaC      0.0198182 0.000148295 133.6401 0.0000
## rhoC        0.0047060 0.014548476   0.3235 0.7465
## thetaC:tmrcaC 1.0223058 0.013460362   75.9494 0.0000
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC      -0.001
## tmrcaC     -0.004 -0.069
## rhoC        0.001  0.012  0.067
## thetaC:tmrcaC -0.048  0.026  0.075 -0.015
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -4.79143530 -0.40162824  0.00873902  0.44671770  4.52028563
##
## Residual standard error: 0.0004791766
## Degrees of freedom: 600 total; 595 residual
vif(g.rep_8)

##          thetaC          tmrcaC          rhoC    thetaC:tmrcaC
## 1.006009     1.015515     1.005156     1.006994

g.rep_8.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.50kb.rep_8, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_8.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.50kb.rep_8
##      AIC      BIC logLik
## -5369.959 -5347.975 2689.98
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##          Phi
## 0.4676478
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0208143 0.00020979 99.21612 0.0000
## thetaC       1.1333322 0.01746884 64.87738 0.0000
## rhoC        -0.0900602 0.08770082 -1.02690 0.3049
##
## Correlation:
##          (Intr) thetaC
## thetaC  0.000
## rhoC   0.000  0.012
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -7.41084900 -0.48902470 -0.01613762  0.49491223  5.48392430
##
## Residual standard error: 0.003091654
## Degrees of freedom: 600 total; 597 residual
anova.diversity <- Anova(m.diversity.rep_8)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.50kb[1, 8] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.inf.50kb[2, 8] <- anova.diversity$VarExp[1] * 100
r2.inf.50kb[3, 8] <- anova.diversity$VarExp[2] * 100
r2.inf.50kb[4, 8] <- anova.diversity$VarExp[3] * 100
r2.inf.50kb[5, 8] <- anova.diversity$VarExp[4] * 100
```

## 2.1.9 Replicate 9

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_9/rs.pair_9.", sep = "")
pi.50kb <- read.table(paste(p, "diversity.50kb.bedgraph", sep = ""), header = T)
pi.50kb$avg <- apply(pi.50kb[4:ncol(pi.50kb)], 1, mean)
tmrca.50kb <- read.table(paste(p, "TMRCAs.50kb.bedgraph", sep = ""), header = T)
tmrca.50kb$avg <- apply(tmrca.50kb[4:ncol(tmrca.50kb)], 1, mean)
rho.50kb <- read.table(paste(p, "rho.50kb.bedgraph", sep = ""), header = T)
theta.50kb <- read.table(paste(p, "theta.50kb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.50kb$sim, theta.50kb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.50kb$sim and theta.50kb$sample_mean
## S = 609380, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9830727

inf.lands.50kb.rep_9 <- as.data.frame(cbind(pi.50kb$avg, theta.50kb$sample_mean, rho.50kb$sample_mean, tmrca.50kb$avg))
names(inf.lands.50kb.rep_9) <- c("diversity", "theta", "rho", "tmrca")

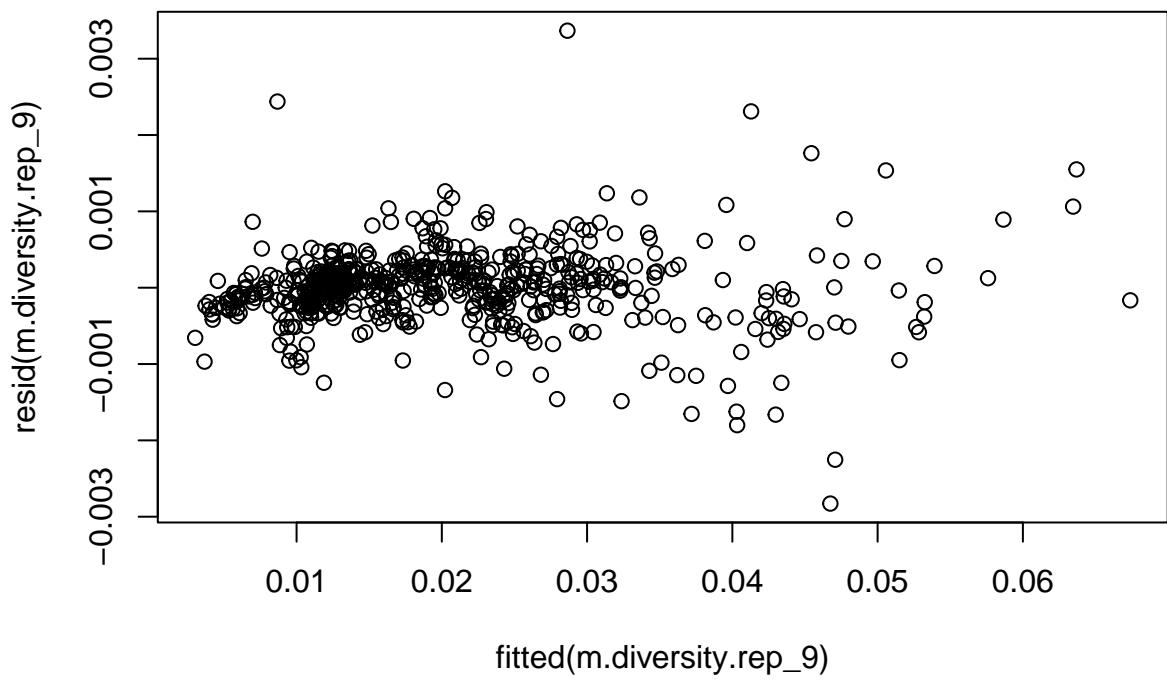
# centering
inf.lands.50kb.rep_9$thetaC <- inf.lands.50kb.rep_9$theta - mean(inf.lands.50kb.rep_9$theta)
inf.lands.50kb.rep_9$tmrcaC <- inf.lands.50kb.rep_9$tmrca - mean(inf.lands.50kb.rep_9$tmrca)
inf.lands.50kb.rep_9$rhoC <- inf.lands.50kb.rep_9$rho - mean(inf.lands.50kb.rep_9$rho)

inf.lands.50kb.rep_9$bin <- 1:nrow(inf.lands.50kb.rep_9)

# for merging:
inf.lands.50kb.rep_9$Replicate <- 9

m.diversity.rep_9 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.50kb.rep_9)

plot(resid(m.diversity.rep_9)~fitted(m.diversity.rep_9))
```

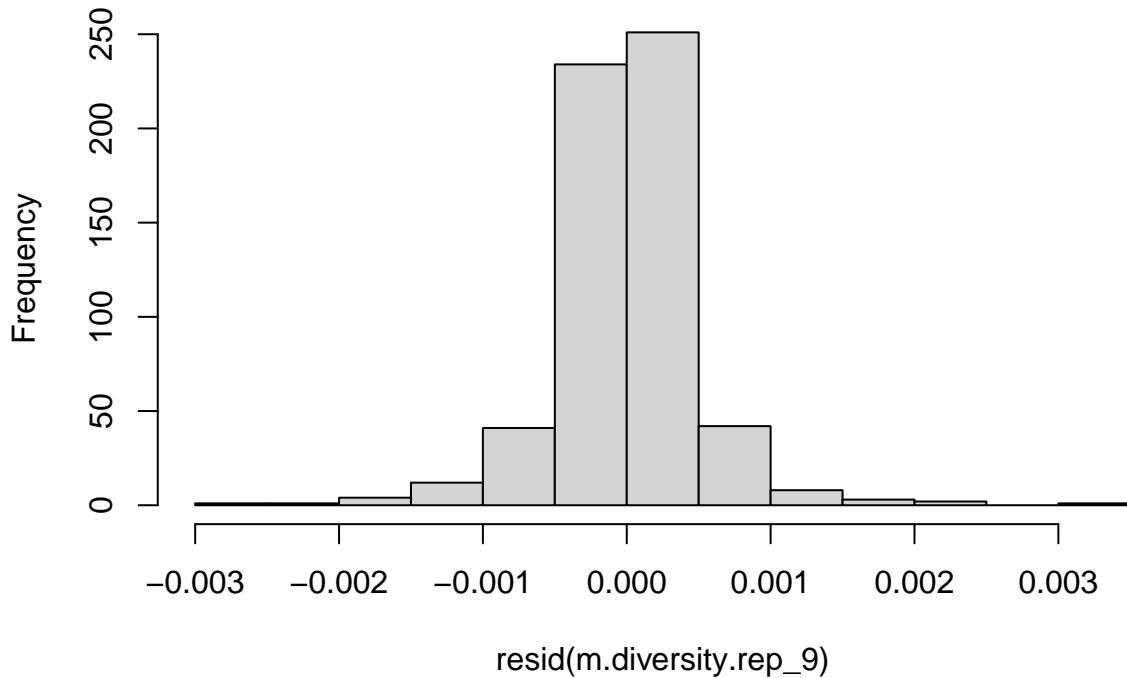


```
dwtest(m.diversity.rep_9)
```

```
##
##  Durbin-Watson test
##
## data: m.diversity.rep_9
## DW = 1.3455, p-value = 2.541e-16
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_9)
```

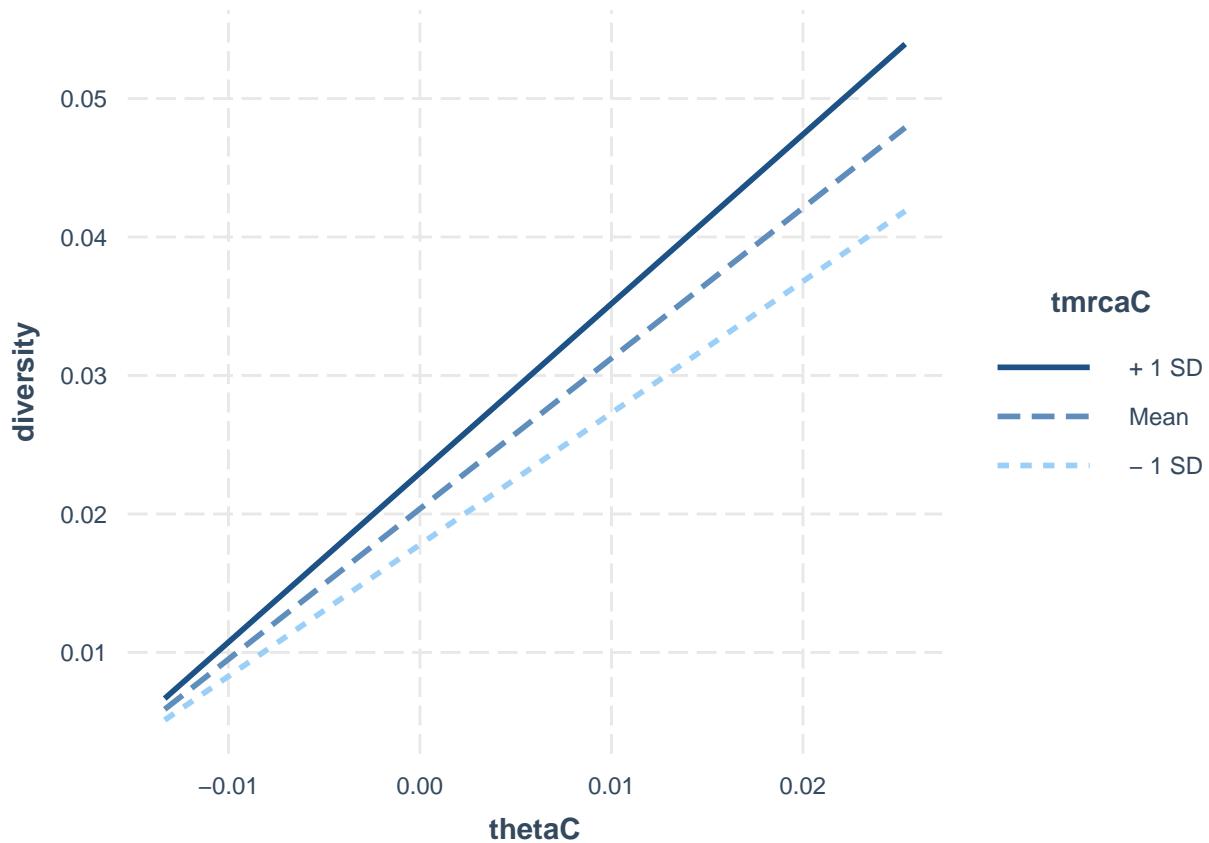
```
##
##  Harrison-McCabe test
##
## data: m.diversity.rep_9
## HMC = 0.52947, p-value = 0.835
hist(resid(m.diversity.rep_9))
```

## Histogram of resid(m.diversity.rep\_9)



```
summary(m.diversity.rep_9)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.50kb.rep_9)
##
## Residuals:
##       Min         1Q      Median         3Q        Max
## -0.0028280 -0.0002274  0.0000078  0.0002235  0.0033670
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.037e-02 2.069e-05 984.748 <2e-16 ***
## thetaC      1.086e+00 2.147e-03 505.918 <2e-16 ***
## rhoC        1.171e-02 1.718e-02  0.682   0.496
## tmrcaC     1.990e-02 1.617e-04 123.090 <2e-16 ***
## thetaC:tmrcaC 1.045e+00 1.408e-02  74.239 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0005043 on 595 degrees of freedom
## Multiple R-squared:  0.998, Adjusted R-squared:  0.998
## F-statistic: 7.306e+04 on 4 and 595 DF,  p-value: < 2.2e-16
interact_plot(m.diversity.rep_9, pred = thetaC, modx= tmrcaC)
```



```
g.rep_9 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
  data = inf.lands.50kb.rep_9, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_9)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep_9
##       AIC     BIC   logLik
##   -7487.186 -7456.408 3750.593
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.412105
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0203835 0.000032571 625.8123 0.0000
## thetaC      1.0864837 0.002863160 379.4701 0.0000
## tmrcaC      0.0194098 0.000164202 118.2072 0.0000
## rhoC        0.0014542 0.015946130   0.0912 0.9274
## thetaC:tmrcaC 0.9860233 0.014806396  66.5944 0.0000
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC      0.003
## tmrcaC     0.001 -0.125
## rhoC       -0.004  0.017  0.041
## thetaC:tmrcaC -0.067 -0.040 -0.014  0.076
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -4.86419788 -0.43551103  0.02063926  0.43146966  6.60989138
##
## Residual standard error: 0.0005120851
## Degrees of freedom: 600 total; 595 residual
vif(g.rep_9)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##      1.018252     1.018249     1.008251     1.008039

g.rep_9.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.50kb.rep_9, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_9.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.50kb.rep_9
##          AIC      BIC    logLik
## -5406.246 -5384.261 2708.123
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.3833499
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0205299 0.00017580 116.77810 0.0000
## thetaC       1.1341848 0.01570929  72.19836 0.0000
## rhoC        -0.1665026 0.09061323  -1.83751 0.0666
##
## Correlation:
##      (Intr) thetaC
## thetaC 0.000
## rhoC   0.001  0.026
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -4.88951873 -0.46241592  0.05059189  0.47484598  6.24257165
##
## Residual standard error: 0.002870881
## Degrees of freedom: 600 total; 597 residual
anova.diversity <- Anova(m.diversity.rep_9)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.50kb[1, 9] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.inf.50kb[2, 9] <- anova.diversity$VarExp[1] * 100
r2.inf.50kb[3, 9] <- anova.diversity$VarExp[2] * 100
r2.inf.50kb[4, 9] <- anova.diversity$VarExp[3] * 100
r2.inf.50kb[5, 9] <- anova.diversity$VarExp[4] * 100
```

### 2.1.10 Replicate 10

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_10/rs.pair_10.", sep = "")
pi.50kb <- read.table(paste(p, "diversity.50kb.bedgraph", sep = ""), header = T)
pi.50kb$avg <- apply(pi.50kb[4:ncol(pi.50kb)], 1, mean)
tmrca.50kb <- read.table(paste(p, "TMRCAs.50kb.bedgraph", sep = ""), header = T)
tmrca.50kb$avg <- apply(tmrca.50kb[4:ncol(tmrca.50kb)], 1, mean)
rho.50kb <- read.table(paste(p, "rho.50kb.bedgraph", sep = ""), header = T)
theta.50kb <- read.table(paste(p, "theta.50kb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.50kb$sim, theta.50kb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.50kb$sim and theta.50kb$sample_mean
## S = 558257, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9844928

inf.lands.50kb.rep_10 <- as.data.frame(cbind(pi.50kb$avg, theta.50kb$sample_mean, rho.50kb$sample_mean,
names(inf.lands.50kb.rep_10) <- c("diversity", "theta", "rho", "tmrca")

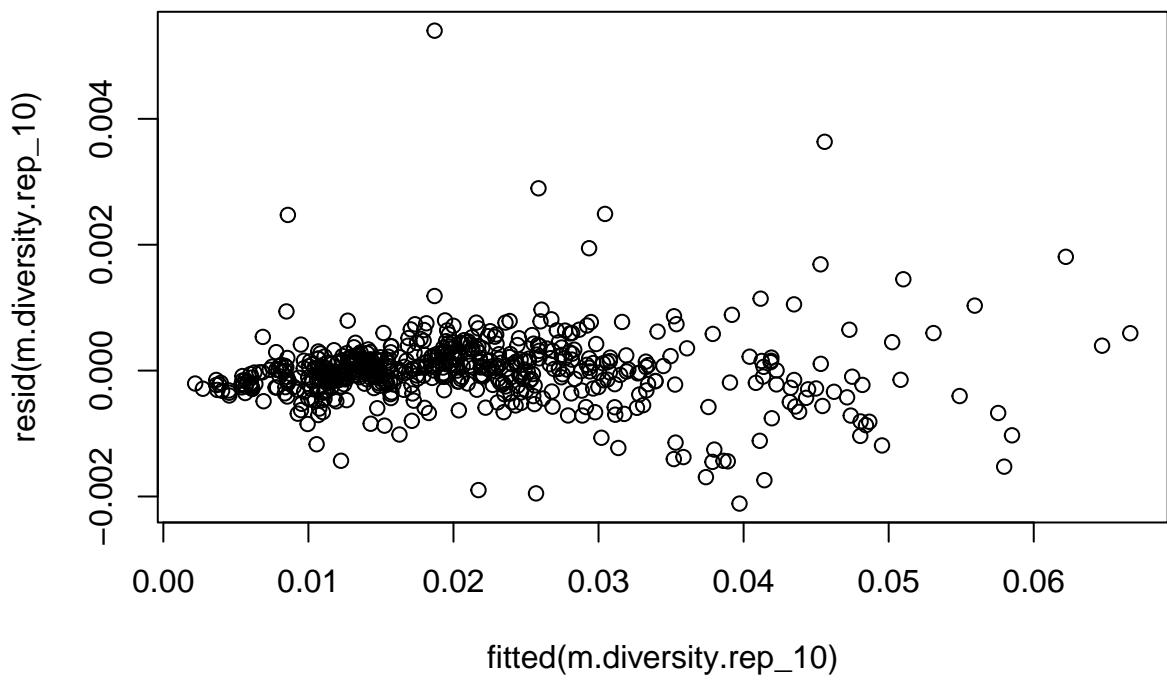
# centering
inf.lands.50kb.rep_10$thetaC <- inf.lands.50kb.rep_10$theta - mean(inf.lands.50kb.rep_10$theta)
inf.lands.50kb.rep_10$tmrcaC <- inf.lands.50kb.rep_10$tmrca - mean(inf.lands.50kb.rep_10$tmrca)
inf.lands.50kb.rep_10$rhoC <- inf.lands.50kb.rep_10$rho - mean(inf.lands.50kb.rep_10$rho)

inf.lands.50kb.rep_10$bin <- 1:nrow(inf.lands.50kb.rep_10)

# for merging:
inf.lands.50kb.rep_10$Replicate <- 10

m.diversity.rep_10 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.50kb.rep_10)

plot(resid(m.diversity.rep_10)~fitted(m.diversity.rep_10))
```

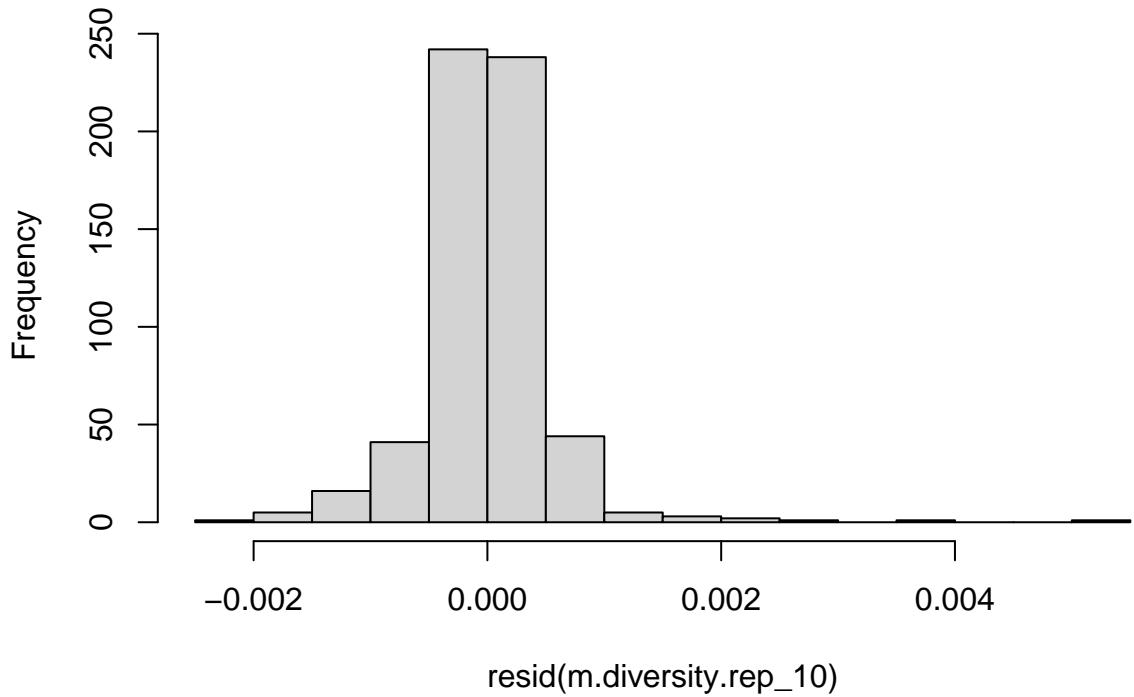


```
dwttest(m.diversity.rep_10)
```

```
##
## Durbin-Watson test
##
## data: m.diversity.rep_10
## DW = 1.3449, p-value = 2.3e-16
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_10)
```

```
##
## Harrison-McCabe test
##
## data: m.diversity.rep_10
## HMC = 0.67092, p-value = 1
hist(resid(m.diversity.rep_10))
```

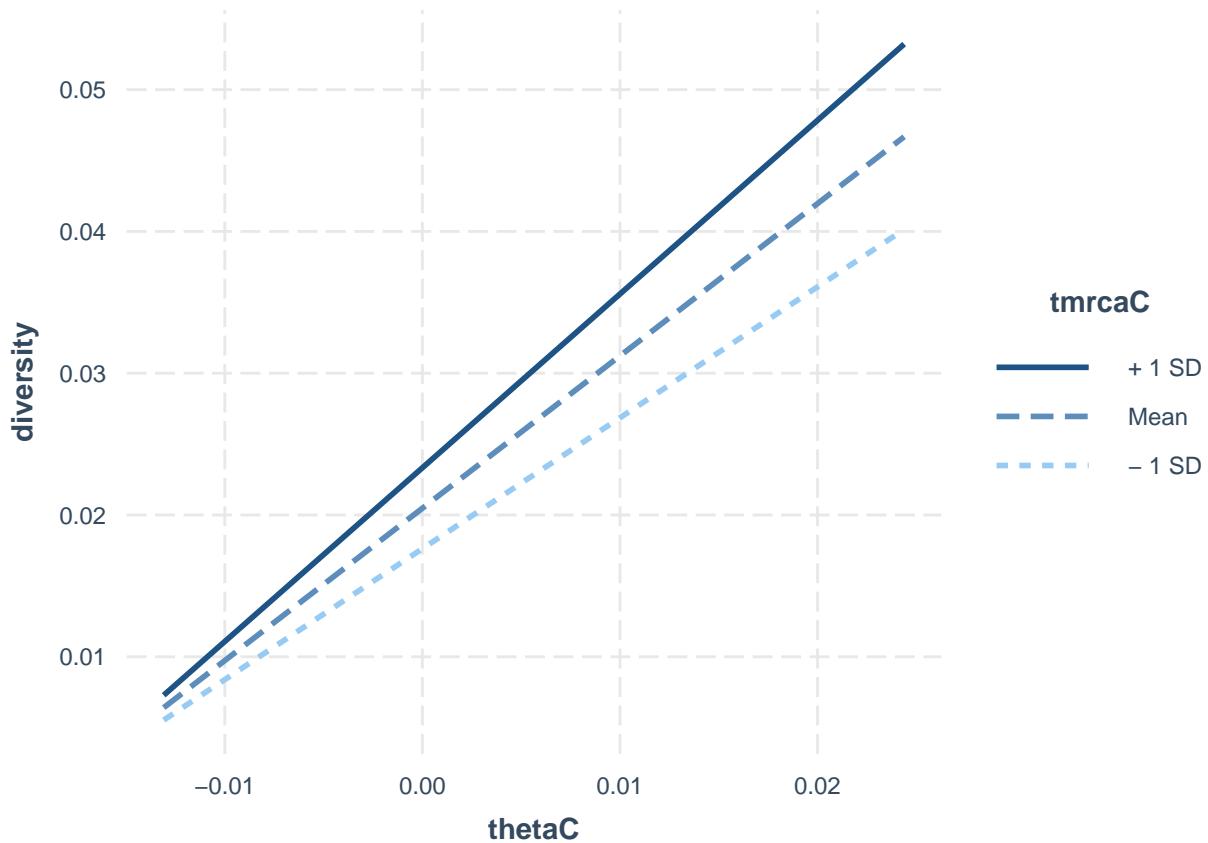
## Histogram of resid(m.diversity.rep\_10)



```
summary(m.diversity.rep_10)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,  
##      data = inf.lands.50kb.rep_10)  
##  
## Residuals:  
##       Min         1Q     Median        3Q       Max  
## -0.0021127 -0.0002121 -0.0000085  0.0001956  0.0054007  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 2.048e-02 2.313e-05 885.243 <2e-16 ***  
## thetaC      1.074e+00 2.407e-03 446.391 <2e-16 ***  
## rhoC       -2.139e-02 1.771e-02 -1.208  0.227  
## tmrcaC      2.070e-02 1.767e-04 117.152 <2e-16 ***  
## thetaC:tmrcaC 1.096e+00 1.562e-02 70.181 <2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.000561 on 595 degrees of freedom  
## Multiple R-squared:  0.9975, Adjusted R-squared:  0.9975  
## F-statistic: 6.053e+04 on 4 and 595 DF,  p-value: < 2.2e-16
```

```
interact_plot(m.diversity.rep_10, pred = thetaC, modx= tmrcaC)
```



```

g.rep_10 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
                  data = inf.lands.50kb.rep_1, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_10)

```

```

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep_1
##          AIC      BIC    logLik
##     -7367.645 -7336.866 3690.822
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.3212747
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0204388 0.000031255 653.9355 0.0000
## thetaC      1.0980191 0.002985790 367.7482 0.0000
## tmrcaC      0.0199958 0.000176128 113.5300 0.0000
## rhoC        0.0035408 0.017040672   0.2078 0.8355
## thetaC:tmrcaC 1.0653107 0.017126226   62.2035 0.0000
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC

```

```

## thetaC      0.010
## tmrcaC     -0.018 -0.155
## rhoC       -0.003  0.009  0.012
## thetaC:tmrcaC -0.096 -0.101  0.181  0.042
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -5.45341396 -0.37367657  0.05022105  0.36056906  6.43069153
##
## Residual standard error: 0.000544344
## Degrees of freedom: 600 total; 595 residual
vif(g.rep_10)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##      1.030576     1.054551    1.001941     1.041465
g.rep_10.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.50kb.rep_10, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_10.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.50kb.rep_10
##          AIC      BIC   logLik
## -5437.978 -5415.994 2723.989
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.4549714
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0207082 0.00019363 106.94544 0.0000
## thetaC       1.1606422 0.01631116  71.15634 0.0000
## rhoC        -0.1660896 0.08076784  -2.05638 0.0402
##
## Correlation:
##      (Intr) thetaC
## thetaC 0.000
## rhoC   0.001  0.000
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -3.86544315 -0.50573567  0.01449108  0.52601610  6.72401413
##
## Residual standard error: 0.002899699
## Degrees of freedom: 600 total; 597 residual
anova.diversity <- Anova(m.diversity.rep_10)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```

r2.inf.50kb[1, 10] <- anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]
r2.inf.50kb[2, 10] <- anova.diversity$VarExp[1] * 100
r2.inf.50kb[3, 10] <- anova.diversity$VarExp[2] * 100
r2.inf.50kb[4, 10] <- anova.diversity$VarExp[3] * 100
r2.inf.50kb[5, 10] <- anova.diversity$VarExp[4] * 100

r2.inf.50kb$average <- rowMeans(r2.inf.50kb)
r2.inf.50kb <- transform(r2.inf.50kb, sd=apply(r2.inf.50kb, 1, sd, na.rm = TRUE))

```

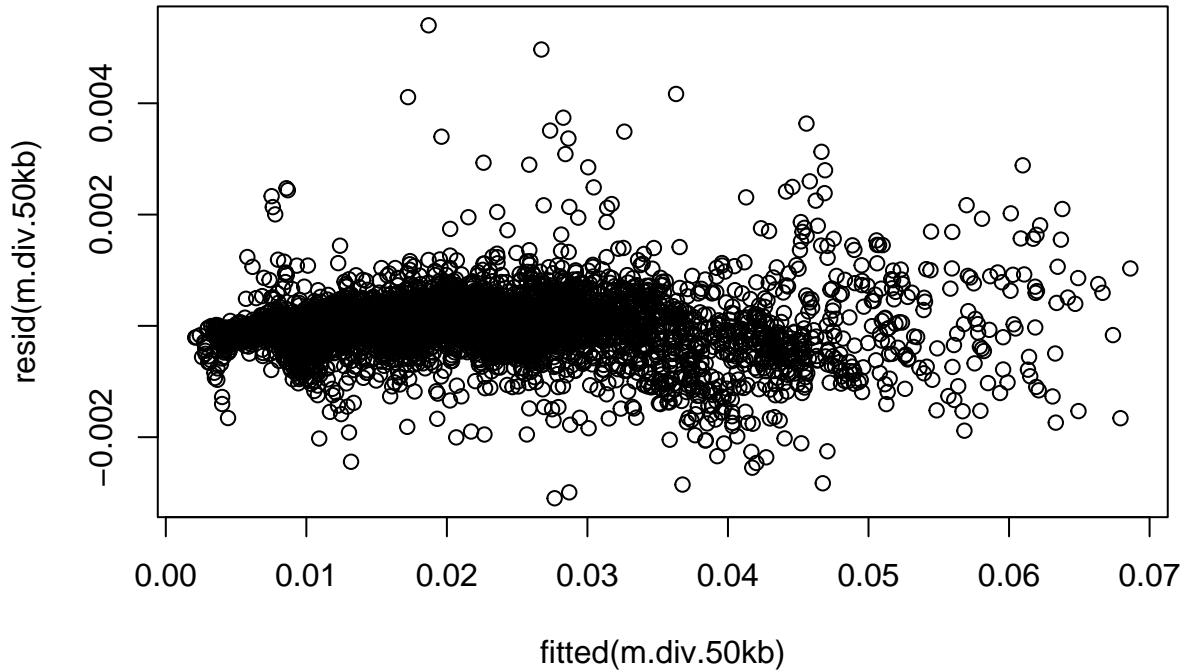
### 2.1.11 all replicates:

```

inf.lands.50kb.all <- rbind(inf.lands.50kb.rep_1, inf.lands.50kb.rep_2, inf.lands.50kb.rep_3, inf.lands.50kb.rep_4)

m.div.50kb <- lm(diversity ~ (thetaC + rhoC + tmrcac + thetaC:tmrcac)*as.factor(Replicate), data = inf.lands.50kb.all)
plot(resid(m.div.50kb)~fitted(m.div.50kb))

```



```

dwtest(m.div.50kb)

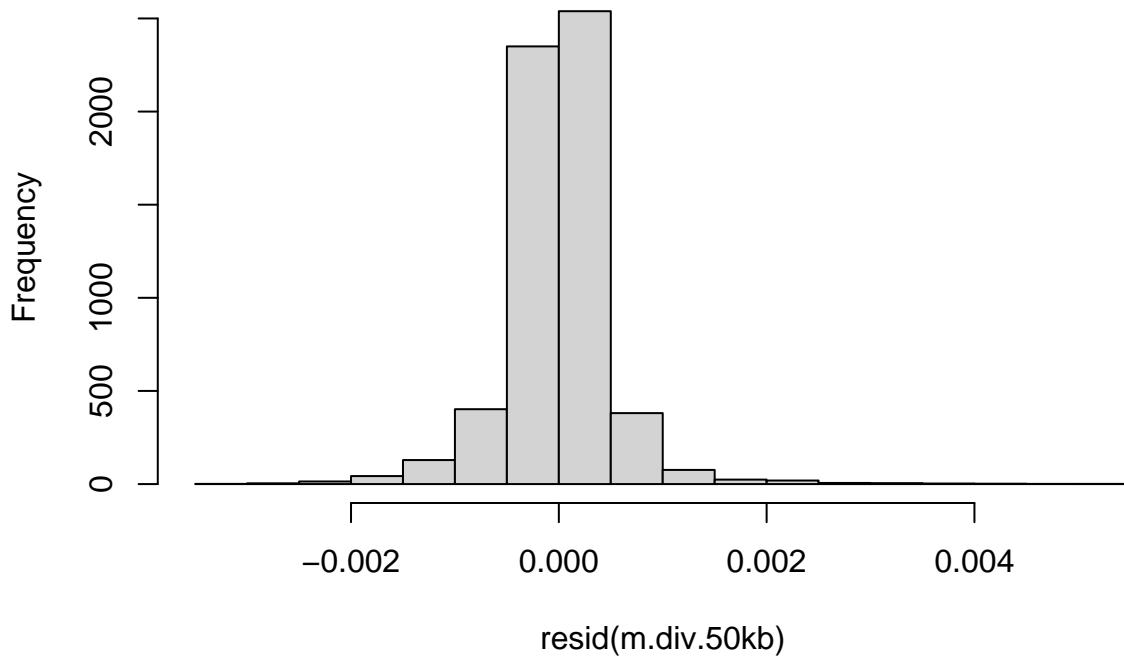
##
##  Durbin-Watson test
##
##  data:  m.div.50kb
##  DW = 1.3249, p-value < 2.2e-16
##  alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)

##
##  Harrison-McCabe test
##
##  data:  m.div.50kb
##  HMC = 0.50366, p-value = 0.658

```

```
hist(resid(m.div.50kb))
```

Histogram of resid(m.div.50kb)



```
m.div.50kb.2 <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC + thetaC:rhoC)*as.factor(Replicate))
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC + thetaC:rhoC + rhoC:tmrcaC)*as.factor(Replicate))
```

```
AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)
```

```
##           df      AIC
## m.div.50kb   51 -73877.32
## m.div.50kb.2 61 -73868.89
## m.div.50kb.3 71 -73992.94
```

```
summary(m.div.50kb)
```

```
##
## Call:
## lm(formula = diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC) *
##       as.factor(Replicate), data = inf.lands.50kb.all)
##
## Residuals:
##      Min        1Q    Median        3Q        Max
## -0.0030973 -0.0002036  0.0000076  0.0002133  0.0054007
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.043e-02 2.101e-05 972.548 < 2e-16 ***
## thetaC      1.096e+00 2.221e-03 493.438 < 2e-16 ***
## rhoC       -4.461e-03 1.650e-02 -0.270 0.786909
## tmrcaC     2.026e-02 1.541e-04 131.441 < 2e-16 ***
## as.factor(Replicate)2 -2.363e-06 2.968e-05 -0.080 0.936530
```

```

## as.factor(Replicate)3      1.266e-04  2.968e-05  4.266  2.02e-05 *** 
## as.factor(Replicate)4      1.793e-04  2.961e-05  6.054  1.50e-09 *** 
## as.factor(Replicate)5      3.524e-05  2.963e-05  1.189  0.234326 
## as.factor(Replicate)6      3.133e-05  2.964e-05  1.057  0.290526 
## as.factor(Replicate)7      3.036e-05  2.964e-05  1.024  0.305728 
## as.factor(Replicate)8      2.651e-04  2.963e-05  8.947  < 2e-16 *** 
## as.factor(Replicate)9      -5.825e-05 2.967e-05 -1.963  0.049696 * 
## as.factor(Replicate)10     4.479e-05  2.975e-05  1.506  0.132197 
## thetaC:tmrcaC             1.100e+00  1.491e-02  73.755 < 2e-16 *** 
## thetaC:as.factor(Replicate)2 -8.685e-03  3.122e-03 -2.782  0.005420 ** 
## thetaC:as.factor(Replicate)3 -1.871e-02  3.093e-03 -6.049  1.54e-09 *** 
## thetaC:as.factor(Replicate)4  2.796e-02  3.119e-03  8.963  < 2e-16 *** 
## thetaC:as.factor(Replicate)5  1.215e-02  3.125e-03  3.889  0.000102 *** 
## thetaC:as.factor(Replicate)6 -1.002e-02  3.094e-03 -3.240  0.001202 ** 
## thetaC:as.factor(Replicate)7 -2.283e-03  3.117e-03 -0.732  0.463905 
## thetaC:as.factor(Replicate)8  1.151e-02  3.113e-03  3.697  0.000220 *** 
## thetaC:as.factor(Replicate)9 -9.252e-03  3.108e-03 -2.977  0.002925 ** 
## thetaC:as.factor(Replicate)10 -2.131e-02  3.120e-03 -6.832  9.20e-12 *** 
## rhoC:as.factor(Replicate)2 -7.206e-03  2.347e-02 -0.307  0.758849 
## rhoC:as.factor(Replicate)3 -9.427e-03  2.345e-02 -0.402  0.687674 
## rhoC:as.factor(Replicate)4 -6.662e-03  2.349e-02 -0.284  0.776732 
## rhoC:as.factor(Replicate)5 -2.473e-03  2.393e-02 -0.103  0.917680 
## rhoC:as.factor(Replicate)6  1.381e-02  2.306e-02  0.599  0.549449 
## rhoC:as.factor(Replicate)7 -3.538e-02  2.343e-02 -1.510  0.131105 
## rhoC:as.factor(Replicate)8 -2.315e-03  2.340e-02 -0.099  0.921183 
## rhoC:as.factor(Replicate)9  1.617e-02  2.398e-02  0.674  0.500029 
## rhoC:as.factor(Replicate)10 -1.693e-02  2.307e-02 -0.734  0.462966 
## tmrcaC:as.factor(Replicate)2 -2.689e-04  2.213e-04 -1.215  0.224342 
## tmrcaC:as.factor(Replicate)3 -1.546e-05  2.144e-04 -0.072  0.942513 
## tmrcaC:as.factor(Replicate)4 -6.536e-04  2.101e-04 -3.111  0.001874 ** 
## tmrcaC:as.factor(Replicate)5 -4.184e-04  2.164e-04 -1.933  0.053249 . 
## tmrcaC:as.factor(Replicate)6 -9.362e-05  2.235e-04 -0.419  0.675348 
## tmrcaC:as.factor(Replicate)7 -4.557e-05  2.224e-04 -0.205  0.837659 
## tmrcaC:as.factor(Replicate)8 -1.258e-04  2.152e-04 -0.584  0.558918 
## tmrcaC:as.factor(Replicate)9 -3.572e-04  2.248e-04 -1.589  0.112145 
## tmrcaC:as.factor(Replicate)10 4.449e-04  2.228e-04  1.997  0.045880 * 
## thetaC:tmrcaC:as.factor(Replicate)2 -3.725e-02  2.033e-02 -1.832  0.067009 . 
## thetaC:tmrcaC:as.factor(Replicate)3 -8.236e-02  1.966e-02 -4.189  2.84e-05 *** 
## thetaC:tmrcaC:as.factor(Replicate)4 -4.519e-02  2.017e-02 -2.241  0.025093 * 
## thetaC:tmrcaC:as.factor(Replicate)5 -3.768e-02  1.986e-02 -1.897  0.057874 . 
## thetaC:tmrcaC:as.factor(Replicate)6 -4.980e-02  2.051e-02 -2.428  0.015191 * 
## thetaC:tmrcaC:as.factor(Replicate)7 -4.418e-02  2.097e-02 -2.107  0.035148 * 
## thetaC:tmrcaC:as.factor(Replicate)8 -2.915e-02  1.990e-02 -1.465  0.142953 
## thetaC:tmrcaC:as.factor(Replicate)9 -5.477e-02  2.063e-02 -2.655  0.007954 ** 
## thetaC:tmrcaC:as.factor(Replicate)10 -3.768e-03  2.060e-02 -0.183  0.854904 
## --- 
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1 
## 
## Residual standard error: 0.0005107 on 5950 degrees of freedom 
## Multiple R-squared:  0.9979, Adjusted R-squared:  0.9979 
## F-statistic: 5.859e+04 on 49 and 5950 DF,  p-value: < 2.2e-16

```

### 2.1.12 Plots

```

scale.3d <- function(x) sprintf("%.3f", x)

rho.plot <- as.data.frame(cbind(inf.lands.50kb.rep_1$bin,
                                sim.rho.50kb$sim,
                                inf.lands.50kb.rep_1$rho,
                                inf.lands.50kb.rep_2$rho,
                                inf.lands.50kb.rep_3$rho,
                                inf.lands.50kb.rep_4$rho,
                                inf.lands.50kb.rep_5$rho,
                                inf.lands.50kb.rep_6$rho,
                                inf.lands.50kb.rep_7$rho,
                                inf.lands.50kb.rep_8$rho,
                                inf.lands.50kb.rep_9$rho,
                                inf.lands.50kb.rep_10$rho))

rho.plot[,3:ncol(rho.plot)] <- 1.53 * rho.plot[,3:ncol(rho.plot)] # scaling because of SCRM NO vs Ne

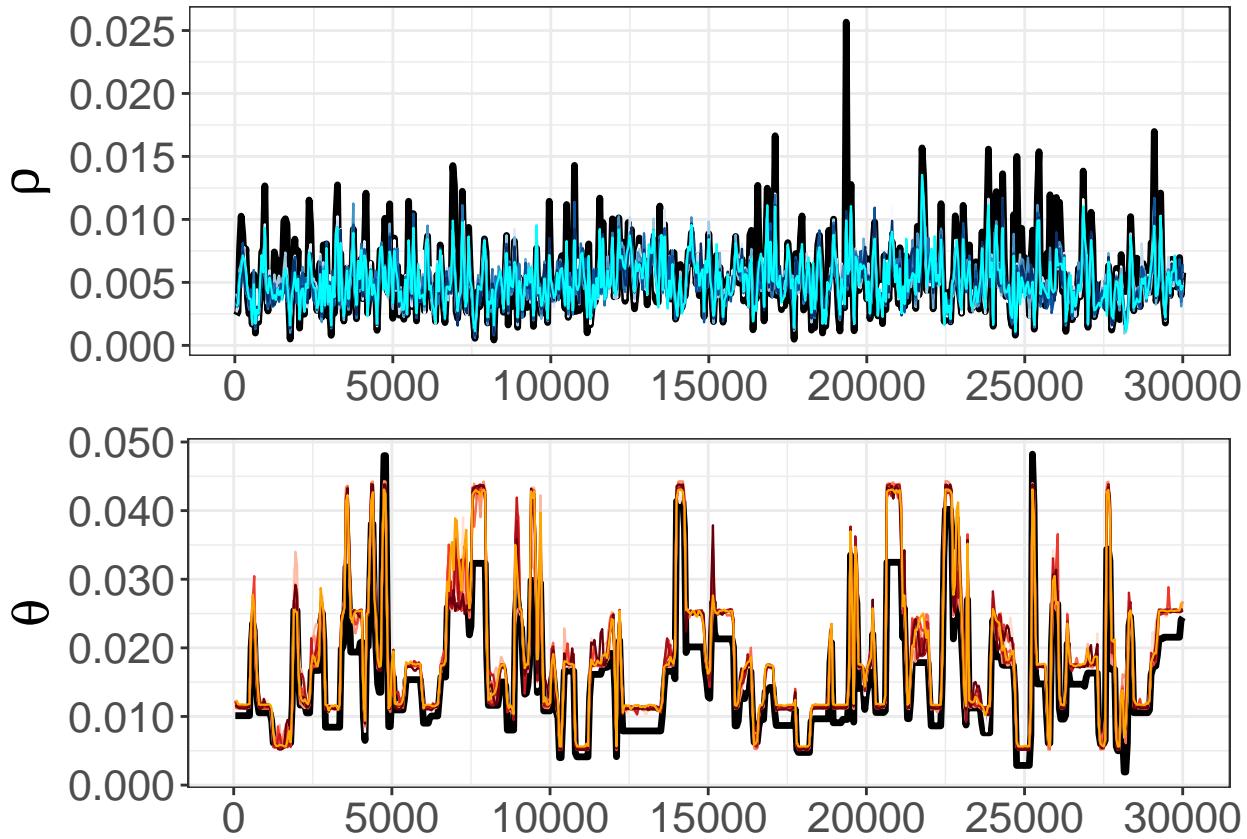
names(rho.plot) <- c("bin", "sim", reps)
molten.rho <- melt(rho.plot, id.vars = "bin")
rho.map.50kb <- ggplot(data = molten.rho, aes(x = bin * 50, y = value, colour = variable)) + theme_bw()
rho.map.50kb <- rho.map.50kb + geom_line(data = molten.rho, aes(size = variable)) + scale_size_manual(values = c("black", brewer.pal(n = 9, name = "Blues")))
rho.map.50kb <- rho.map.50kb + scale_color_manual(values = c("black", brewer.pal(n = 9, name = "Blues")))
rho.map.50kb <- rho.map.50kb + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_breaks())
rho.map.50kb <- rho.map.50kb + labs(title = NULL, x = NULL, y = expression(rho))
rho.map.50kb <- rho.map.50kb + theme(text = element_text(size = 20), axis.title.x = element_text(size = 20))

theta.plot <- as.data.frame(cbind(inf.lands.50kb.rep_1$bin,
                                    sim.theta.50kb$sim,
                                    inf.lands.50kb.rep_1$theta,
                                    inf.lands.50kb.rep_2$theta,
                                    inf.lands.50kb.rep_3$theta,
                                    inf.lands.50kb.rep_4$theta,
                                    inf.lands.50kb.rep_5$theta,
                                    inf.lands.50kb.rep_6$theta,
                                    inf.lands.50kb.rep_7$theta,
                                    inf.lands.50kb.rep_8$theta,
                                    inf.lands.50kb.rep_9$theta,
                                    inf.lands.50kb.rep_10$theta))

names(theta.plot) <- c("bin", "sim", reps)
molten.theta <- melt(theta.plot, id.vars = "bin")
theta.map.50kb <- ggplot(data = molten.theta, aes(x = bin * 50, y = value, colour = variable)) + theme_bw()
theta.map.50kb <- theta.map.50kb + geom_line(data = molten.theta, aes(size = variable)) + scale_size_manual(values = c("black", brewer.pal(n = 9, name = "Reds")))
theta.map.50kb <- theta.map.50kb + scale_color_manual(values = c("black", brewer.pal(n = 9, name = "Reds")))
theta.map.50kb <- theta.map.50kb + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_breaks())
theta.map.50kb <- theta.map.50kb + labs(title = NULL, x = NULL, y = expression(theta))
theta.map.50kb <- theta.map.50kb + theme(text = element_text(size = 20), axis.title.x = element_text(size = 20))

plot_grid(rho.map.50kb, theta.map.50kb, nrow = 2, ncol = 1)

```



## 2.2 200 kb scale

```
r2.inf.200kb <- as.data.frame(matrix(ncol = nreps, nrow = 5))
row.names(r2.inf.200kb) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
colnames(r2.inf.200kb) <- reps

# sim landscapes
sim.rho.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims/dm.sim.rho.2e+05.txt")
sim.theta.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims/dm.sim.theta.2e+05.txt")
sim.lands.200kb <- as.data.frame(cbind(sim.theta.200kb$sim, sim.rho.200kb$sim))
names(sim.lands.200kb ) <- c("theta", "rho")
```

### 2.2.1 Replicate 1

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_1/rs.pair_1.", sep = "")
pi.200kb <- read.table(paste(p, "diversity.200kb.bedgraph", sep = ""), header = T)
pi.200kb$avg <- apply(pi.200kb[4:ncol(pi.200kb)], 1, mean)
tmrca.200kb <- read.table(paste(p, "TMRCA.200kb.bedgraph", sep = ""), header = T)
tmrca.200kb$avg <- apply(tmrca.200kb[4:ncol(tmrca.200kb)], 1, mean)
rho.200kb <- read.table(paste(p, "rho.200kb.bedgraph", sep = ""), header = T)
theta.200kb <- read.table(paste(p, "theta.200kb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.200kb$sim, theta.200kb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
```

```

##  

## data: sim.theta.200kb$sim and theta.200kb$sample_mean  

## S = 8264.3, p-value < 2.2e-16  

## alternative hypothesis: true rho is not equal to 0  

## sample estimates:  

## rho  

## 0.9853072  

inf.lands.200kb.rep_1 <- as.data.frame(cbind(pi.200kb$avg, theta.200kb$sample_mean, rho.200kb$sample_mean))  

names(inf.lands.200kb.rep_1) <- c("diversity", "theta", "rho", "tmrca")  

# centering  

inf.lands.200kb.rep_1$thetaC <- inf.lands.200kb.rep_1$theta - mean(inf.lands.200kb.rep_1$theta)  

inf.lands.200kb.rep_1$tmrcaC <- inf.lands.200kb.rep_1$tmrca - mean(inf.lands.200kb.rep_1$tmrca)  

inf.lands.200kb.rep_1$rhoC <- inf.lands.200kb.rep_1$rho - mean(inf.lands.200kb.rep_1$rho)  

inf.lands.200kb.rep_1$bin <- 1:nrow(inf.lands.200kb.rep_1)  

# for merging:  

inf.lands.200kb.rep_1$Replicate <- 1  

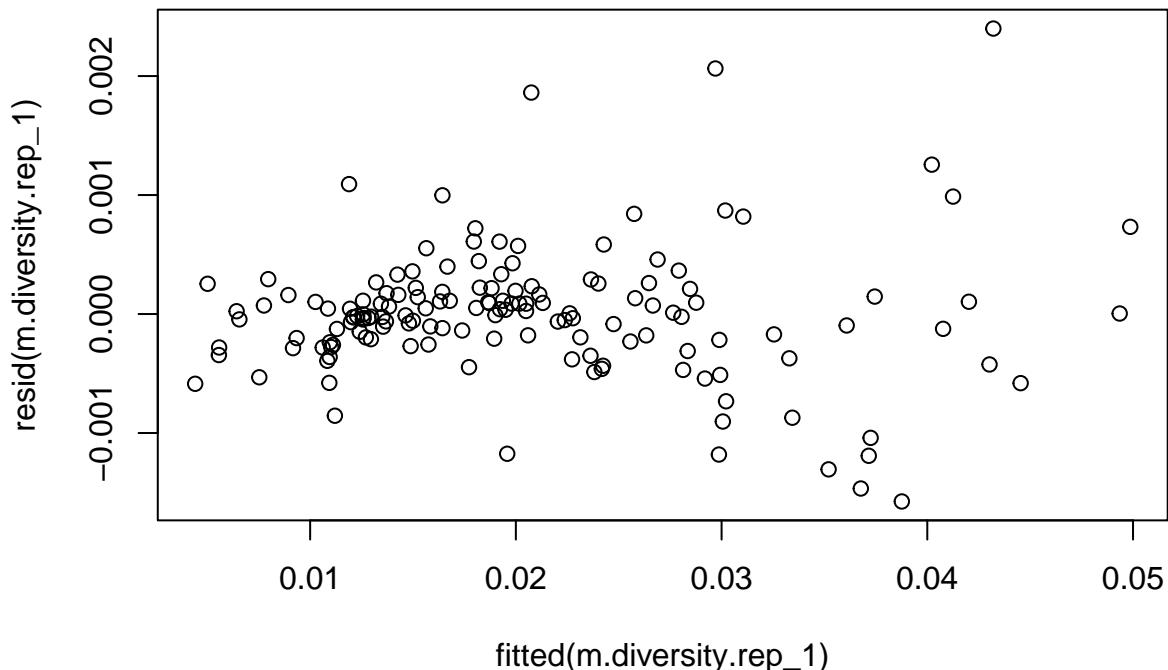
  

m.diversity.rep_1 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.200kb.rep_1)  

plot(resid(m.diversity.rep_1)~fitted(m.diversity.rep_1))

```



```

dwtest(m.diversity.rep_1)
  

##  

## Durbin-Watson test  

##  

## data: m.diversity.rep_1  

## DW = 1.8429, p-value = 0.1407  

## alternative hypothesis: true autocorrelation is greater than 0

```

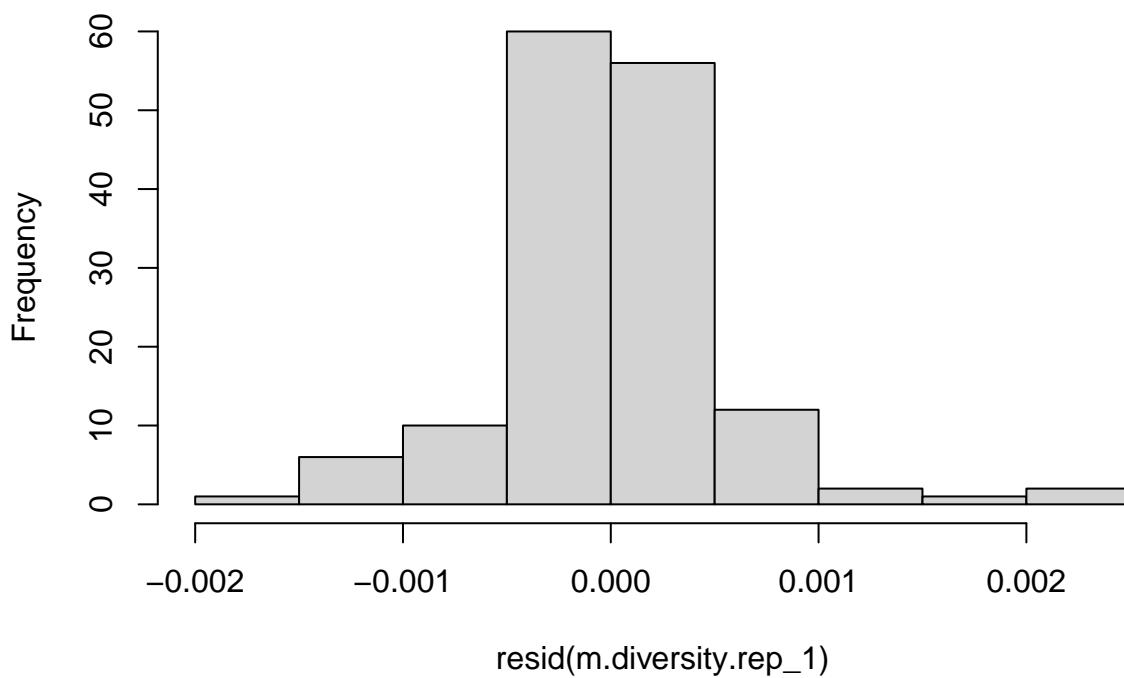
```

hmctest(m.diversity.rep_1)

##
##  Harrison-McCabe test
##
## data: m.diversity.rep_1
## HMC = 0.49224, p-value = 0.444
hist(resid(m.diversity.rep_1))

```

### Histogram of resid(m.diversity.rep\_1)



```
summary(m.diversity.rep_1)
```

```

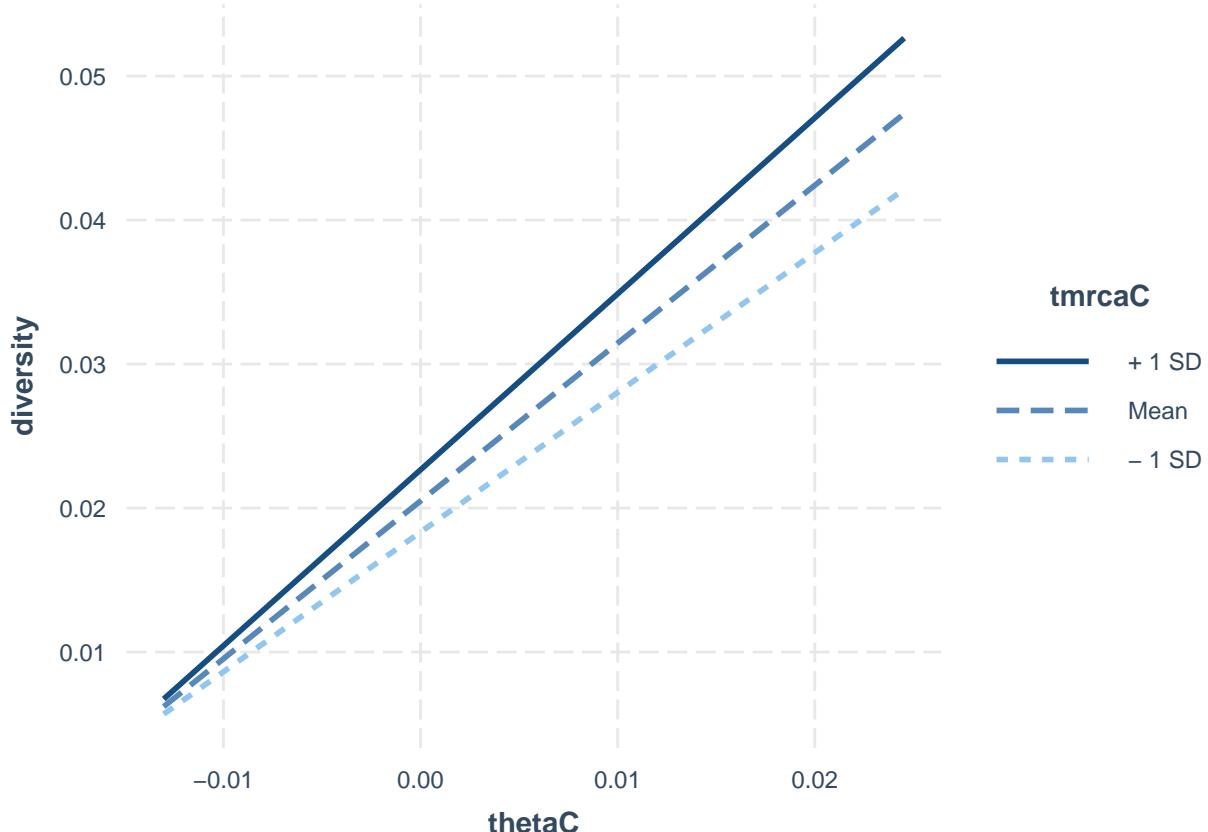
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##      data = inf.lands.200kb.rep_1)
##
## Residuals:
##      Min        1Q    Median        3Q       Max
## -1.575e-03 -2.359e-04 -1.035e-05  1.834e-04  2.399e-03
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.049e-02  4.583e-05 447.178 <2e-16 ***
## thetaC      1.096e+00  5.418e-03 202.263 <2e-16 ***
## rhoC        1.426e-02  6.350e-02   0.225   0.823
## tmrcaC     2.103e-02  5.010e-04  41.966 <2e-16 ***
## thetaC:tmrcaC 1.224e+00  5.186e-02  23.595 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

## 
## Residual standard error: 0.0005573 on 145 degrees of freedom
## Multiple R-squared:  0.9968, Adjusted R-squared:  0.9967
## F-statistic: 1.131e+04 on 4 and 145 DF,  p-value: < 2.2e-16
interact_plot(m.diversity.rep_1, pred = thetaC, modx= tmrcaC)

```



```

g.rep_1 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
                 data = inf.lands.200kb.rep_1, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_1)

```

```

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
## Data: inf.lands.200kb.rep_1
##          AIC      BIC    logLik
## -1814.128 -1793.054  914.0641
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##           Phi
## 0.08562895
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0204958 0.00004989 410.8349 0.0000
## thetaC       1.0967285 0.00562895 194.8371 0.0000

```

```

## tmrcaC      0.0210125 0.00050621  41.5092  0.0000
## rhoC        0.0219683 0.06340360   0.3465  0.7295
## thetaC:tmrcaC 1.2110957 0.05322577  22.7539  0.0000
##
## Correlation:
##              (Intr) thetaC tmrcaC rhoC
## thetaC      -0.001
## tmrcaC     -0.043 -0.110
## rhoC        -0.010 -0.009  0.248
## thetaC:tmrcaC -0.113  0.010  0.375  0.090
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -2.94983846 -0.42035716 -0.01013693  0.33115763  4.40016170
##
## Residual standard error: 0.0005481049
## Degrees of freedom: 150 total; 145 residual
vif(g.rep_1)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##      1.015853     1.249427     1.066075     1.167458

g.rep_1.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.200kb.rep_1, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_1.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.200kb.rep_1
##      AIC      BIC logLik
## -1432.216 -1417.163 721.1082
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.2090144
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0206297 0.00020572 100.27847 0.0000
## thetaC      1.1244227 0.02111497  53.25239 0.0000
## rhoC      -0.5711032 0.21962397  -2.60037 0.0103
##
## Correlation:
##          (Intr) thetaC
## thetaC 0.000
## rhoC  0.001  0.015
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -4.46691260 -0.42444799  0.03262027  0.46216734  3.67858710
##

```

```

## Residual standard error: 0.002021045
## Degrees of freedom: 150 total; 147 residual
anova.diversity <- Anova(m.diversity.rep_1)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.inf.200kb[1, 1] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.inf.200kb[2, 1] <- anova.diversity$VarExp[1] * 100
r2.inf.200kb[3, 1] <- anova.diversity$VarExp[2] * 100
r2.inf.200kb[4, 1] <- anova.diversity$VarExp[3] * 100
r2.inf.200kb[5, 1] <- anova.diversity$VarExp[4] * 100

```

## 2.2.2 Replicate 2

```

p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_2/rs.pair_2.", sep = "")
pi.200kb <- read.table(paste(p, "diversity.200kb.bedgraph", sep = ""), header = T)
pi.200kb$avg <- apply(pi.200kb[4:ncol(pi.200kb)], 1, mean)
tmrca.200kb <- read.table(paste(p, "TMRCA.200kb.bedgraph", sep = ""), header = T)
tmrca.200kb$avg <- apply(tmrca.200kb[4:ncol(tmrca.200kb)], 1, mean)
rho.200kb <- read.table(paste(p, "rho.200kb.bedgraph", sep = ""), header = T)
theta.200kb <- read.table(paste(p, "theta.200kb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.200kb$sim, theta.200kb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.200kb$sim and theta.200kb$sample_mean
## S = 6148.2, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9890693

inf.lands.200kb.rep_2 <- as.data.frame(cbind(pi.200kb$avg, theta.200kb$sample_mean, rho.200kb$sample_mean))
names(inf.lands.200kb.rep_2) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.200kb.rep_2$thetaC <- inf.lands.200kb.rep_2$theta - mean(inf.lands.200kb.rep_2$theta)
inf.lands.200kb.rep_2$tmrcaC <- inf.lands.200kb.rep_2$tmrca - mean(inf.lands.200kb.rep_2$tmrca)
inf.lands.200kb.rep_2$rhoC <- inf.lands.200kb.rep_2$rho - mean(inf.lands.200kb.rep_2$rho)

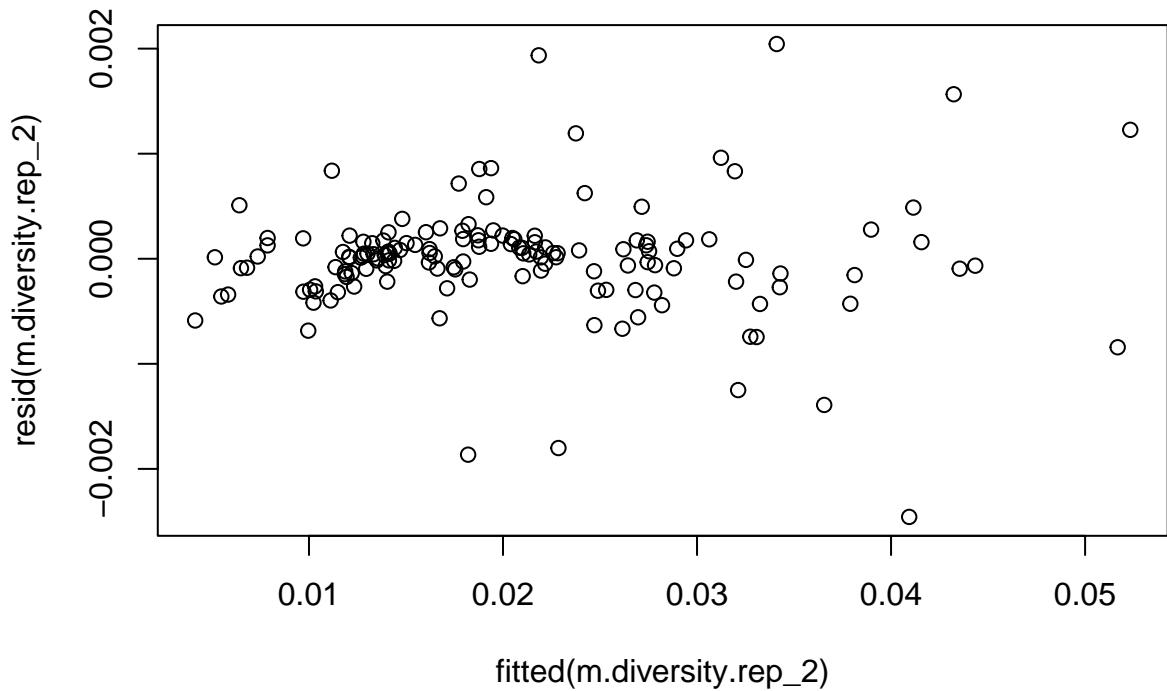
inf.lands.200kb.rep_2$bin <- 1:nrow(inf.lands.200kb.rep_2)

# for merging:
inf.lands.200kb.rep_2$Replicate <- 2

m.diversity.rep_2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.200kb.rep_2)

plot(resid(m.diversity.rep_2)~fitted(m.diversity.rep_2))

```



```

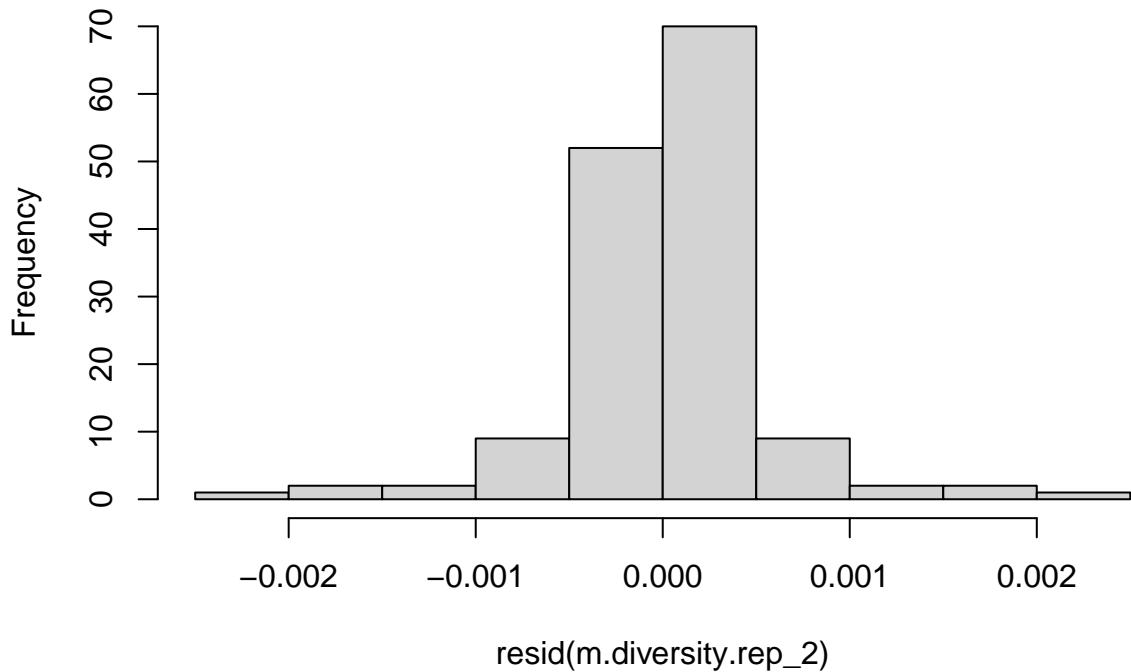
dwtest(m.diversity.rep_2)

##
##  Durbin-Watson test
##
##  data: m.diversity.rep_2
##  DW = 1.7156, p-value = 0.03159
##  alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_2)

##
##  Harrison-McCabe test
##
##  data: m.diversity.rep_2
##  HMC = 0.50531, p-value = 0.555
hist(resid(m.diversity.rep_2))

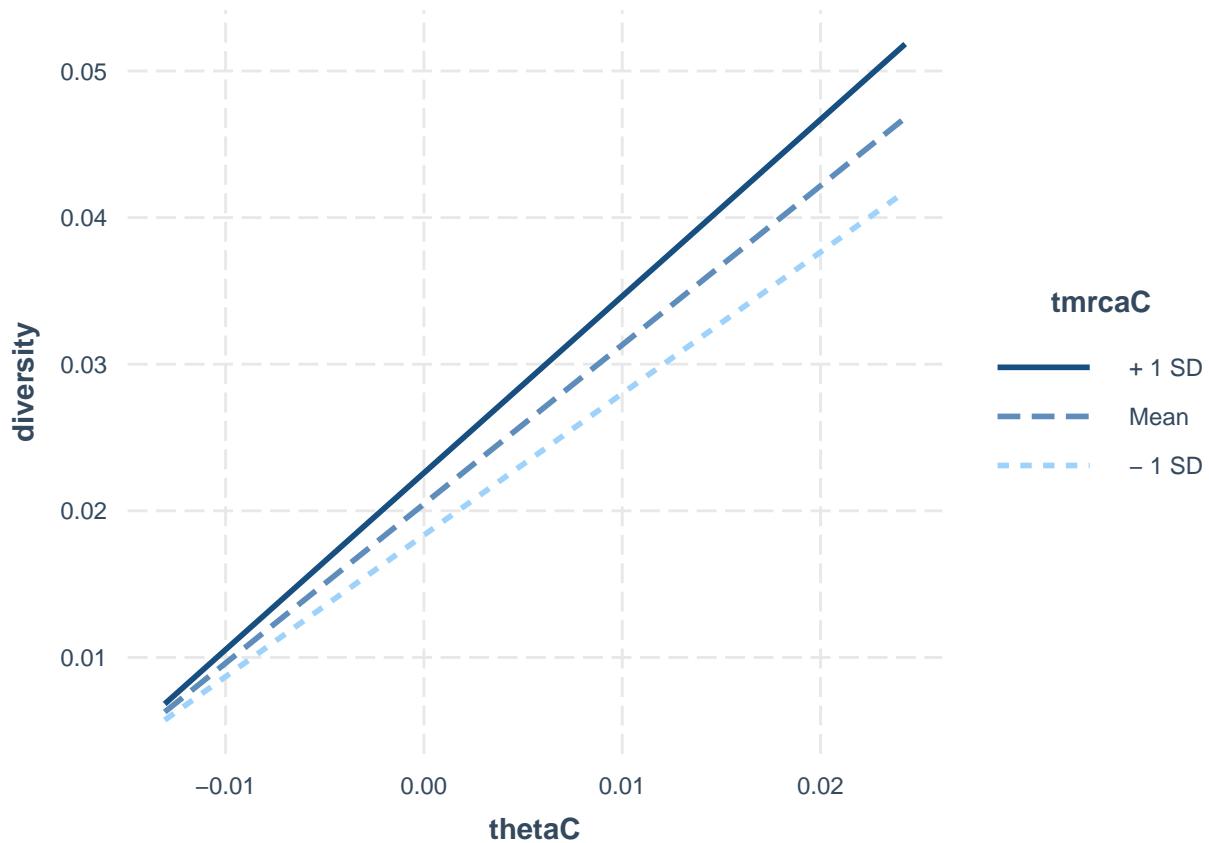
```

## Histogram of resid(m.diversity.rep\_2)



```
summary(m.diversity.rep_2)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##      data = inf.lands.200kb.rep_2)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -2.457e-03 -1.632e-04  2.314e-05  1.700e-04  2.044e-03 
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 2.046e-02 4.515e-05 453.271 <2e-16 ***
## thetaC      1.085e+00 5.297e-03 204.913 <2e-16 ***
## rhoC        9.251e-03 6.537e-02  0.142   0.888  
## tmrcaC      2.050e-02 5.178e-04  39.582 <2e-16 ***
## thetaC:tmrcaC 1.161e+00 4.967e-02  23.381 <2e-16 ***
## ---      
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0005487 on 145 degrees of freedom
## Multiple R-squared:  0.9969, Adjusted R-squared:  0.9968 
## F-statistic: 1.164e+04 on 4 and 145 DF,  p-value: < 2.2e-16
interact_plot(m.diversity.rep_2, pred = thetaC, modx= tmrcaC)
```



```
g.rep_2 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
                 data = inf.lands.200kb.rep_2, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_2)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.200kb.rep_2
##          AIC      BIC    logLik
##     -1821.325 -1800.251  917.6627
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.1654346
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0204681 0.00005329 384.0912 0.0000
## thetaC      1.0868465 0.00566891 191.7207 0.0000
## tmrcaC      0.0204136 0.00053121  38.4284 0.0000
## rhoC        -0.0060738 0.06368644  -0.0954 0.9242
## thetaC:tmrcaC 1.1274440 0.05080579  22.1912 0.0000
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC          0.005
## tmrcaC        -0.054 -0.150
## rhoC          -0.013 -0.022  0.171
## thetaC:tmrcaC -0.108 -0.049  0.491  0.125
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -4.58086608 -0.34056969  0.06376542  0.29976087  3.77133875
##
## Residual standard error: 0.0005405587
## Degrees of freedom: 150 total; 145 residual
vif(g.rep_2)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##      1.023970     1.366753     1.032349     1.320968

g.rep_2.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.200kb.rep_2, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_2.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.200kb.rep_2
##      AIC      BIC    logLik
## -1465.219 -1450.166 737.6095
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.3137584
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0206008 0.00021211 97.12366 0.0000
## thetaC       1.1262748 0.01942595 57.97785 0.0000
## rhoC       -0.3984795 0.20018010 -1.99061 0.0484
##
## Correlation:
##      (Intr) thetaC
## thetaC 0.000
## rhoC   0.002  0.001
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -4.31916797 -0.44159324  0.03266396  0.49987953  3.39180105
##
## Residual standard error: 0.001864311
## Degrees of freedom: 150 total; 147 residual
anova.diversity <- Anova(m.diversity.rep_2)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.200kb[1, 2] <- anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]
r2.inf.200kb[2, 2] <- anova.diversity$VarExp[1] * 100
r2.inf.200kb[3, 2] <- anova.diversity$VarExp[2] * 100
r2.inf.200kb[4, 2] <- anova.diversity$VarExp[3] * 100
r2.inf.200kb[5, 2] <- anova.diversity$VarExp[4] * 100
```

### 2.2.3 Replicate 3

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_3/rs.pair_3.", sep = "")
pi.200kb <- read.table(paste(p, "diversity.200kb.bedgraph", sep = ""), header = T)
pi.200kb$avg <- apply(pi.200kb[4:ncol(pi.200kb)], 1, mean)
tmrca.200kb <- read.table(paste(p, "TMRCA.200kb.bedgraph", sep = ""), header = T)
tmrca.200kb$avg <- apply(tmrca.200kb[4:ncol(tmrca.200kb)], 1, mean)
rho.200kb <- read.table(paste(p, "rho.200kb.bedgraph", sep = ""), header = T)
theta.200kb <- read.table(paste(p, "theta.200kb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.200kb$sim, theta.200kb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.200kb$sim and theta.200kb$sample_mean
## S = 9791.4, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9825924

inf.lands.200kb.rep_3 <- as.data.frame(cbind(pi.200kb$avg, theta.200kb$sample_mean, rho.200kb$sample_mean))
names(inf.lands.200kb.rep_3) <- c("diversity", "theta", "rho", "tmrca")

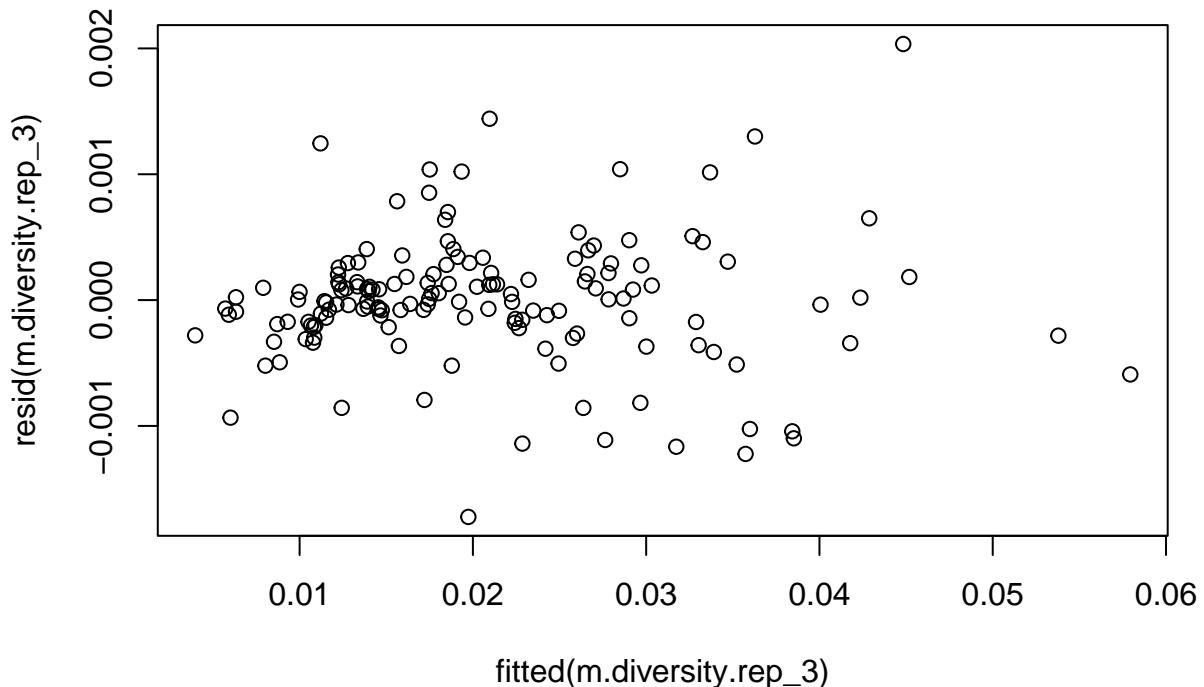
# centering
inf.lands.200kb.rep_3$thetaC <- inf.lands.200kb.rep_3$theta - mean(inf.lands.200kb.rep_3$theta)
inf.lands.200kb.rep_3$tmrcaC <- inf.lands.200kb.rep_3$tmrca - mean(inf.lands.200kb.rep_3$tmrca)
inf.lands.200kb.rep_3$rhoC <- inf.lands.200kb.rep_3$rho - mean(inf.lands.200kb.rep_3$rho)

inf.lands.200kb.rep_3$bin <- 1:nrow(inf.lands.200kb.rep_3)

# for merging:
inf.lands.200kb.rep_3$Replicate <- 3

m.diversity.rep_3 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.200kb.rep_3)

plot(resid(m.diversity.rep_3)~fitted(m.diversity.rep_3))
```



```

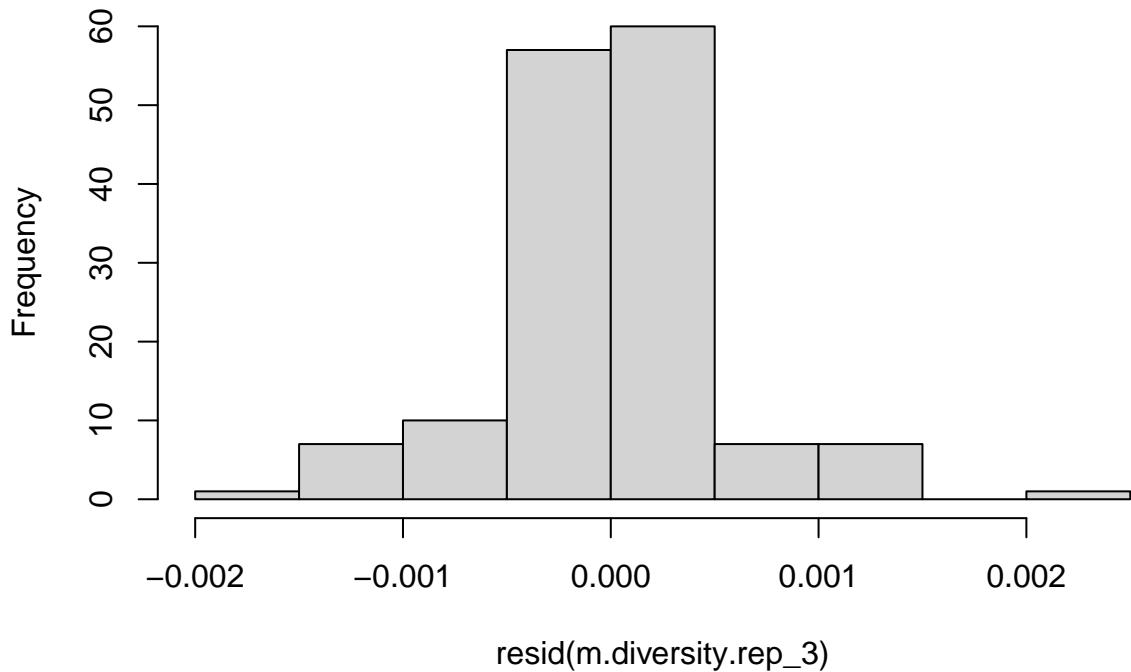
dwtest(m.diversity.rep_3)

##
## Durbin-Watson test
##
## data: m.diversity.rep_3
## DW = 1.7271, p-value = 0.03626
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_3)

##
## Harrison-McCabe test
##
## data: m.diversity.rep_3
## HMC = 0.49269, p-value = 0.437
hist(resid(m.diversity.rep_3))

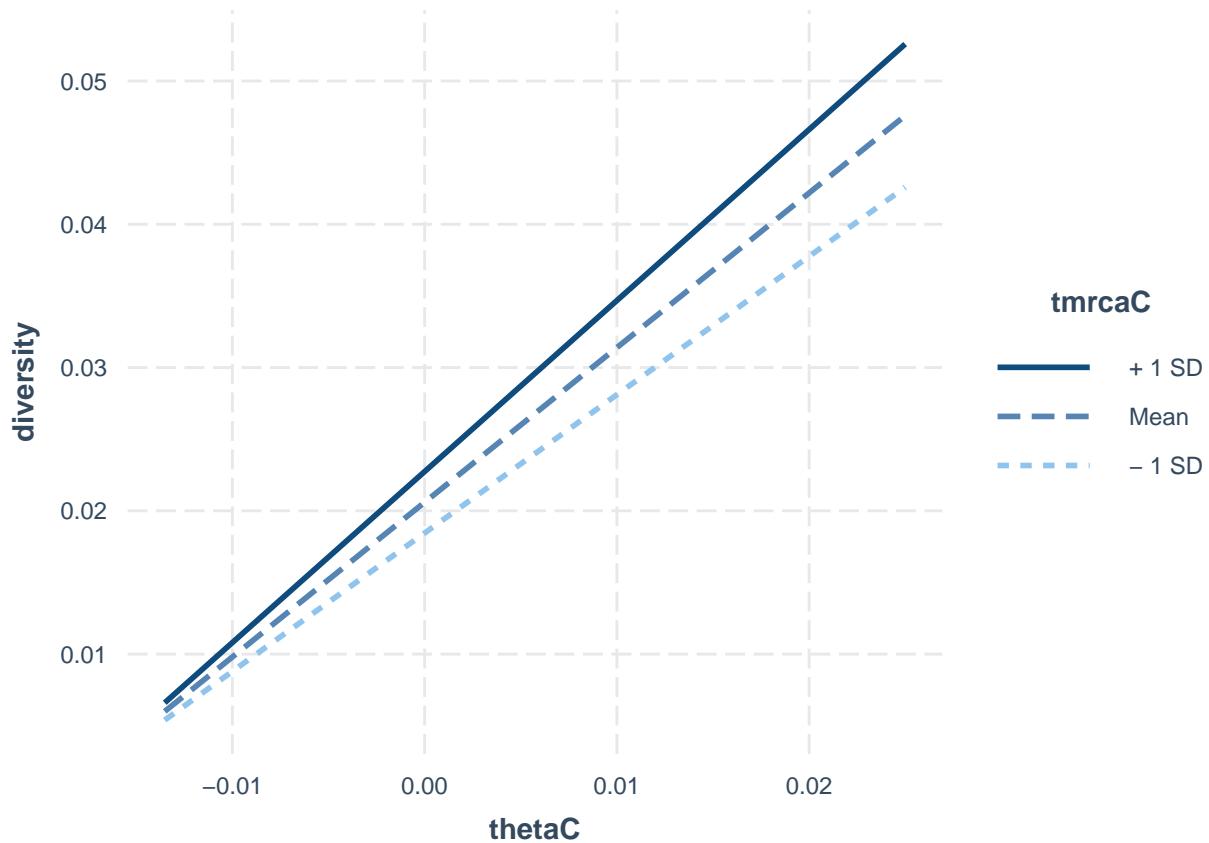
```

## Histogram of resid(m.diversity.rep\_3)



```
summary(m.diversity.rep_3)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,  
##      data = inf.lands.200kb.rep_3)  
##  
## Residuals:  
##       Min        1Q     Median        3Q       Max  
## -1.723e-03 -1.975e-04 -2.090e-06  2.053e-04  2.035e-03  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 2.060e-02 4.271e-05 482.307 <2e-16 ***  
## thetaC      1.079e+00 4.918e-03 219.494 <2e-16 ***  
## rhoC       3.612e-02 6.152e-02   0.587   0.558  
## tmrcaC     2.055e-02 4.262e-04  48.218 <2e-16 ***  
## thetaC:tmrcaC 1.092e+00 3.816e-02  28.629 <2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0005196 on 145 degrees of freedom  
## Multiple R-squared:  0.9974, Adjusted R-squared:  0.9973  
## F-statistic: 1.387e+04 on 4 and 145 DF,  p-value: < 2.2e-16  
interact_plot(m.diversity.rep_3, pred = thetaC, modx= tmrcaC)
```



```
g.rep_3 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
  data = inf.lands.200kb.rep_3, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_3)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.200kb.rep_3
##       AIC      BIC    logLik
##   -1837.259 -1816.184  925.6294
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.1534496
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0206000 0.00004979 413.7691 0.0000
## thetaC      1.0808335 0.00523730 206.3723 0.0000
## tmrcaC     0.0205864 0.00043609  47.2067 0.0000
## rhoC        0.0431677 0.06142122   0.7028 0.4833
## thetaC:tmrcaC 1.0712178 0.03947149  27.1390 0.0000
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC          0.006
## tmrcaC        -0.020 -0.153
## rhoC          -0.009 -0.025  0.167
## thetaC:tmrcaC -0.101 -0.061  0.181  0.089
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -3.38419912 -0.35874981 -0.00849962  0.40321853  4.03279383
##
## Residual standard error: 0.0005116005
## Degrees of freedom: 150 total; 145 residual
vif(g.rep_3)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##     1.025025    1.081264    1.032608    1.039063
g.rep_3.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.200kb.rep_3, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_3.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.200kb.rep_3
##      AIC      BIC logLik
## -1403.367 -1388.314 706.6834
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.2774686
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0207429 0.00024772 83.73477 0.000
## thetaC       1.1273552 0.02313319 48.73324 0.000
## rhoC        -0.5122430 0.25571026 -2.00322 0.047
##
## Correlation:
##      (Intr) thetaC
## thetaC 0.000
## rhoC   0.001  0.003
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -3.57656146 -0.41478403  0.08100049  0.42358182  3.69818275
##
## Residual standard error: 0.002264567
## Degrees of freedom: 150 total; 147 residual
anova.diversity <- Anova(m.diversity.rep_3)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.200kb[1, 3] <- anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]
r2.inf.200kb[2, 3] <- anova.diversity$VarExp[1] * 100
r2.inf.200kb[3, 3] <- anova.diversity$VarExp[2] * 100
r2.inf.200kb[4, 3] <- anova.diversity$VarExp[3] * 100
r2.inf.200kb[5, 3] <- anova.diversity$VarExp[4] * 100
```

## 2.2.4 Replicate 4

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_4/rs.pair_4.", sep = "")
pi.200kb <- read.table(paste(p, "diversity.200kb.bedgraph", sep = ""), header = T)
pi.200kb$avg <- apply(pi.200kb[4:ncol(pi.200kb)], 1, mean)
tmrca.200kb <- read.table(paste(p, "TMRCA.200kb.bedgraph", sep = ""), header = T)
tmrca.200kb$avg <- apply(tmrca.200kb[4:ncol(tmrca.200kb)], 1, mean)
rho.200kb <- read.table(paste(p, "rho.200kb.bedgraph", sep = ""), header = T)
theta.200kb <- read.table(paste(p, "theta.200kb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.200kb$sim, theta.200kb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.200kb$sim and theta.200kb$sample_mean
## S = 9866.4, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.982459

inf.lands.200kb.rep_4 <- as.data.frame(cbind(pi.200kb$avg, theta.200kb$sample_mean, rho.200kb$sample_mean))
names(inf.lands.200kb.rep_4) <- c("diversity", "theta", "rho", "tmrca")

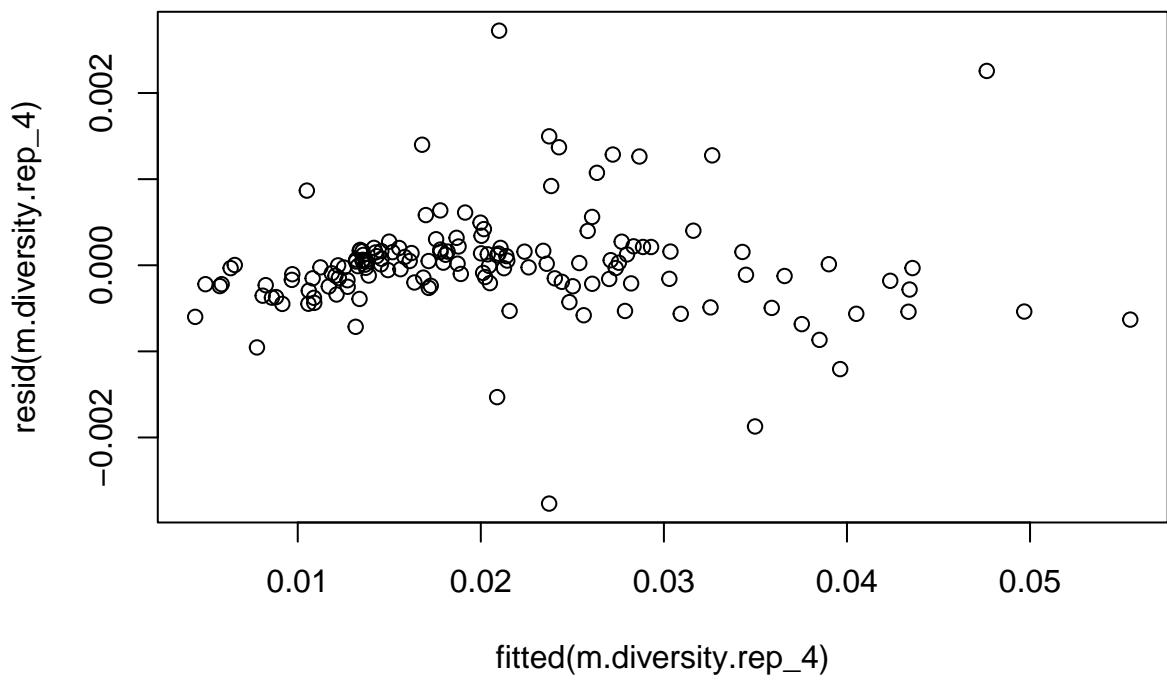
# centering
inf.lands.200kb.rep_4$thetaC <- inf.lands.200kb.rep_4$theta - mean(inf.lands.200kb.rep_4$theta)
inf.lands.200kb.rep_4$tmrcaC <- inf.lands.200kb.rep_4$tmrca - mean(inf.lands.200kb.rep_4$tmrca)
inf.lands.200kb.rep_4$rhoC <- inf.lands.200kb.rep_4$rho - mean(inf.lands.200kb.rep_4$rho)

inf.lands.200kb.rep_4$bin <- 1:nrow(inf.lands.200kb.rep_4)

# for merging:
inf.lands.200kb.rep_4$Replicate <- 4

m.diversity.rep_4 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.200kb.rep_4)

plot(resid(m.diversity.rep_4)~fitted(m.diversity.rep_4))
```

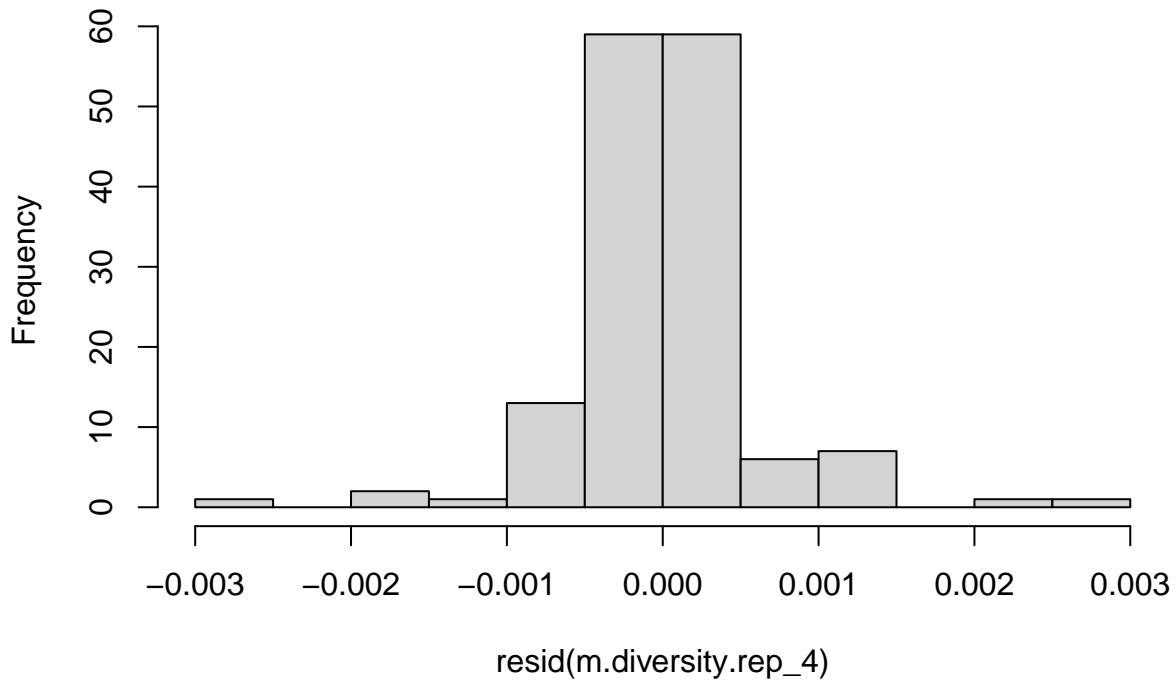


```
dwtest(m.diversity.rep_4)
```

```
##
##  Durbin-Watson test
##
## data: m.diversity.rep_4
## DW = 1.6283, p-value = 0.00823
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_4)
```

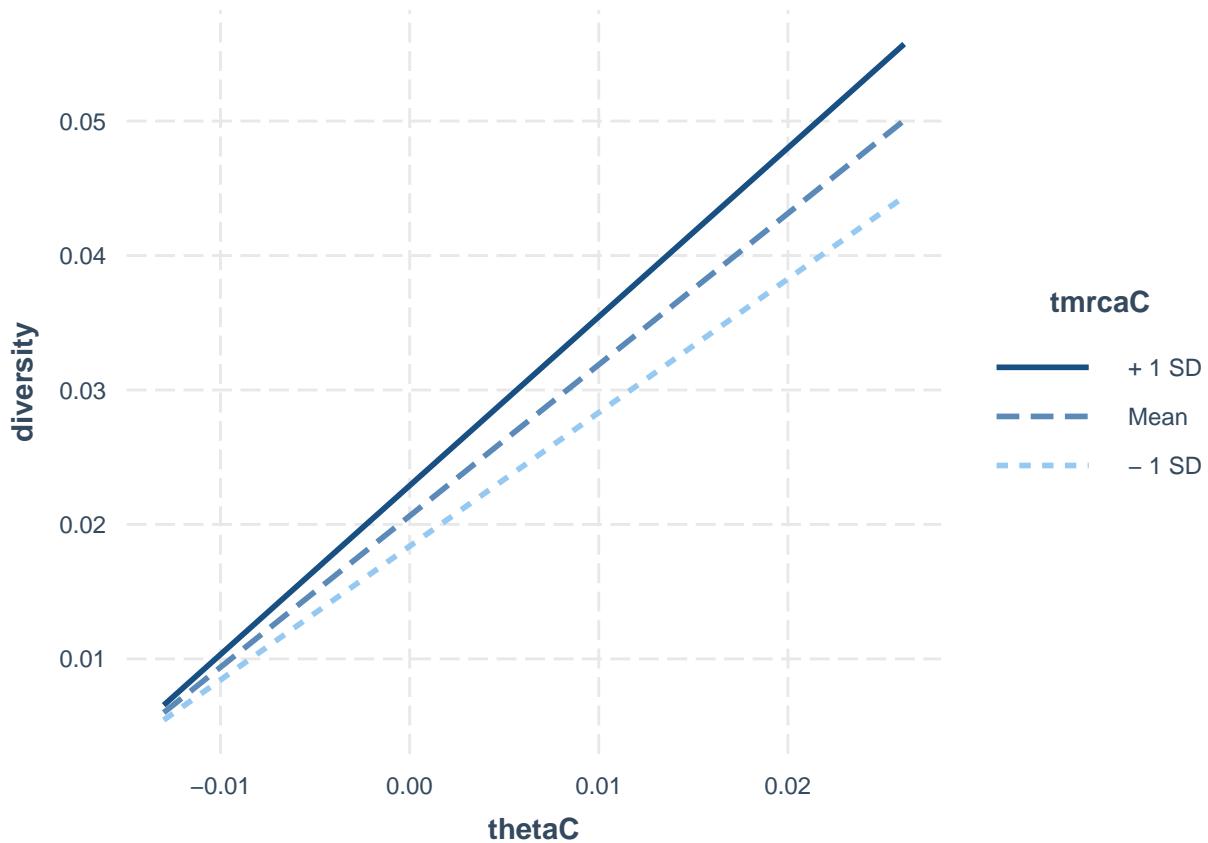
```
##
##  Harrison-McCabe test
##
## data: m.diversity.rep_4
## HMC = 0.54628, p-value = 0.782
hist(resid(m.diversity.rep_4))
```

## Histogram of resid(m.diversity.rep\_4)



```
summary(m.diversity.rep_4)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.200kb.rep_4)
##
## Residuals:
##      Min        1Q    Median        3Q       Max
## -2.768e-03 -2.282e-04 -4.140e-06  1.588e-04  2.724e-03
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.063e-02 4.965e-05 415.535 <2e-16 ***
## thetaC       1.125e+00 5.855e-03 192.138 <2e-16 ***
## rhoC         6.411e-02 7.349e-02   0.872   0.384
## tmrcaC       1.975e-02 4.667e-04  42.319 <2e-16 ***
## thetaC:tmrcaC 1.146e+00 5.168e-02  22.178 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0006075 on 145 degrees of freedom
## Multiple R-squared:  0.9963, Adjusted R-squared:  0.9962
## F-statistic:  9799 on 4 and 145 DF,  p-value: < 2.2e-16
interact_plot(m.diversity.rep_4, pred = thetaC, modx= tmrcaC)
```



```
g.rep_4 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
  data = inf.lands.200kb.rep_4, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_4)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.200kb.rep_4
##       AIC     BIC   logLik
##   -1792.908 -1771.834 903.4542
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.1996946
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0206346 0.00006076 339.6014 0.0000
## thetaC      1.1223743 0.00626603 179.1204 0.0000
## tmrcaC      0.0198270 0.00047759  41.5143 0.0000
## rhoC        0.0706769 0.07071306   0.9995 0.3192
## thetaC:tmrcaC 1.1216837 0.05373238  20.8754 0.0000
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC      -0.003
## tmrcaC     -0.012 -0.039
## rhoC       -0.002  0.018  0.182
## thetaC:tmrcaC -0.040  0.064  0.264  0.027
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -4.63571446 -0.38925930 -0.02298232  0.24825431  4.56473653
##
## Residual standard error: 0.0005980989
## Degrees of freedom: 150 total; 145 residual
vif(g.rep_4)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##      1.008269     1.115533    1.035414     1.081806
g.rep_4.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.200kb.rep_4, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_4.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.200kb.rep_4
##          AIC      BIC  logLik
## -1406.204 -1391.151 708.1021
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.2791937
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0206898 0.00024597 84.11461 0.0000
## thetaC       1.1309856 0.02340816 48.31587 0.0000
## rhoC        -0.4082832 0.24994231 -1.63351 0.1045
##
## Correlation:
##      (Intr) thetaC
## thetaC 0.00
## rhoC   0.00  0.02
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -4.9242575 -0.4591282  0.0538119  0.4694468  4.4837294
##
## Residual standard error: 0.002244411
## Degrees of freedom: 150 total; 147 residual
anova.diversity <- Anova(m.diversity.rep_4)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.200kb[1, 4] <- anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]
r2.inf.200kb[2, 4] <- anova.diversity$VarExp[1] * 100
r2.inf.200kb[3, 4] <- anova.diversity$VarExp[2] * 100
r2.inf.200kb[4, 4] <- anova.diversity$VarExp[3] * 100
r2.inf.200kb[5, 4] <- anova.diversity$VarExp[4] * 100
```

## 2.2.5 Replicate 5

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_5/rs.pair_5.", sep = "")
pi.200kb <- read.table(paste(p, "diversity.200kb.bedgraph", sep = ""), header = T)
pi.200kb$avg <- apply(pi.200kb[4:ncol(pi.200kb)], 1, mean)
tmrca.200kb <- read.table(paste(p, "TMRCA.200kb.bedgraph", sep = ""), header = T)
tmrca.200kb$avg <- apply(tmrca.200kb[4:ncol(tmrca.200kb)], 1, mean)
rho.200kb <- read.table(paste(p, "rho.200kb.bedgraph", sep = ""), header = T)
theta.200kb <- read.table(paste(p, "theta.200kb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.200kb$sim, theta.200kb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.200kb$sim and theta.200kb$sample_mean
## S = 7360.3, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9869145

inf.lands.200kb.rep_5 <- as.data.frame(cbind(pi.200kb$avg, theta.200kb$sample_mean, rho.200kb$sample_mean))
names(inf.lands.200kb.rep_5) <- c("diversity", "theta", "rho", "tmrca")

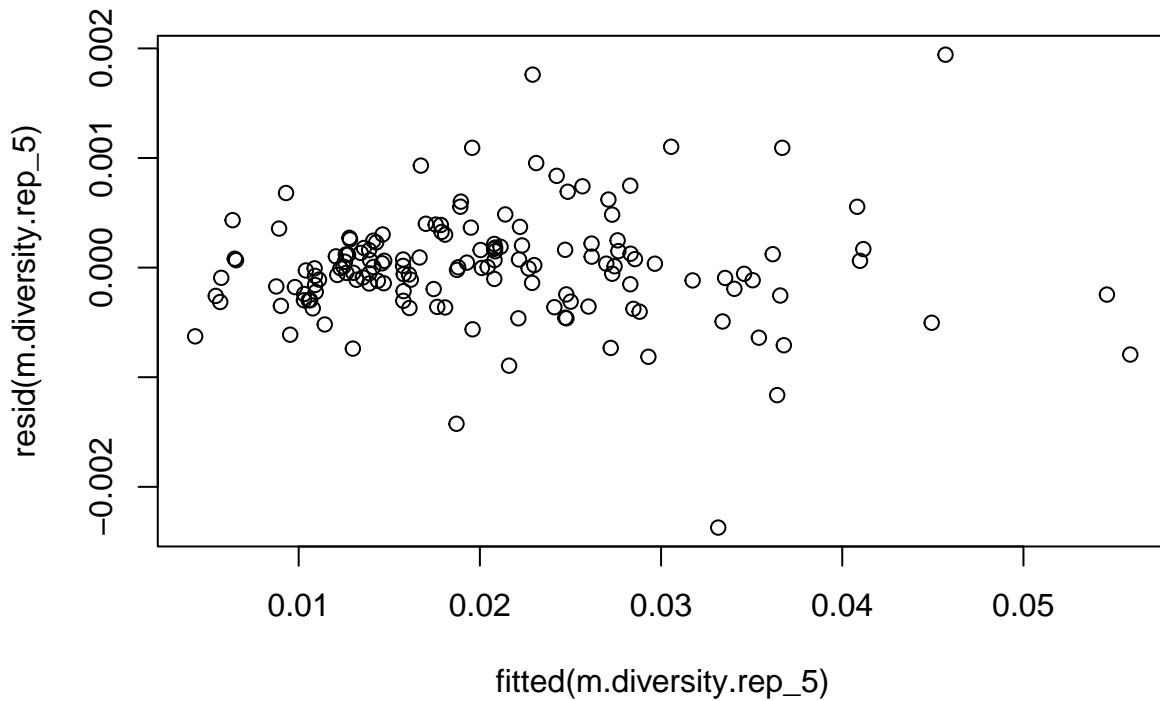
# centering
inf.lands.200kb.rep_5$thetaC <- inf.lands.200kb.rep_5$theta - mean(inf.lands.200kb.rep_5$theta)
inf.lands.200kb.rep_5$tmrcaC <- inf.lands.200kb.rep_5$tmrca - mean(inf.lands.200kb.rep_5$tmrca)
inf.lands.200kb.rep_5$rhoC <- inf.lands.200kb.rep_5$rho - mean(inf.lands.200kb.rep_5$rho)

inf.lands.200kb.rep_5$bin <- 1:nrow(inf.lands.200kb.rep_5)

# for merging:
inf.lands.200kb.rep_5$Replicate <- 5

m.diversity.rep_5 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.200kb.rep_5)

plot(resid(m.diversity.rep_5)~fitted(m.diversity.rep_5))
```

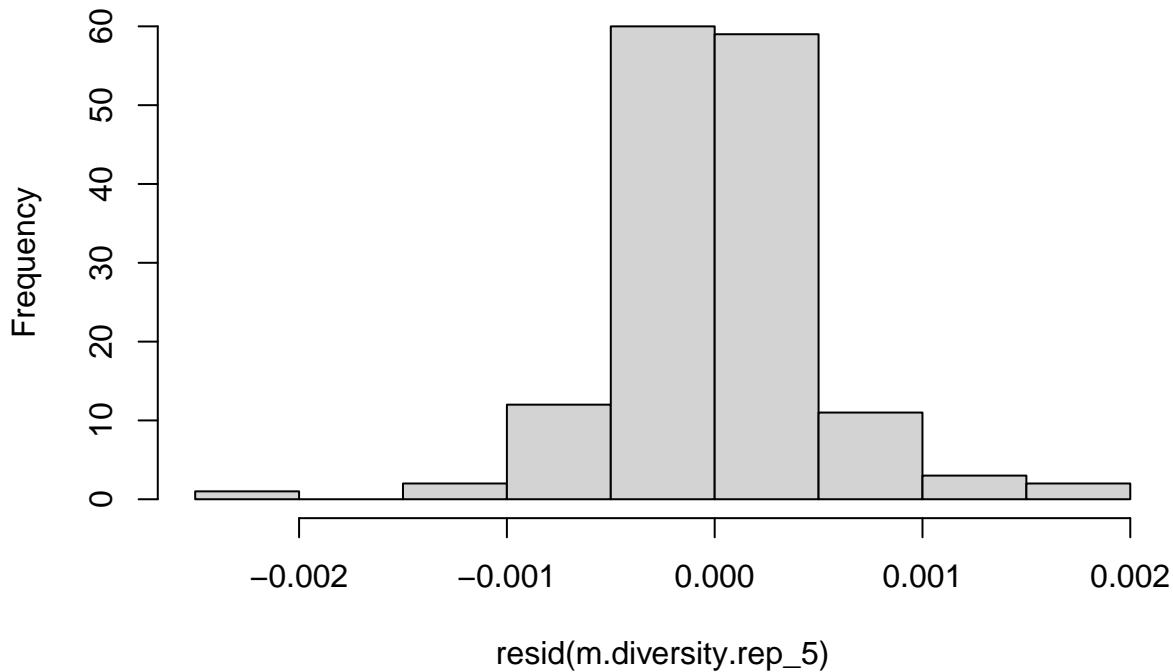


```
dwtest(m.diversity.rep_5)
```

```
##
##  Durbin-Watson test
##
## data: m.diversity.rep_5
## DW = 1.473, p-value = 0.0003904
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_5)
```

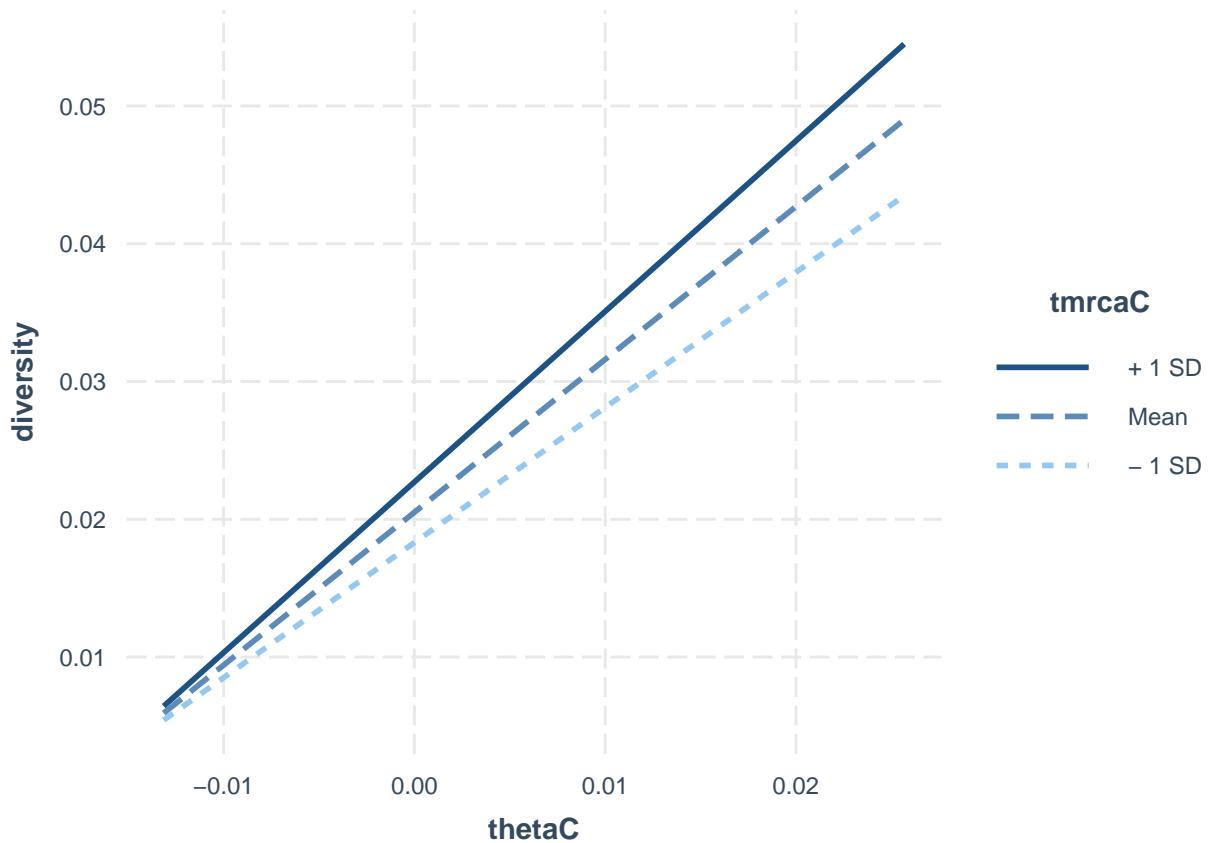
```
##
##  Harrison-McCabe test
##
## data: m.diversity.rep_5
## HMC = 0.42356, p-value = 0.095
hist(resid(m.diversity.rep_5))
```

## Histogram of resid(m.diversity.rep\_5)



```
summary(m.diversity.rep_5)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,  
##      data = inf.lands.200kb.rep_5)  
##  
## Residuals:  
##       Min         1Q     Median        3Q       Max  
## -0.0023718 -0.0002435  0.0000000  0.0001819  0.0019428  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 2.051e-02 4.143e-05 495.020 <2e-16 ***  
## thetaC      1.109e+00 4.896e-03 226.607 <2e-16 ***  
## rhoC        8.631e-02 6.272e-02   1.376  0.171  
## tmrcaC      2.045e-02 4.162e-04  49.148 <2e-16 ***  
## thetaC:tmrcaC 1.199e+00 3.896e-02  30.786 <2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0005067 on 145 degrees of freedom  
## Multiple R-squared:  0.9974, Adjusted R-squared:  0.9973  
## F-statistic: 1.37e+04 on 4 and 145 DF,  p-value: < 2.2e-16  
interact_plot(m.diversity.rep_5, pred = thetaC, modx= tmrcaC)
```



```
g.rep_5 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
                 data = inf.lands.200kb.rep_5, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_5)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.200kb.rep_5
##          AIC      BIC    logLik
## -1853.508 -1832.434  933.7542
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##     Phi
## 0.2890306
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0205091 0.00005581 367.4517 0.0000
## thetaC       1.1068824 0.00529802 208.9238 0.0000
## tmrcaC       0.0206087 0.00042265  48.7607 0.0000
## rhoC         0.0912157 0.06030229   1.5126 0.1325
## thetaC:tmrcaC 1.1670320 0.03885841  30.0329 0.0000
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC      -0.001
## tmrcaC     -0.009 -0.098
## rhoC       -0.006 -0.045  0.198
## thetaC:tmrcaC -0.038  0.025  0.256  0.166
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -4.69081849 -0.45570753 -0.04325154  0.33563272  4.08749773
##
## Residual standard error: 0.0005001316
## Degrees of freedom: 150 total; 145 residual
vif(g.rep_5)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##      1.013524    1.111015    1.057373    1.089764

g.rep_5.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.200kb.rep_5, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_5.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.200kb.rep_5
##          AIC      BIC  logLik
## -1410.762 -1395.709 710.3812
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.2658747
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0205716 0.00023791 86.46709 0.0000
## thetaC       1.1258771 0.02302967 48.88811 0.0000
## rhoC        -0.6236980 0.25913685 -2.40683 0.0173
##
## Correlation:
##      (Intr) thetaC
## thetaC  0.000
## rhoC   0.000 -0.032
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -3.2105114 -0.4827096  0.0393999  0.4735940  3.9755306
##
## Residual standard error: 0.002201973
## Degrees of freedom: 150 total; 147 residual
anova.diversity <- Anova(m.diversity.rep_5)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.200kb[1, 5] <- anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]
r2.inf.200kb[2, 5] <- anova.diversity$VarExp[1] * 100
r2.inf.200kb[3, 5] <- anova.diversity$VarExp[2] * 100
r2.inf.200kb[4, 5] <- anova.diversity$VarExp[3] * 100
r2.inf.200kb[5, 5] <- anova.diversity$VarExp[4] * 100
```

## 2.2.6 Replicate 6

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_6/rs.pair_6.", sep = "")
pi.200kb <- read.table(paste(p, "diversity.200kb.bedgraph", sep = ""), header = T)
pi.200kb$avg <- apply(pi.200kb[4:ncol(pi.200kb)], 1, mean)
tmrca.200kb <- read.table(paste(p, "TMRCA.200kb.bedgraph", sep = ""), header = T)
tmrca.200kb$avg <- apply(tmrca.200kb[4:ncol(tmrca.200kb)], 1, mean)
rho.200kb <- read.table(paste(p, "rho.200kb.bedgraph", sep = ""), header = T)
theta.200kb <- read.table(paste(p, "theta.200kb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.200kb$sim, theta.200kb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.200kb$sim and theta.200kb$sample_mean
## S = 7436.3, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## 0.9867794

inf.lands.200kb.rep_6 <- as.data.frame(cbind(pi.200kb$avg, theta.200kb$sample_mean, rho.200kb$sample_mean))
names(inf.lands.200kb.rep_6) <- c("diversity", "theta", "rho", "tmrca")

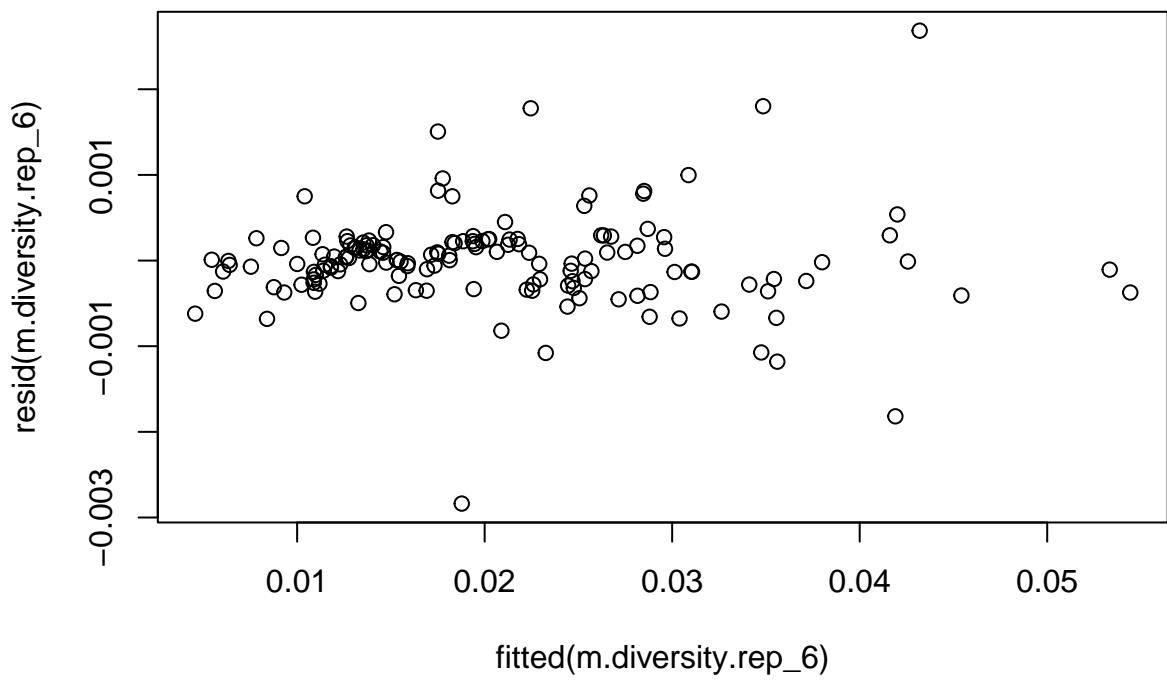
# centering
inf.lands.200kb.rep_6$thetaC <- inf.lands.200kb.rep_6$theta - mean(inf.lands.200kb.rep_6$theta)
inf.lands.200kb.rep_6$tmrcaC <- inf.lands.200kb.rep_6$tmrca - mean(inf.lands.200kb.rep_6$tmrca)
inf.lands.200kb.rep_6$rhoC <- inf.lands.200kb.rep_6$rho - mean(inf.lands.200kb.rep_6$rho)

inf.lands.200kb.rep_6$bin <- 1:nrow(inf.lands.200kb.rep_6)

# for merging:
inf.lands.200kb.rep_6$Replicate <- 6

m.diversity.rep_6 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.200kb.rep_6)

plot(resid(m.diversity.rep_6)~fitted(m.diversity.rep_6))
```

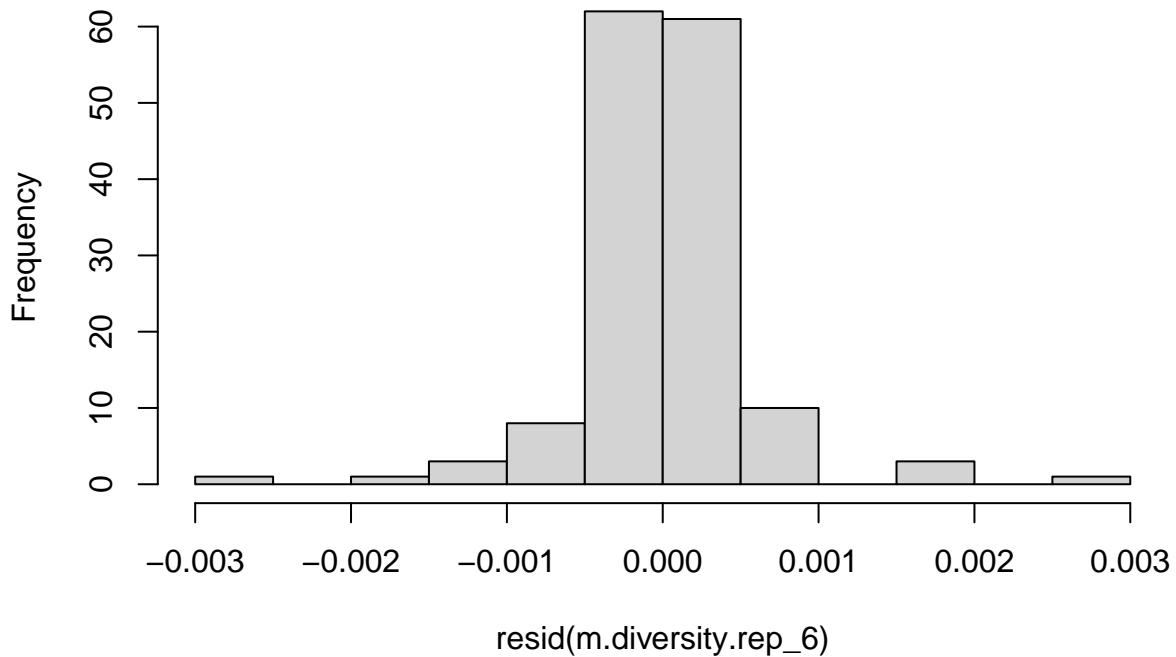


```
dwtest(m.diversity.rep_6)
```

```
##
##  Durbin-Watson test
##
## data: m.diversity.rep_6
## DW = 1.6828, p-value = 0.01928
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_6)
```

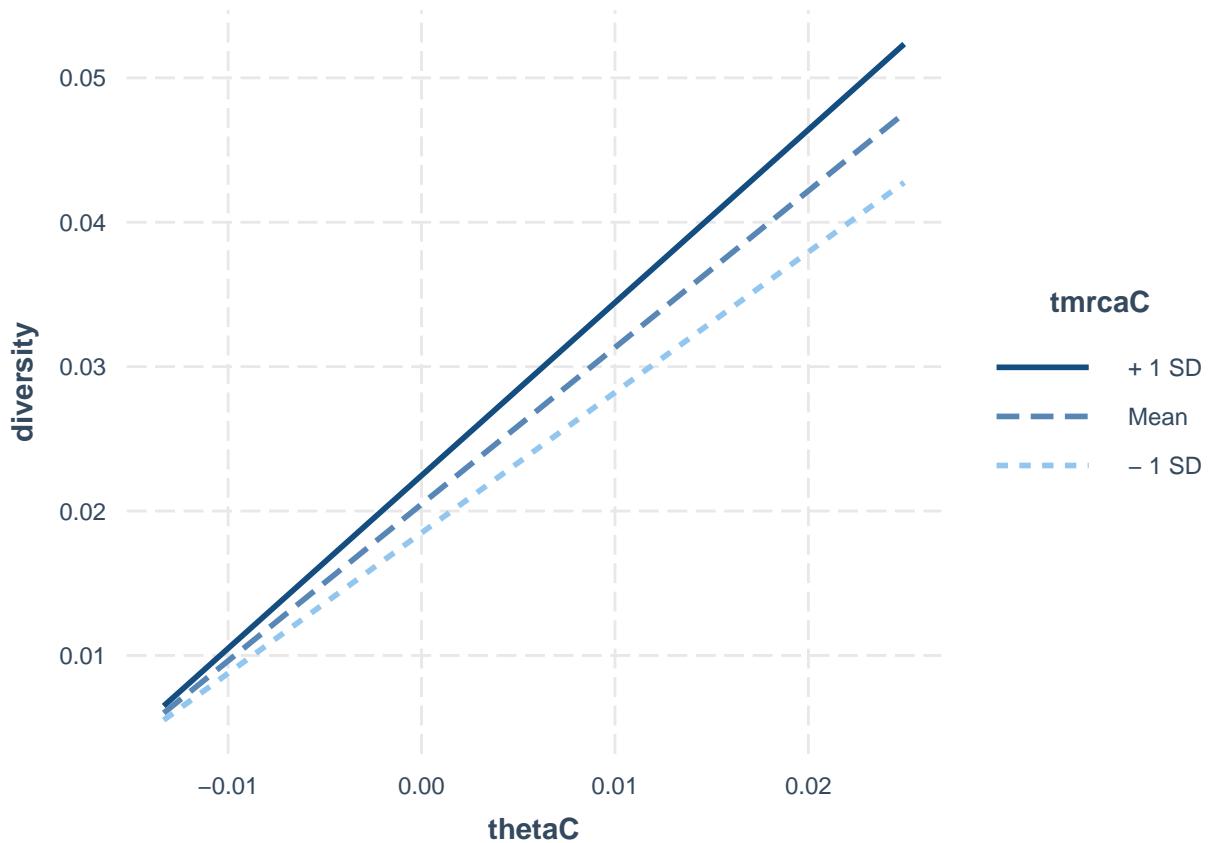
```
##
##  Harrison-McCabe test
##
## data: m.diversity.rep_6
## HMC = 0.48734, p-value = 0.416
hist(resid(m.diversity.rep_6))
```

## Histogram of resid(m.diversity.rep\_6)



```
summary(m.diversity.rep_6)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.200kb.rep_6)
##
## Residuals:
##       Min         1Q      Median         3Q        Max
## -2.837e-03 -2.547e-04  3.600e-07  2.011e-04  2.684e-03
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.048e-02 4.657e-05 439.670 <2e-16 ***
## thetaC      1.085e+00 5.404e-03 200.771 <2e-16 ***
## rhoC        4.915e-02 6.439e-02   0.763   0.447
## tmrcaC      2.024e-02 5.329e-04  37.991 <2e-16 ***
## thetaC:tmrcaC 1.146e+00 4.835e-02  23.708 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.000568 on 145 degrees of freedom
## Multiple R-squared:  0.9967, Adjusted R-squared:  0.9966
## F-statistic: 1.106e+04 on 4 and 145 DF,  p-value: < 2.2e-16
interact_plot(m.diversity.rep_6, pred = thetaC, modx= tmrcaC)
```



```
g.rep_6 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
  data = inf.lands.200kb.rep_6, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_6)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.200kb.rep_6
##       AIC      BIC    logLik
##   -1811.57 -1790.496  912.7851
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.1730188
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0204792 0.00005540 369.6328 0.0000
## thetaC      1.0855830 0.00577130 188.1002 0.0000
## tmrcaC      0.0203230 0.000054805 37.0823 0.0000
## rhoC        0.0441005 0.06334022  0.6962 0.4874
## thetaC:tmrcaC 1.1199378 0.04982885 22.4757 0.0000
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC          0.002
## tmrcaC        -0.023 -0.109
## rhoC          -0.008 -0.005  0.340
## thetaC:tmrcaC -0.080 -0.023  0.278  0.116
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -5.126866241 -0.430648507 -0.002042255  0.325479464  4.863421007
##
## Residual standard error: 0.0005591586
## Degrees of freedom: 150 total; 145 residual
vif(g.rep_6)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##     1.013289    1.224420    1.132487    1.084133

g.rep_6.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.200kb.rep_6, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_6.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.200kb.rep_6
##      AIC      BIC logLik
## -1450.868 -1435.815 730.4341
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.3062371
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0205840 0.00022012 93.51378 0e+00
## thetaC       1.1123598 0.02006909 55.42651 0e+00
## rhoC        -0.7401946 0.19645270 -3.76780 2e-04
##
## Correlation:
##      (Intr) thetaC
## thetaC 0.000
## rhoC   0.002  0.031
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -3.19333658 -0.46017960  0.02519769  0.43441985  3.88632753
##
## Residual standard error: 0.001950655
## Degrees of freedom: 150 total; 147 residual
anova.diversity <- Anova(m.diversity.rep_6)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.200kb[1, 6] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.inf.200kb[2, 6] <- anova.diversity$VarExp[1] * 100
r2.inf.200kb[3, 6] <- anova.diversity$VarExp[2] * 100
r2.inf.200kb[4, 6] <- anova.diversity$VarExp[3] * 100
r2.inf.200kb[5, 6] <- anova.diversity$VarExp[4] * 100
```

## 2.2.7 Replicate 7

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_7/rs.pair_7.", sep = "")
pi.200kb <- read.table(paste(p, "diversity.200kb.bedgraph", sep = ""), header = T)
pi.200kb$avg <- apply(pi.200kb[4:ncol(pi.200kb)], 1, mean)
tmrca.200kb <- read.table(paste(p, "TMRCA.200kb.bedgraph", sep = ""), header = T)
tmrca.200kb$avg <- apply(tmrca.200kb[4:ncol(tmrca.200kb)], 1, mean)
rho.200kb <- read.table(paste(p, "rho.200kb.bedgraph", sep = ""), header = T)
theta.200kb <- read.table(paste(p, "theta.200kb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.200kb$sim, theta.200kb$sample_mean, method = "spearman")

## Warning in cor.test.default(sim.theta.200kb$sim, theta.200kb$sample_mean, :
## Cannot compute exact p-value with ties

##
## Spearman's rank correlation rho
##
## data: sim.theta.200kb$sim and theta.200kb$sample_mean
## S = 7134.3, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## 0.9873163

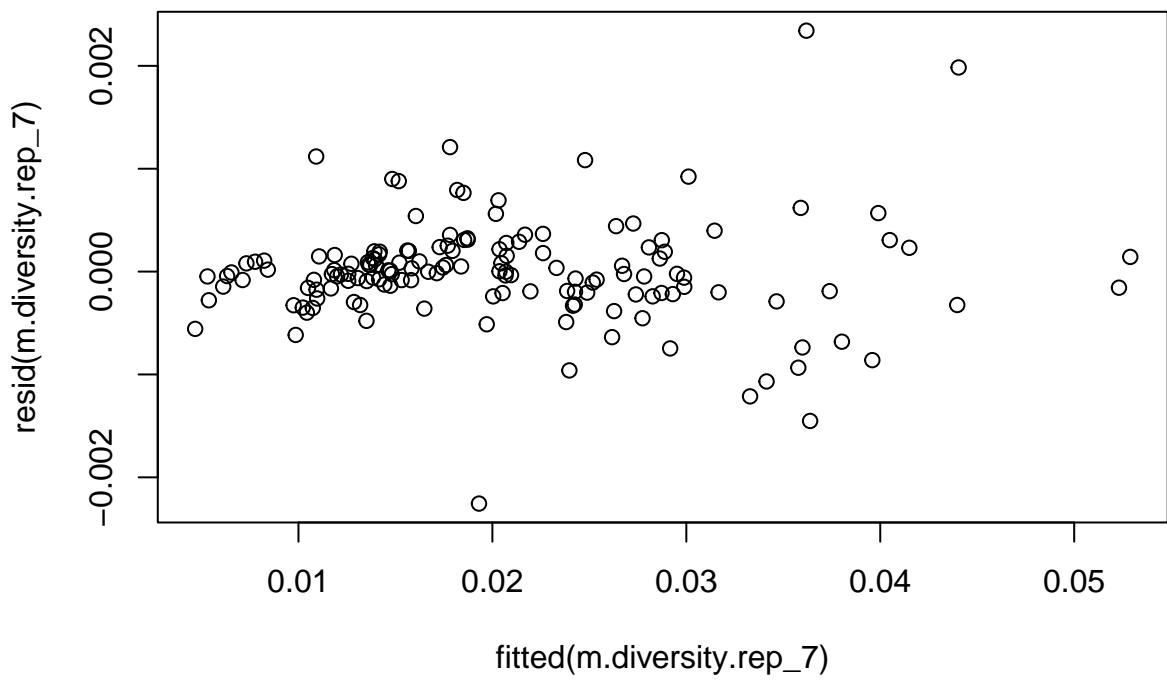
inf.lands.200kb.rep_7 <- as.data.frame(cbind(pi.200kb$avg, theta.200kb$sample_mean, rho.200kb$sample_mean))
names(inf.lands.200kb.rep_7) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.200kb.rep_7$thetaC <- inf.lands.200kb.rep_7$theta - mean(inf.lands.200kb.rep_7$theta)
inf.lands.200kb.rep_7$tmrcaC <- inf.lands.200kb.rep_7$tmrca - mean(inf.lands.200kb.rep_7$tmrca)
inf.lands.200kb.rep_7$rhoC <- inf.lands.200kb.rep_7$rho - mean(inf.lands.200kb.rep_7$rho)

inf.lands.200kb.rep_7$bin <- 1:nrow(inf.lands.200kb.rep_7)

# for merging:
inf.lands.200kb.rep_7$Replicate <- 7

m.diversity.rep_7 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.200kb.rep_7)
plot(resid(m.diversity.rep_7)~fitted(m.diversity.rep_7))
```

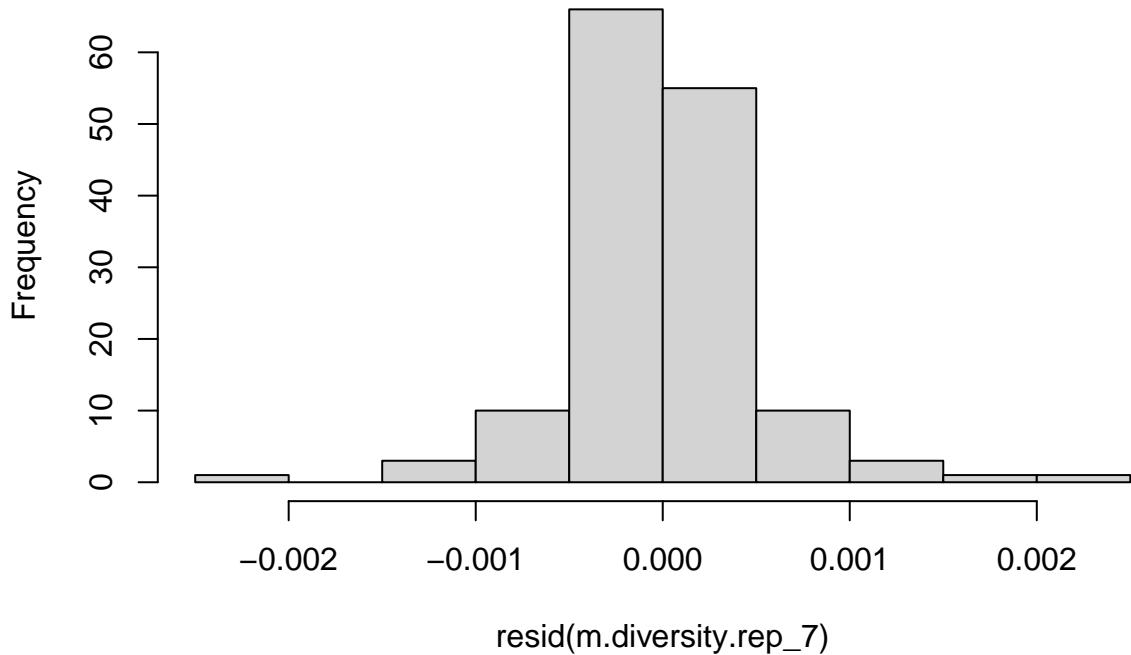


```
dwtest(m.diversity.rep_7)
```

```
##
##  Durbin-Watson test
##
## data: m.diversity.rep_7
## DW = 1.6673, p-value = 0.01553
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_7)
```

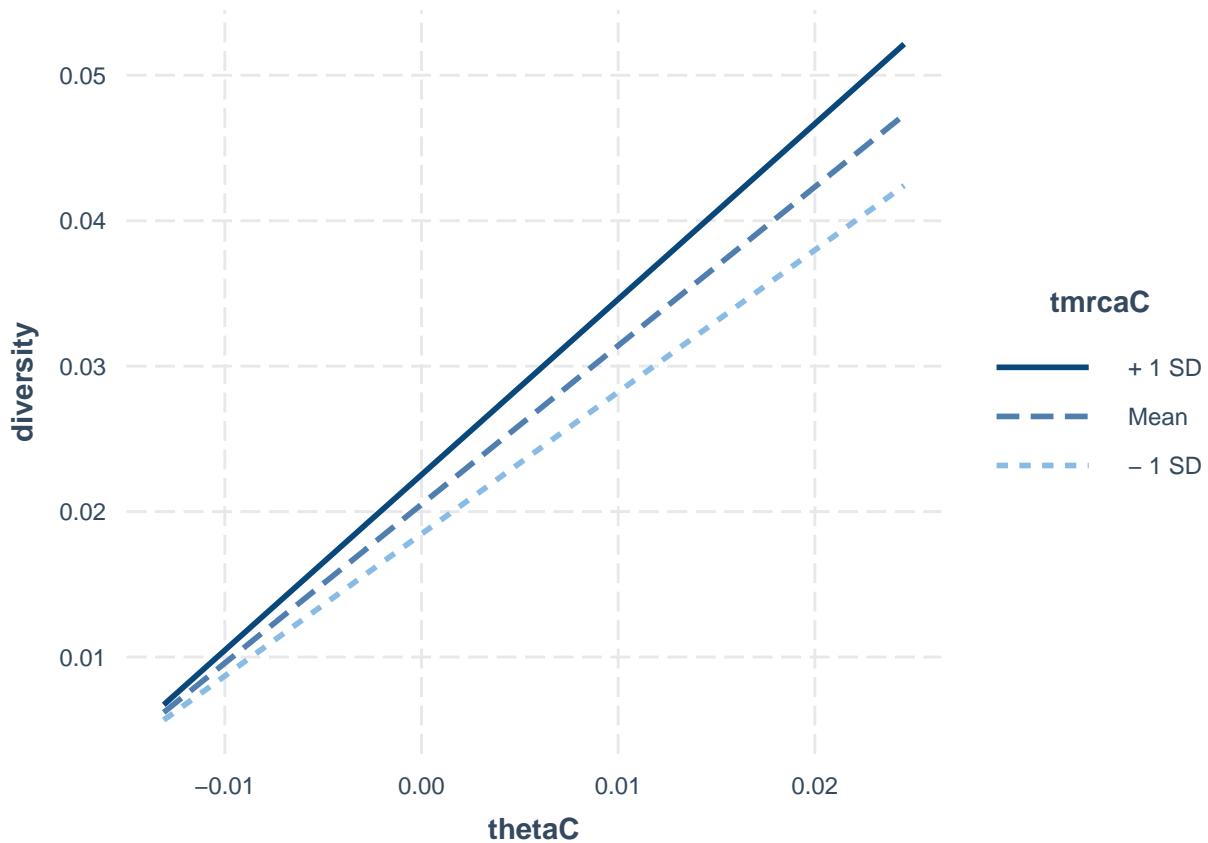
```
##
##  Harrison-McCabe test
##
## data: m.diversity.rep_7
## HMC = 0.43605, p-value = 0.147
hist(resid(m.diversity.rep_7))
```

## Histogram of resid(m.diversity.rep\_7)



```
summary(m.diversity.rep_7)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##      data = inf.lands.200kb.rep_7)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -2.255e-03 -2.038e-04 -2.189e-05  1.931e-04  2.342e-03
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 0.0204967  0.0000427 480.036 <2e-16 ***
## thetaC       1.0913523  0.0049822 219.050 <2e-16 ***
## rhoC        -0.0194028  0.0611569 -0.317   0.752    
## tmrcaC       0.0204993  0.0004700  43.612 <2e-16 ***
## thetaC:tmrcaC 1.1606406  0.0451718  25.694 <2e-16 ***
## ---      
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0005216 on 145 degrees of freedom
## Multiple R-squared:  0.9972, Adjusted R-squared:  0.9971 
## F-statistic: 1.281e+04 on 4 and 145 DF,  p-value: < 2.2e-16
interact_plot(m.diversity.rep_7, pred = thetaC, modx= tmrcaC)
```



```
g.rep_7 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
  data = inf.lands.200kb.rep_7, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_7)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.200kb.rep_7
##       AIC     BIC   logLik
##   -1837.873 -1816.799 925.9367
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.1935696
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0204997 0.00005196 394.5197 0.0000
## thetaC      1.0931140 0.00535150 204.2630 0.0000
## tmrcaC      0.0203603 0.00047964  42.4489 0.0000
## rhoC        -0.0138547 0.06038474  -0.2294 0.8189
## thetaC:tmrcaC 1.1234814 0.04563517  24.6188 0.0000
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC      -0.002
## tmrcaC     -0.021 -0.082
## rhoC       -0.003 -0.022  0.167
## thetaC:tmrcaC -0.060  0.039  0.329  0.078
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -4.36585180 -0.42077188 -0.01421357  0.38381511  4.57664531
##
## Residual standard error: 0.0005142079
## Degrees of freedom: 150 total; 145 residual
vif(g.rep_7)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##      1.011928     1.158318     1.029312     1.127670
g.rep_7.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.200kb.rep_7, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_7.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.200kb.rep_7
##          AIC      BIC    logLik
## -1444.025 -1428.971 727.0123
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.2825213
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0205796 0.00021783 94.47441 0.0000
## thetaC       1.1122060 0.02050319 54.24550 0.0000
## rhoC        -0.4602880 0.22027764 -2.08958 0.0384
##
## Correlation:
##      (Intr) thetaC
## thetaC  0.000
## rhoC   0.002 -0.007
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -3.4561092 -0.4625831  0.1353834  0.5540699  4.0615520
##
## Residual standard error: 0.001980566
## Degrees of freedom: 150 total; 147 residual
anova.diversity <- Anova(m.diversity.rep_7)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.200kb[1, 7] <- anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]
r2.inf.200kb[2, 7] <- anova.diversity$VarExp[1] * 100
r2.inf.200kb[3, 7] <- anova.diversity$VarExp[2] * 100
r2.inf.200kb[4, 7] <- anova.diversity$VarExp[3] * 100
r2.inf.200kb[5, 7] <- anova.diversity$VarExp[4] * 100
```

## 2.2.8 Replicate 8

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_8/rs.pair_8.", sep = "")
pi.200kb <- read.table(paste(p, "diversity.200kb.bedgraph", sep = ""), header = T)
pi.200kb$avg <- apply(pi.200kb[4:ncol(pi.200kb)], 1, mean)
tmrca.200kb <- read.table(paste(p, "TMRCA.200kb.bedgraph", sep = ""), header = T)
tmrca.200kb$avg <- apply(tmrca.200kb[4:ncol(tmrca.200kb)], 1, mean)
rho.200kb <- read.table(paste(p, "rho.200kb.bedgraph", sep = ""), header = T)
theta.200kb <- read.table(paste(p, "theta.200kb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.200kb$sim, theta.200kb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.200kb$sim and theta.200kb$sample_mean
## S = 6883.3, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.98777626

inf.lands.200kb.rep_8 <- as.data.frame(cbind(pi.200kb$avg, theta.200kb$sample_mean, rho.200kb$sample_mean))
names(inf.lands.200kb.rep_8) <- c("diversity", "theta", "rho", "tmrca")

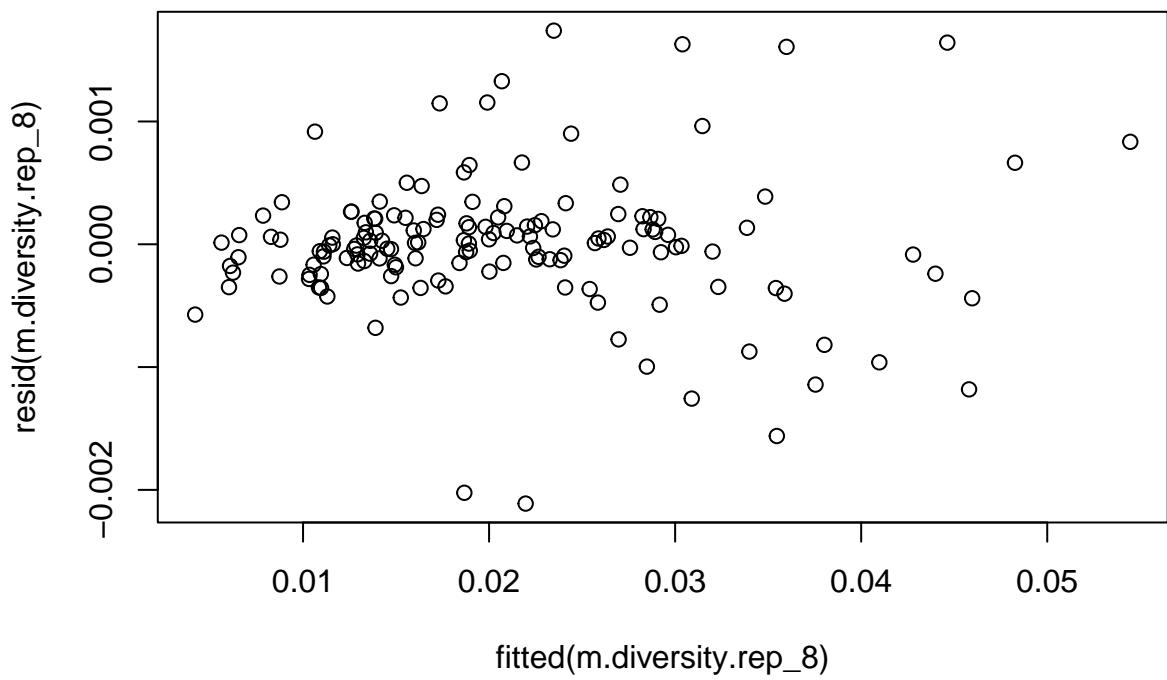
# centering
inf.lands.200kb.rep_8$thetaC <- inf.lands.200kb.rep_8$theta - mean(inf.lands.200kb.rep_8$theta)
inf.lands.200kb.rep_8$tmrcaC <- inf.lands.200kb.rep_8$tmrca - mean(inf.lands.200kb.rep_8$tmrca)
inf.lands.200kb.rep_8$rhoC <- inf.lands.200kb.rep_8$rho - mean(inf.lands.200kb.rep_8$rho)

inf.lands.200kb.rep_8$bin <- 1:nrow(inf.lands.200kb.rep_8)

# for merging:
inf.lands.200kb.rep_8$Replicate <- 8

m.diversity.rep_8 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.200kb.rep_8)

plot(resid(m.diversity.rep_8)~fitted(m.diversity.rep_8))
```

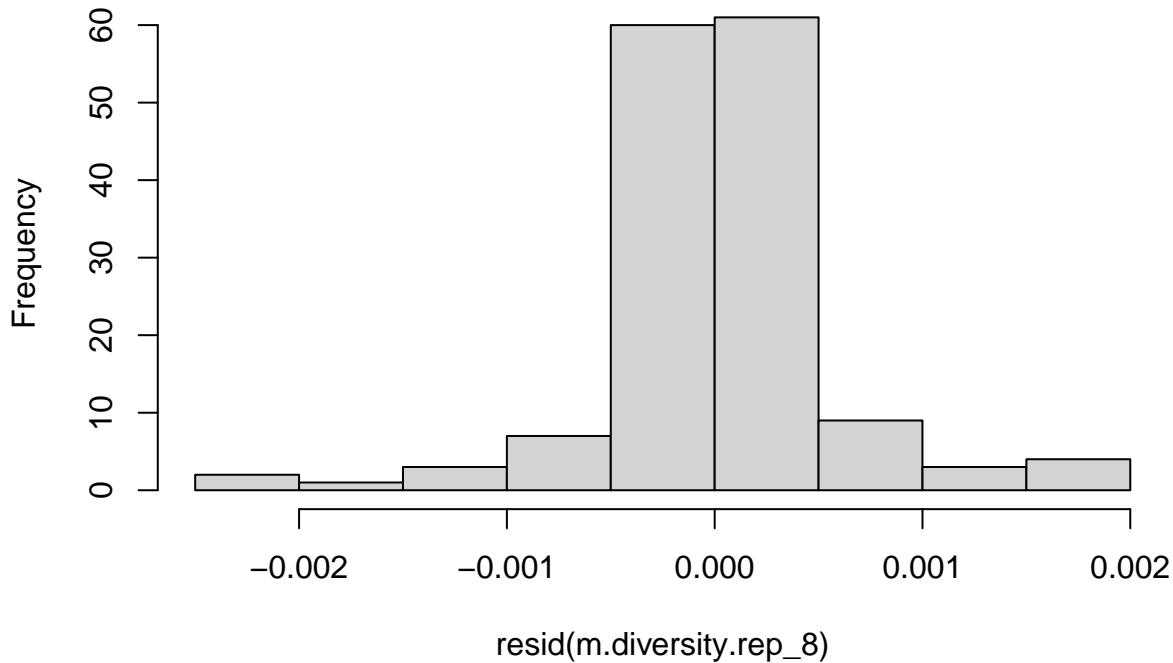


```
dwtest(m.diversity.rep_8)
```

```
##
##  Durbin-Watson test
##
## data: m.diversity.rep_8
## DW = 1.5909, p-value = 0.004238
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_8)
```

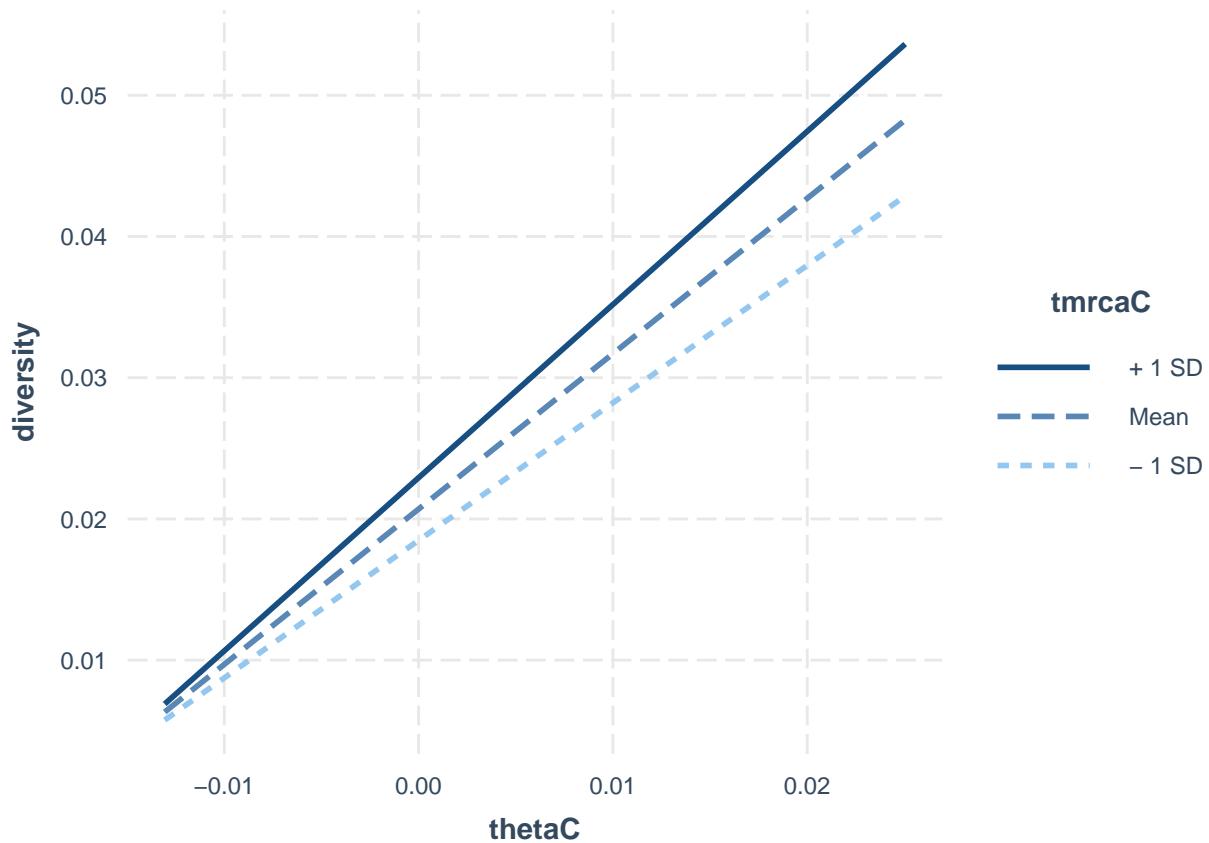
```
##
##  Harrison-McCabe test
##
## data: m.diversity.rep_8
## HMC = 0.45552, p-value = 0.208
hist(resid(m.diversity.rep_8))
```

## Histogram of resid(m.diversity.rep\_8)



```
summary(m.diversity.rep_8)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,  
##      data = inf.lands.200kb.rep_8)  
##  
## Residuals:  
##       Min        1Q     Median        3Q       Max  
## -2.112e-03 -1.846e-04  7.690e-06  1.961e-04  1.739e-03  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 2.070e-02 4.624e-05 447.65 <2e-16 ***  
## thetaC      1.100e+00 5.401e-03 203.69 <2e-16 ***  
## rhoC        6.479e-02 6.610e-02   0.98  0.329  
## tmrcaC      2.076e-02 4.865e-04   42.68 <2e-16 ***  
## thetaC:tmrcaC 1.181e+00 4.604e-02   25.64 <2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0005639 on 145 degrees of freedom  
## Multiple R-squared:  0.9968, Adjusted R-squared:  0.9967  
## F-statistic: 1.124e+04 on 4 and 145 DF,  p-value: < 2.2e-16  
interact_plot(m.diversity.rep_8, pred = thetaC, modx= tmrcaC)
```



```
g.rep_8 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
  data = inf.lands.200kb.rep_8, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_8)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.200kb.rep_8
##          AIC      BIC    logLik
##     -1816.857 -1795.783  915.4287
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.2325221
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0207042 0.00005859 353.3963 0.0000
## thetaC      1.0990491 0.00584866 187.9147 0.0000
## tmrcaC      0.0207188 0.00049940  41.4878 0.0000
## rhoC        0.0549165 0.06405597   0.8573 0.3927
## thetaC:tmrcaC 1.1364878 0.04655992  24.4091 0.0000
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC      -0.001
## tmrcaC     -0.026 -0.121
## rhoC       -0.003 -0.003  0.185
## thetaC:tmrcaC -0.074  0.014  0.351  0.043
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -3.78620355 -0.37183043 -0.03601008  0.33263464  3.19188937
##
## Residual standard error: 0.0005563072
## Degrees of freedom: 150 total; 145 residual
vif(g.rep_8)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##      1.019264     1.202188    1.036381     1.145973

g.rep_8.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.200kb.rep_8, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_8.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.200kb.rep_8
##          AIC      BIC  logLik
## -1429.786 -1414.733 719.8932
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.3033588
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0208111 0.00023518 88.49129 0.0000
## thetaC       1.1297636 0.02165099 52.18069 0.0000
## rhoC        -0.4075453 0.22773180 -1.78958 0.0756
##
## Correlation:
##      (Intr) thetaC
## thetaC 0.000
## rhoC   0.000  0.018
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -4.25604299 -0.41587461  0.04359114  0.48798012  3.54428535
##
## Residual standard error: 0.002090655
## Degrees of freedom: 150 total; 147 residual
anova.diversity <- Anova(m.diversity.rep_8)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.200kb[1, 8] <- anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]
r2.inf.200kb[2, 8] <- anova.diversity$VarExp[1] * 100
r2.inf.200kb[3, 8] <- anova.diversity$VarExp[2] * 100
r2.inf.200kb[4, 8] <- anova.diversity$VarExp[3] * 100
r2.inf.200kb[5, 8] <- anova.diversity$VarExp[4] * 100
```

## 2.2.9 Replicate 9

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_9/rs.pair_9.", sep = "")
pi.200kb <- read.table(paste(p, "diversity.200kb.bedgraph", sep = ""), header = T)
pi.200kb$avg <- apply(pi.200kb[4:ncol(pi.200kb)], 1, mean)
tmrca.200kb <- read.table(paste(p, "TMRCA.200kb.bedgraph", sep = ""), header = T)
tmrca.200kb$avg <- apply(tmrca.200kb[4:ncol(tmrca.200kb)], 1, mean)
rho.200kb <- read.table(paste(p, "rho.200kb.bedgraph", sep = ""), header = T)
theta.200kb <- read.table(paste(p, "theta.200kb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.200kb$sim, theta.200kb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.200kb$sim and theta.200kb$sample_mean
## S = 7233.3, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9871403

inf.lands.200kb.rep_9 <- as.data.frame(cbind(pi.200kb$avg, theta.200kb$sample_mean, rho.200kb$sample_mean))
names(inf.lands.200kb.rep_9) <- c("diversity", "theta", "rho", "tmrca")

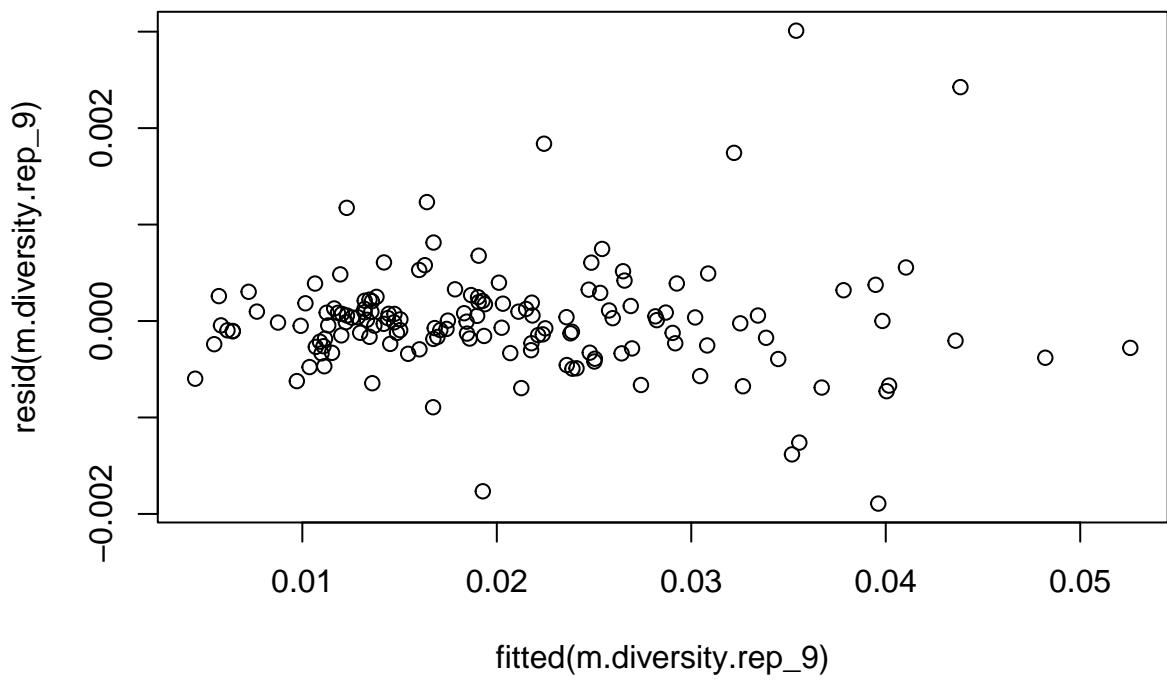
# centering
inf.lands.200kb.rep_9$thetaC <- inf.lands.200kb.rep_9$theta - mean(inf.lands.200kb.rep_9$theta)
inf.lands.200kb.rep_9$tmrcaC <- inf.lands.200kb.rep_9$tmrca - mean(inf.lands.200kb.rep_9$tmrca)
inf.lands.200kb.rep_9$rhoC <- inf.lands.200kb.rep_9$rho - mean(inf.lands.200kb.rep_9$rho)

inf.lands.200kb.rep_9$bin <- 1:nrow(inf.lands.200kb.rep_9)

# for merging:
inf.lands.200kb.rep_9$Replicate <- 9

m.diversity.rep_9 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.200kb.rep_9)

plot(resid(m.diversity.rep_9)~fitted(m.diversity.rep_9))
```

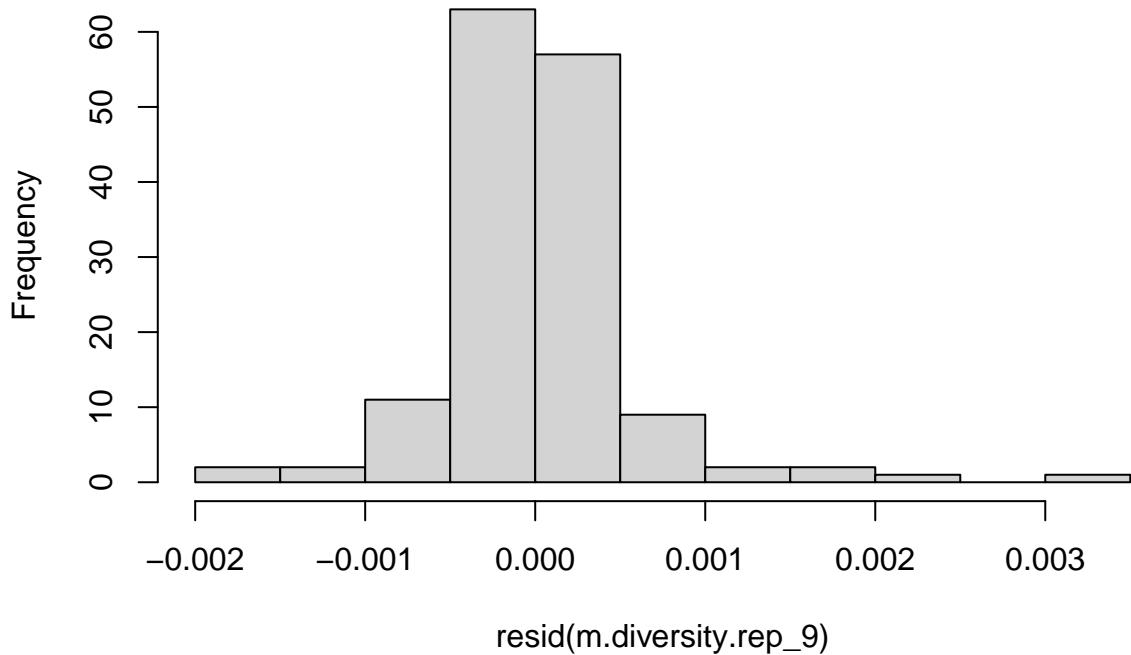


```
dwtest(m.diversity.rep_9)
```

```
##
##  Durbin-Watson test
##
## data: m.diversity.rep_9
## DW = 1.6772, p-value = 0.01787
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_9)
```

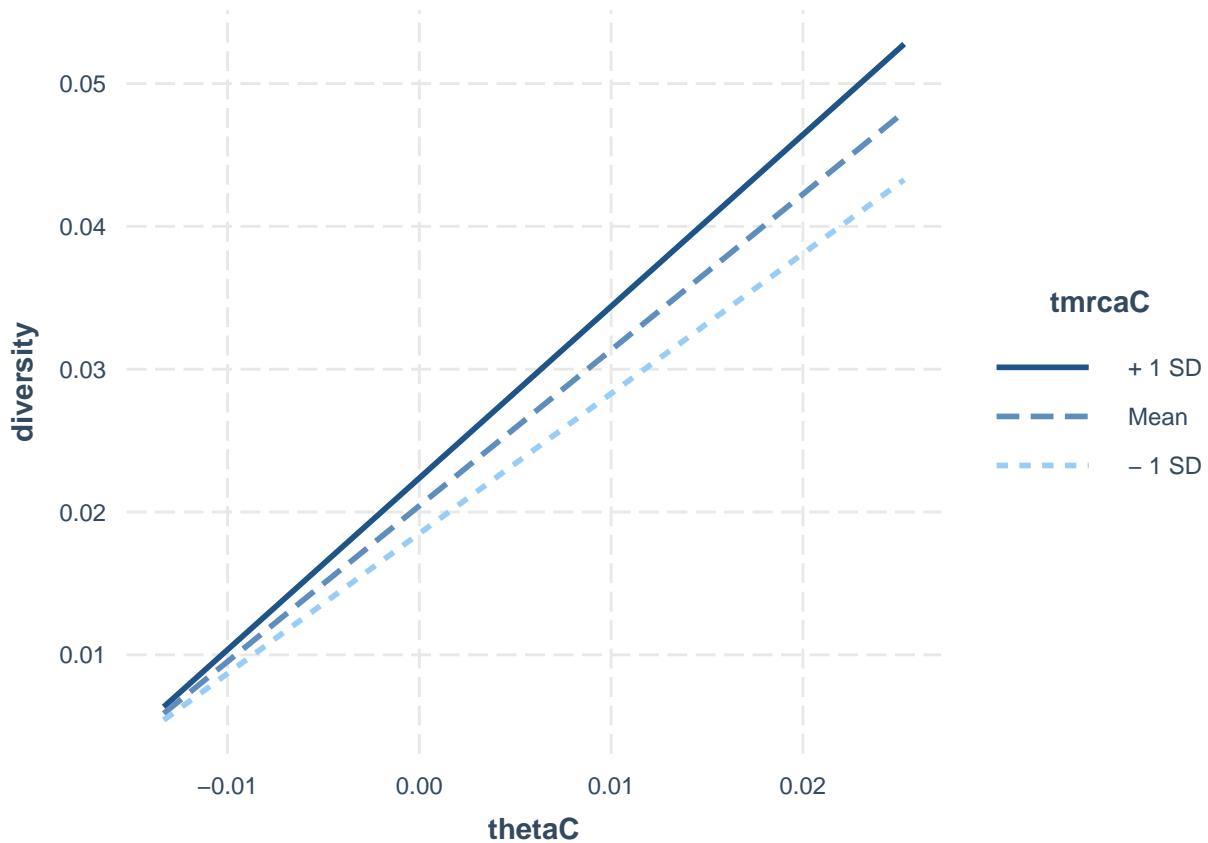
```
##
##  Harrison-McCabe test
##
## data: m.diversity.rep_9
## HMC = 0.38369, p-value = 0.023
hist(resid(m.diversity.rep_9))
```

## Histogram of resid(m.diversity.rep\_9)



```
summary(m.diversity.rep_9)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.200kb.rep_9)
##
## Residuals:
##       Min         1Q      Median         3Q        Max
## -0.0018926 -0.0002394 -0.0000149  0.0001830  0.0030102
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.044e-02 4.788e-05 426.832 <2e-16 ***
## thetaC      1.091e+00 5.584e-03 195.371 <2e-16 ***
## rhoC        1.218e-01 7.409e-02   1.643   0.102
## tmrcaC     2.096e-02 5.758e-04  36.402 <2e-16 ***
## thetaC:tmrcaC 1.200e+00 5.571e-02  21.530 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.000584 on 145 degrees of freedom
## Multiple R-squared:  0.9965, Adjusted R-squared:  0.9964
## F-statistic: 1.02e+04 on 4 and 145 DF,  p-value: < 2.2e-16
interact_plot(m.diversity.rep_9, pred = thetaC, modx= tmrcaC)
```



```
g.rep_9 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
  data = inf.lands.200kb.rep_9, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_9)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.200kb.rep_9
##          AIC      BIC    logLik
##     -1804.101 -1783.026  909.0504
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.2058788
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0204394 0.00005911 345.7760 0.0000
## thetaC       1.0918715 0.00599966 181.9888 0.0000
## tmrcaC      0.0210780 0.00059395  35.4877 0.0000
## rhoC        0.1568335 0.07270121   2.1572 0.0326
## thetaC:tmrcaC 1.1467223 0.05773633  19.8614 0.0000
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC      -0.006
## tmrcaC     -0.029 -0.067
## rhoC       -0.008  0.011  0.270
## thetaC:tmrcaC -0.076  0.077  0.351  0.110
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -3.22090386 -0.40412235 -0.03092443  0.30494856  5.19848696
##
## Residual standard error: 0.000576945
## Degrees of freedom: 150 total; 145 residual
vif(g.rep_9)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##      1.017102     1.228533    1.079801     1.153832
g.rep_9.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.200kb.rep_9, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_9.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.200kb.rep_9
##          AIC      BIC  logLik
## -1464.018 -1448.965 737.009
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.3448494
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0205379 0.00022295 92.11977 0.0000
## thetaC       1.1066746 0.01936981 57.13401 0.0000
## rhoC        -0.4865608 0.21452090 -2.26813 0.0248
##
## Correlation:
##      (Intr) thetaC
## thetaC 0.000
## rhoC   0.002  0.028
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -4.01675167 -0.35192121 -0.05519082  0.39502917  4.12501538
##
## Residual standard error: 0.00189327
## Degrees of freedom: 150 total; 147 residual
anova.diversity <- Anova(m.diversity.rep_9)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.200kb[1, 9] <- anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]
r2.inf.200kb[2, 9] <- anova.diversity$VarExp[1] * 100
r2.inf.200kb[3, 9] <- anova.diversity$VarExp[2] * 100
r2.inf.200kb[4, 9] <- anova.diversity$VarExp[3] * 100
r2.inf.200kb[5, 9] <- anova.diversity$VarExp[4] * 100
```

## 2.2.10 Replicate 10

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_10/rs.pair_10.", sep = "")
pi.200kb <- read.table(paste(p, "diversity.200kb.bedgraph", sep = ""), header = T)
pi.200kb$avg <- apply(pi.200kb[4:ncol(pi.200kb)], 1, mean)
tmrca.200kb <- read.table(paste(p, "TMRCA.200kb.bedgraph", sep = ""), header = T)
tmrca.200kb$avg <- apply(tmrca.200kb[4:ncol(tmrca.200kb)], 1, mean)
rho.200kb <- read.table(paste(p, "rho.200kb.bedgraph", sep = ""), header = T)
theta.200kb <- read.table(paste(p, "theta.200kb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.200kb$sim, theta.200kb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.200kb$sim and theta.200kb$sample_mean
## S = 6266.2, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9888595

inf.lands.200kb.rep_10 <- as.data.frame(cbind(pi.200kb$avg, theta.200kb$sample_mean, rho.200kb$sample_mean))
names(inf.lands.200kb.rep_10) <- c("diversity", "theta", "rho", "tmrca")

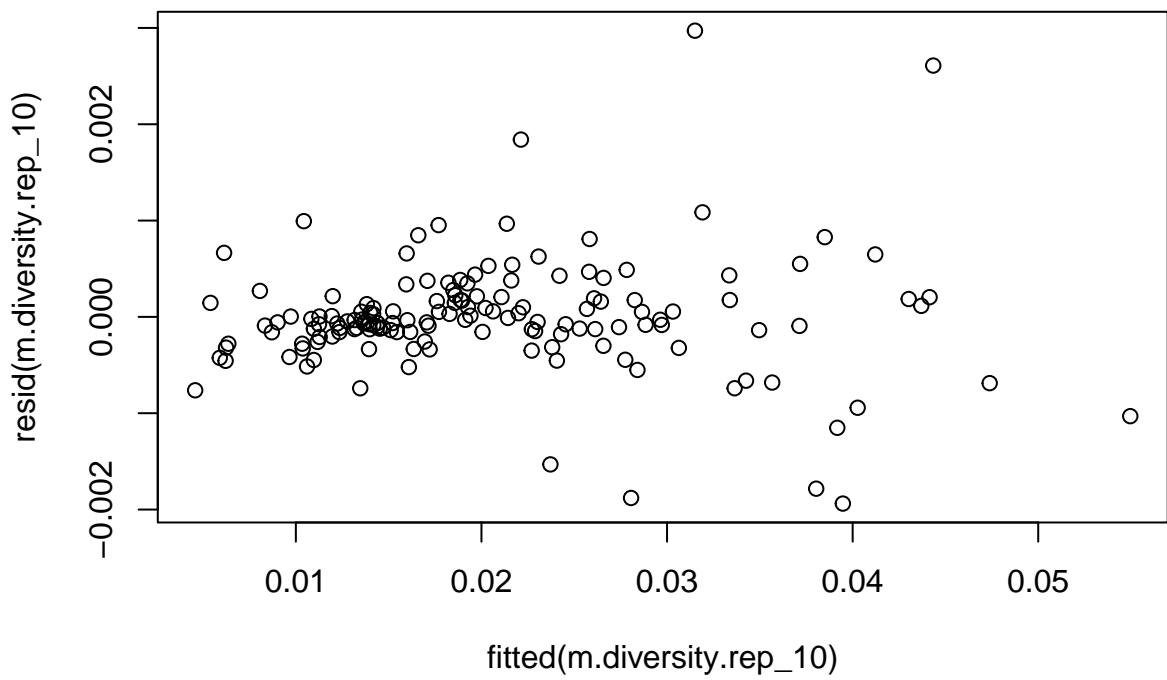
# centering
inf.lands.200kb.rep_10$thetaC <- inf.lands.200kb.rep_10$theta - mean(inf.lands.200kb.rep_10$theta)
inf.lands.200kb.rep_10$tmrcaC <- inf.lands.200kb.rep_10$tmrca - mean(inf.lands.200kb.rep_10$tmrca)
inf.lands.200kb.rep_10$rhoC <- inf.lands.200kb.rep_10$rho - mean(inf.lands.200kb.rep_10$rho)

inf.lands.200kb.rep_10$bin <- 1:nrow(inf.lands.200kb.rep_10)

# for merging:
inf.lands.200kb.rep_10$Replicate <- 10

m.diversity.rep_10 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.200kb.rep_10)

plot(resid(m.diversity.rep_10)~fitted(m.diversity.rep_10))
```

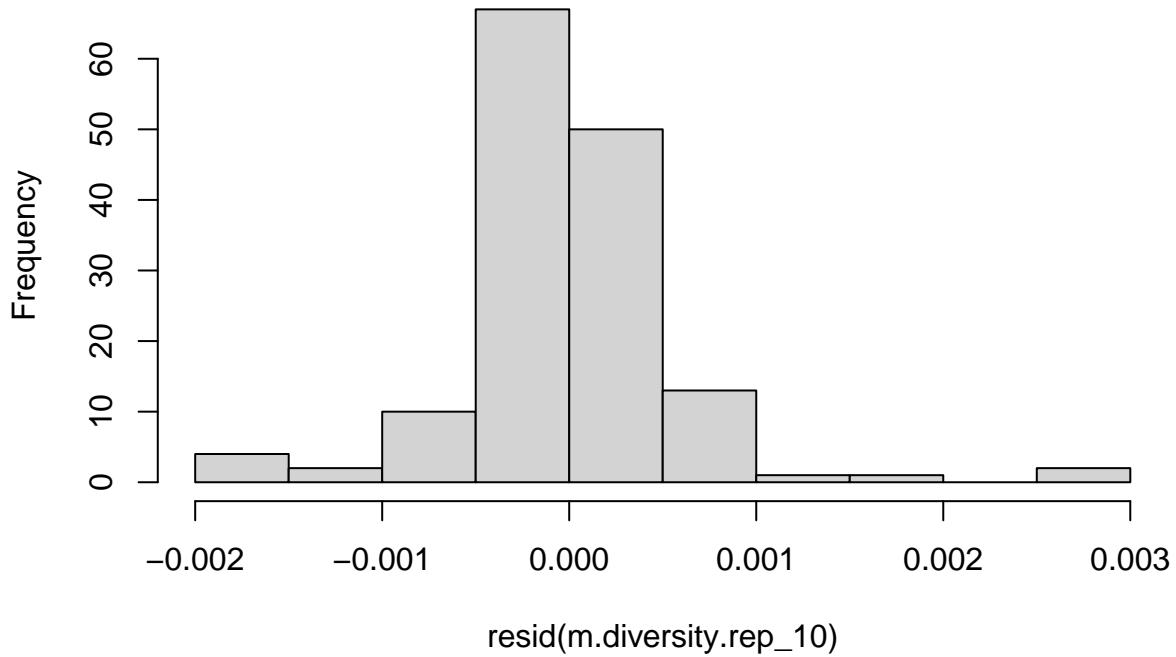


```
dwtest(m.diversity.rep_10)
```

```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_10  
## DW = 1.777, p-value = 0.06912  
## alternative hypothesis: true autocorrelation is greater than 0  
hmctest(m.diversity.rep_10)
```

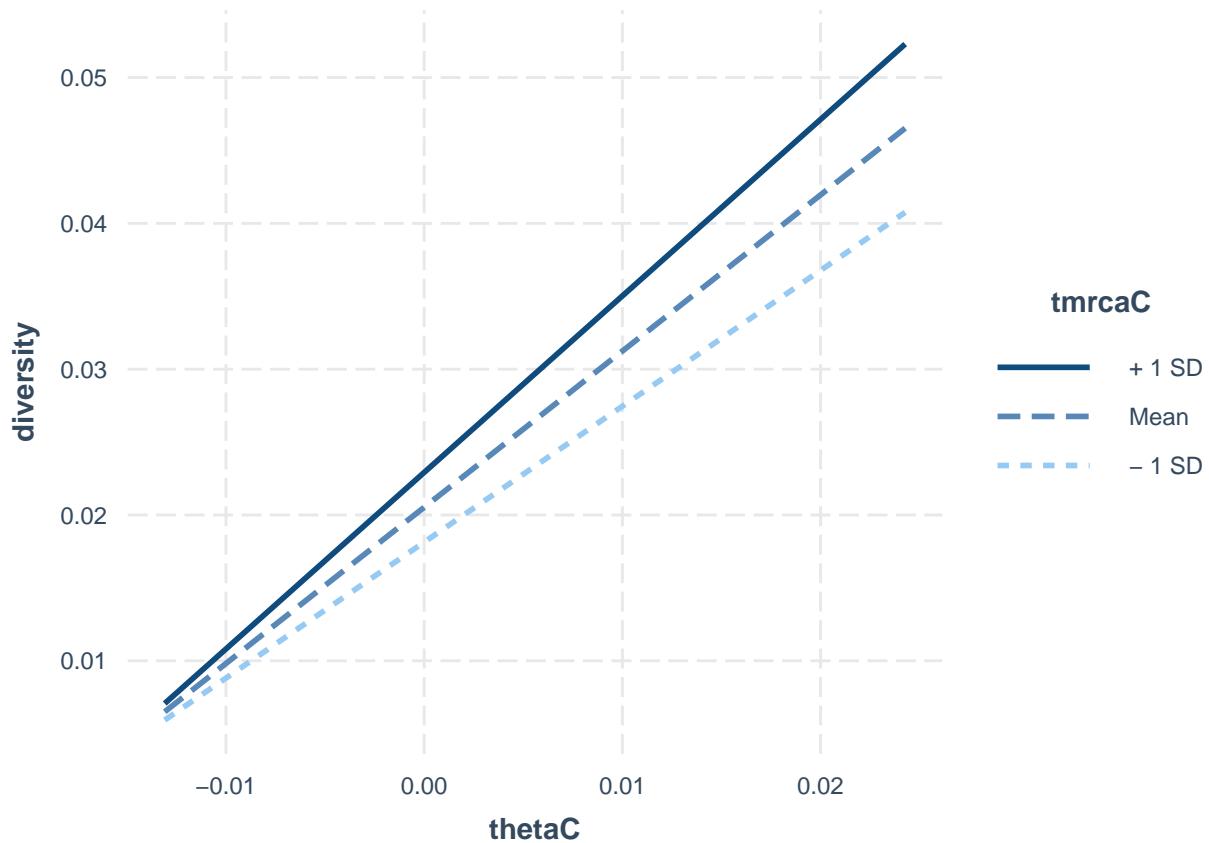
```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_10  
## HMC = 0.6193, p-value = 0.983  
hist(resid(m.diversity.rep_10))
```

## Histogram of resid(m.diversity.rep\_10)



```
summary(m.diversity.rep_10)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.200kb.rep_10)
##
## Residuals:
##       Min         1Q     Median         3Q        Max
## -1.938e-03 -1.748e-04 -4.971e-05  1.828e-04  2.971e-03
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.053e-02 5.021e-05 408.838 <2e-16 ***
## thetaC      1.071e+00 5.803e-03 184.625 <2e-16 ***
## rhoC        1.995e-02 7.054e-02   0.283   0.778
## tmrcaC     2.204e-02 5.689e-04  38.738 <2e-16 ***
## thetaC:tmrcaC 1.283e+00 5.870e-02  21.866 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0006067 on 145 degrees of freedom
## Multiple R-squared:  0.9963, Adjusted R-squared:  0.9962
## F-statistic:  9827 on 4 and 145 DF,  p-value: < 2.2e-16
interact_plot(m.diversity.rep_10, pred = thetaC, modx= tmrcaC)
```



```

g.rep_10 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
                  data = inf.lands.200kb.rep_1, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_10)

```

```

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.200kb.rep_1
##          AIC      BIC    logLik
##     -1814.128 -1793.054  914.0641
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.08562895
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0204958 0.00004989 410.8349 0.0000
## thetaC      1.0967285 0.00562895 194.8371 0.0000
## tmrcaC      0.0210125 0.00050621  41.5092 0.0000
## rhoC        0.0219683 0.06340360   0.3465 0.7295
## thetaC:tmrcaC 1.2110957 0.05322577  22.7539 0.0000
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC

```

```

## thetaC      -0.001
## tmrcaC     -0.043 -0.110
## rhoC       -0.010 -0.009  0.248
## thetaC:tmrcaC -0.113  0.010  0.375  0.090
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -2.94983846 -0.42035716 -0.01013693  0.33115763  4.40016170
##
## Residual standard error: 0.0005481049
## Degrees of freedom: 150 total; 145 residual
vif(g.rep_10)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##      1.015853     1.249427     1.066075     1.167458
g.rep_10.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.200kb.rep_10, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_10.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.200kb.rep_10
##          AIC      BIC    logLik
## -1442.284 -1427.23  726.1418
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.3304014
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0207131 0.00023459 88.29634 0.0000
## thetaC       1.1352063 0.02089711 54.32360 0.0000
## rhoC        -0.5008572 0.21144100 -2.36878 0.0191
##
## Correlation:
##      (Intr) thetaC
## thetaC  0.000
## rhoC   0.002 -0.030
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -2.75464197 -0.53844834  0.02521541  0.52547583  4.31476850
##
## Residual standard error: 0.002024422
## Degrees of freedom: 150 total; 147 residual
anova.diversity <- Anova(m.diversity.rep_10)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```

r2.inf.200kb[1, 10] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] * 100
r2.inf.200kb[2, 10] <- anova.diversity$VarExp[1] * 100
r2.inf.200kb[3, 10] <- anova.diversity$VarExp[2] * 100
r2.inf.200kb[4, 10] <- anova.diversity$VarExp[3] * 100
r2.inf.200kb[5, 10] <- anova.diversity$VarExp[4] * 100

r2.inf.200kb$average <- rowMeans(r2.inf.200kb)
r2.inf.200kb <- transform(r2.inf.200kb, sd=apply(r2.inf.200kb, 1, sd, na.rm = TRUE))

```

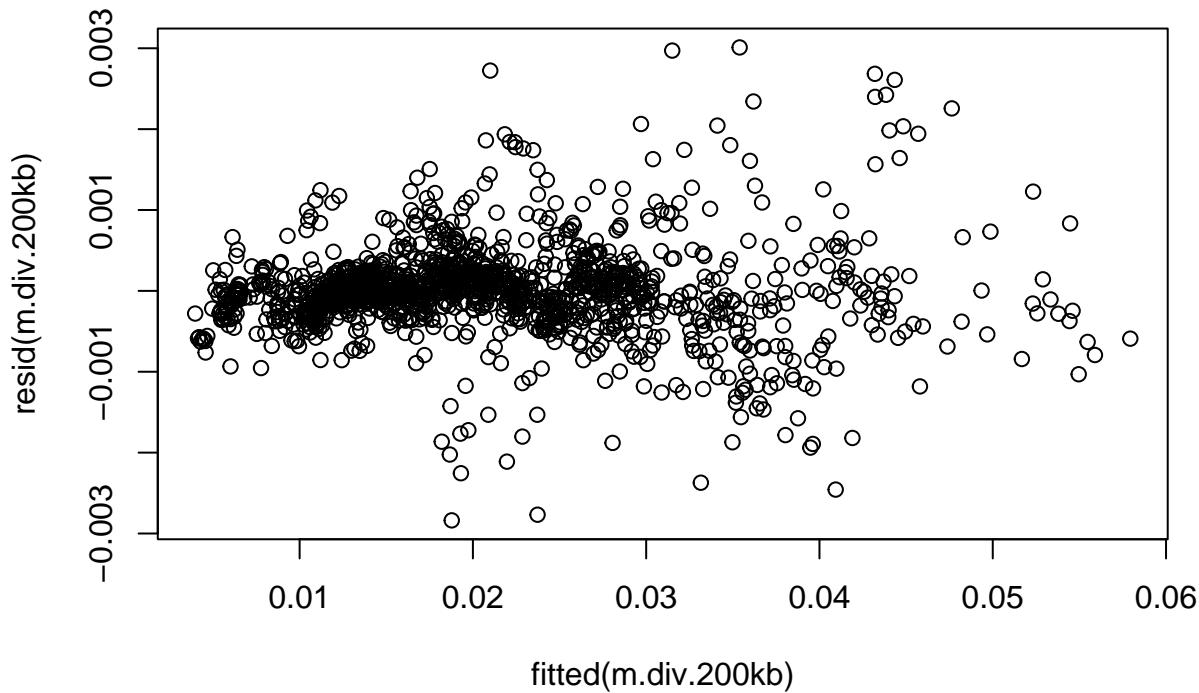
### 2.2.11 all replicates:

```

inf.lands.200kb.all <- rbind(inf.lands.200kb.rep_1, inf.lands.200kb.rep_2, inf.lands.200kb.rep_3, inf.lands.200kb.rep_4)

m.div.200kb <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC)*as.factor(Replicate), data = inf.lands.200kb.all)
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```



```

dwtest(m.div.200kb)

##
##  Durbin-Watson test
##
##  data:  m.div.200kb
##  DW = 1.6825, p-value = 8.31e-12
##  alternative hypothesis: true autocorrelation is greater than 0

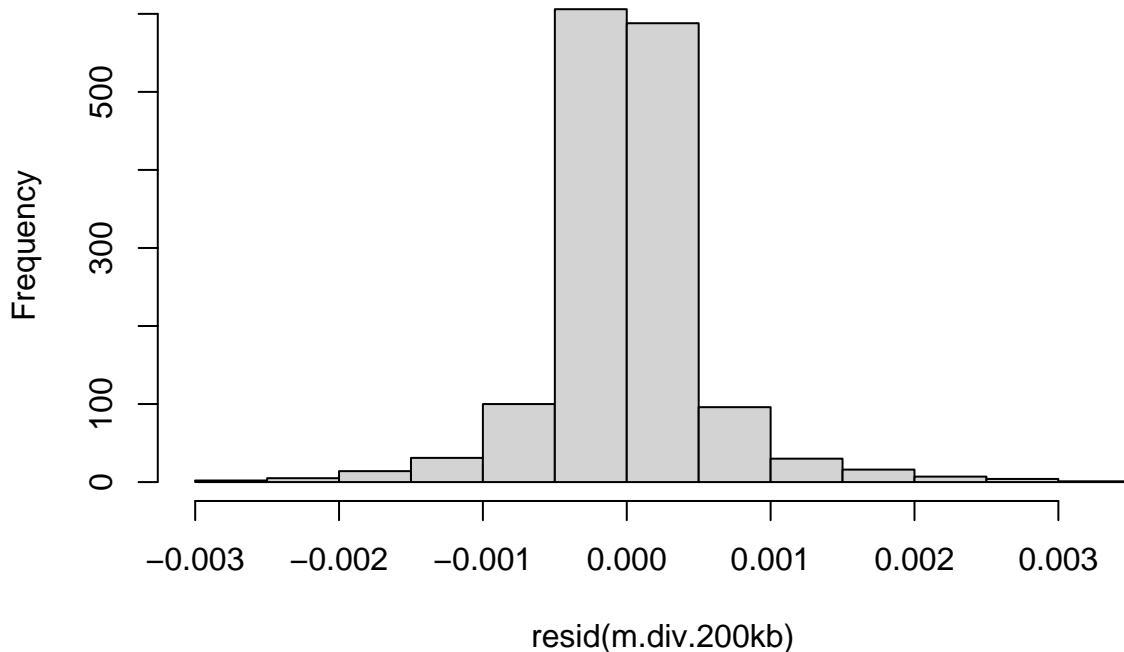
hmctest(m.div.200kb)

##
##  Harrison-McCabe test
##
##  data:  m.div.200kb
##  HMC = 0.48172, p-value = 0.149

```

```
hist(resid(m.div.200kb))
```

Histogram of resid(m.div.200kb)



```
m.div.200kb.2 <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC + thetaC:rhoC)*as.factor(Replicate), data = inf.lands.200kb.all)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC + thetaC:rhoC + rhoC:tmrcaC)*as.factor(Replicate), data = inf.lands.200kb.all)
```

```
AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)
```

```
##                df      AIC
## m.div.200kb    51 -18158.03
## m.div.200kb.2  61 -18155.65
## m.div.200kb.3  71 -18154.31
```

```
summary(m.div.200kb)
```

```
##
## Call:
## lm(formula = diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC) *
##     as.factor(Replicate), data = inf.lands.200kb.all)
##
## Residuals:
##      Min        1Q        Median         3Q        Max 
## -2.837e-03 -2.188e-04 -6.580e-06  1.836e-04  3.010e-03 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 2.049e-02 4.600e-05 445.509 < 2e-16 ***
## thetaC       1.096e+00 5.439e-03 201.508 < 2e-16 ***
## rhoC         1.426e-02 6.373e-02   0.224 0.822950  
## tmrcaC       2.103e-02 5.029e-04  41.809 < 2e-16 ***
## as.factor(Replicate)2 -3.060e-05 6.507e-05  -0.470 0.638292
```

```

## as.factor(Replicate)3      1.025e-04  6.504e-05  1.576 0.115287
## as.factor(Replicate)4      1.385e-04  6.486e-05  2.136 0.032875 *
## as.factor(Replicate)5      1.180e-05  6.487e-05  0.182 0.855637
## as.factor(Replicate)6      -1.818e-05 6.496e-05 -0.280 0.779594
## as.factor(Replicate)7      2.154e-06  6.491e-05  0.033 0.973535
## as.factor(Replicate)8      2.053e-04  6.496e-05  3.160 0.001611 **
## as.factor(Replicate)9      -5.912e-05 6.496e-05 -0.910 0.362922
## as.factor(Replicate)10     3.230e-05  6.526e-05  0.495 0.620766
## thetaC:tmrcaC             1.224e+00  5.205e-02  23.507 < 2e-16 ***
## thetaC:as.factor(Replicate)2 -1.053e-02 7.664e-03 -1.374 0.169687
## thetaC:as.factor(Replicate)3 -1.650e-02 7.590e-03 -2.174 0.029886 *
## thetaC:as.factor(Replicate)4 2.909e-02 7.659e-03  3.799 0.000151 ***
## thetaC:as.factor(Replicate)5 1.351e-02 7.668e-03  1.762 0.078268 .
## thetaC:as.factor(Replicate)6 -1.096e-02 7.610e-03 -1.441 0.149866
## thetaC:as.factor(Replicate)7 -4.595e-03 7.624e-03 -0.603 0.546846
## thetaC:as.factor(Replicate)8 4.142e-03 7.634e-03  0.543 0.587471
## thetaC:as.factor(Replicate)9 -4.972e-03 7.628e-03 -0.652 0.514662
## thetaC:as.factor(Replicate)10 -2.460e-02 7.629e-03 -3.225 0.001289 **
## rhoC:as.factor(Replicate)2 -5.012e-03 9.221e-02 -0.054 0.956658
## rhoC:as.factor(Replicate)3 2.185e-02 9.191e-02  0.238 0.812089
## rhoC:as.factor(Replicate)4 4.984e-02 9.296e-02  0.536 0.591924
## rhoC:as.factor(Replicate)5 7.204e-02 9.411e-02  0.766 0.444095
## rhoC:as.factor(Replicate)6 3.489e-02 8.991e-02  0.388 0.698042
## rhoC:as.factor(Replicate)7 -3.367e-02 9.146e-02 -0.368 0.712840
## rhoC:as.factor(Replicate)8 5.053e-02 9.144e-02  0.553 0.580613
## rhoC:as.factor(Replicate)9 1.075e-01 9.538e-02  1.127 0.259957
## rhoC:as.factor(Replicate)10 5.683e-03 9.106e-02  0.062 0.950247
## tmrcaC:as.factor(Replicate)2 -5.309e-04 7.291e-04 -0.728 0.466627
## tmrcaC:as.factor(Replicate)3 -4.744e-04 6.808e-04 -0.697 0.486026
## tmrcaC:as.factor(Replicate)4 -1.276e-03 6.615e-04 -1.930 0.053851 .
## tmrcaC:as.factor(Replicate)5 -5.725e-04 6.812e-04 -0.840 0.400788
## tmrcaC:as.factor(Replicate)6 -7.813e-04 7.269e-04 -1.075 0.282629
## tmrcaC:as.factor(Replicate)7 -5.267e-04 7.121e-04 -0.740 0.459573
## tmrcaC:as.factor(Replicate)8 -2.644e-04 6.970e-04 -0.379 0.704532
## tmrcaC:as.factor(Replicate)9 -6.463e-05 7.464e-04 -0.087 0.931011
## tmrcaC:as.factor(Replicate)10 1.011e-03 7.267e-04  1.391 0.164432
## thetaC:tmrcaC:as.factor(Replicate)2 -6.224e-02 7.262e-02 -0.857 0.391526
## thetaC:tmrcaC:as.factor(Replicate)3 -1.311e-01 6.631e-02 -1.978 0.048172 *
## thetaC:tmrcaC:as.factor(Replicate)4 -7.738e-02 7.053e-02 -1.097 0.272721
## thetaC:tmrcaC:as.factor(Replicate)5 -2.416e-02 6.752e-02 -0.358 0.720504
## thetaC:tmrcaC:as.factor(Replicate)6 -7.740e-02 7.054e-02 -1.097 0.272752
## thetaC:tmrcaC:as.factor(Replicate)7 -6.291e-02 7.111e-02 -0.885 0.376449
## thetaC:tmrcaC:as.factor(Replicate)8 -4.279e-02 6.925e-02 -0.618 0.536691
## thetaC:tmrcaC:as.factor(Replicate)9 -2.404e-02 7.454e-02 -0.322 0.747141
## thetaC:tmrcaC:as.factor(Replicate)10 5.990e-02 7.509e-02  0.798 0.425121
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0005594 on 1450 degrees of freedom
## Multiple R-squared:  0.9968, Adjusted R-squared:  0.9967
## F-statistic:  9292 on 49 and 1450 DF,  p-value: < 2.2e-16

```

### 2.2.12 Plots

```

scale.3d <- function(x) sprintf("%.3f", x)

rho.plot <- as.data.frame(cbind(inf.lands.200kb.rep_1$bin,
                                sim.rho.200kb$sim,
                                inf.lands.200kb.rep_1$rho,
                                inf.lands.200kb.rep_2$rho,
                                inf.lands.200kb.rep_3$rho,
                                inf.lands.200kb.rep_4$rho,
                                inf.lands.200kb.rep_5$rho,
                                inf.lands.200kb.rep_6$rho,
                                inf.lands.200kb.rep_7$rho,
                                inf.lands.200kb.rep_8$rho,
                                inf.lands.200kb.rep_9$rho,
                                inf.lands.200kb.rep_10$rho))

rho.plot[,3:ncol(rho.plot)] <- 1.53 * rho.plot[,3:ncol(rho.plot)] # scaling because of SCRM NO vs Ne

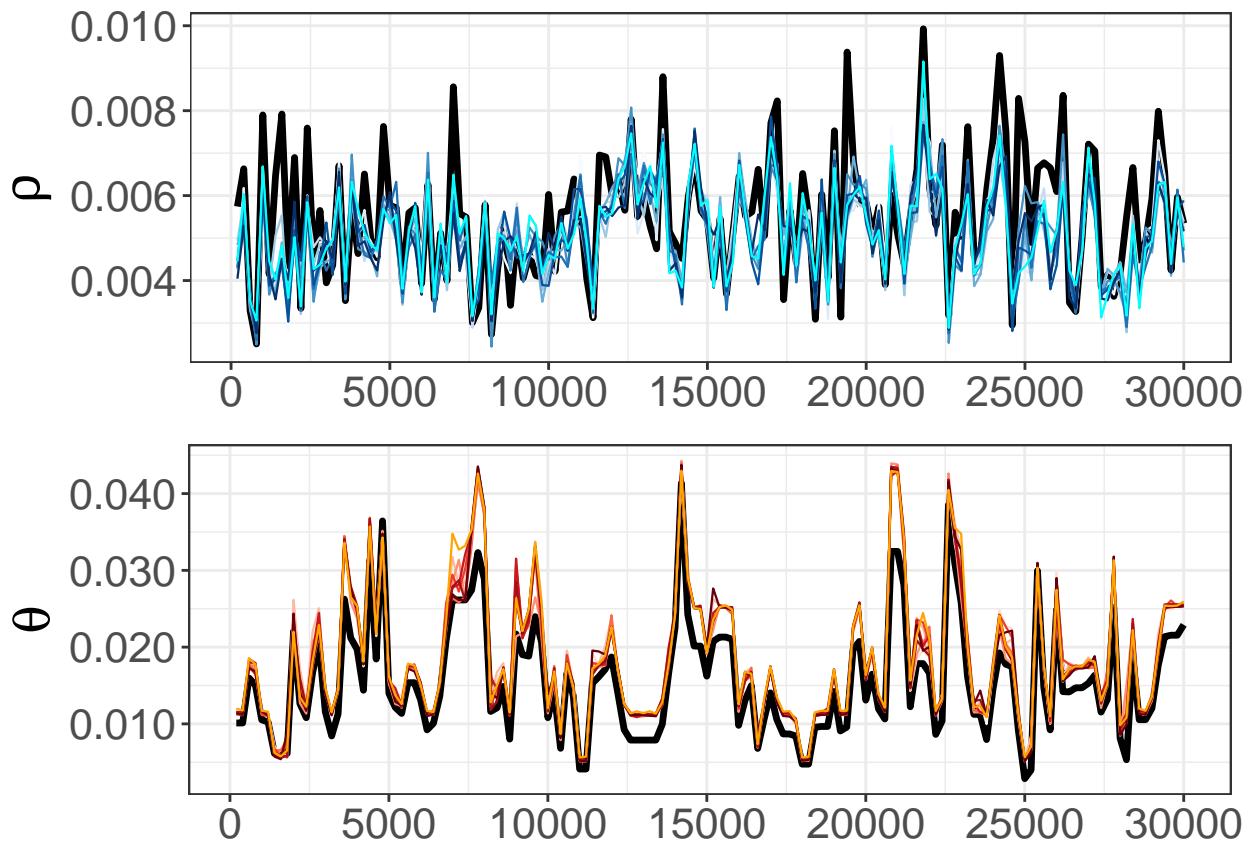
names(rho.plot) <- c("bin", "sim", reps)
molten.rho <- melt(rho.plot, id.vars = "bin")
rho.map.200kb <- ggplot(data = molten.rho, aes(x = bin * 200, y = value, colour = variable)) + theme_bw()
rho.map.200kb <- rho.map.200kb + geom_line(data = molten.rho, aes(size = variable)) + scale_size_manual()
rho.map.200kb <- rho.map.200kb + scale_color_manual(values = c("black", brewer.pal(n = 9, name = "Blues"))
rho.map.200kb <- rho.map.200kb + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_breaks())
rho.map.200kb <- rho.map.200kb + labs(title = NULL, x = NULL, y = expression(rho))
rho.map.200kb <- rho.map.200kb + theme(text = element_text(size = 20), axis.title.x = element_text(size = 20))

theta.plot <- as.data.frame(cbind(inf.lands.200kb.rep_1$bin,
                                    sim.theta.200kb$sim,
                                    inf.lands.200kb.rep_1$theta,
                                    inf.lands.200kb.rep_2$theta,
                                    inf.lands.200kb.rep_3$theta,
                                    inf.lands.200kb.rep_4$theta,
                                    inf.lands.200kb.rep_5$theta,
                                    inf.lands.200kb.rep_6$theta,
                                    inf.lands.200kb.rep_7$theta,
                                    inf.lands.200kb.rep_8$theta,
                                    inf.lands.200kb.rep_9$theta,
                                    inf.lands.200kb.rep_10$theta))

names(theta.plot) <- c("bin", "sim", reps)
molten.theta <- melt(theta.plot, id.vars = "bin")
theta.map.200kb <- ggplot(data = molten.theta, aes(x = bin * 200, y = value, colour = variable)) + theme_bw()
theta.map.200kb <- theta.map.200kb + geom_line(data = molten.theta, aes(size = variable)) + scale_size_manual()
theta.map.200kb <- theta.map.200kb + scale_color_manual(values = c("black", brewer.pal(n = 9, name = "Reds"))
theta.map.200kb <- theta.map.200kb + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_breaks())
theta.map.200kb <- theta.map.200kb + labs(title = NULL, x = NULL, y = expression(theta))
theta.map.200kb <- theta.map.200kb + theme(text = element_text(size = 20), axis.title.x = element_text(size = 20))

plot_grid(rho.map.200kb, theta.map.200kb, nrow = 2, ncol = 1)

```



## 2.3 1 Mb scale

```
r2.inf.1Mb <- as.data.frame(matrix(ncol = nreps, nrow = 5))
row.names(r2.inf.1Mb) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
colnames(r2.inf.1Mb) <- reps

# sim landscapes
sim.rho.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims/dm.sim.rho.1e+06.txt")
sim.theta.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims/dm.sim.theta.1e+06.txt")
sim.lands.1Mb <- as.data.frame(cbind(sim.theta.1Mb$sim, sim.rho.1Mb$sim))
names(sim.lands.1Mb) <- c("theta", "rho")
```

### 2.3.1 Replicate 1

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_1/rs.pair_1.", sep = "")
pi.1Mb <- read.table(paste(p, "diversity.1Mb.bedgraph", sep = ""), header = T)
pi.1Mb$avg <- apply(pi.1Mb[4:ncol(pi.1Mb)], 1, mean)
tmrca.1Mb <- read.table(paste(p, "TMRCA.1Mb.bedgraph", sep = ""), header = T)
tmrca.1Mb$avg <- apply(tmrca.1Mb[4:ncol(tmrca.1Mb)], 1, mean)
rho.1Mb <- read.table(paste(p, "rho.1Mb.bedgraph", sep = ""), header = T)
theta.1Mb <- read.table(paste(p, "theta.1Mb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.1Mb$sim, theta.1Mb$sample_mean, method = "spearman")

## Spearman's rank correlation rho
```

```

##  

## data: sim.theta.1Mb$sim and theta.1Mb$sample_mean  

## S = 94, p-value < 2.2e-16  

## alternative hypothesis: true rho is not equal to 0  

## sample estimates:  

## rho  

## 0.9790879  

inf.lands.1Mb.rep_1 <- as.data.frame(cbind(pi.1Mb$avg, theta.1Mb$sample_mean, rho.1Mb$sample_mean, tmrca.1Mb$sample_mean))
names(inf.lands.1Mb.rep_1) <- c("diversity", "theta", "rho", "tmrca")  

# centering
inf.lands.1Mb.rep_1$thetaC <- inf.lands.1Mb.rep_1$theta - mean(inf.lands.1Mb.rep_1$theta)
inf.lands.1Mb.rep_1$tmrcaC <- inf.lands.1Mb.rep_1$tmrca - mean(inf.lands.1Mb.rep_1$tmrca)
inf.lands.1Mb.rep_1$rhoC <- inf.lands.1Mb.rep_1$rho - mean(inf.lands.1Mb.rep_1$rho)  

inf.lands.1Mb.rep_1$bin <- 1:nrow(inf.lands.1Mb.rep_1)  

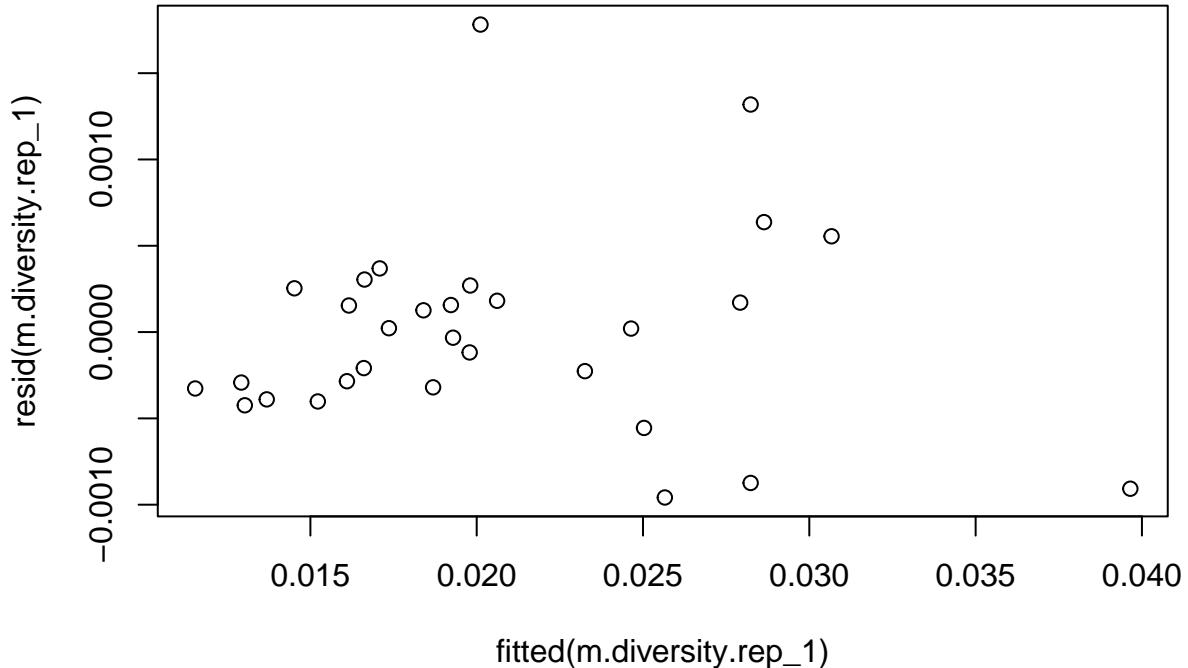
# for merging:
inf.lands.1Mb.rep_1$Replicate <- 1  

m.diversity.rep_1 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.1Mb.rep_1)  

plot(resid(m.diversity.rep_1)~fitted(m.diversity.rep_1))

```



```

dwtest(m.diversity.rep_1)  

##  

## Durbin-Watson test  

##  

## data: m.diversity.rep_1  

## DW = 1.9667, p-value = 0.4252  

## alternative hypothesis: true autocorrelation is greater than 0

```

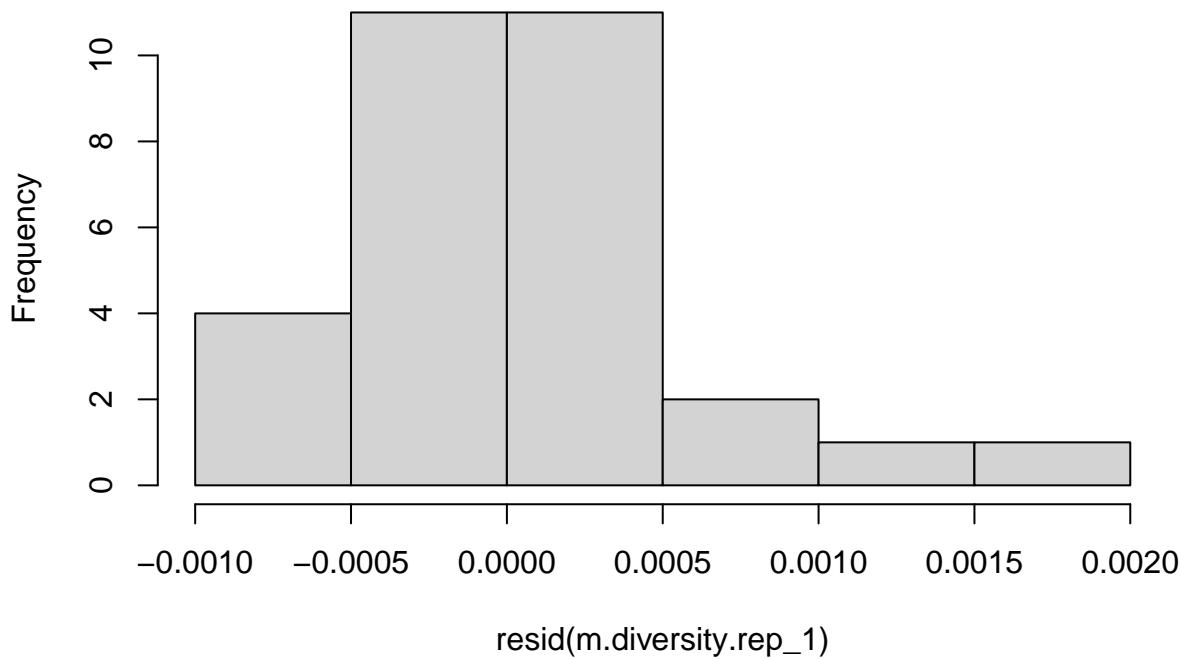
```

hmctest(m.diversity.rep_1)

##
##  Harrison-McCabe test
##
## data: m.diversity.rep_1
## HMC = 0.46606, p-value = 0.418
hist(resid(m.diversity.rep_1))

```

### Histogram of resid(m.diversity.rep\_1)



```

summary(m.diversity.rep_1)

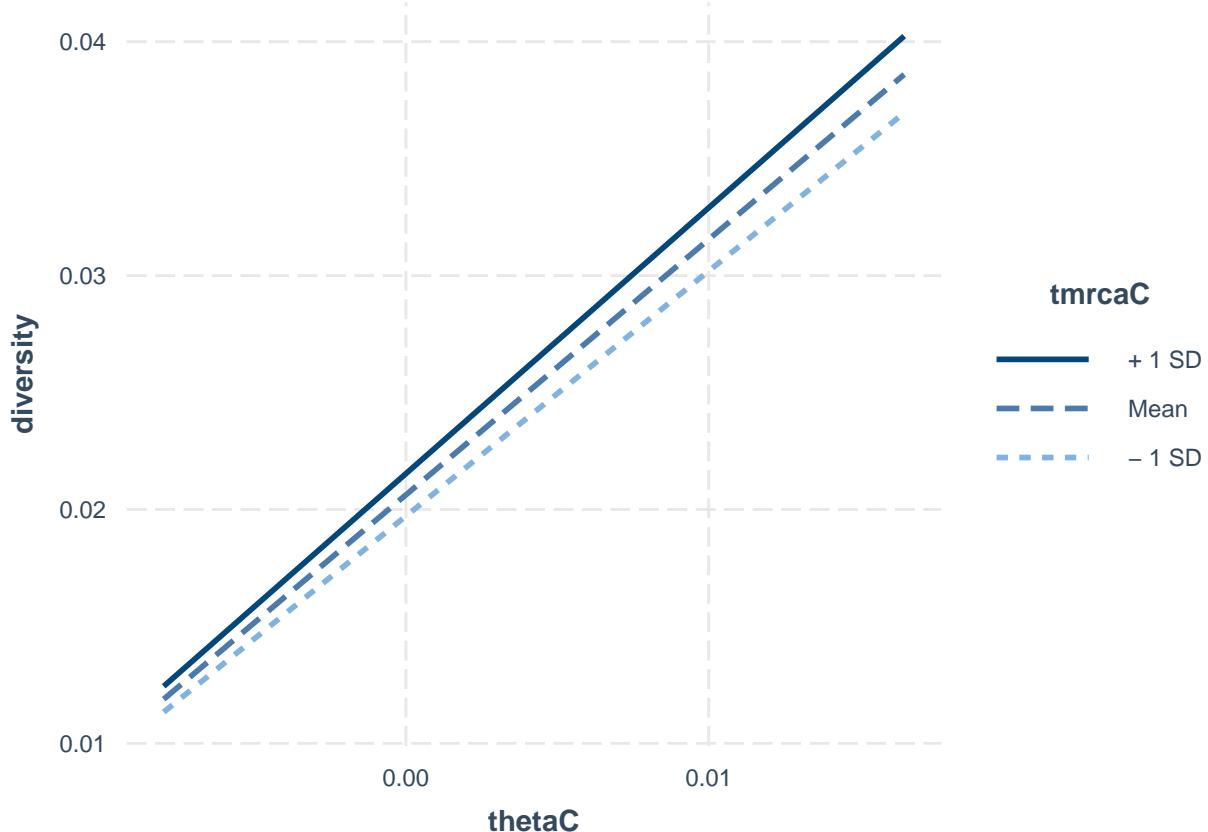
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##      data = inf.lands.1Mb.rep_1)
##
## Residuals:
##      Min        1Q    Median        3Q       Max
## -0.0009583 -0.0003251 -0.0000061  0.0002355  0.0017816
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.020625  0.000115 179.401 < 2e-16 ***
## thetaC      1.092123  0.021125  51.697 < 2e-16 ***
## rhoC        0.003099  0.351525   0.009   0.993
## tmrcaC     0.016704  0.002985   5.596 8.05e-06 ***
## thetaC:tmrcaC 0.819285  0.498125   1.645    0.113
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

## 
## Residual standard error: 0.0006297 on 25 degrees of freedom
## Multiple R-squared:  0.9917, Adjusted R-squared:  0.9904
## F-statistic: 749.1 on 4 and 25 DF,  p-value: < 2.2e-16
interact_plot(m.diversity.rep_1, pred = thetaC, modx= tmrcaC)

```



```

g.rep_1 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
                 data = inf.lands.1Mb.rep_1, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_1)

```

```

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep_1
##       AIC      BIC logLik
##   -348.56 -338.7516 181.28
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.0188108
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0206248 0.0001171 176.16584 0.0000
## thetaC      1.0920063 0.0211898  51.53453 0.0000

```

```

## tmrcaC      0.0168279 0.0029670  5.67164  0.0000
## rhoC        0.0007886 0.3523958  0.00224  0.9982
## thetaC:tmrcaC 0.8389718 0.4973907  1.68675  0.1041
##
## Correlation:
##              (Intr) thetaC tmrcaC rhoC
## thetaC      -0.001
## tmrcaC      0.001 -0.171
## rhoC        0.000 -0.021  0.376
## thetaC:tmrcaC 0.004 -0.283  0.575 -0.003
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -1.67095844 -0.56781078 -0.01108315  0.40839933  3.09944720
##
## Residual standard error: 0.0005748314
## Degrees of freedom: 30 total; 25 residual
vif(g.rep_1)

##          thetaC         tmrcaC         rhoC thetaC:tmrcaC
##          1.087501      1.898249      1.271394      1.717045

g.rep_1.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.1Mb.rep_1, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_1.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.1Mb.rep_1
## AIC      BIC  logLik
## -329.2361 -322.2301 169.618
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##          Phi
## -0.3222673
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0206090 0.0001242 165.95945 0.0000
## thetaC       1.0935838 0.0263685  41.47310 0.0000
## rhoC        -0.9523384 0.3871228  -2.46004 0.0206
##
## Correlation:
##          (Intr) thetaC
## thetaC  0.002
## rhoC   -0.001 -0.056
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -2.3284963 -0.5352289  0.1792210  0.6290505  1.9096098
##

```

```

## Residual standard error: 0.0008939388
## Degrees of freedom: 30 total; 27 residual
anova.diversity <- Anova(m.diversity.rep_1)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.inf.1Mb[1, 1] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
r2.inf.1Mb[2, 1] <- anova.diversity$VarExp[1] * 100
r2.inf.1Mb[3, 1] <- anova.diversity$VarExp[2] * 100
r2.inf.1Mb[4, 1] <- anova.diversity$VarExp[3] * 100
r2.inf.1Mb[5, 1] <- anova.diversity$VarExp[4] * 100

```

### 2.3.2 Replicate 2

```

p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_2/rs.pair_2.", sep = "")
pi.1Mb <- read.table(paste(p, "diversity.1Mb.bedgraph", sep = ""), header = T)
pi.1Mb$avg <- apply(pi.1Mb[4:ncol(pi.1Mb)], 1, mean)
tmrca.1Mb <- read.table(paste(p, "TMRCA.1Mb.bedgraph", sep = ""), header = T)
tmrca.1Mb$avg <- apply(tmrca.1Mb[4:ncol(tmrca.1Mb)], 1, mean)
rho.1Mb <- read.table(paste(p, "rho.1Mb.bedgraph", sep = ""), header = T)
theta.1Mb <- read.table(paste(p, "theta.1Mb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.1Mb$sim, theta.1Mb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.1Mb$sim and theta.1Mb$sample_mean
## S = 114, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## 0.9746385

inf.lands.1Mb.rep_2 <- as.data.frame(cbind(pi.1Mb$avg, theta.1Mb$sample_mean, rho.1Mb$sample_mean, tmrca.1Mb$avg))
names(inf.lands.1Mb.rep_2) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.1Mb.rep_2$thetaC <- inf.lands.1Mb.rep_2$theta - mean(inf.lands.1Mb.rep_2$theta)
inf.lands.1Mb.rep_2$tmrcaC <- inf.lands.1Mb.rep_2$tmrca - mean(inf.lands.1Mb.rep_2$tmrca)
inf.lands.1Mb.rep_2$rhoC <- inf.lands.1Mb.rep_2$rho - mean(inf.lands.1Mb.rep_2$rho)

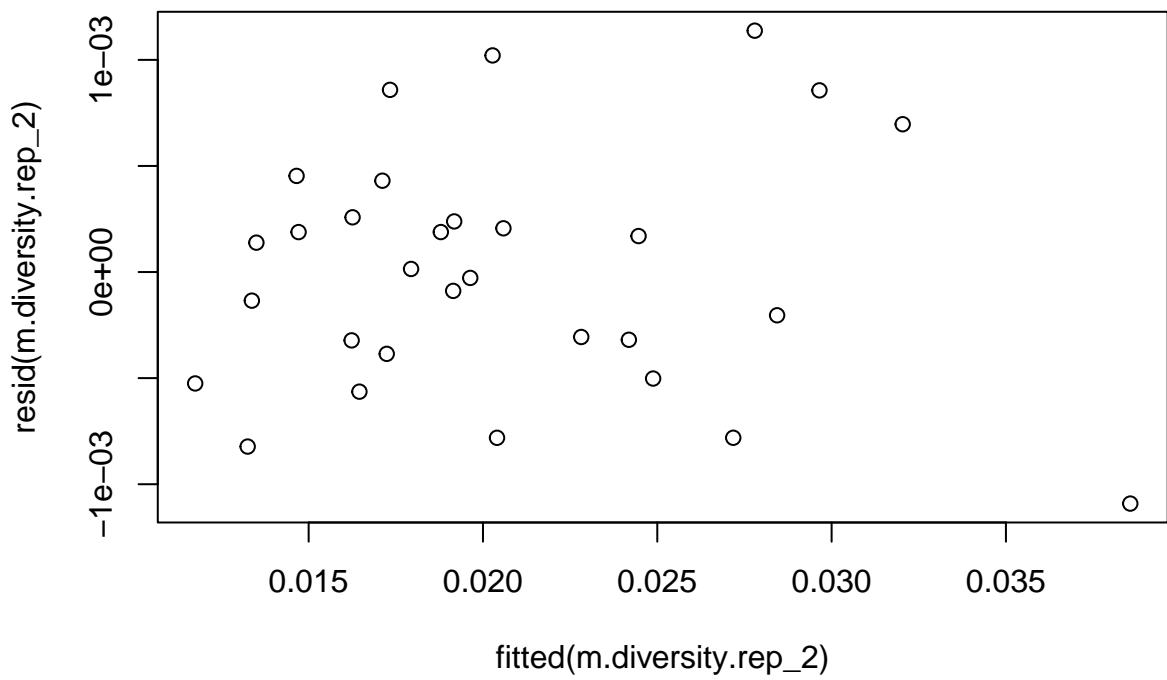
inf.lands.1Mb.rep_2$bin <- 1:nrow(inf.lands.1Mb.rep_2)

# for merging:
inf.lands.1Mb.rep_2$Replicate <- 2

m.diversity.rep_2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.1Mb.rep_2)

plot(resid(m.diversity.rep_2)~fitted(m.diversity.rep_2))

```

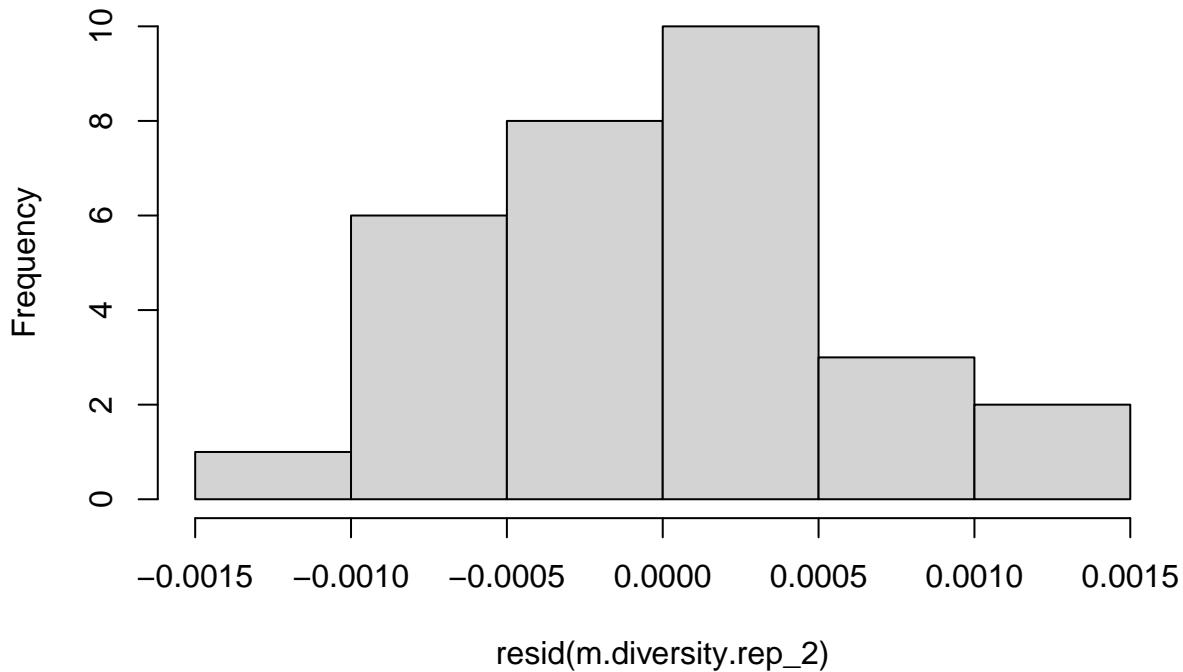


```
dwtest(m.diversity.rep_2)
```

```
##
##  Durbin-Watson test
##
## data: m.diversity.rep_2
## DW = 1.966, p-value = 0.4212
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_2)
```

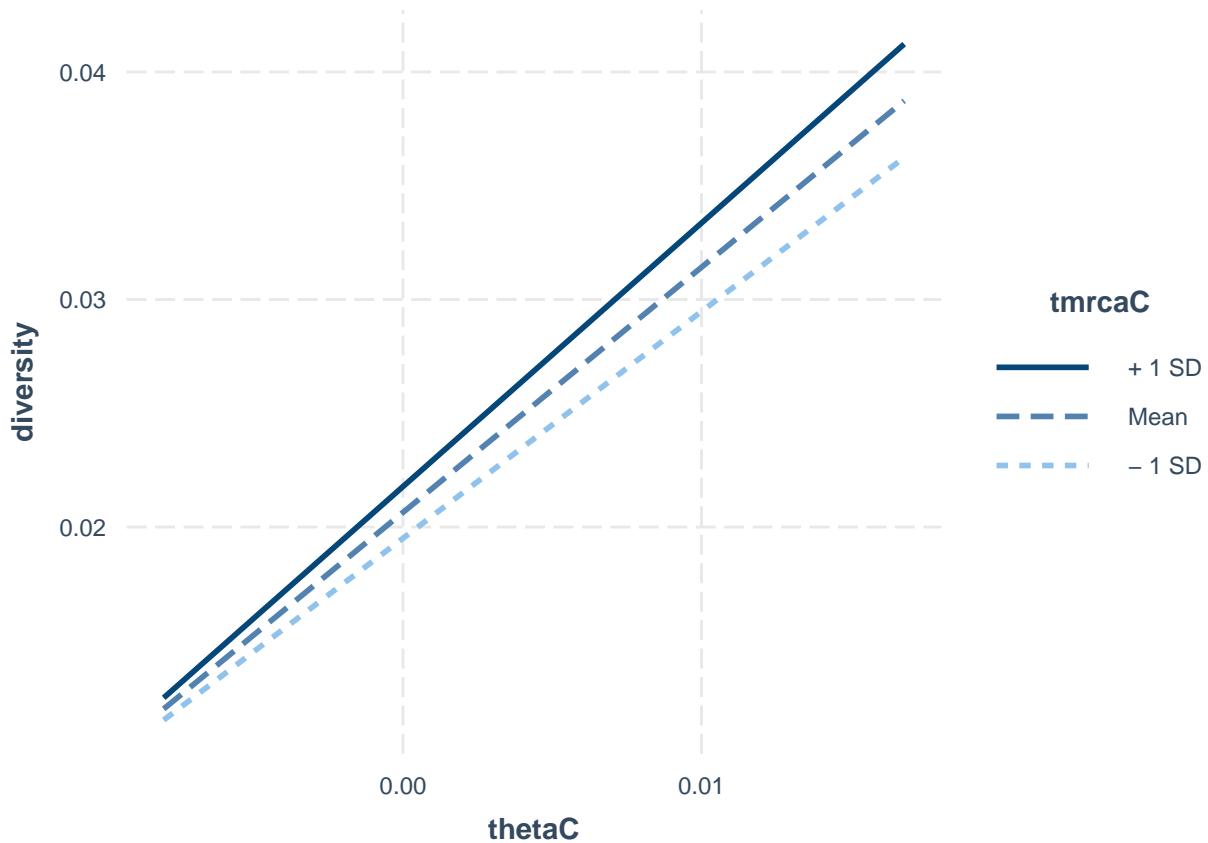
```
##
##  Harrison-McCabe test
##
## data: m.diversity.rep_2
## HMC = 0.4866, p-value = 0.476
hist(resid(m.diversity.rep_2))
```

## Histogram of resid(m.diversity.rep\_2)



```
summary(m.diversity.rep_2)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.1Mb.rep_2)
##
## Residuals:
##       Min         1Q      Median        3Q       Max
## -1.091e-03 -3.697e-04 -6.640e-06  2.531e-04  1.138e-03
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.0206424  0.0001134 182.048 < 2e-16 ***
## thetaC      1.0774623  0.0197421  54.577 < 2e-16 ***
## rhoC        0.3474698  0.4535646   0.766  0.4508
## tmrcaC      0.0195388  0.0026090   7.489 7.66e-08 ***
## thetaC:tmrcaC 1.3891871  0.5019294   2.768  0.0105 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0006138 on 25 degrees of freedom
## Multiple R-squared:  0.9919, Adjusted R-squared:  0.9906
## F-statistic: 765.1 on 4 and 25 DF,  p-value: < 2.2e-16
interact_plot(m.diversity.rep_2, pred = thetaC, modx= tmrcaC)
```



```

g.rep_2 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
                 data = inf.lands.1Mb.rep_2, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_2)

```

```

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep_2
##          AIC      BIC    logLik
##     -350.0905 -340.2821 182.0452
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.01325283
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0206428 0.0001148 179.80497 0.0000
## thetaC      1.0773596 0.0197550  54.53607 0.0000
## tmrcaC      0.0195384 0.0026060    7.49753 0.0000
## rhoC        0.3372081 0.4548652   0.74134 0.4654
## thetaC:tmrcaC 1.3998089 0.5015497   2.79097 0.0099
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC

```

```

## thetaC      -0.015
## tmrcaC      0.078  0.012
## rhoC       -0.056  0.004  0.165
## thetaC:tmrcaC  0.150 -0.097  0.527 -0.369
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -1.95006224 -0.66519213 -0.01401553  0.44798577  2.03312007
##
## Residual standard error: 0.0005603058
## Degrees of freedom: 30 total; 25 residual
vif(g.rep_2)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##      1.021369     1.764385     1.468410     2.007938

g.rep_2.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.1Mb.rep_2, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_2.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.1Mb.rep_2
##      AIC      BIC   logLik
## -318.0822 -311.0762 164.0411
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## -0.01297054
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0205937 0.0001941 106.12154 0.0000
## thetaC       1.0716533 0.0343149  31.23000 0.0000
## rhoC       -0.5592219 0.6546032  -0.85429 0.4005
##
## Correlation:
##      (Intr) thetaC
## thetaC  0.000
## rhoC   0.000 -0.081
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -2.0512845 -0.6085269  0.1849871  0.5460123  1.6511980
##
## Residual standard error: 0.00102108
## Degrees of freedom: 30 total; 27 residual
anova.diversity <- Anova(m.diversity.rep_2)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.1Mb[1, 2] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] * 100)
r2.inf.1Mb[2, 2] <- anova.diversity$VarExp[1] * 100
r2.inf.1Mb[3, 2] <- anova.diversity$VarExp[2] * 100
r2.inf.1Mb[4, 2] <- anova.diversity$VarExp[3] * 100
r2.inf.1Mb[5, 2] <- anova.diversity$VarExp[4] * 100
```

### 2.3.3 Replicate 3

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_3/rs.pair_3.", sep = "")
pi.1Mb <- read.table(paste(p, "diversity.1Mb.bedgraph", sep = ""), header = T)
pi.1Mb$avg <- apply(pi.1Mb[4:ncol(pi.1Mb)], 1, mean)
tmrca.1Mb <- read.table(paste(p, "TMRCAs.1Mb.bedgraph", sep = ""), header = T)
tmrca.1Mb$avg <- apply(tmrca.1Mb[4:ncol(tmrca.1Mb)], 1, mean)
rho.1Mb <- read.table(paste(p, "rho.1Mb.bedgraph", sep = ""), header = T)
theta.1Mb <- read.table(paste(p, "theta.1Mb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.1Mb$sim, theta.1Mb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.1Mb$sim and theta.1Mb$sample_mean
## S = 86, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9808676

inf.lands.1Mb.rep_3 <- as.data.frame(cbind(pi.1Mb$avg, theta.1Mb$sample_mean, rho.1Mb$sample_mean, tmrca.1Mb$avg))
names(inf.lands.1Mb.rep_3) <- c("diversity", "theta", "rho", "tmrca")

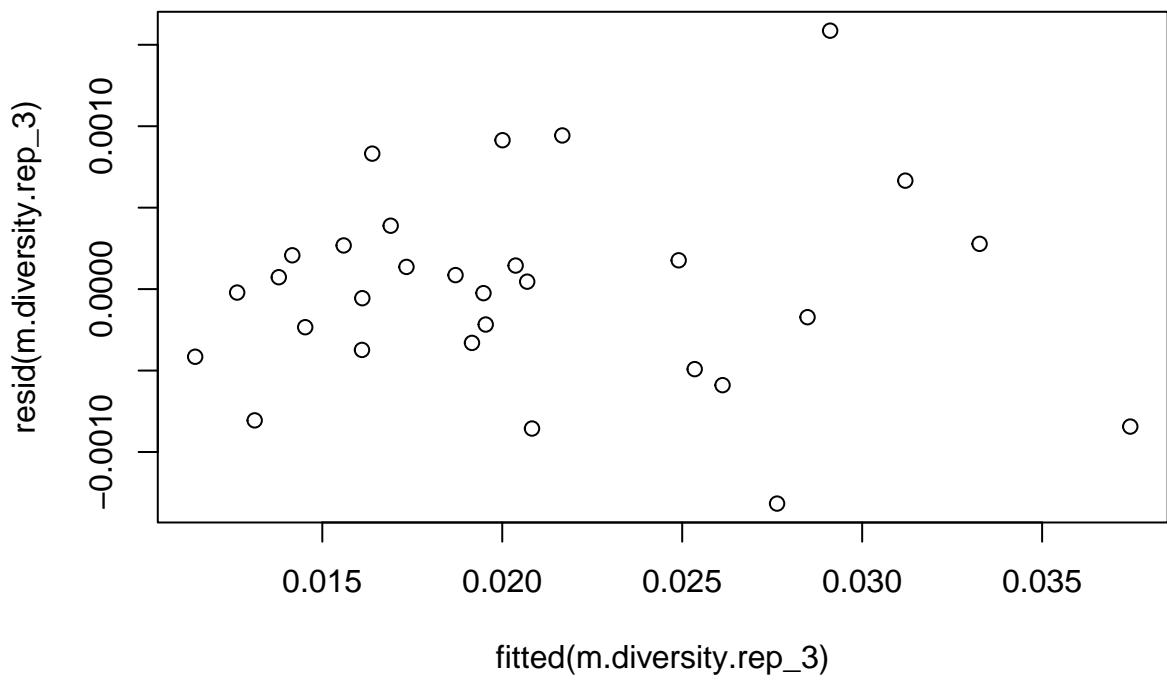
# centering
inf.lands.1Mb.rep_3$thetaC <- inf.lands.1Mb.rep_3$theta - mean(inf.lands.1Mb.rep_3$theta)
inf.lands.1Mb.rep_3$tmrcaC <- inf.lands.1Mb.rep_3$tmrca - mean(inf.lands.1Mb.rep_3$tmrca)
inf.lands.1Mb.rep_3$rhoC <- inf.lands.1Mb.rep_3$rho - mean(inf.lands.1Mb.rep_3$rho)

inf.lands.1Mb.rep_3$bin <- 1:nrow(inf.lands.1Mb.rep_3)

# for merging:
inf.lands.1Mb.rep_3$Replicate <- 3

m.diversity.rep_3 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.1Mb.rep_3)

plot(resid(m.diversity.rep_3)~fitted(m.diversity.rep_3))
```

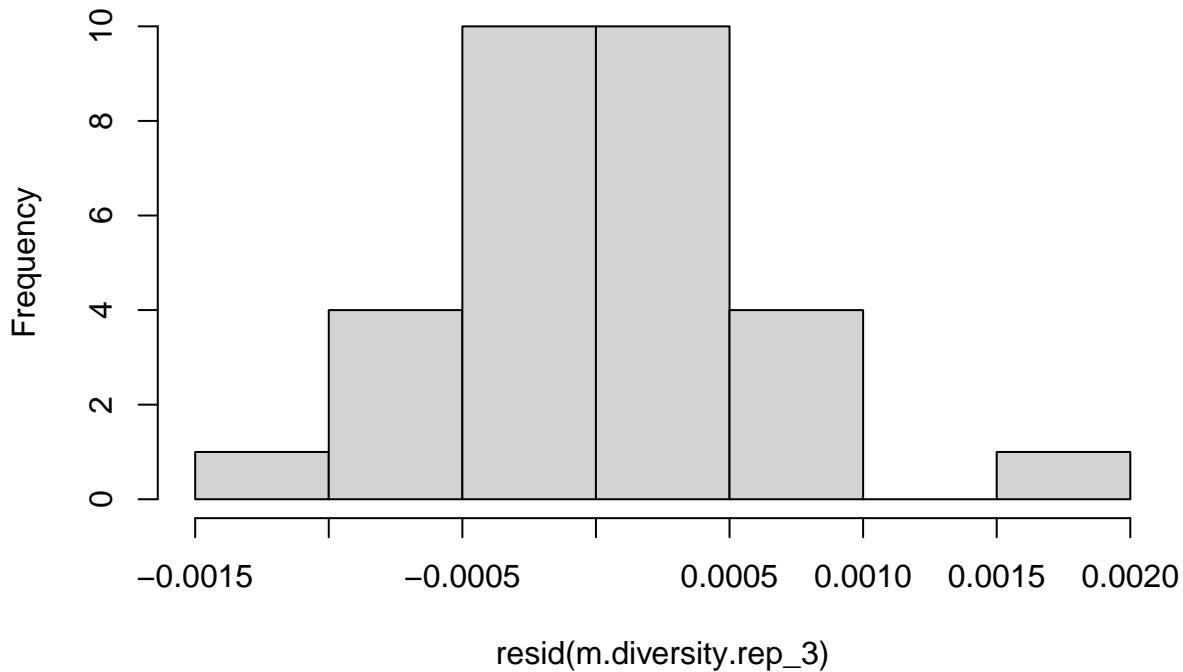


```
dwtest(m.diversity.rep_3)
```

```
##
##  Durbin-Watson test
##
## data: m.diversity.rep_3
## DW = 1.3502, p-value = 0.02515
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_3)
```

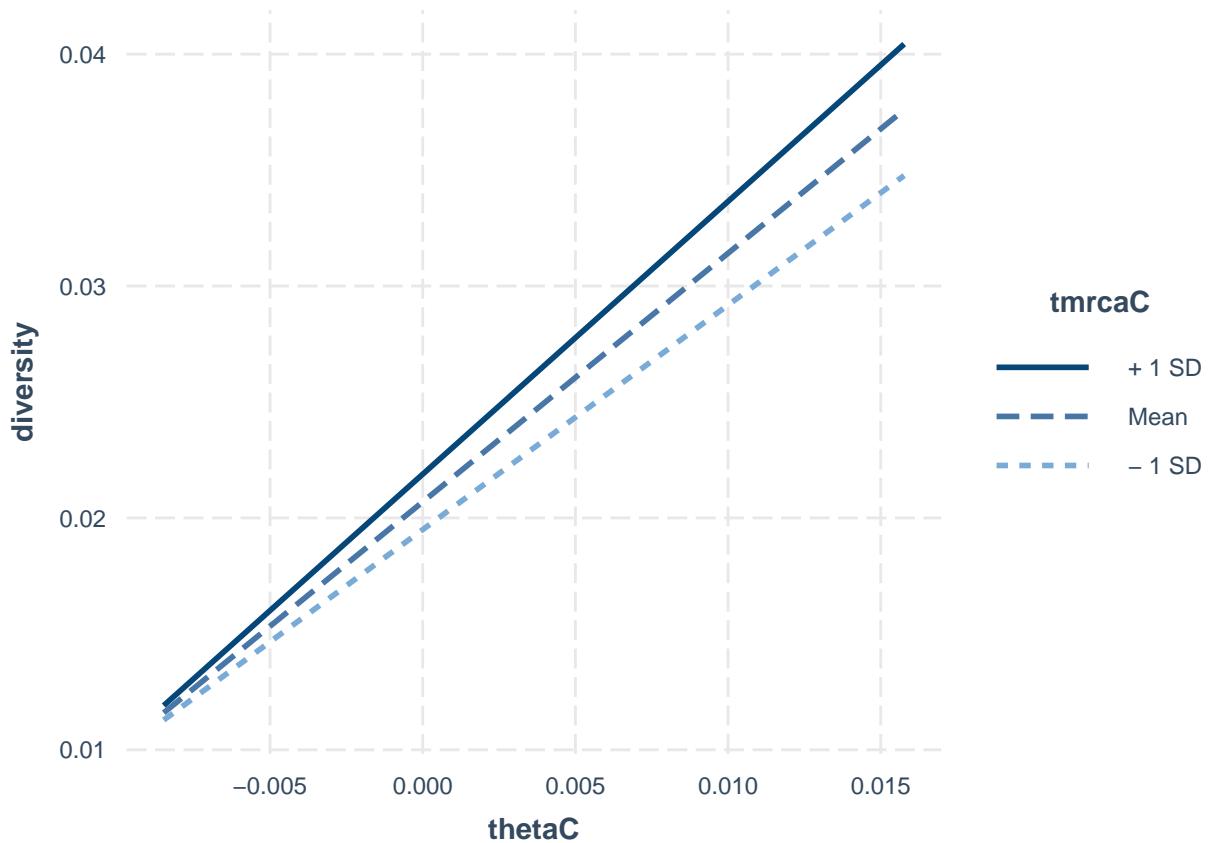
```
##
##  Harrison-McCabe test
##
## data: m.diversity.rep_3
## HMC = 0.51975, p-value = 0.553
hist(resid(m.diversity.rep_3))
```

## Histogram of resid(m.diversity.rep\_3)



```
summary(m.diversity.rep_3)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.1Mb.rep_3)
##
## Residuals:
##       Min         1Q      Median         3Q        Max
## -1.317e-03 -3.626e-04  1.232e-05  2.530e-04  1.587e-03
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.0206899  0.0001206 171.565 < 2e-16 ***
## thetaC       1.0723605  0.0213849  50.146 < 2e-16 ***
## rhoC        0.1501119  0.3861502   0.389  0.70076
## tmrcaC      0.0209333  0.0025600   8.177 1.57e-08 ***
## thetaC:tmrcaC 1.8224106  0.5068011   3.596  0.00139 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0006567 on 25 degrees of freedom
## Multiple R-squared:  0.9915, Adjusted R-squared:  0.9901
## F-statistic: 728.3 on 4 and 25 DF,  p-value: < 2.2e-16
interact_plot(m.diversity.rep_3, pred = thetaC, modx= tmrcaC)
```



```
g.rep_3 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
                  data = inf.lands.1Mb.rep_3, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_3)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep_3
##          AIC      BIC    logLik
## -349.3777 -339.5693 181.6889
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.3277574
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0206863 0.0001662 124.43077 0.0000
## thetaC      1.0693355 0.0206663  51.74291 0.0000
## tmrcaC      0.0216118 0.0022595   9.56486 0.0000
## rhoC        0.0916173 0.3604146   0.25420 0.8014
## thetaC:tmrcaC 1.9813808 0.4596404   4.31072 0.0002
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC          0.024
## tmrcaC        -0.051 -0.272
## rhoC           0.026  0.090  0.062
## thetaC:tmrcaC -0.081 -0.284  0.478 -0.312
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -2.06120732 -0.59725161  0.02282195  0.36381078  2.61148857
##
## Residual standard error: 0.0005989662
## Degrees of freedom: 30 total; 25 residual
vif(g.rep_3)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##     1.119139    1.425723    1.185890    1.564342
g.rep_3.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.1Mb.rep_3, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_3.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.1Mb.rep_3
##      AIC      BIC   logLik
## -311.0899 -304.0839 160.5449
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## -0.06226692
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0207330 0.0002082 99.56794 0.0000
## thetaC       1.1012864 0.0377084 29.20532 0.0000
## rhoC        -0.3177321 0.6160273 -0.51578 0.6102
##
## Correlation:
##      (Intr) thetaC
## thetaC  0.000
## rhoC   -0.001 -0.036
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -2.20029757 -0.55512347  0.03085907  0.50826091  1.89284077
##
## Residual standard error: 0.00114935
## Degrees of freedom: 30 total; 27 residual
anova.diversity <- Anova(m.diversity.rep_3)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.1Mb[1, 3] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] * 100)
r2.inf.1Mb[2, 3] <- anova.diversity$VarExp[1] * 100
r2.inf.1Mb[3, 3] <- anova.diversity$VarExp[2] * 100
r2.inf.1Mb[4, 3] <- anova.diversity$VarExp[3] * 100
r2.inf.1Mb[5, 3] <- anova.diversity$VarExp[4] * 100
```

### 2.3.4 Replicate 4

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_4/rs.pair_4.", sep = "")
pi.1Mb <- read.table(paste(p, "diversity.1Mb.bedgraph", sep = ""), header = T)
pi.1Mb$avg <- apply(pi.1Mb[4:ncol(pi.1Mb)], 1, mean)
tmrca.1Mb <- read.table(paste(p, "TMRCAs.1Mb.bedgraph", sep = ""), header = T)
tmrca.1Mb$avg <- apply(tmrca.1Mb[4:ncol(tmrca.1Mb)], 1, mean)
rho.1Mb <- read.table(paste(p, "rho.1Mb.bedgraph", sep = ""), header = T)
theta.1Mb <- read.table(paste(p, "theta.1Mb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.1Mb$sim, theta.1Mb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.1Mb$sim and theta.1Mb$sample_mean
## S = 80, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9822024

inf.lands.1Mb.rep_4 <- as.data.frame(cbind(pi.1Mb$avg, theta.1Mb$sample_mean, rho.1Mb$sample_mean, tmrca.1Mb$avg))
names(inf.lands.1Mb.rep_4) <- c("diversity", "theta", "rho", "tmrca")

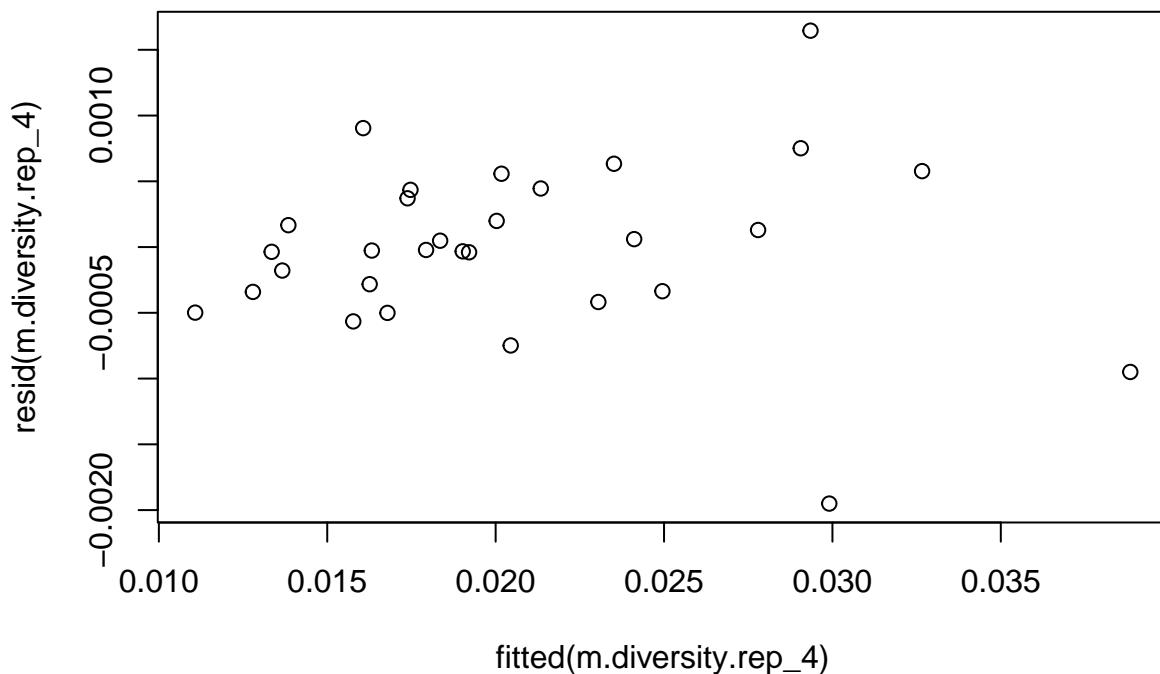
# centering
inf.lands.1Mb.rep_4$thetaC <- inf.lands.1Mb.rep_4$theta - mean(inf.lands.1Mb.rep_4$theta)
inf.lands.1Mb.rep_4$tmrcaC <- inf.lands.1Mb.rep_4$tmrca - mean(inf.lands.1Mb.rep_4$tmrca)
inf.lands.1Mb.rep_4$rhoC <- inf.lands.1Mb.rep_4$rho - mean(inf.lands.1Mb.rep_4$rho)

inf.lands.1Mb.rep_4$bin <- 1:nrow(inf.lands.1Mb.rep_4)

# for merging:
inf.lands.1Mb.rep_4$Replicate <- 4

m.diversity.rep_4 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.1Mb.rep_4)

plot(resid(m.diversity.rep_4)~fitted(m.diversity.rep_4))
```

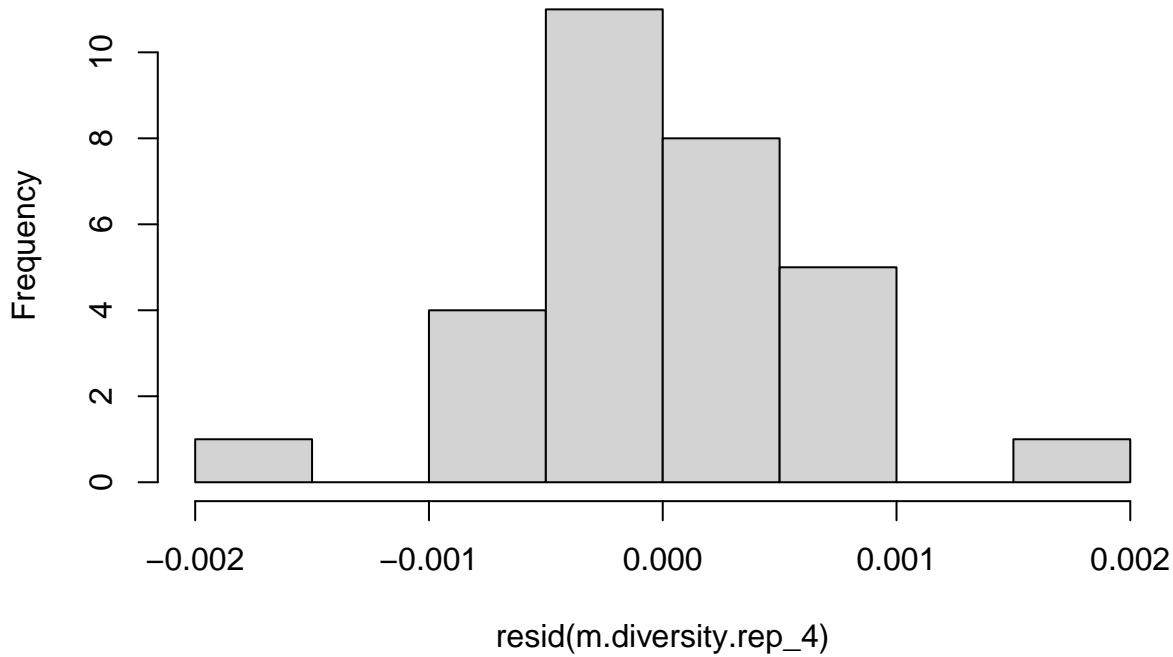


```
dwtest(m.diversity.rep_4)
```

```
##
##  Durbin-Watson test
##
## data: m.diversity.rep_4
## DW = 2.0871, p-value = 0.5863
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_4)
```

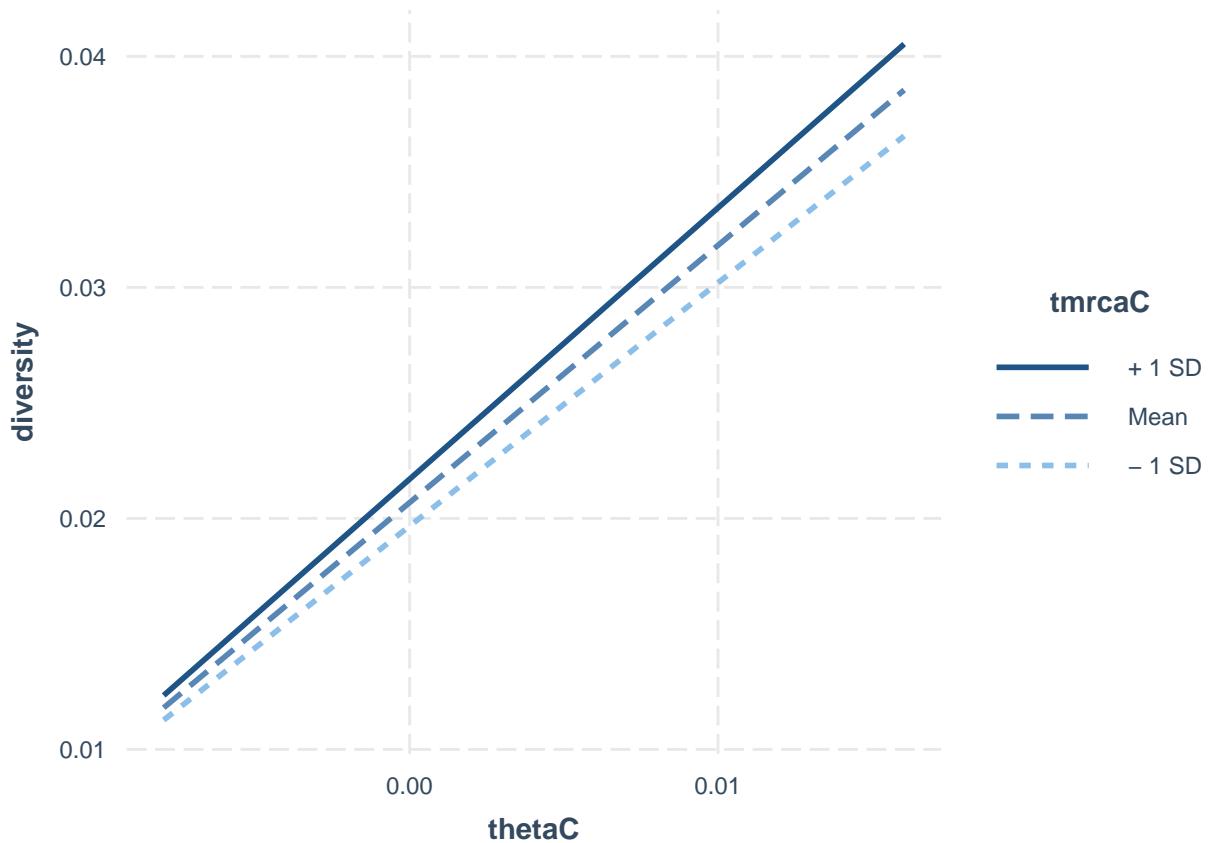
```
##
##  Harrison-McCabe test
##
## data: m.diversity.rep_4
## HMC = 0.42593, p-value = 0.283
hist(resid(m.diversity.rep_4))
```

## Histogram of resid(m.diversity.rep\_4)



```
summary(m.diversity.rep_4)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.1Mb.rep_4)
##
## Residuals:
##       Min         1Q      Median         3Q        Max
## -1.950e-03 -3.397e-04 -2.417e-05  4.190e-04  1.645e-03
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.0206840 0.0001284 161.149 < 2e-16 ***
## thetaC       1.1134126 0.0224842  49.520 < 2e-16 ***
## rhoC        -0.0339570 0.4581591  -0.074   0.942
## tmrcaC       0.0178545 0.0033294   5.363 1.46e-05 ***
## thetaC:tmrcaC 1.0646819 0.6921958   1.538   0.137
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.000703 on 25 degrees of freedom
## Multiple R-squared:  0.9901, Adjusted R-squared:  0.9886
## F-statistic: 628.1 on 4 and 25 DF,  p-value: < 2.2e-16
interact_plot(m.diversity.rep_4, pred = thetaC, modx= tmrcaC)
```



```
g.rep_4 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
                  data = inf.lands.1Mb.rep_4, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_4)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep_4
##          AIC      BIC    logLik
##     -342.0193 -332.2109 178.0096
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## -0.05853672
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0206839 0.0001213 170.49504 0.0000
## thetaC      1.1137846 0.0222646  50.02482 0.0000
## tmrcaC      0.0173804 0.0033848   5.13488 0.0000
## rhoC        -0.0467801 0.4513716  -0.10364 0.9183
## thetaC:tmrcaC 0.9716766 0.6991874   1.38972 0.1769
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC      0.001
## tmrcaC     -0.003 -0.036
## rhoC        0.002  0.016  0.215
## thetaC:tmrcaC -0.006 -0.054  0.653 -0.181
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -3.03132272 -0.49951188 -0.03148496  0.64957883  2.58514901
##
## Residual standard error: 0.0006419926
## Degrees of freedom: 30 total; 25 residual
vif(g.rep_4)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##      1.002978     2.181651    1.293335     2.154008
g.rep_4.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.1Mb.rep_4, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_4.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.1Mb.rep_4
##      AIC      BIC   logLik
## -323.3904 -316.3844 166.6952
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## -0.3430849
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0206798 0.0001348 153.42630 0.0000
## thetaC      1.1175389 0.0287817  38.82807 0.0000
## rhoC      -1.1557791 0.4865494  -2.37546 0.0249
##
## Correlation:
##      (Intr) thetaC
## thetaC 0.004
## rhoC  0.003  0.002
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -2.3370913 -0.2969692  0.1671986  0.5302828  2.0808719
##
## Residual standard error: 0.0009928647
## Degrees of freedom: 30 total; 27 residual
anova.diversity <- Anova(m.diversity.rep_4)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.1Mb[1, 4] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] * 100)
r2.inf.1Mb[2, 4] <- anova.diversity$VarExp[1] * 100
r2.inf.1Mb[3, 4] <- anova.diversity$VarExp[2] * 100
r2.inf.1Mb[4, 4] <- anova.diversity$VarExp[3] * 100
r2.inf.1Mb[5, 4] <- anova.diversity$VarExp[4] * 100
```

### 2.3.5 Replicate 5

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_5/rs.pair_5.", sep = "")
pi.1Mb <- read.table(paste(p, "diversity.1Mb.bedgraph", sep = ""), header = T)
pi.1Mb$avg <- apply(pi.1Mb[4:ncol(pi.1Mb)], 1, mean)
tmrca.1Mb <- read.table(paste(p, "TMRCAs.1Mb.bedgraph", sep = ""), header = T)
tmrca.1Mb$avg <- apply(tmrca.1Mb[4:ncol(tmrca.1Mb)], 1, mean)
rho.1Mb <- read.table(paste(p, "rho.1Mb.bedgraph", sep = ""), header = T)
theta.1Mb <- read.table(paste(p, "theta.1Mb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.1Mb$sim, theta.1Mb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.1Mb$sim and theta.1Mb$sample_mean
## S = 76, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9830923

inf.lands.1Mb.rep_5 <- as.data.frame(cbind(pi.1Mb$avg, theta.1Mb$sample_mean, rho.1Mb$sample_mean, tmrca.1Mb$avg))
names(inf.lands.1Mb.rep_5) <- c("diversity", "theta", "rho", "tmrca")

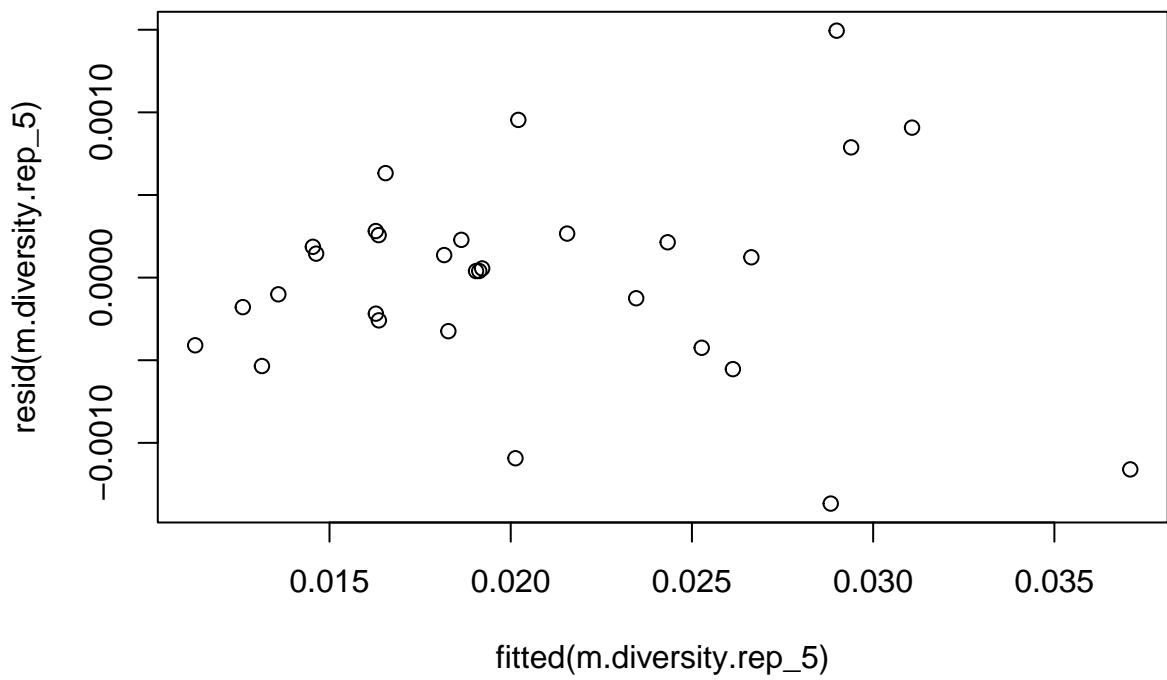
# centering
inf.lands.1Mb.rep_5$thetaC <- inf.lands.1Mb.rep_5$theta - mean(inf.lands.1Mb.rep_5$theta)
inf.lands.1Mb.rep_5$tmrcaC <- inf.lands.1Mb.rep_5$tmrca - mean(inf.lands.1Mb.rep_5$tmrca)
inf.lands.1Mb.rep_5$rhoC <- inf.lands.1Mb.rep_5$rho - mean(inf.lands.1Mb.rep_5$rho)

inf.lands.1Mb.rep_5$bin <- 1:nrow(inf.lands.1Mb.rep_5)

# for merging:
inf.lands.1Mb.rep_5$Replicate <- 5

m.diversity.rep_5 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.1Mb.rep_5)

plot(resid(m.diversity.rep_5)~fitted(m.diversity.rep_5))
```

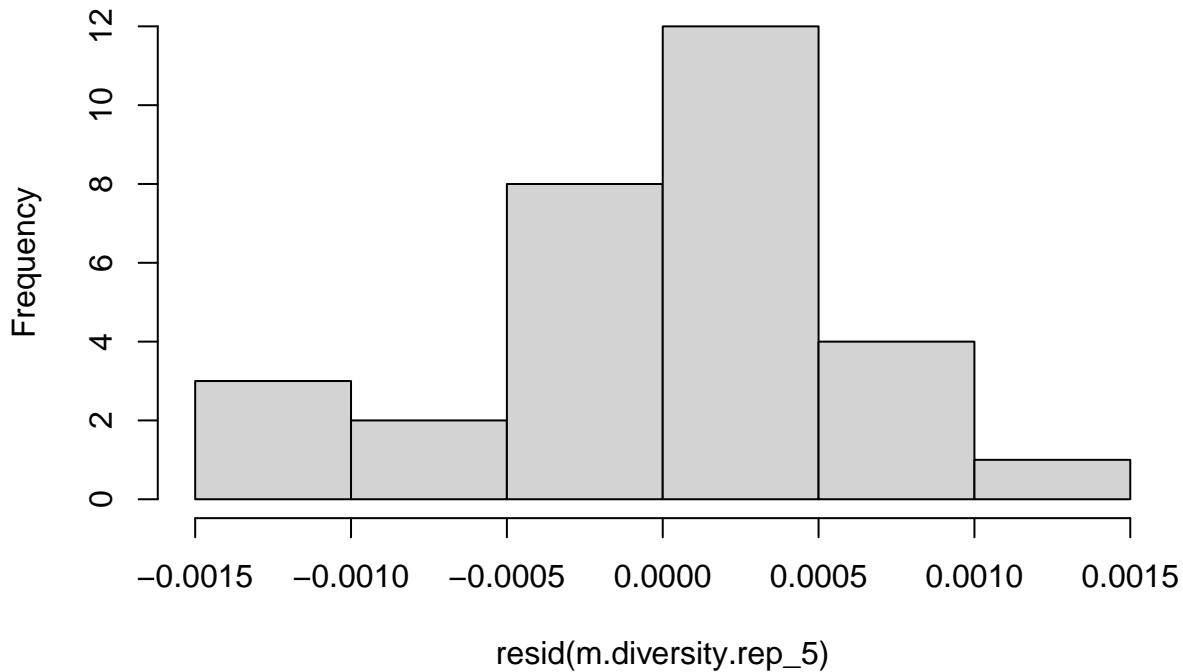


```
dwtest(m.diversity.rep_5)
```

```
##
##  Durbin-Watson test
##
## data: m.diversity.rep_5
## DW = 1.8381, p-value = 0.2796
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_5)
```

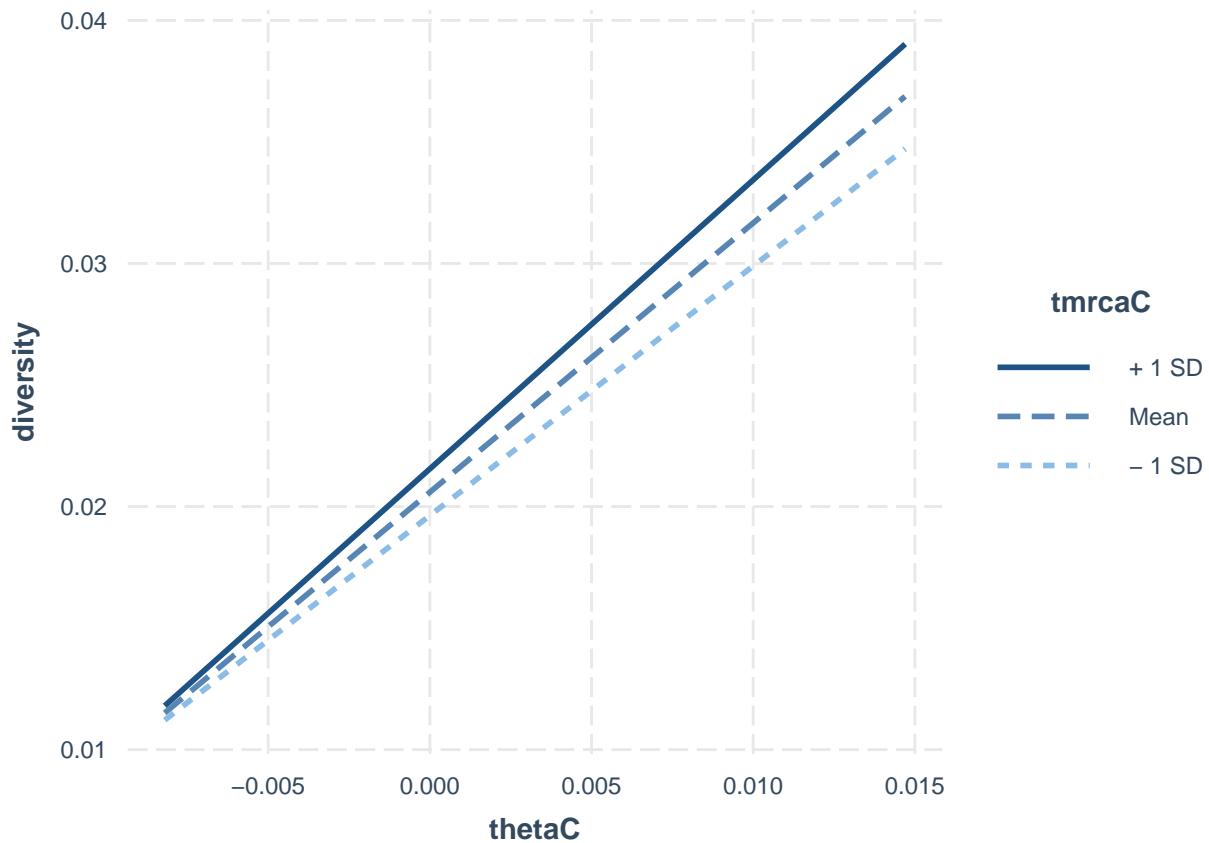
```
##
##  Harrison-McCabe test
##
## data: m.diversity.rep_5
## HMC = 0.49429, p-value = 0.51
hist(resid(m.diversity.rep_5))
```

## Histogram of resid(m.diversity.rep\_5)



```
summary(m.diversity.rep_5)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.1Mb.rep_5)
##
## Residuals:
##       Min         1Q      Median         3Q        Max
## -1.367e-03 -3.078e-04  4.773e-05  2.499e-04  1.494e-03
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.0205901  0.0001215 169.475 < 2e-16 ***
## thetaC      1.1075044  0.0217775  50.855 < 2e-16 ***
## rhoC       -0.1291914  0.4158082  -0.311  0.7586
## tmrcaC      0.0174135  0.0033337   5.224 2.09e-05 ***
## thetaC:tmrcaC 1.4750759  0.6476973   2.277  0.0316 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0006642 on 25 degrees of freedom
## Multiple R-squared:  0.9905, Adjusted R-squared:  0.989
## F-statistic: 650.9 on 4 and 25 DF,  p-value: < 2.2e-16
interact_plot(m.diversity.rep_5, pred = thetaC, modx= tmrcaC)
```



```
g.rep_5 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
  data = inf.lands.1Mb.rep_5, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_5)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep_5
##   AIC      BIC    logLik
## -345.5754 -335.767 179.7877
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.09742974
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept) 0.0205933 0.0001336 154.16894 0.0000
## thetaC      1.1072954 0.0218882  50.58862 0.0000
## tmrcaC      0.0179569 0.0032649   5.50000 0.0000
## rhoC        -0.1181976 0.4172436  -0.28328 0.7793
## thetaC:tmrcaC 1.6258812 0.6398768   2.54093 0.0176
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC          0.002
## tmrcaC         0.033  0.055
## rhoC          -0.002  0.016  0.365
## thetaC:tmrcaC  0.058  0.056  0.609 -0.028
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -2.2002408 -0.4979867  0.0723577  0.3822209  2.4009759
##
## Residual standard error: 0.0006068364
## Degrees of freedom: 30 total; 25 residual
vif(g.rep_5)

##      thetaC        tmrcaC        rhoC thetaC:tmrcaC
##      1.003874     2.071251     1.303671     1.797134
g.rep_5.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.1Mb.rep_5, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_5.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.1Mb.rep_5
##      AIC      BIC    logLik
## -327.0266 -320.0206 168.5133
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## -0.151117
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0205697 0.0001476 139.31706 0.0000
## thetaC       1.0982569 0.0293493  37.42021 0.0000
## rhoC        -1.2150813 0.4706686  -2.58161 0.0156
##
## Correlation:
##      (Intr) thetaC
## thetaC  0.001
## rhoC   -0.002 -0.018
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -1.9762372 -0.5677260  0.1592677  0.6160406  2.4429343
##
## Residual standard error: 0.0008894714
## Degrees of freedom: 30 total; 27 residual
anova.diversity <- Anova(m.diversity.rep_5)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.1Mb[1, 5] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] * 100)
r2.inf.1Mb[2, 5] <- anova.diversity$VarExp[1] * 100
r2.inf.1Mb[3, 5] <- anova.diversity$VarExp[2] * 100
r2.inf.1Mb[4, 5] <- anova.diversity$VarExp[3] * 100
r2.inf.1Mb[5, 5] <- anova.diversity$VarExp[4] * 100
```

### 2.3.6 Replicate 6

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_6/rs.pair_6.", sep = "")
pi.1Mb <- read.table(paste(p, "diversity.1Mb.bedgraph", sep = ""), header = T)
pi.1Mb$avg <- apply(pi.1Mb[4:ncol(pi.1Mb)], 1, mean)
tmrca.1Mb <- read.table(paste(p, "TMRCAs.1Mb.bedgraph", sep = ""), header = T)
tmrca.1Mb$avg <- apply(tmrca.1Mb[4:ncol(tmrca.1Mb)], 1, mean)
rho.1Mb <- read.table(paste(p, "rho.1Mb.bedgraph", sep = ""), header = T)
theta.1Mb <- read.table(paste(p, "theta.1Mb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.1Mb$sim, theta.1Mb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.1Mb$sim and theta.1Mb$sample_mean
## S = 84, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9813126

inf.lands.1Mb.rep_6 <- as.data.frame(cbind(pi.1Mb$avg, theta.1Mb$sample_mean, rho.1Mb$sample_mean, tmrca.1Mb$avg))
names(inf.lands.1Mb.rep_6) <- c("diversity", "theta", "rho", "tmrca")

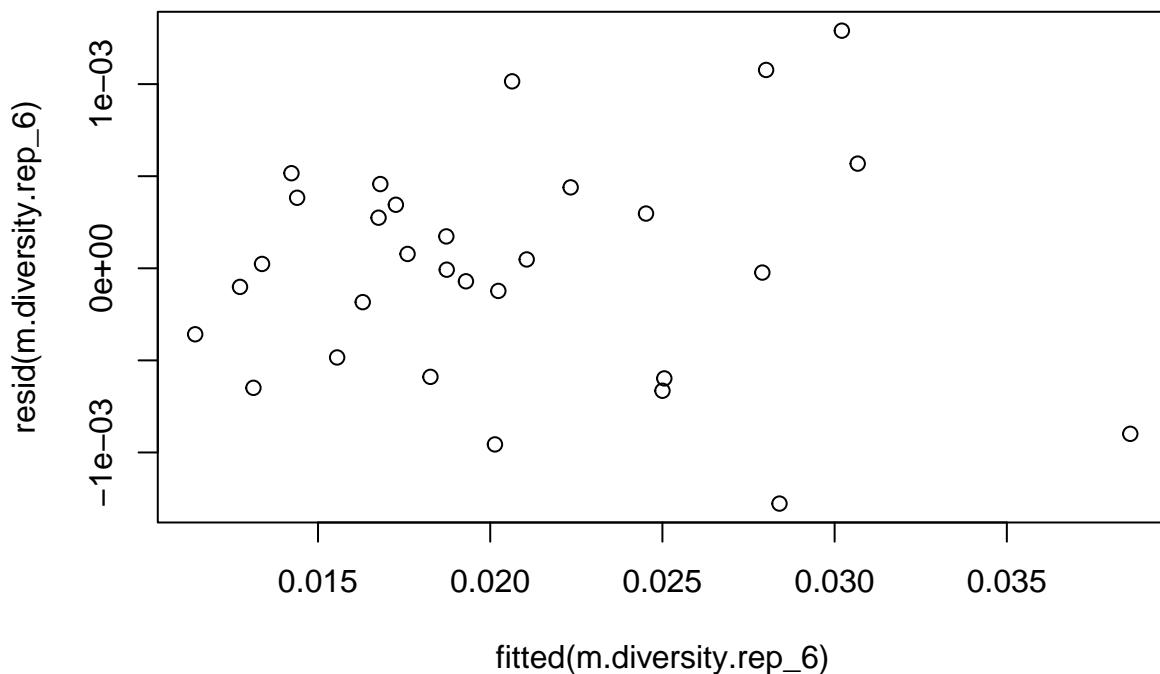
# centering
inf.lands.1Mb.rep_6$thetaC <- inf.lands.1Mb.rep_6$theta - mean(inf.lands.1Mb.rep_6$theta)
inf.lands.1Mb.rep_6$tmrcaC <- inf.lands.1Mb.rep_6$tmrca - mean(inf.lands.1Mb.rep_6$tmrca)
inf.lands.1Mb.rep_6$rhoC <- inf.lands.1Mb.rep_6$rho - mean(inf.lands.1Mb.rep_6$rho)

inf.lands.1Mb.rep_6$bin <- 1:nrow(inf.lands.1Mb.rep_6)

# for merging:
inf.lands.1Mb.rep_6$Replicate <- 6

m.diversity.rep_6 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.1Mb.rep_6)

plot(resid(m.diversity.rep_6)~fitted(m.diversity.rep_6))
```

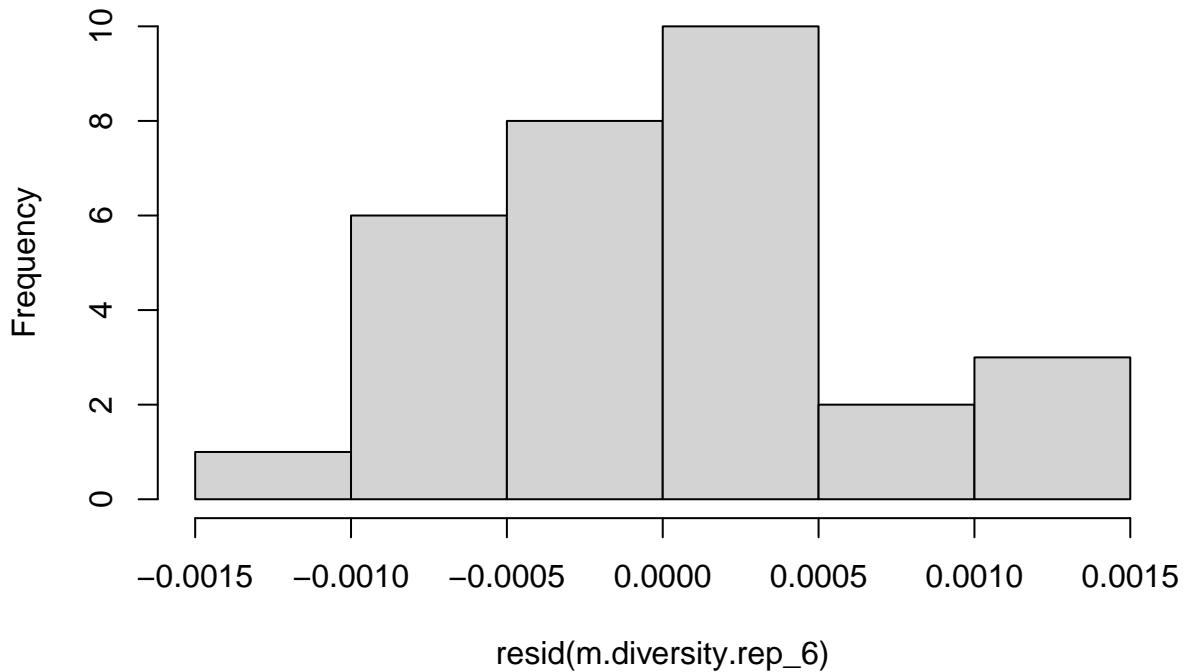


```
dwtest(m.diversity.rep_6)
```

```
##
##  Durbin-Watson test
##
## data: m.diversity.rep_6
## DW = 1.7678, p-value = 0.2162
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_6)
```

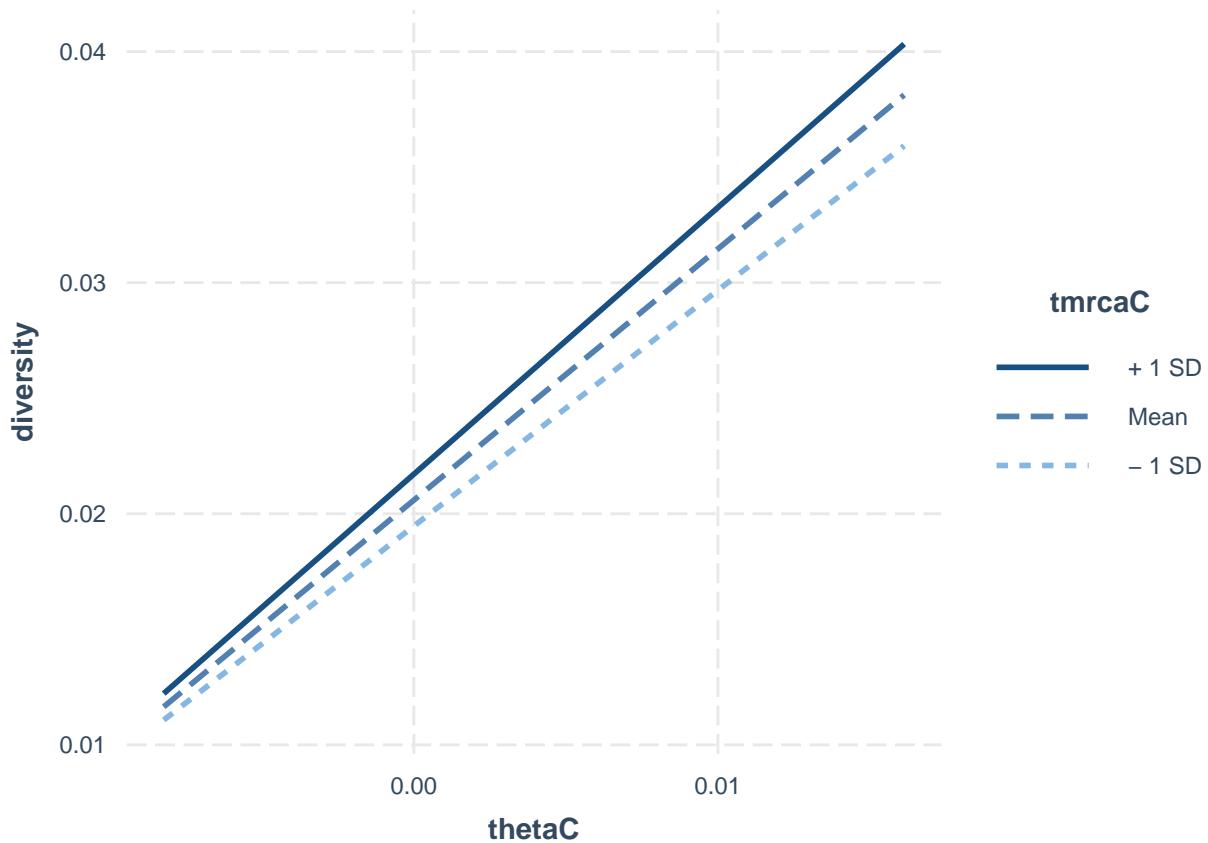
```
##
##  Harrison-McCabe test
##
## data: m.diversity.rep_6
## HMC = 0.38206, p-value = 0.181
hist(resid(m.diversity.rep_6))
```

## Histogram of resid(m.diversity.rep\_6)



```
summary(m.diversity.rep_6)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,  
##      data = inf.lands.1Mb.rep_6)  
##  
## Residuals:  
##       Min         1Q     Median        3Q       Max  
## -1.277e-03 -4.527e-04  7.960e-06  3.734e-04  1.290e-03  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 0.0205897  0.0001193 172.524 < 2e-16 ***  
## thetaC      1.0872234  0.0212487  51.167 < 2e-16 ***  
## rhoC        0.3998838  0.3697035   1.082  0.2897  
## tmrcaC      0.0196732  0.0028089   7.004 2.43e-07 ***  
## thetaC:tmrcaC 1.1711909  0.4979919   2.352  0.0269 *  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0006531 on 25 degrees of freedom  
## Multiple R-squared:  0.9911, Adjusted R-squared:  0.9897  
## F-statistic: 694.4 on 4 and 25 DF,  p-value: < 2.2e-16  
interact_plot(m.diversity.rep_6, pred = thetaC, modx= tmrcaC)
```



```
g.rep_6 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
                  data = inf.lands.1Mb.rep_6, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_6)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep_6
##          AIC      BIC    logLik
##     -346.8212 -337.0128 180.4106
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.1358209
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0205924 0.0001363 151.13216 0.0000
## thetaC      1.0860890 0.0213756  50.80966 0.0000
## tmrcaC      0.0198458 0.0027501   7.21651 0.0000
## rhoC        0.3466959 0.3730361   0.92939 0.3616
## thetaC:tmrcaC 1.3137006 0.4935342   2.66182 0.0134
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC      -0.007
## tmrcaC      0.000 -0.065
## rhoC       -0.010  0.040  0.485
## thetaC:tmrcaC 0.033 -0.186  0.336 -0.157
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -2.09674866 -0.76764130  0.02681106  0.64010637  2.02153252
##
## Residual standard error: 0.0005969812
## Degrees of freedom: 30 total; 25 residual
vif(g.rep_6)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##     1.036142     1.691913     1.539768     1.360141
g.rep_6.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.1Mb.rep_6, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_6.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.1Mb.rep_6
##      AIC      BIC   logLik
## -317.8306 -310.8246 163.9153
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## -0.04598612
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0205747 0.0001889 108.91122 0.0000
## thetaC       1.0881740 0.0343243  31.70273 0.0000
## rhoC        -0.8461274 0.4782870  -1.76908 0.0882
##
## Correlation:
##      (Intr) thetaC
## thetaC  0.000
## rhoC   -0.001 -0.001
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -1.7855991 -0.6320726  0.1751760  0.5604975  2.9148885
##
## Residual standard error: 0.001026338
## Degrees of freedom: 30 total; 27 residual
anova.diversity <- Anova(m.diversity.rep_6)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.1Mb[1, 6] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] * 100)
r2.inf.1Mb[2, 6] <- anova.diversity$VarExp[1] * 100
r2.inf.1Mb[3, 6] <- anova.diversity$VarExp[2] * 100
r2.inf.1Mb[4, 6] <- anova.diversity$VarExp[3] * 100
r2.inf.1Mb[5, 6] <- anova.diversity$VarExp[4] * 100
```

### 2.3.7 Replicate 7

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_7/rs.pair_7.", sep = "")
pi.1Mb <- read.table(paste(p, "diversity.1Mb.bedgraph", sep = ""), header = T)
pi.1Mb$avg <- apply(pi.1Mb[4:ncol(pi.1Mb)], 1, mean)
tmrca.1Mb <- read.table(paste(p, "TMRCAs.1Mb.bedgraph", sep = ""), header = T)
tmrca.1Mb$avg <- apply(tmrca.1Mb[4:ncol(tmrca.1Mb)], 1, mean)
rho.1Mb <- read.table(paste(p, "rho.1Mb.bedgraph", sep = ""), header = T)
theta.1Mb <- read.table(paste(p, "theta.1Mb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.1Mb$sim, theta.1Mb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.1Mb$sim and theta.1Mb$sample_mean
## S = 112, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9750834

inf.lands.1Mb.rep_7 <- as.data.frame(cbind(pi.1Mb$avg, theta.1Mb$sample_mean, rho.1Mb$sample_mean, tmrca.1Mb$avg))
names(inf.lands.1Mb.rep_7) <- c("diversity", "theta", "rho", "tmrca")

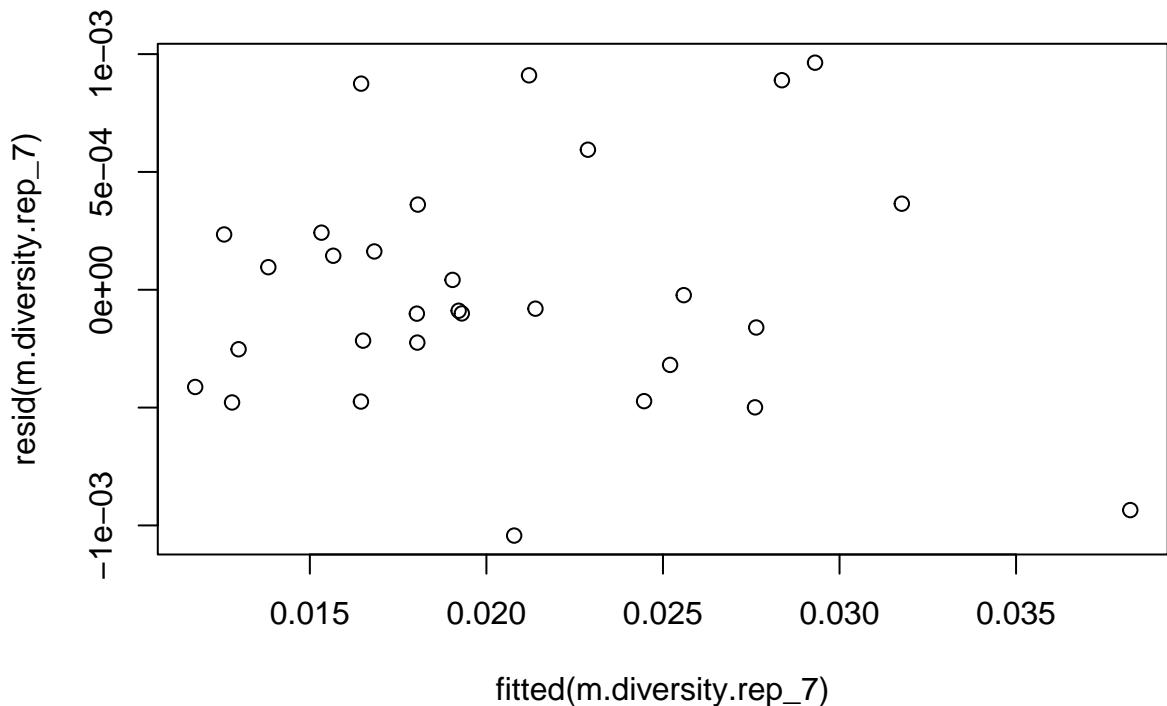
# centering
inf.lands.1Mb.rep_7$thetaC <- inf.lands.1Mb.rep_7$theta - mean(inf.lands.1Mb.rep_7$theta)
inf.lands.1Mb.rep_7$tmrcaC <- inf.lands.1Mb.rep_7$tmrca - mean(inf.lands.1Mb.rep_7$tmrca)
inf.lands.1Mb.rep_7$rhoC <- inf.lands.1Mb.rep_7$rho - mean(inf.lands.1Mb.rep_7$rho)

inf.lands.1Mb.rep_7$bin <- 1:nrow(inf.lands.1Mb.rep_7)

# for merging:
inf.lands.1Mb.rep_7$Replicate <- 7

m.diversity.rep_7 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.1Mb.rep_7)

plot(resid(m.diversity.rep_7)~fitted(m.diversity.rep_7))
```



```

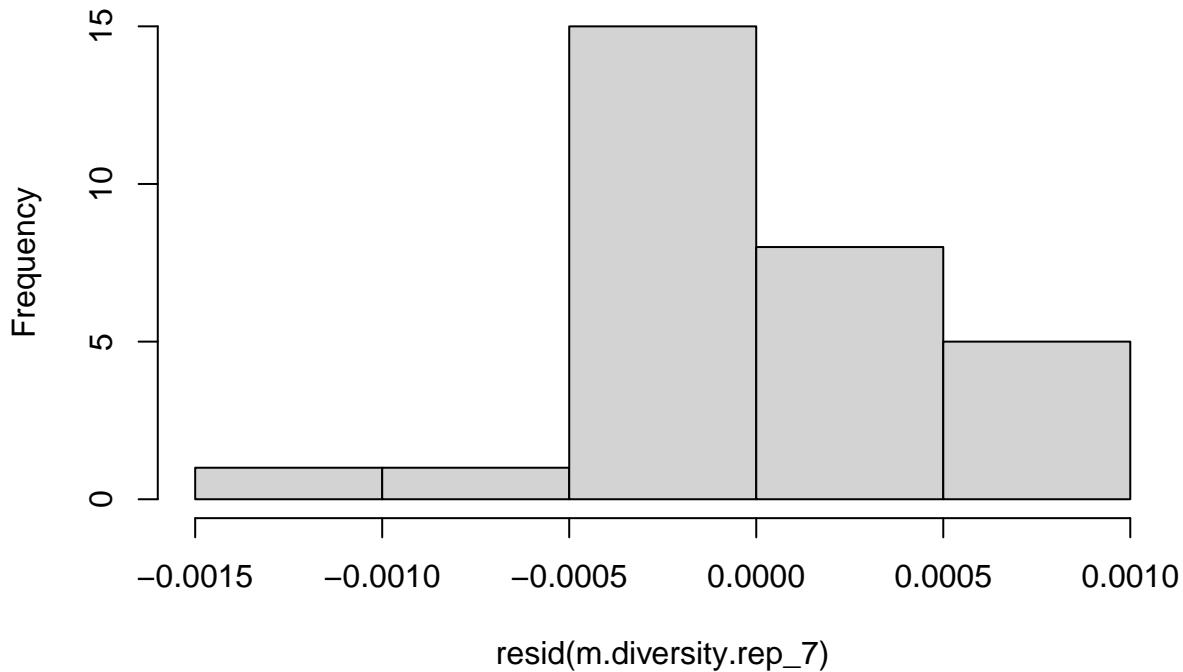
dwtest(m.diversity.rep_7)

##
##  Durbin-Watson test
##
## data: m.diversity.rep_7
## DW = 1.6938, p-value = 0.1634
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_7)

##
##  Harrison-McCabe test
##
## data: m.diversity.rep_7
## HMC = 0.40789, p-value = 0.245
hist(resid(m.diversity.rep_7))

```

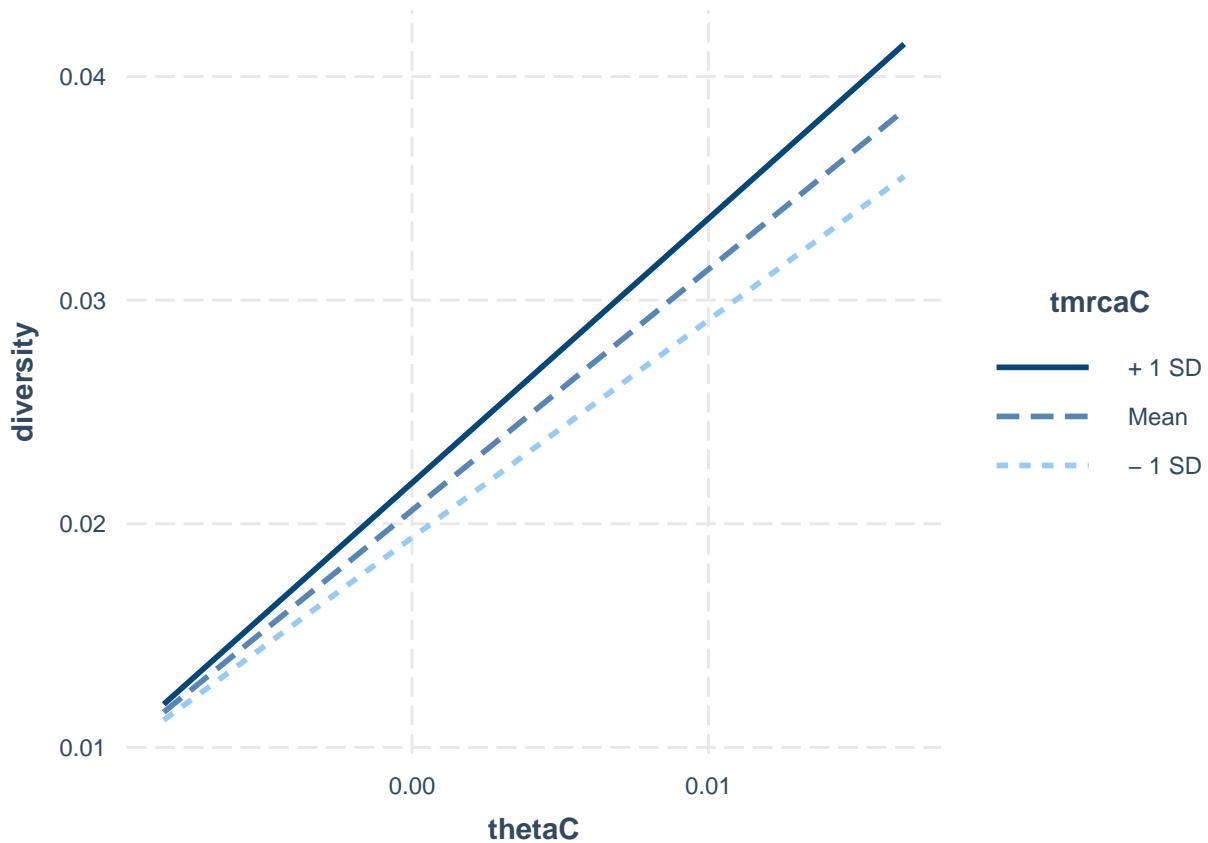
## Histogram of resid(m.diversity.rep\_7)



```
summary(m.diversity.rep_7)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,  
##      data = inf.lands.1Mb.rep_7)  
##  
## Residuals:  
##       Min         1Q     Median        3Q       Max  
## -0.0010431 -0.0003022 -0.0000846  0.0002404  0.0009636  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 0.0206041  0.0001001 205.827 < 2e-16 ***  
## thetaC      1.0776129  0.0174765  61.661 < 2e-16 ***  
## rhoC        0.0680221  0.3366597   0.202  0.841513  
## tmrcaC      0.0238615  0.0027851   8.568 6.58e-09 ***  
## thetaC:tmrcaC 2.0280640  0.4774338   4.248 0.000262 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0005471 on 25 degrees of freedom  
## Multiple R-squared:  0.9937, Adjusted R-squared:  0.9927  
## F-statistic: 992.7 on 4 and 25 DF,  p-value: < 2.2e-16
```

```
interact_plot(m.diversity.rep_7, pred = thetaC, modx= tmrcaC)
```



```
g.rep_7 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
                  data = inf.lands.1Mb.rep_7, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_7)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep_7
##          AIC      BIC    logLik
## -357.7791 -347.9708 185.8896
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.1726746
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept) 0.0206041 0.0001184 174.02851 0.0000
## thetaC      1.0780510 0.0175352  61.47931 0.0000
## tmrcaC      0.0233774 0.0026923   8.68312 0.0000
## rhoC        -0.0447197 0.3354118  -0.13333 0.8950
## thetaC:tmrcaC 2.0331470 0.4572788   4.44619 0.0002
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC      -0.005
## tmrcaC      0.022 -0.097
## rhoC       -0.009 -0.074  0.228
## thetaC:tmrcaC  0.046 -0.103  0.586 -0.198
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -2.1497675 -0.5506932 -0.1283266  0.4700014  1.9723133
##
## Residual standard error: 0.0005001377
## Degrees of freedom: 30 total; 25 residual
vif(g.rep_7)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##     1.020214     1.873531     1.290005     1.862508
g.rep_7.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.1Mb.rep_7, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_7.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.1Mb.rep_7
##          AIC      BIC  logLik
## -319.9699 -312.9639 164.985
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.1179429
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0205818 0.0002149 95.79213 0.0000
## thetaC       1.0897560 0.0336214 32.41258 0.0000
## rhoC        -0.8110199 0.5672255 -1.42980 0.1642
##
## Correlation:
## (Intr) thetaC
## thetaC -0.001
## rhoC   0.002 -0.097
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -2.37431230 -0.29863999  0.01070772  0.55844318  2.30950358
##
## Residual standard error: 0.0009960966
## Degrees of freedom: 30 total; 27 residual
anova.diversity <- Anova(m.diversity.rep_7)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.1Mb[1, 7] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] * 100)
r2.inf.1Mb[2, 7] <- anova.diversity$VarExp[1] * 100
r2.inf.1Mb[3, 7] <- anova.diversity$VarExp[2] * 100
r2.inf.1Mb[4, 7] <- anova.diversity$VarExp[3] * 100
r2.inf.1Mb[5, 7] <- anova.diversity$VarExp[4] * 100
```

### 2.3.8 Replicate 8

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_8/rs.pair_8.", sep = "")
pi.1Mb <- read.table(paste(p, "diversity.1Mb.bedgraph", sep = ""), header = T)
pi.1Mb$avg <- apply(pi.1Mb[4:ncol(pi.1Mb)], 1, mean)
tmrca.1Mb <- read.table(paste(p, "TMRCAs.1Mb.bedgraph", sep = ""), header = T)
tmrca.1Mb$avg <- apply(tmrca.1Mb[4:ncol(tmrca.1Mb)], 1, mean)
rho.1Mb <- read.table(paste(p, "rho.1Mb.bedgraph", sep = ""), header = T)
theta.1Mb <- read.table(paste(p, "theta.1Mb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.1Mb$sim, theta.1Mb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.1Mb$sim and theta.1Mb$sample_mean
## S = 80, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9822024

inf.lands.1Mb.rep_8 <- as.data.frame(cbind(pi.1Mb$avg, theta.1Mb$sample_mean, rho.1Mb$sample_mean, tmrca.1Mb$avg))
names(inf.lands.1Mb.rep_8) <- c("diversity", "theta", "rho", "tmrca")

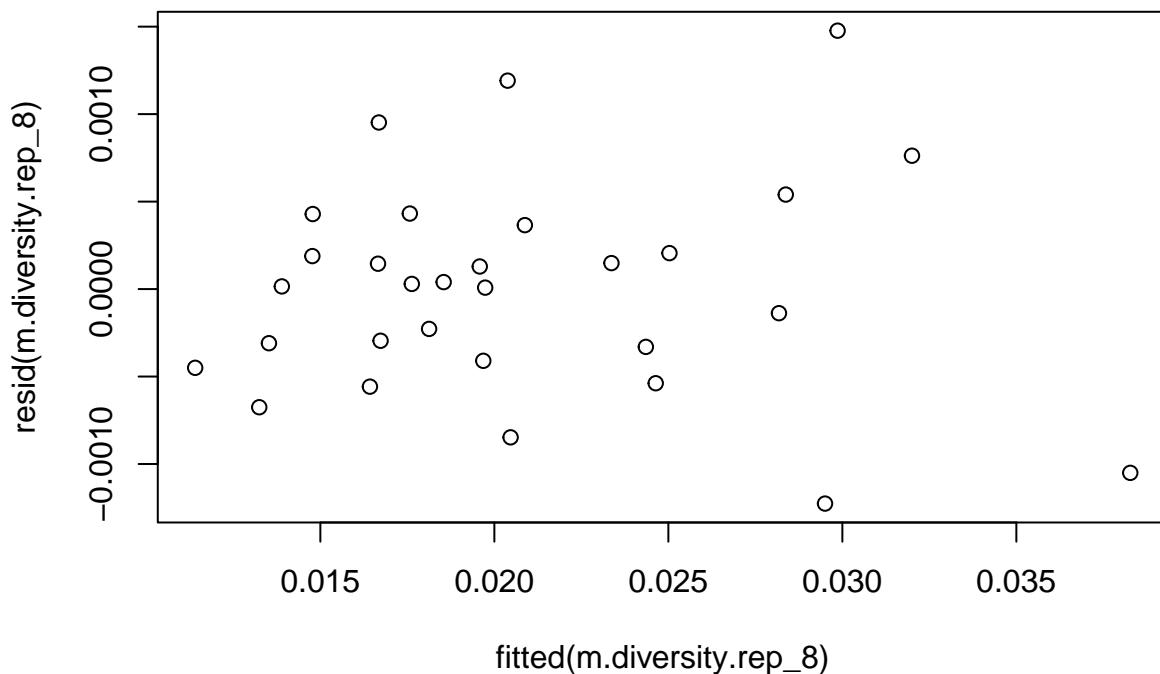
# centering
inf.lands.1Mb.rep_8$thetaC <- inf.lands.1Mb.rep_8$theta - mean(inf.lands.1Mb.rep_8$theta)
inf.lands.1Mb.rep_8$tmrcaC <- inf.lands.1Mb.rep_8$tmrca - mean(inf.lands.1Mb.rep_8$tmrca)
inf.lands.1Mb.rep_8$rhoC <- inf.lands.1Mb.rep_8$rho - mean(inf.lands.1Mb.rep_8$rho)

inf.lands.1Mb.rep_8$bin <- 1:nrow(inf.lands.1Mb.rep_8)

# for merging:
inf.lands.1Mb.rep_8$Replicate <- 8

m.diversity.rep_8 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.1Mb.rep_8)

plot(resid(m.diversity.rep_8)~fitted(m.diversity.rep_8))
```

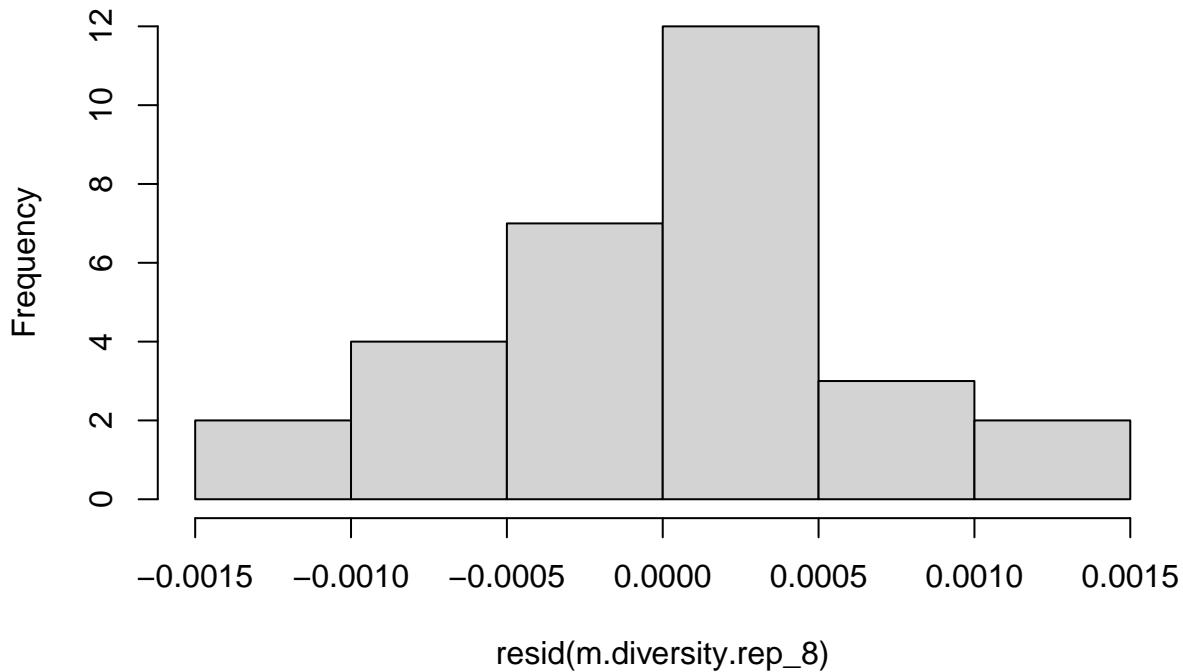


```
dwtest(m.diversity.rep_8)
```

```
##
##  Durbin-Watson test
##
## data: m.diversity.rep_8
## DW = 1.6816, p-value = 0.17
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_8)
```

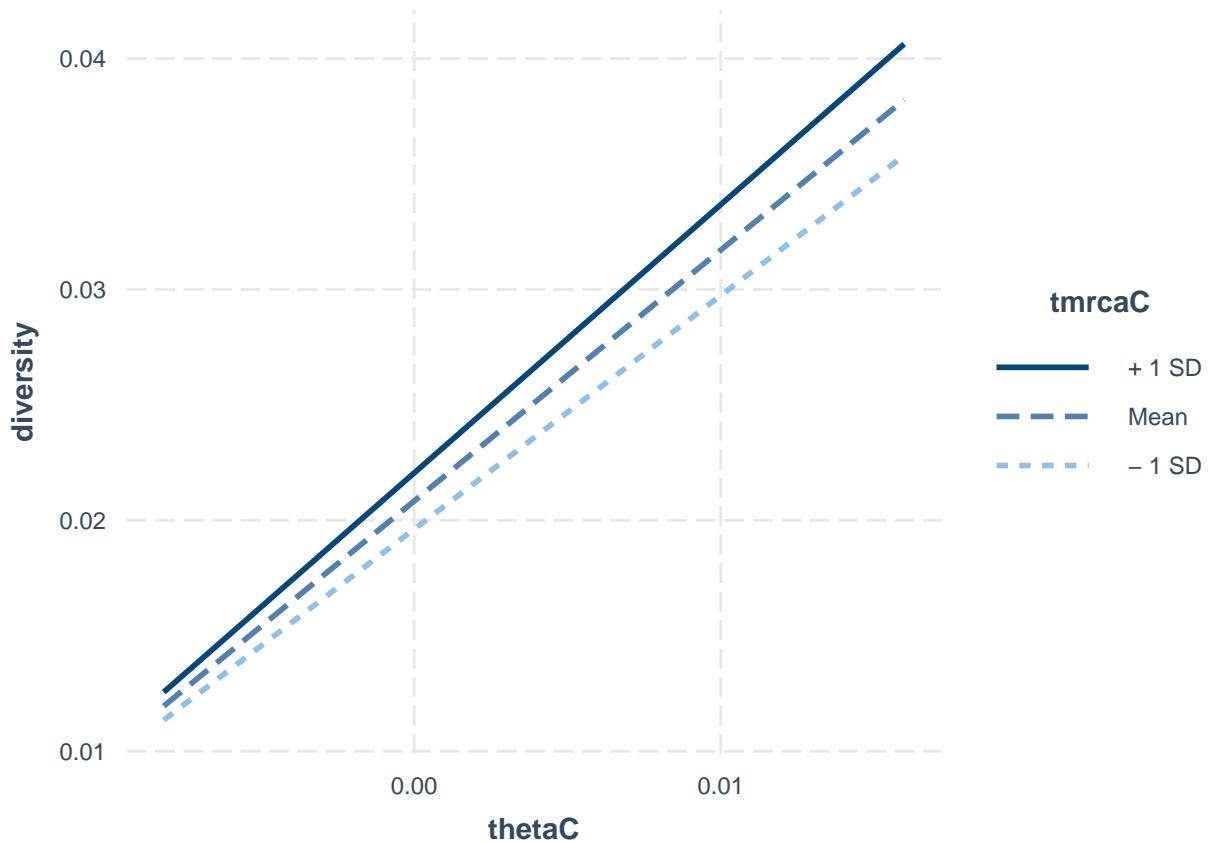
```
##
##  Harrison-McCabe test
##
## data: m.diversity.rep_8
## HMC = 0.45613, p-value = 0.354
hist(resid(m.diversity.rep_8))
```

## Histogram of resid(m.diversity.rep\_8)



```
summary(m.diversity.rep_8)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,  
##      data = inf.lands.1Mb.rep_8)  
##  
## Residuals:  
##       Min         1Q     Median        3Q       Max  
## -1.226e-03 -3.903e-04  2.222e-05  3.255e-04  1.477e-03  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 0.0208365  0.0001224 170.170 < 2e-16 ***  
## thetaC      1.0871732  0.0214774  50.620 < 2e-16 ***  
## rhoC        0.3643104  0.4059648   0.897  0.3781  
## tmrcaC      0.0197018  0.0033310   5.915 3.58e-06 ***  
## thetaC:tmrcaC 1.2143037  0.5213795   2.329   0.0282 *  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0006676 on 25 degrees of freedom  
## Multiple R-squared:  0.9906, Adjusted R-squared:  0.9891  
## F-statistic: 660.6 on 4 and 25 DF,  p-value: < 2.2e-16  
interact_plot(m.diversity.rep_8, pred = thetaC, modx= tmrcaC)
```



```
g.rep_8 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
                  data = inf.lands.1Mb.rep_8, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_8)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep_8
##          AIC      BIC    logLik
##     -345.8378 -336.0294 179.9189
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.1655662
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0208387 0.0001435 145.21451 0.0000
## thetaC      1.0841156 0.0213728  50.72412 0.0000
## tmrcaC      0.0201746 0.0030896   6.52983 0.0000
## rhoC        0.3427329 0.4152276   0.82541 0.4169
## thetaC:tmrcaC 1.3177433 0.4885467   2.69727 0.0123
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC      -0.012
## tmrcaC      0.046 -0.065
## rhoC       -0.024  0.082  0.056
## thetaC:tmrcaC 0.071 -0.140  0.721 -0.279
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -1.96269837 -0.63215676  0.03038078  0.52605973  2.37801009
##
## Residual standard error: 0.0006095428
## Degrees of freedom: 30 total; 25 residual
vif(g.rep_8)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##      1.023443     2.452808    1.275892     2.678721
g.rep_8.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.1Mb.rep_8, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_8.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.1Mb.rep_8
##      AIC      BIC   logLik
## -319.0793 -312.0733 164.5397
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## -0.1415906
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0208035 0.0001699 122.42339 0.0000
## thetaC       1.0823875 0.0328438  32.95562 0.0000
## rhoC        -0.5688595 0.5260339  -1.08141 0.2891
##
## Correlation:
##      (Intr) thetaC
## thetaC  0.001
## rhoC   0.001 -0.012
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -1.87467372 -0.74418645  0.07635072  0.53300754  2.76001890
##
## Residual standard error: 0.001014048
## Degrees of freedom: 30 total; 27 residual
anova.diversity <- Anova(m.diversity.rep_8)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.1Mb[1, 8] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] * 100)
r2.inf.1Mb[2, 8] <- anova.diversity$VarExp[1] * 100
r2.inf.1Mb[3, 8] <- anova.diversity$VarExp[2] * 100
r2.inf.1Mb[4, 8] <- anova.diversity$VarExp[3] * 100
r2.inf.1Mb[5, 8] <- anova.diversity$VarExp[4] * 100
```

### 2.3.9 Replicate 9

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_9/rs.pair_9.", sep = "")
pi.1Mb <- read.table(paste(p, "diversity.1Mb.bedgraph", sep = ""), header = T)
pi.1Mb$avg <- apply(pi.1Mb[4:ncol(pi.1Mb)], 1, mean)
tmrca.1Mb <- read.table(paste(p, "TMRCAs.1Mb.bedgraph", sep = ""), header = T)
tmrca.1Mb$avg <- apply(tmrca.1Mb[4:ncol(tmrca.1Mb)], 1, mean)
rho.1Mb <- read.table(paste(p, "rho.1Mb.bedgraph", sep = ""), header = T)
theta.1Mb <- read.table(paste(p, "theta.1Mb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.1Mb$sim, theta.1Mb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.1Mb$sim and theta.1Mb$sample_mean
## S = 84, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9813126

inf.lands.1Mb.rep_9 <- as.data.frame(cbind(pi.1Mb$avg, theta.1Mb$sample_mean, rho.1Mb$sample_mean, tmrca.1Mb$avg))
names(inf.lands.1Mb.rep_9) <- c("diversity", "theta", "rho", "tmrca")

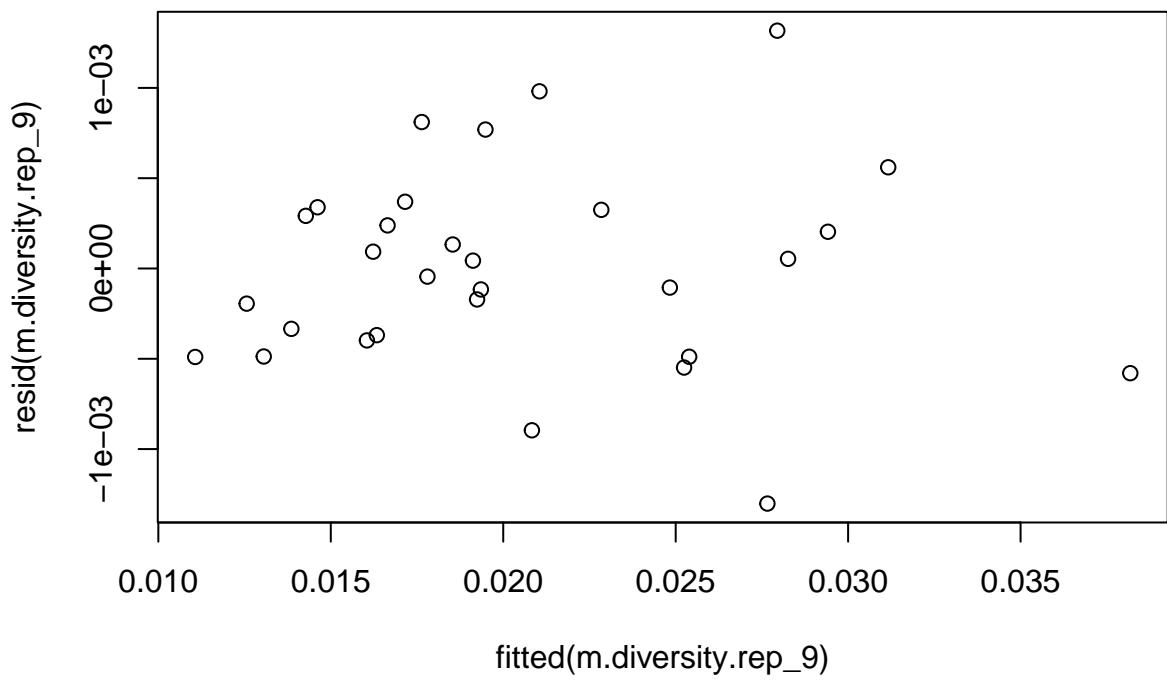
# centering
inf.lands.1Mb.rep_9$thetaC <- inf.lands.1Mb.rep_9$theta - mean(inf.lands.1Mb.rep_9$theta)
inf.lands.1Mb.rep_9$tmrcaC <- inf.lands.1Mb.rep_9$tmrca - mean(inf.lands.1Mb.rep_9$tmrca)
inf.lands.1Mb.rep_9$rhoC <- inf.lands.1Mb.rep_9$rho - mean(inf.lands.1Mb.rep_9$rho)

inf.lands.1Mb.rep_9$bin <- 1:nrow(inf.lands.1Mb.rep_9)

# for merging:
inf.lands.1Mb.rep_9$Replicate <- 9

m.diversity.rep_9 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.1Mb.rep_9)

plot(resid(m.diversity.rep_9)~fitted(m.diversity.rep_9))
```

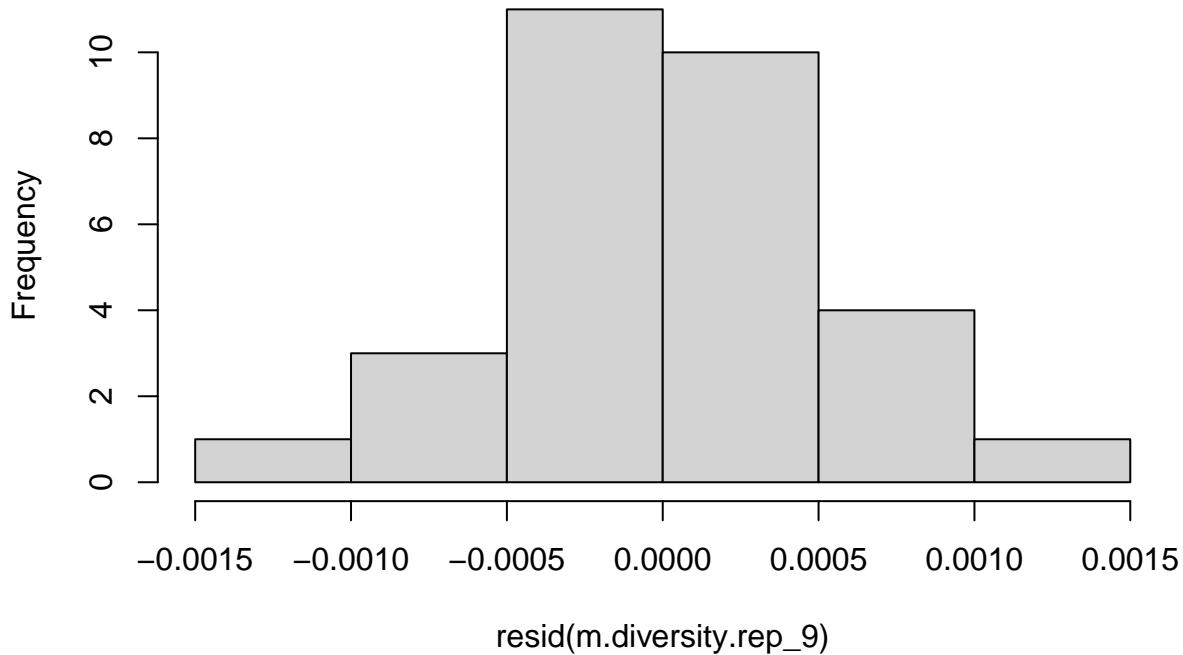


```
dwtest(m.diversity.rep_9)
```

```
##
##  Durbin-Watson test
##
## data: m.diversity.rep_9
## DW = 1.686, p-value = 0.1501
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.diversity.rep_9)
```

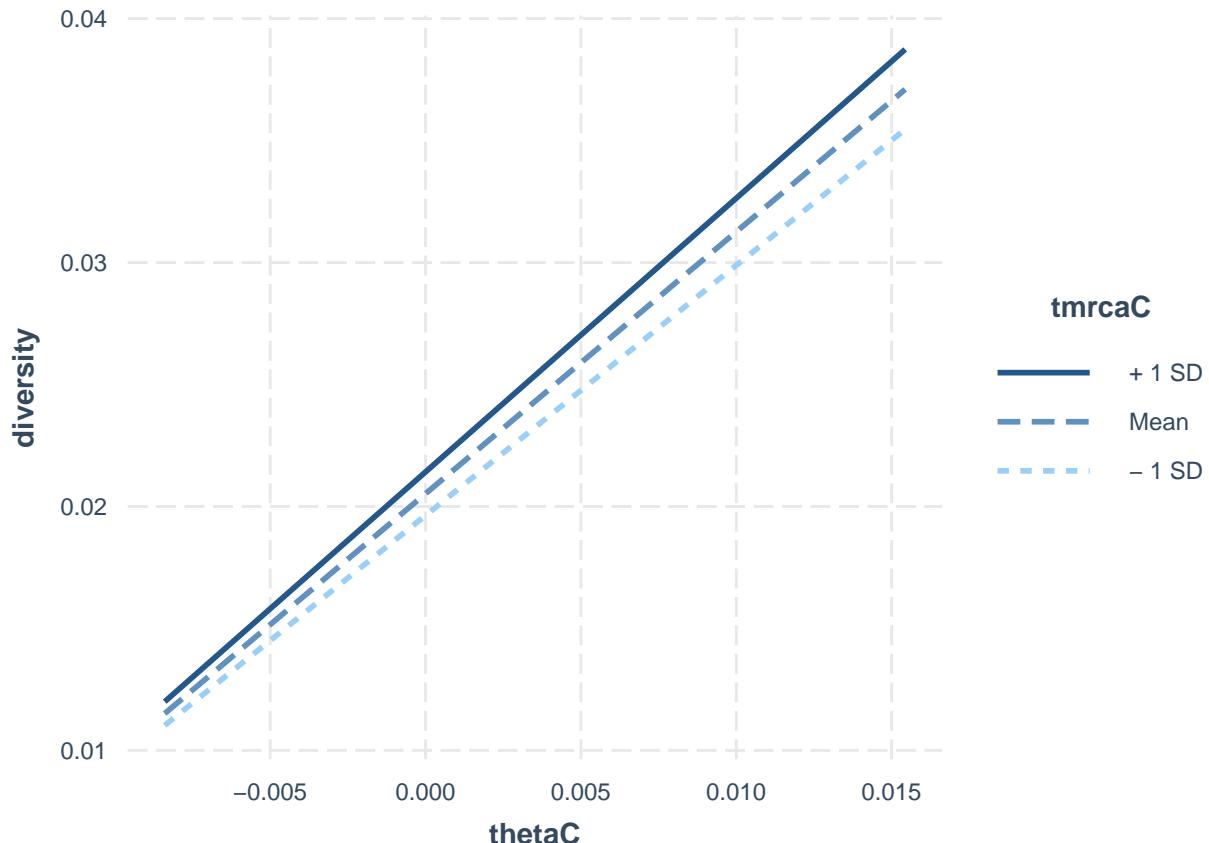
```
##
##  Harrison-McCabe test
##
## data: m.diversity.rep_9
## HMC = 0.49123, p-value = 0.453
hist(resid(m.diversity.rep_9))
```

## Histogram of resid(m.diversity.rep\_9)



```
summary(m.diversity.rep_9)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.1Mb.rep_9)
##
## Residuals:
##       Min         1Q      Median        3Q       Max
## -1.302e-03 -3.910e-04 -8.900e-07  3.164e-04  1.317e-03
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.0205233  0.0001107 185.445 < 2e-16 ***
## thetaC      1.0737054  0.0195206  55.004 < 2e-16 ***
## rhoC        0.1883059  0.3756234   0.501  0.6205
## tmrcaC      0.0183079  0.0027965   6.547 7.39e-07 ***
## thetaC:tmrcaC 0.9925142  0.4598859   2.158   0.0407 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0006061 on 25 degrees of freedom
## Multiple R-squared:  0.9922, Adjusted R-squared:  0.991
## F-statistic: 799.9 on 4 and 25 DF,  p-value: < 2.2e-16
interact_plot(m.diversity.rep_9, pred = thetaC, modx= tmrcaC)
```



```
g.rep_9 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
                 data = inf.lands.1Mb.rep_9, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_9)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep_9
##          AIC      BIC    logLik
##     -351.6229 -341.8146 182.8115
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.1633414
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0205240 0.0001297 158.24435 0.0000
## thetaC       1.0696841 0.0194352  55.03845 0.0000
## tmrcaC      0.0185521 0.0026328   7.04662 0.0000
## rhoC        0.2186371 0.3777124   0.57885 0.5679
## thetaC:tmrcaC 1.0045124 0.4613387   2.17739 0.0391
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC      0.004
## tmrcaC     -0.021 -0.112
## rhoC        0.002  0.012  0.321
## thetaC:tmrcaC -0.022 -0.171  0.296 -0.217
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -2.277428606 -0.752076800 -0.002716583  0.581067342  2.423831154
##
## Residual standard error: 0.0005533147
## Degrees of freedom: 30 total; 25 residual
vif(g.rep_9)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##      1.034584     1.327310    1.266322     1.268614
g.rep_9.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.1Mb.rep_9, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_9.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.1Mb.rep_9
##      AIC      BIC   logLik
## -325.8718 -318.8658 167.9359
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## -0.2006686
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0205144 0.0001444 142.03128 0.0000
## thetaC       1.0817758 0.0289649  37.34776 0.0000
## rhoC        -0.9433213 0.4654231  -2.02680 0.0527
##
## Correlation:
##      (Intr) thetaC
## thetaC  0.001
## rhoC   -0.004 -0.041
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -2.57578335 -0.68638049 -0.02735148  0.65238571  1.96492871
##
## Residual standard error: 0.0009146795
## Degrees of freedom: 30 total; 27 residual
anova.diversity <- Anova(m.diversity.rep_9)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```
r2.inf.1Mb[1, 9] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] * 100)
r2.inf.1Mb[2, 9] <- anova.diversity$VarExp[1] * 100
r2.inf.1Mb[3, 9] <- anova.diversity$VarExp[2] * 100
r2.inf.1Mb[4, 9] <- anova.diversity$VarExp[3] * 100
r2.inf.1Mb[5, 9] <- anova.diversity$VarExp[4] * 100
```

### 2.3.10 Replicate 10

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_10/rs.pair_10.", sep = "")
pi.1Mb <- read.table(paste(p, "diversity.1Mb.bedgraph", sep = ""), header = T)
pi.1Mb$avg <- apply(pi.1Mb[4:ncol(pi.1Mb)], 1, mean)
tmrca.1Mb <- read.table(paste(p, "TMRCA.1Mb.bedgraph", sep = ""), header = T)
tmrca.1Mb$avg <- apply(tmrca.1Mb[4:ncol(tmrca.1Mb)], 1, mean)
rho.1Mb <- read.table(paste(p, "rho.1Mb.bedgraph", sep = ""), header = T)
theta.1Mb <- read.table(paste(p, "theta.1Mb.bedgraph", sep = ""), header = T)

cor.test(sim.theta.1Mb$sim, theta.1Mb$sample_mean, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: sim.theta.1Mb$sim and theta.1Mb$sample_mean
## S = 70, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9844271

inf.lands.1Mb.rep_10 <- as.data.frame(cbind(pi.1Mb$avg, theta.1Mb$sample_mean, rho.1Mb$sample_mean, tmrca.1Mb$avg))
names(inf.lands.1Mb.rep_10) <- c("diversity", "theta", "rho", "tmrca")

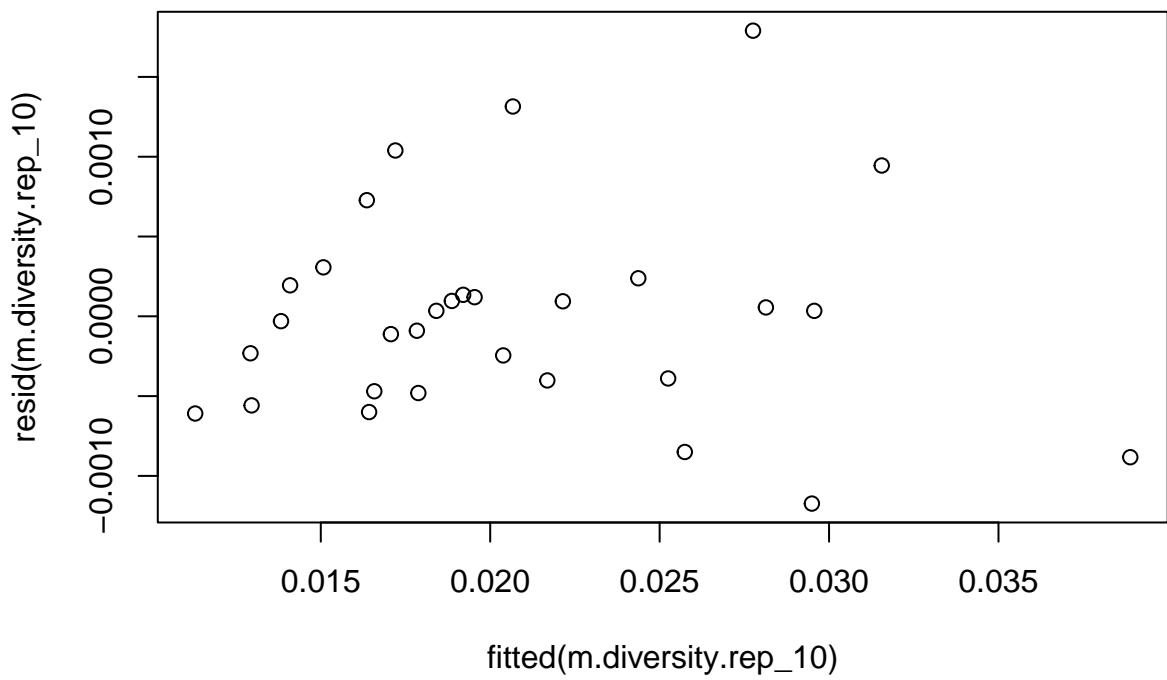
# centering
inf.lands.1Mb.rep_10$thetaC <- inf.lands.1Mb.rep_10$theta - mean(inf.lands.1Mb.rep_10$theta)
inf.lands.1Mb.rep_10$tmrcaC <- inf.lands.1Mb.rep_10$tmrca - mean(inf.lands.1Mb.rep_10$tmrca)
inf.lands.1Mb.rep_10$rhoC <- inf.lands.1Mb.rep_10$rho - mean(inf.lands.1Mb.rep_10$rho)

inf.lands.1Mb.rep_10$bin <- 1:nrow(inf.lands.1Mb.rep_10)

# for merging:
inf.lands.1Mb.rep_10$Replicate <- 10

m.diversity.rep_10 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.1Mb.rep_10)

plot(resid(m.diversity.rep_10)~fitted(m.diversity.rep_10))
```

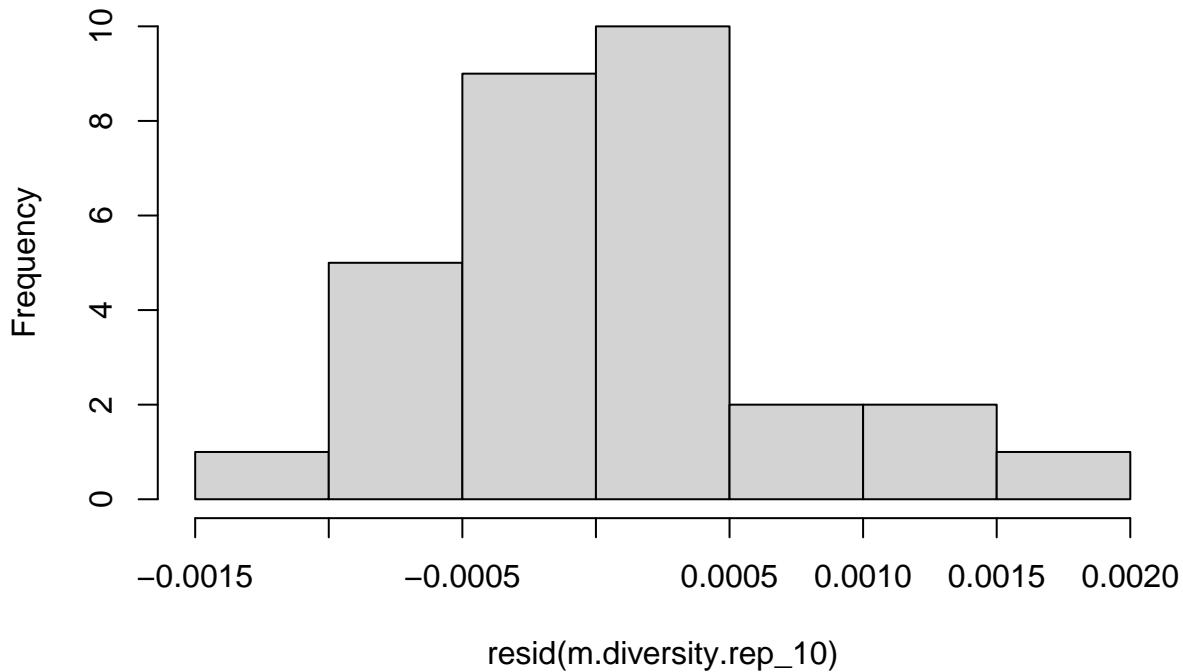


```
dwttest(m.diversity.rep_10)
```

```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_10  
## DW = 1.5209, p-value = 0.06939  
## alternative hypothesis: true autocorrelation is greater than 0  
hmctest(m.diversity.rep_10)
```

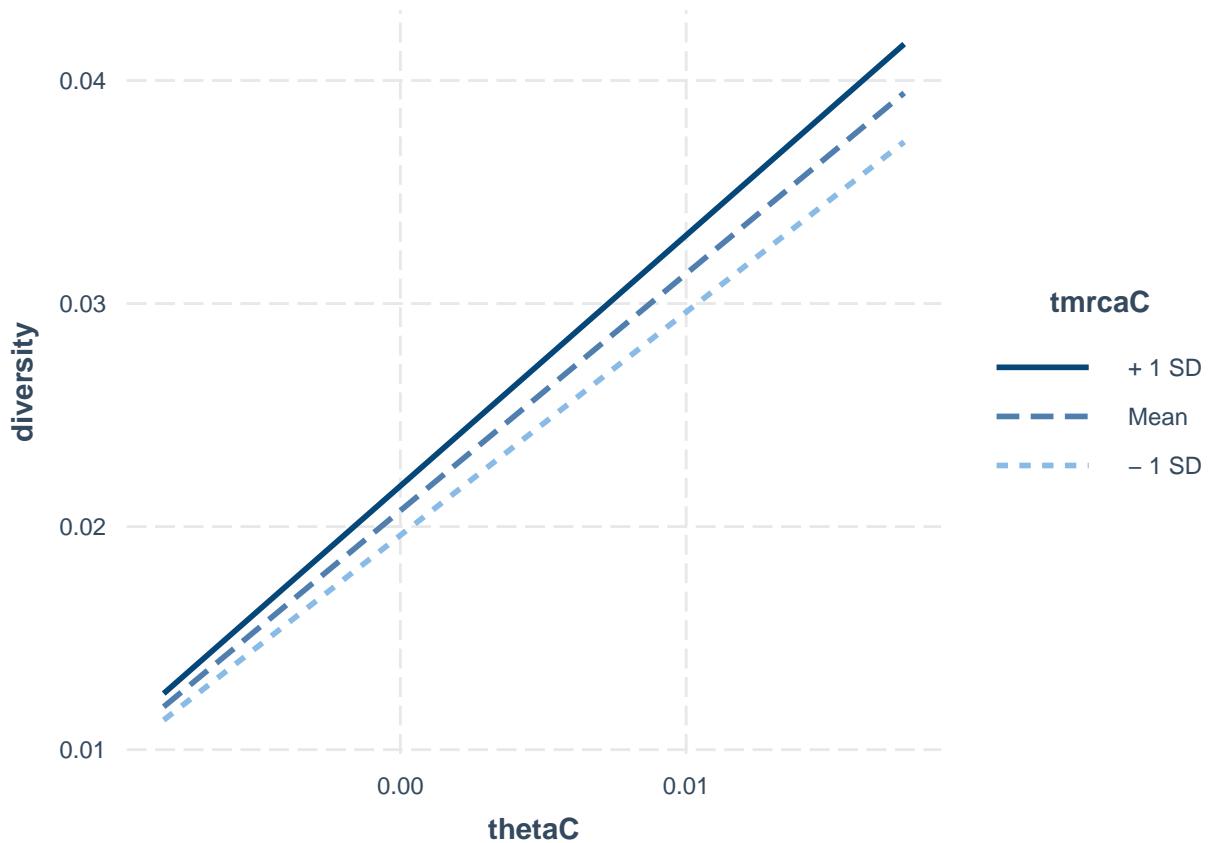
```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_10  
## HMC = 0.59687, p-value = 0.776  
hist(resid(m.diversity.rep_10))
```

## Histogram of resid(m.diversity.rep\_10)



```
summary(m.diversity.rep_10)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.1Mb.rep_10)
##
## Residuals:
##       Min         1Q     Median         3Q        Max
## -0.0011734 -0.0004527  0.0000019  0.0001794  0.0017898
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.0207164  0.0001292 160.343 < 2e-16 ***
## thetaC      1.0619903  0.0218331  48.641 < 2e-16 ***
## rhoC        0.0656389  0.4323685   0.152  0.8806
## tmrcaC      0.0189583  0.0031915   5.940 3.35e-06 ***
## thetaC:tmrcaC 1.0582401  0.5049627   2.096  0.0464 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0007071 on 25 degrees of freedom
## Multiple R-squared:  0.9898, Adjusted R-squared:  0.9882
## F-statistic: 605.8 on 4 and 25 DF,  p-value: < 2.2e-16
interact_plot(m.diversity.rep_10, pred = thetaC, modx= tmrcaC)
```



```
g.rep_10 <- gls(diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC,
                  data = inf.lands.1Mb.rep_1, cor = corAR1(0, ~bin), method = "ML")
```

```
summary(g.rep_10)
```

```
## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + tmrcaC + rhoC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep_1
##       AIC      BIC logLik
##   -348.56 -338.7516 181.28
##
## Correlation Structure: AR(1)
##   Formula: ~bin
##   Parameter estimate(s):
##       Phi
## 0.0188108
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0206248 0.0001171 176.16584 0.0000
## thetaC      1.0920063 0.0211898  51.53453 0.0000
## tmrcaC     0.0168279 0.0029670   5.67164 0.0000
## rhoC        0.0007886 0.3523958   0.00224 0.9982
## thetaC:tmrcaC 0.8389718 0.4973907   1.68675 0.1041
##
## Correlation:
## (Intr) thetaC tmrcaC rhoC
```

```

## thetaC      -0.001
## tmrcaC      0.001 -0.171
## rhoC        0.000 -0.021  0.376
## thetaC:tmrcaC 0.004 -0.283  0.575 -0.003
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -1.67095844 -0.56781078 -0.01108315  0.40839933  3.09944720
##
## Residual standard error: 0.0005748314
## Degrees of freedom: 30 total; 25 residual
vif(g.rep_10)

##      thetaC      tmrcaC      rhoC thetaC:tmrcaC
##      1.087501     1.898249     1.271394     1.717045

g.rep_10.no.tmrca <- gls(diversity ~ thetaC + rhoC,
                           data = inf.lands.1Mb.rep_10, cor = corAR1(0, ~bin), method = "ML")

summary(g.rep_10.no.tmrca)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC
## Data: inf.lands.1Mb.rep_10
##          AIC      BIC    logLik
## -316.9544 -309.9484 163.4772
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## -0.01181332
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.020705 0.0001980 104.59296 0.0000
## thetaC       1.062802 0.0337999  31.44392 0.0000
## rhoC        -0.727976 0.5917022  -1.23031 0.2292
##
## Correlation:
## (Intr) thetaC
## thetaC 0.000
## rhoC   0.000 -0.106
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -2.05588562 -0.66664272 -0.06688445  0.53908458  1.87562405
##
## Residual standard error: 0.001040441
## Degrees of freedom: 30 total; 27 residual
anova.diversity <- Anova(m.diversity.rep_10)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

```

```

r2.inf.1Mb[1, 10] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.inf.1Mb[2, 10] <- anova.diversity$VarExp[1] * 100
r2.inf.1Mb[3, 10] <- anova.diversity$VarExp[2] * 100
r2.inf.1Mb[4, 10] <- anova.diversity$VarExp[3] * 100
r2.inf.1Mb[5, 10] <- anova.diversity$VarExp[4] * 100

r2.inf.1Mb$average <- rowMeans(r2.inf.1Mb)
r2.inf.1Mb <- transform(r2.inf.1Mb, sd=apply(r2.inf.1Mb, 1, sd, na.rm = TRUE))

```

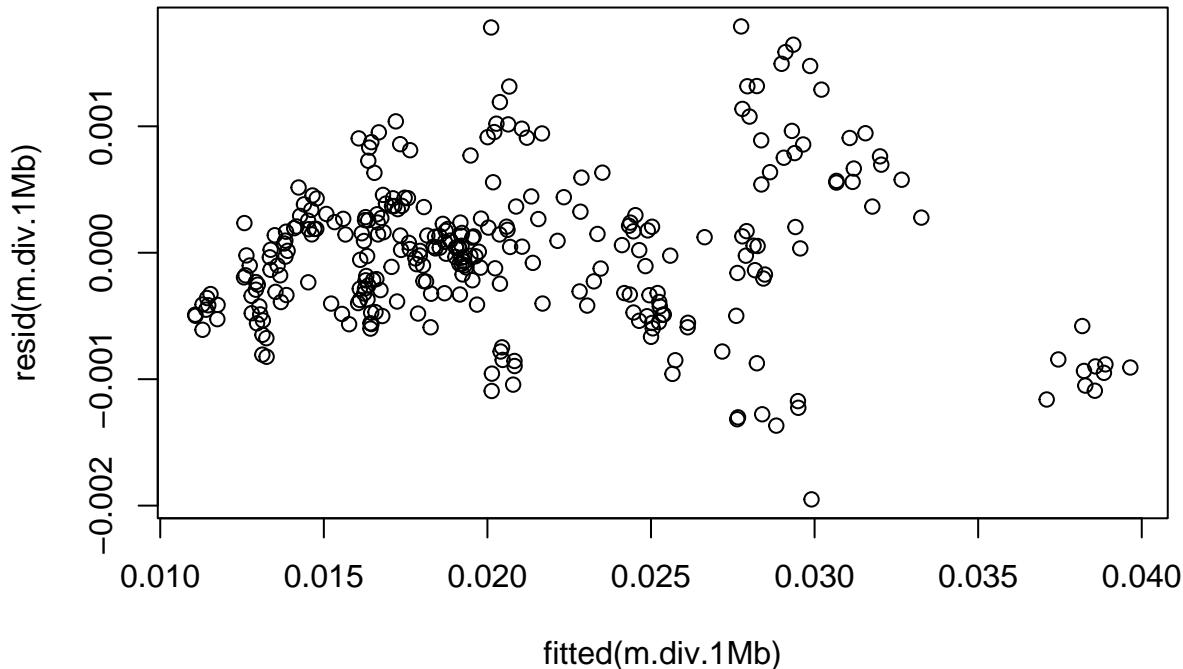
### 2.3.11 all replicates:

```

inf.lands.1Mb.all <- rbind(inf.lands.1Mb.rep_1, inf.lands.1Mb.rep_2, inf.lands.1Mb.rep_3, inf.lands.1Mb.rep_4)

m.div.1Mb <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC)*as.factor(Replicate), data = inf.lands.1Mb.all)
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```



```
dwtest(m.div.1Mb)
```

```

##
## Durbin-Watson test
##
## data: m.div.1Mb
## DW = 1.7602, p-value = 0.001541
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.1Mb)

```

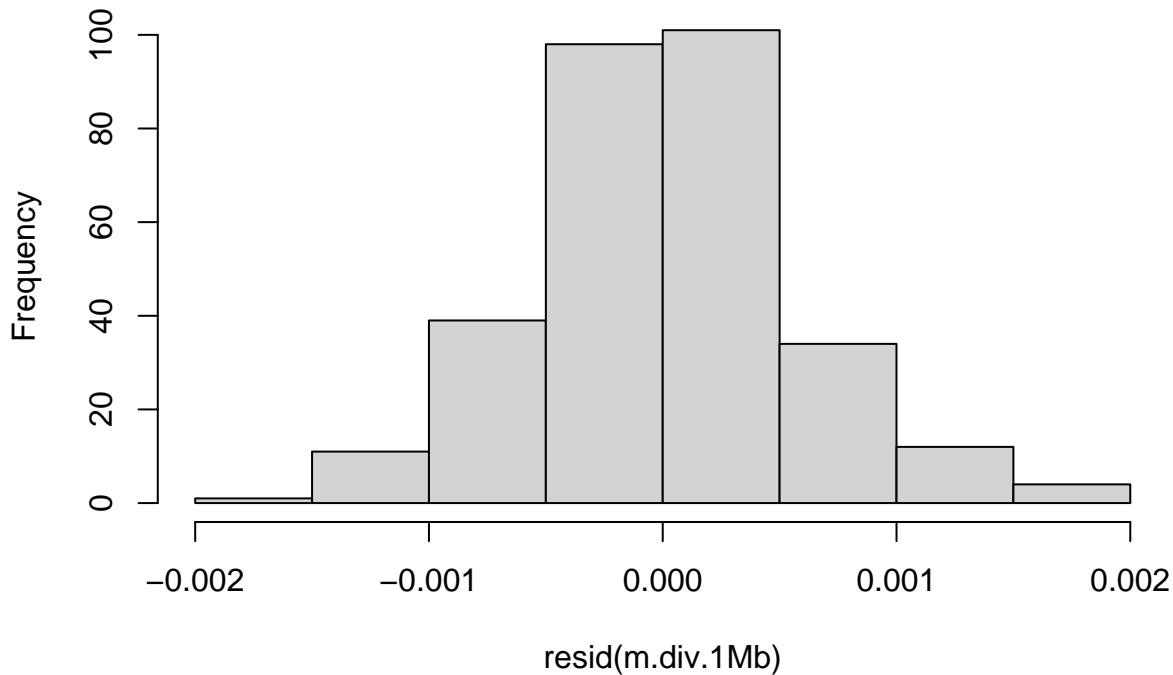
```

##
## Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.51208, p-value = 0.609

```

```
hist(resid(m.div.1Mb))
```

**Histogram of resid(m.div.1Mb)**



```
m.div.1Mb.2 <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC + thetaC:rhoC)*as.factor(Replicate)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC + thetaC:rhoC + rhoC:tmrcaC)*as.factor(Replicate)
```

```
AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)
```

```
##          df      AIC
## m.div.1Mb   51 -3507.758
## m.div.1Mb.2 61 -3522.377
## m.div.1Mb.3 71 -3504.645
```

```
summary(m.div.1Mb)
```

```
##
## Call:
## lm(formula = diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC) *
##     as.factor(Replicate), data = inf.lands.1Mb.all)
##
## Residuals:
##      Min        1Q        Median        3Q       Max
## -0.0019505 -0.0003895  0.0000113  0.0002755  0.0017898
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.062e-02 1.180e-04 174.750 < 2e-16 ***
## thetaC      1.092e+00 2.169e-02  50.357 < 2e-16 ***
## rhoC       3.099e-03 3.609e-01   0.009   0.993
## tmrcaC     1.670e-02 3.065e-03   5.451  1.2e-07 ***
## as.factor(Replicate)2 1.783e-05 1.679e-04   0.106   0.915
```

```

## as.factor(Replicate)3      6.531e-05  1.674e-04  0.390  0.697
## as.factor(Replicate)4      5.942e-05  1.669e-04  0.356  0.722
## as.factor(Replicate)5     -3.449e-05  1.671e-04 -0.206  0.837
## as.factor(Replicate)6     -3.480e-05  1.670e-04 -0.208  0.835
## as.factor(Replicate)7     -2.047e-05  1.671e-04 -0.123  0.903
## as.factor(Replicate)8      2.120e-04  1.673e-04  1.267  0.206
## as.factor(Replicate)9     -1.013e-04  1.669e-04 -0.607  0.545
## as.factor(Replicate)10     9.189e-05  1.670e-04  0.550  0.583
## thetaC:tmrcaC            8.193e-01  5.114e-01  1.602  0.110
## thetaC:as.factor(Replicate)2 -1.466e-02  3.004e-02 -0.488  0.626
## thetaC:as.factor(Replicate)3 -1.976e-02  3.022e-02 -0.654  0.514
## thetaC:as.factor(Replicate)4  2.129e-02  2.996e-02  0.711  0.478
## thetaC:as.factor(Replicate)5  1.538e-02  3.032e-02  0.507  0.612
## thetaC:as.factor(Replicate)6 -4.900e-03  3.021e-02 -0.162  0.871
## thetaC:as.factor(Replicate)7 -1.451e-02  2.995e-02 -0.485  0.628
## thetaC:as.factor(Replicate)8 -4.950e-03  3.005e-02 -0.165  0.869
## thetaC:as.factor(Replicate)9 -1.842e-02  3.006e-02 -0.613  0.541
## thetaC:as.factor(Replicate)10 -3.013e-02  2.947e-02 -1.022  0.308
## rhoC:as.factor(Replicate)2  3.444e-01  5.987e-01  0.575  0.566
## rhoC:as.factor(Replicate)3  1.470e-01  5.241e-01  0.280  0.779
## rhoC:as.factor(Replicate)4 -3.706e-02  5.547e-01 -0.067  0.947
## rhoC:as.factor(Replicate)5 -1.323e-01  5.422e-01 -0.244  0.807
## rhoC:as.factor(Replicate)6  3.968e-01  5.139e-01  0.772  0.441
## rhoC:as.factor(Replicate)7  6.492e-02  5.371e-01  0.121  0.904
## rhoC:as.factor(Replicate)8  3.612e-01  5.336e-01  0.677  0.499
## rhoC:as.factor(Replicate)9  1.852e-01  5.392e-01  0.343  0.732
## rhoC:as.factor(Replicate)10 6.254e-02  5.352e-01  0.117  0.907
## tmrcaC:as.factor(Replicate)2 2.835e-03  4.116e-03  0.689  0.492
## tmrcaC:as.factor(Replicate)3  4.229e-03  3.968e-03  1.066  0.287
## tmrcaC:as.factor(Replicate)4  1.151e-03  4.332e-03  0.266  0.791
## tmrcaC:as.factor(Replicate)5  7.096e-04  4.463e-03  0.159  0.874
## tmrcaC:as.factor(Replicate)6  2.969e-03  4.138e-03  0.718  0.474
## tmrcaC:as.factor(Replicate)7  7.158e-03  4.497e-03  1.592  0.113
## tmrcaC:as.factor(Replicate)8  2.998e-03  4.449e-03  0.674  0.501
## tmrcaC:as.factor(Replicate)9  1.604e-03  4.277e-03  0.375  0.708
## tmrcaC:as.factor(Replicate)10 2.254e-03  4.231e-03  0.533  0.595
## thetaC:tmrcaC:as.factor(Replicate)2 5.699e-01  7.355e-01  0.775  0.439
## thetaC:tmrcaC:as.factor(Replicate)3  1.003e+00  7.144e-01  1.404  0.162
## thetaC:tmrcaC:as.factor(Replicate)4  2.454e-01  8.165e-01  0.301  0.764
## thetaC:tmrcaC:as.factor(Replicate)5  6.558e-01  8.117e-01  0.808  0.420
## thetaC:tmrcaC:as.factor(Replicate)6  3.519e-01  7.102e-01  0.495  0.621
## thetaC:tmrcaC:as.factor(Replicate)7  1.209e+00  7.614e-01  1.588  0.114
## thetaC:tmrcaC:as.factor(Replicate)8  3.950e-01  7.186e-01  0.550  0.583
## thetaC:tmrcaC:as.factor(Replicate)9  1.732e-01  7.086e-01  0.244  0.807
## thetaC:tmrcaC:as.factor(Replicate)10 2.390e-01  6.889e-01  0.347  0.729
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0006464 on 250 degrees of freedom
## Multiple R-squared:  0.9913, Adjusted R-squared:  0.9896
## F-statistic: 582.5 on 49 and 250 DF,  p-value: < 2.2e-16

```

### 2.3.12 Plots

```

scale.3d <- function(x) sprintf("%.3f", x)

rho.plot <- as.data.frame(cbind(inf.lands.1Mb.rep_1$bin,
                                sim.rho.1Mb$sim,
                                inf.lands.1Mb.rep_1$rho,
                                inf.lands.1Mb.rep_2$rho,
                                inf.lands.1Mb.rep_3$rho,
                                inf.lands.1Mb.rep_4$rho,
                                inf.lands.1Mb.rep_5$rho,
                                inf.lands.1Mb.rep_6$rho,
                                inf.lands.1Mb.rep_7$rho,
                                inf.lands.1Mb.rep_8$rho,
                                inf.lands.1Mb.rep_9$rho,
                                inf.lands.1Mb.rep_10$rho))

rho.plot[,3:ncol(rho.plot)] <- 1.53 * rho.plot[,3:ncol(rho.plot)] # scaling because of SCRM NO vs Ne

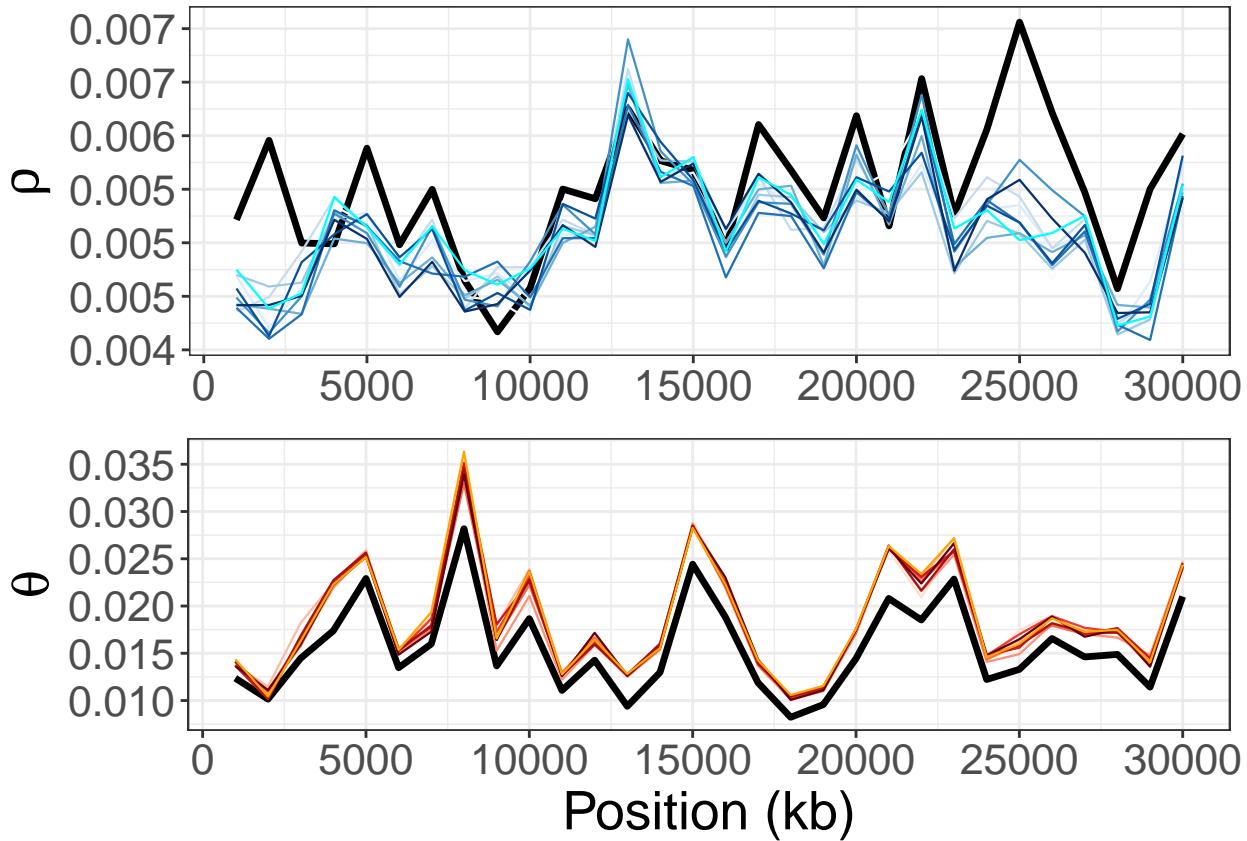
names(rho.plot) <- c("bin", "sim", reps)
molten.rho <- melt(rho.plot, id.vars = "bin")
rho.map.1Mb <- ggplot(data = molten.rho, aes(x = bin * 1000, y = value, colour = variable)) + theme_bw()
rho.map.1Mb <- rho.map.1Mb + geom_line(data = molten.rho, aes(size = variable)) + scale_size_manual(values = c(1, 2, 3, 4, 5, 6, 7, 8, 9, 10))
rho.map.1Mb <- rho.map.1Mb + scale_color_manual(values = c("black", brewer.pal(n = 9, name = "Blues")))
rho.map.1Mb <- rho.map.1Mb + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_breaks())
rho.map.1Mb <- rho.map.1Mb + labs(title = NULL, x = NULL, y = expression(rho))
rho.map.1Mb <- rho.map.1Mb + theme(text = element_text(size = 20), axis.title.x = element_text(size = 20))

theta.plot <- as.data.frame(cbind(inf.lands.1Mb.rep_1$bin,
                                    sim.theta.1Mb$sim,
                                    inf.lands.1Mb.rep_1$theta,
                                    inf.lands.1Mb.rep_2$theta,
                                    inf.lands.1Mb.rep_3$theta,
                                    inf.lands.1Mb.rep_4$theta,
                                    inf.lands.1Mb.rep_5$theta,
                                    inf.lands.1Mb.rep_6$theta,
                                    inf.lands.1Mb.rep_7$theta,
                                    inf.lands.1Mb.rep_8$theta,
                                    inf.lands.1Mb.rep_9$theta,
                                    inf.lands.1Mb.rep_10$theta))

names(theta.plot) <- c("bin", "sim", reps)
molten.theta <- melt(theta.plot, id.vars = "bin")
theta.map.1Mb <- ggplot(data = molten.theta, aes(x = bin * 1000, y = value, colour = variable)) + theme_bw()
theta.map.1Mb <- theta.map.1Mb + geom_line(data = molten.theta, aes(size = variable)) + scale_size_manual(values = c(1, 2, 3, 4, 5, 6, 7, 8, 9, 10))
theta.map.1Mb <- theta.map.1Mb + scale_color_manual(values = c("black", brewer.pal(n = 9, name = "Reds")))
theta.map.1Mb <- theta.map.1Mb + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_breaks())
theta.map.1Mb <- theta.map.1Mb + labs(title = NULL, x = "Position (kb)", y = expression(theta))
theta.map.1Mb <- theta.map.1Mb + theme(text = element_text(size = 20), axis.title.x = element_text(size = 20))

plot_grid(rho.map.1Mb, theta.map.1Mb, nrow = 2, ncol = 1)

```



```
fig2 <- plot_grid(theta.map.50kb, theta.map.200kb, theta.map.1Mb, labels = "AUTO", nrow = 3, ncol = 1)
save_plot("Figure2.pdf", fig2, base_height = 16, base_width = 12)
```

### 3 Real Drosophila data.

We first focus on chr 2L for comparing  $R^2$  with simulations

```
r2.dm.tab <- as.data.frame(matrix(ncol = 6, nrow = 3))
colnames(r2.dm.tab) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA", "bin.size")

# 50kb
# recombination landscapes
rho.dm.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.rho.50kb.bedgraph", header = T)

# diversity
diversity.dm.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.diversity.50kb.bedgraph", header = T)
diversity.dm.50kb$avg <- apply(diversity.dm.50kb[4:ncol(diversity.dm.50kb)], 1, mean)

# mutation landscapes
theta.dm.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.theta.50kb.bedgraph", header = T)

# TMRCA landscapes
tmrca.dm.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.TMRCA.50kb.bedgraph", header = T)
tmrca.dm.50kb$sample_mean <- apply(tmrca.dm.50kb[4:ncol(tmrca.dm.50kb)], 1, mean)

# missing data
missing.prop.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.missing.prop.50kb.bedgraph", header = T)
```

```

intersect.50kb <- apply(missing.prop.50kb[4:ncol(missing.prop.50kb)], 1, function(x) any(x > 0.1))

dm.lands.50kb <- as.data.frame(cbind(diversity.dm.50kb$avg,
                                         theta.dm.50kb$sample_mean,
                                         rho.dm.50kb$sample_mean,
                                         tmrca.dm.50kb$sample_mean))

names(dm.lands.50kb) <- c("diversity", "theta", "rho", "tmrca")
dm.lands.50kb$bin <- 1:nrow(dm.lands.50kb)

# filters based on missing data
dm.lands.50kb <- dm.lands.50kb[which(intersect.50kb == F),]

# OLS

# centering
dm.lands.50kb$thetaC <- dm.lands.50kb$theta - mean(dm.lands.50kb$theta)
dm.lands.50kb$tmrcaC <- dm.lands.50kb$tmrca - mean(dm.lands.50kb$tmrca)
dm.lands.50kb$rhoC <- dm.lands.50kb$rho - mean(dm.lands.50kb$rho)

m.diversity <- lm(diversity ~ thetaC + rhoC + tmrcaC + tmrcaC*thetaC, data = dm.lands.50kb)

# type 2 ANOVA
anova.diversity <- Anova(m.diversity)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.dm.tab[1,] <- c((anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
                     anova.diversity$VarExp[1] * 100,
                     anova.diversity$VarExp[2] * 100,
                     anova.diversity$VarExp[3] * 100,
                     anova.diversity$VarExp[4] * 100, 50)

# 200kb
# recombination landscapes
rho.dm.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.rho.200kb.bedgraph", header = T)

# diversity
diversity.dm.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.diversity.200kb.bedgraph", header = T)
diversity.dm.200kb$avg <- apply(diversity.dm.200kb[4:ncol(diversity.dm.200kb)], 1, mean)

# mutation landscapes
theta.dm.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.theta.200kb.bedgraph", header = T)

# TMRCAs landscapes
tmrca.dm.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.TMRCA.200kb.bedgraph", header = T)
tmrca.dm.200kb$sample_mean <- apply(tmrca.dm.200kb[4:ncol(tmrca.dm.200kb)], 1, mean)

# missing data
missing.prop.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.missing.prop.200kb.bedgraph", header = T)
intersect.200kb <- apply(missing.prop.200kb[4:ncol(missing.prop.200kb)], 1, function(x) any(x > 0.1))

dm.lands.200kb <- as.data.frame(cbind(diversity.dm.200kb$avg,
                                         theta.dm.200kb$sample_mean,
                                         rho.dm.200kb$sample_mean,
                                         tmrca.dm.200kb$sample_mean))

```

```

    theta.dm.200kb$sample_mean,
    rho.dm.200kb$sample_mean,
    tmrca.dm.200kb$sample_mean))

names(dm.lands.200kb) <- c("diversity", "theta", "rho", "tmrca")
dm.lands.200kb$bin <- 1:nrow(dm.lands.200kb)
# filters based on missing data
dm.lands.200kb <- dm.lands.200kb[which(intersect.200kb == F),]

# OLS

dm.lands.200kb$thetaC <- dm.lands.200kb$theta - mean(dm.lands.200kb$theta)
dm.lands.200kb$tmrcaC <- dm.lands.200kb$tmrca - mean(dm.lands.200kb$tmrca)
dm.lands.200kb$rhoC <- dm.lands.200kb$rho - mean(dm.lands.200kb$rho)

m.diversity <- lm(diversity ~ thetaC + rhoC + tmrcaC + tmrcaC*thetaC, data = dm.lands.200kb)

# type 2 ANOVA
anova.diversity <- Anova(m.diversity)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.dm.tab[2,] <- c((anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
                      anova.diversity$VarExp[1] * 100,
                      anova.diversity$VarExp[2] * 100,
                      anova.diversity$VarExp[3] * 100,
                      anova.diversity$VarExp[4] * 100, 200))

# 1Mb
# recombination landscapes
rho.dm.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.rho.1Mb.bedgraph", header = T)

# diversity
diversity.dm.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.diversity.1Mb.bedgraph", header = T)
diversity.dm.1Mb$avg <- apply(diversity.dm.1Mb[4:ncol(diversity.dm.1Mb)], 1, mean)

# mutation landscapes
theta.dm.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.theta.1Mb.bedgraph", header = T)

# TMRCA landscapes
tmrca.dm.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.TMRCA.1Mb.bedgraph", header = T)
tmrca.dm.1Mb$sample_mean <- apply(tmrca.dm.1Mb[4:ncol(tmrca.dm.1Mb)], 1, mean)

# missing data
missing.prop.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.missing.prop.1Mb.bedgraph", header = T)
intersect.1Mb <- apply(missing.prop.1Mb[4:ncol(missing.prop.1Mb)], 1, function(x) any(x > 0.1))

dm.lands.1Mb <- as.data.frame(cbind(diversity.dm.1Mb$avg,
                                         theta.dm.1Mb$sample_mean,
                                         rho.dm.1Mb$sample_mean,
                                         tmrca.dm.1Mb$sample_mean))

names(dm.lands.1Mb) <- c("diversity", "theta", "rho", "tmrca")

```

```

dm.lands.1Mb$bin <- 1:nrow(dm.lands.1Mb)
# filters based on missing data
dm.lands.1Mb <- dm.lands.1Mb[which(intersect.1Mb == F),]

# OLS
dm.lands.1Mb$thetaC <- dm.lands.1Mb$theta - mean(dm.lands.1Mb$theta)
dm.lands.1Mb$tmrcaC <- dm.lands.1Mb$tmrca - mean(dm.lands.1Mb$tmrca)
dm.lands.1Mb$rhoC <- dm.lands.1Mb$rho - mean(dm.lands.1Mb$rho)

m.diversity <- lm(diversity ~ thetaC + rhoC + tmrcaC + tmrcaC*thetaC, data = dm.lands.1Mb)

# type 2 ANOVA
anova.diversity <- Anova(m.diversity)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.dm.tab[3,] <- c((anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
    anova.diversity$VarExp[4]) * 100,
    anova.diversity$VarExp[1] * 100,
    anova.diversity$VarExp[2] * 100,
    anova.diversity$VarExp[3] * 100,
    anova.diversity$VarExp[4] * 100, 1000)

```

We now move on to whole-genome analyses

### 3.1 50 kb windows

```

# Chr 2L

# recombination landscapes
rho.dm.50kb.2L <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.rho.50kb.bedgraph", header = T)

# diversity
diversity.dm.50kb.2L <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.diversity.50kb.bedgraph", header =
diversity.dm.50kb.2L$avg <- apply(diversity.dm.50kb.2L[4:ncol(diversity.dm.50kb.2L)], 1, mean)

# mutation landscapes
theta.dm.50kb.2L <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.theta.50kb.bedgraph", header = T)

# TMRCA landscapes
tmrca.dm.50kb.2L <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.TMRCA.50kb.bedgraph", header = T)
tmrca.dm.50kb.2L$sample_mean <- apply(tmrca.dm.50kb.2L[4:ncol(tmrca.dm.50kb.2L)], 1, mean)

# missing data
missing.prop.50kb.2L <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.missing.prop.50kb.bedgraph", header =
intersect.50kb.2L <- apply(missing.prop.50kb.2L[4:ncol(missing.prop.50kb.2L)], 1, function(x) any(x > 0))

dm.lands.50kb.2L <- as.data.frame(cbind(diversity.dm.50kb.2L$chromStart,
                                            diversity.dm.50kb.2L$chromEnd,
                                            diversity.dm.50kb.2L$avg,
                                            theta.dm.50kb.2L$sample_mean,
                                            rho.dm.50kb.2L$sample_mean,

```

```

tmrca.dm.50kb.2L$sample_mean))
names(dm.lands.50kb.2L) <- c("start", "end", "diversity", "theta", "rho", "tmrca")
dm.lands.50kb.2L$bin <- 1:nrow(dm.lands.50kb.2L)

# filters based on missing data
dm.lands.50kb.2L <- dm.lands.50kb.2L[which(intersect.50kb.2L == F),]

dm.lands.50kb.2L$chr <- "2L"

dm.lands.50kb.2L$thetaC <- dm.lands.50kb.2L$theta - mean(dm.lands.50kb.2L$theta)
dm.lands.50kb.2L$tmrcaC <- dm.lands.50kb.2L$tmrca - mean(dm.lands.50kb.2L$tmrca)
dm.lands.50kb.2L$rhoC <- dm.lands.50kb.2L$rho - mean(dm.lands.50kb.2L$rho)

g.div.dm.50kb.2L <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                           data = dm.lands.50kb.2L, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), nAGQ = 100)

summary(g.div.dm.50kb.2L)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC)
## Data: dm.lands.50kb.2L
##      AIC      BIC logLik
## -4690.441 -4660.219 2353.22
##
## Correlation Structure: ARMA(1,0)
## Formula: ~bin
## Parameter estimate(s):
##     Phi1
## 0.1318436
## Variance function:
## Structure: Power of variance covariate
## Formula: ~tmrcaC
## Parameter estimates:
##     power
## 0.02239814
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0097130 0.00001087 893.9585 0.0000
## thetaC       0.9874554 0.00504783 195.6197 0.0000
## rhoC        0.0017748 0.00146095   1.2148 0.2253
## tmrcaC      0.0126819 0.00021188  59.8534 0.0000
## thetaC:tmrcaC 1.2080584 0.04507126  26.8033 0.0000
##
## Correlation:
##          (Intr) thetaC rhoC    tmrcaC
## thetaC    -0.016
## rhoC      0.027  0.026
## tmrcaC    -0.132 -0.379 -0.456
## thetaC:tmrcaC -0.306  0.061 -0.088  0.402
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -3.60864294 -0.52688547 -0.05949911  0.51229899  4.16571201

```

```

## 
## Residual standard error: 0.0001811126
## Degrees of freedom: 323 total; 318 residual
# Chr 2R

# recombination landscapes
rho.dm.50kb.2R <- read.table("dm_data/dm_chr_maps/2R/dm_30x5x5.rho.50kb.bedgraph", header = T)

# diversity
diversity.dm.50kb.2R <- read.table("dm_data/dm_chr_maps/2R/dm_30x5x5.diversity.50kb.bedgraph", header = T)
diversity.dm.50kb.2R$avg <- apply(diversity.dm.50kb.2R[4:ncol(diversity.dm.50kb.2R)], 1, mean)

# mutation landscapes
theta.dm.50kb.2R <- read.table("dm_data/dm_chr_maps/2R/dm_30x5x5.theta.50kb.bedgraph", header = T)

# TMRCAs landscapes
tmrca.dm.50kb.2R <- read.table("dm_data/dm_chr_maps/2R/dm_30x5x5.TMRCA.50kb.bedgraph", header = T)
tmrca.dm.50kb.2R$sample_mean <- apply(tmrca.dm.50kb.2R[4:ncol(tmrca.dm.50kb.2R)], 1, mean)

# missing data
missing.prop.50kb.2R <- read.table("dm_data/dm_chr_maps/2R/dm_30x5x5.missing.prop.50kb.bedgraph", header = T)
intersect.50kb.2R <- apply(missing.prop.50kb.2R[4:ncol(missing.prop.50kb.2R)], 1, function(x) any(x > 0))

dm.lands.50kb.2R <- as.data.frame(cbind(diversity.dm.50kb.2R$chromStart,
                                            diversity.dm.50kb.2R$chromEnd,
                                            diversity.dm.50kb.2R$avg,
                                            theta.dm.50kb.2R$sample_mean,
                                            rho.dm.50kb.2R$sample_mean,
                                            tmrca.dm.50kb.2R$sample_mean))
names(dm.lands.50kb.2R) <- c("start", "end", "diversity", "theta", "rho", "tmrca")
dm.lands.50kb.2R$bin <- 1:nrow(dm.lands.50kb.2R)

# filters based on missing data
dm.lands.50kb.2R <- dm.lands.50kb.2R[which(intersect.50kb.2R == F),]

dm.lands.50kb.2R$chr <- "2R"

dm.lands.50kb.2R$thetaC <- dm.lands.50kb.2R$theta - mean(dm.lands.50kb.2R$theta)
dm.lands.50kb.2R$tmrcaC <- dm.lands.50kb.2R$tmrca - mean(dm.lands.50kb.2R$tmrca)
dm.lands.50kb.2R$rhoC <- dm.lands.50kb.2R$rho - mean(dm.lands.50kb.2R$rho)

g.div.dm.50kb.2R <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                           data = dm.lands.50kb.2R, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin),
                           summary(g.div.dm.50kb.2R)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC)
##   Data: dm.lands.50kb.2R
##          AIC      BIC    logLik
##     -4473.266 -4443.583 2244.633
##
## Correlation Structure: ARMA(1,0)
## Formula: ~bin
```

```

## Parameter estimate(s):
##      Phi1
## 0.1094586
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~tmrcaC
## Parameter estimates:
##      power
## 0.05919674
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept) 0.0085652 0.00000938 913.0793 0.0000
## thetaC       0.9709055 0.00361092 268.8801 0.0000
## rhoC        0.0001728 0.00149052   0.1160 0.9078
## tmrcaC      0.0116837 0.00019594  59.6303 0.0000
## thetaC:tmrcaC 1.0680644 0.04933969  21.6472 0.0000
##
## Correlation:
##          (Intr) thetaC rhoC   tmrcaC
## thetaC     0.044
## rhoC      -0.003  0.084
## tmrcaC    -0.103 -0.360 -0.381
## thetaC:tmrcaC -0.260 -0.114  0.022  0.341
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -3.56718360 -0.56905223  0.01512333  0.64333847  3.32352563
##
## Residual standard error: 0.0001778837
## Degrees of freedom: 302 total; 297 residual

# recombination landscapes
rho.dm.50kb.3L <- read.table("dm_data/dm_chr_maps/3L/dm_30x5x5.rho.50kb.bedgraph", header = T)

# diversity
diversity.dm.50kb.3L <- read.table("dm_data/dm_chr_maps/3L/dm_30x5x5.diversity.50kb.bedgraph", header = T)
diversity.dm.50kb.3L$avg <- apply(diversity.dm.50kb.3L[4:ncol(diversity.dm.50kb.3L)], 1, mean)

# mutation landscapes
theta.dm.50kb.3L <- read.table("dm_data/dm_chr_maps/3L/dm_30x5x5.theta.50kb.bedgraph", header = T)

# TMRCA landscapes
tmrca.dm.50kb.3L <- read.table("dm_data/dm_chr_maps/3L/dm_30x5x5.TMRCA.50kb.bedgraph", header = T)
tmrca.dm.50kb.3L$sample_mean <- apply(tmrca.dm.50kb.3L[4:ncol(tmrca.dm.50kb.3L)], 1, mean)

# missing data
missing.prop.50kb.3L <- read.table("dm_data/dm_chr_maps/3L/dm_30x5x5.missing.prop.50kb.bedgraph", header = T)
intersect.50kb.3L <- apply(missing.prop.50kb.3L[4:ncol(missing.prop.50kb.3L)], 1, function(x) any(x > 0))

dm.lands.50kb.3L <- as.data.frame(cbind(diversity.dm.50kb.3L$chromStart,
                                            diversity.dm.50kb.3L$chromEnd,
                                            diversity.dm.50kb.3L$avg,
                                            theta.dm.50kb.3L$sample_mean,

```

```

rho.dm.50kb.3L$sample_mean,
tmrca.dm.50kb.3L$sample_mean))
names(dm.lands.50kb.3L) <- c("start", "end", "diversity", "theta", "rho", "tmrca")
dm.lands.50kb.3L$bin <- 1:nrow(dm.lands.50kb.3L)

# filters based on missing data
dm.lands.50kb.3L <- dm.lands.50kb.3L[which(intersect.50kb.3L == F),]

dm.lands.50kb.3L$chr <- "3L"

dm.lands.50kb.3L$thetaC <- dm.lands.50kb.3L$theta - mean(dm.lands.50kb.3L$theta)
dm.lands.50kb.3L$tmrcaC <- dm.lands.50kb.3L$tmrca - mean(dm.lands.50kb.3L$tmrca)
dm.lands.50kb.3L$rhoC <- dm.lands.50kb.3L$rho - mean(dm.lands.50kb.3L$rho)

g.div.dm.50kb.3L <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                           data = dm.lands.50kb.3L, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin),
                           na.action = na.omit)

summary(g.div.dm.50kb.3L)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC)
## Data: dm.lands.50kb.3L
##      AIC      BIC    logLik
## -5025.491 -4994.674 2520.746
##
## Correlation Structure: ARMA(1,0)
## Formula: ~bin
## Parameter estimate(s):
##     Phi1
## 0.2696667
## Variance function:
## Structure: Power of variance covariate
## Formula: ~tmrcaC
## Parameter estimates:
##     power
## 0.06685875
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0089556 0.000012514 715.6471 0.0000
## thetaC       0.9656448 0.004479703 215.5600 0.0000
## rhoC        0.0028522 0.001435660   1.9867 0.0477
## tmrcaC      0.0118244 0.000153683   76.9400 0.0000
## thetaC:tmrcaC 1.0917168 0.030139577  36.2220 0.0000
##
## Correlation:
##          (Intr) thetaC rhoC   tmrcaC
## thetaC   -0.004
## rhoC     0.004  0.150
## tmrcaC   -0.106 -0.427 -0.517
## thetaC:tmrcaC -0.323  0.045 -0.029  0.309
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max

```

```

## -3.70241395 -0.68659890  0.01012415  0.61472090  3.79680208
##
## Residual standard error: 0.0002214495
## Degrees of freedom: 348 total; 343 residual
# Chr 3R

# recombination landscapes
rho.dm.50kb.3R <- read.table("dm_data/dm_chr_maps/3R/dm_30x5x5.rho.50kb.bedgraph", header = T)

# diversity
diversity.dm.50kb.3R <- read.table("dm_data/dm_chr_maps/3R/dm_30x5x5.diversity.50kb.bedgraph", header =
diversity.dm.50kb.3R$avg <- apply(diversity.dm.50kb.3R[4:ncol(diversity.dm.50kb.3R)], 1, mean)

# mutation landscapes
theta.dm.50kb.3R <- read.table("dm_data/dm_chr_maps/3R/dm_30x5x5.theta.50kb.bedgraph", header = T)

# TMRCA landscapes
tmrca.dm.50kb.3R <- read.table("dm_data/dm_chr_maps/3R/dm_30x5x5.TMRCA.50kb.bedgraph", header = T)
tmrca.dm.50kb.3R$sample_mean <- apply(tmrca.dm.50kb.3R[4:ncol(tmrca.dm.50kb.3R)], 1, mean)

# missing data
missing.prop.50kb.3R <- read.table("dm_data/dm_chr_maps/3R/dm_30x5x5.missing.prop.50kb.bedgraph", header =
intersect.50kb.3R <- apply(missing.prop.50kb.3R[4:ncol(missing.prop.50kb.3R)], 1, function(x) any(x > 0))

dm.lands.50kb.3R <- as.data.frame(cbind(diversity.dm.50kb.3R$chromStart,
                                            diversity.dm.50kb.3R$chromEnd,
                                            diversity.dm.50kb.3R$avg,
                                            theta.dm.50kb.3R$sample_mean,
                                            rho.dm.50kb.3R$sample_mean,
                                            tmrca.dm.50kb.3R$sample_mean))
names(dm.lands.50kb.3R) <- c("start", "end", "diversity", "theta", "rho", "tmrca")
dm.lands.50kb.3R$bin <- 1:nrow(dm.lands.50kb.3R)

# filters based on missing data
dm.lands.50kb.3R <- dm.lands.50kb.3R[which(intersect.50kb.3R == F),]

dm.lands.50kb.3R$chr <- "3R"

dm.lands.50kb.3R$thetaC <- dm.lands.50kb.3R$theta - mean(dm.lands.50kb.3R$theta)
dm.lands.50kb.3R$tmrcaC <- dm.lands.50kb.3R$tmrca - mean(dm.lands.50kb.3R$tmrca)
dm.lands.50kb.3R$rhoC <- dm.lands.50kb.3R$rho - mean(dm.lands.50kb.3R$rho)

g.div.dm.50kb.3R <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                           data = dm.lands.50kb.3R, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin),
                           summary(g.div.dm.50kb.3R)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC)
##   Data: dm.lands.50kb.3R
##       AIC      BIC    logLik
##   -6576.594 -6543.846 3296.297
##
## Correlation Structure: ARMA(1,0)

```

```

## Formula: ~bin
## Parameter estimate(s):
##     Phi1
## 0.2356751
## Variance function:
## Structure: Power of variance covariate
## Formula: ~tmrcaC
## Parameter estimates:
##     power
## 0.1042665
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0075334 0.00000895 841.7772 0.0000
## thetaC       0.9644922 0.00331480 290.9655 0.0000
## rhoC        -0.0017265 0.00118208 -1.4606 0.1449
## tmrcaC      0.0106635 0.00013264  80.3973 0.0000
## thetaC:tmrcaC 1.0663698 0.03719362 28.6708 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC      0.003
## rhoC        -0.022  0.107
## tmrcaC      -0.203 -0.346 -0.501
## thetaC:tmrcaC -0.384 -0.089  0.039  0.507
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -3.64020083 -0.59320311  0.03347561  0.68857658  4.67175243
##
## Residual standard error: 0.0002041515
## Degrees of freedom: 443 total; 438 residual

# all together now
dm.lands.50kb <- rbind.data.frame(dm.lands.50kb.2L, dm.lands.50kb.2R, dm.lands.50kb.3L, dm.lands.50kb.3R)

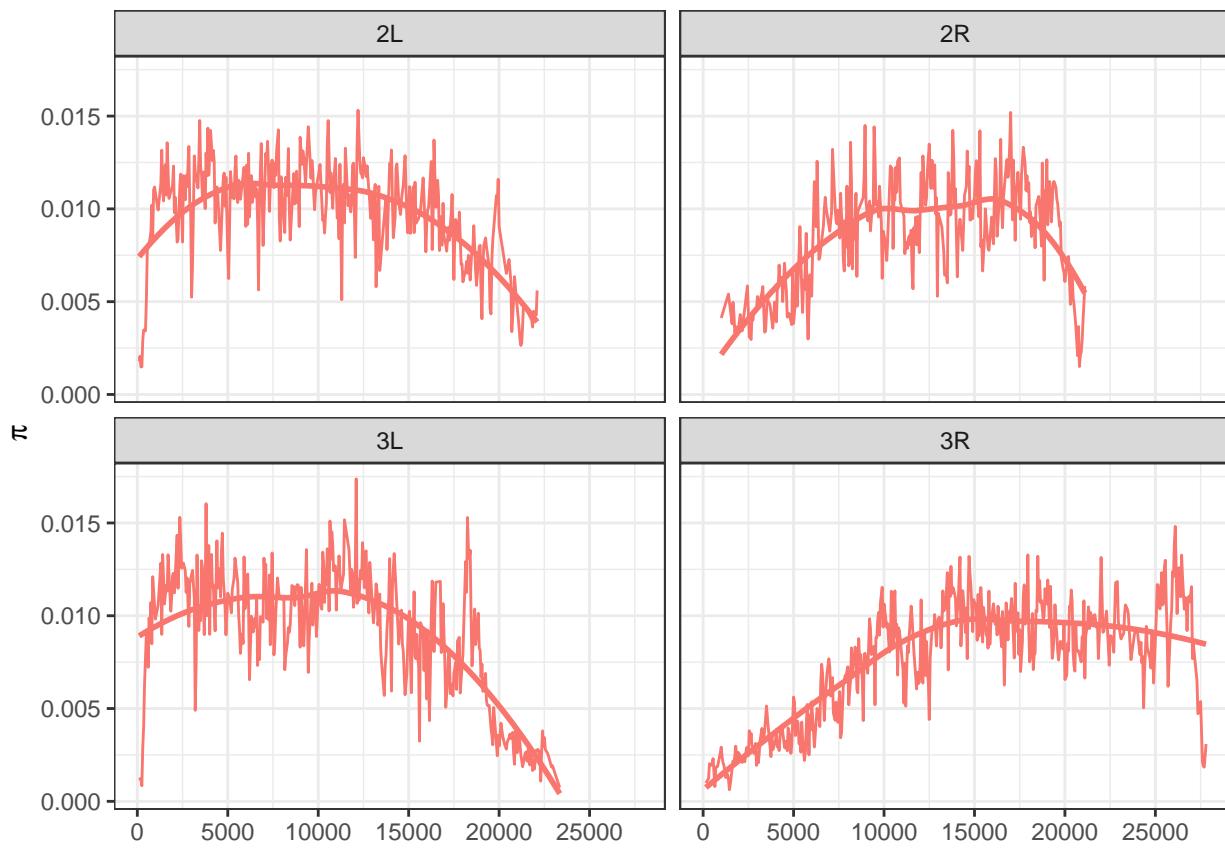
write.table(dm.lands.50kb, "dm_data/dm_chr_maps/dm.maps.50kb.tsv", quote = F, sep = "\t", row.names = F)

# Plots
scale.3d <- function(x) sprintf("%.3f", x) # digits shown in y axis

setTimeLimit(cpu = Inf, elapsed = Inf, transient = F)

molten.diversity <- melt(dm.lands.50kb[c(3,7,8)], id.vars = c("bin", "chr"))
diversity.map <- ggplot(data = molten.diversity, aes(x = bin * 50, y = value)) + facet_wrap(~chr)
diversity.map <- diversity.map + geom_line(data = molten.diversity, colour = "#F8766D")
diversity.map <- diversity.map + geom_smooth(method = "loess", se = F, colour = "#F8766D")
diversity.map <- diversity.map + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_breaks())
diversity.map <- diversity.map + labs(title = NULL, x = NULL, y = expression(pi))
diversity.map <- diversity.map + theme(axis.title.x = element_text(size = 20), axis.title.y = element_text(size = 20))
diversity.map

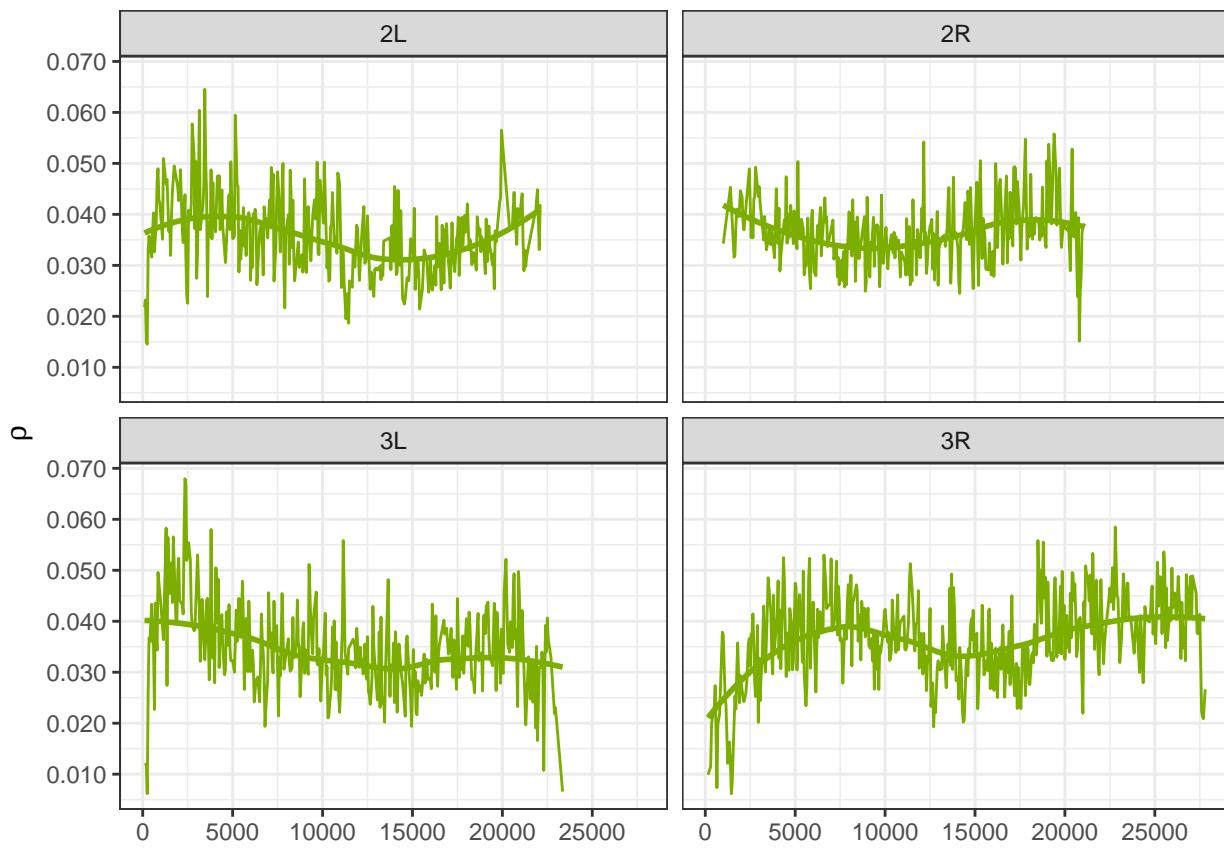
```



```

molten.rho <- melt(dm.lands.50kb[c(5,7,8)], id.vars = c("bin", "chr"))
rho.map <- ggplot(data = molten.rho, aes(x = bin * 50, y = value)) + facet_wrap(~chr)
rho.map <- rho.map + geom_line(data = molten.rho, colour = "#7CAE00")
rho.map <- rho.map + geom_smooth(method = "loess", se = F, colour = "#7CAE00")
rho.map <- rho.map + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_l
rho.map <- rho.map + labs(title = NULL, x = NULL, y = expression(rho))
rho.map <- rho.map + theme(axis.title.x = element_text(size = 20), axis.title.y = element_text(size = 20)
rho.map

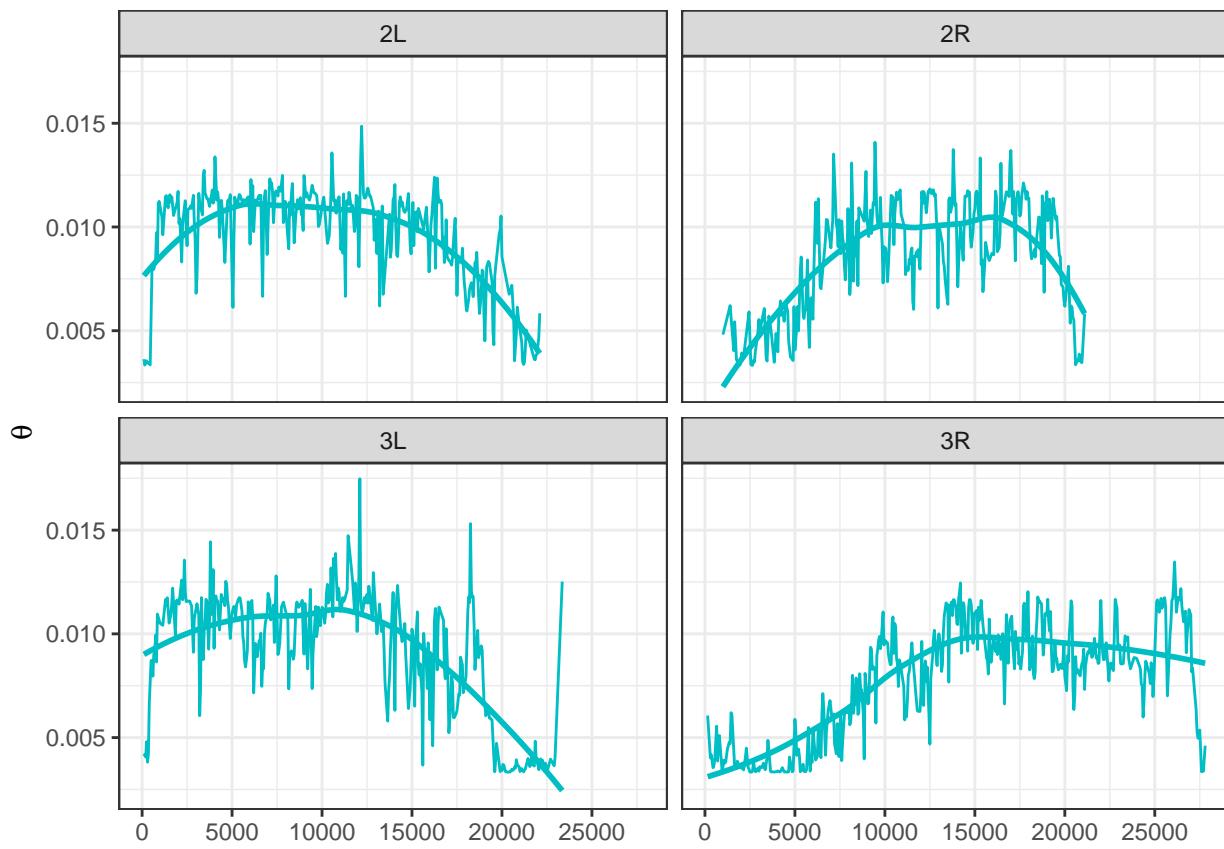
```



```

molten.theta <- melt(dm.lands.50kb[c(4,7,8)], id.vars = c("bin", "chr"))
theta.map <- ggplot(data = molten.theta, aes(x = bin * 50, y = value)) + facet_wrap(~chr)
theta.map <- theta.map + geom_line(data = molten.theta, colour = "#00BFC4")
theta.map <- theta.map + geom_smooth(method = "loess", se = F, colour = "#00BFC4")
theta.map <- theta.map + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_breaks())
theta.map <- theta.map + labs(title = NULL, x = NULL, y = expression(theta))
theta.map <- theta.map + theme(axis.title.x = element_text(size = 20), axis.title.y = element_text(size = 20))
theta.map

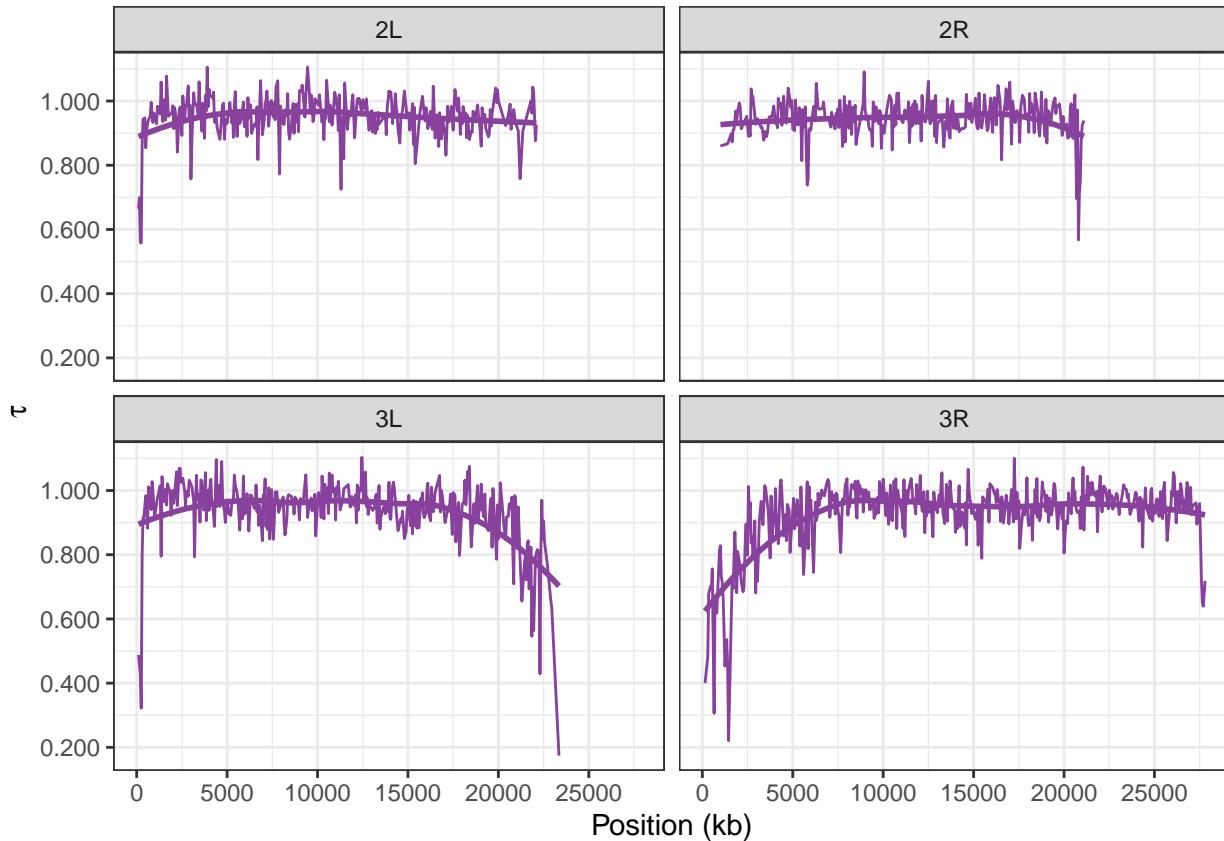
```



```

molten.tmrca <- melt(dm.lands.50kb[c(6,7,8)], id.vars = c("bin", "chr"))
tmrca.map <- ggplot(data = molten.tmrca, aes(x = bin * 50, y = value)) + facet_wrap(~chr)
tmrca.map <- tmrca.map + geom_line(data = molten.tmrca, colour = "#88419d")
tmrca.map <- tmrca.map + geom_smooth(method = "loess", se = F, colour = "#88419d")
tmrca.map <- tmrca.map + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_breaks())
tmrca.map <- tmrca.map + labs(title = NULL, x = "Position (kb)", y = expression(tau))
tmrca.map <- tmrca.map + theme(axis.title.x = element_text(size = 20), axis.title.y = element_text(size = 20))
tmrca.map

```



```
# genome-wide correlations between maps
cor.test(~rho + diversity, data = dm.lands.50kb, method = "spearman")
```

```
##
## Spearman's rank correlation rho
##
## data: rho and diversity
## S = 369190884, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.2197879
```

```
cor.test(~rho + tmrca, data = dm.lands.50kb, method = "spearman")
```

```
##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 245063950, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.4821057
```

```
cor.test(~theta + tmrca, data = dm.lands.50kb, method = "spearman")
```

```
##
## Spearman's rank correlation rho
```

```

## 
## data: theta and tmrca
## S = 254806288, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.4615172

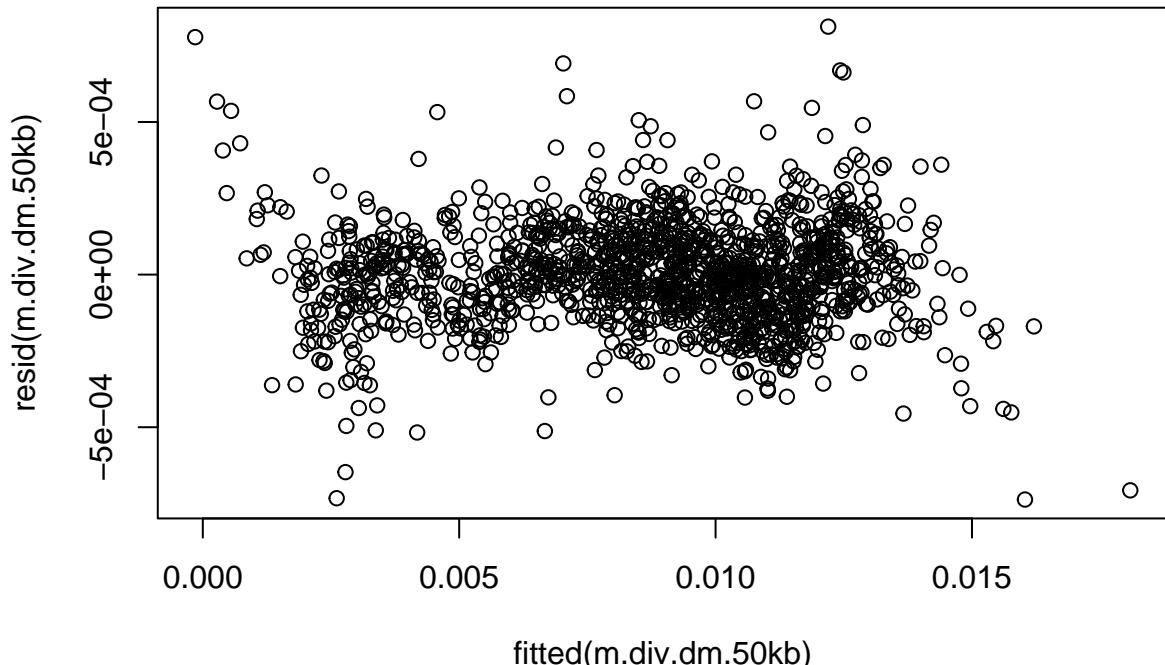
# Linear models
# centering
dm.lands.50kb$thetaC <- dm.lands.50kb$theta - mean(dm.lands.50kb$theta)
dm.lands.50kb$tmrcaC <- dm.lands.50kb$tmrca - mean(dm.lands.50kb$tmrca)
dm.lands.50kb$rhoC <- dm.lands.50kb$rho - mean(dm.lands.50kb$rho)

dm.lands.50kb$bin <- 1:nrow(dm.lands.50kb)

m.div.dm.50kb <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC), data = dm.lands.50kb)

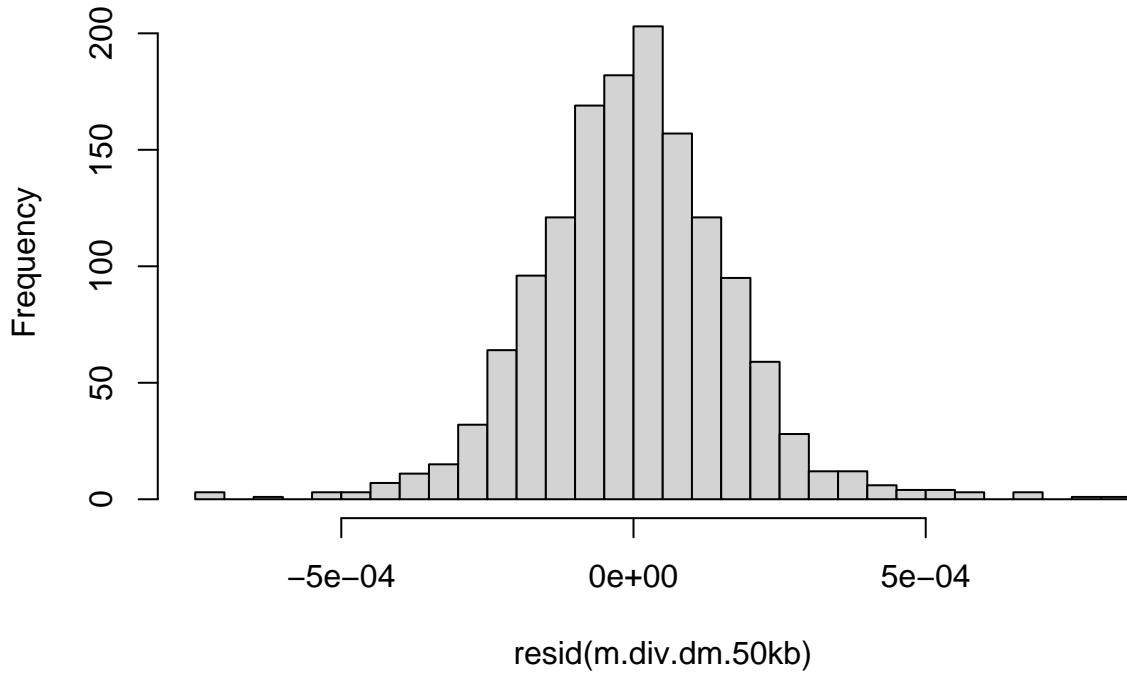
plot(resid(m.div.dm.50kb)~fitted(m.div.dm.50kb))

```



```
hist(resid(m.div.dm.50kb), nclass = 30)
```

## Histogram of resid(m.div.dm.50kb)



```
dwtest(m.div.dm.50kb)

##
##  Durbin-Watson test
##
## data: m.div.dm.50kb
## DW = 1.5747, p-value = 3.694e-16
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.dm.50kb, nsim = 10000)

##
##  Harrison-McCabe test
##
## data: m.div.dm.50kb
## HMC = 0.50534, p-value = 0.6012
summary(m.div.dm.50kb)

##
## Call:
## lm(formula = diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
##     data = dm.lands.50kb)
##
## Residuals:
##       Min        1Q      Median        3Q       Max
## -7.369e-04 -1.007e-04  1.500e-07  9.777e-05  8.124e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 8.603e-03 4.838e-06 1778.154 <2e-16 ***
```

```

## thetaC      9.759e-01  1.822e-03  535.514   <2e-16 ***
## rhoC       1.209e-03  6.874e-04   1.759    0.0788 .
## tmrcaC     1.139e-02  7.780e-05  146.379   <2e-16 ***
## thetaC:tmrcaC 1.065e+00  1.654e-02   64.386   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0001675 on 1411 degrees of freedom
## Multiple R-squared:  0.9973, Adjusted R-squared:  0.9973
## F-statistic: 1.286e+05 on 4 and 1411 DF,  p-value: < 2.2e-16

# type 2 ANOVA
anova.diversity <- Anova(m.div.dm.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
anova.diversity

## Anova Table (Type II tests)
##
## Response: diversity
##           Sum Sq Df  F value Pr(>F) VarExp
## thetaC      0.0081479  1 2.9046e+05 0.000000 0.92684
## rhoC       0.0000001  1 3.0932e+00 0.078838 0.00001
## tmrcaC     0.0004872  1 1.7367e+04 0.000000 0.05542
## thetaC:tmrcaC 0.0001163  1 4.1456e+03 0.000000 0.01323
## Residuals   0.0000396 1411                      0.00450

# GLS
g.div.dm.50kb.1 <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                           data = dm.lands.50kb, weights = varPower(0, ~tmrcaC|chr), cor = corAR1(0, ~bin|ch)

g.div.dm.50kb.2 <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                           data = dm.lands.50kb, weights = varPower(0, ~theta|chr), cor = corAR1(0, ~bin|ch)

g.div.dm.50kb.3 <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                           data = dm.lands.50kb, weights = varPower(0, ~theta|chr), method = "ML")

g.div.dm.50kb.4 <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                           data = dm.lands.50kb, weights = varPower(0, ~tmrcaC|chr), method = "ML")

AIC(g.div.dm.50kb.1, g.div.dm.50kb.2, g.div.dm.50kb.3, g.div.dm.50kb.4)

##          df      AIC
## g.div.dm.50kb.1 11 -20716.73
## g.div.dm.50kb.2 11 -20681.77
## g.div.dm.50kb.3 10 -20620.30
## g.div.dm.50kb.4 10 -20655.40

summary(g.div.dm.50kb.1)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC)
## Data: dm.lands.50kb
##          AIC      BIC logLik
## -20716.73 -20658.92 10369.36
##
```

```

## Correlation Structure: AR(1)
## Formula: ~bin | chr
## Parameter estimate(s):
##     Phi
## 0.2144958
## Variance function:
## Structure: Power of variance covariate, different strata
## Formula: ~tmrcaC | chr
## Parameter estimates:
##      2L      2R      3L      3R
## 0.05445085 0.09431089 0.06301189 0.11582370
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0085894 0.000005516 1557.0928 0.0000
## thetaC       0.9739854 0.002055447  473.8558 0.0000
## rhoC        0.0004325 0.000704757   0.6136 0.5396
## tmrcaC      0.0115855 0.000084597  136.9497 0.0000
## thetaC:tmrcaC 1.0997196 0.018815526   58.4475 0.0000
##
## Correlation:
##          (Intr) thetaC rhoC tmrcaC
## thetaC    0.044
## rhoC     -0.005  0.137
## tmrcaC   -0.143 -0.375 -0.480
## thetaC:tmrcaC -0.289 -0.046  0.003  0.409
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -4.04794537 -0.58184890  0.04817139  0.65222011  4.30624880
##
## Residual standard error: 0.0002182617
## Degrees of freedom: 1416 total; 1411 residual
vif(g.div.dm.50kb.1)

##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
## 1.191539 1.394432 1.938114 1.306769

# Linear model without TMRCA --> rho becomes significant
g.div.dm.50kb.5 <- gls(diversity ~ (thetaC + rhoC),
                           data = dm.lands.50kb, weights = varPower(0, ~thetaC|chr), cor = corAR1(0, ~bin|chr))

summary(g.div.dm.50kb.5)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ (thetaC + rhoC)
## Data: dm.lands.50kb
##      AIC      BIC logLik
## -16799.87 -16752.56 8408.933
##
## Correlation Structure: AR(1)
## Formula: ~bin | chr
## Parameter estimate(s):
##     Phi

```

```

## 0.2247151
## Variance function:
## Structure: Power of variance covariate, different strata
## Formula: ~thetaC | chr
## Parameter estimates:
##          2L      2R      3L      3R
## 0.09783160 0.09779667 0.05144519 0.09035490
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0087332 0.000021244 411.0954     0
## thetaC       1.0944710 0.008181042 133.7814     0
## rhoC        0.0499971 0.002361411  21.1725     0
##
## Correlation:
##      (Intr) thetaC
## thetaC -0.012
## rhoC   -0.003 -0.148
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -12.55241945 -0.53031140  0.01367413  0.61083754  3.01722550
##
## Residual standard error: 0.001130577
## Degrees of freedom: 1416 total; 1413 residual

```

### 3.2 200 kb windows

```

# Chr 2L

# recombination landscapes
rho.dm.200kb.2L <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.rho.200kb.bedgraph", header = T)

# diversity
diversity.dm.200kb.2L <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.diversity.200kb.bedgraph", header = T)
diversity.dm.200kb.2L$avg <- apply(diversity.dm.200kb.2L[4:ncol(diversity.dm.200kb.2L)], 1, mean)

# mutation landscapes
theta.dm.200kb.2L <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.theta.200kb.bedgraph", header = T)

# TMRCA landscapes
tmrca.dm.200kb.2L <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.TMRCA.200kb.bedgraph", header = T)
tmrca.dm.200kb.2L$sample_mean <- apply(tmrca.dm.200kb.2L[4:ncol(tmrca.dm.200kb.2L)], 1, mean)

# missing data
missing.prop.200kb.2L <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.missing.prop.200kb.bedgraph", header = T)
intersect.200kb.2L <- apply(missing.prop.200kb.2L[4:ncol(missing.prop.200kb.2L)], 1, function(x) any(x))

dm.lands.200kb.2L <- as.data.frame(cbind(diversity.dm.200kb.2L$chromStart,
                                             diversity.dm.200kb.2L$chromEnd,
                                             diversity.dm.200kb.2L$avg,
                                             theta.dm.200kb.2L$sample_mean,
                                             rho.dm.200kb.2L$sample_mean,
                                             tmrca.dm.200kb.2L$sample_mean))

```

```

names(dm.lands.200kb.2L) <- c("start", "end", "diversity", "theta", "rho", "tmrca")
dm.lands.200kb.2L$bin <- 1:nrow(dm.lands.200kb.2L)

# filters based on missing data
dm.lands.200kb.2L <- dm.lands.200kb.2L[which(intersect.200kb.2L == F),]

dm.lands.200kb.2L$chr <- "2L"

dm.lands.200kb.2L$thetaC <- dm.lands.200kb.2L$theta - mean(dm.lands.200kb.2L$theta)
dm.lands.200kb.2L$tmrcaC <- dm.lands.200kb.2L$tmrca - mean(dm.lands.200kb.2L$tmrca)
dm.lands.200kb.2L$rhoC <- dm.lands.200kb.2L$rho - mean(dm.lands.200kb.2L$rho)

g.div.dm.200kb.2L <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                             data = dm.lands.200kb.2L, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin))

summary(g.div.dm.200kb.2L)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC)
##   Data: dm.lands.200kb.2L
##          AIC      BIC  logLik
##    -1244.082 -1224.731 630.041
##
## Correlation Structure: ARMA(1,0)
##   Formula: ~bin
##   Parameter estimate(s):
##     Phi1
## 0.1002962
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~tmrcaC
##   Parameter estimates:
##     power
## 0.05640964
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0096851 0.00001590 609.2540 0.0000
## thetaC       0.9912075 0.00852140 116.3197 0.0000
## rhoC        0.0035710 0.00328708   1.0864 0.2807
## tmrcaC      0.0122532 0.00061930  19.7855 0.0000
## thetaC:tmrcaC 1.0357572 0.10202136  10.1524 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC      0.034
## rhoC        0.100  0.195
## tmrcaC     -0.244 -0.449 -0.572
## thetaC:tmrcaC -0.337 -0.112 -0.276  0.696
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -1.8896987 -0.6840157 -0.1976799  0.4999174  3.1380216
##

```

```

## Residual standard error: 0.0001535204
## Degrees of freedom: 83 total; 78 residual
# Chr 2R

# recombination landscapes
rho.dm.200kb.2R <- read.table("dm_data/dm_chr_maps/2R/dm_30x5x5.rho.200kb.bedgraph", header = T)

# diversity
diversity.dm.200kb.2R <- read.table("dm_data/dm_chr_maps/2R/dm_30x5x5.diversity.200kb.bedgraph", header = T)
diversity.dm.200kb.2R$avg <- apply(diversity.dm.200kb.2R[4:ncol(diversity.dm.200kb.2R)], 1, mean)

# mutation landscapes
theta.dm.200kb.2R <- read.table("dm_data/dm_chr_maps/2R/dm_30x5x5.theta.200kb.bedgraph", header = T)

# TMRCAs landscapes
tmrca.dm.200kb.2R <- read.table("dm_data/dm_chr_maps/2R/dm_30x5x5.TMRCA.200kb.bedgraph", header = T)
tmrca.dm.200kb.2R$sample_mean <- apply(tmrca.dm.200kb.2R[4:ncol(tmrca.dm.200kb.2R)], 1, mean)

# missing data
missing.prop.200kb.2R <- read.table("dm_data/dm_chr_maps/2R/dm_30x5x5.missing.prop.200kb.bedgraph", header = T)
intersect.200kb.2R <- apply(missing.prop.200kb.2R[4:ncol(missing.prop.200kb.2R)], 1, function(x) any(x))

dm.lands.200kb.2R <- as.data.frame(cbind(diversity.dm.200kb.2R$chromStart,
                                             diversity.dm.200kb.2R$chromEnd,
                                             diversity.dm.200kb.2R$avg,
                                             theta.dm.200kb.2R$sample_mean,
                                             rho.dm.200kb.2R$sample_mean,
                                             tmrca.dm.200kb.2R$sample_mean))
names(dm.lands.200kb.2R) <- c("start", "end", "diversity", "theta", "rho", "tmrca")
dm.lands.200kb.2R$bin <- 1:nrow(dm.lands.200kb.2R)

# filters based on missing data
dm.lands.200kb.2R <- dm.lands.200kb.2R[which(intersect.200kb.2R == F),]

dm.lands.200kb.2R$chr <- "2R"

dm.lands.200kb.2R$thetaC <- dm.lands.200kb.2R$theta - mean(dm.lands.200kb.2R$theta)
dm.lands.200kb.2R$tmrcaC <- dm.lands.200kb.2R$tmrca - mean(dm.lands.200kb.2R$tmrca)
dm.lands.200kb.2R$rhoC <- dm.lands.200kb.2R$rho - mean(dm.lands.200kb.2R$rho)

g.div.dm.200kb.2R <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                            data = dm.lands.200kb.2R, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin))

summary(g.div.dm.200kb.2R)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC)
## Data: dm.lands.200kb.2R
##          AIC      BIC    logLik
##     -1165.932 -1147.499 590.9659
## 
## Correlation Structure: ARMA(1,0)
## Formula: ~bin
## Parameter estimate(s):

```

```

##      Phi1
## 0.2372428
## Variance function:
##  Structure: Power of variance covariate
##  Formula: ~tmrcaC
## Parameter estimates:
##      power
## 0.06275131
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept) 0.0085392 0.00001264 675.8307 0.0000
## thetaC       0.9699152 0.00505288 191.9530 0.0000
## rhoC        0.0027465 0.00292834   0.9379 0.3516
## tmrcaC      0.0110299 0.00043604  25.2959 0.0000
## thetaC:tmrcaC 0.9373743 0.11041693    8.4894 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC  tmrcaC
## thetaC     0.030
## rhoC      -0.063  0.097
## tmrcaC    -0.153 -0.376 -0.219
## thetaC:tmrcaC -0.290 -0.069  0.120  0.497
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -2.13836840 -0.68198223  0.08032991  0.80898896  2.57448459
##
## Residual standard error: 0.0001098196
## Degrees of freedom: 74 total; 69 residual
# recombination landscapes
rho.dm.200kb.3L <- read.table("dm_data/dm_chr_maps/3L/dm_30x5x5.rho.200kb.bedgraph", header = T)

# diversity
diversity.dm.200kb.3L <- read.table("dm_data/dm_chr_maps/3L/dm_30x5x5.diversity.200kb.bedgraph", header = T)
diversity.dm.200kb.3L$avg <- apply(diversity.dm.200kb.3L[4:ncol(diversity.dm.200kb.3L)], 1, mean)

# mutation landscapes
theta.dm.200kb.3L <- read.table("dm_data/dm_chr_maps/3L/dm_30x5x5.theta.200kb.bedgraph", header = T)

# TMRCAs landscapes
tmrca.dm.200kb.3L <- read.table("dm_data/dm_chr_maps/3L/dm_30x5x5.TMRCA.200kb.bedgraph", header = T)
tmrca.dm.200kb.3L$sample_mean <- apply(tmrca.dm.200kb.3L[4:ncol(tmrca.dm.200kb.3L)], 1, mean)

# missing data
missing.prop.200kb.3L <- read.table("dm_data/dm_chr_maps/3L/dm_30x5x5.missing.prop.200kb.bedgraph", header = T)
intersect.200kb.3L <- apply(missing.prop.200kb.3L[4:ncol(missing.prop.200kb.3L)], 1, function(x) any(x))

dm.lands.200kb.3L <- as.data.frame(cbind(diversity.dm.200kb.3L$chromStart,
                                             diversity.dm.200kb.3L$chromEnd,
                                             diversity.dm.200kb.3L$avg,
                                             theta.dm.200kb.3L$sample_mean,
                                             rho.dm.200kb.3L$sample_mean,
                                             intersect.200kb.3L))

```

```

tmrca.dm.200kb.3L$sample_mean))
names(dm.lands.200kb.3L) <- c("start", "end", "diversity", "theta", "rho", "tmrca")
dm.lands.200kb.3L$bin <- 1:nrow(dm.lands.200kb.3L)

# filters based on missing data
dm.lands.200kb.3L <- dm.lands.200kb.3L[which(intersect.200kb.3L == F),]

dm.lands.200kb.3L$chr <- "3L"

dm.lands.200kb.3L$thetaC <- dm.lands.200kb.3L$theta - mean(dm.lands.200kb.3L$theta)
dm.lands.200kb.3L$tmrcaC <- dm.lands.200kb.3L$tmrca - mean(dm.lands.200kb.3L$tmrca)
dm.lands.200kb.3L$rhoC <- dm.lands.200kb.3L$rho - mean(dm.lands.200kb.3L$rho)

g.div.dm.200kb.3L <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                           data = dm.lands.200kb.3L, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin))

summary(g.div.dm.200kb.3L)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC)
## Data: dm.lands.200kb.3L
##      AIC      BIC    logLik
## -1307.956 -1288.321 661.9781
##
## Correlation Structure: ARMA(1,0)
## Formula: ~bin
## Parameter estimate(s):
##     Phi1
## 0.2105682
## Variance function:
## Structure: Power of variance covariate
## Formula: ~tmrcaC
## Parameter estimates:
##     power
## -0.01470136
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0089474 0.00001816 492.7438 0.0000
## thetaC       0.9811147 0.00736731 133.1713 0.0000
## rhoC        0.0078270 0.00261567   2.9923 0.0037
## tmrcaC      0.0106115 0.00042145  25.1784 0.0000
## thetaC:tmrcaC 0.7871946 0.07703046 10.2193 0.0000
##
## Correlation:
##          (Intr) thetaC rhoC   tmrcaC
## thetaC   0.133
## rhoC    0.079  0.300
## tmrcaC -0.394 -0.661 -0.463
## thetaC:tmrcaC -0.587 -0.238 -0.153  0.680
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -2.89079240 -0.54320978  0.05844326  0.51224633  2.31374278

```

```

## 
## Residual standard error: 0.0001059737
## Degrees of freedom: 86 total; 81 residual
# Chr 3R

# recombination landscapes
rho.dm.200kb.3R <- read.table("dm_data/dm_chr_maps/3R/dm_30x5x5.rho.200kb.bedgraph", header = T)

# diversity
diversity.dm.200kb.3R <- read.table("dm_data/dm_chr_maps/3R/dm_30x5x5.diversity.200kb.bedgraph", header = T)

diversity.dm.200kb.3R$avg <- apply(diversity.dm.200kb.3R[4:ncol(diversity.dm.200kb.3R)], 1, mean)

# mutation landscapes
theta.dm.200kb.3R <- read.table("dm_data/dm_chr_maps/3R/dm_30x5x5.theta.200kb.bedgraph", header = T)

# TMRCA landscapes
tmrca.dm.200kb.3R <- read.table("dm_data/dm_chr_maps/3R/dm_30x5x5.TMRCA.200kb.bedgraph", header = T)
tmrca.dm.200kb.3R$sample_mean <- apply(tmrca.dm.200kb.3R[4:ncol(tmrca.dm.200kb.3R)], 1, mean)

# missing data
missing.prop.200kb.3R <- read.table("dm_data/dm_chr_maps/3R/dm_30x5x5.missing.prop.200kb.bedgraph", header = T)
intersect.200kb.3R <- apply(missing.prop.200kb.3R[4:ncol(missing.prop.200kb.3R)], 1, function(x) any(x))

dm.lands.200kb.3R <- as.data.frame(cbind(diversity.dm.200kb.3R$chromStart,
                                             diversity.dm.200kb.3R$chromEnd,
                                             diversity.dm.200kb.3R$avg,
                                             theta.dm.200kb.3R$sample_mean,
                                             rho.dm.200kb.3R$sample_mean,
                                             tmrca.dm.200kb.3R$sample_mean))
names(dm.lands.200kb.3R) <- c("start", "end", "diversity", "theta", "rho", "tmrca")
dm.lands.200kb.3R$bin <- 1:nrow(dm.lands.200kb.3R)

# filters based on missing data
dm.lands.200kb.3R <- dm.lands.200kb.3R[which(intersect.200kb.3R == F),]

dm.lands.200kb.3R$chr <- "3R"

dm.lands.200kb.3R$thetaC <- dm.lands.200kb.3R$theta - mean(dm.lands.200kb.3R$theta)
dm.lands.200kb.3R$tmrcaC <- dm.lands.200kb.3R$tmrca - mean(dm.lands.200kb.3R$tmrca)
dm.lands.200kb.3R$rhoC <- dm.lands.200kb.3R$rho - mean(dm.lands.200kb.3R$rho)

g.div.dm.200kb.3R <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                            data = dm.lands.200kb.3R, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin))

summary(g.div.dm.200kb.3R)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC)
##   Data: dm.lands.200kb.3R
##       AIC      BIC  logLik
##   -1883.368 -1861.135 949.684
## 
## Correlation Structure: ARMA(1,0)

```

```

## Formula: ~bin
## Parameter estimate(s):
##     Phi1
## 0.09974948
## Variance function:
## Structure: Power of variance covariate
## Formula: ~tmrcaC
## Parameter estimates:
##     power
## 0.1960113
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0075661 0.00001040 727.7696 0.0000
## thetaC       0.9683546 0.00387775 249.7209 0.0000
## rhoC        -0.0041012 0.00175339 -2.3390 0.0211
## tmrcaC      0.0103602 0.00028386 36.4976 0.0000
## thetaC:tmrcaC 0.7922675 0.07387641 10.7242 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC      0.283
## rhoC        0.214  0.306
## tmrcaC     -0.574 -0.559 -0.546
## thetaC:tmrcaC -0.625 -0.374 -0.215  0.781
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -2.78869608 -0.72931864 -0.06801681  0.64535064  2.75174311
##
## Residual standard error: 0.0001631813
## Degrees of freedom: 119 total; 114 residual

# all together now
dm.lands.200kb <- rbind.data.frame(dm.lands.200kb.2L, dm.lands.200kb.2R, dm.lands.200kb.3L, dm.lands.200kb.3R)

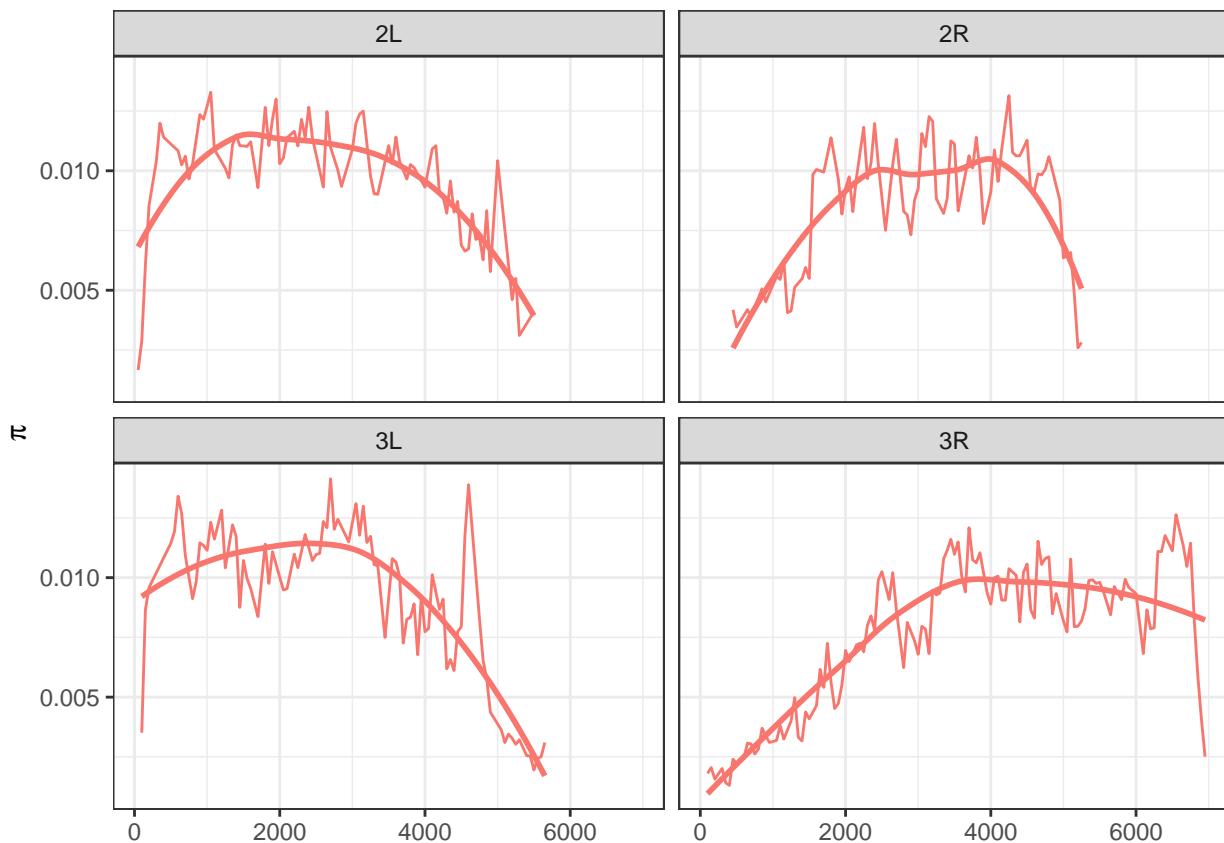
write.table(dm.lands.200kb, "dm_data/dm_chr_maps/dm.maps.200kb.tsv", quote = F, sep = "\t", row.names = FALSE)

# Plots
scale.3d <- function(x) sprintf("%.3f", x) # digits shown in y axis

setTimeLimit(cpu = Inf, elapsed = Inf, transient = F)

molten.diversity <- melt(dm.lands.200kb[c(3,7,8)], id.vars = c("bin", "chr"))
diversity.map <- ggplot(data = molten.diversity, aes(x = bin * 50, y = value)) + facet_wrap(~chr)
diversity.map <- diversity.map + geom_line(data = molten.diversity, colour = "#F8766D")
diversity.map <- diversity.map + geom_smooth(method = "loess", se = F, colour = "#F8766D")
diversity.map <- diversity.map + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_breaks())
diversity.map <- diversity.map + labs(title = NULL, x = NULL, y = expression(pi))
diversity.map <- diversity.map + theme(axis.title.x = element_text(size = 20), axis.title.y = element_text(size = 20))
diversity.map

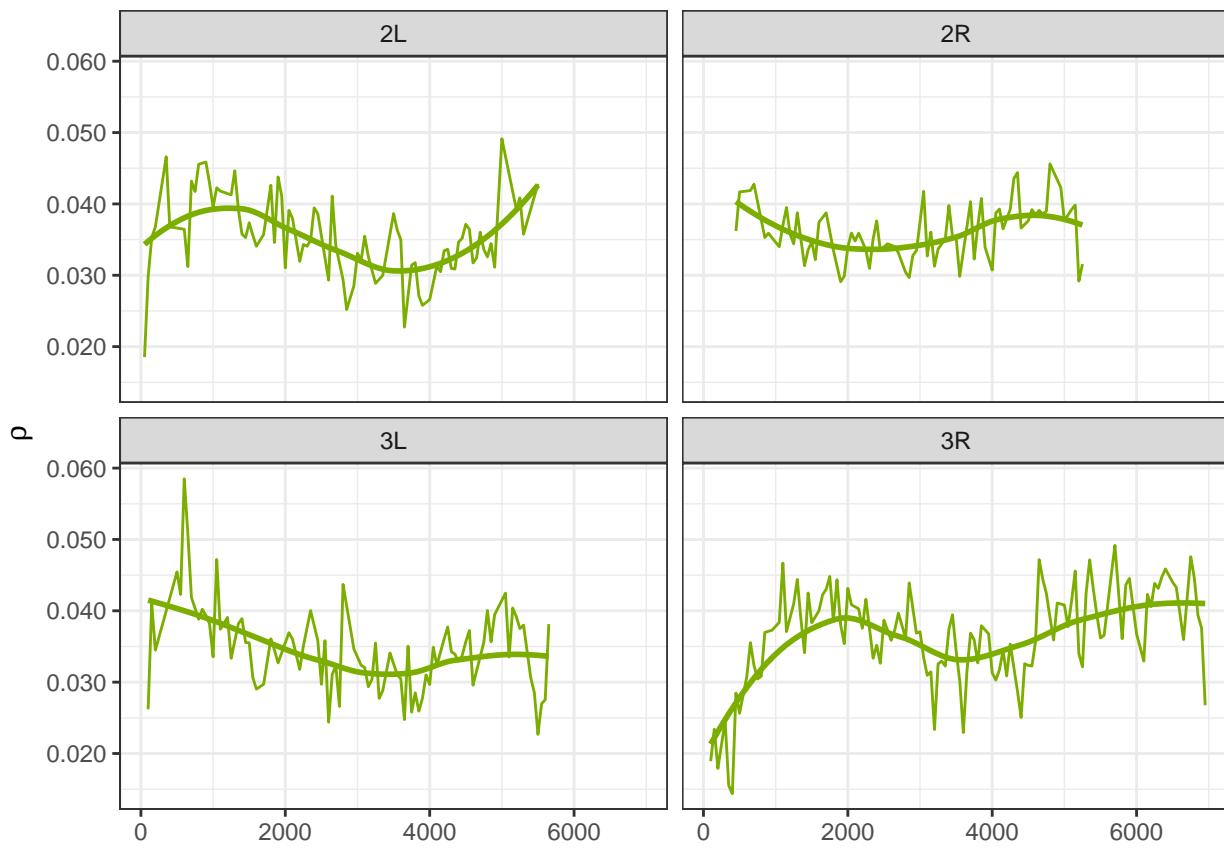
```



```

molten.rho <- melt(dm.lands.200kb[c(5,7,8)], id.vars = c("bin", "chr"))
rho.map <- ggplot(data = molten.rho, aes(x = bin * 50, y = value)) + facet_wrap(~chr)
rho.map <- rho.map + geom_line(data = molten.rho, colour = "#7CAE00")
rho.map <- rho.map + geom_smooth(method = "loess", se = F, colour = "#7CAE00")
rho.map <- rho.map + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_l
rho.map <- rho.map + labs(title = NULL, x = NULL, y = expression(rho))
rho.map <- rho.map + theme(axis.title.x = element_text(size = 20), axis.title.y = element_text(size = 20))
rho.map

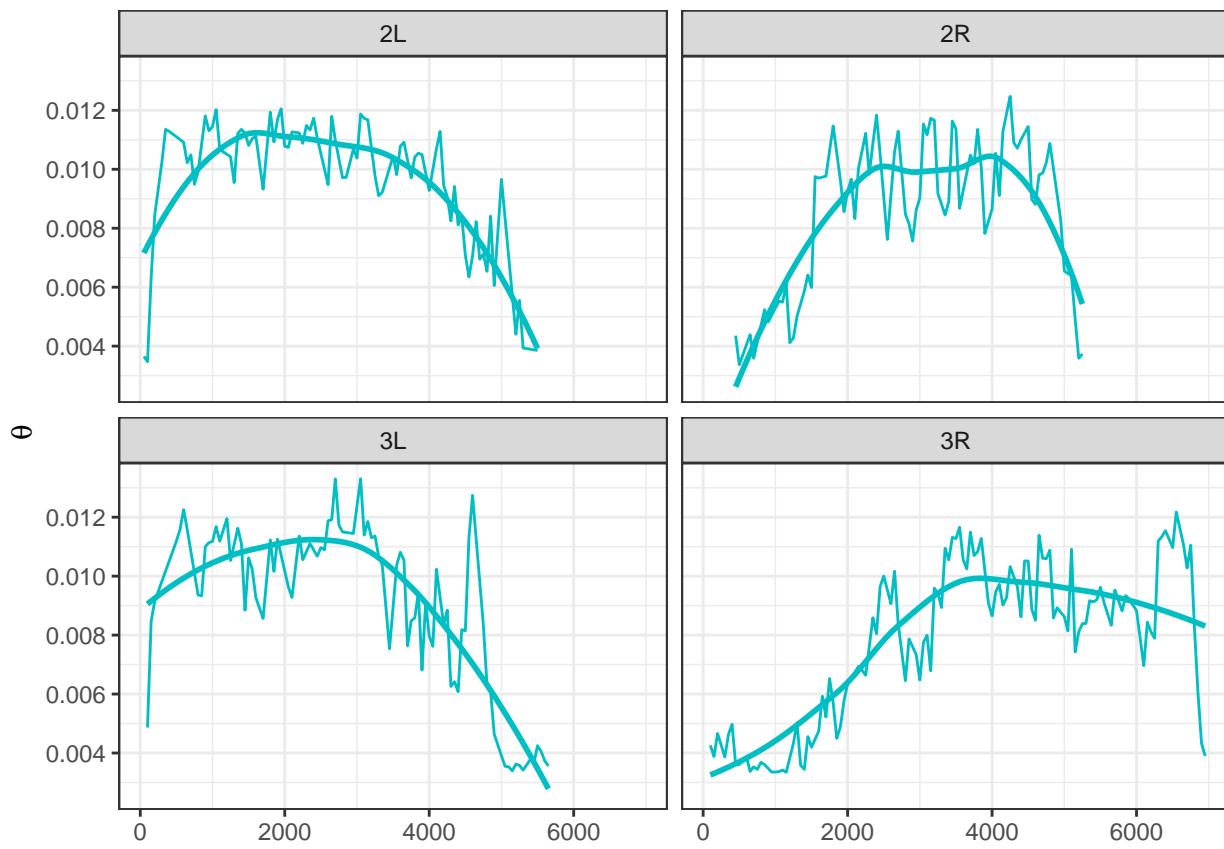
```



```

molten.theta <- melt(dm.lands.200kb[c(4,7,8)], id.vars = c("bin", "chr"))
theta.map <- ggplot(data = molten.theta, aes(x = bin * 50, y = value)) + facet_wrap(~chr)
theta.map <- theta.map + geom_line(data = molten.theta, colour = "#00BFC4")
theta.map <- theta.map + geom_smooth(method = "loess", se = F, colour = "#00BFC4")
theta.map <- theta.map + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_breaks())
theta.map <- theta.map + labs(title = NULL, x = NULL, y = expression(theta))
theta.map <- theta.map + theme(axis.title.x = element_text(size = 20), axis.title.y = element_text(size = 20))
theta.map

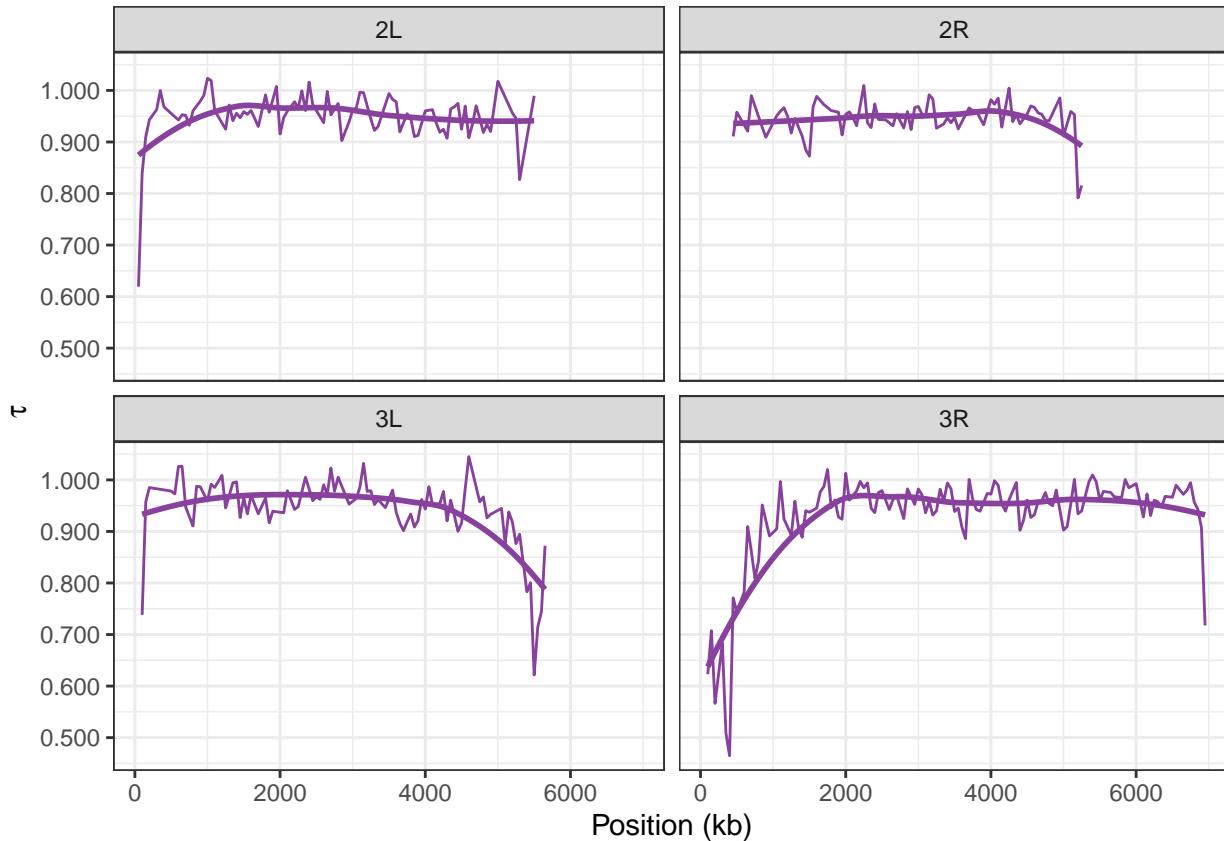
```



```

molten.tmrca <- melt(dm.lands.200kb[c(6,7,8)], id.vars = c("bin", "chr"))
tmrca.map <- ggplot(data = molten.tmrca, aes(x = bin * 50, y = value)) + facet_wrap(~chr)
tmrca.map <- tmrca.map + geom_line(data = molten.tmrca, colour = "#88419d")
tmrca.map <- tmrca.map + geom_smooth(method = "loess", se = F, colour = "#88419d")
tmrca.map <- tmrca.map + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_breaks())
tmrca.map <- tmrca.map + labs(title = NULL, x = "Position (kb)", y = expression(tau))
tmrca.map <- tmrca.map + theme(axis.title.x = element_text(size = 20), axis.title.y = element_text(size = 20))
tmrca.map

```



```
# genome-wide correlations
cor.test(~rho + diversity, data = dm.lands.200kb, method = "spearman")
```

```
##
## Spearman's rank correlation rho
##
## data: rho and diversity
## S = 6652998, p-value = 0.002515
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.1585153
```

```
cor.test(~rho + tmrca, data = dm.lands.200kb, method = "spearman")
```

```
##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 4384696, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.4454147
```

```
cor.test(~theta + tmrca, data = dm.lands.200kb, method = "spearman")
```

```
##
## Spearman's rank correlation rho
```

```

## 
## data: theta and tmrca
## S = 3844174, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.513781

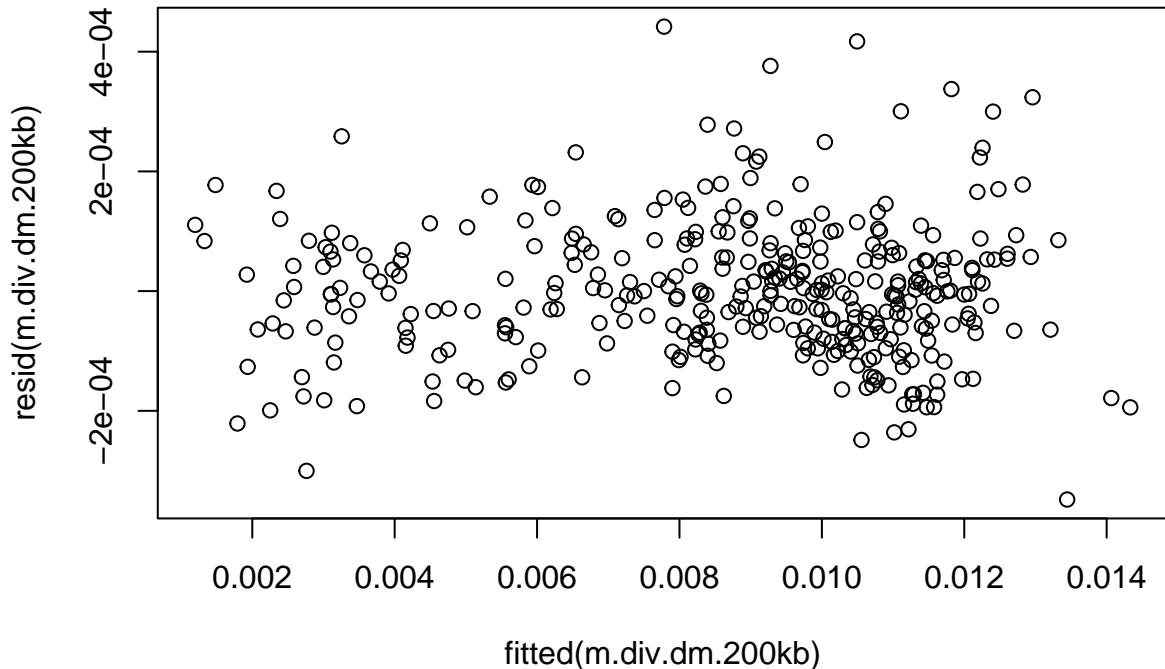
# Linear models
# centering
dm.lands.200kb$thetaC <- dm.lands.200kb$theta - mean(dm.lands.200kb$theta)
dm.lands.200kb$tmrcaC <- dm.lands.200kb$tmrca - mean(dm.lands.200kb$tmrca)
dm.lands.200kb$rhoC <- dm.lands.200kb$rho - mean(dm.lands.200kb$rho)

dm.lands.200kb$bin <- 1:nrow(dm.lands.200kb)

m.div.dm.200kb <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC), data = dm.lands.200kb)

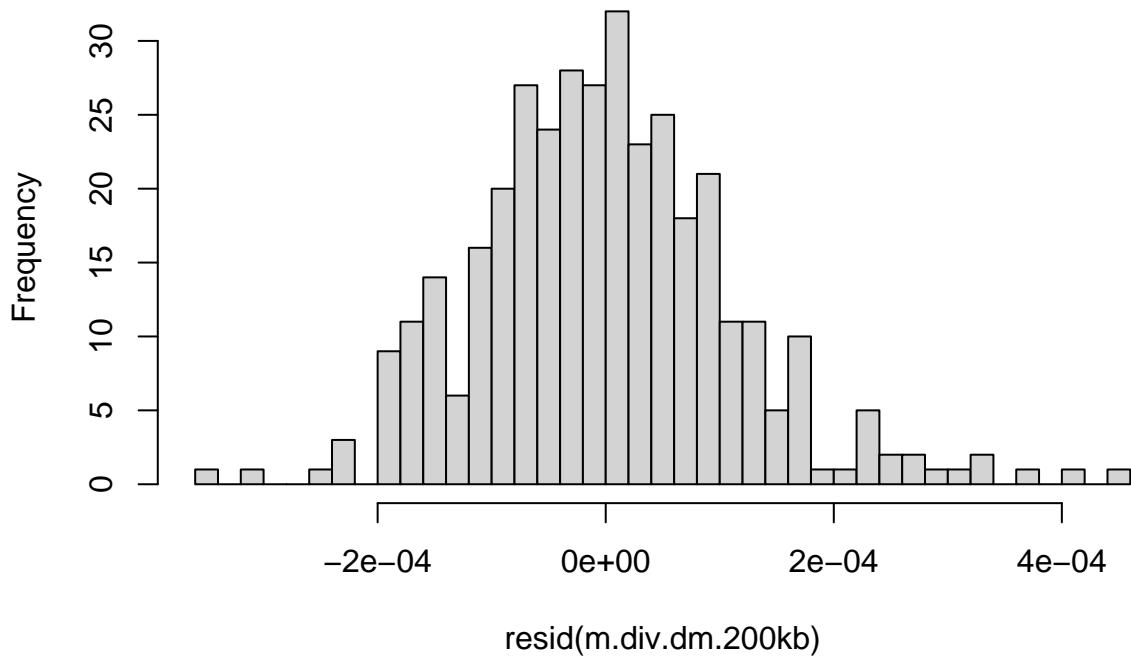
plot(resid(m.div.dm.200kb)~fitted(m.div.dm.200kb))

```



```
hist(resid(m.div.dm.200kb), nclass = 30)
```

## Histogram of resid(m.div.dm.200kb)



```
dwtest(m.div.dm.200kb)
```

```
##  
##  Durbin-Watson test  
##  
## data: m.div.dm.200kb  
## DW = 1.4463, p-value = 3.114e-08  
## alternative hypothesis: true autocorrelation is greater than 0  
hmctest(m.div.dm.200kb, nsim = 10000)
```

```
##
```

```
##  Harrison-McCabe test
```

```
##
```

```
## data: m.div.dm.200kb
```

```
## HMC = 0.56948, p-value = 0.9683
```

```
summary(m.div.dm.200kb)
```

```
##
```

```
## Call:
```

```
## lm(formula = diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),  
##      data = dm.lands.200kb)
```

```
##
```

```
## Residuals:
```

```
##       Min        1Q     Median        3Q       Max  
## -3.481e-04 -6.976e-05 -4.240e-06  6.351e-05  4.418e-04
```

```
##
```

```
## Coefficients:
```

```
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 8.571e-03 7.361e-06 1164.402 <2e-16 ***
```

```

## thetaC      9.802e-01  2.925e-03  335.083   <2e-16 ***
## rhoC       1.652e-03  1.319e-03   1.252     0.211
## tmrcaC     1.104e-02  2.092e-04   52.753   <2e-16 ***
## thetaC:tmrcaC 8.772e-01  4.258e-02   20.604   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0001143 on 357 degrees of freedom
## Multiple R-squared:  0.9985, Adjusted R-squared:  0.9985
## F-statistic: 6.074e+04 on 4 and 357 DF,  p-value: < 2.2e-16

# type 2 ANOVA
anova.diversity <- Anova(m.div.dm.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
anova.diversity

## Anova Table (Type II tests)
##
## Response: diversity
##           Sum Sq Df  F value Pr(>F)  VarExp
## thetaC      0.00165091  1 126265.729 0.00000 0.96688
## rhoC       0.00000002  1      1.567 0.21147 0.00001
## tmrcaC     0.00004631  1    3541.894 0.00000 0.02712
## thetaC:tmrcaC 0.00000555  1     424.530 0.00000 0.00325
## Residuals   0.00000467 357                      0.00273

# GLS
g.div.dm.200kb.1 <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                           data = dm.lands.200kb, weights = varPower(0, ~tmrcaC|chr), cor = corAR1(0, ~bin|chr))
g.div.dm.200kb.2 <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                           data = dm.lands.200kb, weights = varPower(0, ~thetaC|chr), cor = corAR1(0, ~bin|chr))
g.div.dm.200kb.3 <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                           data = dm.lands.200kb, weights = varPower(0, ~thetaC|chr), method = "ML")
g.div.dm.200kb.4 <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                           data = dm.lands.200kb, weights = varPower(0, ~tmrcaC|chr), method = "ML")

AIC(g.div.dm.200kb.1, g.div.dm.200kb.2, g.div.dm.200kb.3, g.div.dm.200kb.4)

##          df      AIC
## g.div.dm.200kb.1 11 -5583.726
## g.div.dm.200kb.2 11 -5586.917
## g.div.dm.200kb.3 10 -5561.165
## g.div.dm.200kb.4 10 -5559.348

summary(g.div.dm.200kb.1)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC)
## Data: dm.lands.200kb
##          AIC      BIC logLik
## -5583.726 -5540.918 2802.863
##
```

```

## Correlation Structure: AR(1)
## Formula: ~bin | chr
## Parameter estimate(s):
##     Phi
## 0.2843776
## Variance function:
## Structure: Power of variance covariate, different strata
## Formula: ~tmrcaC | chr
## Parameter estimates:
##          2L        2R        3L        3R
## -0.041143168 0.074096129 0.001953365 0.075769644
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0085528 0.00000826 1035.3856 0.0000
## thetaC       0.9746365 0.00308267  316.1668 0.0000
## rhoC        0.0005062 0.00134208   0.3772 0.7062
## tmrcaC      0.0111855 0.00019829   56.4105 0.0000
## thetaC:tmrcaC 0.9085940 0.04279033   21.2336 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC tmrcaC
## thetaC    0.133
## rhoC     -0.012  0.189
## tmrcaC   -0.315 -0.455 -0.439
## thetaC:tmrcaC -0.440 -0.196 -0.068  0.727
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -2.9288491 -0.5661772 0.1198220 0.6423762 3.2163952
##
## Residual standard error: 0.0001234783
## Degrees of freedom: 362 total; 357 residual
vif(g.div.dm.200kb.1)

##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
## 1.344037 1.505614 3.925969 2.712069

# Linear model without TMRCA --> rho becomes significant
g.div.dm.200kb.5 <- gls(diversity ~ (thetaC + rhoC),
                           data = dm.lands.200kb, weights = varPower(0, ~thetaC), cor = corAR1(0, ~bin), me
```

```
summary(g.div.dm.200kb.5)
```

```

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ (thetaC + rhoC)
## Data: dm.lands.200kb
##      AIC      BIC logLik
## -4723.291 -4699.941 2367.645
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##     Phi
```

```

## 0.4168254
## Variance function:
## Structure: Power of variance covariate
## Formula: ~thetaC
## Parameter estimates:
## power
## 0.13171
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0086889 0.000030456 285.29066      0
## thetaC       1.0809727 0.011736952  92.09995      0
## rhoC        0.0472191 0.003846123  12.27706      0
##
## Correlation:
##          (Intr) thetaC
## thetaC -0.016
## rhoC   0.048 -0.145
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -5.445432702 -0.523327124 -0.009243674  0.572229138  2.972069433
##
## Residual standard error: 0.0009029211
## Degrees of freedom: 362 total; 359 residual

```

### 3.3 1 Mb windows

```

# Chr 2L

# recombination landscapes
rho.dm.1Mb.2L <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.rho.1Mb.bedgraph", header = T)

# diversity
diversity.dm.1Mb.2L <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.diversity.1Mb.bedgraph", header = T)
diversity.dm.1Mb.2L$avg <- apply(diversity.dm.1Mb.2L[4:ncol(diversity.dm.1Mb.2L)], 1, mean)

# mutation landscapes
theta.dm.1Mb.2L <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.theta.1Mb.bedgraph", header = T)

# TMRCA landscapes
tmrca.dm.1Mb.2L <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.TMRCA.1Mb.bedgraph", header = T)
tmrca.dm.1Mb.2L$sample_mean <- apply(tmrca.dm.1Mb.2L[4:ncol(tmrca.dm.1Mb.2L)], 1, mean)

# missing data
missing.prop.1Mb.2L <- read.table("dm_data/dm_chr_maps/2L/dm_30x5x5.missing.prop.1Mb.bedgraph", header = T)
intersect.1Mb.2L <- apply(missing.prop.1Mb.2L[4:ncol(missing.prop.1Mb.2L)], 1, function(x) any(x > 0.1))

dm.lands.1Mb.2L <- as.data.frame(cbind(diversity.dm.1Mb.2L$chromStart,
                                         diversity.dm.1Mb.2L$chromEnd,
                                         diversity.dm.1Mb.2L$avg,
                                         theta.dm.1Mb.2L$sample_mean,
                                         rho.dm.1Mb.2L$sample_mean,
                                         tmrca.dm.1Mb.2L$sample_mean))

```

```

names(dm.lands.1Mb.2L) <- c("start", "end", "diversity", "theta", "rho", "tmrca")
dm.lands.1Mb.2L$bin <- 1:nrow(dm.lands.1Mb.2L)

# filters based on missing data
dm.lands.1Mb.2L <- dm.lands.1Mb.2L[which(intersect.1Mb.2L == F),]

dm.lands.1Mb.2L$chr <- "2L"

dm.lands.1Mb.2L$thetaC <- dm.lands.1Mb.2L$theta - mean(dm.lands.1Mb.2L$theta)
dm.lands.1Mb.2L$tmrcaC <- dm.lands.1Mb.2L$tmrca - mean(dm.lands.1Mb.2L$tmrca)
dm.lands.1Mb.2L$rhoC <- dm.lands.1Mb.2L$rho - mean(dm.lands.1Mb.2L$rho)

g.div.dm.1Mb.2L <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                           data = dm.lands.1Mb.2L, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), ...)

summary(g.div.dm.1Mb.2L)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC)
##   Data: dm.lands.1Mb.2L
##       AIC     BIC   logLik
##   -299.3268 -291.7713 157.6634
##
## Correlation Structure: ARMA(1,0)
##   Formula: ~bin
## Parameter estimate(s):
##   Phi1
## 0.3144048
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~tmrcaC
## Parameter estimates:
##   power
## -0.04167166
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0101124 0.00002513 402.3734 0.0000
## thetaC      0.9865547 0.02033816  48.5076 0.0000
## rhoC       0.0010558 0.00560117   0.1885 0.8532
## tmrcaC     0.0129654 0.00122549  10.5798 0.0000
## thetaC:tmrcaC 1.8344985 0.31522351    5.8197 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC      -0.006
## rhoC        0.168  0.107
## tmrcaC     -0.247 -0.591 -0.594
## thetaC:tmrcaC -0.447  0.063 -0.394  0.584
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -1.4305539 -0.5991356 -0.1638086  0.5088896  2.4443876
##

```

```

## Residual standard error: 5.223258e-05
## Degrees of freedom: 19 total; 14 residual
# Chr 2R

# recombination landscapes
rho.dm.1Mb.2R <- read.table("dm_data/dm_chr_maps/2R/dm_30x5x5.rho.1Mb.bedgraph", header = T)

# diversity
diversity.dm.1Mb.2R <- read.table("dm_data/dm_chr_maps/2R/dm_30x5x5.diversity.1Mb.bedgraph", header = T)
diversity.dm.1Mb.2R$avg <- apply(diversity.dm.1Mb.2R[4:ncol(diversity.dm.1Mb.2R)], 1, mean)

# mutation landscapes
theta.dm.1Mb.2R <- read.table("dm_data/dm_chr_maps/2R/dm_30x5x5.theta.1Mb.bedgraph", header = T)

# TMRCA landscapes
tmrca.dm.1Mb.2R <- read.table("dm_data/dm_chr_maps/2R/dm_30x5x5.TMRCA.1Mb.bedgraph", header = T)
tmrca.dm.1Mb.2R$sample_mean <- apply(tmrca.dm.1Mb.2R[4:ncol(tmrca.dm.1Mb.2R)], 1, mean)

# missing data
missing.prop.1Mb.2R <- read.table("dm_data/dm_chr_maps/2R/dm_30x5x5.missing.prop.1Mb.bedgraph", header = T)
intersect.1Mb.2R <- apply(missing.prop.1Mb.2R[4:ncol(missing.prop.1Mb.2R)], 1, function(x) any(x > 0.1))

dm.lands.1Mb.2R <- as.data.frame(cbind(diversity.dm.1Mb.2R$chromStart,
                                           diversity.dm.1Mb.2R$chromEnd,
                                           diversity.dm.1Mb.2R$avg,
                                           theta.dm.1Mb.2R$sample_mean,
                                           rho.dm.1Mb.2R$sample_mean,
                                           tmrca.dm.1Mb.2R$sample_mean))
names(dm.lands.1Mb.2R) <- c("start", "end", "diversity", "theta", "rho", "tmrca")
dm.lands.1Mb.2R$bin <- 1:nrow(dm.lands.1Mb.2R)

# filters based on missing data
dm.lands.1Mb.2R <- dm.lands.1Mb.2R[which(intersect.1Mb.2R == F),]

dm.lands.1Mb.2R$chr <- "2R"

dm.lands.1Mb.2R$thetaC <- dm.lands.1Mb.2R$theta - mean(dm.lands.1Mb.2R$theta)
dm.lands.1Mb.2R$tmrcaC <- dm.lands.1Mb.2R$tmrca - mean(dm.lands.1Mb.2R$tmrca)
dm.lands.1Mb.2R$rhoC <- dm.lands.1Mb.2R$rho - mean(dm.lands.1Mb.2R$rho)

g.div.dm.1Mb.2R <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                           data = dm.lands.1Mb.2R, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), na.action = na.omit)

summary(g.div.dm.1Mb.2R)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC)
## Data: dm.lands.1Mb.2R
##      AIC      BIC    logLik
## -260.3174 -253.6517 138.1587
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):

```

```

##      Phi
## -0.0218456
## Variance function:
## Structure: Power of variance covariate
## Formula: ~tmrcaC
## Parameter estimates:
##      power
## -0.286626
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept) 0.0091552 0.0000283 323.2402 0.0000
## thetaC       0.9718147 0.0212995  45.6262 0.0000
## rhoC        0.0083025 0.0084990   0.9769 0.3479
## tmrcaC      0.0103641 0.0019099   5.4266 0.0002
## thetaC:tmrcaC 0.5202501 0.5098563   1.0204 0.3277
##
## Correlation:
##            (Intr) thetaC rhoC    tmrcaC
## thetaC     -0.233
## rhoC       0.302 -0.140
## tmrcaC    -0.353 -0.638 -0.213
## thetaC:tmrcaC -0.803  0.231 -0.355  0.536
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -1.4712709 -0.4619228 -0.3324611  0.4352917  2.9199214
##
## Residual standard error: 1.478574e-05
## Degrees of freedom: 17 total; 12 residual
# recombination landscapes
rho.dm.1Mb.3L <- read.table("dm_data/dm_chr_maps/3L/dm_30x5x5.rho.1Mb.bedgraph", header = T)

# diversity
diversity.dm.1Mb.3L <- read.table("dm_data/dm_chr_maps/3L/dm_30x5x5.diversity.1Mb.bedgraph", header = T)
diversity.dm.1Mb.3L$avg <- apply(diversity.dm.1Mb.3L[4:ncol(diversity.dm.1Mb.3L)], 1, mean)

# mutation landscapes
theta.dm.1Mb.3L <- read.table("dm_data/dm_chr_maps/3L/dm_30x5x5.theta.1Mb.bedgraph", header = T)

# TMRCAs landscapes
tmrca.dm.1Mb.3L <- read.table("dm_data/dm_chr_maps/3L/dm_30x5x5.TMRCA.1Mb.bedgraph", header = T)
tmrca.dm.1Mb.3L$sample_mean <- apply(tmrca.dm.1Mb.3L[4:ncol(tmrca.dm.1Mb.3L)], 1, mean)

# missing data
missing.prop.1Mb.3L <- read.table("dm_data/dm_chr_maps/3L/dm_30x5x5.missing.prop.1Mb.bedgraph", header = T)
intersect.1Mb.3L <- apply(missing.prop.1Mb.3L[4:ncol(missing.prop.1Mb.3L)], 1, function(x) any(x > 0.1))

dm.lands.1Mb.3L <- as.data.frame(cbind(diversity.dm.1Mb.3L$chromStart,
                                         diversity.dm.1Mb.3L$chromEnd,
                                         diversity.dm.1Mb.3L$avg,
                                         theta.dm.1Mb.3L$sample_mean,
                                         rho.dm.1Mb.3L$sample_mean,
                                         
```

```

tmrca.dm.1Mb.3L$sample_mean))
names(dm.lands.1Mb.3L) <- c("start", "end", "diversity", "theta", "rho", "tmrca")
dm.lands.1Mb.3L$bin <- 1:nrow(dm.lands.1Mb.3L)

# filters based on missing data
dm.lands.1Mb.3L <- dm.lands.1Mb.3L[which(intersect.1Mb.3L == F),]

dm.lands.1Mb.3L$chr <- "3L"

dm.lands.1Mb.3L$thetaC <- dm.lands.1Mb.3L$theta - mean(dm.lands.1Mb.3L$theta)
dm.lands.1Mb.3L$tmrcaC <- dm.lands.1Mb.3L$tmrca - mean(dm.lands.1Mb.3L$tmrca)
dm.lands.1Mb.3L$rhoC <- dm.lands.1Mb.3L$rho - mean(dm.lands.1Mb.3L$rho)

g.div.dm.1Mb.3L <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                           data = dm.lands.1Mb.3L, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), na.action = na.omit)

summary(g.div.dm.1Mb.3L)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC)
## Data: dm.lands.1Mb.3L
##      AIC      BIC    logLik
## -348.8084 -340.0801 182.4042
##
## Correlation Structure: ARMA(1,0)
## Formula: ~bin
## Parameter estimate(s):
##     Phi1
## 0.249026
## Variance function:
## Structure: Power of variance covariate
## Formula: ~tmrcaC
## Parameter estimates:
##     power
## 0.3377385
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0091813 0.00002405 381.7940 0.0000
## thetaC       1.0032652 0.01244385  80.6233 0.0000
## rhoC        0.0070903 0.00396199   1.7896 0.0913
## tmrcaC      0.0084717 0.00094627   8.9528 0.0000
## thetaC:tmrcaC 0.3950013 0.16662491   2.3706 0.0298
##
## Correlation:
##          (Intr) thetaC rhoC   tmrcaC
## thetaC   0.400
## rhoC    0.531  0.320
## tmrcaC -0.622 -0.738 -0.571
## thetaC:tmrcaC -0.618 -0.348 -0.438  0.689
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max

```

```

## -2.71883315 -0.45696303  0.01830762  0.69607904  1.69584501
##
## Residual standard error: 0.0002107777
## Degrees of freedom: 22 total; 17 residual
# Chr 3R

# recombination landscapes
rho.dm.1Mb.3R <- read.table("dm_data/dm_chr_maps/3R/dm_30x5x5.rho.1Mb.bedgraph", header = T)

# diversity
diversity.dm.1Mb.3R <- read.table("dm_data/dm_chr_maps/3R/dm_30x5x5.diversity.1Mb.bedgraph", header = T)
diversity.dm.1Mb.3R$avg <- apply(diversity.dm.1Mb.3R[4:ncol(diversity.dm.1Mb.3R)], 1, mean)

# mutation landscapes
theta.dm.1Mb.3R <- read.table("dm_data/dm_chr_maps/3R/dm_30x5x5.theta.1Mb.bedgraph", header = T)

# TMRCA landscapes
tmrca.dm.1Mb.3R <- read.table("dm_data/dm_chr_maps/3R/dm_30x5x5.TMRCA.1Mb.bedgraph", header = T)
tmrca.dm.1Mb.3R$sample_mean <- apply(tmrca.dm.1Mb.3R[4:ncol(tmrca.dm.1Mb.3R)], 1, mean)

# missing data
missing.prop.1Mb.3R <- read.table("dm_data/dm_chr_maps/3R/dm_30x5x5.missing.prop.1Mb.bedgraph", header = T)
intersect.1Mb.3R <- apply(missing.prop.1Mb[4:ncol(missing.prop.1Mb.3R)], 1, function(x) any(x > 0.1))

dm.lands.1Mb.3R <- as.data.frame(cbind(diversity.dm.1Mb.3R$chromStart,
                                         diversity.dm.1Mb.3R$chromEnd,
                                         diversity.dm.1Mb.3R$avg,
                                         theta.dm.1Mb.3R$sample_mean,
                                         rho.dm.1Mb.3R$sample_mean,
                                         tmrca.dm.1Mb.3R$sample_mean))
names(dm.lands.1Mb.3R) <- c("start", "end", "diversity", "theta", "rho", "tmrca")
dm.lands.1Mb.3R$bin <- 1:nrow(dm.lands.1Mb.3R)

# filters based on missing data
dm.lands.1Mb.3R <- dm.lands.1Mb.3R[which(intersect.1Mb.3R == F),]

dm.lands.1Mb.3R$chr <- "3R"

dm.lands.1Mb.3R$thetaC <- dm.lands.1Mb.3R$theta - mean(dm.lands.1Mb.3R$theta)
dm.lands.1Mb.3R$tmrcaC <- dm.lands.1Mb.3R$tmrca - mean(dm.lands.1Mb.3R$tmrca)
dm.lands.1Mb.3R$rhoC <- dm.lands.1Mb.3R$rho - mean(dm.lands.1Mb.3R$rho)

g.div.dm.1Mb.3R <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                           data = dm.lands.1Mb.3R, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), na.action = na.omit)

summary(g.div.dm.1Mb.3R)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC)
##   Data: dm.lands.1Mb.3R
##       AIC      BIC    logLik
##   -324.5017 -316.9462 170.2509
##
## Correlation Structure: ARMA(1,0)

```

```

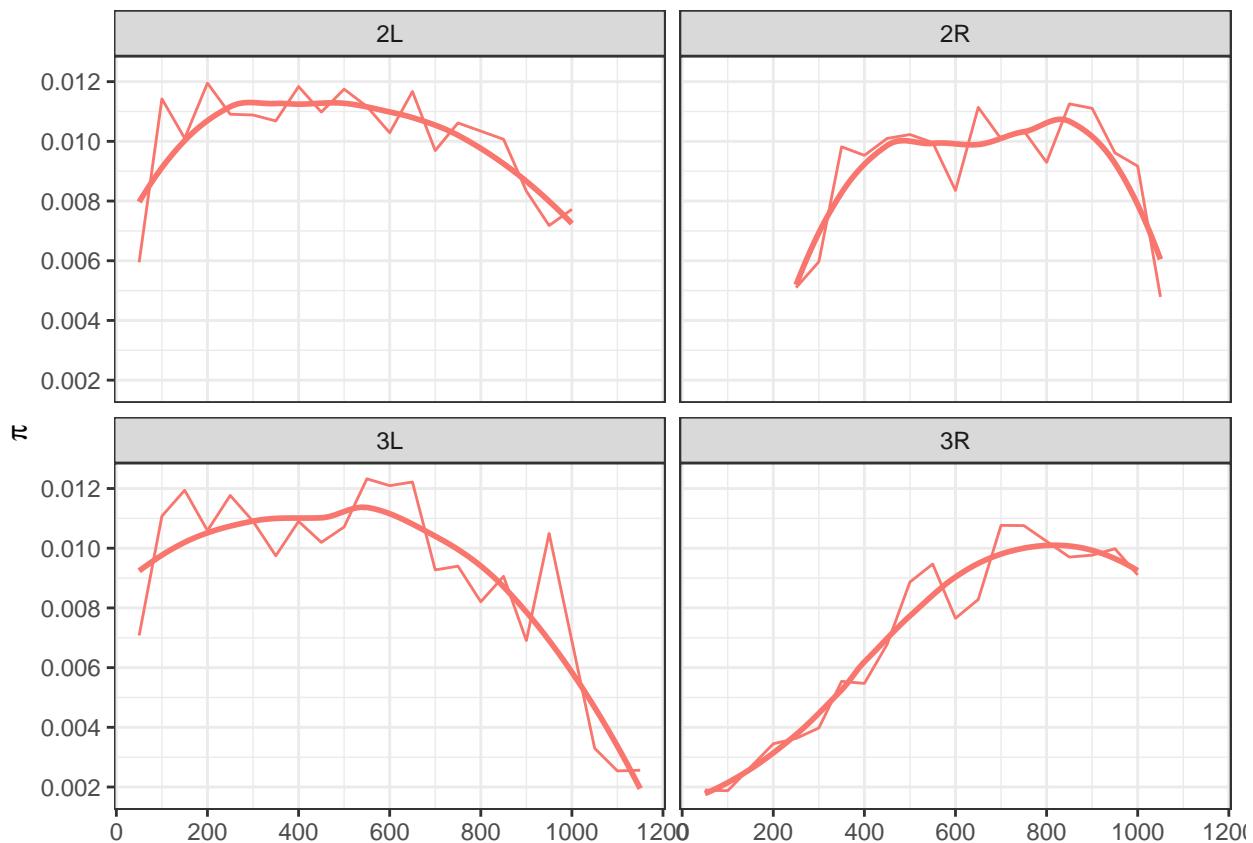
## Formula: ~bin
## Parameter estimate(s):
##     Phi1
## -0.4823527
## Variance function:
## Structure: Power of variance covariate
## Formula: ~tmrcaC
## Parameter estimates:
##     power
## 0.8128992
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0067246 0.00002252 298.66684 0.0000
## thetaC       0.9664707 0.00658600 146.74630 0.0000
## rhoC        0.0031144 0.00241054   1.29200 0.2173
## tmrcaC      0.0094832 0.00049711  19.07661 0.0000
## thetaC:tmrcaC 0.7457601 0.17910163    4.16389 0.0010
##
## Correlation:
##            (Intr) thetaC rhoC  tmrcaC
## thetaC      0.911
## rhoC       -0.280  0.066
## tmrcaC     -0.923 -0.944 -0.023
## thetaC:tmrcaC -0.940 -0.881  0.320  0.856
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -1.7308894 -0.4913490  0.1058365  0.6374128  1.9989782
##
## Residual standard error: 0.0004245867
## Degrees of freedom: 19 total; 14 residual
# all together now
dm.lands.1Mb <- rbind.data.frame(dm.lands.1Mb.2L, dm.lands.1Mb.2R, dm.lands.1Mb.3L, dm.lands.1Mb.3R)

write.table(dm.lands.1Mb, "dm_data/dm_chr_maps/dm.maps.1Mb.tsv", quote = F, sep = "\t", row.names = F, )

# Plots
scale.3d <- function(x) sprintf("%.3f", x) # digits shown in y axis

setTimeLimit(cpu = Inf, elapsed = Inf, transient = F)

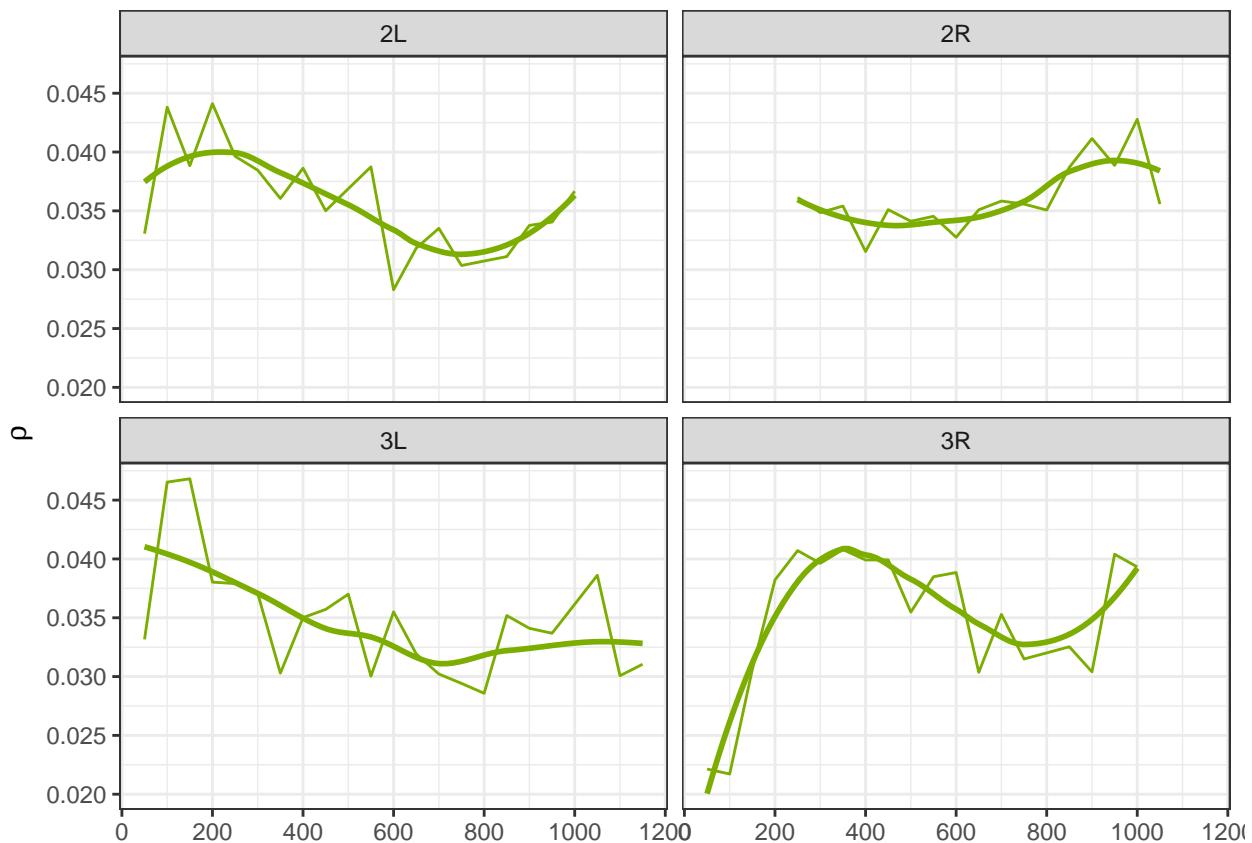
molten.diversity <- melt(dm.lands.1Mb[c(3,7,8)], id.vars = c("bin", "chr"))
diversity.map <- ggplot(data = molten.diversity, aes(x = bin * 50, y = value)) + facet_wrap(~chr)
diversity.map <- diversity.map + geom_line(data = molten.diversity, colour = "#F8766D")
diversity.map <- diversity.map + geom_smooth(method = "loess", se = F, colour = "#F8766D")
diversity.map <- diversity.map + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_breaks())
diversity.map <- diversity.map + labs(title = NULL, x = NULL, y = expression(pi))
diversity.map <- diversity.map + theme(axis.title.x = element_text(size = 20), axis.title.y = element_t
```



```

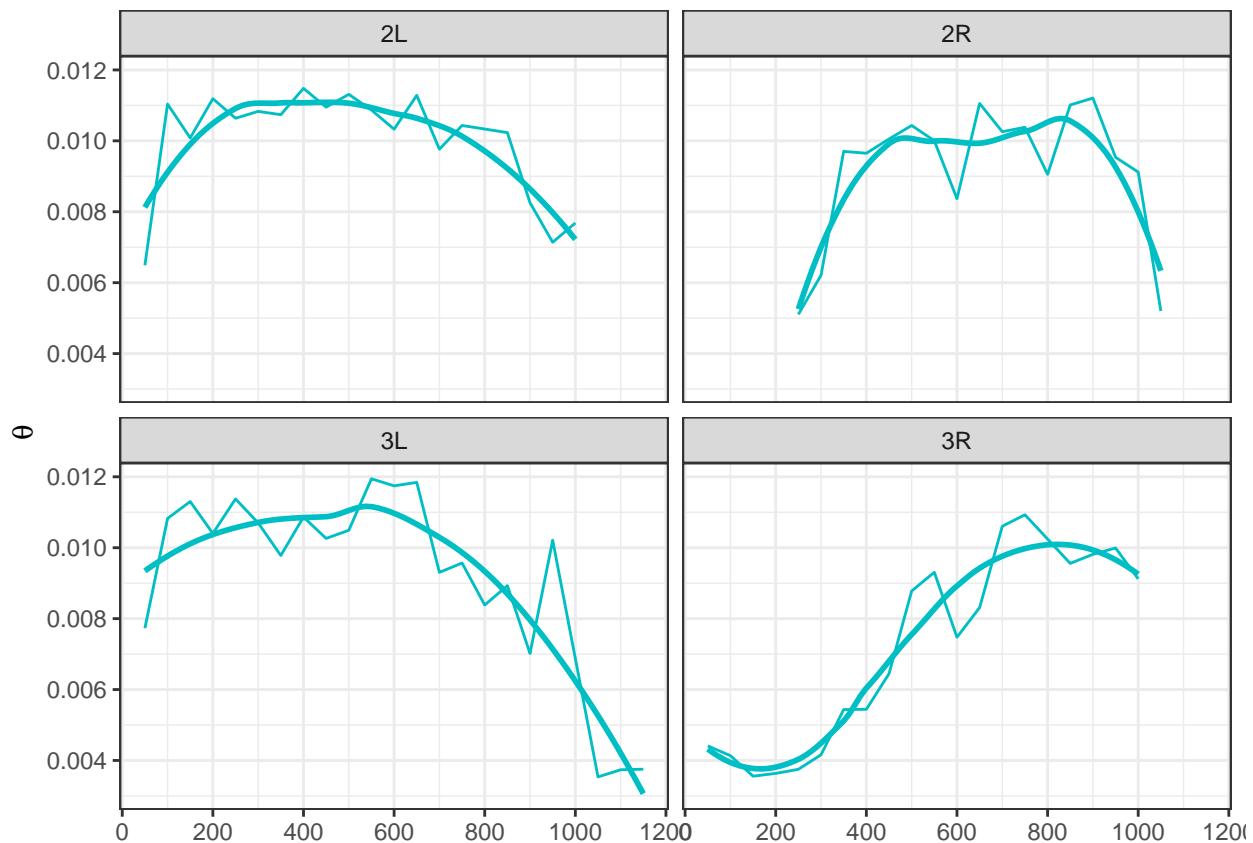
molten.rho <- melt(dm.lands.1Mb[c(5,7,8)], id.vars = c("bin", "chr"))
rho.map <- ggplot(data = molten.rho, aes(x = bin * 50, y = value)) + facet_wrap(~chr)
rho.map <- rho.map + geom_line(data = molten.rho, colour = "#7CAE00")
rho.map <- rho.map + geom_smooth(method = "loess", se = F, colour = "#7CAE00")
rho.map <- rho.map + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_l
rho.map <- rho.map + labs(title = NULL, x = NULL, y = expression(rho))
rho.map <- rho.map + theme(axis.title.x = element_text(size = 20), axis.title.y = element_text(size = 20))
rho.map

```



```

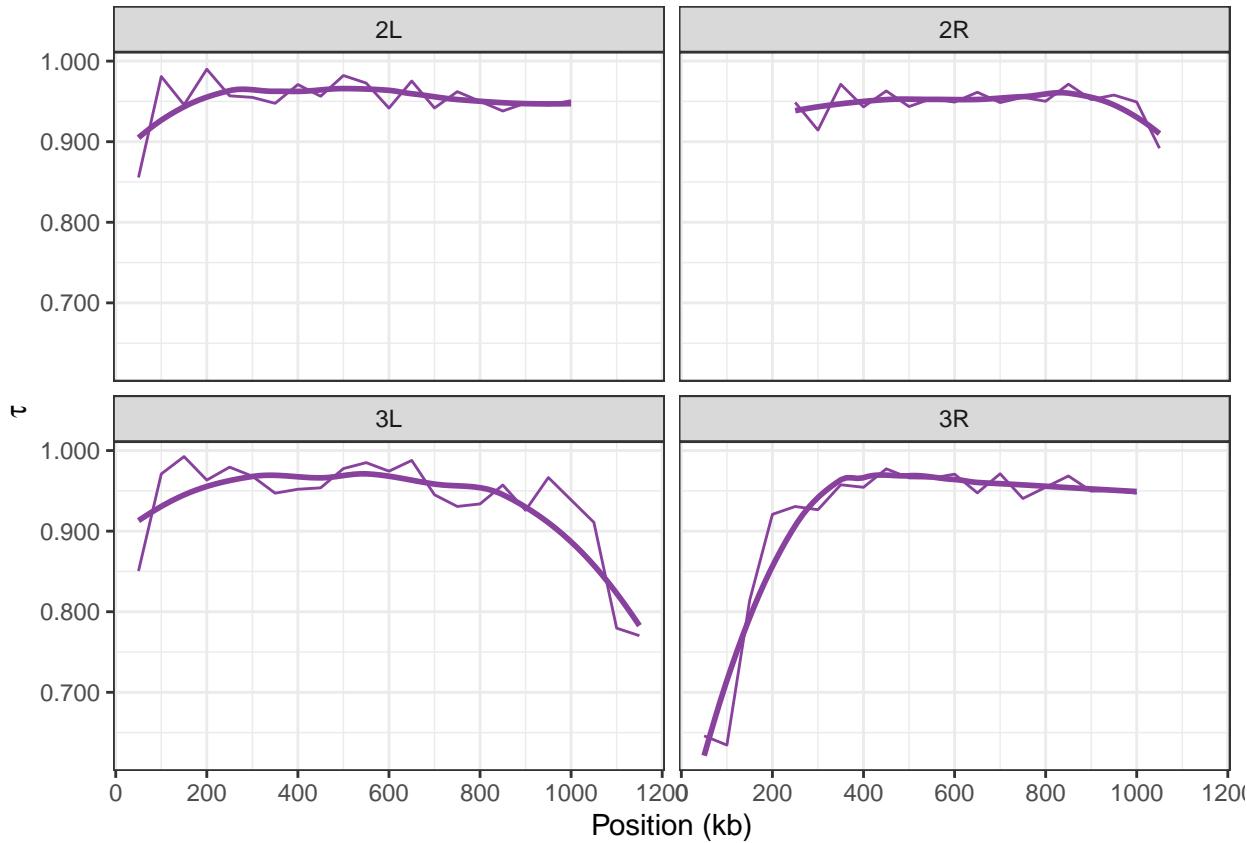
molten.theta <- melt(dm.lands.1Mb[c(4,7,8)], id.vars = c("bin", "chr"))
theta.map <- ggplot(data = molten.theta, aes(x = bin * 50, y = value)) + facet_wrap(~chr)
theta.map <- theta.map + geom_line(data = molten.theta, colour = "#00BFC4")
theta.map <- theta.map + geom_smooth(method = "loess", se = F, colour = "#00BFC4")
theta.map <- theta.map + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_breaks())
theta.map <- theta.map + labs(title = NULL, x = NULL, y = expression(theta))
theta.map <- theta.map + theme(axis.title.x = element_text(size = 20), axis.title.y = element_text(size = 20))
theta.map
  
```



```

molten.tmrca <- melt(dm.lands.1Mb[c(6,7,8)], id.vars = c("bin", "chr"))
tmrca.map <- ggplot(data = molten.tmrca, aes(x = bin * 50, y = value)) + facet_wrap(~chr)
tmrca.map <- tmrca.map + geom_line(data = molten.tmrca, colour = "#88419d")
tmrca.map <- tmrca.map + geom_smooth(method = "loess", se = F, colour = "#88419d")
tmrca.map <- tmrca.map + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_breaks())
tmrca.map <- tmrca.map + labs(title = NULL, x = "Position (kb)", y = expression(tau))
tmrca.map <- tmrca.map + theme(axis.title.x = element_text(size = 20), axis.title.y = element_text(size = 20))
tmrca.map

```



```
# genome-wide correlations
cor.test(~rho + diversity, data = dm.lands.1Mb, method = "spearman")
```

```
##
## Spearman's rank correlation rho
##
## data: rho and diversity
## S = 60404, p-value = 0.07236
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.2060045
cor.test(~rho + tmrca, data = dm.lands.1Mb, method = "spearman")
```

```
##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 42930, p-value = 8.798e-05
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.4356959
cor.test(~theta + tmrca, data = dm.lands.1Mb, method = "spearman")
```

```
##
## Spearman's rank correlation rho
```

```

## 
## data: theta and tmrca
## S = 22964, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.698144

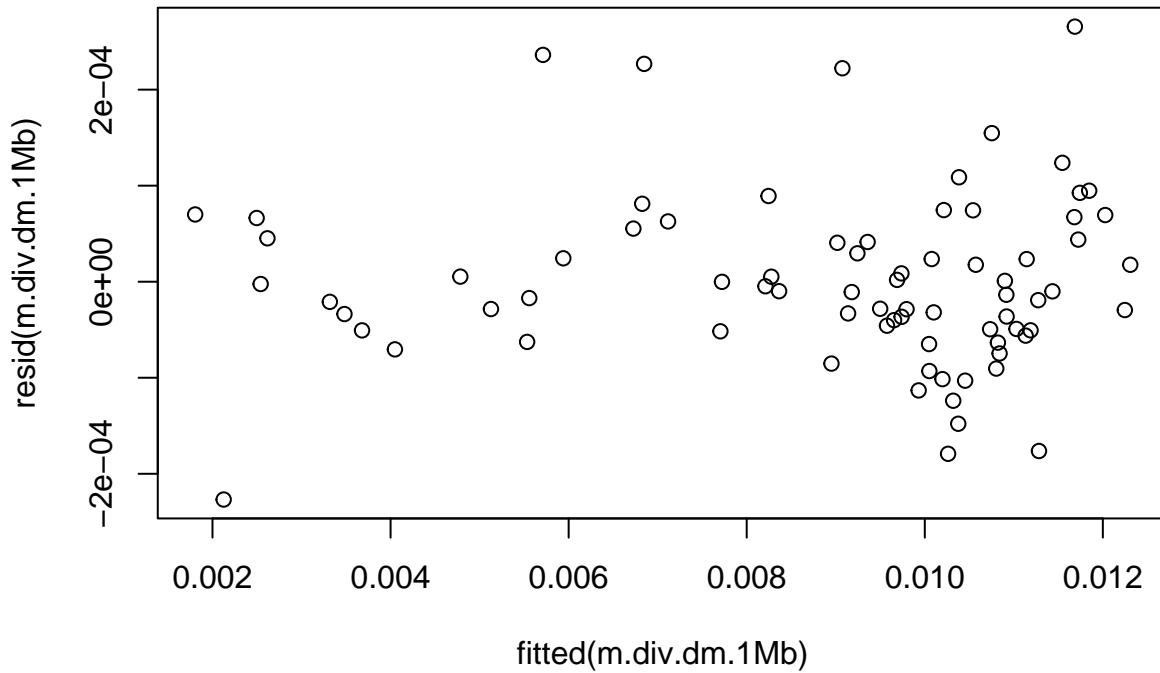
# Linear models
# centering
dm.lands.1Mb$thetaC <- dm.lands.1Mb$theta - mean(dm.lands.1Mb$theta)
dm.lands.1Mb$tmrcaC <- dm.lands.1Mb$tmrca - mean(dm.lands.1Mb$tmrca)
dm.lands.1Mb$rhoC <- dm.lands.1Mb$rho - mean(dm.lands.1Mb$rho)

dm.lands.1Mb$bin <- 1:nrow(dm.lands.1Mb)

m.div.dm.1Mb <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC), data = dm.lands.1Mb)

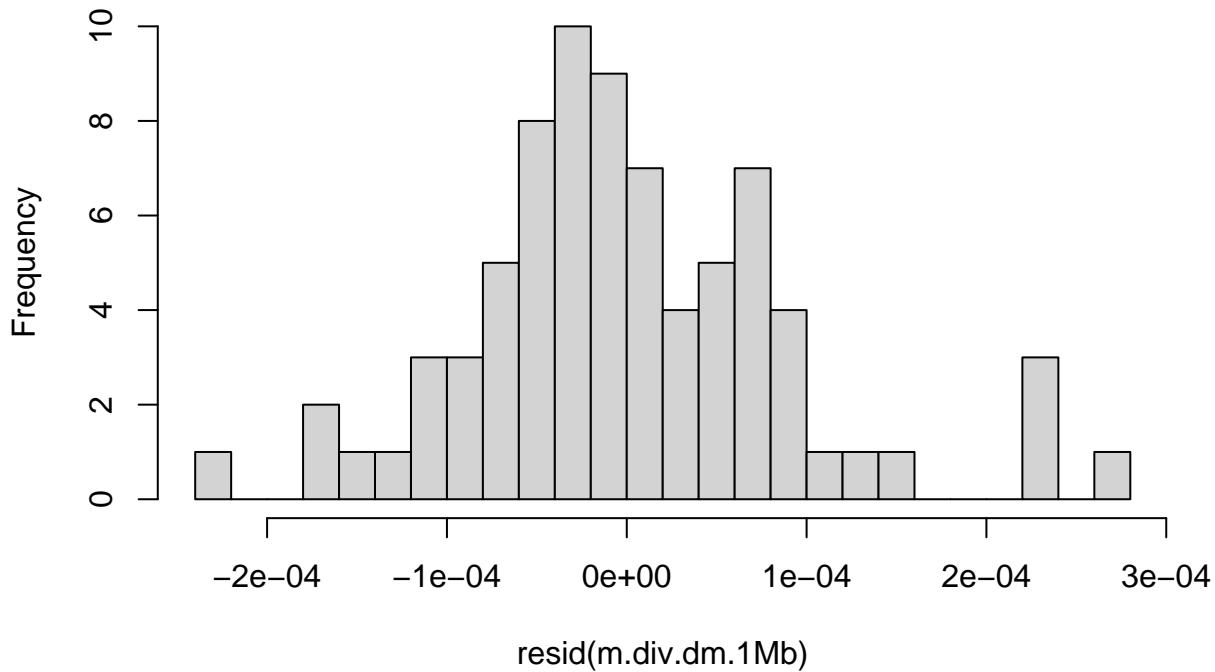
plot(resid(m.div.dm.1Mb)~fitted(m.div.dm.1Mb))

```



```
hist(resid(m.div.dm.1Mb), nclass = 30)
```

## Histogram of resid(m.div.dm.1Mb)



```
dwtest(m.div.dm.1Mb)

##
##  Durbin-Watson test
##
## data: m.div.dm.1Mb
## DW = 1.6563, p-value = 0.03648
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.dm.1Mb, nsim = 10000)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.dm.1Mb
## HMC = 0.72492, p-value = 0.9983
summary(m.div.dm.1Mb)

##
## Call:
## lm(formula = diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
##      data = dm.lands.1Mb)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -2.268e-04 -5.063e-05 -1.004e-05  4.519e-05  2.656e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 8.808e-03 1.551e-05 568.036 < 2e-16 ***
```

```

## thetaC      9.919e-01 6.725e-03 147.497 < 2e-16 ***
## rhoC       6.510e-03 3.034e-03  2.145  0.0353 *
## tmrcaC     9.525e-03 6.035e-04 15.784 < 2e-16 ***
## thetaC:tmrcaC 4.881e-01 1.131e-01   4.315 4.99e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.283e-05 on 72 degrees of freedom
## Multiple R-squared:  0.999, Adjusted R-squared:  0.9989
## F-statistic: 1.74e+04 on 4 and 72 DF,  p-value: < 2.2e-16

# type 2 ANOVA
anova.diversity <- Anova(m.div.dm.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
anova.diversity

## Anova Table (Type II tests)
##
## Response: diversity
##           Sum Sq Df  F value    Pr(>F)  VarExp
## thetaC      2.4658e-04  1 28614.4891 0.000000 0.97371
## rhoC       4.0000e-08  1     4.6028 0.035293 0.00016
## tmrcaC     5.8360e-06  1    677.2706 0.000000 0.02305
## thetaC:tmrcaC 1.6000e-07  1     18.6226 0.000050 0.00063
## Residuals   6.2000e-07 72                   0.00245

# GLS
g.div.dm.1Mb.1 <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                         data = dm.lands.1Mb, weights = varPower(0, ~tmrcaC|chr), cor = corAR1(0, ~bin|chr))

g.div.dm.1Mb.2 <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                         data = dm.lands.1Mb, weights = varPower(0, ~theta|chr), cor = corAR1(0, ~bin|chr))

g.div.dm.1Mb.3 <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                         data = dm.lands.1Mb, weights = varPower(0, ~theta|chr), method = "ML")

g.div.dm.1Mb.4 <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                         data = dm.lands.1Mb, weights = varPower(0, ~tmrcaC|chr), method = "ML")

AIC(g.div.dm.1Mb.1, g.div.dm.1Mb.2, g.div.dm.1Mb.3, g.div.dm.1Mb.4)

##          df      AIC
## g.div.dm.1Mb.1 11 -1228.719
## g.div.dm.1Mb.2 11 -1202.198
## g.div.dm.1Mb.3 10 -1202.415
## g.div.dm.1Mb.4 10 -1222.559

summary(g.div.dm.1Mb.1)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC)
## Data: dm.lands.1Mb
##          AIC      BIC  logLik
## -1228.719 -1202.937 625.3593
##
```

```

## Correlation Structure: AR(1)
## Formula: ~bin | chr
## Parameter estimate(s):
##     Phi
## 0.4040378
## Variance function:
## Structure: Power of variance covariate, different strata
## Formula: ~tmrcaC | chr
## Parameter estimates:
##      2L      2R      3L      3R
## 0.3814217 0.3225539 0.4579989 0.5841943
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0087611 0.00000890 984.6352 0.0000
## thetaC       0.9830140 0.00395599 248.4877 0.0000
## rhoC        0.0012460 0.00207145   0.6015 0.5494
## tmrcaC      0.0103831 0.00051388  20.2055 0.0000
## thetaC:tmrcaC 0.6061715 0.12215915    4.9621 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC      0.225
## rhoC        0.466  0.603
## tmrcaC     -0.364 -0.486 -0.568
## thetaC:tmrcaC -0.286 -0.210 -0.299  0.636
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -1.6371469 -0.3675723  0.2903415  0.9878832  2.4854661
##
## Residual standard error: 0.0004263997
## Degrees of freedom: 77 total; 72 residual
vif(g.div.dm.1Mb.1)

##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
## 1.674634 1.863553 2.423500 1.719226

# Linear model without TMRCA --> rho becomes significant
g.div.dm.1Mb.5 <- gls(diversity ~ (thetaC + rhoC),
                         data = dm.lands.1Mb, weights = varPower(0, ~thetaC|chr), cor = corAR1(0, ~bin|chr))

summary(g.div.dm.1Mb.5)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ (thetaC + rhoC)
## Data: dm.lands.1Mb
##      AIC      BIC      logLik
## -1055.094 -1034.536.5469
##
## Correlation Structure: AR(1)
## Formula: ~bin | chr
## Parameter estimate(s):
##     Phi

```

```

## 0.5243617
## Variance function:
## Structure: Power of variance covariate, different strata
## Formula: ~thetaC | chr
## Parameter estimates:
##      2L      2R      3L      3R
## 0.2518860 0.2065555 0.2564038 0.1788172
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0089103 0.000042565 209.33432     0
## thetaC       1.1056720 0.018207498  60.72619     0
## rhoC        0.0395498 0.006816697   5.80191     0
##
## Correlation:
##          (Intr) thetaC
## thetaC -0.115
## rhoC   0.055 -0.292
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -3.46396737 -0.69180396 -0.06437384  0.58736967  1.68761843
##
## Residual standard error: 0.001151706
## Degrees of freedom: 77 total; 74 residual

```

### 3.4 Evolutionary (Protein) Rates

This is how we generated the table from raw data:

```

# loads data
dm.raw <- read.table("dm_data/dm_misc/dpgp2_Dsimulans_bpp.all.csv", header = TRUE, sep = "\t") %>%
  select(GeneID, MeanNumberSynPos, PiN, PiS, MeanNumberSynPosDiv, dS, dN) %>% na.omit()

# summarises
dm.tbl <- ddply(dm.raw, .variables = "GeneID", .fun = plyr::summarize,
  MeanNumberNonSynPos = sum(3 - MeanNumberSynPos),
  MeanNumberSynPos = sum(MeanNumberSynPos),
  PiN = sum(PiN),
  PiS = sum(PiS),
  MeanNumberNonSynPosDiv = sum(3 - MeanNumberSynPosDiv),
  MeanNumberSynPosDiv = sum(MeanNumberSynPosDiv),
  dN = sum(dN),
  dS = sum(dS))

dm.tbl$PiN <- (dm.tbl$PiN / dm.tbl$MeanNumberNonSynPos)
dm.tbl$PiS <- (dm.tbl$PiS / dm.tbl$MeanNumberSynPos)
dm.tbl$dN <- (dm.tbl$dN / dm.tbl$MeanNumberNonSynPosDiv)
dm.tbl$dS <- (dm.tbl$dS / dm.tbl$MeanNumberSynPosDiv)

# computes ratios
dm.tbl$PiN_PiS <- with(dm.tbl, PiN / PiS)
dm.tbl$dN_dS <- with(dm.tbl, dN / dS)

# we ignore genes with ratios above 1

```

```

dm.tbl <- dm.tbl[dm.tbl$PiN_PiS < 1,]
dm.tbl <- dm.tbl[dm.tbl$dN_dS < 1,]
dm.tbl <- na.omit(dm.tbl)

dm.genes.coord <- read.table("dm_data/dm_misc/Dmel_trans_nooverlaps-final.txt", header = F) %>% select(
  names(dm.genes.coord) <- c("chr", "start", "end", "GeneID")

dm.evol <- merge(dm.genes.coord, dm.tbl, by = "GeneID")
dm.evol <- arrange(dm.evol, chr, start)

# reorder maps to use GR
dm.maps.50kb <- dm.lands.50kb[,c(8,1:6)]

# mapping genes to 50kb windows in ismc maps
dm.lands.gr <- makeGRangesFromDataFrame(dm.maps.50kb)
values(dm.lands.gr) <- select(dm.maps.50kb, diversity, theta, rho, tmrca)
evolrate.gr <- makeGRangesFromDataFrame(dm.evol)
values(evolrate.gr) <- select(dm.evol, PiN, PiS, dN, dS)

hits_1 <- findOverlaps(query = evolrate.gr, subject = dm.lands.gr, type = "within")

evolrate.gr.df <- as.data.frame(evolrate.gr[queryHits(hits_1)], row.names = NULL)
dm.lands.gr.df <- as.data.frame(dm.lands.gr[subjectHits(hits_1)], row.names = NULL)

dm.lands.evolrate <- cbind.data.frame(dm.lands.gr.df[,c(1:3,6:9)], evolrate.gr.df[,c(2:4,6:9)])

names(dm.lands.evolrate)[1] <- "chr"
names(dm.lands.evolrate)[2] <- "start.window"
names(dm.lands.evolrate)[3] <- "end.window"
names(dm.lands.evolrate)[8] <- "start.gene"
names(dm.lands.evolrate)[9] <- "end.gene"
names(dm.lands.evolrate)[10] <- "length.gene"

dm.lands.evolrate <- arrange(dm.lands.evolrate, chr, start.window, start.gene)

dm.lands.evolrate.bins <- ddply(dm.lands.evolrate, .variables = c("chr", "start.window"), .fun = plyr:::
  diversity = mean(diversity),
  theta = mean(theta),
  rho = mean(rho),
  tmrca = mean(tmrca),
  exonic.sites = sum(length.gene),
  PiN.window = sum(PiN*length.gene) / sum(length.gene),
  PiS.window = sum(PiS*length.gene) / sum(length.gene),
  dN.window = sum(dN*length.gene) / sum(length.gene),
  dS.window = sum(dS*length.gene) / sum(length.gene))

dm.lands.evolrate.bins$bin <- 1:nrow(dm.lands.evolrate.bins)

write.table(dm.lands.evolrate.bins, "dm_data/dm_chr_maps/dm_maps_50kb_protein_rates.tsv",
            sep = "\t", quote = F, col.names = T, row.names = F)

```

We can read the table generated and move on with the analyses:

```

dm.lands.evolrate.bins <- read.table("dm_data/dm_chr_maps/dm_maps_50kb_protein_rates.tsv", header = T, )

# linear model in windows with more than 20kb exonic sites
dm.lands.genes <- filter(dm.lands.evolrate.bins, exonic.sites > 2e+4)

# centering
dm.lands.genes$thetaC <- dm.lands.genes$theta - mean(dm.lands.genes$theta)
dm.lands.genes$tmrcaC <- dm.lands.genes$tmrca - mean(dm.lands.genes$tmrca)
dm.lands.genes$rhoC <- dm.lands.genes$rho - mean(dm.lands.genes$rho)

m.dm.cds.1 <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC*tmrcaC), data = dm.lands.genes)
m.dm.cds.2 <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC*tmrcaC + rhoC*tmrcaC), data = dm.lands.genes)

AIC(m.dm.cds.1, m.dm.cds.2)

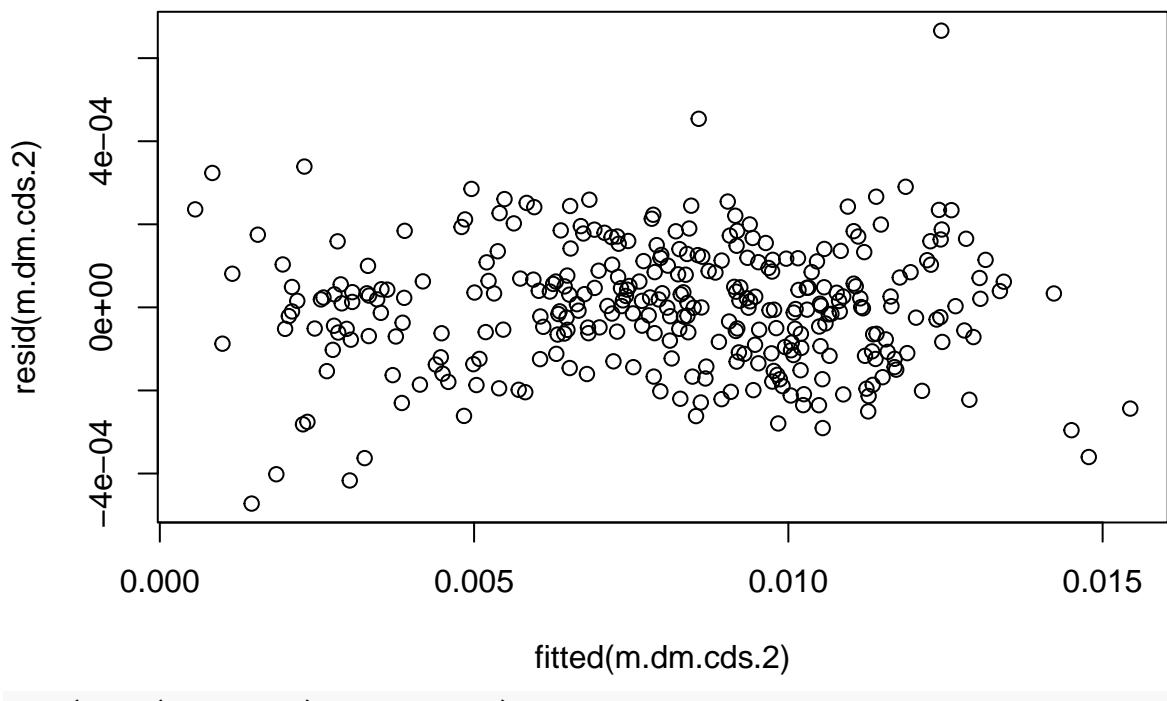
##          df      AIC
## m.dm.cds.1 6 -4778.177
## m.dm.cds.2 7 -4782.425

summary(m.dm.cds.2)

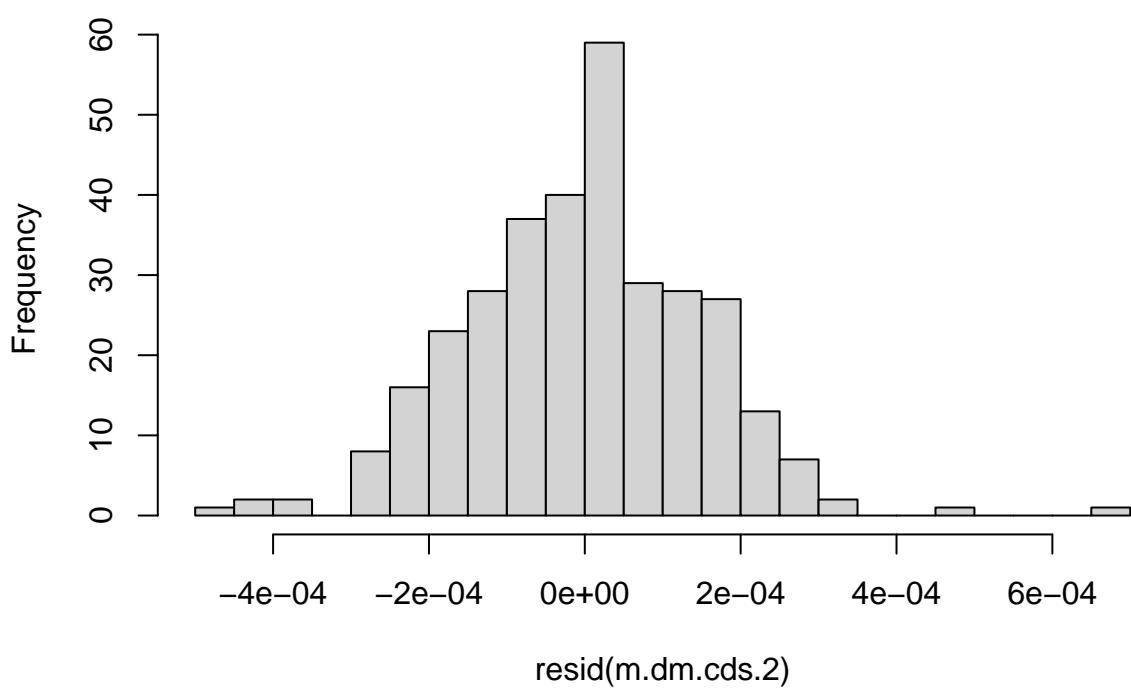
##
## Call:
## lm(formula = diversity ~ (thetaC + rhoC + tmrcaC + thetaC * tmrcaC +
##     rhoC * tmrcaC), data = dm.lands.genes)
##
## Residuals:
##       Min        1Q        Median        3Q        Max
## -4.723e-04 -9.596e-05  3.810e-06  8.994e-05  6.661e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 7.890e-03 9.716e-06 812.013   <2e-16 ***
## thetaC      9.511e-01 3.665e-03 259.551   <2e-16 ***
## rhoC       1.053e-03 1.530e-03  0.688   0.4919
## tmrcaC     1.120e-02 1.964e-04  57.010   <2e-16 ***
## thetaC:tmrcaC 1.079e+00 4.299e-02  25.098   <2e-16 ***
## rhoC:tmrcaC  2.110e-02 8.481e-03  2.488   0.0133 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.000149 on 318 degrees of freedom
## Multiple R-squared:  0.9977, Adjusted R-squared:  0.9977
## F-statistic: 2.785e+04 on 5 and 318 DF, p-value: < 2.2e-16

# picking best OLS for ANOVA
plot(resid(m.dm.cds.2)~fitted(m.dm.cds.2))

```



**Histogram of `resid(m.dm.cds.2)`**



```
##  
## Durbin-Watson test  
##  
## data: m.dm.cds.2  
## DW = 2.0035, p-value = 0.4719
```

```

## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.dm.cds.2, nsim = 10000)

##
##  Harrison-McCabe test
##
## data: m.dm.cds.2
## HMC = 0.41117, p-value = 0.012
summary(m.dm.cds.2)

##
## Call:
## lm(formula = diversity ~ (thetaC + rhoC + tmrcaC + thetaC * tmrcaC +
##     rhoC * tmrcaC), data = dm.lands.genes)
##
## Residuals:
##       Min        1Q      Median        3Q       Max
## -4.723e-04 -9.596e-05  3.810e-06  8.994e-05  6.661e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 7.890e-03 9.716e-06 812.013 <2e-16 ***
## thetaC      9.511e-01 3.665e-03 259.551 <2e-16 ***
## rhoC        1.053e-03 1.530e-03  0.688  0.4919
## tmrcaC      1.120e-02 1.964e-04  57.010 <2e-16 ***
## thetaC:tmrcaC 1.079e+00 4.299e-02  25.098 <2e-16 ***
## rhoC:tmrcaC  2.110e-02 8.481e-03  2.488  0.0133 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.000149 on 318 degrees of freedom
## Multiple R-squared:  0.9977, Adjusted R-squared:  0.9977
## F-statistic: 2.785e+04 on 5 and 318 DF,  p-value: < 2.2e-16

# type 2 anova
anova.diversity.cds <- Anova(m.dm.cds.2)
apiss <- anova.diversity.cds$"Sum Sq"
anova.diversity.cds$VarExp <- apiss / sum(apiss)

anova.diversity.cds

## Anova Table (Type II tests)
##
## Response: diversity
##             Sum Sq Df   F value    Pr(>F)  VarExp
## thetaC      1.544e-03  1 69536.4716 0.000000 0.93236
## rhoC        5.000e-08  1     2.1199 0.146386 0.00003
## tmrcaC      9.078e-05  1   4088.1586 0.000000 0.05482
## thetaC:tmrcaC 1.399e-05  1    629.9096 0.000000 0.00845
## rhoC:tmrcaC  1.400e-07  1     6.1917 0.013347 0.00008
## Residuals    7.060e-06 318                 0.00426

# simple correlations
cor.test(dm.lands.evolrate.bins$theta, dm.lands.evolrate.bins$exonic.sites, method = "spearman")

```

```

## Spearman's rank correlation rho
##
## data: dm.lands.evolrate.bins$theta and dm.lands.evolrate.bins$exonic.sites
## S = 339155743, p-value = 6.388e-06
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.1289611
cor.test(dm.lands.evolrate.bins$tmrca, dm.lands.evolrate.bins$exonic.sites, method = "spearman")

## Spearman's rank correlation rho
##
## data: dm.lands.evolrate.bins$tmrca and dm.lands.evolrate.bins$exonic.sites
## S = 360421366, p-value = 2.034e-12
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.1997488
pcor.test(dm.lands.evolrate.bins$tmrca, dm.lands.evolrate.bins$exonic.sites, dm.lands.evolrate.bins$theta)

##      estimate      p.value statistic    n gp   Method
## 1 -0.1582194 2.912866e-08 -5.583083 1217  1 spearman
pcor.test(dm.lands.evolrate.bins$theta, dm.lands.evolrate.bins$exonic.sites, dm.lands.evolrate.bins$tmrca)

##      estimate      p.value statistic    n gp   Method
## 1 -0.0374759 0.1915716 -1.306672 1217  1 spearman
cor.test(dm.lands.evolrate.bins$PiN, dm.lands.evolrate.bins$theta, method = "spearman")

## Spearman's rank correlation rho
##
## data: dm.lands.evolrate.bins$PiN and dm.lands.evolrate.bins$theta
## S = 192322126, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.3598097
cor.test(dm.lands.evolrate.bins$PiS, dm.lands.evolrate.bins$theta, method = "spearman")

## Spearman's rank correlation rho
##
## data: dm.lands.evolrate.bins$PiS and dm.lands.evolrate.bins$theta
## S = 78488708, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.7387315
pcor.test(dm.lands.evolrate.bins$PiN, dm.lands.evolrate.bins$theta, dm.lands.evolrate.bins$tmrca, method = "spearman")

```

```

##      estimate      p.value statistic     n gp    Method
## 1 0.2711637 6.149318e-22  9.815788 1217  1 spearman
pcor.test(dm.lands.evolrate.bins$PiS, dm.lands.evolrate.bins$theta, dm.lands.evolrate.bins$tmrca, method='spearman')

##      estimate      p.value statistic     n gp    Method
## 1 0.6767774 1.129784e-163 32.03071 1217  1 spearman

# bootstrapping PiN and PiS correlations
boot.tbl <- dm.lands.evolrate.bins %>% dplyr::select(PiN.window, theta, PiS.window, tmrca)
boot.PiN.theta <- boot(boot.tbl,
  statistic = function(boot.tbl, i) {
    pcor.test(boot.tbl[i, "PiN.window"], boot.tbl[i, "theta"], boot.tbl[i, "tmrca"], method='spearman')
  },
  R = 10000
)
boot.ci(boot.PiN.theta, type = "basic")

## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 10000 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = boot.PiN.theta, type = "basic")
##
## Intervals :
## Level      Basic
## 95%   ( 0.2197,  0.3236 )
## Calculations and Intervals on Original Scale
boot.PiS.theta <- boot(boot.tbl,
  statistic = function(boot.tbl, i) {
    pcor.test(boot.tbl[i, "PiS.window"], boot.tbl[i, "theta"], boot.tbl[i, "tmrca"], method='spearman')
  },
  R = 10000
)
boot.ci(boot.PiS.theta, type = "basic")

## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 10000 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = boot.PiS.theta, type = "basic")
##
## Intervals :
## Level      Basic
## 95%   ( 0.6409,  0.7149 )
## Calculations and Intervals on Original Scale

```

## 4 $R^2$ plot with real, simulated (true) and simulated (inferred) data.

```

# true landscapes
r2.sim.avg <- rbind.data.frame(r2.sim.50kb$average, r2.sim.200kb$average, r2.sim.1Mb$average, make.row.names=TRUE)
colnames(r2.sim.avg) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
r2.sim.avg$bin.size <- c(50, 200, 1000)

```

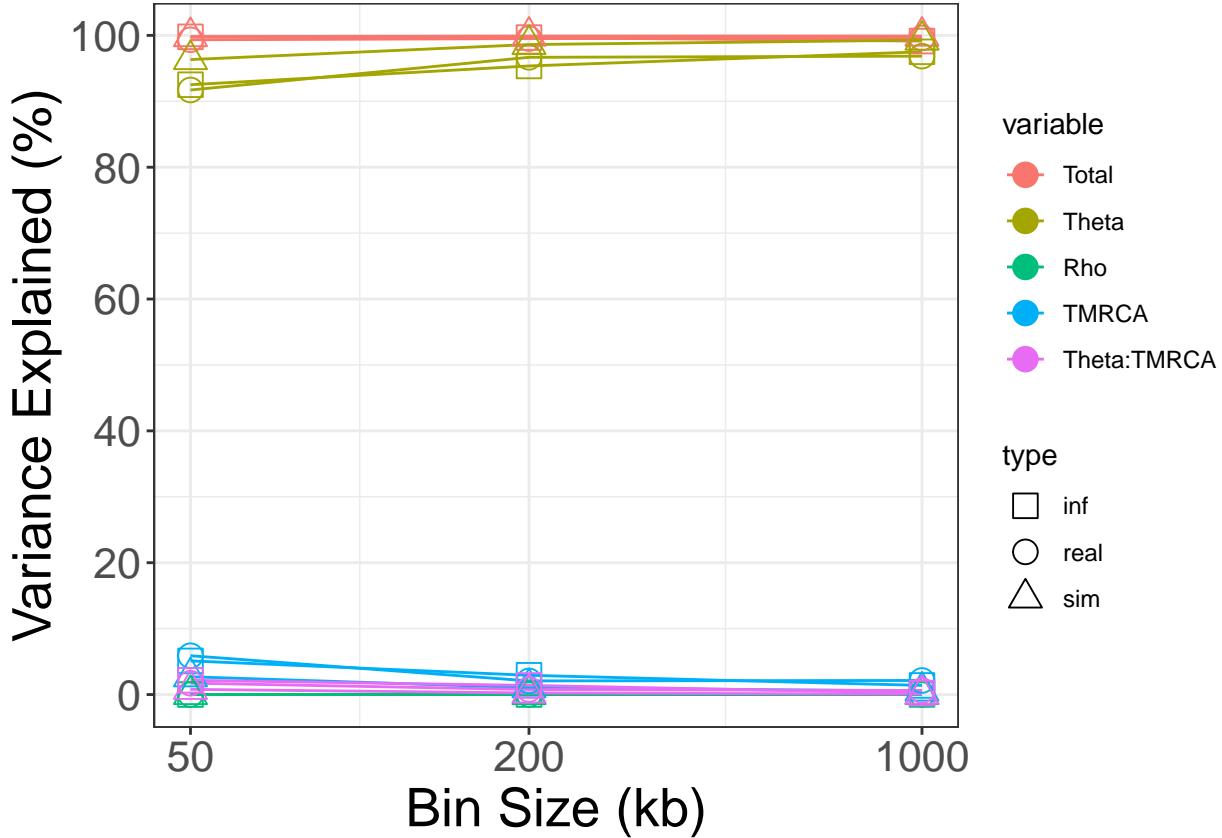
```

# inferred landscapes
r2.inf.avg <- rbind.data.frame(r2.inf.50kb$average, r2.inf.200kb$average, r2.inf.1Mb$average, make.row.names = TRUE)
colnames(r2.inf.avg) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
r2.inf.avg$bin.size <- c(50, 200, 1000)

r2.tab.comb <- rbind.data.frame(r2.dm.tab, r2.sim.avg, r2.inf.avg)
r2.tab.comb$type <- c(rep("real", 3), rep("sim", 3), rep("inf", 3))

molten.r2 <- melt(r2.tab.comb, id.vars = c("bin.size", "type"))
r2.plot <- ggplot(data = molten.r2, aes(x = bin.size, y = value, colour = variable, fill = type))
r2.plot <- r2.plot + geom_line(data = molten.r2)
r2.plot <- r2.plot + geom_point(aes(shape = type, colour = variable), size = 4)
r2.plot <- r2.plot + scale_x_continuous(breaks = c(50, 200, 1000), trans="log10")
r2.plot <- r2.plot + scale_y_continuous(breaks = pretty_breaks())
r2.plot <- r2.plot + scale_shape_manual(values = c(0, 1, 2))
r2.plot <- r2.plot + labs(title = NULL, x = "Bin Size (kb)", y = "Variance Explained (%)") + theme_bw()
r2.plot <- r2.plot + theme(axis.title = element_text(size = 20), axis.text = element_text(size = 16))
r2.plot

```



```
ggsave("Figure4.pdf", r2.plot, device = "pdf")
```

## 5 Simulations with BGS and flat Mutation Landscape in SLiM (iSMC-inferred landscapes)

### 5.1 50 kb scale

```
r2.bgs.50kb <- as.data.frame(matrix(ncol = nreps, nrow = 5))
row.names(r2.bgs.50kb) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
colnames(r2.bgs.50kb) <- reps

sim.theta.50kb <- read.table("dm_bgs_sims/MutationMap_50kb.csv", header = T)
sim.rho.50kb <- read.table("dm_bgs_sims/RecombinationMap_50kb.csv", header = T)
```

#### 5.1.1 Replicate 1

```
rep_1.pi.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.diver")
rep_1.pi.50kb$avg <- apply(rep_1.pi.50kb[4:ncol(rep_1.pi.50kb)], 1, mean)
rep_1.rho.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.rho")
rep_1.theta.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.theta")
rep_1.tmrca.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.TMRCA")
rep_1.tmrca.50kb$avg <- apply(rep_1.tmrca.50kb[4:ncol(rep_1.tmrca.50kb)], 1, mean)

inf.lands.50kb.rep1 <- as.data.frame(cbind(rep_1.pi.50kb$avg, rep_1.theta.50kb$sample_mean, rep_1.tmrca.50kb$avg))
names(inf.lands.50kb.rep1) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.50kb.rep1$thetaC <- inf.lands.50kb.rep1$theta - mean(inf.lands.50kb.rep1$theta)
inf.lands.50kb.rep1$tmrcaC <- inf.lands.50kb.rep1$tmrca - mean(inf.lands.50kb.rep1$tmrca)
inf.lands.50kb.rep1$rhoC <- inf.lands.50kb.rep1$rho - mean(inf.lands.50kb.rep1$rho)

inf.lands.50kb.rep1$bin <- 1:nrow(inf.lands.50kb.rep1)

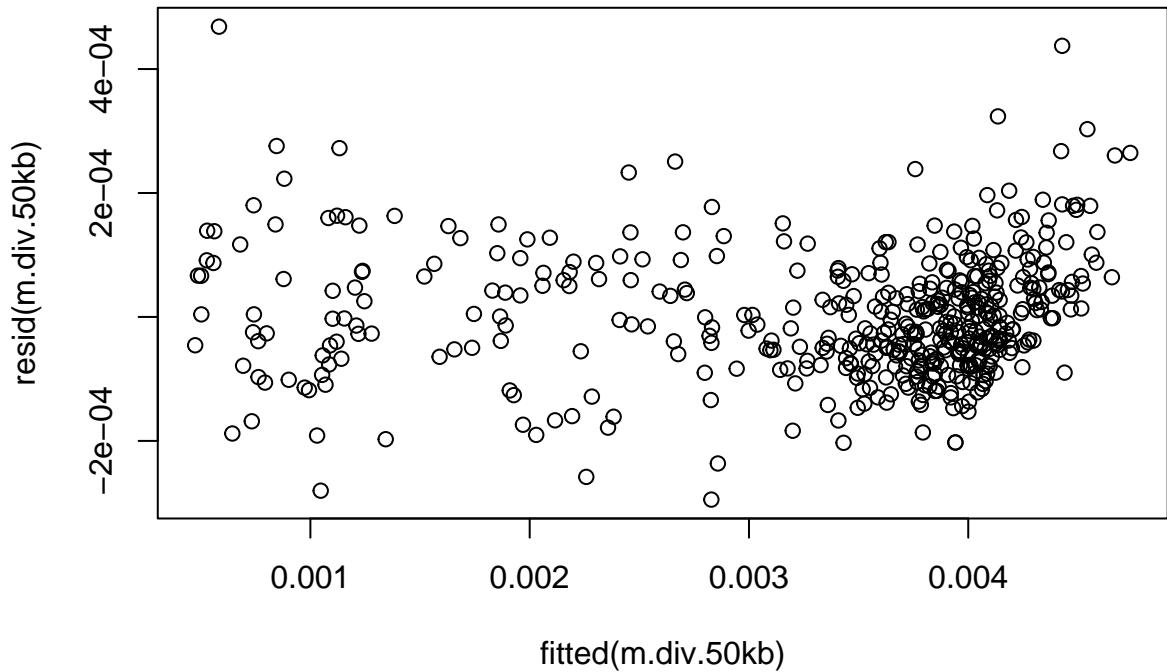
# for merging:
inf.lands.50kb.rep1 <- inf.lands.50kb.rep1
inf.lands.50kb.rep1$Replicate <- 1

m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.50kb.rep1)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.50kb.rep1)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.50kb.rep1)

AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

##          df      AIC
## m.div.50kb     6 -7318.145
## m.div.50kb.2   7 -7451.068
## m.div.50kb.3   8 -7486.698

plot(resid(m.div.50kb)~fitted(m.div.50kb))
```

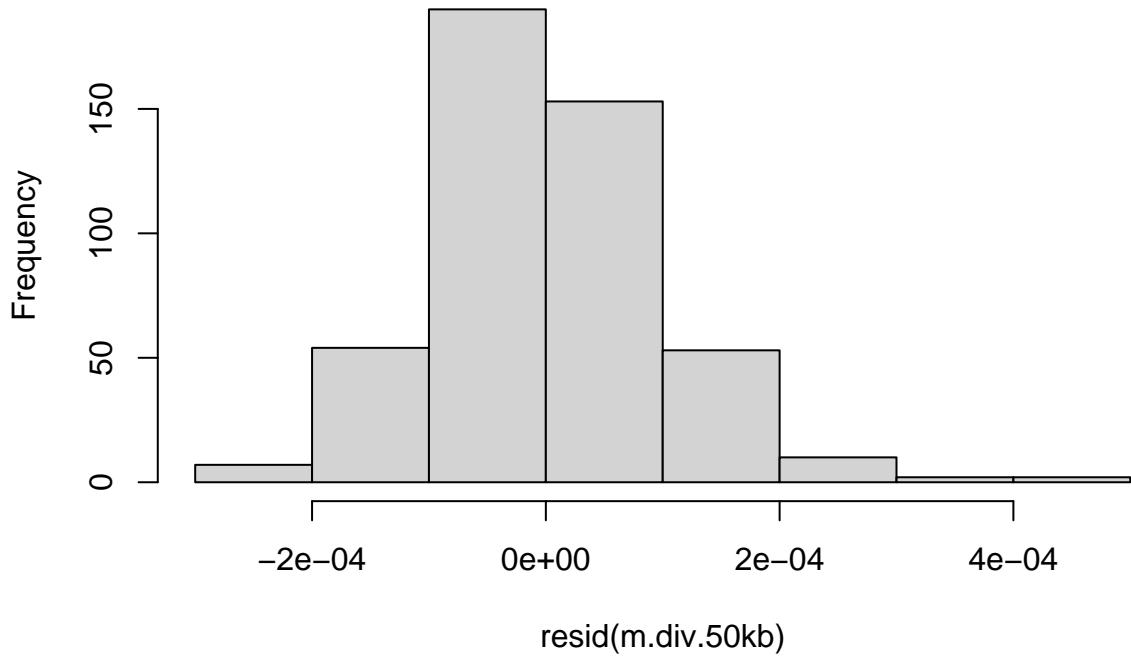


```
dwtest(m.div.50kb)
```

```
##  
## Durbin-Watson test  
##  
## data: m.div.50kb  
## DW = 1.4321, p-value = 1.478e-10  
## alternative hypothesis: true autocorrelation is greater than 0  
hmctest(m.div.50kb)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.div.50kb  
## HMC = 0.52172, p-value = 0.751  
hist(resid(m.div.50kb))
```

## Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.50kb.rep1)
##
## Residuals:
##       Min         1Q     Median        3Q       Max
## -2.947e-04 -6.541e-05 -1.228e-05  5.931e-05  4.683e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.277e-03 4.998e-06 655.616 < 2e-16 ***
## thetaC      1.006e+00 6.702e-03 150.043 < 2e-16 ***
## rhoC       -9.708e-03 2.472e-03 -3.927 9.89e-05 ***
## tmrcaC      4.427e-03 4.633e-05  95.553 < 2e-16 ***
## thetaC:tmrcaC 1.440e+00 4.349e-02  33.119 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0001015 on 466 degrees of freedom
## Multiple R-squared:  0.9913, Adjusted R-squared:  0.9912
## F-statistic: 1.33e+04 on 4 and 466 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.50kb[1, 1] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.50kb[2, 1] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb[3, 1] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb[4, 1] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb[5, 1] <- anova.diversity$VarExp[4] * 100

g.div.50kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep1, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep1, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep1, weights = varPower(0, ~theta), method = "ML")
g.div.50kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep1, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.50kb.1, g.div.50kb.2, g.div.50kb.3, g.div.50kb.4)

##             df      AIC
## g.div.50kb.1 8 -7399.286
## g.div.50kb.2 8 -7355.715
## g.div.50kb.3 7 -7316.900
## g.div.50kb.4 7 -7364.037

summary(g.div.50kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep1
##        AIC      BIC  logLik
##     -7316.9 -7287.816 3665.45
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##       power
##     -0.1014917
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032769 0.00000503 651.9396 0e+00
## thetaC       1.0054351 0.00719805 139.6817 0e+00
## rhoC        -0.0095979 0.00250781 -3.8272 1e-04
## tmrcaC       0.0044287 0.00004609  96.0789 0e+00
## thetaC:tmrcaC 1.4438099 0.04510765  32.0081 0e+00
##
## Correlation:
##            (Intr) thetaC rhoC    tmrcaC
## thetaC     -0.151
## rhoC       0.148 -0.373
## tmrcaC    -0.213 -0.043 -0.406
## thetaC:tmrcaC -0.365  0.276 -0.390  0.587

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -2.8674339 -0.6482883 -0.1174017  0.5737792  4.7306842
## 
## Residual standard error: 5.692921e-05
## Degrees of freedom: 471 total; 466 residual
vif(g.div.50kb.3)

##          thetaC        rhoC        tmrcaC thetaC:tmrcaC
##      1.367234     1.469587     1.859346     1.775887

```

### 5.1.2 Replicate 2

```

rep_2.pi.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.diver")
rep_2.pi.50kb$avg <- apply(rep_2.pi.50kb[4:ncol(rep_2.pi.50kb)], 1, mean)
rep_2.rho.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.rho")
rep_2.theta.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.theta")
rep_2.tmrca.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.TMRCA")
rep_2.tmrca.50kb$avg <- apply(rep_2.tmrca.50kb[4:ncol(rep_2.tmrca.50kb)], 1, mean)

inf.lands.50kb.rep2 <- as.data.frame(cbind(rep_2.pi.50kb$avg, rep_2.theta.50kb$sample_mean, rep_2.tmrca.50kb$avg))
names(inf.lands.50kb.rep2) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.50kb.rep2$thetaC <- inf.lands.50kb.rep2$theta - mean(inf.lands.50kb.rep2$theta)
inf.lands.50kb.rep2$tmrcaC <- inf.lands.50kb.rep2$tmrca - mean(inf.lands.50kb.rep2$tmrca)
inf.lands.50kb.rep2$rhoC <- inf.lands.50kb.rep2$rho - mean(inf.lands.50kb.rep2$rho)

inf.lands.50kb.rep2$bin <- 1:nrow(inf.lands.50kb.rep2)

# for merging:
inf.lands.50kb.rep2 <- inf.lands.50kb.rep2
inf.lands.50kb.rep2$Replicate <- 1

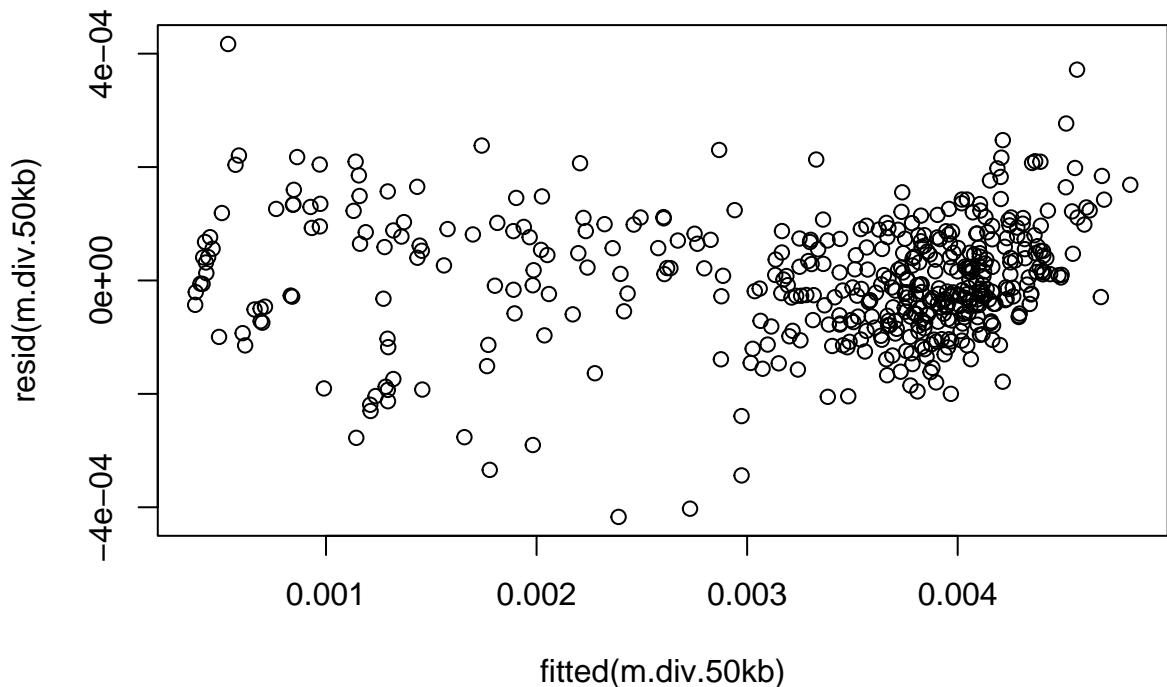
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.50kb.rep2)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.50kb.rep2)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.50kb.rep2)

AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

##          df      AIC
## m.div.50kb    6 -7276.144
## m.div.50kb.2  7 -7410.948
## m.div.50kb.3  8 -7431.395

plot(resid(m.div.50kb)~fitted(m.div.50kb))

```

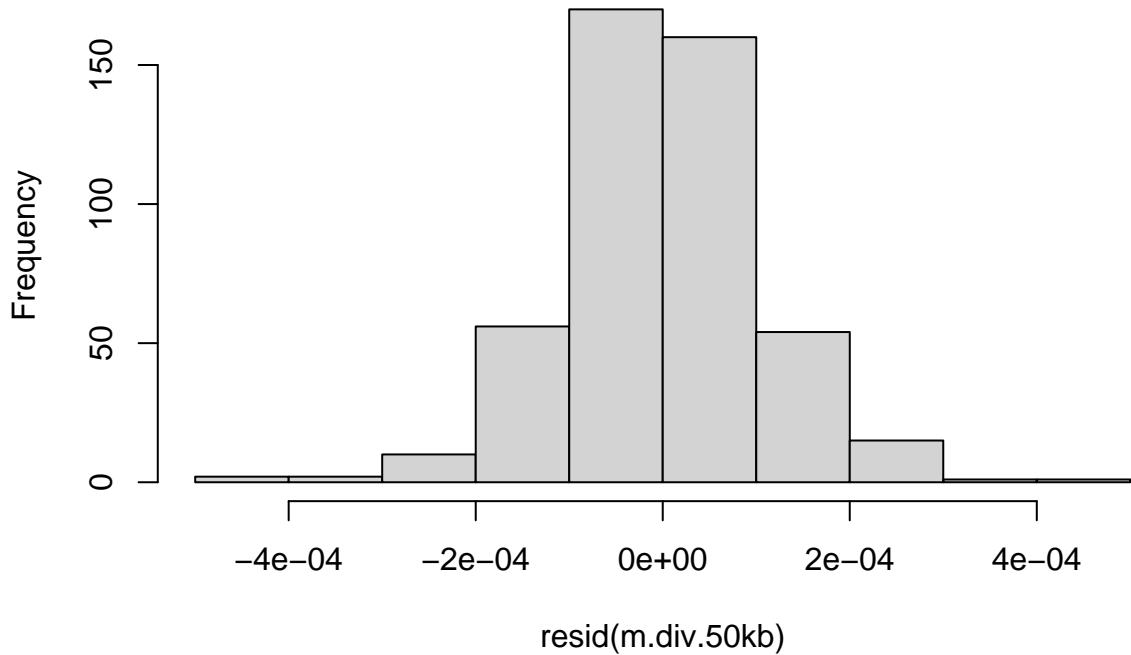


```
dwtest(m.div.50kb)
```

```
##
##  Durbin-Watson test
##
## data: m.div.50kb
## DW = 1.2946, p-value = 3.222e-15
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.50kb
## HMC = 0.54072, p-value = 0.903
hist(resid(m.div.50kb))
```

## Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##     data = inf.lands.50kb.rep2)
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -4.170e-04 -6.312e-05 -6.800e-06  7.111e-05  4.170e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.259e-03 5.004e-06 651.204 <2e-16 ***
## thetaC      1.011e+00 5.917e-03 170.941 <2e-16 ***
## rhoC       -4.534e-03 2.399e-03 -1.891  0.0593 .  
## tmrcaC      4.443e-03 4.698e-05  94.580 <2e-16 ***
## thetaC:tmrcaC 1.398e+00 3.709e-02  37.684 <2e-16 ***
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0001062 on 466 degrees of freedom
## Multiple R-squared:  0.9914, Adjusted R-squared:  0.9913 
## F-statistic: 1.34e+04 on 4 and 466 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.50kb[1, 2] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.50kb[2, 2] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb[3, 2] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb[4, 2] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb[5, 2] <- anova.diversity$VarExp[4] * 100

g.div.50kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep2, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep2, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep2, weights = varPower(0, ~theta), method = "ML")
g.div.50kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep2, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.50kb.1, g.div.50kb.2, g.div.50kb.3, g.div.50kb.4)

##                 df      AIC
## g.div.50kb.1  8 -7357.344
## g.div.50kb.2  8 -7336.580
## g.div.50kb.3  7 -7288.080
## g.div.50kb.4  7 -7305.879

summary(g.div.50kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep2
##          AIC      BIC  logLik
##        -7288.08 -7258.996 3651.04
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
## Parameter estimates:
##   power
## -0.4081818
##
## Coefficients:
##                Value Std.Error t-value p-value
## (Intercept) 0.0032575 0.00000508 641.8553 0.0000
## thetaC       1.0124073 0.00775179 130.6030 0.0000
## rhoC        -0.0040721 0.00246568 -1.6515 0.0993
## tmrcaC       0.0044536 0.00004513  98.6740 0.0000
## thetaC:tmrcaC 1.4273988 0.04122365  34.6257 0.0000
##
## Correlation:
##             (Intr) thetaC rhoC    tmrcaC
## thetaC     -0.304
## rhoC       0.127 -0.379
## tmrcaC    -0.134  0.038 -0.454
## thetaC:tmrcaC -0.236  0.195 -0.380  0.565

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -3.52489862 -0.63206070 -0.05459749  0.67564509  4.32924101
## 
## Residual standard error: 1.020588e-05
## Degrees of freedom: 471 total; 466 residual
vif(g.div.50kb.3)

##          thetaC        rhoC        tmrcaC thetaC:tmrcaC
## 1.229717    1.521322    1.708997    1.550185

```

### 5.1.3 Replicate 3

```

rep_3.pi.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.diver")
rep_3.pi.50kb$avg <- apply(rep_3.pi.50kb[4:ncol(rep_3.pi.50kb)], 1, mean)
rep_3.rho.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.rho")
rep_3.theta.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.theta")
rep_3.tmrca.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.TMRCA")
rep_3.tmrca.50kb$avg <- apply(rep_3.tmrca.50kb[4:ncol(rep_3.tmrca.50kb)], 1, mean)

inf.lands.50kb.rep3 <- as.data.frame(cbind(rep_3.pi.50kb$avg, rep_3.theta.50kb$sample_mean, rep_3.tmrca.50kb$avg))
names(inf.lands.50kb.rep3) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.50kb.rep3$thetaC <- inf.lands.50kb.rep3$theta - mean(inf.lands.50kb.rep3$theta)
inf.lands.50kb.rep3$tmrcaC <- inf.lands.50kb.rep3$tmrca - mean(inf.lands.50kb.rep3$tmrca)
inf.lands.50kb.rep3$rhoC <- inf.lands.50kb.rep3$rho - mean(inf.lands.50kb.rep3$rho)

inf.lands.50kb.rep3$bin <- 1:nrow(inf.lands.50kb.rep3)

# for merging:
inf.lands.50kb.rep3 <- inf.lands.50kb.rep3
inf.lands.50kb.rep3$Replicate <- 1

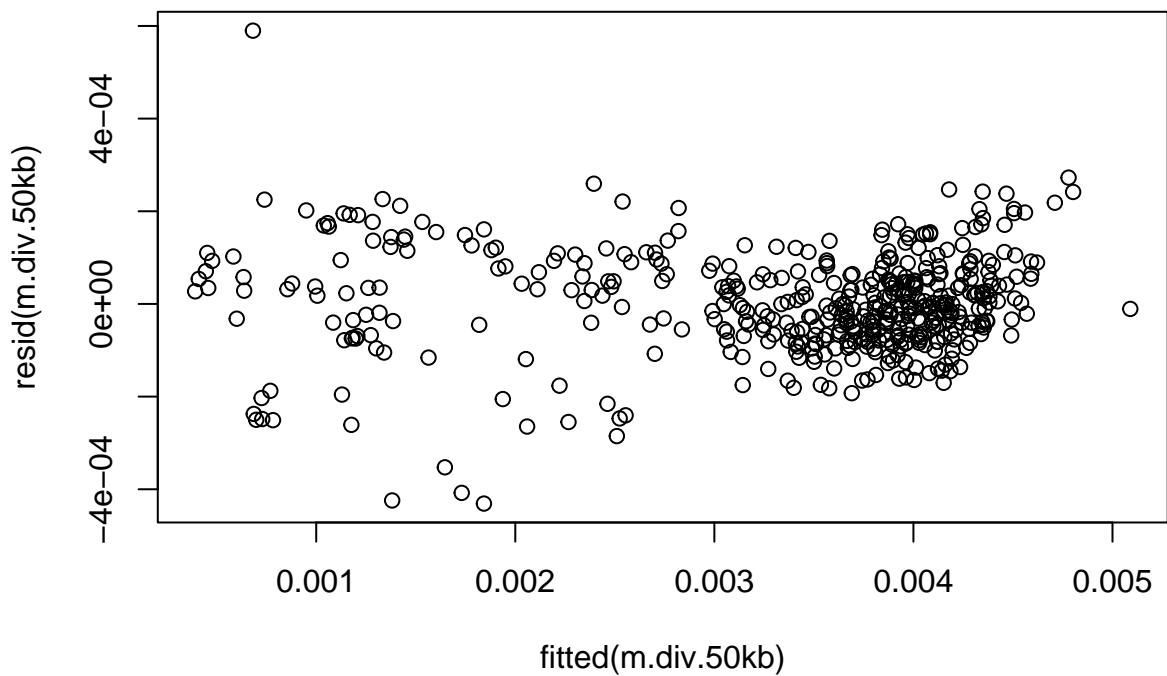
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.50kb.rep3)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.50kb.rep3)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.50kb.rep3)

AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

##          df      AIC
## m.div.50kb     6 -7236.648
## m.div.50kb.2   7 -7340.444
## m.div.50kb.3   8 -7339.716

plot(resid(m.div.50kb)~fitted(m.div.50kb))

```

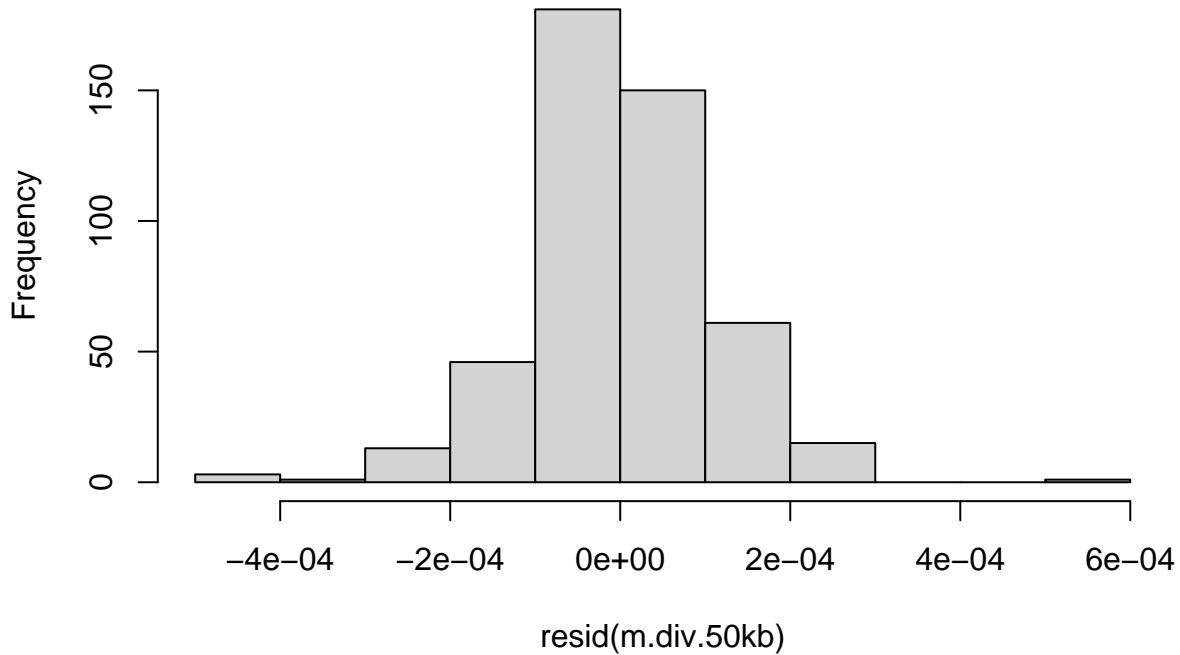


```
dwtest(m.div.50kb)
```

```
##
##  Durbin-Watson test
##
## data: m.div.50kb
## DW = 1.1119, p-value < 2.2e-16
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.50kb
## HMC = 0.52223, p-value = 0.762
hist(resid(m.div.50kb))
```

## Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##     data = inf.lands.50kb.rep3)
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -4.309e-04 -6.593e-05 -3.010e-06  6.406e-05  5.898e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.240e-03 5.846e-06 554.234 <2e-16 ***
## thetaC      9.990e-01 1.080e-02  92.469 <2e-16 ***
## rhoC       -2.159e-02 3.353e-03  -6.439  3e-10 ***
## tmrcaC      4.853e-03 5.411e-05  89.678 <2e-16 ***
## thetaC:tmrcaC 1.564e+00 4.725e-02  33.099 <2e-16 ***
## ---      
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0001107 on 466 degrees of freedom
## Multiple R-squared:  0.9897, Adjusted R-squared:  0.9896 
## F-statistic: 1.12e+04 on 4 and 466 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.50kb[1, 3] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.50kb[2, 3] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb[3, 3] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb[4, 3] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb[5, 3] <- anova.diversity$VarExp[4] * 100

g.div.50kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep3, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep3, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep3, weights = varPower(0, ~theta), method = "ML")
g.div.50kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep3, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.50kb.1, g.div.50kb.2, g.div.50kb.3, g.div.50kb.4)

##             df      AIC
## g.div.50kb.1 8 -7359.900
## g.div.50kb.2 8 -7340.098
## g.div.50kb.3 7 -7288.913
## g.div.50kb.4 7 -7274.406

summary(g.div.50kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep3
##       AIC      BIC  logLik
##   -7288.913 -7259.829 3651.457
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
## Parameter estimates:
##   power
## -1.091799
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032438 0.00000609 532.3525 0e+00
## thetaC       0.9768237 0.01338390  72.9850 0e+00
## rhoC        -0.0119449 0.00322386 -3.7051 2e-04
## tmrcaC       0.0048080 0.00005006  96.0371 0e+00
## thetaC:tmrcaC 1.5193043 0.05851355  25.9650 0e+00
##
## Correlation:
##            (Intr) thetaC rhoC    tmrcaC
## thetaC     -0.529
## rhoC       0.263 -0.501
## tmrcaC    -0.247 -0.034 -0.434
## thetaC:tmrcaC -0.531  0.442 -0.444  0.441

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -2.59963451 -0.68458381 -0.01785194  0.62376484  6.50658904
## 
## Residual standard error: 2.251601e-07
## Degrees of freedom: 471 total; 466 residual
vif(g.div.50kb.3)

##          thetaC        rhoC        tmrcaC thetaC:tmrcaC
##     1.816128    1.836383    1.703670    1.676572

```

### 5.1.4 Replicate 4

```

rep_4.pi.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.diver")
rep_4.pi.50kb$avg <- apply(rep_4.pi.50kb[4:ncol(rep_4.pi.50kb)], 1, mean)
rep_4.rho.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.rho")
rep_4.theta.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.theta")
rep_4.tmrca.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.TMRCA")
rep_4.tmrca.50kb$avg <- apply(rep_4.tmrca.50kb[4:ncol(rep_4.tmrca.50kb)], 1, mean)

inf.lands.50kb.rep4 <- as.data.frame(cbind(rep_4.pi.50kb$avg, rep_4.theta.50kb$sample_mean, rep_4.tmrca.50kb$avg))
names(inf.lands.50kb.rep4) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.50kb.rep4$thetaC <- inf.lands.50kb.rep4$theta - mean(inf.lands.50kb.rep4$theta)
inf.lands.50kb.rep4$tmrcaC <- inf.lands.50kb.rep4$tmrca - mean(inf.lands.50kb.rep4$tmrca)
inf.lands.50kb.rep4$rhoC <- inf.lands.50kb.rep4$rho - mean(inf.lands.50kb.rep4$rho)

inf.lands.50kb.rep4$bin <- 1:nrow(inf.lands.50kb.rep4)

# for merging:
inf.lands.50kb.rep4 <- inf.lands.50kb.rep4
inf.lands.50kb.rep4$Replicate <- 1

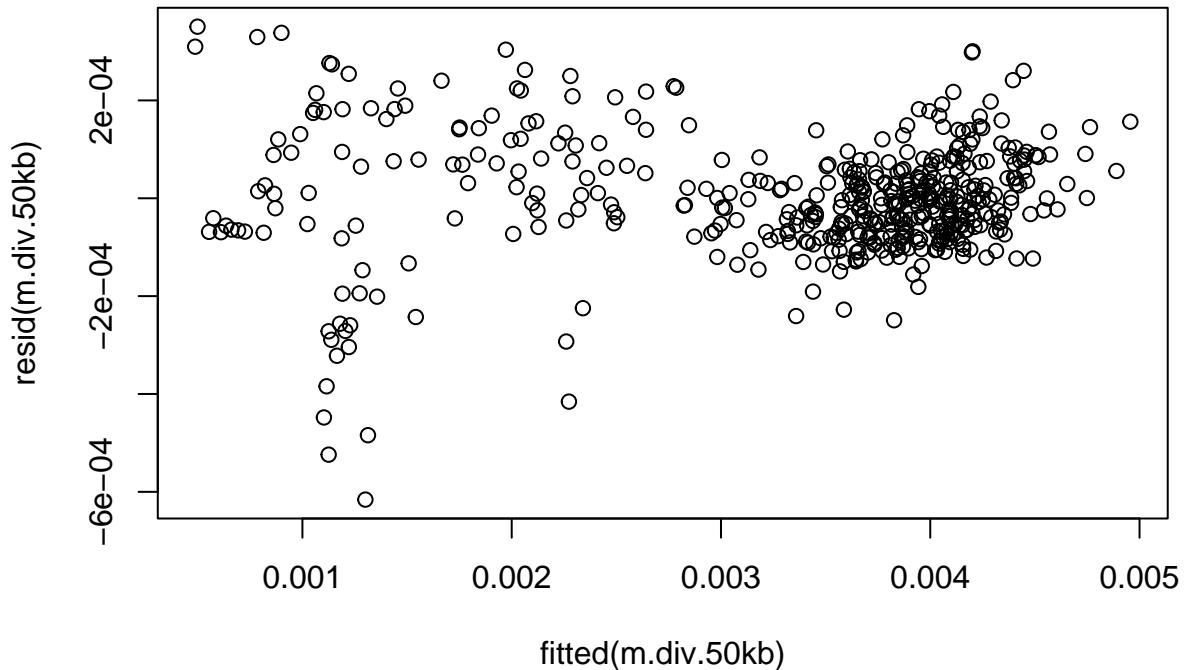
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.50kb.rep4)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.50kb.rep4)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.50kb.rep4)

AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

##          df      AIC
## m.div.50kb     6 -7148.596
## m.div.50kb.2   7 -7314.670
## m.div.50kb.3   8 -7320.485

plot(resid(m.div.50kb)~fitted(m.div.50kb))

```

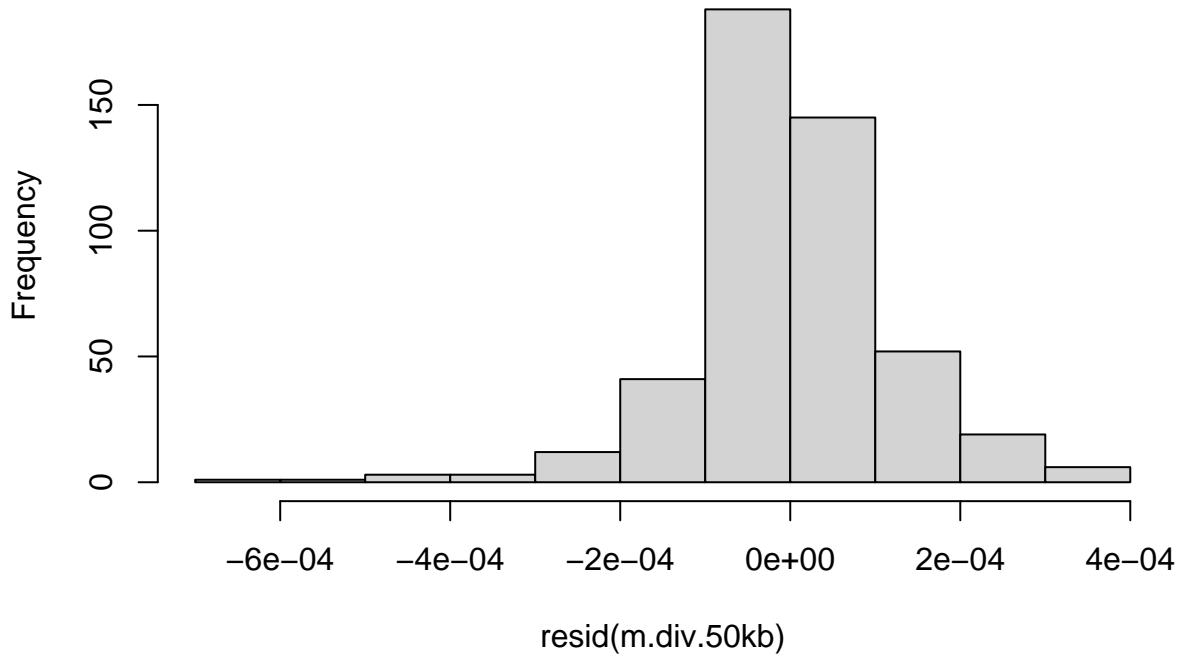


```
dwtest(m.div.50kb)
```

```
##
##  Durbin-Watson test
##
## data: m.div.50kb
## DW = 0.8328, p-value < 2.2e-16
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.50kb
## HMC = 0.30453, p-value < 2.2e-16
hist(resid(m.div.50kb))
```

## Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.50kb.rep4)
##
## Residuals:
##       Min         1Q     Median        3Q       Max
## -6.159e-04 -6.584e-05 -3.550e-06  6.891e-05  3.507e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.272e-03 6.258e-06 522.93 < 2e-16 ***
## thetaC      1.072e+00 9.427e-03 113.76 < 2e-16 ***
## rhoC       -2.087e-02 2.742e-03   -7.61 1.53e-13 ***
## tmrcaC      4.847e-03 6.387e-05   75.89 < 2e-16 ***
## thetaC:tmrcaC 1.500e+00 6.429e-02   23.33 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0001216 on 466 degrees of freedom
## Multiple R-squared:  0.9875, Adjusted R-squared:  0.9874
## F-statistic:  9231 on 4 and 466 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.50kb[1, 4] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.50kb[2, 4] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb[3, 4] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb[4, 4] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb[5, 4] <- anova.diversity$VarExp[4] * 100

g.div.50kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep4, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep4, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep4, weights = varPower(0, ~theta), method = "ML")
g.div.50kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep4, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.50kb.1, g.div.50kb.2, g.div.50kb.3, g.div.50kb.4)

##                 df      AIC
## g.div.50kb.1  8 -7364.127
## g.div.50kb.2  8 -7380.679
## g.div.50kb.3  7 -7328.156
## g.div.50kb.4  7 -7185.307

summary(g.div.50kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep4
##       AIC      BIC  logLik
##   -7328.156 -7299.072 3671.078
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##       power
##   -1.716365
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032745 0.00000641 510.5089 0e+00
## thetaC      1.0530201 0.01402599  75.0764 0e+00
## rhoC      -0.0078260 0.00228445 -3.4258 7e-04
## tmrcaC     0.0047769 0.00004948  96.5484 0e+00
## thetaC:tmrcaC 1.5114666 0.07777455 19.4339 0e+00
##
## Correlation:
##            (Intr) thetaC rhoC    tmrcaC
## thetaC      -0.717
## rhoC       0.208 -0.339
## tmrcaC     0.007 -0.209 -0.292
## thetaC:tmrcaC -0.468  0.403 -0.269 -0.042

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -3.09763551 -0.64794574 -0.02894227  0.67255210  3.68496533
## 
## Residual standard error: 6.320069e-09
## Degrees of freedom: 471 total; 466 residual
vif(g.div.50kb.3)

##          thetaC        rhoC        tmrcaC thetaC:tmrcaC
## 1.428139    1.368975    1.239488    1.223467

```

### 5.1.5 Replicate 5

```

rep_5.pi.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.diver")
rep_5.pi.50kb$avg <- apply(rep_5.pi.50kb[4:ncol(rep_5.pi.50kb)], 1, mean)
rep_5.rho.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.rho")
rep_5.theta.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.theta")
rep_5.tmrca.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.TMRCA")
rep_5.tmrca.50kb$avg <- apply(rep_5.tmrca.50kb[4:ncol(rep_5.tmrca.50kb)], 1, mean)

inf.lands.50kb.rep5 <- as.data.frame(cbind(rep_5.pi.50kb$avg, rep_5.theta.50kb$sample_mean, rep_5.tmrca.50kb$avg))
names(inf.lands.50kb.rep5) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.50kb.rep5$thetaC <- inf.lands.50kb.rep5$theta - mean(inf.lands.50kb.rep5$theta)
inf.lands.50kb.rep5$tmrcaC <- inf.lands.50kb.rep5$tmrca - mean(inf.lands.50kb.rep5$tmrca)
inf.lands.50kb.rep5$rhoC <- inf.lands.50kb.rep5$rho - mean(inf.lands.50kb.rep5$rho)

inf.lands.50kb.rep5$bin <- 1:nrow(inf.lands.50kb.rep5)

# for merging:
inf.lands.50kb.rep5 <- inf.lands.50kb.rep5
inf.lands.50kb.rep5$Replicate <- 1

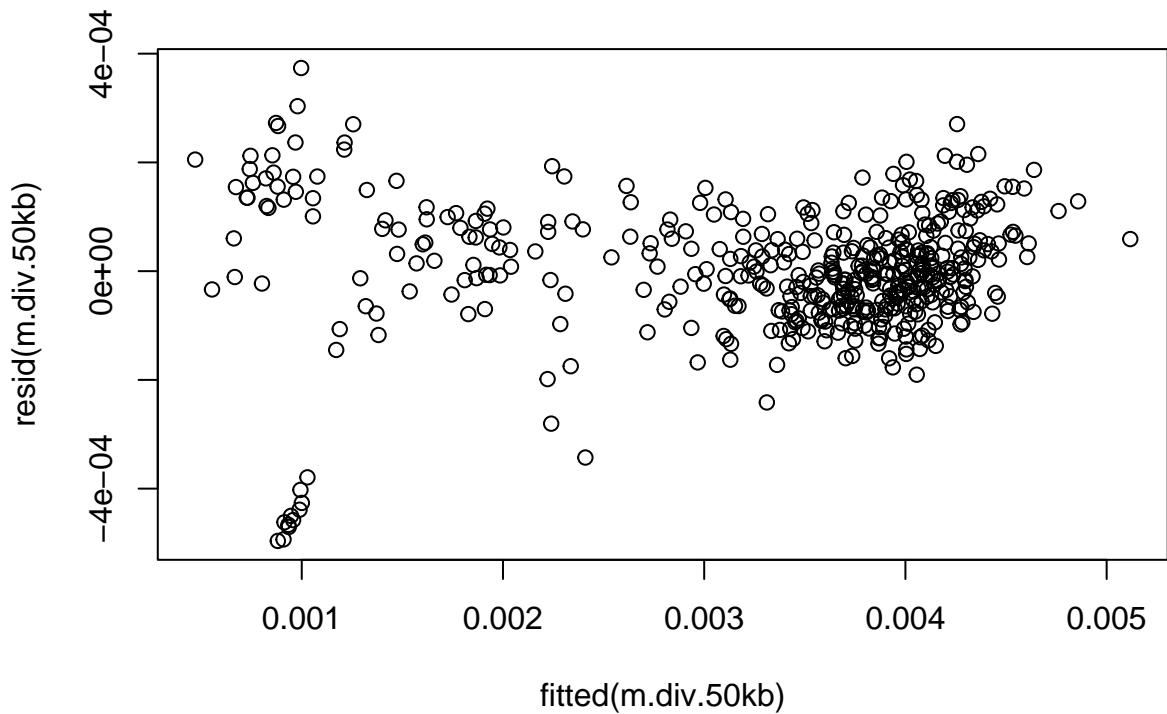
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.50kb.rep5)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.50kb.rep5)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.50kb.rep5)

AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

##          df      AIC
## m.div.50kb     6 -7172.172
## m.div.50kb.2   7 -7341.719
## m.div.50kb.3   8 -7354.145

plot(resid(m.div.50kb)~fitted(m.div.50kb))

```



```

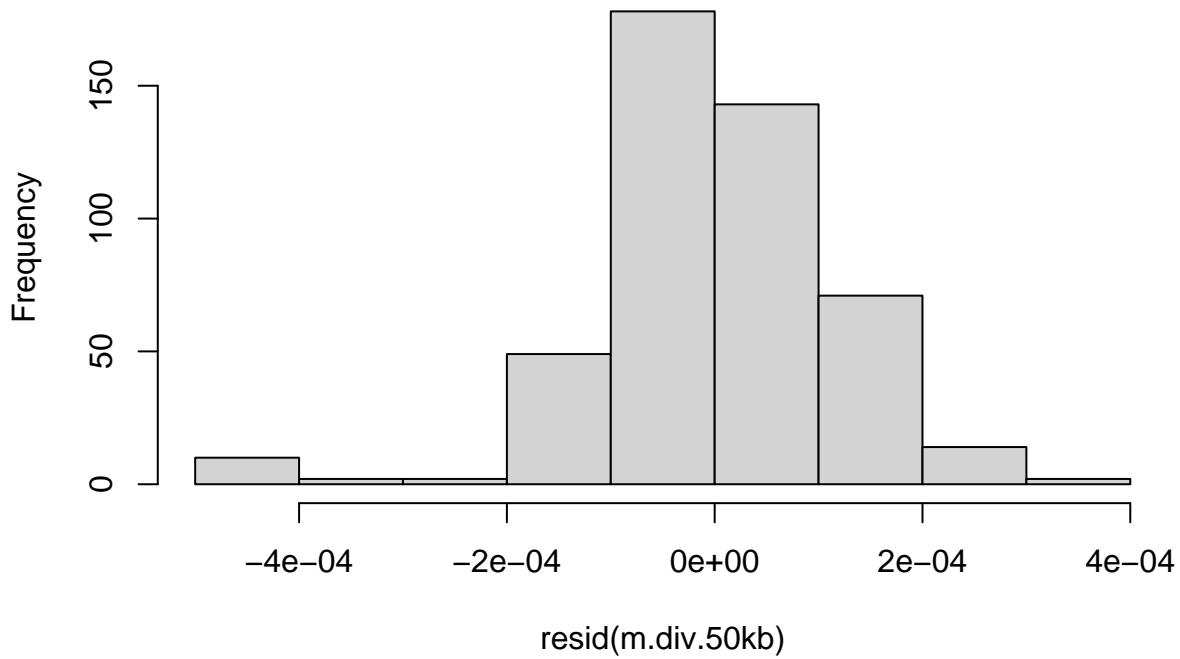
dwtest(m.div.50kb)

##
##  Durbin-Watson test
##
## data: m.div.50kb
## DW = 0.85321, p-value < 2.2e-16
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)

##
##  Harrison-McCabe test
##
## data: m.div.50kb
## HMC = 0.2333, p-value < 2.2e-16
hist(resid(m.div.50kb))

```

## Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##     data = inf.lands.50kb.rep5)
##
## Residuals:
##       Min         1Q      Median         3Q        Max
## -4.961e-04 -6.375e-05 -3.090e-06  6.777e-05  3.736e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.270e-03 5.753e-06 568.437 < 2e-16 ***
## thetaC      1.020e+00 7.027e-03 145.100 < 2e-16 ***
## rhoC       -1.412e-02 2.587e-03 -5.459 7.8e-08 ***
## tmrcaC      4.663e-03 6.224e-05 74.918 < 2e-16 ***
## thetaC:tmrcaC 1.404e+00 5.510e-02 25.477 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0001186 on 466 degrees of freedom
## Multiple R-squared:  0.988, Adjusted R-squared:  0.9879
## F-statistic: 9613 on 4 and 466 DF, p-value: < 2.2e-16

anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.50kb[1, 5] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.50kb[2, 5] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb[3, 5] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb[4, 5] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb[5, 5] <- anova.diversity$VarExp[4] * 100

g.div.50kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep5, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep5, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep5, weights = varPower(0, ~theta), method = "ML")
g.div.50kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep5, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.50kb.1, g.div.50kb.2, g.div.50kb.3, g.div.50kb.4)

##             df      AIC
## g.div.50kb.1 8 -7372.655
## g.div.50kb.2 8 -7396.802
## g.div.50kb.3 7 -7353.762
## g.div.50kb.4 7 -7191.430

summary(g.div.50kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep5
##       AIC      BIC    logLik
##   -7353.762 -7324.678 3683.881
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##       power
##   -1.250143
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032684 0.00000574 568.9219 0.0000
## thetaC      1.0163725 0.01103937  92.0680 0.0000
## rhoC      -0.0081960 0.00256257 -3.1984 0.0015
## tmrcaC     0.0046435 0.00004864  95.4763 0.0000
## thetaC:tmrcaC 1.5350345 0.06594486 23.2775 0.0000
##
## Correlation:
##          (Intr) thetaC rhoC   tmrcaC
## thetaC    -0.668
## rhoC      0.244 -0.335
## tmrcaC   -0.061 -0.092 -0.399
## thetaC:tmrcaC -0.382  0.327 -0.295  0.084

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -2.682153307 -0.700850203 -0.007002239  0.581689051  3.153007219
## 
## Residual standard error: 8.22055e-08
## Degrees of freedom: 471 total; 466 residual
vif(g.div.50kb.3)

##          thetaC        rhoC        tmrcaC thetaC:tmrcaC
##     1.290406    1.468923    1.276986    1.171610

```

### 5.1.6 Replicate 6

```

rep_6.pi.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.diver")
rep_6.pi.50kb$avg <- apply(rep_6.pi.50kb[4:ncol(rep_6.pi.50kb)], 1, mean)
rep_6.rho.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.rho")
rep_6.theta.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.theta")
rep_6.tmrca.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.TMRCA")
rep_6.tmrca.50kb$avg <- apply(rep_6.tmrca.50kb[4:ncol(rep_6.tmrca.50kb)], 1, mean)

inf.lands.50kb.rep6 <- as.data.frame(cbind(rep_6.pi.50kb$avg, rep_6.theta.50kb$sample_mean, rep_6.tmrca.50kb$avg))
names(inf.lands.50kb.rep6) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.50kb.rep6$thetaC <- inf.lands.50kb.rep6$theta - mean(inf.lands.50kb.rep6$theta)
inf.lands.50kb.rep6$tmrcaC <- inf.lands.50kb.rep6$tmrca - mean(inf.lands.50kb.rep6$tmrca)
inf.lands.50kb.rep6$rhoC <- inf.lands.50kb.rep6$rho - mean(inf.lands.50kb.rep6$rho)

inf.lands.50kb.rep6$bin <- 1:nrow(inf.lands.50kb.rep6)

# for merging:
inf.lands.50kb.rep6 <- inf.lands.50kb.rep6
inf.lands.50kb.rep6$Replicate <- 1

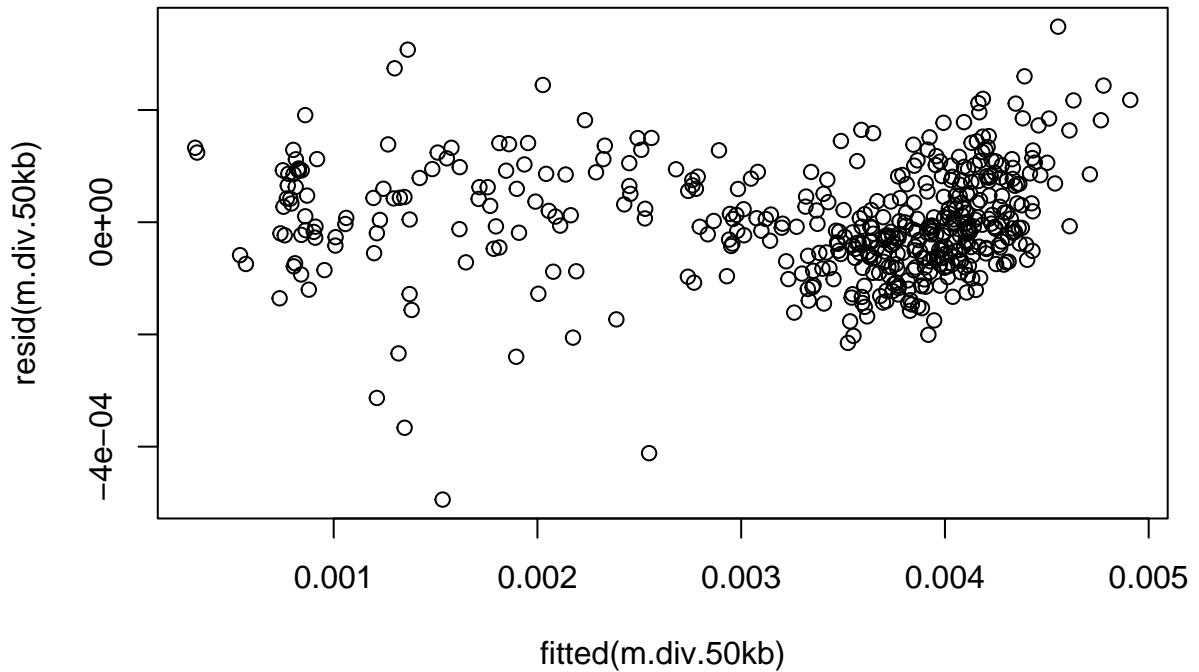
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.50kb.rep6)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.50kb.rep6)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.50kb.rep6)

AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

##          df      AIC
## m.div.50kb     6 -7335.144
## m.div.50kb.2   7 -7498.540
## m.div.50kb.3   8 -7514.166

plot(resid(m.div.50kb)~fitted(m.div.50kb))

```

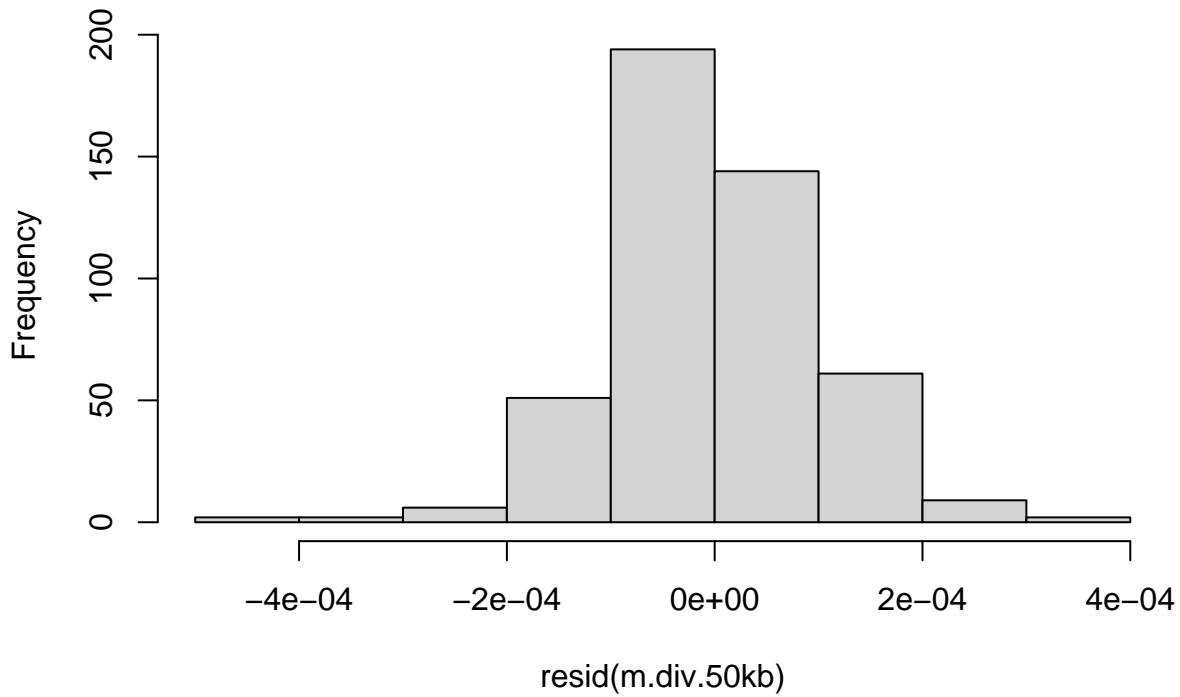


```
dwtest(m.div.50kb)
```

```
##
##  Durbin-Watson test
##
## data: m.div.50kb
## DW = 1.3358, p-value = 9.341e-14
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.50kb
## HMC = 0.47386, p-value = 0.232
hist(resid(m.div.50kb))
```

## Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.50kb.rep6)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -4.943e-04 -5.947e-05 -8.070e-06  6.832e-05  3.485e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.220e-03 5.176e-06 622.042 <2e-16 ***
## thetaC      9.534e-01 9.236e-03 103.226 <2e-16 ***
## rhoC       -5.393e-03 2.447e-03 -2.204  0.028 *  
## tmrcaC      4.525e-03 3.735e-05 121.133 <2e-16 *** 
## thetaC:tmrcaC 1.504e+00 4.103e-02 36.646 <2e-16 *** 
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 9.972e-05 on 466 degrees of freedom
## Multiple R-squared:  0.9921, Adjusted R-squared:  0.9921 
## F-statistic: 1.468e+04 on 4 and 466 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.50kb[1, 6] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.50kb[2, 6] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb[3, 6] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb[4, 6] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb[5, 6] <- anova.diversity$VarExp[4] * 100

g.div.50kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep6, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")

g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep6, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")

g.div.50kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep6, weights = varPower(0, ~theta), method = "ML")

g.div.50kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep6, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.50kb.1, g.div.50kb.2, g.div.50kb.3, g.div.50kb.4)

##             df      AIC
## g.div.50kb.1 8 -7401.361
## g.div.50kb.2 8 -7395.754
## g.div.50kb.3 7 -7343.374
## g.div.50kb.4 7 -7344.669

summary(g.div.50kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep6
##       AIC      BIC  logLik
##   -7343.374 -7314.29 3678.687
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##       power
##   -0.4875493
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032193 0.00000530 607.6494 0.0000
## thetaC       0.9475585 0.01054102  89.8925 0.0000
## rhoC        -0.0045657 0.00232628 -1.9627 0.0503
## tmrcaC       0.0045371 0.00003659 123.9958 0.0000
## thetaC:tmrcaC 1.5262923 0.04601779  33.1674 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC    tmrcaC
## thetaC     -0.324
## rhoC       0.154 -0.468
## tmrcaC    -0.233 -0.058 -0.392
## thetaC:tmrcaC -0.495  0.358 -0.295  0.481

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -4.08862261 -0.60657489 -0.08314079  0.71335416  3.70206913
## 
## Residual standard error: 6.337495e-06
## Degrees of freedom: 471 total; 466 residual
vif(g.div.50kb.3)

##          thetaC        rhoC        tmrcaC thetaC:tmrcaC
##      1.745874     1.684710     1.813824     1.645992

```

### 5.1.7 Replicate 7

```

rep_7.pi.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.diver")
rep_7.pi.50kb$avg <- apply(rep_7.pi.50kb[4:ncol(rep_7.pi.50kb)], 1, mean)
rep_7.rho.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.rho")
rep_7.theta.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.theta")
rep_7.tmrca.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.TMRCA")
rep_7.tmrca.50kb$avg <- apply(rep_7.tmrca.50kb[4:ncol(rep_7.tmrca.50kb)], 1, mean)

inf.lands.50kb.rep7 <- as.data.frame(cbind(rep_7.pi.50kb$avg, rep_7.theta.50kb$sample_mean, rep_7.tmrca.50kb$avg))
names(inf.lands.50kb.rep7) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.50kb.rep7$thetaC <- inf.lands.50kb.rep7$theta - mean(inf.lands.50kb.rep7$theta)
inf.lands.50kb.rep7$tmrcaC <- inf.lands.50kb.rep7$tmrca - mean(inf.lands.50kb.rep7$tmrca)
inf.lands.50kb.rep7$rhoC <- inf.lands.50kb.rep7$rho - mean(inf.lands.50kb.rep7$rho)

inf.lands.50kb.rep7$bin <- 1:nrow(inf.lands.50kb.rep7)

# for merging:
inf.lands.50kb.rep7 <- inf.lands.50kb.rep7
inf.lands.50kb.rep7$Replicate <- 1

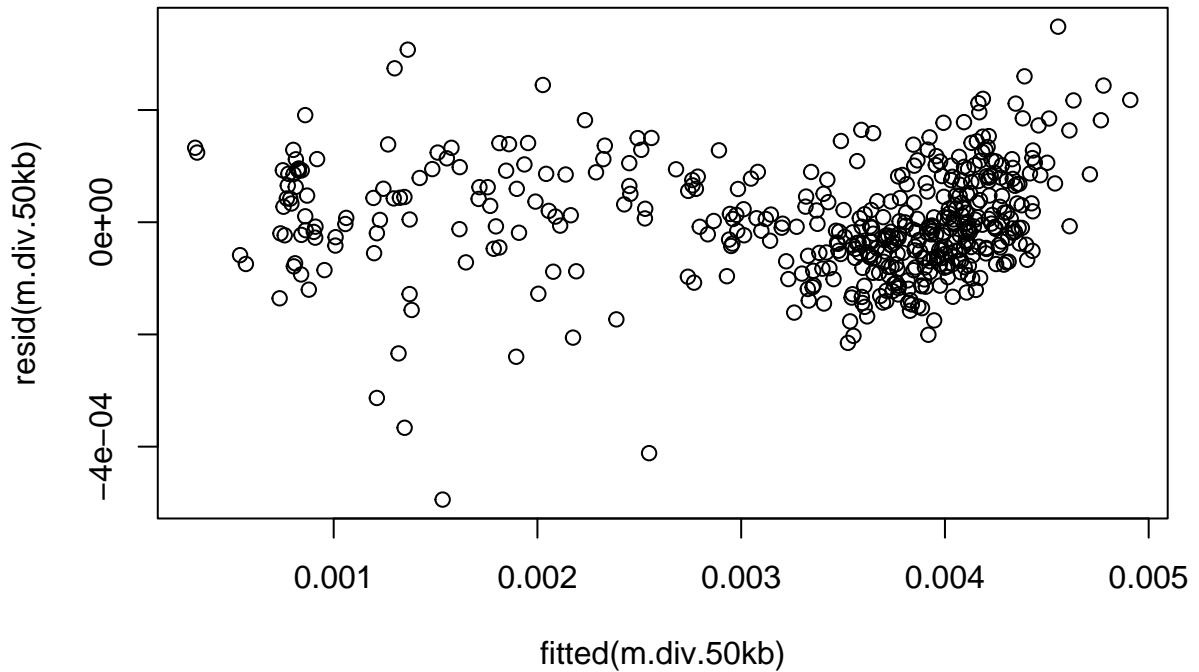
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.50kb.rep7)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.50kb.rep7)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.50kb.rep7)

AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

##          df      AIC
## m.div.50kb    6 -7335.144
## m.div.50kb.2  7 -7498.540
## m.div.50kb.3  8 -7514.166

plot(resid(m.div.50kb)~fitted(m.div.50kb))

```

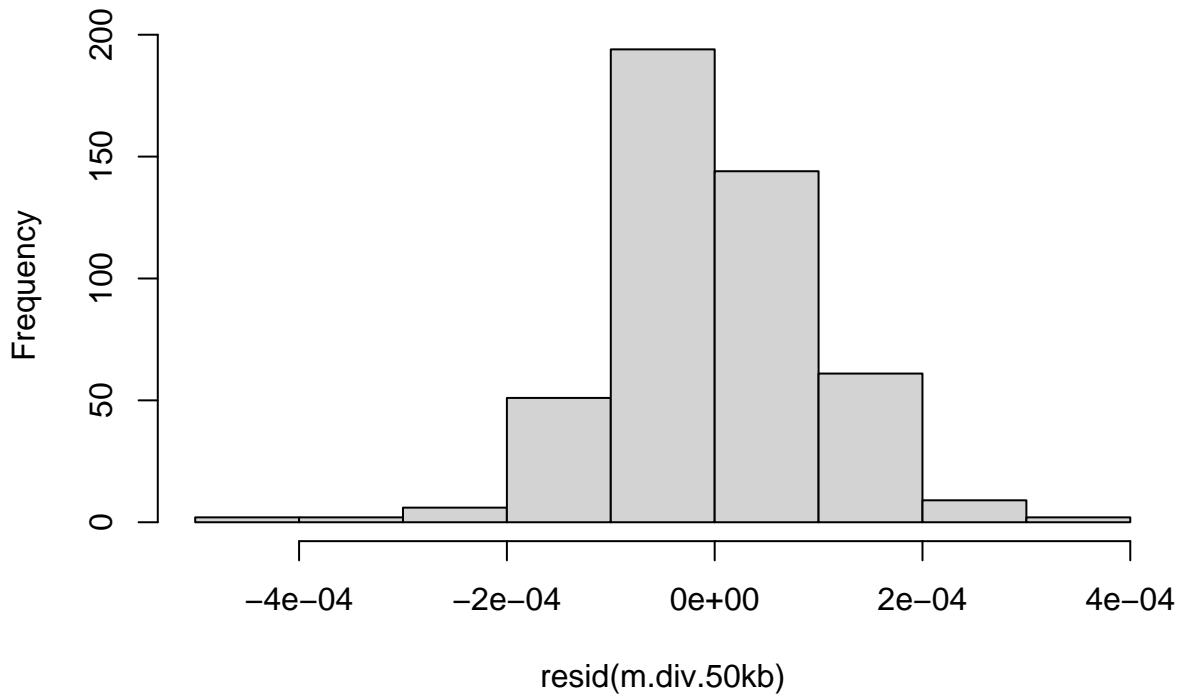


```
dwtest(m.div.50kb)
```

```
##
##  Durbin-Watson test
##
## data: m.div.50kb
## DW = 1.3358, p-value = 9.341e-14
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.50kb
## HMC = 0.47386, p-value = 0.238
hist(resid(m.div.50kb))
```

## Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##     data = inf.lands.50kb.rep7)
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -4.943e-04 -5.947e-05 -8.070e-06  6.832e-05  3.485e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.220e-03 5.176e-06 622.042 <2e-16 ***
## thetaC      9.534e-01 9.236e-03 103.226 <2e-16 ***
## rhoC       -5.393e-03 2.447e-03 -2.204  0.028 *  
## tmrcaC      4.525e-03 3.735e-05 121.133 <2e-16 ***
## thetaC:tmrcaC 1.504e+00 4.103e-02 36.646 <2e-16 ***
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 9.972e-05 on 466 degrees of freedom
## Multiple R-squared:  0.9921, Adjusted R-squared:  0.9921 
## F-statistic: 1.468e+04 on 4 and 466 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.50kb[1, 7] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.50kb[2, 7] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb[3, 7] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb[4, 7] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb[5, 7] <- anova.diversity$VarExp[4] * 100

g.div.50kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep7, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep7, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep7, weights = varPower(0, ~theta), method = "ML")
g.div.50kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep7, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.50kb.1, g.div.50kb.2, g.div.50kb.3, g.div.50kb.4)

##             df      AIC
## g.div.50kb.1 8 -7401.361
## g.div.50kb.2 8 -7395.754
## g.div.50kb.3 7 -7343.374
## g.div.50kb.4 7 -7344.669

summary(g.div.50kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep7
##       AIC      BIC  logLik
##   -7343.374 -7314.29 3678.687
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##       power
##   -0.4875493
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032193 0.00000530 607.6494 0.0000
## thetaC       0.9475585 0.01054102  89.8925 0.0000
## rhoC        -0.0045657 0.00232628 -1.9627 0.0503
## tmrcaC       0.0045371 0.00003659 123.9958 0.0000
## thetaC:tmrcaC 1.5262923 0.04601779  33.1674 0.0000
##
## Correlation:
##          (Intr) thetaC rhoC    tmrcaC
## thetaC     -0.324
## rhoC       0.154 -0.468
## tmrcaC    -0.233 -0.058 -0.392
## thetaC:tmrcaC -0.495  0.358 -0.295  0.481

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -4.08862261 -0.60657489 -0.08314079  0.71335416  3.70206913
## 
## Residual standard error: 6.337495e-06
## Degrees of freedom: 471 total; 466 residual
vif(g.div.50kb.3)

##          thetaC        rhoC        tmrcaC thetaC:tmrcaC
##      1.745874     1.684710     1.813824     1.645992

```

### 5.1.8 Replicate 8

```

rep_8.pi.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.diver")
rep_8.pi.50kb$avg <- apply(rep_8.pi.50kb[4:ncol(rep_8.pi.50kb)], 1, mean)
rep_8.rho.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.rho")
rep_8.theta.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.theta")
rep_8.tmrca.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.TMRCA")
rep_8.tmrca.50kb$avg <- apply(rep_8.tmrca.50kb[4:ncol(rep_8.tmrca.50kb)], 1, mean)

inf.lands.50kb.rep8 <- as.data.frame(cbind(rep_8.pi.50kb$avg, rep_8.theta.50kb$sample_mean, rep_8.tmrca.50kb$avg))
names(inf.lands.50kb.rep8) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.50kb.rep8$thetaC <- inf.lands.50kb.rep8$theta - mean(inf.lands.50kb.rep8$theta)
inf.lands.50kb.rep8$tmrcaC <- inf.lands.50kb.rep8$tmrca - mean(inf.lands.50kb.rep8$tmrca)
inf.lands.50kb.rep8$rhoC <- inf.lands.50kb.rep8$rho - mean(inf.lands.50kb.rep8$rho)

inf.lands.50kb.rep8$bin <- 1:nrow(inf.lands.50kb.rep8)

# for merging:
inf.lands.50kb.rep8 <- inf.lands.50kb.rep8
inf.lands.50kb.rep8$Replicate <- 1

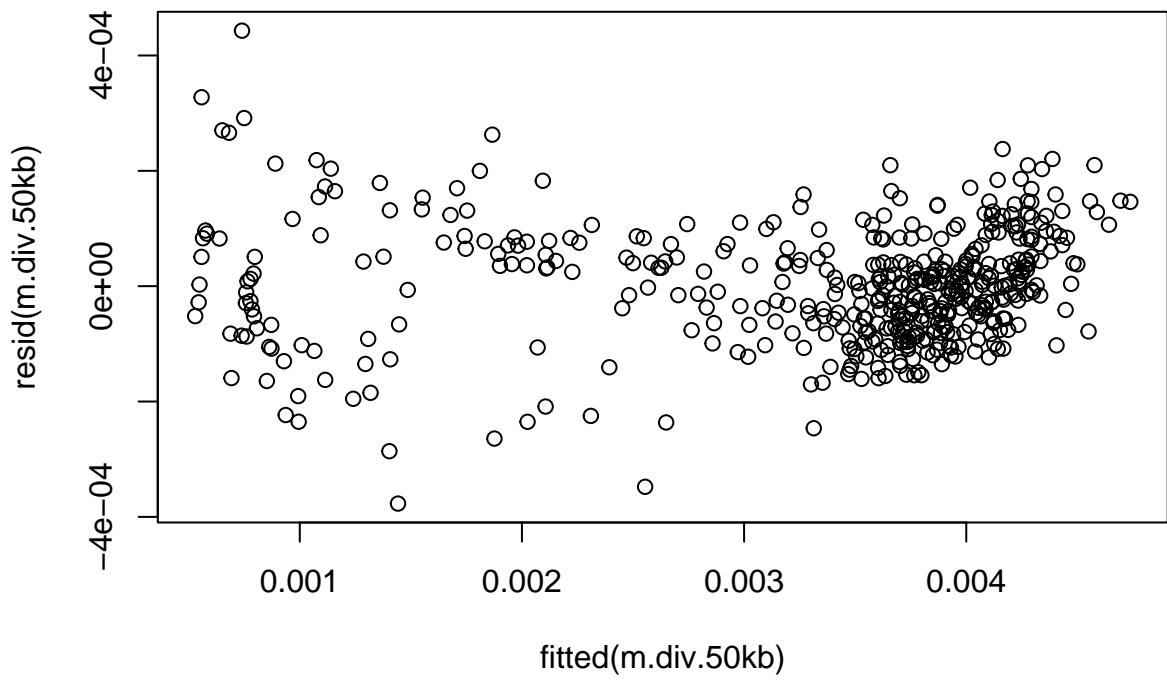
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.50kb.rep8)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.50kb.rep8)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.50kb.rep8)

AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

##           df      AIC
## m.div.50kb    6 -7306.572
## m.div.50kb.2  7 -7395.464
## m.div.50kb.3  8 -7417.026

plot(resid(m.div.50kb)~fitted(m.div.50kb))

```

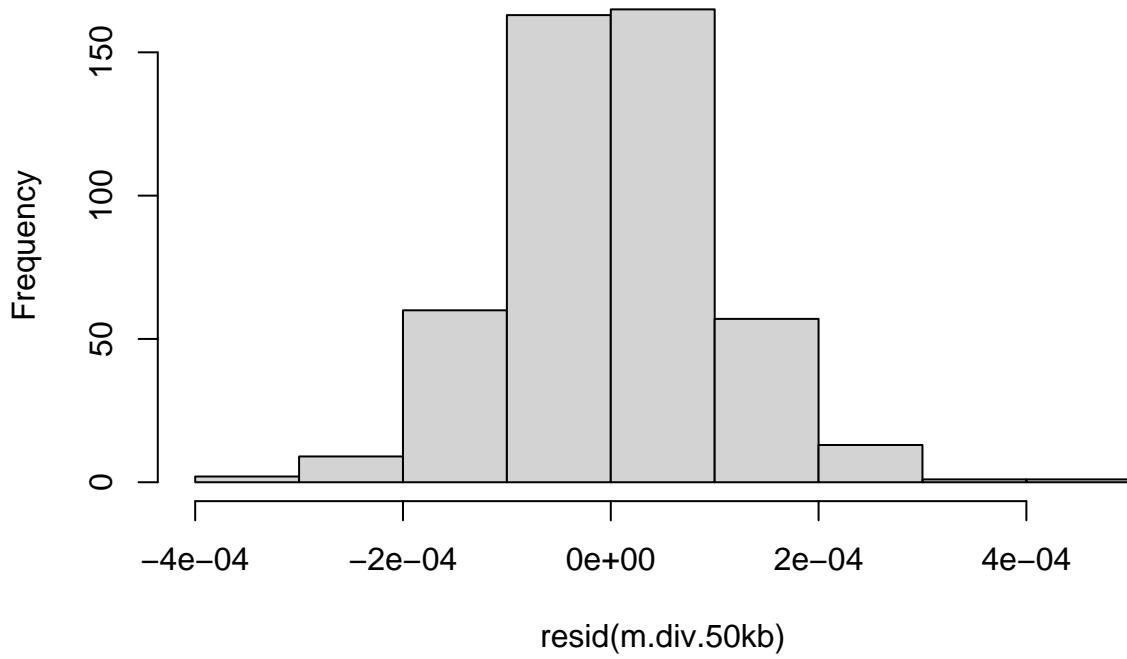


```
dwtest(m.div.50kb)
```

```
##
##  Durbin-Watson test
##
## data: m.div.50kb
## DW = 1.1894, p-value < 2.2e-16
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.50kb
## HMC = 0.43038, p-value = 0.015
hist(resid(m.div.50kb))
```

## Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##     data = inf.lands.50kb.rep8)
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -3.769e-04 -6.997e-05  7.200e-07  6.476e-05  4.430e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.222e-03 5.257e-06 612.845 <2e-16 ***
## thetaC      1.024e+00 7.003e-03 146.273 <2e-16 ***
## rhoC       -2.032e-02 2.326e-03 -8.735 <2e-16 ***
## tmrcaC      4.540e-03 4.741e-05  95.750 <2e-16 ***
## thetaC:tmrcaC 1.539e+00 5.006e-02  30.742 <2e-16 ***
## ---      
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0001028 on 466 degrees of freedom
## Multiple R-squared:  0.9913, Adjusted R-squared:  0.9912 
## F-statistic: 1.329e+04 on 4 and 466 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.50kb[1, 8] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.50kb[2, 8] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb[3, 8] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb[4, 8] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb[5, 8] <- anova.diversity$VarExp[4] * 100

g.div.50kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep8, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep8, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep8, weights = varPower(0, ~theta), method = "ML")
g.div.50kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep8, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.50kb.1, g.div.50kb.2, g.div.50kb.3, g.div.50kb.4)

##             df      AIC
## g.div.50kb.1 8 -7416.341
## g.div.50kb.2 8 -7387.986
## g.div.50kb.3 7 -7327.716
## g.div.50kb.4 7 -7355.330

summary(g.div.50kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep8
##        AIC      BIC    logLik
##   -7327.716 -7298.632 3670.858
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##     power
## -0.734904
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032208 0.00000559 575.7028 0
## thetaC       1.0152924 0.01030530  98.5214 0
## rhoC        -0.0180657 0.00260902 -6.9243 0
## tmrcaC       0.0045590 0.00004496 101.4012 0
## thetaC:tmrcaC 1.5987953 0.05970086  26.7801 0
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC     -0.465
## rhoC       0.232 -0.300
## tmrcaC    -0.208 -0.109 -0.454
## thetaC:tmrcaC -0.500  0.342 -0.328  0.416

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -2.80727802 -0.69707408 -0.02648353  0.58385802  5.31468972
## 
## Residual standard error: 1.572529e-06
## Degrees of freedom: 471 total; 466 residual
vif(g.div.50kb.3)

##          thetaC        rhoC        tmrcaC thetaC:tmrcaC
##      1.424254     1.490470     1.682699     1.481909

```

### 5.1.9 Replicate 9

```

rep_9.pi.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.diver")
rep_9.pi.50kb$avg <- apply(rep_9.pi.50kb[4:ncol(rep_9.pi.50kb)], 1, mean)
rep_9.rho.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.rho")
rep_9.theta.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.theta")
rep_9.tmrca.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.TMRCA")
rep_9.tmrca.50kb$avg <- apply(rep_9.tmrca.50kb[4:ncol(rep_9.tmrca.50kb)], 1, mean)

inf.lands.50kb.rep9 <- as.data.frame(cbind(rep_9.pi.50kb$avg, rep_9.theta.50kb$sample_mean, rep_9.tmrca.50kb$avg))
names(inf.lands.50kb.rep9) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.50kb.rep9$thetaC <- inf.lands.50kb.rep9$theta - mean(inf.lands.50kb.rep9$theta)
inf.lands.50kb.rep9$tmrcaC <- inf.lands.50kb.rep9$tmrca - mean(inf.lands.50kb.rep9$tmrca)
inf.lands.50kb.rep9$rhoC <- inf.lands.50kb.rep9$rho - mean(inf.lands.50kb.rep9$rho)

inf.lands.50kb.rep9$bin <- 1:nrow(inf.lands.50kb.rep9)

# for merging:
inf.lands.50kb.rep9 <- inf.lands.50kb.rep9
inf.lands.50kb.rep9$Replicate <- 1

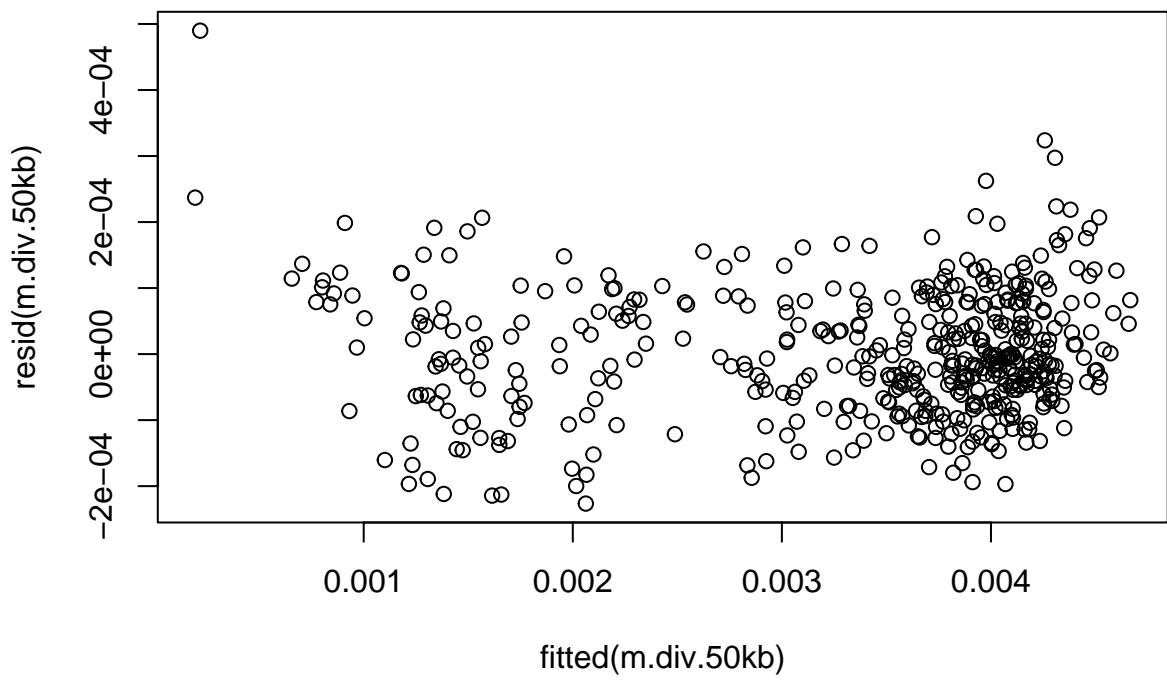
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.50kb.rep9)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.50kb.rep9)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.50kb.rep9)

AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

##          df      AIC
## m.div.50kb    6 -7369.759
## m.div.50kb.2  7 -7424.115
## m.div.50kb.3  8 -7428.899

plot(resid(m.div.50kb)~fitted(m.div.50kb))

```

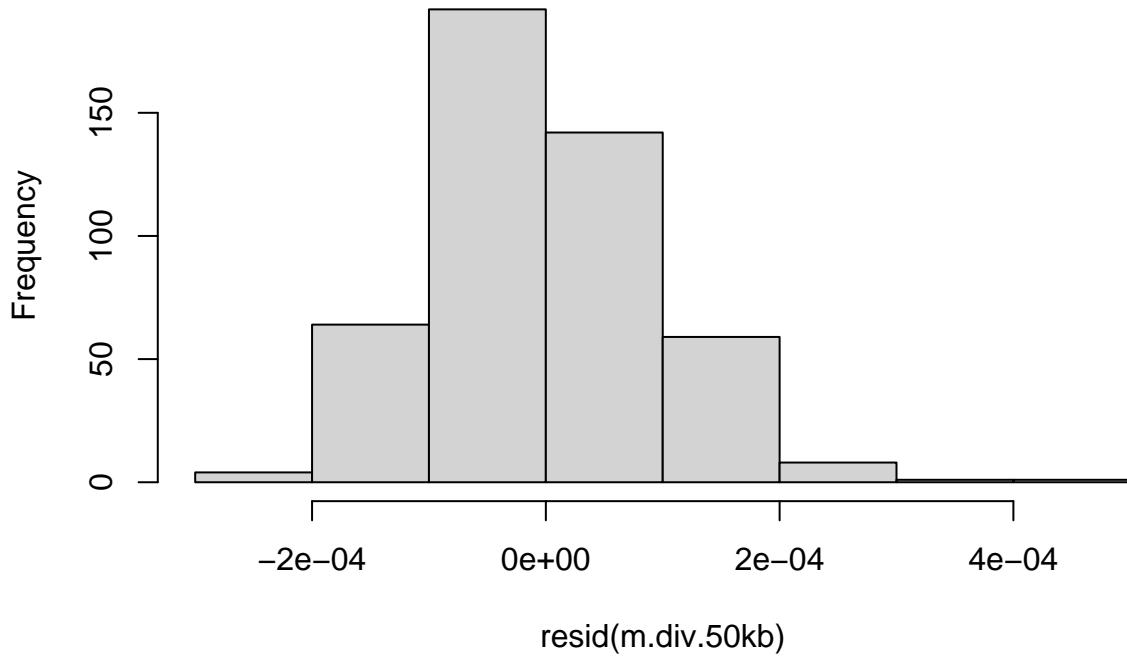


```
dwtest(m.div.50kb)
```

```
##
##  Durbin-Watson test
##
## data: m.div.50kb
## DW = 1.2528, p-value < 2.2e-16
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.50kb
## HMC = 0.46539, p-value = 0.154
hist(resid(m.div.50kb))
```

## Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##     data = inf.lands.50kb.rep9)
##
## Residuals:
##       Min         1Q      Median         3Q        Max
## -2.264e-04 -6.316e-05 -1.027e-05  6.801e-05  4.899e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.248e-03 5.227e-06 621.439 <2e-16 ***
## thetaC      1.007e+00 1.036e-02  97.243 <2e-16 ***
## rhoC       -1.100e-02 3.402e-03 -3.235 0.0013 **
## tmrcaC      4.379e-03 4.958e-05  88.332 <2e-16 ***
## thetaC:tmrcaC 1.555e+00 5.186e-02  29.995 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.612e-05 on 466 degrees of freedom
## Multiple R-squared:  0.9917, Adjusted R-squared:  0.9917
## F-statistic: 1.396e+04 on 4 and 466 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.50kb[1, 9] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.50kb[2, 9] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb[3, 9] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb[4, 9] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb[5, 9] <- anova.diversity$VarExp[4] * 100

g.div.50kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep9, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep9, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep9, weights = varPower(0, ~theta), method = "ML")
g.div.50kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep9, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.50kb.1, g.div.50kb.2, g.div.50kb.3, g.div.50kb.4)

##             df      AIC
## g.div.50kb.1 8 -7451.009
## g.div.50kb.2 8 -7439.797
## g.div.50kb.3 7 -7376.047
## g.div.50kb.4 7 -7383.267

summary(g.div.50kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep9
##       AIC      BIC  logLik
##   -7376.047 -7346.963 3695.024
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##       power
##   -0.4270749
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032474 0.00000528 614.7741 0.0000
## thetaC      1.0062408 0.01106024  90.9782 0.0000
## rhoC      -0.0102097 0.00323678 -3.1543 0.0017
## tmrcaC     0.0043865 0.00004812  91.1520 0.0000
## thetaC:tmrcaC 1.5757705 0.05403968 29.1595 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC    tmrcaC
## thetaC     -0.243
## rhoC      0.170 -0.643
## tmrcaC    -0.350  0.002 -0.396
## thetaC:tmrcaC -0.544  0.245 -0.301  0.648

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -2.2113836 -0.6525291 -0.1192687  0.7100956  5.1287732
## 
## Residual standard error: 8.453983e-06
## Degrees of freedom: 471 total; 466 residual
vif(g.div.50kb.3)

##          thetaC         rhoC        tmrcaC thetaC:tmrcaC
## 2.305163     2.465079    2.509466     2.033860

```

### 5.1.10 Replicate 10

```

rep_10.pi.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_5.dti")
rep_10.pi.50kb$avg <- apply(rep_10.pi.50kb[4:ncol(rep_10.pi.50kb)], 1, mean)
rep_10.rho.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_5.rti")
rep_10.theta.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_5.ti")
rep_10.tmrca.50kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_5.tmrca")
rep_10.tmrca.50kb$avg <- apply(rep_10.tmrca.50kb[4:ncol(rep_10.tmrca.50kb)], 1, mean)

inf.lands.50kb.rep10 <- as.data.frame(cbind(rep_10.pi.50kb$avg, rep_10.theta.50kb$sample_mean, rep_10.tmrca.50kb$avg))
names(inf.lands.50kb.rep10) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.50kb.rep10$thetaC <- inf.lands.50kb.rep10$theta - mean(inf.lands.50kb.rep10$theta)
inf.lands.50kb.rep10$tmrcaC <- inf.lands.50kb.rep10$tmrca - mean(inf.lands.50kb.rep10$tmrca)
inf.lands.50kb.rep10$rhoC <- inf.lands.50kb.rep10$rho - mean(inf.lands.50kb.rep10$rho)

inf.lands.50kb.rep10$bin <- 1:nrow(inf.lands.50kb.rep10)

# for merging:
inf.lands.50kb.rep10 <- inf.lands.50kb.rep10
inf.lands.50kb.rep10$Replicate <- 1

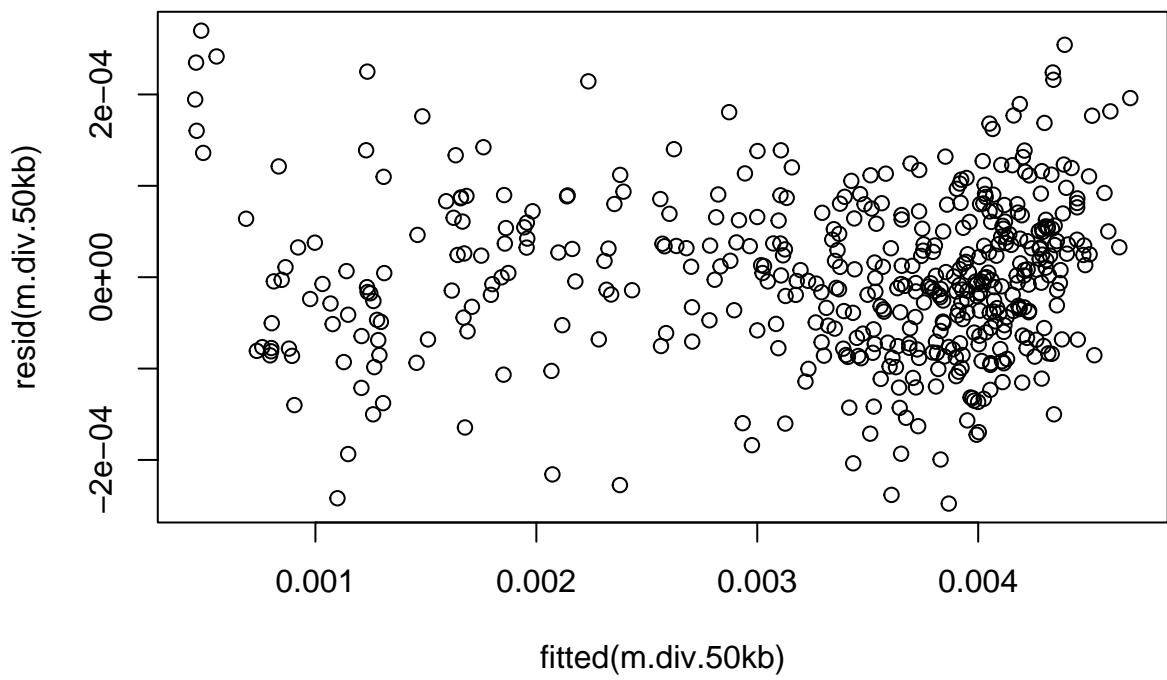
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.50kb.rep10)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.50kb.rep10)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.50kb.rep10)

AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

##          df      AIC
## m.div.50kb     6 -7460.959
## m.div.50kb.2   7 -7475.549
## m.div.50kb.3   8 -7483.607

plot(resid(m.div.50kb)~fitted(m.div.50kb))

```

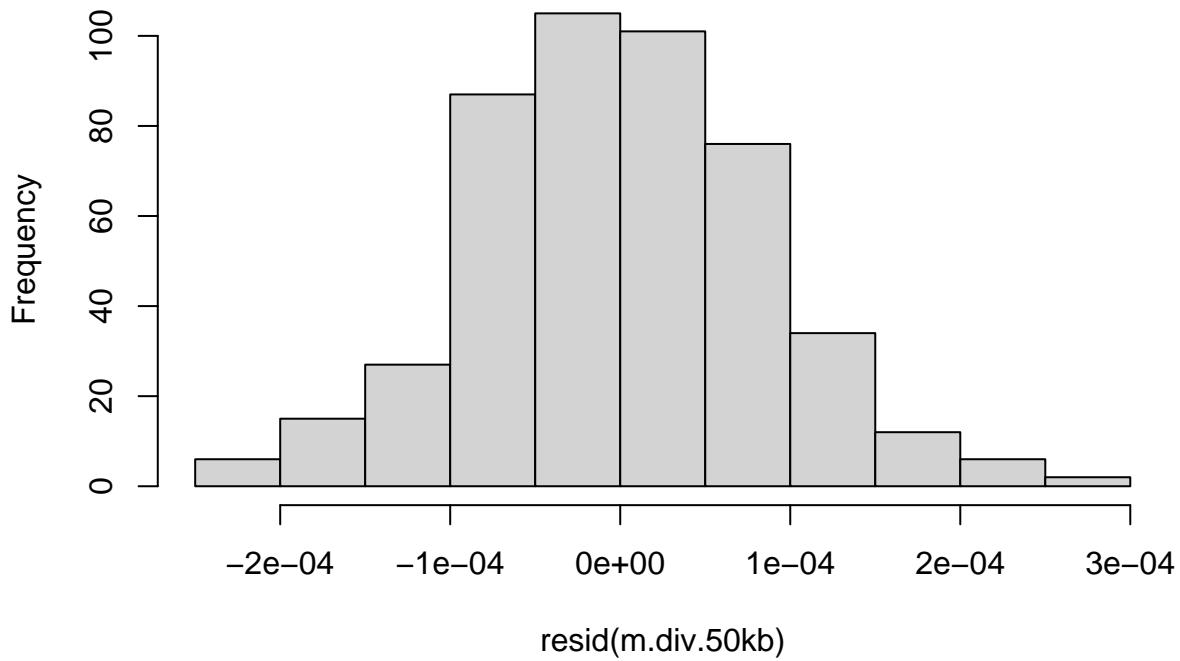


```
dwtest(m.div.50kb)
```

```
##
##  Durbin-Watson test
##
## data: m.div.50kb
## DW = 1.5178, p-value = 3.811e-08
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.50kb
## HMC = 0.53736, p-value = 0.886
hist(resid(m.div.50kb))
```

## Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.50kb.rep10)
##
## Residuals:
##       Min         1Q     Median        3Q       Max
## -2.478e-04 -6.053e-05 -2.924e-06  5.485e-05  2.698e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.198e-03 5.109e-06 625.860 <2e-16 ***
## thetaC      9.866e-01 8.927e-03 110.518 <2e-16 ***
## rhoC      -7.779e-03 2.350e-03 -3.311  0.001 **
## tmrcaC     4.495e-03 4.372e-05 102.823 <2e-16 ***
## thetaC:tmrcaC 1.665e+00 4.678e-02 35.582 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.725e-05 on 466 degrees of freedom
## Multiple R-squared:  0.9935, Adjusted R-squared:  0.9934
## F-statistic: 1.774e+04 on 4 and 466 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.50kb[1, 10] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.50kb[2, 10] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb[3, 10] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb[4, 10] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb[5, 10] <- anova.diversity$VarExp[4] * 100

g.div.50kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep10, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep10, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep10, weights = varPower(0, ~theta), method = "ML")
g.div.50kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.50kb.rep10, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.50kb.1, g.div.50kb.2, g.div.50kb.3, g.div.50kb.4)

##             df      AIC
## g.div.50kb.1 8 -7484.624
## g.div.50kb.2 8 -7485.078
## g.div.50kb.3 7 -7459.832
## g.div.50kb.4 7 -7459.998

summary(g.div.50kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep10
##          AIC      BIC    logLik
##        -7459.832 -7430.748 3736.916
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##     power
##     -0.1592648
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0031967 0.00000514 621.9328 0.0000
## thetaC       0.9849415 0.00928349 106.0960 0.0000
## rhoC        -0.0075689 0.00236213 -3.2043 0.0014
## tmrcaC       0.0045075 0.00004366 103.2465 0.0000
## thetaC:tmrcaC 1.6785292 0.04770442 35.1860 0.0000
##
## Correlation:
##           (Intr) thetaC rhoC   tmrcaC
## thetaC     -0.269
## rhoC       0.302 -0.536
## tmrcaC    -0.434 -0.104 -0.319
## thetaC:tmrcaC -0.623  0.370 -0.480  0.698

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -2.91439880 -0.70455045 -0.02126716  0.64062857  2.97141938
## 
## Residual standard error: 3.517815e-05
## Degrees of freedom: 471 total; 466 residual
vif(g.div.50kb.3)

```

```

##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
##      2.216705   1.751910    3.009599     3.171116

```

## 5.2 200 kb scale

```

r2.bgs.200kb <- as.data.frame(matrix(ncol = nreps, nrow = 5))
row.names(r2.bgs.200kb) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
colnames(r2.bgs.200kb) <- reps

sim.theta.200kb <- read.table("dm_bgs_sims/MutationMap_200kb.csv", header = T)
sim.rho.200kb <- read.table("dm_bgs_sims/RecombinationMap_200kb.csv", header = T)

```

### 5.2.1 Replicate 1

```

rep_1.pi.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.dive")
rep_1.pi.200kb$avg <- apply(rep_1.pi.200kb[4:ncol(rep_1.pi.200kb)], 1, mean)
rep_1.rho.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.rho")
rep_1.theta.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.theta")
rep_1.tmrca.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.TMRCA")
rep_1.tmrca.200kb$avg <- apply(rep_1.tmrca.200kb[4:ncol(rep_1.tmrca.200kb)], 1, mean)

inf.lands.200kb.rep1 <- as.data.frame(cbind(rep_1.pi.200kb$avg, rep_1.theta.200kb$sample_mean, rep_1.tmrca.200kb$avg))
names(inf.lands.200kb.rep1) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.200kb.rep1$thetaC <- inf.lands.200kb.rep1$theta - mean(inf.lands.200kb.rep1$theta)
inf.lands.200kb.rep1$tmrcaC <- inf.lands.200kb.rep1$tmrca - mean(inf.lands.200kb.rep1$tmrca)
inf.lands.200kb.rep1$rhoC <- inf.lands.200kb.rep1$rho - mean(inf.lands.200kb.rep1$rho)

inf.lands.200kb.rep1$bin <- 1:nrow(inf.lands.200kb.rep1)

# for merging:
inf.lands.200kb.rep1 <- inf.lands.200kb.rep1
inf.lands.200kb.rep1$Replicate <- 1

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.200kb.rep1)
m.div.200kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.200kb.rep1)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.200kb.rep1)

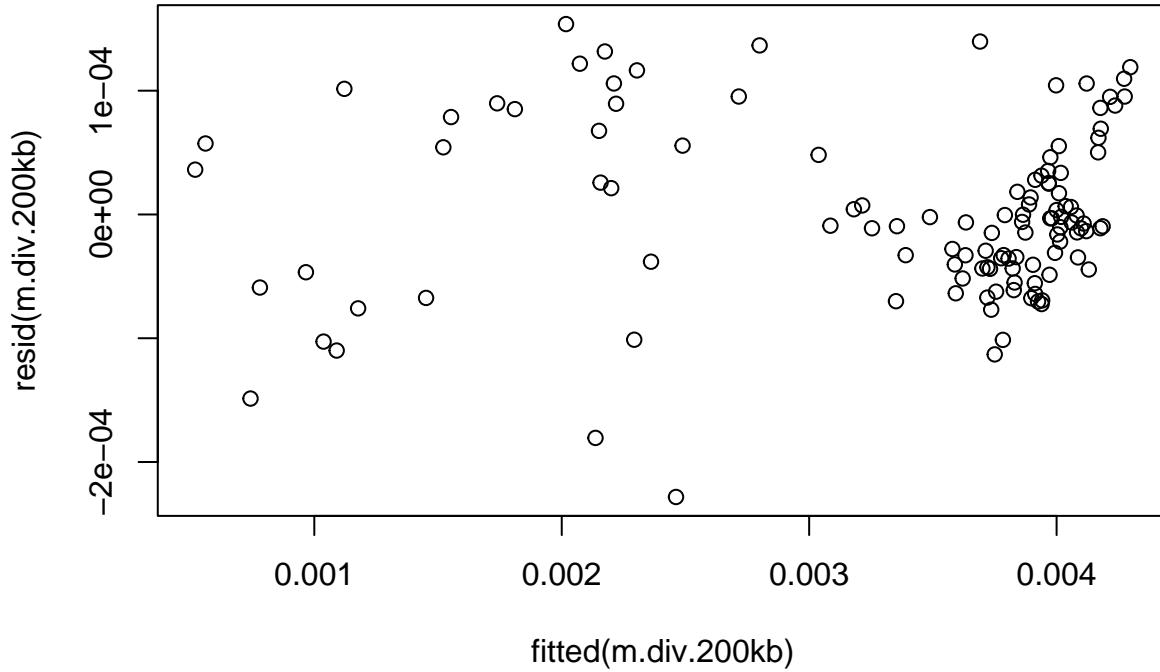
AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)

##          df      AIC
## m.div.200kb     6 -1914.977
## m.div.200kb.2   7 -1944.689

```

```
## m.div.200kb.3 8 -1949.080
```

```
plot(resid(m.div.200kb)~fitted(m.div.200kb))
```



```
dwttest(m.div.200kb)
```

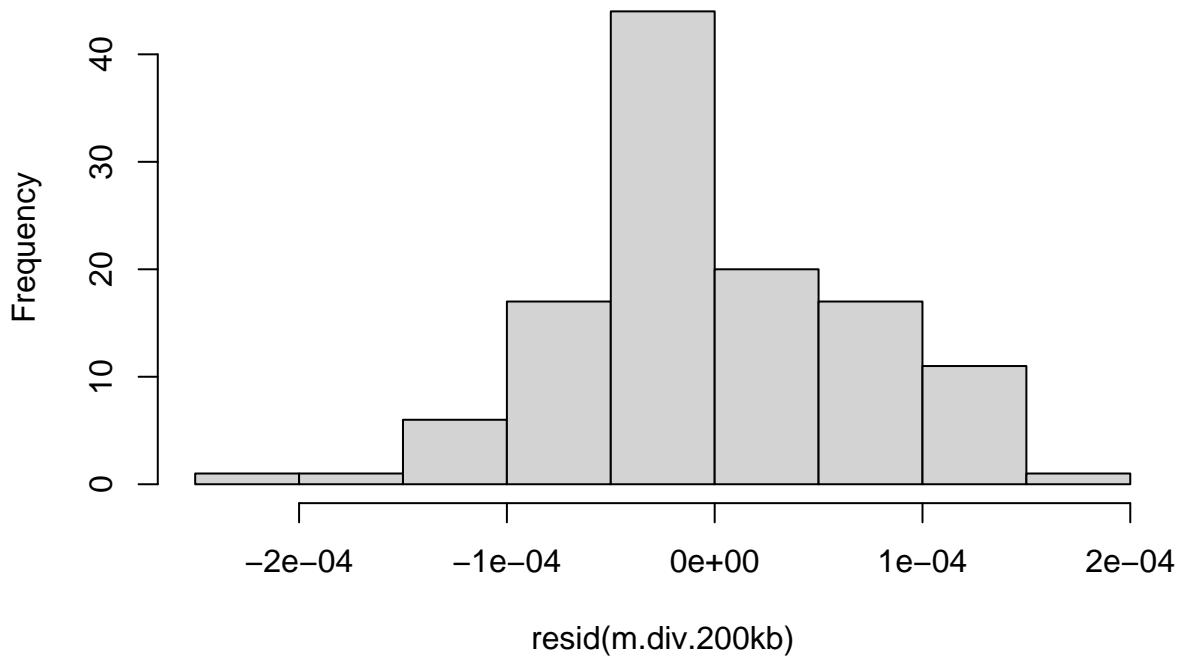
```
##  
## Durbin-Watson test  
##  
## data: m.div.200kb  
## DW = 1.2584, p-value = 1.066e-05  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmctest(m.div.200kb)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.div.200kb  
## HMC = 0.44852, p-value = 0.223
```

```
hist(resid(m.div.200kb))
```

## Histogram of resid(m.div.200kb)



```
summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.200kb.rep1)
##
## Residuals:
##       Min         1Q     Median         3Q        Max
## -2.283e-04 -4.365e-05 -6.902e-06  4.766e-05  1.538e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.281e-03 7.378e-06 444.748 <2e-16 ***
## thetaC      9.974e-01 9.968e-03 100.055 <2e-16 ***
## rhoC       -4.104e-03 3.993e-03 -1.028   0.306
## tmrcaC      4.264e-03 9.788e-05  43.569 <2e-16 ***
## thetaC:tmrcaC 1.296e+00 9.192e-02  14.098 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.032e-05 on 113 degrees of freedom
## Multiple R-squared:  0.9953, Adjusted R-squared:  0.9951
## F-statistic:  5984 on 4 and 113 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.200kb[1, 1] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.200kb[2, 1] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb[3, 1] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb[4, 1] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb[5, 1] <- anova.diversity$VarExp[4] * 100

g.div.200kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep1, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep1, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep1, weights = varPower(0, ~theta), method = "ML")
g.div.200kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep1, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.200kb.1, g.div.200kb.2, g.div.200kb.3, g.div.200kb.4)

##                 df      AIC
## g.div.200kb.1 8 -1929.159
## g.div.200kb.2 8 -1933.494
## g.div.200kb.3 7 -1926.365
## g.div.200kb.4 7 -1917.258

summary(g.div.200kb.3)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
## Data: inf.lands.200kb.rep1
##          AIC      BIC    logLik
## -1926.365 -1906.971 970.1827
##
## Variance function:
## Structure: Power of variance covariate
## Formula: ~theta
## Parameter estimates:
##       power
## -1.080861
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032885 0.00000834 394.2498 0.0000
## thetaC       0.9708036 0.01721523  56.3921 0.0000
## rhoC        0.0033041 0.00402510   0.8209 0.4134
## tmrcaC      0.0042215 0.00008753  48.2274 0.0000
## thetaC:tmrcaC 1.2036805 0.11732841 10.2591 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC     -0.639
## rhoC       0.349 -0.467
## tmrcaC    -0.180 -0.069 -0.485
## thetaC:tmrcaC -0.584  0.488 -0.484  0.339

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -2.99907520 -0.66401443 -0.03059178  0.50174113  2.54737837
## 
## Residual standard error: 1.462783e-07
## Degrees of freedom: 118 total; 113 residual
vif(g.div.200kb.3)

##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
## 1.831093 1.973108 1.688173    1.625769

```

## 5.2.2 Replicate 2

```

rep_2.pi.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.dive")
rep_2.pi.200kb$avg <- apply(rep_2.pi.200kb[4:ncol(rep_2.pi.200kb)], 1, mean)
rep_2.rho.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.rho")
rep_2.theta.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.theta")
rep_2.tmrca.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.tmrca")
rep_2.tmrca.200kb$avg <- apply(rep_2.tmrca.200kb[4:ncol(rep_2.tmrca.200kb)], 1, mean)

inf.lands.200kb.rep2 <- as.data.frame(cbind(rep_2.pi.200kb$avg, rep_2.theta.200kb$sample_mean, rep_2.tmrca.200kb$avg))
names(inf.lands.200kb.rep2) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.200kb.rep2$thetaC <- inf.lands.200kb.rep2$theta - mean(inf.lands.200kb.rep2$theta)
inf.lands.200kb.rep2$tmrcaC <- inf.lands.200kb.rep2$tmrca - mean(inf.lands.200kb.rep2$tmrca)
inf.lands.200kb.rep2$rhoC <- inf.lands.200kb.rep2$rho - mean(inf.lands.200kb.rep2$rho)

inf.lands.200kb.rep2$bin <- 1:nrow(inf.lands.200kb.rep2)

# for merging:
inf.lands.200kb.rep2 <- inf.lands.200kb.rep2
inf.lands.200kb.rep2$Replicate <- 1

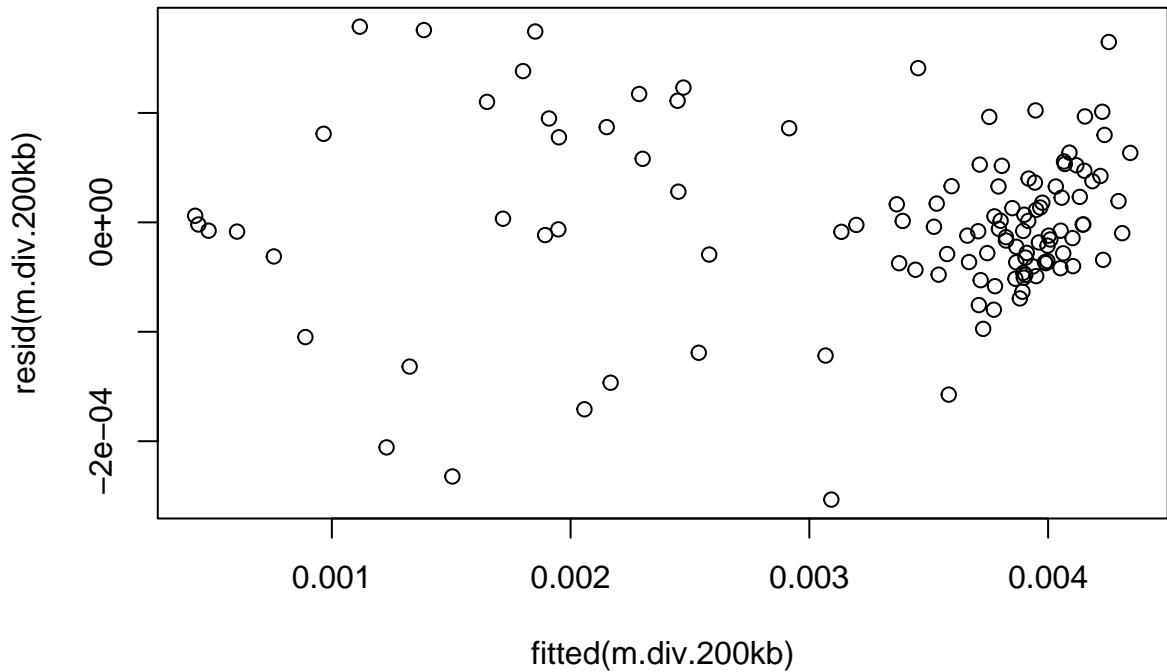
m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.200kb.rep2)
m.div.200kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.200kb.rep2)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.200kb.rep2)

AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)

##      df      AIC
## m.div.200kb     6 -1887.453
## m.div.200kb.2   7 -1919.176
## m.div.200kb.3   8 -1920.353

plot(resid(m.div.200kb)~fitted(m.div.200kb))

```

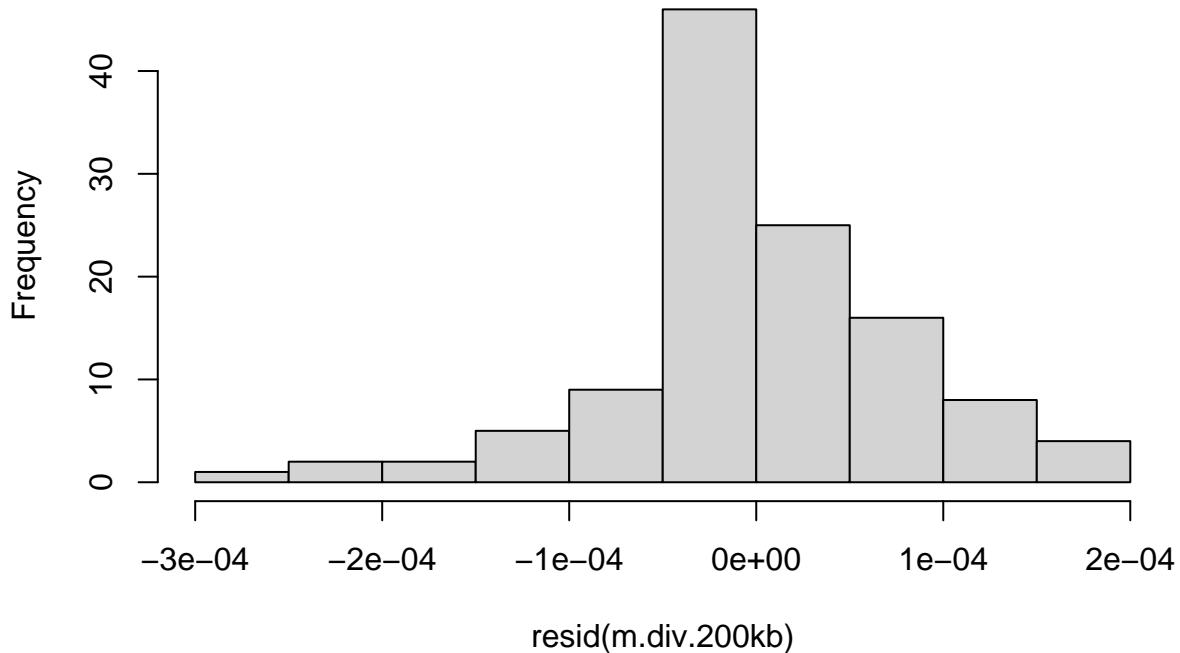


```
dwtest(m.div.200kb)
```

```
##
##  Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.063, p-value = 5.447e-08
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.49635, p-value = 0.495
hist(resid(m.div.200kb))
```

## Histogram of resid(m.div.200kb)



```
summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.200kb.rep2)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -2.533e-04 -3.652e-05 -6.176e-06  4.179e-05  1.788e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.262e-03 7.579e-06 430.439 <2e-16 ***
## thetaC      9.986e-01 8.965e-03 111.396 <2e-16 ***
## rhoC        8.743e-04 4.151e-03   0.211   0.834  
## tmrcaC      4.301e-03 1.082e-04  39.768 <2e-16 ***
## thetaC:tmrcaC 1.155e+00 8.152e-02  14.172 <2e-16 ***
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.902e-05 on 113 degrees of freedom
## Multiple R-squared:  0.9946, Adjusted R-squared:  0.9944 
## F-statistic:  5214 on 4 and 113 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.200kb[1, 2] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.200kb[2, 2] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb[3, 2] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb[4, 2] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb[5, 2] <- anova.diversity$VarExp[4] * 100

g.div.200kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep2, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep2, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep2, weights = varPower(0, ~theta), method = "ML")
g.div.200kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep2, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.200kb.1, g.div.200kb.2, g.div.200kb.3, g.div.200kb.4)

##                 df      AIC
## g.div.200kb.1  8 -1917.295
## g.div.200kb.2  8 -1916.677
## g.div.200kb.3  7 -1903.456
## g.div.200kb.4  7 -1896.019

summary(g.div.200kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.200kb.rep2
##          AIC      BIC    logLik
##        -1903.456 -1884.061 958.7279
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##     power
##     -1.085434
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032643 0.00000853 382.8006 0.0000
## thetaC       0.9899751 0.01622286  61.0235 0.0000
## rhoC        0.0069842 0.00405325   1.7231 0.0876
## tmrcaC      0.0042272 0.00009516  44.4238 0.0000
## thetaC:tmrcaC 1.1253916 0.11680302   9.6350 0.0000
##
## Correlation:
##           (Intr) thetaC rhoC   tmrcaC
## thetaC     -0.654
## rhoC       0.247 -0.385
## tmrcaC    -0.083 -0.021 -0.561
## thetaC:tmrcaC -0.395  0.329 -0.409  0.237

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -3.51891730 -0.57824590 -0.03723372  0.70670288  2.40975217
## 
## Residual standard error: 1.488727e-07
## Degrees of freedom: 118 total; 113 residual
vif(g.div.200kb.3)

##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
## 1.363138 1.985520 1.622713    1.260591

```

### 5.2.3 Replicate 3

```

rep_3.pi.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.dive")
rep_3.pi.200kb$avg <- apply(rep_3.pi.200kb[4:ncol(rep_3.pi.200kb)], 1, mean)
rep_3.rho.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.rho")
rep_3.theta.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.theta")
rep_3.tmrca.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.TMRCA")
rep_3.tmrca.200kb$avg <- apply(rep_3.tmrca.200kb[4:ncol(rep_3.tmrca.200kb)], 1, mean)

inf.lands.200kb.rep3 <- as.data.frame(cbind(rep_3.pi.200kb$avg, rep_3.theta.200kb$sample_mean, rep_3.tmrca.200kb$avg))
names(inf.lands.200kb.rep3) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.200kb.rep3$thetaC <- inf.lands.200kb.rep3$theta - mean(inf.lands.200kb.rep3$theta)
inf.lands.200kb.rep3$tmrcaC <- inf.lands.200kb.rep3$tmrca - mean(inf.lands.200kb.rep3$tmrca)
inf.lands.200kb.rep3$rhoC <- inf.lands.200kb.rep3$rho - mean(inf.lands.200kb.rep3$rho)

inf.lands.200kb.rep3$bin <- 1:nrow(inf.lands.200kb.rep3)

# for merging:
inf.lands.200kb.rep3 <- inf.lands.200kb.rep3
inf.lands.200kb.rep3$Replicate <- 1

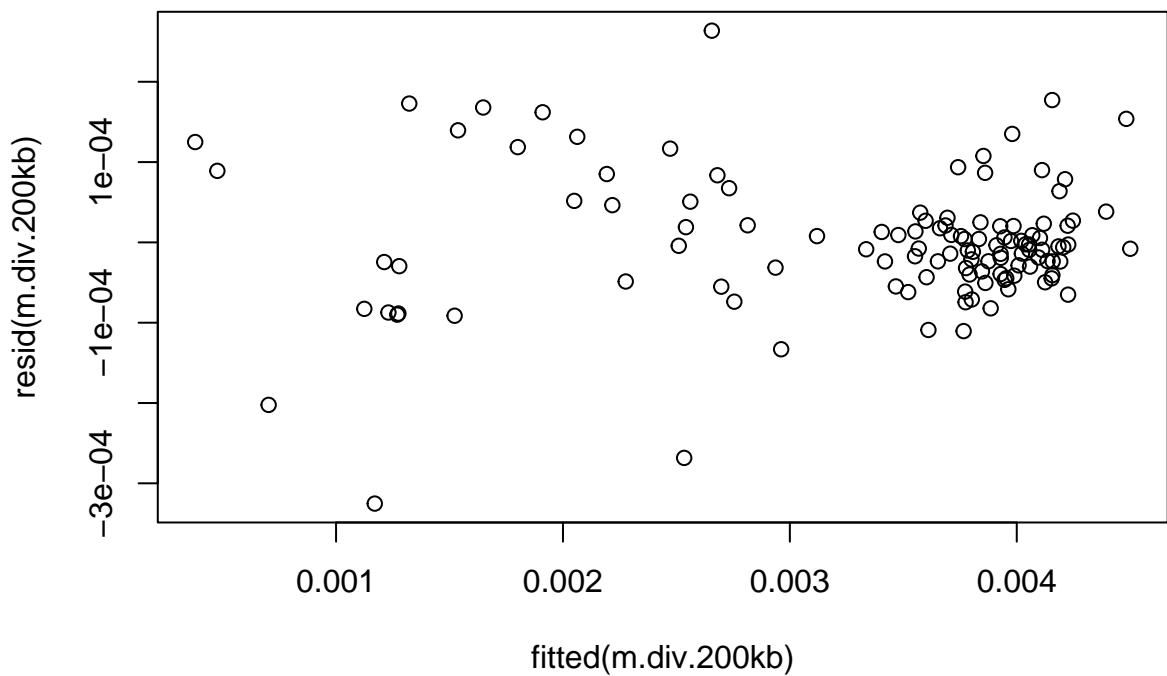
m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.200kb.rep3)
m.div.200kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.200kb.rep3)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.200kb.rep3)

AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)

##      df      AIC
## m.div.200kb     6 -1876.293
## m.div.200kb.2   7 -1898.010
## m.div.200kb.3   8 -1902.143

plot(resid(m.div.200kb)~fitted(m.div.200kb))

```

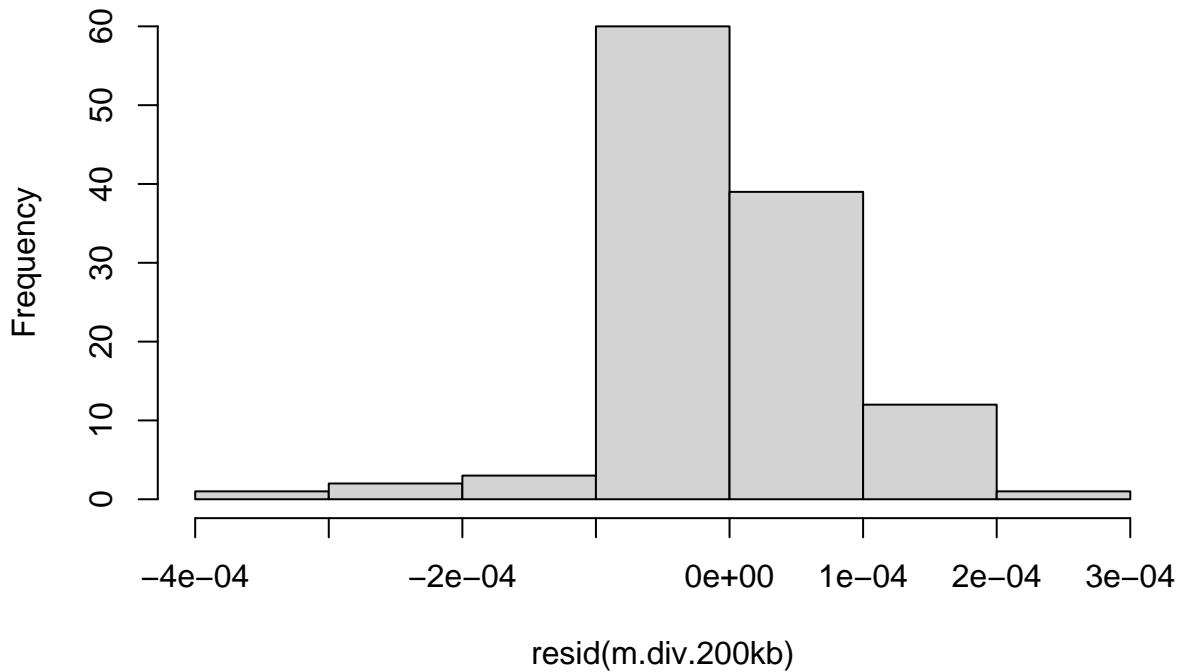


```
dwtest(m.div.200kb)
```

```
##
##  Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.1111, p-value = 1.783e-07
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.46233, p-value = 0.294
hist(resid(m.div.200kb))
```

## Histogram of resid(m.div.200kb)



```
summary(m.div.200kb)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.200kb.rep3)
##
## Residuals:
##      Min        1Q    Median        3Q       Max
## -3.252e-04 -4.059e-05 -6.880e-06  2.642e-05  2.636e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.242e-03 9.601e-06 337.658 < 2e-16 ***
## thetaC      9.685e-01 1.825e-02  53.057 < 2e-16 ***
## rhoC       -2.030e-02 5.679e-03 -3.575 0.000517 ***
## tmrcaC      4.991e-03 1.229e-04  40.605 < 2e-16 ***
## thetaC:tmrcaC 1.520e+00 9.968e-02  15.248 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.285e-05 on 113 degrees of freedom
## Multiple R-squared:  0.9935, Adjusted R-squared:  0.9932
## F-statistic:  4302 on 4 and 113 DF,  p-value: < 2.2e-16
anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
```

```
r2.bgs.200kb[1, 3] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.200kb[2, 3] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb[3, 3] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb[4, 3] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb[5, 3] <- anova.diversity$VarExp[4] * 100

g.div.200kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep3, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")

g.div.200kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep3, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")

g.div.200kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep3, weights = varPower(0, ~theta), method = "ML")

g.div.200kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep3, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.200kb.1, g.div.200kb.2, g.div.200kb.3, g.div.200kb.4)

```

```

##             df      AIC
## g.div.200kb.1 8 -1922.374
## g.div.200kb.2 8 -1930.481
## g.div.200kb.3 7 -1924.104
## g.div.200kb.4 7 -1894.752

summary(g.div.200kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.200kb.rep3
##          AIC      BIC    logLik
##        -1924.104 -1904.709 969.0518
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
## Parameter estimates:
##   power
## -2.126211
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032622 0.00001028 317.2138 0.0000
## thetaC       0.9224921 0.02375101  38.8401 0.0000
## rhoC        0.0027288 0.00490482   0.5564 0.5791
## tmrcaC      0.0046998 0.00010351  45.4062 0.0000
## thetaC:tmrcaC 1.1347165 0.14316037    7.9262 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC     -0.743
## rhoC       0.398 -0.416
## tmrcaC    -0.206 -0.122 -0.565
## thetaC:tmrcaC -0.646  0.503 -0.522  0.260

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -2.50460278 -0.67087750 -0.06109084  0.52042110  4.19078904
## 
## Residual standard error: 4.250353e-10
## Degrees of freedom: 118 total; 113 residual
vif(g.div.200kb.3)

##          thetaC        rhoC        tmrcaC thetaC:tmrcaC
##      1.848355    2.367957    1.945836    1.628937

```

## 5.2.4 Replicate 4

```

rep_4.pi.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.dive")
rep_4.pi.200kb$avg <- apply(rep_4.pi.200kb[4:ncol(rep_4.pi.200kb)], 1, mean)
rep_4.rho.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.rho")
rep_4.theta.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.theta")
rep_4.tmrca.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.tmrca")
rep_4.tmrca.200kb$avg <- apply(rep_4.tmrca.200kb[4:ncol(rep_4.tmrca.200kb)], 1, mean)

inf.lands.200kb.rep4 <- as.data.frame(cbind(rep_4.pi.200kb$avg, rep_4.theta.200kb$sample_mean, rep_4.tmrca.200kb$avg))
names(inf.lands.200kb.rep4) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.200kb.rep4$thetaC <- inf.lands.200kb.rep4$theta - mean(inf.lands.200kb.rep4$theta)
inf.lands.200kb.rep4$tmrcaC <- inf.lands.200kb.rep4$tmrca - mean(inf.lands.200kb.rep4$tmrca)
inf.lands.200kb.rep4$rhoC <- inf.lands.200kb.rep4$rho - mean(inf.lands.200kb.rep4$rho)

inf.lands.200kb.rep4$bin <- 1:nrow(inf.lands.200kb.rep4)

# for merging:
inf.lands.200kb.rep4 <- inf.lands.200kb.rep4
inf.lands.200kb.rep4$Replicate <- 1

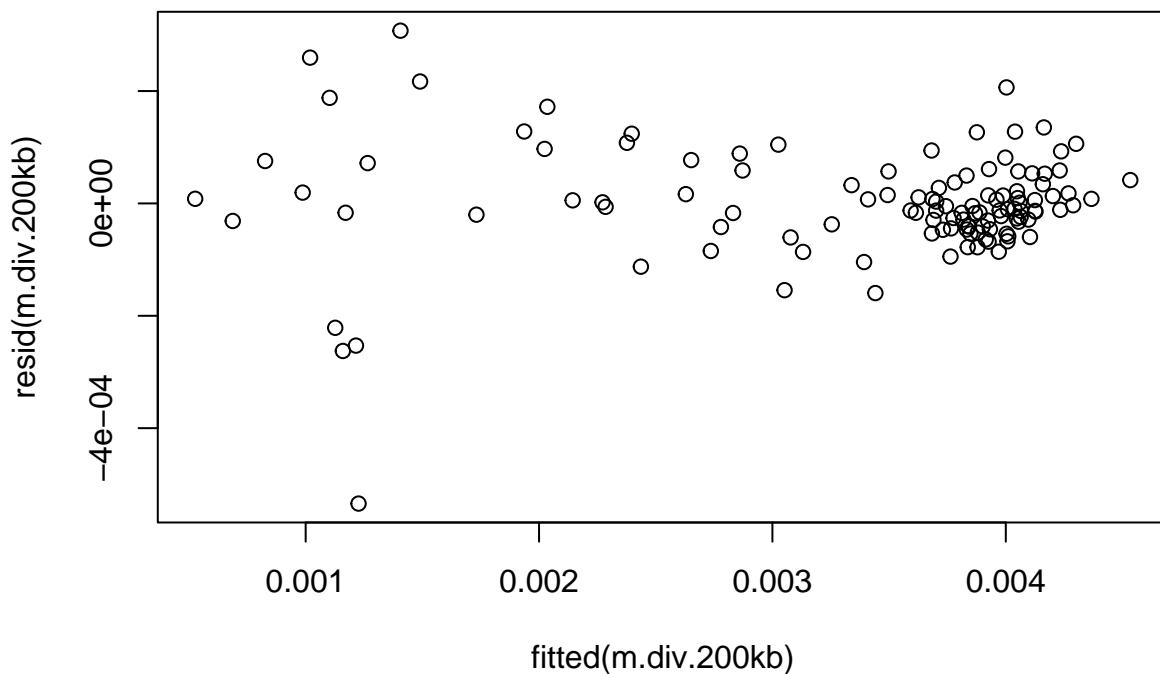
m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.200kb.rep4)
m.div.200kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.200kb.rep4)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.200kb.rep4)

AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)

##          df      AIC
## m.div.200kb     6 -1827.605
## m.div.200kb.2   7 -1873.540
## m.div.200kb.3   8 -1871.569

plot(resid(m.div.200kb)~fitted(m.div.200kb))

```

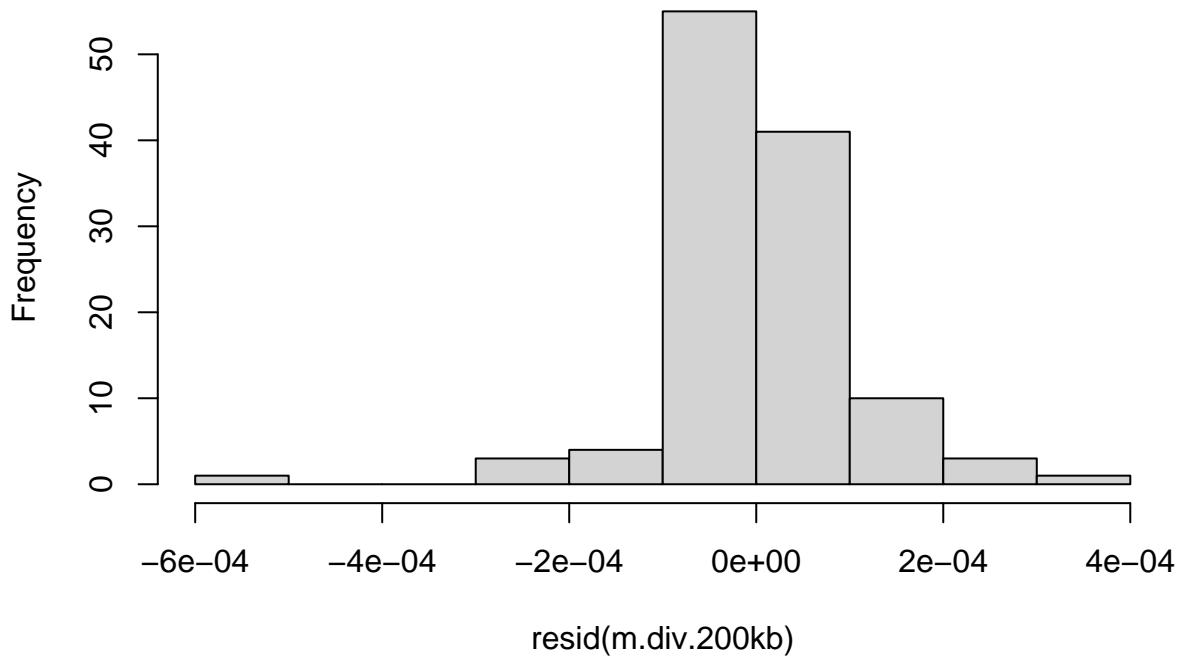


```
dwtest(m.div.200kb)
```

```
##
##  Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.3604, p-value = 0.0001091
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.2301, p-value < 2.2e-16
hist(resid(m.div.200kb))
```

## Histogram of resid(m.div.200kb)



```
summary(m.div.200kb)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.200kb.rep4)
##
## Residuals:
##      Min        1Q    Median        3Q       Max
## -5.342e-04 -4.098e-05 -7.900e-06  4.752e-05  3.074e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.276e-03 1.143e-05 286.660 < 2e-16 ***
## thetaC      1.045e+00 1.761e-02  59.334 < 2e-16 ***
## rhoC       -2.233e-02 5.132e-03 -4.350 2.99e-05 ***
## tmrcaC      5.026e-03 1.709e-04  29.414 < 2e-16 ***
## thetaC:tmrcaC 1.339e+00 1.551e-01   8.634 4.35e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0001018 on 113 degrees of freedom
## Multiple R-squared:  0.9904, Adjusted R-squared:  0.9901
## F-statistic: 2915 on 4 and 113 DF,  p-value: < 2.2e-16
anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
```

```
r2.bgs.200kb[1, 4] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.200kb[2, 4] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb[3, 4] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb[4, 4] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb[5, 4] <- anova.diversity$VarExp[4] * 100

g.div.200kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep4, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep4, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep4, weights = varPower(0, ~theta), method = "ML")
g.div.200kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep4, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.200kb.1, g.div.200kb.2, g.div.200kb.3, g.div.200kb.4)

##                 df      AIC
## g.div.200kb.1 8 -1855.917
## g.div.200kb.2 8 -1925.934
## g.div.200kb.3 7 -1927.927
## g.div.200kb.4 7 -1847.741

summary(g.div.200kb.3)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
## Data: inf.lands.200kb.rep4
##          AIC      BIC    logLik
## -1927.927 -1908.532 970.9635
##
## Variance function:
## Structure: Power of variance covariate
## Formula: ~theta
## Parameter estimates:
##       power
## -2.669007
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032818 0.00001095 299.72122 0.0000
## thetaC      1.0207123 0.02542774  40.14169 0.0000
## rhoC      -0.0009231 0.00320329 -0.28818 0.7737
## tmrcaC     0.0047770 0.00010882  43.89864 0.0000
## thetaC:tmrcaC 1.2979389 0.18863144   6.88082 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC     -0.848
## rhoC      0.274 -0.302
## tmrcaC    0.155 -0.357 -0.311
## thetaC:tmrcaC -0.544  0.455 -0.271 -0.311

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -2.02838223 -0.65770633 -0.02151832  0.58911537  2.66454244
## 
## Residual standard error: 1.912967e-11
## Degrees of freedom: 118 total; 113 residual
vif(g.div.200kb.3)

```

```

##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
## 1.554579 1.528687 1.603813    1.410626

```

### 5.2.5 Replicate 5

```

rep_5.pi.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.dive")
rep_5.pi.200kb$avg <- apply(rep_5.pi.200kb[4:ncol(rep_5.pi.200kb)], 1, mean)
rep_5.rho.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.rho")
rep_5.theta.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.theta")
rep_5.tmrca.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.tmrca")
rep_5.tmrca.200kb$avg <- apply(rep_5.tmrca.200kb[4:ncol(rep_5.tmrca.200kb)], 1, mean)

inf.lands.200kb.rep5 <- as.data.frame(cbind(rep_5.pi.200kb$avg, rep_5.theta.200kb$sample_mean, rep_5.tmrca.200kb$avg))
names(inf.lands.200kb.rep5) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.200kb.rep5$thetaC <- inf.lands.200kb.rep5$theta - mean(inf.lands.200kb.rep5$theta)
inf.lands.200kb.rep5$tmrcaC <- inf.lands.200kb.rep5$tmrca - mean(inf.lands.200kb.rep5$tmrca)
inf.lands.200kb.rep5$rhoC <- inf.lands.200kb.rep5$rho - mean(inf.lands.200kb.rep5$rho)

inf.lands.200kb.rep5$bin <- 1:nrow(inf.lands.200kb.rep5)

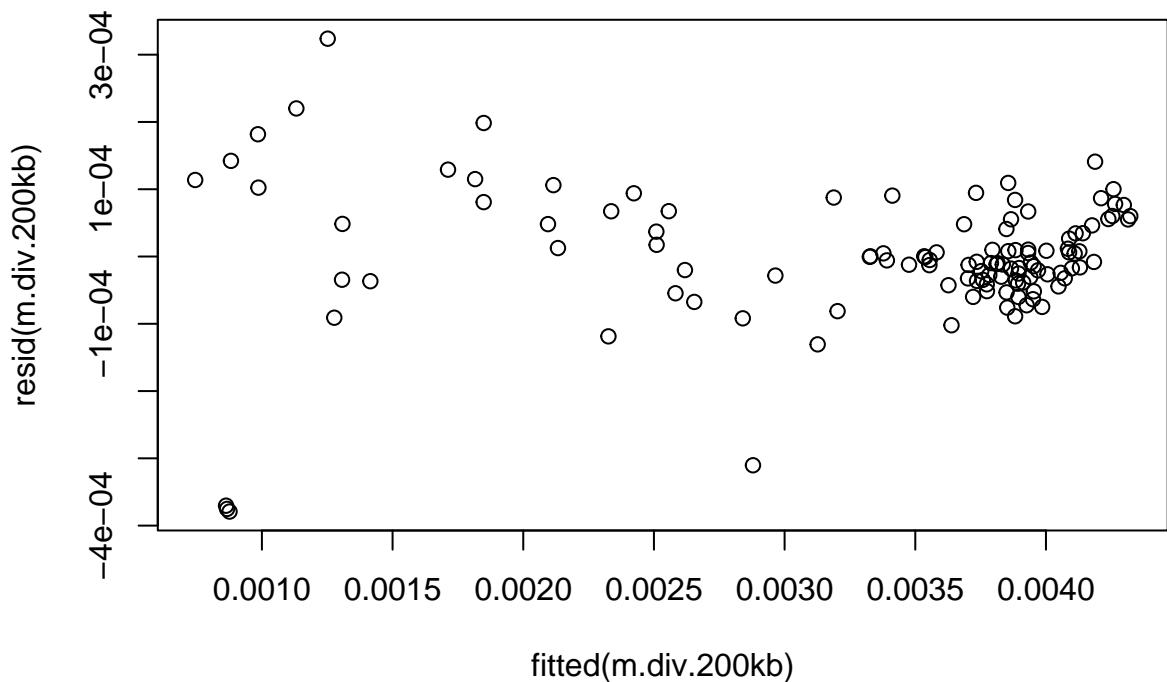
# for merging:
inf.lands.200kb.rep5 <- inf.lands.200kb.rep5
inf.lands.200kb.rep5$Replicate <- 1

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.200kb.rep5)
m.div.200kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.200kb.rep5)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.200kb.rep5)

AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)

##      df      AIC
## m.div.200kb     6 -1832.288
## m.div.200kb.2   7 -1908.006
## m.div.200kb.3   8 -1906.692
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```

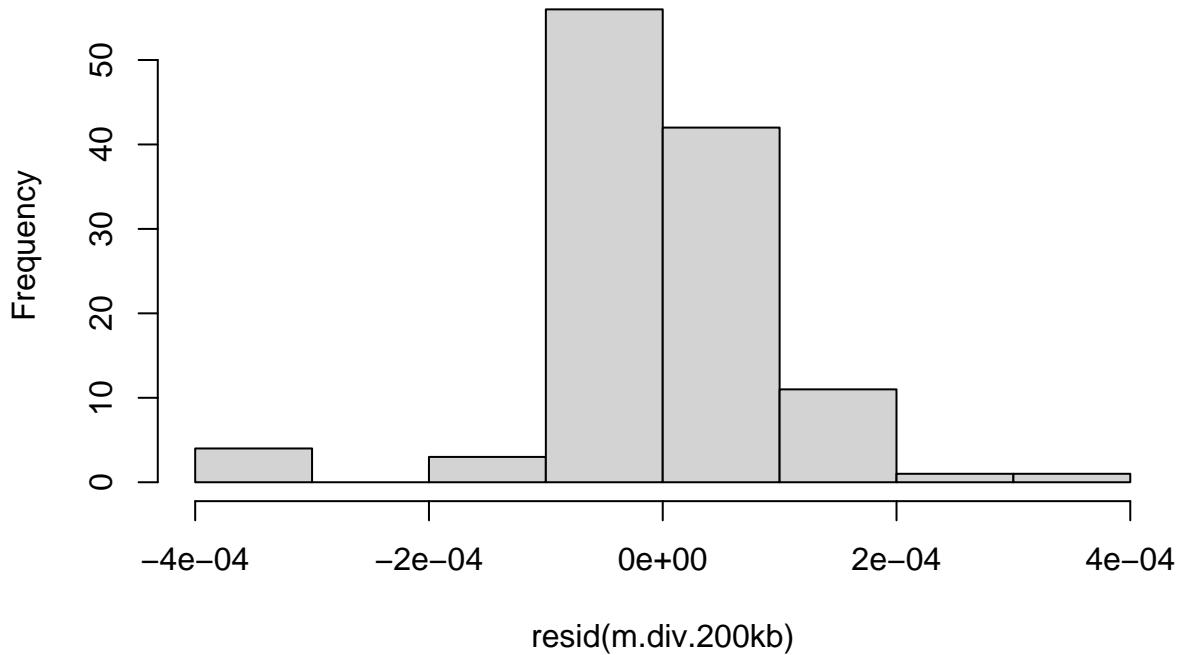


```
dwtest(m.div.200kb)
```

```
##
##  Durbin-Watson test
##
##  data: m.div.200kb
##  DW = 0.92809, p-value = 6.318e-10
##  alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb)
```

```
##
##  Harrison-McCabe test
##
##  data: m.div.200kb
##  HMC = 0.11675, p-value < 2.2e-16
hist(resid(m.div.200kb))
```

## Histogram of resid(m.div.200kb)



```
summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.200kb.rep5)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -3.791e-04 -3.534e-05 -6.800e-06  5.343e-05  3.238e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.283e-03 1.059e-05 310.058 < 2e-16 ***
## thetaC      9.887e-01 1.432e-02  69.023 < 2e-16 ***
## rhoC       -1.473e-02 5.029e-03 -2.928  0.00413 ** 
## tmrcaC      4.787e-03 1.789e-04  26.750 < 2e-16 ***
## thetaC:tmrcaC 8.767e-01 1.750e-01   5.009 2.04e-06 ***
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.983e-05 on 113 degrees of freedom
## Multiple R-squared:  0.9905, Adjusted R-squared:  0.9902 
## F-statistic: 2954 on 4 and 113 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.200kb[1, 5] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.200kb[2, 5] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb[3, 5] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb[4, 5] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb[5, 5] <- anova.diversity$VarExp[4] * 100

g.div.200kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep5, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep5, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep5, weights = varPower(0, ~theta), method = "ML")
g.div.200kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep5, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.200kb.1, g.div.200kb.2, g.div.200kb.3, g.div.200kb.4)

##                 df      AIC
## g.div.200kb.1 8 -1904.235
## g.div.200kb.2 8 -1966.271
## g.div.200kb.3 7 -1957.545
## g.div.200kb.4 7 -1877.048

summary(g.div.200kb.3)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
## Data: inf.lands.200kb.rep5
##          AIC      BIC   logLik
## -1957.545 -1938.15 985.7726
##
## Variance function:
## Structure: Power of variance covariate
## Formula: ~theta
## Parameter estimates:
##       power
## -2.391887
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032774 0.00001096 299.03645 0.0000
## thetaC       0.9895543 0.02287693  43.25556 0.0000
## rhoC        0.0066653 0.00365417   1.82403 0.0708
## tmrcaC      0.0042963 0.00012657  33.94444 0.0000
## thetaC:tmrcaC 1.5492412 0.25844201   5.99454 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC     -0.904
## rhoC       0.342 -0.341
## tmrcaC    0.348 -0.416 -0.313
## thetaC:tmrcaC -0.627  0.574 -0.266 -0.618

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -2.51067986 -0.72940766 -0.08537948  0.66721967  2.52110876
## 
## Residual standard error: 7.541972e-11
## Degrees of freedom: 118 total; 113 residual
vif(g.div.200kb.3)

##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
## 1.770022 2.101209 3.007245    2.679306

```

## 5.2.6 Replicate 6

```

rep_6.pi.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.dive")
rep_6.pi.200kb$avg <- apply(rep_6.pi.200kb[4:ncol(rep_6.pi.200kb)], 1, mean)
rep_6.rho.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.rho")
rep_6.theta.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.theta")
rep_6.tmrca.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.tmrca")
rep_6.tmrca.200kb$avg <- apply(rep_6.tmrca.200kb[4:ncol(rep_6.tmrca.200kb)], 1, mean)

inf.lands.200kb.rep6 <- as.data.frame(cbind(rep_6.pi.200kb$avg, rep_6.theta.200kb$sample_mean, rep_6.tmrca.200kb$avg))
names(inf.lands.200kb.rep6) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.200kb.rep6$thetaC <- inf.lands.200kb.rep6$theta - mean(inf.lands.200kb.rep6$theta)
inf.lands.200kb.rep6$tmrcaC <- inf.lands.200kb.rep6$tmrca - mean(inf.lands.200kb.rep6$tmrca)
inf.lands.200kb.rep6$rhoC <- inf.lands.200kb.rep6$rho - mean(inf.lands.200kb.rep6$rho)

inf.lands.200kb.rep6$bin <- 1:nrow(inf.lands.200kb.rep6)

# for merging:
inf.lands.200kb.rep6 <- inf.lands.200kb.rep6
inf.lands.200kb.rep6$Replicate <- 1

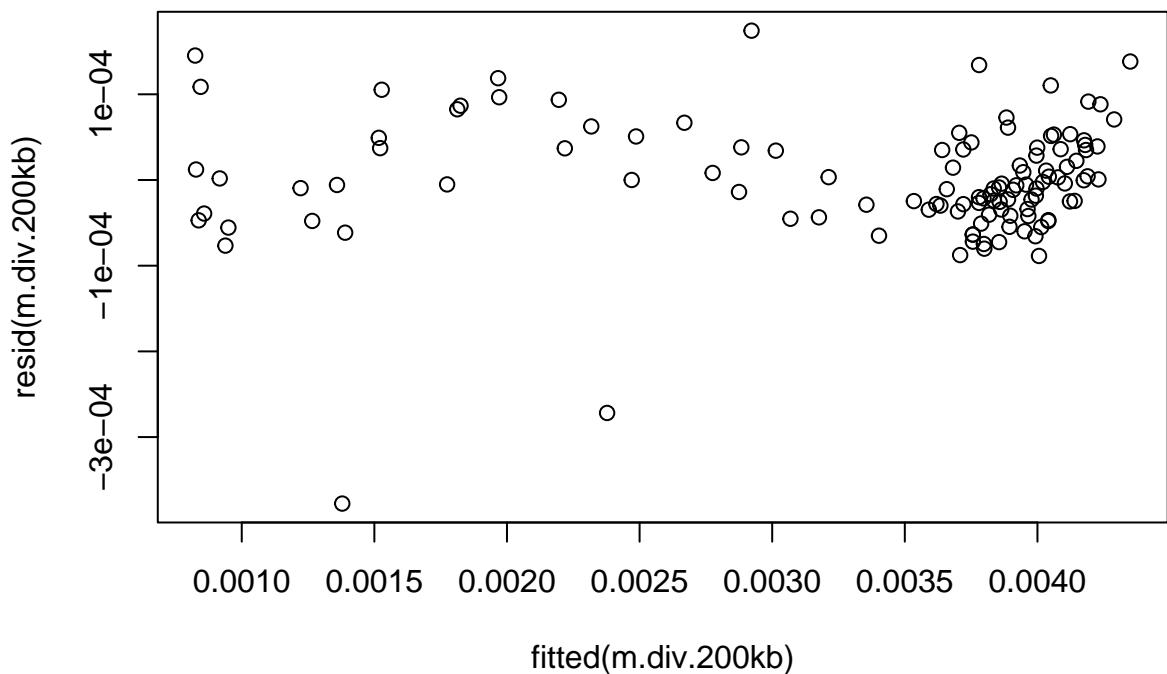
m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.200kb.rep6)
m.div.200kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.200kb.rep6)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.200kb.rep6)

AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)

##      df      AIC
## m.div.200kb     6 -1911.034
## m.div.200kb.2   7 -1936.062
## m.div.200kb.3   8 -1935.098

plot(resid(m.div.200kb)~fitted(m.div.200kb))

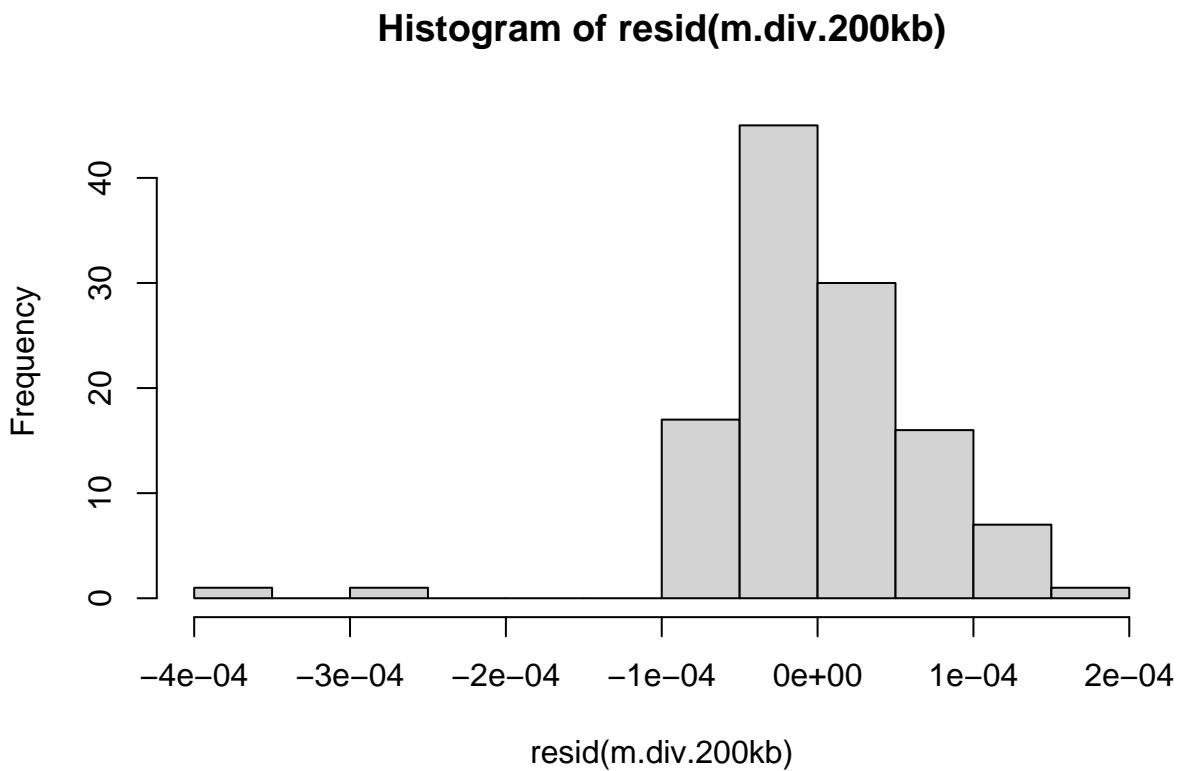
```



```
dwtest(m.div.200kb)
```

```
##
##  Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.5065, p-value = 0.001877
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.3467, p-value = 0.013
hist(resid(m.div.200kb))
```



```

summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.200kb.rep6)
##
## Residuals:
##       Min        1Q     Median        3Q       Max
## -3.776e-04 -3.617e-05 -5.260e-06  3.802e-05  1.743e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.232e-03 8.240e-06 392.222 <2e-16 ***
## thetaC       9.288e-01 1.516e-02   61.272 <2e-16 ***
## rhoC         4.115e-04 3.911e-03    0.105   0.916  
## tmrcaC       4.368e-03 6.441e-05   67.810 <2e-16 ***
## thetaC:tmrcaC 1.264e+00 8.898e-02   14.208 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Residual standard error: 7.151e-05 on 113 degrees of freedom
## Multiple R-squared:  0.9955, Adjusted R-squared:  0.9953 
## F-statistic:  6262 on 4 and 113 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.200kb[1, 6] <- (anova.diversity$VarExp[1] + anova.diversit

```

```

r2.bgs.200kb[2, 6] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb[3, 6] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb[4, 6] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb[5, 6] <- anova.diversity$VarExp[4] * 100

g.div.200kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep6, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep6, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep6, weights = varPower(0, ~theta), method = "ML")
g.div.200kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep6, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.200kb.1, g.div.200kb.2, g.div.200kb.3, g.div.200kb.4)

##                 df      AIC
## g.div.200kb.1 8 -1920.492
## g.div.200kb.2 8 -1940.555
## g.div.200kb.3 7 -1936.838
## g.div.200kb.4 7 -1914.435

summary(g.div.200kb.3)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
## Data: inf.lands.200kb.rep6
##          AIC      BIC   logLik
## -1936.838 -1917.444 975.4192
##
## Variance function:
## Structure: Power of variance covariate
## Formula: ~theta
## Parameter estimates:
##       power
## -1.630375
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032306 0.00000894 361.3092 0.0000
## thetaC       0.9172863 0.02050378  44.7374 0.0000
## rhoC        0.0022991 0.00298926   0.7691 0.4434
## tmrcaC      0.0043875 0.00005702  76.9426 0.0000
## thetaC:tmrcaC 1.3282349 0.11467784  11.5823 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC     -0.665
## rhoC       0.227 -0.361
## tmrcaC    -0.112 -0.204 -0.404
## thetaC:tmrcaC -0.650  0.440 -0.318  0.249

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -3.6868115 -0.5651622 -0.1157522  0.6510378  3.6401674
## 
## Residual standard error: 6.533835e-09
## Degrees of freedom: 118 total; 113 residual
vif(g.div.200kb.3)

##          thetaC        rhoC        tmrcaC thetaC:tmrcaC
##      1.776494     1.583826     1.627773     1.457581

```

### 5.2.7 Replicate 7

```

rep_7.pi.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.dive")
rep_7.pi.200kb$avg <- apply(rep_7.pi.200kb[4:ncol(rep_7.pi.200kb)], 1, mean)
rep_7.rho.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.rho")
rep_7.theta.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.theta")
rep_7.tmrca.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.TMRCA")
rep_7.tmrca.200kb$avg <- apply(rep_7.tmrca.200kb[4:ncol(rep_7.tmrca.200kb)], 1, mean)

inf.lands.200kb.rep7 <- as.data.frame(cbind(rep_7.pi.200kb$avg, rep_7.theta.200kb$sample_mean, rep_7.tmrca.200kb$avg))
names(inf.lands.200kb.rep7) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.200kb.rep7$thetaC <- inf.lands.200kb.rep7$theta - mean(inf.lands.200kb.rep7$theta)
inf.lands.200kb.rep7$tmrcaC <- inf.lands.200kb.rep7$tmrca - mean(inf.lands.200kb.rep7$tmrca)
inf.lands.200kb.rep7$rhoC <- inf.lands.200kb.rep7$rho - mean(inf.lands.200kb.rep7$rho)

inf.lands.200kb.rep7$bin <- 1:nrow(inf.lands.200kb.rep7)

# for merging:
inf.lands.200kb.rep7 <- inf.lands.200kb.rep7
inf.lands.200kb.rep7$Replicate <- 1

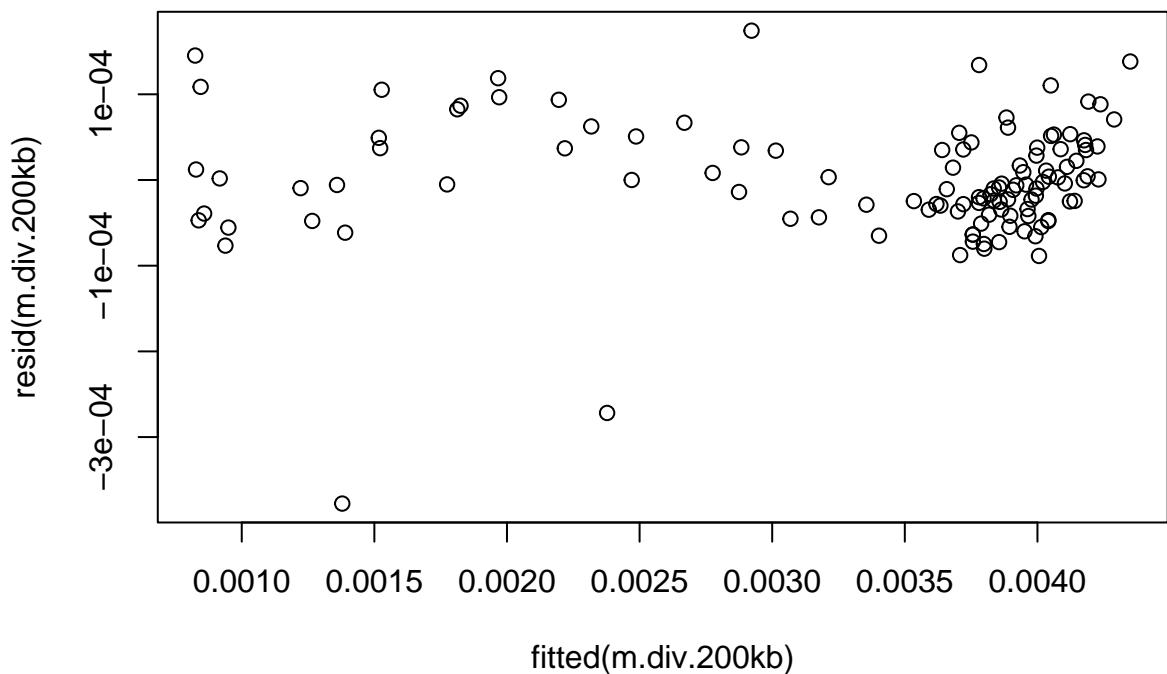
m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.200kb.rep7)
m.div.200kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.200kb.rep7)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.200kb.rep7)

AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)

##          df      AIC
## m.div.200kb     6 -1911.034
## m.div.200kb.2   7 -1936.062
## m.div.200kb.3   8 -1935.098

plot(resid(m.div.200kb)~fitted(m.div.200kb))

```

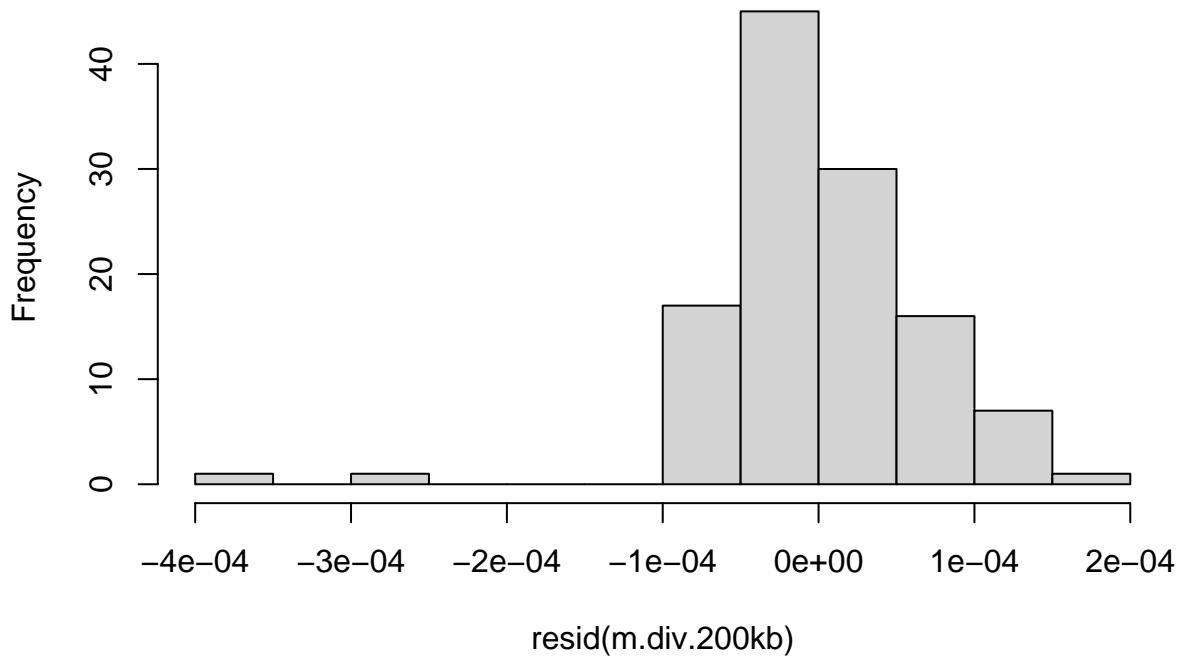


```
dwtest(m.div.200kb)
```

```
##
##  Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.5065, p-value = 0.001877
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.3467, p-value = 0.005
hist(resid(m.div.200kb))
```

## Histogram of resid(m.div.200kb)



```
summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.200kb.rep7)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -3.776e-04 -3.617e-05 -5.260e-06  3.802e-05  1.743e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.232e-03 8.240e-06 392.222 <2e-16 ***
## thetaC      9.288e-01 1.516e-02  61.272 <2e-16 ***
## rhoC        4.115e-04 3.911e-03   0.105   0.916  
## tmrcaC      4.368e-03 6.441e-05  67.810 <2e-16 ***
## thetaC:tmrcaC 1.264e+00 8.898e-02  14.208 <2e-16 ***
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 7.151e-05 on 113 degrees of freedom
## Multiple R-squared:  0.9955, Adjusted R-squared:  0.9953 
## F-statistic: 6262 on 4 and 113 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.200kb[1, 7] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.200kb[2, 7] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb[3, 7] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb[4, 7] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb[5, 7] <- anova.diversity$VarExp[4] * 100

g.div.200kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep7, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep7, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep7, weights = varPower(0, ~theta), method = "ML")
g.div.200kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep7, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.200kb.1, g.div.200kb.2, g.div.200kb.3, g.div.200kb.4)

##                 df      AIC
## g.div.200kb.1  8 -1920.492
## g.div.200kb.2  8 -1940.555
## g.div.200kb.3  7 -1936.838
## g.div.200kb.4  7 -1914.435

summary(g.div.200kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.200kb.rep7
##       AIC      BIC  logLik
##   -1936.838 -1917.444 975.4192
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##       power
##   -1.630375
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032306 0.00000894 361.3092 0.0000
## thetaC       0.9172863 0.02050378  44.7374 0.0000
## rhoC        0.0022991 0.00298926   0.7691 0.4434
## tmrcaC      0.0043875 0.00005702  76.9426 0.0000
## thetaC:tmrcaC 1.3282349 0.11467784  11.5823 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC     -0.665
## rhoC       0.227 -0.361
## tmrcaC    -0.112 -0.204 -0.404
## thetaC:tmrcaC -0.650  0.440 -0.318  0.249

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -3.6868115 -0.5651622 -0.1157522  0.6510378  3.6401674
## 
## Residual standard error: 6.533835e-09
## Degrees of freedom: 118 total; 113 residual
vif(g.div.200kb.3)

##          thetaC        rhoC        tmrcaC thetaC:tmrcaC
##      1.776494     1.583826     1.627773     1.457581

```

## 5.2.8 Replicate 8

```

rep_8.pi.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.dive")
rep_8.pi.200kb$avg <- apply(rep_8.pi.200kb[4:ncol(rep_8.pi.200kb)], 1, mean)
rep_8.rho.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.rho")
rep_8.theta.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.theta")
rep_8.tmrca.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.tmrca")
rep_8.tmrca.200kb$avg <- apply(rep_8.tmrca.200kb[4:ncol(rep_8.tmrca.200kb)], 1, mean)

inf.lands.200kb.rep8 <- as.data.frame(cbind(rep_8.pi.200kb$avg, rep_8.theta.200kb$sample_mean, rep_8.tmrca.200kb$avg))
names(inf.lands.200kb.rep8) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.200kb.rep8$thetaC <- inf.lands.200kb.rep8$theta - mean(inf.lands.200kb.rep8$theta)
inf.lands.200kb.rep8$tmrcaC <- inf.lands.200kb.rep8$tmrca - mean(inf.lands.200kb.rep8$tmrca)
inf.lands.200kb.rep8$rhoC <- inf.lands.200kb.rep8$rho - mean(inf.lands.200kb.rep8$rho)

inf.lands.200kb.rep8$bin <- 1:nrow(inf.lands.200kb.rep8)

# for merging:
inf.lands.200kb.rep8 <- inf.lands.200kb.rep8
inf.lands.200kb.rep8$Replicate <- 1

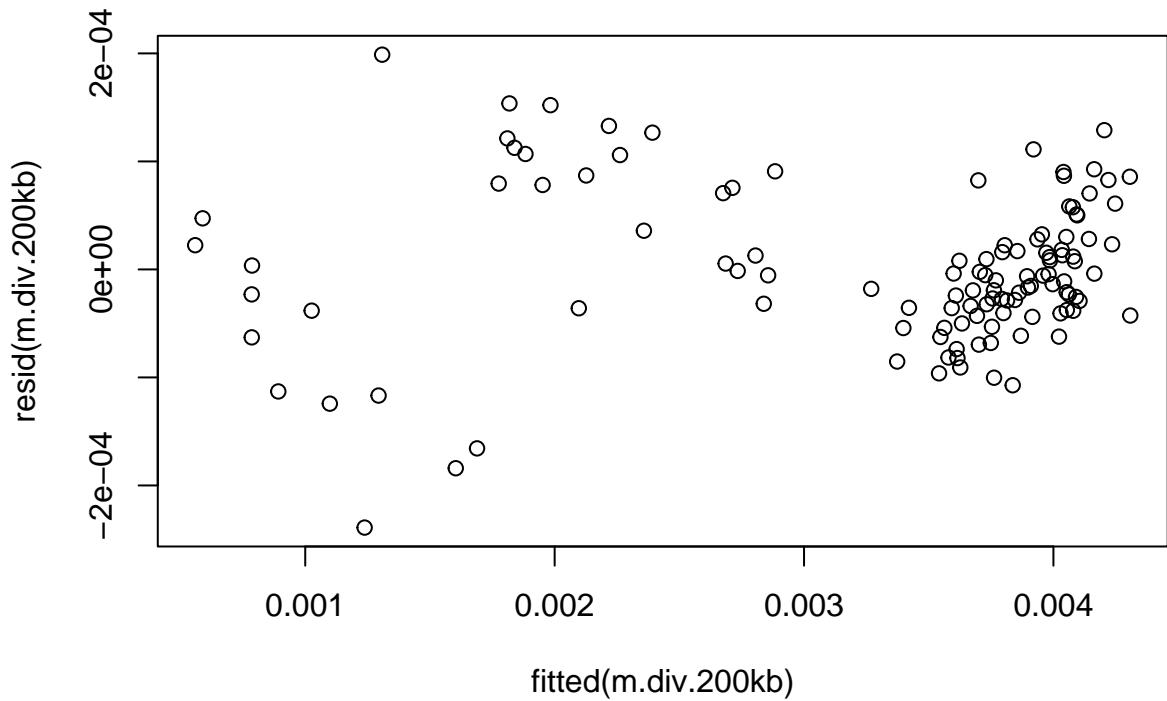
m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.200kb.rep8)
m.div.200kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.200kb.rep8)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.200kb.rep8)

AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)

##          df      AIC
## m.div.200kb    6 -1905.50
## m.div.200kb.2  7 -1923.90
## m.div.200kb.3  8 -1925.21

plot(resid(m.div.200kb)~fitted(m.div.200kb))

```

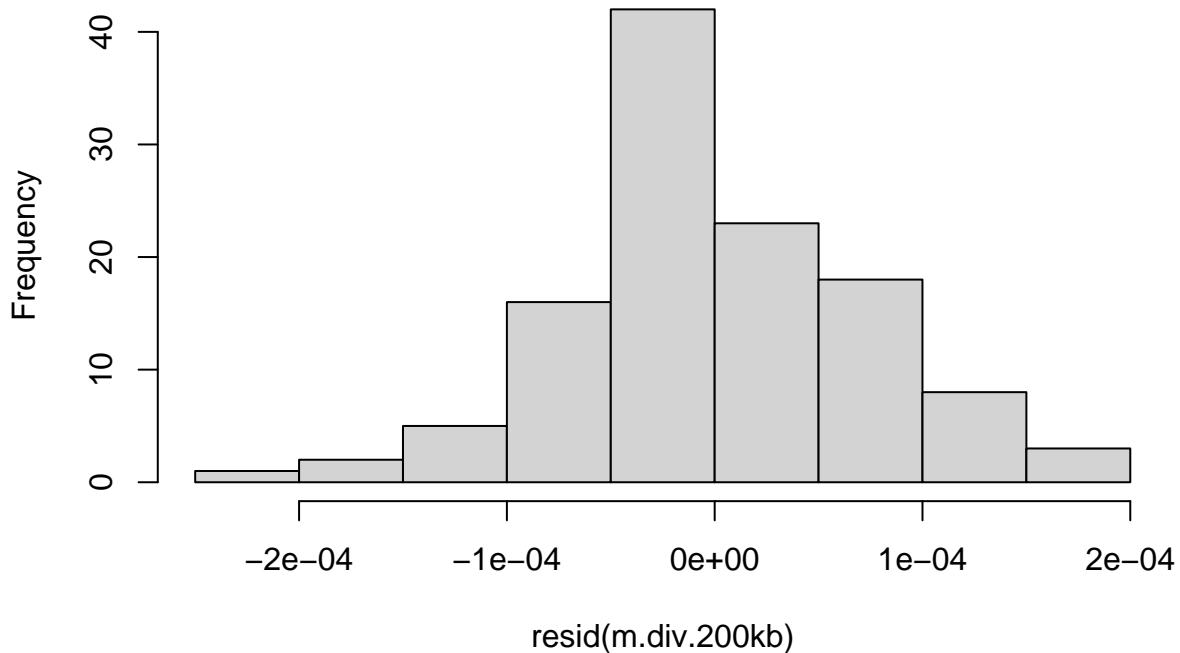


```
dwtest(m.div.200kb)
```

```
##
## Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.2303, p-value = 5.166e-06
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb)
```

```
##
## Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.37056, p-value = 0.03
hist(resid(m.div.200kb))
```

## Histogram of resid(m.div.200kb)



```
summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.200kb.rep8)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -2.390e-04 -3.825e-05 -5.591e-06  4.443e-05  1.988e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.221e-03 8.322e-06 387.016 < 2e-16 ***
## thetaC      1.017e+00 1.094e-02  92.962 < 2e-16 ***
## rhoC       -2.092e-02 3.786e-03 -5.526 2.13e-07 ***
## tmrcaC      4.560e-03 1.005e-04  45.393 < 2e-16 ***
## thetaC:tmrcaC 1.522e+00 1.131e-01  13.456 < 2e-16 ***
## ---      
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 7.32e-05 on 113 degrees of freedom
## Multiple R-squared:  0.9951, Adjusted R-squared:  0.9949 
## F-statistic: 5732 on 4 and 113 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.200kb[1, 8] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.200kb[2, 8] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb[3, 8] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb[4, 8] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb[5, 8] <- anova.diversity$VarExp[4] * 100

g.div.200kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep8, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep8, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep8, weights = varPower(0, ~theta), method = "ML")
g.div.200kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep8, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.200kb.1, g.div.200kb.2, g.div.200kb.3, g.div.200kb.4)

##                 df      AIC
## g.div.200kb.1  8 -1932.600
## g.div.200kb.2  8 -1937.089
## g.div.200kb.3  7 -1937.377
## g.div.200kb.4  7 -1918.893

summary(g.div.200kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.200kb.rep8
##          AIC      BIC  logLik
##        -1937.377 -1917.982 975.6885
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
## Parameter estimates:
##   power
## -1.878383
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032344 0.00000985 328.4171 0.0000
## thetaC       0.9627689 0.02185825  44.0460 0.0000
## rhoC        -0.0082138 0.00386613 -2.1245 0.0358
## tmrcaC       0.0045252 0.00008179  55.3261 0.0000
## thetaC:tmrcaC 1.5036433 0.13840840 10.8638 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC     -0.784
## rhoC       0.358 -0.351
## tmrcaC    -0.030 -0.234 -0.483
## thetaC:tmrcaC -0.638  0.482 -0.338  0.067

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -1.9946307 -0.6775280 -0.1141325  0.6237563  3.1278548
## 
## Residual standard error: 1.530777e-09
## Degrees of freedom: 118 total; 113 residual
vif(g.div.200kb.3)

##          thetaC         rhoC        tmrcaC thetaC:tmrcaC
## 1.811248     1.875762     1.743492     1.375969

```

### 5.2.9 Replicate 9

```

rep_9.pi.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.dive")
rep_9.pi.200kb$avg <- apply(rep_9.pi.200kb[4:ncol(rep_9.pi.200kb)], 1, mean)
rep_9.rho.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.rho")
rep_9.theta.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.theta")
rep_9.tmrca.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.tmrca")
rep_9.tmrca.200kb$avg <- apply(rep_9.tmrca.200kb[4:ncol(rep_9.tmrca.200kb)], 1, mean)

inf.lands.200kb.rep9 <- as.data.frame(cbind(rep_9.pi.200kb$avg, rep_9.theta.200kb$sample_mean, rep_9.tmrca.200kb$avg))
names(inf.lands.200kb.rep9) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.200kb.rep9$thetaC <- inf.lands.200kb.rep9$theta - mean(inf.lands.200kb.rep9$theta)
inf.lands.200kb.rep9$tmrcaC <- inf.lands.200kb.rep9$tmrca - mean(inf.lands.200kb.rep9$tmrca)
inf.lands.200kb.rep9$rhoC <- inf.lands.200kb.rep9$rho - mean(inf.lands.200kb.rep9$rho)

inf.lands.200kb.rep9$bin <- 1:nrow(inf.lands.200kb.rep9)

# for merging:
inf.lands.200kb.rep9 <- inf.lands.200kb.rep9
inf.lands.200kb.rep9$Replicate <- 1

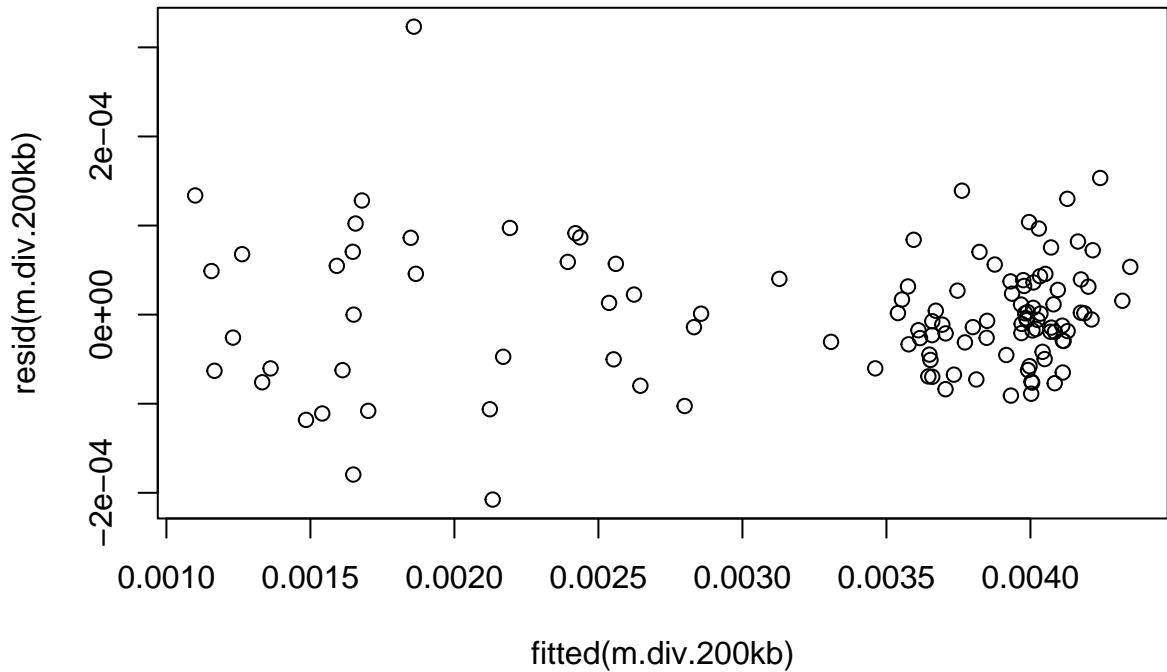
m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.200kb.rep9)
m.div.200kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.200kb.rep9)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.200kb.rep9)

AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)

##          df      AIC
## m.div.200kb    6 -1906.537
## m.div.200kb.2  7 -1906.701
## m.div.200kb.3  8 -1910.859

plot(resid(m.div.200kb)~fitted(m.div.200kb))

```

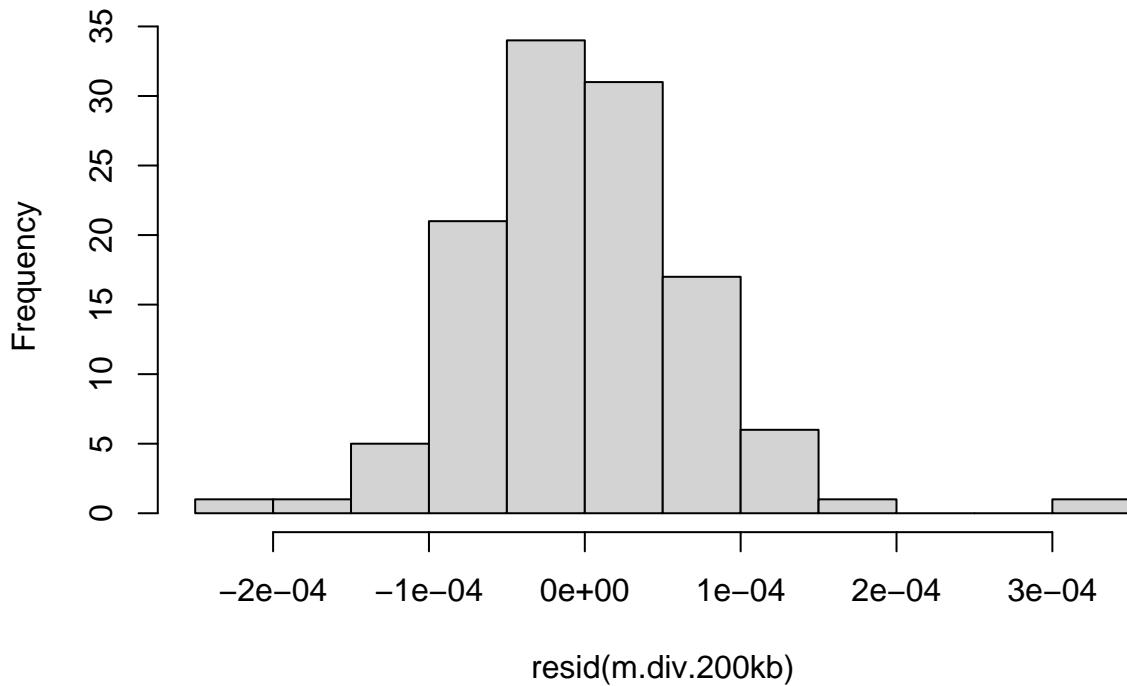


```
dwtest(m.div.200kb)
```

```
##
##  Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.2787, p-value = 2.2e-05
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.35665, p-value = 0.006
hist(resid(m.div.200kb))
```

## Histogram of resid(m.div.200kb)



```
summary(m.div.200kb)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,  
##      data = inf.lands.200kb.rep9)  
##  
## Residuals:  
##      Min        1Q    Median        3Q       Max  
## -2.076e-04 -4.682e-05 -6.010e-06  3.996e-05  3.232e-04  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 3.266e-03 8.920e-06 366.151 <2e-16 ***  
## thetaC      9.871e-01 1.741e-02  56.693 <2e-16 ***  
## rhoC       9.046e-04 5.911e-03   0.153   0.879  
## tmrcaC     4.050e-03 1.058e-04  38.264 <2e-16 ***  
## thetaC:tmrcaC 1.218e+00 1.156e-01  10.530 <2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 7.288e-05 on 113 degrees of freedom  
## Multiple R-squared:  0.9946, Adjusted R-squared:  0.9944  
## F-statistic:  5230 on 4 and 113 DF,  p-value: < 2.2e-16
```

```
anova.diversity <- Anova(m.div.200kb)  
apiss <- anova.diversity$"Sum Sq"  
anova.diversity$VarExp <- apiss / sum(apiss)
```

```
r2.bgs.200kb[1, 9] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.200kb[2, 9] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb[3, 9] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb[4, 9] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb[5, 9] <- anova.diversity$VarExp[4] * 100

g.div.200kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep9, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep9, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep9, weights = varPower(0, ~theta), method = "ML")
g.div.200kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep9, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.200kb.1, g.div.200kb.2, g.div.200kb.3, g.div.200kb.4)

##                 df      AIC
## g.div.200kb.1 8 -1931.011
## g.div.200kb.2 8 -1922.265
## g.div.200kb.3 7 -1916.833
## g.div.200kb.4 7 -1924.388

summary(g.div.200kb.3)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
## Data: inf.lands.200kb.rep9
##          AIC      BIC    logLik
## -1916.833 -1897.438 965.4164
##
## Variance function:
## Structure: Power of variance covariate
## Formula: ~theta
## Parameter estimates:
##       power
## -1.082583
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032663 0.00000920 354.9684 0.0000
## thetaC       0.9842793 0.02012000  48.9204 0.0000
## rhoC        0.0029596 0.00501867   0.5897 0.5566
## tmrcaC      0.0040304 0.00009727  41.4361 0.0000
## thetaC:tmrcaC 1.2099218 0.12627567   9.5816 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC     -0.462
## rhoC      0.248 -0.556
## tmrcaC    -0.319 -0.110 -0.435
## thetaC:tmrcaC -0.676  0.345 -0.338  0.492

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -1.9751365 -0.6158304 -0.1083347  0.6213443  4.6377522
## 
## Residual standard error: 1.478625e-07
## Degrees of freedom: 118 total; 113 residual
vif(g.div.200kb.3)

##          thetaC        rhoC        tmrcaC thetaC:tmrcaC
##      2.436334     2.397958     2.387627     1.772638

```

### 5.2.10 Replicate 10

```

rep_10.pi.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_5.d
rep_10.pi.200kb$avg <- apply(rep_10.pi.200kb[4:ncol(rep_10.pi.200kb)], 1, mean)
rep_10.rho.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_5.
rep_10.theta.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_5.
rep_10.tmrca.200kb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_5.
rep_10.tmrca.200kb$avg <- apply(rep_10.tmrca.200kb[4:ncol(rep_10.tmrca.200kb)], 1, mean)

inf.lands.200kb.rep10 <- as.data.frame(cbind(rep_10.pi.200kb$avg, rep_10.theta.200kb$sample_mean, rep_10.
names(inf.lands.200kb.rep10) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.200kb.rep10$thetaC <- inf.lands.200kb.rep10$theta - mean(inf.lands.200kb.rep10$theta)
inf.lands.200kb.rep10$tmrcaC <- inf.lands.200kb.rep10$tmrca - mean(inf.lands.200kb.rep10$tmrca)
inf.lands.200kb.rep10$rhoC <- inf.lands.200kb.rep10$rho - mean(inf.lands.200kb.rep10$rho)

inf.lands.200kb.rep10$bin <- 1:nrow(inf.lands.200kb.rep10)

# for merging:
inf.lands.200kb.rep10 <- inf.lands.200kb.rep10
inf.lands.200kb.rep10$Replicate <- 1

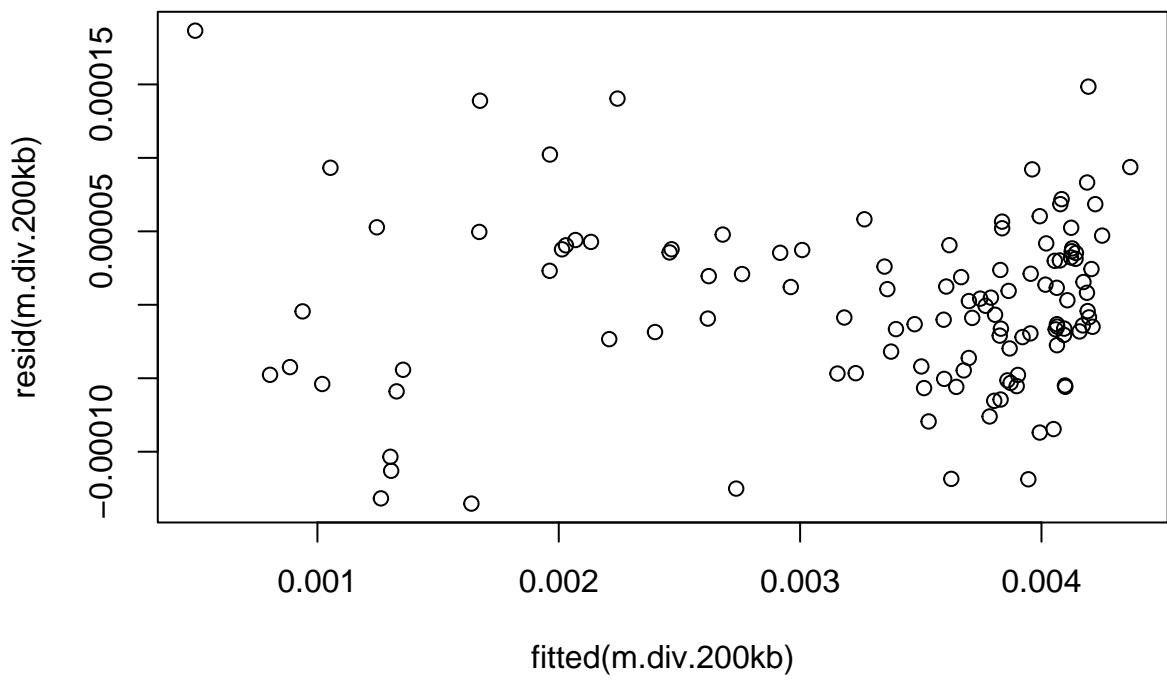
m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.200kb.rep10)
m.div.200kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.200kb.rep10)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.200kb.rep10)

AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)

##          df      AIC
## m.div.200kb     6 -1953.891
## m.div.200kb.2   7 -1957.296
## m.div.200kb.3   8 -1956.404

plot(resid(m.div.200kb)~fitted(m.div.200kb))

```

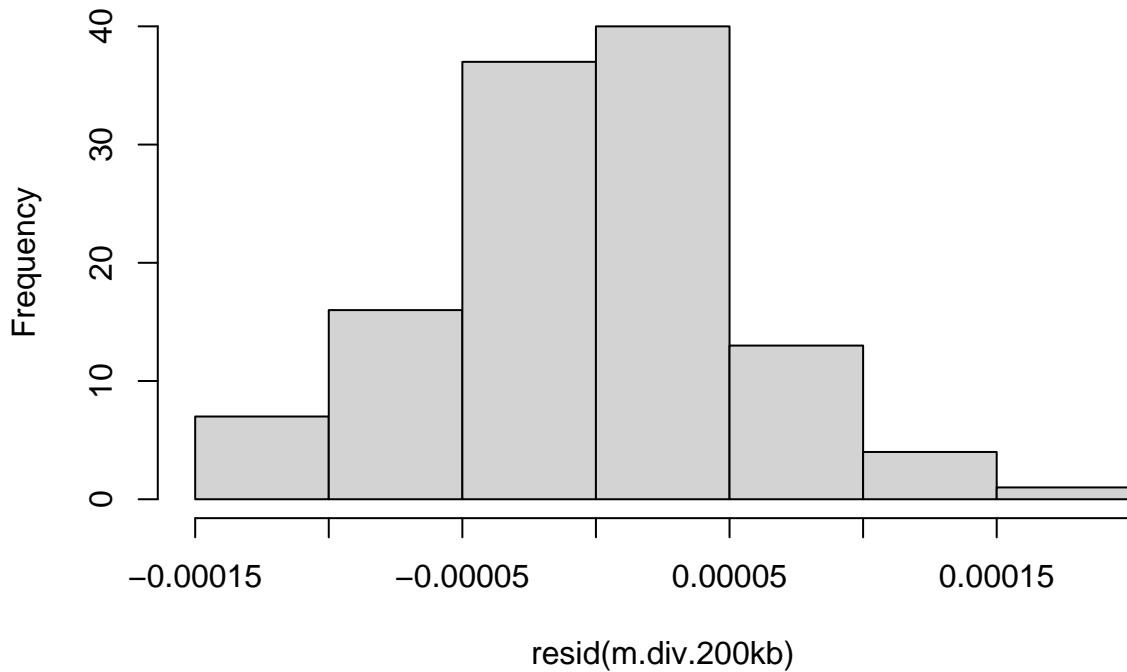


```
dwtest(m.div.200kb)
```

```
##
##  Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.4907, p-value = 0.001364
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.4609, p-value = 0.302
hist(resid(m.div.200kb))
```

## Histogram of resid(m.div.200kb)



```
summary(m.div.200kb)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.200kb.rep10)
##
## Residuals:
##      Min        1Q    Median        3Q       Max
## -1.353e-04 -4.230e-05 -2.486e-06  3.708e-05  1.866e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.208e-03 8.005e-06 400.71 <2e-16 ***
## thetaC      9.757e-01 1.418e-02   68.82 <2e-16 ***
## rhoC       -4.932e-03 3.681e-03   -1.34   0.183
## tmrcaC     4.336e-03 8.327e-05   52.08 <2e-16 ***
## thetaC:tmrcaC 1.504e+00 8.914e-02   16.87 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.963e-05 on 113 degrees of freedom
## Multiple R-squared:  0.9966, Adjusted R-squared:  0.9965
## F-statistic:  8373 on 4 and 113 DF,  p-value: < 2.2e-16
anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
```

```
r2.bgs.200kb[1, 10] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) / 3
```

```

r2.bgs.200kb[2, 10] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb[3, 10] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb[4, 10] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb[5, 10] <- anova.diversity$VarExp[4] * 100

g.div.200kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep10, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), na.action = na.omit)
g.div.200kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep10, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), na.action = na.omit)
g.div.200kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep10, weights = varPower(0, ~theta), method = "ML")
g.div.200kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep10, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.200kb.1, g.div.200kb.2, g.div.200kb.3, g.div.200kb.4)

```

```

##             df      AIC
## g.div.200kb.1 8 -1956.857
## g.div.200kb.2 8 -1961.174
## g.div.200kb.3 7 -1962.059
## g.div.200kb.4 7 -1954.326

```

```
summary(g.div.200kb.3)
```

```

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.200kb.rep10
##          AIC      BIC    logLik
## -1962.059 -1942.664 988.0295
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
## Parameter estimates:
##   power
## -1.050657
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032026 0.00000819 390.9569 0.0000
## thetaC       0.9673050 0.01663839  58.1369 0.0000
## rhoC        -0.0036182 0.00342358 -1.0568 0.2928
## tmrcaC       0.0044132 0.00008237  53.5765 0.0000
## thetaC:tmrcaC 1.5967041 0.09757204 16.3644 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC     -0.442
## rhoC       0.392 -0.493
## tmrcaC    -0.447 -0.247 -0.319
## thetaC:tmrcaC -0.732  0.327 -0.496  0.612

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -2.44406069 -0.66547647 -0.04305055  0.56882100  2.81110079
## 
## Residual standard error: 1.454558e-07
## Degrees of freedom: 118 total; 113 residual
vif(g.div.200kb.3)

```

```

##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
##      2.391981   1.820450   2.860658    2.619865

```

### 5.3 1 Mb scale

```

r2.bgs.1Mb <- as.data.frame(matrix(ncol = nreps, nrow = 5))
row.names(r2.bgs.1Mb) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
colnames(r2.bgs.1Mb) <- reps

sim.theta.1Mb <- read.table("dm_bgs_sims/MutationMap_1000kb.csv", header = T)
sim.rho.1Mb <- read.table("dm_bgs_sims/RecombinationMap_1000kb.csv", header = T)

```

#### 5.3.1 Replicate 1

```

rep_1.pi.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.diversity")
rep_1.pi.1Mb$avg <- apply(rep_1.pi.1Mb[4:ncol(rep_1.pi.1Mb)], 1, mean)
rep_1.rho.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.rho.1Mb")
rep_1.theta.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.theta.1Mb")
rep_1.tmrca.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.TMRCA.1Mb")
rep_1.tmrca.1Mb$avg <- apply(rep_1.tmrca.1Mb[4:ncol(rep_1.tmrca.1Mb)], 1, mean)

inf.lands.1Mb.rep1 <- as.data.frame(cbind(rep_1.pi.1Mb$avg, rep_1.theta.1Mb$sample_mean, rep_1.tmrca.1Mb$avg))
names(inf.lands.1Mb.rep1) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.1Mb.rep1$thetaC <- inf.lands.1Mb.rep1$theta - mean(inf.lands.1Mb.rep1$theta)
inf.lands.1Mb.rep1$tmrcaC <- inf.lands.1Mb.rep1$tmrca - mean(inf.lands.1Mb.rep1$tmrca)
inf.lands.1Mb.rep1$rhoC <- inf.lands.1Mb.rep1$rho - mean(inf.lands.1Mb.rep1$rho)

inf.lands.1Mb.rep1$bin <- 1:nrow(inf.lands.1Mb.rep1)

# for merging:
inf.lands.1Mb.rep1 <- inf.lands.1Mb.rep1
inf.lands.1Mb.rep1$Replicate <- 1

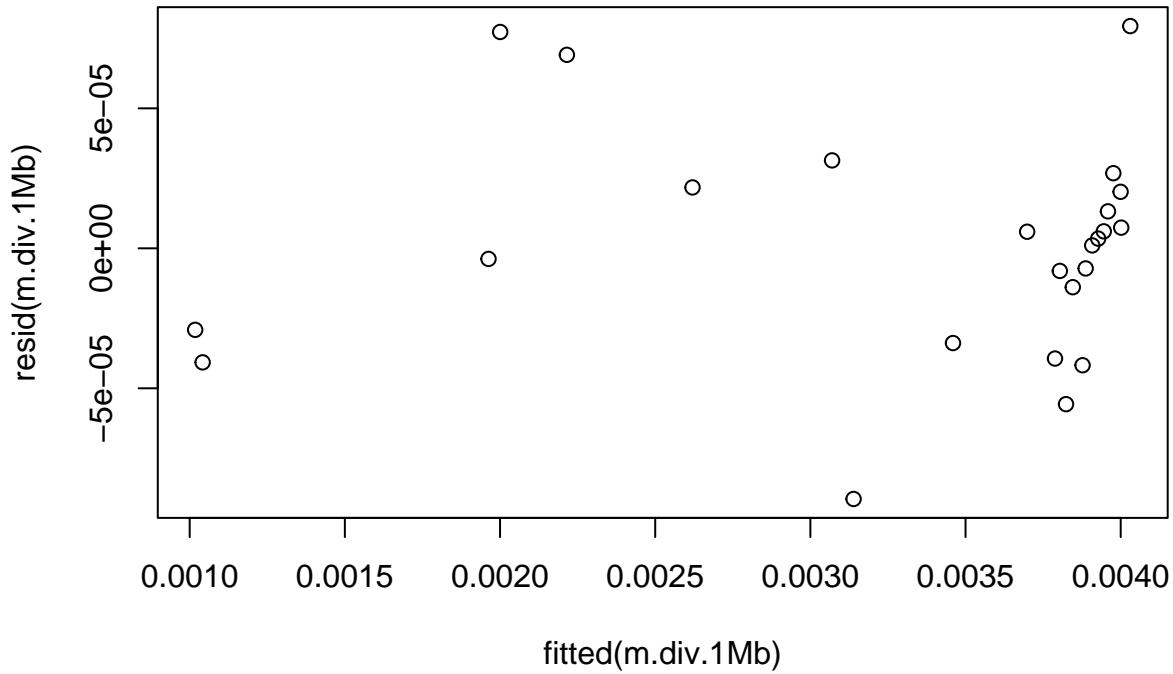
m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.1Mb.rep1)
m.div.1Mb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.1Mb.rep1)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.1Mb.rep1)

AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)

```

	df	AIC
m.div.1Mb	6	-406.0092
m.div.1Mb.2	7	-430.3498

```
## m.div.1Mb.3 8 -429.6365
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))
```

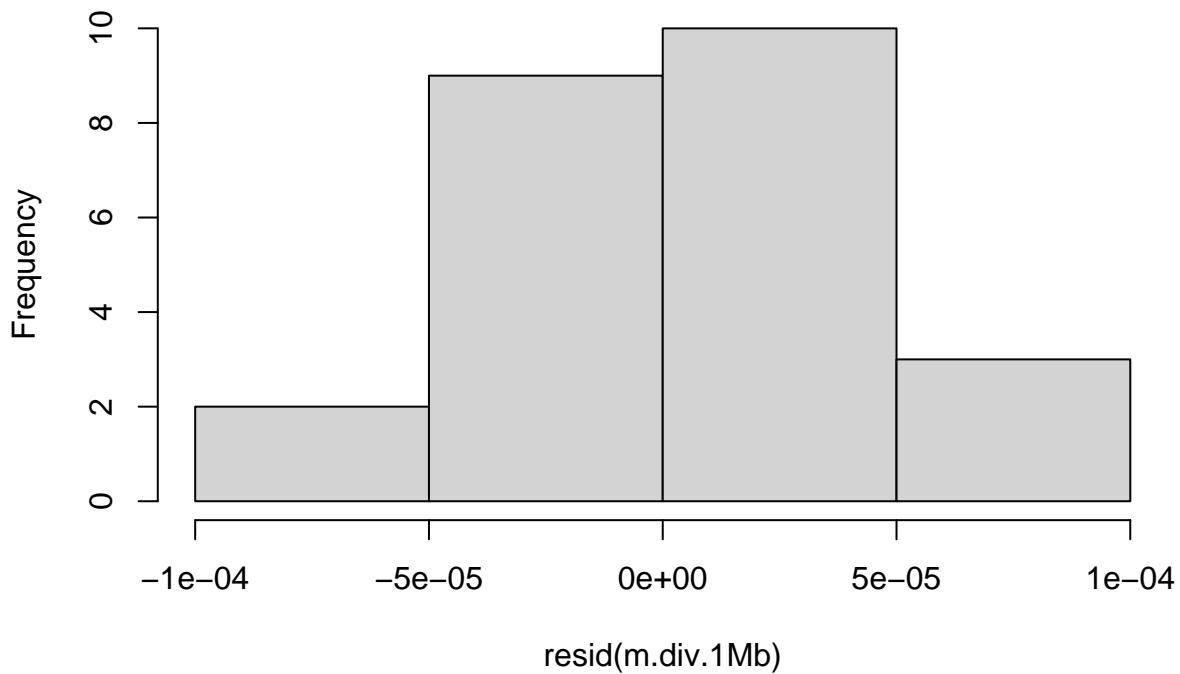


```
dwtest(m.div.1Mb)
```

```
##
##  Durbin-Watson test
##
## data: m.div.1Mb
## DW = 1.5555, p-value = 0.08007
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.1Mb)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.45959, p-value = 0.384
hist(resid(m.div.1Mb))
```

## Histogram of resid(m.div.1Mb)



```
summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##     data = inf.lands.1Mb.rep1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -8.953e-05 -3.030e-05  2.250e-06  2.058e-05  7.938e-05
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.254e-03 1.291e-05 251.954 < 2e-16 ***
## thetaC      9.715e-01 1.576e-02  61.645 < 2e-16 ***
## rhoC       -9.396e-03 8.296e-03  -1.133 0.271502  
## tmrcaC      4.173e-03 2.523e-04  16.540 9.75e-13 ***
## thetaC:tmrcaC 9.890e-01 2.369e-01   4.175 0.000513 *** 
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 4.492e-05 on 19 degrees of freedom
## Multiple R-squared:  0.9982, Adjusted R-squared:  0.9978 
## F-statistic: 2604 on 4 and 19 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.1Mb[1, 1] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.1Mb[2, 1] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb[3, 1] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb[4, 1] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb[5, 1] <- anova.diversity$VarExp[4] * 100

g.div.1Mb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep1, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep1, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep1, weights = varPower(0, ~theta), method = "ML")
g.div.1Mb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep1, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.1Mb.1, g.div.1Mb.2, g.div.1Mb.3, g.div.1Mb.4)

##             df      AIC
## g.div.1Mb.1 8 -404.0002
## g.div.1Mb.2 8 -409.1515
## g.div.1Mb.3 7 -410.3386
## g.div.1Mb.4 7 -404.4055

summary(g.div.1Mb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep1
##       AIC      BIC  logLik
##   -410.3386 -402.0922 212.1693
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##       power
##   -2.023167
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032718 0.00001510 216.74597 0.0000
## thetaC       0.9215871 0.03309801  27.84419 0.0000
## rhoC        0.0120765 0.00797878   1.51358 0.1466
## tmrcaC      0.0039579 0.00019161  20.65590 0.0000
## thetaC:tmrcaC 0.6717915 0.25595339   2.62466 0.0167
##
## Correlation:
##           (Intr) thetaC rhoC   tmrcaC
## thetaC     -0.784
## rhoC      0.548 -0.526
## tmrcaC    -0.243 -0.106 -0.551
## thetaC:tmrcaC -0.726  0.554 -0.634  0.360

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -2.4378441 -0.7324371  0.1090189  0.7573097  1.4770720
## 
## Residual standard error: 3.880261e-10
## Degrees of freedom: 24 total; 19 residual
vif(g.div.1Mb.3)

##          thetaC         rhoC        tmrcaC thetaC:tmrcaC
##      2.427407     2.973115     2.239180     2.020861

```

### 5.3.2 Replicate 2

```

rep_2.pi.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.diversity")
rep_2.pi.1Mb$avg <- apply(rep_2.pi.1Mb[4:ncol(rep_2.pi.1Mb)], 1, mean)
rep_2.rho.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.rho")
rep_2.theta.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.theta")
rep_2.tmrca.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.TMRCA")
rep_2.tmrca.1Mb$avg <- apply(rep_2.tmrca.1Mb[4:ncol(rep_2.tmrca.1Mb)], 1, mean)

inf.lands.1Mb.rep2 <- as.data.frame(cbind(rep_2.pi.1Mb$avg, rep_2.theta.1Mb$sample_mean, rep_2.tmrca.1Mb$avg))
names(inf.lands.1Mb.rep2) <- c("diversity", "theta", "tmrca", "rho")

# centering
inf.lands.1Mb.rep2$thetaC <- inf.lands.1Mb.rep2$theta - mean(inf.lands.1Mb.rep2$theta)
inf.lands.1Mb.rep2$tmrcaC <- inf.lands.1Mb.rep2$tmrca - mean(inf.lands.1Mb.rep2$tmrca)
inf.lands.1Mb.rep2$rhoC <- inf.lands.1Mb.rep2$rho - mean(inf.lands.1Mb.rep2$rho)

inf.lands.1Mb.rep2$bin <- 1:nrow(inf.lands.1Mb.rep2)

# for merging:
inf.lands.1Mb.rep2 <- inf.lands.1Mb.rep2
inf.lands.1Mb.rep2$Replicate <- 1

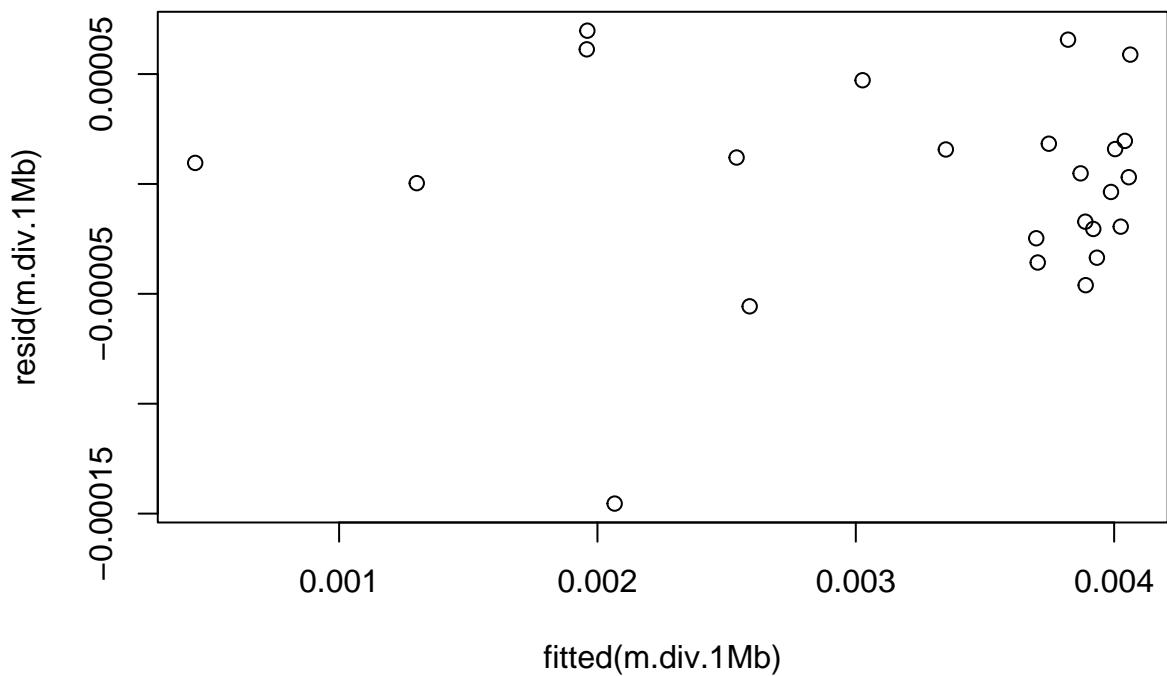
m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.1Mb.rep2)
m.div.1Mb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.1Mb.rep2)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.1Mb.rep2)

AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)

##          df      AIC
## m.div.1Mb     6 -399.3496
## m.div.1Mb.2   7 -400.4083
## m.div.1Mb.3   8 -404.4321

plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```

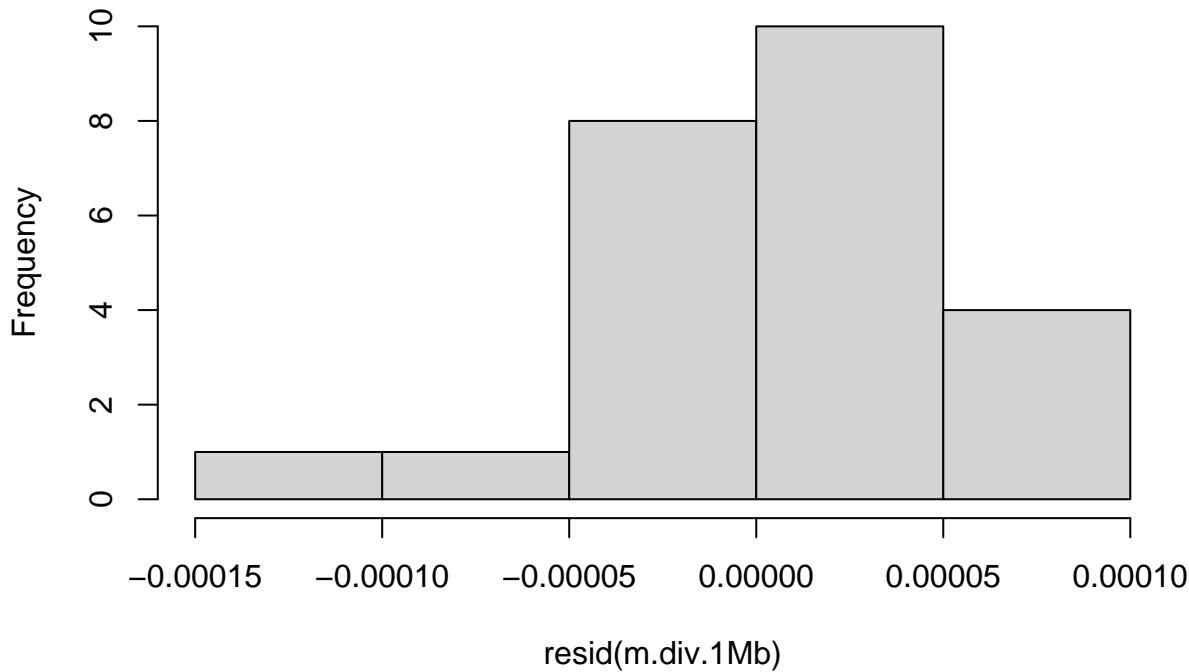


```
dwtest(m.div.1Mb)
```

```
##  
##  Durbin-Watson test  
##  
##  data: m.div.1Mb  
##  DW = 1.9912, p-value = 0.4076  
##  alternative hypothesis: true autocorrelation is greater than 0  
hmctest(m.div.1Mb)
```

```
##  
##  Harrison-McCabe test  
##  
##  data: m.div.1Mb  
##  HMC = 0.30667, p-value = 0.075  
hist(resid(m.div.1Mb))
```

## Histogram of resid(m.div.1Mb)



```
summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##     data = inf.lands.1Mb.rep2)
##
## Residuals:
##       Min         1Q      Median         3Q        Max
## -1.454e-04 -2.155e-05  3.937e-06  1.863e-05  6.974e-05
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.212e-03 1.309e-05 245.351 < 2e-16 ***
## thetaC      1.004e+00 1.562e-02  64.253 < 2e-16 ***
## rhoC       -8.039e-03 8.127e-03 -0.989 0.335038
## tmrcaC      4.377e-03 2.656e-04 16.477 1.04e-12 ***
## thetaC:tmrcaC 1.422e+00 3.310e-01   4.297 0.000389 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.16e-05 on 19 degrees of freedom
## Multiple R-squared:  0.9979, Adjusted R-squared:  0.9975
## F-statistic: 2268 on 4 and 19 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.1Mb[1, 2] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.1Mb[2, 2] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb[3, 2] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb[4, 2] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb[5, 2] <- anova.diversity$VarExp[4] * 100

g.div.1Mb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep2, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")

g.div.1Mb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep2, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")

g.div.1Mb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep2, weights = varPower(0, ~theta), method = "ML")

g.div.1Mb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep2, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.1Mb.1, g.div.1Mb.2, g.div.1Mb.3, g.div.1Mb.4)

##           df      AIC
## g.div.1Mb.1 8 -400.8891
## g.div.1Mb.2 8 -398.2412
## g.div.1Mb.3 7 -400.2042
## g.div.1Mb.4 7 -402.8436

summary(g.div.1Mb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep2
##       AIC      BIC    logLik
##   -400.2042 -391.9578 207.1021
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##       power
##   -1.212998
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032150 0.0000175 184.14687 0.0000
## thetaC       1.0011436 0.0318203  31.46238 0.0000
## rhoC        -0.0029708 0.0095617  -0.31070 0.7594
## tmrcaC       0.0042837 0.0002888  14.83268 0.0000
## thetaC:tmrcaC 1.2596398 0.4834910   2.60530 0.0174
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC     -0.811
## rhoC      0.368 -0.444
## tmrcaC    0.227 -0.293 -0.505
## thetaC:tmrcaC -0.732  0.654 -0.334 -0.348

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -2.3171033 -0.6352535  0.0043190  0.4947650  1.9662715
## 
## Residual standard error: 4.267979e-08
## Degrees of freedom: 24 total; 19 residual
vif(g.div.1Mb.3)

##          thetaC         rhoC        tmrcaC thetaC:tmrcaC
##      2.484863     3.135203     2.875812     2.075453

```

### 5.3.3 Replicate 3

```

rep_3.pi.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.diversity")
rep_3.pi.1Mb$avg <- apply(rep_3.pi.1Mb[4:ncol(rep_3.pi.1Mb)], 1, mean)
rep_3.rho.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.rho.1Mb")
rep_3.theta.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.theta.1Mb")
rep_3.tmrca.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.TMRCA.1Mb")
rep_3.tmrca.1Mb$avg <- apply(rep_3.tmrca.1Mb[4:ncol(rep_3.tmrca.1Mb)], 1, mean)

inf.lands.1Mb.rep3 <- as.data.frame(cbind(rep_3.pi.1Mb$avg, rep_3.theta.1Mb$sample_mean, rep_3.tmrca.1Mb$avg))
names(inf.lands.1Mb.rep3) <- c("diversity", "theta", "tmrca", "rho")

cor.test(~theta+tmrca, data = inf.lands.1Mb.rep3, method = "spearman")

## 
## Spearman's rank correlation rho
## 
## data: theta and tmrca
## S = 440, p-value = 3.288e-06
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.8086957

cor.test(~theta+rho, data = inf.lands.1Mb.rep3, method = "spearman")

## 
## Spearman's rank correlation rho
## 
## data: theta and rho
## S = 770, p-value = 0.0005364
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.6652174

cor.test(~rho+tmrca, data = inf.lands.1Mb.rep3, method = "spearman")

## 
## Spearman's rank correlation rho
## 
## data: rho and tmrca
## S = 754, p-value = 0.0004483

```

```

## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.6721739
# centering
inf.lands.1Mb.rep3$thetaC <- inf.lands.1Mb.rep3$theta - mean(inf.lands.1Mb.rep3$theta)
inf.lands.1Mb.rep3$tmrcaC <- inf.lands.1Mb.rep3$tmrca - mean(inf.lands.1Mb.rep3$tmrca)
inf.lands.1Mb.rep3$rhoC <- inf.lands.1Mb.rep3$rho - mean(inf.lands.1Mb.rep3$rho)

inf.lands.1Mb.rep3$bin <- 1:nrow(inf.lands.1Mb.rep3)

# for merging:
inf.lands.1Mb.rep3 <- inf.lands.1Mb.rep3
inf.lands.1Mb.rep3$Replicate <- 1

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.1Mb.rep3)
m.div.1Mb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.1Mb.rep3)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.1Mb.rep3)

AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)

##          df      AIC
## m.div.1Mb    6 -409.5885
## m.div.1Mb.2   7 -421.5471
## m.div.1Mb.3   8 -425.6301
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```

```
dwtest(m.div.1Mb)
```

```

## 
## Durbin-Watson test
## 
```

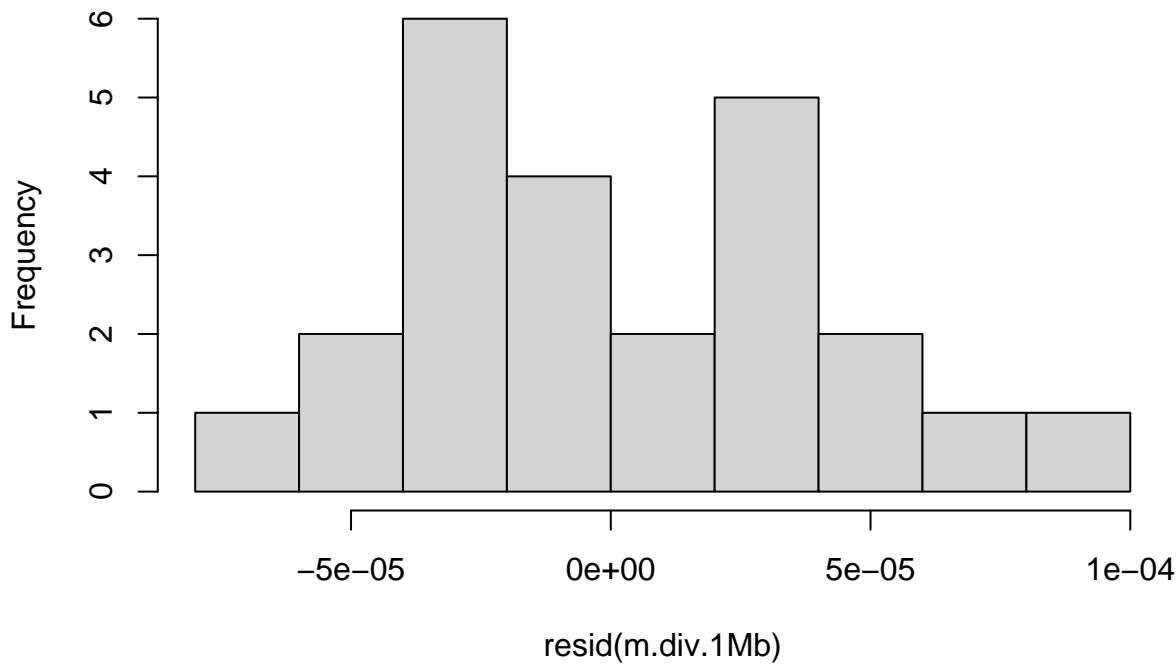
```

## data: m.div.1Mb
## DW = 1.5916, p-value = 0.08878
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.1Mb)

##
##  Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.49696, p-value = 0.489
hist(resid(m.div.1Mb))

```

### Histogram of resid(m.div.1Mb)



```
summary(m.div.1Mb)
```

```

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.1Mb.rep3)
##
## Residuals:
##      Min        1Q     Median        3Q       Max 
## -6.175e-05 -2.983e-05 -9.534e-06  2.798e-05  8.075e-05 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.226e-03 1.424e-05 226.584 < 2e-16 ***
## thetaC      8.712e-01 3.284e-02  26.531 < 2e-16 ***
## rhoC       -1.881e-02 8.705e-03 -2.161   0.0437 *  
## tmrcaC      5.277e-03 1.800e-04  29.312 < 2e-16 ***
## 
```

```

## thetaC:tmrcaC  1.378e+00  2.275e-01   6.057 7.96e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.169e-05 on 19 degrees of freedom
## Multiple R-squared:  0.9984, Adjusted R-squared:  0.998
## F-statistic:  2900 on 4 and 19 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.1Mb[1, 3] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
r2.bgs.1Mb[2, 3] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb[3, 3] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb[4, 3] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb[5, 3] <- anova.diversity$VarExp[4] * 100

g.div.1Mb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep3, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep3, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep3, weights = varPower(0, ~theta), method = "ML")
g.div.1Mb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep3, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.1Mb.1, g.div.1Mb.2, g.div.1Mb.3, g.div.1Mb.4)

##          df      AIC
## g.div.1Mb.1 8 -412.9887
## g.div.1Mb.2 8 -421.6118
## g.div.1Mb.3 7 -422.9079
## g.div.1Mb.4 7 -407.8511
summary(g.div.1Mb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep3
##   AIC      BIC    logLik
## -422.9079 -414.6615 218.4539
##
## 
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##     power
## -3.724078
##
## Coefficients:
##              Value Std.Error t-value p-value

```

```

## (Intercept) 0.0032933 0.0000184 178.77408 0.0000
## thetaC 0.7870738 0.0431431 18.24332 0.0000
## rhoC 0.0273497 0.0075170 3.63836 0.0017
## tmrcaC 0.0046109 0.0001840 25.06263 0.0000
## thetaC:tmrcaC -0.2390013 0.3660344 -0.65295 0.5216
##
## Correlation:
## (Intr) thetaC rhoC tmrcaC
## thetaC -0.860
## rhoC 0.566 -0.397
## tmrcaC 0.089 -0.454 -0.450
## thetaC:tmrcaC -0.831 0.651 -0.650 -0.037
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -1.9969434 -0.7226474 -0.1659388  0.8513819  1.7336059
##
## Residual standard error: 2.191358e-14
## Degrees of freedom: 24 total; 19 residual
vif(g.div.1Mb.3)

##      thetaC       rhoC       tmrcaC thetaC:tmrcaC
## 3.317025 3.688734 3.131145 2.561962

```

### 5.3.4 Replicate 4

```

rep_4.pi.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.diversity")
rep_4.pi.1Mb$avg <- apply(rep_4.pi.1Mb[4:ncol(rep_4.pi.1Mb)], 1, mean)
rep_4.rho.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.rho.1Mb")
rep_4.theta.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.theta.1Mb")
rep_4.tmrca.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.TMRCA.1Mb")
rep_4.tmrca.1Mb$avg <- apply(rep_4.tmrca.1Mb[4:ncol(rep_4.tmrca.1Mb)], 1, mean)

inf.lands.1Mb.rep4 <- as.data.frame(cbind(rep_4.pi.1Mb$avg, rep_4.theta.1Mb$sample_mean, rep_4.tmrca.1Mb$avg))
names(inf.lands.1Mb.rep4) <- c("diversity", "theta", "tmrca", "rho")

cor.test(~theta+tmrca, data = inf.lands.1Mb.rep4, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 500, p-value = 9.977e-06
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.7826087

cor.test(~theta+rho, data = inf.lands.1Mb.rep4, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho

```

```

## S = 940, p-value = 0.002813
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.5913043
cor.test(~rho+tmrca, data = inf.lands.1Mb.rep4, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 902, p-value = 0.00201
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.6078261

# centering
inf.lands.1Mb.rep4$thetaC <- inf.lands.1Mb.rep4$theta - mean(inf.lands.1Mb.rep4$theta)
inf.lands.1Mb.rep4$tmrcaC <- inf.lands.1Mb.rep4$tmrca - mean(inf.lands.1Mb.rep4$tmrca)
inf.lands.1Mb.rep4$rhoC <- inf.lands.1Mb.rep4$rho - mean(inf.lands.1Mb.rep4$rho)

inf.lands.1Mb.rep4$bin <- 1:nrow(inf.lands.1Mb.rep4)

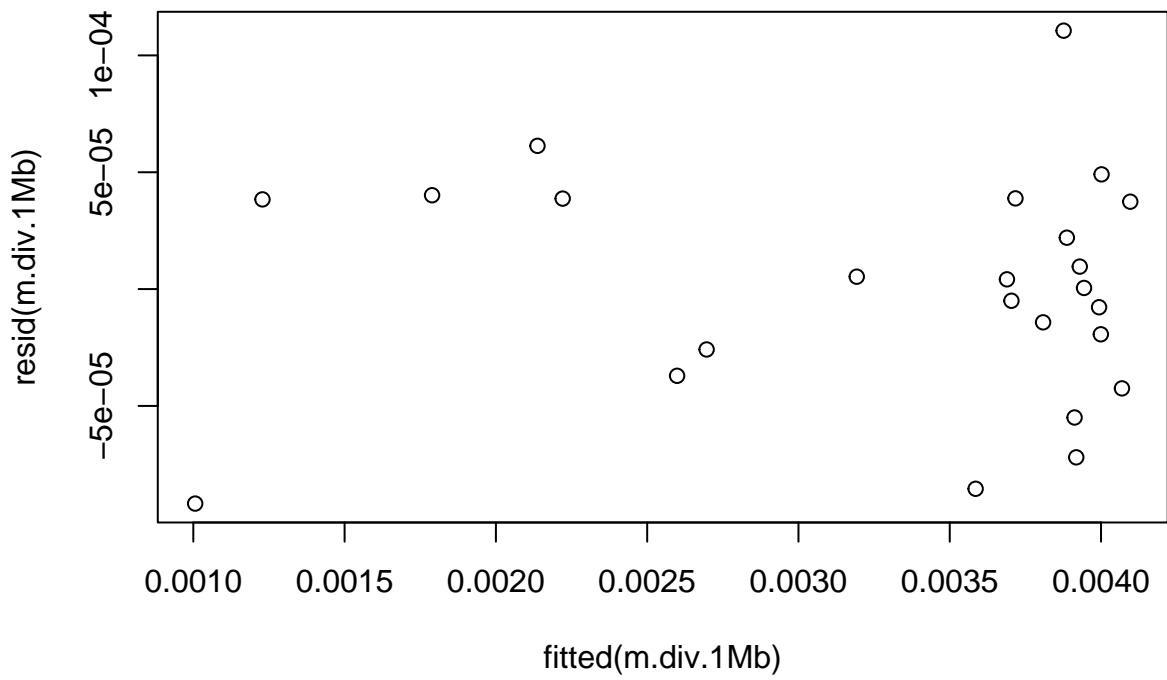
# for merging:
inf.lands.1Mb.rep4 <- inf.lands.1Mb.rep4
inf.lands.1Mb.rep4$Replicate <- 1

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.1Mb.rep4)
m.div.1Mb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.1Mb.rep4)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.1Mb.rep4)

AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)

##          df      AIC
## m.div.1Mb    6 -397.3660
## m.div.1Mb.2   7 -427.2283
## m.div.1Mb.3   8 -446.7941
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```

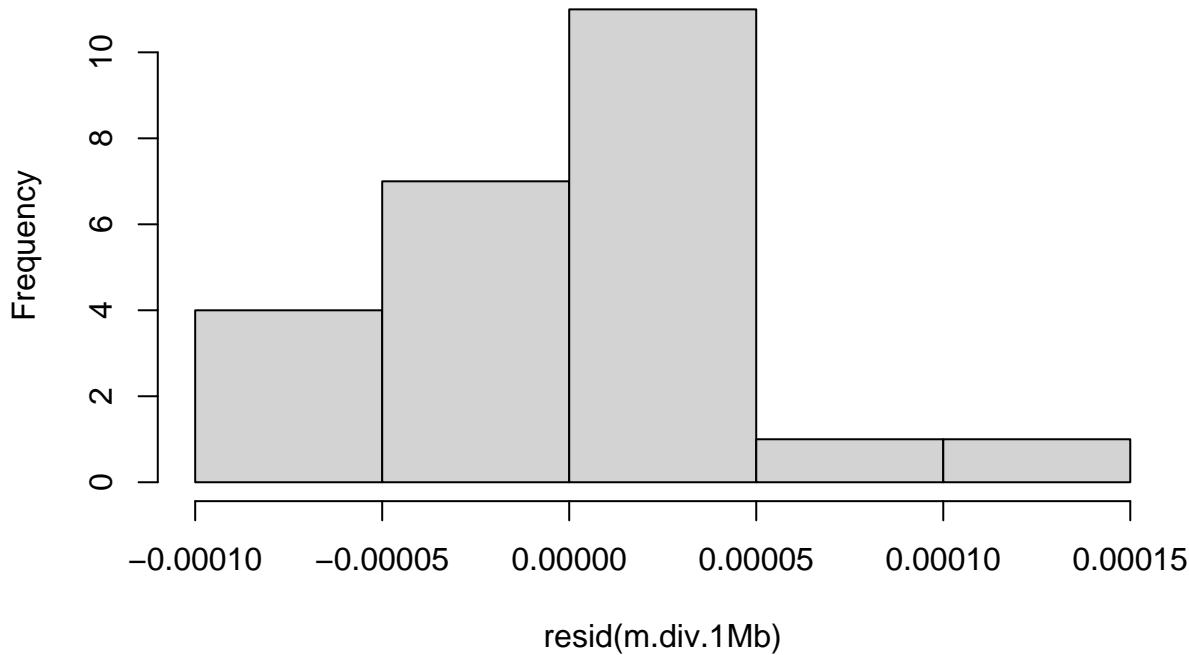


```
dwtest(m.div.1Mb)
```

```
##
##  Durbin-Watson test
##
## data: m.div.1Mb
## DW = 1.3655, p-value = 0.02222
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.1Mb)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.48067, p-value = 0.443
hist(resid(m.div.1Mb))
```

## Histogram of resid(m.div.1Mb)



```
summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.1Mb.rep4)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -9.179e-05 -2.866e-05  2.328e-06  3.847e-05  1.106e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.238e-03 1.922e-05 168.487 < 2e-16 ***
## thetaC      1.010e+00 3.264e-02  30.927 < 2e-16 ***
## rhoC        -4.312e-02 8.617e-03 -5.004 7.88e-05 ***
## tmrcaC      5.734e-03 3.744e-04 15.312 3.83e-12 ***
## thetaC:tmrcaC 1.420e+00 4.169e-01   3.406  0.00296 ** 
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 5.378e-05 on 19 degrees of freedom
## Multiple R-squared:  0.9974, Adjusted R-squared:  0.9968 
## F-statistic: 1813 on 4 and 19 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.1Mb[1, 4] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
```

```

r2.bgs.1Mb[2, 4] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb[3, 4] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb[4, 4] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb[5, 4] <- anova.diversity$VarExp[4] * 100

g.div.1Mb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep4, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep4, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep4, weights = varPower(0, ~theta), method = "ML")
g.div.1Mb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep4, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.1Mb.1, g.div.1Mb.2, g.div.1Mb.3, g.div.1Mb.4)

##           df      AIC
## g.div.1Mb.1 8 -404.8346
## g.div.1Mb.2 8 -424.5156
## g.div.1Mb.3 7 -422.1707
## g.div.1Mb.4 7 -400.0480

summary(g.div.1Mb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep4
##       AIC      BIC  logLik
##   -422.1707 -413.9243 218.0853
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##       power
##   -4.737286
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032689 0.0000159 205.75108 0.0000
## thetaC       0.9760242 0.0361547  26.99576 0.0000
## rhoC        0.0039813 0.0046685   0.85280 0.4044
## tmrcaC      0.0047403 0.0002452  19.33405 0.0000
## thetaC:tmrcaC 0.8318990 0.4600537   1.80826 0.0864
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC     -0.883
## rhoC      0.383 -0.230
## tmrcaC    0.246 -0.494 -0.334
## thetaC:tmrcaC -0.601 0.469 -0.337 -0.505

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -2.6711787 -0.6405707  0.1119790  0.6454920  1.4954806
## 
## Residual standard error: 7.05933e-17
## Degrees of freedom: 24 total; 19 residual
vif(g.div.1Mb.3)

##          thetaC         rhoC        tmrcaC thetaC:tmrcaC
##      1.724453     2.187442     2.913950     2.187653

```

### 5.3.5 Replicate 5

```

rep_5.pi.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.diversity")
rep_5.pi.1Mb$avg <- apply(rep_5.pi.1Mb[4:ncol(rep_5.pi.1Mb)], 1, mean)
rep_5.rho.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.rho.1Mb")
rep_5.theta.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.theta.1Mb")
rep_5.tmrca.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.TMRCA.1Mb")
rep_5.tmrca.1Mb$avg <- apply(rep_5.tmrca.1Mb[4:ncol(rep_5.tmrca.1Mb)], 1, mean)

inf.lands.1Mb.rep5 <- as.data.frame(cbind(rep_5.pi.1Mb$avg, rep_5.theta.1Mb$sample_mean, rep_5.tmrca.1Mb$avg))
names(inf.lands.1Mb.rep5) <- c("diversity", "theta", "tmrca", "rho")

cor.test(~theta+tmrca, data = inf.lands.1Mb.rep5, method = "spearman")

## 
## Spearman's rank correlation rho
## 
## data: theta and tmrca
## S = 268, p-value = 2.67e-06
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.8834783

cor.test(~theta+rho, data = inf.lands.1Mb.rep5, method = "spearman")

## 
## Spearman's rank correlation rho
## 
## data: theta and rho
## S = 1460, p-value = 0.08
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.3652174

cor.test(~rho+tmrca, data = inf.lands.1Mb.rep5, method = "spearman")

## 
## Spearman's rank correlation rho
## 
## data: rho and tmrca
## S = 1062, p-value = 0.007459

```

```

## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.5382609

# centering
inf.lands.1Mb.rep5$thetaC <- inf.lands.1Mb.rep5$theta - mean(inf.lands.1Mb.rep5$theta)
inf.lands.1Mb.rep5$tmrcaC <- inf.lands.1Mb.rep5$tmrca - mean(inf.lands.1Mb.rep5$tmrca)
inf.lands.1Mb.rep5$rhoC <- inf.lands.1Mb.rep5$rho - mean(inf.lands.1Mb.rep5$rho)

inf.lands.1Mb.rep5$bin <- 1:nrow(inf.lands.1Mb.rep5)

# for merging:
inf.lands.1Mb.rep5 <- inf.lands.1Mb.rep5
inf.lands.1Mb.rep5$Replicate <- 1

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.1Mb.rep5)
m.div.1Mb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.1Mb.rep5)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.1Mb.rep5)

AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)

##          df      AIC
## m.div.1Mb     6 -382.7189
## m.div.1Mb.2   7 -416.9266
## m.div.1Mb.3   8 -419.8725

plot(resid(m.div.1Mb)~fitted(m.div.1Mb))



```

dwtest(m.div.1Mb)

```

## 
## Durbin-Watson test
##

```

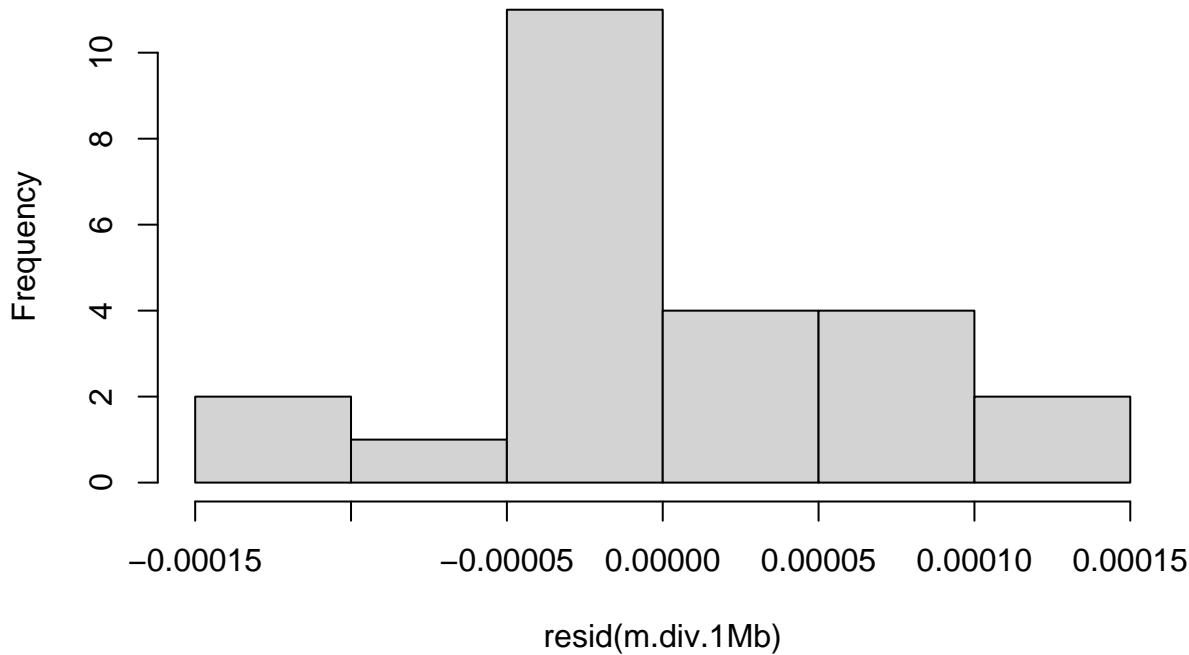
```

## data: m.div.1Mb
## DW = 1.7255, p-value = 0.1405
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.1Mb)

##
##  Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.138, p-value = 0.003
hist(resid(m.div.1Mb))

```

### Histogram of resid(m.div.1Mb)



```
summary(m.div.1Mb)
```

```

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.1Mb.rep5)
##
## Residuals:
##      Min        1Q    Median        3Q       Max 
## -1.491e-04 -3.724e-05 -6.155e-06  3.251e-05  1.498e-04 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.254e-03 2.031e-05 160.184 < 2e-16 ***
## thetaC      9.496e-01 3.075e-02  30.884 < 2e-16 ***
## rhoC       -3.654e-02 1.253e-02 -2.916  0.00886 **  
## tmrcaC      5.750e-03 5.084e-04 11.310   7e-10 ***
## 
```

```

## thetaC:tmrcaC  3.073e-01  4.749e-01   0.647  0.52524
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.297e-05 on 19 degrees of freedom
## Multiple R-squared:  0.9954, Adjusted R-squared:  0.9945
## F-statistic:  1034 on 4 and 19 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.1Mb[1, 5] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
r2.bgs.1Mb[2, 5] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb[3, 5] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb[4, 5] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb[5, 5] <- anova.diversity$VarExp[4] * 100

g.div.1Mb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep5, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep5, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep5, weights = varPower(0, ~theta), method = "ML")
g.div.1Mb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep5, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.1Mb.1, g.div.1Mb.2, g.div.1Mb.3, g.div.1Mb.4)

##          df      AIC
## g.div.1Mb.1 8 -405.5094
## g.div.1Mb.2 8 -416.4060
## g.div.1Mb.3 7 -417.3755
## g.div.1Mb.4 7 -404.1949

summary(g.div.1Mb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep5
##       AIC      BIC    logLik
##   -417.3755 -409.1291 215.6878
##
## 
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##     power
## -3.557677
##
## Coefficients:
##             Value Std.Error t-value p-value

```

```

## (Intercept) 0.0032539 0.0000171 190.36062 0.0000
## thetaC 0.9547500 0.0341476 27.95952 0.0000
## rhoC 0.0135203 0.0067801 1.99412 0.0607
## tmrcaC 0.0041562 0.0003606 11.52515 0.0000
## thetaC:tmrcaC 1.5129197 0.6394793 2.36586 0.0288
##
## Correlation:
## (Intr) thetaC rhoC tmrcaC
## thetaC -0.934
## rhoC 0.246 -0.150
## tmrcaC 0.417 -0.495 -0.425
## thetaC:tmrcaC -0.608 0.546 -0.103 -0.770
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -1.8935863 -0.7573840  0.2241411  0.7328966  1.5503079
##
## Residual standard error: 5.423247e-14
## Degrees of freedom: 24 total; 19 residual
vif(g.div.1Mb.3)

##          thetaC         rhoC        tmrcaC thetaC:tmrcaC
## 1.686193     3.183125     7.798430     5.560645

```

### 5.3.6 Replicate 6

```

rep_6.pi.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.diversity")
rep_6.pi.1Mb$avg <- apply(rep_6.pi.1Mb[4:ncol(rep_6.pi.1Mb)], 1, mean)
rep_6.rho.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.rho.1Mb")
rep_6.theta.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.theta.1Mb")
rep_6.tmrca.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.TMRCA.1Mb")
rep_6.tmrca.1Mb$avg <- apply(rep_6.tmrca.1Mb[4:ncol(rep_6.tmrca.1Mb)], 1, mean)

inf.lands.1Mb.rep6 <- as.data.frame(cbind(rep_6.pi.1Mb$avg, rep_6.theta.1Mb$sample_mean, rep_6.tmrca.1Mb$avg))
names(inf.lands.1Mb.rep6) <- c("diversity", "theta", "tmrca", "rho")

cor.test(~theta+tmrca, data = inf.lands.1Mb.rep6, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 442, p-value = 3.392e-06
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## 0.8078261

cor.test(~theta+rho, data = inf.lands.1Mb.rep6, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho

```

```

## S = 550, p-value = 2.535e-05
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.7608696
cor.test(~rho+tmrca, data = inf.lands.1Mb.rep6, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 392, p-value = 2.091e-06
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.8295652

# centering
inf.lands.1Mb.rep6$thetaC <- inf.lands.1Mb.rep6$theta - mean(inf.lands.1Mb.rep6$theta)
inf.lands.1Mb.rep6$tmrcaC <- inf.lands.1Mb.rep6$tmrca - mean(inf.lands.1Mb.rep6$tmrca)
inf.lands.1Mb.rep6$rhoC <- inf.lands.1Mb.rep6$rho - mean(inf.lands.1Mb.rep6$rho)

inf.lands.1Mb.rep6$bin <- 1:nrow(inf.lands.1Mb.rep6)

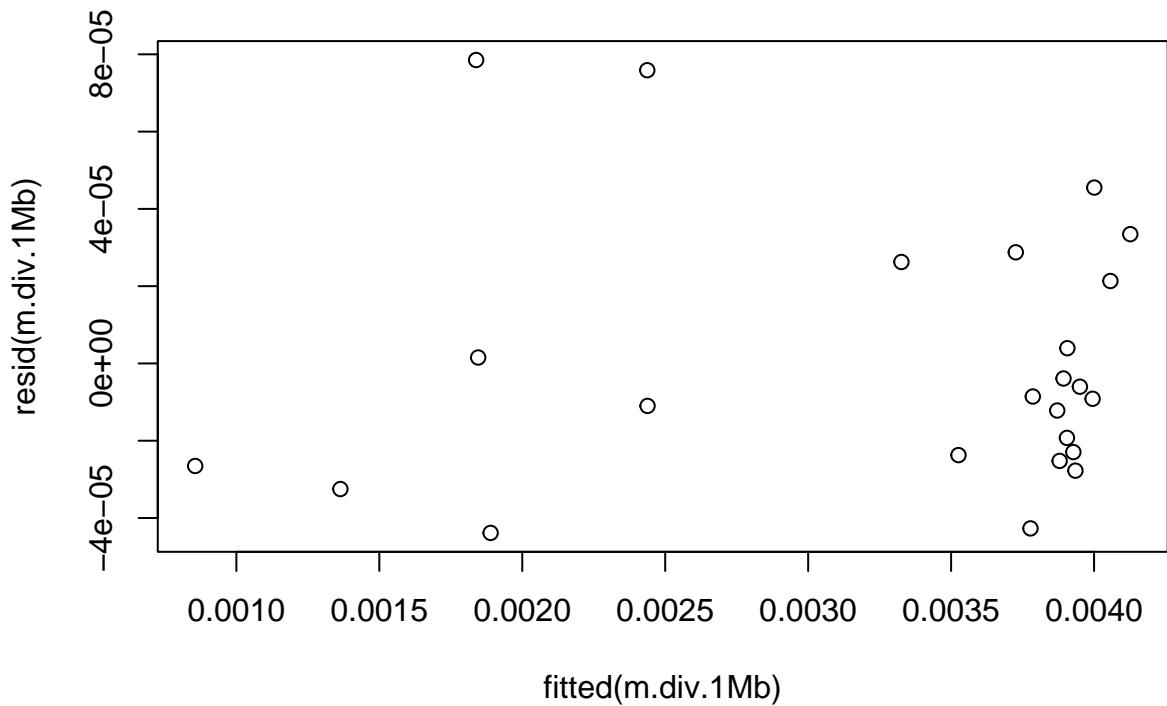
# for merging:
inf.lands.1Mb.rep6 <- inf.lands.1Mb.rep6
inf.lands.1Mb.rep6$Replicate <- 1

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.1Mb.rep6)
m.div.1Mb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.1Mb.rep6)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.1Mb.rep6)

AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)

##          df      AIC
## m.div.1Mb    6 -415.3703
## m.div.1Mb.2   7 -417.0328
## m.div.1Mb.3   8 -415.8507
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```

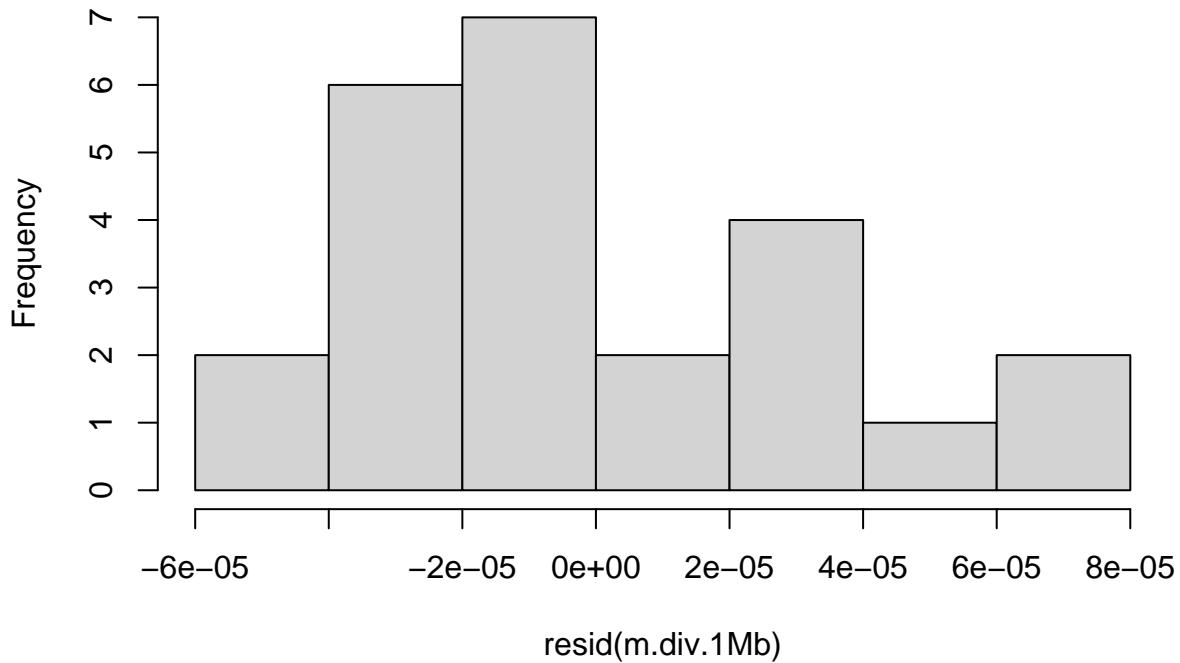


```
dwtest(m.div.1Mb)
```

```
##  
##  Durbin-Watson test  
##  
##  data:  m.div.1Mb  
##  DW = 1.6421, p-value = 0.08247  
##  alternative hypothesis: true autocorrelation is greater than 0  
hmctest(m.div.1Mb)
```

```
##  
##  Harrison-McCabe test  
##  
##  data:  m.div.1Mb  
##  HMC = 0.44033, p-value = 0.349  
hist(resid(m.div.1Mb))
```

## Histogram of resid(m.div.1Mb)



```
summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.1Mb.rep6)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -4.385e-05 -2.409e-05 -8.850e-06  2.257e-05  7.852e-05
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.221e-03 1.452e-05 221.916 < 2e-16 ***
## thetaC      8.720e-01 2.701e-02  32.287 < 2e-16 ***
## rhoC       -2.162e-03 6.894e-03 -0.314  0.75725  
## tmrcaC      4.418e-03 7.076e-05  62.438 < 2e-16 ***
## thetaC:tmrcaC 8.861e-01 2.794e-01   3.172  0.00502 ** 
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 3.696e-05 on 19 degrees of freedom
## Multiple R-squared:  0.9989, Adjusted R-squared:  0.9987 
## F-statistic:  4266 on 4 and 19 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.1Mb[1, 6] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
```

```

r2.bgs.1Mb[2, 6] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb[3, 6] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb[4, 6] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb[5, 6] <- anova.diversity$VarExp[4] * 100

g.div.1Mb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep6, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep6, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep6, weights = varPower(0, ~theta), method = "ML")
g.div.1Mb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep6, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.1Mb.1, g.div.1Mb.2, g.div.1Mb.3, g.div.1Mb.4)

##           df      AIC
## g.div.1Mb.1 8 -419.5980
## g.div.1Mb.2 8 -414.2332
## g.div.1Mb.3 7 -416.0917
## g.div.1Mb.4 7 -420.2497

summary(g.div.1Mb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep6
##       AIC      BIC    logLik
##   -416.0917 -407.8454 215.0459
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##     power
## -1.520312
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0032272 0.0000172 187.11448 0.0000
## thetaC       0.8493976 0.0323282  26.27419 0.0000
## rhoC        0.0010118 0.0057291   0.17661 0.8617
## tmrcaC      0.0044253 0.0000679   65.21370 0.0000
## thetaC:tmrcaC 0.7973603 0.3536114    2.25491 0.0361
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC     -0.786
## rhoC      0.436 -0.580
## tmrcaC    -0.057 -0.130 -0.388
## thetaC:tmrcaC -0.886 0.706 -0.483 0.109

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -1.4816278 -0.6660409 -0.3104259  0.5962878  2.2696281
## 
## Residual standard error: 6.080401e-09
## Degrees of freedom: 24 total; 19 residual
vif(g.div.1Mb.3)

##          thetaC         rhoC        tmrcaC thetaC:tmrcaC
##      3.222770     2.256455     1.632443     2.180967

```

### 5.3.7 Replicate 7

```

rep_7.pi.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.diversity")
rep_7.pi.1Mb$avg <- apply(rep_7.pi.1Mb[4:ncol(rep_7.pi.1Mb)], 1, mean)
rep_7.rho.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.rho.1Mb")
rep_7.theta.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.theta.1Mb")
rep_7.tmrca.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.TMRCA.1Mb")
rep_7.tmrca.1Mb$avg <- apply(rep_7.tmrca.1Mb[4:ncol(rep_7.tmrca.1Mb)], 1, mean)

inf.lands.1Mb.rep7 <- as.data.frame(cbind(rep_7.pi.1Mb$avg, rep_7.theta.1Mb$sample_mean, rep_7.tmrca.1Mb$avg))
names(inf.lands.1Mb.rep7) <- c("diversity", "theta", "tmrca", "rho")

cor.test(~theta+tmrca, data = inf.lands.1Mb.rep7, method = "spearman")

## 
## Spearman's rank correlation rho
## 
## data: theta and tmrca
## S = 442, p-value = 3.392e-06
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.8078261

cor.test(~theta+rho, data = inf.lands.1Mb.rep7, method = "spearman")

## 
## Spearman's rank correlation rho
## 
## data: theta and rho
## S = 550, p-value = 2.535e-05
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.7608696

cor.test(~rho+tmrca, data = inf.lands.1Mb.rep7, method = "spearman")

## 
## Spearman's rank correlation rho
## 
## data: rho and tmrca
## S = 392, p-value = 2.091e-06

```

```

## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.8295652
# centering
inf.lands.1Mb.rep7$thetaC <- inf.lands.1Mb.rep7$theta - mean(inf.lands.1Mb.rep7$theta)
inf.lands.1Mb.rep7$tmrcaC <- inf.lands.1Mb.rep7$tmrca - mean(inf.lands.1Mb.rep7$tmrca)
inf.lands.1Mb.rep7$rhoC <- inf.lands.1Mb.rep7$rho - mean(inf.lands.1Mb.rep7$rho)

inf.lands.1Mb.rep7$bin <- 1:nrow(inf.lands.1Mb.rep7)

# for merging:
inf.lands.1Mb.rep7 <- inf.lands.1Mb.rep7
inf.lands.1Mb.rep7$Replicate <- 1

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.1Mb.rep7)
m.div.1Mb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.1Mb.rep7)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.1Mb.rep7)

AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)

##          df      AIC
## m.div.1Mb    6 -415.3703
## m.div.1Mb.2   7 -417.0328
## m.div.1Mb.3   8 -415.8507
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))


```

```

dwtest(m.div.1Mb)

##
## Durbin-Watson test

```

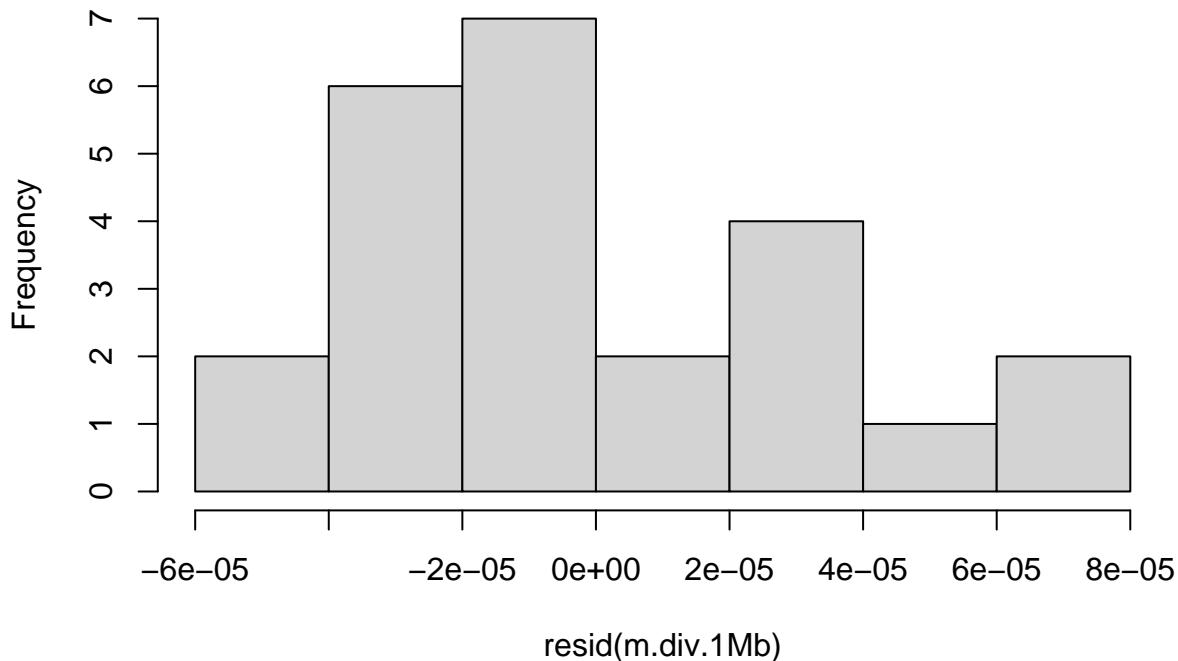
```

## 
## data: m.div.1Mb
## DW = 1.6421, p-value = 0.08247
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.1Mb)

## 
##  Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.44033, p-value = 0.345
hist(resid(m.div.1Mb))

```

### Histogram of resid(m.div.1Mb)



```

summary(m.div.1Mb)

## 
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.1Mb.rep7)
## 
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -4.385e-05 -2.409e-05 -8.850e-06  2.257e-05  7.852e-05 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.221e-03  1.452e-05 221.916 < 2e-16 ***
## thetaC      8.720e-01  2.701e-02  32.287 < 2e-16 ***
## rhoC       -2.162e-03  6.894e-03  -0.314  0.75725  
## 
```

```

## tmrcaC      4.418e-03  7.076e-05  62.438  < 2e-16 ***
## thetaC:tmrcaC 8.861e-01  2.794e-01   3.172  0.00502 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.696e-05 on 19 degrees of freedom
## Multiple R-squared:  0.9989, Adjusted R-squared:  0.9987
## F-statistic:  4266 on 4 and 19 DF,  p-value: < 2.2e-16
anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.1Mb[1, 7] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
r2.bgs.1Mb[2, 7] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb[3, 7] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb[4, 7] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb[5, 7] <- anova.diversity$VarExp[4] * 100

g.div.1Mb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep7, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep7, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep7, weights = varPower(0, ~theta), method = "ML")
g.div.1Mb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep7, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.1Mb.1, g.div.1Mb.2, g.div.1Mb.3, g.div.1Mb.4)

##          df      AIC
## g.div.1Mb.1 8 -419.5980
## g.div.1Mb.2 8 -414.2332
## g.div.1Mb.3 7 -416.0917
## g.div.1Mb.4 7 -420.2497
summary(g.div.1Mb.3)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
## Data: inf.lands.1Mb.rep7
##          AIC      BIC    logLik
## -416.0917 -407.8454 215.0459
##
## Variance function:
## Structure: Power of variance covariate
## Formula: ~theta
## Parameter estimates:
##     power
## -1.520312
##
## Coefficients:
```

```

##          Value Std.Error   t-value p-value
## (Intercept) 0.0032272 0.0000172 187.11448 0.0000
## thetaC      0.8493976 0.0323282  26.27419 0.0000
## rhoC       0.0010118 0.0057291   0.17661 0.8617
## tmrcaC     0.0044253 0.0000679  65.21370 0.0000
## thetaC:tmrcaC 0.7973603 0.3536114   2.25491 0.0361
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC      -0.786
## rhoC        0.436 -0.580
## tmrcaC     -0.057 -0.130 -0.388
## thetaC:tmrcaC -0.886  0.706 -0.483  0.109
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -1.4816278 -0.6660409 -0.3104259  0.5962878  2.2696281
##
## Residual standard error: 6.080401e-09
## Degrees of freedom: 24 total; 19 residual
vif(g.div.1Mb.3)

##           thetaC         rhoC         tmrcaC thetaC:tmrcaC
## 3.222770    2.256455    1.632443    2.180967

```

### 5.3.8 Replicate 8

```

rep_8.pi.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.divers")
rep_8.pi.1Mb$avg <- apply(rep_8.pi.1Mb[4:ncol(rep_8.pi.1Mb)], 1, mean)
rep_8.rho.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.rho.1Mb")
rep_8.theta.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.theta.1Mb")
rep_8.tmrca.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.TMRCA.1Mb")
rep_8.tmrca.1Mb$avg <- apply(rep_8.tmrca.1Mb[4:ncol(rep_8.tmrca.1Mb)], 1, mean)

inf.lands.1Mb.rep8 <- as.data.frame(cbind(rep_8.pi.1Mb$avg, rep_8.theta.1Mb$sample_mean, rep_8.tmrca.1Mb$avg))
names(inf.lands.1Mb.rep8) <- c("diversity", "theta", "tmrca", "rho")

cor.test(~theta+tmrca, data = inf.lands.1Mb.rep8, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 318, p-value = 2.389e-06
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.8617391

cor.test(~theta+rho, data = inf.lands.1Mb.rep8, method = "spearman")

##
## Spearman's rank correlation rho
##

```

```

## data: theta and rho
## S = 1174, p-value = 0.01624
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.4895652

cor.test(~rho+tmrca, data = inf.lands.1Mb.rep8, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 698, p-value = 0.0002294
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.6965217

# centering
inf.lands.1Mb.rep8$thetaC <- inf.lands.1Mb.rep8$theta - mean(inf.lands.1Mb.rep8$theta)
inf.lands.1Mb.rep8$tmrcaC <- inf.lands.1Mb.rep8$tmrca - mean(inf.lands.1Mb.rep8$tmrca)
inf.lands.1Mb.rep8$rhoC <- inf.lands.1Mb.rep8$rho - mean(inf.lands.1Mb.rep8$rho)

inf.lands.1Mb.rep8$bin <- 1:nrow(inf.lands.1Mb.rep8)

# for merging:
inf.lands.1Mb.rep8 <- inf.lands.1Mb.rep8
inf.lands.1Mb.rep8$Replicate <- 1

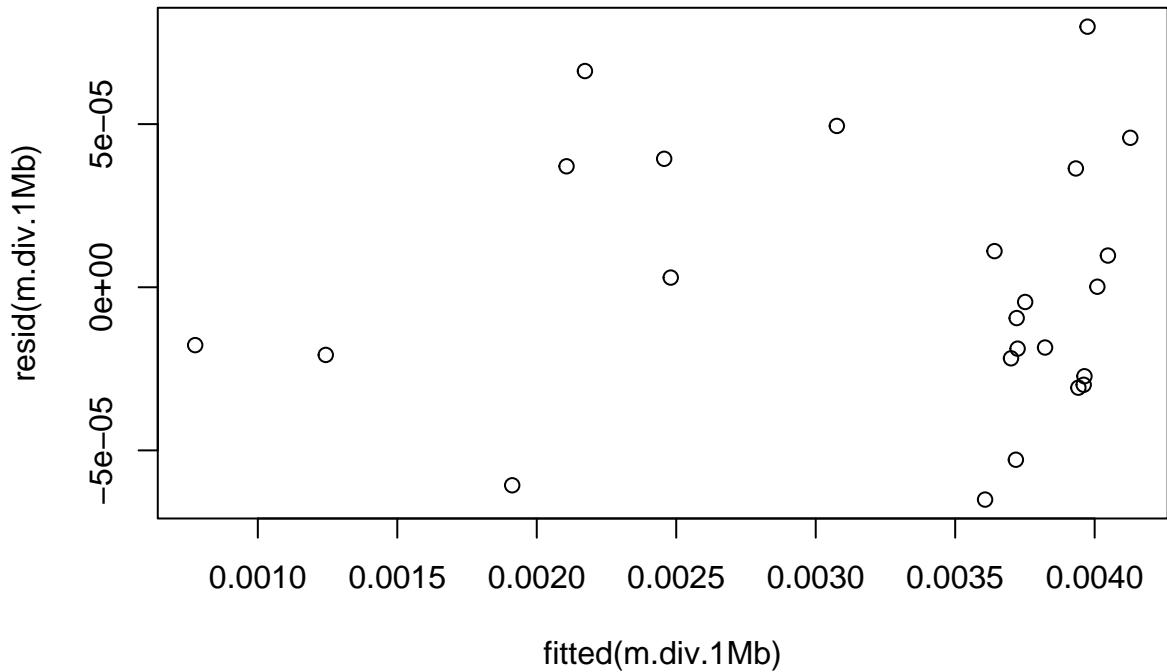
m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.1Mb.rep8)
m.div.1Mb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.1Mb.rep8)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.1Mb.rep8)

AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)

##          df      AIC
## m.div.1Mb     6 -408.1140
## m.div.1Mb.2   7 -431.5240
## m.div.1Mb.3   8 -437.7876

plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```



```

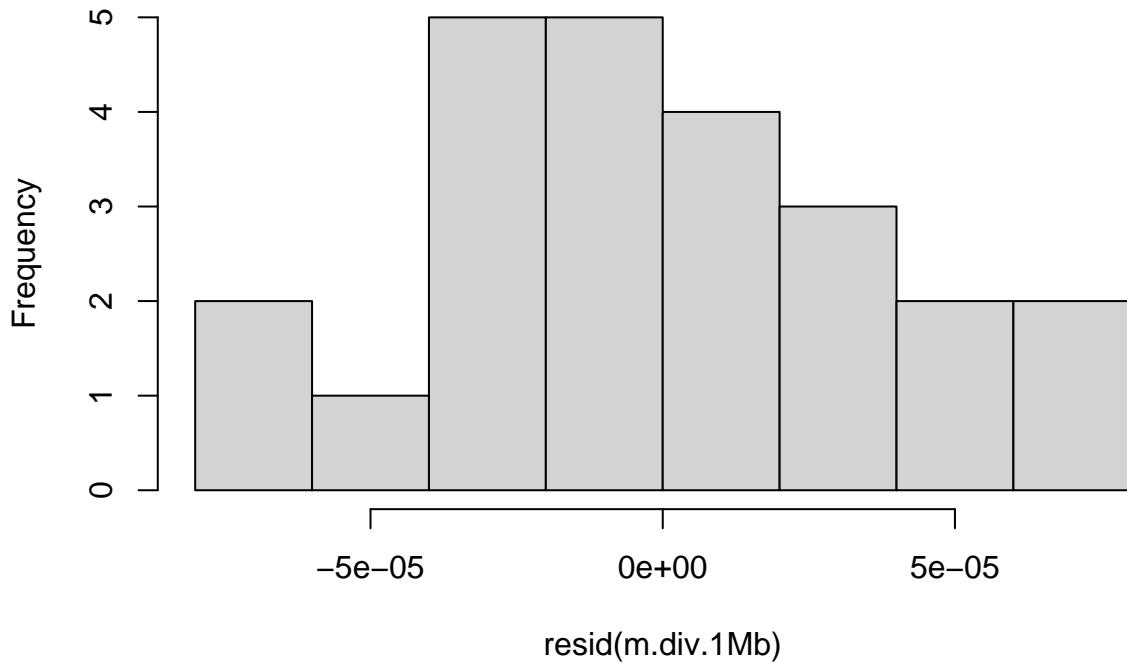
dwtest(m.div.1Mb)

##
##  Durbin-Watson test
##
## data: m.div.1Mb
## DW = 1.8179, p-value = 0.2531
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.1Mb)

##
##  Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.49032, p-value = 0.501
hist(resid(m.div.1Mb))

```

## Histogram of resid(m.div.1Mb)



```
summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.1Mb.rep8)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -6.508e-05 -2.315e-05 -6.980e-06  3.657e-05  7.987e-05
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.187e-03 1.665e-05 191.449 < 2e-16 ***
## thetaC      9.816e-01 2.185e-02  44.935 < 2e-16 ***
## rhoC       -3.638e-02 6.222e-03 -5.847 1.24e-05 ***
## tmrcaC      4.835e-03 2.131e-04  22.685 3.19e-15 ***
## thetaC:tmrcaC 1.624e+00 4.018e-01   4.042 0.000696 ***
## ---      
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 4.299e-05 on 19 degrees of freedom
## Multiple R-squared:  0.9984, Adjusted R-squared:  0.9981 
## F-statistic: 2956 on 4 and 19 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.1Mb[1, 8] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
```

```

r2.bgs.1Mb[2, 8] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb[3, 8] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb[4, 8] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb[5, 8] <- anova.diversity$VarExp[4] * 100

g.div.1Mb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep8, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")

g.div.1Mb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep8, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")

g.div.1Mb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep8, weights = varPower(0, ~theta), method = "ML")

g.div.1Mb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep8, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.1Mb.1, g.div.1Mb.2, g.div.1Mb.3, g.div.1Mb.4)

##           df      AIC
## g.div.1Mb.1 8 -406.1310
## g.div.1Mb.2 8 -404.6132
## g.div.1Mb.3 7 -406.5578
## g.div.1Mb.4 7 -406.1844

summary(g.div.1Mb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep8
##       AIC      BIC  logLik
##   -406.5578 -398.3115 210.2789
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##     power
## 0.7018945
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0031854 0.0000159 199.91712 0e+00
## thetaC       0.9850537 0.0158532  62.13591 0e+00
## rhoC        -0.0389530 0.0050369 -7.73357 0e+00
## tmrcaC       0.0048569 0.0002006  24.20959 0e+00
## thetaC:tmrcaC 1.6762142 0.3731008   4.49266 2e-04
##
## Correlation:
##          (Intr) thetaC rhoC    tmrcaC
## thetaC    -0.347
## rhoC      0.456  0.137
## tmrcaC   -0.340 -0.343 -0.667
## thetaC:tmrcaC -0.827  0.553 -0.545  0.414

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -1.87875767 -0.65584520 -0.04899389  0.92099803  1.99185455
## 
## Residual standard error: 0.00201201
## Degrees of freedom: 24 total; 19 residual
vif(g.div.1Mb.3)

##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
##      3.805533    2.448838    2.910652    4.725060

```

### 5.3.9 Replicate 9

```

rep_9.pi.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.diversity")
rep_9.pi.1Mb$avg <- apply(rep_9.pi.1Mb[4:ncol(rep_9.pi.1Mb)], 1, mean)
rep_9.rho.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.rho.1Mb")
rep_9.theta.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.theta.1Mb")
rep_9.tmrca.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.TMRCA.1Mb")
rep_9.tmrca.1Mb$avg <- apply(rep_9.tmrca.1Mb[4:ncol(rep_9.tmrca.1Mb)], 1, mean)

inf.lands.1Mb.rep9 <- as.data.frame(cbind(rep_9.pi.1Mb$avg, rep_9.theta.1Mb$sample_mean, rep_9.tmrca.1Mb$avg))
names(inf.lands.1Mb.rep9) <- c("diversity", "theta", "tmrca", "rho")

cor.test(~theta+tmrca, data = inf.lands.1Mb.rep9, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 206, p-value = 2.614e-06
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9104348

cor.test(~theta+rho, data = inf.lands.1Mb.rep9, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho
## S = 192, p-value = 2.54e-06
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9165217

cor.test(~rho+tmrca, data = inf.lands.1Mb.rep9, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 178, p-value = 2.448e-06

```

```

## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.9226087

# centering
inf.lands.1Mb.rep9$thetaC <- inf.lands.1Mb.rep9$theta - mean(inf.lands.1Mb.rep9$theta)
inf.lands.1Mb.rep9$tmrcaC <- inf.lands.1Mb.rep9$tmrca - mean(inf.lands.1Mb.rep9$tmrca)
inf.lands.1Mb.rep9$rhoC <- inf.lands.1Mb.rep9$rho - mean(inf.lands.1Mb.rep9$rho)

inf.lands.1Mb.rep9$bin <- 1:nrow(inf.lands.1Mb.rep9)

# for merging:
inf.lands.1Mb.rep9 <- inf.lands.1Mb.rep9
inf.lands.1Mb.rep9$Replicate <- 1

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.1Mb.rep9)
m.div.1Mb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.1Mb.rep9)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.1Mb.rep9)

AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)

##          df      AIC
## m.div.1Mb    6 -406.1573
## m.div.1Mb.2   7 -408.0519
## m.div.1Mb.3   8 -408.6284

plot(resid(m.div.1Mb)~fitted(m.div.1Mb))


```

```

dwtest(m.div.1Mb)

## 
## Durbin-Watson test
## 
```

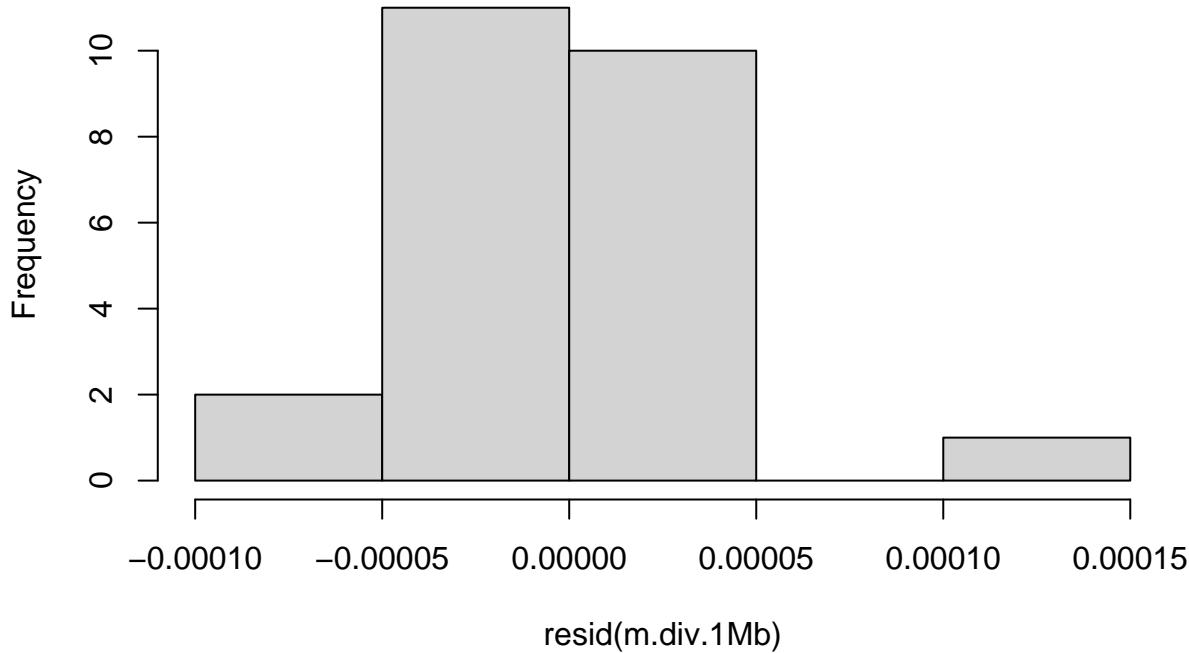
```

## data: m.div.1Mb
## DW = 1.3992, p-value = 0.03732
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.1Mb)

##
##  Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.19756, p-value = 0.014
hist(resid(m.div.1Mb))

```

### Histogram of resid(m.div.1Mb)



```
summary(m.div.1Mb)
```

```

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##     data = inf.lands.1Mb.rep9)
##
## Residuals:
##      Min        1Q        Median         3Q        Max 
## -8.630e-05 -2.169e-05 -1.068e-05  2.216e-05  1.198e-04 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.239e-03 1.633e-05 198.380 < 2e-16 ***
## thetaC       9.538e-01 3.045e-02  31.321 < 2e-16 ***
## rhoC        -2.836e-03 1.216e-02  -0.233 0.818000  
## tmrcaC       4.134e-03 2.838e-04  14.568 9.19e-12 ***
```

```

## thetaC:tmrcaC  1.118e+00  2.777e-01   4.024  0.000725 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.478e-05 on 19 degrees of freedom
## Multiple R-squared:  0.998, Adjusted R-squared:  0.9976
## F-statistic:  2400 on 4 and 19 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.1Mb[1, 9] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
r2.bgs.1Mb[2, 9] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb[3, 9] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb[4, 9] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb[5, 9] <- anova.diversity$VarExp[4] * 100

g.div.1Mb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep9, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep9, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep9, weights = varPower(0, ~theta), method = "ML")
g.div.1Mb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep9, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.1Mb.1, g.div.1Mb.2, g.div.1Mb.3, g.div.1Mb.4)

##          df      AIC
## g.div.1Mb.1 8 -410.8860
## g.div.1Mb.2 8 -414.3732
## g.div.1Mb.3 7 -414.5030
## g.div.1Mb.4 7 -410.7982
summary(g.div.1Mb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep9
##       AIC      BIC  logLik
## -414.503 -406.2567 214.2515
##
## 
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##     power
## -2.373641
##
## Coefficients:
##             Value Std.Error t-value p-value

```

```

## (Intercept) 0.0032415 0.00001434 226.07447 0.0000
## thetaC 0.9424435 0.03770148 24.99752 0.0000
## rhoC 0.0042696 0.00765516 0.55775 0.5835
## tmrcaC 0.0040464 0.00022530 17.95980 0.0000
## thetaC:tmrcaC 1.0584478 0.24614326 4.30013 0.0004
##
## Correlation:
## (Intr) thetaC rhoC tmrcaC
## thetaC -0.552
## rhoC 0.394 -0.374
## tmrcaC -0.226 -0.436 -0.480
## thetaC:tmrcaC -0.760 0.308 -0.462 0.352
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -1.7340864 -0.8630162 -0.1808558  0.9468456  1.8219562
##
## Residual standard error: 4.687009e-11
## Degrees of freedom: 24 total; 19 residual
vif(g.div.1Mb.3)

##      thetaC       rhoC       tmrcaC thetaC:tmrcaC
## 3.416953 2.885606 3.824060 1.644120

```

### 5.3.10 Replicate 10

```

rep_10.pi.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_5.div")
rep_10.pi.1Mb$avg <- apply(rep_10.pi.1Mb[4:ncol(rep_10.pi.1Mb)], 1, mean)
rep_10.rho.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_5.rho")
rep_10.theta.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_5.theta")
rep_10.tmrca.1Mb <- read.table("dm_bgs_sims/10r/Homogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_5.tmrca")
rep_10.tmrca.1Mb$avg <- apply(rep_10.tmrca.1Mb[4:ncol(rep_10.tmrca.1Mb)], 1, mean)

inf.lands.1Mb.rep10 <- as.data.frame(cbind(rep_10.pi.1Mb$avg, rep_10.theta.1Mb$sample_mean, rep_10.tmrca.1Mb$avg))
names(inf.lands.1Mb.rep10) <- c("diversity", "theta", "tmrca", "rho")

cor.test(~theta+tmrca, data = inf.lands.1Mb.rep10, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and tmrca
## S = 302, p-value = 2.503e-06
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## 0.8686957

cor.test(~theta+rho, data = inf.lands.1Mb.rep10, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: theta and rho

```

```

## S = 830, p-value = 0.00101
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.6391304
cor.test(~rho+tmrca, data = inf.lands.1Mb.rep10, method = "spearman")

##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 796, p-value = 0.000711
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.653913

# centering
inf.lands.1Mb.rep10$thetaC <- inf.lands.1Mb.rep10$theta - mean(inf.lands.1Mb.rep10$theta)
inf.lands.1Mb.rep10$tmrcaC <- inf.lands.1Mb.rep10$tmrca - mean(inf.lands.1Mb.rep10$tmrca)
inf.lands.1Mb.rep10$rhoC <- inf.lands.1Mb.rep10$rho - mean(inf.lands.1Mb.rep10$rho)

inf.lands.1Mb.rep10$bin <- 1:nrow(inf.lands.1Mb.rep10)

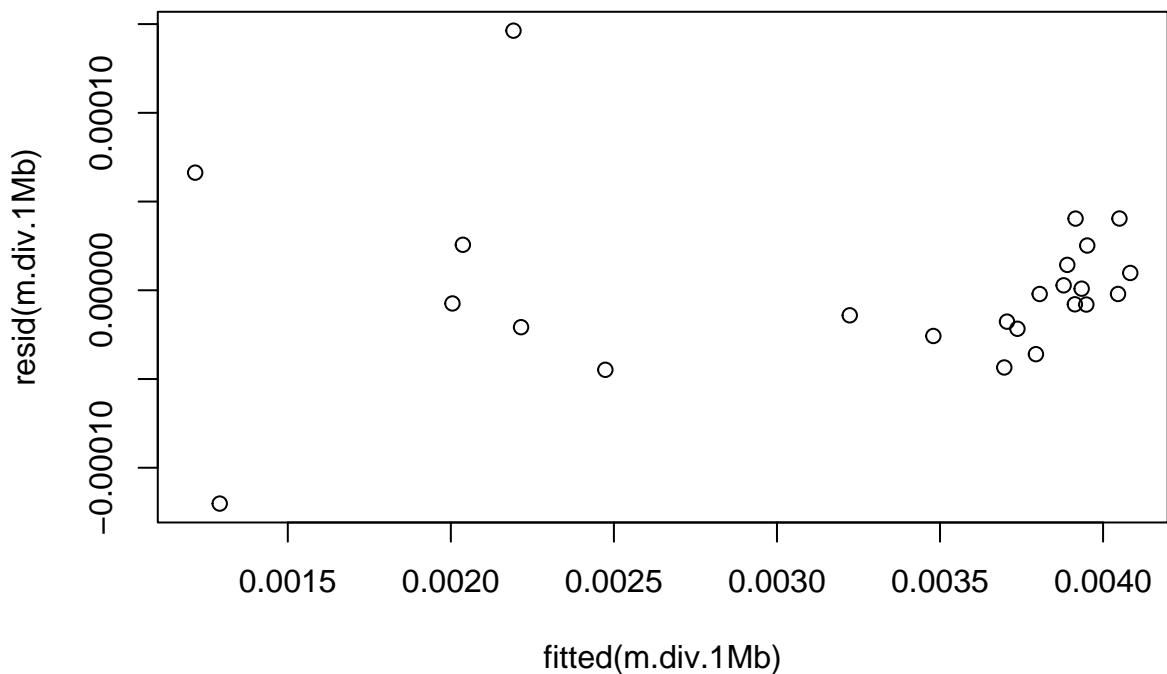
# for merging:
inf.lands.1Mb.rep10 <- inf.lands.1Mb.rep10
inf.lands.1Mb.rep10$Replicate <- 1

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.1Mb.rep10)
m.div.1Mb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.1Mb.rep10)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.1Mb.rep10)

AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)

##          df      AIC
## m.div.1Mb     6 -398.4287
## m.div.1Mb.2   7 -403.8113
## m.div.1Mb.3   8 -416.8144
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```

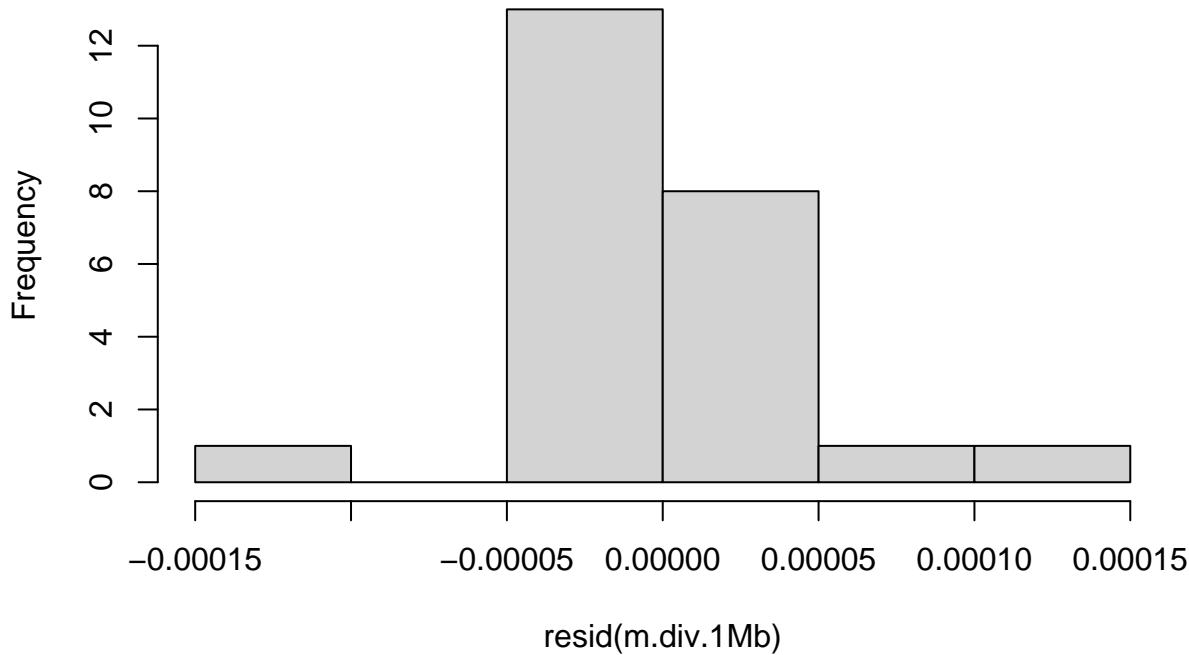


```
dwtest(m.div.1Mb)
```

```
##
##  Durbin-Watson test
##
## data: m.div.1Mb
## DW = 1.0519, p-value = 0.001454
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.1Mb)
```

```
##
##  Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.51438, p-value = 0.531
hist(resid(m.div.1Mb))
```

## Histogram of resid(m.div.1Mb)



```
summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.1Mb.rep10)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -1.202e-04 -2.103e-05 -4.762e-06  1.704e-05  1.463e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.232e-03 2.255e-05 143.313 < 2e-16 ***
## thetaC       8.964e-01 4.162e-02  21.537 8.26e-15 ***
## rhoC        7.052e-03 1.312e-02   0.538  0.5971    
## tmrcaC      3.986e-03 2.222e-04  17.942 2.27e-13 ***
## thetaC:tmrcaC 6.957e-01 3.632e-01    1.915  0.0706 .  
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 5.26e-05 on 19 degrees of freedom
## Multiple R-squared:  0.9974, Adjusted R-squared:  0.9969 
## F-statistic: 1824 on 4 and 19 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.1Mb[1, 10] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.1Mb[2, 10] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb[3, 10] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb[4, 10] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb[5, 10] <- anova.diversity$VarExp[4] * 100

g.div.1Mb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep10, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep10, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep10, weights = varPower(0, ~theta), method = "ML")
g.div.1Mb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep10, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.1Mb.1, g.div.1Mb.2, g.div.1Mb.3, g.div.1Mb.4)

##           df      AIC
## g.div.1Mb.1 8 -427.2196
## g.div.1Mb.2 8 -416.1866
## g.div.1Mb.3 7 -412.5449
## g.div.1Mb.4 7 -426.7420

summary(g.div.1Mb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep10
##       AIC      BIC  logLik
##   -412.5449 -404.2985 213.2724
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##       power
##   -6.942024
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0031813 0.0000185 171.77091 0.0000
## thetaC       0.9219060 0.0533941 17.26607 0.0000
## rhoC        -0.0047991 0.0038578 -1.24402 0.2286
## tmrcaC       0.0041277 0.0002063 20.00655 0.0000
## thetaC:tmrcaC 2.2865764 0.3720056   6.14662 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC     -0.790
## rhoC      0.314 -0.127
## tmrcaC    0.212 -0.606 -0.220
## thetaC:tmrcaC -0.402  0.077 -0.364 -0.253

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -2.37591517 -0.48916830 -0.07381683  0.49448374  1.97637780
## 
## Residual standard error: 2.783215e-22
## Degrees of freedom: 24 total; 19 residual
vif(g.div.1Mb.3)

##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
##      1.951920    1.602199    2.330619    1.459781

```

## 5.4 all replicates:

```

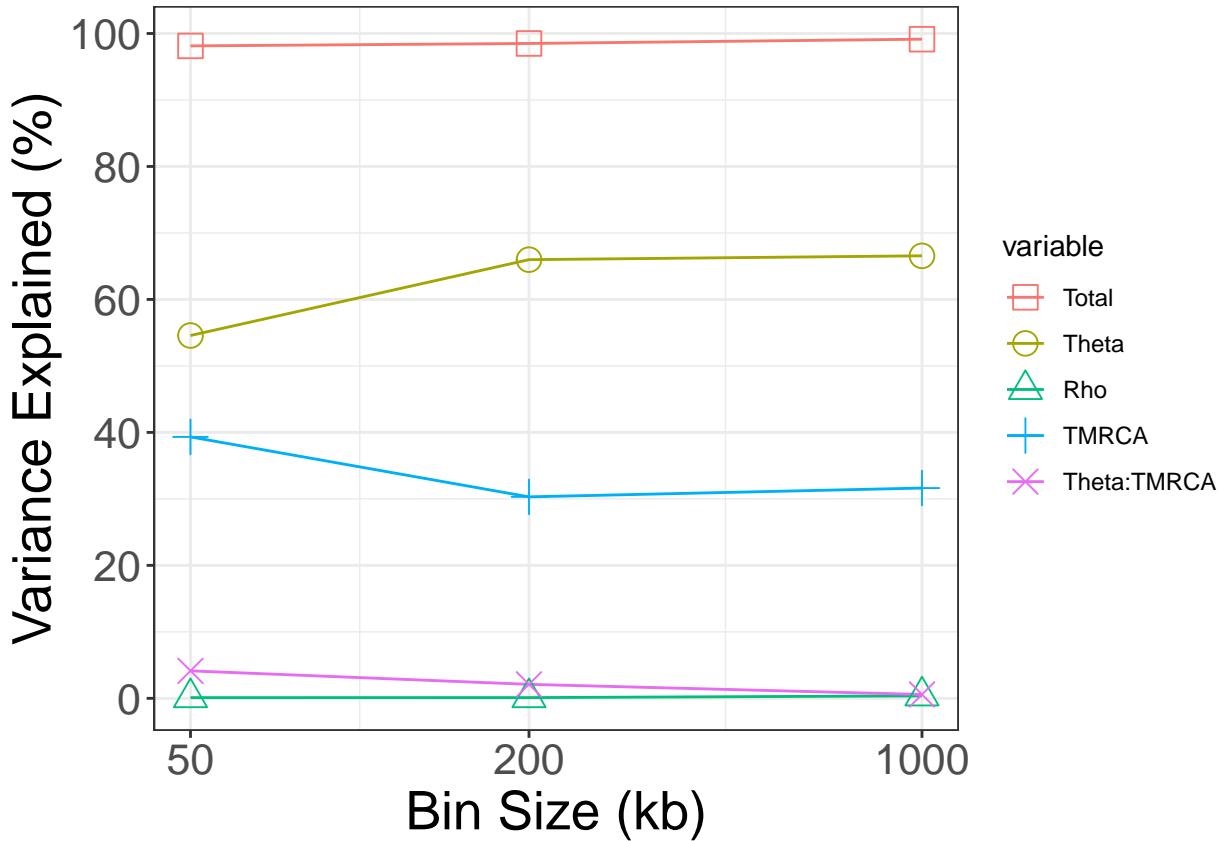
r2.bgs.50kb$average <- apply(r2.bgs.50kb, 1, mean)
r2.bgs.200kb$average <- apply(r2.bgs.200kb, 1, mean)
r2.bgs.1Mb$average <- apply(r2.bgs.1Mb, 1, mean)

# inferred landscapes
r2.inf.avg <- rbind.data.frame(r2.bgs.50kb$average, r2.bgs.200kb$average, r2.bgs.1Mb$average, make.row.colnames(r2.inf.avg) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
r2.inf.avg$bin.size <- c(50, 200, 1000)

r2.tab.comb <- rbind.data.frame(r2.inf.avg)

molten.r2 <- melt(r2.tab.comb, id.vars = "bin.size")
r2.plot <- ggplot(data = molten.r2, aes(x = bin.size, y = value, colour = variable))
r2.plot <- r2.plot + geom_line(data = molten.r2)
r2.plot <- r2.plot + geom_point(aes(shape = variable), size = 4)
r2.plot <- r2.plot + scale_x_continuous(breaks = c(50, 200, 1000), trans="log10")
r2.plot <- r2.plot + scale_y_continuous(breaks = pretty_breaks())
r2.plot <- r2.plot + scale_shape_manual(values = c(0, 1, 2, 3, 4))
r2.plot <- r2.plot + labs(title = NULL, x = "Bin Size (kb)", y = "Variance Explained (%)") + theme_bw()
r2.plot <- r2.plot + theme(axis.title = element_text(size = 20), axis.text = element_text(size = 16))
r2.plot

```



```
ggsave("Figure7.pdf", r2.plot, device = "pdf", )
```

## 6 Simulations with BGS and Gamma Mutation Landscape in SLiM (iSMC-inferred landscapes)

```
cor.table <- as.data.frame(matrix(ncol = 3, nrow = nreps))
row.names(cor.table) <- reps
colnames(cor.table) <- c("50kb", "200kb", "1Mb")
```

### 6.1 50 kb scale

```
r2.bgs.50kb <- as.data.frame(matrix(ncol = nreps, nrow = 5))
row.names(r2.bgs.50kb) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
colnames(r2.bgs.50kb) <- reps

r2.bgs.50kb.true <- as.data.frame(matrix(ncol = nreps, nrow = 5))
row.names(r2.bgs.50kb.true) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
colnames(r2.bgs.50kb.true) <- reps

sim.theta.50kb <- read.table("dm_bgs_sims/MutationMap_50kb.csv", sep = ",", header = T)
sim.rho.50kb <- read.table("dm_bgs_sims/RecombinationMap_50kb.csv", sep = ",", header = T)
```

### 6.1.1 Replicate 1

```

rep1.sim.tmrca.50kb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep1_w50000.csv", sep = ",", header = T)

rep_1.pi.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.dim")
rep_1.pi.50kb$avg <- apply(rep_1.pi.50kb[4:ncol(rep_1.pi.50kb)], 1, mean)
rep_1.rho.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.dim")
rep_1.theta.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.dim")
rep_1.tmrca.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.dim")
rep_1.tmrca.50kb$avg <- apply(rep_1.tmrca.50kb[4:ncol(rep_1.tmrca.50kb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.50kb.rep1 <- as.data.frame(cbind(rep_1.pi.50kb$avg, sim.theta.50kb$Rate, rep1.sim.tmrca.50kb))
names(true.lands.50kb.rep1) <- c("diversity", "theta", "tmrca", "rho")
true.lands.50kb.rep1$thetaC <- true.lands.50kb.rep1$theta - mean(true.lands.50kb.rep1$theta)
true.lands.50kb.rep1$tmrcaC <- true.lands.50kb.rep1$tmrca - mean(true.lands.50kb.rep1$tmrca)
true.lands.50kb.rep1$rhoC <- true.lands.50kb.rep1$rho - mean(true.lands.50kb.rep1$rho, na.rm = T)
true.lands.50kb.rep1$Replicate <- 1
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.50kb.rep1)
anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.50kb.true[1, 1] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.50kb.true[2, 1] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb.true[3, 1] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb.true[4, 1] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb.true[5, 1] <- anova.diversity$VarExp[4] * 100

inf.lands.50kb.rep1 <- as.data.frame(cbind(rep_1.pi.50kb$avg, rep_1.theta.50kb$sample_mean, rep_1.tmrca.50kb))
names(inf.lands.50kb.rep1) <- c("diversity", "theta", "tmrca", "rho")

cor.table[1, 1] <- cor.test(sim.theta.50kb$Rate, rep_1.theta.50kb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.50kb.rep1$thetaC <- inf.lands.50kb.rep1$theta - mean(inf.lands.50kb.rep1$theta)
inf.lands.50kb.rep1$tmrcaC <- inf.lands.50kb.rep1$tmrca - mean(inf.lands.50kb.rep1$tmrca)
inf.lands.50kb.rep1$rhoC <- inf.lands.50kb.rep1$rho - mean(inf.lands.50kb.rep1$rho)

inf.lands.50kb.rep1$bin <- 1:nrow(inf.lands.50kb.rep1)

# for merging:
inf.lands.50kb.rep1 <- inf.lands.50kb.rep1
inf.lands.50kb.rep1$Replicate <- 1

m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.50kb.rep1)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.50kb.rep1)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.50kb.rep1)

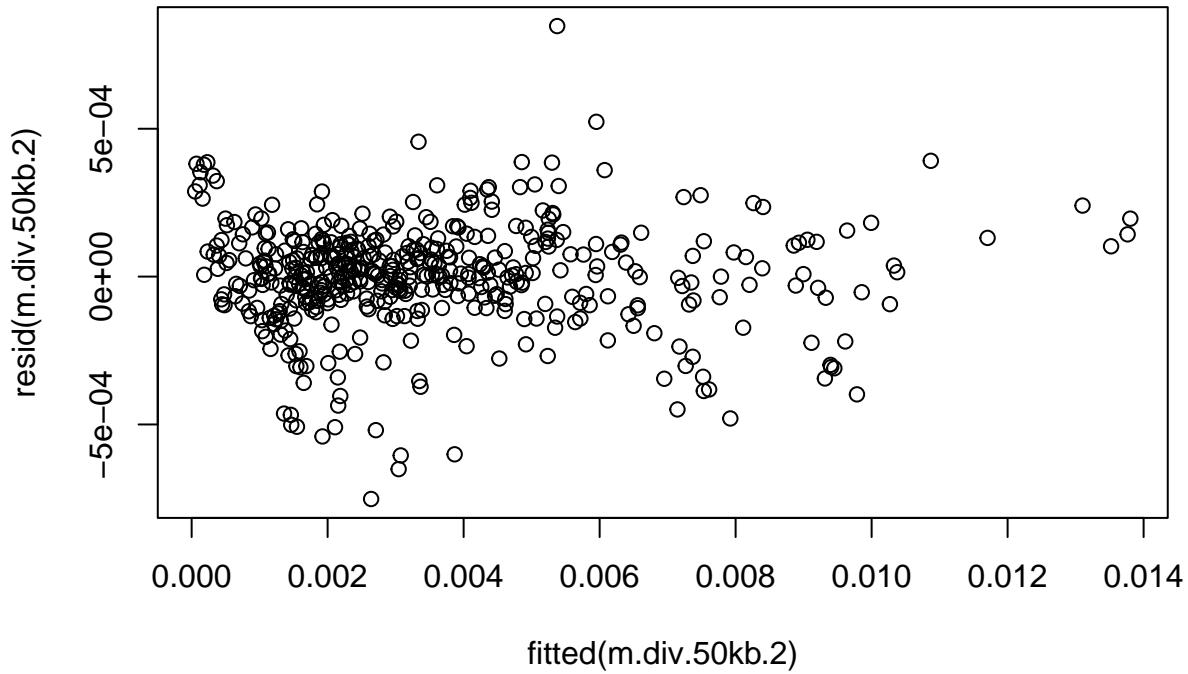
AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

##           df      AIC
## m.div.50kb     6 -6711.225
## m.div.50kb.2   7 -6769.917

```

```
## m.div.50kb.3 8 -6773.287
```

```
plot(resid(m.div.50kb.2)~fitted(m.div.50kb.2))
```



```
dwttest(m.div.50kb.2)
```

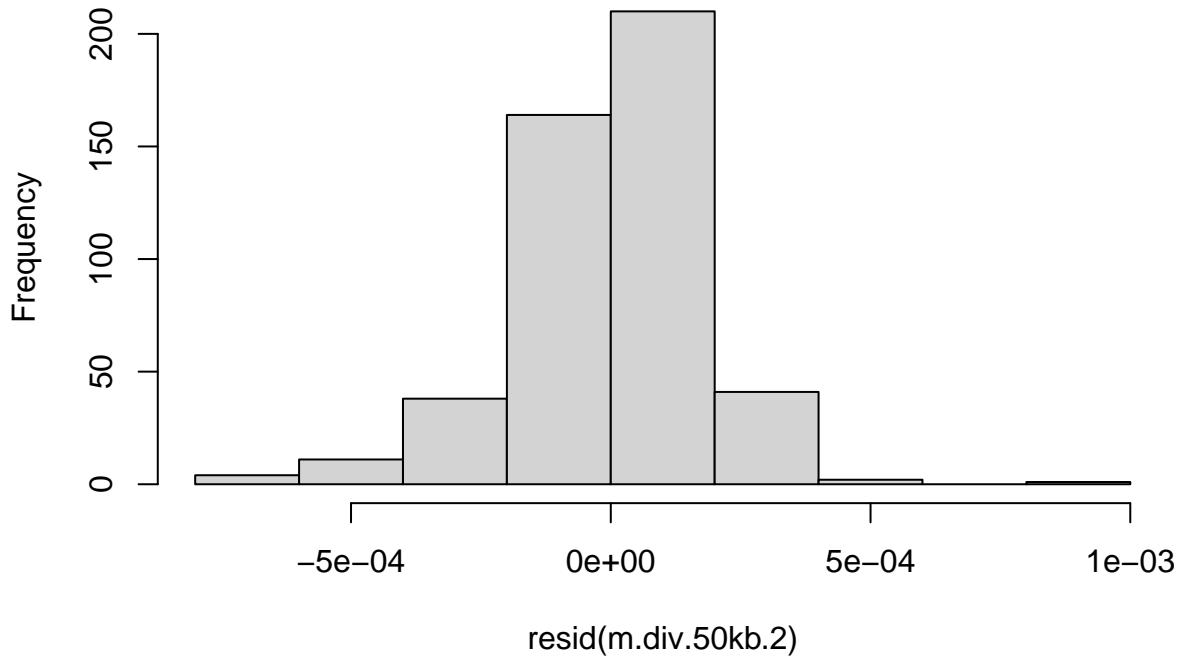
```
##  
## Durbin-Watson test  
##  
## data: m.div.50kb.2  
## DW = 0.87081, p-value < 2.2e-16  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmctest(m.div.50kb.2)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.div.50kb.2  
## HMC = 0.44862, p-value = 0.056
```

```
hist(resid(m.div.50kb.2))
```

## Histogram of resid(m.div.50kb.2)



```
summary(m.div.50kb.2)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC +
##     rhoC:tmrcaC, data = inf.lands.50kb.rep1)
##
## Residuals:
##      Min        1Q    Median        3Q       Max 
## -7.520e-04 -7.777e-05  9.490e-06  1.025e-04  8.472e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.408e-03 9.997e-06 340.914 < 2e-16 ***
## thetaC      1.101e+00 5.095e-03 216.158 < 2e-16 ***
## rhoC        3.964e-02 5.571e-03  7.115 4.27e-12 ***
## tmrcaC      4.483e-03 8.032e-05 55.823 < 2e-16 ***
## thetaC:tmrcaC 1.359e+00 2.844e-02  47.792 < 2e-16 ***
## rhoC:tmrcaC  2.809e-01 3.513e-02   7.997 1.02e-14 ***
## ---      
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0001815 on 465 degrees of freedom
## Multiple R-squared:  0.9949, Adjusted R-squared:  0.9948 
## F-statistic: 1.8e+04 on 5 and 465 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.50kb.2)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
```

```

r2.bgs.50kb[1, 1] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.bgs.50kb[2, 1] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb[3, 1] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb[4, 1] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb[5, 1] <- anova.diversity$VarExp[4] * 100

g.div.50kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep1, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep1, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep1, weights = varPower(0, ~theta), method = "ML")
g.div.50kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep1, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.50kb.1, g.div.50kb.2, g.div.50kb.3, g.div.50kb.4)

##           df      AIC
## g.div.50kb.1 8 -6931.989
## g.div.50kb.2 8 -6938.978
## g.div.50kb.3 7 -6759.275
## g.div.50kb.4 7 -6765.627
summary(g.div.50kb.3)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
## Data: inf.lands.50kb.rep1
##          AIC      BIC  logLik
## -6759.275 -6730.191 3386.638
##
## Variance function:
## Structure: Power of variance covariate
## Formula: ~theta
## Parameter estimates:
##     power
## 0.4736601
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0034561 0.000009204 375.4931      0
## thetaC       1.1086892 0.005953385 186.2284      0
## rhoC        0.0521215 0.005177600 10.0667      0
## tmrcaC      0.0039010 0.000044082  88.4950      0
## thetaC:tmrcaC 1.3464303 0.028940376  46.5243      0
##
## Correlation:
## (Intr) thetaC rhoC   tmrcaC
## thetaC    0.479
## rhoC     0.007 -0.287
## tmrcaC   -0.099 -0.069 -0.335

```

```

## thetaC:tmrcaC -0.188 -0.187 -0.033  0.524
##
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -4.34679876 -0.51809214  0.05652429  0.54157338  4.29208524
##
## Residual standard error: 0.002974804
## Degrees of freedom: 471 total; 466 residual
vif(g.div.50kb.3)

##          thetaC         rhoC        tmrcaC thetaC:tmrcaC
## 1.145853     1.284479     1.614090     1.447901

```

### 6.1.2 Replicate 2

```

rep2.sim.tmrca.50kb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep2_w50000.csv", sep = ",", header = T)

rep_2.pi.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.di")
rep_2.pi.50kb$avg <- apply(rep_2.pi.50kb[4:ncol(rep_2.pi.50kb)], 1, mean)
rep_2.rho.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.r")
rep_2.theta.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5")
rep_2.tmrca.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5")
rep_2.tmrca.50kb$avg <- apply(rep_2.tmrca.50kb[4:ncol(rep_2.tmrca.50kb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.50kb.rep2 <- as.data.frame(cbind(rep_1.pi.50kb$avg, sim.theta.50kb$Rate, rep2.sim.tmrca.50kb))
names(true.lands.50kb.rep2) <- c("diversity", "theta", "tmrca", "rho")
true.lands.50kb.rep2$thetaC <- true.lands.50kb.rep2$theta - mean(true.lands.50kb.rep2$theta)
true.lands.50kb.rep2$tmrcaC <- true.lands.50kb.rep2$tmrca - mean(true.lands.50kb.rep2$tmrca)
true.lands.50kb.rep2$rhoC <- true.lands.50kb.rep2$rho - mean(true.lands.50kb.rep2$rho, na.rm = T)
true.lands.50kb.rep2$Replicate <- 1
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.50kb.rep2)
anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.50kb.true[1, 2] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.50kb.true[2, 2] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb.true[3, 2] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb.true[4, 2] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb.true[5, 2] <- anova.diversity$VarExp[4] * 100

inf.lands.50kb.rep2 <- as.data.frame(cbind(rep_2.pi.50kb$avg, rep_2.theta.50kb$sample_mean, rep_2.tmrca.50kb))
names(inf.lands.50kb.rep2) <- c("diversity", "theta", "tmrca", "rho")

cor.table[2, 1] <- cor.test(sim.theta.50kb$Rate, rep_2.theta.50kb$sample_mean, method = "spearman")$est

# centering
inf.lands.50kb.rep2$thetaC <- inf.lands.50kb.rep2$theta - mean(inf.lands.50kb.rep2$theta)
inf.lands.50kb.rep2$tmrcaC <- inf.lands.50kb.rep2$tmrca - mean(inf.lands.50kb.rep2$tmrca)
inf.lands.50kb.rep2$rhoC <- inf.lands.50kb.rep2$rho - mean(inf.lands.50kb.rep2$rho)

inf.lands.50kb.rep2$bin <- 1:nrow(inf.lands.50kb.rep2)

```

```

# for merging:
inf.lands.50kb.rep2 <- inf.lands.50kb.rep2
inf.lands.50kb.rep2$Replicate <- 1

m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.50kb.rep2)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.50kb.rep2)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.50kb.rep2)

AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

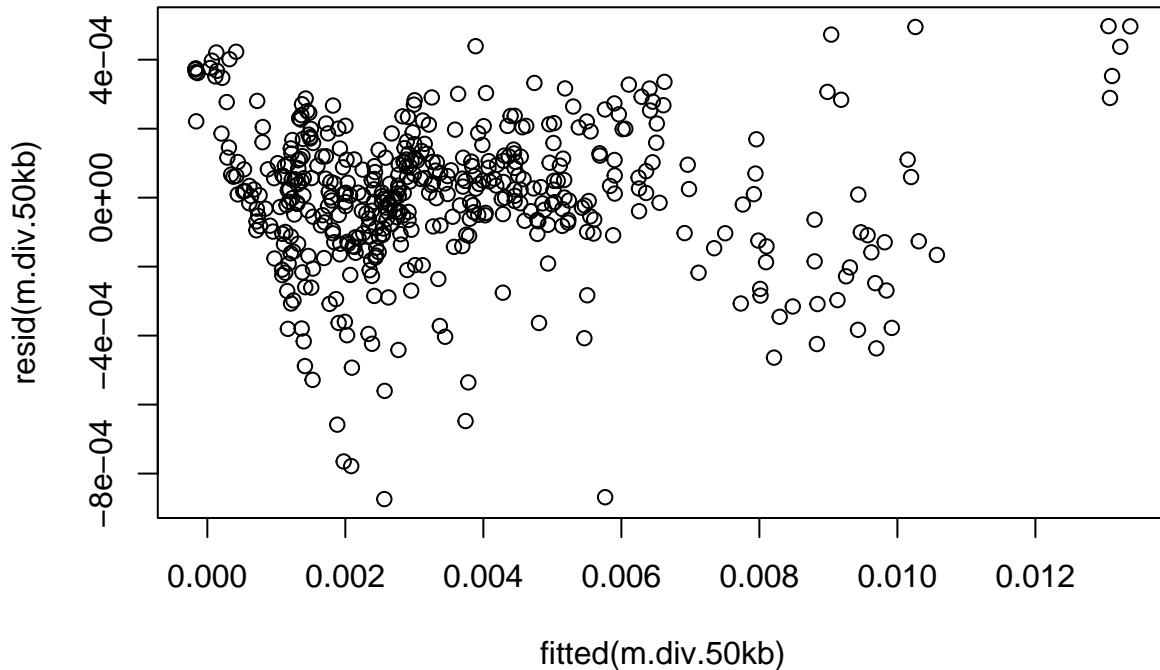
```

```

##          df      AIC
## m.div.50kb     6 -6649.218
## m.div.50kb.2   7 -6767.980
## m.div.50kb.3   8 -6779.854

```

```
plot(resid(m.div.50kb)~fitted(m.div.50kb))
```



```
dwtest(m.div.50kb)
```

```

##
##  Durbin-Watson test
##
## data: m.div.50kb
## DW = 0.92098, p-value < 2.2e-16
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)

```

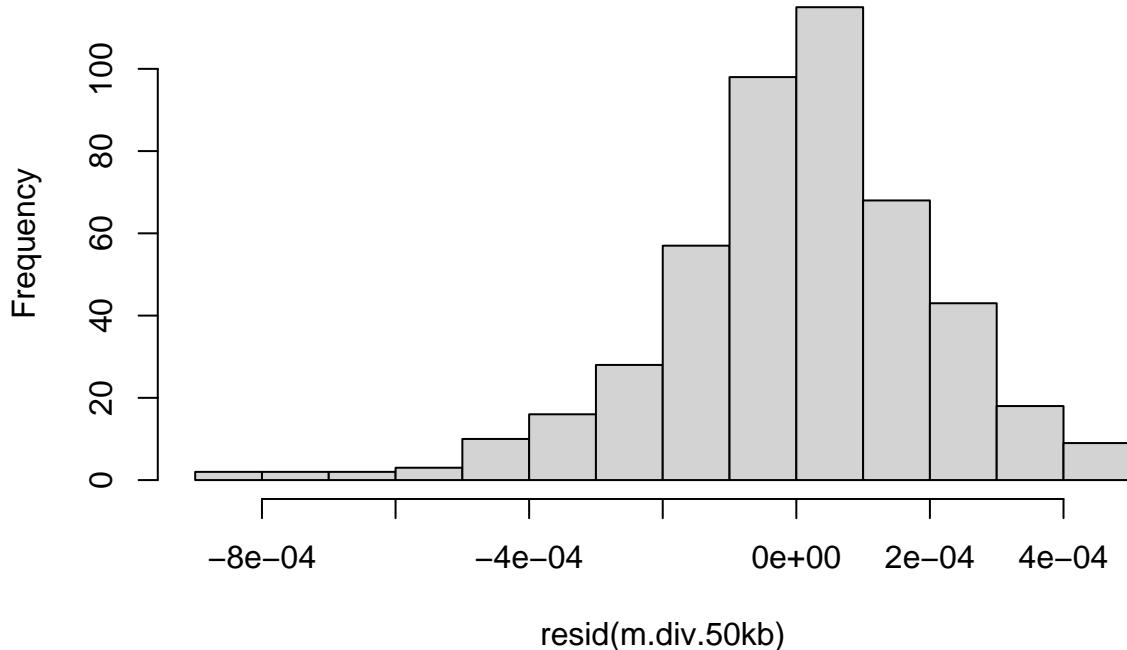
```

##
##  Harrison-McCabe test
##
## data: m.div.50kb
## HMC = 0.4077, p-value = 0.001

```

```
hist(resid(m.div.50kb))
```

Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,  
##      data = inf.lands.50kb.rep2)  
##  
## Residuals:  
##       Min        1Q     Median        3Q       Max  
## -8.740e-04 -1.030e-04  1.349e-05  1.126e-04  4.971e-04  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 3.476e-03 9.569e-06 363.28 <2e-16 ***  
## thetaC      1.275e+00 6.422e-03 198.57 <2e-16 ***  
## rhoC        1.169e-02 5.106e-03   2.29  0.0225 *  
## tmrcaC      3.372e-03 3.228e-05 104.47 <2e-16 ***  
## thetaC:tmrcaC 1.241e+00 2.277e-02   54.51 <2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0002066 on 466 degrees of freedom  
## Multiple R-squared:  0.9935, Adjusted R-squared:  0.9934  
## F-statistic: 1.781e+04 on 4 and 466 DF,  p-value: < 2.2e-16  
anova.diversity <- Anova(m.div.50kb)  
apiss <- anova.diversity$"Sum Sq"  
anova.diversity$VarExp <- apiss / sum(apiss)
```

```

r2.bgs.50kb[1, 2] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.bgs.50kb[2, 2] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb[3, 2] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb[4, 2] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb[5, 2] <- anova.diversity$VarExp[4] * 100

g.div.50kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep2, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep2, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep2, weights = varPower(0, ~theta), method = "ML")
g.div.50kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep2, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.50kb.1, g.div.50kb.2, g.div.50kb.3, g.div.50kb.4)

##           df      AIC
## g.div.50kb.1 8 -6821.900
## g.div.50kb.2 8 -6850.592
## g.div.50kb.3 7 -6682.201
## g.div.50kb.4 7 -6679.873
summary(g.div.50kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep2
##   AIC      BIC logLik
## -6682.201 -6653.117 3348.1
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
## Parameter estimates:
##   power
## 0.3935279
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0034782 0.000009638 360.8871 0e+00
## thetaC       1.2721750 0.007190662 176.9204 0e+00
## rhoC        0.0171851 0.004879366  3.5220 5e-04
## tmrcaC      0.0033612 0.000032505 103.4068 0e+00
## thetaC:tmrcaC 1.2081616 0.025105154  48.1240 0e+00
##
## Correlation:
##            (Intr) thetaC rhoC    tmrcaC
## thetaC     0.398
## rhoC      0.009 -0.199
## tmrcaC   -0.049 -0.033 -0.345

```

```

## thetaC:tmrcaC -0.116 -0.226 -0.055  0.389
##
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -4.49301470 -0.46880229  0.07118776  0.57332632  2.12179443
##
## Residual standard error: 0.002103018
## Degrees of freedom: 471 total; 466 residual
vif(g.div.50kb.3)

##      thetaC       rhoC      tmrcaC thetaC:tmrcaC
## 1.106155 1.196856 1.344242    1.246553

```

### 6.1.3 Replicate 3

```

rep3.sim.tmrca.50kb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep3_w50000.csv", sep = ",", header = T)

rep_3.pi.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.di")
rep_3.pi.50kb$avg <- apply(rep_3.pi.50kb[4:ncol(rep_3.pi.50kb)], 1, mean)
rep_3.rho.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.r")
rep_3.theta.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5")
rep_3.tmrca.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5")
rep_3.tmrca.50kb$avg <- apply(rep_3.tmrca.50kb[4:ncol(rep_3.tmrca.50kb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.50kb.rep3 <- as.data.frame(cbind(rep_1.pi.50kb$avg, sim.theta.50kb$Rate, rep3.sim.tmrca.50kb))
names(true.lands.50kb.rep3) <- c("diversity", "theta", "tmrca", "rho")
true.lands.50kb.rep3$thetaC <- true.lands.50kb.rep3$theta - mean(true.lands.50kb.rep3$theta)
true.lands.50kb.rep3$tmrcaC <- true.lands.50kb.rep3$tmrca - mean(true.lands.50kb.rep3$tmrca)
true.lands.50kb.rep3$rhoC <- true.lands.50kb.rep3$rho - mean(true.lands.50kb.rep3$rho, na.rm = T)
true.lands.50kb.rep3$Replicate <- 1
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.50kb.rep3)
anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.50kb.true[1, 3] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.50kb.true[2, 3] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb.true[3, 3] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb.true[4, 3] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb.true[5, 3] <- anova.diversity$VarExp[4] * 100

inf.lands.50kb.rep3 <- as.data.frame(cbind(rep_3.pi.50kb$avg, rep_3.theta.50kb$sample_mean, rep_3.tmrca.50kb))
names(inf.lands.50kb.rep3) <- c("diversity", "theta", "tmrca", "rho")

cor.table[3, 1] <- cor.test(sim.theta.50kb$Rate, rep_3.theta.50kb$sample_mean, method = "spearman")$est

# centering
inf.lands.50kb.rep3$thetaC <- inf.lands.50kb.rep3$theta - mean(inf.lands.50kb.rep3$theta)
inf.lands.50kb.rep3$tmrcaC <- inf.lands.50kb.rep3$tmrca - mean(inf.lands.50kb.rep3$tmrca)
inf.lands.50kb.rep3$rhoC <- inf.lands.50kb.rep3$rho - mean(inf.lands.50kb.rep3$rho)

inf.lands.50kb.rep3$bin <- 1:nrow(inf.lands.50kb.rep3)

```

```

# for merging:
inf.lands.50kb.rep3 <- inf.lands.50kb.rep3
inf.lands.50kb.rep3$Replicate <- 1

m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.50kb.rep3)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.50kb.rep3)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.50kb.rep3)

AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

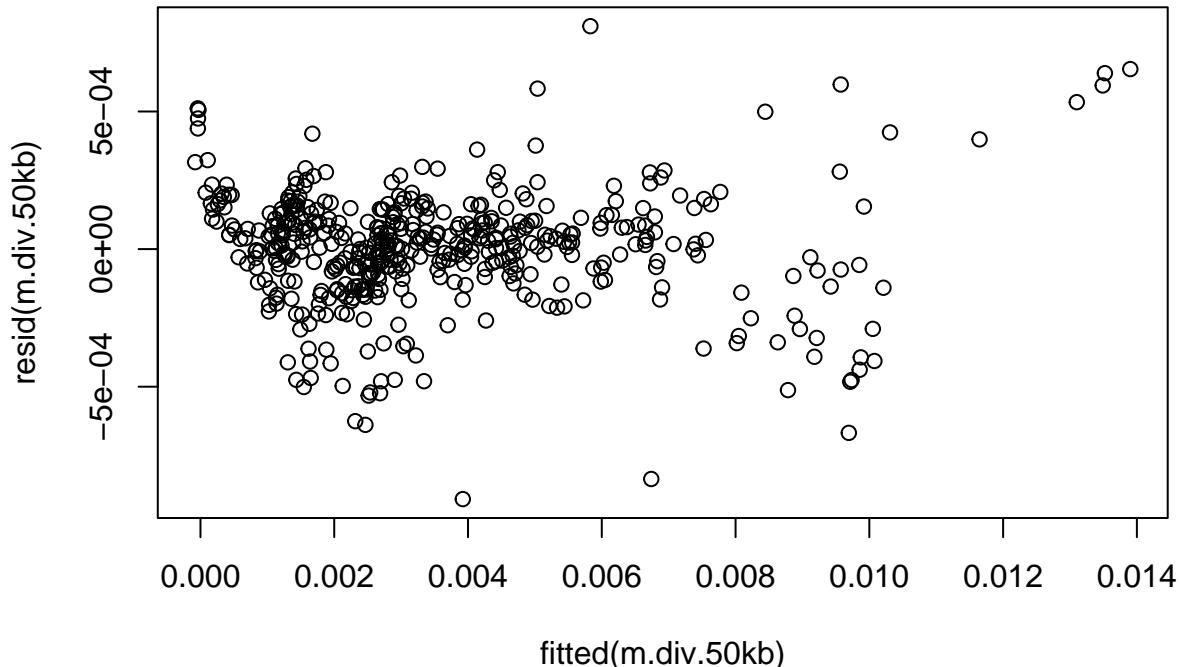
```

```

##          df      AIC
## m.div.50kb    6 -6637.516
## m.div.50kb.2  7 -6780.842
## m.div.50kb.3  8 -6801.784

```

```
plot(resid(m.div.50kb)~fitted(m.div.50kb))
```



```
dwtest(m.div.50kb)
```

```

##
##  Durbin-Watson test
##
##  data:  m.div.50kb
##  DW = 0.89865, p-value < 2.2e-16
##  alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)

```

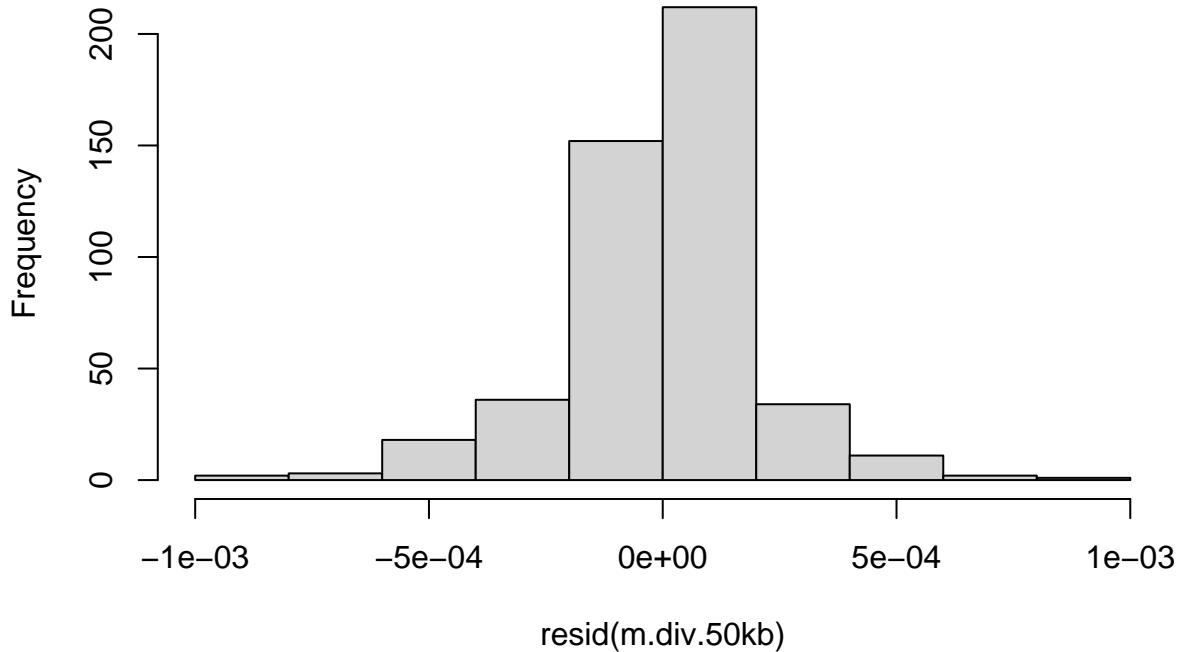
```

##
##  Harrison-McCabe test
##
##  data:  m.div.50kb
##  HMC = 0.50047, p-value = 0.523

```

```
hist(resid(m.div.50kb))
```

Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,  
##      data = inf.lands.50kb.rep3)  
##  
## Residuals:  
##      Min       1Q   Median       3Q      Max  
## -9.084e-04 -8.949e-05  1.918e-05  1.054e-04  8.099e-04  
##  
## Coefficients:  
##              Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 3.505e-03 9.676e-06 362.237 <2e-16 ***  
## thetaC       1.312e+00 6.449e-03 203.462 <2e-16 ***  
## rhoC         1.097e-02 5.153e-03   2.129  0.0338 *  
## tmrcaC       3.237e-03 3.487e-05  92.838 <2e-16 ***  
## thetaC:tmrcaC 1.186e+00 2.390e-02  49.600 <2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0002091 on 466 degrees of freedom  
## Multiple R-squared:  0.9932, Adjusted R-squared:  0.9931  
## F-statistic: 1.694e+04 on 4 and 466 DF,  p-value: < 2.2e-16  
anova.diversity <- Anova(m.div.50kb)  
apiss <- anova.diversity$"Sum Sq"  
anova.diversity$VarExp <- apiss / sum(apiss)
```

```

r2.bgs.50kb[1, 3] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.bgs.50kb[2, 3] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb[3, 3] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb[4, 3] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb[5, 3] <- anova.diversity$VarExp[4] * 100

g.div.50kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep3, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep3, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep3, weights = varPower(0, ~theta), method = "ML")
g.div.50kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep3, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.50kb.1, g.div.50kb.2, g.div.50kb.3, g.div.50kb.4)

##           df      AIC
## g.div.50kb.1 8 -6826.837
## g.div.50kb.2 8 -6854.552
## g.div.50kb.3 7 -6699.473
## g.div.50kb.4 7 -6676.519
summary(g.div.50kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep3
##       AIC     BIC   logLik
## -6699.473 -6670.389 3356.736
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
## Parameter estimates:
##   power
## 0.4942882
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0035078 0.000009699 361.6599 0e+00
## thetaC       1.3054348 0.007242851 180.2377 0e+00
## rhoC        0.0189783 0.004825241   3.9331 1e-04
## tmrcaC      0.0032306 0.000033681   95.9174 0e+00
## thetaC:tmrcaC 1.1145749 0.025369938   43.9329 0e+00
##
## Correlation:
##            (Intr) thetaC rhoC    tmrcaC
## thetaC      0.486
## rhoC       0.002 -0.177
## tmrcaC    -0.030  0.002 -0.372

```

```

## thetaC:tmrcaC -0.096 -0.152 -0.018  0.312
##
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -4.41121799 -0.49190945  0.06406712  0.57664950  3.48192284
##
## Residual standard error: 0.003822243
## Degrees of freedom: 471 total; 466 residual
vif(g.div.50kb.3)

##      thetaC       rhoC      tmrcaC thetaC:tmrcaC
## 1.059040 1.212741 1.302453   1.145266

```

#### 6.1.4 Replicate 4

```

rep4.sim.tmrca.50kb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep4_w50000.csv", sep = ",", header = T)

rep_4.pi.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.di")
rep_4.pi.50kb$avg <- apply(rep_4.pi.50kb[4:ncol(rep_4.pi.50kb)], 1, mean)
rep_4.rho.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.r")
rep_4.theta.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.t")
rep_4.tmrca.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.tmrca")
rep_4.tmrca.50kb$avg <- apply(rep_4.tmrca.50kb[4:ncol(rep_4.tmrca.50kb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.50kb.rep4 <- as.data.frame(cbind(rep_1.pi.50kb$avg, sim.theta.50kb$Rate, rep4.sim.tmrca.50kb))
names(true.lands.50kb.rep4) <- c("diversity", "theta", "tmrca", "rho")
true.lands.50kb.rep4$thetaC <- true.lands.50kb.rep4$theta - mean(true.lands.50kb.rep4$theta)
true.lands.50kb.rep4$tmrcaC <- true.lands.50kb.rep4$tmrca - mean(true.lands.50kb.rep4$tmrca)
true.lands.50kb.rep4$rhoC <- true.lands.50kb.rep4$rho - mean(true.lands.50kb.rep4$rho, na.rm = T)
true.lands.50kb.rep4$Replicate <- 1
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.50kb.rep4)
anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.50kb.true[1, 4] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.50kb.true[2, 4] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb.true[3, 4] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb.true[4, 4] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb.true[5, 4] <- anova.diversity$VarExp[4] * 100

inf.lands.50kb.rep4 <- as.data.frame(cbind(rep_4.pi.50kb$avg, rep_4.theta.50kb$sample_mean, rep_4.tmrca.50kb$sample_mean))
names(inf.lands.50kb.rep4) <- c("diversity", "theta", "tmrca", "rho")

cor.table[4, 1] <- cor.test(sim.theta.50kb$Rate, rep_4.theta.50kb$sample_mean, method = "spearman")$estimate
# centering
inf.lands.50kb.rep4$thetaC <- inf.lands.50kb.rep4$theta - mean(inf.lands.50kb.rep4$theta)
inf.lands.50kb.rep4$tmrcaC <- inf.lands.50kb.rep4$tmrca - mean(inf.lands.50kb.rep4$tmrca)
inf.lands.50kb.rep4$rhoC <- inf.lands.50kb.rep4$rho - mean(inf.lands.50kb.rep4$rho)

inf.lands.50kb.rep4$bin <- 1:nrow(inf.lands.50kb.rep4)

```

```

# for merging:
inf.lands.50kb.rep4 <- inf.lands.50kb.rep4
inf.lands.50kb.rep4$Replicate <- 1

m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.50kb.rep4)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.50kb.rep4)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.50kb.rep4)

AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

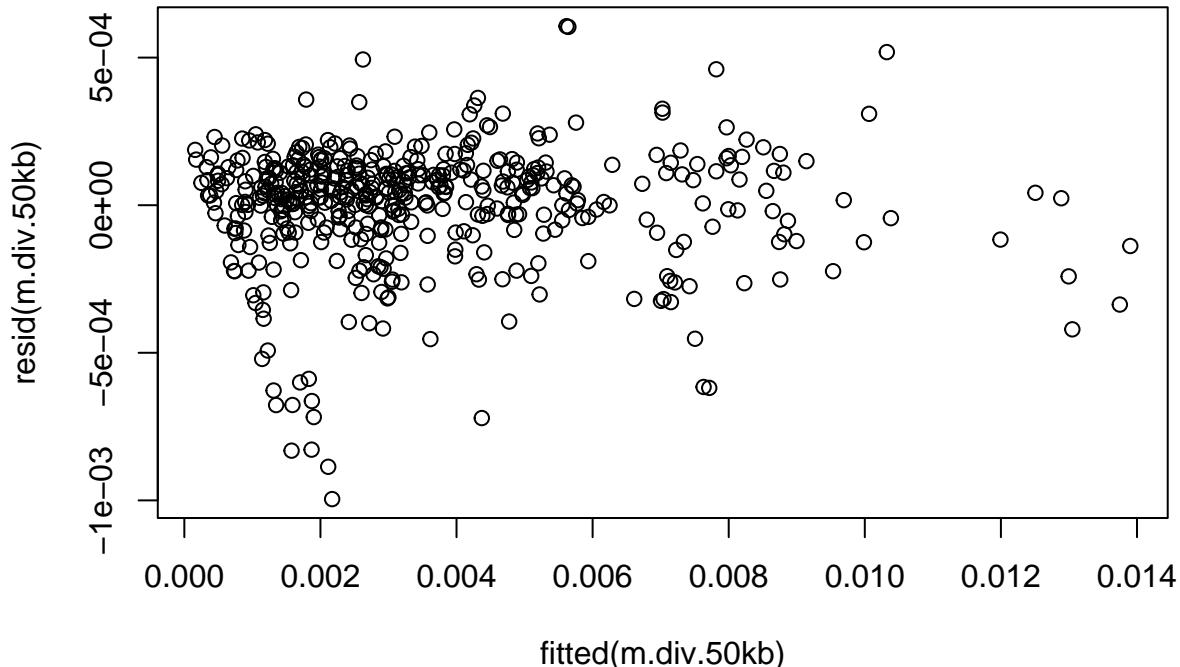
```

```

##          df      AIC
## m.div.50kb     6 -6651.111
## m.div.50kb.2   7 -6649.680
## m.div.50kb.3   8 -6651.347

```

```
plot(resid(m.div.50kb)~fitted(m.div.50kb))
```



```
dwtest(m.div.50kb)
```

```

##
##  Durbin-Watson test
##
##  data:  m.div.50kb
##  DW = 0.94293, p-value < 2.2e-16
##  alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.50kb)

```

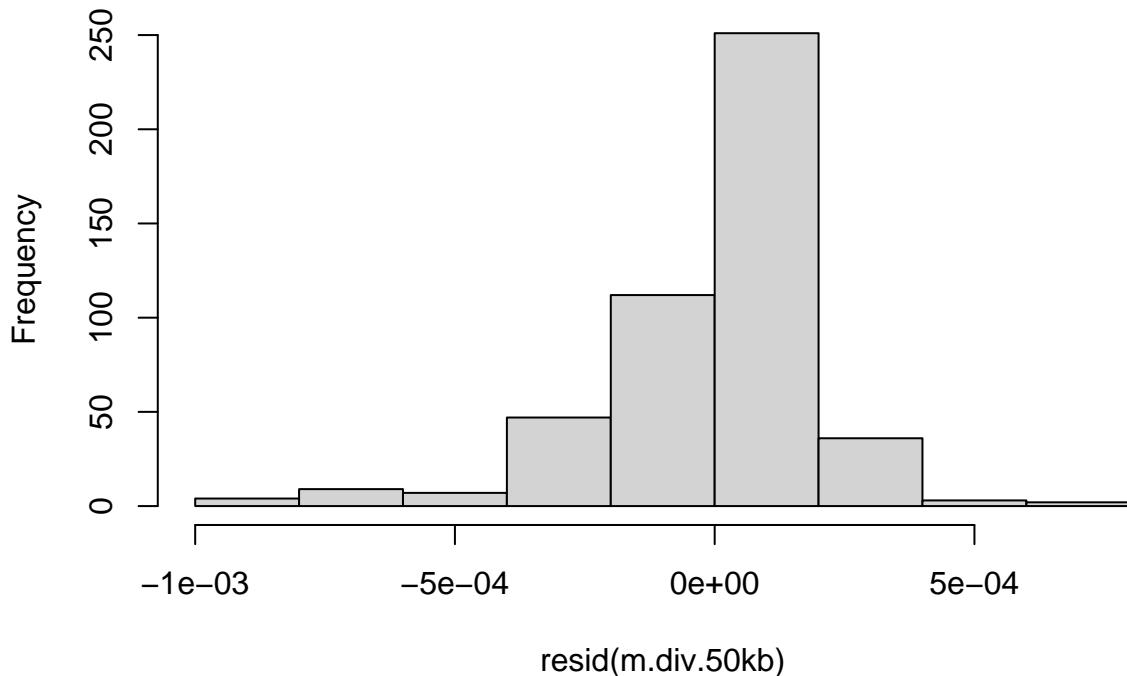
```

##
##  Harrison-McCabe test
##
##  data:  m.div.50kb
##  HMC = 0.43008, p-value = 0.011

```

```
hist(resid(m.div.50kb))
```

Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,  
##      data = inf.lands.50kb.rep4)  
##  
## Residuals:  
##       Min        1Q     Median        3Q       Max  
## -9.957e-04 -7.736e-05  4.142e-05  1.167e-04  6.064e-04  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 3.439e-03 9.716e-06 353.943 <2e-16 ***  
## thetaC      1.066e+00 5.131e-03 207.727 <2e-16 ***  
## rhoC        4.166e-02 4.872e-03   8.552 <2e-16 ***  
## tmrcaC      4.753e-03 6.204e-05  76.620 <2e-16 ***  
## thetaC:tmrcaC 1.514e+00 2.990e-02  50.617 <2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0002061 on 466 degrees of freedom  
## Multiple R-squared:  0.9934, Adjusted R-squared:  0.9933  
## F-statistic: 1.742e+04 on 4 and 466 DF,  p-value: < 2.2e-16  
anova.diversity <- Anova(m.div.50kb)  
apiss <- anova.diversity$"Sum Sq"  
anova.diversity$VarExp <- apiss / sum(apiss)
```

```

r2.bgs.50kb[1, 4] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.bgs.50kb[2, 4] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb[3, 4] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb[4, 4] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb[5, 4] <- anova.diversity$VarExp[4] * 100

g.div.50kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep4, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep4, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep4, weights = varPower(0, ~theta), method = "ML")
g.div.50kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep4, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.50kb.1, g.div.50kb.2, g.div.50kb.3, g.div.50kb.4)

##           df      AIC
## g.div.50kb.1 8 -6872.472
## g.div.50kb.2 8 -6875.271
## g.div.50kb.3 7 -6654.881
## g.div.50kb.4 7 -6700.650
summary(g.div.50kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep4
##   AIC      BIC  logLik
## -6654.881 -6625.797 3334.44
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
## Parameter estimates:
##   power
## 0.1527489
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0034372 0.00000977 351.7078     0
## thetaC       1.0643723 0.00545768 195.0228     0
## rhoC        0.0438922 0.00488900  8.9777     0
## tmrcaC      0.0047503 0.00006318  75.1824     0
## thetaC:tmrcaC 1.5397661 0.03235723  47.5865     0
##
## Correlation:
##            (Intr) thetaC rhoC    tmrcaC
## thetaC      0.191
## rhoC       -0.009 -0.265
## tmrcaC     -0.080 -0.204 -0.145

```

```

## thetaC:tmrcaC -0.232 -0.173  0.053  0.356
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -5.2015408 -0.3778042  0.2017817  0.5787508  2.8135238
##
## Residual standard error: 0.0004990653
## Degrees of freedom: 471 total; 466 residual
vif(g.div.50kb.3)

##          thetaC         rhoC        tmrcaC thetaC:tmrcaC
## 1.157157    1.133423    1.236016    1.166786

```

### 6.1.5 Replicate 5

```

rep5.sim.tmrca.50kb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep5_w50000.csv", sep = ",", header = T)

rep_5.pi.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.di")
rep_5.pi.50kb$avg <- apply(rep_5.pi.50kb[4:ncol(rep_5.pi.50kb)], 1, mean)
rep_5.rho.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.r")
rep_5.theta.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5")
rep_5.tmrca.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5")
rep_5.tmrca.50kb$avg <- apply(rep_5.tmrca.50kb[4:ncol(rep_5.tmrca.50kb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.50kb.rep5 <- as.data.frame(cbind(rep_1.pi.50kb$avg, sim.theta.50kb$Rate, rep5.sim.tmrca.50kb))
names(true.lands.50kb.rep5) <- c("diversity", "theta", "tmrca", "rho")
true.lands.50kb.rep5$thetaC <- true.lands.50kb.rep5$theta - mean(true.lands.50kb.rep5$theta)
true.lands.50kb.rep5$tmrcaC <- true.lands.50kb.rep5$tmrca - mean(true.lands.50kb.rep5$tmrca)
true.lands.50kb.rep5$rhoC <- true.lands.50kb.rep5$rho - mean(true.lands.50kb.rep5$rho, na.rm = T)
true.lands.50kb.rep5$Replicate <- 1
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.50kb.rep5)
anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.50kb.true[1, 5] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] + anova.diversity$VarExp[4]) * 100
r2.bgs.50kb.true[2, 5] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb.true[3, 5] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb.true[4, 5] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb.true[5, 5] <- anova.diversity$VarExp[4] * 100

inf.lands.50kb.rep5 <- as.data.frame(cbind(rep_5.pi.50kb$avg, rep_5.theta.50kb$sample_mean, rep_5.tmrca.50kb$sample_mean))
names(inf.lands.50kb.rep5) <- c("diversity", "theta", "tmrca", "rho")

cor.table[5, 1] <- cor.test(sim.theta.50kb$Rate, rep_5.theta.50kb$sample_mean, method = "spearman")$estimate
cor.table[1, 5] <- cor.test(sim.theta.50kb$Rate, rep_5.theta.50kb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.50kb.rep5$thetaC <- inf.lands.50kb.rep5$theta - mean(inf.lands.50kb.rep5$theta)
inf.lands.50kb.rep5$tmrcaC <- inf.lands.50kb.rep5$tmrca - mean(inf.lands.50kb.rep5$tmrca)
inf.lands.50kb.rep5$rhoC <- inf.lands.50kb.rep5$rho - mean(inf.lands.50kb.rep5$rho)

inf.lands.50kb.rep5$bin <- 1:nrow(inf.lands.50kb.rep5)

```

```

# for merging:
inf.lands.50kb.rep5 <- inf.lands.50kb.rep5
inf.lands.50kb.rep5$Replicate <- 1

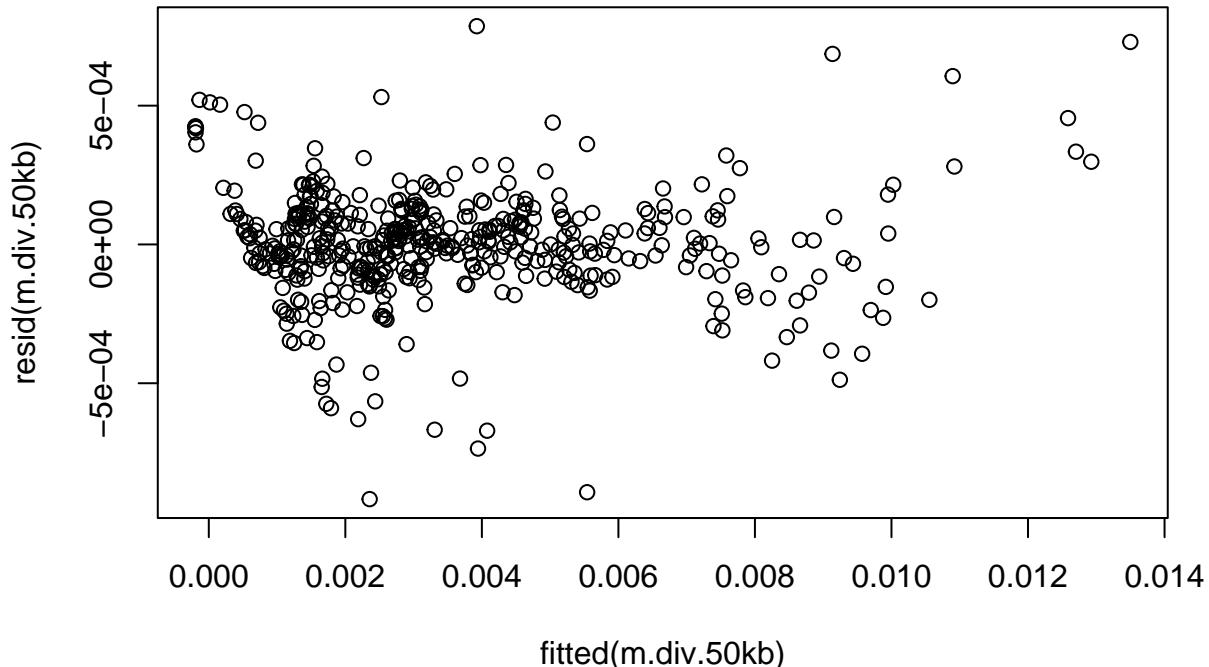
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.50kb.rep5)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.50kb.rep5)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.50kb.rep5)

AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

##           df      AIC
## m.div.50kb     6 -6679.244
## m.div.50kb.2   7 -6802.716
## m.div.50kb.3   8 -6811.009

plot(resid(m.div.50kb)~fitted(m.div.50kb))

```



```

dwtest(m.div.50kb)

##
##  Durbin-Watson test
##
##  data:  m.div.50kb
##  DW = 0.98276, p-value < 2.2e-16
##  alternative hypothesis: true autocorrelation is greater than 0

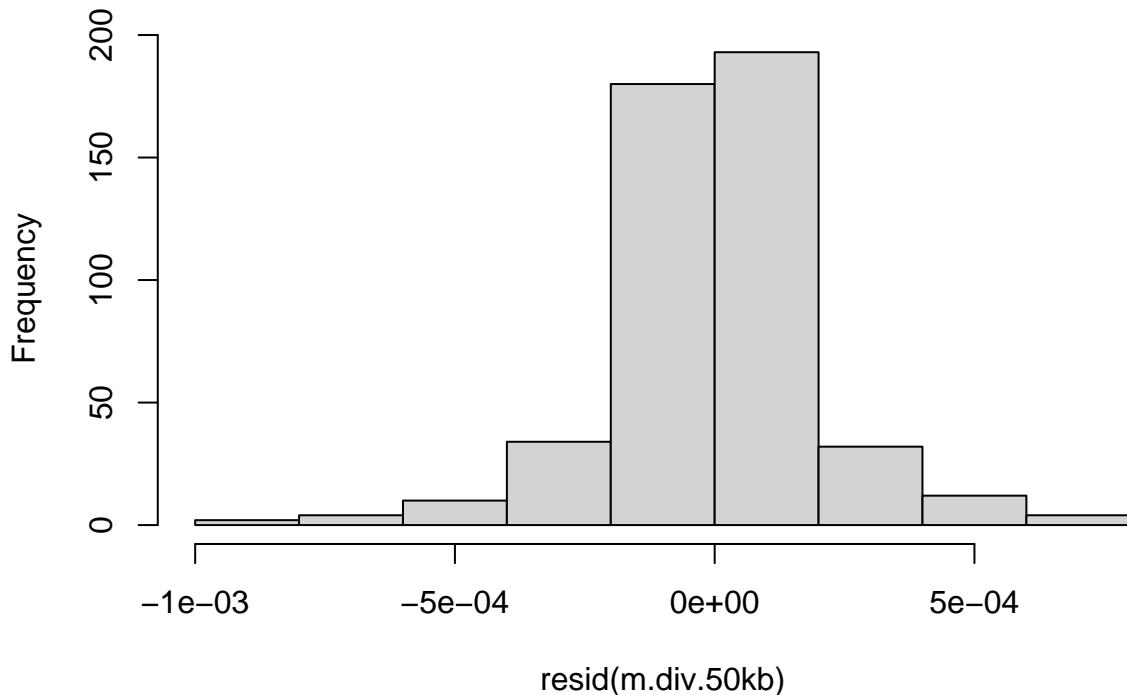
hmctest(m.div.50kb)

##
##  Harrison-McCabe test
##
##  data:  m.div.50kb
##  HMC = 0.39935, p-value = 0.002

```

```
hist(resid(m.div.50kb))
```

Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,  
##      data = inf.lands.50kb.rep5)  
##  
## Residuals:  
##      Min       1Q   Median       3Q      Max  
## -9.174e-04 -8.788e-05  7.320e-06  9.869e-05  7.862e-04  
##  
## Coefficients:  
##              Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 3.452e-03 9.312e-06 370.741 <2e-16 ***  
## thetaC       1.288e+00 6.186e-03 208.139 <2e-16 ***  
## rhoC         8.740e-03 4.922e-03  1.776  0.0764 .  
## tmrcaC       3.336e-03 3.447e-05  96.761 <2e-16 ***  
## thetaC:tmrcaC 1.241e+00 2.398e-02  51.749 <2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0002001 on 466 degrees of freedom  
## Multiple R-squared:  0.9936, Adjusted R-squared:  0.9936  
## F-statistic: 1.81e+04 on 4 and 466 DF,  p-value: < 2.2e-16  
anova.diversity <- Anova(m.div.50kb)  
apiss <- anova.diversity$"Sum Sq"  
anova.diversity$VarExp <- apiss / sum(apiss)
```

```

r2.bgs.50kb[1, 5] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.bgs.50kb[2, 5] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb[3, 5] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb[4, 5] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb[5, 5] <- anova.diversity$VarExp[4] * 100

g.div.50kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep5, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep5, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep5, weights = varPower(0, ~theta), method = "ML")
g.div.50kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep5, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.50kb.1, g.div.50kb.2, g.div.50kb.3, g.div.50kb.4)

##           df      AIC
## g.div.50kb.1 8 -6839.185
## g.div.50kb.2 8 -6876.135
## g.div.50kb.3 7 -6721.049
## g.div.50kb.4 7 -6709.999
summary(g.div.50kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep5
##   AIC      BIC    logLik
## -6721.049 -6691.965 3367.525
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
## Parameter estimates:
##   power
## 0.4471777
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0034552 0.000009444 365.8683 0.0000
## thetaC       1.2814136 0.007104489 180.3667 0.0000
## rhoC        0.0136620 0.004733547   2.8862 0.0041
## tmrcaC      0.0033220 0.000035485   93.6164 0.0000
## thetaC:tmrcaC 1.1970833 0.027229278   43.9631 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC     0.452
## rhoC      0.005 -0.222
## tmrcaC   -0.079 -0.075 -0.327

```

```

## thetaC:tmrcaC -0.159 -0.203 -0.022  0.489
##
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -4.43775897 -0.45599876  0.02430307  0.53146119  3.77882686
##
## Residual standard error: 0.002814922
## Degrees of freedom: 471 total; 466 residual
vif(g.div.50kb.3)

##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
## 1.106175 1.220884 1.519047    1.385262

```

### 6.1.6 Replicate 6

```

rep6.sim.tmrca.50kb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep6_w50000.csv", sep = ",", header = T)

rep_6.pi.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.di")
rep_6.pi.50kb$avg <- apply(rep_6.pi.50kb[4:ncol(rep_6.pi.50kb)], 1, mean)
rep_6.rho.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.r")
rep_6.theta.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5")
rep_6.tmrca.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5")
rep_6.tmrca.50kb$avg <- apply(rep_6.tmrca.50kb[4:ncol(rep_6.tmrca.50kb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.50kb.rep6 <- as.data.frame(cbind(rep_1.pi.50kb$avg, sim.theta.50kb$Rate, rep6.sim.tmrca.50kb))
names(true.lands.50kb.rep6) <- c("diversity", "theta", "tmrca", "rho")
true.lands.50kb.rep6$thetaC <- true.lands.50kb.rep6$theta - mean(true.lands.50kb.rep6$theta)
true.lands.50kb.rep6$tmrcaC <- true.lands.50kb.rep6$tmrca - mean(true.lands.50kb.rep6$tmrca)
true.lands.50kb.rep6$rhoC <- true.lands.50kb.rep6$rho - mean(true.lands.50kb.rep6$rho, na.rm = T)
true.lands.50kb.rep6$Replicate <- 1
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.50kb.rep6)
anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.50kb.true[1, 6] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.50kb.true[2, 6] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb.true[3, 6] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb.true[4, 6] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb.true[5, 6] <- anova.diversity$VarExp[4] * 100

inf.lands.50kb.rep6 <- as.data.frame(cbind(rep_6.pi.50kb$avg, rep_6.theta.50kb$sample_mean, rep_6.tmrca.50kb))
names(inf.lands.50kb.rep6) <- c("diversity", "theta", "tmrca", "rho")

cor.table[6, 1] <- cor.test(sim.theta.50kb$Rate, rep_6.theta.50kb$sample_mean, method = "spearman")$est

# centering
inf.lands.50kb.rep6$thetaC <- inf.lands.50kb.rep6$theta - mean(inf.lands.50kb.rep6$theta)
inf.lands.50kb.rep6$tmrcaC <- inf.lands.50kb.rep6$tmrca - mean(inf.lands.50kb.rep6$tmrca)
inf.lands.50kb.rep6$rhoC <- inf.lands.50kb.rep6$rho - mean(inf.lands.50kb.rep6$rho)

inf.lands.50kb.rep6$bin <- 1:nrow(inf.lands.50kb.rep6)

```

```

# for merging:
inf.lands.50kb.rep6 <- inf.lands.50kb.rep6
inf.lands.50kb.rep6$Replicate <- 1

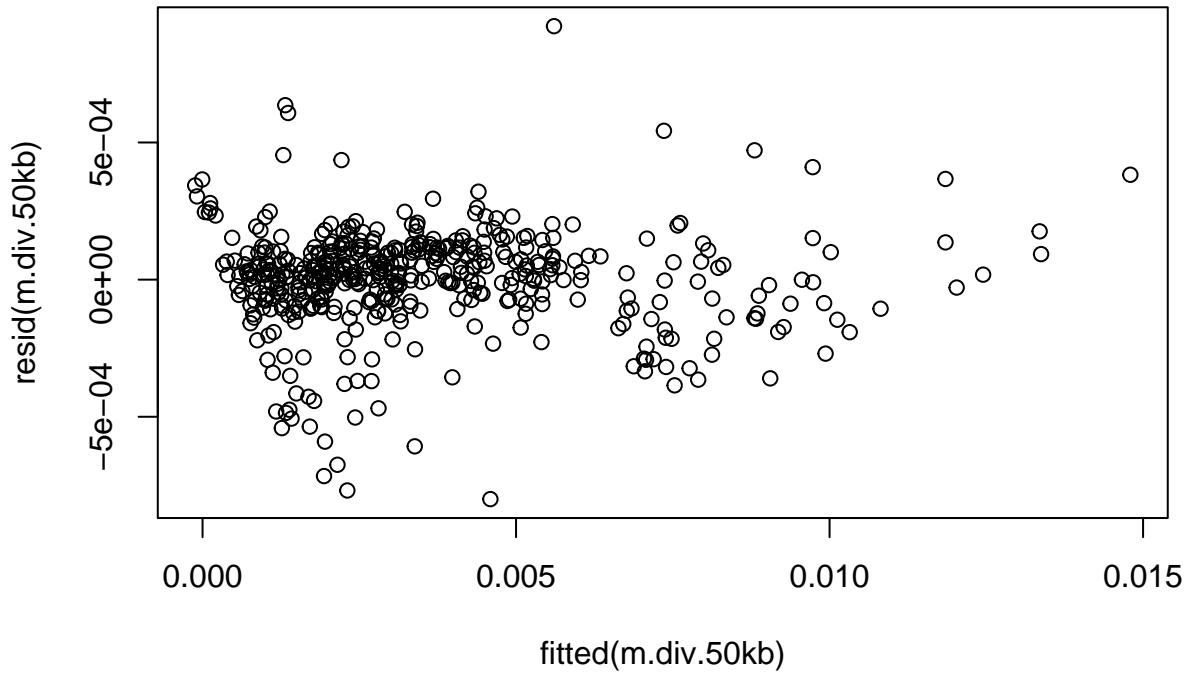
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.50kb.rep6)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.50kb.rep6)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.50kb.rep6)

AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

##           df      AIC
## m.div.50kb     6 -6743.728
## m.div.50kb.2   7 -6802.823
## m.div.50kb.3   8 -6805.058

plot(resid(m.div.50kb)~fitted(m.div.50kb))

```



```

dwtest(m.div.50kb)

##
##  Durbin-Watson test
##
##  data:  m.div.50kb
##  DW = 0.93612, p-value < 2.2e-16
##  alternative hypothesis: true autocorrelation is greater than 0

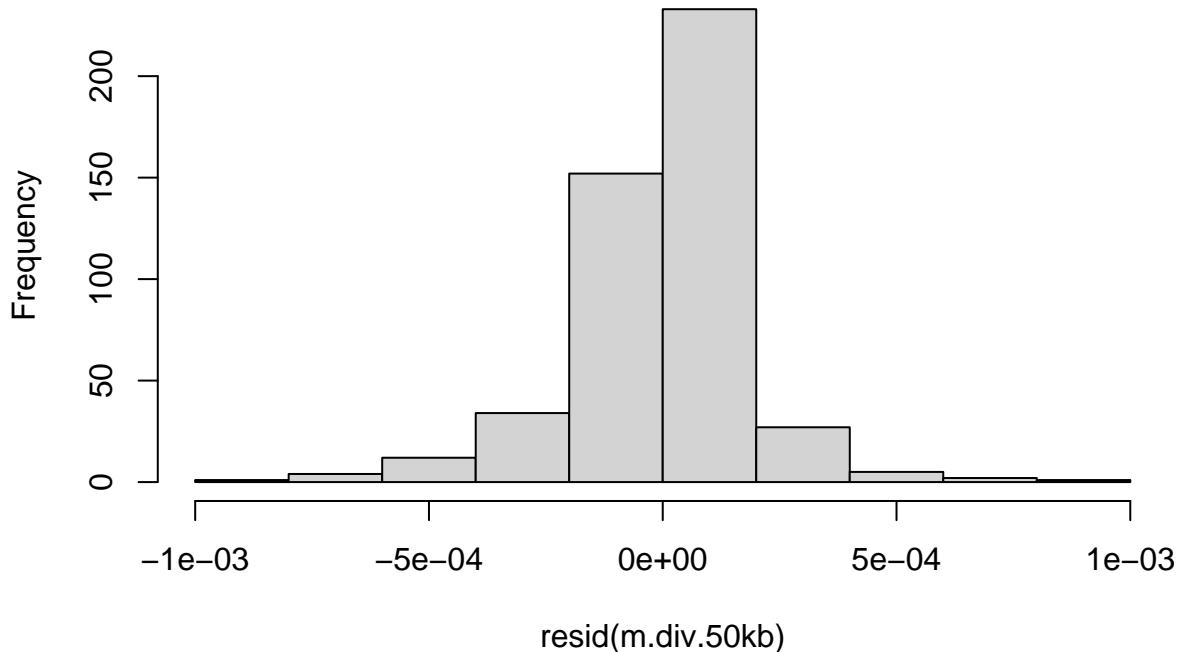
hmctest(m.div.50kb)

##
##  Harrison-McCabe test
##
##  data:  m.div.50kb
##  HMC = 0.4347, p-value = 0.017

```

```
hist(resid(m.div.50kb))
```

Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,  
##      data = inf.lands.50kb.rep6)  
##  
## Residuals:  
##       Min        1Q     Median        3Q       Max  
## -8.002e-04 -7.326e-05  1.942e-05  9.821e-05  9.241e-04  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 3.404e-03 8.832e-06 385.358 < 2e-16 ***  
## thetaC       1.105e+00 5.059e-03 218.484 < 2e-16 ***  
## rhoC         1.667e-02 3.878e-03   4.299 2.09e-05 ***  
## tmrcaC       4.233e-03 4.493e-05  94.200 < 2e-16 ***  
## thetaC:tmrcaC 1.423e+00 2.353e-02  60.461 < 2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0001868 on 466 degrees of freedom  
## Multiple R-squared:  0.9947, Adjusted R-squared:  0.9947  
## F-statistic: 2.194e+04 on 4 and 466 DF,  p-value: < 2.2e-16  
anova.diversity <- Anova(m.div.50kb)  
apiss <- anova.diversity$"Sum Sq"  
anova.diversity$VarExp <- apiss / sum(apiss)
```

```

r2.bgs.50kb[1, 6] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.bgs.50kb[2, 6] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb[3, 6] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb[4, 6] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb[5, 6] <- anova.diversity$VarExp[4] * 100

g.div.50kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep6, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep6, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep6, weights = varPower(0, ~theta), method = "ML")
g.div.50kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep6, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.50kb.1, g.div.50kb.2, g.div.50kb.3, g.div.50kb.4)

##           df      AIC
## g.div.50kb.1 8 -6946.467
## g.div.50kb.2 8 -6948.943
## g.div.50kb.3 7 -6762.528
## g.div.50kb.4 7 -6828.222
summary(g.div.50kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep6
##   AIC      BIC    logLik
## -6762.528 -6733.444 3388.264
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
## Parameter estimates:
##   power
## 0.271011
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0034030 0.000008909 381.9809     0
## thetaC       1.1044051 0.005512915 200.3305     0
## rhoC        0.0164441 0.003809512   4.3166     0
## tmrcaC      0.0042366 0.000046267   91.5698     0
## thetaC:tmrcaC 1.4328627 0.026527219   54.0148     0
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC      0.338
## rhoC        0.010 -0.168
## tmrcaC     -0.131 -0.232 -0.273

```

```

## thetaC:tmrcaC -0.257 -0.299 -0.014  0.493
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -4.1829268 -0.3945907  0.1090670  0.5609412  4.5102796
##
## Residual standard error: 0.0009014532
## Degrees of freedom: 471 total; 466 residual
vif(g.div.50kb.3)

##          thetaC          rhoC      tmrcaC thetaC:tmrcaC
##     1.167726     1.160985     1.500100     1.400350

```

### 6.1.7 Replicate 7

```

rep7.sim.tmrca.50kb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep7_w50000.csv", sep = ",", header = T)

rep_7.pi.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep7/dm2L_bgs_rep7_5.di")
rep_7.pi.50kb$avg <- apply(rep_7.pi.50kb[4:ncol(rep_7.pi.50kb)], 1, mean)
rep_7.rho.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep7/dm2L_bgs_rep7_5.r")
rep_7.theta.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep7/dm2L_bgs_rep7_5")
rep_7.tmrca.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep7/dm2L_bgs_rep7_5")
rep_7.tmrca.50kb$avg <- apply(rep_7.tmrca.50kb[4:ncol(rep_7.tmrca.50kb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.50kb.rep7 <- as.data.frame(cbind(rep_1.pi.50kb$avg, sim.theta.50kb$Rate, rep7.sim.tmrca.50kb))
names(true.lands.50kb.rep7) <- c("diversity", "theta", "tmrca", "rho")
true.lands.50kb.rep7$thetaC <- true.lands.50kb.rep7$theta - mean(true.lands.50kb.rep7$theta)
true.lands.50kb.rep7$tmrcaC <- true.lands.50kb.rep7$tmrca - mean(true.lands.50kb.rep7$tmrca)
true.lands.50kb.rep7$rhoC <- true.lands.50kb.rep7$rho - mean(true.lands.50kb.rep7$rho, na.rm = T)
true.lands.50kb.rep7$Replicate <- 1
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.50kb.rep7)
anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.50kb.true[1, 7] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.50kb.true[2, 7] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb.true[3, 7] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb.true[4, 7] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb.true[5, 7] <- anova.diversity$VarExp[4] * 100

inf.lands.50kb.rep7 <- as.data.frame(cbind(rep_7.pi.50kb$avg, rep_7.theta.50kb$sample_mean, rep_7.tmrca.50kb))
names(inf.lands.50kb.rep7) <- c("diversity", "theta", "tmrca", "rho")

cor.table[7, 1] <- cor.test(sim.theta.50kb$Rate, rep_7.theta.50kb$sample_mean, method = "spearman")$est

# centering
inf.lands.50kb.rep7$thetaC <- inf.lands.50kb.rep7$theta - mean(inf.lands.50kb.rep7$theta)
inf.lands.50kb.rep7$tmrcaC <- inf.lands.50kb.rep7$tmrca - mean(inf.lands.50kb.rep7$tmrca)
inf.lands.50kb.rep7$rhoC <- inf.lands.50kb.rep7$rho - mean(inf.lands.50kb.rep7$rho)

inf.lands.50kb.rep7$bin <- 1:nrow(inf.lands.50kb.rep7)

```

```

# for merging:
inf.lands.50kb.rep7 <- inf.lands.50kb.rep7
inf.lands.50kb.rep7$Replicate <- 1

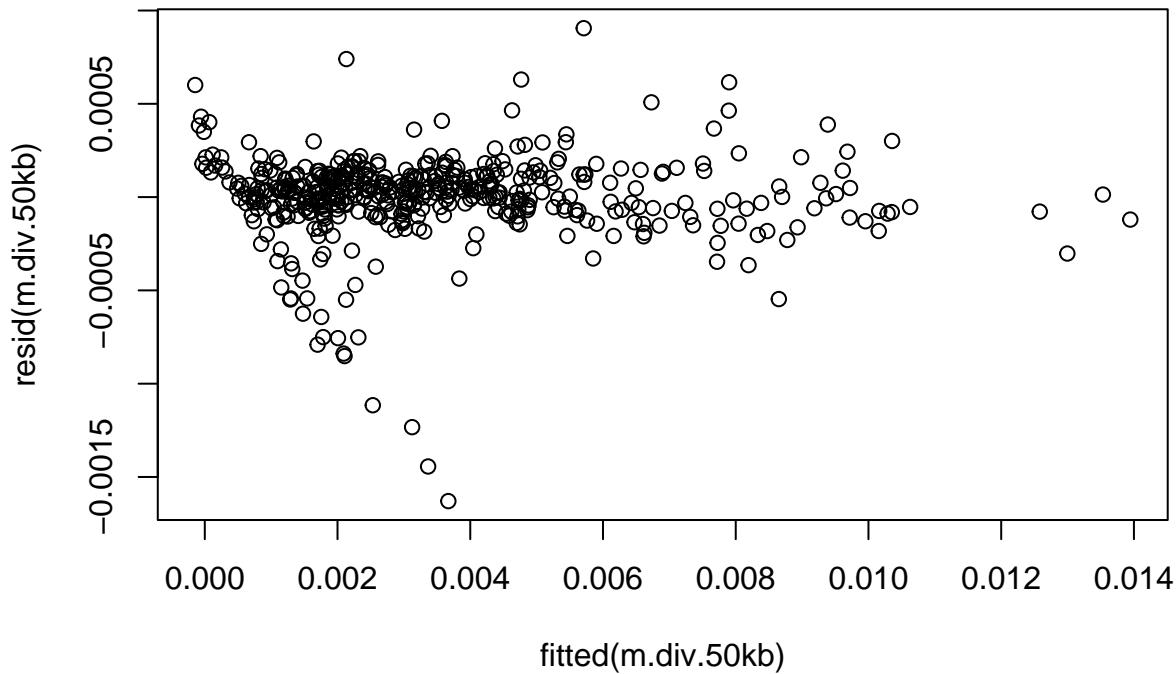
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.50kb.rep7)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.50kb.rep7)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.50kb.rep7)

AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

##           df      AIC
## m.div.50kb     6 -6529.539
## m.div.50kb.2   7 -6563.670
## m.div.50kb.3   8 -6563.389

plot(resid(m.div.50kb)~fitted(m.div.50kb))

```



```

dwtest(m.div.50kb)

##
##  Durbin-Watson test
##
##  data:  m.div.50kb
##  DW = 0.80944, p-value < 2.2e-16
##  alternative hypothesis: true autocorrelation is greater than 0

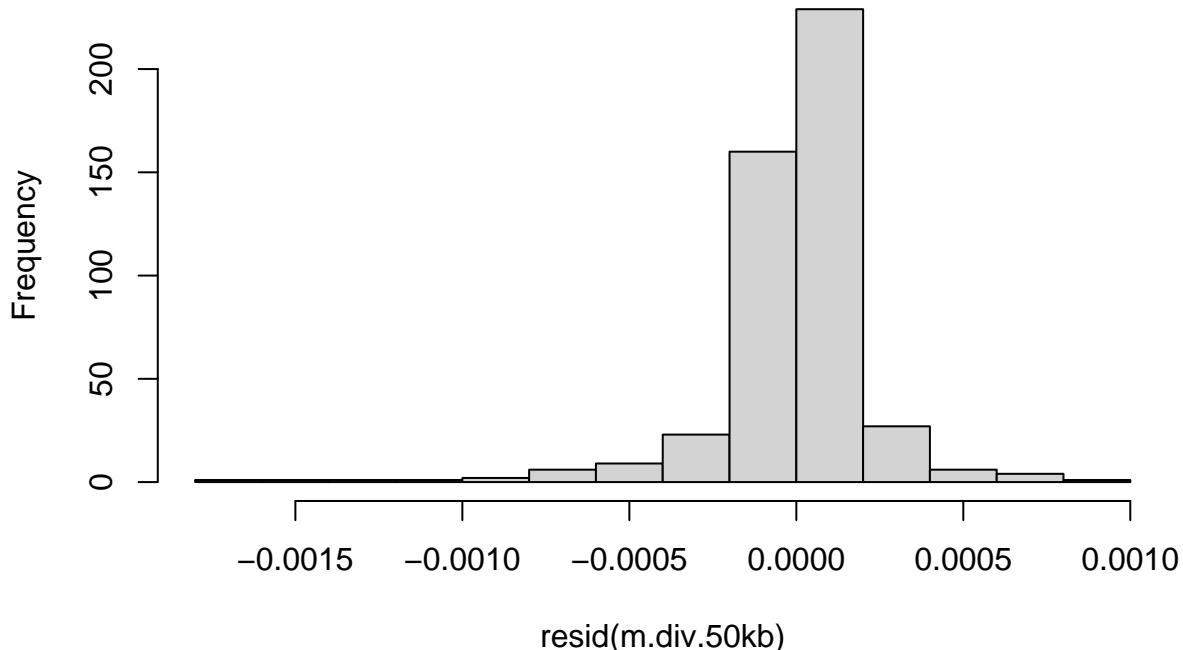
hmctest(m.div.50kb)

##
##  Harrison-McCabe test
##
##  data:  m.div.50kb
##  HMC = 0.3513, p-value < 2.2e-16

```

```
hist(resid(m.div.50kb))
```

Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,  
##      data = inf.lands.50kb.rep7)  
##  
## Residuals:  
##      Min       1Q   Median       3Q      Max  
## -1.629e-03 -6.430e-05  2.768e-05  1.120e-04  9.053e-04  
##  
## Coefficients:  
##              Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 3.322e-03 1.142e-05 290.772 < 2e-16 ***  
## thetaC       1.111e+00 6.786e-03 163.749 < 2e-16 ***  
## rhoC         2.980e-02 5.600e-03  5.321 1.61e-07 ***  
## tmrcaC       4.170e-03 6.401e-05  65.143 < 2e-16 ***  
## thetaC:tmrcaC 1.512e+00 3.838e-02  39.399 < 2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0002345 on 466 degrees of freedom  
## Multiple R-squared:  0.9912, Adjusted R-squared:  0.9912  
## F-statistic: 1.317e+04 on 4 and 466 DF,  p-value: < 2.2e-16  
anova.diversity <- Anova(m.div.50kb)  
apiss <- anova.diversity$"Sum Sq"  
anova.diversity$VarExp <- apiss / sum(apiss)
```

```

r2.bgs.50kb[1, 7] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.bgs.50kb[2, 7] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb[3, 7] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb[4, 7] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb[5, 7] <- anova.diversity$VarExp[4] * 100

g.div.50kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep7, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep7, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep7, weights = varPower(0, ~theta), method = "ML")
g.div.50kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep7, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.50kb.1, g.div.50kb.2, g.div.50kb.3, g.div.50kb.4)

##           df      AIC
## g.div.50kb.1 8 -6771.554
## g.div.50kb.2 8 -6847.669
## g.div.50kb.3 7 -6555.954
## g.div.50kb.4 7 -6550.583
summary(g.div.50kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep7
##   AIC      BIC    logLik
## -6555.954 -6526.87 3284.977
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
## Parameter estimates:
##   power
## 0.4318893
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0033169 0.00001198 276.85158     0
## thetaC       1.1018671 0.00780478 141.17848     0
## rhoC        0.0317114 0.00550514  5.76032     0
## tmrcaC      0.0042223 0.00007282  57.98213     0
## thetaC:tmrcaC 1.5680797 0.04561954  34.37299     0
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC      0.500
## rhoC       -0.021 -0.250
## tmrcaC     -0.280 -0.329 -0.170

```

```

## thetaC:tmrcaC -0.372 -0.336  0.061  0.754
##
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -6.1376825 -0.2653249  0.1119443  0.4879379  3.3805282
##
## Residual standard error: 0.002942983
## Degrees of freedom: 471 total; 466 residual
vif(g.div.50kb.3)

##          thetaC         rhoC        tmrcaC thetaC:tmrcaC
## 1.260102     1.239715     2.733275     2.542584

```

### 6.1.8 Replicate 8

```

rep8.sim.tmrca.50kb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep8_w50000.csv", sep = ",", header = T)

rep_8.pi.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.di")
rep_8.pi.50kb$avg <- apply(rep_8.pi.50kb[4:ncol(rep_8.pi.50kb)], 1, mean)
rep_8.rho.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.r")
rep_8.theta.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5")
rep_8.tmrca.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5")
rep_8.tmrca.50kb$avg <- apply(rep_8.tmrca.50kb[4:ncol(rep_8.tmrca.50kb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.50kb.rep8 <- as.data.frame(cbind(rep_1.pi.50kb$avg, sim.theta.50kb$Rate, rep8.sim.tmrca.50kb))
names(true.lands.50kb.rep8) <- c("diversity", "theta", "tmrca", "rho")
true.lands.50kb.rep8$thetaC <- true.lands.50kb.rep8$theta - mean(true.lands.50kb.rep8$theta)
true.lands.50kb.rep8$tmrcaC <- true.lands.50kb.rep8$tmrca - mean(true.lands.50kb.rep8$tmrca)
true.lands.50kb.rep8$rhoC <- true.lands.50kb.rep8$rho - mean(true.lands.50kb.rep8$rho, na.rm = T)
true.lands.50kb.rep8$Replicate <- 1
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.50kb.rep8)
anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.50kb.true[1, 8] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.50kb.true[2, 8] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb.true[3, 8] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb.true[4, 8] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb.true[5, 8] <- anova.diversity$VarExp[4] * 100

inf.lands.50kb.rep8 <- as.data.frame(cbind(rep_8.pi.50kb$avg, rep_8.theta.50kb$sample_mean, rep_8.tmrca.50kb))
names(inf.lands.50kb.rep8) <- c("diversity", "theta", "tmrca", "rho")

cor.table[8, 1] <- cor.test(sim.theta.50kb$Rate, rep_8.theta.50kb$sample_mean, method = "spearman")$est

# centering
inf.lands.50kb.rep8$thetaC <- inf.lands.50kb.rep8$theta - mean(inf.lands.50kb.rep8$theta)
inf.lands.50kb.rep8$tmrcaC <- inf.lands.50kb.rep8$tmrca - mean(inf.lands.50kb.rep8$tmrca)
inf.lands.50kb.rep8$rhoC <- inf.lands.50kb.rep8$rho - mean(inf.lands.50kb.rep8$rho)

inf.lands.50kb.rep8$bin <- 1:nrow(inf.lands.50kb.rep8)

```

```

# for merging:
inf.lands.50kb.rep8 <- inf.lands.50kb.rep8
inf.lands.50kb.rep8$Replicate <- 1

m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.50kb.rep8)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.50kb.rep8)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.50kb.rep8)

AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

##           df      AIC
## m.div.50kb     6 -6664.906
## m.div.50kb.2   7 -6820.661
## m.div.50kb.3   8 -6830.462

plot(resid(m.div.50kb)~fitted(m.div.50kb))



```

dwtest(m.div.50kb)

```

##
##  Durbin-Watson test
##
##  data: m.div.50kb
##  DW = 0.81053, p-value < 2.2e-16
##  alternative hypothesis: true autocorrelation is greater than 0

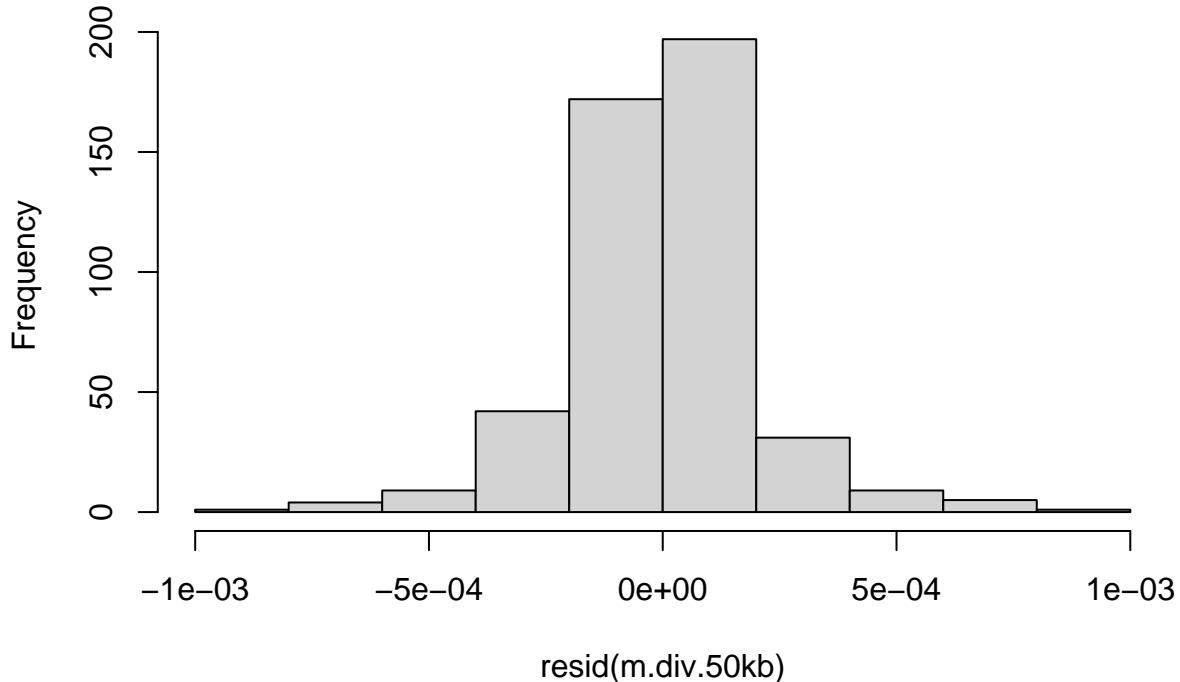
hmctest(m.div.50kb)

##
##  Harrison-McCabe test
##
##  data: m.div.50kb
##  HMC = 0.39763, p-value < 2.2e-16

```

```
hist(resid(m.div.50kb))
```

Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,  
##      data = inf.lands.50kb.rep8)  
##  
## Residuals:  
##       Min        1Q     Median        3Q       Max  
## -8.849e-04 -1.035e-04  4.480e-06  1.033e-04  8.415e-04  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 3.424e-03 9.459e-06 361.965 <2e-16 ***  
## thetaC       1.242e+00 6.563e-03 189.277 <2e-16 ***  
## rhoC         8.381e-03 5.300e-03   1.581    0.115  
## tmrcaC       3.389e-03 3.343e-05 101.373 <2e-16 ***  
## thetaC:tmrcaC 1.306e+00 2.597e-02  50.287 <2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0002031 on 466 degrees of freedom  
## Multiple R-squared:  0.9934, Adjusted R-squared:  0.9934  
## F-statistic: 1.766e+04 on 4 and 466 DF,  p-value: < 2.2e-16  
anova.diversity <- Anova(m.div.50kb)  
apiss <- anova.diversity$"Sum Sq"  
anova.diversity$VarExp <- apiss / sum(apiss)
```

```

r2.bgs.50kb[1, 8] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.bgs.50kb[2, 8] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb[3, 8] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb[4, 8] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb[5, 8] <- anova.diversity$VarExp[4] * 100

g.div.50kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep8, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep8, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep8, weights = varPower(0, ~theta), method = "ML")
g.div.50kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep8, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.50kb.1, g.div.50kb.2, g.div.50kb.3, g.div.50kb.4)

##           df      AIC
## g.div.50kb.1 8 -6889.362
## g.div.50kb.2 8 -6915.099
## g.div.50kb.3 7 -6750.478
## g.div.50kb.4 7 -6740.369

summary(g.div.50kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep8
##       AIC      BIC    logLik
##   -6750.478 -6721.394 3382.239
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
## Parameter estimates:
##   power
## 0.6457134
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0034302 0.000009656 355.2515 0.0000
## thetaC       1.2470563 0.007332157 170.0804 0.0000
## rhoC        0.0133119 0.004692246   2.8370 0.0048
## tmrcaC      0.0033566 0.000033544 100.0652 0.0000
## thetaC:tmrcaC 1.1613759 0.027531291   42.1838 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC      0.601
## rhoC       0.001 -0.161
## tmrcaC     -0.067 -0.062 -0.360

```

```

## thetaC:tmrcaC -0.143 -0.262 -0.027  0.525
##
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -4.24874158 -0.53347725  0.04182428  0.53332121  3.79069374
##
## Residual standard error: 0.008905455
## Degrees of freedom: 471 total; 466 residual
vif(g.div.50kb.3)

##      thetaC       rhoC      tmrcaC thetaC:tmrcaC
## 1.107570 1.226780 1.655377 1.528324

```

### 6.1.9 Replicate 9

```

rep9.sim.tmrca.50kb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep9_w50000.csv", sep = ",", header = T)

rep_9.pi.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.di")
rep_9.pi.50kb$avg <- apply(rep_9.pi.50kb[4:ncol(rep_9.pi.50kb)], 1, mean)
rep_9.rho.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.r")
rep_9.theta.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5")
rep_9.tmrca.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5")
rep_9.tmrca.50kb$avg <- apply(rep_9.tmrca.50kb[4:ncol(rep_9.tmrca.50kb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.50kb.rep9 <- as.data.frame(cbind(rep_1.pi.50kb$avg, sim.theta.50kb$Rate, rep9.sim.tmrca.50kb))
names(true.lands.50kb.rep9) <- c("diversity", "theta", "tmrca", "rho")
true.lands.50kb.rep9$thetaC <- true.lands.50kb.rep9$theta - mean(true.lands.50kb.rep9$theta)
true.lands.50kb.rep9$tmrcaC <- true.lands.50kb.rep9$tmrca - mean(true.lands.50kb.rep9$tmrca)
true.lands.50kb.rep9$rhoC <- true.lands.50kb.rep9$rho - mean(true.lands.50kb.rep9$rho, na.rm = T)
true.lands.50kb.rep9$Replicate <- 1
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.50kb.rep9)
anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.50kb.true[1, 9] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.50kb.true[2, 9] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb.true[3, 9] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb.true[4, 9] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb.true[5, 9] <- anova.diversity$VarExp[4] * 100

inf.lands.50kb.rep9 <- as.data.frame(cbind(rep_9.pi.50kb$avg, rep_9.theta.50kb$sample_mean, rep_9.tmrca.50kb))
names(inf.lands.50kb.rep9) <- c("diversity", "theta", "tmrca", "rho")

cor.table[9, 1] <- cor.test(sim.theta.50kb$Rate, rep_9.theta.50kb$sample_mean, method = "spearman")$est

# centering
inf.lands.50kb.rep9$thetaC <- inf.lands.50kb.rep9$theta - mean(inf.lands.50kb.rep9$theta)
inf.lands.50kb.rep9$tmrcaC <- inf.lands.50kb.rep9$tmrca - mean(inf.lands.50kb.rep9$tmrca)
inf.lands.50kb.rep9$rhoC <- inf.lands.50kb.rep9$rho - mean(inf.lands.50kb.rep9$rho)

inf.lands.50kb.rep9$bin <- 1:nrow(inf.lands.50kb.rep9)

```

```

# for merging:
inf.lands.50kb.rep9 <- inf.lands.50kb.rep9
inf.lands.50kb.rep9$Replicate <- 1

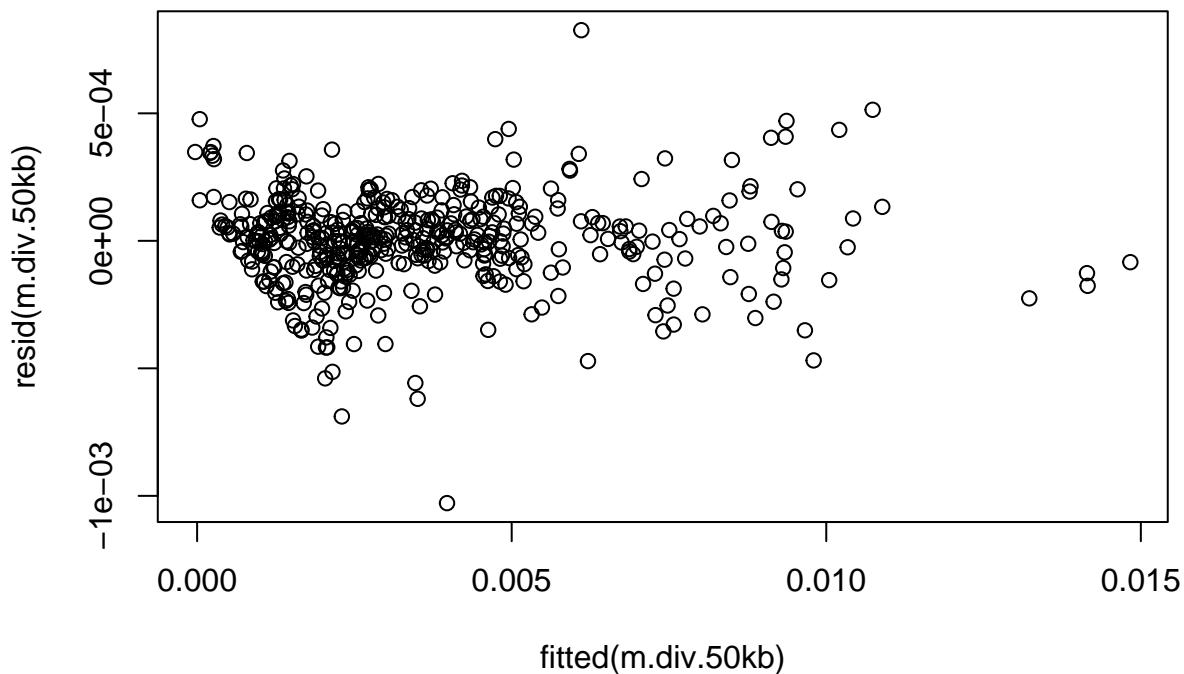
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.50kb.rep9)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.50kb.rep9)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.50kb.rep9)

AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

##           df      AIC
## m.div.50kb     6 -6772.620
## m.div.50kb.2   7 -6788.142
## m.div.50kb.3   8 -6788.032

plot(resid(m.div.50kb)~fitted(m.div.50kb))

```



```

dwtest(m.div.50kb)

##
##  Durbin-Watson test
##
##  data:  m.div.50kb
##  DW = 1.2553, p-value < 2.2e-16
##  alternative hypothesis: true autocorrelation is greater than 0

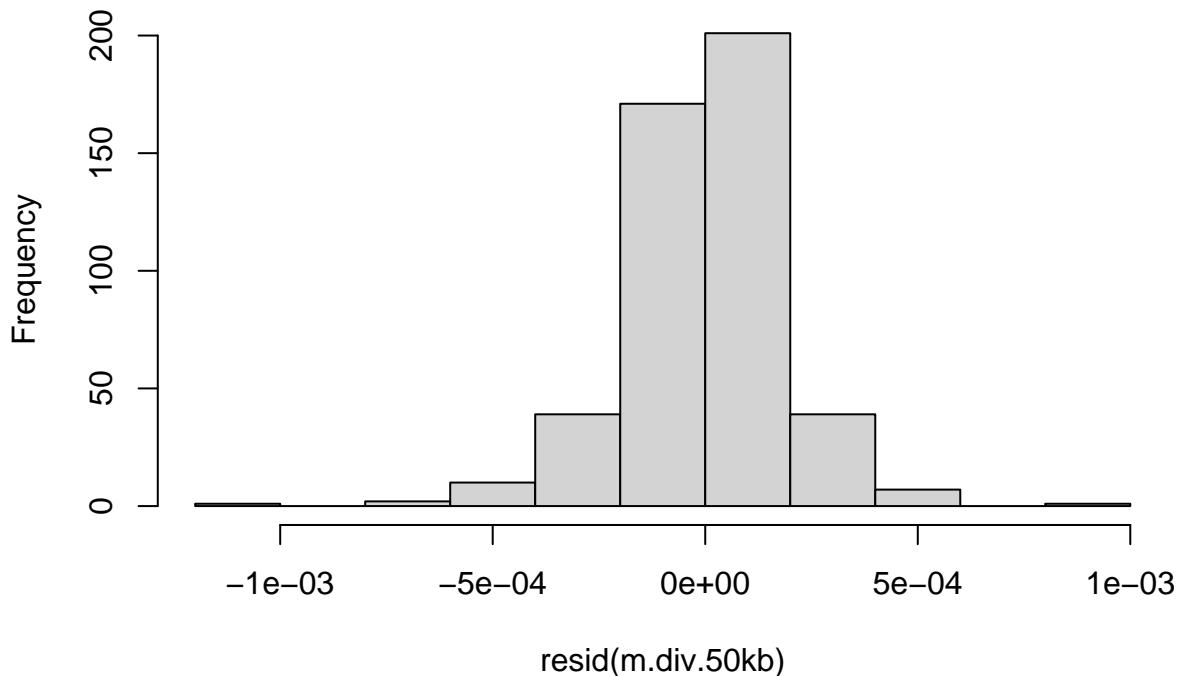
hmctest(m.div.50kb)

##
##  Harrison-McCabe test
##
##  data:  m.div.50kb
##  HMC = 0.48698, p-value = 0.353

```

```
hist(resid(m.div.50kb))
```

Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,  
##      data = inf.lands.50kb.rep9)  
##  
## Residuals:  
##       Min        1Q     Median        3Q       Max  
## -1.028e-03 -7.795e-05  1.040e-05  9.457e-05  8.260e-04  
##  
## Coefficients:  
##              Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 3.386e-03 8.797e-06 384.938 < 2e-16 ***  
## thetaC       1.197e+00 6.055e-03 197.676 < 2e-16 ***  
## rhoC         1.895e-02 4.699e-03   4.032 6.45e-05 ***  
## tmrcaC       3.897e-03 4.056e-05  96.094 < 2e-16 ***  
## thetaC:tmrcaC 1.553e+00 2.874e-02  54.050 < 2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0001812 on 466 degrees of freedom  
## Multiple R-squared:  0.9949, Adjusted R-squared:  0.9948  
## F-statistic: 2.265e+04 on 4 and 466 DF,  p-value: < 2.2e-16  
anova.diversity <- Anova(m.div.50kb)  
apiss <- anova.diversity$"Sum Sq"  
anova.diversity$VarExp <- apiss / sum(apiss)
```

```

r2.bgs.50kb[1, 9] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.bgs.50kb[2, 9] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb[3, 9] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb[4, 9] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb[5, 9] <- anova.diversity$VarExp[4] * 100

g.div.50kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep9, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep9, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep9, weights = varPower(0, ~theta), method = "ML")
g.div.50kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep9, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.50kb.1, g.div.50kb.2, g.div.50kb.3, g.div.50kb.4)

##           df      AIC
## g.div.50kb.1 8 -6844.364
## g.div.50kb.2 8 -6903.791
## g.div.50kb.3 7 -6804.377
## g.div.50kb.4 7 -6772.655
summary(g.div.50kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep9
##       AIC     BIC   logLik
## -6804.377 -6775.293 3409.189
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
## Parameter estimates:
##   power
## 0.3817603
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0033889 0.00000899 376.7816     0
## thetaC       1.1924109 0.00675297 176.5759     0
## rhoC        0.0198466 0.00465667  4.2620     0
## tmrcaC      0.0038946 0.00004397  88.5678     0
## thetaC:tmrcaC 1.5343949 0.03313194  46.3116     0
##
## Correlation:
##            (Intr) thetaC rhoC    tmrcaC
## thetaC      0.467
## rhoC      -0.010 -0.194
## tmrcaC    -0.241 -0.326 -0.296

```

```

## thetaC:tmrcaC -0.361 -0.430  0.030  0.663
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -5.23766061 -0.47972109  0.04058785  0.53646388  4.07355376
##
## Residual standard error: 0.001714965
## Degrees of freedom: 471 total; 466 residual
vif(g.div.50kb.3)

##      thetaC       rhoC      tmrcaC thetaC:tmrcaC
## 1.313079 1.298832 2.228784    2.083348

```

### 6.1.10 Replicate 10

```

rep10.sim.tmrca.50kb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep10_w50000.csv", sep = ",", header = T)

rep_10.pi.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_50kb.csv")
rep_10.pi.50kb$avg <- apply(rep_10.pi.50kb[4:ncol(rep_10.pi.50kb)], 1, mean)
rep_10.rho.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_50kb.csv")
rep_10.theta.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_50kb.csv")
rep_10.tmrca.50kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_50kb.csv")
rep_10.tmrca.50kb$avg <- apply(rep_10.tmrca.50kb[4:ncol(rep_10.tmrca.50kb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.50kb.rep10 <- as.data.frame(cbind(rep_10.pi.50kb$avg, sim.theta.50kb$Rate, rep10.sim.tmrca.50kb$Rate))
names(true.lands.50kb.rep10) <- c("diversity", "theta", "tmrca", "rho")
true.lands.50kb.rep10$thetaC <- true.lands.50kb.rep10$theta - mean(true.lands.50kb.rep10$theta)
true.lands.50kb.rep10$tmrcaC <- true.lands.50kb.rep10$tmrca - mean(true.lands.50kb.rep10$tmrca)
true.lands.50kb.rep10$rhoC <- true.lands.50kb.rep10$rho - mean(true.lands.50kb.rep10$rho, na.rm = T)
true.lands.50kb.rep10$Replicate <- 1
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.50kb.rep10)
anova.diversity <- Anova(m.div.50kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.50kb.true[1, 10] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.50kb.true[2, 10] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb.true[3, 10] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb.true[4, 10] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb.true[5, 10] <- anova.diversity$VarExp[4] * 100

inf.lands.50kb.rep10 <- as.data.frame(cbind(rep_10.pi.50kb$avg, rep_10.theta.50kb$sample_mean, rep10.theta.50kb$sample_mean))
names(inf.lands.50kb.rep10) <- c("diversity", "theta", "tmrca", "rho")

cor.table[10, 1] <- cor.test(sim.theta.50kb$Rate, rep_10.theta.50kb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.50kb.rep10$thetaC <- inf.lands.50kb.rep10$theta - mean(inf.lands.50kb.rep10$theta)
inf.lands.50kb.rep10$tmrcaC <- inf.lands.50kb.rep10$tmrca - mean(inf.lands.50kb.rep10$tmrca)
inf.lands.50kb.rep10$rhoC <- inf.lands.50kb.rep10$rho - mean(inf.lands.50kb.rep10$rho)

inf.lands.50kb.rep10$bin <- 1:nrow(inf.lands.50kb.rep10)

```

```

# for merging:
inf.lands.50kb.rep10 <- inf.lands.50kb.rep10
inf.lands.50kb.rep10$Replicate <- 1

m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.50kb.rep10)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.50kb.rep10)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.50kb.rep10)

AIC(m.div.50kb, m.div.50kb.2, m.div.50kb.3)

##           df      AIC
## m.div.50kb     6 -6830.551
## m.div.50kb.2   7 -6838.420
## m.div.50kb.3   8 -6849.626

plot(resid(m.div.50kb)~fitted(m.div.50kb))



```

dwtest(m.div.50kb)

```

## 
##  Durbin-Watson test
## 
##  data: m.div.50kb
##  DW = 1.1672, p-value < 2.2e-16
##  alternative hypothesis: true autocorrelation is greater than 0

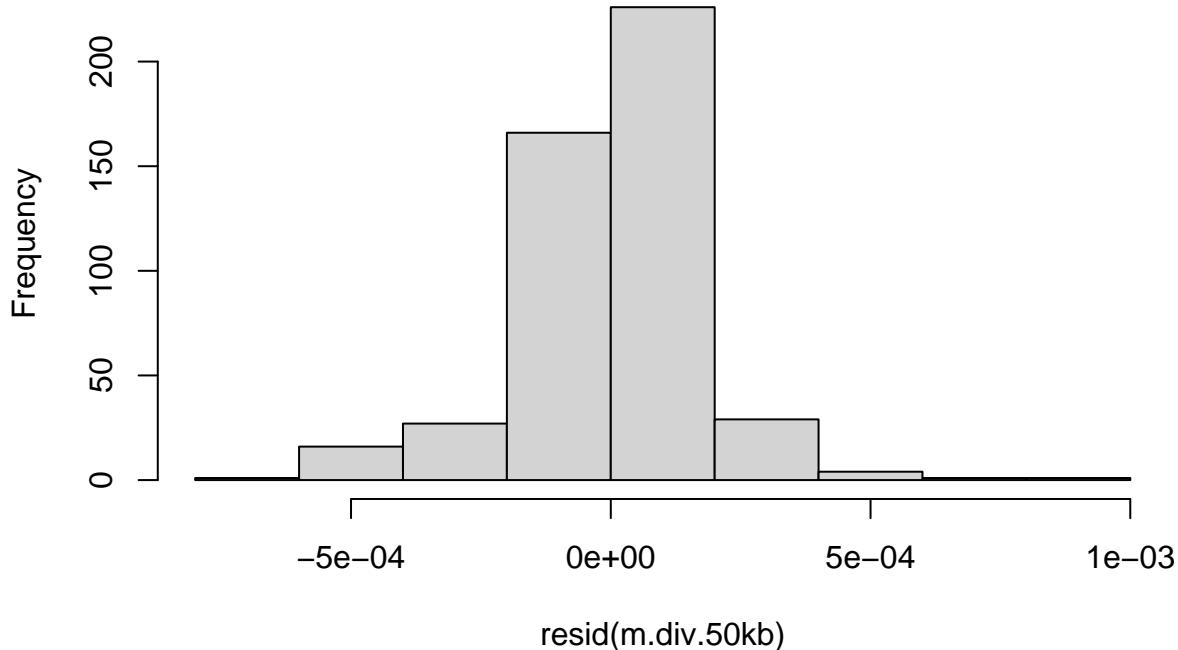
hmctest(m.div.50kb)

## 
##  Harrison-McCabe test
## 
##  data: m.div.50kb
##  HMC = 0.47978, p-value = 0.31

```

```
hist(resid(m.div.50kb))
```

Histogram of resid(m.div.50kb)



```
summary(m.div.50kb)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,  
##      data = inf.lands.50kb.rep10)  
##  
## Residuals:  
##       Min         1Q     Median        3Q       Max  
## -6.172e-04 -6.760e-05  1.266e-05  9.275e-05  8.769e-04  
##  
## Coefficients:  
##              Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 3.443e-03 8.020e-06 429.318 < 2e-16 ***  
## thetaC       1.068e+00 4.356e-03 245.081 < 2e-16 ***  
## rhoC         3.865e-02 5.193e-03   7.442 4.84e-13 ***  
## tmrcaC       4.432e-03 4.816e-05  92.015 < 2e-16 ***  
## thetaC:tmrcaC 1.413e+00 2.399e-02  58.877 < 2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0001704 on 466 degrees of freedom  
## Multiple R-squared:  0.9955, Adjusted R-squared:  0.9955  
## F-statistic: 2.585e+04 on 4 and 466 DF,  p-value: < 2.2e-16  
anova.diversity <- Anova(m.div.50kb)  
apiss <- anova.diversity$"Sum Sq"  
anova.diversity$VarExp <- apiss / sum(apiss)
```

```

r2.bgs.50kb[1, 10] <- anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]
r2.bgs.50kb[2, 10] <- anova.diversity$VarExp[1] * 100
r2.bgs.50kb[3, 10] <- anova.diversity$VarExp[2] * 100
r2.bgs.50kb[4, 10] <- anova.diversity$VarExp[3] * 100
r2.bgs.50kb[5, 10] <- anova.diversity$VarExp[4] * 100

g.div.50kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep10, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep10, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.50kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep10, weights = varPower(0, ~theta), method = "ML")
g.div.50kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                       data = inf.lands.50kb.rep10, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.50kb.1, g.div.50kb.2, g.div.50kb.3, g.div.50kb.4)

##           df      AIC
## g.div.50kb.1 8 -6942.468
## g.div.50kb.2 8 -6997.019
## g.div.50kb.3 7 -6868.321
## g.div.50kb.4 7 -6861.577
summary(g.div.50kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.50kb.rep10
##       AIC      BIC    logLik
##   -6868.321 -6839.237 3441.161
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
## Parameter estimates:
##   power
## 0.3740056
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0034424 0.000008084 425.8315     0
## thetaC       1.0686825 0.004873670 219.2768     0
## rhoC        0.0443179 0.004804829  9.2236     0
## tmrcaC      0.0044039 0.000048558  90.6934     0
## thetaC:tmrcaC 1.4173157 0.026661837  53.1590     0
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC      0.393
## rhoC       0.009 -0.275
## tmrcaC    -0.107 -0.100 -0.390

```

```

## thetaC:tmrcaC -0.233 -0.151 -0.021  0.463
##
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -3.62765088 -0.45676308  0.09593681  0.61915114  3.79738407
##
## Residual standard error: 0.001457433
## Degrees of freedom: 471 total; 466 residual
vif(g.div.50kb.3)

##      thetaC       rhoC      tmrcaC thetaC:tmrcaC
##     1.147519    1.373197    1.611565    1.328148

```

## 6.2 200 kb scale

```

r2.bgs.200kb <- as.data.frame(matrix(ncol = nreps, nrow = 5))
row.names(r2.bgs.200kb) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
colnames(r2.bgs.200kb) <- reps

r2.bgs.200kb.true <- as.data.frame(matrix(ncol = nreps, nrow = 5))
row.names(r2.bgs.200kb.true) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
colnames(r2.bgs.200kb.true) <- reps

sim.theta.200kb <- read.table("dm_bgs_sims/MutationMap_200kb.csv", sep = ",", header = T)
sim.rho.200kb <- read.table("dm_bgs_sims/RecombinationMap_200kb.csv", sep = ",", header = T)

```

### 6.2.1 Replicate 1

```

rep1.sim.tmrca.200kb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep1_w200000.csv", sep = ",", header = T)

rep_1.pi.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.d")
rep_1.pi.200kb$avg <- apply(rep_1.pi.200kb[4:ncol(rep_1.pi.200kb)], 1, mean)
rep_1.rho.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.d")
rep_1.theta.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.d")
rep_1.tmrca.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.d")
rep_1.tmrca.200kb$avg <- apply(rep_1.tmrca.200kb[4:ncol(rep_1.tmrca.200kb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.200kb.rep1 <- as.data.frame(cbind(rep_1.pi.200kb$avg, sim.theta.200kb$Rate, rep1.sim.tmrca.200kb$Rate))
names(true.lands.200kb.rep1) <- c("diversity", "theta", "tmrca", "rho")
true.lands.200kb.rep1$thetaC <- true.lands.200kb.rep1$theta - mean(true.lands.200kb.rep1$theta)
true.lands.200kb.rep1$tmrcaC <- true.lands.200kb.rep1$tmrca - mean(true.lands.200kb.rep1$tmrca)
true.lands.200kb.rep1$rhoC <- true.lands.200kb.rep1$rho - mean(true.lands.200kb.rep1$rho, na.rm = T)
true.lands.200kb.rep1$Replicate <- 1
m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.200kb.rep1)
anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.200kb.true[1, 1] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.200kb.true[2, 1] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb.true[3, 1] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb.true[4, 1] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb.true[5, 1] <- anova.diversity$VarExp[4] * 100

```

```

inf.lands.200kb.rep1 <- as.data.frame(cbind(rep_1.pi.200kb$avg, rep_1.theta.200kb$sample_mean, rep_1.tmrca))
names(inf.lands.200kb.rep1) <- c("diversity", "theta", "tmrca", "rho")

cor.table[1, 2] <- cor.test(sim.theta.200kb$Rate, rep_1.theta.200kb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.200kb.rep1$thetaC <- inf.lands.200kb.rep1$theta - mean(inf.lands.200kb.rep1$theta)
inf.lands.200kb.rep1$tmrcaC <- inf.lands.200kb.rep1$tmrca - mean(inf.lands.200kb.rep1$tmrca)
inf.lands.200kb.rep1$rhoC <- inf.lands.200kb.rep1$rho - mean(inf.lands.200kb.rep1$rho)

inf.lands.200kb.rep1$bin <- 1:nrow(inf.lands.200kb.rep1)

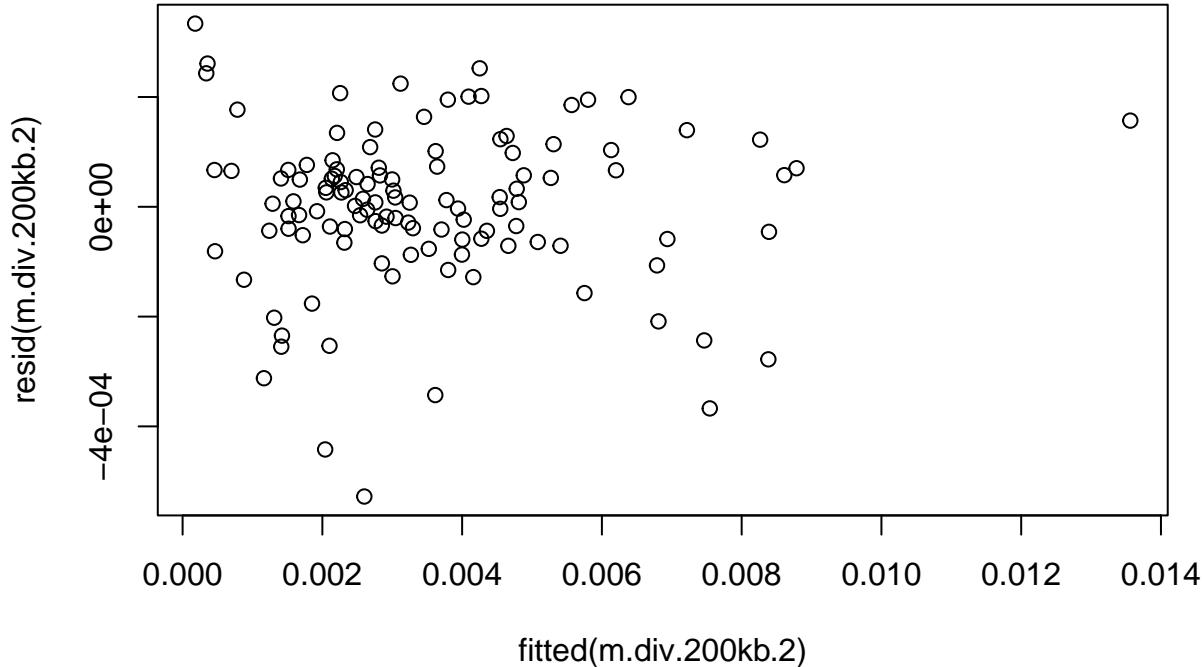
# for merging:
inf.lands.200kb.rep1 <- inf.lands.200kb.rep1
inf.lands.200kb.rep1$Replicate <- 1

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.200kb.rep1)
m.div.200kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.200kb.rep1)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.200kb.rep1)

AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)

##          df      AIC
## m.div.200kb    6 -1724.393
## m.div.200kb.2  7 -1740.570
## m.div.200kb.3  8 -1739.520
plot(resid(m.div.200kb.2)~fitted(m.div.200kb.2))

```



```
dwtest(m.div.200kb.2)
```

```
##
```

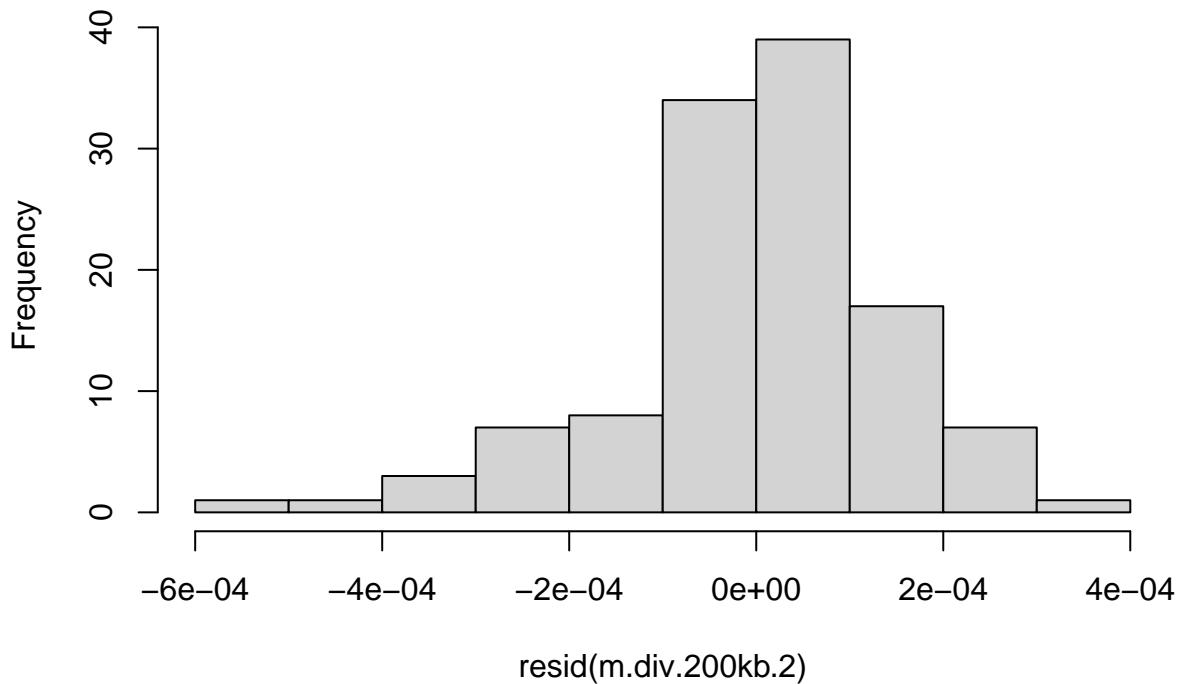
```

## Durbin-Watson test
##
## data: m.div.200kb.2
## DW = 1.167, p-value = 1.002e-06
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb.2)

##
## Harrison-McCabe test
##
## data: m.div.200kb.2
## HMC = 0.38434, p-value = 0.028
hist(resid(m.div.200kb.2))

```

**Histogram of resid(m.div.200kb.2)**



```

summary(m.div.200kb.2)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC +
##      rhoC:tmrcaC, data = inf.lands.200kb.rep1)
##
## Residuals:
##      Min        1Q    Median        3Q       Max 
## -5.278e-04 -5.856e-05  9.240e-06  7.099e-05  3.337e-04 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.415e-03 1.769e-05 193.085 < 2e-16 ***
## thetaC      1.094e+00 1.019e-02 107.387 < 2e-16 ***
## 
```

```

## rhoC          3.098e-02  1.007e-02   3.077  0.00262 **
## tmrcaC        4.599e-03  1.787e-04  25.740  < 2e-16 ***
## thetaC:tmrcaC 1.336e+00  6.156e-02  21.699  < 2e-16 ***
## rhoC:tmrcaC   3.240e-01  7.502e-02   4.319  3.41e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0001466 on 112 degrees of freedom
## Multiple R-squared:  0.9957, Adjusted R-squared:  0.9955
## F-statistic:  5132 on 5 and 112 DF,  p-value: < 2.2e-16
anova.diversity <- Anova(m.div.200kb.2)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.200kb[1, 1] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]
r2.bgs.200kb[2, 1] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb[3, 1] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb[4, 1] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb[5, 1] <- anova.diversity$VarExp[4] * 100

g.div.200kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep1, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep1, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep1, weights = varPower(0, ~theta), method = "ML")
g.div.200kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep1, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.200kb.1, g.div.200kb.2, g.div.200kb.3, g.div.200kb.4)

##             df      AIC
## g.div.200kb.1 8 -1766.542
## g.div.200kb.2 8 -1764.701
## g.div.200kb.3 7 -1743.945
## g.div.200kb.4 7 -1752.612
summary(g.div.200kb.3)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
## Data: inf.lands.200kb.rep1
##       AIC      BIC    logLik
##     -1743.945 -1724.551 878.9727
##
## Variance function:
## Structure: Power of variance covariate
## Formula: ~theta
## Parameter estimates:
##       power
## 0.7361752

```

```

## 
## Coefficients:
##              Value Std. Error t-value p-value
## (Intercept) 0.0034707 0.00001499 231.50685     0
## thetaC      1.1083561 0.01144751  96.82072     0
## rhoC        0.0495004 0.00837259   5.91220     0
## tmrcaC      0.0038521 0.00007797  49.40405     0
## thetaC:tmrcaC 1.3100299 0.05918971  22.13273     0
##
## Correlation:
##            (Intr) thetaC rhoC  tmrcaC
## thetaC      0.563
## rhoC        0.004 -0.373
## tmrcaC     -0.076  0.027 -0.377
## thetaC:tmrcaC -0.149 -0.092 -0.098  0.550
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -3.34897044 -0.50845520 -0.03176751  0.64399094  2.60457466
##
## Residual standard error: 0.01046373
## Degrees of freedom: 118 total; 113 residual
vif(g.div.200kb.3)

```

	thetaC	rhoC	tmrcaC	thetaC:tmrcaC
##	1.190126	1.391290	1.695926	1.471880

## 6.2.2 Replicate 2

```

rep2.sim.tmrca.200kb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep2_w200000.csv", sep = ",", header = T)

rep_2.pi.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.d")
rep_2.pi.200kb$avg <- apply(rep_2.pi.200kb[4:ncol(rep_2.pi.200kb)], 1, mean)
rep_2.rho.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.d")
rep_2.theta.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.d")
rep_2.tmrca.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.d")
rep_2.tmrca.200kb$avg <- apply(rep_2.tmrca.200kb[4:ncol(rep_2.tmrca.200kb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.200kb.rep2 <- as.data.frame(cbind(rep_1.pi.200kb$avg, sim.theta.200kb$Rate, rep2.sim.tmrca.200kb))
names(true.lands.200kb.rep2) <- c("diversity", "theta", "tmrca", "rho")
true.lands.200kb.rep2$thetaC <- true.lands.200kb.rep2$theta - mean(true.lands.200kb.rep2$theta)
true.lands.200kb.rep2$tmrcaC <- true.lands.200kb.rep2$tmrca - mean(true.lands.200kb.rep2$tmrca)
true.lands.200kb.rep2$rhoC <- true.lands.200kb.rep2$rho - mean(true.lands.200kb.rep2$rho, na.rm = T)
true.lands.200kb.rep2$Replicate <- 1
m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.200kb.rep2)
anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.200kb.true[1, 2] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.200kb.true[2, 2] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb.true[3, 2] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb.true[4, 2] <- anova.diversity$VarExp[3] * 100

```

```

r2.bgs.200kb.true[5, 2] <- anova.diversity$VarExp[4] * 100

inf.lands.200kb.rep2 <- as.data.frame(cbind(rep_2.pi.200kb$avg, rep_2.theta.200kb$sample_mean, rep_2.tmrca.200kb$sample_mean))
names(inf.lands.200kb.rep2) <- c("diversity", "theta", "tmrca", "rho")

cor.table[2, 2] <- cor.test(sim.theta.200kb$Rate, rep_2.theta.200kb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.200kb.rep2$thetaC <- inf.lands.200kb.rep2$theta - mean(inf.lands.200kb.rep2$theta)
inf.lands.200kb.rep2$tmrcaC <- inf.lands.200kb.rep2$tmrca - mean(inf.lands.200kb.rep2$tmrca)
inf.lands.200kb.rep2$rhoC <- inf.lands.200kb.rep2$rho - mean(inf.lands.200kb.rep2$rho)

inf.lands.200kb.rep2$bin <- 1:nrow(inf.lands.200kb.rep2)

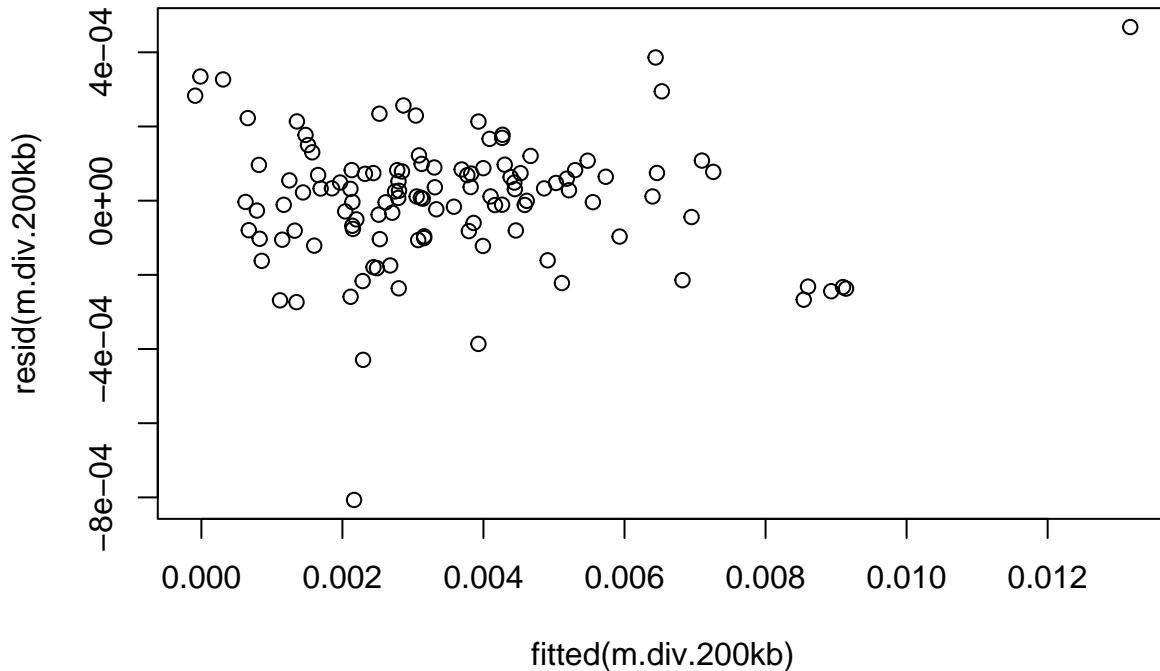
# for merging:
inf.lands.200kb.rep2 <- inf.lands.200kb.rep2
inf.lands.200kb.rep2$Replicate <- 1

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.200kb.rep2)
m.div.200kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.200kb.rep2)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.200kb.rep2)

AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)

##          df      AIC
## m.div.200kb     6 -1700.943
## m.div.200kb.2   7 -1724.292
## m.div.200kb.3   8 -1728.465
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```



```

dwtest(m.div.200kb)

##
##  Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.4796, p-value = 0.001381
## alternative hypothesis: true autocorrelation is greater than 0

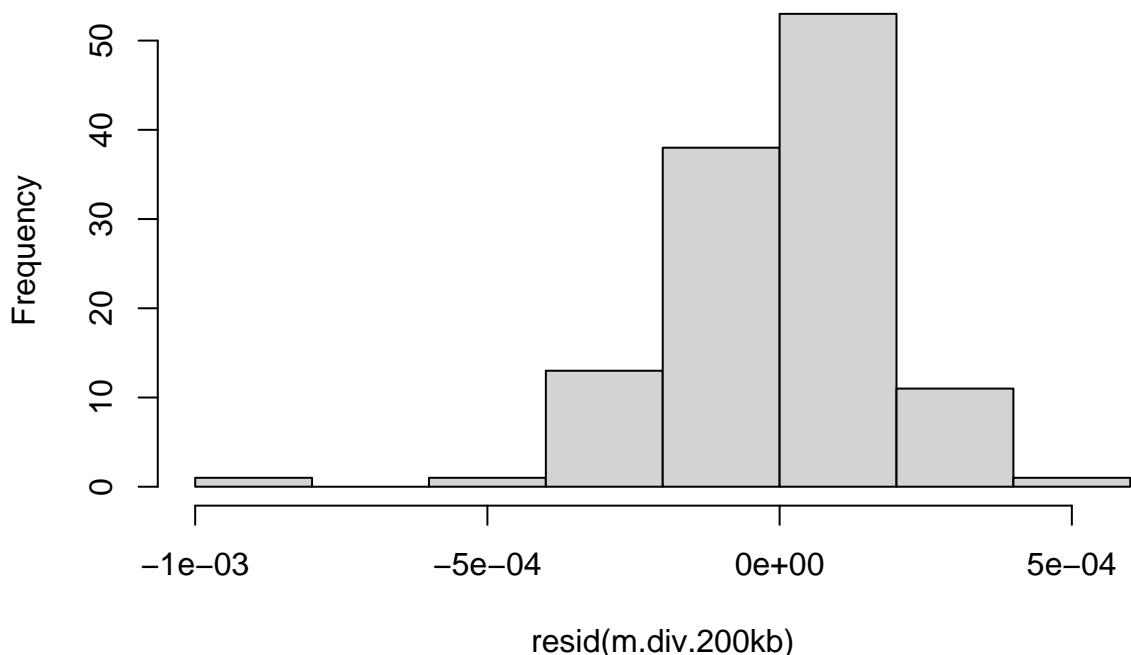
hmctest(m.div.200kb)

##
##  Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.31601, p-value = 0.001

hist(resid(m.div.200kb))

```

**Histogram of resid(m.div.200kb)**



```

summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.200kb.rep2)
##
## Residuals:
##       Min        1Q     Median        3Q       Max
## -8.069e-04 -8.170e-05  1.681e-05  8.234e-05  4.681e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.681e-05  8.234e-05   2.03    0.045 *
## thetaC      -8.069e-04  8.170e-05  -9.88   <2e-16 ***
## rhoC        4.681e-04  8.234e-05   5.63    0.000 ***
## tmrcaC      1.681e-05  8.234e-05   0.20    0.839
## thetaC:tmrcaC 1.681e-05  8.234e-05   0.20    0.839
##
```

```

##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.490e-03 1.608e-05 217.015 <2e-16 ***
## thetaC      1.270e+00 1.302e-02  97.564 <2e-16 ***
## rhoC        1.464e-02 9.533e-03   1.536   0.127
## tmrcaC     3.319e-03 6.107e-05  54.351 <2e-16 ***
## thetaC:tmrcaC 1.234e+00 4.611e-02  26.756 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0001742 on 113 degrees of freedom
## Multiple R-squared:  0.9939, Adjusted R-squared:  0.9937
## F-statistic:  4640 on 4 and 113 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.200kb[1, 2] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]
r2.bgs.200kb[2, 2] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb[3, 2] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb[4, 2] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb[5, 2] <- anova.diversity$VarExp[4] * 100

g.div.200kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep2, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep2, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep2, weights = varPower(0, ~theta), method = "ML")
g.div.200kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep2, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.200kb.1, g.div.200kb.2, g.div.200kb.3, g.div.200kb.4)

##          df      AIC
## g.div.200kb.1 8 -1726.678
## g.div.200kb.2 8 -1710.004
## g.div.200kb.3 7 -1704.923
## g.div.200kb.4 7 -1719.743

summary(g.div.200kb.3)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
## Data: inf.lands.200kb.rep2
##          AIC      BIC    logLik
## -1704.923 -1685.528 859.4613
##
## Variance function:
## Structure: Power of variance covariate
## Formula: ~theta
## Parameter estimates:
```

```

##      power
## 0.3678003
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept) 0.0034912 0.00001612 216.52518 0.0000
## thetaC       1.2689894 0.01421513  89.27034 0.0000
## rhoC        0.0205454 0.00923486   2.22477 0.0281
## tmrcaC      0.0033095 0.00005994  55.21633 0.0000
## thetaC:tmrcaC 1.1986237 0.05096523  23.51846 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC      0.314
## rhoC        0.006 -0.302
## tmrcaC     -0.020  0.079 -0.408
## thetaC:tmrcaC -0.087 -0.224 -0.018  0.173
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -4.90801162 -0.54193854  0.09032308  0.52513685  2.21280365
##
## Residual standard error: 0.0014917
## Degrees of freedom: 118 total; 113 residual
vif(g.div.200kb.3)

```

	thetaC	rhoC	tmrcaC	thetaC:tmrcaC
##	1.168684	1.316209	1.240963	1.095538

### 6.2.3 Replicate 3

```

rep3.sim.tmrca.200kb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep3_w200000.csv", sep = ",", header = T)

rep_3.pi.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.d")
rep_3.pi.200kb$avg <- apply(rep_3.pi.200kb[4:ncol(rep_3.pi.200kb)], 1, mean)
rep_3.rho.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.d")
rep_3.theta.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.d")
rep_3.tmrca.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.d")
rep_3.tmrca.200kb$avg <- apply(rep_3.tmrca.200kb[4:ncol(rep_3.tmrca.200kb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.200kb.rep3 <- as.data.frame(cbind(rep_1.pi.200kb$avg, sim.theta.200kb$Rate, rep3.sim.tmrca.200kb))
names(true.lands.200kb.rep3) <- c("diversity", "theta", "tmrca", "rho")
true.lands.200kb.rep3$thetaC <- true.lands.200kb.rep3$theta - mean(true.lands.200kb.rep3$theta)
true.lands.200kb.rep3$tmrcaC <- true.lands.200kb.rep3$tmrca - mean(true.lands.200kb.rep3$tmrca)
true.lands.200kb.rep3$rhoC <- true.lands.200kb.rep3$rho - mean(true.lands.200kb.rep3$rho, na.rm = T)
true.lands.200kb.rep3$Replicate <- 1
m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.200kb.rep3)
anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.200kb.true[1, 3] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.bgs.200kb.true[2, 3] <- anova.diversity$VarExp[1] * 100

```

```

r2.bgs.200kb.true[3, 3] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb.true[4, 3] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb.true[5, 3] <- anova.diversity$VarExp[4] * 100

inf.lands.200kb.rep3 <- as.data.frame(cbind(rep_3.pi.200kb$avg, rep_3.theta.200kb$sample_mean, rep_3.tmrca.200kb$tmrca, rep_3.rho.200kb$rho))
names(inf.lands.200kb.rep3) <- c("diversity", "theta", "tmrca", "rho")

cor.table[3, 2] <- cor.test(sim.theta.200kb$Rate, rep_3.theta.200kb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.200kb.rep3$thetaC <- inf.lands.200kb.rep3$theta - mean(inf.lands.200kb.rep3$theta)
inf.lands.200kb.rep3$tmrcaC <- inf.lands.200kb.rep3$tmrca - mean(inf.lands.200kb.rep3$tmrca)
inf.lands.200kb.rep3$rhoC <- inf.lands.200kb.rep3$rho - mean(inf.lands.200kb.rep3$rho)

inf.lands.200kb.rep3$bin <- 1:nrow(inf.lands.200kb.rep3)

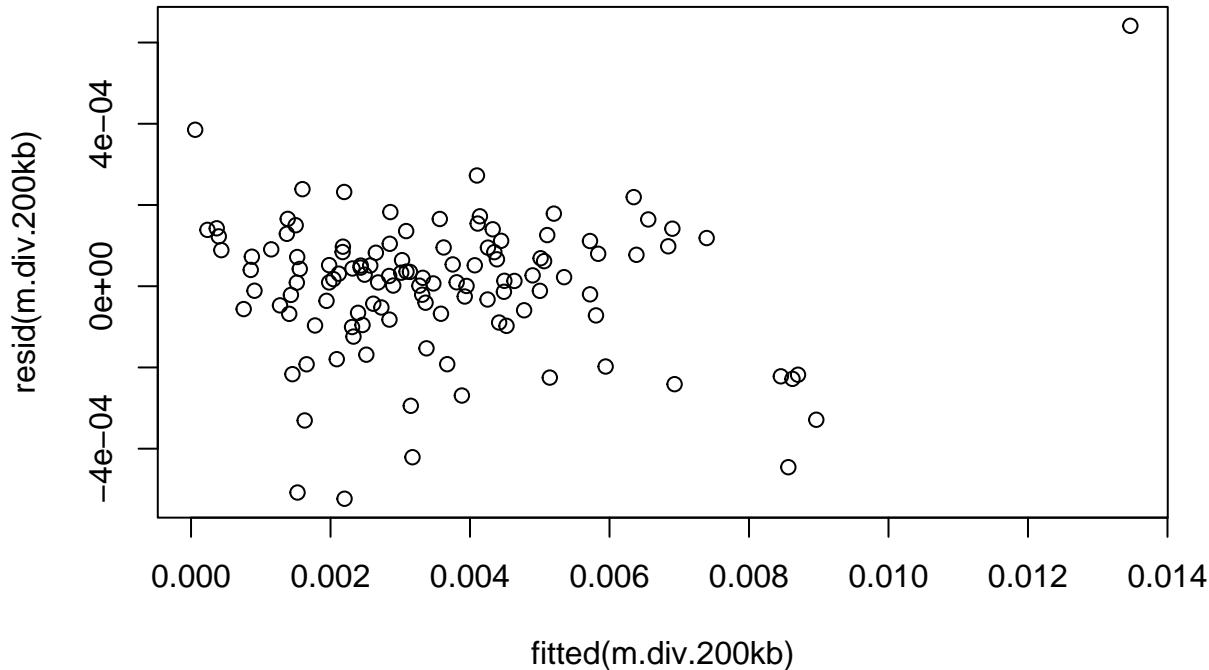
# for merging:
inf.lands.200kb.rep3 <- inf.lands.200kb.rep3
inf.lands.200kb.rep3$Replicate <- 1

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.200kb.rep3)
m.div.200kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.200kb.rep3)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.200kb.rep3)

AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)

##          df      AIC
## m.div.200kb     6 -1707.314
## m.div.200kb.2   7 -1754.542
## m.div.200kb.3   8 -1764.055
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```



```

dwtest(m.div.200kb)

##
##  Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.3035, p-value = 3.818e-05
## alternative hypothesis: true autocorrelation is greater than 0

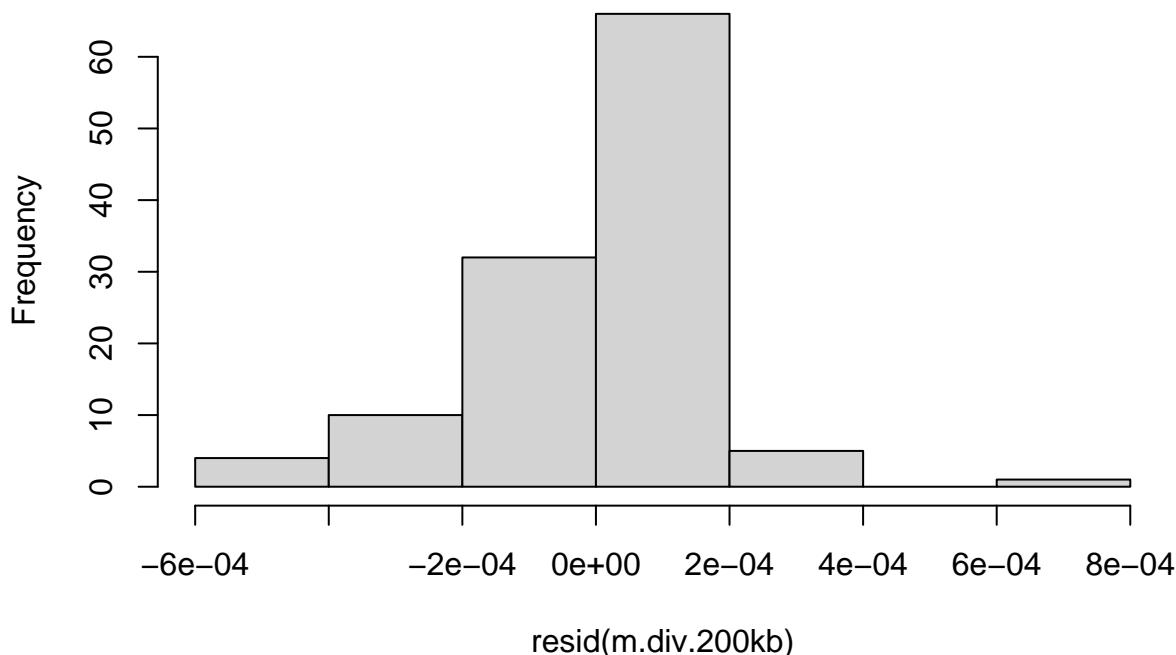
hmctest(m.div.200kb)

##
##  Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.44743, p-value = 0.226

hist(resid(m.div.200kb))

```

**Histogram of resid(m.div.200kb)**



```

summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.200kb.rep3)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -5.233e-04 -6.723e-05  2.374e-05  9.394e-05  6.412e-04
##
## Coefficients:

```

```

##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.519e-03 1.563e-05 225.098 <2e-16 ***
## thetaC      1.304e+00 1.266e-02 103.074 <2e-16 ***
## rhoC        1.509e-02 9.182e-03  1.643   0.103
## tmrcaC     3.196e-03 6.524e-05 48.993 <2e-16 ***
## thetaC:tmrcaC 1.178e+00 4.759e-02 24.752 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0001695 on 113 degrees of freedom
## Multiple R-squared:  0.9941, Adjusted R-squared:  0.9939
## F-statistic:  4792 on 4 and 113 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.200kb[1, 3] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]
r2.bgs.200kb[2, 3] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb[3, 3] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb[4, 3] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb[5, 3] <- anova.diversity$VarExp[4] * 100

g.div.200kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep3, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep3, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep3, weights = varPower(0, ~theta), method = "ML")
g.div.200kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep3, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.200kb.1, g.div.200kb.2, g.div.200kb.3, g.div.200kb.4)

##          df      AIC
## g.div.200kb.1 8 -1726.196
## g.div.200kb.2 8 -1733.453
## g.div.200kb.3 7 -1719.642
## g.div.200kb.4 7 -1713.673

summary(g.div.200kb.3)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
## Data: inf.lands.200kb.rep3
##          AIC      BIC    logLik
## -1719.642 -1700.247 866.8209
##
## Variance function:
## Structure: Power of variance covariate
## Formula: ~theta
## Parameter estimates:
```

```

##      power
## 0.5394141
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept) 0.0035215 0.00001564 225.20991 0.0000
## thetaC       1.3024097 0.01384062  94.10053 0.0000
## rhoC        0.0250918 0.00888843   2.82298 0.0056
## tmrcaC      0.0032052 0.00006146  52.14774 0.0000
## thetaC:tmrcaC 1.0588155 0.05105686  20.73797 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC      0.444
## rhoC       -0.003 -0.311
## tmrcaC     -0.004  0.137 -0.447
## thetaC:tmrcaC -0.064 -0.175  0.023  0.090
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -4.0617345 -0.4658902  0.1165599  0.5723830  3.1881386
##
## Residual standard error: 0.003946494
## Degrees of freedom: 118 total; 113 residual
vif(g.div.200kb.3)

##          thetaC          rhoC          tmrcaC thetaC:tmrcaC
## 1.142896    1.358502    1.266648    1.046199

```

#### 6.2.4 Replicate 4

```

rep4.sim.tmrca.200kb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep4_w200000.csv", sep = ",", header = T)

rep_4.pi.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.d")
rep_4.pi.200kb$avg <- apply(rep_4.pi.200kb[4:ncol(rep_4.pi.200kb)], 1, mean)
rep_4.rho.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.d")
rep_4.theta.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.d")
rep_4.tmrca.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.d")
rep_4.tmrca.200kb$avg <- apply(rep_4.tmrca.200kb[4:ncol(rep_4.tmrca.200kb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.200kb.rep4 <- as.data.frame(cbind(rep_4.pi.200kb$avg, sim.theta.200kb$Rate, rep4.sim.tmrca.200kb))
names(true.lands.200kb.rep4) <- c("diversity", "theta", "tmrca", "rho")
true.lands.200kb.rep4$thetaC <- true.lands.200kb.rep4$theta - mean(true.lands.200kb.rep4$theta)
true.lands.200kb.rep4$tmrcaC <- true.lands.200kb.rep4$tmrca - mean(true.lands.200kb.rep4$tmrca)
true.lands.200kb.rep4$rhoC <- true.lands.200kb.rep4$rho - mean(true.lands.200kb.rep4$rho, na.rm = T)
true.lands.200kb.rep4$Replicate <- 1
m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.200kb.rep4)
anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.200kb.true[1, 4] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.200kb.true[2, 4] <- anova.diversity$VarExp[1] * 100

```

```

r2.bgs.200kb.true[3, 4] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb.true[4, 4] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb.true[5, 4] <- anova.diversity$VarExp[4] * 100

inf.lands.200kb.rep4 <- as.data.frame(cbind(rep_4.pi.200kb$avg, rep_4.theta.200kb$sample_mean, rep_4.tmrca.200kb$tmrca, rep_4.rho.200kb$rho))
names(inf.lands.200kb.rep4) <- c("diversity", "theta", "tmrca", "rho")

cor.table[4, 2] <- cor.test(sim.theta.200kb$Rate, rep_4.theta.200kb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.200kb.rep4$thetaC <- inf.lands.200kb.rep4$theta - mean(inf.lands.200kb.rep4$theta)
inf.lands.200kb.rep4$tmrcaC <- inf.lands.200kb.rep4$tmrca - mean(inf.lands.200kb.rep4$tmrca)
inf.lands.200kb.rep4$rhoC <- inf.lands.200kb.rep4$rho - mean(inf.lands.200kb.rep4$rho)

inf.lands.200kb.rep4$bin <- 1:nrow(inf.lands.200kb.rep4)

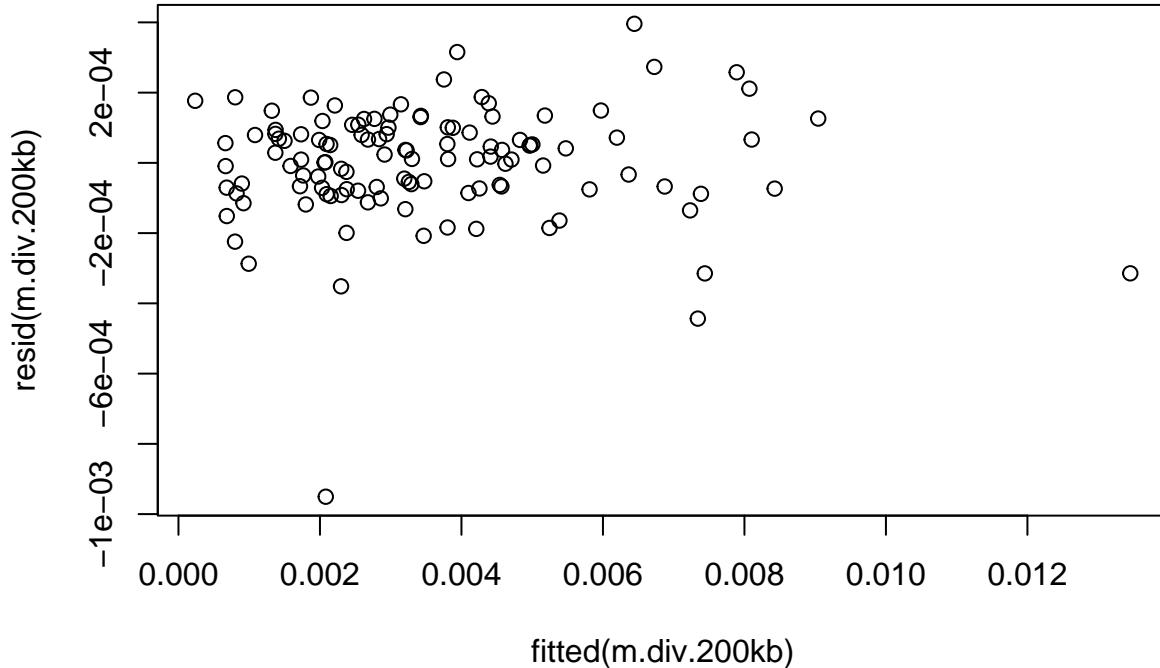
# for merging:
inf.lands.200kb.rep4 <- inf.lands.200kb.rep4
inf.lands.200kb.rep4$Replicate <- 1

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.200kb.rep4)
m.div.200kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.200kb.rep4)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.200kb.rep4)

AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)

##          df      AIC
## m.div.200kb     6 -1713.378
## m.div.200kb.2   7 -1712.955
## m.div.200kb.3   8 -1711.494
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```



```

dwtest(m.div.200kb)

##
##  Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.3999, p-value = 0.0002898
## alternative hypothesis: true autocorrelation is greater than 0

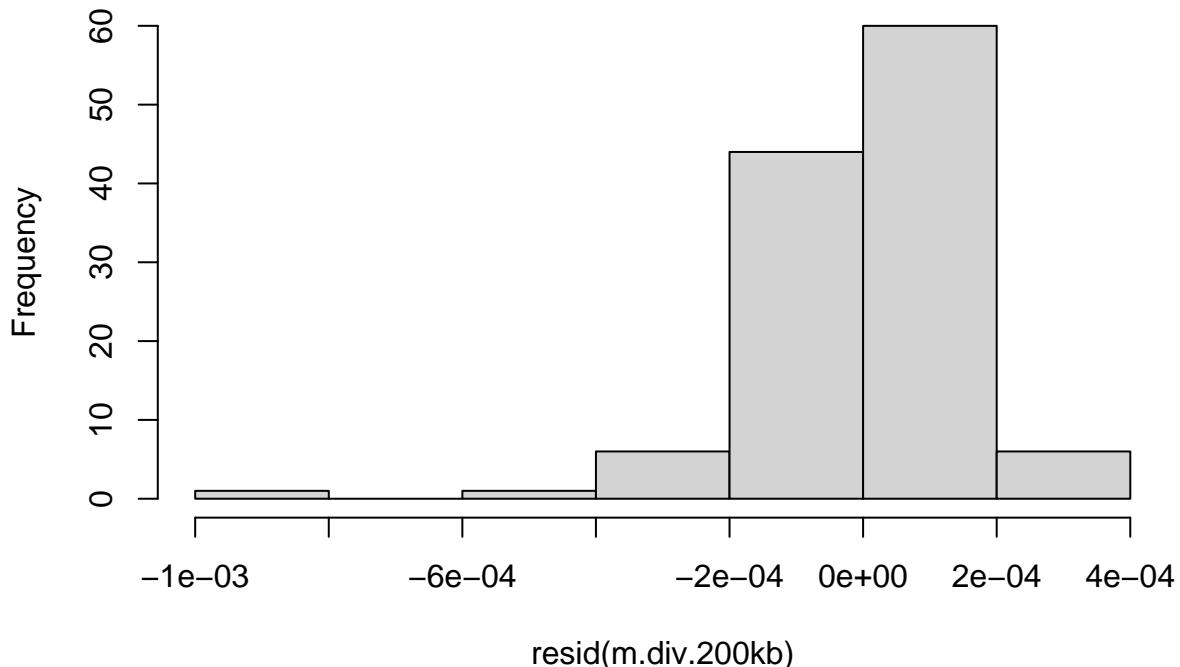
hmctest(m.div.200kb)

##
##  Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.54457, p-value = 0.769

hist(resid(m.div.200kb))

```

**Histogram of resid(m.div.200kb)**



```

summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.200kb.rep4)
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -9.505e-04 -7.323e-05  1.451e-05  9.198e-05  3.959e-04 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept)  1.451e-05  9.198e-05  1.588    0.121    
## thetaC      -9.505e-04 -7.323e-05 -1.308    0.200    
## rhoC        3.959e-04  3.959e-04  1.000    0.317    
## tmrcaC     -1.451e-05 -1.451e-05 -0.000    1.000    
## thetaC:tmrcaC 1.451e-05  9.198e-05  1.588    0.121    
## 
```

```

##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.0034540  0.0000156 221.409 < 2e-16 ***
## thetaC      1.0510911  0.0098390 106.829 < 2e-16 ***
## rhoC        0.0457967  0.0086872  5.272 6.56e-07 ***
## tmrcaC      0.0050692  0.0001243  40.793 < 2e-16 ***
## thetaC:tmrcaC 1.4832766  0.0629216 23.573 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0001652 on 113 degrees of freedom
## Multiple R-squared:  0.9944, Adjusted R-squared:  0.9942
## F-statistic:  5034 on 4 and 113 DF,  p-value: < 2.2e-16
anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.200kb[1, 4] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]
r2.bgs.200kb[2, 4] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb[3, 4] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb[4, 4] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb[5, 4] <- anova.diversity$VarExp[4] * 100

g.div.200kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep4, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep4, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep4, weights = varPower(0, ~theta), method = "ML")
g.div.200kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep4, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.200kb.1, g.div.200kb.2, g.div.200kb.3, g.div.200kb.4)

##          df      AIC
## g.div.200kb.1 8 -1734.204
## g.div.200kb.2 8 -1714.992
## g.div.200kb.3 7 -1711.444
## g.div.200kb.4 7 -1731.676
summary(g.div.200kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.200kb.rep4
##       AIC      BIC    logLik
##   -1711.444 -1692.05 862.7222
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
```

```

##      power
## 0.03207734
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept) 0.0034535 0.00001562 221.09509     0
## thetaC       1.0511893 0.00995135 105.63281     0
## rhoC        0.0461182 0.00870646  5.29701     0
## tmrcaC      0.0050657 0.00012452  40.68200     0
## thetaC:tmrcaC 1.4907778 0.06401702  23.28721     0
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC      0.065
## rhoC       -0.019 -0.338
## tmrcaC     -0.038 -0.172 -0.220
## thetaC:tmrcaC -0.228 -0.170  0.085  0.171
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -5.95926937 -0.46066423  0.09235141  0.57624590  2.39702801
##
## Residual standard error: 0.0001948346
## Degrees of freedom: 118 total; 113 residual
vif(g.div.200kb.3)

```

	thetaC	rhoC	tmrcaC	thetaC:tmrcaC
##	1.229295	1.247833	1.162730	1.058662

### 6.2.5 Replicate 5

```

rep5.sim.tmrca.200kb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep5_w200000.csv", sep = ",", header = T)

rep_5.pi.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.d")
rep_5.pi.200kb$avg <- apply(rep_5.pi.200kb[4:ncol(rep_5.pi.200kb)], 1, mean)
rep_5.rho.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.d")
rep_5.theta.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.d")
rep_5.tmrca.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.d")
rep_5.tmrca.200kb$avg <- apply(rep_5.tmrca.200kb[4:ncol(rep_5.tmrca.200kb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.200kb.rep5 <- as.data.frame(cbind(rep_1.pi.200kb$avg, sim.theta.200kb$Rate, rep5.sim.tmrca.200kb))
names(true.lands.200kb.rep5) <- c("diversity", "theta", "tmrca", "rho")
true.lands.200kb.rep5$thetaC <- true.lands.200kb.rep5$theta - mean(true.lands.200kb.rep5$theta)
true.lands.200kb.rep5$tmrcaC <- true.lands.200kb.rep5$tmrca - mean(true.lands.200kb.rep5$tmrca)
true.lands.200kb.rep5$rhoC <- true.lands.200kb.rep5$rho - mean(true.lands.200kb.rep5$rho, na.rm = T)
true.lands.200kb.rep5$Replicate <- 1
m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.200kb.rep5)
anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.200kb.true[1, 5] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.200kb.true[2, 5] <- anova.diversity$VarExp[1] * 100

```

```

r2.bgs.200kb.true[3, 5] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb.true[4, 5] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb.true[5, 5] <- anova.diversity$VarExp[4] * 100

inf.lands.200kb.rep5 <- as.data.frame(cbind(rep_5.pi.200kb$avg, rep_5.theta.200kb$sample_mean, rep_5.tmrca.200kb$sample_mean))
names(inf.lands.200kb.rep5) <- c("diversity", "theta", "tmrca", "rho")

cor.table[5, 2] <- cor.test(sim.theta.200kb$Rate, rep_5.theta.200kb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.200kb.rep5$thetaC <- inf.lands.200kb.rep5$theta - mean(inf.lands.200kb.rep5$theta)
inf.lands.200kb.rep5$tmrcaC <- inf.lands.200kb.rep5$tmrca - mean(inf.lands.200kb.rep5$tmrca)
inf.lands.200kb.rep5$rhoC <- inf.lands.200kb.rep5$rho - mean(inf.lands.200kb.rep5$rho)

inf.lands.200kb.rep5$bin <- 1:nrow(inf.lands.200kb.rep5)

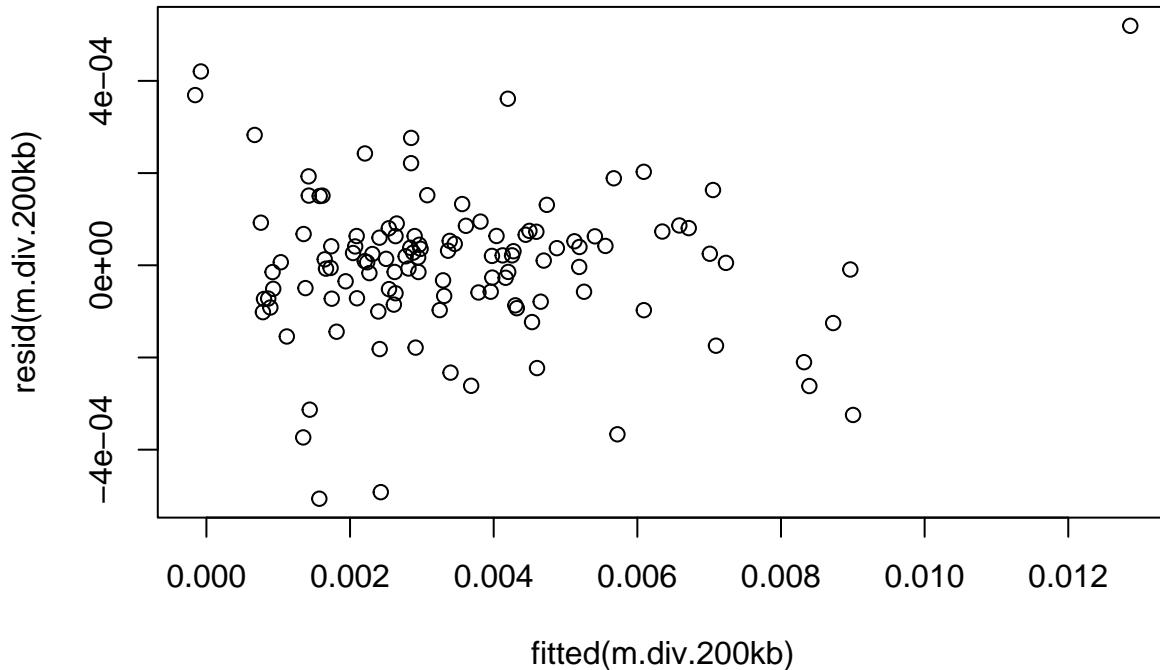
# for merging:
inf.lands.200kb.rep5 <- inf.lands.200kb.rep5
inf.lands.200kb.rep5$Replicate <- 1

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.200kb.rep5)
m.div.200kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.200kb.rep5)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.200kb.rep5)

AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)

##          df      AIC
## m.div.200kb     6 -1719.223
## m.div.200kb.2   7 -1752.807
## m.div.200kb.3   8 -1753.702
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```



```

dwtest(m.div.200kb)

##
##  Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.3237, p-value = 6.006e-05
## alternative hypothesis: true autocorrelation is greater than 0

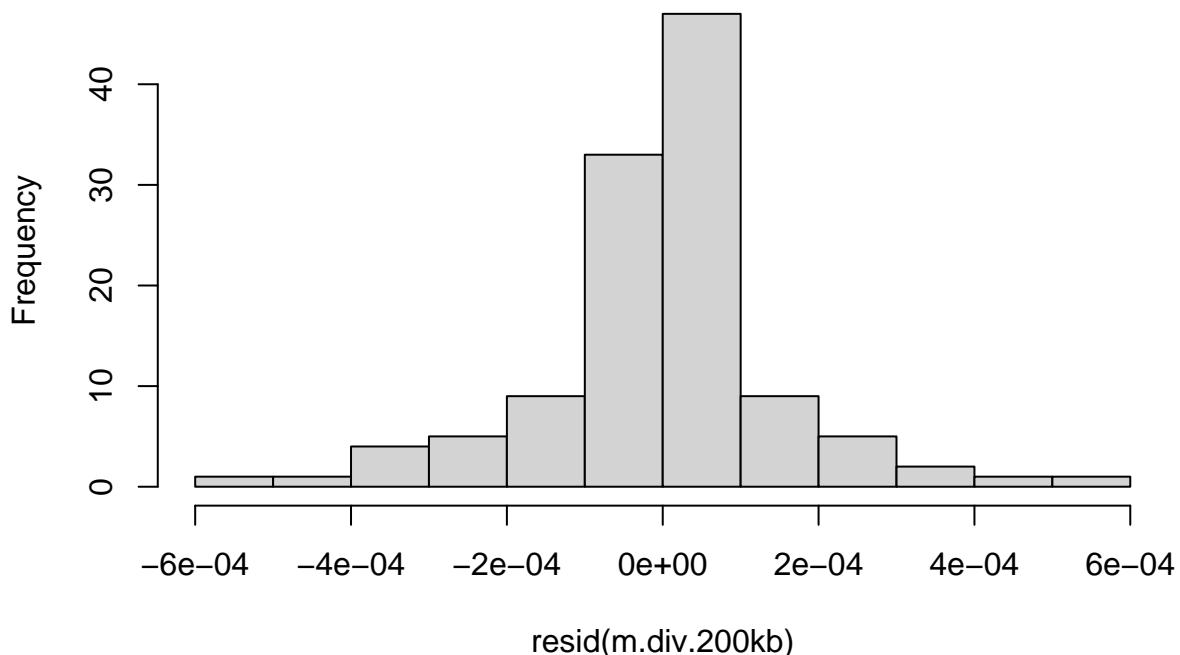
hmctest(m.div.200kb)

##
##  Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.38497, p-value = 0.041

hist(resid(m.div.200kb))

```

**Histogram of resid(m.div.200kb)**



```

summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.200kb.rep5)
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -5.064e-04 -7.206e-05  1.342e-05  6.558e-05  5.195e-04 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept)  1.342e-05  6.558e-05    2.04   0.041 *  
## thetaC      -5.064e-04  5.195e-04   -9.71   <2e-16 ***
## rhoC        -7.206e-05  6.558e-05   -1.09   0.280    
## tmrcaC      1.342e-05  6.558e-05    2.04   0.041 *  
## thetaC:tmrcaC 6.558e-05  6.558e-05    1.00   0.317    
## 
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```

##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.461e-03 1.497e-05 231.248 <2e-16 ***
## thetaC      1.289e+00 1.202e-02 107.250 <2e-16 ***
## rhoC        5.476e-03 8.877e-03  0.617   0.539
## tmrcaC     3.298e-03 6.213e-05 53.084 <2e-16 ***
## thetaC:tmrcaC 1.196e+00 4.528e-02 26.410 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0001612 on 113 degrees of freedom
## Multiple R-squared:  0.9947, Adjusted R-squared:  0.9945
## F-statistic:  5272 on 4 and 113 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.200kb[1, 5] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]
r2.bgs.200kb[2, 5] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb[3, 5] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb[4, 5] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb[5, 5] <- anova.diversity$VarExp[4] * 100

g.div.200kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep5, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep5, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep5, weights = varPower(0, ~theta), method = "ML")
g.div.200kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep5, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.200kb.1, g.div.200kb.2, g.div.200kb.3, g.div.200kb.4)

##          df      AIC
## g.div.200kb.1 8 -1755.478
## g.div.200kb.2 8 -1740.007
## g.div.200kb.3 7 -1725.582
## g.div.200kb.4 7 -1749.740

summary(g.div.200kb.3)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
## Data: inf.lands.200kb.rep5
##          AIC      BIC    logLik
## -1725.582 -1706.187 869.7909
##
## Variance function:
## Structure: Power of variance covariate
## Formula: ~theta
## Parameter estimates:
```

```

##      power
## 0.4273153
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept) 0.0034638 0.00001505 230.12028 0.0000
## thetaC       1.2857552 0.01337872  96.10447 0.0000
## rhoC        0.0119472 0.00874229   1.36660 0.1745
## tmrcaC      0.0032822 0.00006202  52.92532 0.0000
## thetaC:tmrcaC 1.1470417 0.05046751  22.72832 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC     0.368
## rhoC      0.004 -0.344
## tmrcaC    -0.053  0.016 -0.393
## thetaC:tmrcaC -0.148 -0.190 -0.011  0.342
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -3.75640462 -0.47240720  0.07496887  0.41643045  2.69009455
##
## Residual standard error: 0.001969146
## Degrees of freedom: 118 total; 113 residual
vif(g.div.200kb.3)

```

	thetaC	rhoC	tmrcaC	thetaC:tmrcaC
##	1.190932	1.375450	1.374444	1.190572

## 6.2.6 Replicate 6

```

rep6.sim.tmrca.200kb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep6_w200000.csv", sep = ",", header = T)

rep_6.pi.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.d")
rep_6.pi.200kb$avg <- apply(rep_6.pi.200kb[4:ncol(rep_6.pi.200kb)], 1, mean)
rep_6.rho.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.d")
rep_6.theta.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.d")
rep_6.tmrca.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.d")
rep_6.tmrca.200kb$avg <- apply(rep_6.tmrca.200kb[4:ncol(rep_6.tmrca.200kb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.200kb.rep6 <- as.data.frame(cbind(rep_1.pi.200kb$avg, sim.theta.200kb$Rate, rep6.sim.tmrca.200kb))
names(true.lands.200kb.rep6) <- c("diversity", "theta", "tmrca", "rho")
true.lands.200kb.rep6$thetaC <- true.lands.200kb.rep6$theta - mean(true.lands.200kb.rep6$theta)
true.lands.200kb.rep6$tmrcaC <- true.lands.200kb.rep6$tmrca - mean(true.lands.200kb.rep6$tmrca)
true.lands.200kb.rep6$rhoC <- true.lands.200kb.rep6$rho - mean(true.lands.200kb.rep6$rho, na.rm = T)
true.lands.200kb.rep6$Replicate <- 1
m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.200kb.rep6)
anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.200kb.true[1, 6] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.200kb.true[2, 6] <- anova.diversity$VarExp[1] * 100

```

```

r2.bgs.200kb.true[3, 6] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb.true[4, 6] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb.true[5, 6] <- anova.diversity$VarExp[4] * 100

inf.lands.200kb.rep6 <- as.data.frame(cbind(rep_6.pi.200kb$avg, rep_6.theta.200kb$sample_mean, rep_6.tmrca.200kb$tmrca, rep_6.rho.200kb$rho))
names(inf.lands.200kb.rep6) <- c("diversity", "theta", "tmrca", "rho")

cor.table[6, 2] <- cor.test(sim.theta.200kb$Rate, rep_6.theta.200kb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.200kb.rep6$thetaC <- inf.lands.200kb.rep6$theta - mean(inf.lands.200kb.rep6$theta)
inf.lands.200kb.rep6$tmrcaC <- inf.lands.200kb.rep6$tmrca - mean(inf.lands.200kb.rep6$tmrca)
inf.lands.200kb.rep6$rhoC <- inf.lands.200kb.rep6$rho - mean(inf.lands.200kb.rep6$rho)

inf.lands.200kb.rep6$bin <- 1:nrow(inf.lands.200kb.rep6)

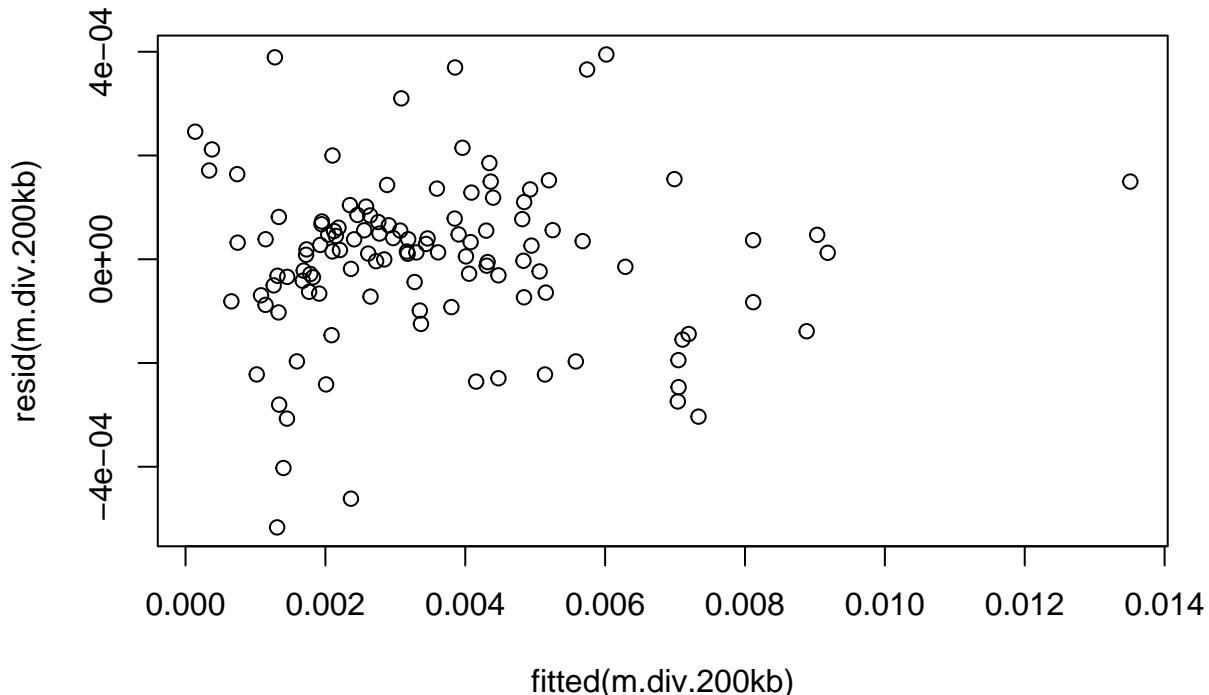
# for merging:
inf.lands.200kb.rep6 <- inf.lands.200kb.rep6
inf.lands.200kb.rep6$Replicate <- 1

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.200kb.rep6)
m.div.200kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.200kb.rep6)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.200kb.rep6)

AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)

##          df      AIC
## m.div.200kb    6 -1721.284
## m.div.200kb.2  7 -1738.537
## m.div.200kb.3  8 -1737.848
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```



```

dwtest(m.div.200kb)

##
##  Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.1428, p-value = 6.441e-07
## alternative hypothesis: true autocorrelation is greater than 0

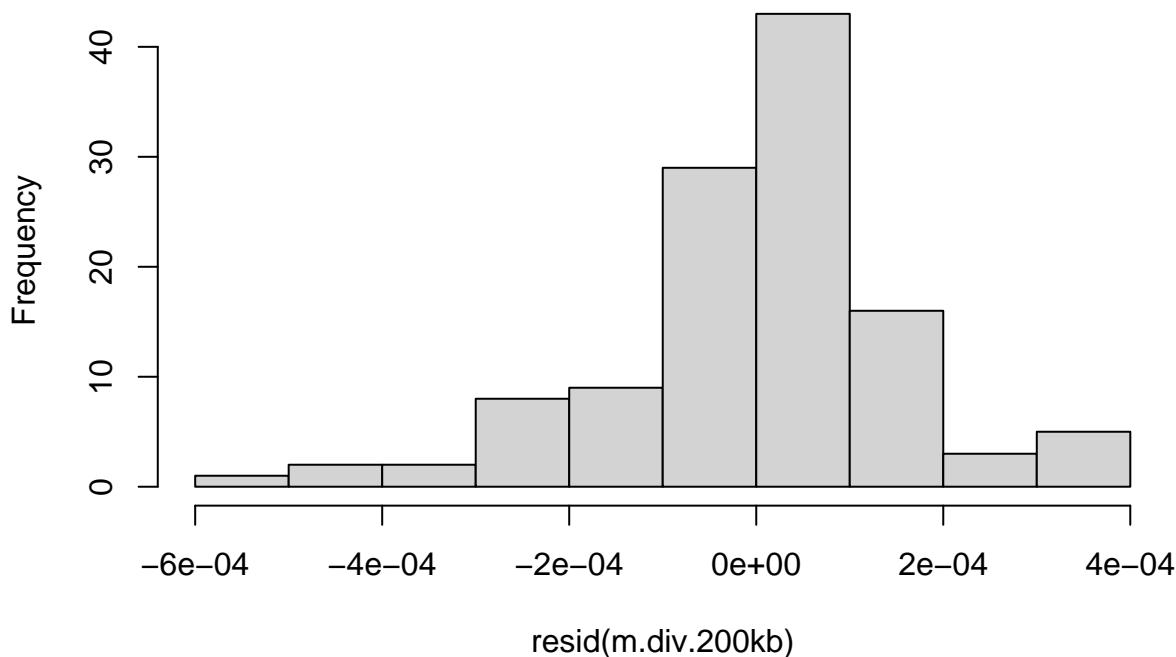
hmctest(m.div.200kb)

##
##  Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.37066, p-value = 0.029

hist(resid(m.div.200kb))

```

**Histogram of resid(m.div.200kb)**



```

summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.200kb.rep6)
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -5.169e-04 -6.868e-05  1.496e-05  7.251e-05  3.947e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept)  1.000e+00  1.000e-01  1.000e+00  1.000e+00  1.000e+00
## thetaC      1.000e-04  1.000e-05  1.000e+00  1.000e+00  1.000e+00
## rhoC        1.000e-04  1.000e-05  1.000e+00  1.000e+00  1.000e+00
## tmrcaC     -1.000e-04 -1.000e-05 -1.000e+00 -1.000e+00 -1.000e+00
## thetaC:tmrcaC 1.000e-04  1.000e-05  1.000e+00  1.000e+00  1.000e+00
## 
```

```

##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.420e-03 1.512e-05 226.13 <2e-16 ***
## thetaC      1.101e+00 1.019e-02 107.98 <2e-16 ***
## rhoC        1.707e-02 7.262e-03   2.35  0.0205 *
## tmrcaC      4.264e-03 8.815e-05  48.37 <2e-16 ***
## thetaC:tmrcaC 1.417e+00 5.145e-02   27.55 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0001598 on 113 degrees of freedom
## Multiple R-squared:  0.995, Adjusted R-squared:  0.9949
## F-statistic:  5662 on 4 and 113 DF, p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.200kb[1, 6] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]
r2.bgs.200kb[2, 6] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb[3, 6] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb[4, 6] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb[5, 6] <- anova.diversity$VarExp[4] * 100

g.div.200kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep6, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep6, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep6, weights = varPower(0, ~theta), method = "ML")
g.div.200kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep6, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.200kb.1, g.div.200kb.2, g.div.200kb.3, g.div.200kb.4)

##          df      AIC
## g.div.200kb.1 8 -1750.916
## g.div.200kb.2 8 -1746.207
## g.div.200kb.3 7 -1722.532
## g.div.200kb.4 7 -1738.724

summary(g.div.200kb.3)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
## Data: inf.lands.200kb.rep6
##          AIC      BIC logLik
## -1722.532 -1703.137 868.266
##
## Variance function:
## Structure: Power of variance covariate
## Formula: ~theta
## Parameter estimates:
```

```

##      power
## 0.2643174
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept) 0.0034189 0.00001529 223.64371 0.0000
## thetaC       1.1060883 0.01089476 101.52477 0.0000
## rhoC        0.0170656 0.00717873  2.37724 0.0191
## tmrcaC      0.0042514 0.00008988  47.30080 0.0000
## thetaC:tmrcaC 1.4159442 0.05773371  24.52543 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC      0.297
## rhoC        0.011 -0.220
## tmrcaC     -0.115 -0.201 -0.326
## thetaC:tmrcaC -0.265 -0.294 -0.019  0.420
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -3.8683483 -0.4416453  0.1205680  0.5114539  2.3563921
##
## Residual standard error: 0.0007276808
## Degrees of freedom: 118 total; 113 residual
vif(g.div.200kb.3)

##          thetaC         rhoC         tmrcaC thetaC:tmrcaC
## 1.202416    1.242707    1.436129    1.292643

```

### 6.2.7 Replicate 7

```

rep7.sim.tmrca.200kb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep7_w200000.csv", sep = ",", header = T)

rep_7.pi.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep7/dm2L_bgs_rep7_5.d")
rep_7.pi.200kb$avg <- apply(rep_7.pi.200kb[4:ncol(rep_7.pi.200kb)], 1, mean)
rep_7.rho.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep7/dm2L_bgs_rep7_5.d")
rep_7.theta.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep7/dm2L_bgs_rep7_5.d")
rep_7.tmrca.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep7/dm2L_bgs_rep7_5.d")
rep_7.tmrca.200kb$avg <- apply(rep_7.tmrca.200kb[4:ncol(rep_7.tmrca.200kb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.200kb.rep7 <- as.data.frame(cbind(rep_1.pi.200kb$avg, sim.theta.200kb$Rate, rep7.sim.tmrca.200kb))
names(true.lands.200kb.rep7) <- c("diversity", "theta", "tmrca", "rho")
true.lands.200kb.rep7$thetaC <- true.lands.200kb.rep7$theta - mean(true.lands.200kb.rep7$theta)
true.lands.200kb.rep7$tmrcaC <- true.lands.200kb.rep7$tmrca - mean(true.lands.200kb.rep7$tmrca)
true.lands.200kb.rep7$rhoC <- true.lands.200kb.rep7$rho - mean(true.lands.200kb.rep7$rho, na.rm = T)
true.lands.200kb.rep7$Replicate <- 1
m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.200kb.rep7)
anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.200kb.true[1, 7] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.200kb.true[2, 7] <- anova.diversity$VarExp[1] * 100

```

```

r2.bgs.200kb.true[3, 7] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb.true[4, 7] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb.true[5, 7] <- anova.diversity$VarExp[4] * 100

inf.lands.200kb.rep7 <- as.data.frame(cbind(rep_7.pi.200kb$avg, rep_7.theta.200kb$sample_mean, rep_7.tmrca.200kb$sample_mean))
names(inf.lands.200kb.rep7) <- c("diversity", "theta", "tmrca", "rho")

cor.table[7, 2] <- cor.test(sim.theta.200kb$Rate, rep_7.theta.200kb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.200kb.rep7$thetaC <- inf.lands.200kb.rep7$theta - mean(inf.lands.200kb.rep7$theta)
inf.lands.200kb.rep7$tmrcaC <- inf.lands.200kb.rep7$tmrca - mean(inf.lands.200kb.rep7$tmrca)
inf.lands.200kb.rep7$rhoC <- inf.lands.200kb.rep7$rho - mean(inf.lands.200kb.rep7$rho)

inf.lands.200kb.rep7$bin <- 1:nrow(inf.lands.200kb.rep7)

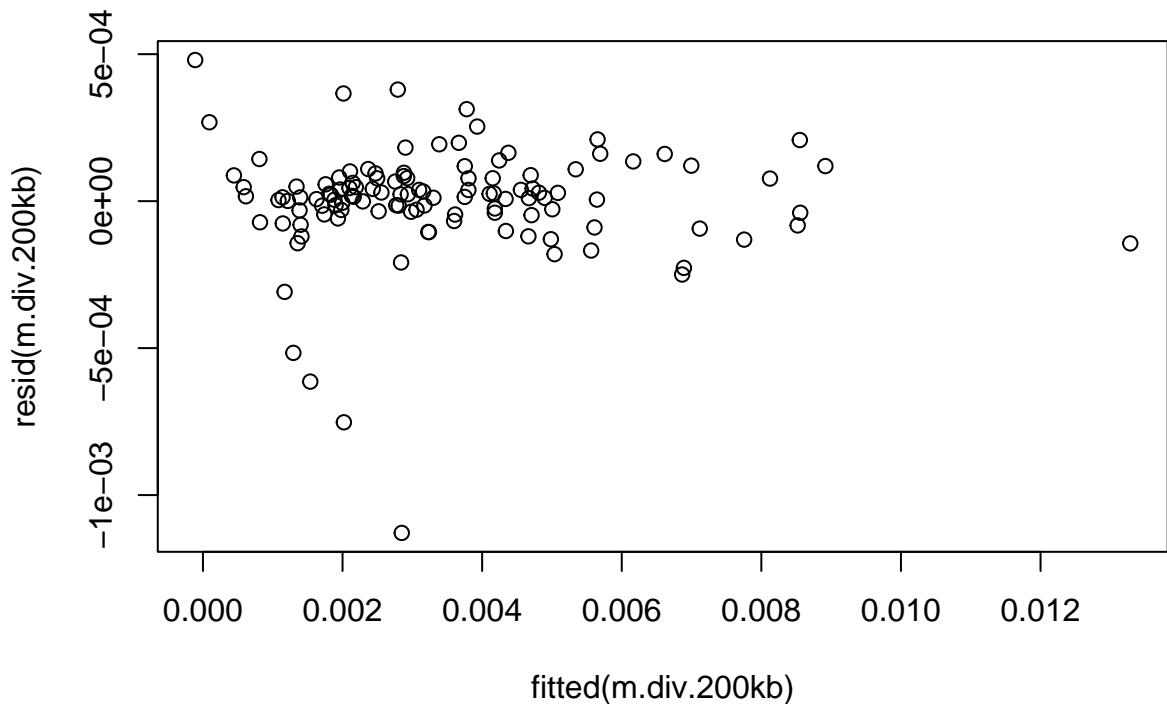
# for merging:
inf.lands.200kb.rep7 <- inf.lands.200kb.rep7
inf.lands.200kb.rep7$Replicate <- 1

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.200kb.rep7)
m.div.200kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.200kb.rep7)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.200kb.rep7)

AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)

##          df      AIC
## m.div.200kb     6 -1675.014
## m.div.200kb.2   7 -1686.944
## m.div.200kb.3   8 -1685.792
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```

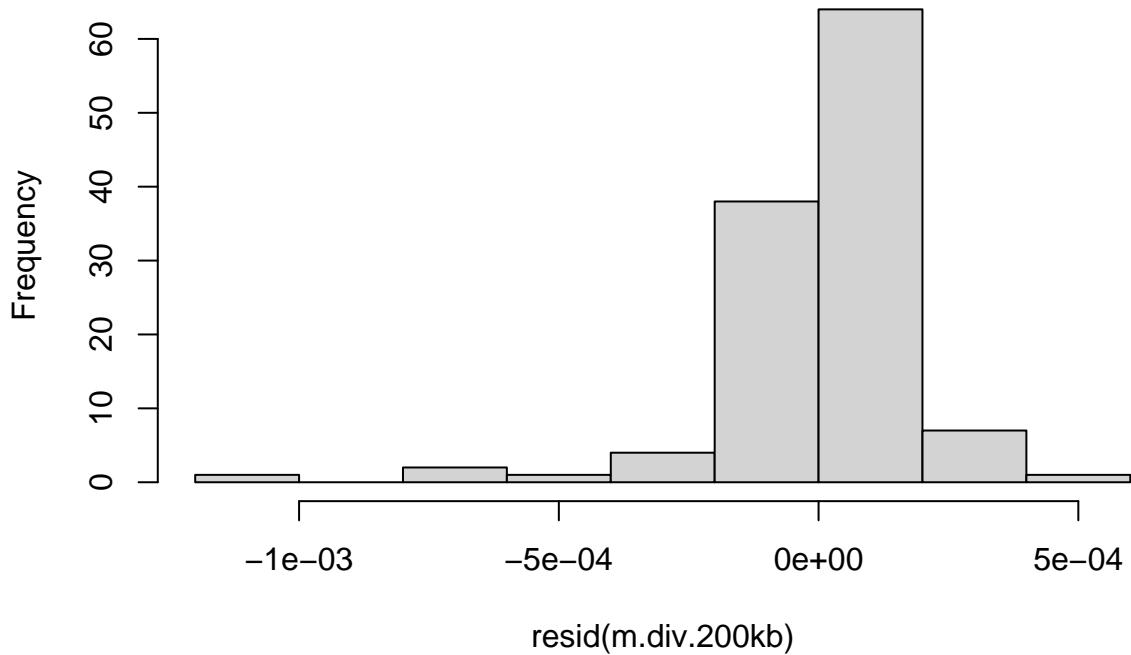


```
dwtest(m.div.200kb)
```

```
##  
## Durbin-Watson test  
##  
## data: m.div.200kb  
## DW = 1.4537, p-value = 0.0008495  
## alternative hypothesis: true autocorrelation is greater than 0  
hmctest(m.div.200kb)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.div.200kb  
## HMC = 0.2727, p-value < 2.2e-16  
hist(resid(m.div.200kb))
```

## Histogram of resid(m.div.200kb)



```
summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.200kb.rep7)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -1.129e-03 -4.377e-05  1.575e-05  7.812e-05  4.801e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.341e-03  1.908e-05 175.137 <2e-16 ***
## thetaC       1.104e+00  1.358e-02  81.322 <2e-16 ***
## rhoC        2.579e-02  1.041e-02  2.477  0.0147 *  
## tmrcaC      4.301e-03  1.323e-04 32.515 <2e-16 ***
## thetaC:tmrcaC 1.493e+00  8.184e-02 18.247 <2e-16 ***
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0001944 on 113 degrees of freedom
## Multiple R-squared:  0.9923, Adjusted R-squared:  0.9921 
## F-statistic: 3652 on 4 and 113 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.200kb[1, 7] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.200kb[2, 7] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb[3, 7] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb[4, 7] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb[5, 7] <- anova.diversity$VarExp[4] * 100

g.div.200kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep7, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep7, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep7, weights = varPower(0, ~theta), method = "ML")
g.div.200kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep7, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.200kb.1, g.div.200kb.2, g.div.200kb.3, g.div.200kb.4)

##                 df      AIC
## g.div.200kb.1  8 -1699.268
## g.div.200kb.2  8 -1683.987
## g.div.200kb.3  7 -1674.195
## g.div.200kb.4  7 -1698.505

summary(g.div.200kb.3)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
## Data: inf.lands.200kb.rep7
##          AIC      BIC    logLik
## -1674.195 -1654.801 844.0976
##
## Variance function:
## Structure: Power of variance covariate
## Formula: ~theta
## Parameter estimates:
##       power
## 0.2235436
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0033379 0.00001961 170.23653 0.0000
## thetaC      1.1020624 0.01463631  75.29644 0.0000
## rhoC       0.0269409 0.01057491   2.54762 0.0122
## tmrcaC     0.0043212 0.00014132  30.57810 0.0000
## thetaC:tmrcaC 1.5314588 0.09352710  16.37449 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC      0.309
## rhoC       -0.017 -0.333
## tmrcaC     -0.248 -0.333 -0.236
## thetaC:tmrcaC -0.396 -0.376  0.054  0.631

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -5.6176121 -0.2278995  0.1068782  0.4264629  2.6382834
## 
## Residual standard error: 0.0007080388
## Degrees of freedom: 118 total; 113 residual
vif(g.div.200kb.3)

##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
## 1.430415 1.377155 2.059089 1.818743

```

## 6.2.8 Replicate 8

```

rep8.sim.tmrca.200kb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep8_w200000.csv", sep = ",", header = T)

rep_8.pi.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.d")
rep_8.pi.200kb$avg <- apply(rep_8.pi.200kb[4:ncol(rep_8.pi.200kb)], 1, mean)
rep_8.rho.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.d")
rep_8.theta.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.d")
rep_8.tmrca.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.d")
rep_8.tmrca.200kb$avg <- apply(rep_8.tmrca.200kb[4:ncol(rep_8.tmrca.200kb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.200kb.rep8 <- as.data.frame(cbind(rep_1.pi.200kb$avg, sim.theta.200kb$Rate, rep8.sim.tmrca.200kb))
names(true.lands.200kb.rep8) <- c("diversity", "theta", "tmrca", "rho")
true.lands.200kb.rep8$thetaC <- true.lands.200kb.rep8$theta - mean(true.lands.200kb.rep8$theta)
true.lands.200kb.rep8$tmrcaC <- true.lands.200kb.rep8$tmrca - mean(true.lands.200kb.rep8$tmrca)
true.lands.200kb.rep8$rhoC <- true.lands.200kb.rep8$rho - mean(true.lands.200kb.rep8$rho, na.rm = T)
true.lands.200kb.rep8$Replicate <- 1
m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.200kb.rep8)
anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$Sum Sq
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.200kb.true[1, 8] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.200kb.true[2, 8] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb.true[3, 8] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb.true[4, 8] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb.true[5, 8] <- anova.diversity$VarExp[4] * 100

inf.lands.200kb.rep8 <- as.data.frame(cbind(rep_8.pi.200kb$avg, rep_8.theta.200kb$sample_mean, rep_8.tmrca.200kb))
names(inf.lands.200kb.rep8) <- c("diversity", "theta", "tmrca", "rho")

cor.table[8, 2] <- cor.test(sim.theta.200kb$Rate, rep_8.theta.200kb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.200kb.rep8$thetaC <- inf.lands.200kb.rep8$theta - mean(inf.lands.200kb.rep8$theta)
inf.lands.200kb.rep8$tmrcaC <- inf.lands.200kb.rep8$tmrca - mean(inf.lands.200kb.rep8$tmrca)
inf.lands.200kb.rep8$rhoC <- inf.lands.200kb.rep8$rho - mean(inf.lands.200kb.rep8$rho)

inf.lands.200kb.rep8$bin <- 1:nrow(inf.lands.200kb.rep8)

# for merging:

```

```

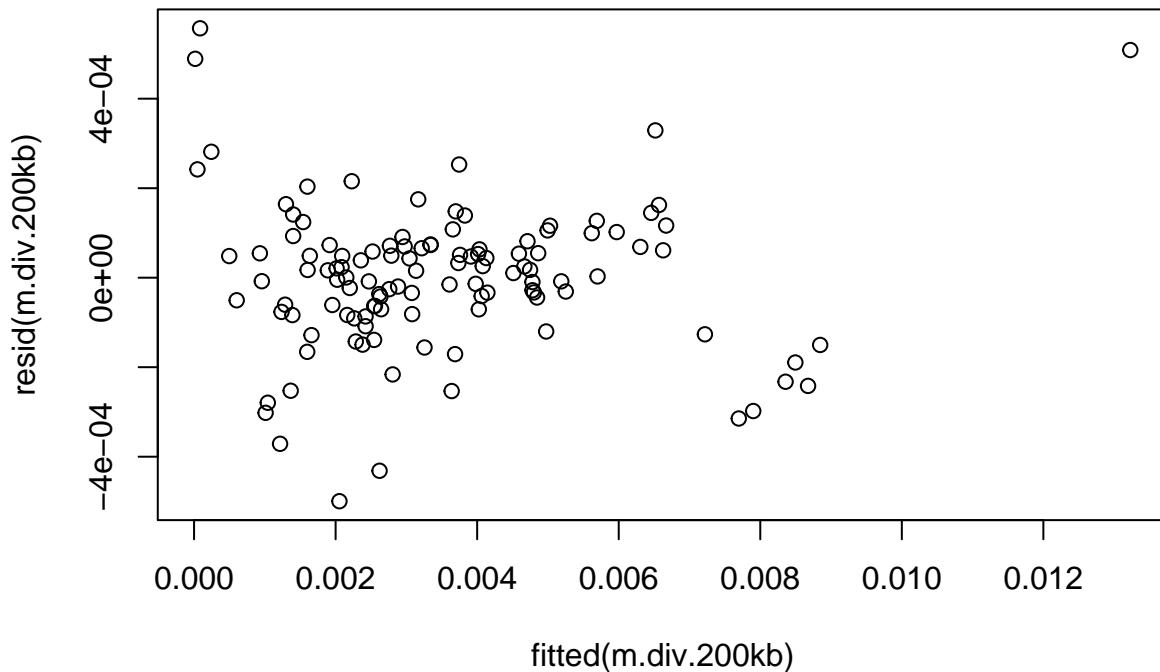
inf.lands.200kb.rep8 <- inf.lands.200kb.rep8
inf.lands.200kb.rep8$Replicate <- 1

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.200kb.rep8)
m.div.200kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.200kb.rep8)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.200kb.rep8)

AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)

##           df      AIC
## m.div.200kb    6 -1711.201
## m.div.200kb.2  7 -1752.777
## m.div.200kb.3  8 -1754.136
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```



```

dwtest(m.div.200kb)

##
##  Durbin-Watson test
##
##  data:  m.div.200kb
##  DW = 1.4172, p-value = 0.0004208
##  alternative hypothesis: true autocorrelation is greater than 0

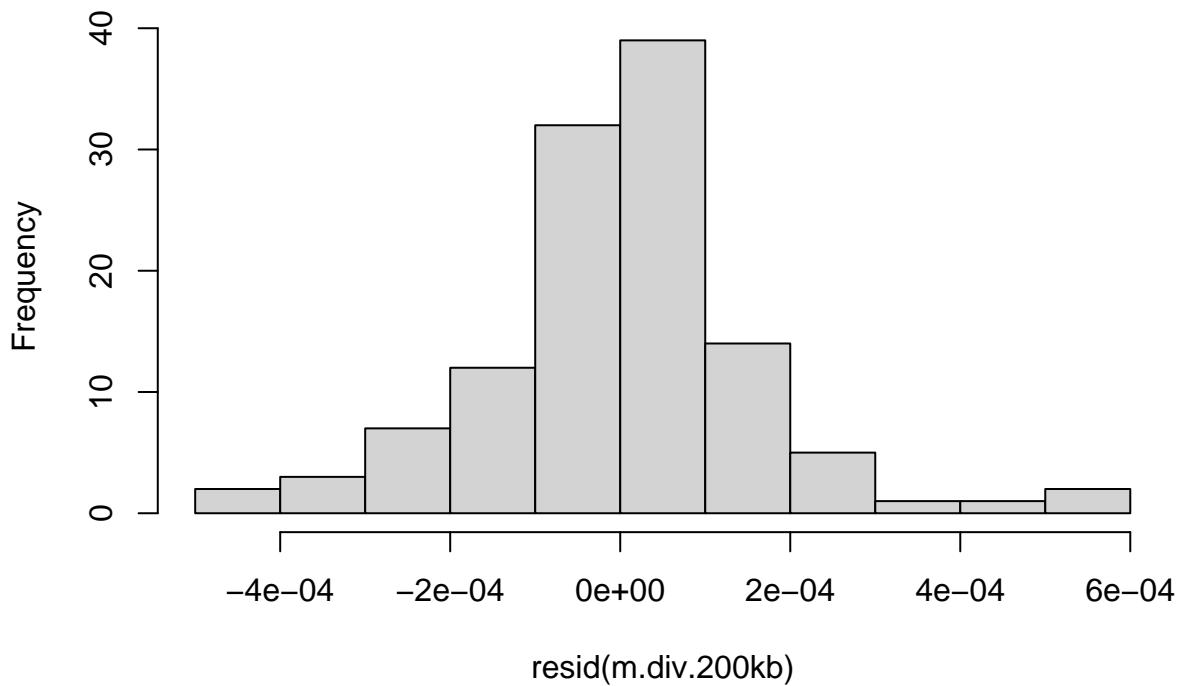
hmctest(m.div.200kb)

##
##  Harrison-McCabe test
##
##  data:  m.div.200kb
##  HMC = 0.36722, p-value = 0.022

hist(resid(m.div.200kb))

```

## Histogram of resid(m.div.200kb)



```
summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.200kb.rep8)
##
## Residuals:
##       Min         1Q     Median        3Q       Max
## -4.995e-04 -7.501e-05  1.296e-05  7.253e-05  5.573e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.435e-03 1.548e-05 221.813 <2e-16 ***
## thetaC      1.237e+00 1.300e-02  95.133 <2e-16 ***
## rhoC        9.601e-03 9.644e-03   0.996   0.322
## tmrcaC      3.336e-03 6.085e-05  54.824 <2e-16 ***
## thetaC:tmrcaC 1.303e+00 5.161e-02  25.255 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0001668 on 113 degrees of freedom
## Multiple R-squared:  0.9943, Adjusted R-squared:  0.9941
## F-statistic: 4932 on 4 and 113 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.200kb[1, 8] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.200kb[2, 8] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb[3, 8] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb[4, 8] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb[5, 8] <- anova.diversity$VarExp[4] * 100

g.div.200kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep8, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep8, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep8, weights = varPower(0, ~theta), method = "ML")
g.div.200kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep8, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.200kb.1, g.div.200kb.2, g.div.200kb.3, g.div.200kb.4)

##                 df      AIC
## g.div.200kb.1  8 -1755.740
## g.div.200kb.2  8 -1748.646
## g.div.200kb.3  7 -1738.511
## g.div.200kb.4  7 -1746.257

summary(g.div.200kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.200kb.rep8
##          AIC      BIC  logLik
##        -1738.511 -1719.117 876.2557
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##     power
## 0.9408611
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0034413 0.00001606 214.34353 0.0000
## thetaC       1.2493957 0.01435473  87.03720 0.0000
## rhoC        0.0146563 0.00812362   1.80415 0.0739
## tmrcaC      0.0032989 0.00005854  56.35435 0.0000
## thetaC:tmrcaC 1.0505342 0.05573402 18.84906 0.0000
##
## Correlation:
##            (Intr) thetaC rhoC    tmrcaC
## thetaC      0.669
## rhoC       -0.030 -0.307
## tmrcaC     -0.024  0.044 -0.398
## thetaC:tmrcaC -0.138 -0.320  0.016  0.489

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -3.28659664 -0.55199225  0.07202289  0.46452382  2.73812395
## 
## Residual standard error: 0.03959627
## Degrees of freedom: 118 total; 113 residual
vif(g.div.200kb.3)

##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
## 1.256856 1.355579 1.701715 1.595889

```

### 6.2.9 Replicate 9

```

rep9.sim.tmrca.200kb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep9_w200000.csv", sep = ",", header = T)

rep_9.pi.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.d")
rep_9.pi.200kb$avg <- apply(rep_9.pi.200kb[4:ncol(rep_9.pi.200kb)], 1, mean)
rep_9.rho.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.d")
rep_9.theta.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.d")
rep_9.tmrca.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.d")
rep_9.tmrca.200kb$avg <- apply(rep_9.tmrca.200kb[4:ncol(rep_9.tmrca.200kb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.200kb.rep9 <- as.data.frame(cbind(rep_1.pi.200kb$avg, sim.theta.200kb$Rate, rep9.sim.tmrca.200kb))
names(true.lands.200kb.rep9) <- c("diversity", "theta", "tmrca", "rho")
true.lands.200kb.rep9$thetaC <- true.lands.200kb.rep9$theta - mean(true.lands.200kb.rep9$theta)
true.lands.200kb.rep9$tmrcaC <- true.lands.200kb.rep9$tmrca - mean(true.lands.200kb.rep9$tmrca)
true.lands.200kb.rep9$rhoC <- true.lands.200kb.rep9$rho - mean(true.lands.200kb.rep9$rho, na.rm = T)
true.lands.200kb.rep9$Replicate <- 1
m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.200kb.rep9)
anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$Sum Sq
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.200kb.true[1, 9] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.200kb.true[2, 9] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb.true[3, 9] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb.true[4, 9] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb.true[5, 9] <- anova.diversity$VarExp[4] * 100

inf.lands.200kb.rep9 <- as.data.frame(cbind(rep_9.pi.200kb$avg, rep_9.theta.200kb$sample_mean, rep_9.tmrca.200kb))
names(inf.lands.200kb.rep9) <- c("diversity", "theta", "tmrca", "rho")

cor.table[9, 2] <- cor.test(sim.theta.200kb$Rate, rep_9.theta.200kb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.200kb.rep9$thetaC <- inf.lands.200kb.rep9$theta - mean(inf.lands.200kb.rep9$theta)
inf.lands.200kb.rep9$tmrcaC <- inf.lands.200kb.rep9$tmrca - mean(inf.lands.200kb.rep9$tmrca)
inf.lands.200kb.rep9$rhoC <- inf.lands.200kb.rep9$rho - mean(inf.lands.200kb.rep9$rho)

inf.lands.200kb.rep9$bin <- 1:nrow(inf.lands.200kb.rep9)

# for merging:

```

```

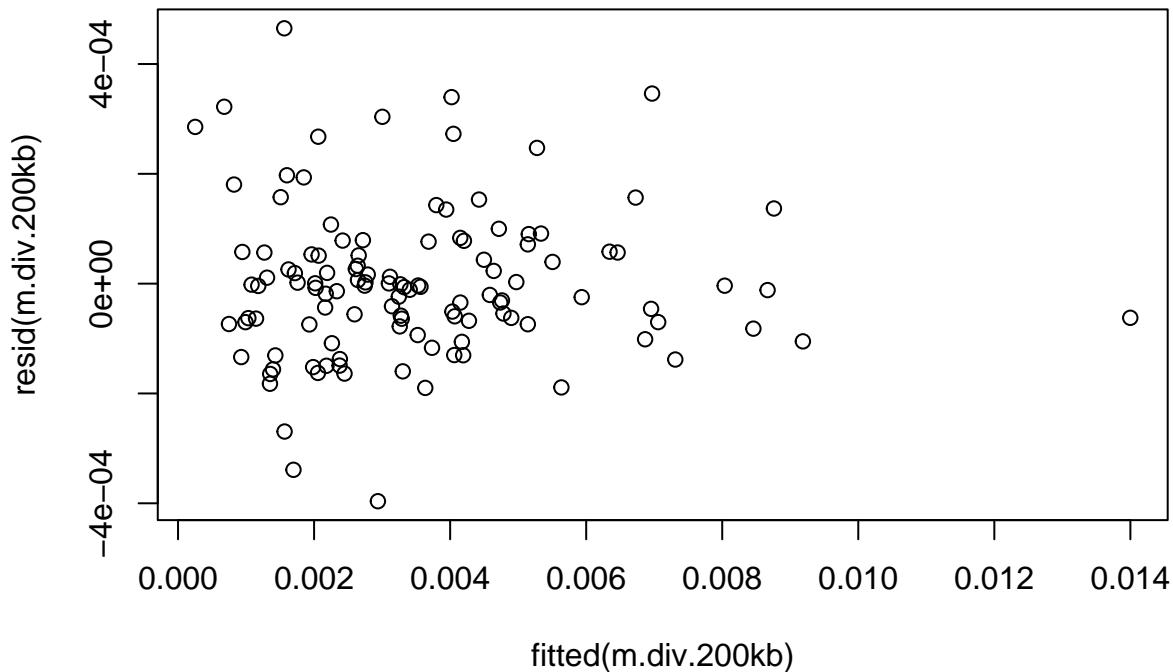
inf.lands.200kb.rep9 <- inf.lands.200kb.rep9
inf.lands.200kb.rep9$Replicate <- 1

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.200kb.rep9)
m.div.200kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.200kb.rep9)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.200kb.rep9)

AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)

##           df      AIC
## m.div.200kb   6 -1753.774
## m.div.200kb.2 7 -1752.849
## m.div.200kb.3 8 -1750.851
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```



```

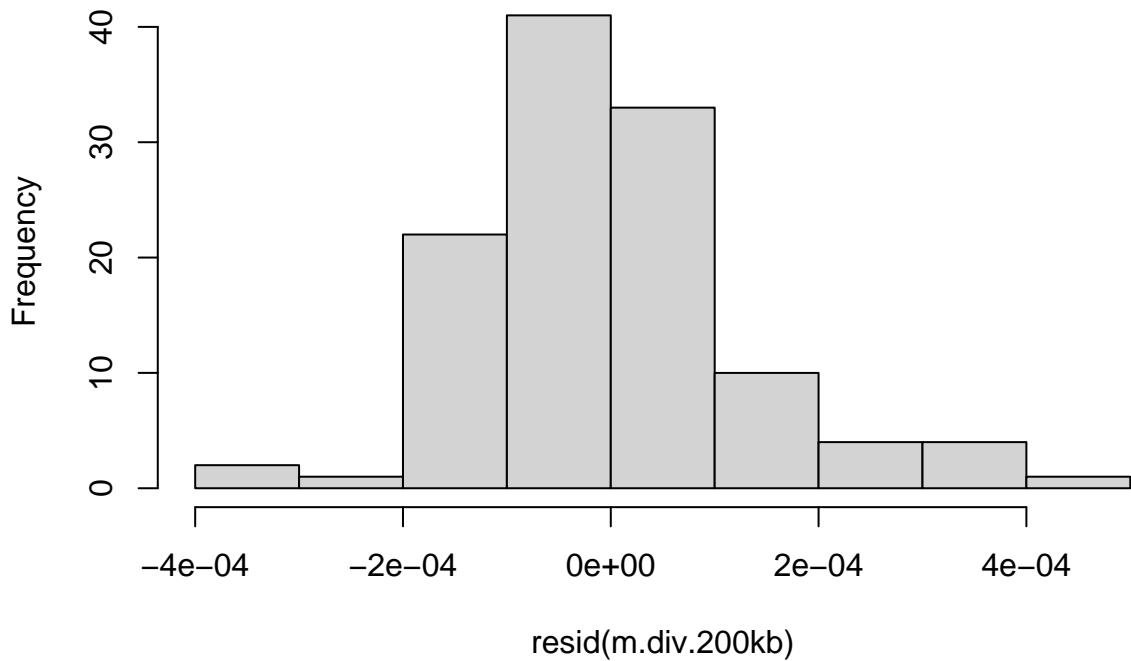
dwtest(m.div.200kb)

##
##  Durbin-Watson test
##
##  data:  m.div.200kb
##  DW = 1.9167, p-value = 0.2774
##  alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb)

##
##  Harrison-McCabe test
##
##  data:  m.div.200kb
##  HMC = 0.31553, p-value = 0.002
hist(resid(m.div.200kb))

```

## Histogram of resid(m.div.200kb)



```
summary(m.div.200kb)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,  
##      data = inf.lands.200kb.rep9)  
##  
## Residuals:  
##      Min       1Q   Median       3Q      Max  
## -3.962e-04 -7.380e-05 -6.080e-06  5.746e-05  4.650e-04  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 3.408e-03 1.349e-05 252.580 < 2e-16 ***  
## thetaC      1.189e+00 1.137e-02 104.514 < 2e-16 ***  
## rhoC        2.129e-02 8.117e-03  2.623 0.00991 **  
## tmrcaC      3.851e-03 7.068e-05  54.487 < 2e-16 ***  
## thetaC:tmrcaC 1.520e+00 5.234e-02 29.035 < 2e-16 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0001392 on 113 degrees of freedom  
## Multiple R-squared:  0.9961, Adjusted R-squared:  0.9959  
## F-statistic: 7167 on 4 and 113 DF,  p-value: < 2.2e-16
```

```
anova.diversity <- Anova(m.div.200kb)  
apiss <- anova.diversity$"Sum Sq"  
anova.diversity$VarExp <- apiss / sum(apiss)
```

```
r2.bgs.200kb[1, 9] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.200kb[2, 9] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb[3, 9] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb[4, 9] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb[5, 9] <- anova.diversity$VarExp[4] * 100

g.div.200kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep9, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep9, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.200kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep9, weights = varPower(0, ~theta), method = "ML")
g.div.200kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep9, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.200kb.1, g.div.200kb.2, g.div.200kb.3, g.div.200kb.4)

##                 df      AIC
## g.div.200kb.1  8 -1763.451
## g.div.200kb.2  8 -1750.490
## g.div.200kb.3  7 -1752.426
## g.div.200kb.4  7 -1765.407

summary(g.div.200kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.200kb.rep9
##       AIC      BIC    logLik
##   -1752.426 -1733.031 883.2129
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##       power
## 0.1388582
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0034089 0.00001363 250.13516 0.0000
## thetaC       1.1896415 0.01189557 100.00708 0.0000
## rhoC        0.0210014 0.00826443   2.54118 0.0124
## tmrcaC      0.0038498 0.00007232   53.23173 0.0000
## thetaC:tmrcaC 1.5109710 0.05625278   26.86038 0.0000
##
## Correlation:
##          (Intr) thetaC rhoC   tmrcaC
## thetaC    0.246
## rhoC     -0.026 -0.309
## tmrcaC   -0.140 -0.243 -0.369
## thetaC:tmrcaC -0.338 -0.452  0.086  0.405

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -2.76264494 -0.52309076 -0.04576363  0.42768957  3.47227913
## 
## Residual standard error: 0.0003107247
## Degrees of freedom: 118 total; 113 residual
vif(g.div.200kb.3)

##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
## 1.472047 1.461443 1.584082    1.445190

```

### 6.2.10 Replicate 10

```

rep10.sim.tmrca.200kb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep10_w200000.csv", sep = ",", header = T)

rep_10.pi.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_pi.csv")
rep_10.pi.200kb$avg <- apply(rep_10.pi.200kb[4:ncol(rep_10.pi.200kb)], 1, mean)
rep_10.rho.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_rho.csv")
rep_10.theta.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_theta.csv")
rep_10.tmrca.200kb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_tmrca.csv")
rep_10.tmrca.200kb$avg <- apply(rep_10.tmrca.200kb[4:ncol(rep_10.tmrca.200kb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.200kb.rep10 <- as.data.frame(cbind(rep_1.pi.200kb$avg, sim.theta.200kb$Rate, rep10.sim.tmrca.200kb$Rate))
names(true.lands.200kb.rep10) <- c("diversity", "theta", "tmrca", "rho")
true.lands.200kb.rep10$thetaC <- true.lands.200kb.rep10$theta - mean(true.lands.200kb.rep10$theta)
true.lands.200kb.rep10$tmrcaC <- true.lands.200kb.rep10$tmrca - mean(true.lands.200kb.rep10$tmrca)
true.lands.200kb.rep10$rhoC <- true.lands.200kb.rep10$rho - mean(true.lands.200kb.rep10$rho, na.rm = T)
true.lands.200kb.rep10$Replicate <- 1
m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.200kb.rep10)
anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$Sum Sq
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.200kb.true[1, 10] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.200kb.true[2, 10] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb.true[3, 10] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb.true[4, 10] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb.true[5, 10] <- anova.diversity$VarExp[4] * 100

inf.lands.200kb.rep10 <- as.data.frame(cbind(rep_10.pi.200kb$avg, rep_10.theta.200kb$sample_mean, rep_10.theta.200kb$sample_mean))
names(inf.lands.200kb.rep10) <- c("diversity", "theta", "tmrca", "rho")

cor.table[10, 2] <- cor.test(sim.theta.200kb$Rate, rep_10.theta.200kb$sample_mean, method = "spearman")

# centering
inf.lands.200kb.rep10$thetaC <- inf.lands.200kb.rep10$theta - mean(inf.lands.200kb.rep10$theta)
inf.lands.200kb.rep10$tmrcaC <- inf.lands.200kb.rep10$tmrca - mean(inf.lands.200kb.rep10$tmrca)
inf.lands.200kb.rep10$rhoC <- inf.lands.200kb.rep10$rho - mean(inf.lands.200kb.rep10$rho)

inf.lands.200kb.rep10$bin <- 1:nrow(inf.lands.200kb.rep10)

# for merging:

```

```

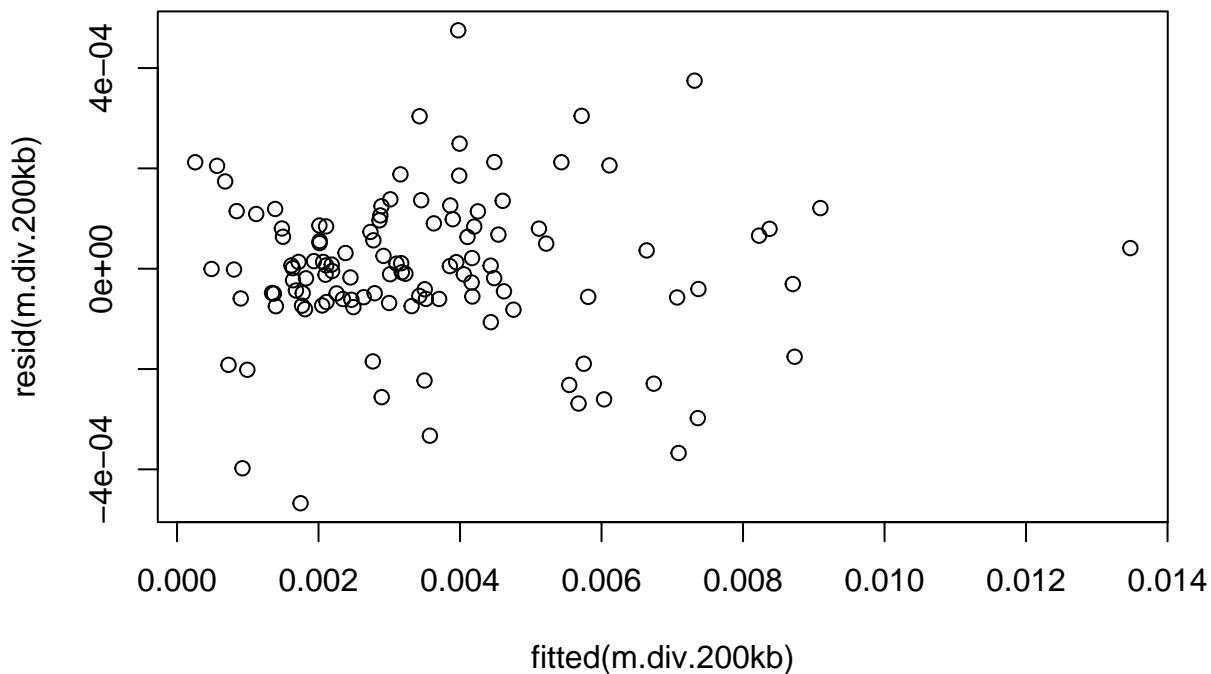
inf.lands.200kb.rep10 <- inf.lands.200kb.rep10
inf.lands.200kb.rep10$Replicate <- 1

m.div.200kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.200kb.rep10)
m.div.200kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.200kb.rep10)
m.div.200kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.200kb.rep10)

AIC(m.div.200kb, m.div.200kb.2, m.div.200kb.3)

##           df      AIC
## m.div.200kb    6 -1734.618
## m.div.200kb.2  7 -1735.599
## m.div.200kb.3  8 -1737.127
plot(resid(m.div.200kb)~fitted(m.div.200kb))

```



```

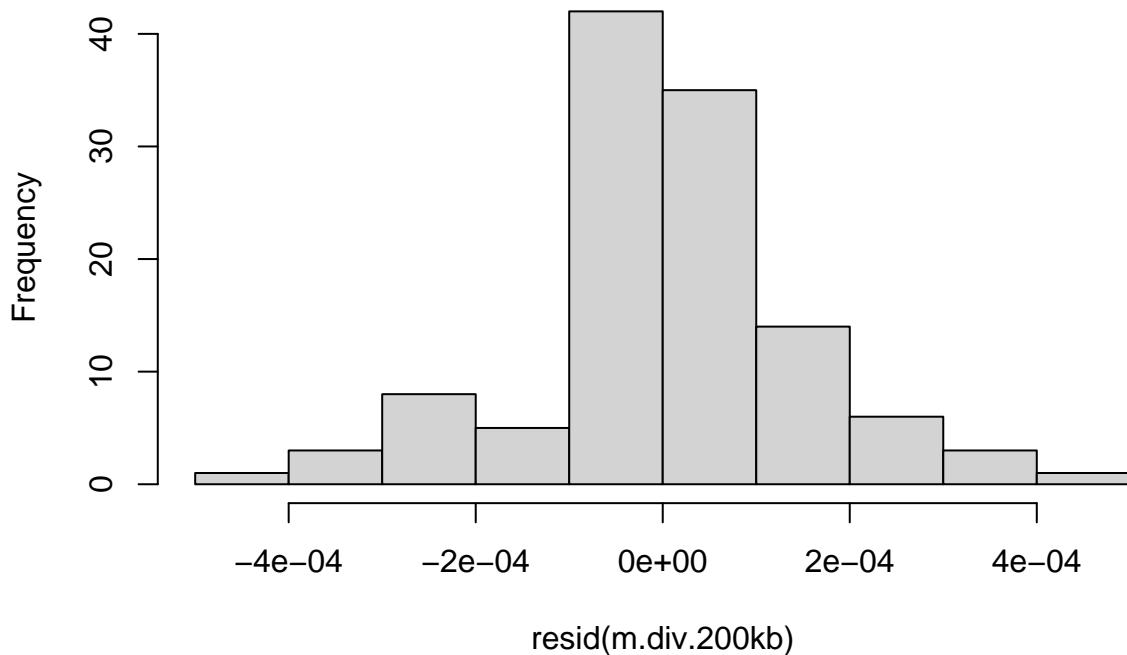
dwtest(m.div.200kb)

##
##  Durbin-Watson test
##
##  data:  m.div.200kb
##  DW = 1.2969, p-value = 3.058e-05
##  alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.200kb)

##
##  Harrison-McCabe test
##
##  data:  m.div.200kb
##  HMC = 0.39016, p-value = 0.029
hist(resid(m.div.200kb))

```

## Histogram of resid(m.div.200kb)



```
summary(m.div.200kb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.200kb.rep10)
##
## Residuals:
##       Min         1Q     Median         3Q        Max
## -4.675e-04 -5.994e-05  2.700e-07  8.305e-05  4.753e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.461e-03 1.419e-05 244.019 < 2e-16 ***
## thetaC      1.063e+00 9.242e-03 115.002 < 2e-16 ***
## rhoC        3.280e-02 1.017e-02   3.224  0.00165 **
## tmrcaC      4.528e-03 1.033e-04  43.821 < 2e-16 ***
## thetaC:tmrcaC 1.330e+00 5.244e-02  25.371 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.000151 on 113 degrees of freedom
## Multiple R-squared:  0.9954, Adjusted R-squared:  0.9953
## F-statistic: 6149 on 4 and 113 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.200kb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.200kb[1, 10] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.200kb[2, 10] <- anova.diversity$VarExp[1] * 100
r2.bgs.200kb[3, 10] <- anova.diversity$VarExp[2] * 100
r2.bgs.200kb[4, 10] <- anova.diversity$VarExp[3] * 100
r2.bgs.200kb[5, 10] <- anova.diversity$VarExp[4] * 100

g.div.200kb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep10, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), na.action = na.omit)
g.div.200kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep10, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), na.action = na.omit)
g.div.200kb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep10, weights = varPower(0, ~theta), method = "ML")
g.div.200kb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                        data = inf.lands.200kb.rep10, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.200kb.1, g.div.200kb.2, g.div.200kb.3, g.div.200kb.4)

```

```

##             df      AIC
## g.div.200kb.1 8 -1746.826
## g.div.200kb.2 8 -1760.403
## g.div.200kb.3 7 -1740.621
## g.div.200kb.4 7 -1734.608

summary(g.div.200kb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.200kb.rep10
##          AIC      BIC    logLik
##        -1740.621 -1721.226 877.3105
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
## Parameter estimates:
##   power
## 0.4149818
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0034619 0.00001437 240.98955 0e+00
## thetaC       1.0667145 0.01021663 104.40964 0e+00
## rhoC        0.0388858 0.00943343   4.12213 1e-04
## tmrcaC      0.0044840 0.00010213   43.90449 0e+00
## thetaC:tmrcaC 1.3172353 0.05899803  22.32677 0e+00
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC     0.362
## rhoC      0.007 -0.354
## tmrcaC   -0.087 -0.026 -0.469
## thetaC:tmrcaC -0.228 -0.117 -0.017  0.381

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -3.925337793 -0.433792136  0.008606498  0.591307894  3.278902328
## 
## Residual standard error: 0.001603282
## Degrees of freedom: 118 total; 113 residual
vif(g.div.200kb.3)

##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
## 1.210381 1.593301 1.623969    1.219199

```

### 6.3 1 Mb scale

```

r2.bgs.1Mb <- as.data.frame(matrix(ncol = nreps, nrow = 5))
row.names(r2.bgs.1Mb) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
colnames(r2.bgs.1Mb) <- reps

r2.bgs.1Mb.true <- as.data.frame(matrix(ncol = nreps, nrow = 5))
row.names(r2.bgs.1Mb.true) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
colnames(r2.bgs.1Mb.true) <- reps

sim.theta.1Mb <- read.table("dm_bgs_sims/MutationMap_1000kb.csv", sep = ",", header = T)
sim.rho.1Mb <- read.table("dm_bgs_sims/RecombinationMap_1000kb.csv", sep = ",", header = T)

```

#### 6.3.1 Replicate 1

```

rep1.sim.tmrca.1Mb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep1_w1000000.csv", sep = ",", header = T)

rep_1.pi.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.div")
rep_1.pi.1Mb$avg <- apply(rep_1.pi.1Mb[4:ncol(rep_1.pi.1Mb)], 1, mean)
rep_1.rho.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.rho")
rep_1.theta.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.theta")
rep_1.tmrca.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep1/dm2L_bgs_rep1_5.tmrca")
rep_1.tmrca.1Mb$avg <- apply(rep_1.tmrca.1Mb[4:ncol(rep_1.tmrca.1Mb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.1Mb.rep1 <- as.data.frame(cbind(rep_1.pi.1Mb$avg, sim.theta.1Mb$Rate, rep1.sim.tmrca.1Mb$Ave))
names(true.lands.1Mb.rep1) <- c("diversity", "theta", "tmrca", "rho")
true.lands.1Mb.rep1$thetaC <- true.lands.1Mb.rep1$theta - mean(true.lands.1Mb.rep1$theta)
true.lands.1Mb.rep1$tmrcaC <- true.lands.1Mb.rep1$tmrca - mean(true.lands.1Mb.rep1$tmrca)
true.lands.1Mb.rep1$rhoC <- true.lands.1Mb.rep1$rho - mean(true.lands.1Mb.rep1$rho, na.rm = T)
true.lands.1Mb.rep1$Replicate <- 1
m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.1Mb.rep1)
anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.1Mb.true[1, 1] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.1Mb.true[2, 1] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb.true[3, 1] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb.true[4, 1] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb.true[5, 1] <- anova.diversity$VarExp[4] * 100

```

```

inf.lands.1Mb.rep1 <- as.data.frame(cbind(rep_1.pi.1Mb$avg, rep_1.theta.1Mb$sample_mean, rep_1.tmrca.1Mb$tmrca))
names(inf.lands.1Mb.rep1) <- c("diversity", "theta", "tmrca", "rho")

cor.table[1, 3] <- cor.test(sim.theta.1Mb$Rate, rep_1.theta.1Mb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.1Mb.rep1$thetaC <- inf.lands.1Mb.rep1$theta - mean(inf.lands.1Mb.rep1$theta)
inf.lands.1Mb.rep1$tmrcaC <- inf.lands.1Mb.rep1$tmrca - mean(inf.lands.1Mb.rep1$tmrca)
inf.lands.1Mb.rep1$rhoC <- inf.lands.1Mb.rep1$rho - mean(inf.lands.1Mb.rep1$rho)

inf.lands.1Mb.rep1$bin <- 1:nrow(inf.lands.1Mb.rep1)

# for merging:
inf.lands.1Mb.rep1 <- inf.lands.1Mb.rep1
inf.lands.1Mb.rep1$Replicate <- 1

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.1Mb.rep1)
m.div.1Mb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.1Mb.rep1)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.1Mb.rep1)

AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)

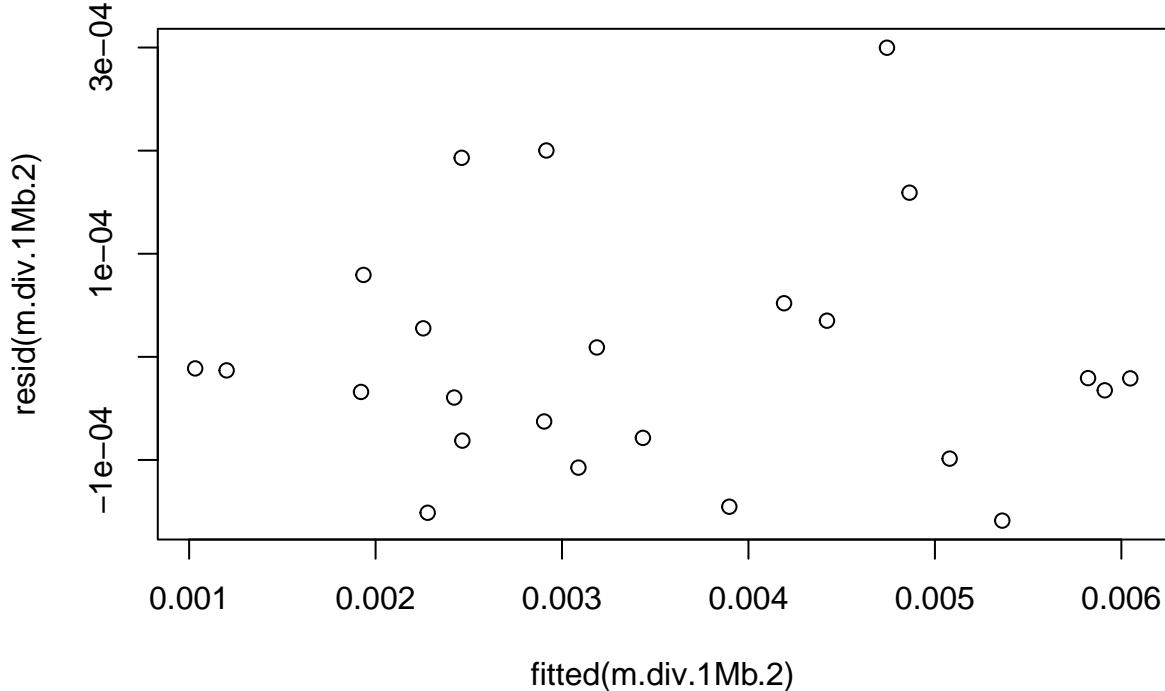
```

```

##          df      AIC
## m.div.1Mb     6 -350.1912
## m.div.1Mb.2   7 -353.4005
## m.div.1Mb.3   8 -351.4502

```

```
plot(resid(m.div.1Mb.2)~fitted(m.div.1Mb.2))
```



```
dwtest(m.div.1Mb.2)
```

```
##
```

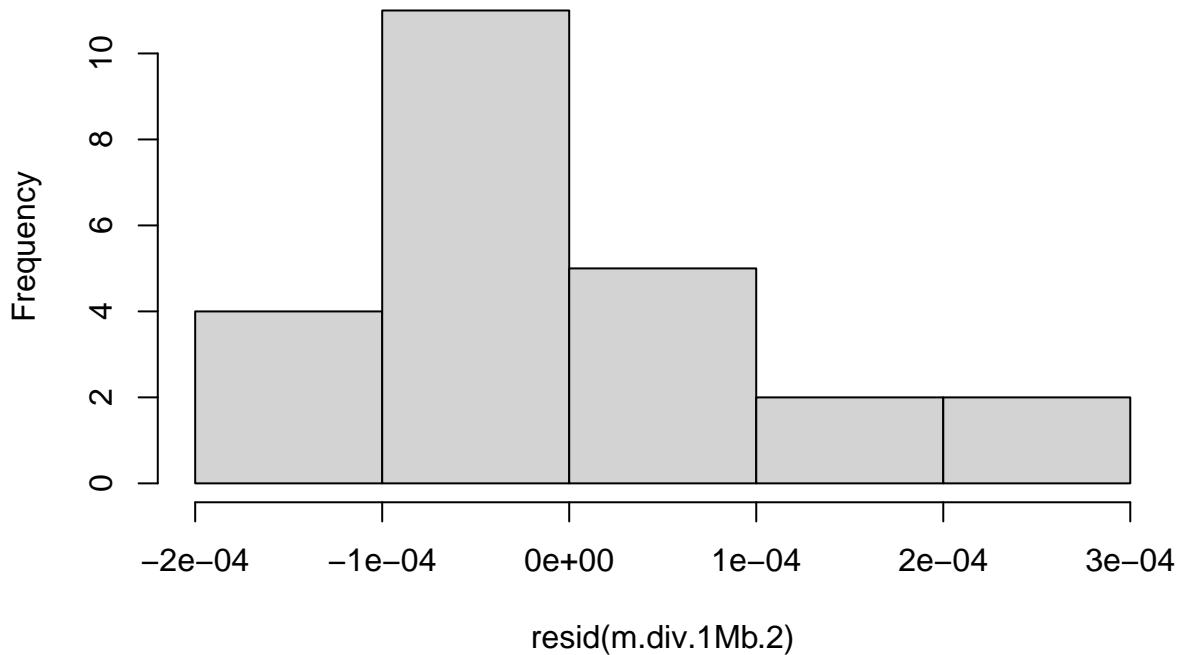
```

## Durbin-Watson test
##
## data: m.div.1Mb.2
## DW = 2.0504, p-value = 0.4914
## alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.1Mb.2)

##
## Harrison-McCabe test
##
## data: m.div.1Mb.2
## HMC = 0.57197, p-value = 0.694
hist(resid(m.div.1Mb.2))

```

**Histogram of resid(m.div.1Mb.2)**



```

summary(m.div.1Mb.2)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC +
##     rhoC:tmrcaC, data = inf.lands.1Mb.rep1)
##
## Residuals:
##      Min        1Q    Median        3Q       Max
## -1.588e-04 -7.924e-05 -2.075e-05  3.932e-05  2.998e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.342e-03 5.732e-05 58.303 < 2e-16 ***
## thetaC      9.934e-01 7.341e-02 13.532 7.13e-11 ***

```

```

## rhoC          3.751e-02  3.528e-02   1.063   0.3018
## tmrcaC       5.305e-03  6.288e-04   8.436  1.14e-07 ***
## thetaC:tmrcaC 2.105e+00  9.052e-01   2.325   0.0319 *
## rhoC:tmrcaC  5.481e-01  2.624e-01   2.089   0.0512 .
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0001325 on 18 degrees of freedom
## Multiple R-squared:  0.994, Adjusted R-squared:  0.9923
## F-statistic: 594.7 on 5 and 18 DF, p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb.2)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.1Mb[1, 1] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
r2.bgs.1Mb[2, 1] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb[3, 1] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb[4, 1] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb[5, 1] <- anova.diversity$VarExp[4] * 100

g.div.1Mb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep1, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep1, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep1, weights = varPower(0, ~theta), method = "ML")
g.div.1Mb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep1, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.1Mb.1, g.div.1Mb.2, g.div.1Mb.3, g.div.1Mb.4)

##           df      AIC
## g.div.1Mb.1 8 -347.5891
## g.div.1Mb.2 8 -348.1816
## g.div.1Mb.3 7 -348.6342
## g.div.1Mb.4 7 -348.6639

summary(g.div.1Mb.3)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
## Data: inf.lands.1Mb.rep1
##      AIC      BIC    logLik
## -348.6342 -340.3878 181.3171
##
## Variance function:
## Structure: Power of variance covariate
## Formula: ~theta
## Parameter estimates:
##     power
## 0.4951664

```

```

## 
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept) 0.0034361 0.0000408 84.27643 0.0000
## thetaC      1.0132773 0.0824669 12.28708 0.0000
## rhoC        0.0755056 0.0307041  2.45914 0.0237
## tmrcaC     0.0040537 0.0002377 17.05650 0.0000
## thetaC:tmrcaC 2.0534919 1.0009642  2.05151 0.0543
## 
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC      0.678
## rhoC        -0.286 -0.638
## tmrcaC     -0.346 -0.298 -0.275
## thetaC:tmrcaC -0.685 -0.871  0.418  0.505
## 
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -1.4032965 -0.4764999 -0.2622762  0.2758051  3.3133189
## 
## Residual standard error: 0.002225736
## Degrees of freedom: 24 total; 19 residual
vif(g.div.1Mb.3)

```

```

##      thetaC       rhoC       tmrcaC thetaC:tmrcaC
## 6.680534 2.811830 2.189128    5.727340

```

### 6.3.2 Replicate 2

```

rep2.sim.tmrca.1Mb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep2_w1000000.csv", sep = ",", header = T)

rep_2.pi.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.div")
rep_2.pi.1Mb$avg <- apply(rep_2.pi.1Mb[4:ncol(rep_2.pi.1Mb)], 1, mean)
rep_2.rho.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.rho")
rep_2.theta.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.theta")
rep_2.tmrca.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep2/dm2L_bgs_rep2_5.tmrca")
rep_2.tmrca.1Mb$avg <- apply(rep_2.tmrca.1Mb[4:ncol(rep_2.tmrca.1Mb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.1Mb.rep2 <- as.data.frame(cbind(rep_1.pi.1Mb$avg, sim.theta.1Mb$Rate, rep2.sim.tmrca.1Mb$Ave))
names(true.lands.1Mb.rep2) <- c("diversity", "theta", "tmrca", "rho")
true.lands.1Mb.rep2$thetaC <- true.lands.1Mb.rep2$theta - mean(true.lands.1Mb.rep2$theta)
true.lands.1Mb.rep2$tmrcaC <- true.lands.1Mb.rep2$tmrca - mean(true.lands.1Mb.rep2$tmrca)
true.lands.1Mb.rep2$rhoC <- true.lands.1Mb.rep2$rho - mean(true.lands.1Mb.rep2$rho, na.rm = T)
true.lands.1Mb.rep2$Replicate <- 1
m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.1Mb.rep2)
anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.1Mb.true[1, 2] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.1Mb.true[2, 2] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb.true[3, 2] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb.true[4, 2] <- anova.diversity$VarExp[3] * 100

```

```

r2.bgs.1Mb.true[5, 2] <- anova.diversity$VarExp[4] * 100

inf.lands.1Mb.rep2 <- as.data.frame(cbind(rep_2.pi.1Mb$avg, rep_2.theta.1Mb$sample_mean, rep_2.tmrca.1Mb$tmrca))
names(inf.lands.1Mb.rep2) <- c("diversity", "theta", "tmrca", "rho")

cor.table[2, 3] <- cor.test(sim.theta.1Mb$Rate, rep_2.theta.1Mb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.1Mb.rep2$thetaC <- inf.lands.1Mb.rep2$theta - mean(inf.lands.1Mb.rep2$theta)
inf.lands.1Mb.rep2$tmrcaC <- inf.lands.1Mb.rep2$tmrca - mean(inf.lands.1Mb.rep2$tmrca)
inf.lands.1Mb.rep2$rhoC <- inf.lands.1Mb.rep2$rho - mean(inf.lands.1Mb.rep2$rho)

inf.lands.1Mb.rep2$bin <- 1:nrow(inf.lands.1Mb.rep2)

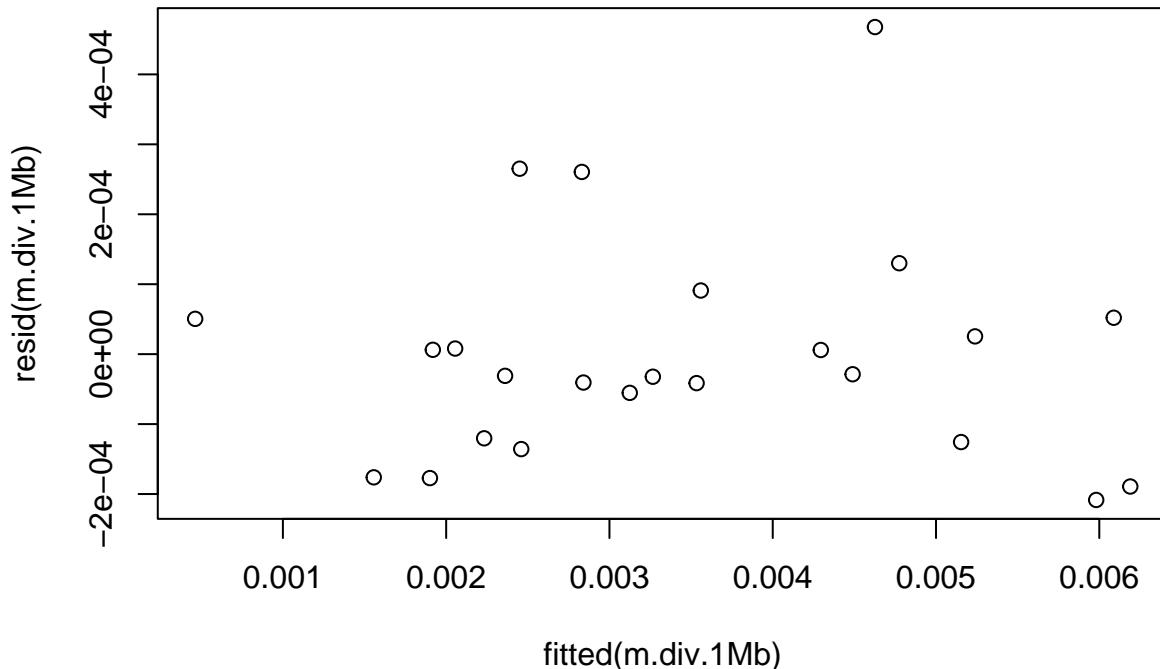
# for merging:
inf.lands.1Mb.rep2 <- inf.lands.1Mb.rep2
inf.lands.1Mb.rep2$Replicate <- 1

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.1Mb.rep2)
m.div.1Mb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.1Mb.rep2)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.1Mb.rep2)

AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)

##          df      AIC
## m.div.1Mb     6 -340.4890
## m.div.1Mb.2   7 -338.4960
## m.div.1Mb.3   8 -340.4696
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```



```

dwtest(m.div.1Mb)

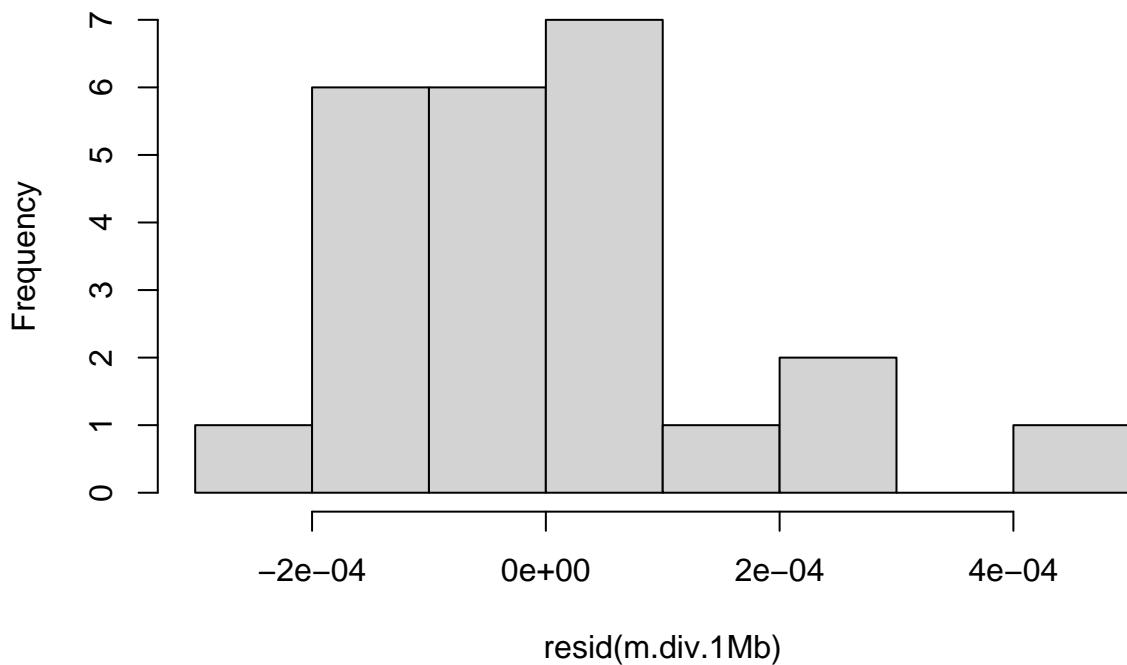
##
##  Durbin-Watson test
##
## data: m.div.1Mb
## DW = 2.2615, p-value = 0.5747
## alternative hypothesis: true autocorrelation is greater than 0

hmctest(m.div.1Mb)

##
##  Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.50859, p-value = 0.546
hist(resid(m.div.1Mb))

```

**Histogram of resid(m.div.1Mb)**



```

summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.1Mb.rep2)
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -2.085e-04 -1.217e-04 -2.989e-05  5.085e-05  4.677e-04 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept)  1.135e-03  1.135e-03  1.000   0.317    
## thetaC      -2.085e-04  1.135e-04 -1.822   0.375    
## rhoC        -1.217e-04  1.135e-04 -1.075   0.285    
## tmrcaC      -2.989e-05  1.135e-05 -2.631   0.059 *  
## thetaC:tmrcaC 5.085e-05  1.135e-05  4.464   0.000 ***
## 
```

```

##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.476e-03 3.592e-05 96.792 < 2e-16 ***
## thetaC      1.305e+00 5.560e-02 23.465 1.71e-15 ***
## rhoC        8.429e-03 3.289e-02  0.256   0.8005
## tmrcaC     3.602e-03 2.238e-04 16.094 1.59e-12 ***
## thetaC:tmrcaC 5.490e-01 2.724e-01  2.016   0.0582 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0001759 on 19 degrees of freedom
## Multiple R-squared:  0.9897, Adjusted R-squared:  0.9876
## F-statistic: 457.9 on 4 and 19 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.1Mb[1, 2] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
r2.bgs.1Mb[2, 2] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb[3, 2] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb[4, 2] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb[5, 2] <- anova.diversity$VarExp[4] * 100

g.div.1Mb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep2, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep2, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep2, weights = varPower(0, ~theta), method = "ML")
g.div.1Mb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep2, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.1Mb.1, g.div.1Mb.2, g.div.1Mb.3, g.div.1Mb.4)

##          df      AIC
## g.div.1Mb.1 8 -338.4110
## g.div.1Mb.2 8 -339.3155
## g.div.1Mb.3 7 -340.4491
## g.div.1Mb.4 7 -338.4931

summary(g.div.1Mb.3)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
## Data: inf.lands.1Mb.rep2
##          AIC      BIC logLik
## -340.4491 -332.2027 177.2246
##
## Variance function:
## Structure: Power of variance covariate
## Formula: ~theta
## Parameter estimates:
```

```

##      power
## 1.281934
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept) 0.0034897 0.00003930 88.78892 0.0000
## thetaC       1.3432539 0.06488550 20.70191 0.0000
## rhoC        0.0248667 0.02714294  0.91614 0.3711
## tmrcaC      0.0034959 0.00019680 17.76351 0.0000
## thetaC:tmrcaC 0.7237951 0.27108673  2.66998 0.0151
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC      0.495
## rhoC       -0.089 -0.609
## tmrcaC      0.091  0.581 -0.543
## thetaC:tmrcaC -0.021 -0.448  0.052 -0.310
##
## Standardized residuals:
##      Min     Q1     Med     Q3     Max
## -1.3253500 -0.4724077 -0.2657178  0.3816227  2.4010863
##
## Residual standard error: 0.2910646
## Degrees of freedom: 24 total; 19 residual
vif(g.div.1Mb.3)

```

##	thetaC	rhoC	tmrcaC	thetaC:tmrcaC
##	2.340049	1.981495	1.704582	1.430447

### 6.3.3 Replicate 3

```

rep3.sim.tmrca.1Mb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep3_w1000000.csv", sep = ",", header = T)

rep_3.pi.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.div")
rep_3.pi.1Mb$avg <- apply(rep_3.pi.1Mb[4:ncol(rep_3.pi.1Mb)], 1, mean)
rep_3.rho.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.rho")
rep_3.theta.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.theta")
rep_3.tmrca.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep3/dm2L_bgs_rep3_5.tmrca")
rep_3.tmrca.1Mb$avg <- apply(rep_3.tmrca.1Mb[4:ncol(rep_3.tmrca.1Mb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.1Mb.rep3 <- as.data.frame(cbind(rep_1.pi.1Mb$avg, sim.theta.1Mb$Rate, rep3.sim.tmrca.1Mb$Avg))
names(true.lands.1Mb.rep3) <- c("diversity", "theta", "tmrca", "rho")
true.lands.1Mb.rep3$thetaC <- true.lands.1Mb.rep3$theta - mean(true.lands.1Mb.rep3$theta)
true.lands.1Mb.rep3$tmrcaC <- true.lands.1Mb.rep3$tmrca - mean(true.lands.1Mb.rep3$tmrca)
true.lands.1Mb.rep3$rhoC <- true.lands.1Mb.rep3$rho - mean(true.lands.1Mb.rep3$rho, na.rm = T)
true.lands.1Mb.rep3$Replicate <- 1
m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.1Mb.rep3)
anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.1Mb.true[1, 3] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.bgs.1Mb.true[2, 3] <- anova.diversity$VarExp[1] * 100

```

```

r2.bgs.1Mb.true[3, 3] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb.true[4, 3] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb.true[5, 3] <- anova.diversity$VarExp[4] * 100

inf.lands.1Mb.rep3 <- as.data.frame(cbind(rep_3.pi.1Mb$avg, rep_3.theta.1Mb$sample_mean, rep_3.tmrca.1Mb$tmrca))
names(inf.lands.1Mb.rep3) <- c("diversity", "theta", "tmrca", "rho")

cor.table[3, 3] <- cor.test(sim.theta.1Mb$Rate, rep_3.theta.1Mb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.1Mb.rep3$thetaC <- inf.lands.1Mb.rep3$theta - mean(inf.lands.1Mb.rep3$theta)
inf.lands.1Mb.rep3$tmrcaC <- inf.lands.1Mb.rep3$tmrca - mean(inf.lands.1Mb.rep3$tmrca)
inf.lands.1Mb.rep3$rhoC <- inf.lands.1Mb.rep3$rho - mean(inf.lands.1Mb.rep3$rho)

inf.lands.1Mb.rep3$bin <- 1:nrow(inf.lands.1Mb.rep3)

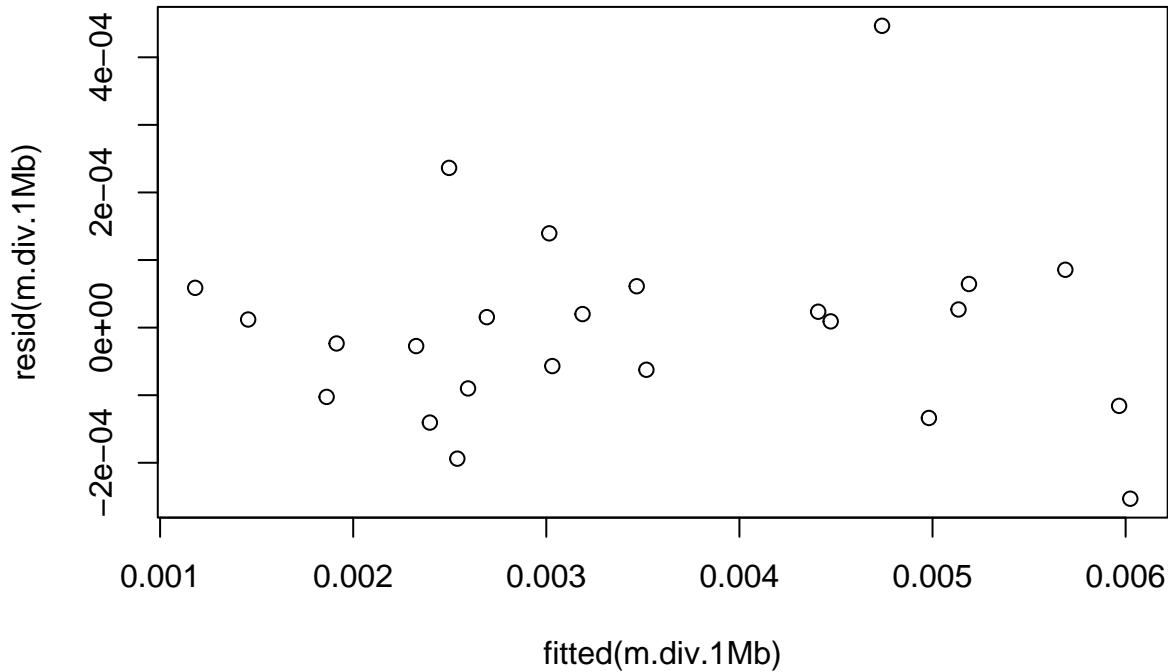
# for merging:
inf.lands.1Mb.rep3 <- inf.lands.1Mb.rep3
inf.lands.1Mb.rep3$Replicate <- 1

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.1Mb.rep3)
m.div.1Mb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.1Mb.rep3)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.1Mb.rep3)

AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)

##          df      AIC
## m.div.1Mb     6 -345.5820
## m.div.1Mb.2   7 -346.9896
## m.div.1Mb.3   8 -348.3194
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```



```

dwtest(m.div.1Mb)

##
##  Durbin-Watson test
##
## data: m.div.1Mb
## DW = 2.5052, p-value = 0.8416
## alternative hypothesis: true autocorrelation is greater than 0

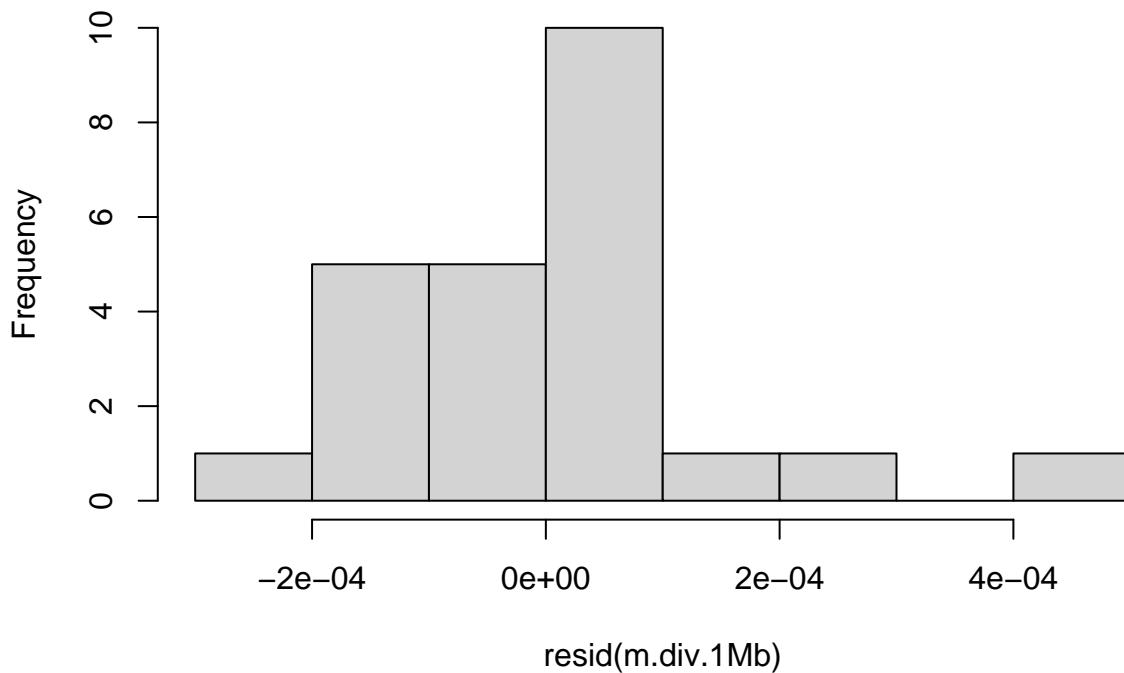
hmctest(m.div.1Mb)

##
##  Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.52869, p-value = 0.578

hist(resid(m.div.1Mb))

```

### Histogram of resid(m.div.1Mb)



```

summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.1Mb.rep3)
##
## Residuals:
##       Min        1Q     Median        3Q       Max
## -2.532e-04 -9.316e-05  1.061e-05  5.944e-05  4.466e-04
##
## Coefficients:

```

```

##             Estimate Std. Error t value Pr(>|t|) 
## (Intercept) 3.517e-03 3.231e-05 108.850 < 2e-16 ***
## thetaC      1.323e+00 4.594e-02  28.788 < 2e-16 ***
## rhoC       -7.069e-03 3.016e-02  -0.234  0.81719
## tmrcaC     3.670e-03 2.069e-04  17.732 2.81e-13 ***
## thetaC:tmrcaC 7.505e-01 1.650e-01    4.549  0.00022 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0001582 on 19 degrees of freedom
## Multiple R-squared:  0.9905, Adjusted R-squared:  0.9885 
## F-statistic: 495.2 on 4 and 19 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.1Mb[1, 3] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
r2.bgs.1Mb[2, 3] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb[3, 3] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb[4, 3] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb[5, 3] <- anova.diversity$VarExp[4] * 100

g.div.1Mb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep3, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep3, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep3, weights = varPower(0, ~theta), method = "ML")
g.div.1Mb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep3, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.1Mb.1, g.div.1Mb.2, g.div.1Mb.3, g.div.1Mb.4)

##          df      AIC
## g.div.1Mb.1 8 -345.3677
## g.div.1Mb.2 8 -347.1405
## g.div.1Mb.3 7 -346.0258
## g.div.1Mb.4 7 -344.4834

summary(g.div.1Mb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep3
##           AIC      BIC logLik
## -346.0258 -337.7794 180.0129
##
## Variance function:
## Structure: Power of variance covariate
## Formula: ~theta
## Parameter estimates:
```

```

##      power
## 1.225993
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept) 0.0035246 0.00003454 102.03989 0.0000
## thetaC       1.3580663 0.05237639  25.92898 0.0000
## rhoC        0.0073311 0.02720431   0.26948 0.7905
## tmrcaC      0.0035822 0.00018732  19.12301 0.0000
## thetaC:tmrcaC 0.8272546 0.18843140    4.39022 0.0003
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC      0.526
## rhoC       -0.045 -0.573
## tmrcaC     0.033  0.393 -0.627
## thetaC:tmrcaC 0.009 -0.072  0.033 -0.049
##
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -1.54924816 -0.55078534 -0.07541142  0.29979596  2.70092421
##
## Residual standard error: 0.1890319
## Degrees of freedom: 24 total; 19 residual
vif(g.div.1Mb.3)

```

	thetaC	rhoC	tmrcaC	thetaC:tmrcaC
##	1.497949	2.078778	1.653891	1.006384

### 6.3.4 Replicate 4

```

rep4.sim.tmrca.1Mb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep4_w1000000.csv", sep = ",", header = T)

rep_4.pi.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.div")
rep_4.pi.1Mb$avg <- apply(rep_4.pi.1Mb[4:ncol(rep_4.pi.1Mb)], 1, mean)
rep_4.rho.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.rho")
rep_4.theta.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.theta")
rep_4.tmrca.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep4/dm2L_bgs_rep4_5.tmrca")
rep_4.tmrca.1Mb$avg <- apply(rep_4.tmrca.1Mb[4:ncol(rep_4.tmrca.1Mb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.1Mb.rep4 <- as.data.frame(cbind(rep_4.pi.1Mb$avg, sim.theta.1Mb$Rate, rep4.sim.tmrca.1Mb$Avg))
names(true.lands.1Mb.rep4) <- c("diversity", "theta", "tmrca", "rho")
true.lands.1Mb.rep4$thetaC <- true.lands.1Mb.rep4$theta - mean(true.lands.1Mb.rep4$theta)
true.lands.1Mb.rep4$tmrcaC <- true.lands.1Mb.rep4$tmrca - mean(true.lands.1Mb.rep4$tmrca)
true.lands.1Mb.rep4$rhoC <- true.lands.1Mb.rep4$rho - mean(true.lands.1Mb.rep4$rho, na.rm = T)
true.lands.1Mb.rep4$Replicate <- 1
m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.1Mb.rep4)
anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.1Mb.true[1, 4] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.1Mb.true[2, 4] <- anova.diversity$VarExp[1] * 100

```

```

r2.bgs.1Mb.true[3, 4] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb.true[4, 4] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb.true[5, 4] <- anova.diversity$VarExp[4] * 100

inf.lands.1Mb.rep4 <- as.data.frame(cbind(rep_4.pi.1Mb$avg, rep_4.theta.1Mb$sample_mean, rep_4.tmrca.1Mb$tmrca))
names(inf.lands.1Mb.rep4) <- c("diversity", "theta", "tmrca", "rho")

cor.table[4, 3] <- cor.test(sim.theta.1Mb$Rate, rep_4.theta.1Mb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.1Mb.rep4$thetaC <- inf.lands.1Mb.rep4$theta - mean(inf.lands.1Mb.rep4$theta)
inf.lands.1Mb.rep4$tmrcaC <- inf.lands.1Mb.rep4$tmrca - mean(inf.lands.1Mb.rep4$tmrca)
inf.lands.1Mb.rep4$rhoC <- inf.lands.1Mb.rep4$rho - mean(inf.lands.1Mb.rep4$rho)

inf.lands.1Mb.rep4$bin <- 1:nrow(inf.lands.1Mb.rep4)

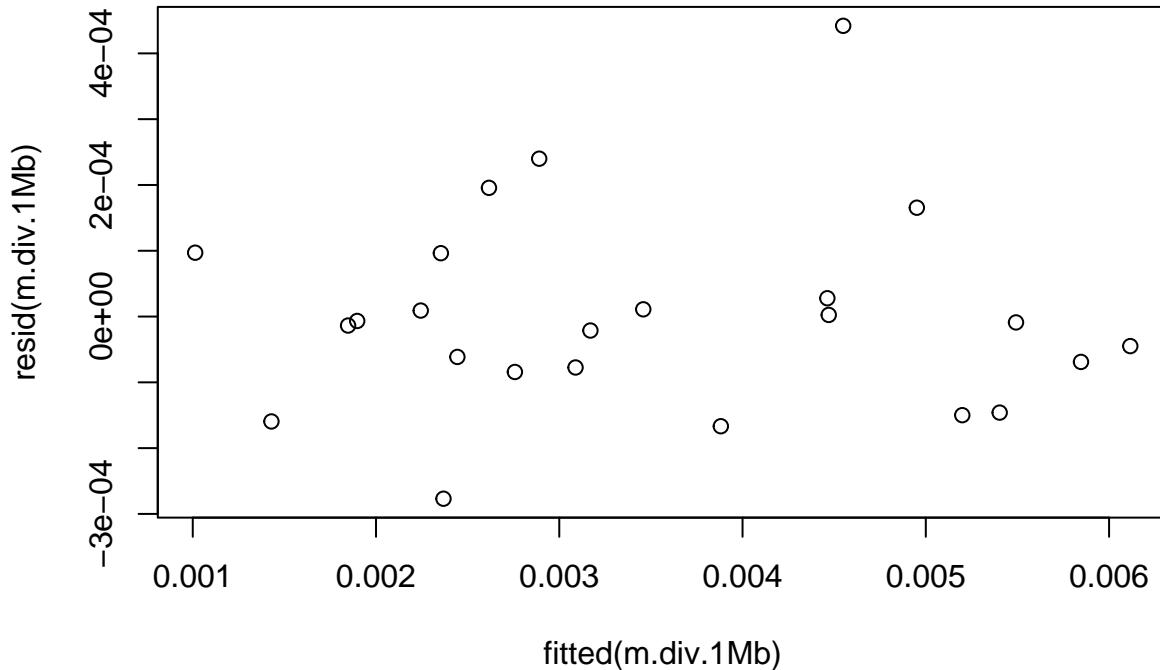
# for merging:
inf.lands.1Mb.rep4 <- inf.lands.1Mb.rep4
inf.lands.1Mb.rep4$Replicate <- 1

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.1Mb.rep4)
m.div.1Mb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.1Mb.rep4)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.1Mb.rep4)

AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)

##          df      AIC
## m.div.1Mb     6 -342.6901
## m.div.1Mb.2   7 -343.4354
## m.div.1Mb.3   8 -341.7061
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```



```

dwtest(m.div.1Mb)

##
##  Durbin-Watson test
##
## data: m.div.1Mb
## DW = 1.8262, p-value = 0.2127
## alternative hypothesis: true autocorrelation is greater than 0

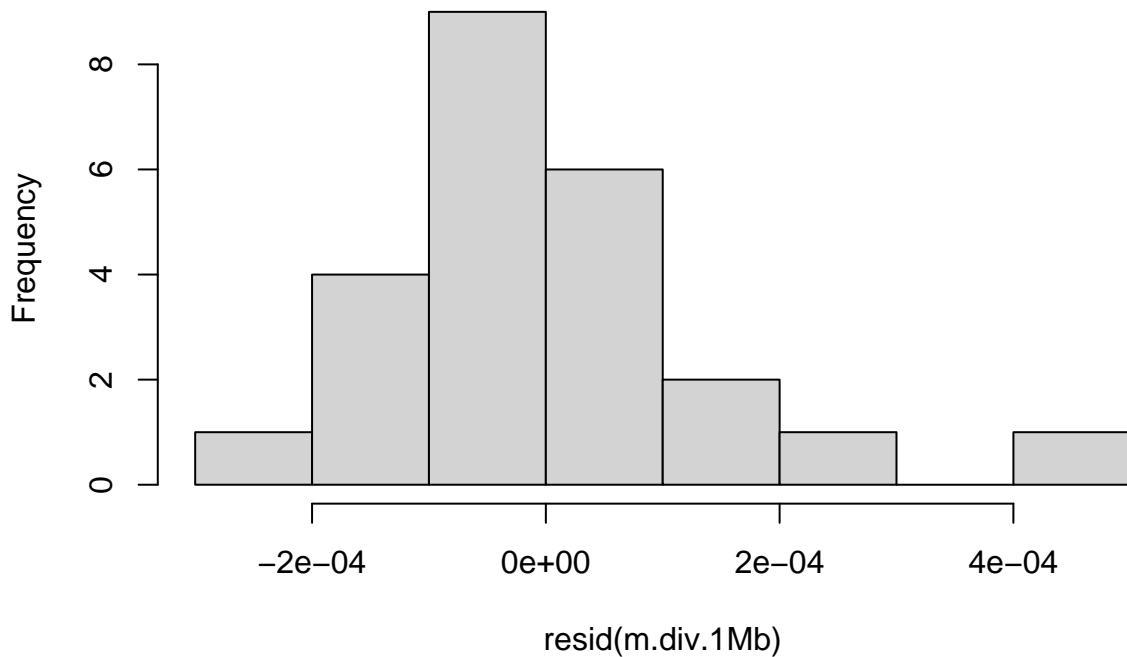
hmctest(m.div.1Mb)

##
##  Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.67938, p-value = 0.889

hist(resid(m.div.1Mb))

```

### Histogram of resid(m.div.1Mb)



```

summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.1Mb.rep4)
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -2.769e-04 -7.914e-05 -1.131e-05  4.493e-05  4.419e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept)  1.131e-05  1.131e-05    1.000  0.3173    
## thetaC      -2.769e-04  1.131e-05  -2.435  0.0197 *  
## rhoC        -7.914e-05  1.131e-05  -0.700  0.4807    
## tmrcaC      4.493e-05  1.131e-05   0.400  0.6907    
## thetaC:tmrcaC 4.419e-04  1.131e-05   3.900  0.0001 ** 
## 
```

```

##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.458e-03 3.683e-05 93.894 < 2e-16 ***
## thetaC      1.003e+00 4.174e-02 24.022 1.11e-15 ***
## rhoC        5.858e-02 3.134e-02   1.869  0.07708 .
## tmrcaC     5.291e-03 4.059e-04 13.037 6.31e-11 ***
## thetaC:tmrcaC 1.875e+00 6.290e-01    2.981  0.00768 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.000168 on 19 degrees of freedom
## Multiple R-squared:  0.9896, Adjusted R-squared:  0.9874
## F-statistic: 452.5 on 4 and 19 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.1Mb[1, 4] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
r2.bgs.1Mb[2, 4] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb[3, 4] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb[4, 4] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb[5, 4] <- anova.diversity$VarExp[4] * 100

g.div.1Mb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep4, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep4, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep4, weights = varPower(0, ~theta), method = "ML")
g.div.1Mb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep4, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.1Mb.1, g.div.1Mb.2, g.div.1Mb.3, g.div.1Mb.4)

##          df      AIC
## g.div.1Mb.1 8 -343.6387
## g.div.1Mb.2 8 -338.7066
## g.div.1Mb.3 7 -340.7065
## g.div.1Mb.4 7 -345.6369

summary(g.div.1Mb.3)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
## Data: inf.lands.1Mb.rep4
##          AIC      BIC  logLik
## -340.7065 -332.4601 177.3532
##
## Variance function:
## Structure: Power of variance covariate
## Formula: ~theta
## Parameter estimates:
```

```

##      power
## 0.07850966
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept) 0.0034577 0.0000368 94.00350 0.0000
## thetaC       1.0040631 0.0422359 23.77274 0.0000
## rhoC        0.0592684 0.0315630  1.87778 0.0758
## tmrcaC      0.0052834 0.0004080 12.95035 0.0000
## thetaC:tmrcaC 1.8738540 0.6211915  3.01655 0.0071
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC      0.166
## rhoC       -0.003 -0.578
## tmrcaC     -0.195 -0.025 -0.433
## thetaC:tmrcaC -0.361 -0.367  0.013  0.537
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -1.8895276 -0.5306627 -0.0678023  0.2944035  2.9182328
##
## Residual standard error: 0.000234782
## Degrees of freedom: 24 total; 19 residual
vif(g.div.1Mb.3)

##          thetaC         rhoC         tmrcaC thetaC:tmrcaC
## 1.908607    2.160469    1.976808    1.713511

```

### 6.3.5 Replicate 5

```

rep5.sim.tmrca.1Mb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep5_w1000000.csv", sep = ",", header = T)

rep_5.pi.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.div")
rep_5.pi.1Mb$avg <- apply(rep_5.pi.1Mb[4:ncol(rep_5.pi.1Mb)], 1, mean)
rep_5.rho.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.rho")
rep_5.theta.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.theta")
rep_5.tmrca.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep5/dm2L_bgs_rep5_5.tmrca")
rep_5.tmrca.1Mb$avg <- apply(rep_5.tmrca.1Mb[4:ncol(rep_5.tmrca.1Mb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.1Mb.rep5 <- as.data.frame(cbind(rep_1.pi.1Mb$avg, sim.theta.1Mb$Rate, rep5.sim.tmrca.1Mb$Ave))
names(true.lands.1Mb.rep5) <- c("diversity", "theta", "tmrca", "rho")
true.lands.1Mb.rep5$thetaC <- true.lands.1Mb.rep5$theta - mean(true.lands.1Mb.rep5$theta)
true.lands.1Mb.rep5$tmrcaC <- true.lands.1Mb.rep5$tmrca - mean(true.lands.1Mb.rep5$tmrca)
true.lands.1Mb.rep5$rhoC <- true.lands.1Mb.rep5$rho - mean(true.lands.1Mb.rep5$rho, na.rm = T)
true.lands.1Mb.rep5$Replicate <- 1
m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.1Mb.rep5)
anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.1Mb.true[1, 5] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.1Mb.true[2, 5] <- anova.diversity$VarExp[1] * 100

```

```

r2.bgs.1Mb.true[3, 5] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb.true[4, 5] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb.true[5, 5] <- anova.diversity$VarExp[4] * 100

inf.lands.1Mb.rep5 <- as.data.frame(cbind(rep_5.pi.1Mb$avg, rep_5.theta.1Mb$sample_mean, rep_5.tmrca.1Mb$tmrca))
names(inf.lands.1Mb.rep5) <- c("diversity", "theta", "tmrca", "rho")

cor.table[5, 3] <- cor.test(sim.theta.1Mb$Rate, rep_5.theta.1Mb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.1Mb.rep5$thetaC <- inf.lands.1Mb.rep5$theta - mean(inf.lands.1Mb.rep5$theta)
inf.lands.1Mb.rep5$tmrcaC <- inf.lands.1Mb.rep5$tmrca - mean(inf.lands.1Mb.rep5$tmrca)
inf.lands.1Mb.rep5$rhoC <- inf.lands.1Mb.rep5$rho - mean(inf.lands.1Mb.rep5$rho)

inf.lands.1Mb.rep5$bin <- 1:nrow(inf.lands.1Mb.rep5)

# for merging:
inf.lands.1Mb.rep5 <- inf.lands.1Mb.rep5
inf.lands.1Mb.rep5$Replicate <- 1

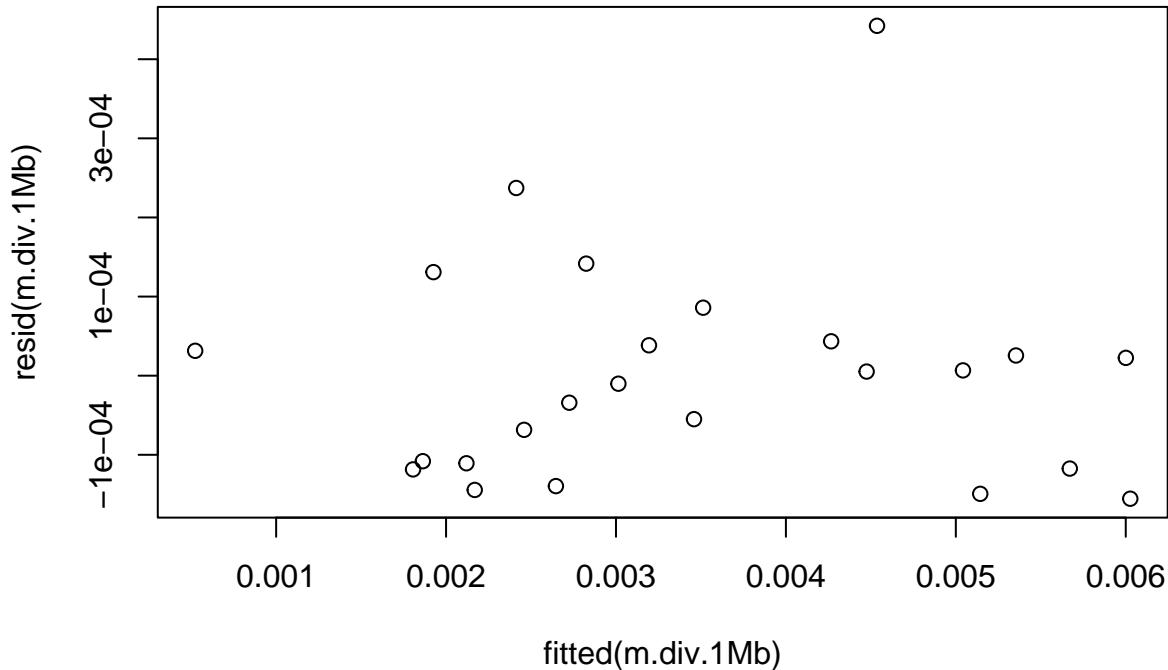
m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.1Mb.rep5)
m.div.1Mb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.1Mb.rep5)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.1Mb.rep5)

AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)

##          df      AIC
## m.div.1Mb     6 -346.9226
## m.div.1Mb.2   7 -345.5662
## m.div.1Mb.3   8 -347.9807

plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```



```

dwtest(m.div.1Mb)

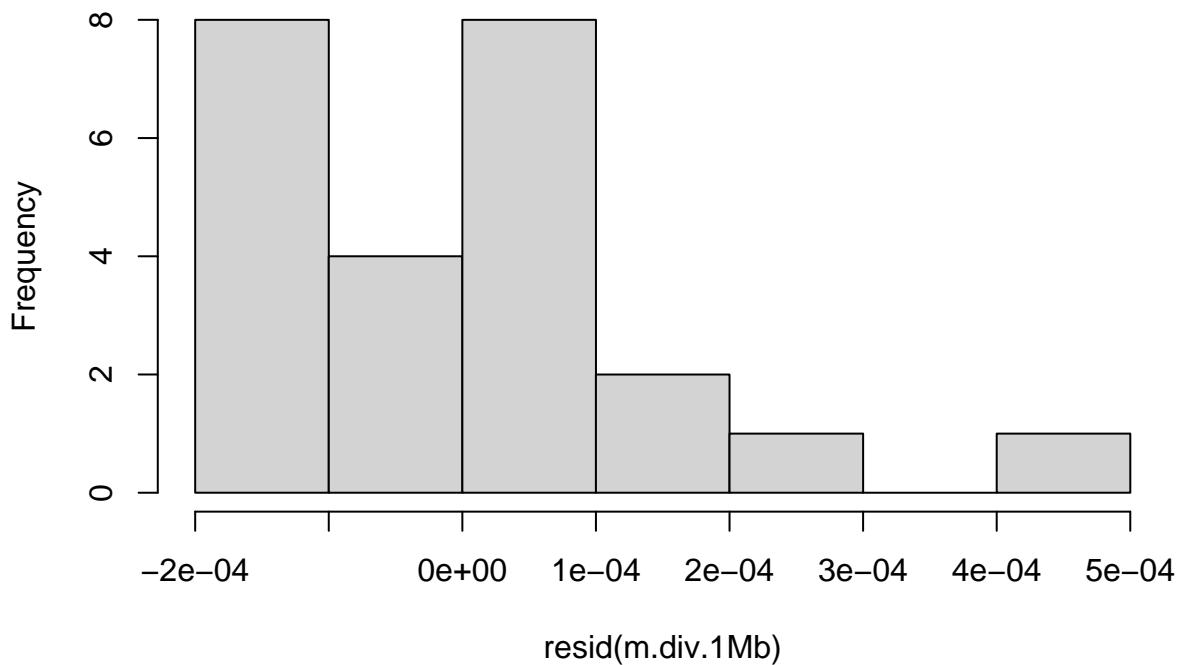
##
##  Durbin-Watson test
##
## data: m.div.1Mb
## DW = 2.3054, p-value = 0.6445
## alternative hypothesis: true autocorrelation is greater than 0

hmctest(m.div.1Mb)

##
##  Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.58123, p-value = 0.692
hist(resid(m.div.1Mb))

```

### Histogram of resid(m.div.1Mb)



```

summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.1Mb.rep5)
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -1.555e-04 -1.124e-04 -2.460e-06  3.966e-05  4.422e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept)  1.00000   0.00000    Inf 0.0000000    
## thetaC      0.00000   0.00000    Inf 0.0000000    
## rhoC       -0.00000   0.00000    Inf 0.0000000    
## tmrcaC     -0.00000   0.00000    Inf 0.0000000    
## thetaC:tmrcaC 0.00000   0.00000    Inf 0.0000000    
## 
```

```

##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.463e-03 3.141e-05 110.243 < 2e-16 ***
## thetaC      1.311e+00 4.668e-02  28.076 < 2e-16 ***
## rhoC       -1.091e-02 2.788e-02  -0.391  0.69992
## tmrcaC     3.365e-03 1.899e-04  17.720 2.84e-13 ***
## thetaC:tmrcaC 7.466e-01 2.170e-01   3.441  0.00274 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0001538 on 19 degrees of freedom
## Multiple R-squared:  0.9917, Adjusted R-squared:  0.9899
## F-statistic: 564.1 on 4 and 19 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.1Mb[1, 5] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
r2.bgs.1Mb[2, 5] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb[3, 5] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb[4, 5] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb[5, 5] <- anova.diversity$VarExp[4] * 100

g.div.1Mb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep5, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep5, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep5, weights = varPower(0, ~theta), method = "ML")
g.div.1Mb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep5, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.1Mb.1, g.div.1Mb.2, g.div.1Mb.3, g.div.1Mb.4)

##          df      AIC
## g.div.1Mb.1 8 -345.3251
## g.div.1Mb.2 8 -345.5873
## g.div.1Mb.3 7 -345.9151
## g.div.1Mb.4 7 -345.0317

summary(g.div.1Mb.3)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
## Data: inf.lands.1Mb.rep5
##          AIC      BIC logLik
## -345.9151 -337.6687 179.9576
##
## Variance function:
## Structure: Power of variance covariate
## Formula: ~theta
## Parameter estimates:
```

```

##      power
## 1.118503
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept) 0.0034688 0.00003433 101.02877 0.0000
## thetaC       1.3283474 0.05424610  24.48743 0.0000
## rhoC        0.0084012 0.02639289   0.31831 0.7537
## tmrcaC      0.0032478 0.00017056  19.04241 0.0000
## thetaC:tmrcaC 0.8841209 0.20550441    4.30220 0.0004
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC      0.479
## rhoC       -0.052 -0.647
## tmrcaC      0.056  0.455 -0.535
## thetaC:tmrcaC -0.040 -0.216 -0.002 -0.176
##
## Standardized residuals:
##      Min     Q1     Med     Q3     Max
## -1.2131276 -0.7213807 -0.1575783  0.3239893  2.7480924
##
## Residual standard error: 0.1012663
## Degrees of freedom: 24 total; 19 residual
vif(g.div.1Mb.3)

##          thetaC         rhoC         tmrcaC thetaC:tmrcaC
## 1.898829 2.087085 1.486258 1.121324

```

### 6.3.6 Replicate 6

```

rep6.sim.tmrca.1Mb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep6_w1000000.csv", sep = ",", header = T)

rep_6.pi.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.div")
rep_6.pi.1Mb$avg <- apply(rep_6.pi.1Mb[4:ncol(rep_6.pi.1Mb)], 1, mean)
rep_6.rho.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.rho")
rep_6.theta.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.theta")
rep_6.tmrca.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep6/dm2L_bgs_rep6_5.tmrca")
rep_6.tmrca.1Mb$avg <- apply(rep_6.tmrca.1Mb[4:ncol(rep_6.tmrca.1Mb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.1Mb.rep6 <- as.data.frame(cbind(rep_1.pi.1Mb$avg, sim.theta.1Mb$Rate, rep6.sim.tmrca.1Mb$Avg))
names(true.lands.1Mb.rep6) <- c("diversity", "theta", "tmrca", "rho")
true.lands.1Mb.rep6$thetaC <- true.lands.1Mb.rep6$theta - mean(true.lands.1Mb.rep6$theta)
true.lands.1Mb.rep6$tmrcaC <- true.lands.1Mb.rep6$tmrca - mean(true.lands.1Mb.rep6$tmrca)
true.lands.1Mb.rep6$rhoC <- true.lands.1Mb.rep6$rho - mean(true.lands.1Mb.rep6$rho, na.rm = T)
true.lands.1Mb.rep6$Replicate <- 1
m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.1Mb.rep6)
anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.1Mb.true[1, 6] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.1Mb.true[2, 6] <- anova.diversity$VarExp[1] * 100

```

```

r2.bgs.1Mb.true[3, 6] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb.true[4, 6] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb.true[5, 6] <- anova.diversity$VarExp[4] * 100

inf.lands.1Mb.rep6 <- as.data.frame(cbind(rep_6.pi.1Mb$avg, rep_6.theta.1Mb$sample_mean, rep_6.tmrca.1Mb$tmrca))
names(inf.lands.1Mb.rep6) <- c("diversity", "theta", "tmrca", "rho")

cor.table[6, 3] <- cor.test(sim.theta.1Mb$Rate, rep_6.theta.1Mb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.1Mb.rep6$thetaC <- inf.lands.1Mb.rep6$theta - mean(inf.lands.1Mb.rep6$theta)
inf.lands.1Mb.rep6$tmrcaC <- inf.lands.1Mb.rep6$tmrca - mean(inf.lands.1Mb.rep6$tmrca)
inf.lands.1Mb.rep6$rhoC <- inf.lands.1Mb.rep6$rho - mean(inf.lands.1Mb.rep6$rho)

inf.lands.1Mb.rep6$bin <- 1:nrow(inf.lands.1Mb.rep6)

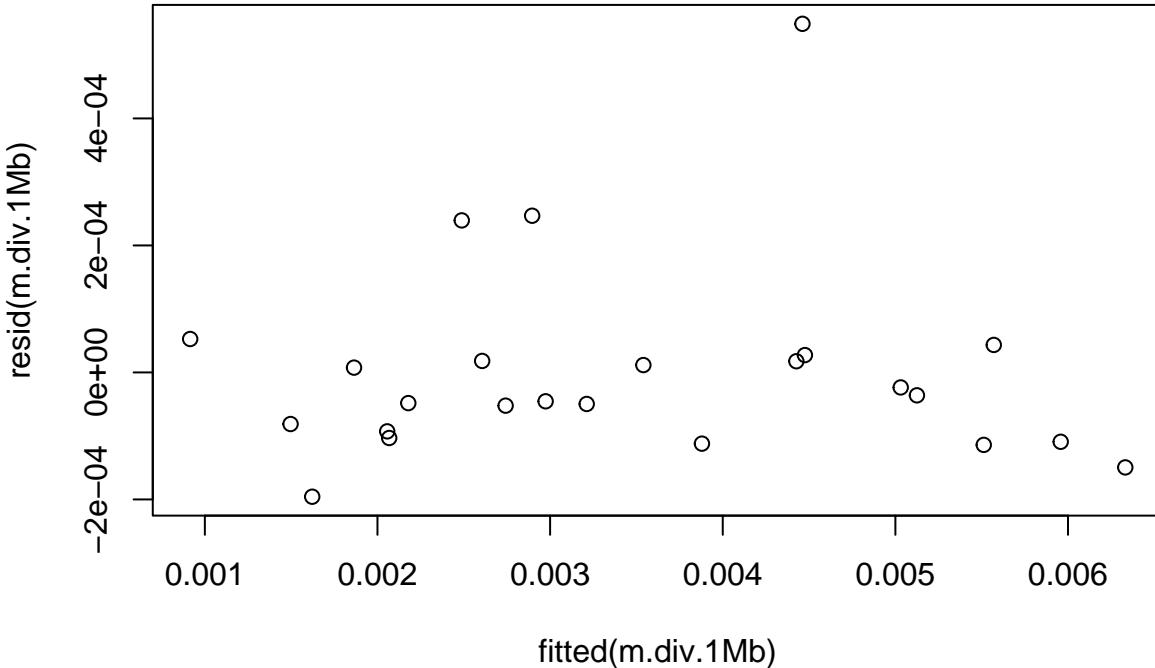
# for merging:
inf.lands.1Mb.rep6 <- inf.lands.1Mb.rep6
inf.lands.1Mb.rep6$Replicate <- 1

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.1Mb.rep6)
m.div.1Mb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.1Mb.rep6)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.1Mb.rep6)

AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)

##          df      AIC
## m.div.1Mb     6 -341.5943
## m.div.1Mb.2   7 -342.4713
## m.div.1Mb.3   8 -343.2357
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```



```

dwtest(m.div.1Mb)

##
##  Durbin-Watson test
##
## data: m.div.1Mb
## DW = 2.1636, p-value = 0.4919
## alternative hypothesis: true autocorrelation is greater than 0

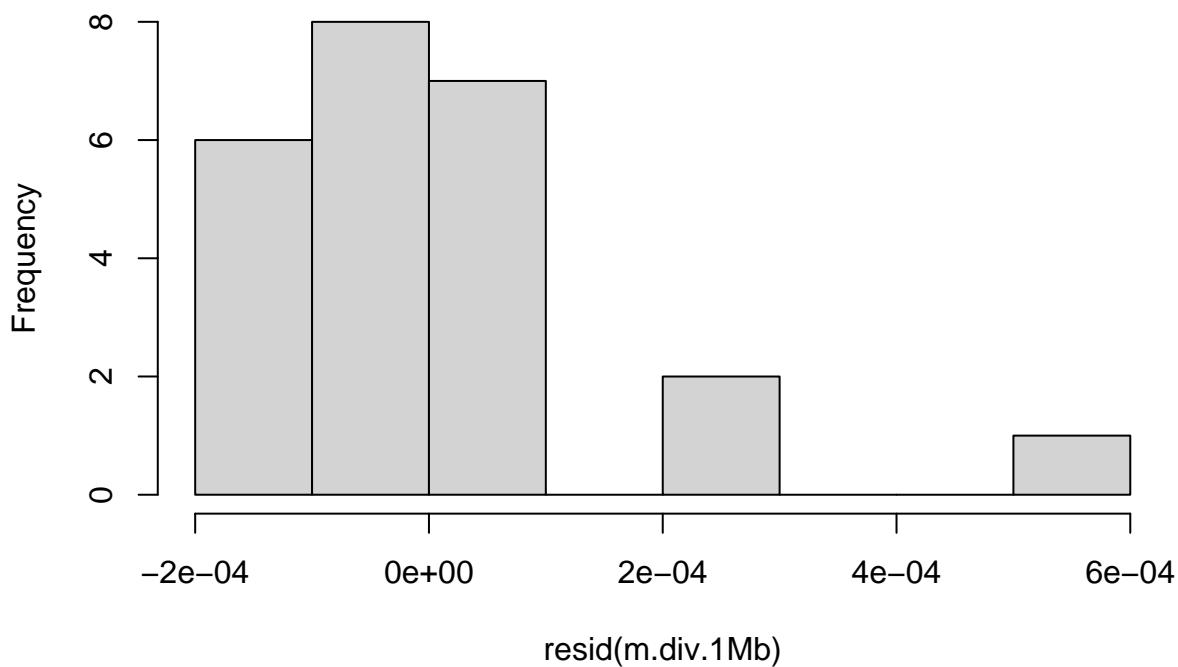
hmctest(m.div.1Mb)

##
##  Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.65357, p-value = 0.837

hist(resid(m.div.1Mb))

```

### Histogram of resid(m.div.1Mb)



```

summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.1Mb.rep6)
##
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -1.957e-04 -9.541e-05 -4.075e-05  2.041e-05  5.490e-04 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept)  1.000e+00  1.000e-01  1.000  0.3162    
## thetaC      -1.957e-04  1.000e-01 -1.957  0.3162    
## rhoC        -9.541e-05  1.000e-01 -9.541  0.3162    
## tmrcaC     -4.075e-05  1.000e-01 -4.075  0.3162    
## thetaC:tmrcaC 2.041e-05  1.000e-01  2.041  0.3162    
## 
```

```

##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.457e-03 3.707e-05 93.270 < 2e-16 ***
## thetaC      1.115e+00 4.504e-02 24.757 6.38e-16 ***
## rhoC        2.697e-02 2.765e-02  0.975   0.342
## tmrcaC     4.032e-03 2.537e-04 15.894 1.98e-12 ***
## thetaC:tmrcaC 7.433e-01 4.689e-01   1.585   0.129
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0001719 on 19 degrees of freedom
## Multiple R-squared:  0.9901, Adjusted R-squared:  0.988
## F-statistic: 475.1 on 4 and 19 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.1Mb[1, 6] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
r2.bgs.1Mb[2, 6] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb[3, 6] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb[4, 6] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb[5, 6] <- anova.diversity$VarExp[4] * 100

g.div.1Mb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep6, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep6, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep6, weights = varPower(0, ~theta), method = "ML")
g.div.1Mb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep6, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.1Mb.1, g.div.1Mb.2, g.div.1Mb.3, g.div.1Mb.4)

##          df      AIC
## g.div.1Mb.1 8 -341.9099
## g.div.1Mb.2 8 -343.7706
## g.div.1Mb.3 7 -342.0432
## g.div.1Mb.4 7 -343.8311

summary(g.div.1Mb.3)

## Generalized least squares fit by maximum likelihood
## Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
## Data: inf.lands.1Mb.rep6
##          AIC      BIC logLik
## -342.0432 -333.7968 178.0216
##
## Variance function:
## Structure: Power of variance covariate
## Formula: ~theta
## Parameter estimates:
```

```

##      power
## 3.130632
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept) 0.0035759 0.0000507 70.55075 0.0000
## thetaC       1.2887546 0.0524764 24.55877 0.0000
## rhoC        0.0174945 0.0150458  1.16275 0.2593
## tmrcaC      0.0042388 0.0002674 15.85209 0.0000
## thetaC:tmrcaC 0.9962534 0.3461699  2.87793 0.0096
##
## Correlation:
##            (Intr) thetaC rhoC   tmrcaC
## thetaC     0.898
## rhoC      -0.264 -0.504
## tmrcaC    0.062  0.099 -0.443
## thetaC:tmrcaC -0.417 -0.518 -0.211  0.635
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -1.4121973 -0.7867277 -0.4832574  0.1781136  2.8300575
##
## Residual standard error: 11371.55
## Degrees of freedom: 24 total; 19 residual
vif(g.div.1Mb.3)

```

```

##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
## 4.311521 2.306290 2.925110  5.296967

```

### 6.3.7 Replicate 7

```

rep7.sim.tmrca.1Mb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep7_w1000000.csv", sep = ",", header = T)

rep_7.pi.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep7/dm2L_bgs_rep7_5.div")
rep_7.pi.1Mb$avg <- apply(rep_7.pi.1Mb[4:ncol(rep_7.pi.1Mb)], 1, mean)
rep_7.rho.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep7/dm2L_bgs_rep7_5.rho")
rep_7.theta.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep7/dm2L_bgs_rep7_5.theta")
rep_7.tmrca.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep7/dm2L_bgs_rep7_5.tmrca")
rep_7.tmrca.1Mb$avg <- apply(rep_7.tmrca.1Mb[4:ncol(rep_7.tmrca.1Mb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.1Mb.rep7 <- as.data.frame(cbind(rep_1.pi.1Mb$avg, sim.theta.1Mb$Rate, rep7.sim.tmrca.1Mb$Ave))
names(true.lands.1Mb.rep7) <- c("diversity", "theta", "tmrca", "rho")
true.lands.1Mb.rep7$thetaC <- true.lands.1Mb.rep7$theta - mean(true.lands.1Mb.rep7$theta)
true.lands.1Mb.rep7$tmrcaC <- true.lands.1Mb.rep7$tmrca - mean(true.lands.1Mb.rep7$tmrca)
true.lands.1Mb.rep7$rhoC <- true.lands.1Mb.rep7$rho - mean(true.lands.1Mb.rep7$rho, na.rm = T)
true.lands.1Mb.rep7$Replicate <- 1
m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.1Mb.rep7)
anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.1Mb.true[1, 7] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.bgs.1Mb.true[2, 7] <- anova.diversity$VarExp[1] * 100

```

```

r2.bgs.1Mb.true[3, 7] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb.true[4, 7] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb.true[5, 7] <- anova.diversity$VarExp[4] * 100

inf.lands.1Mb.rep7 <- as.data.frame(cbind(rep_7.pi.1Mb$avg, rep_7.theta.1Mb$sample_mean, rep_7.tmrca.1Mb$tmrca))
names(inf.lands.1Mb.rep7) <- c("diversity", "theta", "tmrca", "rho")

cor.table[7, 3] <- cor.test(sim.theta.1Mb$Rate, rep_7.theta.1Mb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.1Mb.rep7$thetaC <- inf.lands.1Mb.rep7$theta - mean(inf.lands.1Mb.rep7$theta)
inf.lands.1Mb.rep7$tmrcaC <- inf.lands.1Mb.rep7$tmrca - mean(inf.lands.1Mb.rep7$tmrca)
inf.lands.1Mb.rep7$rhoC <- inf.lands.1Mb.rep7$rho - mean(inf.lands.1Mb.rep7$rho)

inf.lands.1Mb.rep7$bin <- 1:nrow(inf.lands.1Mb.rep7)

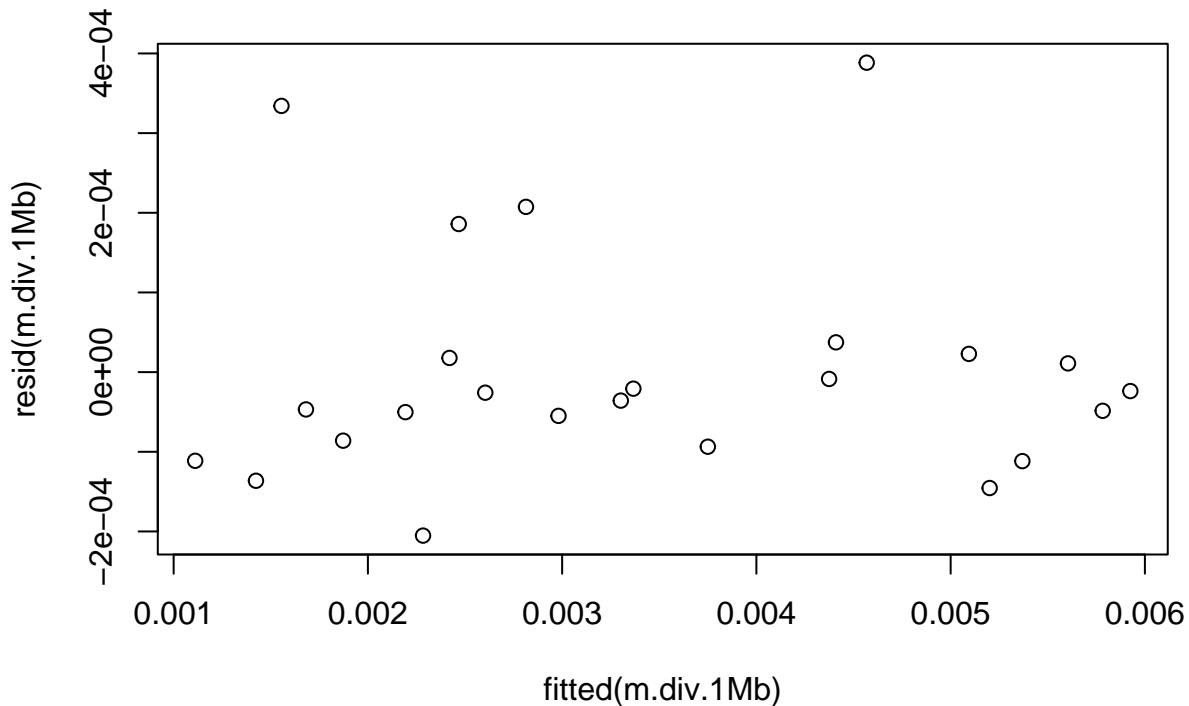
# for merging:
inf.lands.1Mb.rep7 <- inf.lands.1Mb.rep7
inf.lands.1Mb.rep7$Replicate <- 1

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.1Mb.rep7)
m.div.1Mb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.1Mb.rep7)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC)^2, data = inf.lands.1Mb.rep7)

AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)

##           df      AIC
## m.div.1Mb     6 -345.4274
## m.div.1Mb.2   7 -343.4288
## m.div.1Mb.3   8 -342.2231
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```



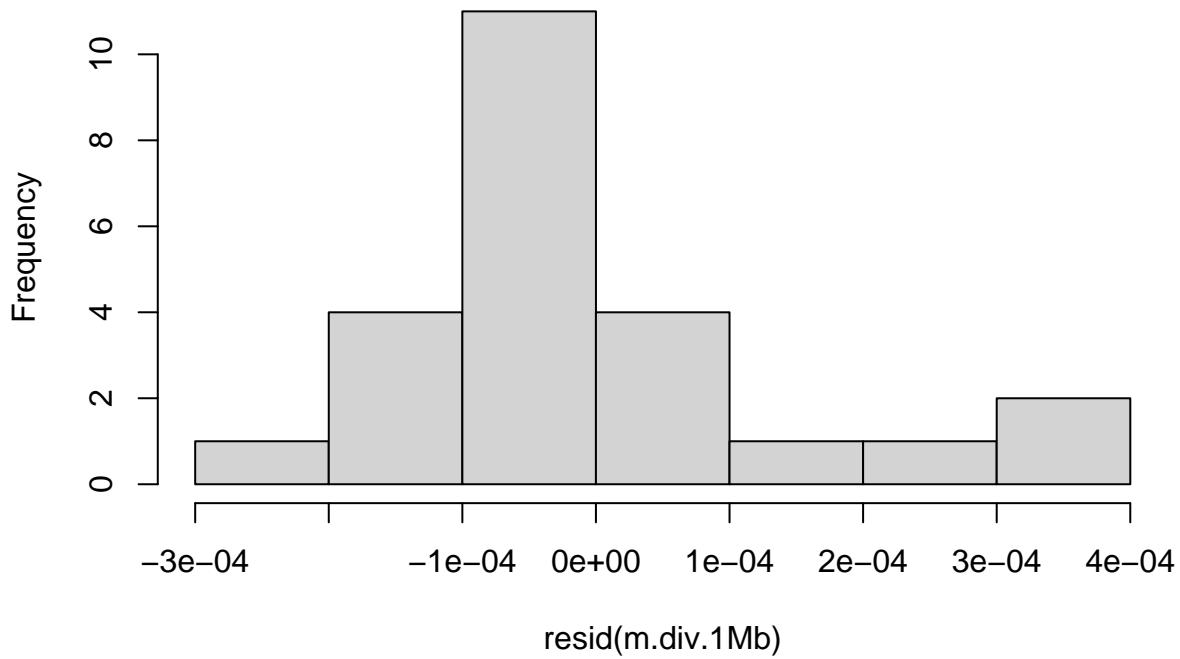
```
dwtest(m.div.1Mb)
```

```
##  
## Durbin-Watson test  
##  
## data: m.div.1Mb  
## DW = 2.1895, p-value = 0.5182  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmctest(m.div.1Mb)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.div.1Mb  
## HMC = 0.49501, p-value = 0.474  
hist(resid(m.div.1Mb))
```

## Histogram of resid(m.div.1Mb)



```
summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##     data = inf.lands.1Mb.rep7)
##
## Residuals:
##      Min        1Q    Median        3Q       Max
## -2.052e-04 -8.794e-05 -3.079e-05  1.908e-05  3.884e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.351e-03 5.037e-05 66.526 < 2e-16 ***
## thetaC      1.086e+00 5.359e-02 20.259 2.52e-14 ***
## rhoC        2.736e-02 3.012e-02  0.908  0.3752
## tmrcaC      4.505e-03 5.883e-04  7.658 3.19e-07 ***
## thetaC:tmrcaC 1.624e+00 8.673e-01  1.873  0.0766 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0001587 on 19 degrees of freedom
## Multiple R-squared:  0.9912, Adjusted R-squared:  0.9893
## F-statistic: 534.8 on 4 and 19 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.1Mb[1, 7] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
```

```

r2.bgs.1Mb[2, 7] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb[3, 7] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb[4, 7] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb[5, 7] <- anova.diversity$VarExp[4] * 100

g.div.1Mb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep7, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep7, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep7, weights = varPower(0, ~theta), method = "ML")
g.div.1Mb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep7, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.1Mb.1, g.div.1Mb.2, g.div.1Mb.3, g.div.1Mb.4)

##             df      AIC
## g.div.1Mb.1 8 -343.8782
## g.div.1Mb.2 8 -342.3197
## g.div.1Mb.3 7 -343.7752
## g.div.1Mb.4 7 -345.6709

summary(g.div.1Mb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep7
##       AIC      BIC    logLik
##   -343.7752 -335.5288 178.8876
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##       power
##   -0.6249336
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0033351 0.0000523 63.73232 0.0000
## thetaC      1.0522911 0.0496791 21.18178 0.0000
## rhoC       0.0194373 0.0287308  0.67653 0.5069
## tmrcaC     0.0048610 0.0006046  8.04002 0.0000
## thetaC:tmrcaC 2.1186592 0.9123559  2.32219 0.0315
##
## Correlation:
##           (Intr) thetaC rhoC   tmrcaC
## thetaC      0.429
## rhoC       0.161 -0.143
## tmrcaC    -0.656 -0.631 -0.462
## thetaC:tmrcaC -0.770 -0.725 -0.247  0.861

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -1.3170115 -0.6371261 -0.1942405  0.1843185  2.7685824
## 
## Residual standard error: 3.639405e-06
## Degrees of freedom: 24 total; 19 residual
vif(g.div.1Mb.3)

##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
## 3.127304 2.123346 5.921703   4.937703

```

### 6.3.8 Replicate 8

```

rep8.sim.tmrca.1Mb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep8_w1000000.csv", sep = ",", header = T)

rep_8.pi.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.div")
rep_8.pi.1Mb$avg <- apply(rep_8.pi.1Mb[4:ncol(rep_8.pi.1Mb)], 1, mean)
rep_8.rho.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.rho")
rep_8.theta.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.theta")
rep_8.tmrca.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep8/dm2L_bgs_rep8_5.tmrca")
rep_8.tmrca.1Mb$avg <- apply(rep_8.tmrca.1Mb[4:ncol(rep_8.tmrca.1Mb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.1Mb.rep8 <- as.data.frame(cbind(rep_1.pi.1Mb$avg, sim.theta.1Mb$Rate, rep8.sim.tmrca.1Mb$Avg))
names(true.lands.1Mb.rep8) <- c("diversity", "theta", "tmrca", "rho")
true.lands.1Mb.rep8$thetaC <- true.lands.1Mb.rep8$theta - mean(true.lands.1Mb.rep8$theta)
true.lands.1Mb.rep8$tmrcaC <- true.lands.1Mb.rep8$tmrca - mean(true.lands.1Mb.rep8$tmrca)
true.lands.1Mb.rep8$rhoC <- true.lands.1Mb.rep8$rho - mean(true.lands.1Mb.rep8$rho, na.rm = T)
true.lands.1Mb.rep8$Replicate <- 1
m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.1Mb.rep8)
anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$Sum Sq
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.1Mb.true[1, 8] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.bgs.1Mb.true[2, 8] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb.true[3, 8] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb.true[4, 8] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb.true[5, 8] <- anova.diversity$VarExp[4] * 100

inf.lands.1Mb.rep8 <- as.data.frame(cbind(rep_8.pi.1Mb$avg, rep_8.theta.1Mb$sample_mean, rep_8.tmrca.1Mb$Avg))
names(inf.lands.1Mb.rep8) <- c("diversity", "theta", "tmrca", "rho")

cor.table[8, 3] <- cor.test(sim.theta.1Mb$Rate, rep_8.theta.1Mb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.1Mb.rep8$thetaC <- inf.lands.1Mb.rep8$theta - mean(inf.lands.1Mb.rep8$theta)
inf.lands.1Mb.rep8$tmrcaC <- inf.lands.1Mb.rep8$tmrca - mean(inf.lands.1Mb.rep8$tmrca)
inf.lands.1Mb.rep8$rhoC <- inf.lands.1Mb.rep8$rho - mean(inf.lands.1Mb.rep8$rho)

inf.lands.1Mb.rep8$bin <- 1:nrow(inf.lands.1Mb.rep8)

# for merging:

```

```

inf.lands.1Mb.rep8 <- inf.lands.1Mb.rep8
inf.lands.1Mb.rep8$Replicate <- 1

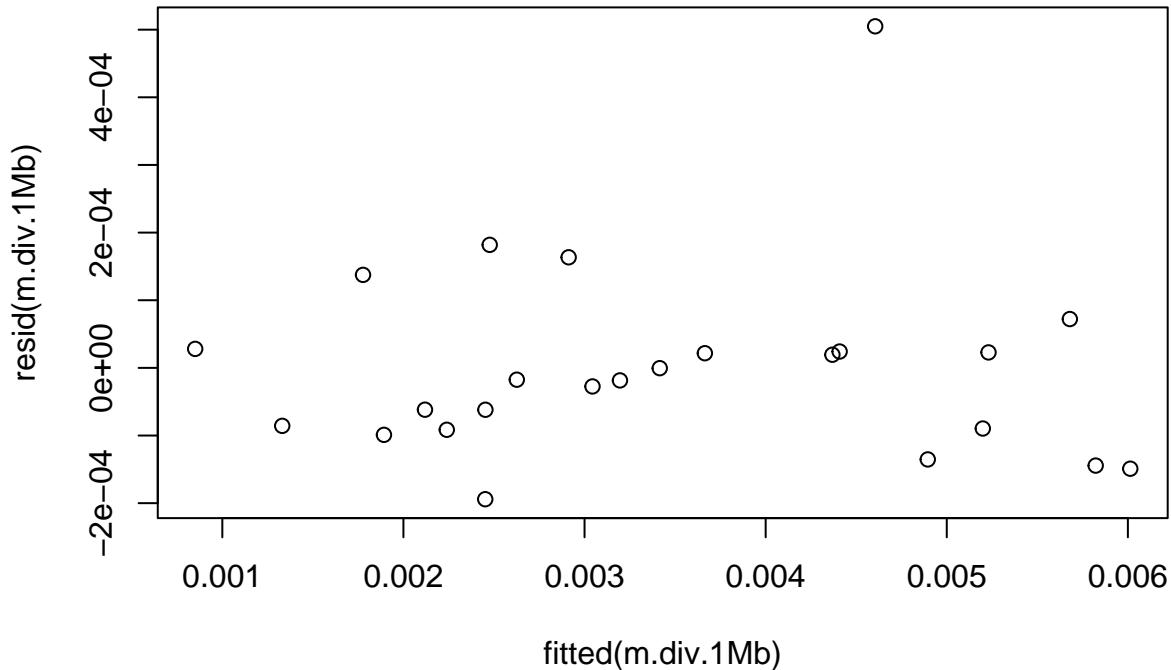
m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.1Mb.rep8)
m.div.1Mb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.1Mb.rep8)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.1Mb.rep8)

AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)

##           df      AIC
## m.div.1Mb    6 -345.1858
## m.div.1Mb.2  7 -343.4070
## m.div.1Mb.3  8 -345.1559

plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```



```

dwtest(m.div.1Mb)

##
##  Durbin-Watson test
##
##  data:  m.div.1Mb
##  DW = 2.3323, p-value = 0.6935
##  alternative hypothesis: true autocorrelation is greater than 0

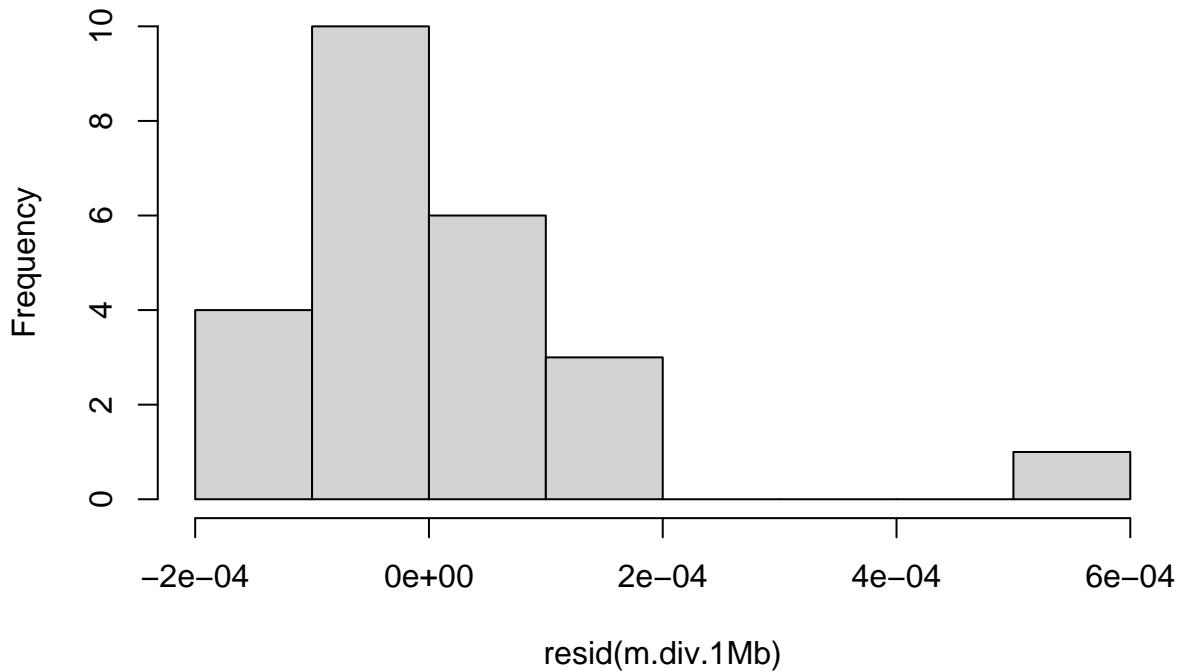
hmctest(m.div.1Mb)

##
##  Harrison-McCabe test
##
##  data:  m.div.1Mb
##  HMC = 0.65145, p-value = 0.854

hist(resid(m.div.1Mb))

```

## Histogram of resid(m.div.1Mb)



```
summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.1Mb.rep8)
##
## Residuals:
##       Min         1Q     Median        3Q       Max
## -1.941e-04 -9.009e-05 -1.798e-05  2.516e-05  5.049e-04
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.428e-03 3.304e-05 103.752 < 2e-16 ***
## thetaC      1.264e+00 5.490e-02  23.029 2.42e-15 ***
## rhoC       -6.271e-03 3.593e-02  -0.175  0.8633
## tmrcaC      3.564e-03 2.162e-04  16.485 1.03e-12 ***
## thetaC:tmrcaC 8.224e-01 2.892e-01   2.844  0.0104 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0001595 on 19 degrees of freedom
## Multiple R-squared:  0.9909, Adjusted R-squared:  0.989
## F-statistic: 515.7 on 4 and 19 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.1Mb[1, 8] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
```

```

r2.bgs.1Mb[2, 8] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb[3, 8] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb[4, 8] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb[5, 8] <- anova.diversity$VarExp[4] * 100

g.div.1Mb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep8, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep8, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep8, weights = varPower(0, ~theta), method = "ML")
g.div.1Mb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep8, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.1Mb.1, g.div.1Mb.2, g.div.1Mb.3, g.div.1Mb.4)

##             df      AIC
## g.div.1Mb.1 8 -344.1779
## g.div.1Mb.2 8 -346.5652
## g.div.1Mb.3 7 -346.9859
## g.div.1Mb.4 7 -343.9414

summary(g.div.1Mb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep8
##       AIC      BIC  logLik
##   -346.9859 -338.7395 180.493
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##     power
## 1.844674
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0034418 0.00003793 90.73488 0.0000
## thetaC       1.2870866 0.06260981 20.55727 0.0000
## rhoC        0.0283001 0.02906012  0.97385 0.3424
## tmrcaC      0.0033891 0.00018982 17.85469 0.0000
## thetaC:tmrcaC 1.0438448 0.28464931  3.66713 0.0016
##
## Correlation:
##           (Intr) thetaC rhoC    tmrcaC
## thetaC      0.665
## rhoC       -0.170 -0.687
## tmrcaC      0.167  0.532 -0.679
## thetaC:tmrcaC -0.163 -0.449  0.284 -0.114

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3       Max
## -1.4834747 -0.6354580 -0.2279145  0.1515981  2.7918383
## 
## Residual standard error: 7.052248
## Degrees of freedom: 24 total; 19 residual
vif(g.div.1Mb.3)

##          thetaC         rhoC        tmrcaC thetaC:tmrcaC
##      2.256212     2.567824     1.937620     1.291249

```

### 6.3.9 Replicate 9

```

rep9.sim.tmrca.1Mb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep9_w1000000.csv", sep = ",", header = T)

rep_9.pi.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.div")
rep_9.pi.1Mb$avg <- apply(rep_9.pi.1Mb[4:ncol(rep_9.pi.1Mb)], 1, mean)
rep_9.rho.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.rho")
rep_9.theta.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.theta")
rep_9.tmrca.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep9/dm2L_bgs_rep9_5.tmrca")
rep_9.tmrca.1Mb$avg <- apply(rep_9.tmrca.1Mb[4:ncol(rep_9.tmrca.1Mb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.1Mb.rep9 <- as.data.frame(cbind(rep_1.pi.1Mb$avg, sim.theta.1Mb$Rate, rep9.sim.tmrca.1Mb$Ave))
names(true.lands.1Mb.rep9) <- c("diversity", "theta", "tmrca", "rho")
true.lands.1Mb.rep9$thetaC <- true.lands.1Mb.rep9$theta - mean(true.lands.1Mb.rep9$theta)
true.lands.1Mb.rep9$tmrcaC <- true.lands.1Mb.rep9$tmrca - mean(true.lands.1Mb.rep9$tmrca)
true.lands.1Mb.rep9$rhoC <- true.lands.1Mb.rep9$rho - mean(true.lands.1Mb.rep9$rho, na.rm = T)
true.lands.1Mb.rep9$Replicate <- 1
m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.1Mb.rep9)
anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$Sum Sq
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.1Mb.true[1, 9] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.bgs.1Mb.true[2, 9] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb.true[3, 9] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb.true[4, 9] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb.true[5, 9] <- anova.diversity$VarExp[4] * 100

inf.lands.1Mb.rep9 <- as.data.frame(cbind(rep_9.pi.1Mb$avg, rep_9.theta.1Mb$sample_mean, rep_9.tmrca.1Mb$sample_mean))
names(inf.lands.1Mb.rep9) <- c("diversity", "theta", "tmrca", "rho")

cor.table[9, 3] <- cor.test(sim.theta.1Mb$Rate, rep_9.theta.1Mb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.1Mb.rep9$thetaC <- inf.lands.1Mb.rep9$theta - mean(inf.lands.1Mb.rep9$theta)
inf.lands.1Mb.rep9$tmrcaC <- inf.lands.1Mb.rep9$tmrca - mean(inf.lands.1Mb.rep9$tmrca)
inf.lands.1Mb.rep9$rhoC <- inf.lands.1Mb.rep9$rho - mean(inf.lands.1Mb.rep9$rho)

inf.lands.1Mb.rep9$bin <- 1:nrow(inf.lands.1Mb.rep9)

# for merging:

```

```

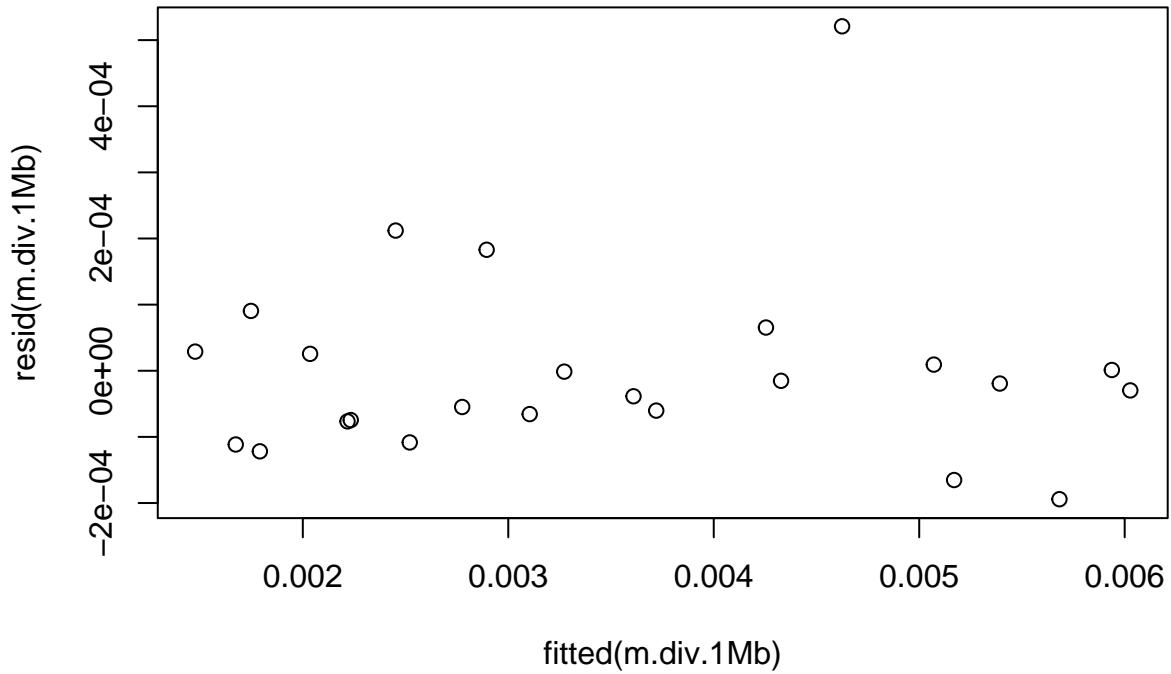
inf.lands.1Mb.rep9 <- inf.lands.1Mb.rep9
inf.lands.1Mb.rep9$Replicate <- 1

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.1Mb.rep9)
m.div.1Mb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.1Mb.rep9)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.1Mb.rep9)

AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)

##           df      AIC
## m.div.1Mb    6 -344.7058
## m.div.1Mb.2  7 -345.4784
## m.div.1Mb.3  8 -344.8491
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```



```

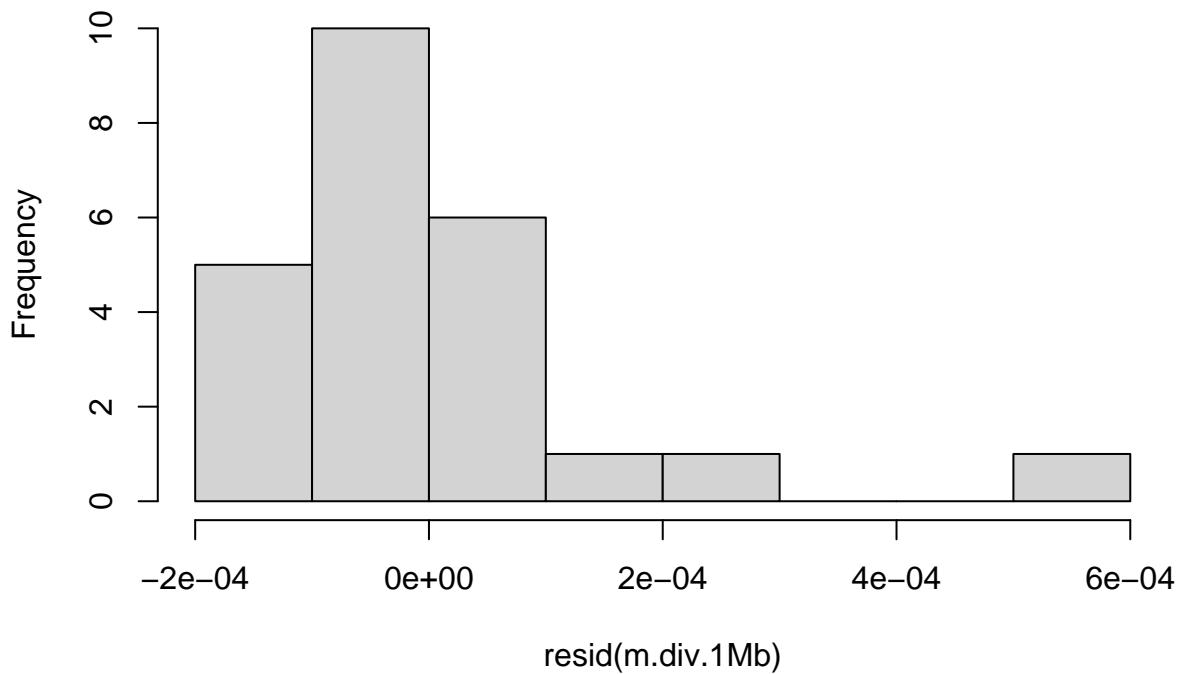
dwtest(m.div.1Mb)

##
##  Durbin-Watson test
##
##  data:  m.div.1Mb
##  DW = 2.6206, p-value = 0.8798
##  alternative hypothesis: true autocorrelation is greater than 0
hmctest(m.div.1Mb)

##
##  Harrison-McCabe test
##
##  data:  m.div.1Mb
##  HMC = 0.64661, p-value = 0.858
hist(resid(m.div.1Mb))

```

## Histogram of resid(m.div.1Mb)



```
summary(m.div.1Mb)

##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##      data = inf.lands.1Mb.rep9)
##
## Residuals:
##       Min     1Q   Median     3Q    Max 
## -1.942e-04 -7.503e-05 -2.451e-05  2.644e-05  5.209e-04
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 3.453e-03 3.751e-05 92.060 < 2e-16 ***
## thetaC      1.216e+00 5.336e-02 22.783 2.94e-15 ***
## rhoC       -6.052e-03 3.346e-02 -0.181  0.8584  
## tmrcaC      3.807e-03 2.487e-04 15.304 3.87e-12 ***
## thetaC:tmrcaC 9.750e-01 3.713e-01  2.626  0.0166 *  
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0001611 on 19 degrees of freedom
## Multiple R-squared:  0.9903, Adjusted R-squared:  0.9883 
## F-statistic: 486.3 on 4 and 19 DF,  p-value: < 2.2e-16

anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$"Sum Sq"
anova.diversity$VarExp <- apiss / sum(apiss)

r2.bgs.1Mb[1, 9] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3] +
```

```

r2.bgs.1Mb[2, 9] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb[3, 9] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb[4, 9] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb[5, 9] <- anova.diversity$VarExp[4] * 100

g.div.1Mb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep9, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep9, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep9, weights = varPower(0, ~theta), method = "ML")
g.div.1Mb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep9, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.1Mb.1, g.div.1Mb.2, g.div.1Mb.3, g.div.1Mb.4)

##           df      AIC
## g.div.1Mb.1 8 -347.5106
## g.div.1Mb.2 8 -349.8511
## g.div.1Mb.3 7 -346.0547
## g.div.1Mb.4 7 -343.4336

summary(g.div.1Mb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep9
##       AIC      BIC  logLik
##   -346.0547 -337.8083 180.0274
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
##   Parameter estimates:
##     power
## 1.916343
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0034744 0.0000413 84.07203 0.0000
## thetaC      1.2936613 0.0586924 22.04139 0.0000
## rhoC       -0.0029089 0.0268341 -0.10840 0.9148
## tmrcaC      0.0037363 0.0002296 16.27063 0.0000
## thetaC:tmrcaC 1.1021921 0.3485437  3.16228 0.0051
##
## Correlation:
##          (Intr) thetaC rhoC    tmrcaC
## thetaC      0.742
## rhoC       -0.235 -0.684
## tmrcaC      0.020  0.220 -0.494
## thetaC:tmrcaC -0.342 -0.372  0.181  0.448

```

```

## 
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -1.37197717 -0.54593737 -0.36858902  0.09647638  2.59397338
## 
## Residual standard error: 10.76124
## Degrees of freedom: 24 total; 19 residual
vif(g.div.1Mb.3)

##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
## 2.137369 2.606907 2.189951    1.876093

```

### 6.3.10 Replicate 10

```

rep10.sim.tmrca.1Mb <- read.table("dm_bgs_sims/10r/dm2L_bgs_rep10_w1000000.csv", sep = ",", header = T)

rep_10.pi.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_5.csv")
rep_10.pi.1Mb$avg <- apply(rep_10.pi.1Mb[4:ncol(rep_10.pi.1Mb)], 1, mean)
rep_10.rho.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_5.csv")
rep_10.theta.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_5.csv")
rep_10.tmrca.1Mb <- read.table("dm_bgs_sims/10r/NonHomogeneous/iSMC/NonHomogeneous/rep10/dm2L_bgs_rep10_5.csv")
rep_10.tmrca.1Mb$avg <- apply(rep_10.tmrca.1Mb[4:ncol(rep_10.tmrca.1Mb)], 1, mean)

# first the linear modeling with the true (simulated) landscapes
true.lands.1Mb.rep10 <- as.data.frame(cbind(rep_1.pi.1Mb$avg, sim.theta.1Mb$Rate, rep10.sim.tmrca.1Mb$Age))
names(true.lands.1Mb.rep10) <- c("diversity", "theta", "tmrca", "rho")
true.lands.1Mb.rep10$thetaC <- true.lands.1Mb.rep10$theta - mean(true.lands.1Mb.rep10$theta)
true.lands.1Mb.rep10$tmrcaC <- true.lands.1Mb.rep10$tmrca - mean(true.lands.1Mb.rep10$tmrca)
true.lands.1Mb.rep10$rhoC <- true.lands.1Mb.rep10$rho - mean(true.lands.1Mb.rep10$rho, na.rm = T)
true.lands.1Mb.rep10$Replicate <- 1
m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = true.lands.1Mb.rep10)
anova.diversity <- Anova(m.div.1Mb)
apiss <- anova.diversity$Sum Sq
anova.diversity$VarExp <- apiss / sum(apiss)
r2.bgs.1Mb.true[1, 10] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3]) * 100
r2.bgs.1Mb.true[2, 10] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb.true[3, 10] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb.true[4, 10] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb.true[5, 10] <- anova.diversity$VarExp[4] * 100

inf.lands.1Mb.rep10 <- as.data.frame(cbind(rep_10.pi.1Mb$avg, rep_10.theta.1Mb$sample_mean, rep_10.tmrca.1Mb$Age))
names(inf.lands.1Mb.rep10) <- c("diversity", "theta", "tmrca", "rho")

cor.table[10, 3] <- cor.test(sim.theta.1Mb$Rate, rep_10.theta.1Mb$sample_mean, method = "spearman")$estimate

# centering
inf.lands.1Mb.rep10$thetaC <- inf.lands.1Mb.rep10$theta - mean(inf.lands.1Mb.rep10$theta)
inf.lands.1Mb.rep10$tmrcaC <- inf.lands.1Mb.rep10$tmrca - mean(inf.lands.1Mb.rep10$tmrca)
inf.lands.1Mb.rep10$rhoC <- inf.lands.1Mb.rep10$rho - mean(inf.lands.1Mb.rep10$rho)

inf.lands.1Mb.rep10$bin <- 1:nrow(inf.lands.1Mb.rep10)

# for merging:

```

```

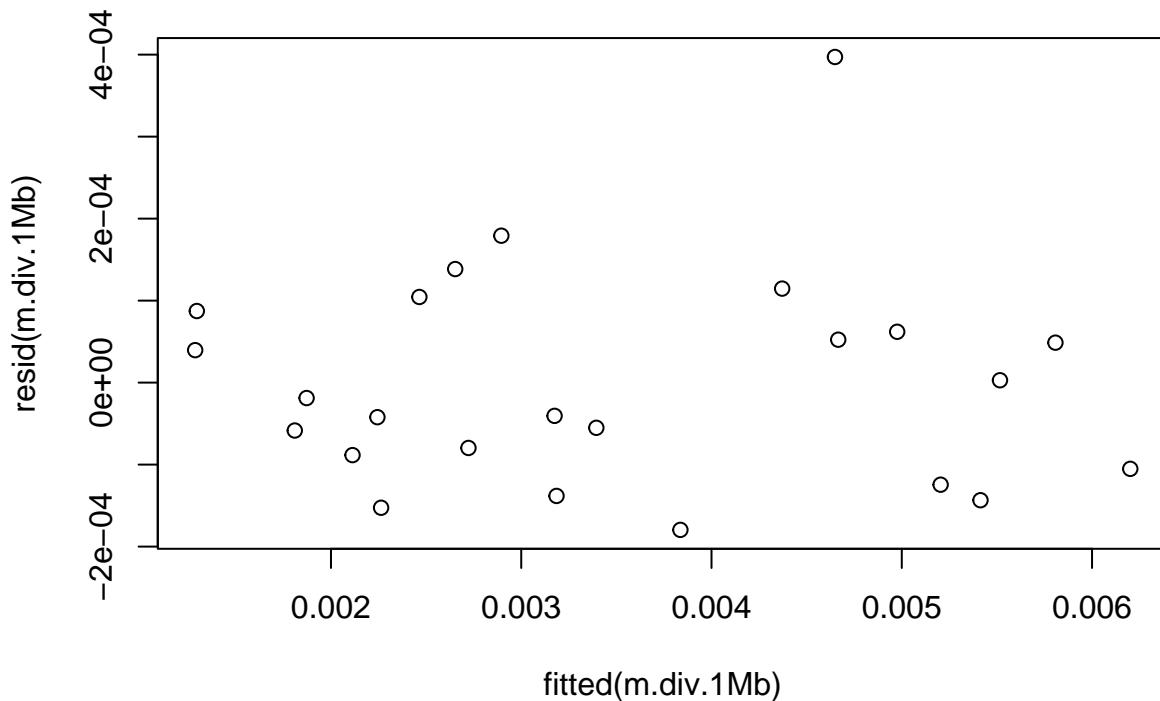
inf.lands.1Mb.rep10 <- inf.lands.1Mb.rep10
inf.lands.1Mb.rep10$Replicate <- 1

m.div.1Mb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = inf.lands.1Mb.rep10)
m.div.1Mb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = inf.lands.1Mb.rep10)
m.div.1Mb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = inf.lands.1Mb.rep10)

AIC(m.div.1Mb, m.div.1Mb.2, m.div.1Mb.3)

##           df      AIC
## m.div.1Mb    6 -349.8858
## m.div.1Mb.2  7 -353.7635
## m.div.1Mb.3  8 -351.7726
plot(resid(m.div.1Mb)~fitted(m.div.1Mb))

```



```

dwtest(m.div.1Mb)

##
##  Durbin-Watson test
##
## data: m.div.1Mb
## DW = 2.0448, p-value = 0.4006
## alternative hypothesis: true autocorrelation is greater than 0

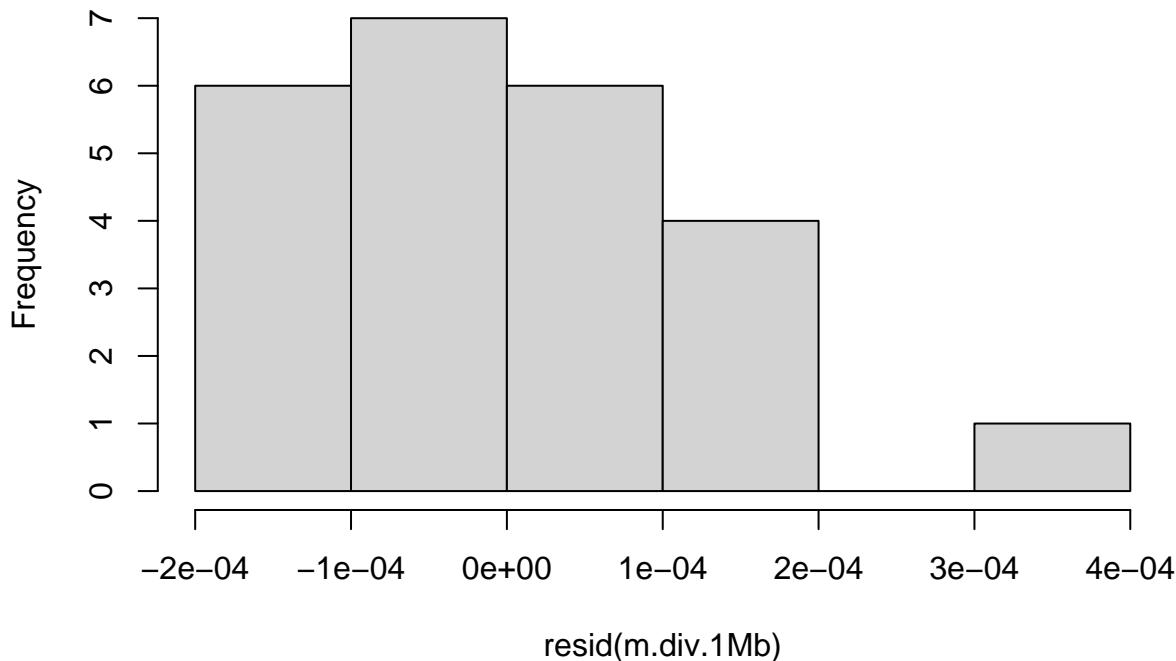
hmctest(m.div.1Mb)

##
##  Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.61476, p-value = 0.79

```

```
hist(resid(m.div.1Mb))
```

**Histogram of resid(m.div.1Mb)**



```
summary(m.div.1Mb)
```

```
##  
## Call:  
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,  
##      data = inf.lands.1Mb.rep10)  
##  
## Residuals:  
##      Min       1Q   Median       3Q      Max  
## -1.796e-04 -9.261e-05 -2.968e-05  6.834e-05  3.971e-04  
##  
## Coefficients:  
##              Estimate Std. Error t value Pr(>|t|)  
## (Intercept) 3.457e-03 3.521e-05 98.178 < 2e-16 ***  
## thetaC       1.015e+00 4.199e-02 24.171 9.92e-16 ***  
## rhoC         4.850e-02 3.237e-02  1.498  0.1505  
## tmrcaC       4.783e-03 3.222e-04 14.844 6.62e-12 ***  
## thetaC:tmrcaC 1.310e+00 5.763e-01   2.273  0.0348 *  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## Residual standard error: 0.0001446 on 19 degrees of freedom  
## Multiple R-squared:  0.9925, Adjusted R-squared:  0.9909  
## F-statistic: 624.7 on 4 and 19 DF,  p-value: < 2.2e-16  
anova.diversity <- Anova(m.div.1Mb)  
apiss <- anova.diversity$"Sum Sq"  
anova.diversity$VarExp <- apiss / sum(apiss)
```

```

r2.bgs.1Mb[1, 10] <- (anova.diversity$VarExp[1] + anova.diversity$VarExp[2] + anova.diversity$VarExp[3])
r2.bgs.1Mb[2, 10] <- anova.diversity$VarExp[1] * 100
r2.bgs.1Mb[3, 10] <- anova.diversity$VarExp[2] * 100
r2.bgs.1Mb[4, 10] <- anova.diversity$VarExp[3] * 100
r2.bgs.1Mb[5, 10] <- anova.diversity$VarExp[4] * 100

g.div.1Mb.1 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep10, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep10, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.1Mb.3 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep10, weights = varPower(0, ~theta), method = "ML")
g.div.1Mb.4 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                      data = inf.lands.1Mb.rep10, weights = varPower(0, ~tmrcaC), method = "ML")

AIC(g.div.1Mb.1, g.div.1Mb.2, g.div.1Mb.3, g.div.1Mb.4)

##           df      AIC
## g.div.1Mb.1 8 -347.2457
## g.div.1Mb.2 8 -348.1811
## g.div.1Mb.3 7 -348.8246
## g.div.1Mb.4 7 -349.0469
summary(g.div.1Mb.3)

## Generalized least squares fit by maximum likelihood
##   Model: diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC
##   Data: inf.lands.1Mb.rep10
##       AIC     BIC   logLik
##   -348.8246 -340.5782 181.4123
##
## Variance function:
##   Structure: Power of variance covariate
##   Formula: ~theta
## Parameter estimates:
##   power
## 0.7454269
##
## Coefficients:
##             Value Std.Error t-value p-value
## (Intercept) 0.0034586 0.0000353 97.87553 0.0000
## thetaC       1.0353207 0.0442649 23.38920 0.0000
## rhoC        0.0439740 0.0290366  1.51444 0.1464
## tmrcaC      0.0047829 0.0003101 15.42616 0.0000
## thetaC:tmrcaC 1.3035906 0.5316560  2.45194 0.0241
##
## Correlation:
##          (Intr) thetaC rhoC    tmrcaC
## thetaC      0.520
## rhoC       -0.109 -0.611
## tmrcaC     -0.182  0.060 -0.527

```

```

## thetaC:tmrcaC -0.498 -0.504  0.190  0.390
##
## Standardized residuals:
##      Min       Q1       Med       Q3      Max
## -1.3571009 -0.7800013 -0.1949018  0.4014887  2.8468855
##
## Residual standard error: 0.009233511
## Degrees of freedom: 24 total; 19 residual
vif(g.div.1Mb.3)

##          thetaC         rhoC      tmrcaC thetaC:tmrcaC
##        2.161747    2.693198    2.158165     1.824506

```

## 6.4 all replicates:

```

write.table(cor.table, "cor.mutation.bgs.tsv", quote = F, sep = "\t")

# true (simulated) landscapes
r2.bgs.50kb.true$average <- apply(r2.bgs.50kb.true, 1, mean)
r2.bgs.200kb.true$average <- apply(r2.bgs.200kb.true, 1, mean)
r2.bgs.1Mb.true$average <- apply(r2.bgs.1Mb.true, 1, mean)

r2.true.avg <- rbind.data.frame(r2.bgs.50kb.true$average, r2.bgs.200kb.true$average, r2.bgs.1Mb.true$average)
colnames(r2.true.avg) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
r2.true.avg$bin.size <- c(50, 200, 1000)

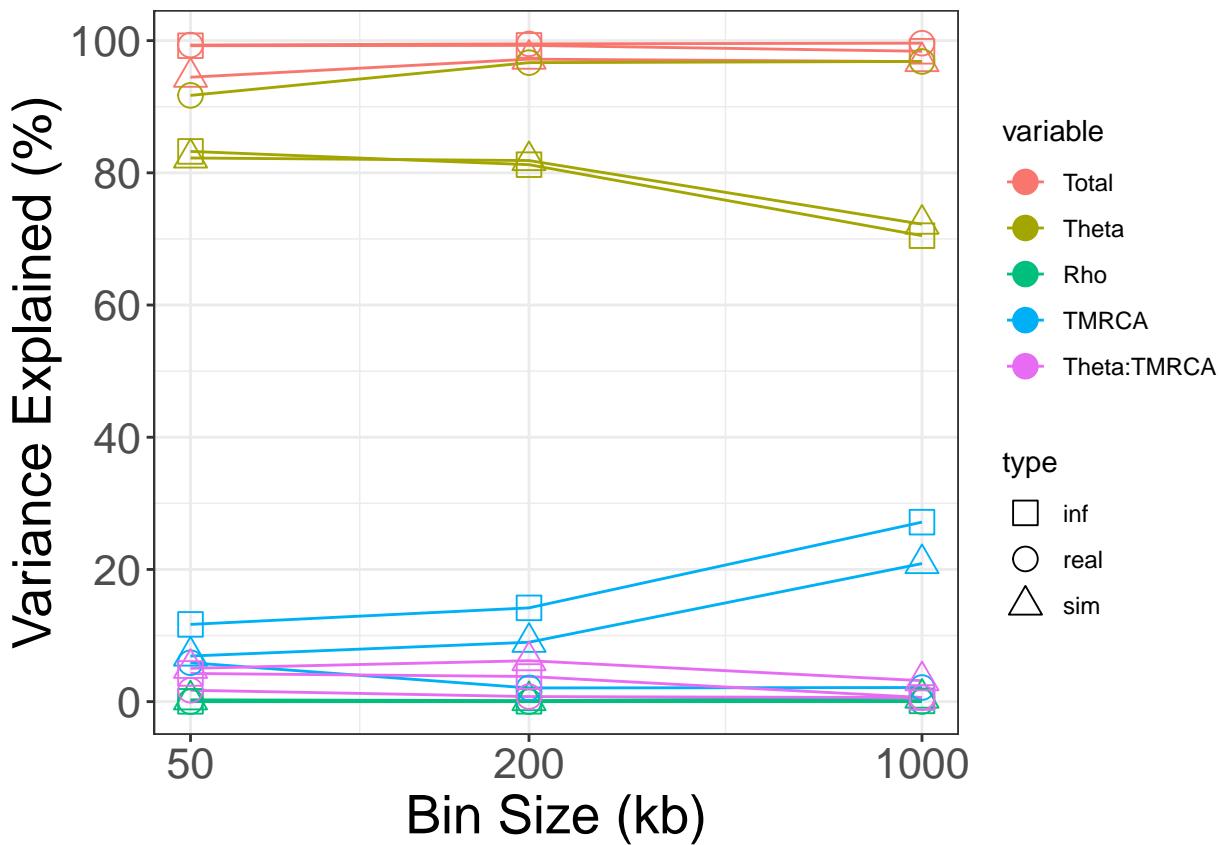
# inferred landscapes
r2.bgs.50kb$average <- apply(r2.bgs.50kb, 1, mean)
r2.bgs.200kb$average <- apply(r2.bgs.200kb, 1, mean)
r2.bgs.1Mb$average <- apply(r2.bgs.1Mb, 1, mean)

r2.inf.avg <- rbind.data.frame(r2.bgs.50kb$average, r2.bgs.200kb$average, r2.bgs.1Mb$average, make.row.r2)
colnames(r2.inf.avg) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
r2.inf.avg$bin.size <- c(50, 200, 1000)

r2.tab.comb <- rbind.data.frame(r2.dm.tab, r2.true.avg, r2.inf.avg)
r2.tab.comb$type <- c(rep("real", 3), rep("sim", 3), rep("inf", 3))

molten.r2 <- melt(r2.tab.comb, id.vars = c("bin.size", "type"))
r2.plot <- ggplot(data = molten.r2, aes(x = bin.size, y = value, colour = variable, fill = type))
r2.plot <- r2.plot + geom_line(data = molten.r2)
r2.plot <- r2.plot + geom_point(aes(shape = type, colour = variable), size = 4)
r2.plot <- r2.plot + scale_x_continuous(breaks = c(50, 200, 1000), trans="log10")
r2.plot <- r2.plot + scale_y_continuous(breaks = pretty_breaks())
r2.plot <- r2.plot + scale_shape_manual(values = c(0, 1, 2))
r2.plot <- r2.plot + labs(title = NULL, x = "Bin Size (kb)", y = "Variance Explained (%)") + theme_bw()
r2.plot <- r2.plot + theme(axis.title = element_text(size = 20), axis.text = element_text(size = 16))
r2.plot

```



```
ggsave("Figure8.pdf", r2.plot, device = "pdf")
```

```
molten.r2 <- melt(r2.tab.comb, id.vars = c("bin.size", "type")) r2.plot <- ggplot(data = molten.r2, aes(x = bin.size, y = value, colour = variable, fill = type)) r2.plot <- r2.plot + geom_line(data = molten.r2) r2.plot <- r2.plot + geom_point(aes(shape = type, colour = variable), size = 4) r2.plot <- r2.plot + scale_x_continuous(breaks = c(50, 200, 1000), trans = "log10") r2.plot <- r2.plot + scale_y_continuous(breaks = pretty_breaks()) r2.plot <- r2.plot + scale_shape_manual(values = c(0, 1, 2)) r2.plot <- r2.plot + labs(title = NULL, x = "Bin Size (kb)", y = "Variance Explained (%)") + theme_bw() r2.plot <- r2.plot + theme(axis.title = element_text(size = 20), axis.text = element_text(size = 16)) r2.plot
```