

What shapes genome-wide diversity?

A case study in *Drosophila melanogaster*

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November 1st 2020

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

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)
```

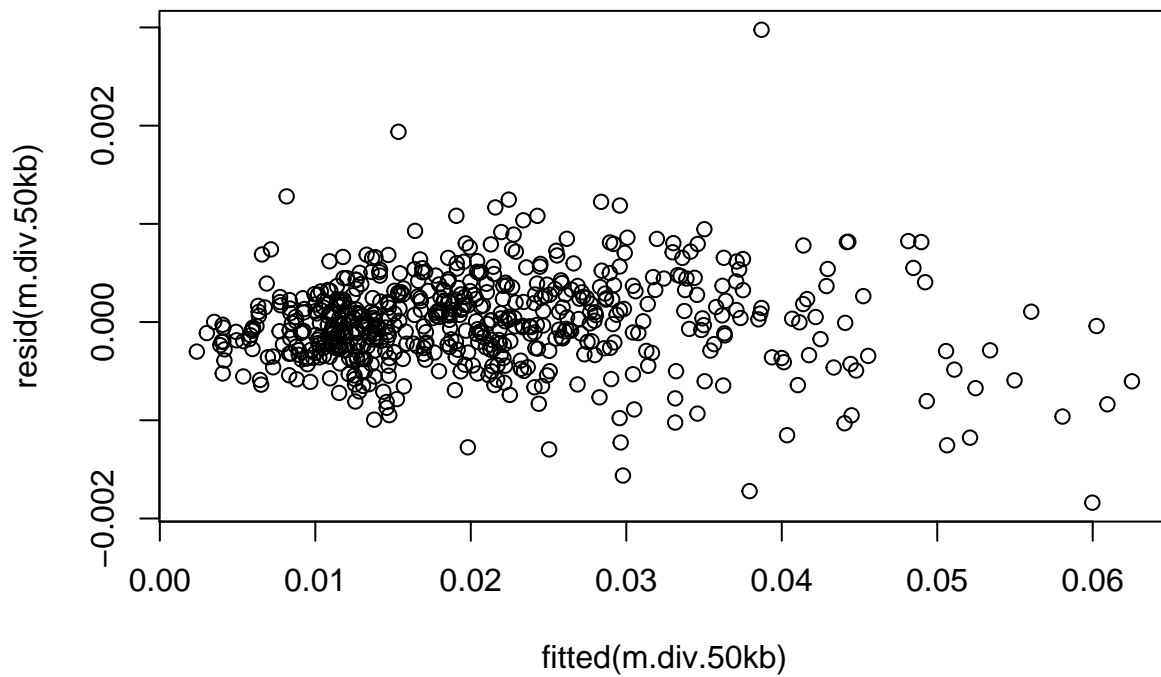
```
sim.lands.50kb$bin <- 1:nrow(sim.lands.50kb)
```

```
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))
```



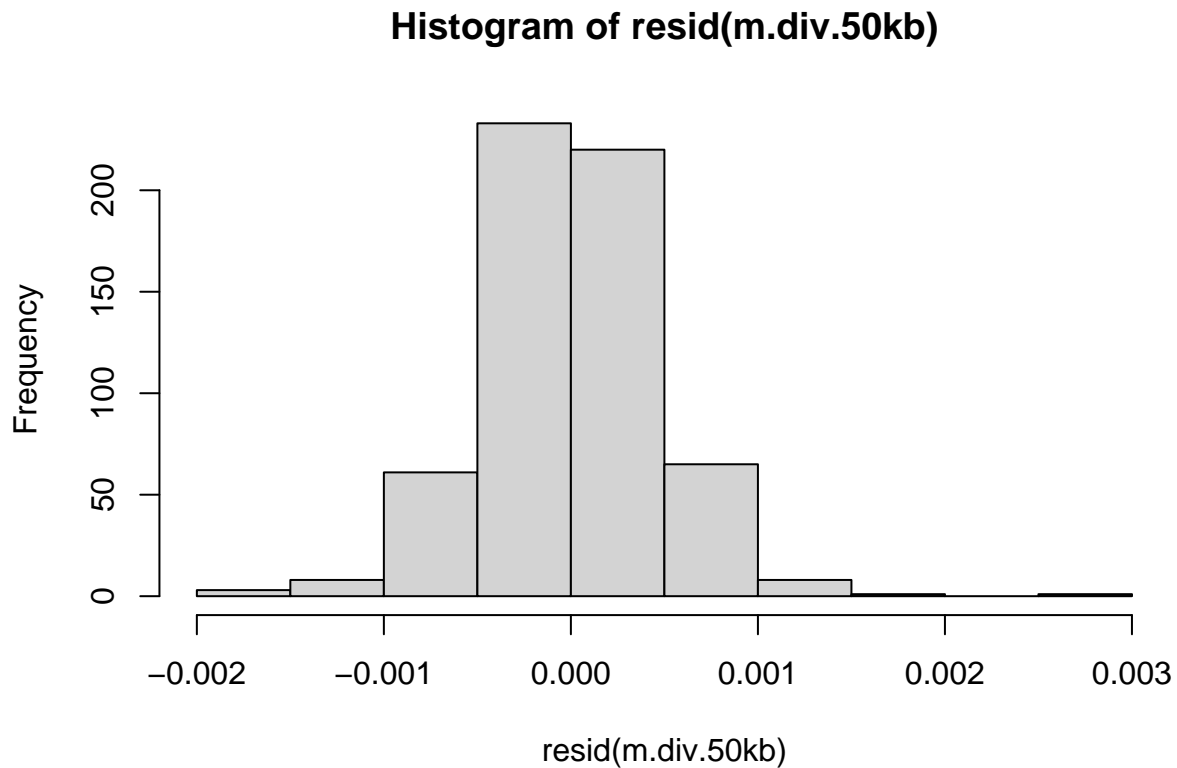
```
dwtest(m.div.50kb)
```

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

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

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

```
hist(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 = "REML")
g.div.50kb.2 <- gls(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
                    data = sim.lands.50kb, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "REML")
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
## -2.955335882 -0.608690299 0.006577071 0.610719662 4.719725049
##
## 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 = TRUE)
rep_2.tmrca.50kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_2/sim.tmrca.50k.map", header = TRUE)

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

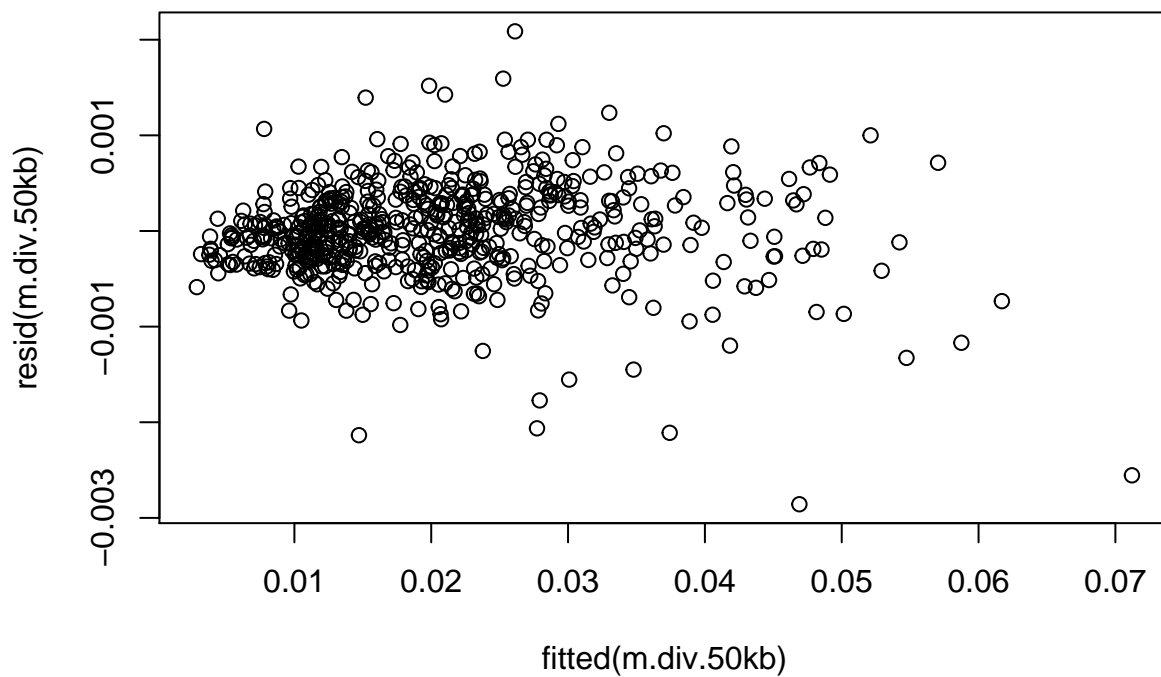
m.div.50kb <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.50kb)
m.div.50kb.2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC + rhoC:tmrcaC, data = sim.lands.50kb)
m.div.50kb.3 <- lm(diversity ~ (thetaC + rhoC + tmrcaC) ^ 2, data = sim.lands.50kb)

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)
```

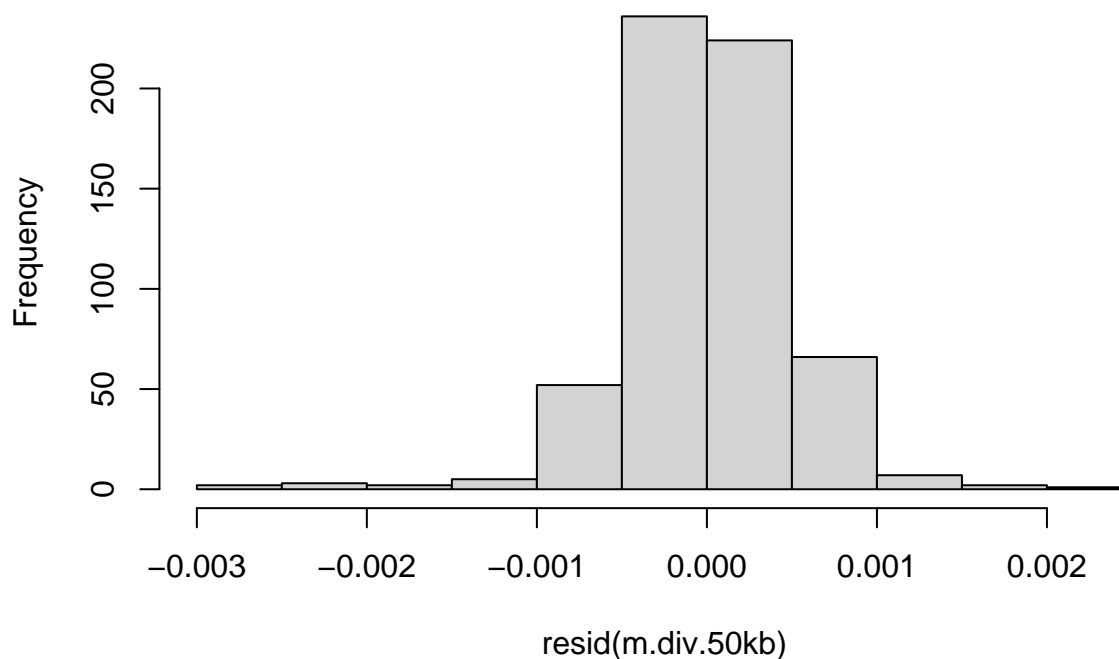
```
##  
## Durbin-Watson test  
##  
## data: m.div.50kb  
## DW = 1.9715, p-value = 0.3445  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.div.50kb  
## HMC = 0.51438, p-value = 0.704
```

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

```

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

sim.lands.50kb <- as.data.frame(cbind(rep_3.pi.50kb$pi, sim.theta.50kb$sim, sim.rho.50kb$sim, rep_3.tmrca.50kb$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 = 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

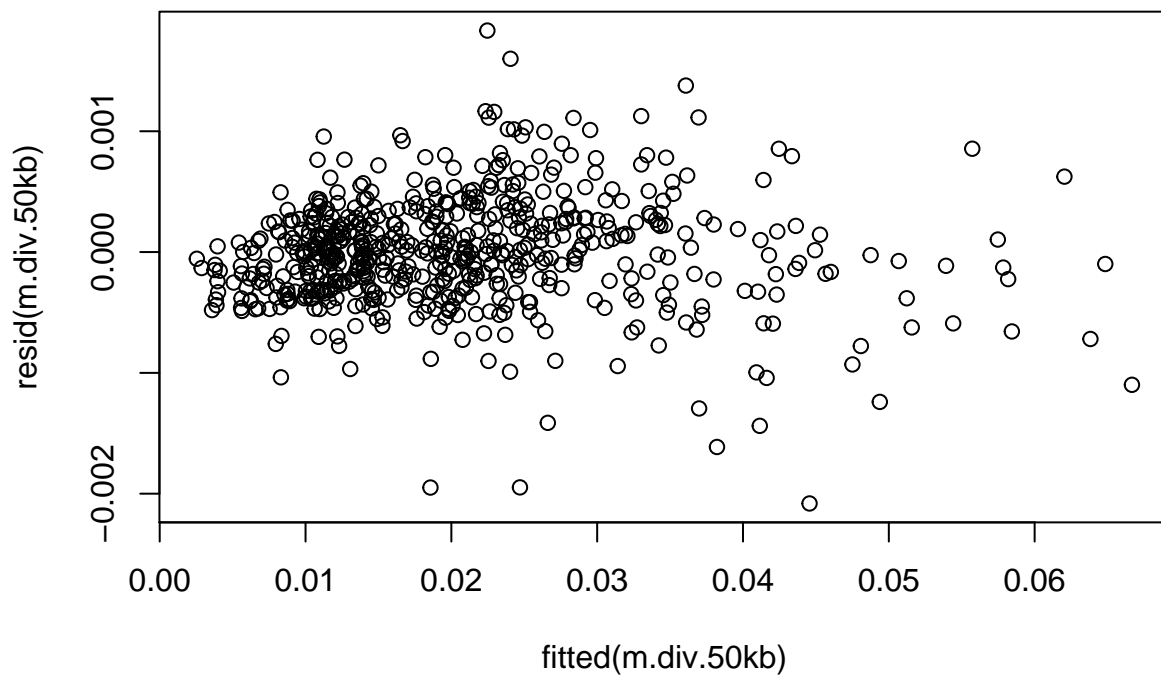
```

```
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.01710883
```

```
# 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)

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



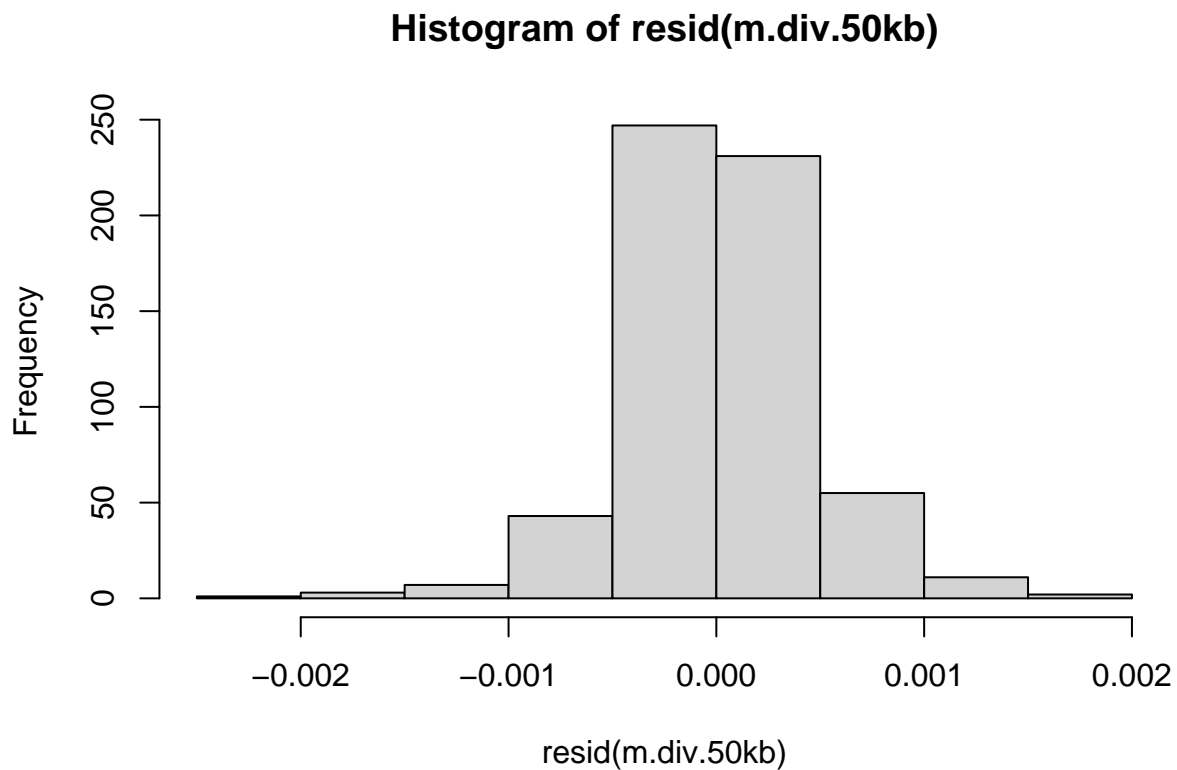
```
dwtest(m.div.50kb)
```

```
##
## 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 = 0.563
```

```
hist(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$sim, rep_4.tmrca.50kb$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 = 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")
```

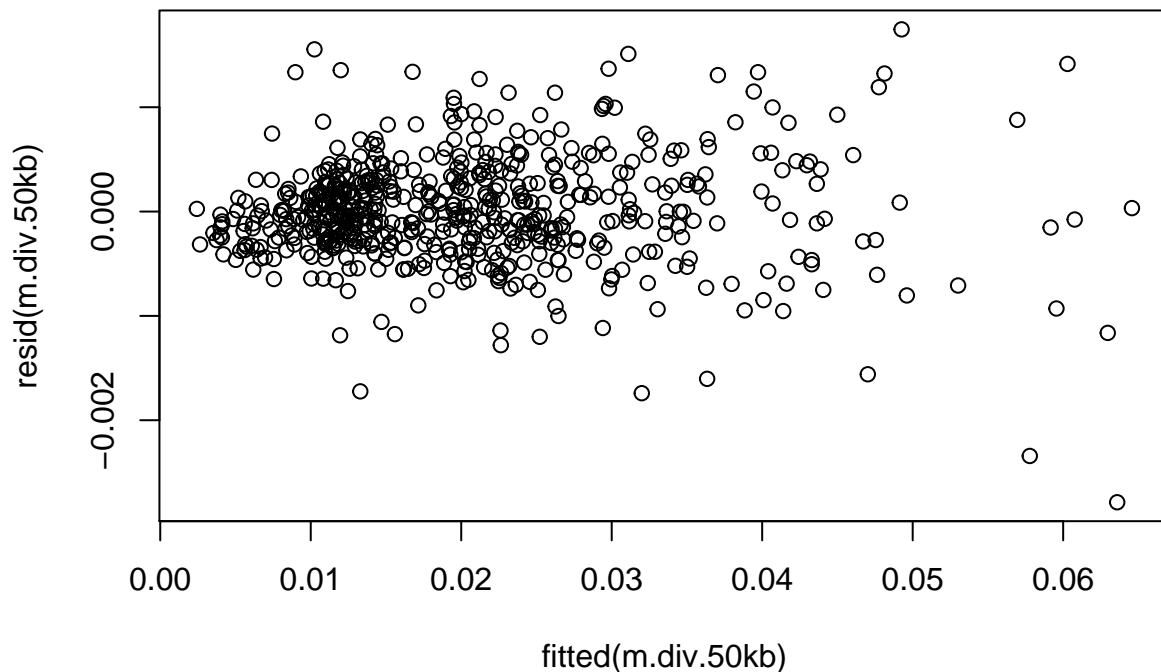
```
##  
## Spearman's rank correlation rho  
##  
## data: rho and tmrca  
## S = 37039432, p-value = 0.4801  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## -0.02887597
```

```
# 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)
```

```
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)
```

```
##
```

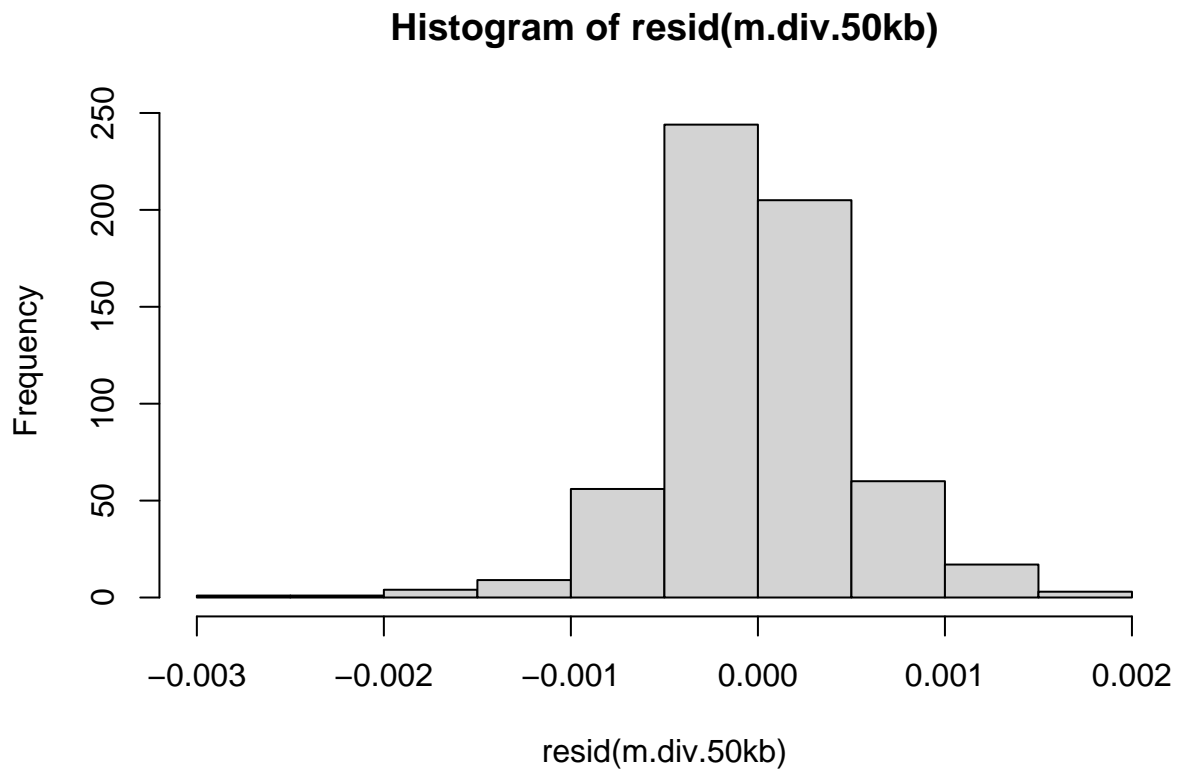


```
## Durbin-Watson test
##
## data: m.div.50kb
## DW = 2.0985, p-value = 0.8779
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##
## Harrison-McCabe test
##
## data: m.div.50kb
## HMC = 0.53836, p-value = 0.911
```

```
hist(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$VarExp[3]) / sum(apiss)
r2.sim.50kb[2, 4] <- anova.diversity$VarExp[1] / sum(apiss)
r2.sim.50kb[3, 4] <- anova.diversity$VarExp[2] / sum(apiss)
r2.sim.50kb[4, 4] <- anova.diversity$VarExp[3] / sum(apiss)
r2.sim.50kb[5, 4] <- anova.diversity$VarExp[4] / sum(apiss)
```

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

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

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

# 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)

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

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

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

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

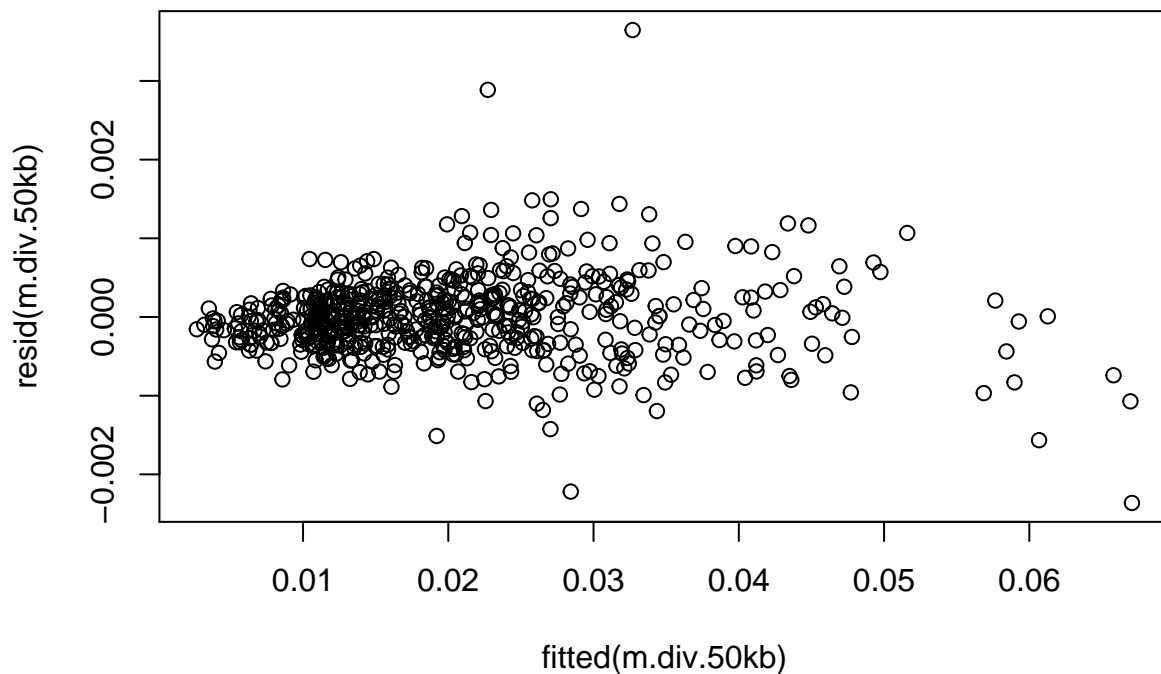
```
##
## Spearman's rank correlation rho
##
```

```
## 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)

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



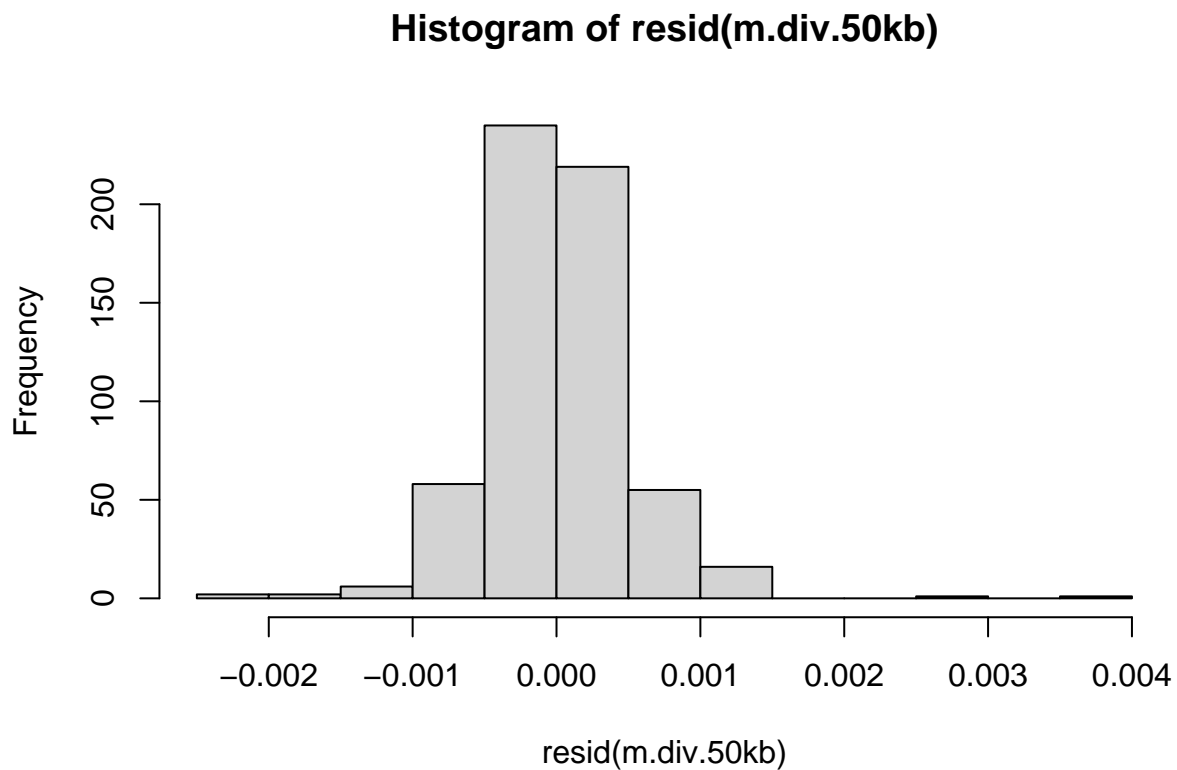
```
dwtest(m.div.50kb)
```

```
##
## 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 = 0.1
```

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

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")
```

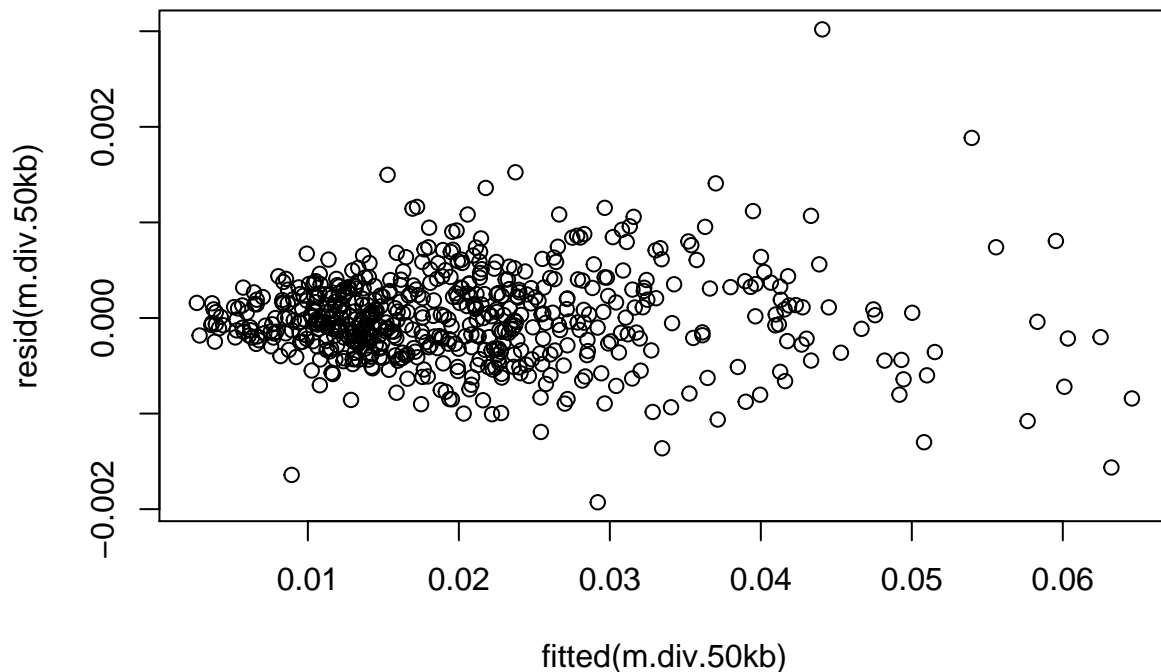
```
##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 36196758, p-value = 0.8936
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## -0.005468293
```

```
# 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)
```

```
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)
```

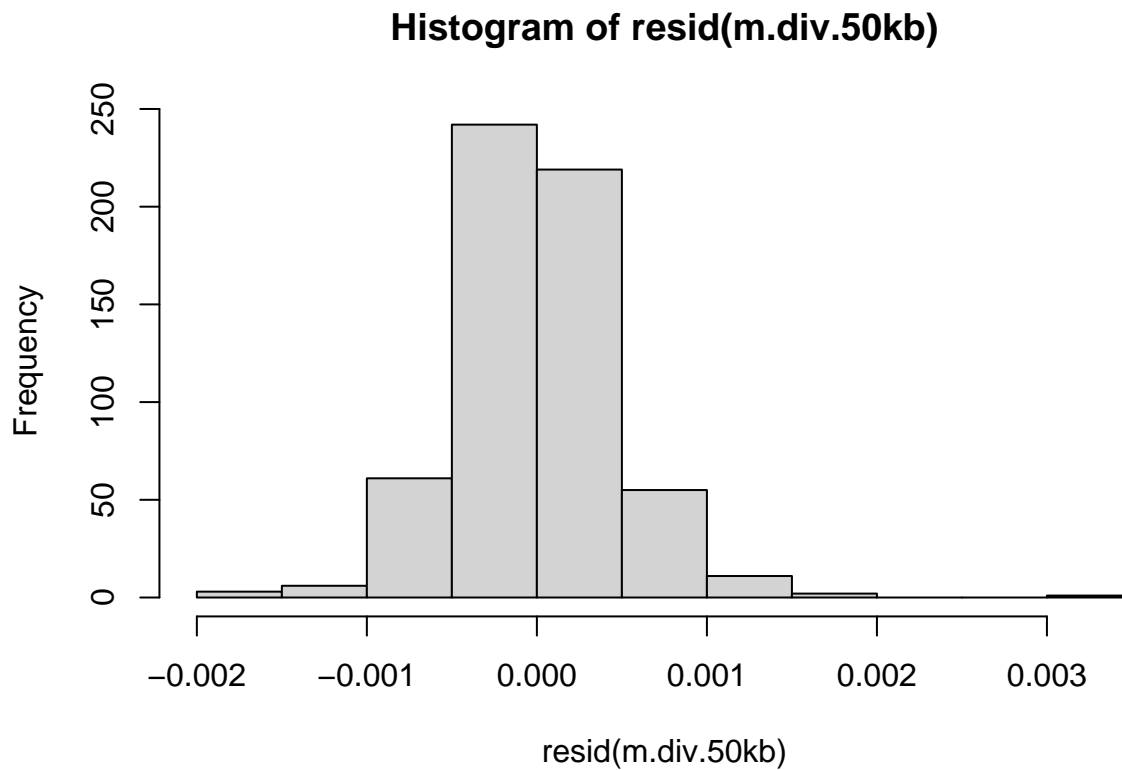
```
##
```

```
## 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 = 0.232
```

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

sim.lands.50kb <- as.data.frame(cbind(rep_8.pi.50kb$pi, sim.theta.50kb$sim, sim.rho.50kb$sim, rep_8.tmrca.50kb$tmrca))
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 = c(0.0101175988992442, 0.0101175988992442, :
## 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 = c(0.0101175988992442, 0.0101175988992442, :  
## 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")
```

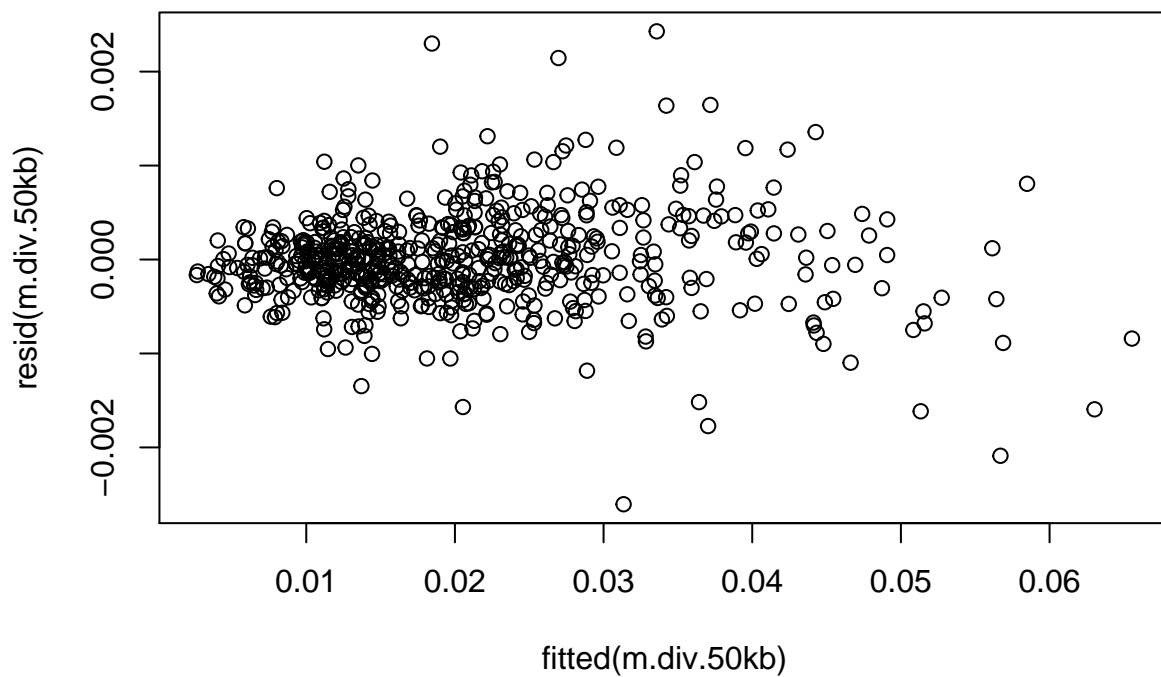
```
##  
## Spearman's rank correlation rho  
##  
## data: rho and tmrca  
## S = 37073930, p-value = 0.4656  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## -0.02983425
```

```
# 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)
```

```
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)
```

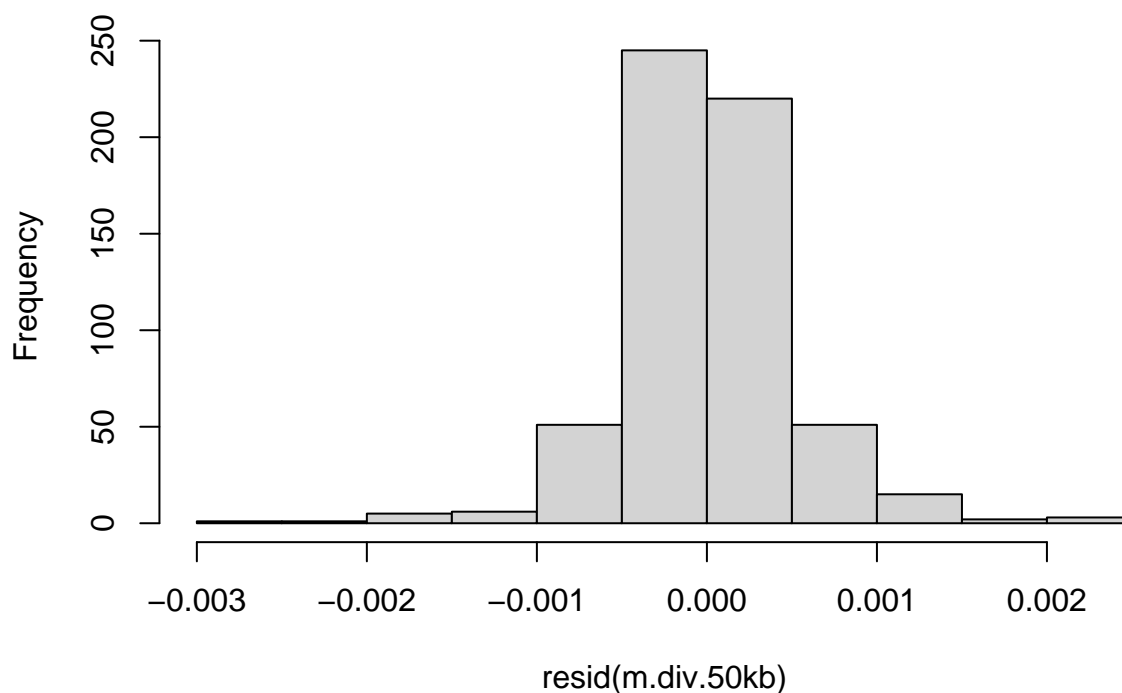
```
##  
## Durbin-Watson test  
##  
## data: m.div.50kb  
## DW = 2.0323, p-value = 0.6384  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.div.50kb  
## HMC = 0.48525, p-value = 0.325
```

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

sim.lands.50kb <- as.data.frame(cbind(rep_9.pi.50kb$pi, sim.theta.50kb$sim, sim.rho.50kb$sim, rep_9.tmrca.50kb$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 = 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

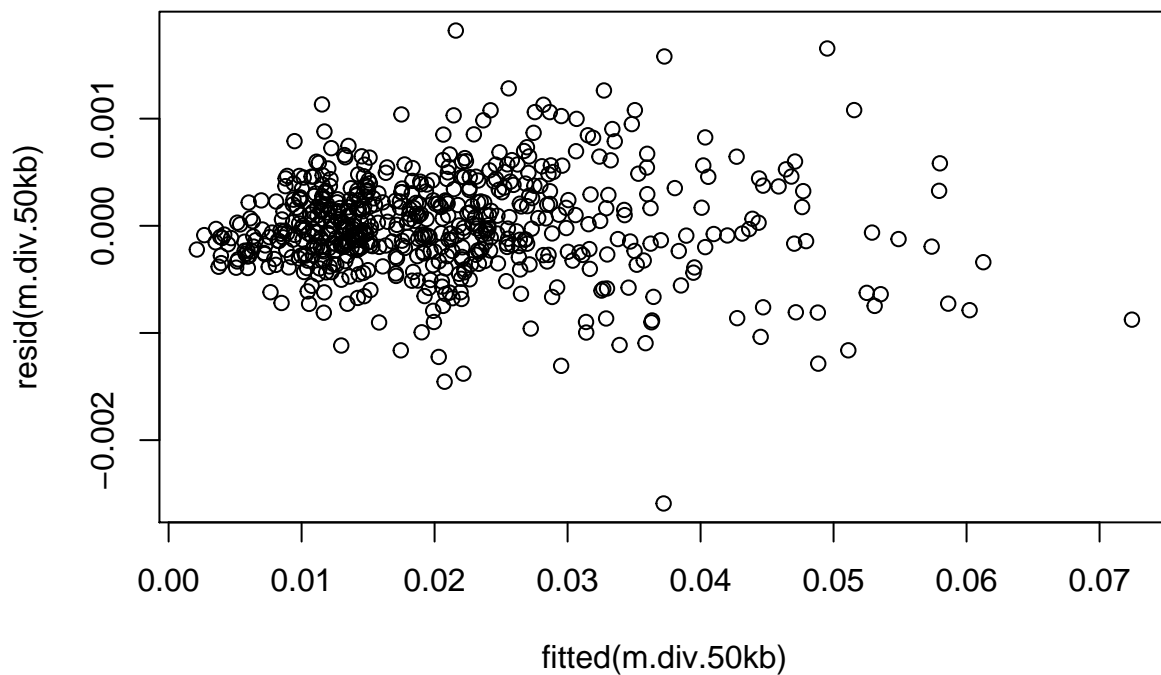
```

```
## 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)

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



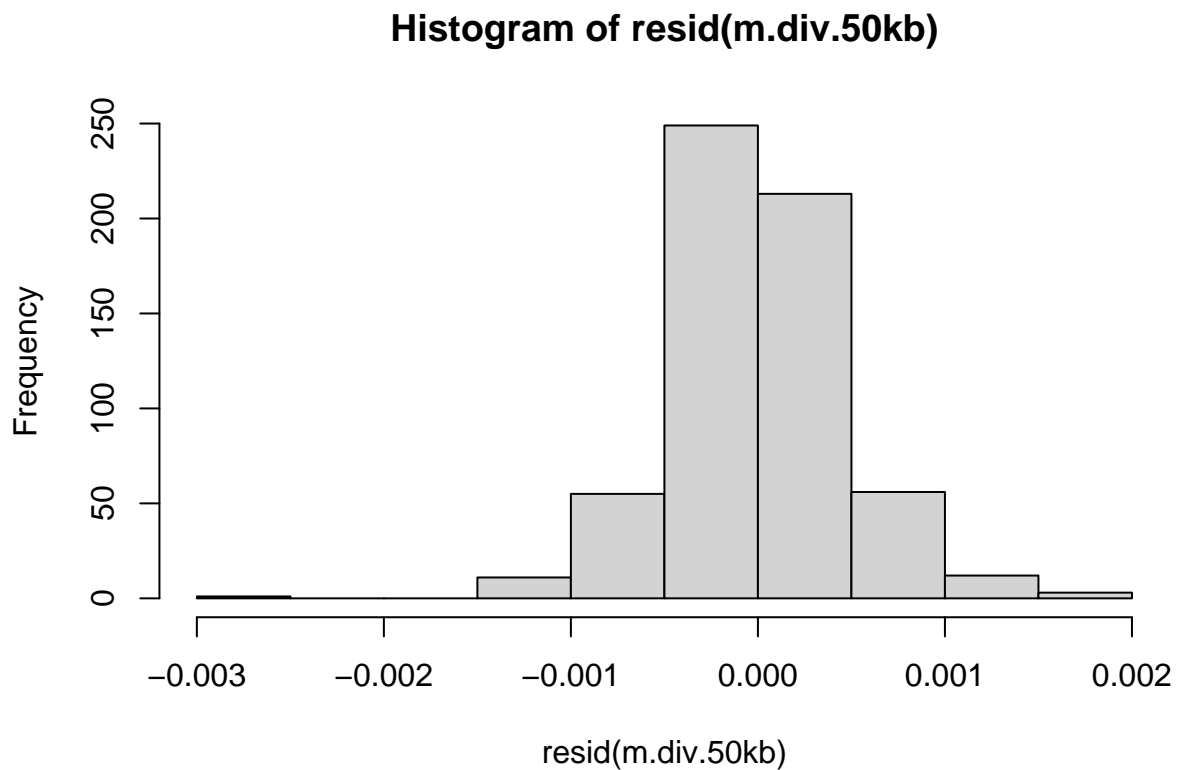
```
dwtest(m.div.50kb)
```

```
##
## 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 = 0.975
```

```
hist(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")
```

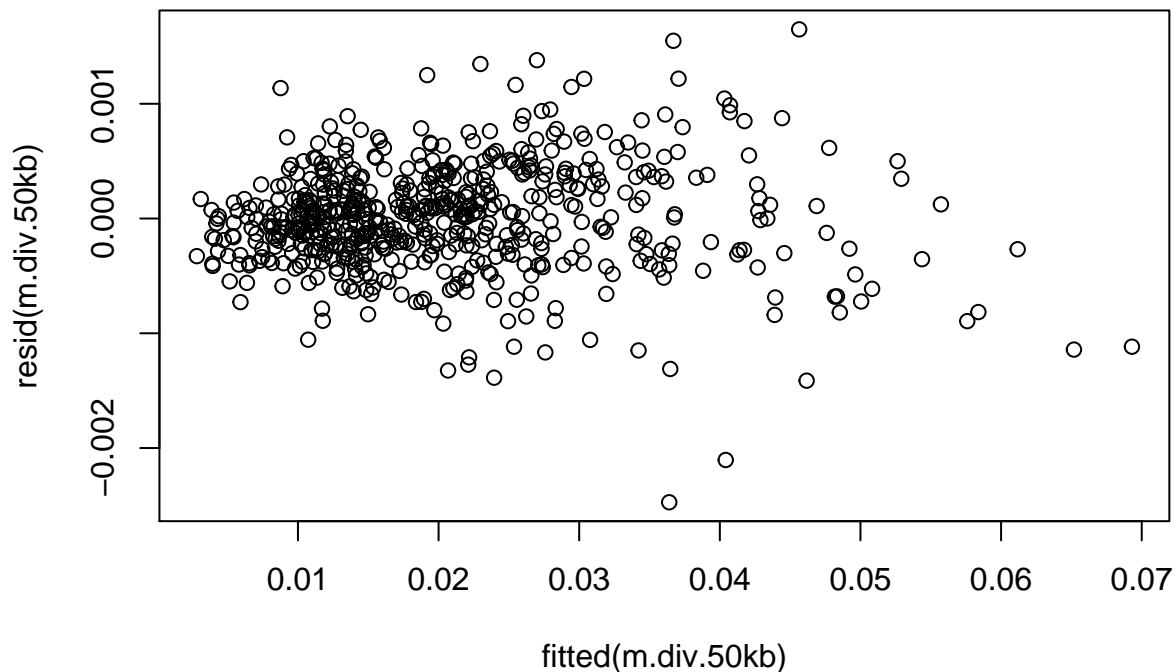
```
##  
## Spearman's rank correlation rho  
##  
## data: rho and tmrca  
## S = 36687846, p-value = 0.6403  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## -0.01910966
```

```
# 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)
```

```
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)
```

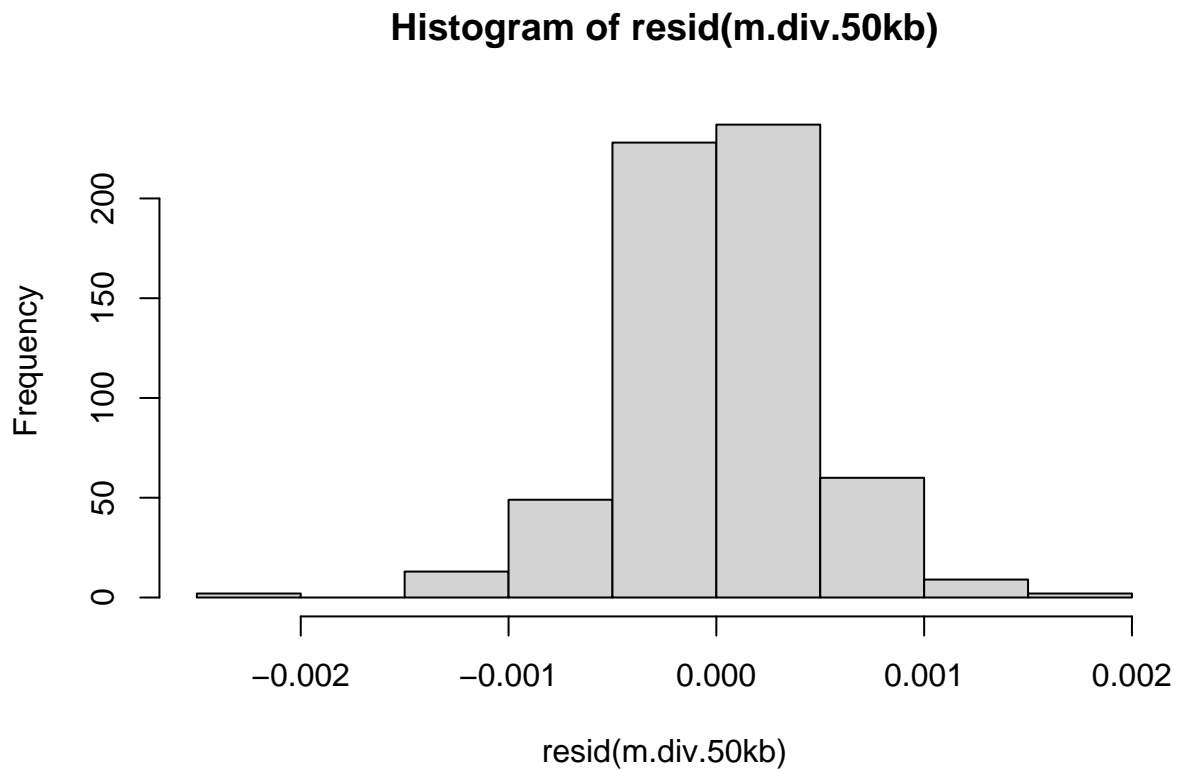
```
##
```

```
## 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 = 0.01
```

```
hist(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))
```

1.2 200 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$sim, rep_1.tmrca.200kb$tmrca))
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
```

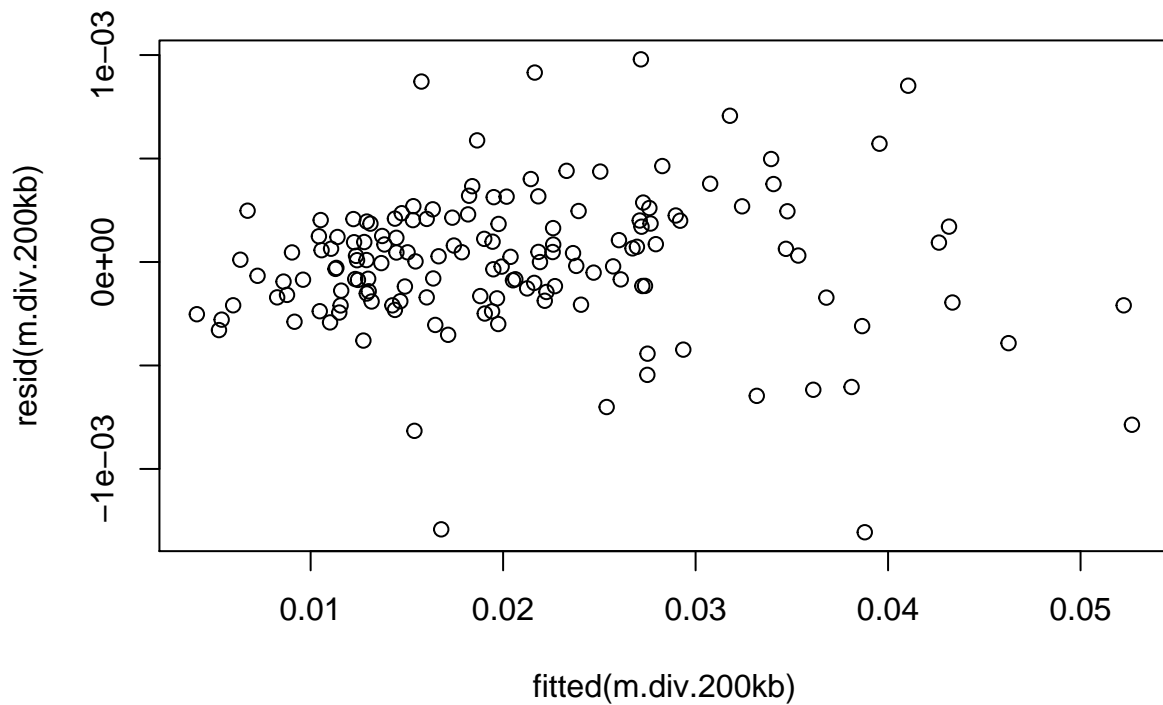
```
cor.test(~rho+tmrca, data = sim.lands.200kb, method = "spearman")
```

```
##
## 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)

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)
```

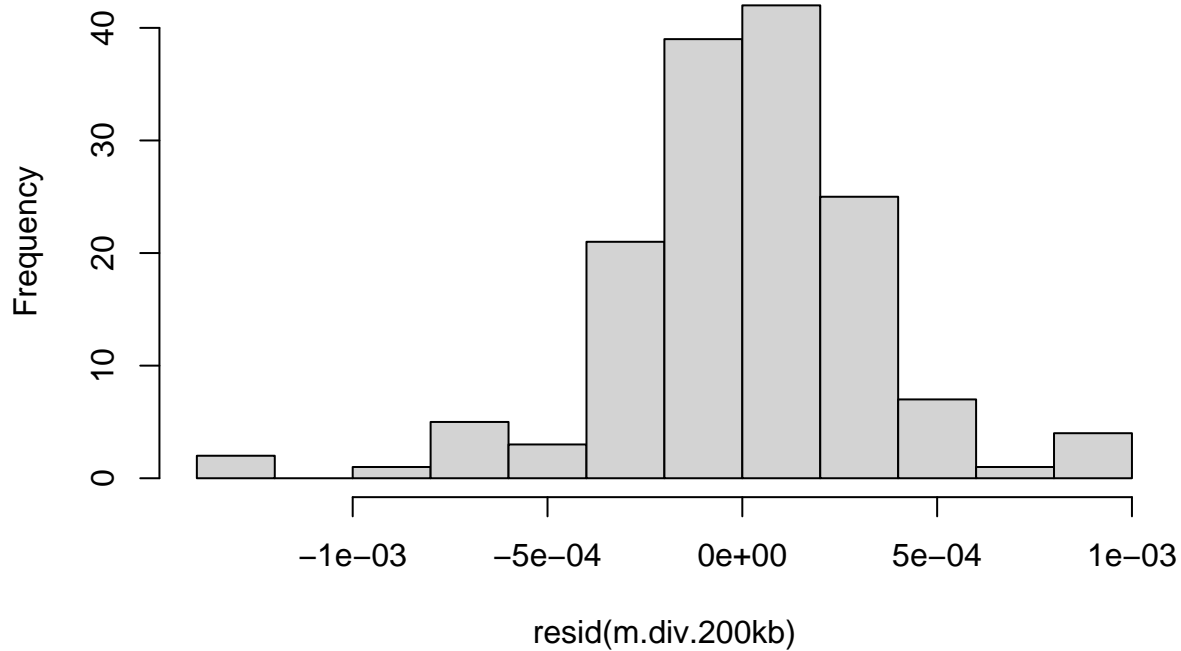
```
##  
## Durbin-Watson test  
##  
## data: m.div.200kb  
## DW = 1.9751, p-value = 0.4234  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.div.200kb  
## HMC = 0.49982, p-value = 0.515
```

```
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$sim, rep_2.tmrca.200kb$tmrca),
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

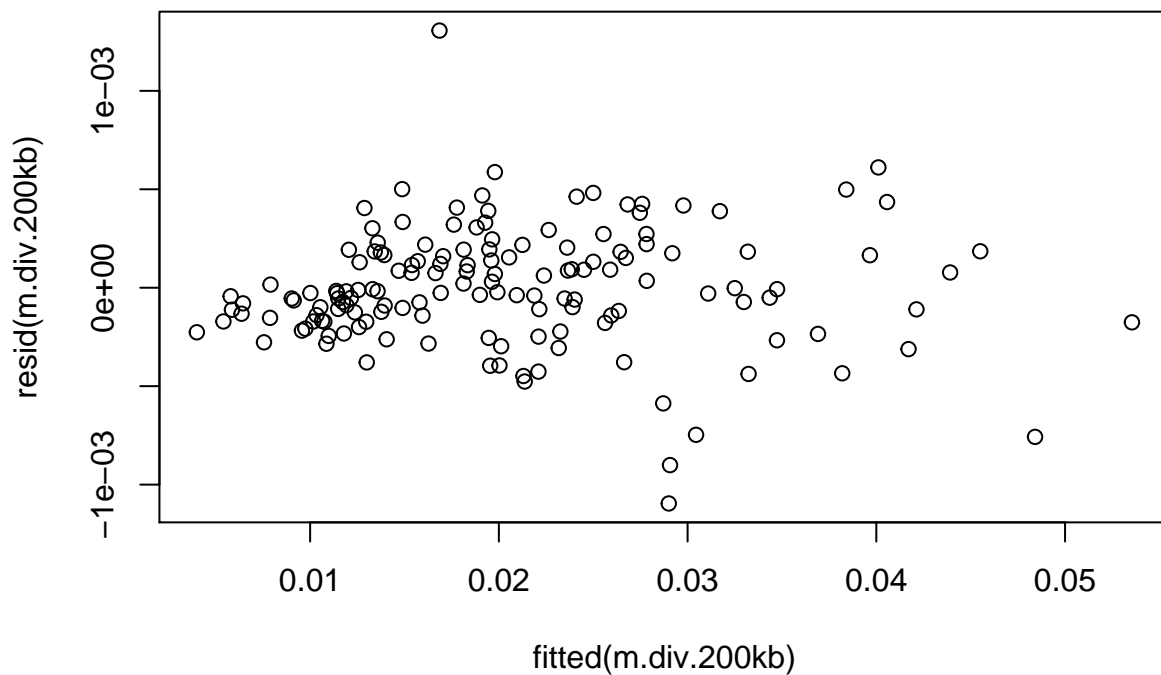
```

```
## 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)

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)
```

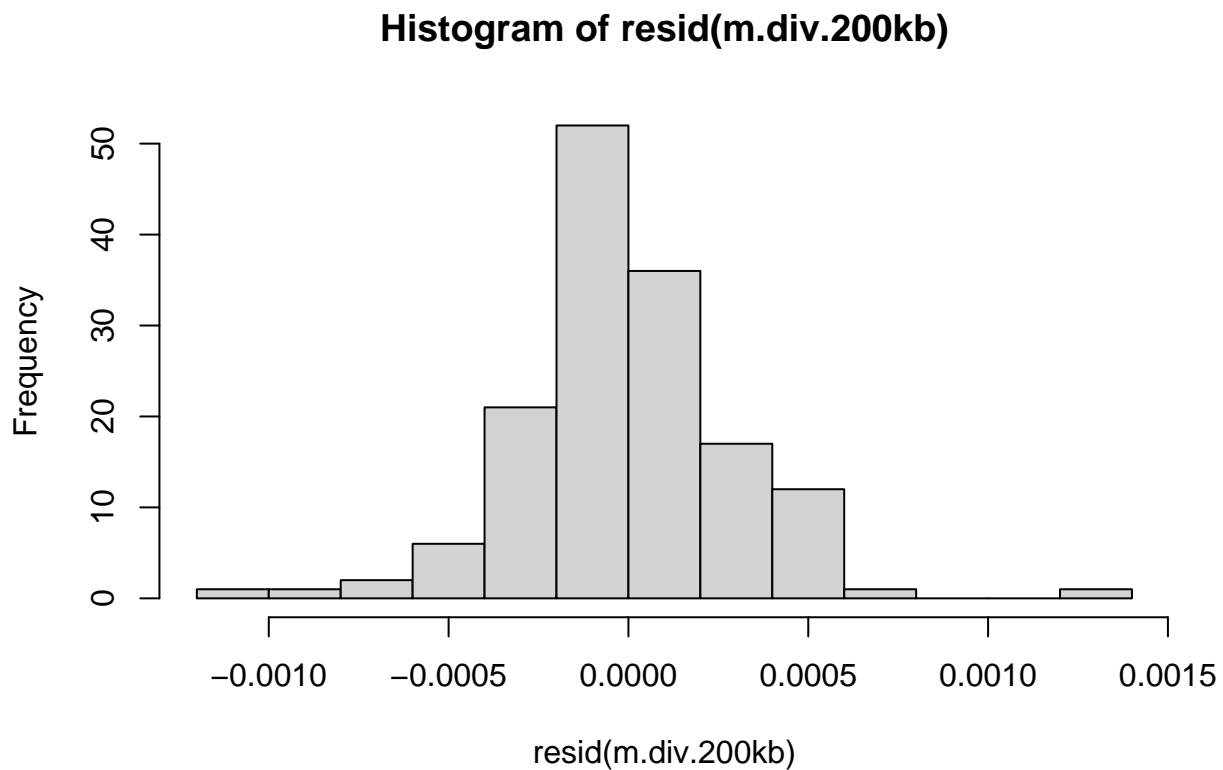
```
##
## Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.5928, p-value = 0.005174
## alternative hypothesis: true autocorrelation is greater than 0
```



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

```
##  
## Harrison-McCabe test  
##  
## data: m.div.200kb  
## HMC = 0.59119, p-value = 0.924
```

```
hist(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", head=1)
rep_3.tmrca.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_3/sim.tmrca.200k.map", header=1)

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

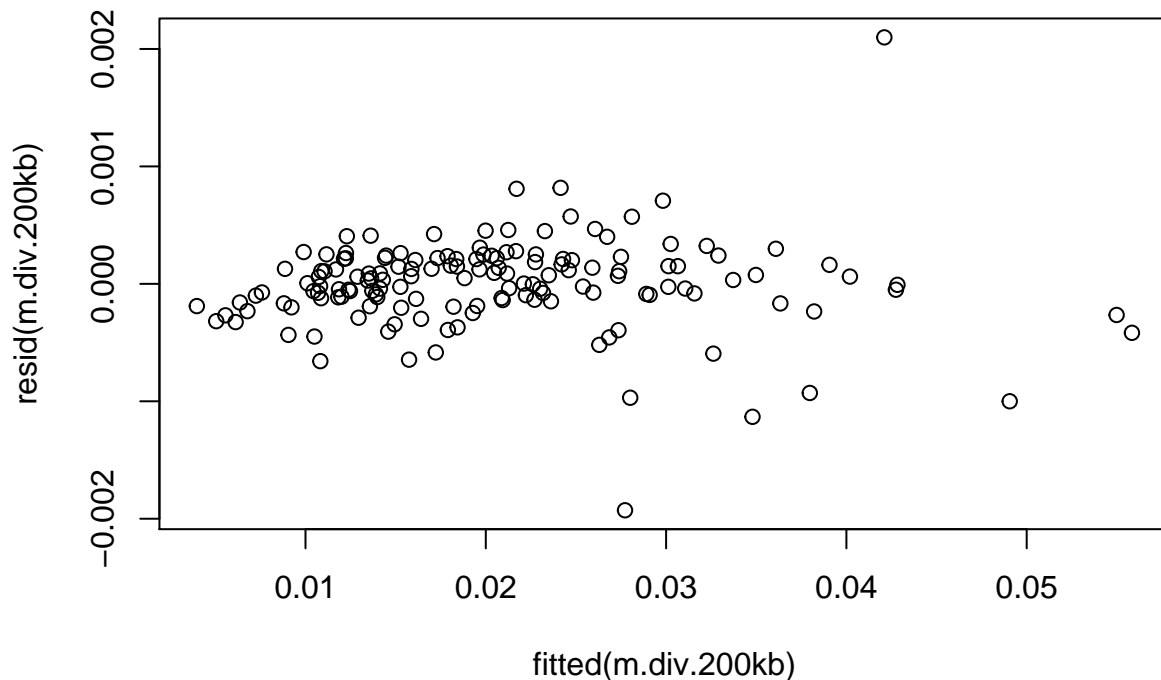
```
##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 594376, p-value = 0.4902
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.05671541
```

```
# 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)
```

```
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)
```

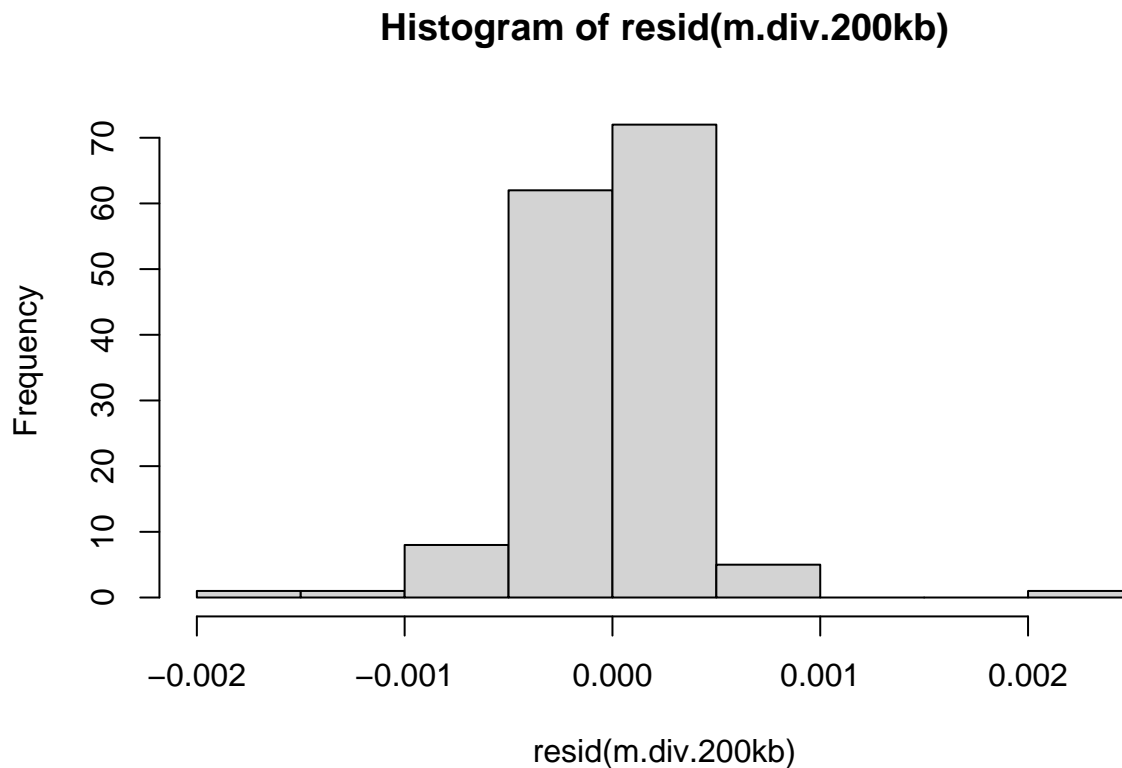
```
##
```

```
## 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 = 0.236
```

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

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

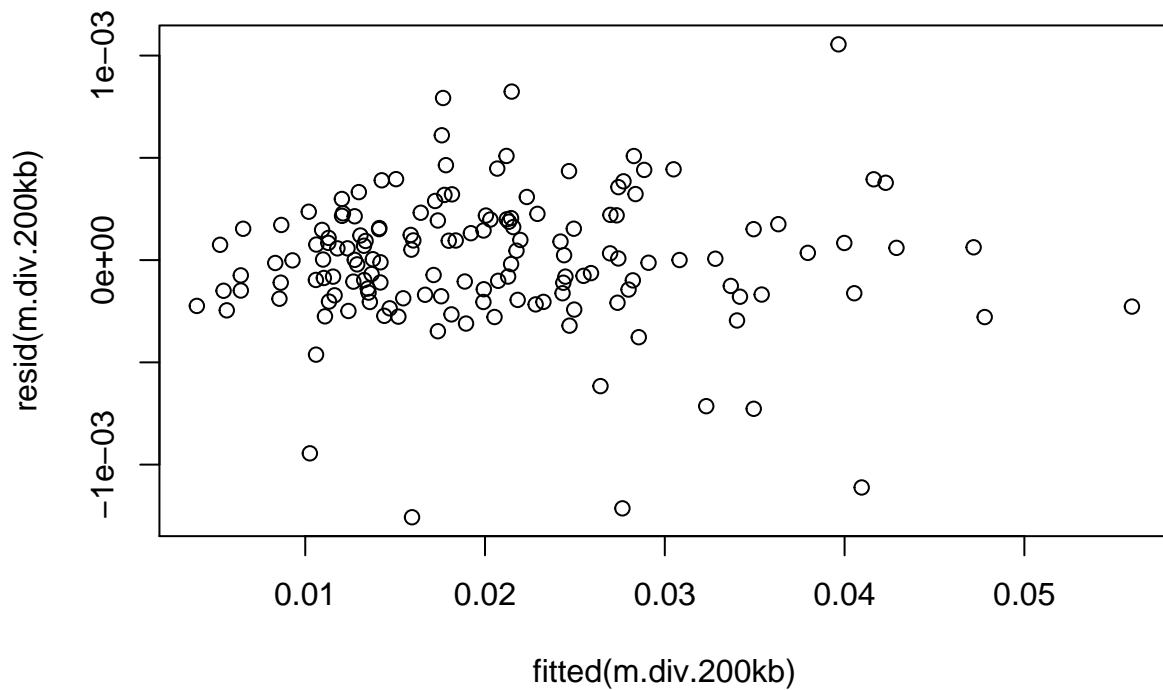
```
cor.test(~rho+tmrca, data = sim.lands.200kb, method = "spearman")
```

```
##
## 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)

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)
```

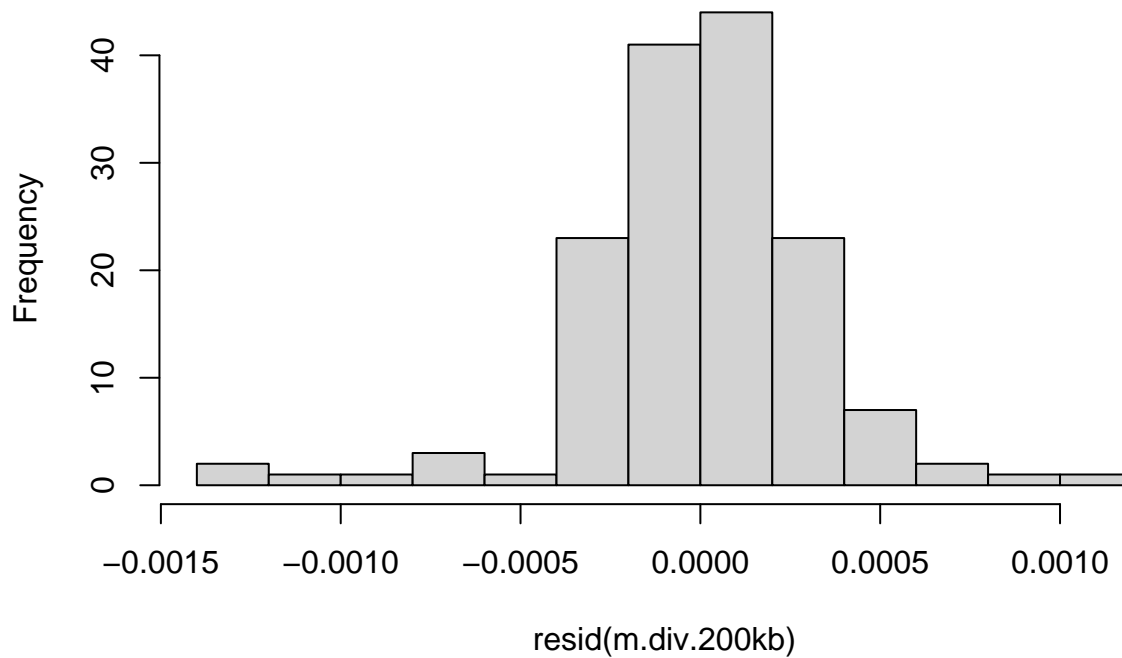
```
##
## Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.9887, p-value = 0.4477
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##
## Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.4058, p-value = 0.052
```

```
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       0.0244436  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$sim, rep_5.tmrca.200kb$tmrca),
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

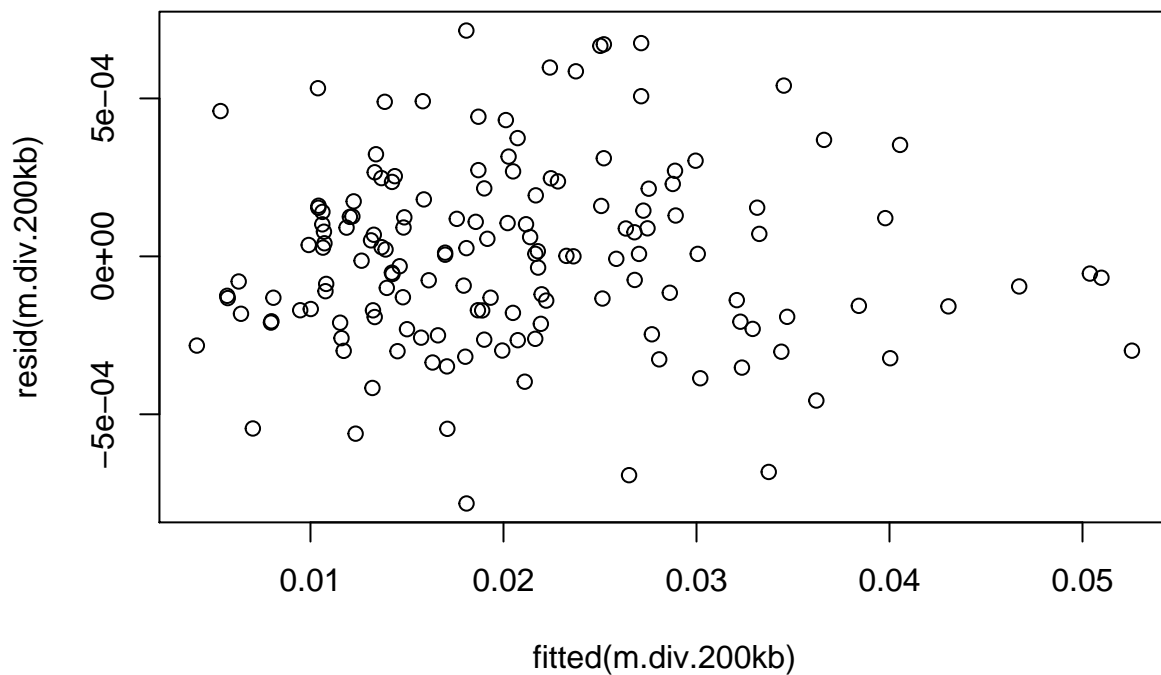
```

```
## 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)

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



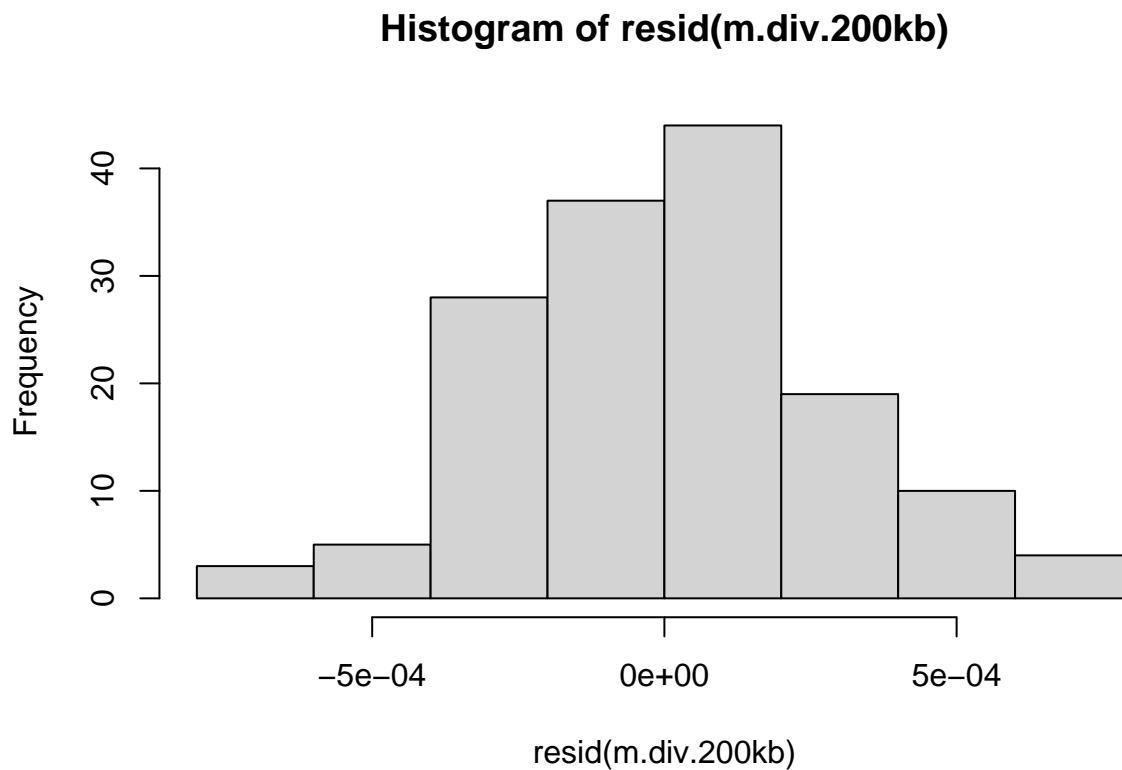
```
dwtest(m.div.200kb)
```

```
##
## 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 = 0.098
```

```
hist(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$VarExp[3] + anova.diversity$VarExp[4]) / anova.diversity$VarExp[5]
r2.sim.200kb[2, 5] <- anova.diversity$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, as.is=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, as.is=TRUE)

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

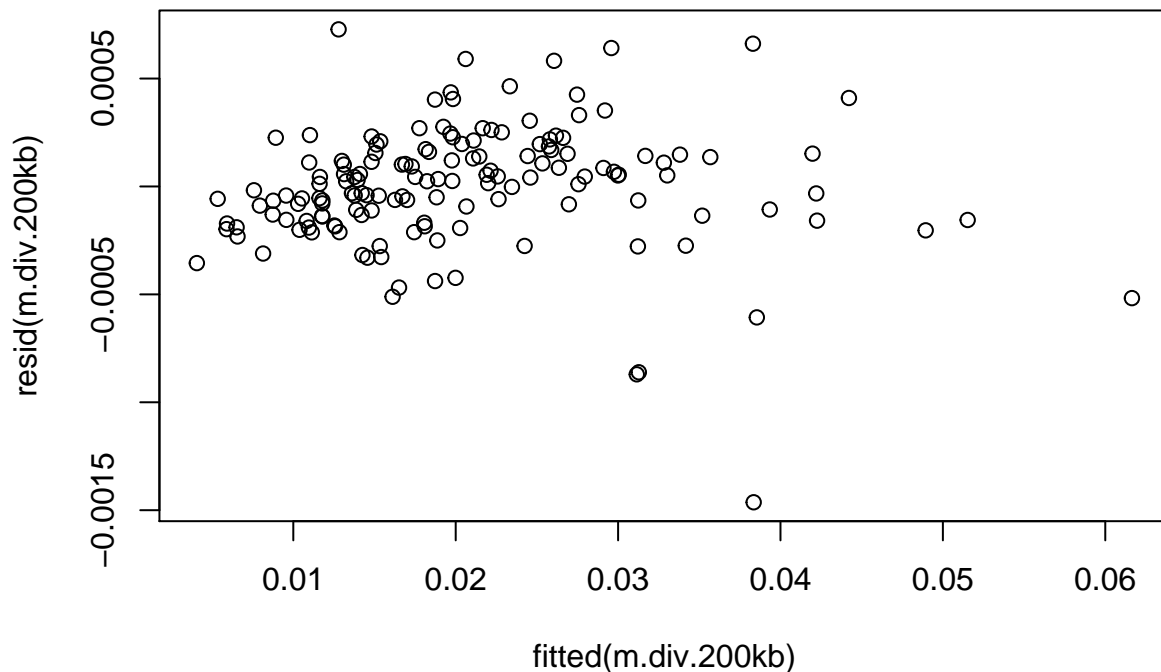
```
##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 606554, p-value = 0.3401
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.07836615
```

```
# 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)
```

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



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

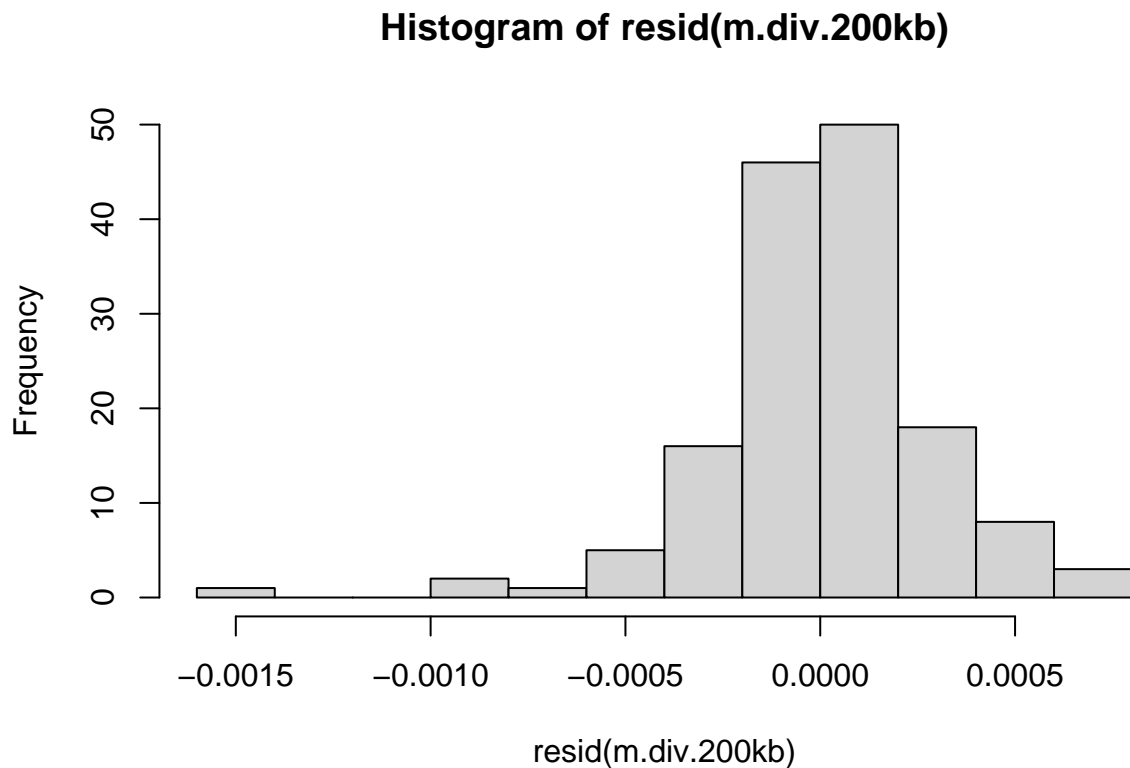
```
##
```

```
## 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 = 0.948
```

```
hist(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$VarExp[3]) / anova.diversity$VarExp[4]
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, as.is = 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, as.is = TRUE)

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

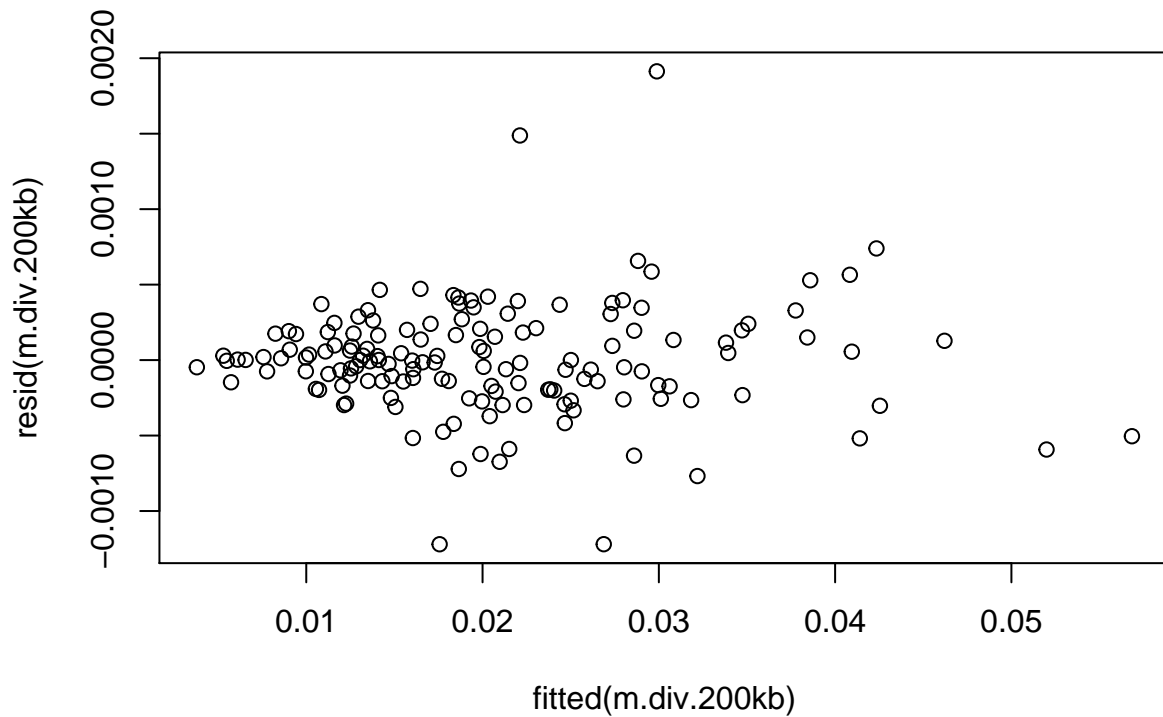
```
cor.test(~rho+tmrca, data = sim.lands.200kb, method = "spearman")
```

```
##
## 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)

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)
```

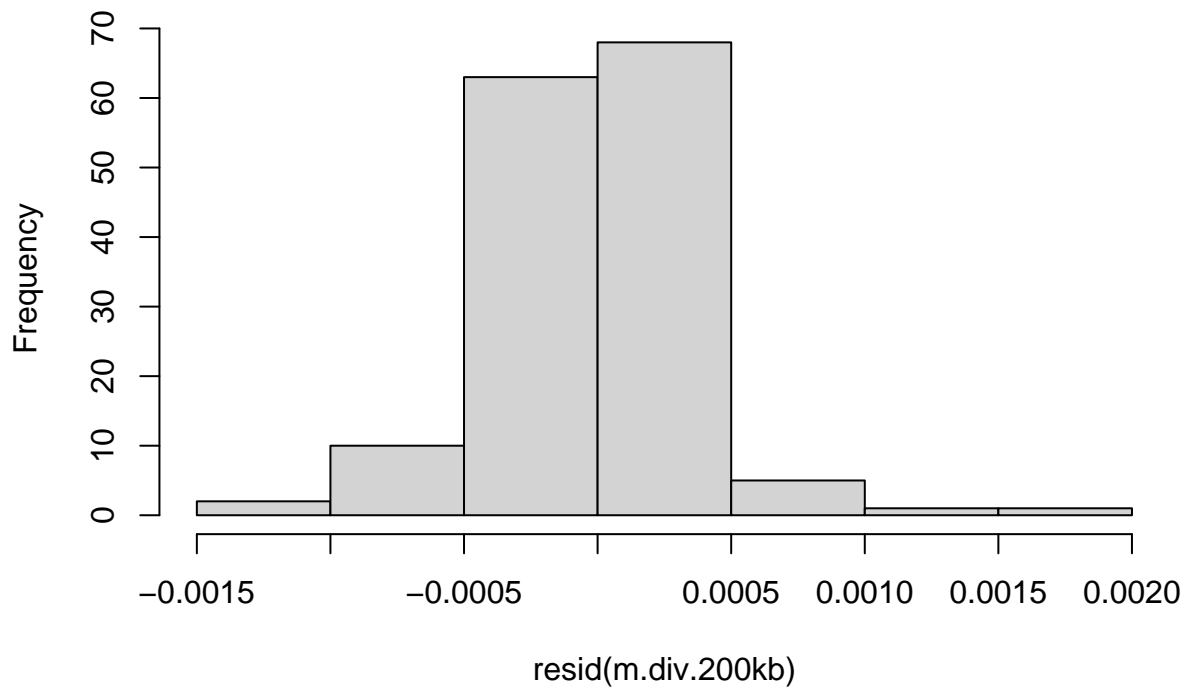
```
##
## Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.9801, p-value = 0.4361
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##
## Harrison-McCabe test
##
## data: m.div.200kb
## HMC = 0.40495, p-value = 0.035
```

```
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$sim, rep_8.tmrca.200kb$tmrca))
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

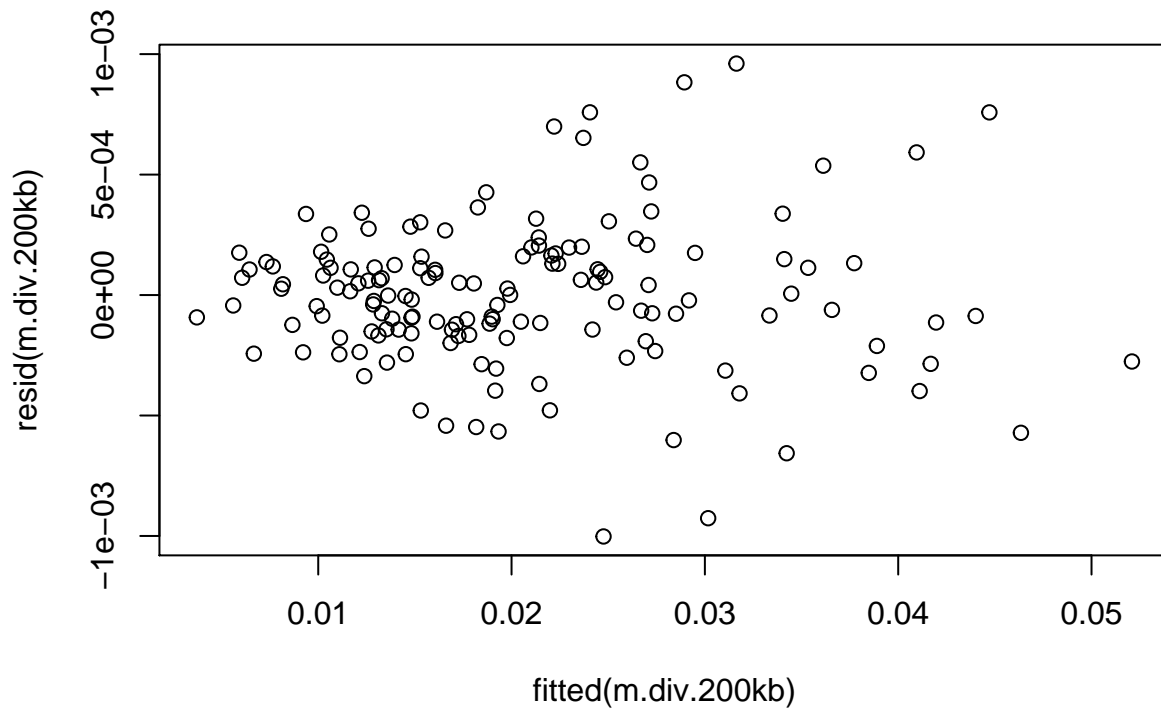
```

```
## 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)

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



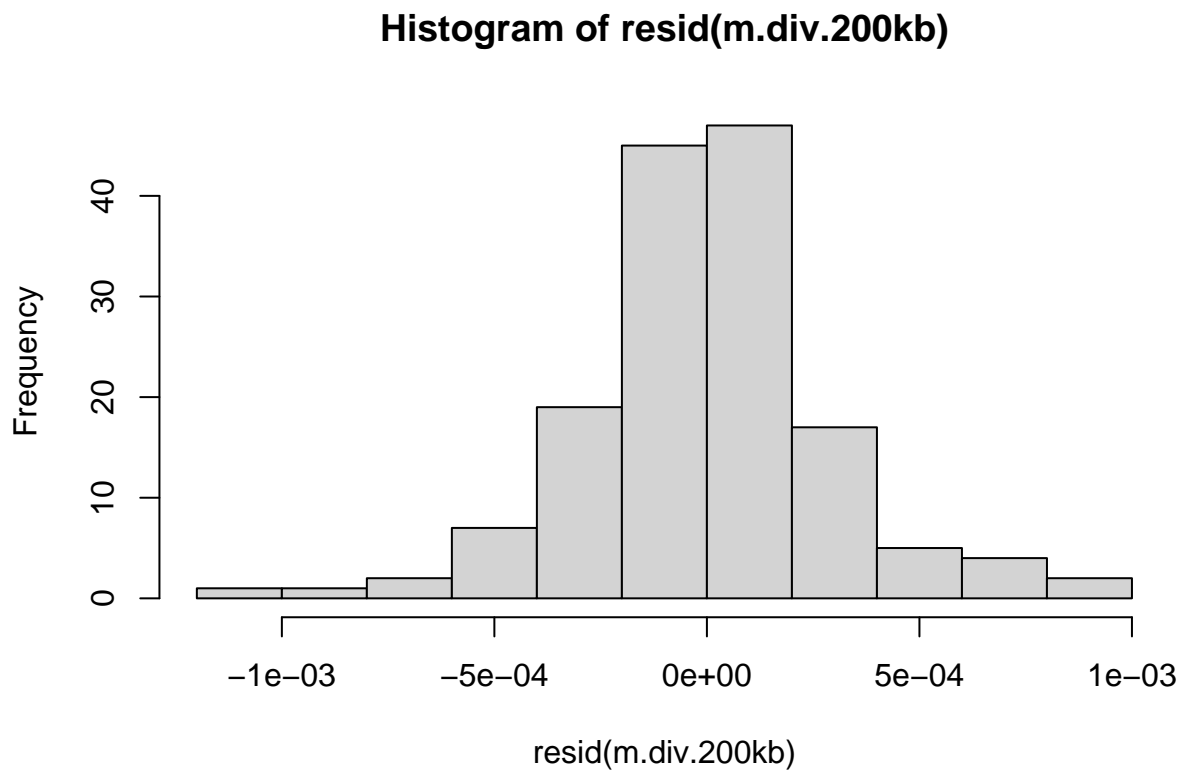
```
dwtest(m.div.200kb)
```

```
##
## 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 = 0.775
```

```
hist(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$VarExp[3] + anova.diversity$VarExp[4]) / sum(apiss)
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", header=TRUE, as.is=TRUE)
rep_9.tmrca.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_9/sim.tmrca.200k.map", header=TRUE, as.is=TRUE)

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

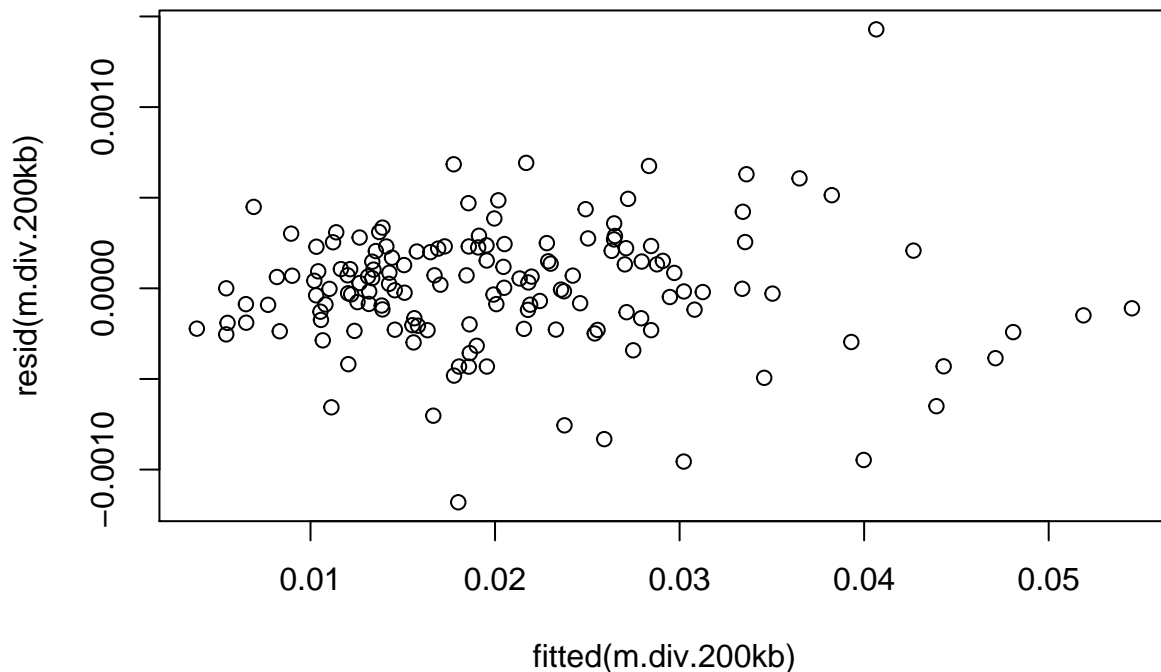
```
##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 597682, p-value = 0.4463
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.062593
```

```
# 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)
```

```
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)
```

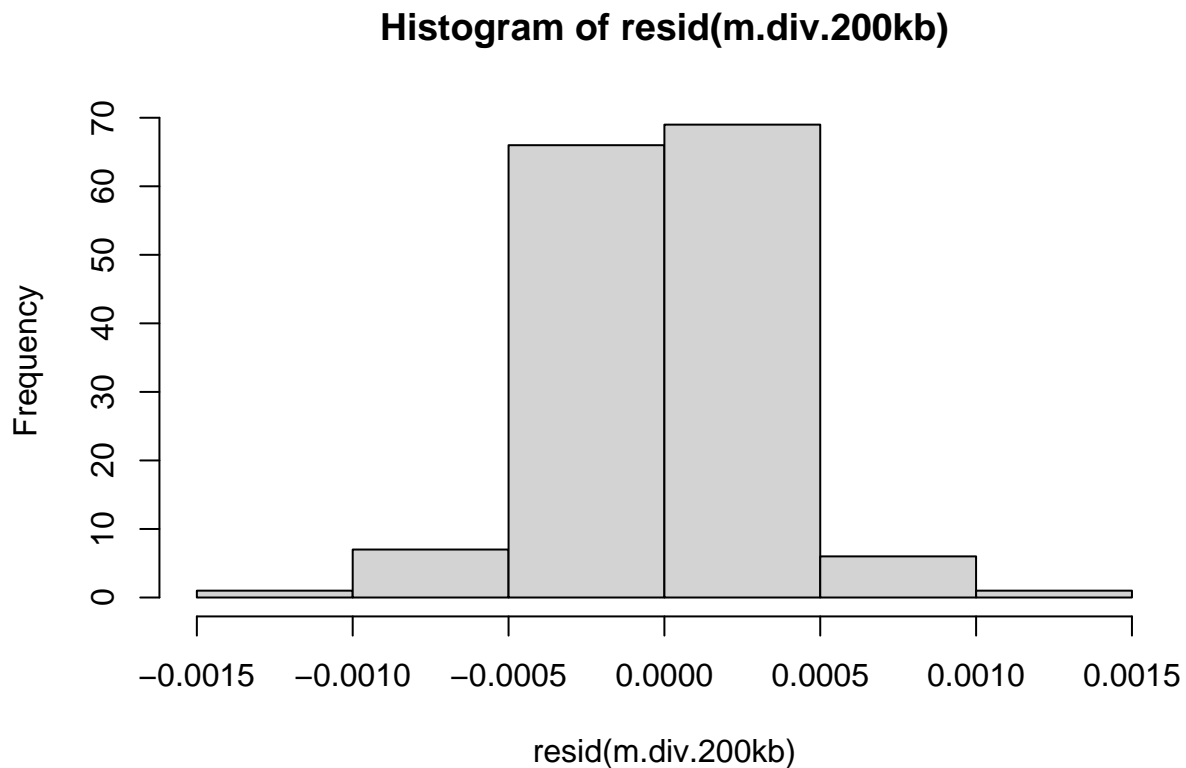
```
##
```

```
## 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 = 0.091
```

```
hist(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", 1
rep_10.tmrca.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_10/sim.tmrca.200k.map", head=1)

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

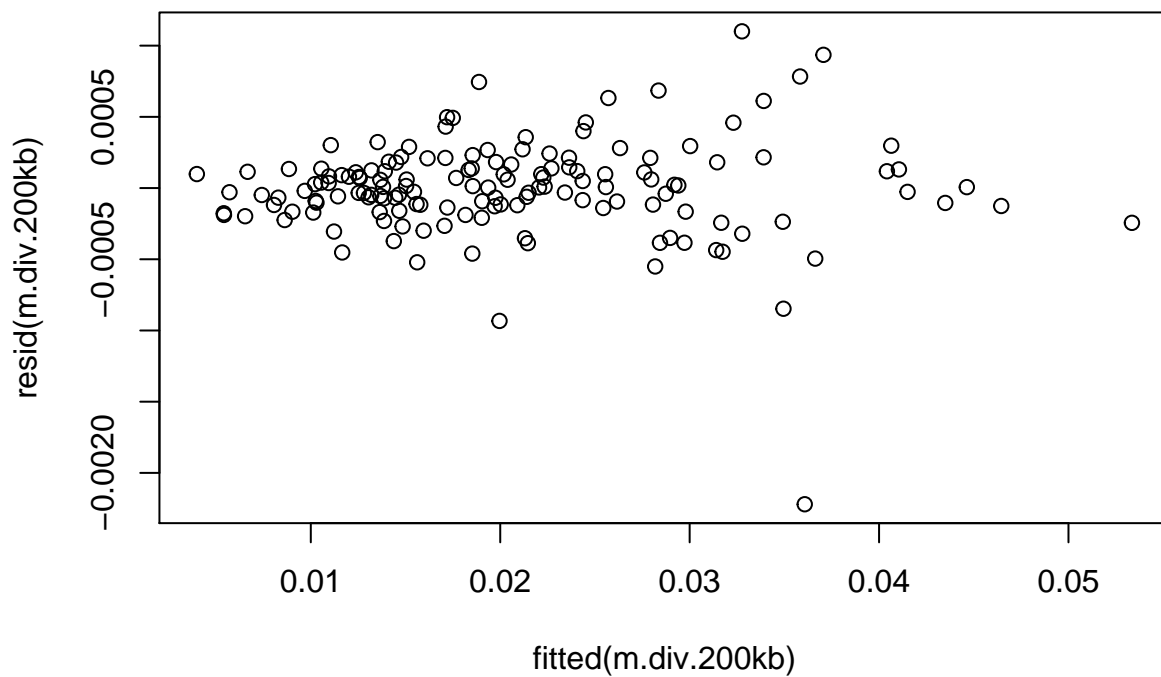
```
cor.test(~rho+tmrca, data = sim.lands.200kb, method = "spearman")
```

```
##
## 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)

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)
```

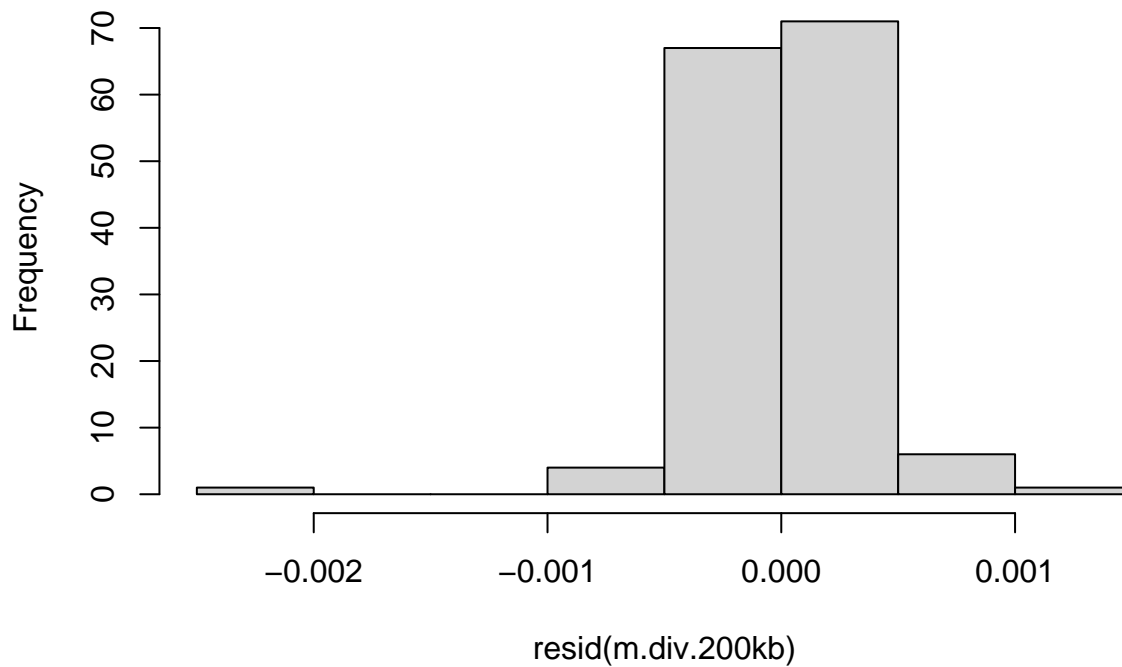
```
##  
## Durbin-Watson test  
##  
## data: m.div.200kb  
## DW = 2.1646, p-value = 0.8354  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.div.200kb  
## HMC = 0.41358, 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
## -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$VarExp[3] + anova.diversity$VarExp[4]) * 100
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))

```

1.3 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
```

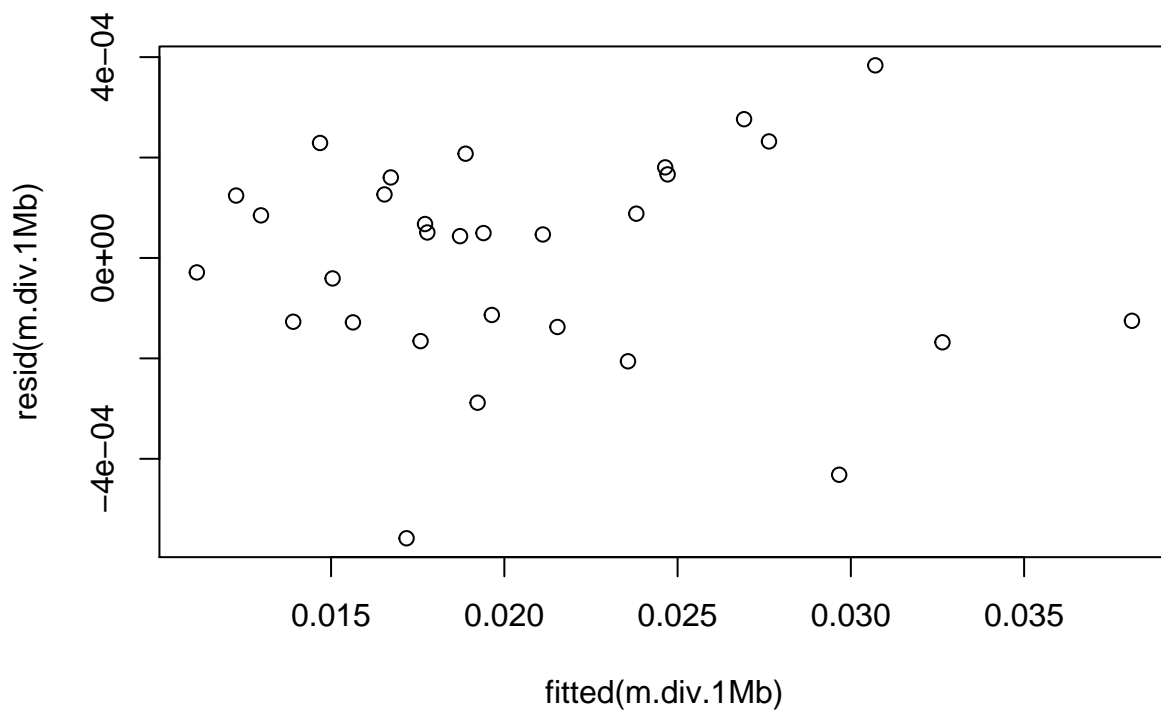
```
cor.test(~rho+tmrca, data = sim.lands.1Mb, method = "spearman")
```

```
##
## 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)

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)
```

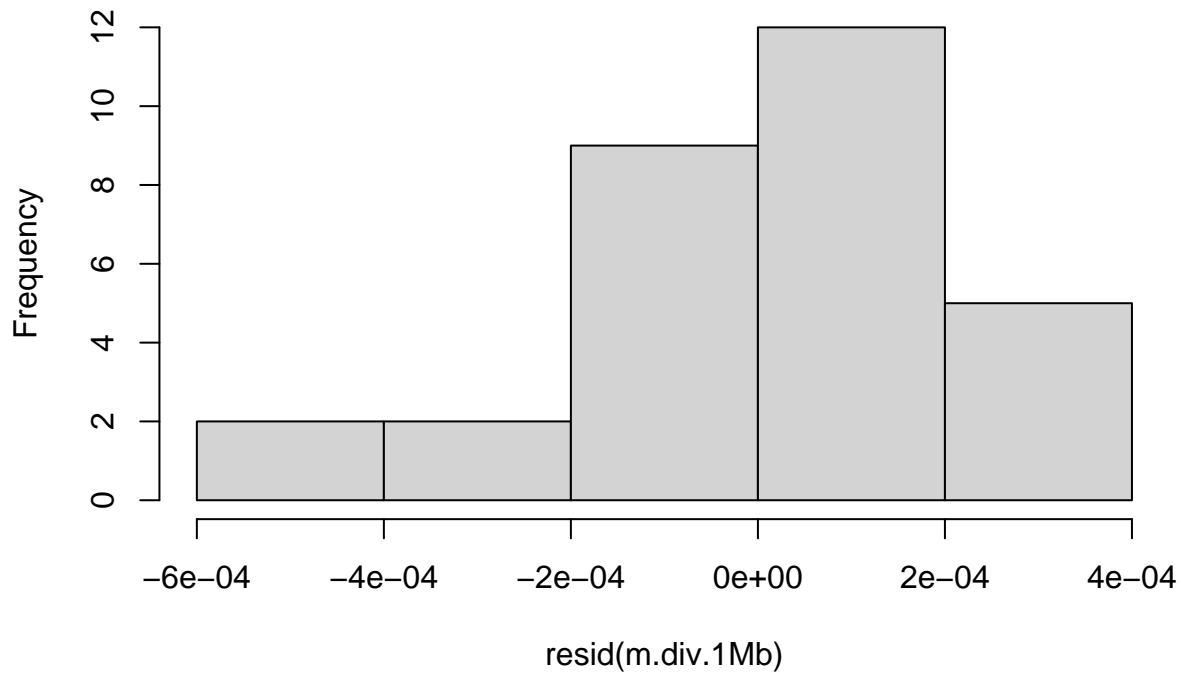
```
##
## Durbin-Watson test
##
## data: m.div.1Mb
## DW = 1.5295, p-value = 0.09374
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##
## Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.59412, p-value = 0.744
```

```
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
```

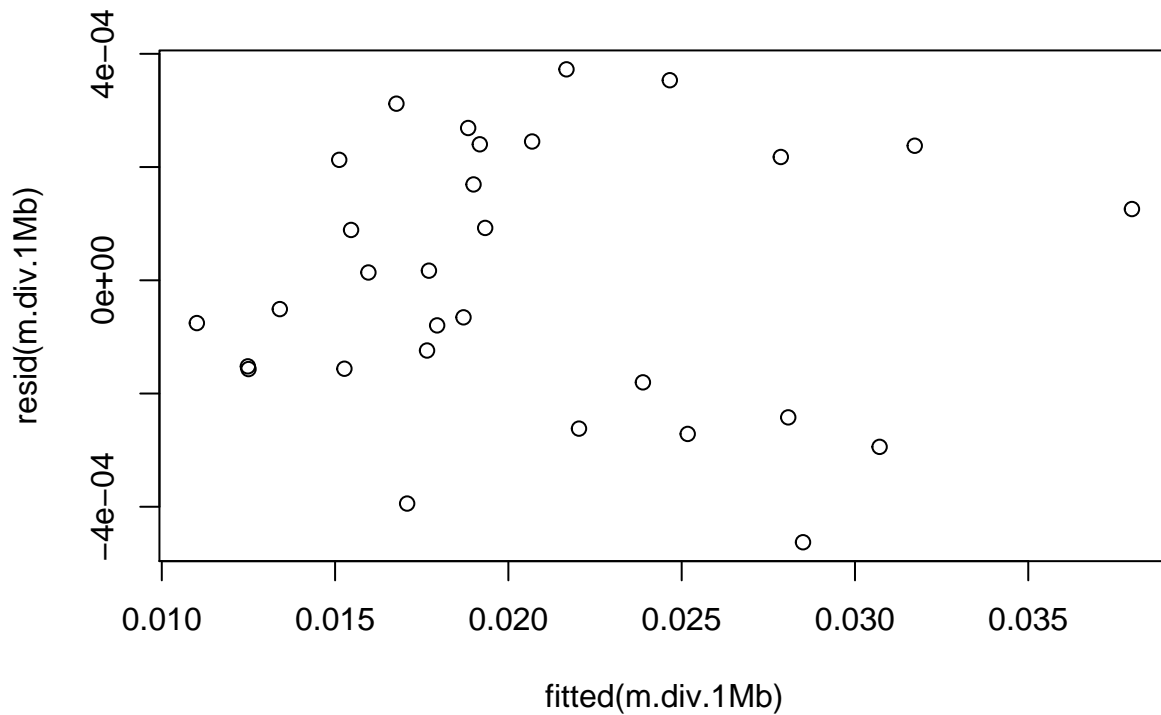
```
cor.test(~diversity+rho, data = sim.lands.200kb, method = "spearman")
```

```
##
## 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)

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)
```

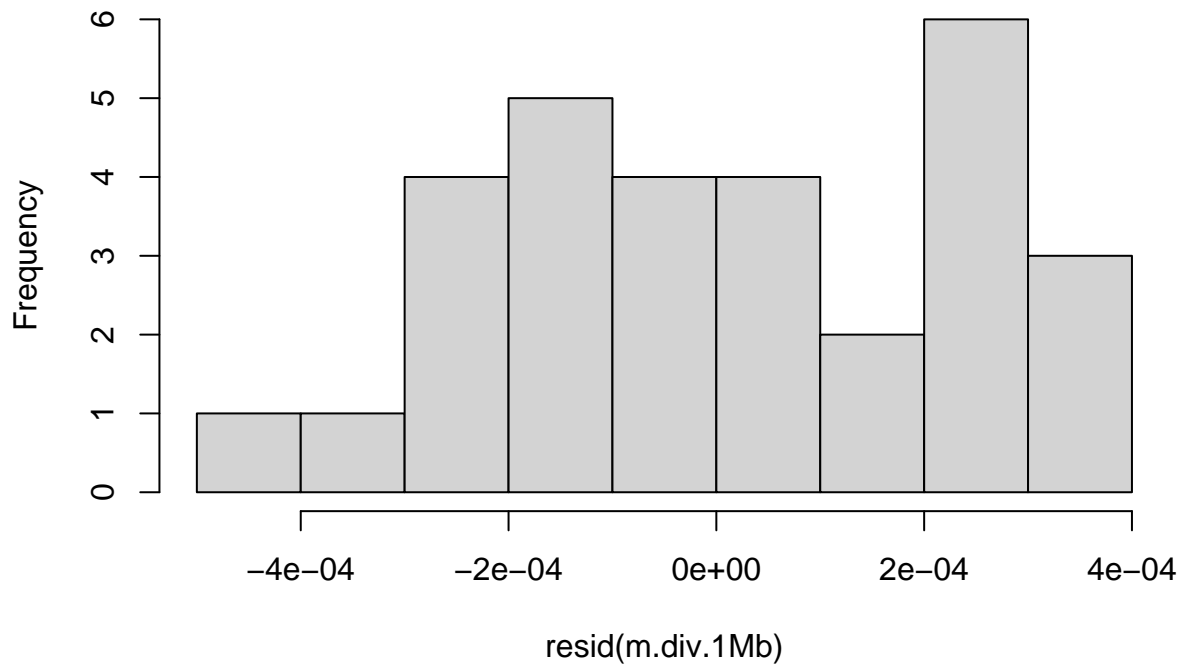
```
##
## Durbin-Watson test
##
## data: m.div.1Mb
## DW = 2.6531, p-value = 0.9631
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##
## Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.51119, p-value = 0.527
```

```
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")
```

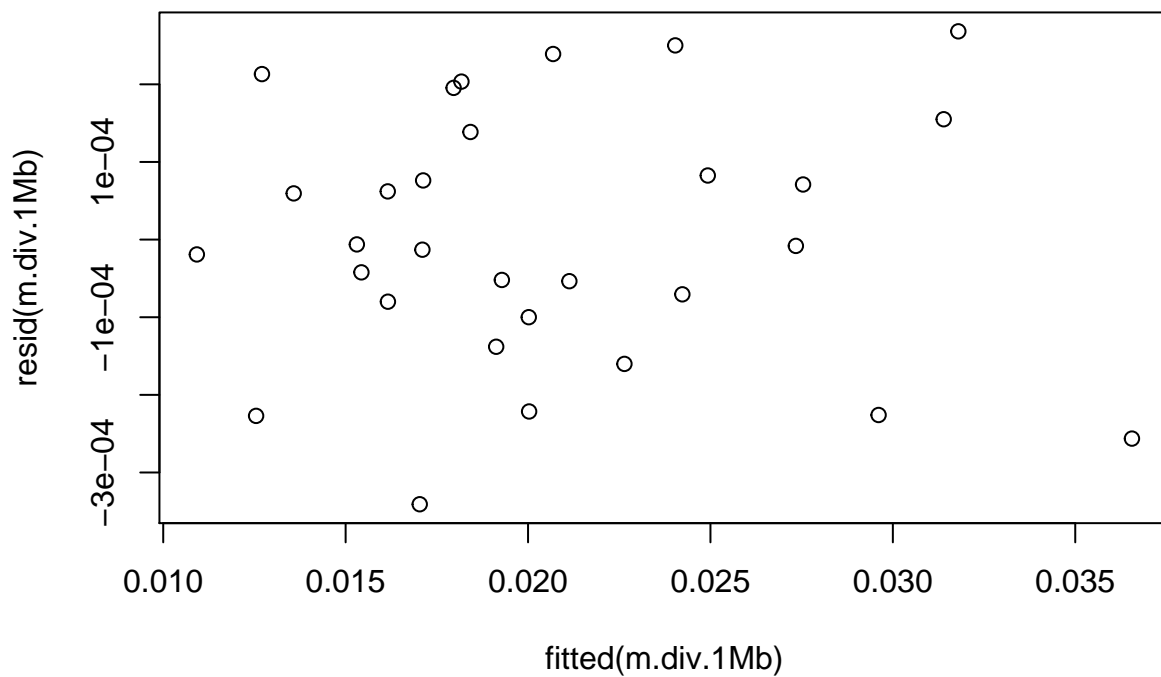
```
##
## Spearman's rank correlation rho
##
## data: diversity and rho
## S = 596694, p-value = 0.4591
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.06083648
```

```
# 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)
```

```
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)
```

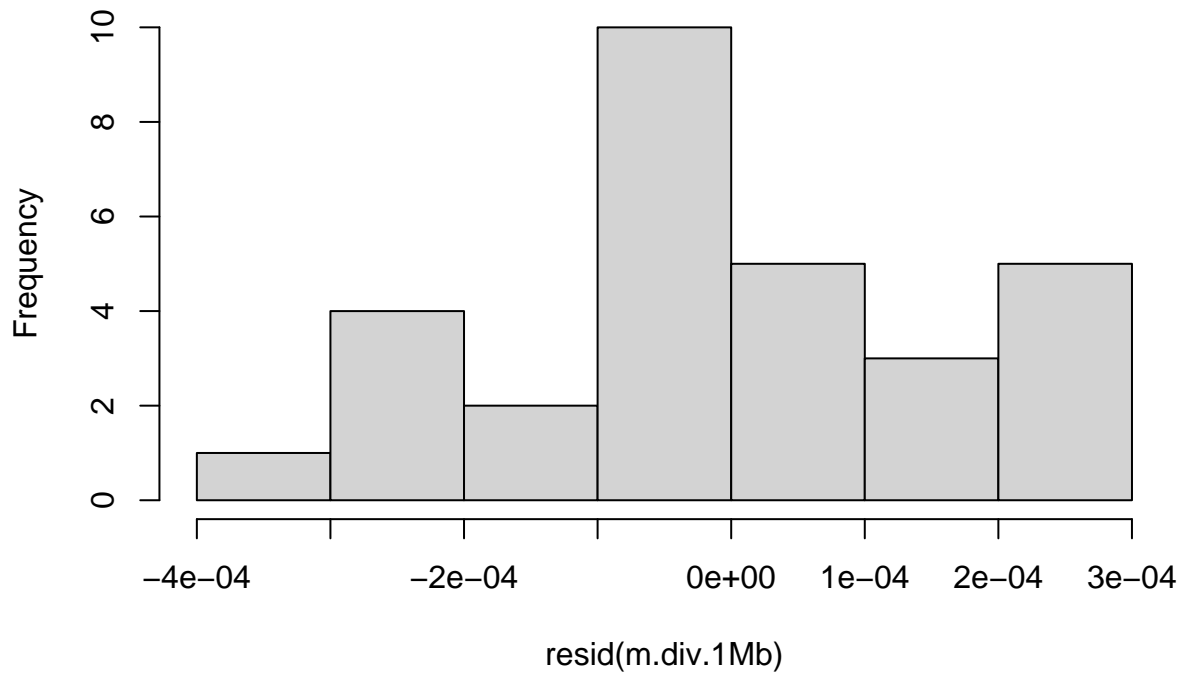
```
##
## Durbin-Watson test
##
## data: m.div.1Mb
## DW = 2.3611, p-value = 0.8304
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##
## Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.69982, p-value = 0.943
```

```
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.1Mb.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")
```

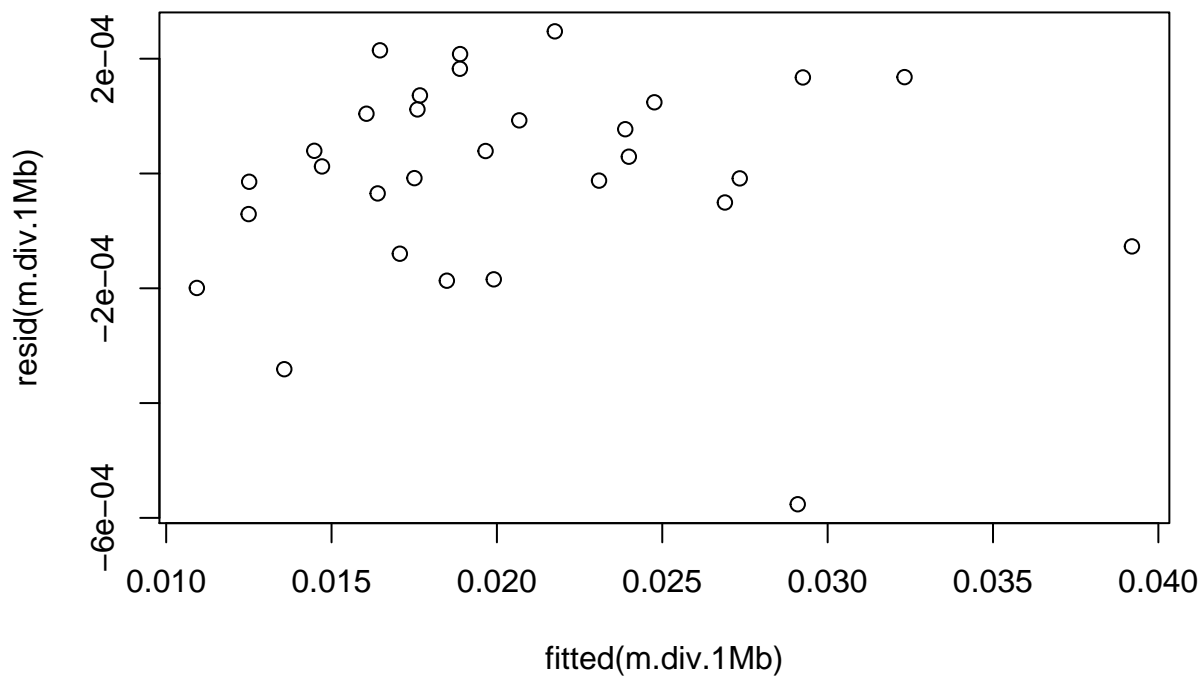
```
##
## Spearman's rank correlation rho
##
## data: diversity and rho
## S = 596694, p-value = 0.4591
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.06083648
```

```
# 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)
```

```
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)
```

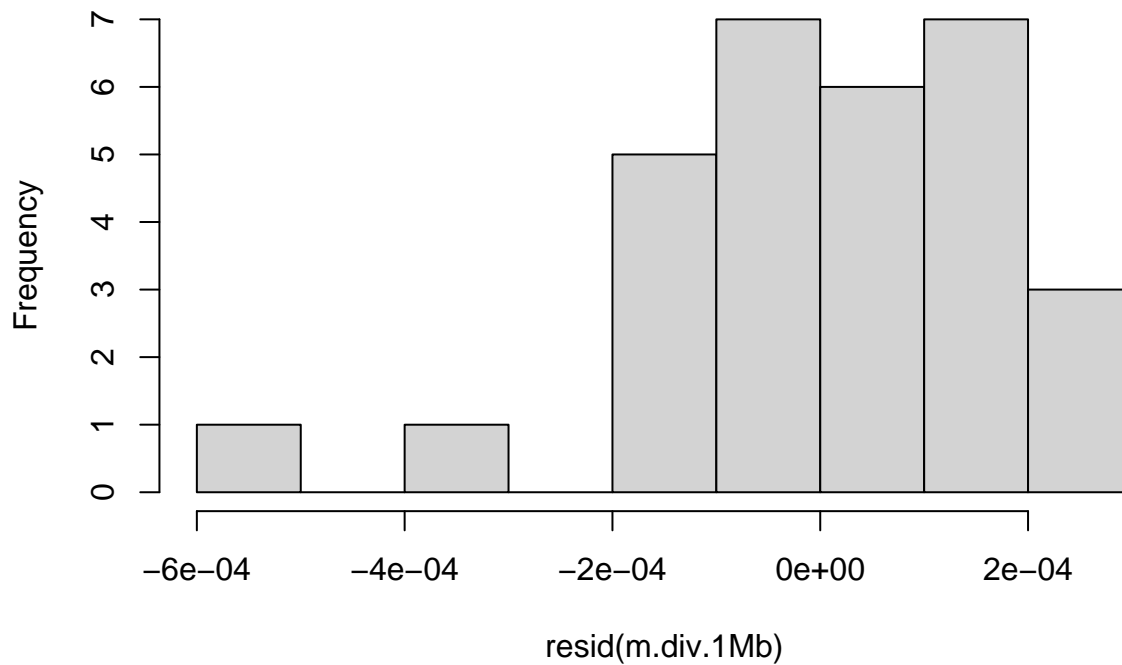
```
##
## Durbin-Watson test
##
## data: m.div.1Mb
## DW = 2.4044, p-value = 0.8773
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##
## Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.39065, p-value = 0.199
```

```
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.1Mb.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

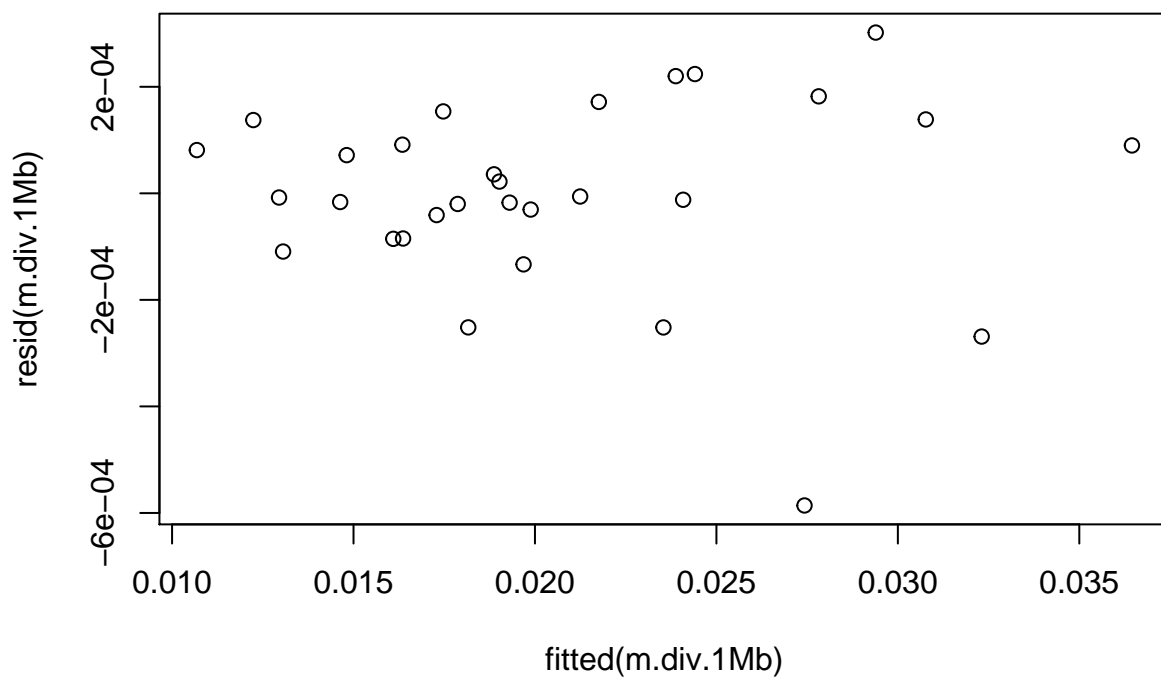
```

```
## 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)

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



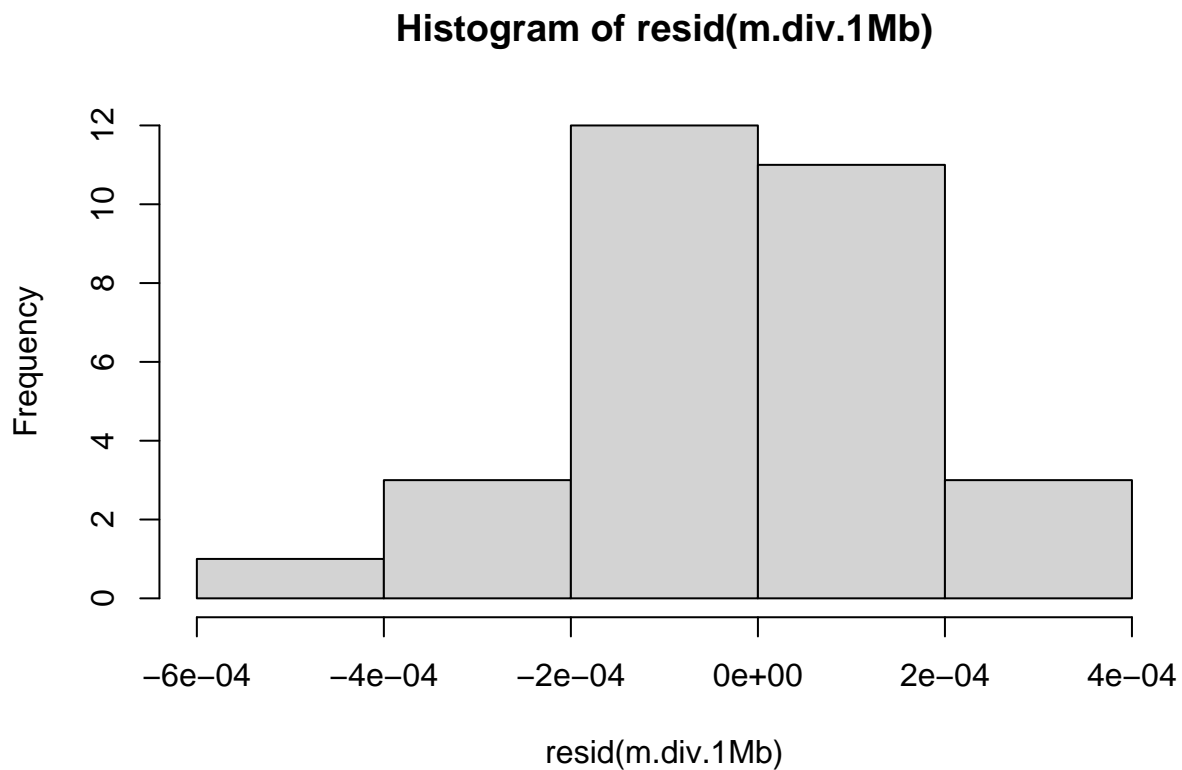
```
dwtest(m.div.1Mb)
```

```
##
## 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 = 0.11
```

```
hist(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$VarExp[3] + anova.diversity$VarExp[4]) / anova.diversity$VarExp[5]
r2.sim.1Mb[2, 5] <- anova.diversity$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, as.is = 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, as.is = 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")
```

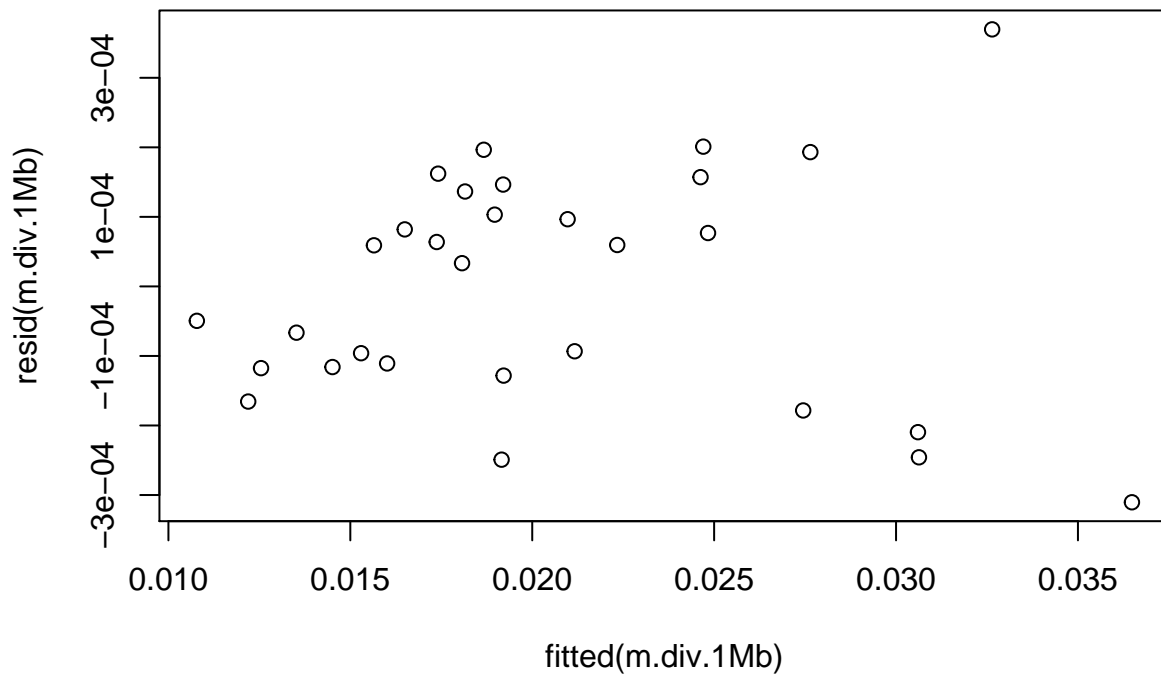
```
##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 4268, p-value = 0.7906
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.05050056
```

```
# 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)
```

```
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)
```

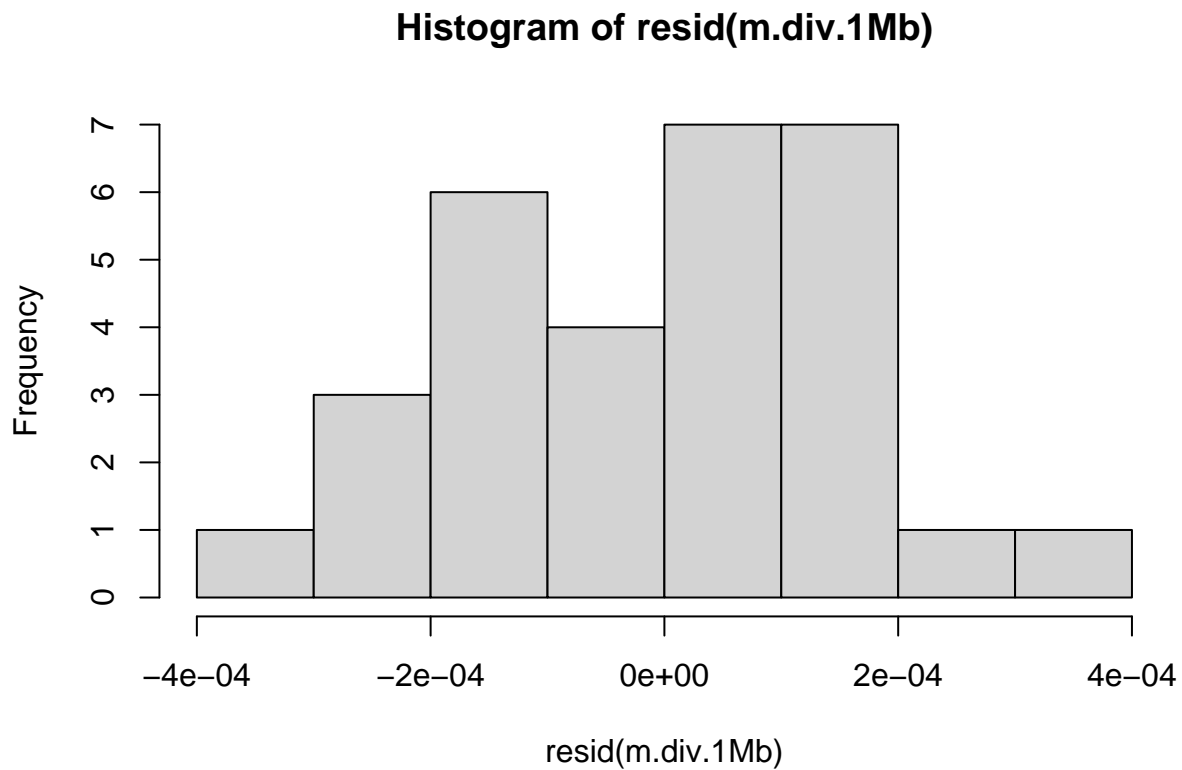
```
##
```

```
## 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 = 0.864
```

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

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
```

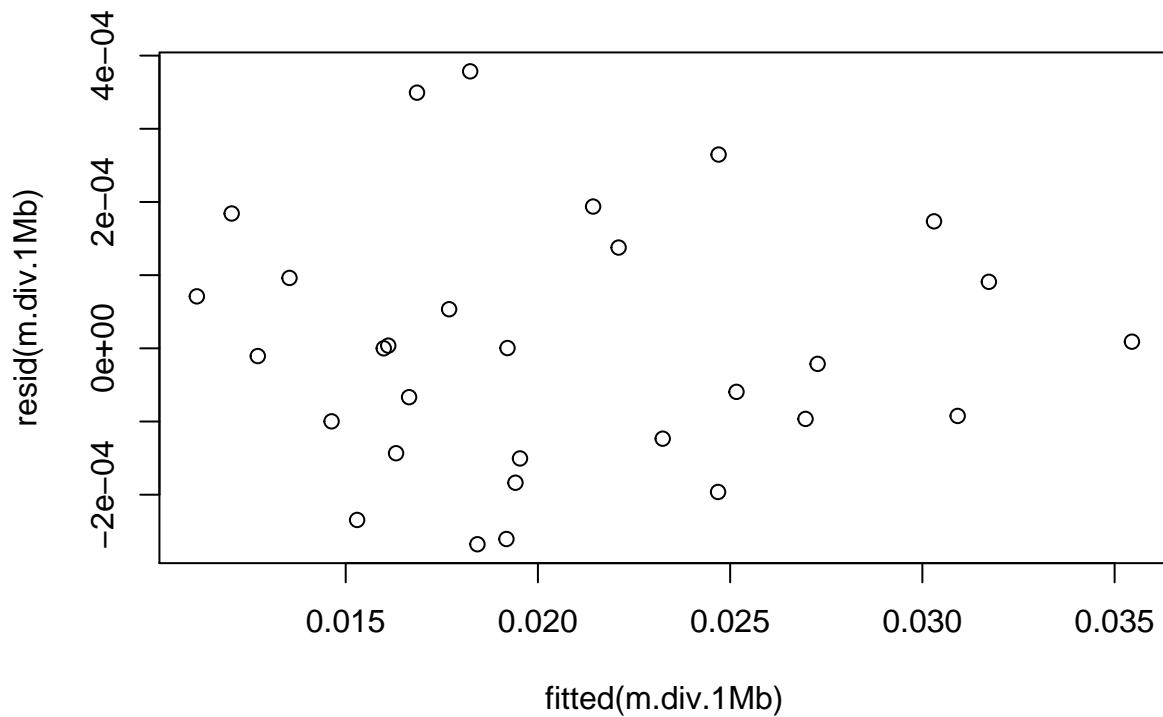
```
cor.test(~rho+tmrca, data = sim.lands.1Mb, method = "spearman")
```

```
##
## 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)

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)
```

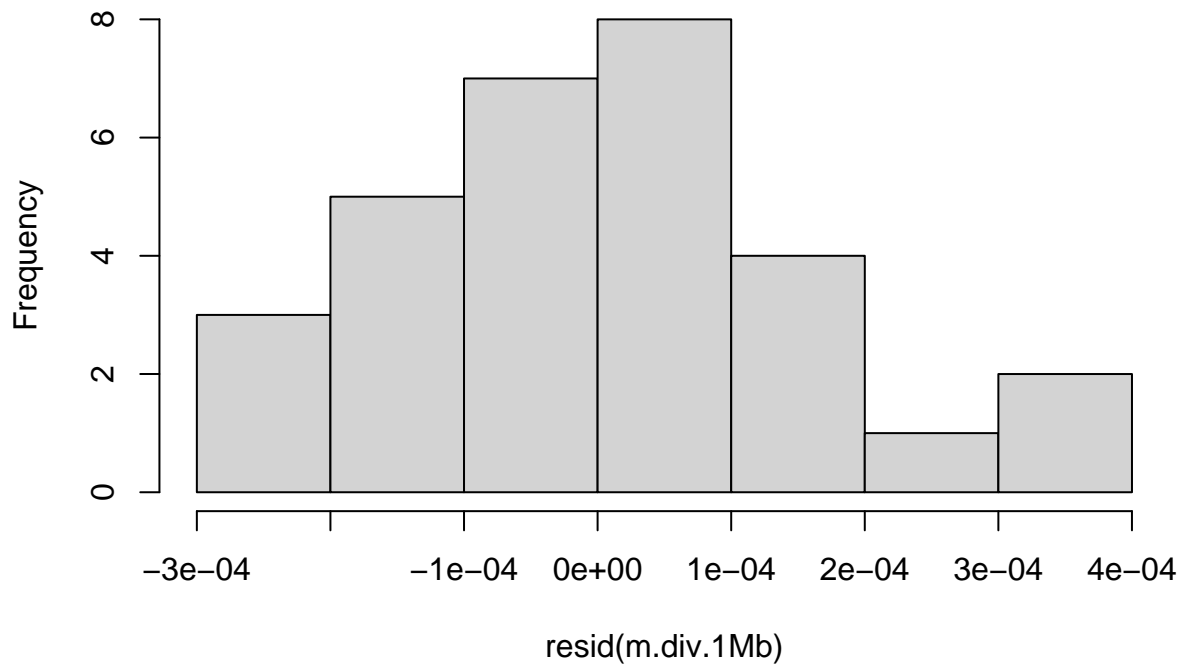
```
##
## Durbin-Watson test
##
## data: m.div.1Mb
## DW = 1.9852, p-value = 0.4718
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##
## Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.65923, p-value = 0.888
```

```
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

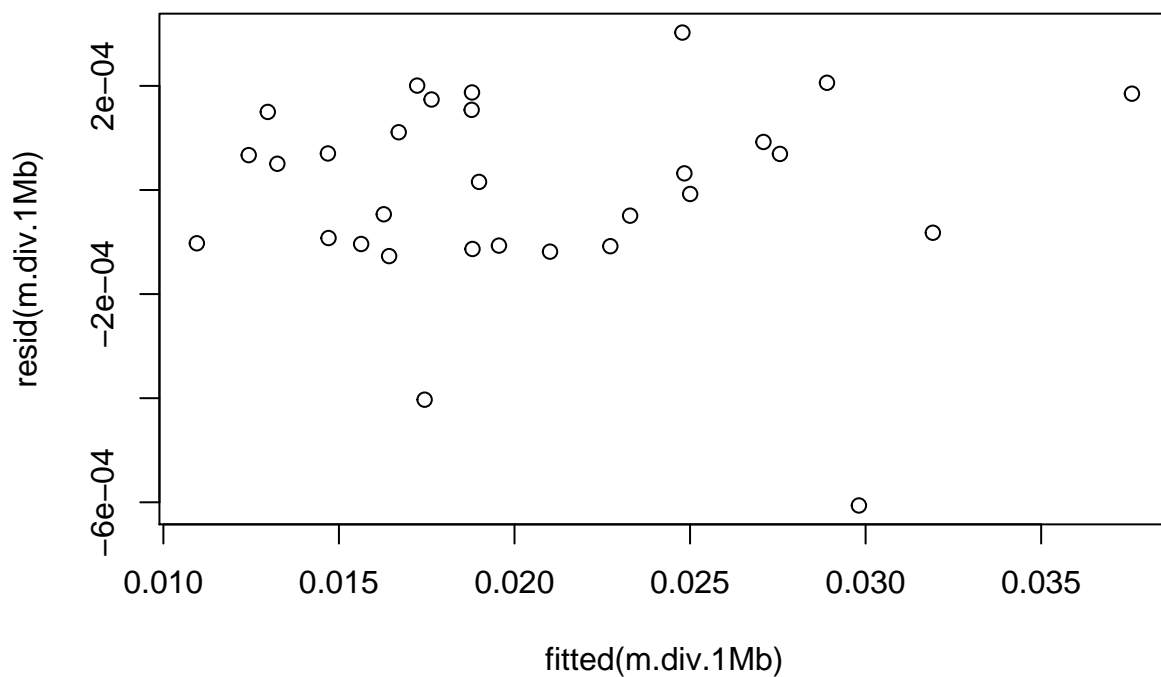
```

```
## 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)

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)
```

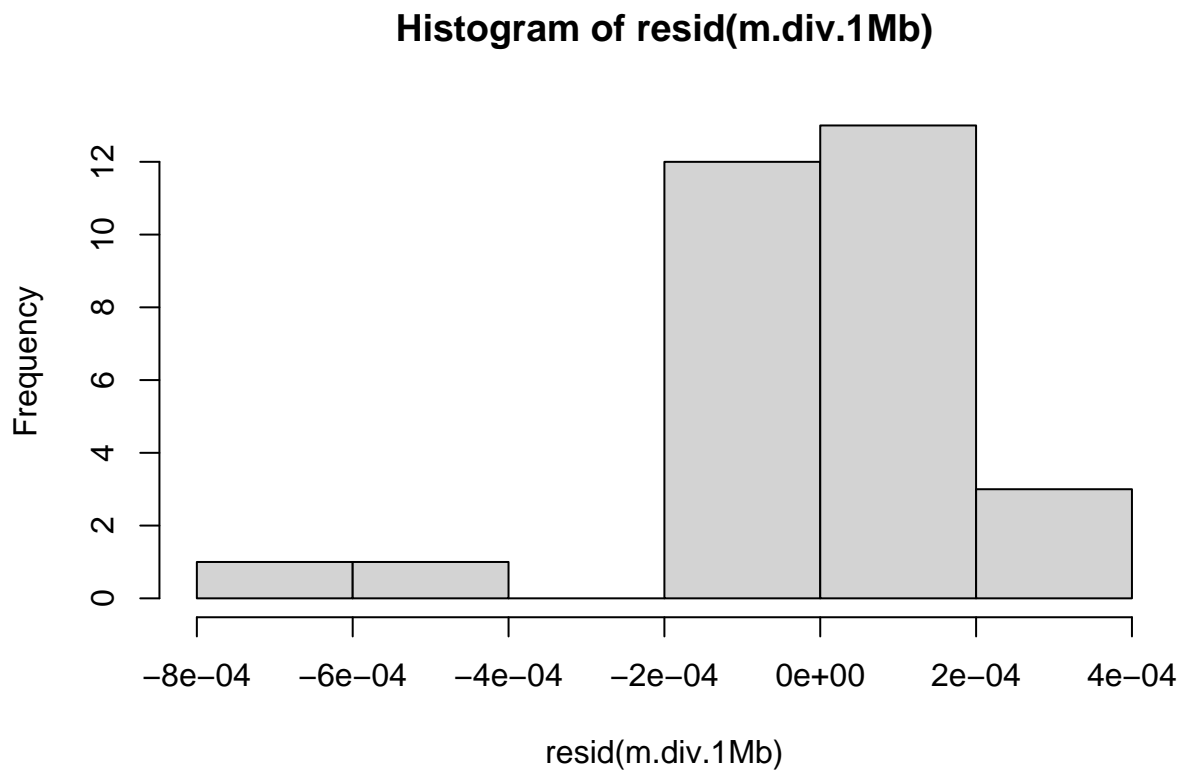
```
##
## Durbin-Watson test
##
## data: m.div.1Mb
## DW = 2.4886, p-value = 0.9089
## alternative hypothesis: true autocorrelation is greater than 0
```



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

```
##  
## Harrison-McCabe test  
##  
## data: m.div.1Mb  
## HMC = 0.6984, p-value = 0.937
```

```
hist(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$VarExp[3] + anova.diversity$VarExp[4]) / anova.diversity$VarExp[1]
r2.sim.1Mb[2, 8] <- anova.diversity$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, as.is = 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, as.is = 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")
```

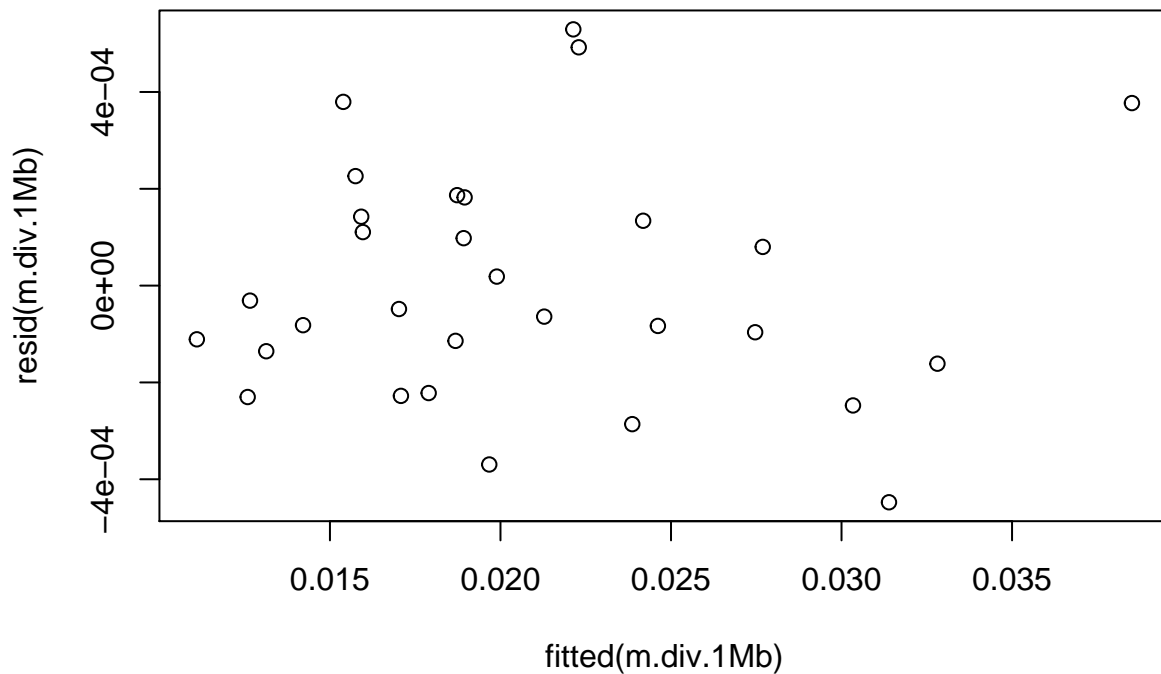
```
##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 4996, p-value = 0.5562
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## -0.1114572
```

```
# 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)
```

```
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)
```

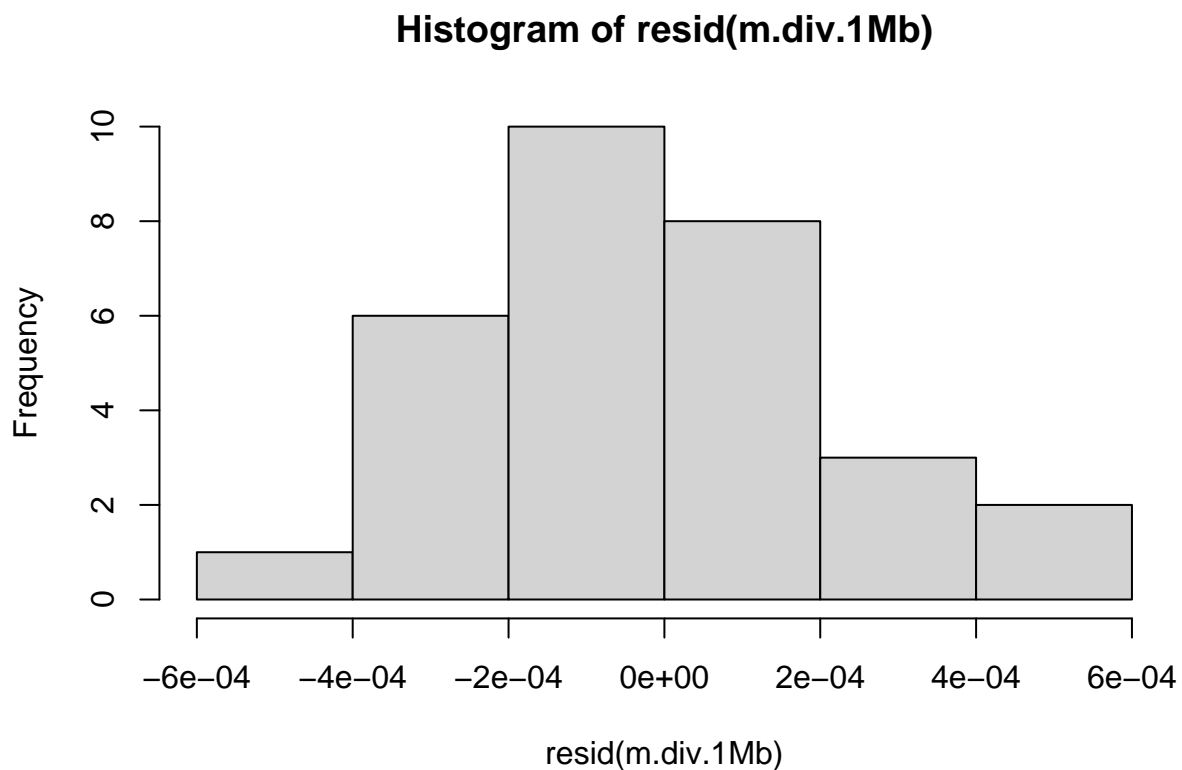
```
##
```

```
## 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 = 0.677
```

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

sim.lands.1Mb <- as.data.frame(cbind(rep_10.pi.1Mb$pi, sim.theta.1Mb$sim, sim.rho.1Mb$sim, rep_10.tmrca.1Mb$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 = 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
```

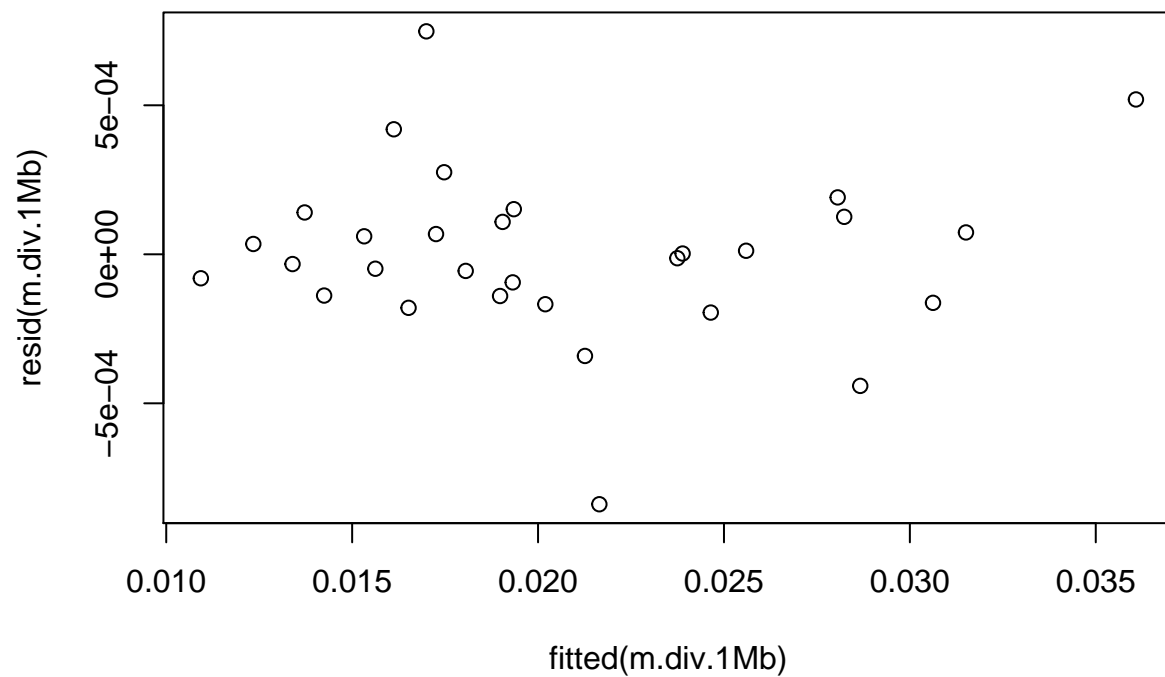
```
cor.test(~rho+tmrca, data = sim.lands.1Mb, method = "spearman")
```

```
##
## 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)

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)
```

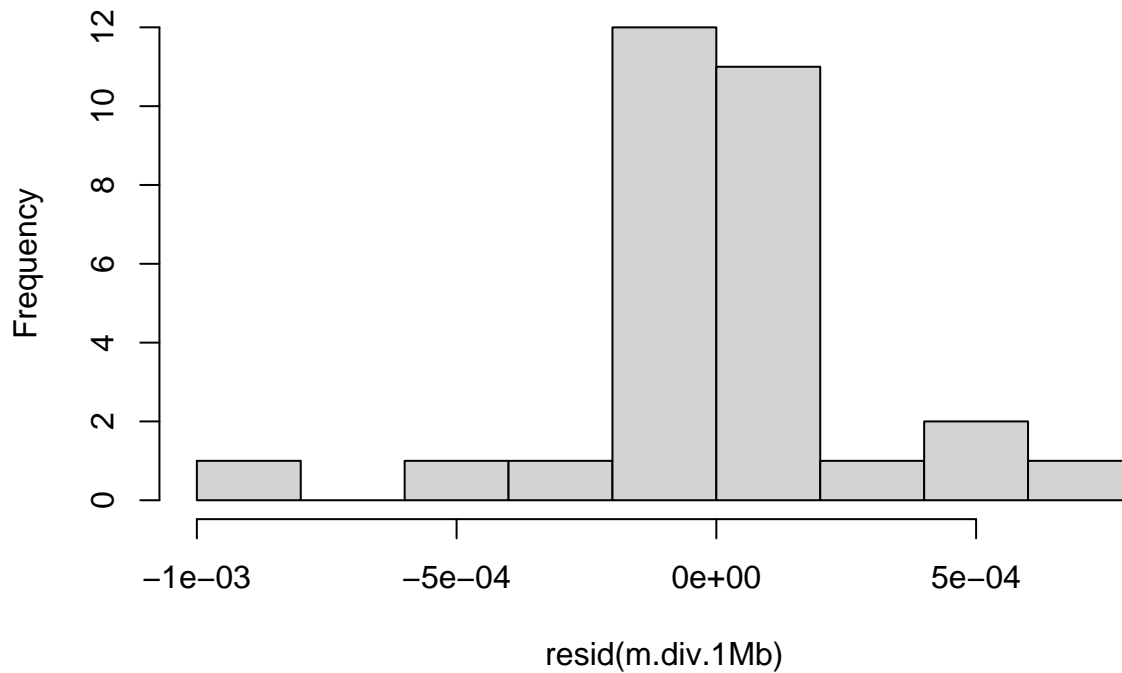
```
##
## Durbin-Watson test
##
## data: m.div.1Mb
## DW = 2.2351, p-value = 0.7114
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##
## Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.50343, p-value = 0.519
```

```
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))

```

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.50k <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims/dm.sim.rho.50000.txt")
sim.theta.50k <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims/dm.sim.theta.50000.txt")
sim.lands.50k <- as.data.frame(cbind(sim.theta.50k$sim, sim.rho.50k$sim))
names(sim.lands.50k) <- 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.50k <- read.table(paste(p, "diversity.50kb.bedgraph", sep = ""), header = T)
pi.50k$avg <- apply(pi.50k[4:ncol(pi.50k)], 1, mean)
tmrca.50k <- read.table(paste(p, "TMRCA.50kb.bedgraph", sep = ""), header = T)
tmrca.50k$avg <- apply(tmrca.50k[4:ncol(tmrca.50k)], 1, mean)
rho.50k <- read.table(paste(p, "rho.50kb.bedgraph", sep = ""), header = T)
theta.50k <- read.table(paste(p, "theta.50kb.bedgraph", sep = ""), header = T)

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

# centering
inf.lands.50k.rep_1$thetaC <- inf.lands.50k.rep_1$theta - mean(inf.lands.50k.rep_1$theta)

```

```

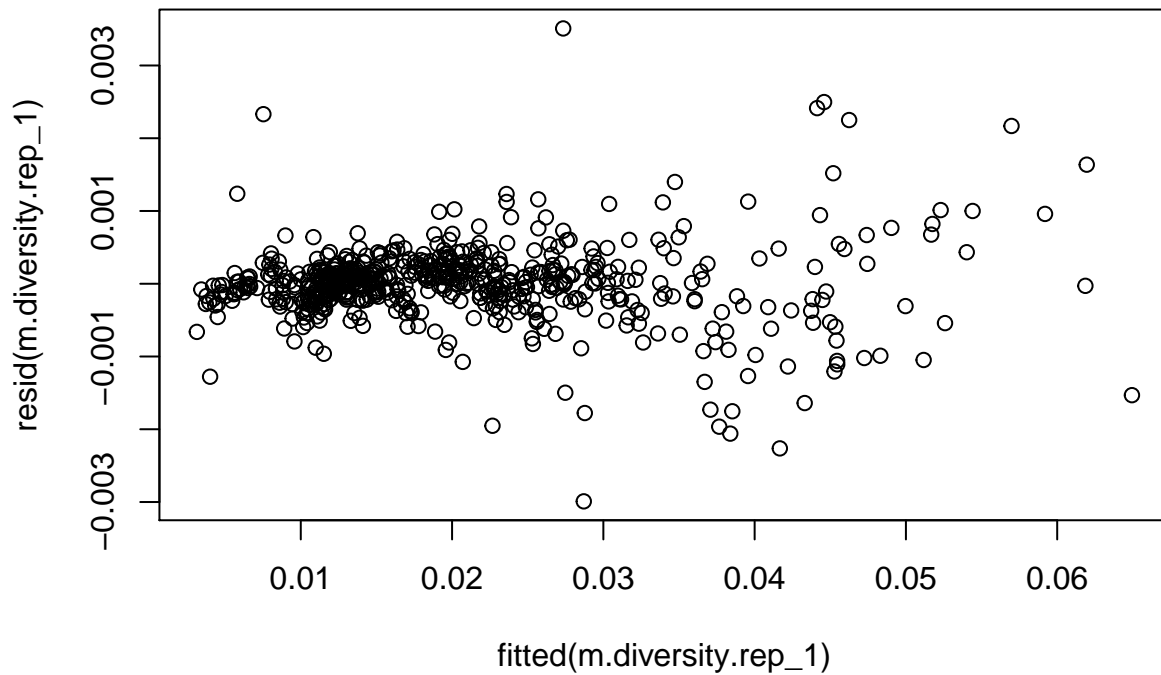
inf.lands.50k.rep_1$tmrcaC <- inf.lands.50k.rep_1$tmrca - mean(inf.lands.50k.rep_1$tmrca)
inf.lands.50k.rep_1$rhoC <- inf.lands.50k.rep_1$rho - mean(inf.lands.50k.rep_1$rho)

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

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

```

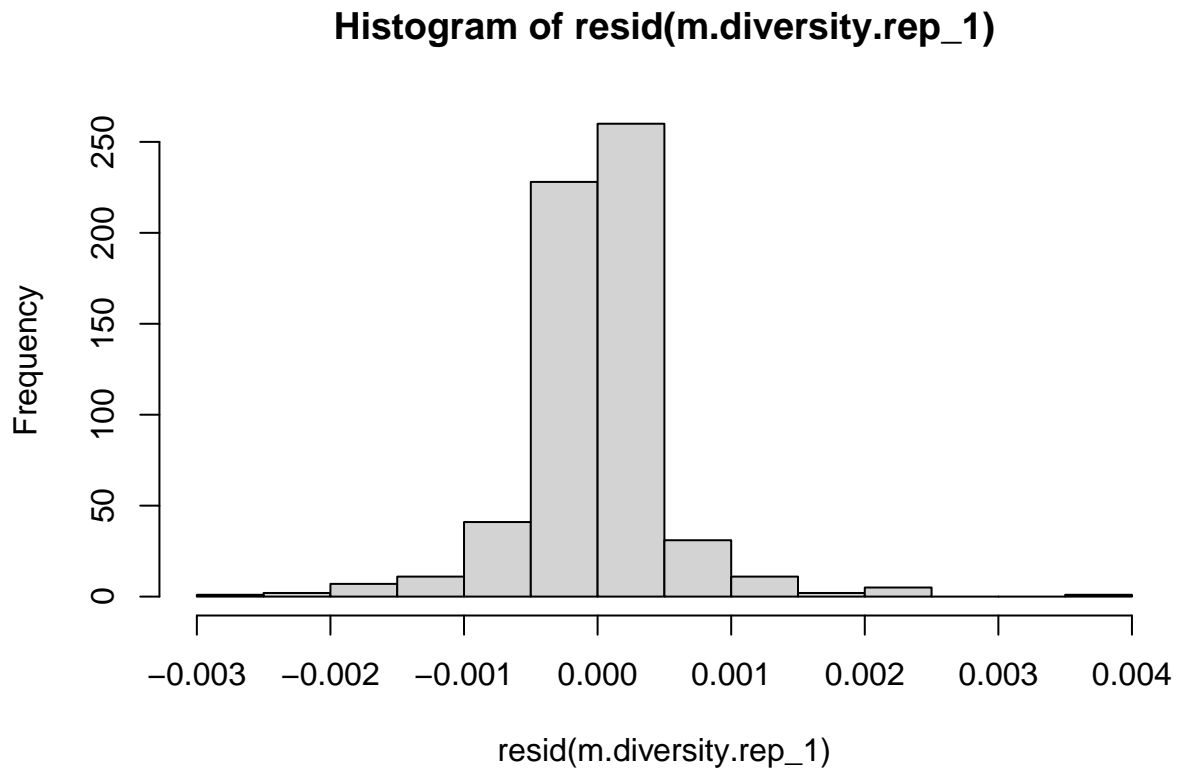
```
hmcctest(m.diversity.rep_1)
```

```

##
## Harrison-McCabe test
##
## data: m.diversity.rep_1
## HMC = 0.61568, p-value = 1

```

```
hist(resid(m.diversity.rep_1))
```

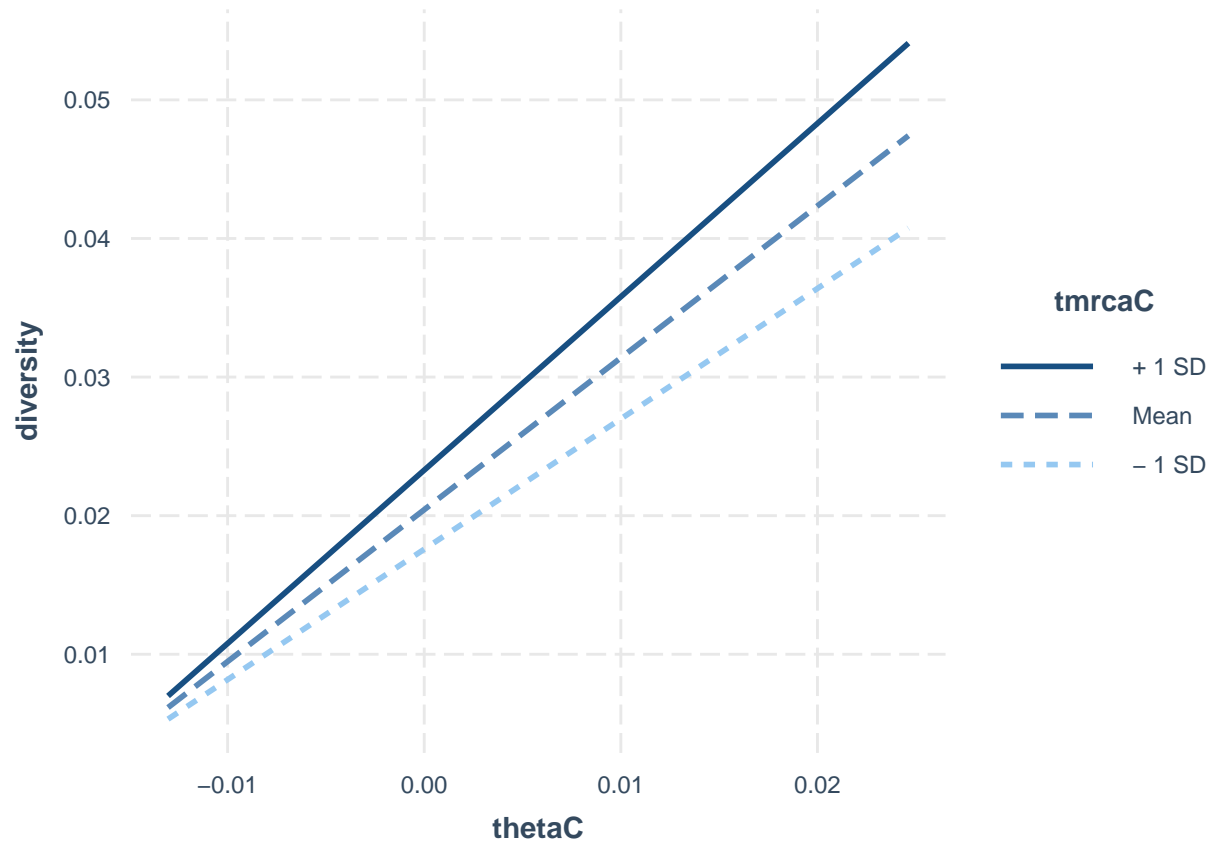


```
summary(m.diversity.rep_1)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.50k.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.50k.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.50k.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.50k.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.50k.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
```

```
## -4.88116215 -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.50k <- read.table(paste(p, "diversity.50kb.bedgraph", sep = ""), header = T)
pi.50k$avg <- apply(pi.50k[4:ncol(pi.50k)], 1, mean)
tmrca.50k <- read.table(paste(p, "TMRCA.50kb.bedgraph", sep = ""), header = T)
tmrca.50k$avg <- apply(tmrca.50k[4:ncol(tmrca.50k)], 1, mean)
rho.50k <- read.table(paste(p, "rho.50kb.bedgraph", sep = ""), header = T)
theta.50k <- read.table(paste(p, "theta.50kb.bedgraph", sep = ""), header = T)

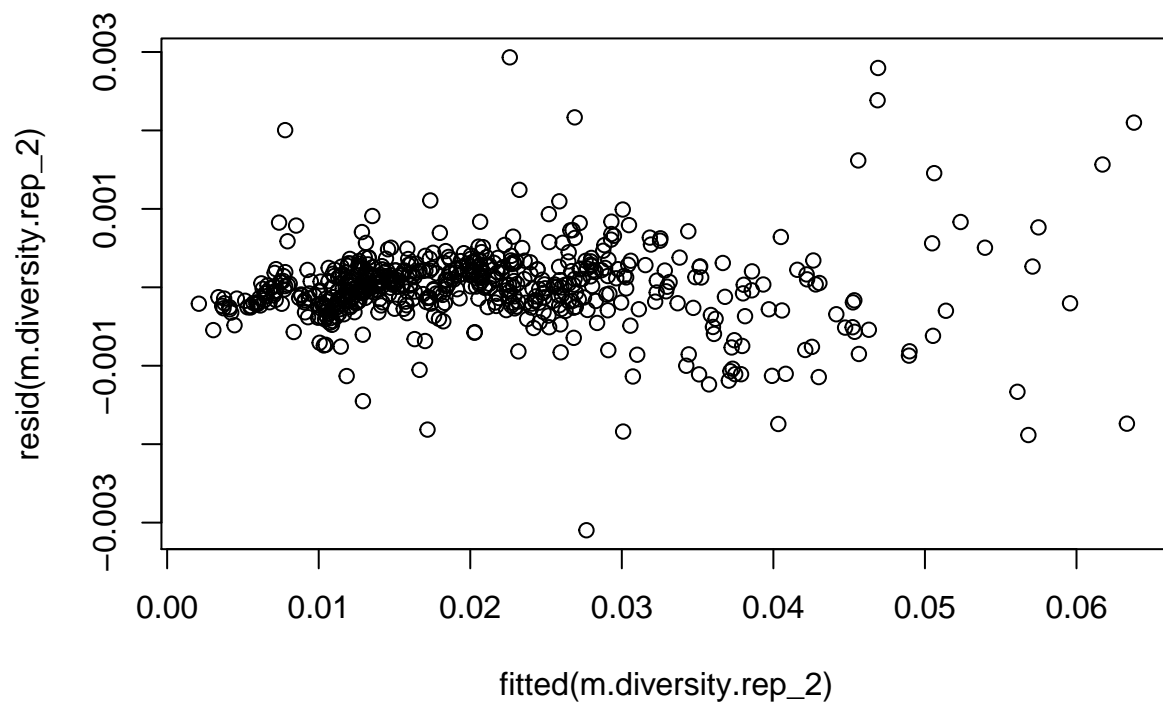
inf.lands.50k.rep_2 <- as.data.frame(cbind(pi.50k$avg, theta.50k$sample_mean, rho.50k$sample_mean, tmrca.50k$sample_mean))
names(inf.lands.50k.rep_2) <- c("diversity", "theta", "rho", "tmrca")

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

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

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

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



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

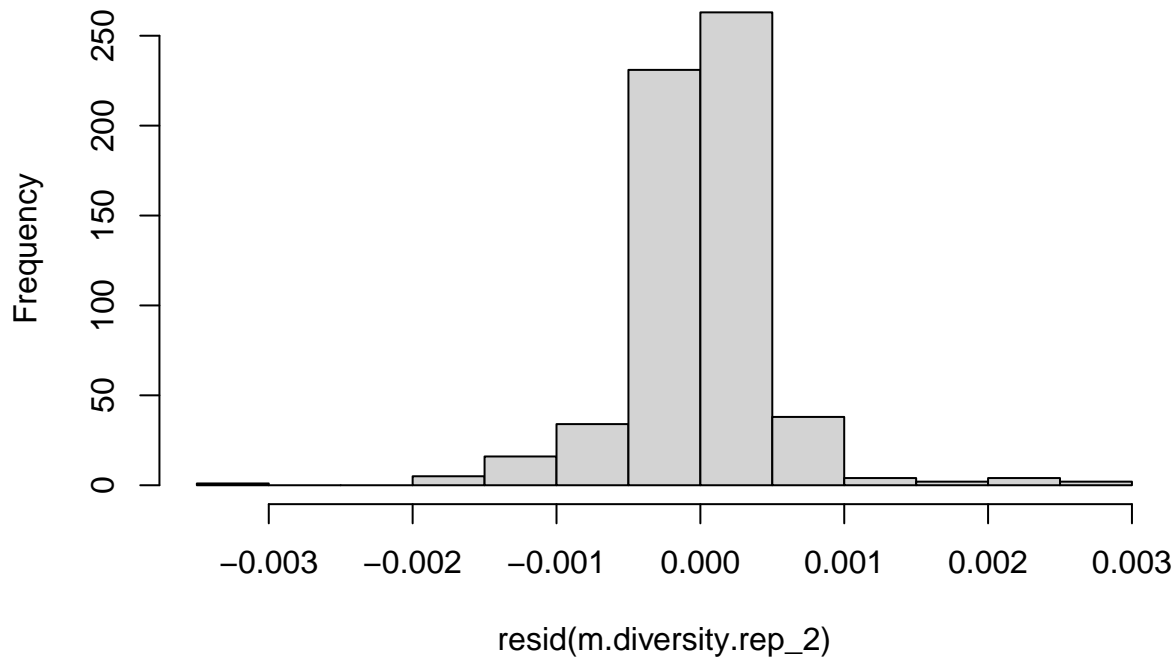
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_2  
## DW = 1.3609, p-value = 1.173e-15  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(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)

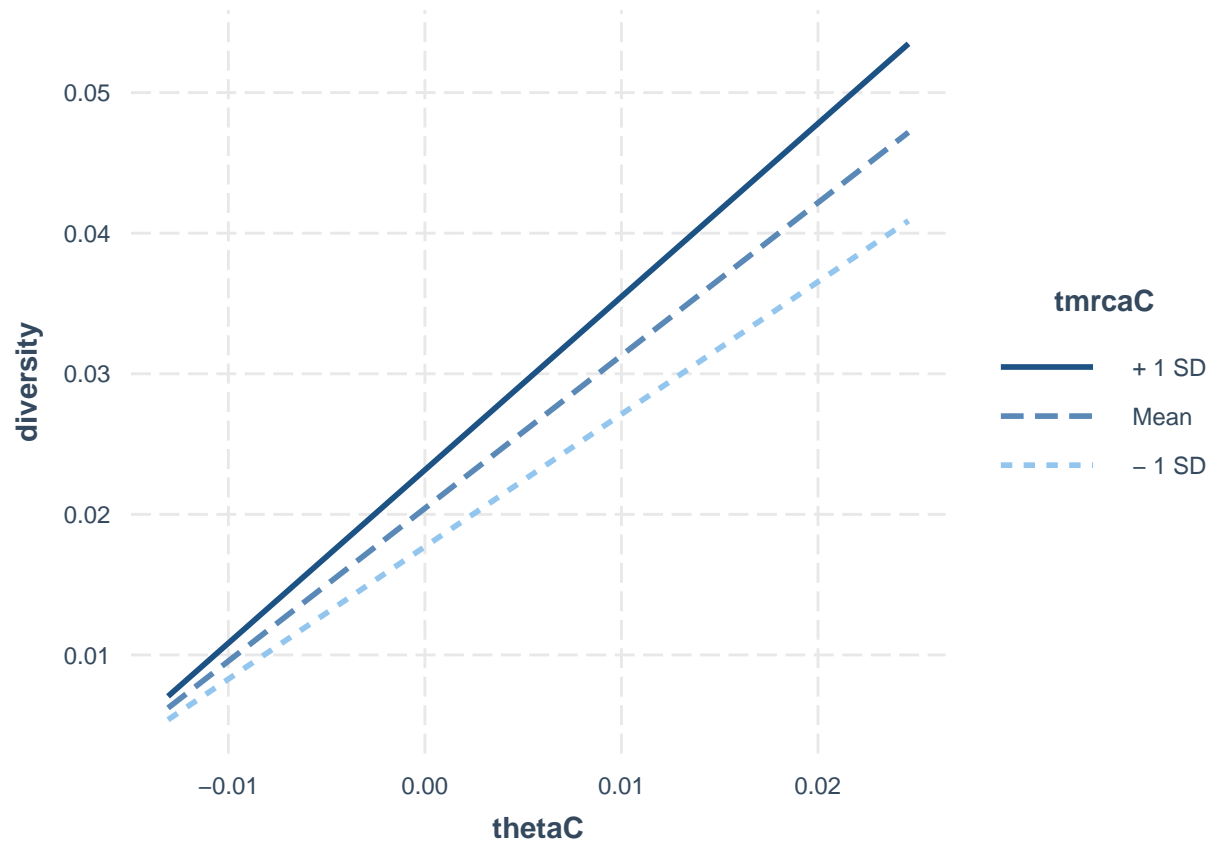


```
summary(m.diversity.rep_2)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.50k.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.50k.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.50k.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.50k.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.50k.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.50k <- read.table(paste(p, "diversity.50kb.bedgraph", sep = ""), header = T)
pi.50k$avg <- apply(pi.50k[4:ncol(pi.50k)], 1, mean)
tmrca.50k <- read.table(paste(p, "TMRCA.50kb.bedgraph", sep = ""), header = T)
tmrca.50k$avg <- apply(tmrca.50k[4:ncol(tmrca.50k)], 1, mean)
rho.50k <- read.table(paste(p, "rho.50kb.bedgraph", sep = ""), header = T)
theta.50k <- read.table(paste(p, "theta.50kb.bedgraph", sep = ""), header = T)

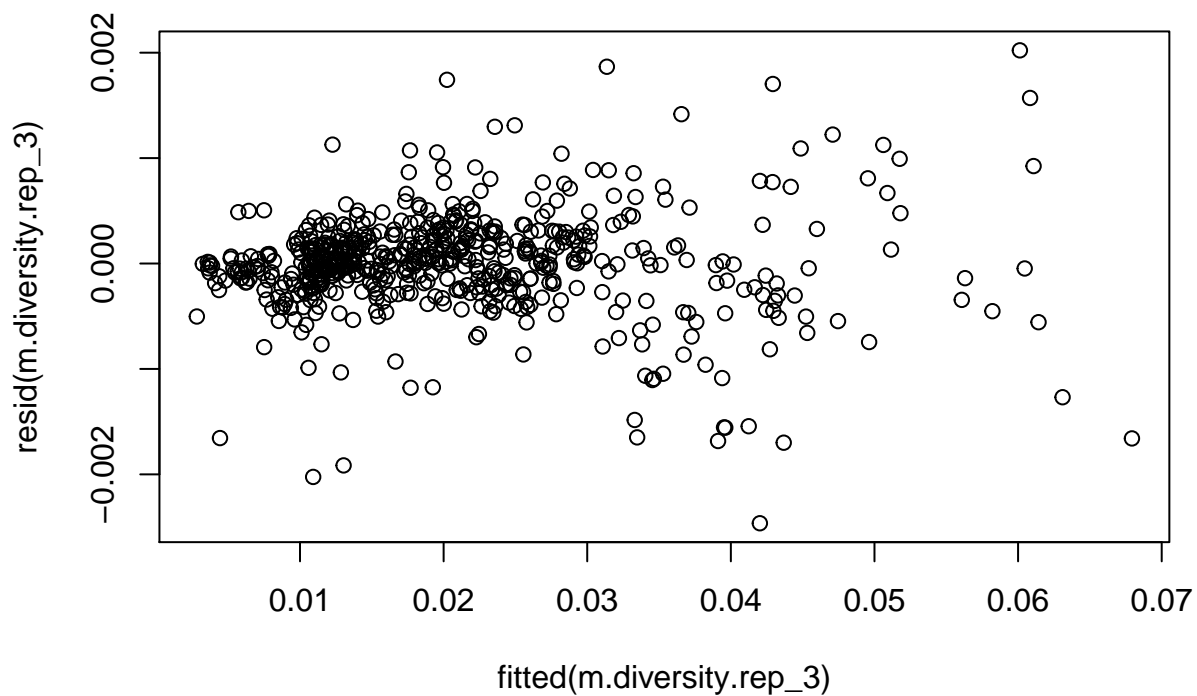
inf.lands.50k.rep_3 <- as.data.frame(cbind(pi.50k$avg, theta.50k$sample_mean, rho.50k$sample_mean, tmrca.50k$sample_mean))
names(inf.lands.50k.rep_3) <- c("diversity", "theta", "rho", "tmrca")

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

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

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

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



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

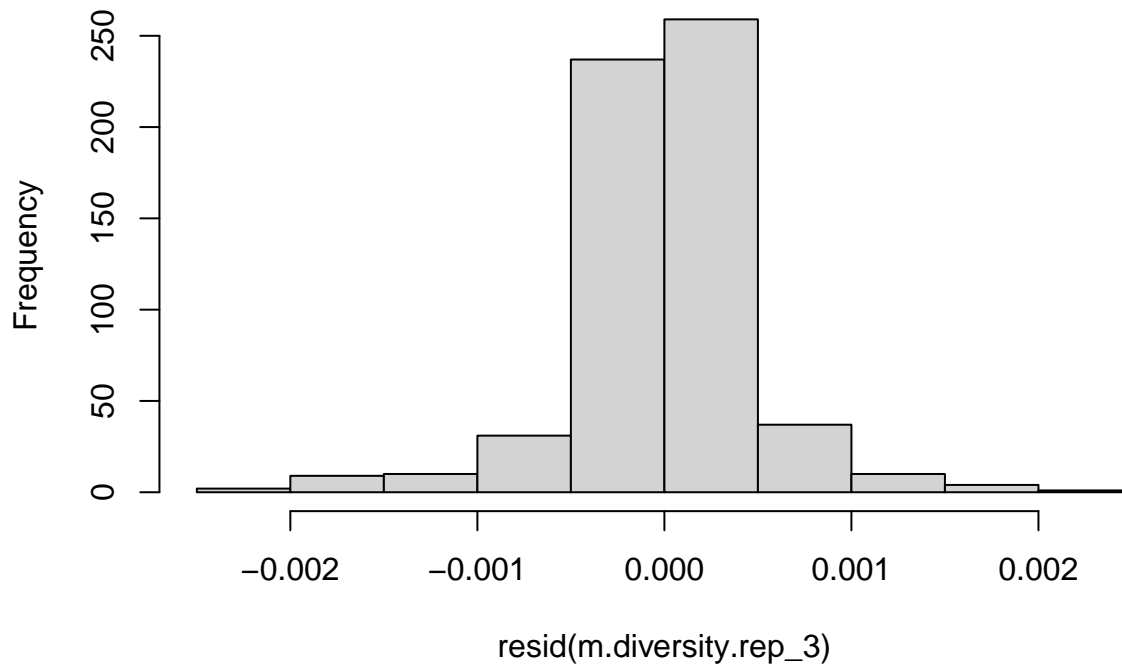
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_3  
## DW = 1.4619, p-value = 1.133e-11  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_3)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_3  
## HMC = 0.52153, p-value = 0.786
```

```
hist(resid(m.diversity.rep_3))
```

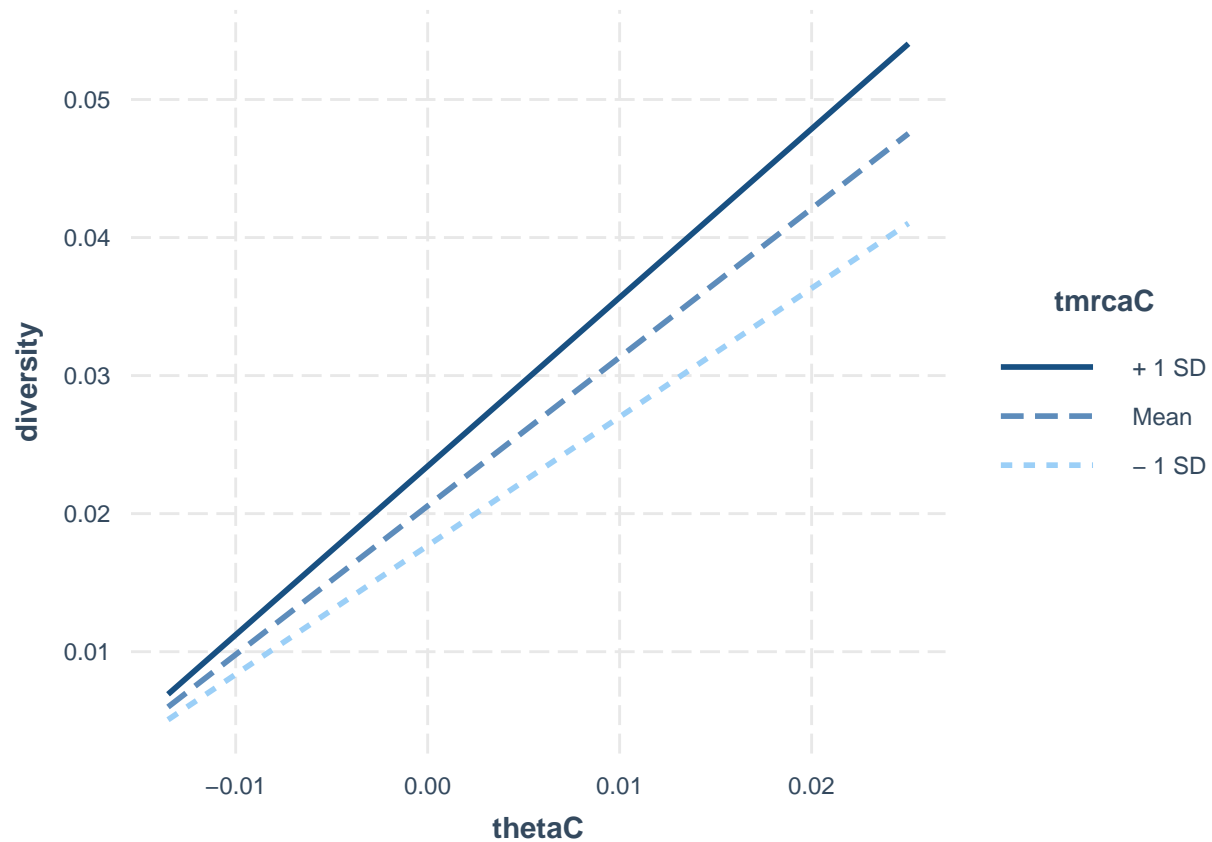
Histogram of resid(m.diversity.rep_3)



```
summary(m.diversity.rep_3)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.50k.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.50k.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.50k.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.50k.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.50k.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.50k <- read.table(paste(p, "diversity.50kb.bedgraph", sep = ""), header = T)
pi.50k$avg <- apply(pi.50k[4:ncol(pi.50k)], 1, mean)
tmrca.50k <- read.table(paste(p, "TMRCA.50kb.bedgraph", sep = ""), header = T)
tmrca.50k$avg <- apply(tmrca.50k[4:ncol(tmrca.50k)], 1, mean)
rho.50k <- read.table(paste(p, "rho.50kb.bedgraph", sep = ""), header = T)
theta.50k <- read.table(paste(p, "theta.50kb.bedgraph", sep = ""), header = T)

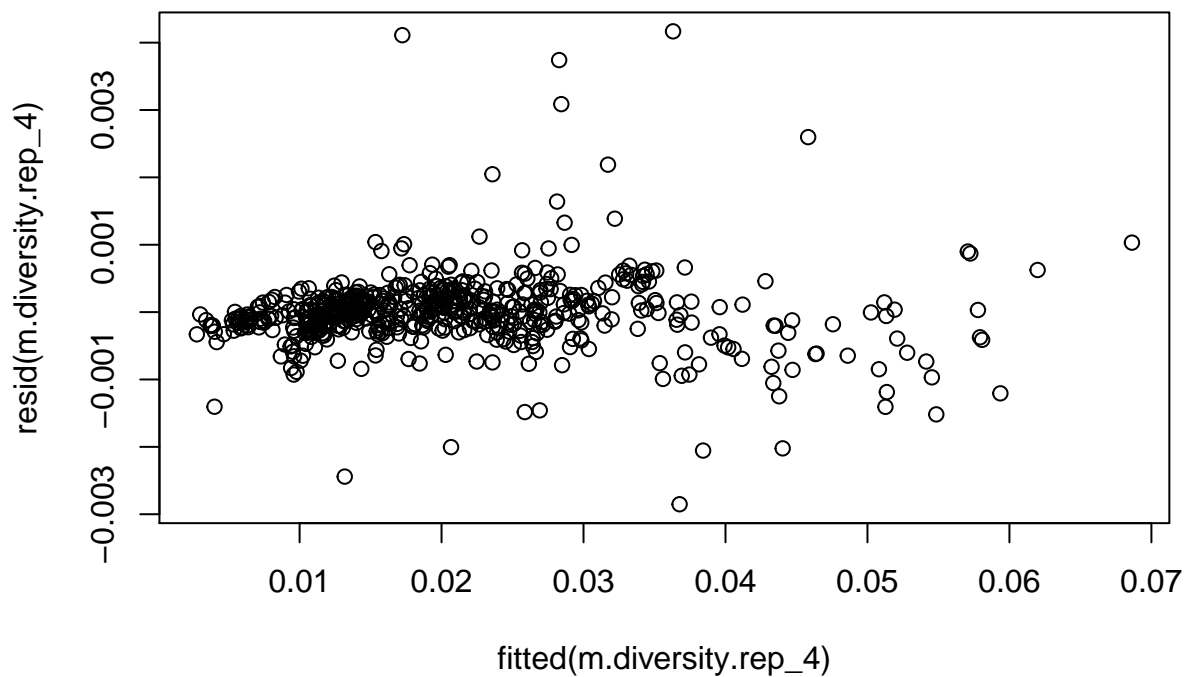
inf.lands.50k.rep_4 <- as.data.frame(cbind(pi.50k$avg, theta.50k$sample_mean, rho.50k$sample_mean, tmrca.50k$sample_mean))
names(inf.lands.50k.rep_4) <- c("diversity", "theta", "rho", "tmrca")

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

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

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

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

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

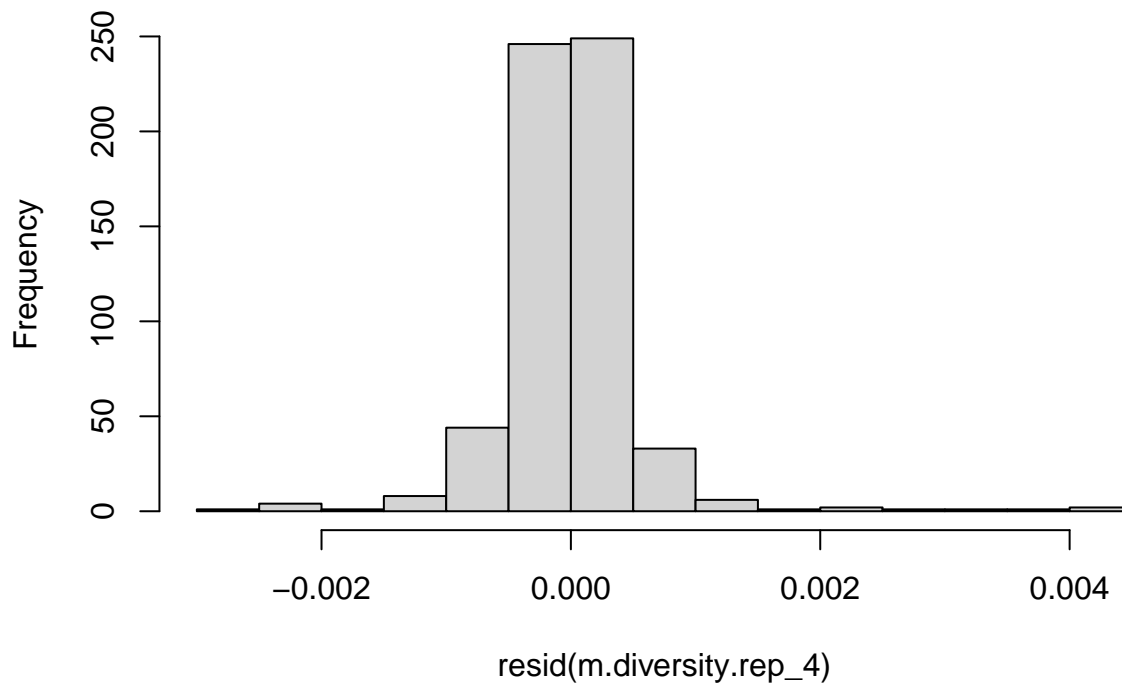
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_4  
## DW = 0.96213, p-value < 2.2e-16  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_4)
```

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

```
hist(resid(m.diversity.rep_4))
```

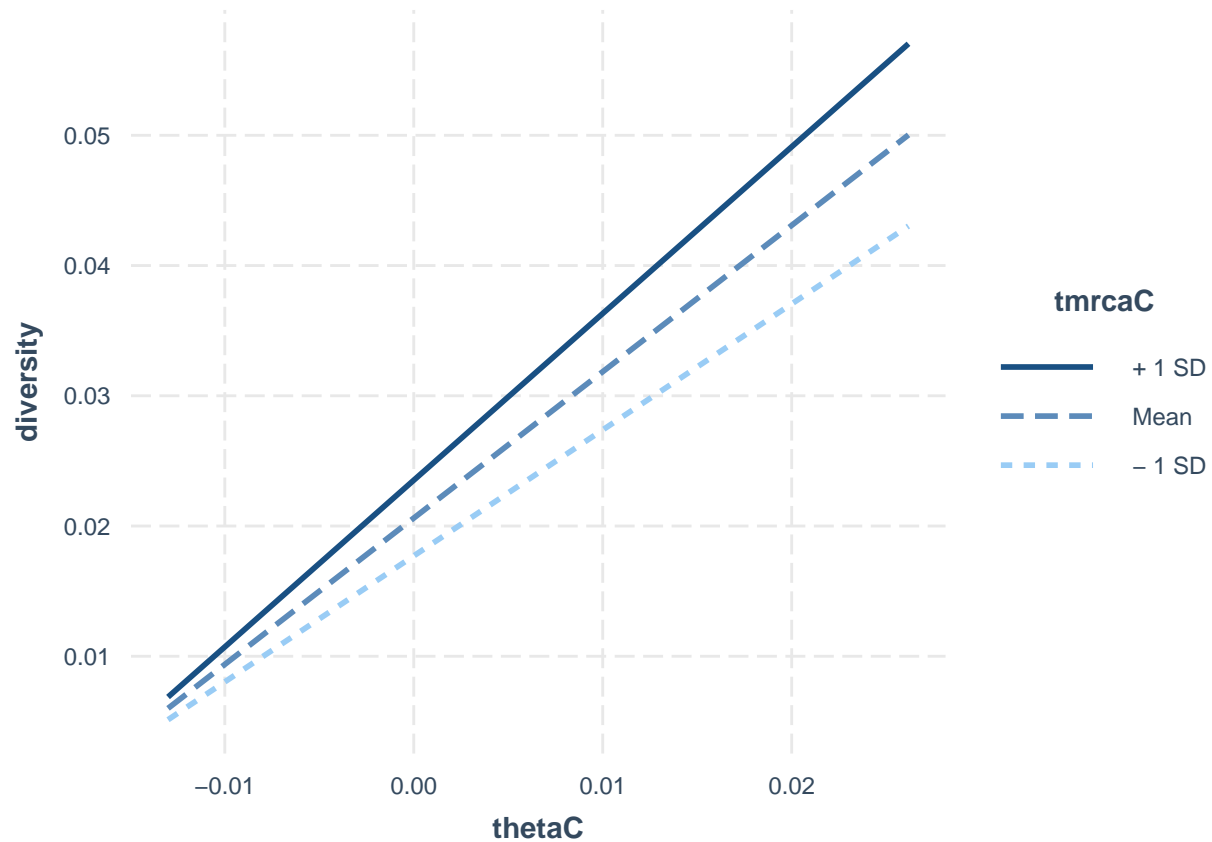
Histogram of resid(m.diversity.rep_4)



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

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.50k.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.50k.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.50k.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.50k.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.50k.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.50k <- read.table(paste(p, "diversity.50kb.bedgraph", sep = ""), header = T)
pi.50k$avg <- apply(pi.50k[4:ncol(pi.50k)], 1, mean)
tmrca.50k <- read.table(paste(p, "TMRCA.50kb.bedgraph", sep = ""), header = T)
tmrca.50k$avg <- apply(tmrca.50k[4:ncol(tmrca.50k)], 1, mean)
rho.50k <- read.table(paste(p, "rho.50kb.bedgraph", sep = ""), header = T)
theta.50k <- read.table(paste(p, "theta.50kb.bedgraph", sep = ""), header = T)

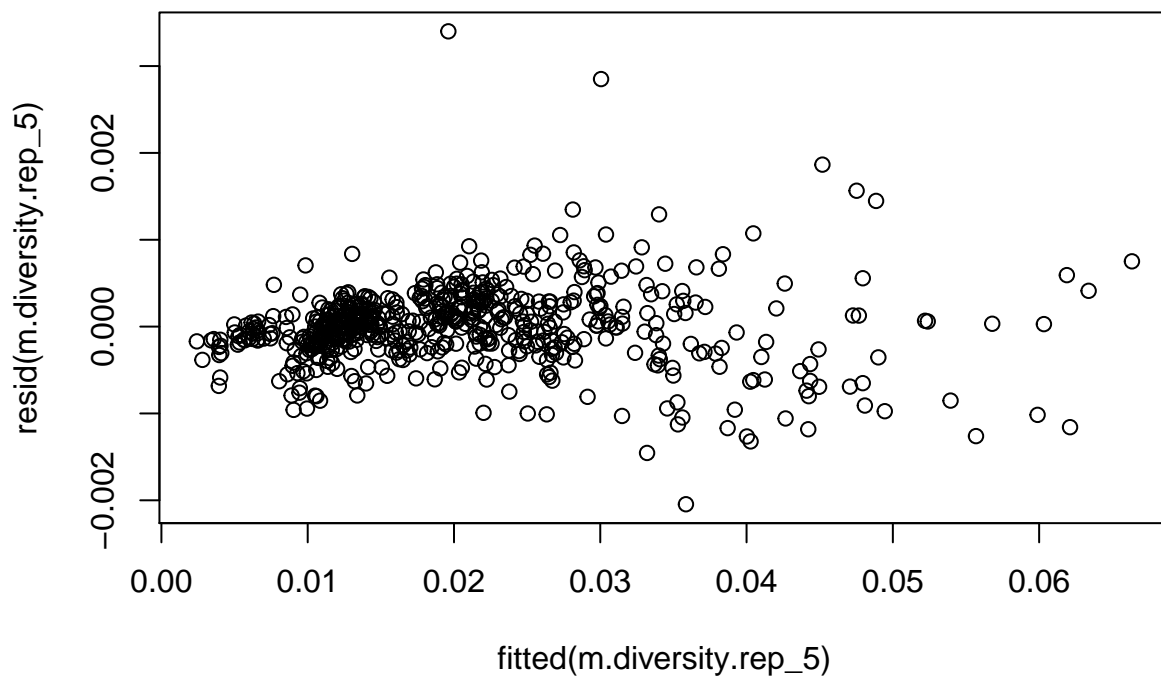
inf.lands.50k.rep_5 <- as.data.frame(cbind(pi.50k$avg, theta.50k$sample_mean, rho.50k$sample_mean, tmrca.50k$sample_mean))
names(inf.lands.50k.rep_5) <- c("diversity", "theta", "rho", "tmrca")

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

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

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

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



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

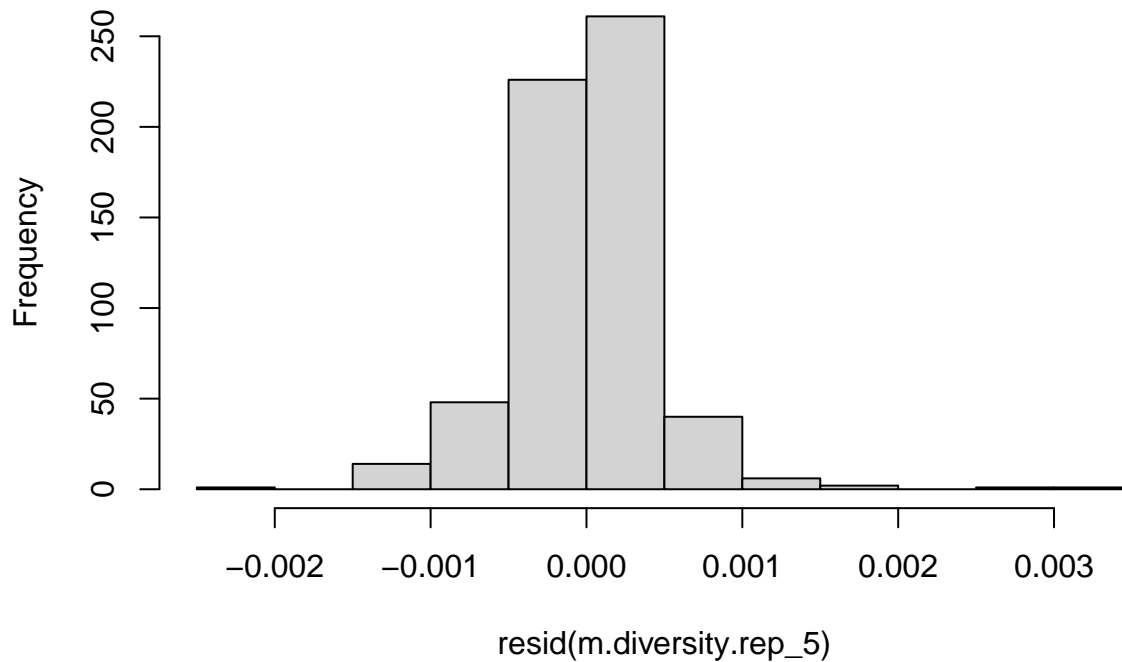
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_5  
## DW = 1.4275, p-value = 5.886e-13  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_5)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_5  
## HMC = 0.55418, p-value = 0.977
```

```
hist(resid(m.diversity.rep_5))
```

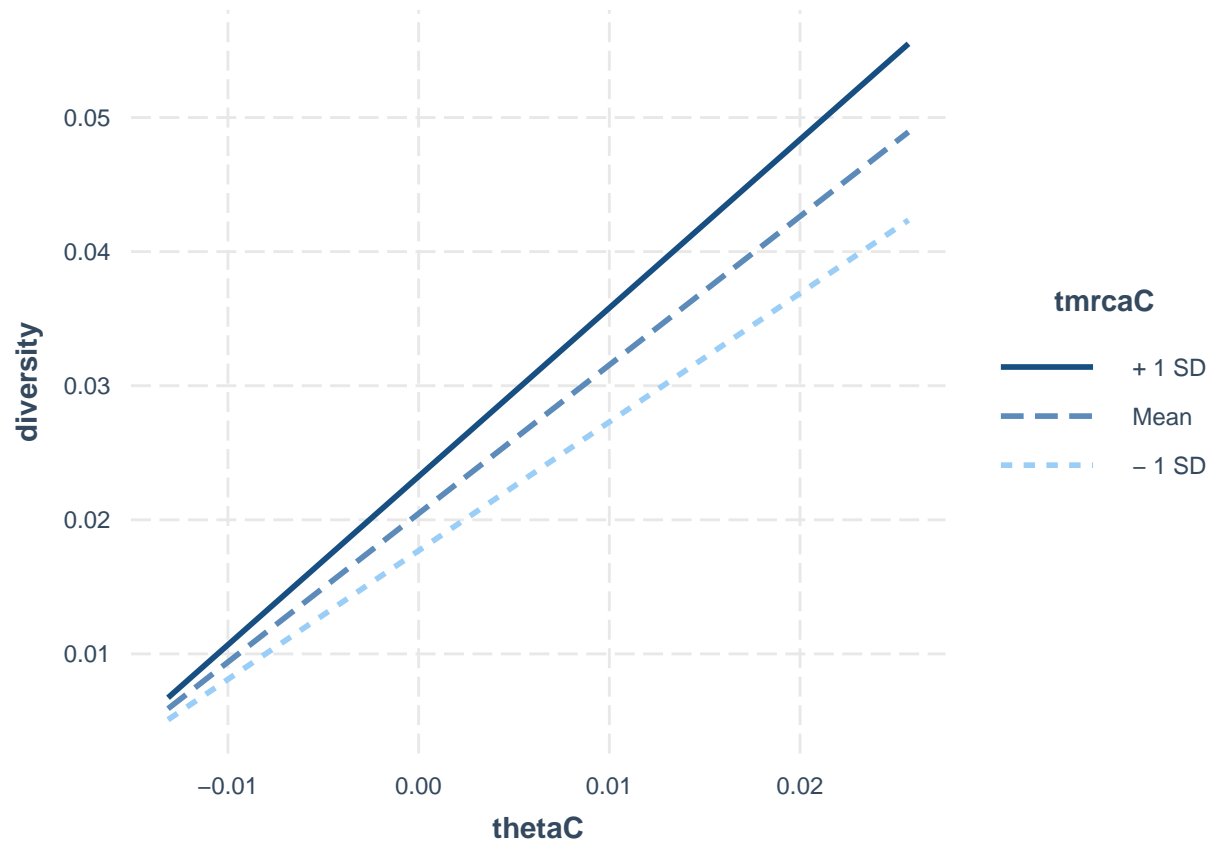
Histogram of resid(m.diversity.rep_5)



```
summary(m.diversity.rep_5)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.50k.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.50k.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.50k.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
## -4.3488500193 -0.4439991672  0.0002670608  0.4775851240  7.1344633176
##
## 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.50k.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.50k.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.50k <- read.table(paste(p, "diversity.50kb.bedgraph", sep = ""), header = T)
pi.50k$avg <- apply(pi.50k[4:ncol(pi.50k)], 1, mean)
tmrca.50k <- read.table(paste(p, "TMRCA.50kb.bedgraph", sep = ""), header = T)
tmrca.50k$avg <- apply(tmrca.50k[4:ncol(tmrca.50k)], 1, mean)
rho.50k <- read.table(paste(p, "rho.50kb.bedgraph", sep = ""), header = T)
theta.50k <- read.table(paste(p, "theta.50kb.bedgraph", sep = ""), header = T)

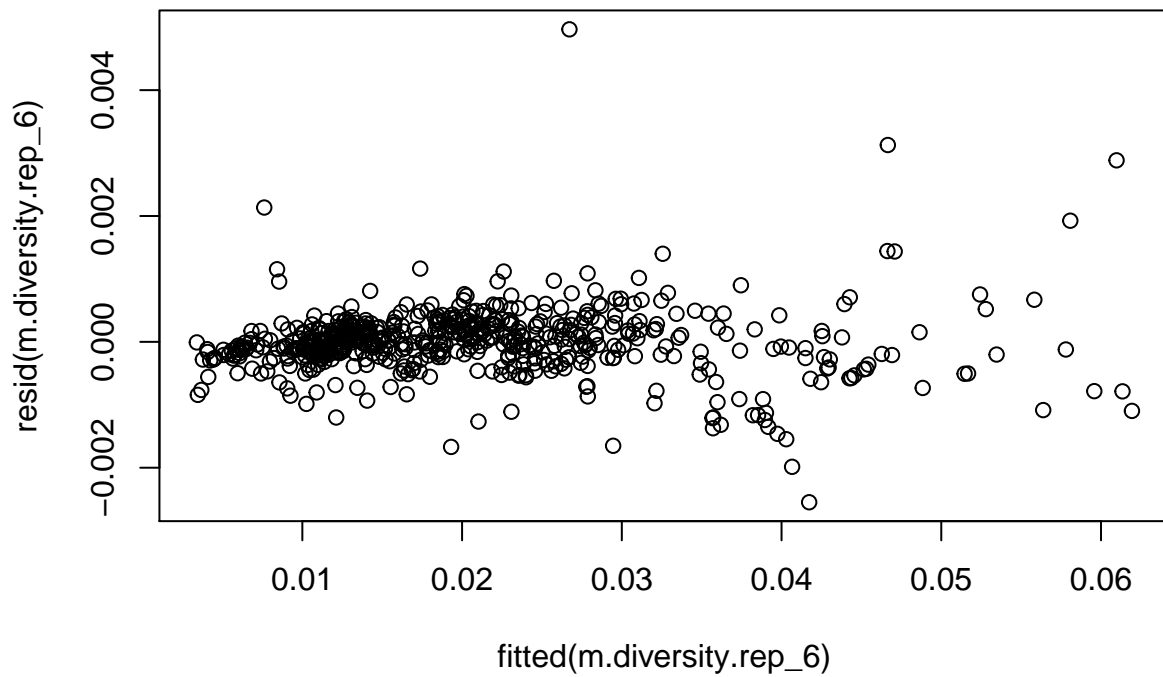
inf.lands.50k.rep_6 <- as.data.frame(cbind(pi.50k$avg, theta.50k$sample_mean, rho.50k$sample_mean, tmrca.50k$sample_mean))
names(inf.lands.50k.rep_6) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.50k.rep_6$thetaC <- inf.lands.50k.rep_6$theta - mean(inf.lands.50k.rep_6$theta)
inf.lands.50k.rep_6$tmrcaC <- inf.lands.50k.rep_6$tmrca - mean(inf.lands.50k.rep_6$tmrca)
inf.lands.50k.rep_6$rhoC <- inf.lands.50k.rep_6$rho - mean(inf.lands.50k.rep_6$rho)

inf.lands.50k.rep_6$bin <- 1:nrow(inf.lands.50k.rep_6)

m.diversity.rep_6 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.50k.rep_6)

plot(resid(m.diversity.rep_6)~fitted(m.diversity.rep_6))
```



```
dwtest(m.diversity.rep_6)
```

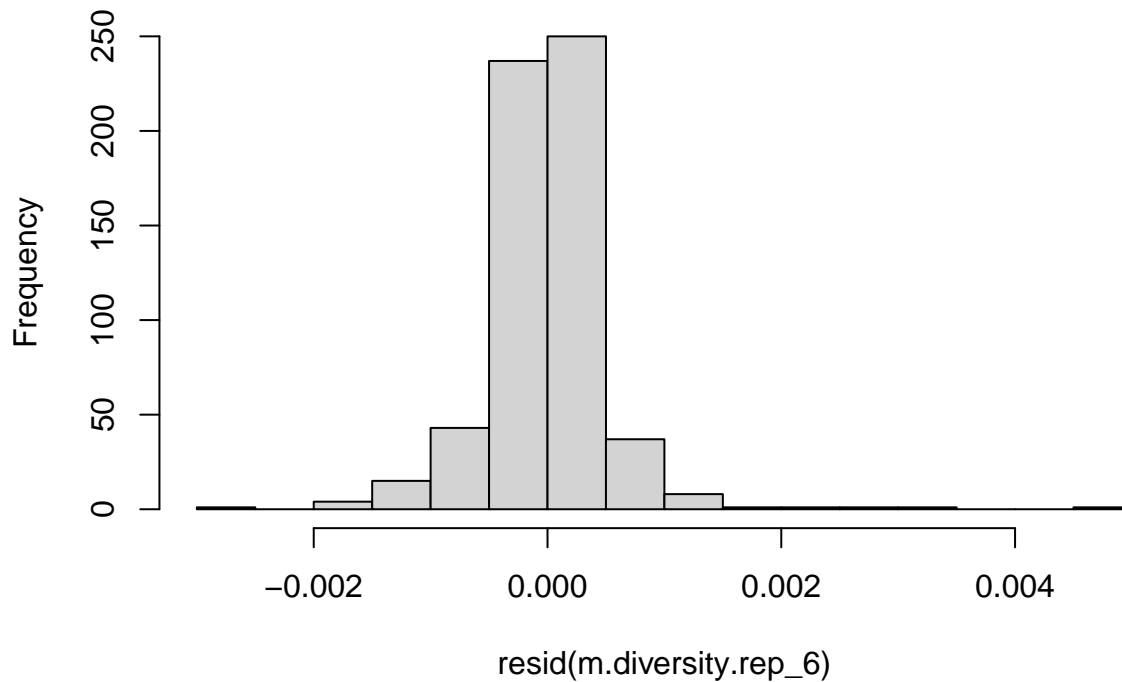
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_6  
## DW = 1.4152, p-value = 1.956e-13  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_6)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_6  
## HMC = 0.5501, p-value = 0.949
```

```
hist(resid(m.diversity.rep_6))
```

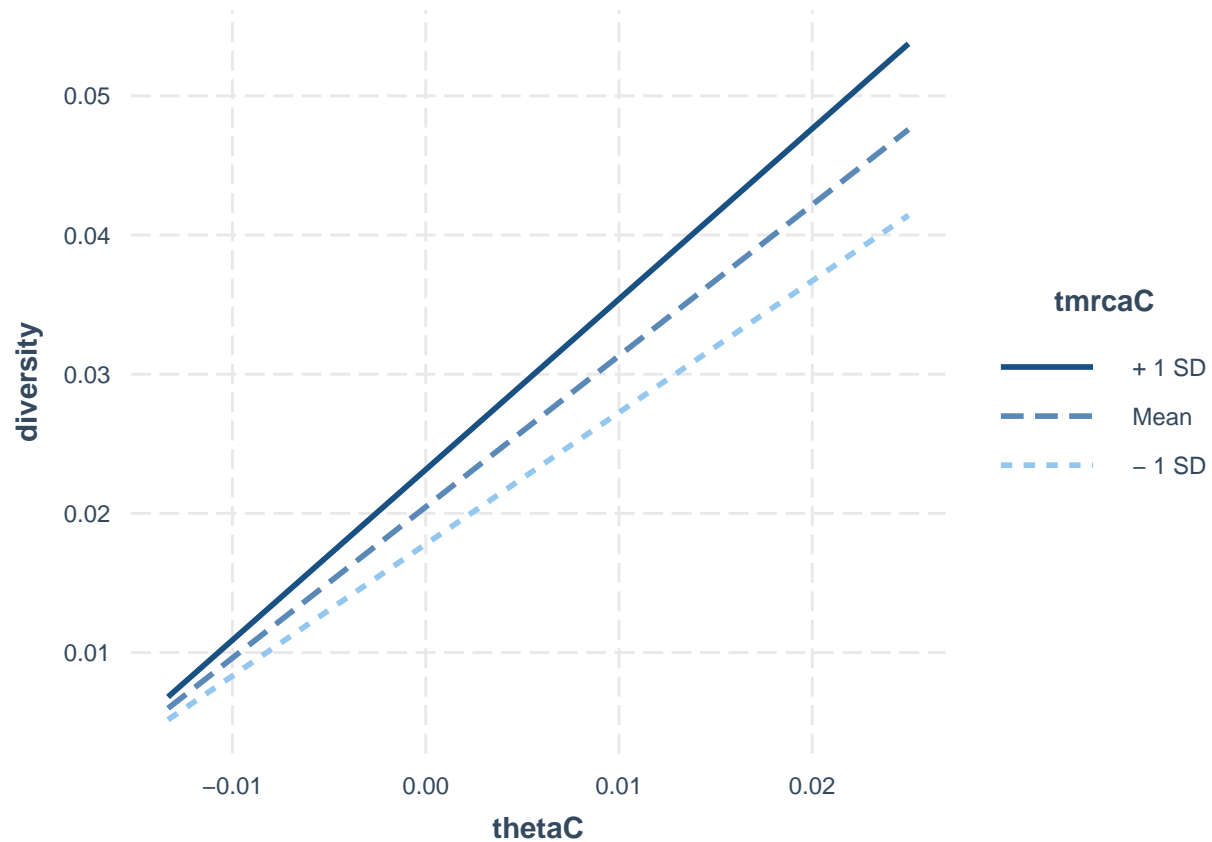
Histogram of resid(m.diversity.rep_6)



```
summary(m.diversity.rep_6)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.50k.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.50k.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.50k.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.50k.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.50k.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 112.72154 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
## -4.246615322 -0.484784795 -0.004012755 0.502253353 5.520109925
##
```

```
## 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.50k <- read.table(paste(p, "diversity.50kb.bedgraph", sep = ""), header = T)
pi.50k$avg <- apply(pi.50k[4:ncol(pi.50k)], 1, mean)
tmrca.50k <- read.table(paste(p, "TMRCA.50kb.bedgraph", sep = ""), header = T)
tmrca.50k$avg <- apply(tmrca.50k[4:ncol(tmrca.50k)], 1, mean)
rho.50k <- read.table(paste(p, "rho.50kb.bedgraph", sep = ""), header = T)
theta.50k <- read.table(paste(p, "theta.50kb.bedgraph", sep = ""), header = T)

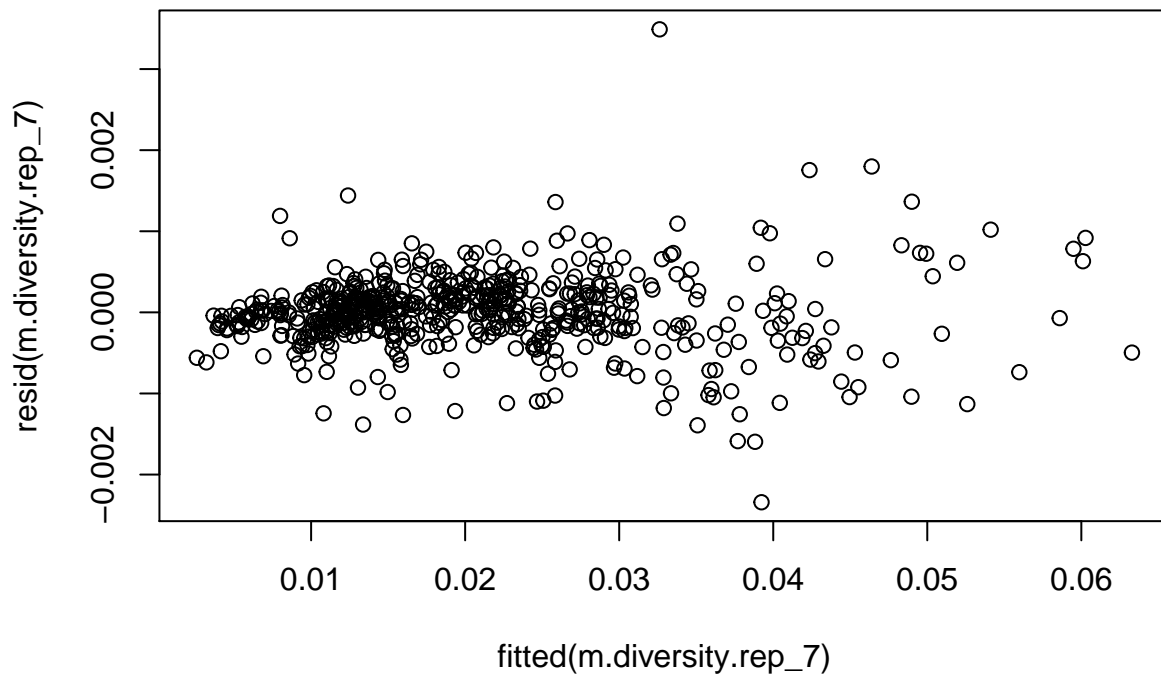
inf.lands.50k.rep_7 <- as.data.frame(cbind(pi.50k$avg, theta.50k$sample_mean, rho.50k$sample_mean, tmrca.50k$sample_mean))
names(inf.lands.50k.rep_7) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.50k.rep_7$thetaC <- inf.lands.50k.rep_7$theta - mean(inf.lands.50k.rep_7$theta)
inf.lands.50k.rep_7$tmrcaC <- inf.lands.50k.rep_7$tmrca - mean(inf.lands.50k.rep_7$tmrca)
inf.lands.50k.rep_7$rhoC <- inf.lands.50k.rep_7$rho - mean(inf.lands.50k.rep_7$rho)

inf.lands.50k.rep_7$bin <- 1:nrow(inf.lands.50k.rep_7)

m.diversity.rep_7 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.50k.rep_7)

plot(resid(m.diversity.rep_7)~fitted(m.diversity.rep_7))
```



```
dwtest(m.diversity.rep_7)
```

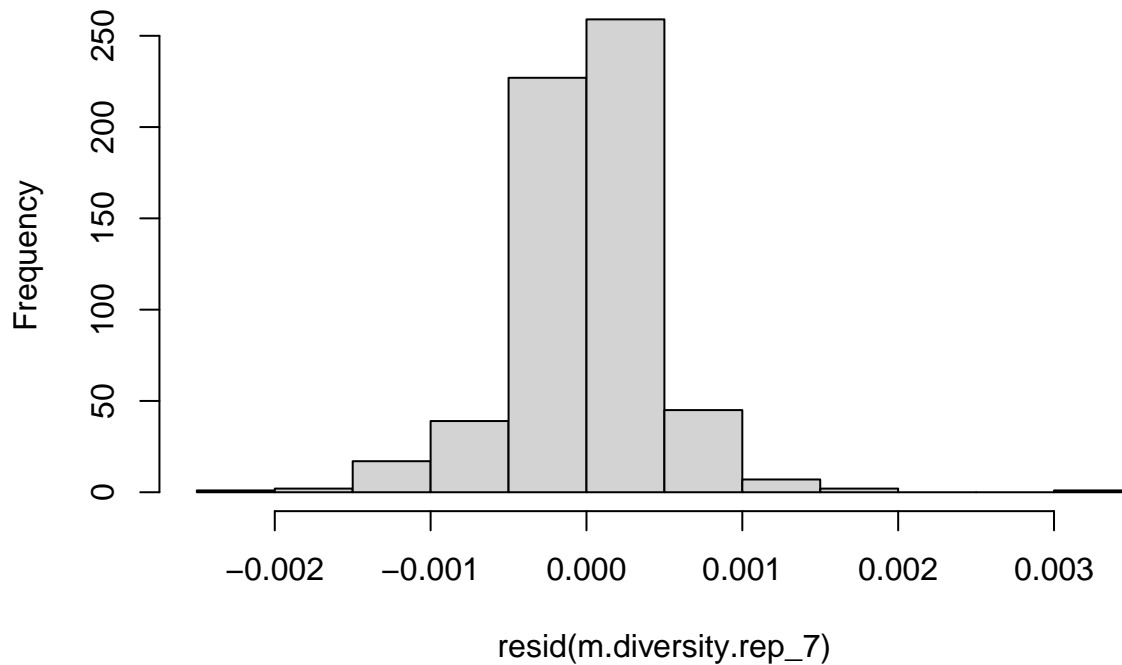
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_7  
## DW = 1.2084, p-value < 2.2e-16  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_7)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_7  
## HMC = 0.58586, p-value = 1
```

```
hist(resid(m.diversity.rep_7))
```

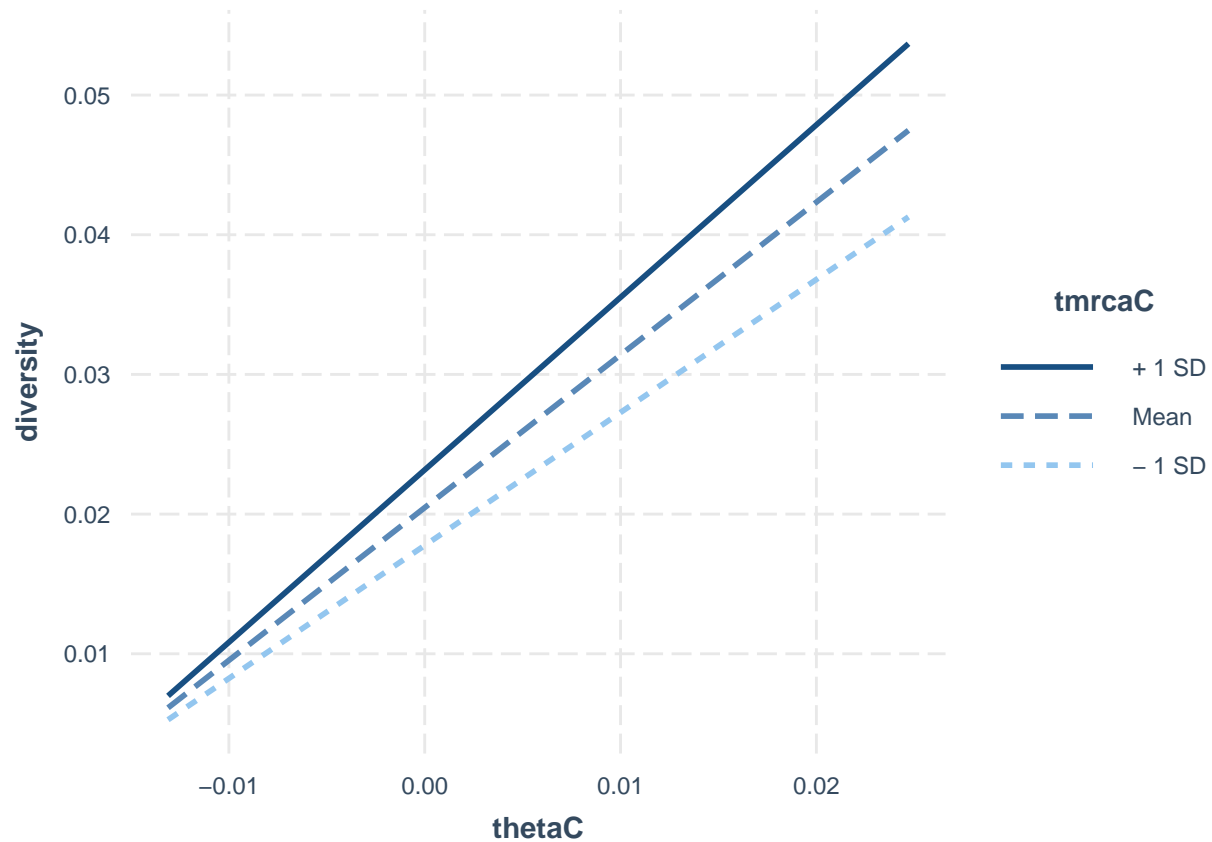

Histogram of resid(m.diversity.rep_7)



```
summary(m.diversity.rep_7)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.50k.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.50k.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.50k.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.50k.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.50k.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.50k <- read.table(paste(p, "diversity.50kb.bedgraph", sep = ""), header = T)
pi.50k$avg <- apply(pi.50k[4:ncol(pi.50k)], 1, mean)
tmrca.50k <- read.table(paste(p, "TMRCA.50kb.bedgraph", sep = ""), header = T)
tmrca.50k$avg <- apply(tmrca.50k[4:ncol(tmrca.50k)], 1, mean)
rho.50k <- read.table(paste(p, "rho.50kb.bedgraph", sep = ""), header = T)
theta.50k <- read.table(paste(p, "theta.50kb.bedgraph", sep = ""), header = T)

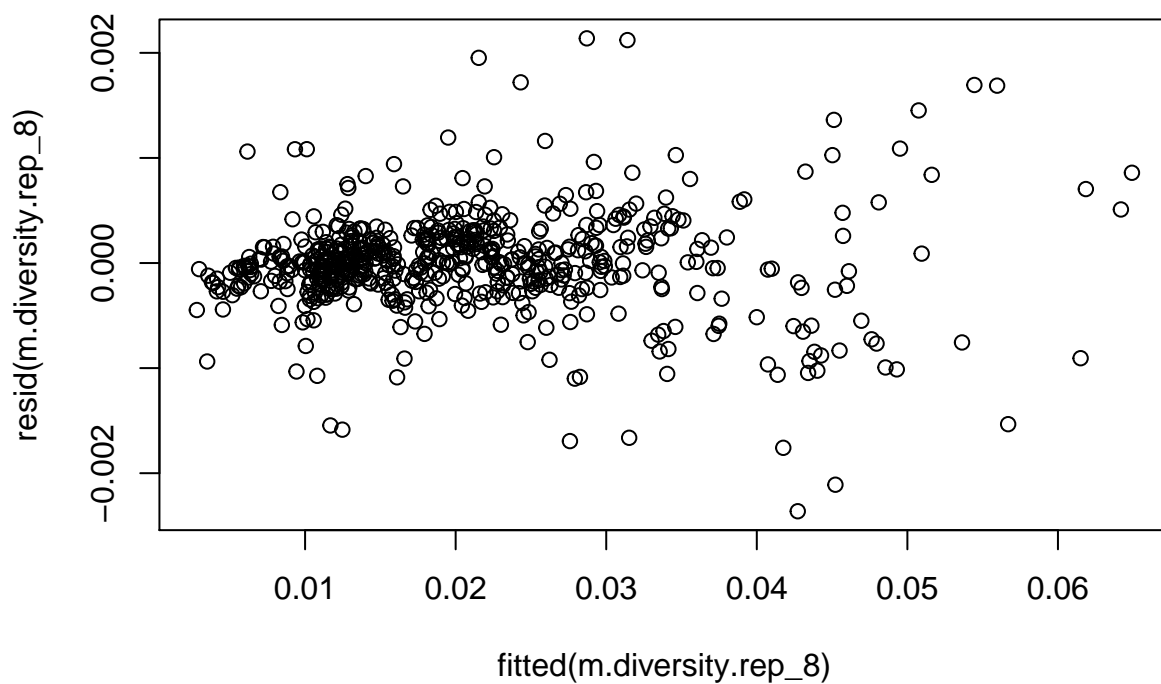
inf.lands.50k.rep_8 <- as.data.frame(cbind(pi.50k$avg, theta.50k$sample_mean, rho.50k$sample_mean, tmrca.50k$sample_mean))
names(inf.lands.50k.rep_8) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.50k.rep_8$thetaC <- inf.lands.50k.rep_8$theta - mean(inf.lands.50k.rep_8$theta)
inf.lands.50k.rep_8$tmrcaC <- inf.lands.50k.rep_8$tmrca - mean(inf.lands.50k.rep_8$tmrca)
inf.lands.50k.rep_8$rhoC <- inf.lands.50k.rep_8$rho - mean(inf.lands.50k.rep_8$rho)

inf.lands.50k.rep_8$bin <- 1:nrow(inf.lands.50k.rep_8)

m.diversity.rep_8 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.50k.rep_8)

plot(resid(m.diversity.rep_8)~fitted(m.diversity.rep_8))
```



```
dwtest(m.diversity.rep_8)
```

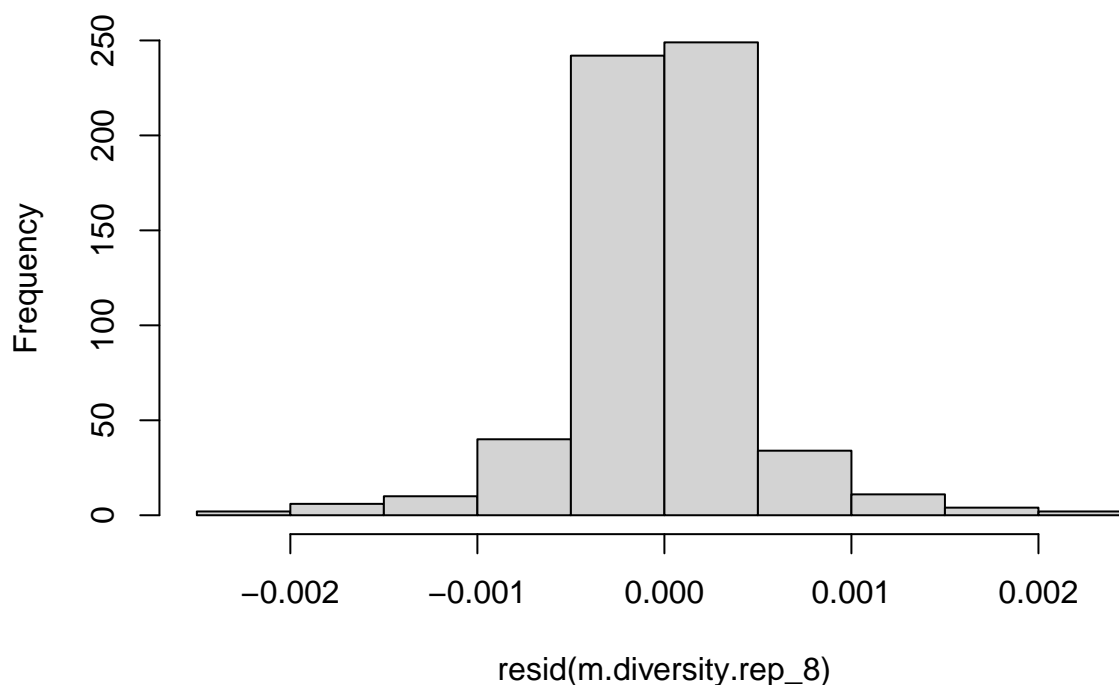
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_8  
## DW = 1.3796, p-value = 6.877e-15  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_8)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_8  
## HMC = 0.62278, p-value = 1
```

```
hist(resid(m.diversity.rep_8))
```

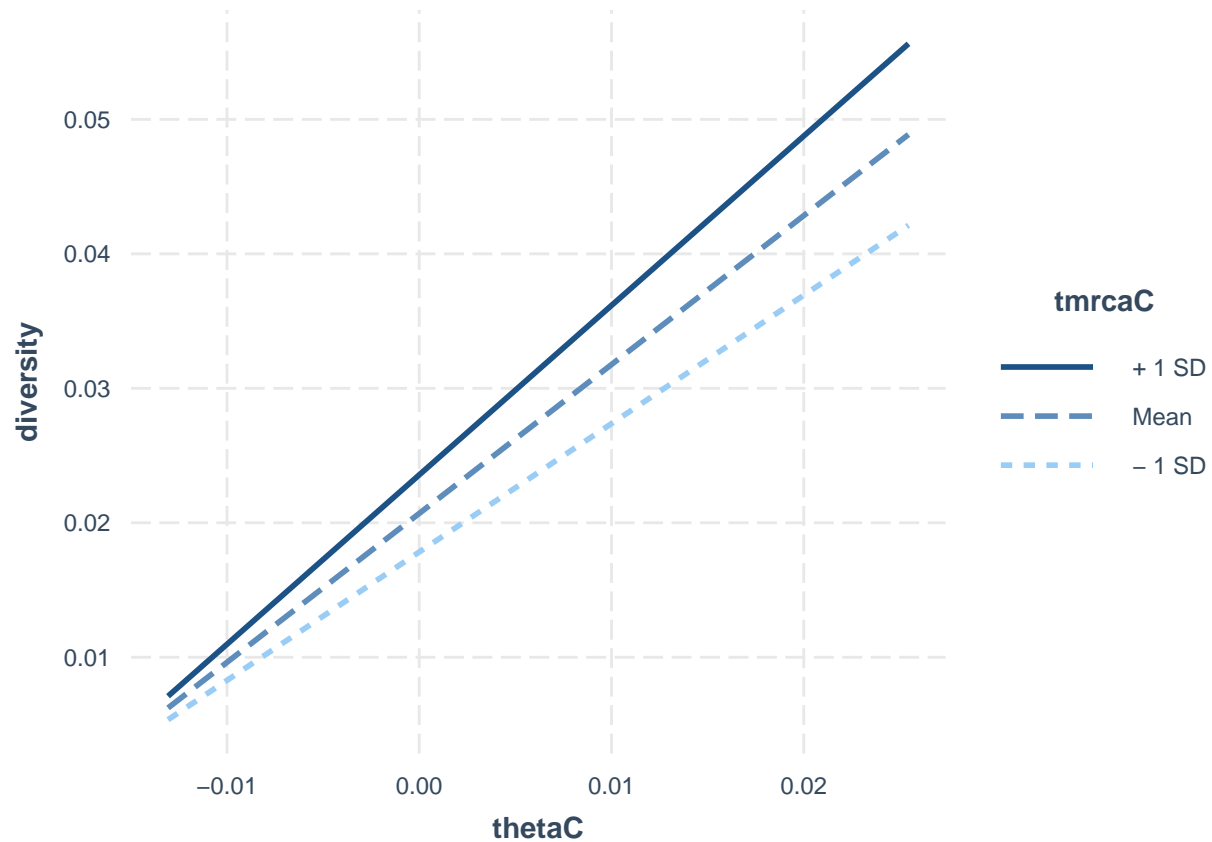
Histogram of resid(m.diversity.rep_8)



```
summary(m.diversity.rep_8)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.50k.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.50k.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.50k.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.50k.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.50k.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
## -7.41084899 -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.50k <- read.table(paste(p, "diversity.50kb.bedgraph", sep = ""), header = T)
pi.50k$avg <- apply(pi.50k[4:ncol(pi.50k)], 1, mean)
tmrca.50k <- read.table(paste(p, "TMRCA.50kb.bedgraph", sep = ""), header = T)
tmrca.50k$avg <- apply(tmrca.50k[4:ncol(tmrca.50k)], 1, mean)
rho.50k <- read.table(paste(p, "rho.50kb.bedgraph", sep = ""), header = T)
theta.50k <- read.table(paste(p, "theta.50kb.bedgraph", sep = ""), header = T)

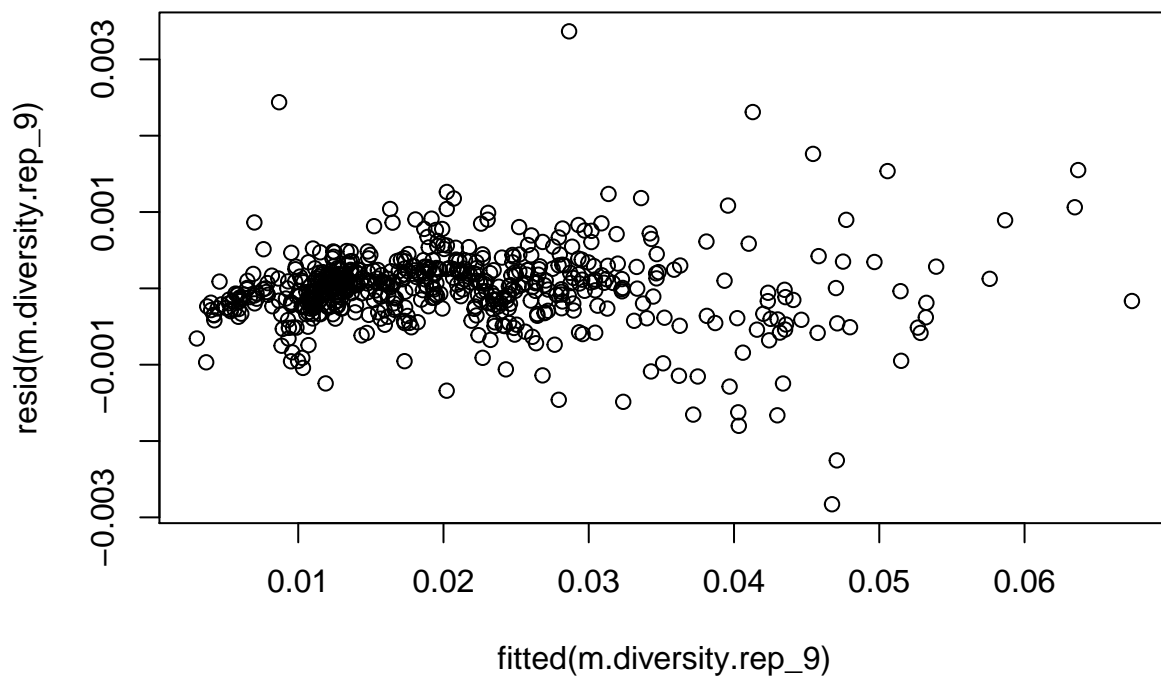
inf.lands.50k.rep_9 <- as.data.frame(cbind(pi.50k$avg, theta.50k$sample_mean, rho.50k$sample_mean, tmrca.50k$sample_mean))
names(inf.lands.50k.rep_9) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.50k.rep_9$thetaC <- inf.lands.50k.rep_9$theta - mean(inf.lands.50k.rep_9$theta)
inf.lands.50k.rep_9$tmrcaC <- inf.lands.50k.rep_9$tmrca - mean(inf.lands.50k.rep_9$tmrca)
inf.lands.50k.rep_9$rhoC <- inf.lands.50k.rep_9$rho - mean(inf.lands.50k.rep_9$rho)

inf.lands.50k.rep_9$bin <- 1:nrow(inf.lands.50k.rep_9)

m.diversity.rep_9 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.50k.rep_9)

plot(resid(m.diversity.rep_9)~fitted(m.diversity.rep_9))
```



```
dwtest(m.diversity.rep_9)
```

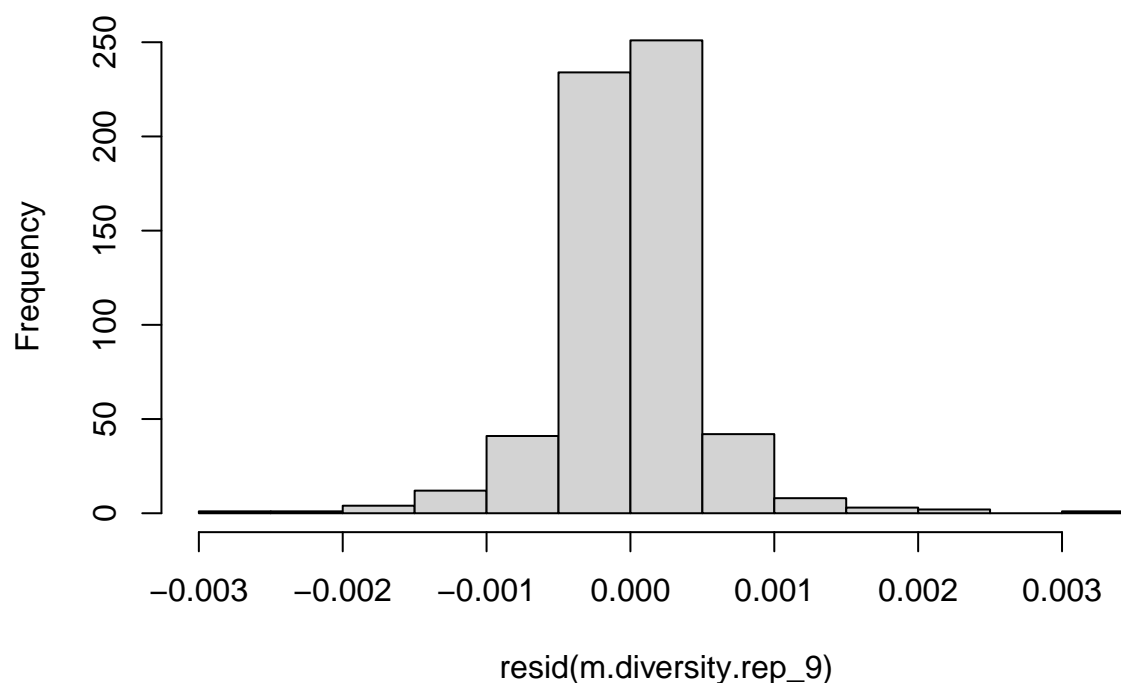
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_9  
## DW = 1.3455, p-value = 2.541e-16  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_9)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_9  
## HMC = 0.52947, p-value = 0.841
```

```
hist(resid(m.diversity.rep_9))
```

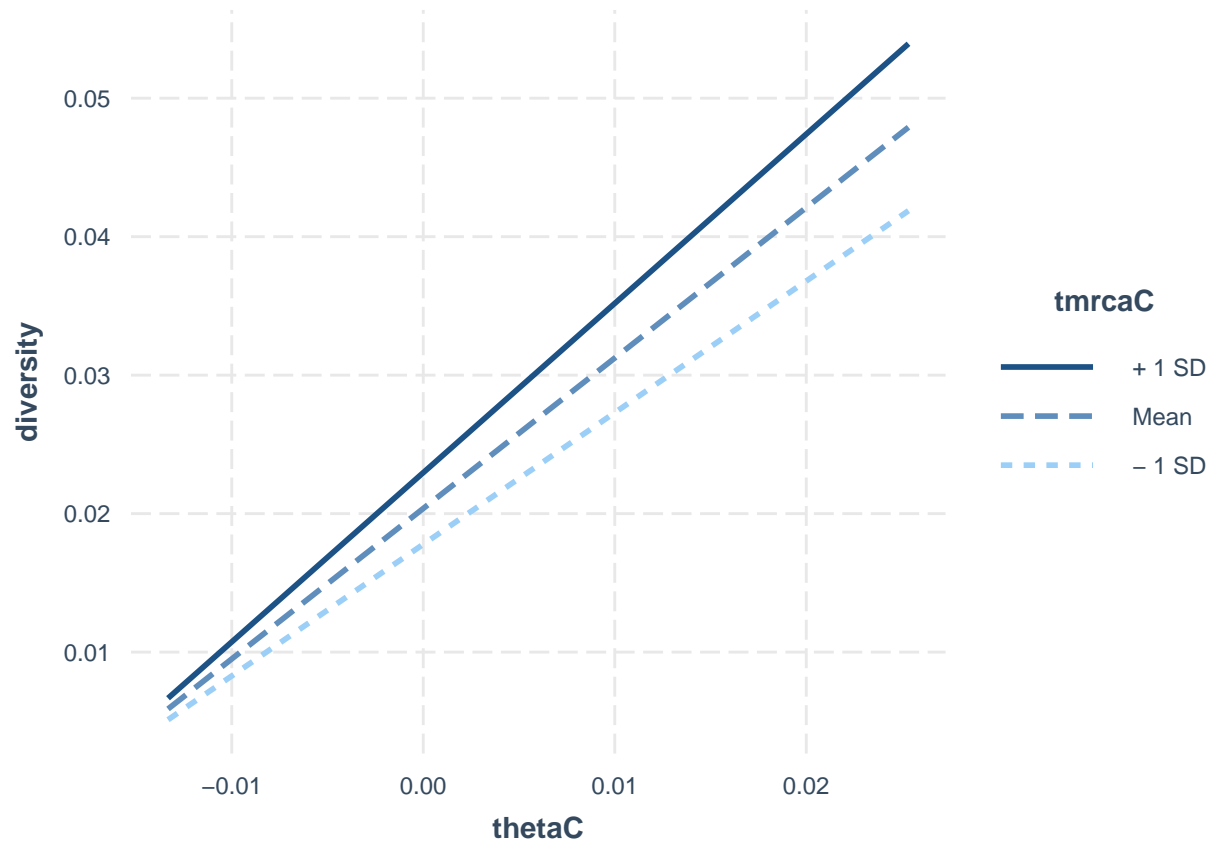
Histogram of resid(m.diversity.rep_9)



```
summary(m.diversity.rep_9)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.50k.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.50k.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.50k.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 6.60989139
##
## 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.50k.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.50k.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

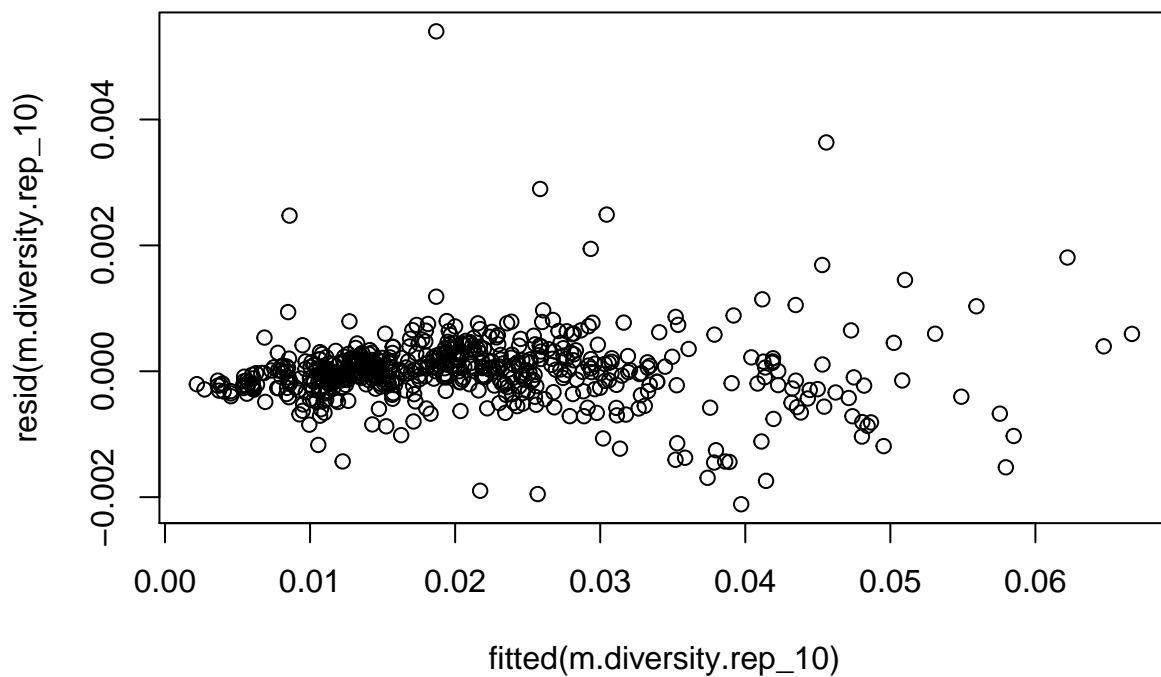
```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_10/rs.pair_10.", sep = "")
pi.50k <- read.table(paste(p, "diversity.50kb.bedgraph", sep = ""), header = T)
pi.50k$avg <- apply(pi.50k[4:ncol(pi.50k)], 1, mean)
tmrca.50k <- read.table(paste(p, "TMRCA.50kb.bedgraph", sep = ""), header = T)
tmrca.50k$avg <- apply(tmrca.50k[4:ncol(tmrca.50k)], 1, mean)
rho.50k <- read.table(paste(p, "rho.50kb.bedgraph", sep = ""), header = T)
theta.50k <- read.table(paste(p, "theta.50kb.bedgraph", sep = ""), header = T)

inf.lands.50k.rep_10 <- as.data.frame(cbind(pi.50k$avg, theta.50k$sample_mean, rho.50k$sample_mean, tmrca.50k$avg))
names(inf.lands.50k.rep_10) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.50k.rep_10$thetaC <- inf.lands.50k.rep_10$theta - mean(inf.lands.50k.rep_10$theta)
inf.lands.50k.rep_10$tmrcaC <- inf.lands.50k.rep_10$tmrca - mean(inf.lands.50k.rep_10$tmrca)
inf.lands.50k.rep_10$rhoC <- inf.lands.50k.rep_10$rho - mean(inf.lands.50k.rep_10$rho)

inf.lands.50k.rep_10$bin <- 1:nrow(inf.lands.50k.rep_10)

m.diversity.rep_10 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.50k.rep_10)
plot(resid(m.diversity.rep_10)~fitted(m.diversity.rep_10))
```



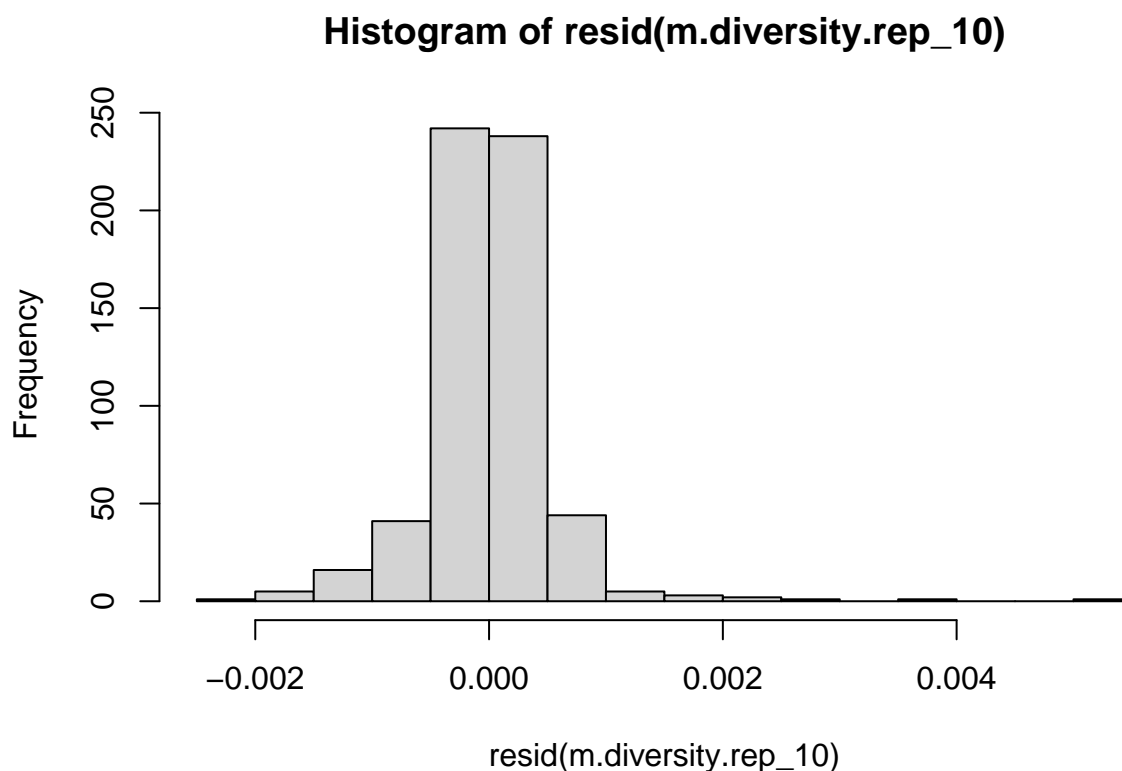
```
dwtest(m.diversity.rep_10)
```

```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_10  
## DW = 1.3449, p-value = 2.3e-16  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_10)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_10  
## HMC = 0.67092, p-value = 1
```

```
hist(resid(m.diversity.rep_10))
```

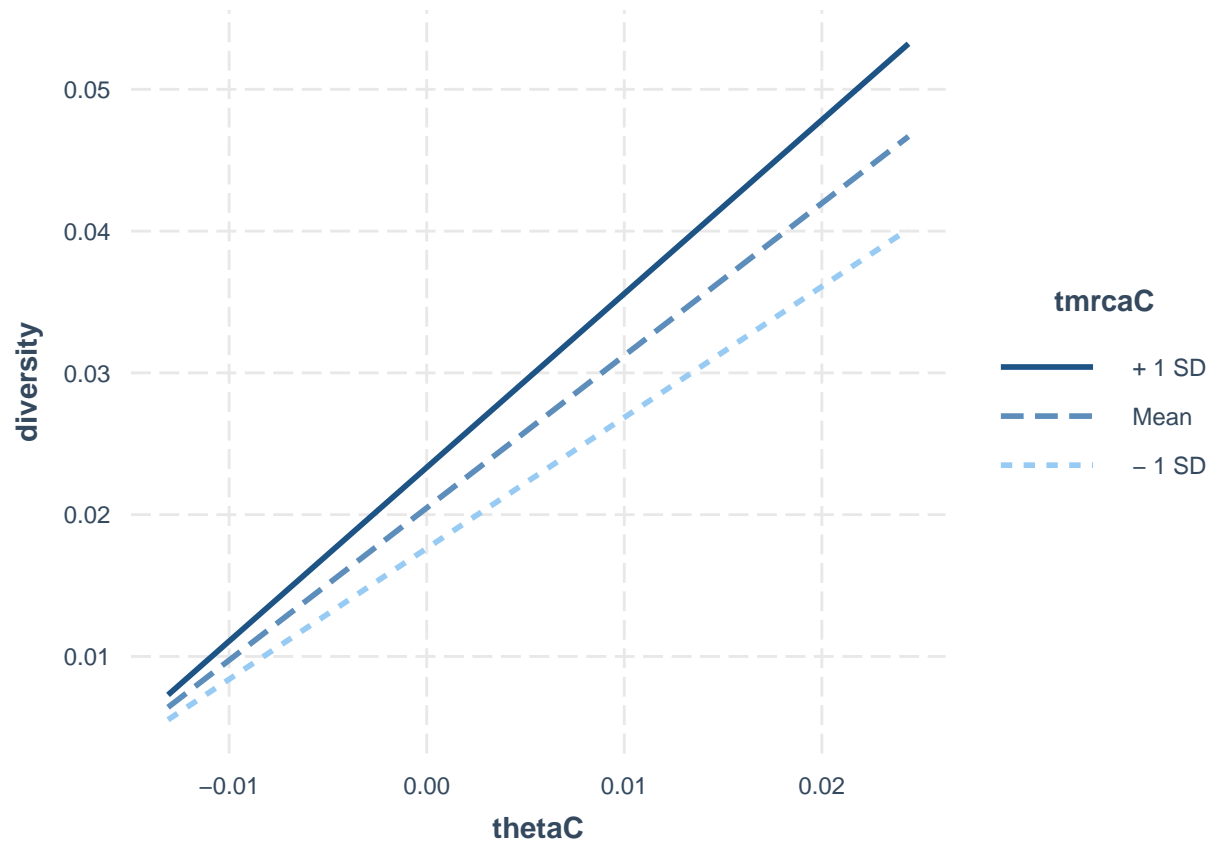


```
summary(m.diversity.rep_10)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.50k.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.50k.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.50k.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.50k.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.50k.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 6.72401412
##
```

```
## 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$VarExp[3] + anova.diversity$VarExp[4] + anova.diversity$VarExp[5]) / anova.diversity$VarExp[1]
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 Plots

```
scale.3d <- function(x) sprintf("%.3f", x)

rho.plot <- as.data.frame(cbind(inf.lands.50k.rep_1$bin,
                                sim.rho.50k$sim,
                                inf.lands.50k.rep_1$rho,
                                inf.lands.50k.rep_2$rho,
                                inf.lands.50k.rep_3$rho,
                                inf.lands.50k.rep_4$rho,
                                inf.lands.50k.rep_5$rho,
                                inf.lands.50k.rep_6$rho,
                                inf.lands.50k.rep_7$rho,
                                inf.lands.50k.rep_8$rho,
                                inf.lands.50k.rep_9$rho,
                                inf.lands.50k.rep_10$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(1, 2, 3, 4, 5, 6, 7, 8, 9, 10))
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.50k.rep_1$bin,
                                sim.theta.50k$sim,
                                inf.lands.50k.rep_1$theta,
                                inf.lands.50k.rep_2$theta,
                                inf.lands.50k.rep_3$theta,
                                inf.lands.50k.rep_4$theta,
                                inf.lands.50k.rep_5$theta))
```

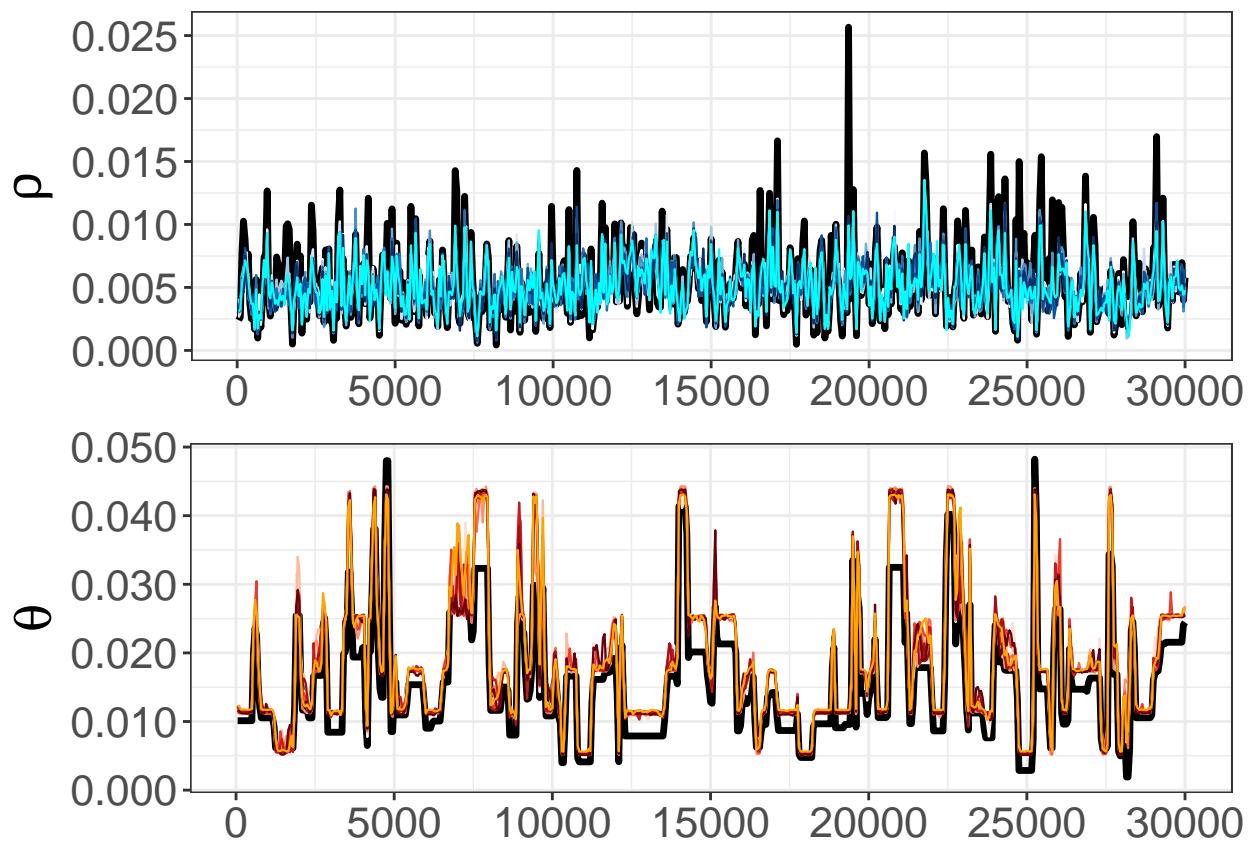
```

      inf.lands.50k.rep_6$theta,
      inf.lands.50k.rep_7$theta,
      inf.lands.50k.rep_8$theta,
      inf.lands.50k.rep_9$theta,
      inf.lands.50k.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_l
theta.map.50kb <- theta.map.50kb + geom_line(data = molten.theta, aes(size = variable)) + scale_size_ma
theta.map.50kb <- theta.map.50kb + scale_color_manual(values = c("black", brewer.pal(n = 9, name = "Red
theta.map.50kb <- theta.map.50kb + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(bro
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(siz

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.200k <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims/dm.sim.rho.2e+05.txt")
sim.theta.200k <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims/dm.sim.theta.2e+05.txt")
sim.lands.200k <- as.data.frame(cbind(sim.theta.200k$sim, sim.rho.200k$sim))
names(sim.lands.200k) <- 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.200k <- read.table(paste(p, "diversity.200kb.bedgraph", sep = ""), header = T)
pi.200k$avg <- apply(pi.200k[4:ncol(pi.200k)], 1, mean)
tmrca.200k <- read.table(paste(p, "TMRCA.200kb.bedgraph", sep = ""), header = T)
tmrca.200k$avg <- apply(tmrca.200k[4:ncol(tmrca.200k)], 1, mean)
rho.200k <- read.table(paste(p, "rho.200kb.bedgraph", sep = ""), header = T)
theta.200k <- read.table(paste(p, "theta.200kb.bedgraph", sep = ""), header = T)

inf.lands.200k.rep_1 <- as.data.frame(cbind(pi.200k$avg, theta.200k$sample_mean, rho.200k$sample_mean,
names(inf.lands.200k.rep_1) <- c("diversity", "theta", "rho", "tmrca")

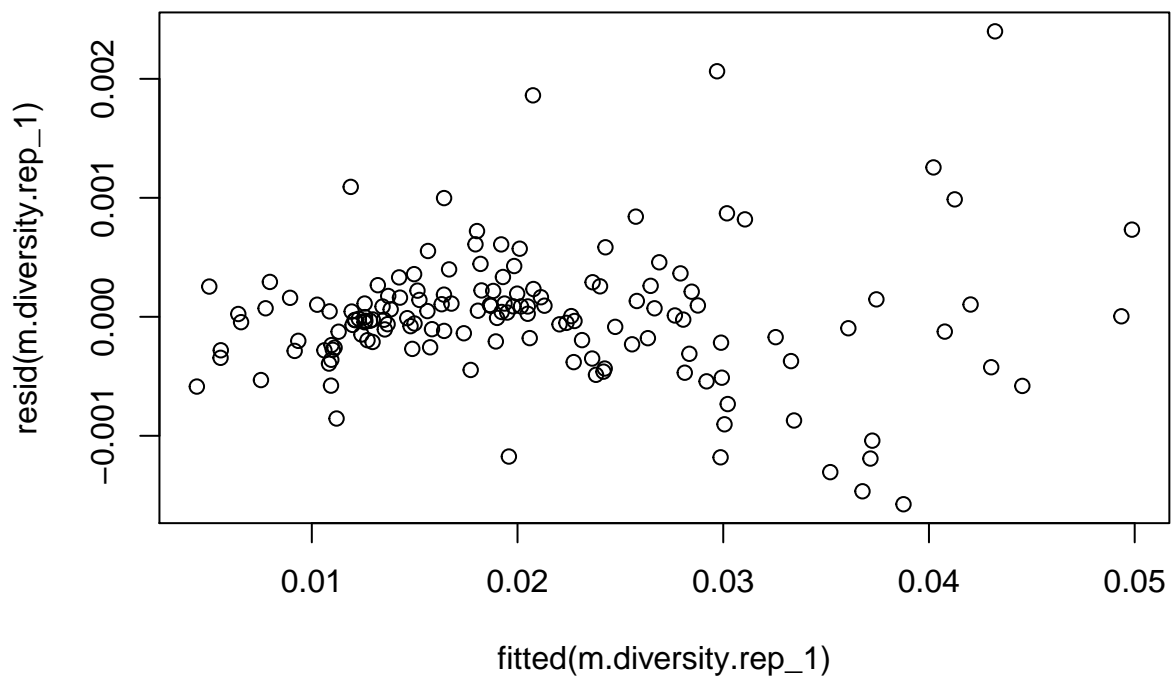
# centering
inf.lands.200k.rep_1$thetaC <- inf.lands.200k.rep_1$theta - mean(inf.lands.200k.rep_1$theta)
inf.lands.200k.rep_1$tmrcaC <- inf.lands.200k.rep_1$tmrca - mean(inf.lands.200k.rep_1$tmrca)
inf.lands.200k.rep_1$rhoC <- inf.lands.200k.rep_1$rho - mean(inf.lands.200k.rep_1$rho)

inf.lands.200k.rep_1$bin <- 1:nrow(inf.lands.200k.rep_1)

m.diversity.rep_1 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.200k.rep_1)

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

```



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

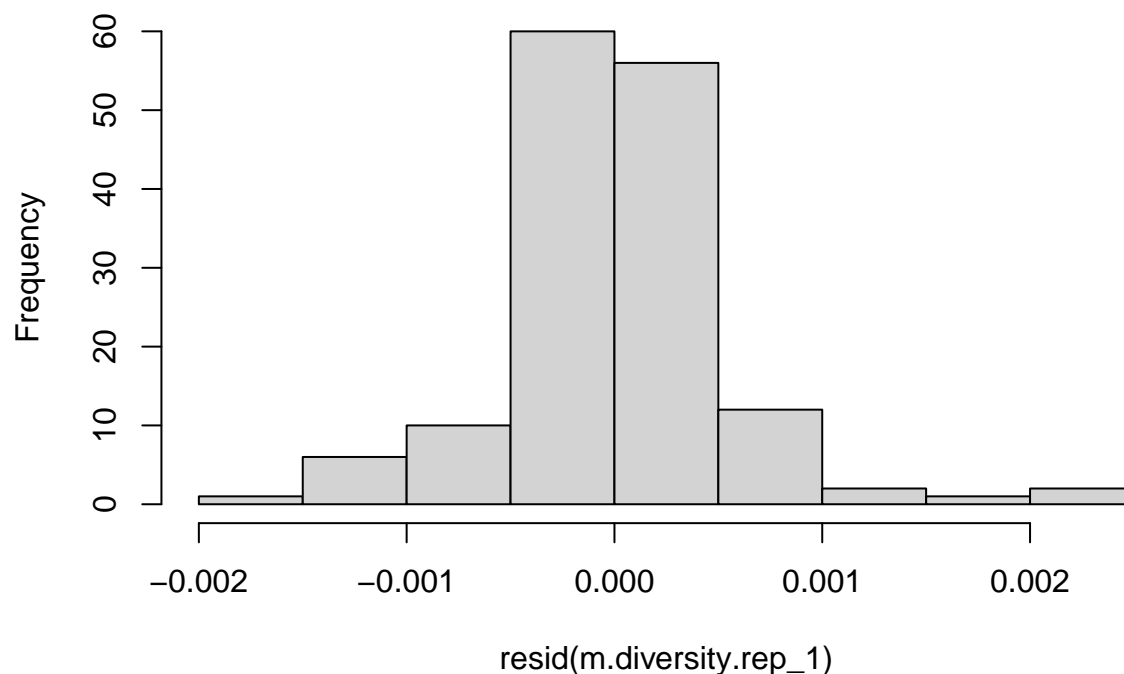
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_1  
## DW = 1.8429, p-value = 0.1407  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_1)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_1  
## HMC = 0.49224, p-value = 0.464
```

```
hist(resid(m.diversity.rep_1))
```

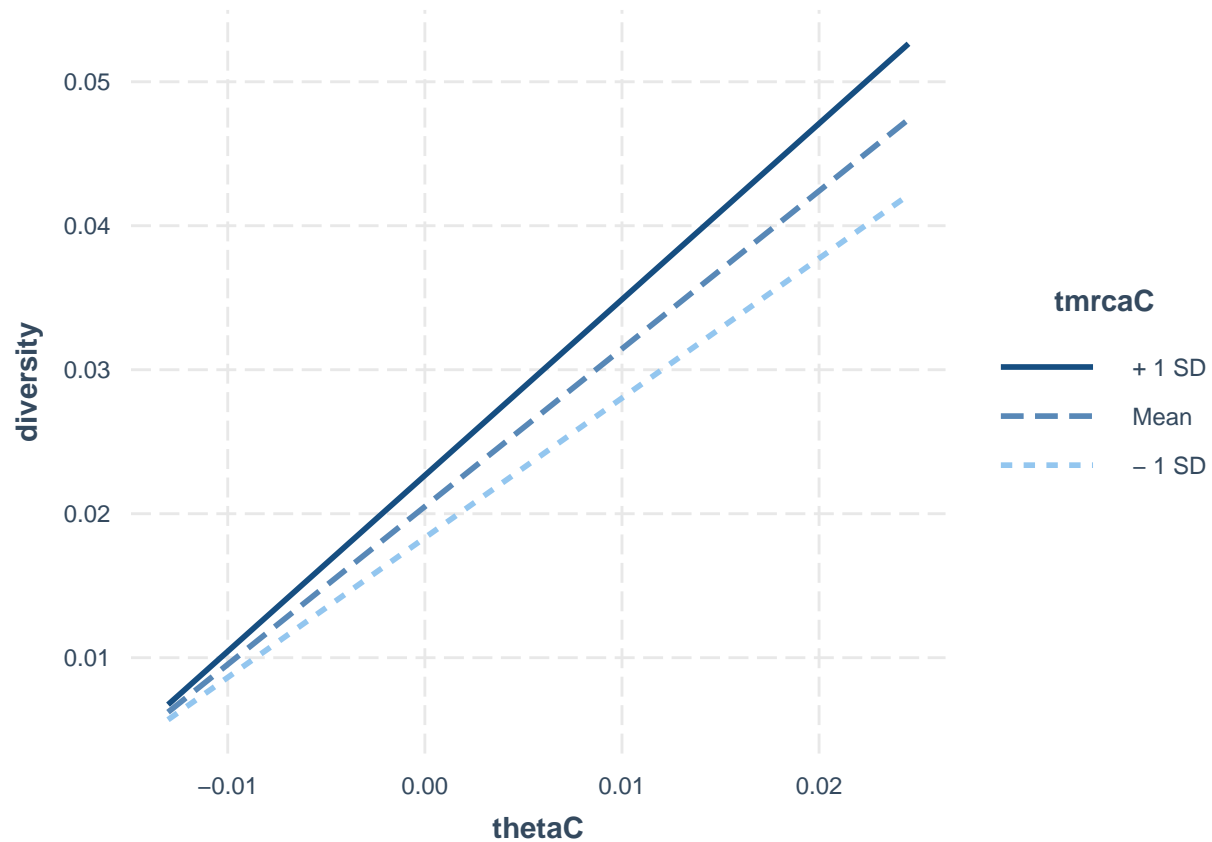
Histogram of resid(m.diversity.rep_1)



```
summary(m.diversity.rep_1)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.200k.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.200k.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.200k.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.200k.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.200k.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$VarExp[3] + anova.diversity$VarExp[4]) / anova.diversity$VarExp[1]
r2.inf.200kb[2, 1] <- anova.diversity$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.200k <- read.table(paste(p, "diversity.200kb.bedgraph", sep = ""), header = T)
pi.200k$avg <- apply(pi.200k[4:ncol(pi.200k)], 1, mean)
tmrca.200k <- read.table(paste(p, "TMRCA.200kb.bedgraph", sep = ""), header = T)
tmrca.200k$avg <- apply(tmrca.200k[4:ncol(tmrca.200k)], 1, mean)
rho.200k <- read.table(paste(p, "rho.200kb.bedgraph", sep = ""), header = T)
theta.200k <- read.table(paste(p, "theta.200kb.bedgraph", sep = ""), header = T)

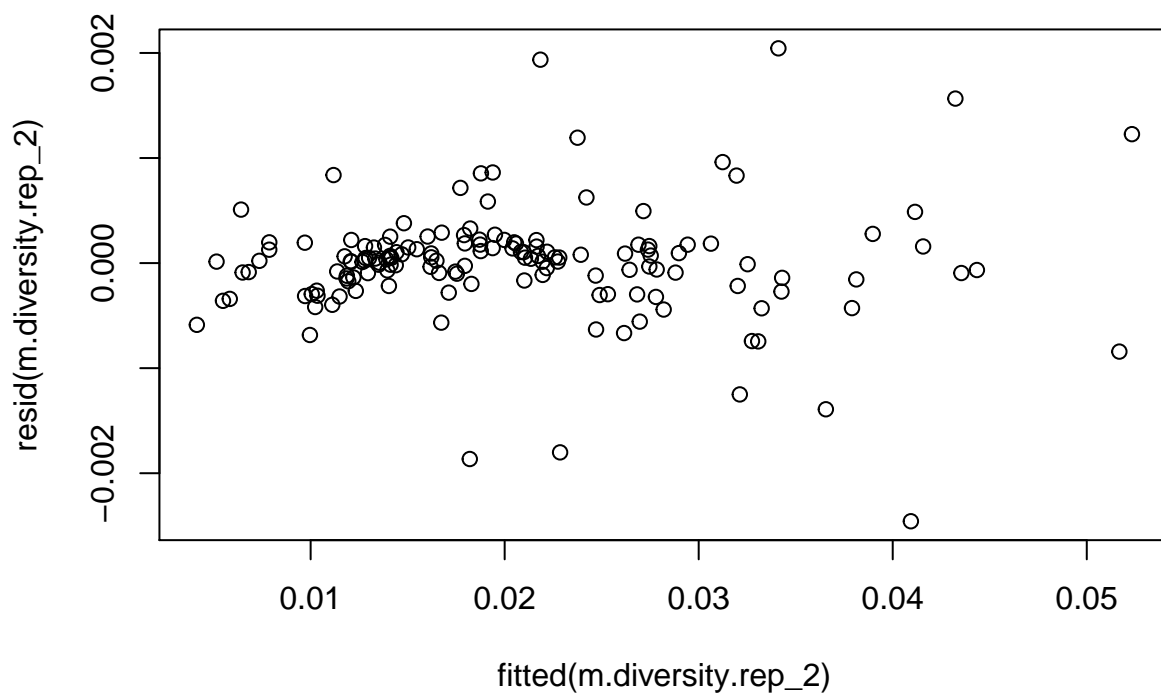
inf.lands.200k.rep_2 <- as.data.frame(cbind(pi.200k$avg, theta.200k$sample_mean, rho.200k$sample_mean, tmrca.200k$sample_mean))
names(inf.lands.200k.rep_2) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.200k.rep_2$thetaC <- inf.lands.200k.rep_2$theta - mean(inf.lands.200k.rep_2$theta)
inf.lands.200k.rep_2$tmrcaC <- inf.lands.200k.rep_2$tmrca - mean(inf.lands.200k.rep_2$tmrca)
inf.lands.200k.rep_2$rhoC <- inf.lands.200k.rep_2$rho - mean(inf.lands.200k.rep_2$rho)

inf.lands.200k.rep_2$bin <- 1:nrow(inf.lands.200k.rep_2)

m.diversity.rep_2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.200k.rep_2)

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



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

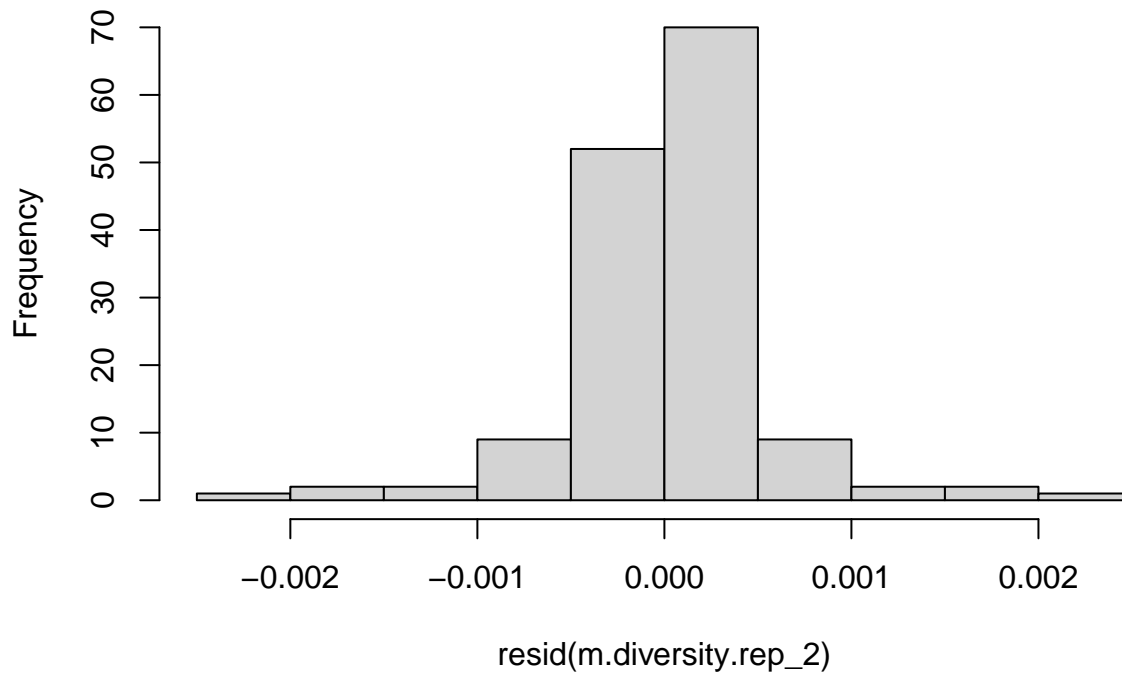
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_2  
## DW = 1.7156, p-value = 0.03159  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(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))
```

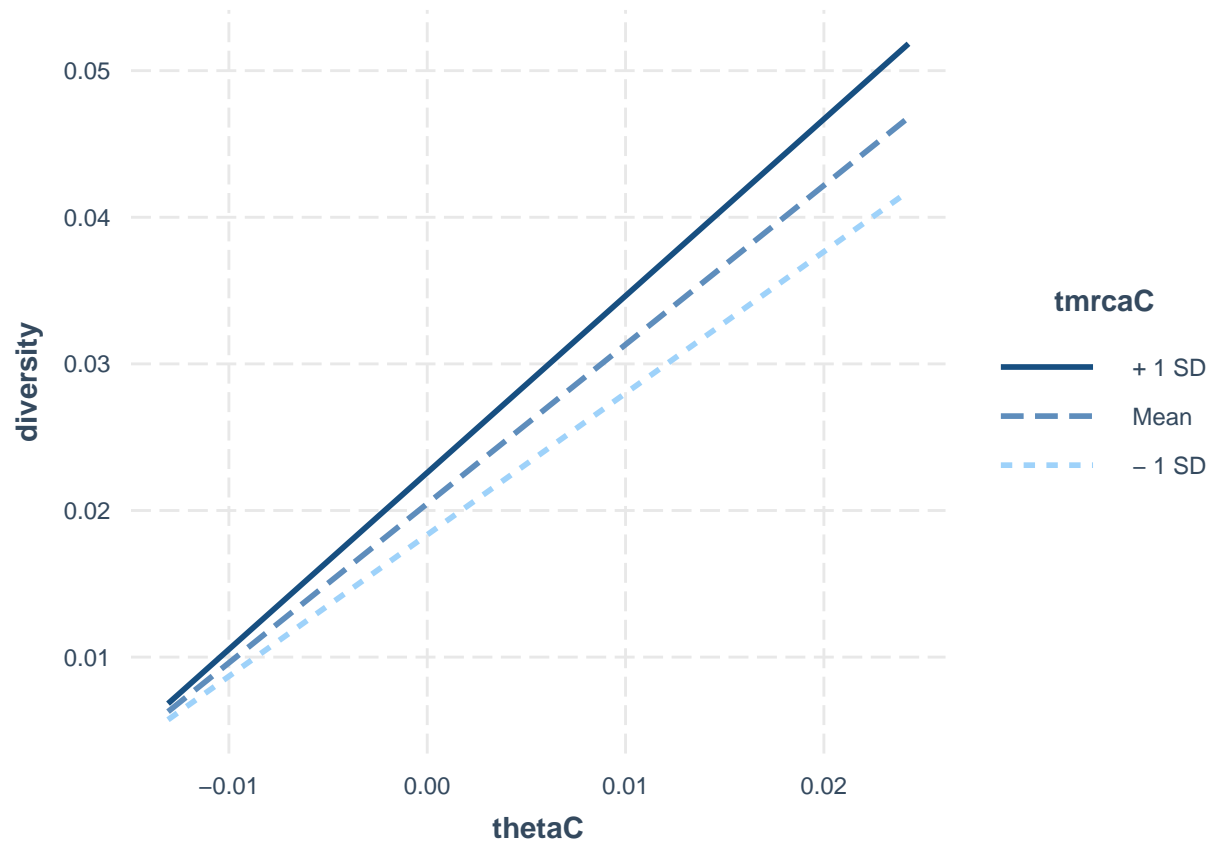
Histogram of resid(m.diversity.rep_2)



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

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.200k.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.200k.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.200k.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.200k.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.200k.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$VarExp[3] + anova.diversity$VarExp[4]) / anova.diversity$VarExp[1]
r2.inf.200kb[2, 2] <- anova.diversity$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

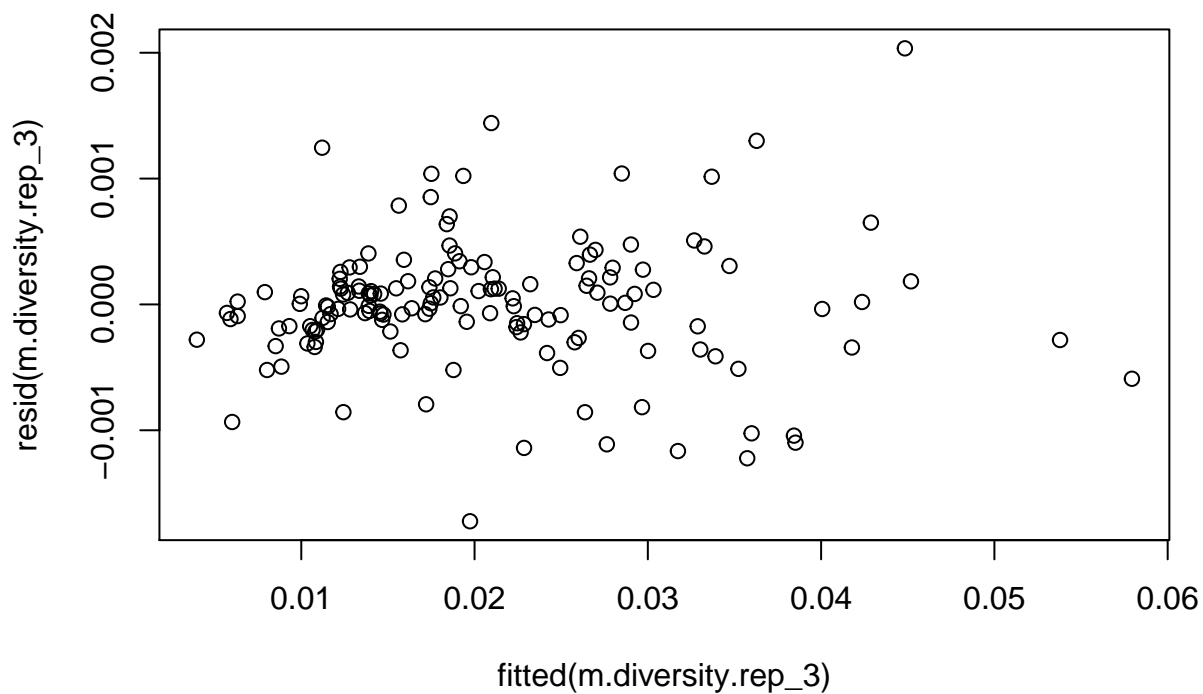
```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_3/rs.pair_3.", sep = "")
pi.200k <- read.table(paste(p, "diversity.200kb.bedgraph", sep = ""), header = T)
pi.200k$avg <- apply(pi.200k[4:ncol(pi.200k)], 1, mean)
tmrca.200k <- read.table(paste(p, "TMRCA.200kb.bedgraph", sep = ""), header = T)
tmrca.200k$avg <- apply(tmrca.200k[4:ncol(tmrca.200k)], 1, mean)
rho.200k <- read.table(paste(p, "rho.200kb.bedgraph", sep = ""), header = T)
theta.200k <- read.table(paste(p, "theta.200kb.bedgraph", sep = ""), header = T)

inf.lands.200k.rep_3 <- as.data.frame(cbind(pi.200k$avg, theta.200k$sample_mean, rho.200k$sample_mean, tmrca.200k$avg))
names(inf.lands.200k.rep_3) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.200k.rep_3$thetaC <- inf.lands.200k.rep_3$theta - mean(inf.lands.200k.rep_3$theta)
inf.lands.200k.rep_3$tmrcaC <- inf.lands.200k.rep_3$tmrca - mean(inf.lands.200k.rep_3$tmrca)
inf.lands.200k.rep_3$rhoC <- inf.lands.200k.rep_3$rho - mean(inf.lands.200k.rep_3$rho)

inf.lands.200k.rep_3$bin <- 1:nrow(inf.lands.200k.rep_3)

m.diversity.rep_3 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.200k.rep_3)
plot(resid(m.diversity.rep_3)~fitted(m.diversity.rep_3))
```



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

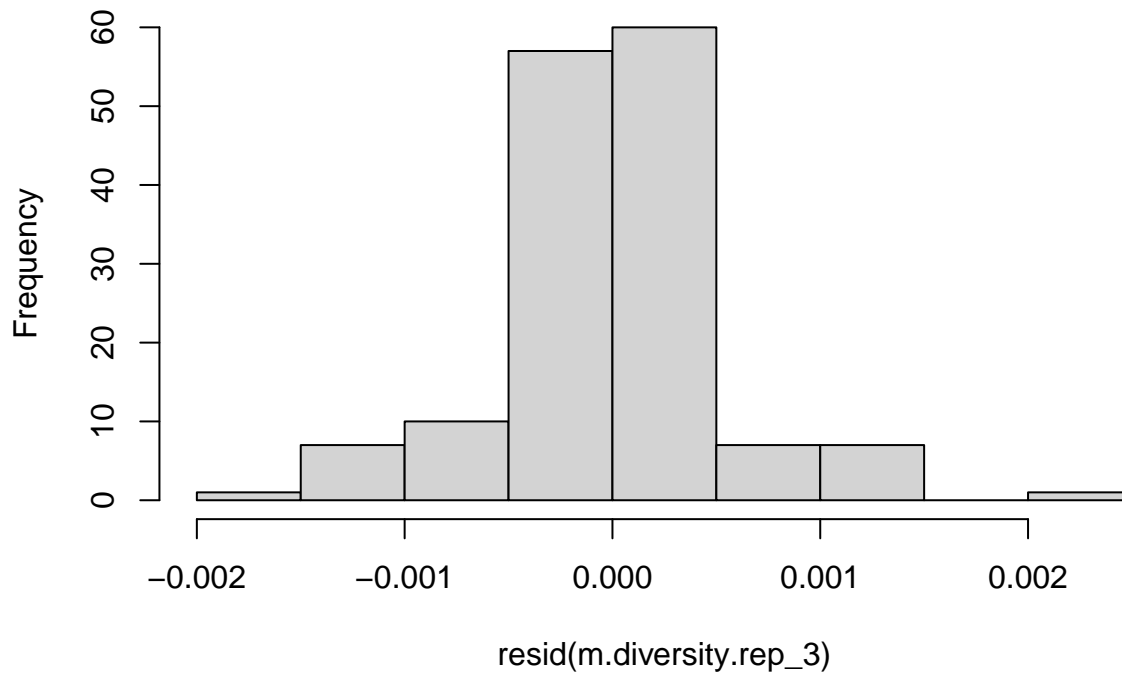
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_3  
## DW = 1.7271, p-value = 0.03626  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_3)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_3  
## HMC = 0.49269, p-value = 0.458
```

```
hist(resid(m.diversity.rep_3))
```

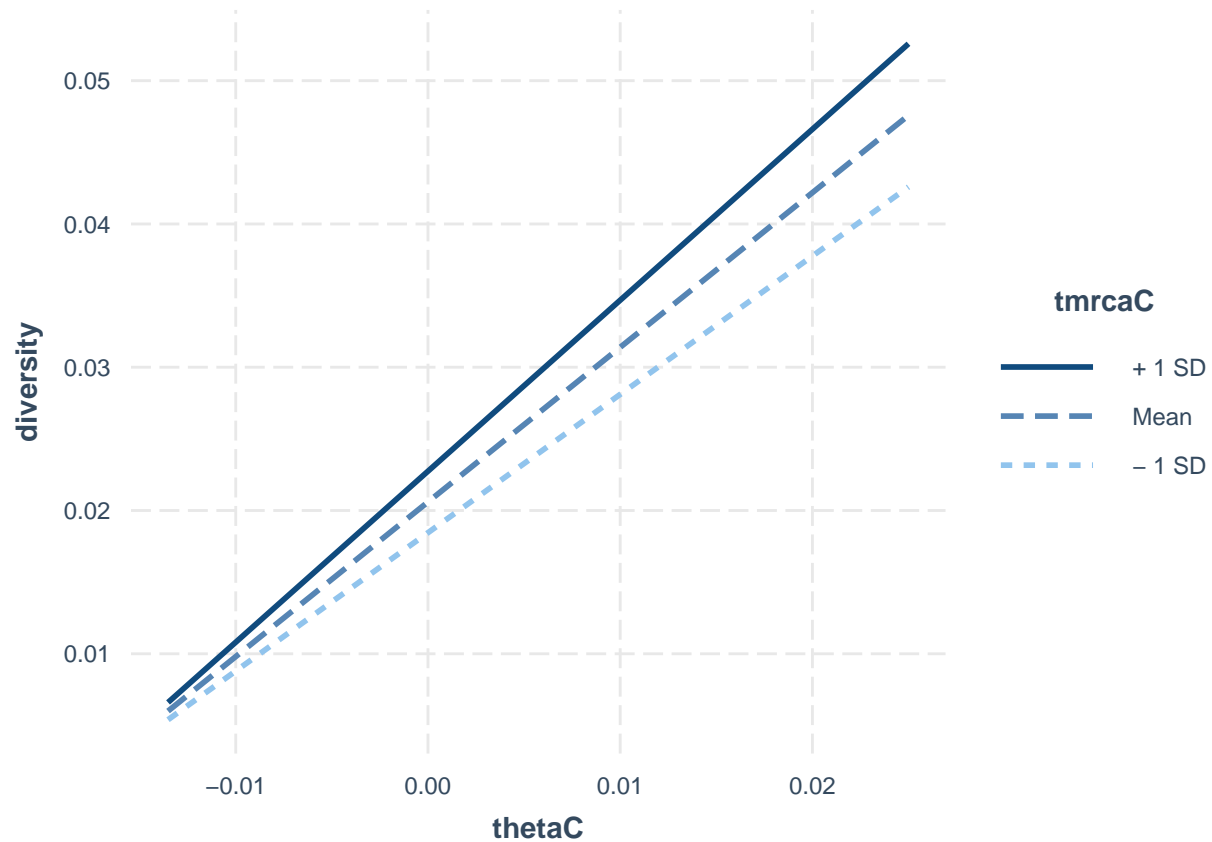

Histogram of resid(m.diversity.rep_3)



```
summary(m.diversity.rep_3)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.200k.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.200k.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.200k.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.200k.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.200k.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

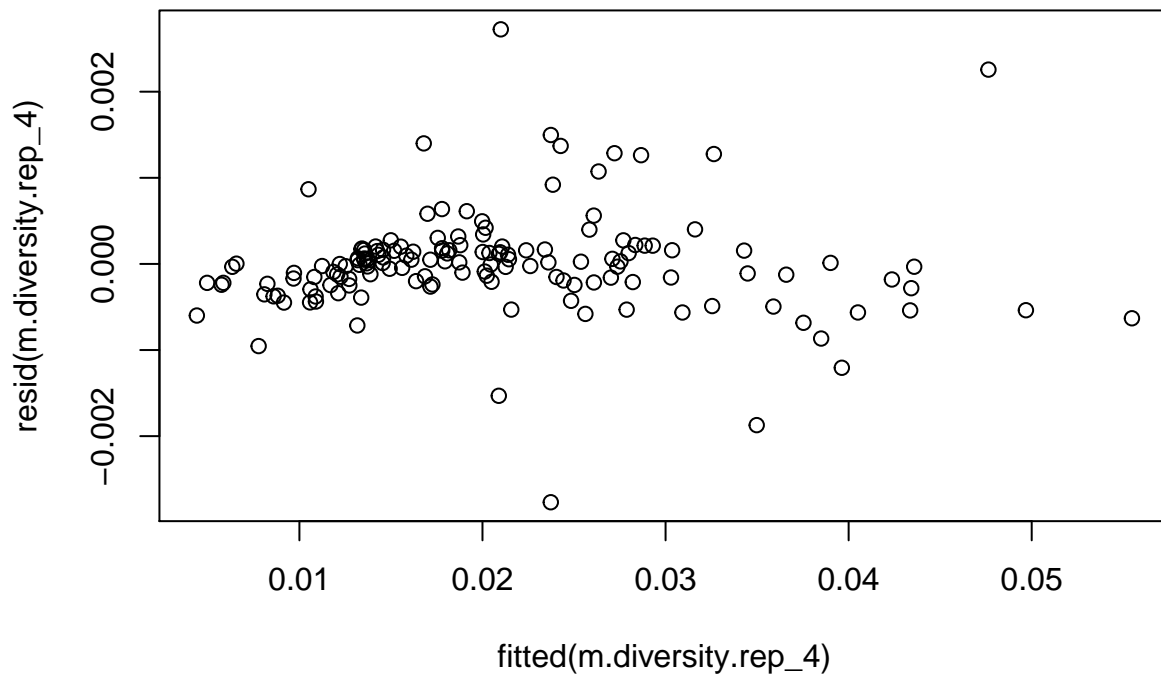
```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_4/rs.pair_4.", sep = "")
pi.200k <- read.table(paste(p, "diversity.200kb.bedgraph", sep = ""), header = T)
pi.200k$avg <- apply(pi.200k[4:ncol(pi.200k)], 1, mean)
tmrca.200k <- read.table(paste(p, "TMRCA.200kb.bedgraph", sep = ""), header = T)
tmrca.200k$avg <- apply(tmrca.200k[4:ncol(tmrca.200k)], 1, mean)
rho.200k <- read.table(paste(p, "rho.200kb.bedgraph", sep = ""), header = T)
theta.200k <- read.table(paste(p, "theta.200kb.bedgraph", sep = ""), header = T)

inf.lands.200k.rep_4 <- as.data.frame(cbind(pi.200k$avg, theta.200k$sample_mean, rho.200k$sample_mean,
names(inf.lands.200k.rep_4) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.200k.rep_4$thetaC <- inf.lands.200k.rep_4$theta - mean(inf.lands.200k.rep_4$theta)
inf.lands.200k.rep_4$tmrcaC <- inf.lands.200k.rep_4$tmrca - mean(inf.lands.200k.rep_4$tmrca)
inf.lands.200k.rep_4$rhoC <- inf.lands.200k.rep_4$rho - mean(inf.lands.200k.rep_4$rho)

inf.lands.200k.rep_4$bin <- 1:nrow(inf.lands.200k.rep_4)

m.diversity.rep_4 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.200k.rep_4)
plot(resid(m.diversity.rep_4)~fitted(m.diversity.rep_4))
```



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

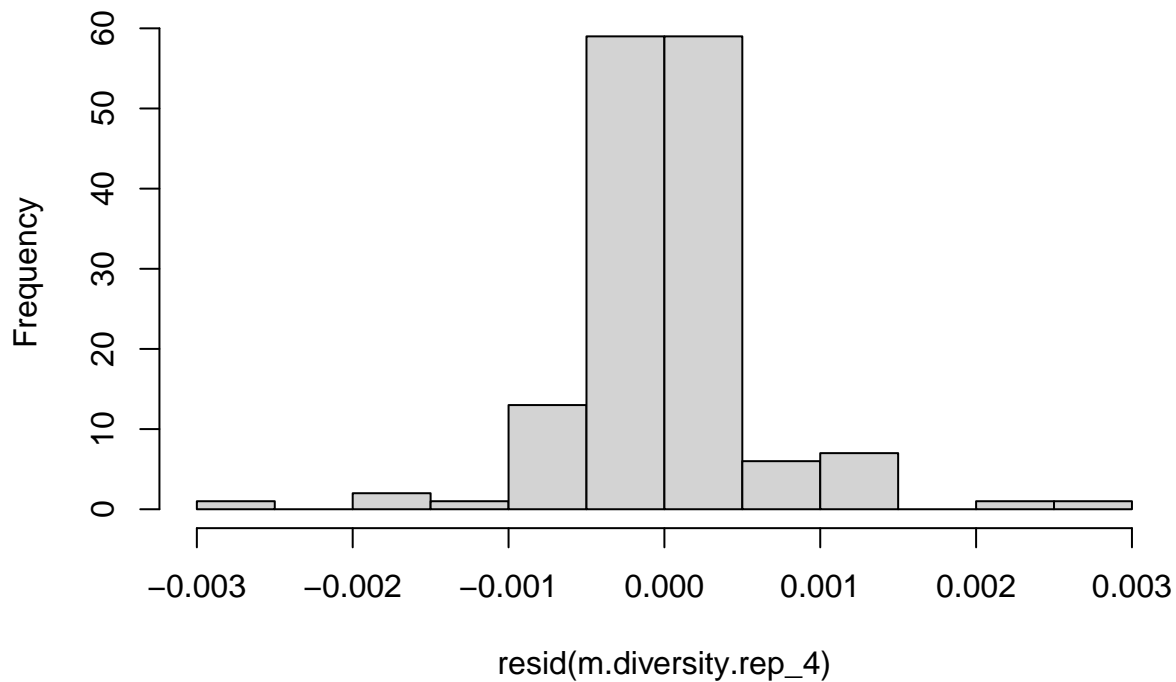
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_4  
## DW = 1.6283, p-value = 0.00823  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_4)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_4  
## HMC = 0.54628, p-value = 0.802
```

```
hist(resid(m.diversity.rep_4))
```

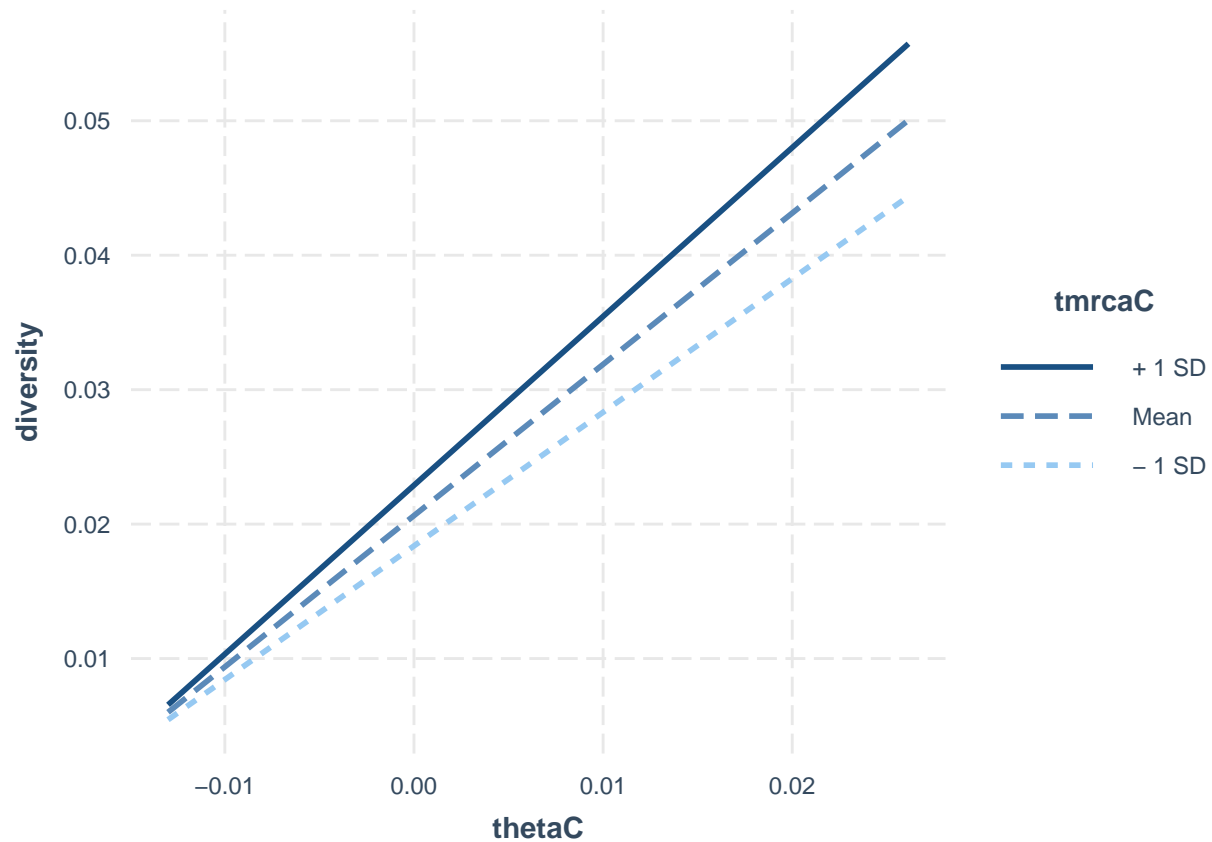
Histogram of resid(m.diversity.rep_4)



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

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.200k.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.200k.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.200k.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.200k.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.200k.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$VarExp[3] + anova.diversity$VarExp[4]) / anova.diversity$VarExp[1]
r2.inf.200kb[2, 4] <- anova.diversity$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.200k <- read.table(paste(p, "diversity.200kb.bedgraph", sep = ""), header = T)
pi.200k$avg <- apply(pi.200k[4:ncol(pi.200k)], 1, mean)
tmrca.200k <- read.table(paste(p, "TMRCA.200kb.bedgraph", sep = ""), header = T)
tmrca.200k$avg <- apply(tmrca.200k[4:ncol(tmrca.200k)], 1, mean)
rho.200k <- read.table(paste(p, "rho.200kb.bedgraph", sep = ""), header = T)
theta.200k <- read.table(paste(p, "theta.200kb.bedgraph", sep = ""), header = T)

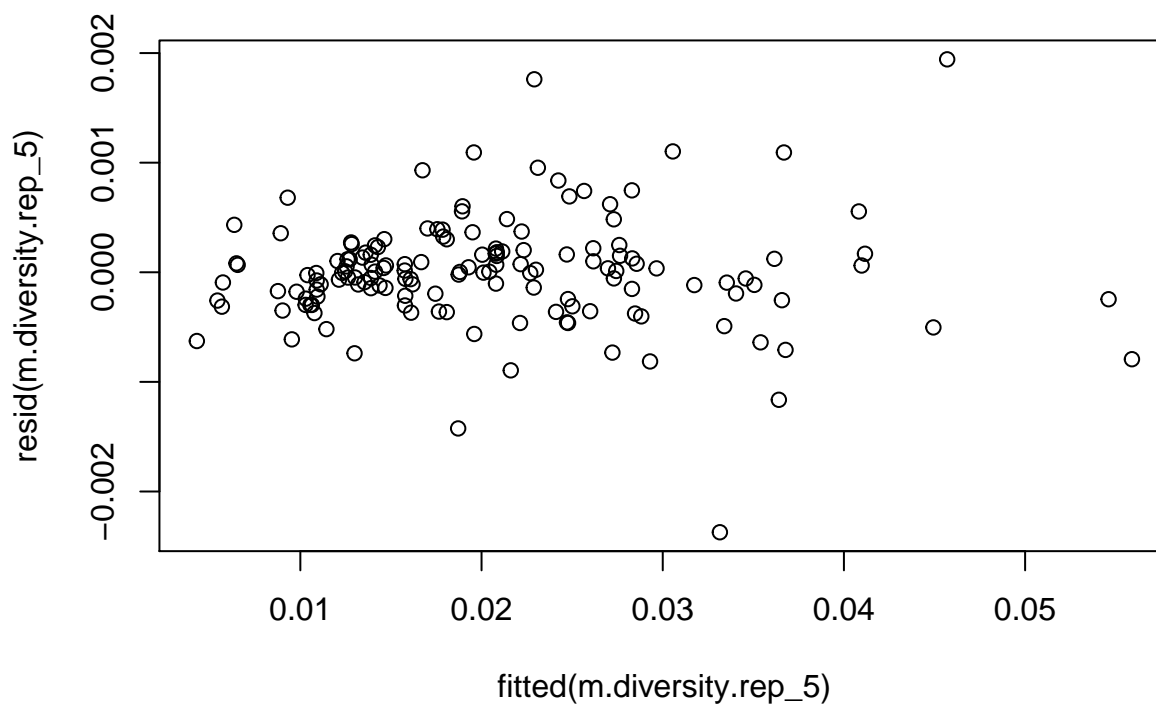
inf.lands.200k.rep_5 <- as.data.frame(cbind(pi.200k$avg, theta.200k$sample_mean, rho.200k$sample_mean, tmrca.200k$avg))
names(inf.lands.200k.rep_5) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.200k.rep_5$thetaC <- inf.lands.200k.rep_5$theta - mean(inf.lands.200k.rep_5$theta)
inf.lands.200k.rep_5$tmrcaC <- inf.lands.200k.rep_5$tmrca - mean(inf.lands.200k.rep_5$tmrca)
inf.lands.200k.rep_5$rhoC <- inf.lands.200k.rep_5$rho - mean(inf.lands.200k.rep_5$rho)

inf.lands.200k.rep_5$bin <- 1:nrow(inf.lands.200k.rep_5)

m.diversity.rep_5 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.200k.rep_5)

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



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

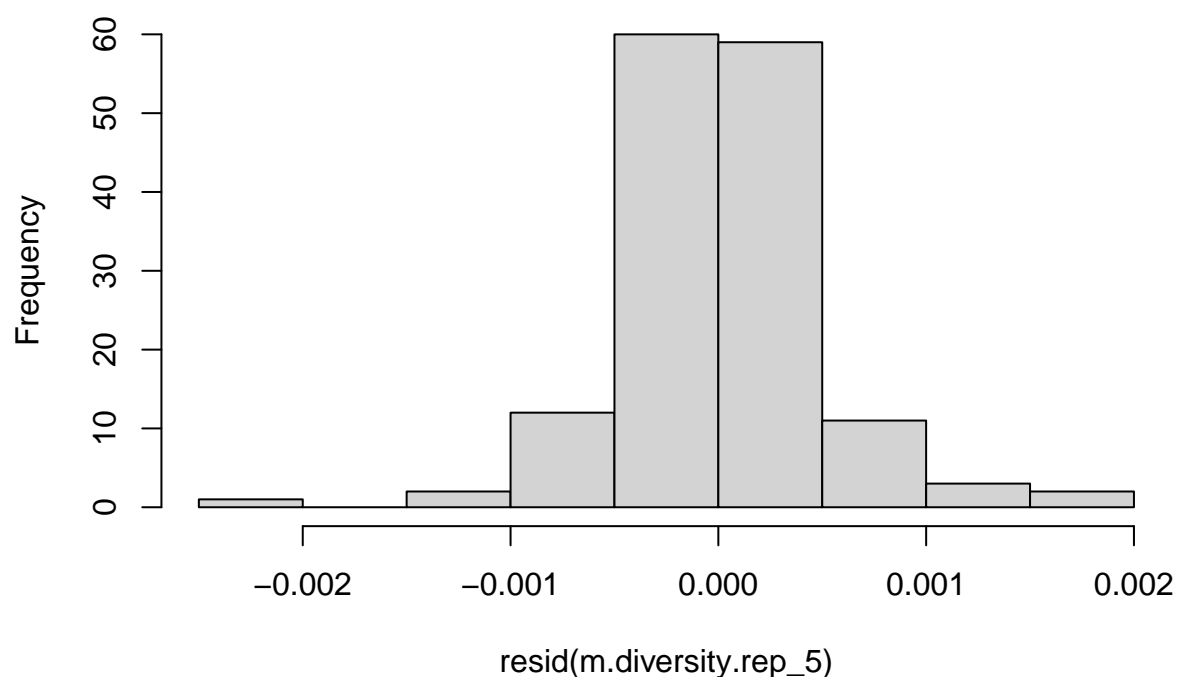
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_5  
## DW = 1.473, p-value = 0.0003904  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_5)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_5  
## HMC = 0.42356, p-value = 0.102
```

```
hist(resid(m.diversity.rep_5))
```

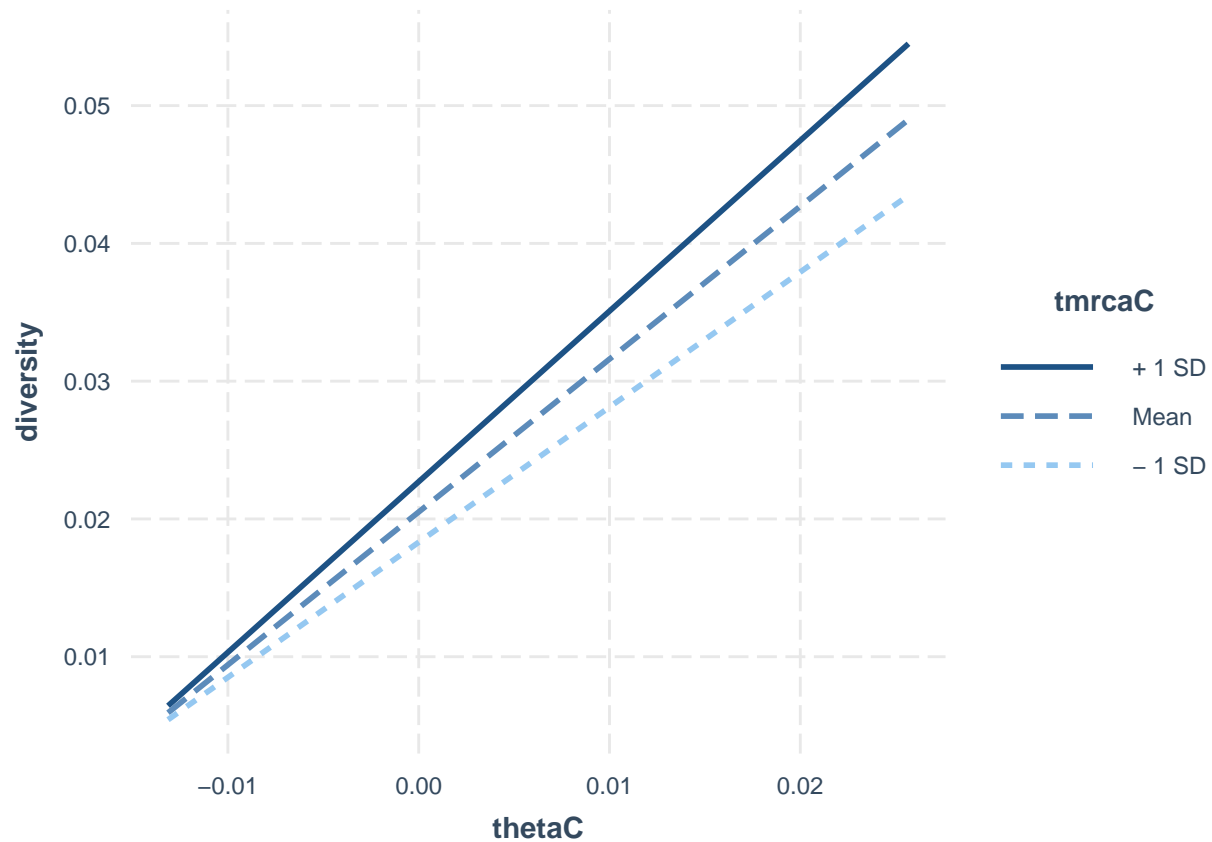
Histogram of resid(m.diversity.rep_5)



```
summary(m.diversity.rep_5)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.200k.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.200k.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.200k.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.200k.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.200k.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$VarExp[3] + anova.diversity$VarExp[4] + anova.diversity$VarExp[5]) / anova.diversity$VarExp[1]
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.200k <- read.table(paste(p, "diversity.200kb.bedgraph", sep = ""), header = T)
pi.200k$avg <- apply(pi.200k[4:ncol(pi.200k)], 1, mean)
tmrca.200k <- read.table(paste(p, "TMRCA.200kb.bedgraph", sep = ""), header = T)
tmrca.200k$avg <- apply(tmrca.200k[4:ncol(tmrca.200k)], 1, mean)
rho.200k <- read.table(paste(p, "rho.200kb.bedgraph", sep = ""), header = T)
theta.200k <- read.table(paste(p, "theta.200kb.bedgraph", sep = ""), header = T)

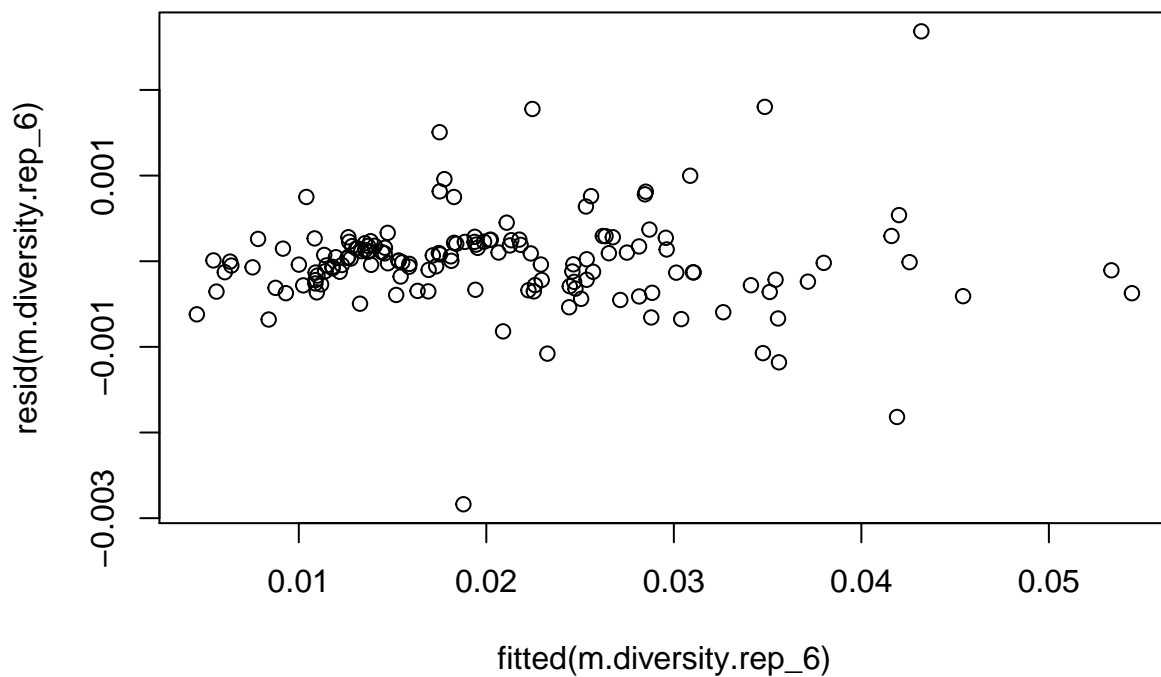
inf.lands.200k.rep_6 <- as.data.frame(cbind(pi.200k$avg, theta.200k$sample_mean, rho.200k$sample_mean, tmrca.200k$avg))
names(inf.lands.200k.rep_6) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.200k.rep_6$thetaC <- inf.lands.200k.rep_6$theta - mean(inf.lands.200k.rep_6$theta)
inf.lands.200k.rep_6$tmrcaC <- inf.lands.200k.rep_6$tmrca - mean(inf.lands.200k.rep_6$tmrca)
inf.lands.200k.rep_6$rhoC <- inf.lands.200k.rep_6$rho - mean(inf.lands.200k.rep_6$rho)

inf.lands.200k.rep_6$bin <- 1:nrow(inf.lands.200k.rep_6)

m.diversity.rep_6 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.200k.rep_6)

plot(resid(m.diversity.rep_6)~fitted(m.diversity.rep_6))
```



```
dwtest(m.diversity.rep_6)
```

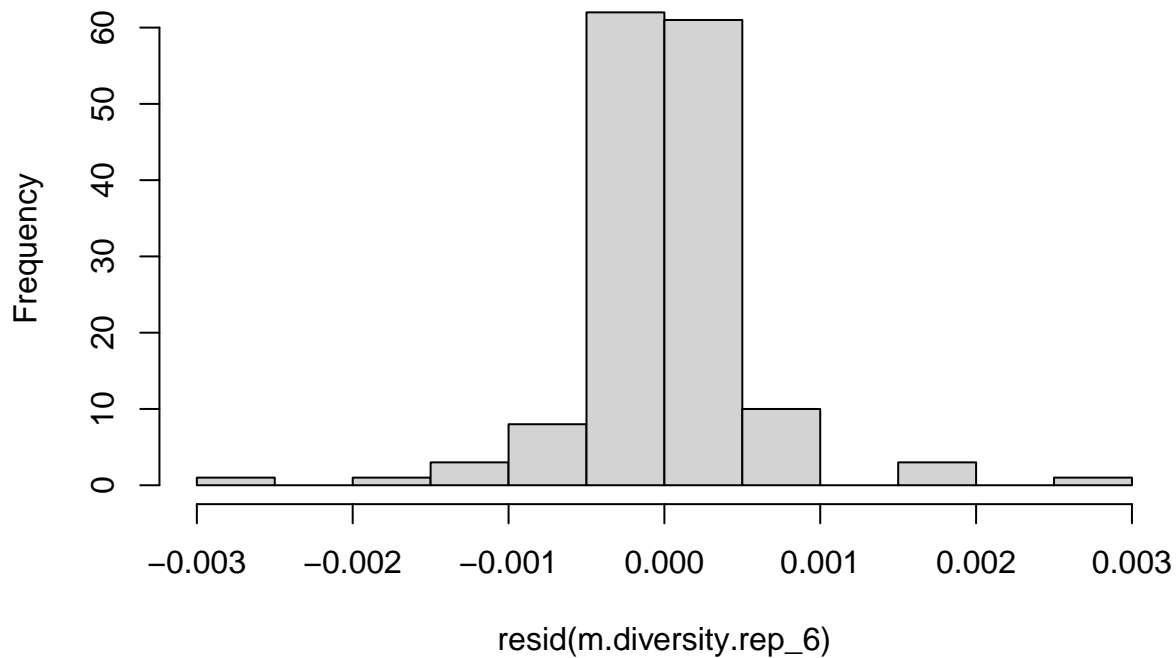
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_6  
## DW = 1.6828, p-value = 0.01928  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_6)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_6  
## HMC = 0.48734, p-value = 0.42
```

```
hist(resid(m.diversity.rep_6))
```

Histogram of resid(m.diversity.rep_6)

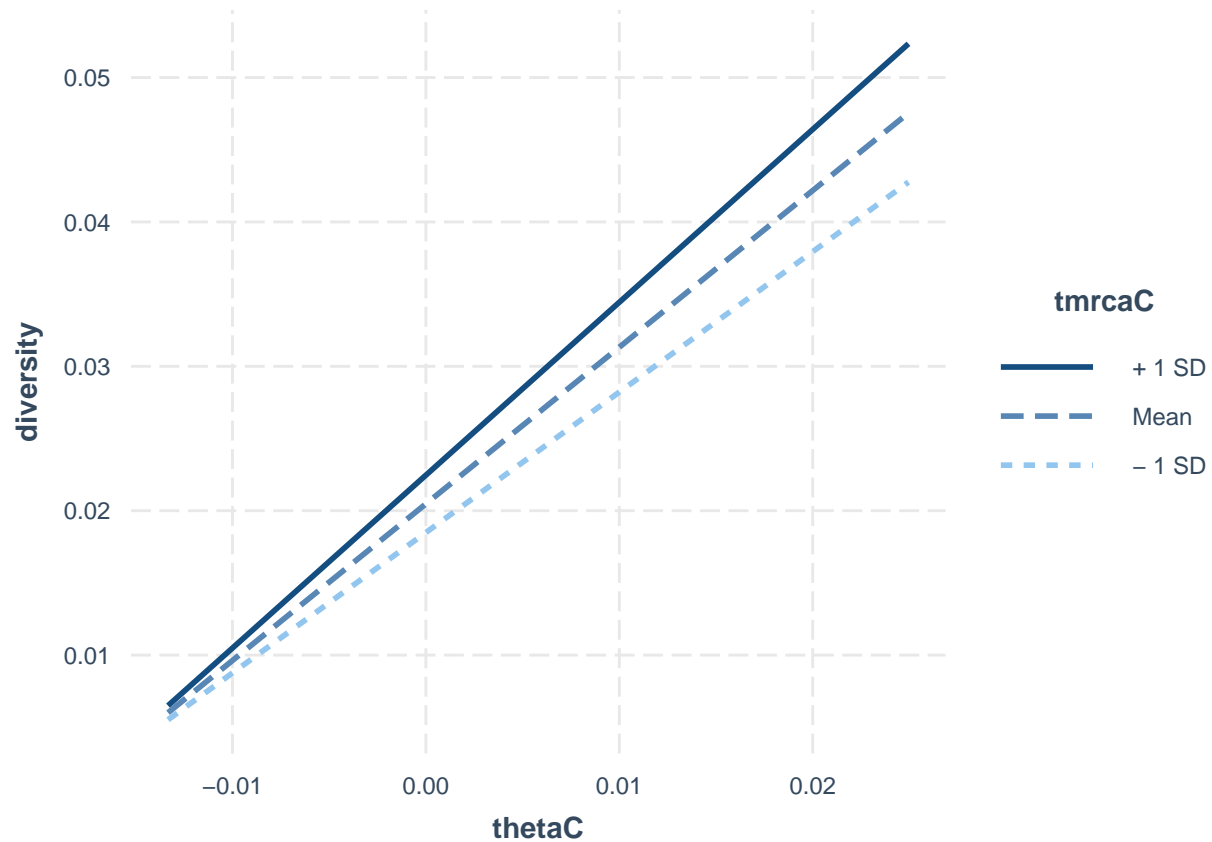


```
summary(m.diversity.rep_6)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.200k.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.200k.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.200k.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 0.00054805  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.200k.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.200k.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$VarExp[3] +
r2.inf.200kb[2, 6] <- anova.diversity$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

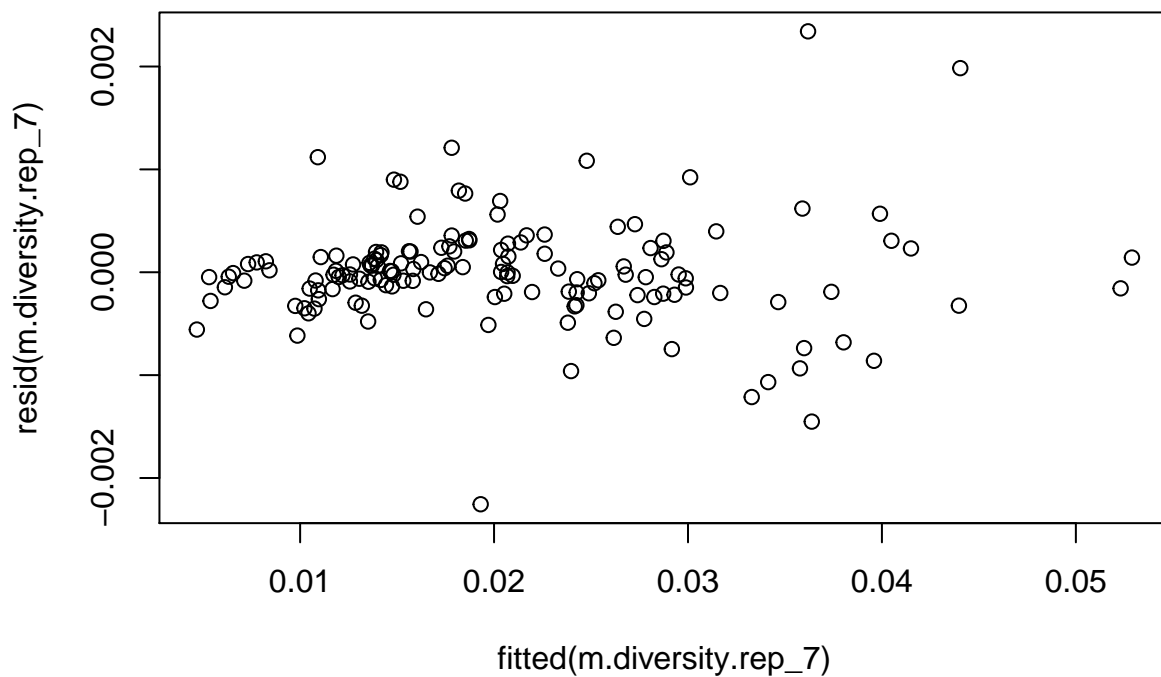
```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_7/rs.pair_7.", sep = "")
pi.200k <- read.table(paste(p, "diversity.200kb.bedgraph", sep = ""), header = T)
pi.200k$avg <- apply(pi.200k[4:ncol(pi.200k)], 1, mean)
tmrca.200k <- read.table(paste(p, "TMRCA.200kb.bedgraph", sep = ""), header = T)
tmrca.200k$avg <- apply(tmrca.200k[4:ncol(tmrca.200k)], 1, mean)
rho.200k <- read.table(paste(p, "rho.200kb.bedgraph", sep = ""), header = T)
theta.200k <- read.table(paste(p, "theta.200kb.bedgraph", sep = ""), header = T)

inf.lands.200k.rep_7 <- as.data.frame(cbind(pi.200k$avg, theta.200k$sample_mean, rho.200k$sample_mean,
names(inf.lands.200k.rep_7) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.200k.rep_7$thetaC <- inf.lands.200k.rep_7$theta - mean(inf.lands.200k.rep_7$theta)
inf.lands.200k.rep_7$tmrcaC <- inf.lands.200k.rep_7$tmrca - mean(inf.lands.200k.rep_7$tmrca)
inf.lands.200k.rep_7$rhoC <- inf.lands.200k.rep_7$rho - mean(inf.lands.200k.rep_7$rho)

inf.lands.200k.rep_7$bin <- 1:nrow(inf.lands.200k.rep_7)

m.diversity.rep_7 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.200k.rep_7)
plot(resid(m.diversity.rep_7)~fitted(m.diversity.rep_7))
```



```
dwtest(m.diversity.rep_7)
```

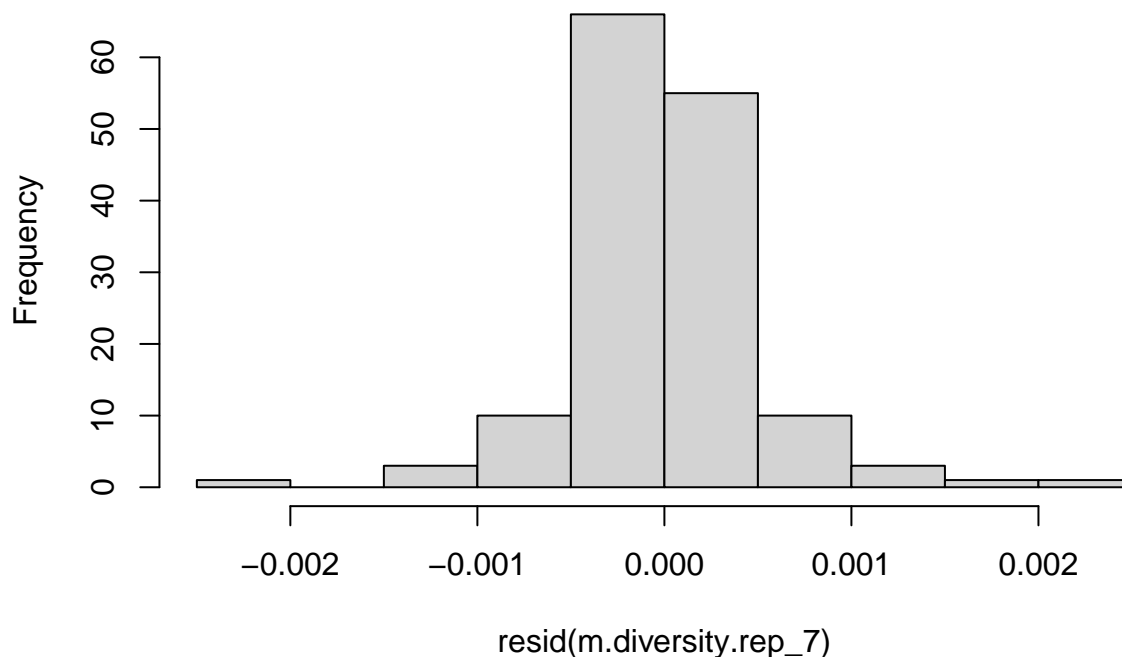
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_7  
## DW = 1.6673, p-value = 0.01553  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_7)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_7  
## HMC = 0.43605, p-value = 0.148
```

```
hist(resid(m.diversity.rep_7))
```

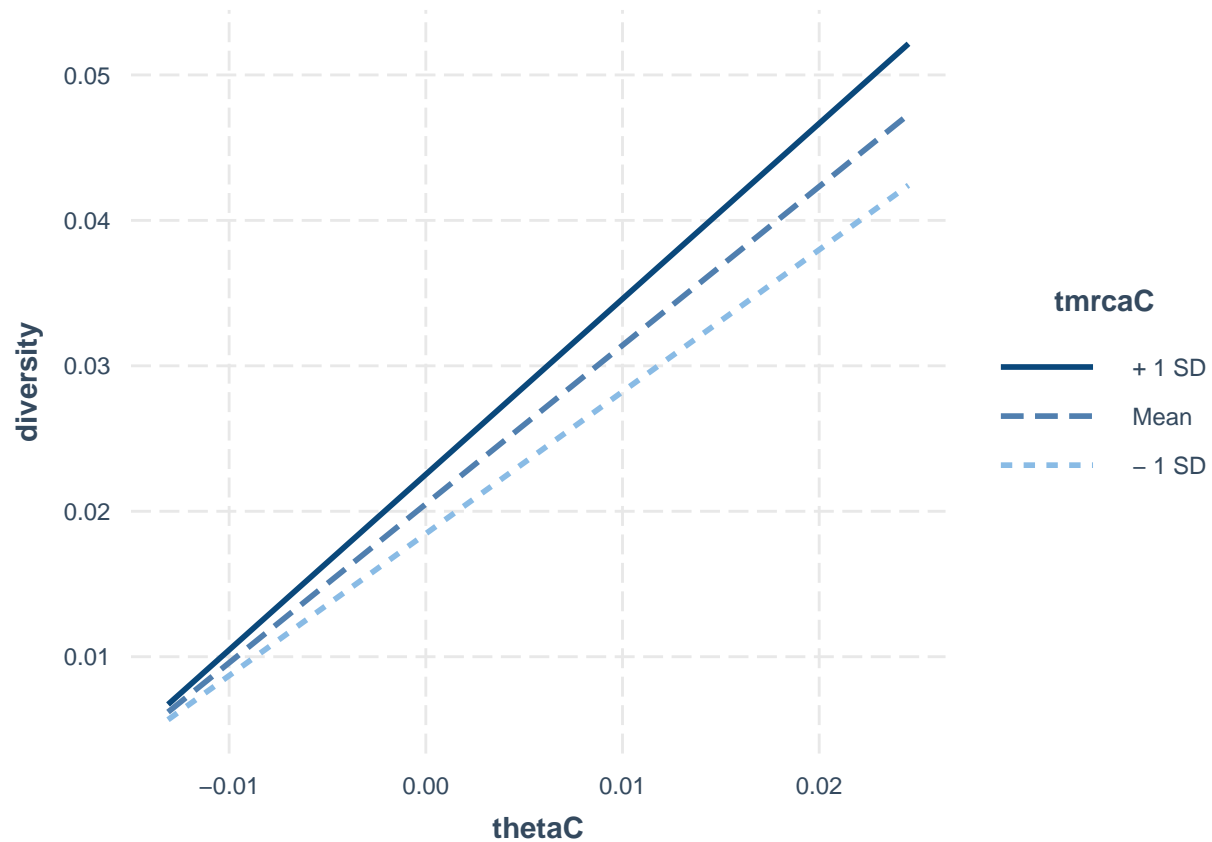
Histogram of resid(m.diversity.rep_7)



```
summary(m.diversity.rep_7)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.200k.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.200k.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.200k.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.200k.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.200k.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.200k <- read.table(paste(p, "diversity.200kb.bedgraph", sep = ""), header = T)
pi.200k$avg <- apply(pi.200k[4:ncol(pi.200k)], 1, mean)
tmrca.200k <- read.table(paste(p, "TMRCA.200kb.bedgraph", sep = ""), header = T)
tmrca.200k$avg <- apply(tmrca.200k[4:ncol(tmrca.200k)], 1, mean)
rho.200k <- read.table(paste(p, "rho.200kb.bedgraph", sep = ""), header = T)
theta.200k <- read.table(paste(p, "theta.200kb.bedgraph", sep = ""), header = T)

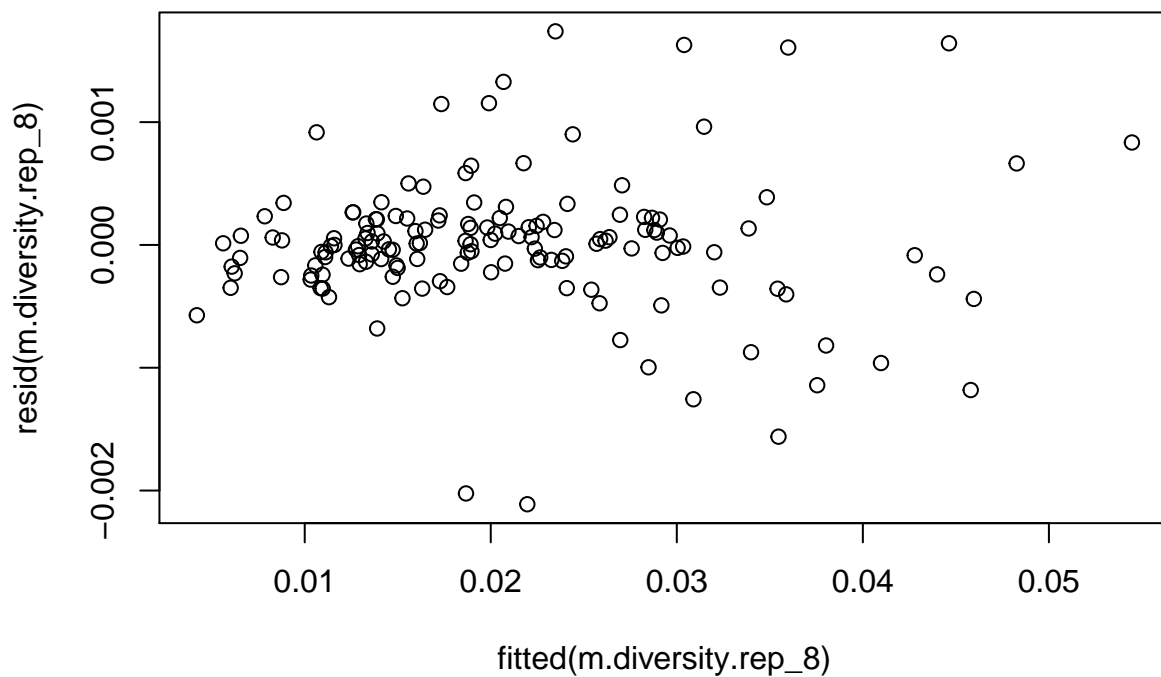
inf.lands.200k.rep_8 <- as.data.frame(cbind(pi.200k$avg, theta.200k$sample_mean, rho.200k$sample_mean,
names(inf.lands.200k.rep_8) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.200k.rep_8$thetaC <- inf.lands.200k.rep_8$theta - mean(inf.lands.200k.rep_8$theta)
inf.lands.200k.rep_8$tmrcaC <- inf.lands.200k.rep_8$tmrca - mean(inf.lands.200k.rep_8$tmrca)
inf.lands.200k.rep_8$rhoC <- inf.lands.200k.rep_8$rho - mean(inf.lands.200k.rep_8$rho)

inf.lands.200k.rep_8$bin <- 1:nrow(inf.lands.200k.rep_8)

m.diversity.rep_8 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.200k.rep_8)

plot(resid(m.diversity.rep_8)~fitted(m.diversity.rep_8))
```

```
dwtest(m.diversity.rep_8)
```

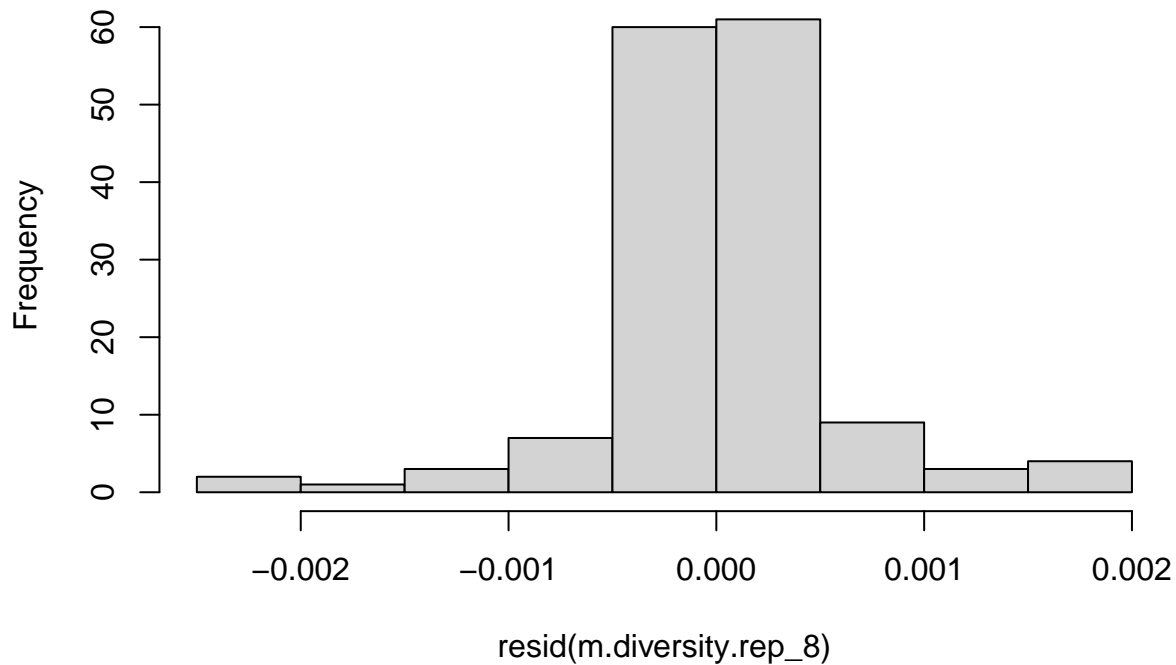
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_8  
## DW = 1.5909, p-value = 0.004238  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_8)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_8  
## HMC = 0.45552, p-value = 0.245
```

```
hist(resid(m.diversity.rep_8))
```

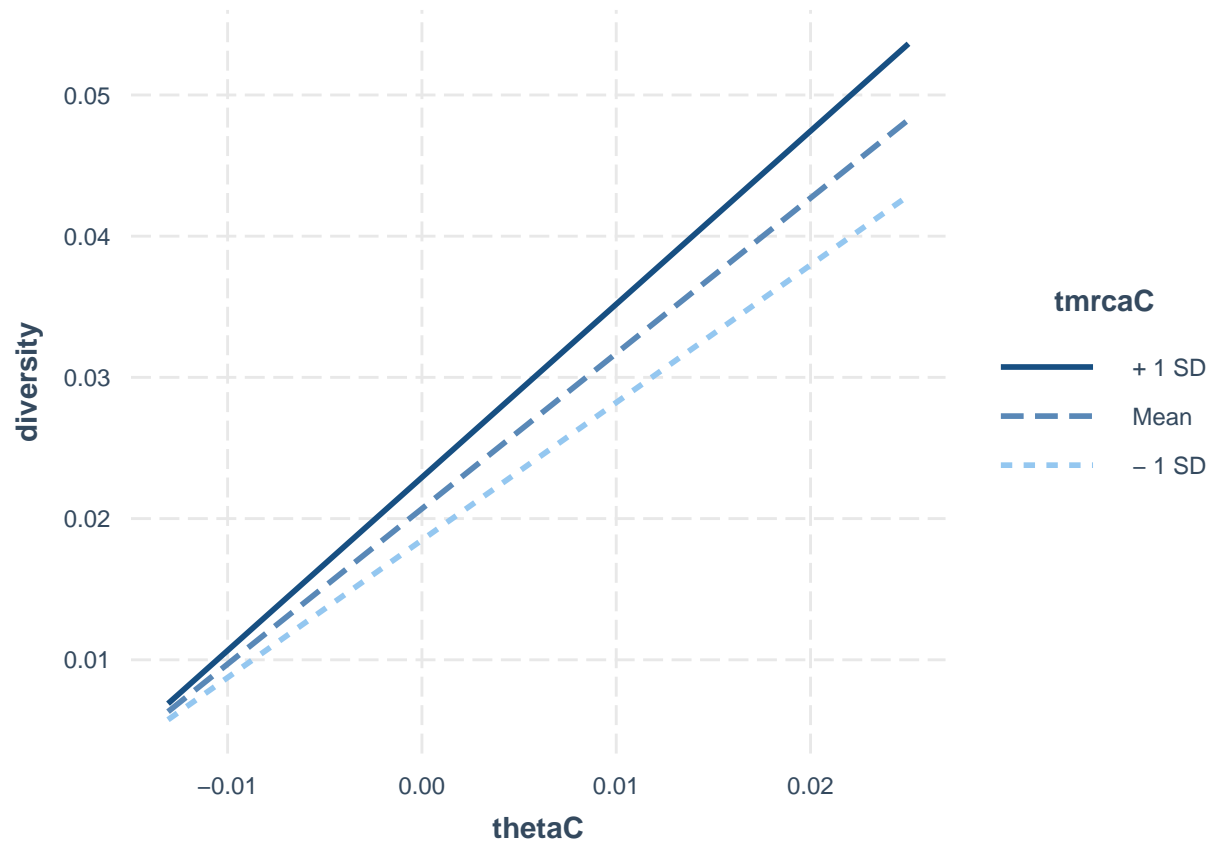
Histogram of resid(m.diversity.rep_8)



```
summary(m.diversity.rep_8)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.200k.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.200k.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.200k.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.200k.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.200k.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$VarExp[3] + anova.diversity$VarExp[4] + anova.diversity$VarExp[5]) / anova.diversity$VarExp[1]
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

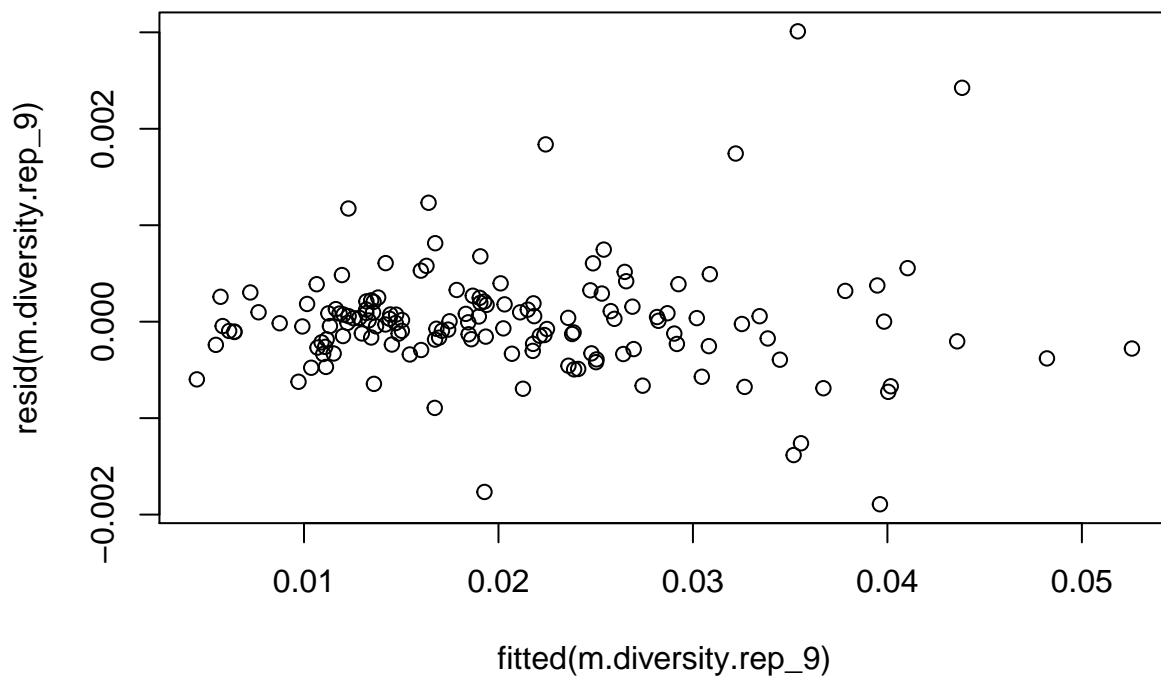
```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_9/rs.pair_9.", sep = "")
pi.200k <- read.table(paste(p, "diversity.200kb.bedgraph", sep = ""), header = T)
pi.200k$avg <- apply(pi.200k[4:ncol(pi.200k)], 1, mean)
tmrca.200k <- read.table(paste(p, "TMRCA.200kb.bedgraph", sep = ""), header = T)
tmrca.200k$avg <- apply(tmrca.200k[4:ncol(tmrca.200k)], 1, mean)
rho.200k <- read.table(paste(p, "rho.200kb.bedgraph", sep = ""), header = T)
theta.200k <- read.table(paste(p, "theta.200kb.bedgraph", sep = ""), header = T)

inf.lands.200k.rep_9 <- as.data.frame(cbind(pi.200k$avg, theta.200k$sample_mean, rho.200k$sample_mean, tmrca.200k$avg))
names(inf.lands.200k.rep_9) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.200k.rep_9$thetaC <- inf.lands.200k.rep_9$theta - mean(inf.lands.200k.rep_9$theta)
inf.lands.200k.rep_9$tmrcaC <- inf.lands.200k.rep_9$tmrca - mean(inf.lands.200k.rep_9$tmrca)
inf.lands.200k.rep_9$rhoC <- inf.lands.200k.rep_9$rho - mean(inf.lands.200k.rep_9$rho)

inf.lands.200k.rep_9$bin <- 1:nrow(inf.lands.200k.rep_9)

m.diversity.rep_9 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.200k.rep_9)
plot(resid(m.diversity.rep_9)~fitted(m.diversity.rep_9))
```



```
dwtest(m.diversity.rep_9)
```

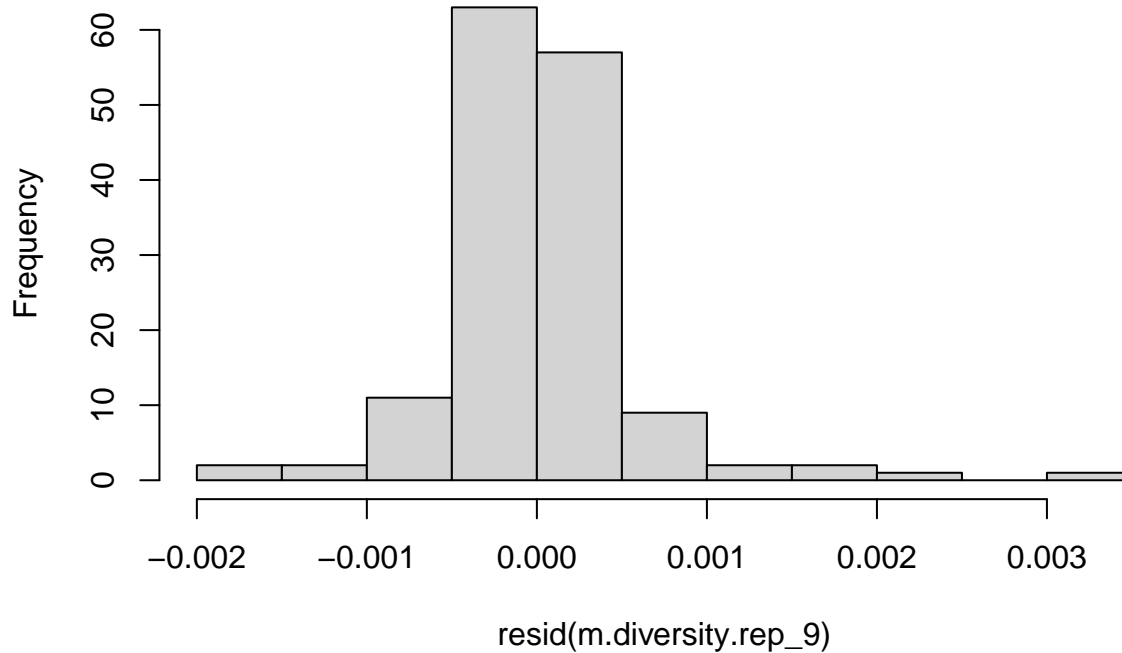
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_9  
## DW = 1.6772, p-value = 0.01787  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_9)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_9  
## HMC = 0.38369, p-value = 0.021
```

```
hist(resid(m.diversity.rep_9))
```

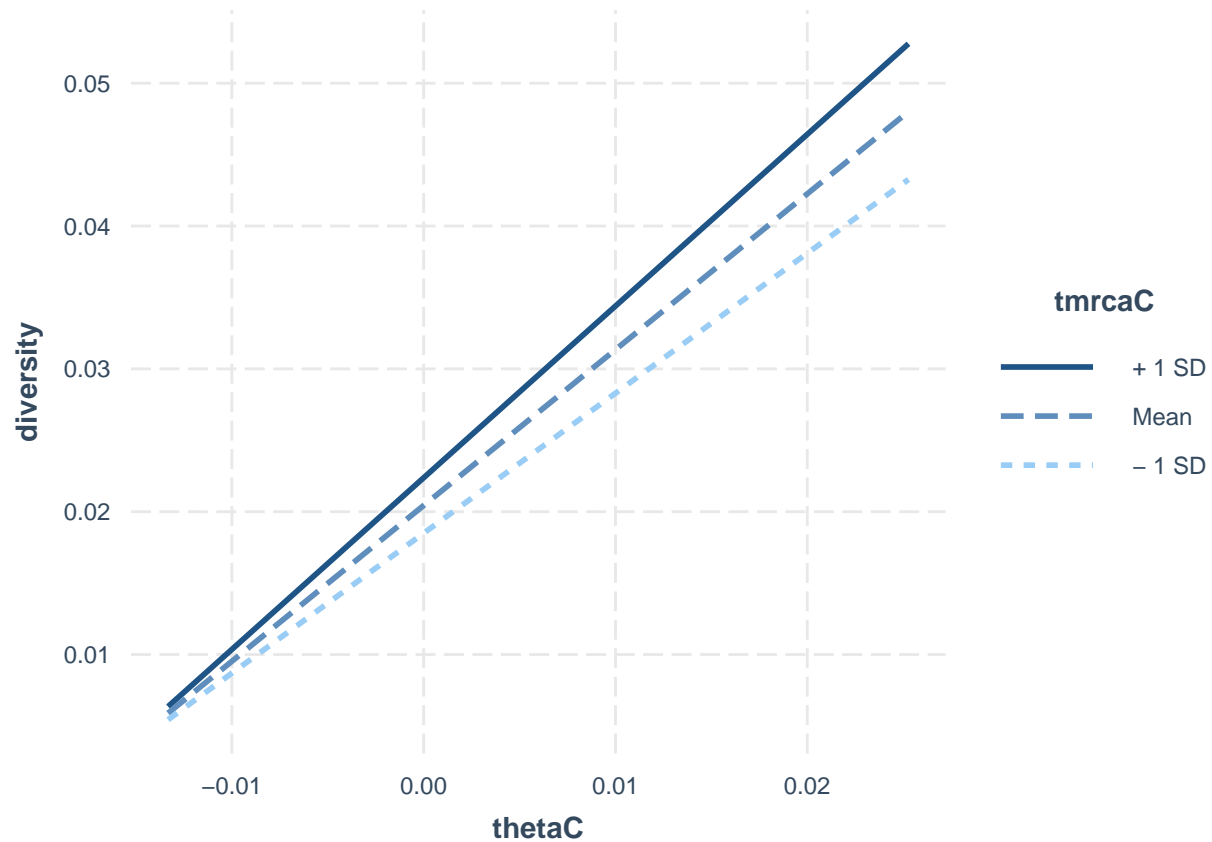
Histogram of resid(m.diversity.rep_9)



```
summary(m.diversity.rep_9)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.200k.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.200k.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.200k.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.200k.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.200k.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

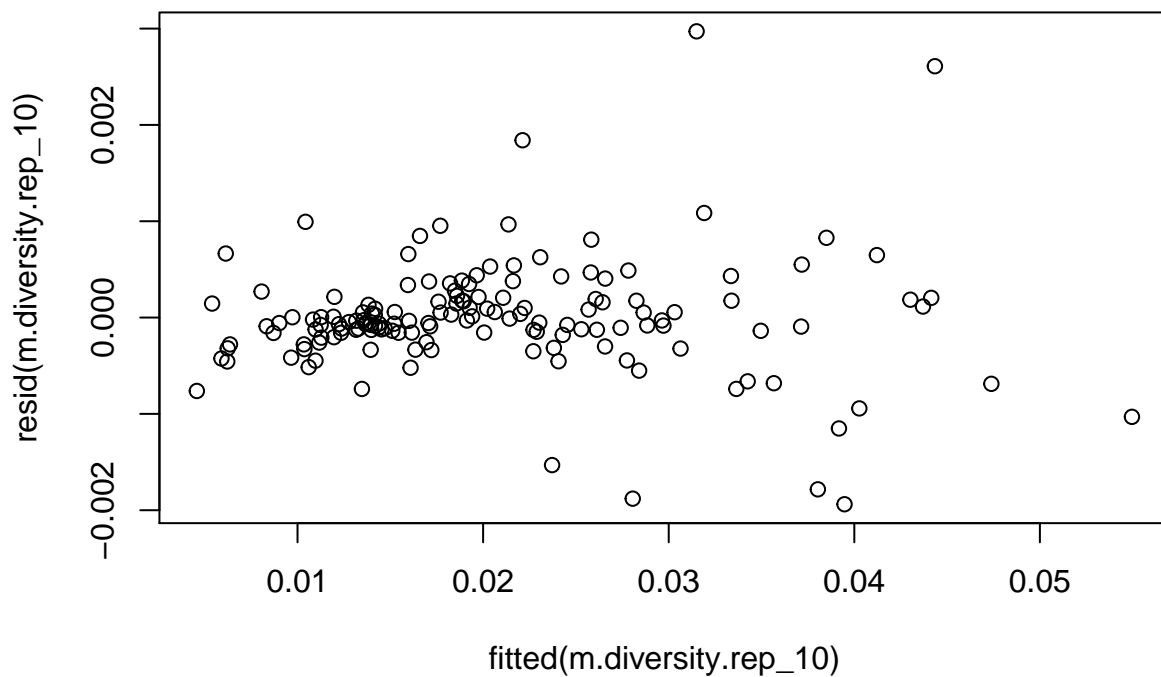
```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_10/rs.pair_10.", sep = "")
pi.200k <- read.table(paste(p, "diversity.200kb.bedgraph", sep = ""), header = T)
pi.200k$avg <- apply(pi.200k[4:ncol(pi.200k)], 1, mean)
tmrca.200k <- read.table(paste(p, "TMRCA.200kb.bedgraph", sep = ""), header = T)
tmrca.200k$avg <- apply(tmrca.200k[4:ncol(tmrca.200k)], 1, mean)
rho.200k <- read.table(paste(p, "rho.200kb.bedgraph", sep = ""), header = T)
theta.200k <- read.table(paste(p, "theta.200kb.bedgraph", sep = ""), header = T)

inf.lands.200k.rep_10 <- as.data.frame(cbind(pi.200k$avg, theta.200k$sample_mean, rho.200k$sample_mean,
names(inf.lands.200k.rep_10) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.200k.rep_10$thetaC <- inf.lands.200k.rep_10$theta - mean(inf.lands.200k.rep_10$theta)
inf.lands.200k.rep_10$tmrcaC <- inf.lands.200k.rep_10$tmrca - mean(inf.lands.200k.rep_10$tmrca)
inf.lands.200k.rep_10$rhoC <- inf.lands.200k.rep_10$rho - mean(inf.lands.200k.rep_10$rho)

inf.lands.200k.rep_10$bin <- 1:nrow(inf.lands.200k.rep_10)

m.diversity.rep_10 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.200k.rep_
plot(resid(m.diversity.rep_10)~fitted(m.diversity.rep_10))
```



```
dwtest(m.diversity.rep_10)
```

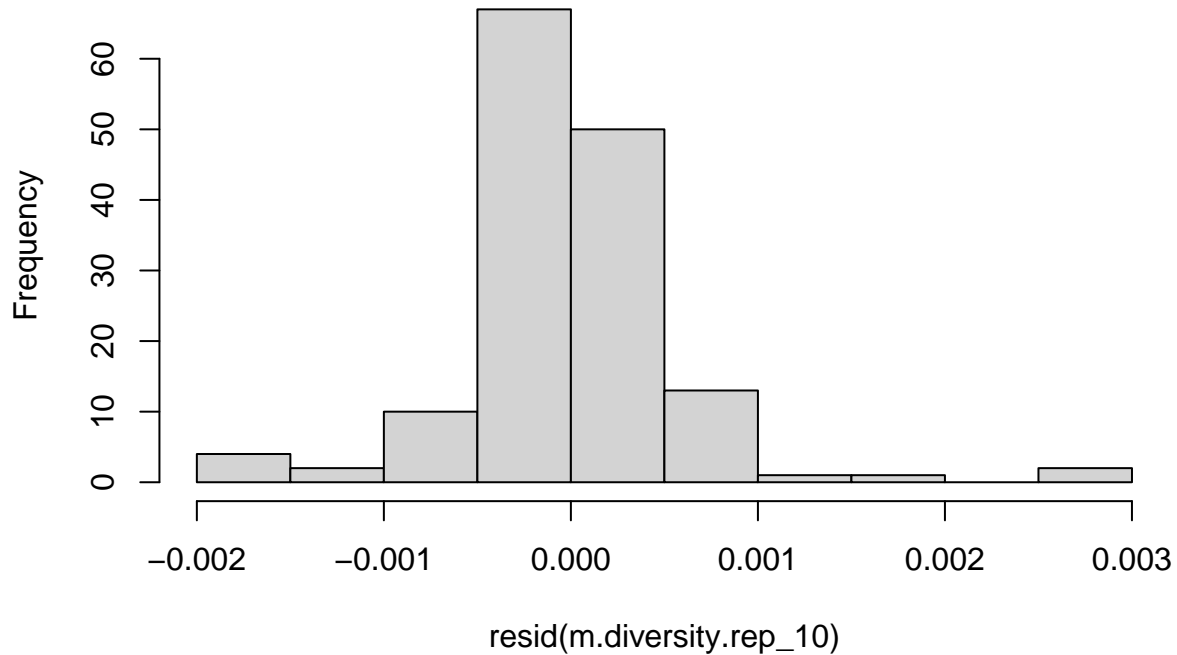
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_10  
## DW = 1.777, p-value = 0.06912  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_10)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_10  
## HMC = 0.6193, p-value = 0.989
```

```
hist(resid(m.diversity.rep_10))
```

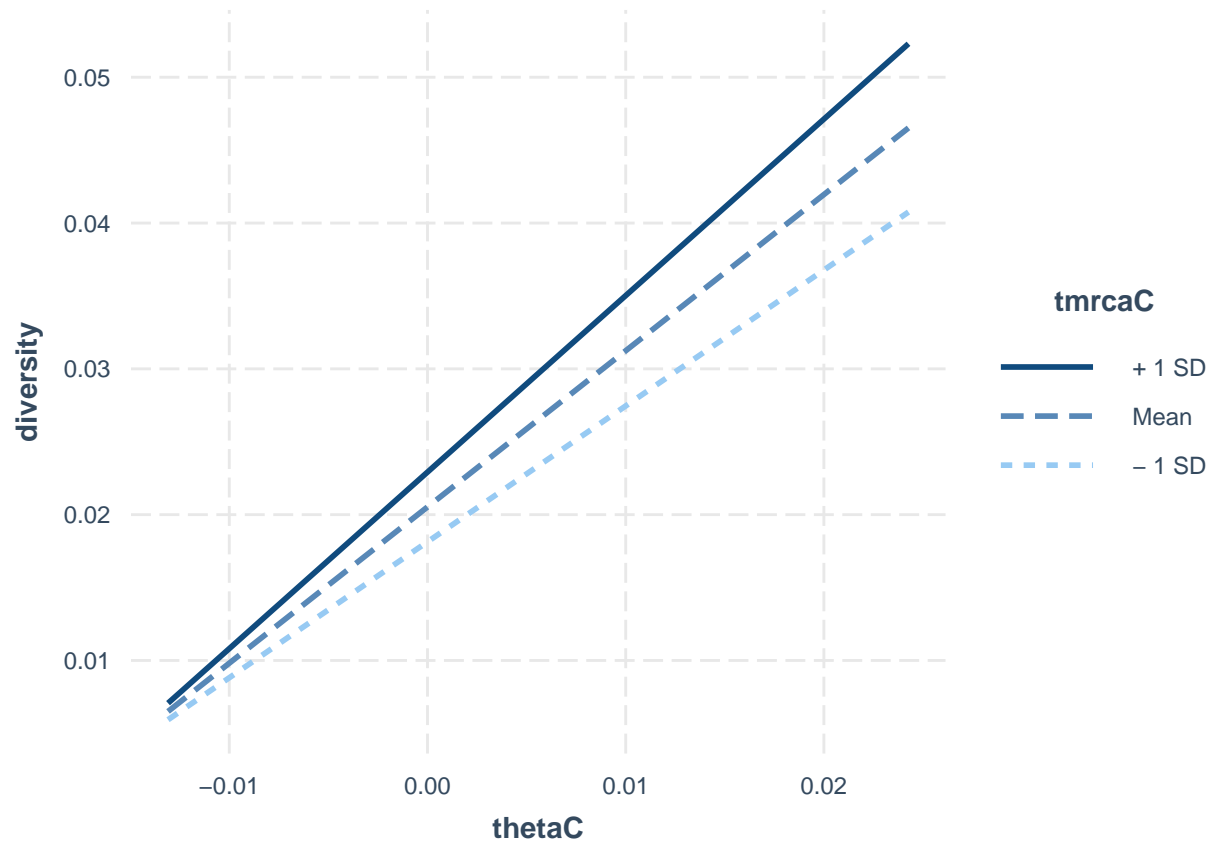
Histogram of resid(m.diversity.rep_10)



```
summary(m.diversity.rep_10)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.200k.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.200k.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.200k.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.200k.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.200k.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
## -2.75464196 -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$VarExp[3] + anova.diversity$VarExp[4] + anova.diversity$VarExp[5])
r2.inf.200kb[2, 10] <- anova.diversity$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 Plots

```
scale.3d <- function(x) sprintf("%.3f", x)

rho.plot <- as.data.frame(cbind(inf.lands.200k.rep_1$bin,
                                sim.rho.200k$sim,
                                inf.lands.200k.rep_1$rho,
                                inf.lands.200k.rep_2$rho,
                                inf.lands.200k.rep_3$rho,
                                inf.lands.200k.rep_4$rho,
                                inf.lands.200k.rep_5$rho,
                                inf.lands.200k.rep_6$rho,
                                inf.lands.200k.rep_7$rho,
                                inf.lands.200k.rep_8$rho,
                                inf.lands.200k.rep_9$rho,
                                inf.lands.200k.rep_10$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(values = c(1, 2, 3, 4, 5, 6, 7, 8, 9, 10))
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.200k.rep_1$bin,
                                sim.theta.200k$sim,
                                inf.lands.200k.rep_1$theta,
                                inf.lands.200k.rep_2$theta,
                                inf.lands.200k.rep_3$theta,
                                inf.lands.200k.rep_4$theta,
                                inf.lands.200k.rep_5$theta,
                                inf.lands.200k.rep_6$theta))
```

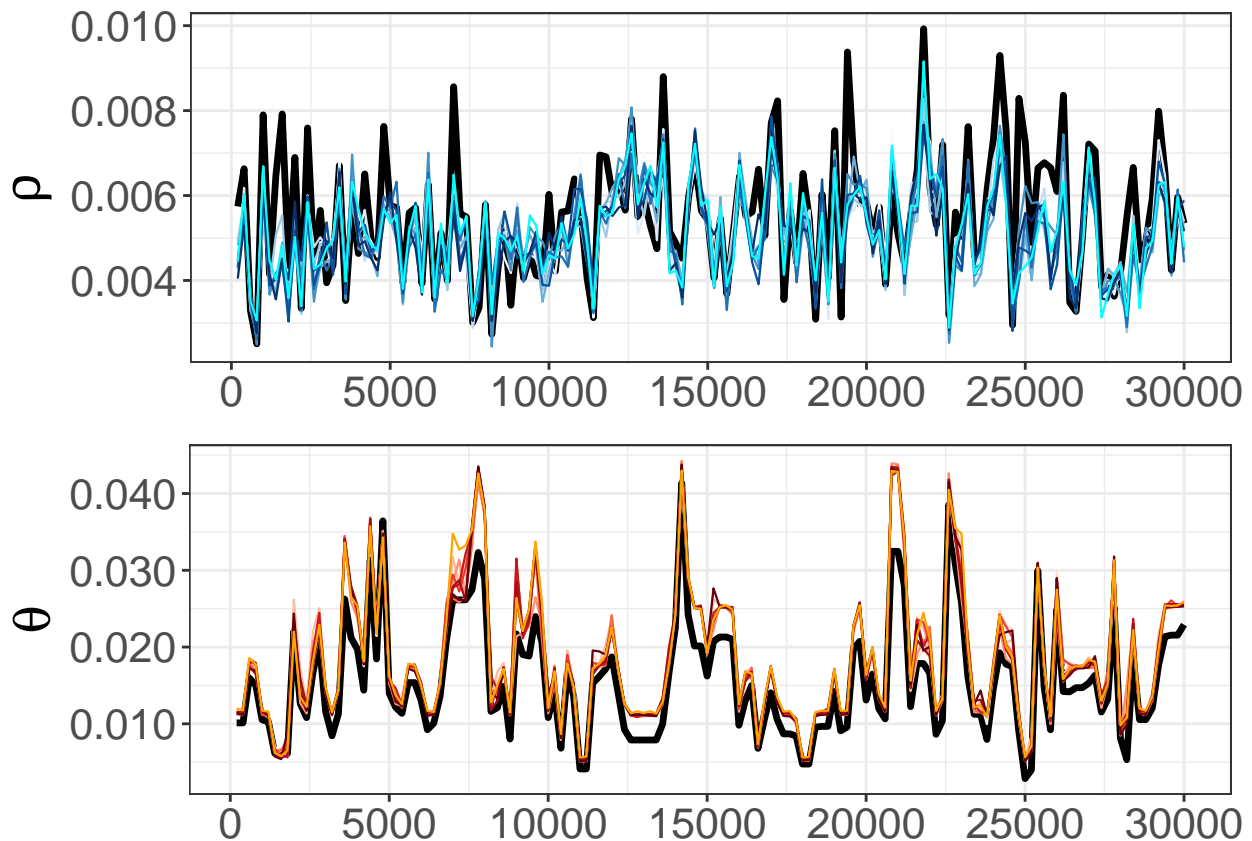
```

      inf.lands.200k.rep_7$theta,
      inf.lands.200k.rep_8$theta,
      inf.lands.200k.rep_9$theta,
      inf.lands.200k.rep_10$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(
theta.map.200kb <- theta.map.200kb + geom_line(data = molten.theta, aes(size = variable)) + scale_size_
theta.map.200kb <- theta.map.200kb + scale_color_manual(values = c("black", brewer.pal(n = 9, name = "R
theta.map.200kb <- theta.map.200kb + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(
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(

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.1M <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims/dm.sim.rho.1e+06.txt")
sim.theta.1M <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims/dm.sim.theta.1e+06.txt")
sim.lands.1M <- as.data.frame(cbind(sim.theta.1M$sim, sim.rho.1M$sim))
names(sim.lands.1M) <- 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.1M <- read.table(paste(p, "diversity.1Mb.bedgraph", sep = ""), header = T)
pi.1M$avg <- apply(pi.1M[4:ncol(pi.1M)], 1, mean)
tmrca.1M <- read.table(paste(p, "TMRCA.1Mb.bedgraph", sep = ""), header = T)
tmrca.1M$avg <- apply(tmrca.1M[4:ncol(tmrca.1M)], 1, mean)
rho.1M <- read.table(paste(p, "rho.1Mb.bedgraph", sep = ""), header = T)
theta.1M <- read.table(paste(p, "theta.1Mb.bedgraph", sep = ""), header = T)

inf.lands.1M.rep_1 <- as.data.frame(cbind(pi.1M$avg, theta.1M$sample_mean, rho.1M$sample_mean, tmrca.1M$avg))
names(inf.lands.1M.rep_1) <- c("diversity", "theta", "rho", "tmrca")

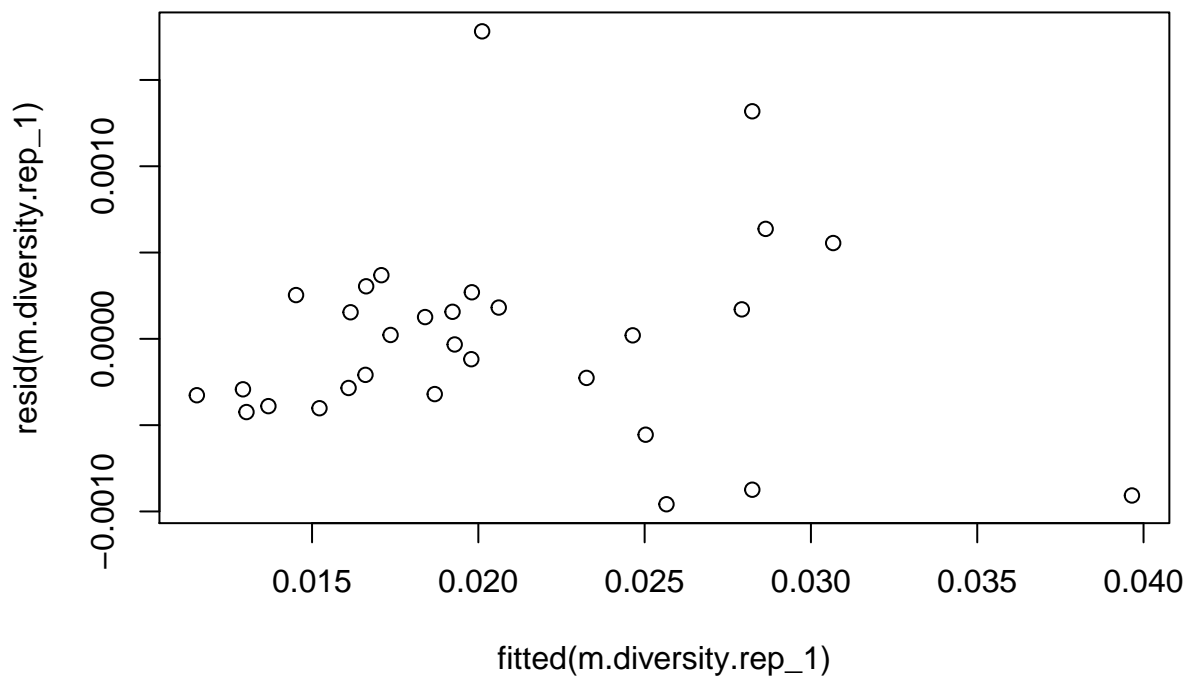
# centering
inf.lands.1M.rep_1$thetaC <- inf.lands.1M.rep_1$theta - mean(inf.lands.1M.rep_1$theta)
inf.lands.1M.rep_1$tmrcaC <- inf.lands.1M.rep_1$tmrca - mean(inf.lands.1M.rep_1$tmrca)
inf.lands.1M.rep_1$rhoC <- inf.lands.1M.rep_1$rho - mean(inf.lands.1M.rep_1$rho)

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

m.diversity.rep_1 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.1M.rep_1)

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

```



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

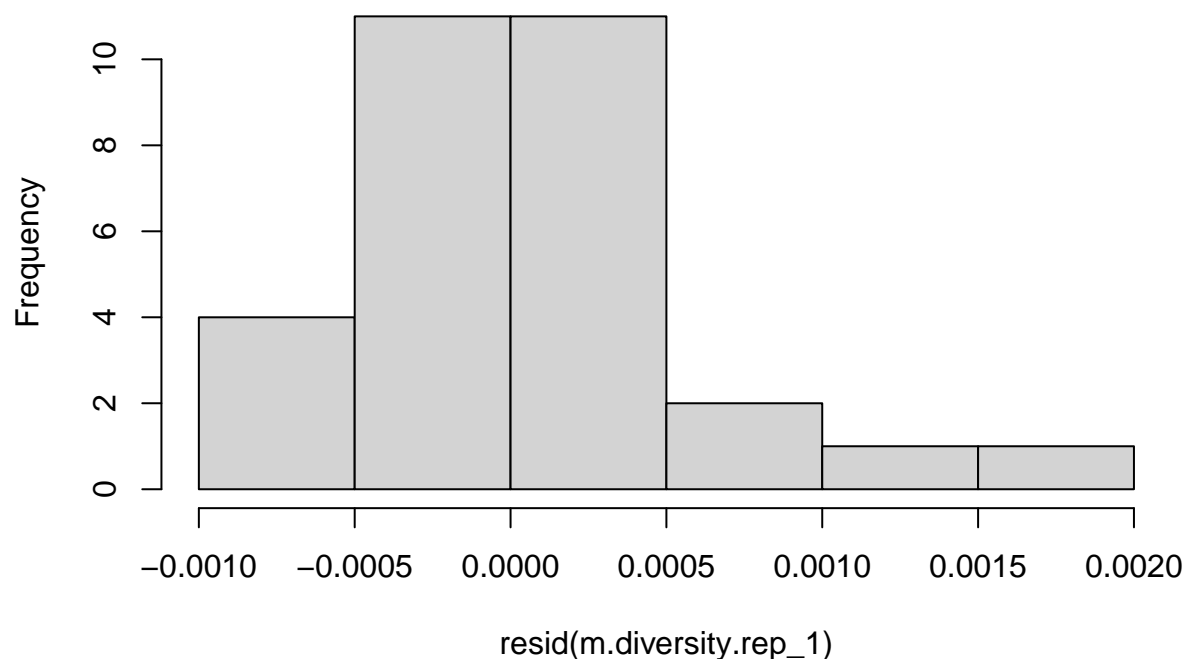
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_1  
## DW = 1.9667, p-value = 0.4252  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_1)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_1  
## HMC = 0.46606, p-value = 0.374
```

```
hist(resid(m.diversity.rep_1))
```

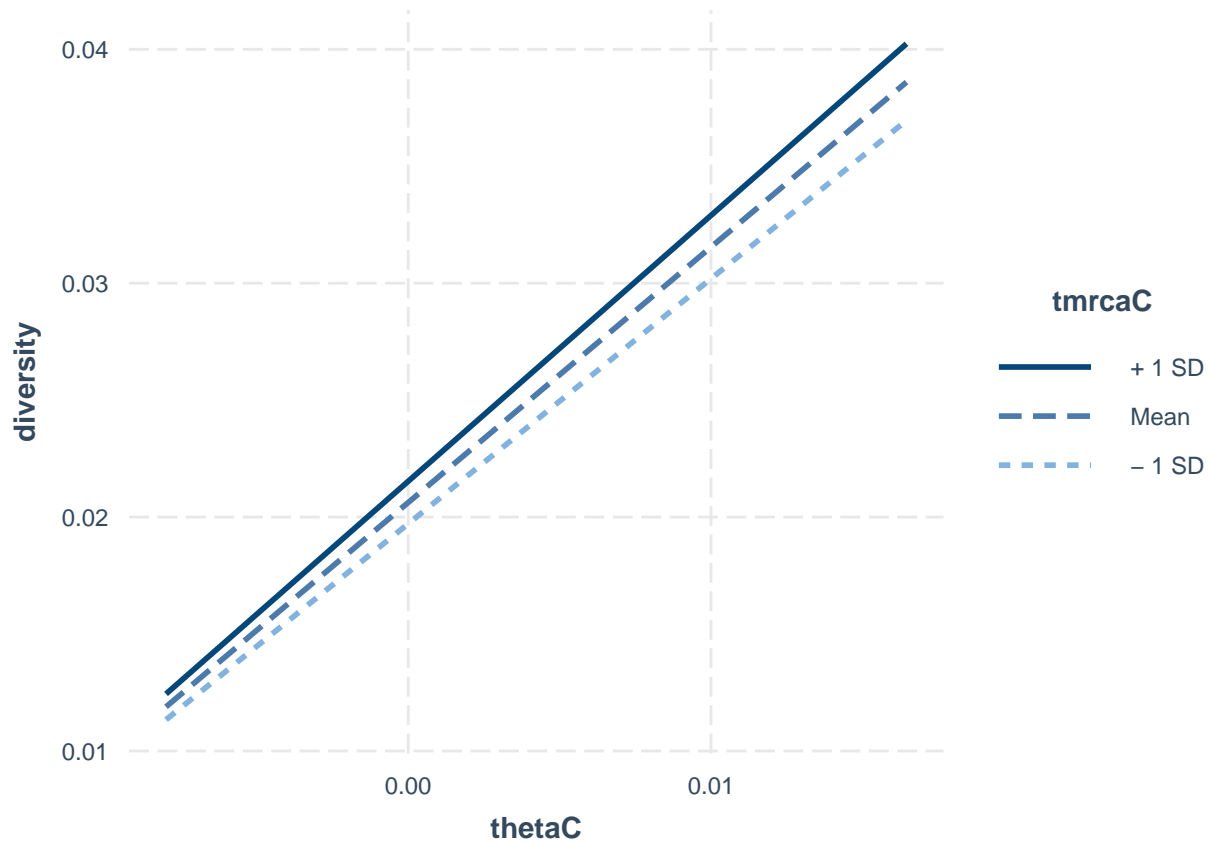
Histogram of resid(m.diversity.rep_1)



```
summary(m.diversity.rep_1)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.1M.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.1M.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.1M.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.1M.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.1M.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$VarExp[3] + anova.diversity$VarExp[4]) / anova.diversity$VarExp[1]
r2.inf.1Mb[2, 1] <- anova.diversity$VarExp[1] / anova.diversity$VarExp[1]
r2.inf.1Mb[3, 1] <- anova.diversity$VarExp[2] / anova.diversity$VarExp[1]
r2.inf.1Mb[4, 1] <- anova.diversity$VarExp[3] / anova.diversity$VarExp[1]
r2.inf.1Mb[5, 1] <- anova.diversity$VarExp[4] / anova.diversity$VarExp[1]
```

2.3.2 Replicate 2

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

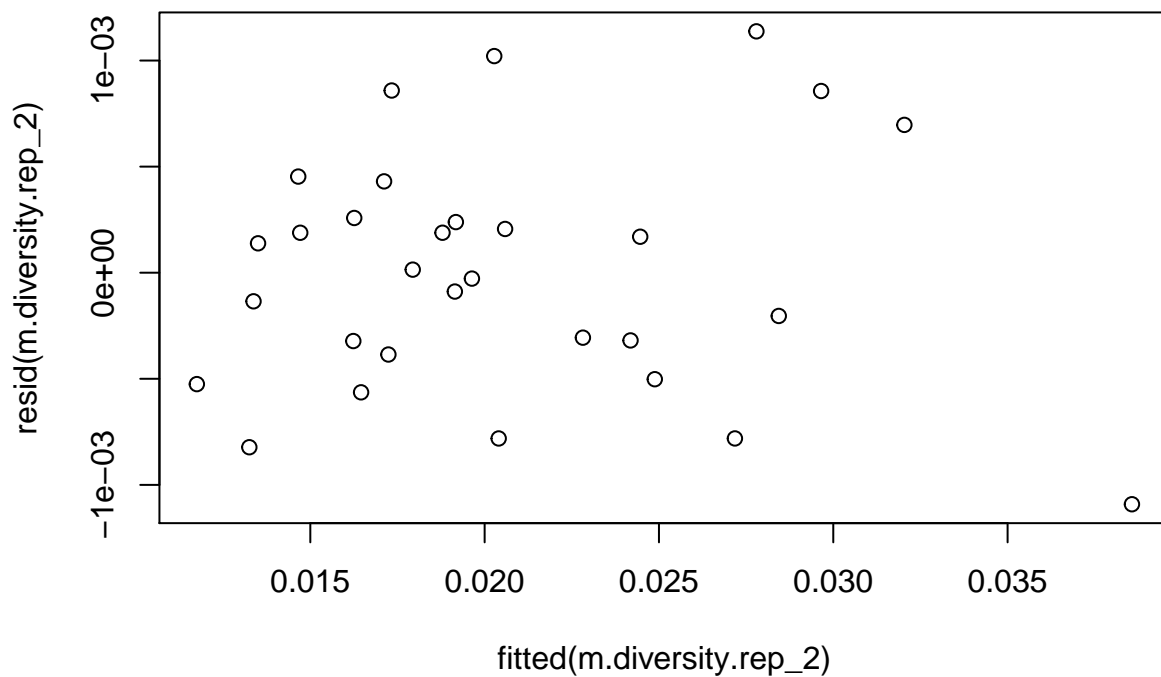
inf.lands.1M.rep_2 <- as.data.frame(cbind(pi.1M$avg, theta.1M$sample_mean, rho.1M$sample_mean, tmrca.1M$sample_mean))
names(inf.lands.1M.rep_2) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.1M.rep_2$thetaC <- inf.lands.1M.rep_2$theta - mean(inf.lands.1M.rep_2$theta)
inf.lands.1M.rep_2$tmrcaC <- inf.lands.1M.rep_2$tmrca - mean(inf.lands.1M.rep_2$tmrca)
inf.lands.1M.rep_2$rhoC <- inf.lands.1M.rep_2$rho - mean(inf.lands.1M.rep_2$rho)

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

m.diversity.rep_2 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.1M.rep_2)

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



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

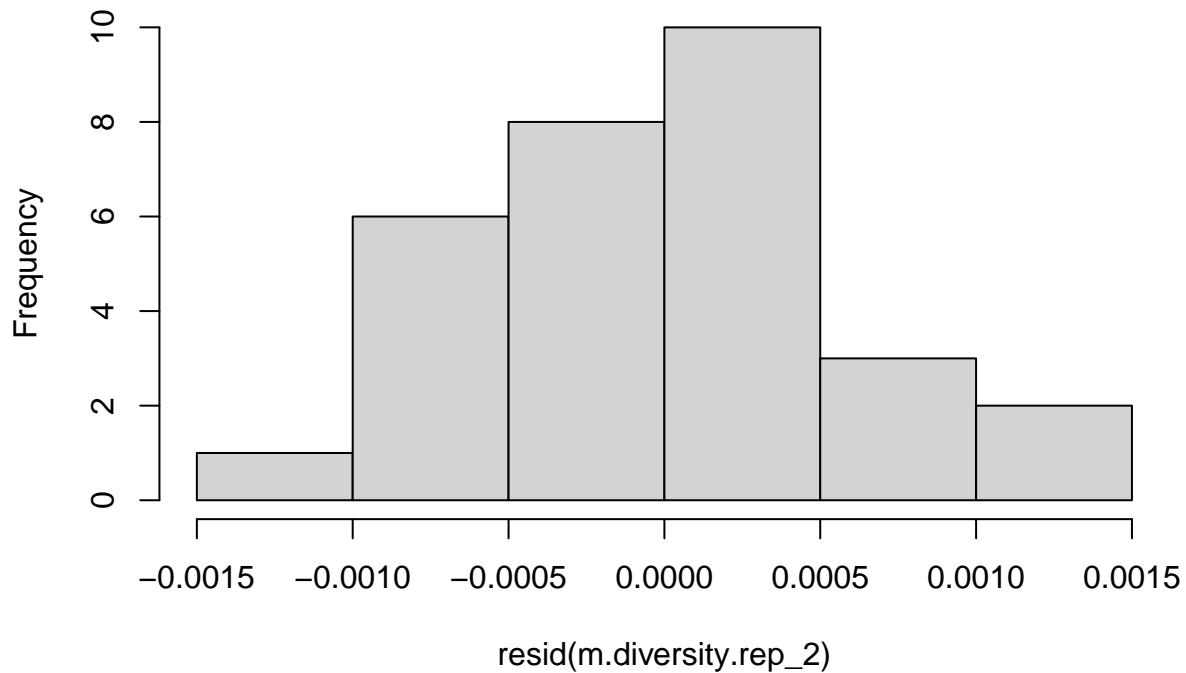
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_2  
## DW = 1.966, p-value = 0.4212  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_2)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_2  
## HMC = 0.4866, p-value = 0.49
```

```
hist(resid(m.diversity.rep_2))
```

Histogram of resid(m.diversity.rep_2)

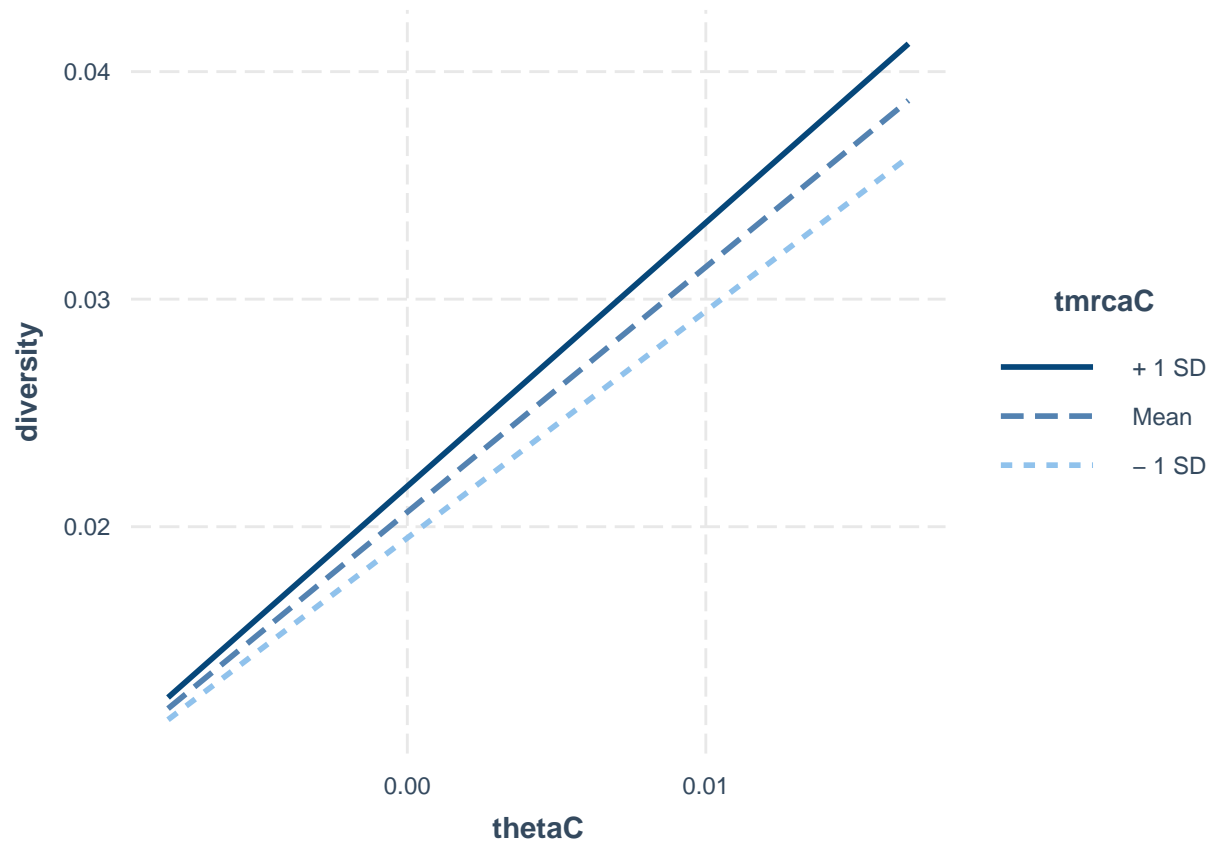


```
summary(m.diversity.rep_2)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.1M.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.1M.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.1M.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.1M.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.1M.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$VarExp[3] + anova.diversity$VarExp[4]) / anova.diversity$VarExp[1]
r2.inf.1Mb[2, 2] <- anova.diversity$VarExp[1] / anova.diversity$VarExp[1]
r2.inf.1Mb[3, 2] <- anova.diversity$VarExp[2] / anova.diversity$VarExp[1]
r2.inf.1Mb[4, 2] <- anova.diversity$VarExp[3] / anova.diversity$VarExp[1]
r2.inf.1Mb[5, 2] <- anova.diversity$VarExp[4] / anova.diversity$VarExp[1]
```

2.3.3 Replicate 3

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

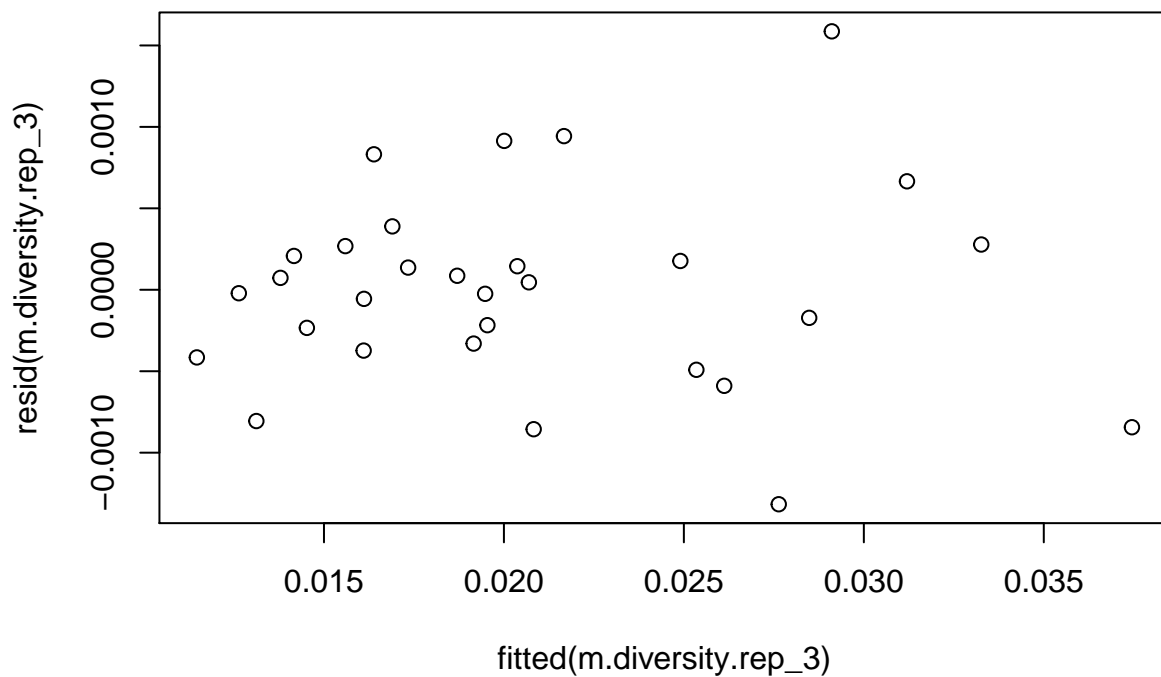
inf.lands.1M.rep_3 <- as.data.frame(cbind(pi.1M$avg, theta.1M$sample_mean, rho.1M$sample_mean, tmrca.1M$sample_mean))
names(inf.lands.1M.rep_3) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.1M.rep_3$thetaC <- inf.lands.1M.rep_3$theta - mean(inf.lands.1M.rep_3$theta)
inf.lands.1M.rep_3$tmrcaC <- inf.lands.1M.rep_3$tmrca - mean(inf.lands.1M.rep_3$tmrca)
inf.lands.1M.rep_3$rhoC <- inf.lands.1M.rep_3$rho - mean(inf.lands.1M.rep_3$rho)

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

m.diversity.rep_3 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.1M.rep_3)

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



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

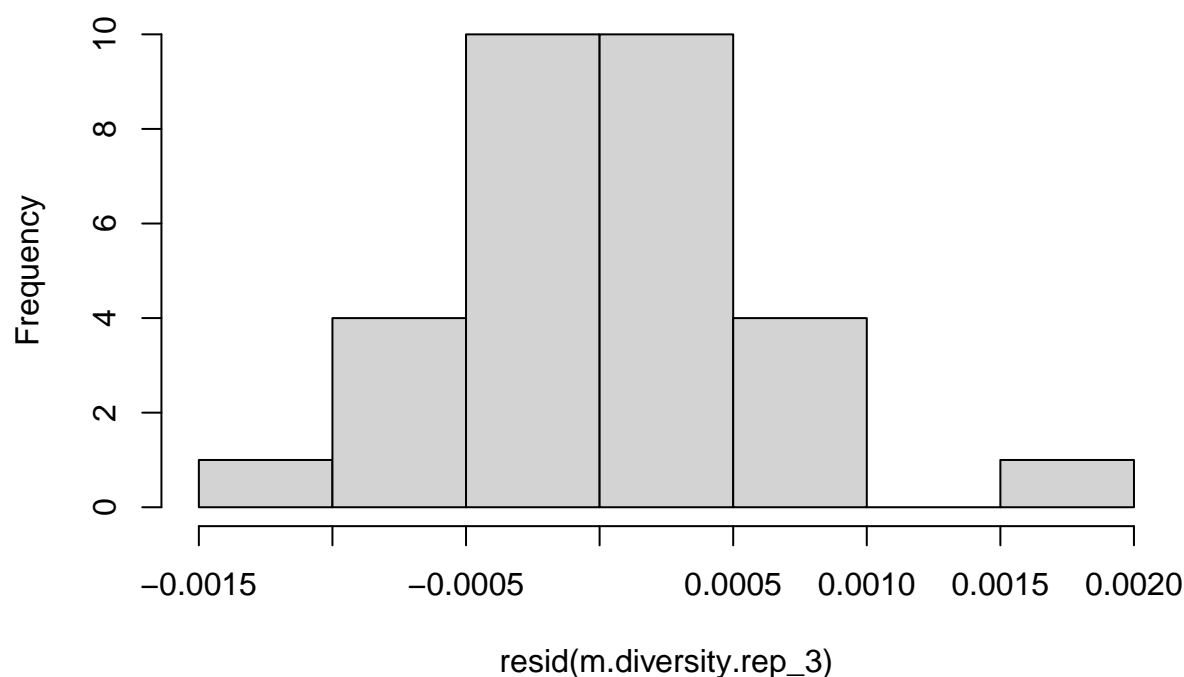
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_3  
## DW = 1.3502, p-value = 0.02515  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_3)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_3  
## HMC = 0.51975, p-value = 0.572
```

```
hist(resid(m.diversity.rep_3))
```

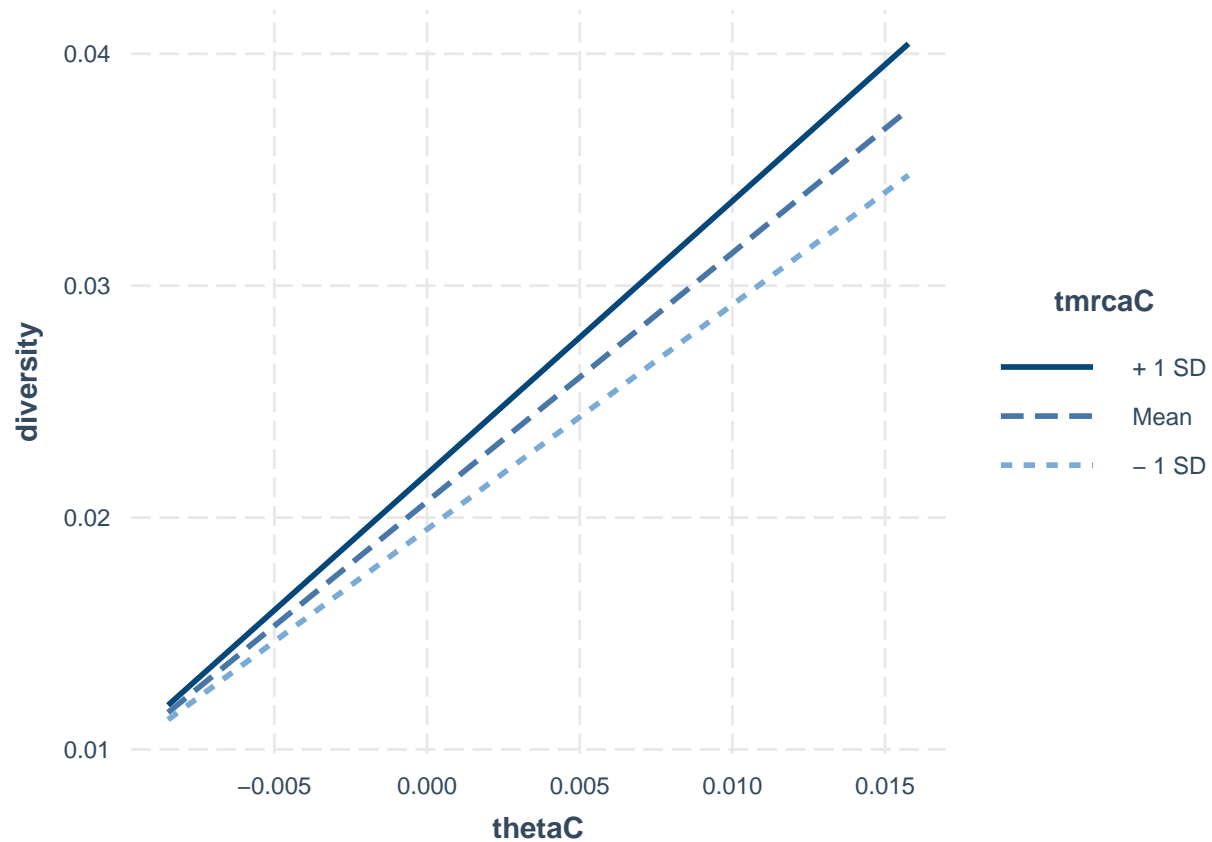
Histogram of resid(m.diversity.rep_3)



```
summary(m.diversity.rep_3)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.1M.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.1M.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.1M.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.1M.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.1M.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$VarExp[3] + anova.diversity$VarExp[4]) / anova.diversity$VarExp[1]
r2.inf.1Mb[2, 3] <- anova.diversity$VarExp[1] / anova.diversity$VarExp[1]
r2.inf.1Mb[3, 3] <- anova.diversity$VarExp[2] / anova.diversity$VarExp[1]
r2.inf.1Mb[4, 3] <- anova.diversity$VarExp[3] / anova.diversity$VarExp[1]
r2.inf.1Mb[5, 3] <- anova.diversity$VarExp[4] / anova.diversity$VarExp[1]
```

2.3.4 Replicate 4

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

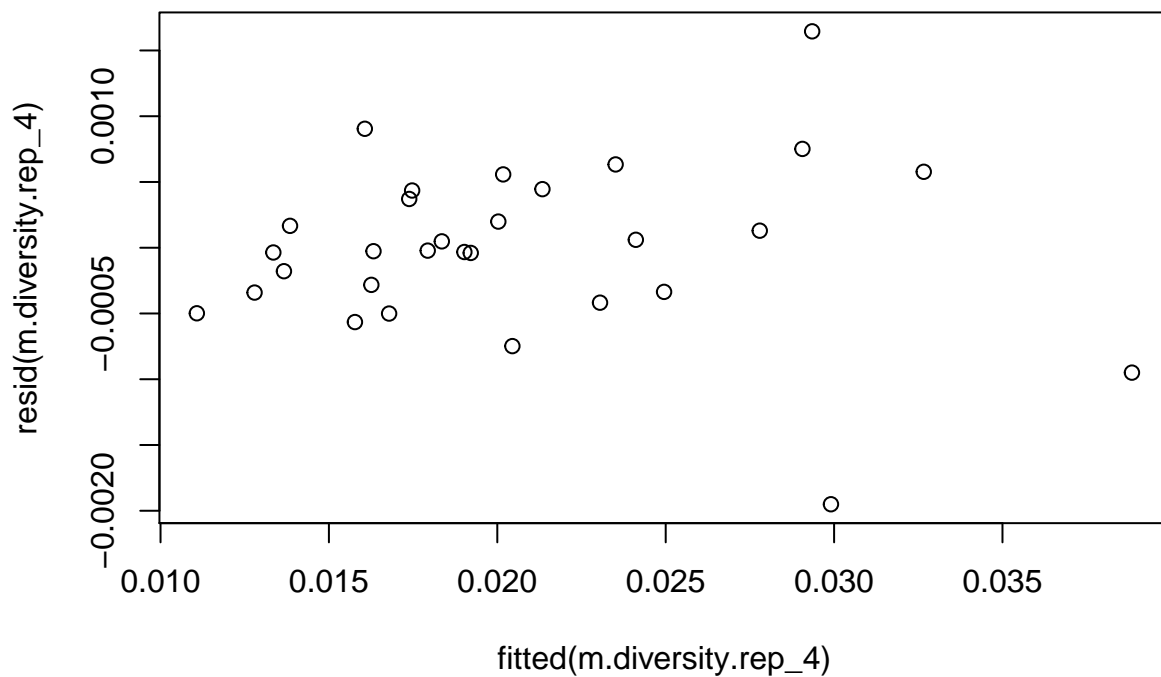
inf.lands.1M.rep_4 <- as.data.frame(cbind(pi.1M$avg, theta.1M$sample_mean, rho.1M$sample_mean, tmrca.1M$sample_mean))
names(inf.lands.1M.rep_4) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.1M.rep_4$thetaC <- inf.lands.1M.rep_4$theta - mean(inf.lands.1M.rep_4$theta)
inf.lands.1M.rep_4$tmrcaC <- inf.lands.1M.rep_4$tmrca - mean(inf.lands.1M.rep_4$tmrca)
inf.lands.1M.rep_4$rhoC <- inf.lands.1M.rep_4$rho - mean(inf.lands.1M.rep_4$rho)

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

m.diversity.rep_4 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.1M.rep_4)

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

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

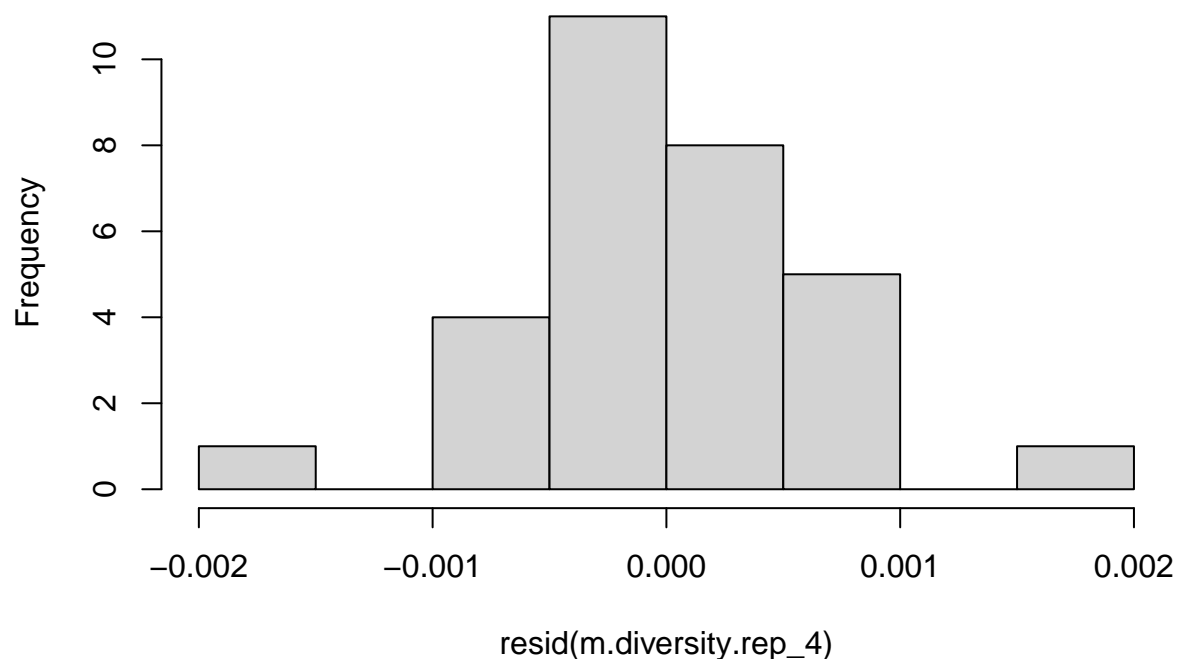
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_4  
## DW = 2.0871, p-value = 0.5863  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_4)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_4  
## HMC = 0.42593, p-value = 0.282
```

```
hist(resid(m.diversity.rep_4))
```

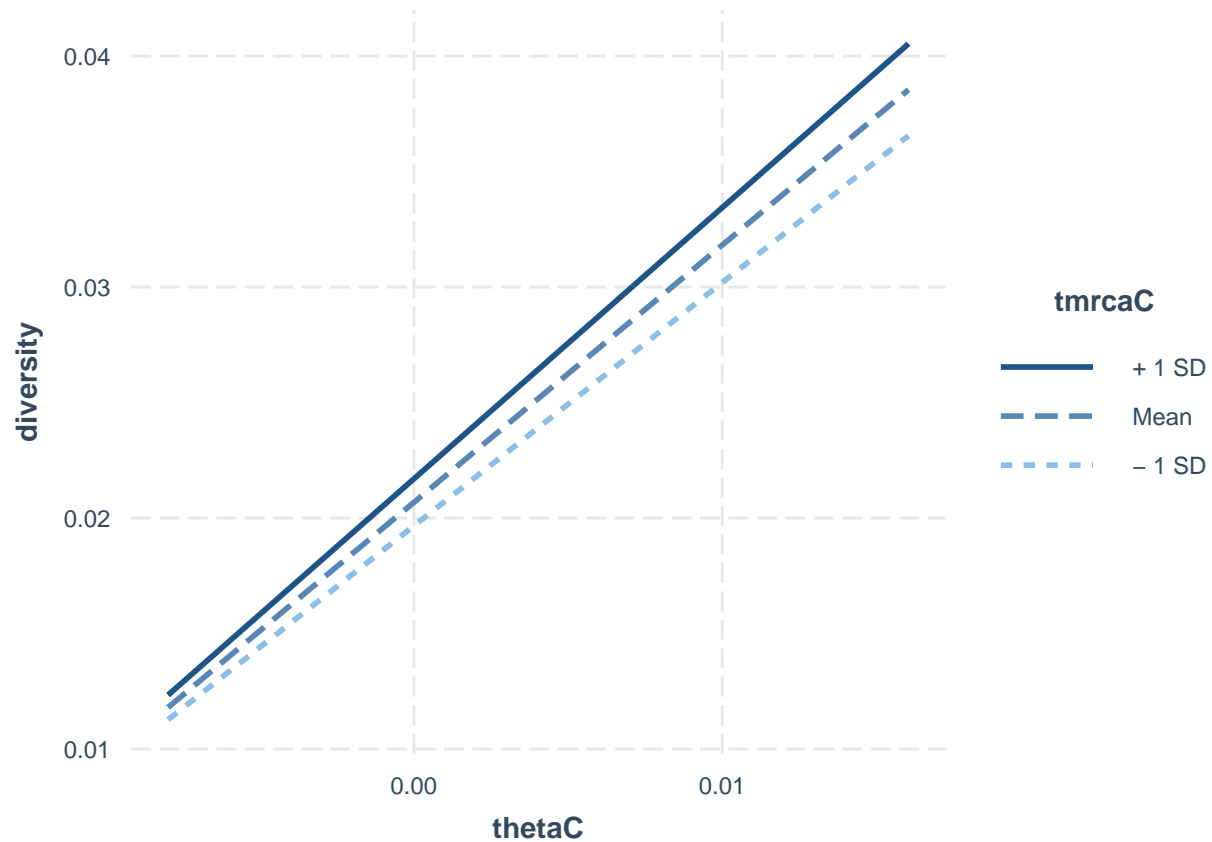
Histogram of resid(m.diversity.rep_4)



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

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.1M.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.1M.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.1M.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.1M.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.1M.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$VarExp[3] + anova.diversity$VarExp[4]) / anova.diversity$VarExp[1]
r2.inf.1Mb[2, 4] <- anova.diversity$VarExp[1] / anova.diversity$VarExp[1]
r2.inf.1Mb[3, 4] <- anova.diversity$VarExp[2] / anova.diversity$VarExp[1]
r2.inf.1Mb[4, 4] <- anova.diversity$VarExp[3] / anova.diversity$VarExp[1]
r2.inf.1Mb[5, 4] <- anova.diversity$VarExp[4] / anova.diversity$VarExp[1]
```

2.3.5 Replicate 5

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

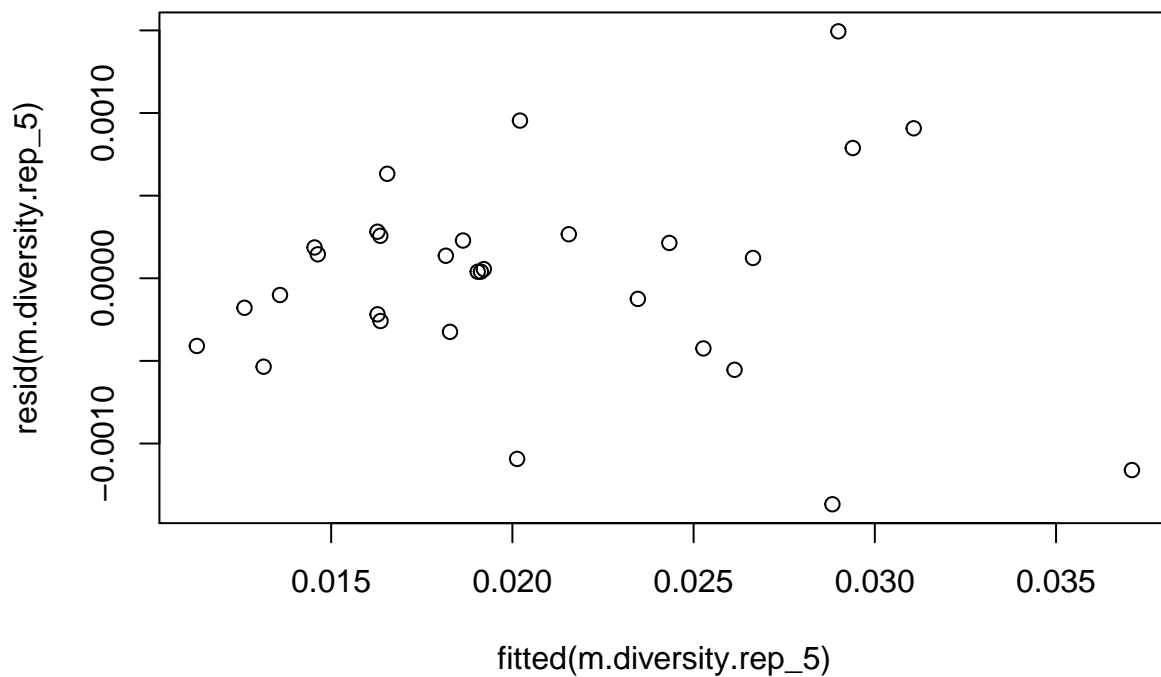
inf.lands.1M.rep_5 <- as.data.frame(cbind(pi.1M$avg, theta.1M$sample_mean, rho.1M$sample_mean, tmrca.1M$sample_mean))
names(inf.lands.1M.rep_5) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.1M.rep_5$thetaC <- inf.lands.1M.rep_5$theta - mean(inf.lands.1M.rep_5$theta)
inf.lands.1M.rep_5$tmrcaC <- inf.lands.1M.rep_5$tmrca - mean(inf.lands.1M.rep_5$tmrca)
inf.lands.1M.rep_5$rhoC <- inf.lands.1M.rep_5$rho - mean(inf.lands.1M.rep_5$rho)

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

m.diversity.rep_5 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.1M.rep_5)

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



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

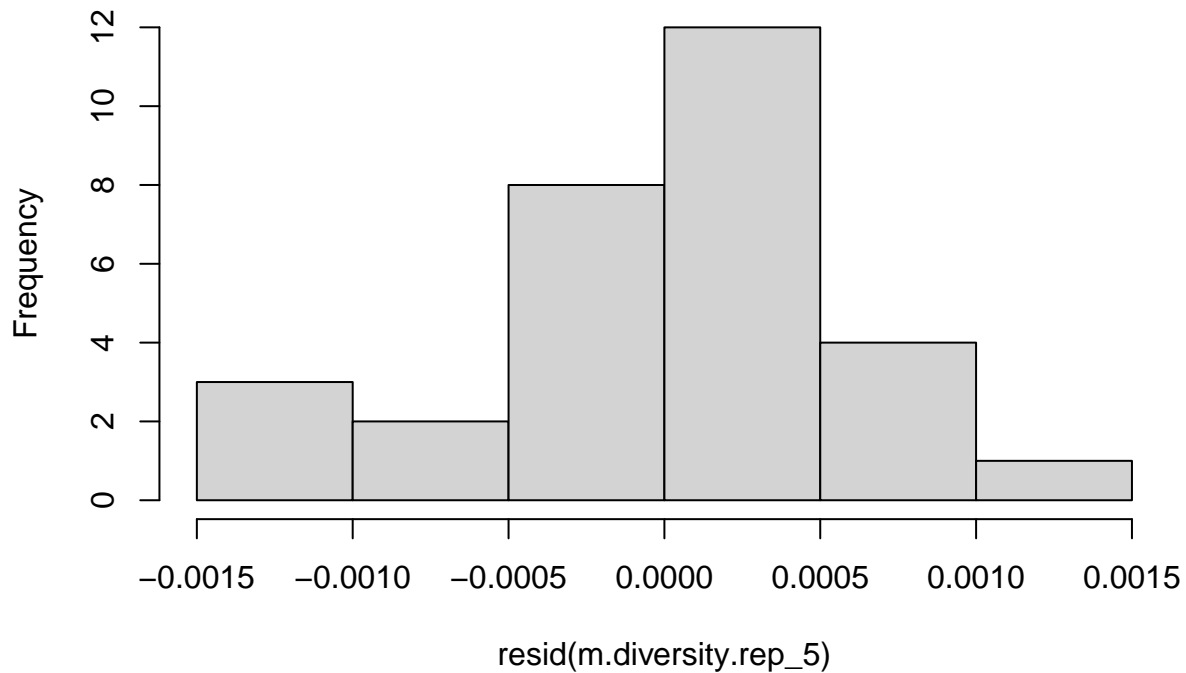
```
##
## Durbin-Watson test
##
## data: m.diversity.rep_5
## DW = 1.8381, p-value = 0.2796
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_5)
```

```
##
## Harrison-McCabe test
##
## data: m.diversity.rep_5
## HMC = 0.49429, p-value = 0.504
```

```
hist(resid(m.diversity.rep_5))
```

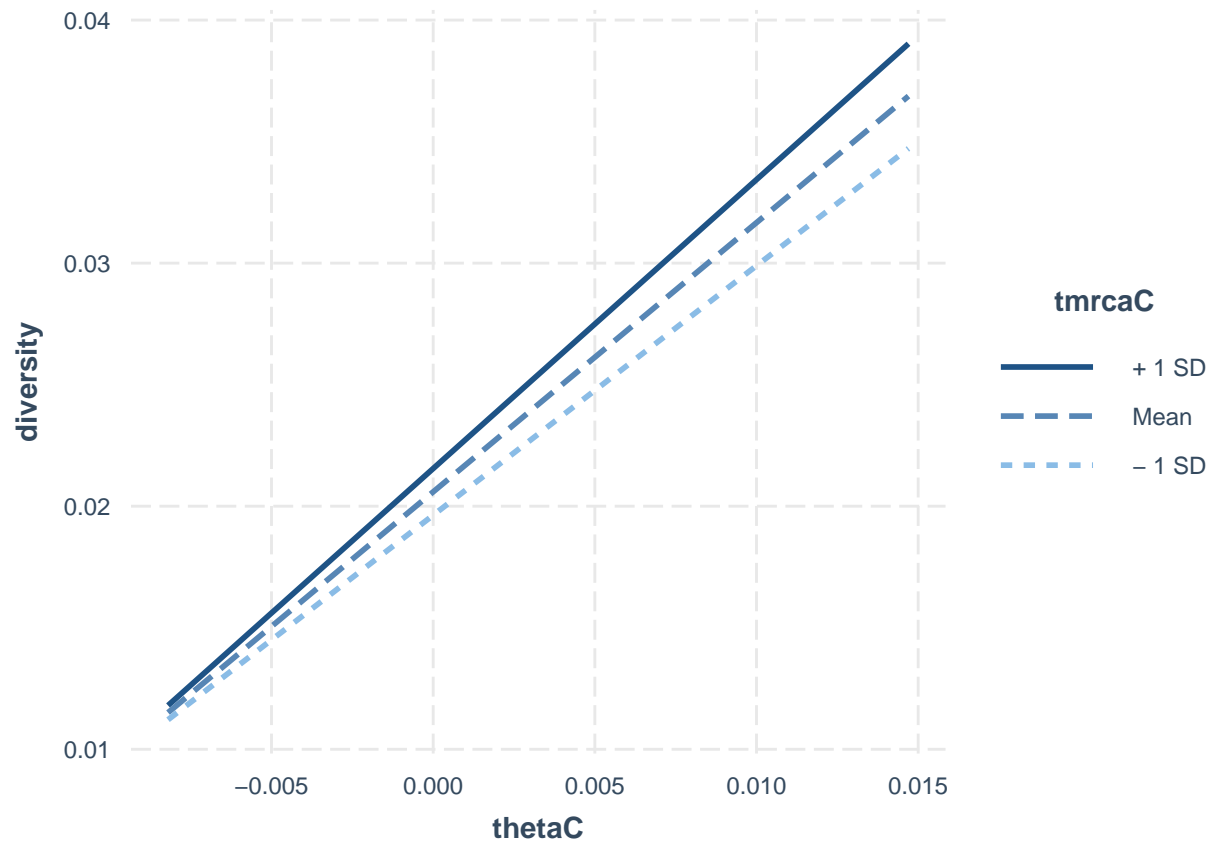
Histogram of resid(m.diversity.rep_5)



```
summary(m.diversity.rep_5)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.1M.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.1M.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.1M.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.1M.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.1M.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$VarExp[3] + anova.diversity$VarExp[4]) / anova.diversity$VarExp[5]
r2.inf.1Mb[2, 5] <- anova.diversity$VarExp[1] / anova.diversity$VarExp[5]
r2.inf.1Mb[3, 5] <- anova.diversity$VarExp[2] / anova.diversity$VarExp[5]
r2.inf.1Mb[4, 5] <- anova.diversity$VarExp[3] / anova.diversity$VarExp[5]
r2.inf.1Mb[5, 5] <- anova.diversity$VarExp[4] / anova.diversity$VarExp[5]
```

2.3.6 Replicate 6

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_6/rs.pair_6.", sep = "")
pi.1M <- read.table(paste(p, "diversity.1Mb.bedgraph", sep = ""), header = T)
pi.1M$avg <- apply(pi.1M[4:ncol(pi.1M)], 1, mean)
tmrca.1M <- read.table(paste(p, "TMRCA.1Mb.bedgraph", sep = ""), header = T)
tmrca.1M$avg <- apply(tmrca.1M[4:ncol(tmrca.1M)], 1, mean)
rho.1M <- read.table(paste(p, "rho.1Mb.bedgraph", sep = ""), header = T)
theta.1M <- read.table(paste(p, "theta.1Mb.bedgraph", sep = ""), header = T)

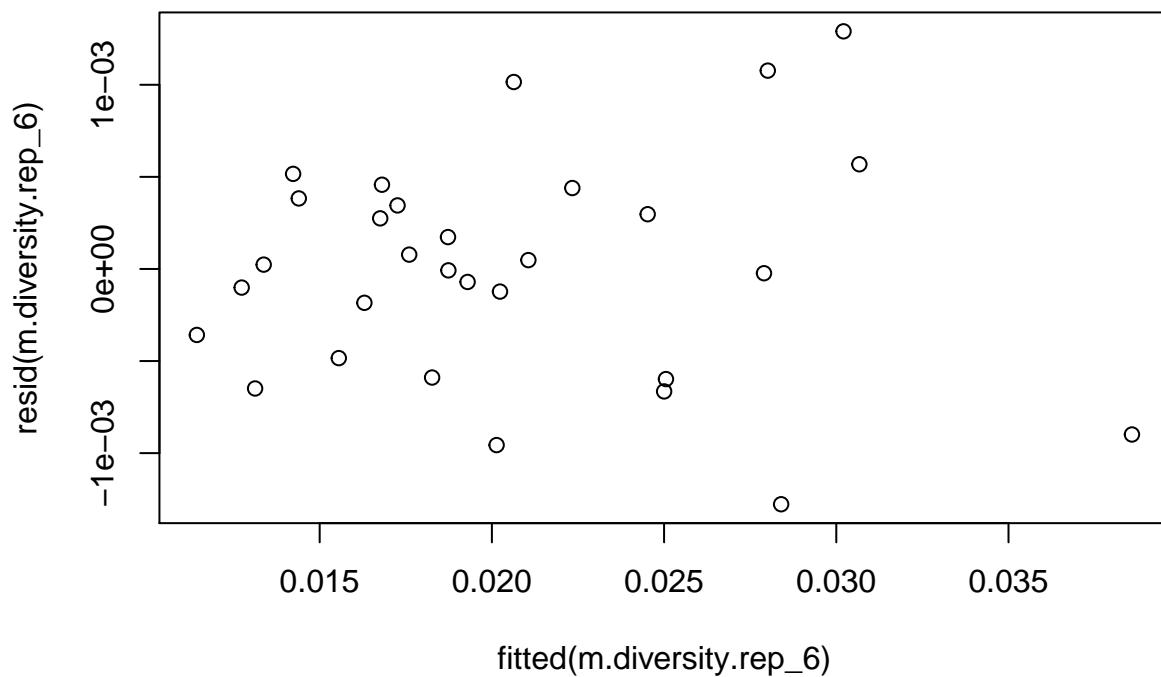
inf.lands.1M.rep_6 <- as.data.frame(cbind(pi.1M$avg, theta.1M$sample_mean, rho.1M$sample_mean, tmrca.1M$sample_mean))
names(inf.lands.1M.rep_6) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.1M.rep_6$thetaC <- inf.lands.1M.rep_6$theta - mean(inf.lands.1M.rep_6$theta)
inf.lands.1M.rep_6$tmrcaC <- inf.lands.1M.rep_6$tmrca - mean(inf.lands.1M.rep_6$tmrca)
inf.lands.1M.rep_6$rhoC <- inf.lands.1M.rep_6$rho - mean(inf.lands.1M.rep_6$rho)

inf.lands.1M.rep_6$bin <- 1:nrow(inf.lands.1M.rep_6)

m.diversity.rep_6 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.1M.rep_6)

plot(resid(m.diversity.rep_6)~fitted(m.diversity.rep_6))
```



```
dwtest(m.diversity.rep_6)
```

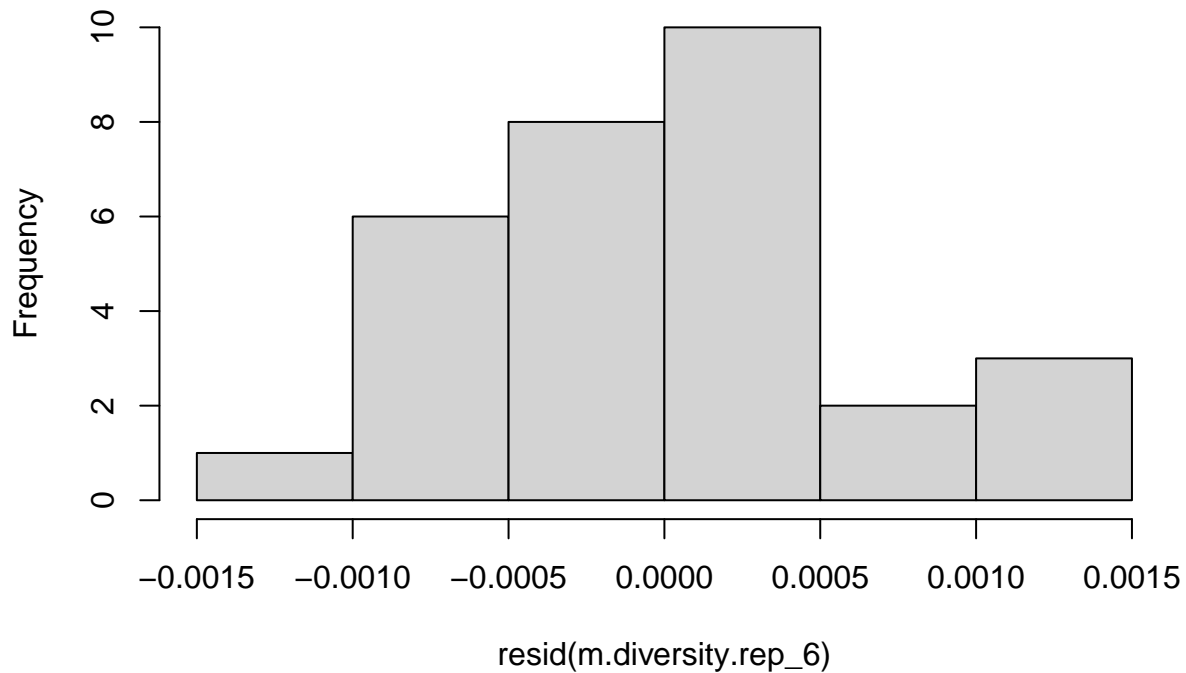
```
##
## Durbin-Watson test
##
## data:  m.diversity.rep_6
## DW = 1.7678, p-value = 0.2162
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_6)
```

```
##
## Harrison-McCabe test
##
## data:  m.diversity.rep_6
## HMC = 0.38206, p-value = 0.178
```

```
hist(resid(m.diversity.rep_6))
```

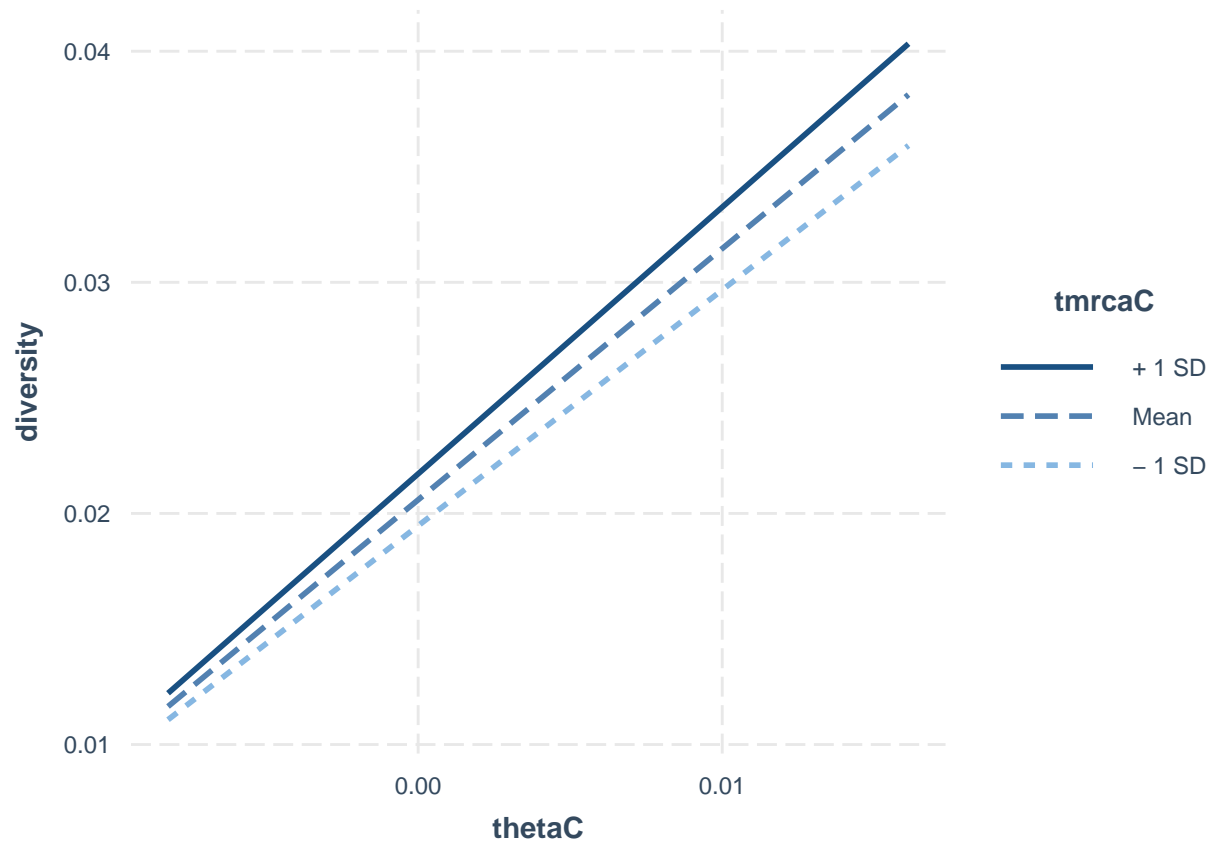
Histogram of resid(m.diversity.rep_6)



```
summary(m.diversity.rep_6)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.1M.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.1M.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.1M.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.1M.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.1M.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$VarExp[3] +
r2.inf.1Mb[2, 6] <- anova.diversity$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.1M <- read.table(paste(p, "diversity.1Mb.bedgraph", sep = ""), header = T)
pi.1M$avg <- apply(pi.1M[4:ncol(pi.1M)], 1, mean)
tmrca.1M <- read.table(paste(p, "TMRCA.1Mb.bedgraph", sep = ""), header = T)
tmrca.1M$avg <- apply(tmrca.1M[4:ncol(tmrca.1M)], 1, mean)
rho.1M <- read.table(paste(p, "rho.1Mb.bedgraph", sep = ""), header = T)
theta.1M <- read.table(paste(p, "theta.1Mb.bedgraph", sep = ""), header = T)

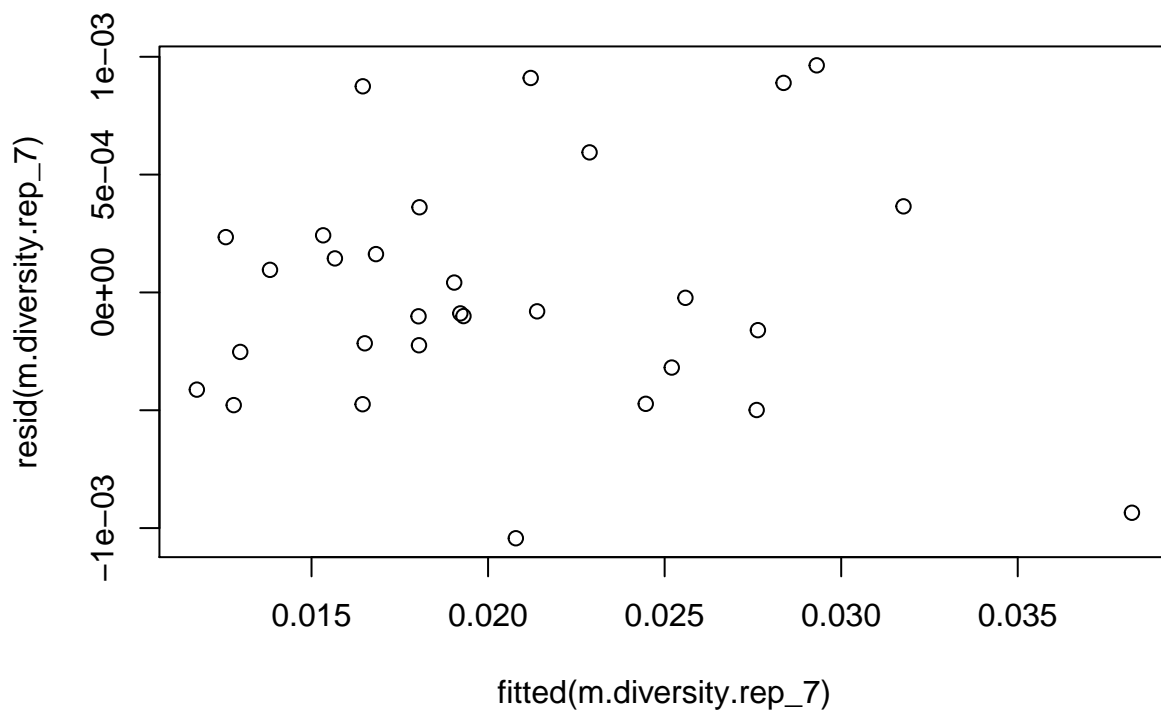
inf.lands.1M.rep_7 <- as.data.frame(cbind(pi.1M$avg, theta.1M$sample_mean, rho.1M$sample_mean, tmrca.1M$sample_mean))
names(inf.lands.1M.rep_7) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.1M.rep_7$thetaC <- inf.lands.1M.rep_7$theta - mean(inf.lands.1M.rep_7$theta)
inf.lands.1M.rep_7$tmrcaC <- inf.lands.1M.rep_7$tmrca - mean(inf.lands.1M.rep_7$tmrca)
inf.lands.1M.rep_7$rhoC <- inf.lands.1M.rep_7$rho - mean(inf.lands.1M.rep_7$rho)

inf.lands.1M.rep_7$bin <- 1:nrow(inf.lands.1M.rep_7)

m.diversity.rep_7 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.1M.rep_7)

plot(resid(m.diversity.rep_7)~fitted(m.diversity.rep_7))
```



```
dwtest(m.diversity.rep_7)
```

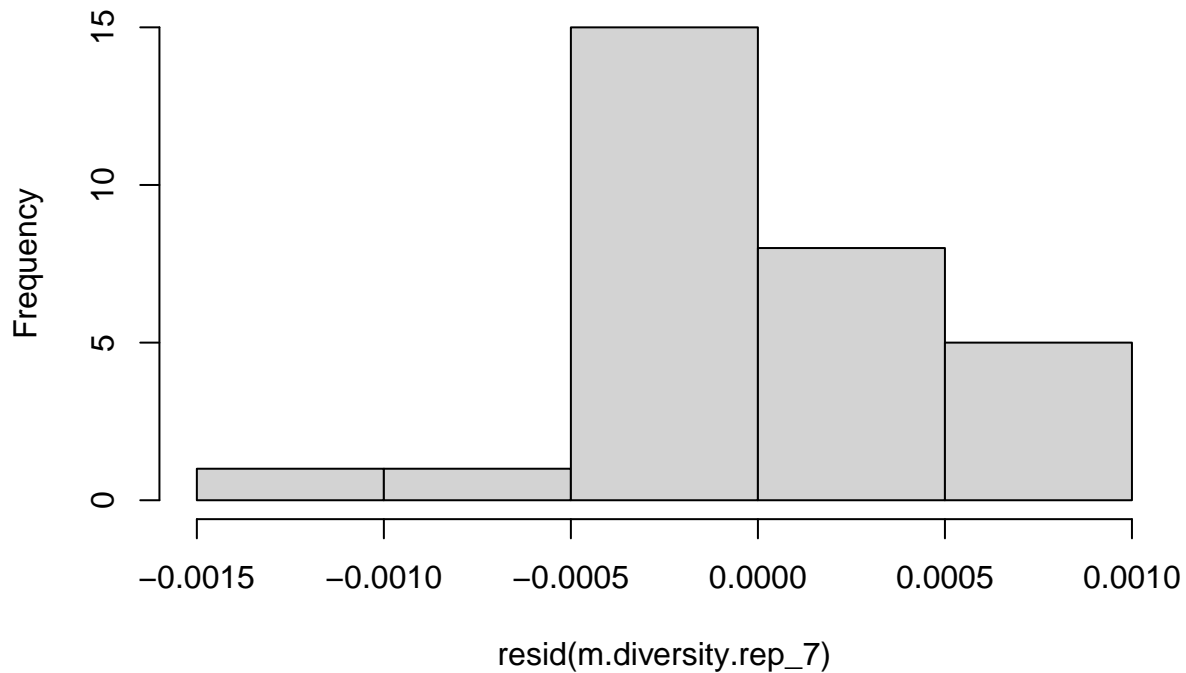
```
##
## Durbin-Watson test
##
## data: m.diversity.rep_7
## DW = 1.6938, p-value = 0.1634
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_7)
```

```
##
## Harrison-McCabe test
##
## data: m.diversity.rep_7
## HMC = 0.40789, p-value = 0.228
```

```
hist(resid(m.diversity.rep_7))
```

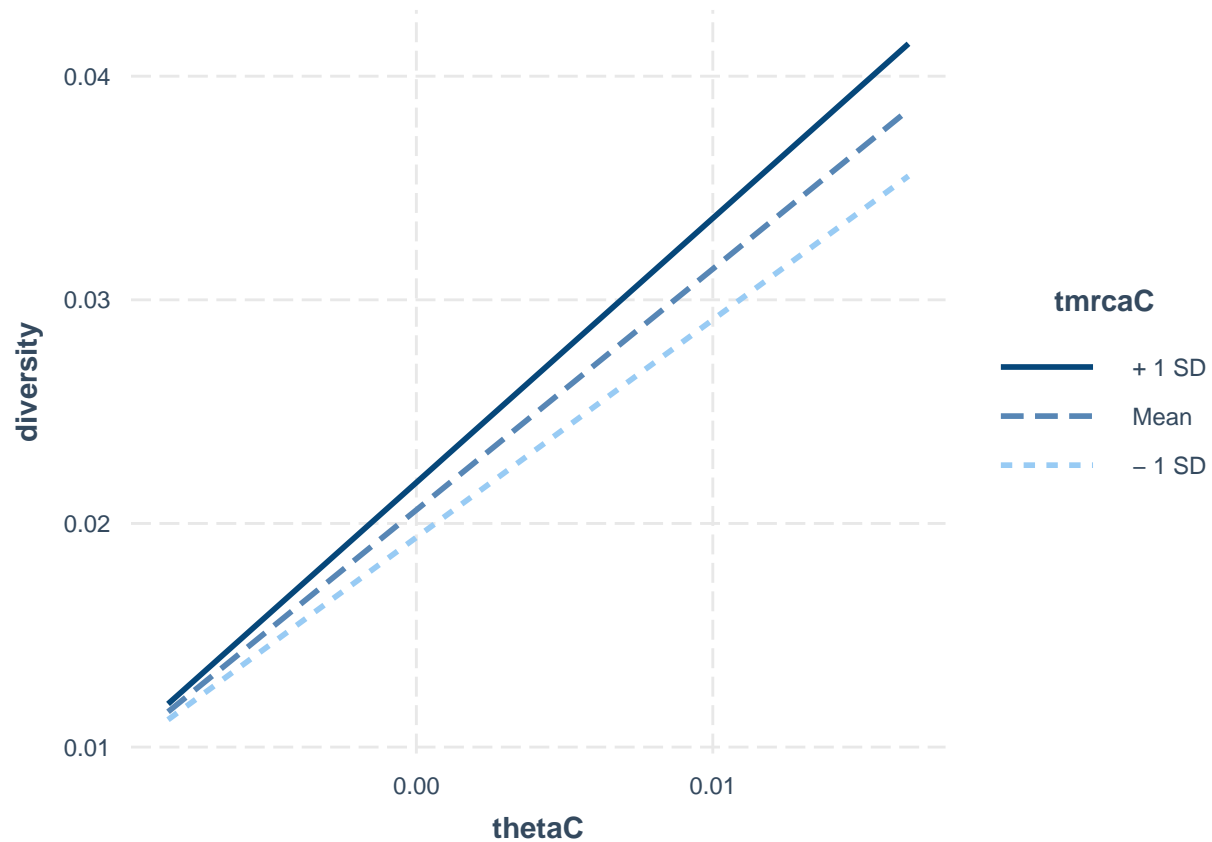

Histogram of resid(m.diversity.rep_7)



```
summary(m.diversity.rep_7)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.1M.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.1M.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.1M.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.1M.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.1M.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$VarExp[3] +
r2.inf.1Mb[2, 7] <- anova.diversity$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.1M <- read.table(paste(p, "diversity.1Mb.bedgraph", sep = ""), header = T)
pi.1M$avg <- apply(pi.1M[4:ncol(pi.1M)], 1, mean)
tmrca.1M <- read.table(paste(p, "TMRCA.1Mb.bedgraph", sep = ""), header = T)
tmrca.1M$avg <- apply(tmrca.1M[4:ncol(tmrca.1M)], 1, mean)
rho.1M <- read.table(paste(p, "rho.1Mb.bedgraph", sep = ""), header = T)
theta.1M <- read.table(paste(p, "theta.1Mb.bedgraph", sep = ""), header = T)

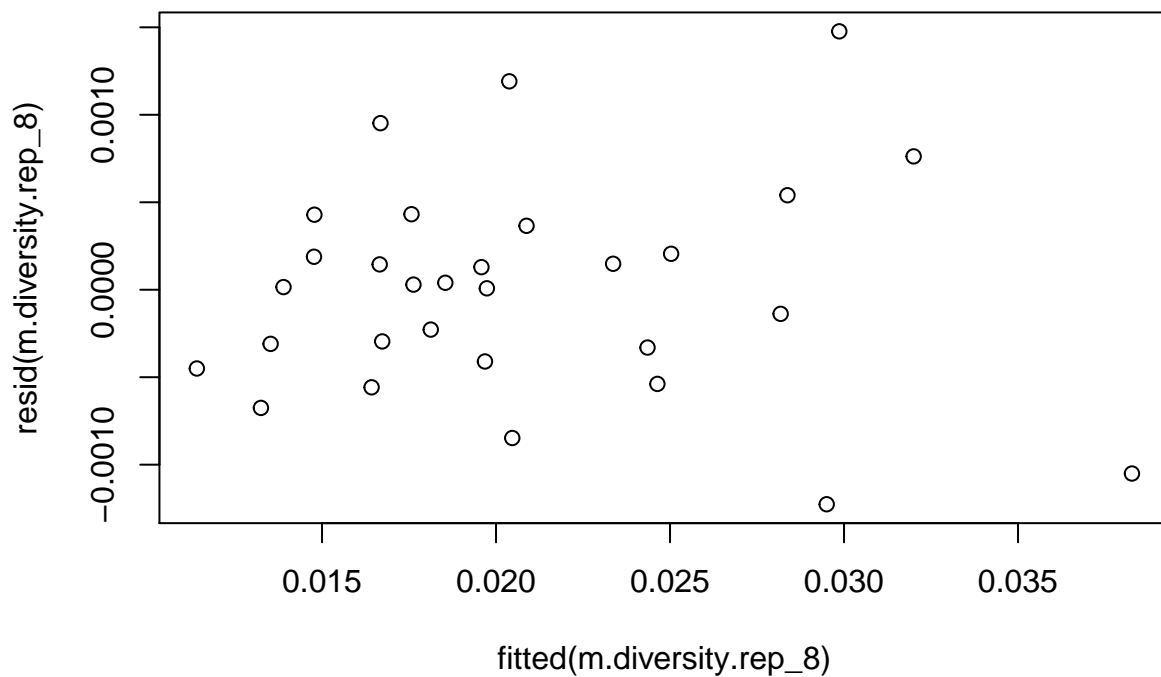
inf.lands.1M.rep_8 <- as.data.frame(cbind(pi.1M$avg, theta.1M$sample_mean, rho.1M$sample_mean, tmrca.1M$sample_mean))
names(inf.lands.1M.rep_8) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.1M.rep_8$thetaC <- inf.lands.1M.rep_8$theta - mean(inf.lands.1M.rep_8$theta)
inf.lands.1M.rep_8$tmrcaC <- inf.lands.1M.rep_8$tmrca - mean(inf.lands.1M.rep_8$tmrca)
inf.lands.1M.rep_8$rhoC <- inf.lands.1M.rep_8$rho - mean(inf.lands.1M.rep_8$rho)

inf.lands.1M.rep_8$bin <- 1:nrow(inf.lands.1M.rep_8)

m.diversity.rep_8 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.1M.rep_8)

plot(resid(m.diversity.rep_8)~fitted(m.diversity.rep_8))
```



```
dwtest(m.diversity.rep_8)
```

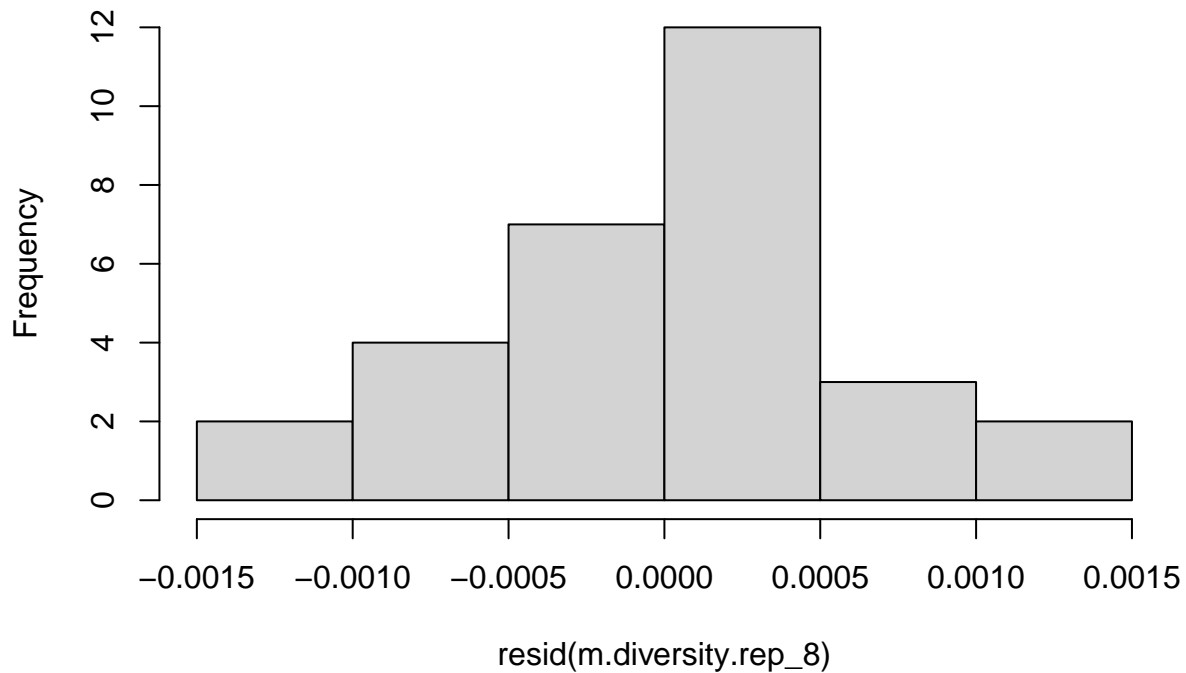
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_8  
## DW = 1.6816, p-value = 0.17  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_8)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_8  
## HMC = 0.45613, p-value = 0.395
```

```
hist(resid(m.diversity.rep_8))
```

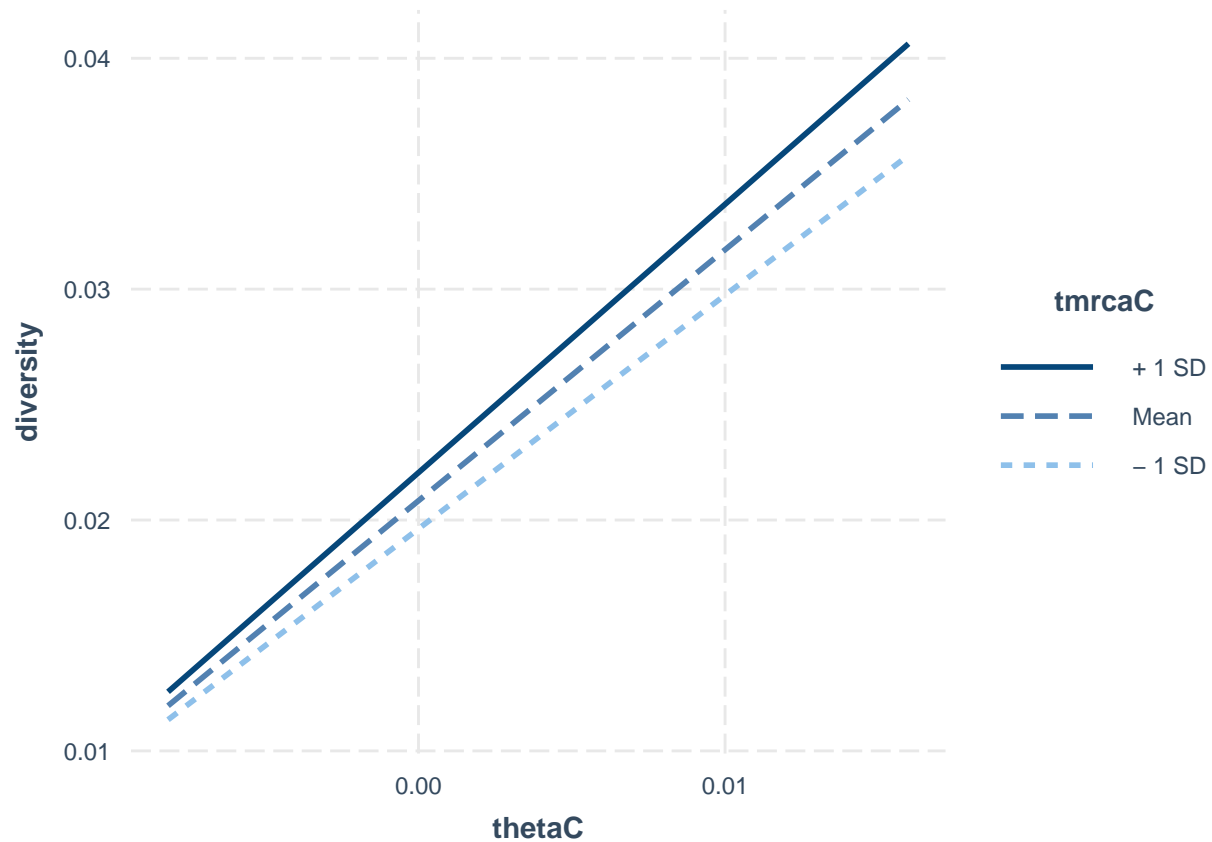
Histogram of resid(m.diversity.rep_8)



```
summary(m.diversity.rep_8)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.1M.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.1M.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.1M.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.1M.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.1M.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$VarExp[3] +
r2.inf.1Mb[2, 8] <- anova.diversity$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.1M <- read.table(paste(p, "diversity.1Mb.bedgraph", sep = ""), header = T)
pi.1M$avg <- apply(pi.1M[4:ncol(pi.1M)], 1, mean)
tmrca.1M <- read.table(paste(p, "TMRCA.1Mb.bedgraph", sep = ""), header = T)
tmrca.1M$avg <- apply(tmrca.1M[4:ncol(tmrca.1M)], 1, mean)
rho.1M <- read.table(paste(p, "rho.1Mb.bedgraph", sep = ""), header = T)
theta.1M <- read.table(paste(p, "theta.1Mb.bedgraph", sep = ""), header = T)

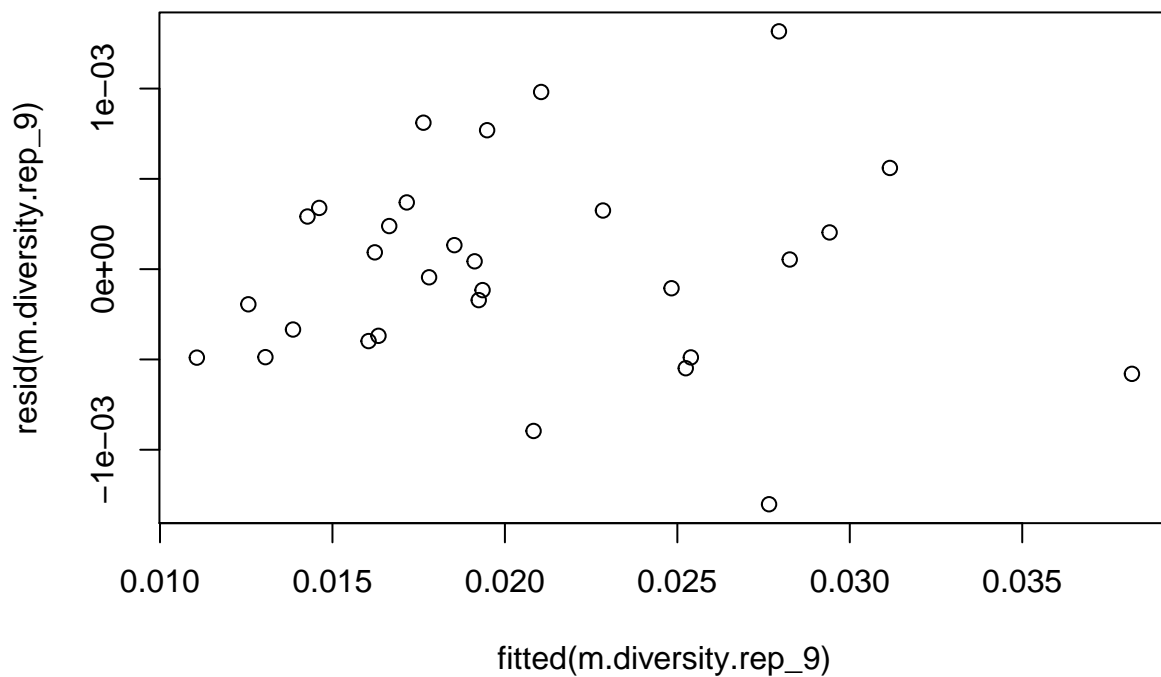
inf.lands.1M.rep_9 <- as.data.frame(cbind(pi.1M$avg, theta.1M$sample_mean, rho.1M$sample_mean, tmrca.1M$sample_mean))
names(inf.lands.1M.rep_9) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.1M.rep_9$thetaC <- inf.lands.1M.rep_9$theta - mean(inf.lands.1M.rep_9$theta)
inf.lands.1M.rep_9$tmrcaC <- inf.lands.1M.rep_9$tmrca - mean(inf.lands.1M.rep_9$tmrca)
inf.lands.1M.rep_9$rhoC <- inf.lands.1M.rep_9$rho - mean(inf.lands.1M.rep_9$rho)

inf.lands.1M.rep_9$bin <- 1:nrow(inf.lands.1M.rep_9)

m.diversity.rep_9 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.1M.rep_9)

plot(resid(m.diversity.rep_9)~fitted(m.diversity.rep_9))
```



```
dwtest(m.diversity.rep_9)
```

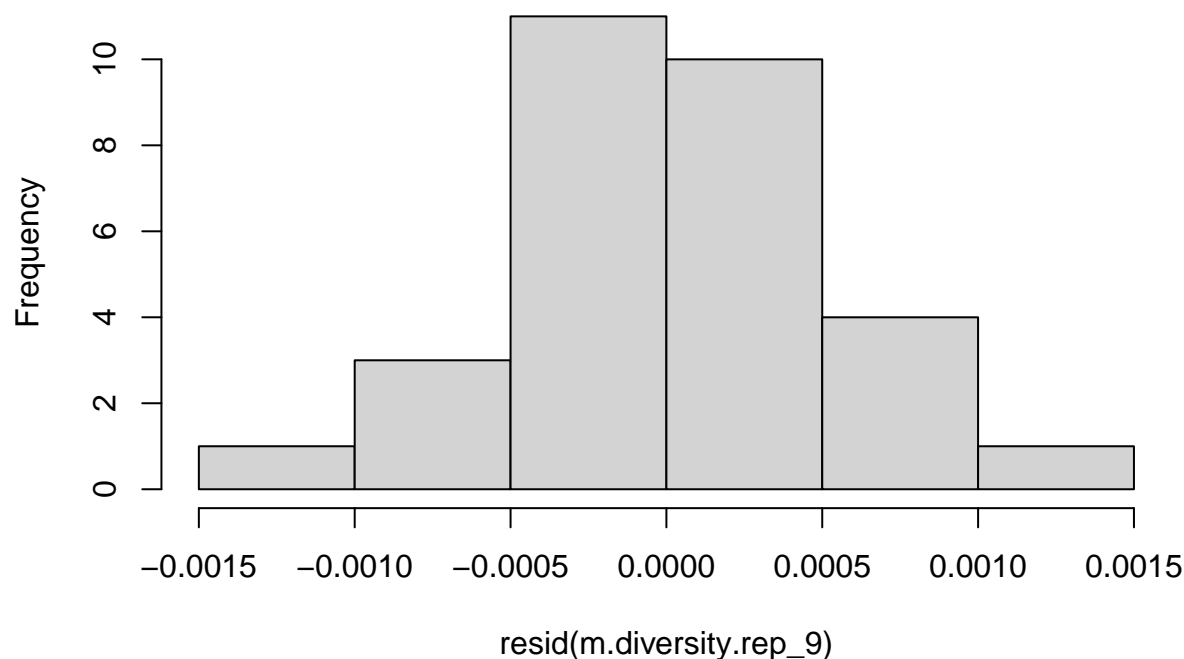
```
##
## Durbin-Watson test
##
## data: m.diversity.rep_9
## DW = 1.686, p-value = 0.1501
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.diversity.rep_9)
```

```
##
## Harrison-McCabe test
##
## data: m.diversity.rep_9
## HMC = 0.49123, p-value = 0.476
```

```
hist(resid(m.diversity.rep_9))
```

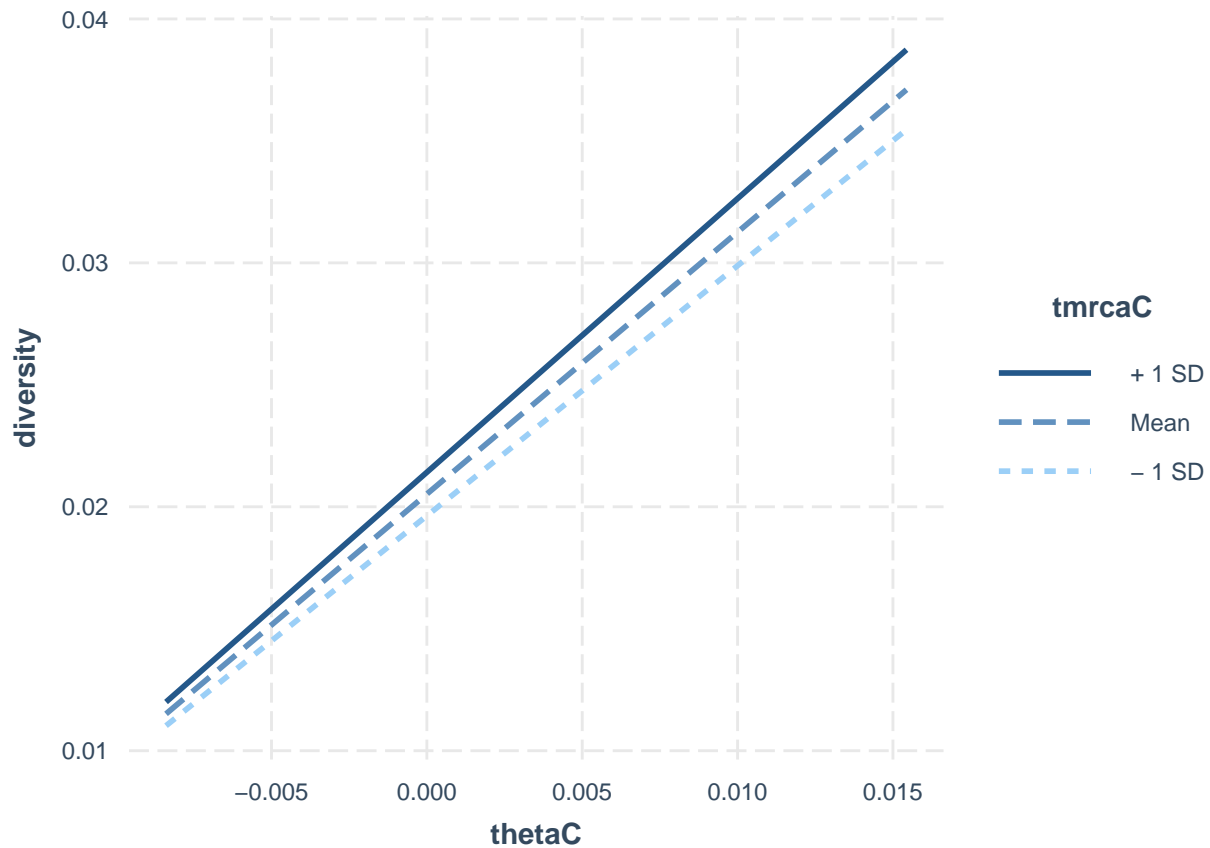
Histogram of resid(m.diversity.rep_9)



```
summary(m.diversity.rep_9)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.1M.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.1M.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.1M.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 0.581067343 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.1M.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.1M.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$VarExp[3] + anova.diversity$VarExp[4]) / anova.diversity$VarExp[1]
r2.inf.1Mb[2, 9] <- anova.diversity$VarExp[1] / anova.diversity$VarExp[1]
r2.inf.1Mb[3, 9] <- anova.diversity$VarExp[2] / anova.diversity$VarExp[1]
r2.inf.1Mb[4, 9] <- anova.diversity$VarExp[3] / anova.diversity$VarExp[1]
r2.inf.1Mb[5, 9] <- anova.diversity$VarExp[4] / anova.diversity$VarExp[1]
```

2.3.10 Replicate 10

```
p <- paste("dm_data/dm_chr_maps/2L/dm_coal_sims/rep_10/rs.pair_10.", sep = "")
pi.1M <- read.table(paste(p, "diversity.1Mb.bedgraph", sep = ""), header = T)
pi.1M$avg <- apply(pi.1M[4:ncol(pi.1M)], 1, mean)
tmrca.1M <- read.table(paste(p, "TMRCA.1Mb.bedgraph", sep = ""), header = T)
tmrca.1M$avg <- apply(tmrca.1M[4:ncol(tmrca.1M)], 1, mean)
rho.1M <- read.table(paste(p, "rho.1Mb.bedgraph", sep = ""), header = T)
theta.1M <- read.table(paste(p, "theta.1Mb.bedgraph", sep = ""), header = T)

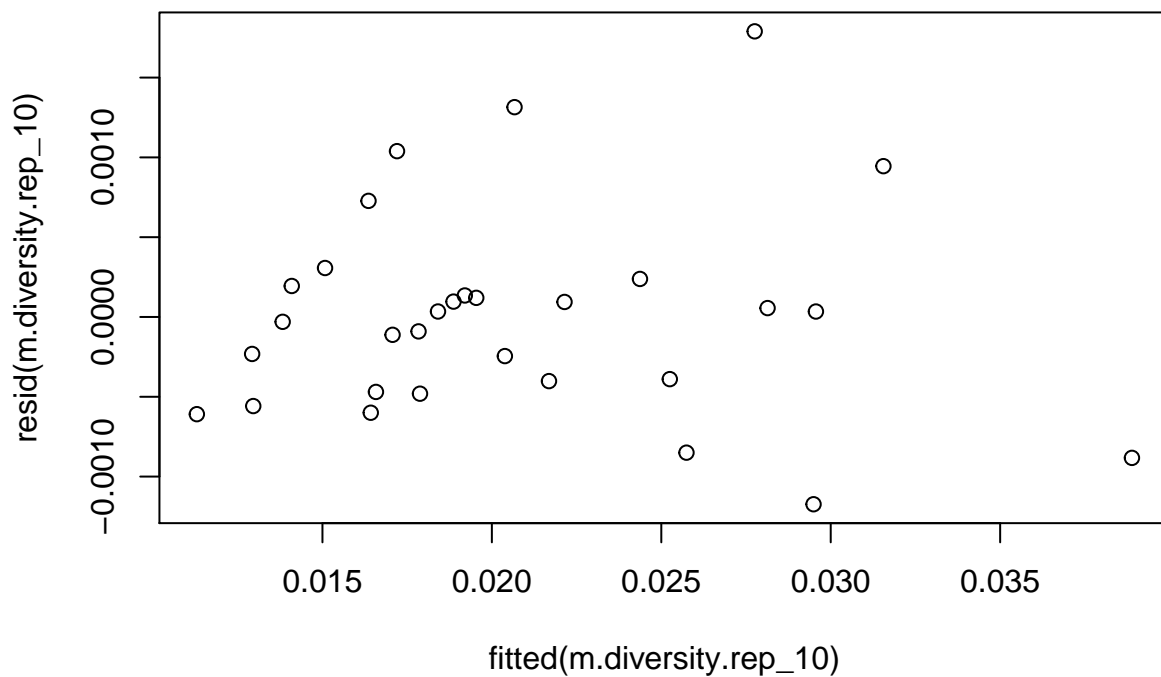
inf.lands.1M.rep_10 <- as.data.frame(cbind(pi.1M$avg, theta.1M$sample_mean, rho.1M$sample_mean, tmrca.1M$sample_mean))
names(inf.lands.1M.rep_10) <- c("diversity", "theta", "rho", "tmrca")

# centering
inf.lands.1M.rep_10$thetaC <- inf.lands.1M.rep_10$theta - mean(inf.lands.1M.rep_10$theta)
inf.lands.1M.rep_10$tmrcaC <- inf.lands.1M.rep_10$tmrca - mean(inf.lands.1M.rep_10$tmrca)
inf.lands.1M.rep_10$rhoC <- inf.lands.1M.rep_10$rho - mean(inf.lands.1M.rep_10$rho)

inf.lands.1M.rep_10$bin <- 1:nrow(inf.lands.1M.rep_10)

m.diversity.rep_10 <- lm(diversity ~ thetaC + rhoC + tmrcaC + thetaC*tmrcaC, data = inf.lands.1M.rep_10)

plot(resid(m.diversity.rep_10)~fitted(m.diversity.rep_10))
```



```
dwtest(m.diversity.rep_10)
```

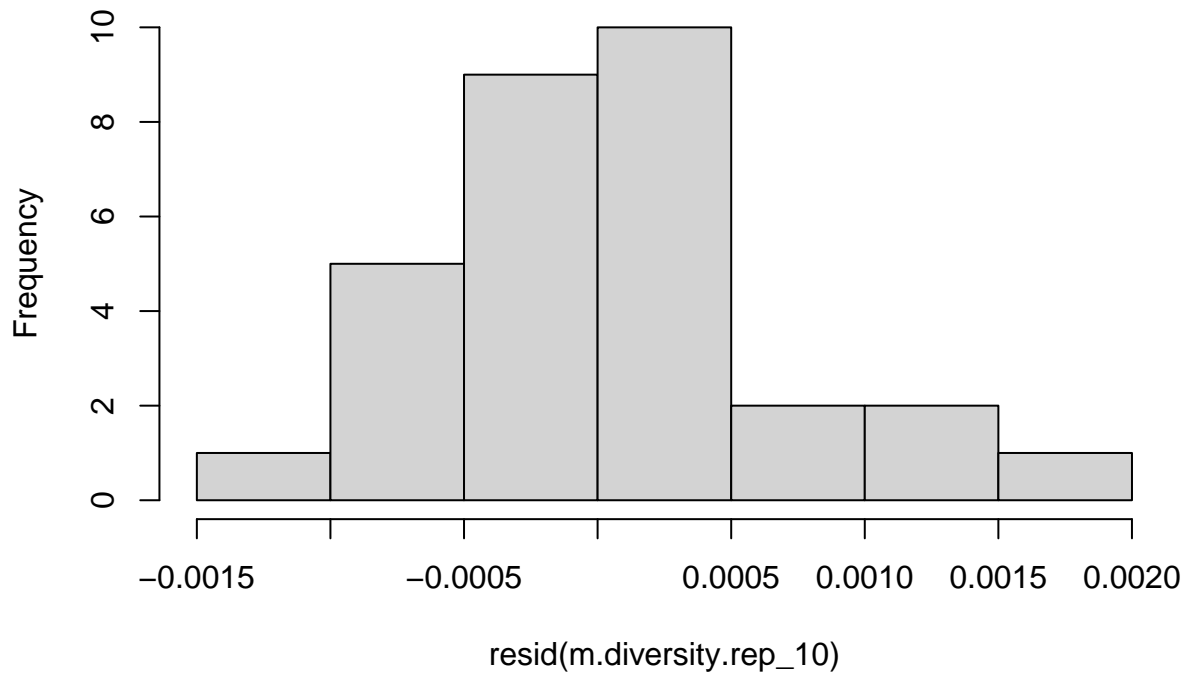
```
##
## Durbin-Watson test
##
## data: m.diversity.rep_10
## DW = 1.5209, p-value = 0.06939
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmctest(m.diversity.rep_10)
```

```
##
## Harrison-McCabe test
##
## data: m.diversity.rep_10
## HMC = 0.59687, p-value = 0.748
```

```
hist(resid(m.diversity.rep_10))
```

Histogram of resid(m.diversity.rep_10)

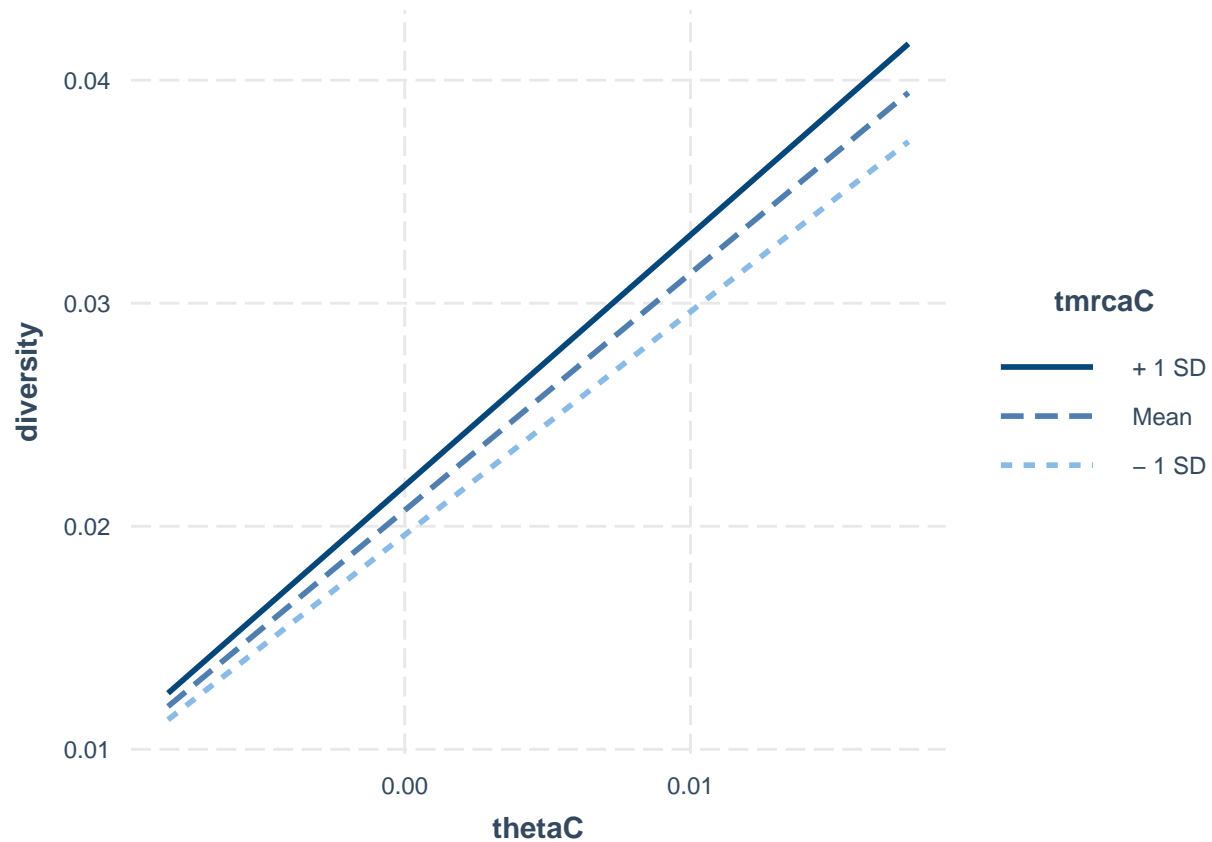


```
summary(m.diversity.rep_10)
```

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC * tmrcaC,
##     data = inf.lands.1M.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.1M.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.1M.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.1M.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.1M.rep_10
## AIC BIC logLik
## -316.9544 -309.9484 163.4772
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
## Phi
## -0.01181333
##
## 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 Plots

```
scale.3d <- function(x) sprintf("%.3f", x)

rho.plot <- as.data.frame(cbind(inf.lands.1M.rep_1$bin,
                                sim.rho.1M$sim,
                                inf.lands.1M.rep_1$rho,
                                inf.lands.1M.rep_2$rho,
                                inf.lands.1M.rep_3$rho,
                                inf.lands.1M.rep_4$rho,
                                inf.lands.1M.rep_5$rho,
                                inf.lands.1M.rep_6$rho,
                                inf.lands.1M.rep_7$rho,
                                inf.lands.1M.rep_8$rho,
                                inf.lands.1M.rep_9$rho,
                                inf.lands.1M.rep_10$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 = 100)
rho.map.1Mb <- rho.map.1Mb + scale_color_manual(values = c("black", brewer.pal(n = 9, name = "Blues")), legend = FALSE)
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.1M.rep_1$bin,
                                sim.theta.1M$sim,
                                inf.lands.1M.rep_1$theta,
                                inf.lands.1M.rep_2$theta,
                                inf.lands.1M.rep_3$theta,
                                inf.lands.1M.rep_4$theta,
                                inf.lands.1M.rep_5$theta,
                                inf.lands.1M.rep_6$theta,
```

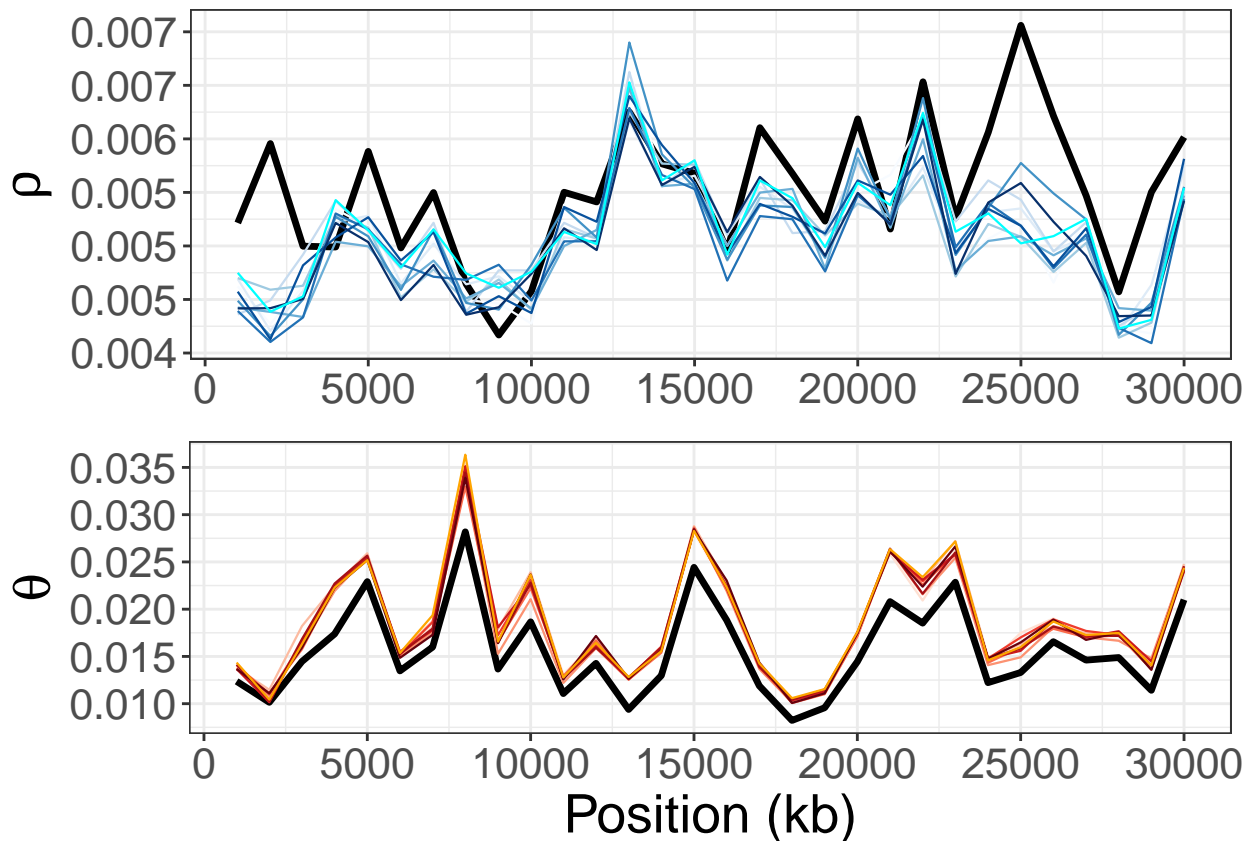
```

inf.lands.1M.rep_7$theta,
inf.lands.1M.rep_8$theta,
inf.lands.1M.rep_9$theta,
inf.lands.1M.rep_10$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(
theta.map.1Mb <- theta.map.1Mb + geom_line(data = molten.theta, aes(size = variable)) + scale_size_manu
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(brea
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

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("fig2.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)

# TMRCA 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))

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 = T)
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 = T)
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), method = "REML")

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)
```

```
# TMRCA 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),
                        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 = T)
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 = T)
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")
```

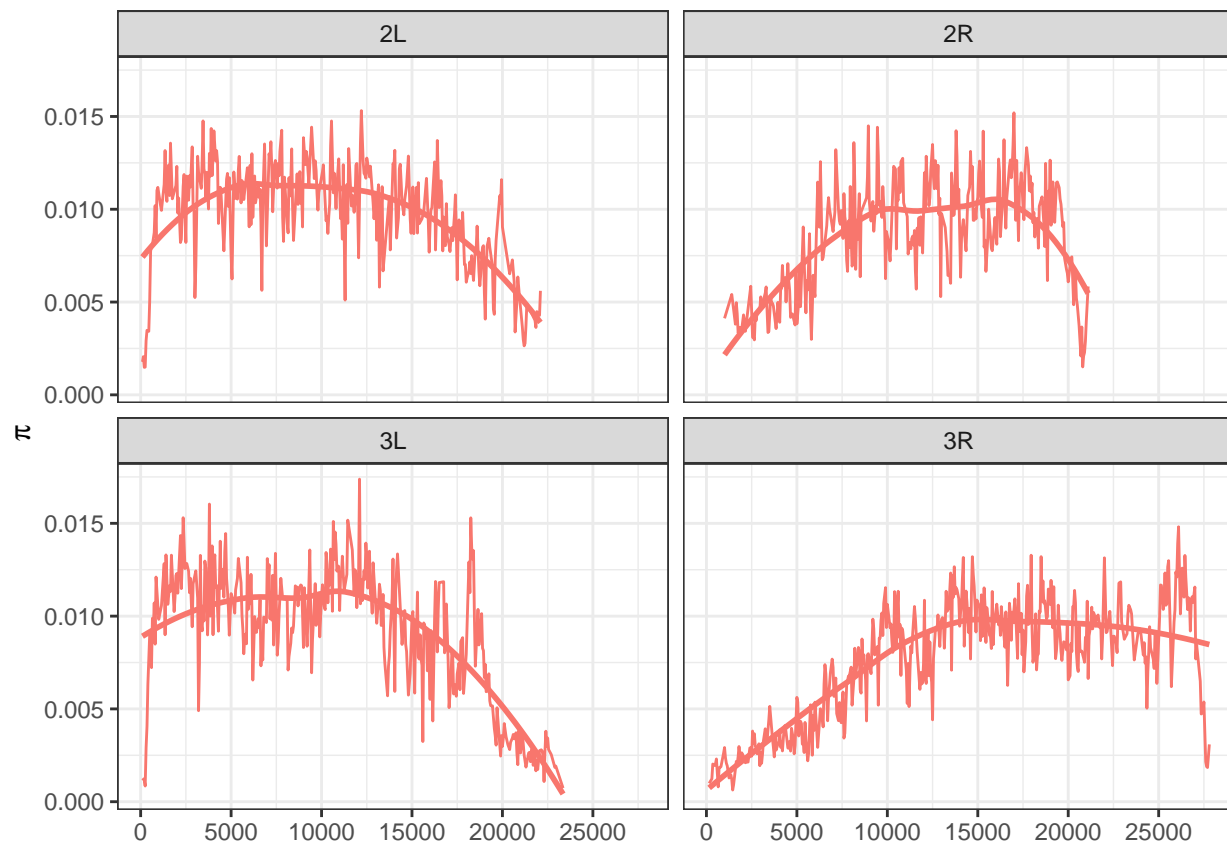
```
diversity.map <- diversity.map + geom_smooth(method = "loess", se = F, colour = "#F8766D")
```

```
diversity.map <- diversity.map + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = scale.3d)
```

```
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))
```

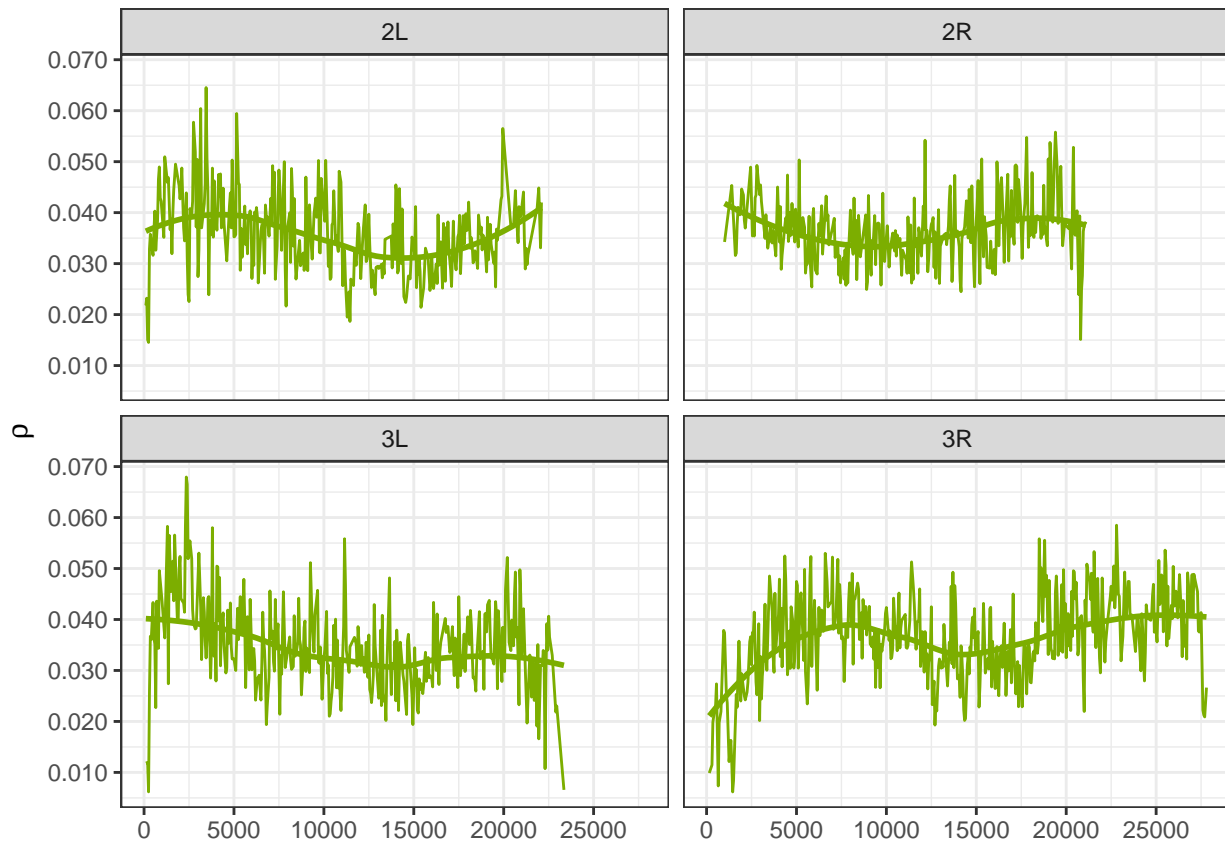
```
diversity.map
```



```

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_breaks())
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

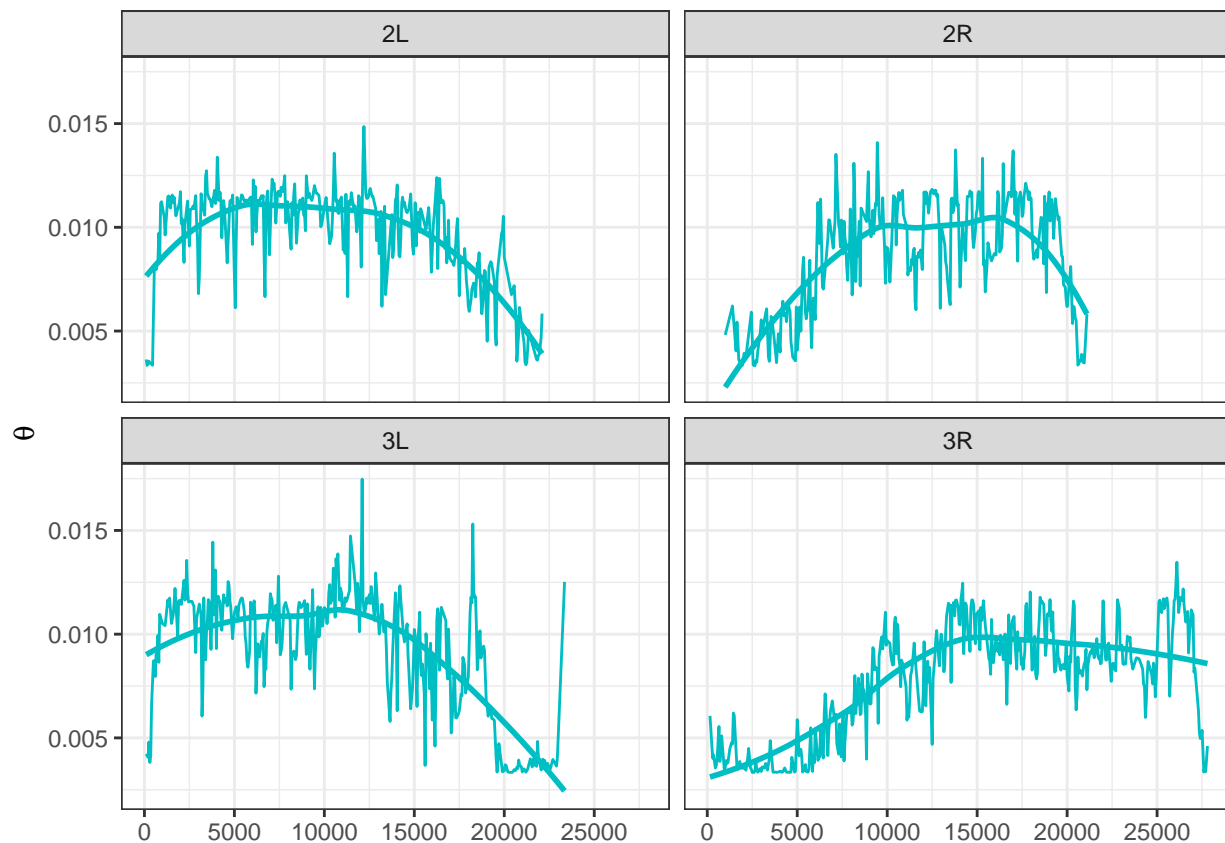
```



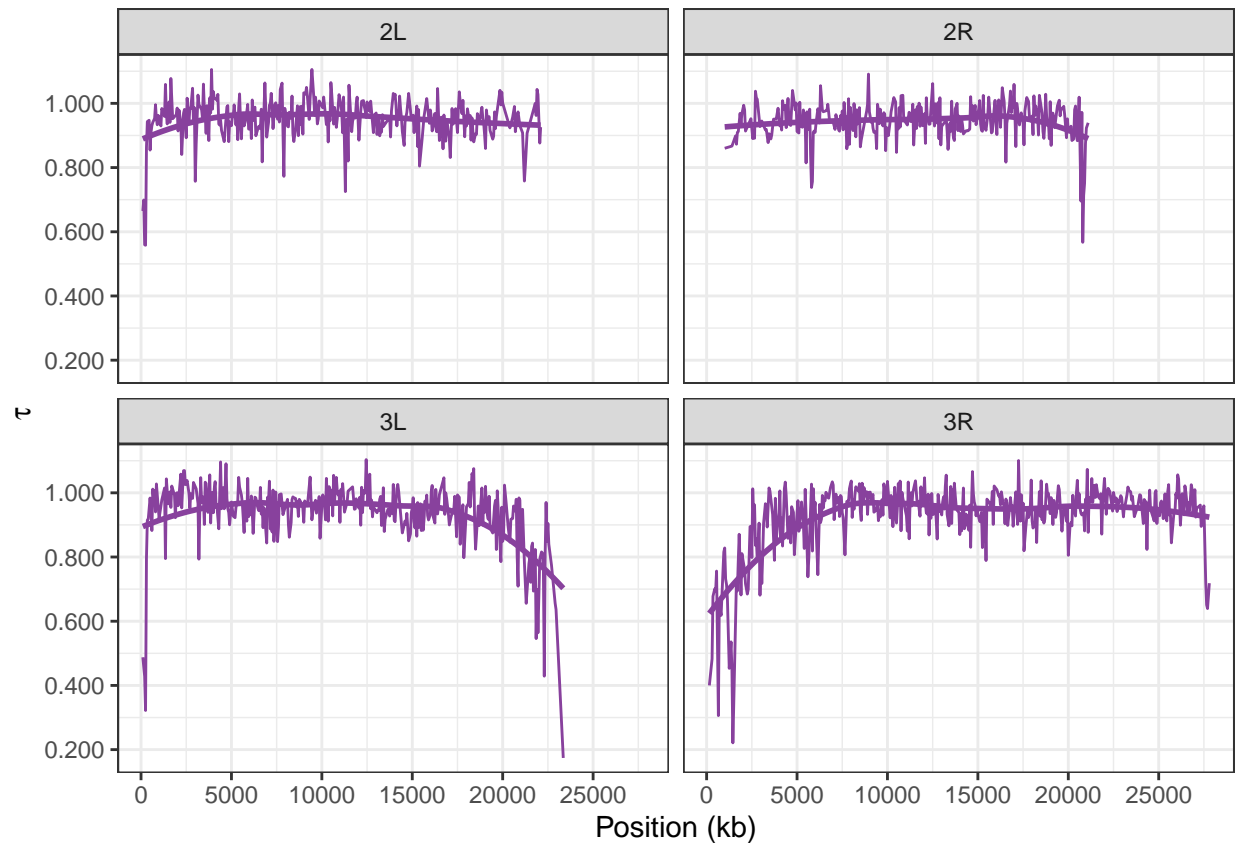
```

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
```

```
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

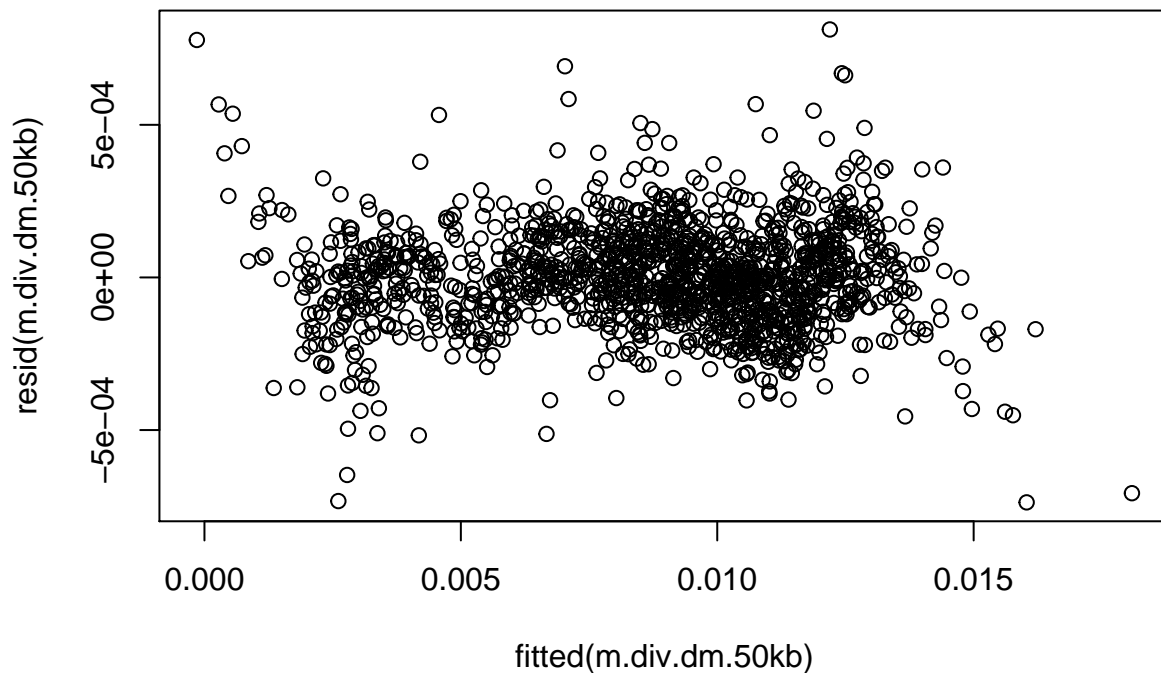
# Linear models
# centering
dm.lands.50kb$thetaC <- dm.lands.50kb$theta - mean(dm.lands.50kb$theta)
dm.lands.50kb$tmrcaC <- dm.lands.50kb$tmrca - mean(dm.lands.50kb$tmrca)
dm.lands.50kb$rhoC <- dm.lands.50kb$rho - mean(dm.lands.50kb$rho)

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

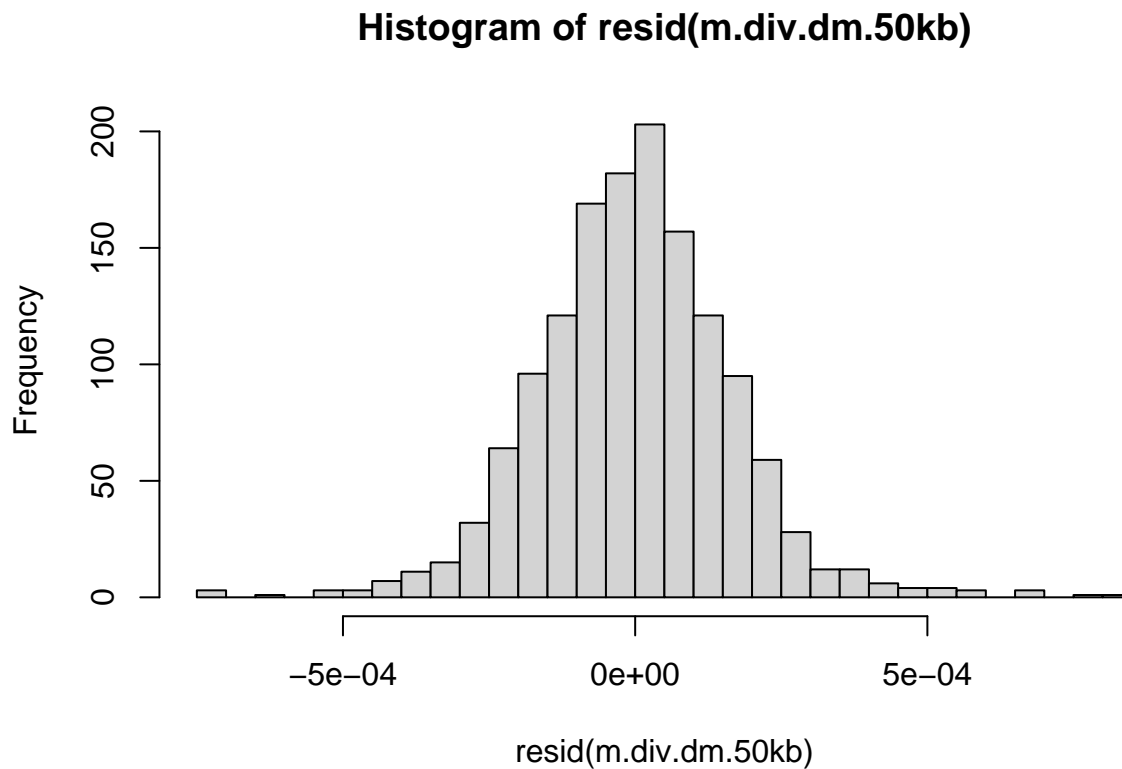
m.div.dm.50kb <- lm( diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC), data = dm.lands.50kb)

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

```



```
hist(resid(m.div.dm.50kb), nclass = 30)
```



```
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
```

```
hmcetest(m.div.dm.50kb, nsim = 10000)
```

```
##
## Harrison-McCabe test
##
## data: m.div.dm.50kb
## HMC = 0.50534, p-value = 0.612
```

```
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), cor = corAR1(0, ~bin), metho

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

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

g.div.dm.50kb.4 <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                        data = dm.lands.50kb, weights = varPower(0, ~tmrcaC), 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 8 -20696.84
## g.div.dm.50kb.2 8 -20665.50
## g.div.dm.50kb.3 7 -20598.95
## g.div.dm.50kb.4 7 -20633.25
```

```
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
## -20696.84 -20654.8 10356.42
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.2163965
## Variance function:
## Structure: Power of variance covariate
## Formula: ~tmrcaC
## Parameter estimates:
##      power
## 0.08046753
##
## Coefficients:
##              Value   Std.Error   t-value p-value
## (Intercept)  0.0085945 0.000005650 1521.0864  0.0000
## thetaC       0.9737833 0.002113767  460.6863  0.0000
## rhoC         0.0008230 0.000712400   1.1553  0.2482
## tmrcaC       0.0115585 0.000085458  135.2542  0.0000
## thetaC:tmrcaC 1.0971658 0.018670392   58.7650  0.0000
##
## Correlation:
##              (Intr) thetaC rhoC   tmrcaC
## thetaC       0.007
## rhoC         0.017  0.128
## tmrcaC       -0.141 -0.382 -0.480
## thetaC:tmrcaC -0.292 -0.043 -0.005  0.396
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -4.26921553 -0.59360044  0.01253385  0.62706410  4.57544814
##
## Residual standard error: 0.0002176236
## Degrees of freedom: 1416 total; 1411 residual
```

```
vif(g.div.dm.50kb.1)
```

```
##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
##      1.202225      1.387189      1.922827      1.281102
```

```
# Linear model without TMRCA --> rho becomes significant
g.div.dm.50kb.5 <- gls(多样性 ~ (thetaC + rhoC),
                      data = dm.lands.50kb, weights = varPower(0, ~thetaC), cor = corAR1(0, ~bin), method = "REML")
summary(g.div.dm.50kb.5)
```

```
## Generalized least squares fit by maximum likelihood
## Model: 多样性 ~ (thetaC + rhoC)
## Data: dm.lands.50kb
##      AIC      BIC    logLik
## -16786.87 -16755.33 8399.434
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.2357723
## Variance function:
## Structure: Power of variance covariate
## Formula: ~thetaC
## Parameter estimates:
##      power
## 0.1061783
##
## Coefficients:
##              Value   Std.Error t-value p-value
## (Intercept) 0.0087412 0.000021878 399.5389      0
## thetaC      1.0958162 0.008482038 129.1926      0
## rhoC        0.0498994 0.002390500  20.8740      0
##
## Correlation:
##      (Intr) thetaC
## thetaC -0.027
## rhoC    0.018 -0.144
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -14.672817411 -0.541914681  0.001243193  0.590679794  3.237494412
##
## Residual standard error: 0.001314897
## 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 == 0))

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)
```

```
# TMRCA 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 == 0))
```

```
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)

# TMRCA 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 == 0))

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$sample_mean,
                                         tmrca.dm.200kb.3L$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 != 0))
```

```
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
## 0.09974947
## 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 = 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.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")
```

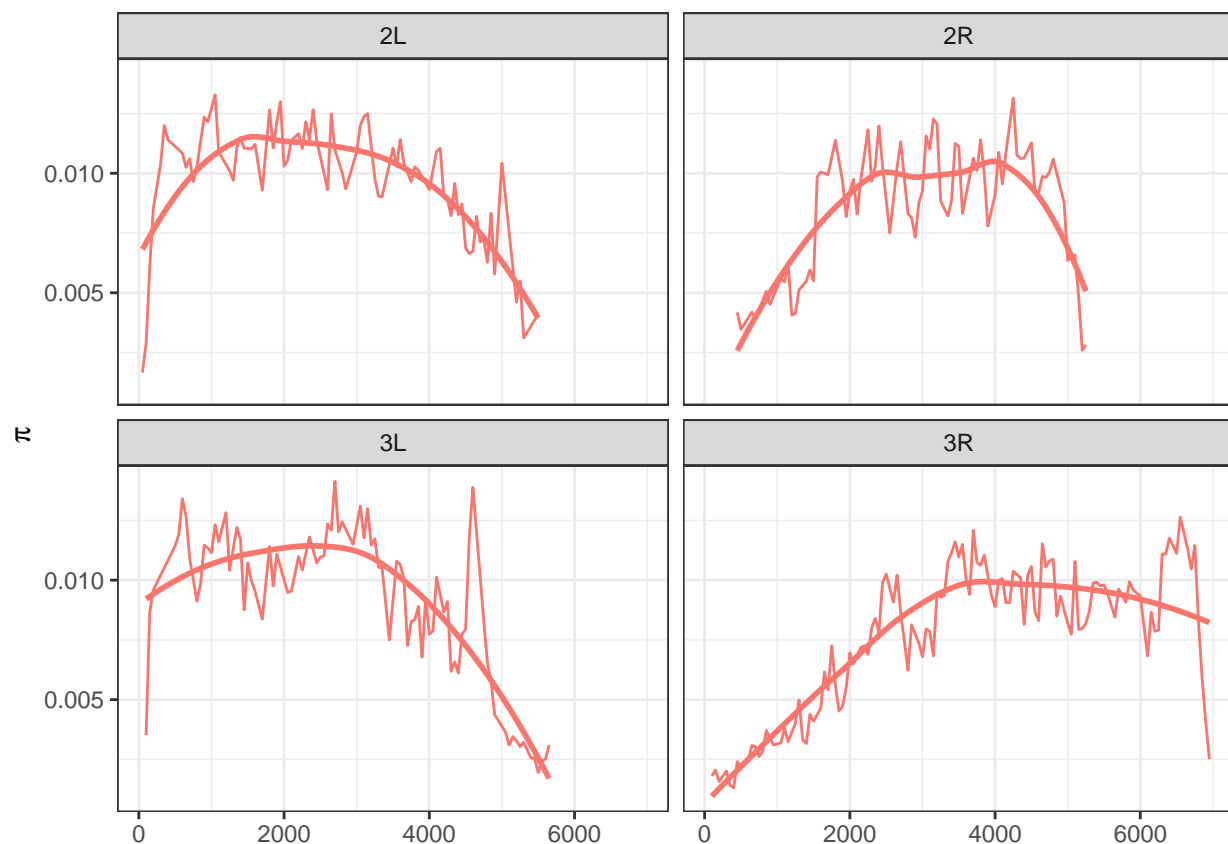
```
diversity.map <- diversity.map + geom_smooth(method = "loess", se = F, colour = "#F8766D")
```

```
diversity.map <- diversity.map + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = scale.3d)
```

```
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_breaks())
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

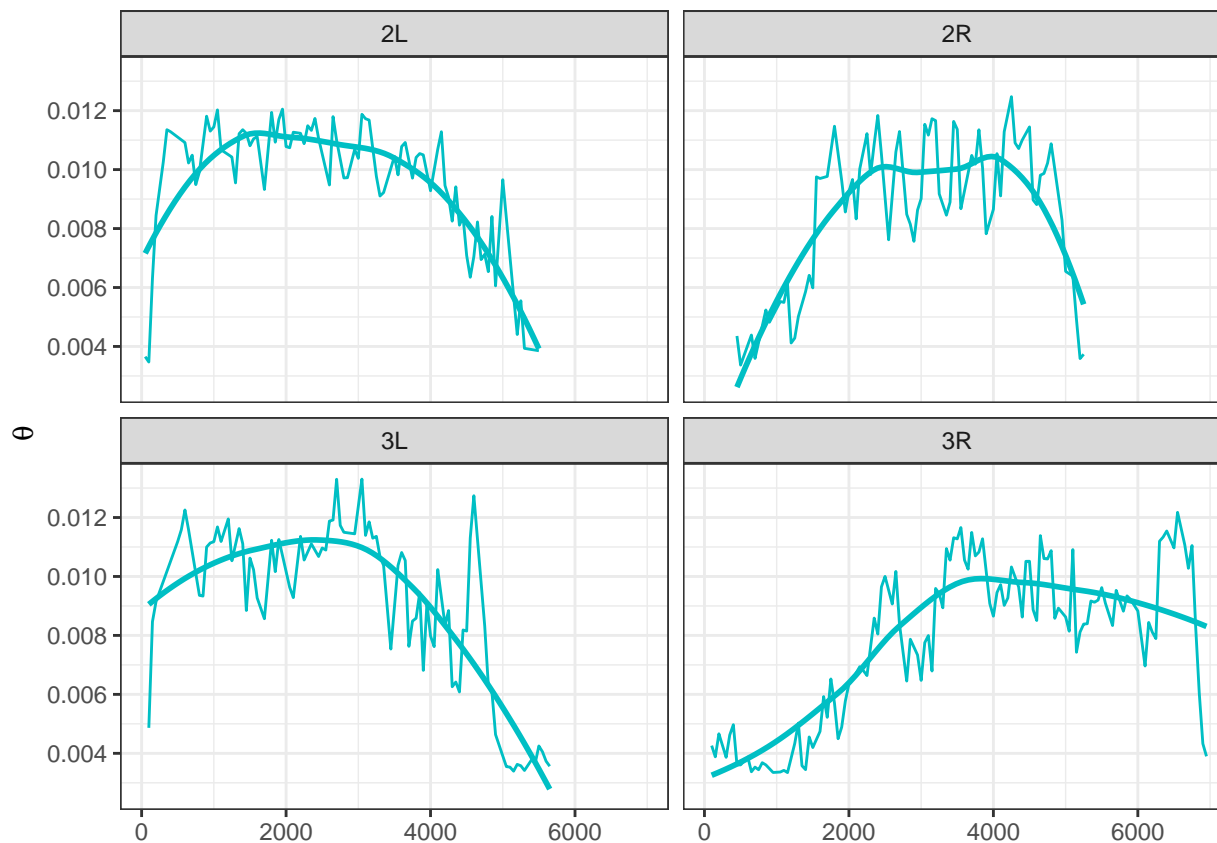
```



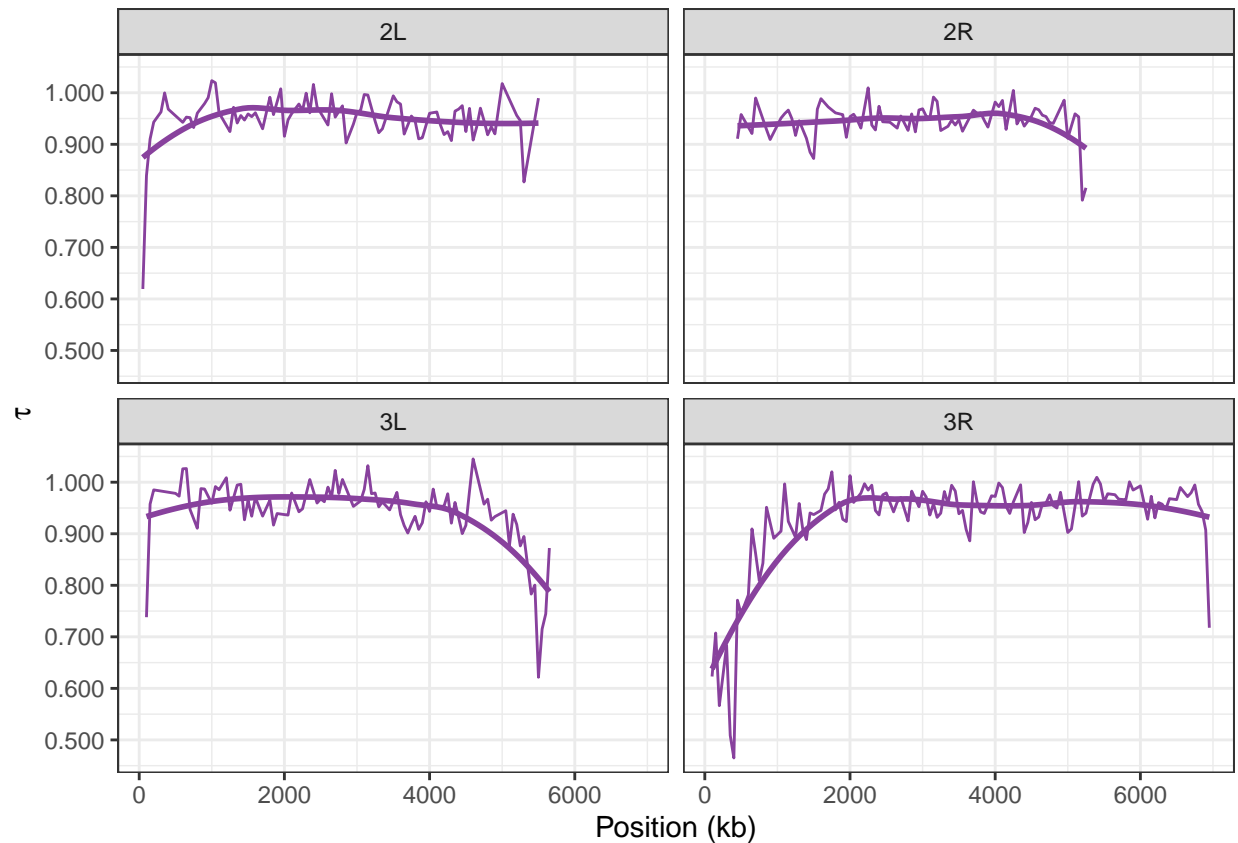
```

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

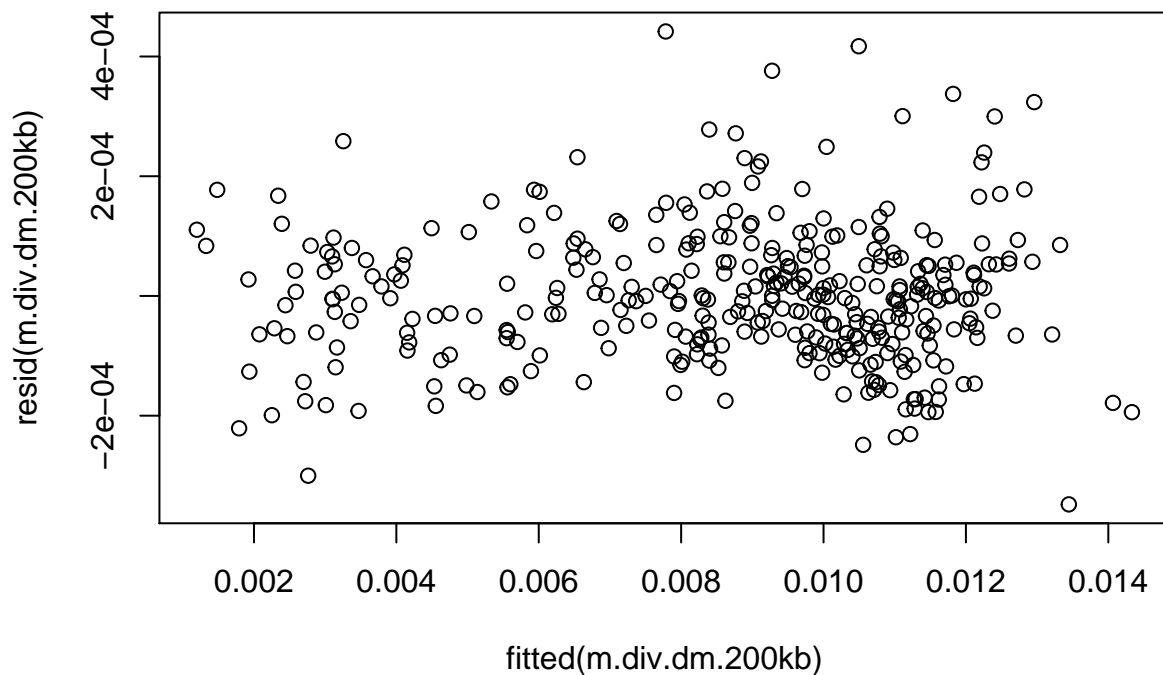
# Linear models
# centering
dm.lands.200kb$thetaC <- dm.lands.200kb$theta - mean(dm.lands.200kb$theta)
dm.lands.200kb$tmrcaC <- dm.lands.200kb$tmrca - mean(dm.lands.200kb$tmrca)
dm.lands.200kb$rhoC <- dm.lands.200kb$rho - mean(dm.lands.200kb$rho)

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

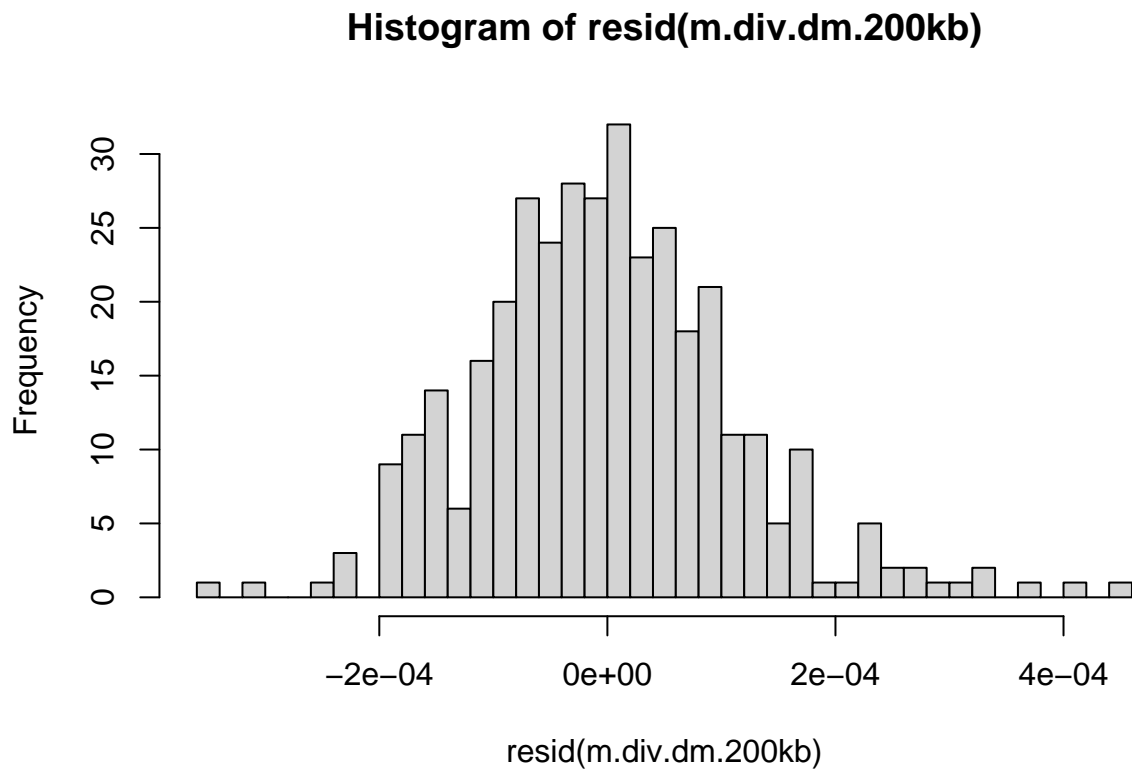
m.div.dm.200kb <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC), data = dm.lands.200kb)

plot(resid(m.div.dm.200kb)~fitted(m.div.dm.200kb))

```



```
hist(resid(m.div.dm.200kb), nclass = 30)
```



```
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 = 0.968
```

```
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), cor = corAR1(0, ~bin), me

g.div.dm.200kb.2 <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                        data = dm.lands.200kb, weights = varPower(0, ~thetaC), cor = corAR1(0, ~bin), me

g.div.dm.200kb.3 <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                        data = dm.lands.200kb, weights = varPower(0, ~thetaC), method = "ML")

g.div.dm.200kb.4 <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                        data = dm.lands.200kb, weights = varPower(0, ~tmrcaC), 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 8 -5564.108
## g.div.dm.200kb.2 8 -5563.492
## g.div.dm.200kb.3 7 -5536.110
## g.div.dm.200kb.4 7 -5537.965
```

```
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
## -5564.108 -5532.975 2790.054
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.2896372
## Variance function:
## Structure: Power of variance covariate
## Formula: ~tmrcaC
## Parameter estimates:
##      power
## 0.03964606
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept)  0.0085678 0.00000898  953.9536  0.0000
## thetaC       0.9760493 0.00342411  285.0517  0.0000
## rhoC         0.0019105 0.00143739   1.3292  0.1846
## tmrcaC       0.0110746 0.00021059   52.5885  0.0000
## thetaC:tmrcaC 0.8983514 0.04429364  20.2817  0.0000
##
## Correlation:
##              (Intr) thetaC rhoC   tmrcaC
## thetaC       0.088
## rhoC         0.052  0.215
## tmrcaC       -0.317 -0.483 -0.479
## thetaC:tmrcaC -0.439 -0.212 -0.108  0.709
##
## Standardized residuals:
##              Min      Q1      Med      Q3      Max
## -2.874213470 -0.626419730 -0.008542897  0.558130746  3.859934979
##
## Residual standard error: 0.0001322223
## Degrees of freedom: 362 total; 357 residual
```

```
vif(g.div.dm.200kb.1)
```

```
##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
##      1.383201      1.526405      3.805781      2.477671
```

```
# 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  2.972069432
##
## 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), method = "REML")

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),
  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
## -0.02184561
## 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)

# TMRCA 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), method = "REML")

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),
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
## -0.4823526
## 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 298.66683 0.0000
## thetaC       0.9664707 0.00658600 146.74629 0.0000
## rhoC         0.0031144 0.00241054   1.29200 0.2173
## tmrcaC       0.0094832 0.00049711  19.07661 0.0000
## thetaC:tmrcaC 0.7457601 0.17910164   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 1.9989783
##
## 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, c
```

```
# 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")
```

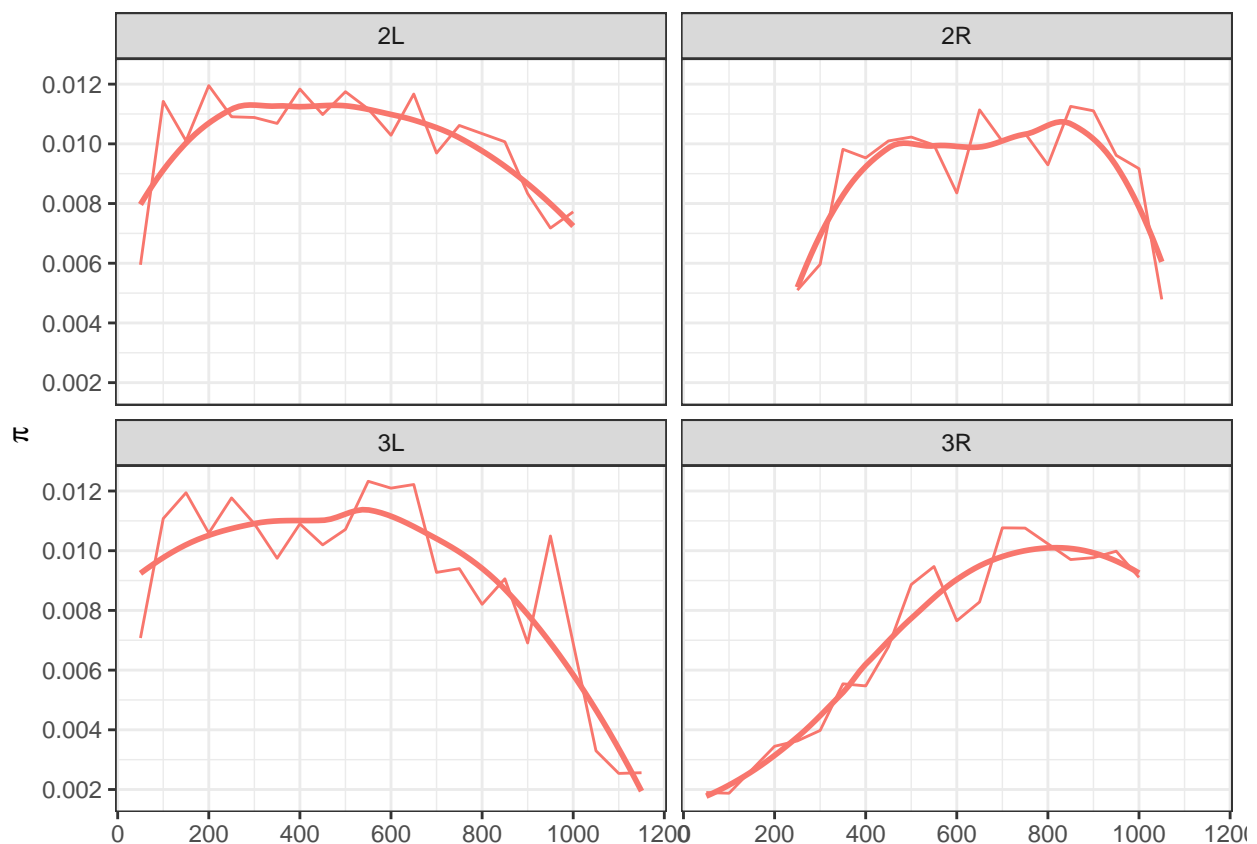
```
diversity.map <- diversity.map + geom_smooth(method = "loess", se = F, colour = "#F8766D")
```

```
diversity.map <- diversity.map + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(break
```

```
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
```

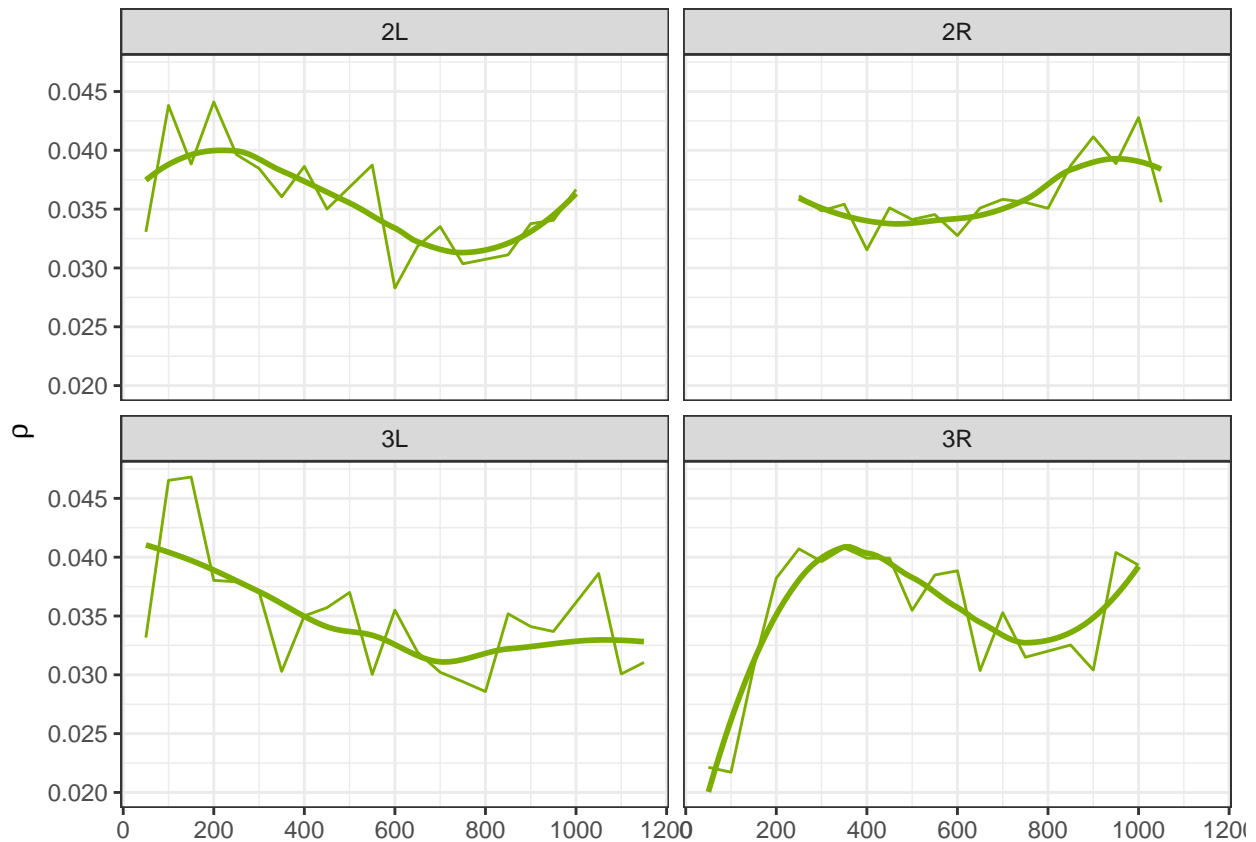
```
diversity.map
```



```

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_breaks())
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

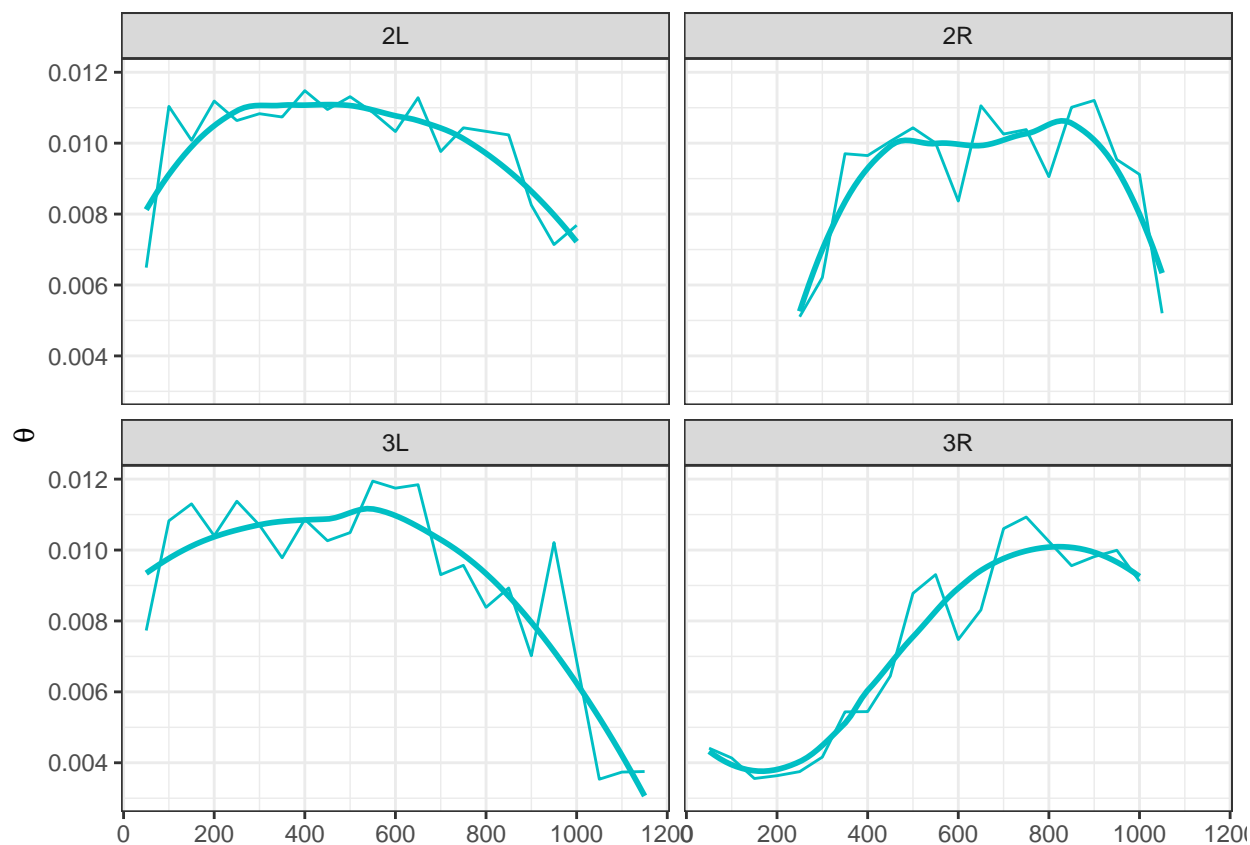
```



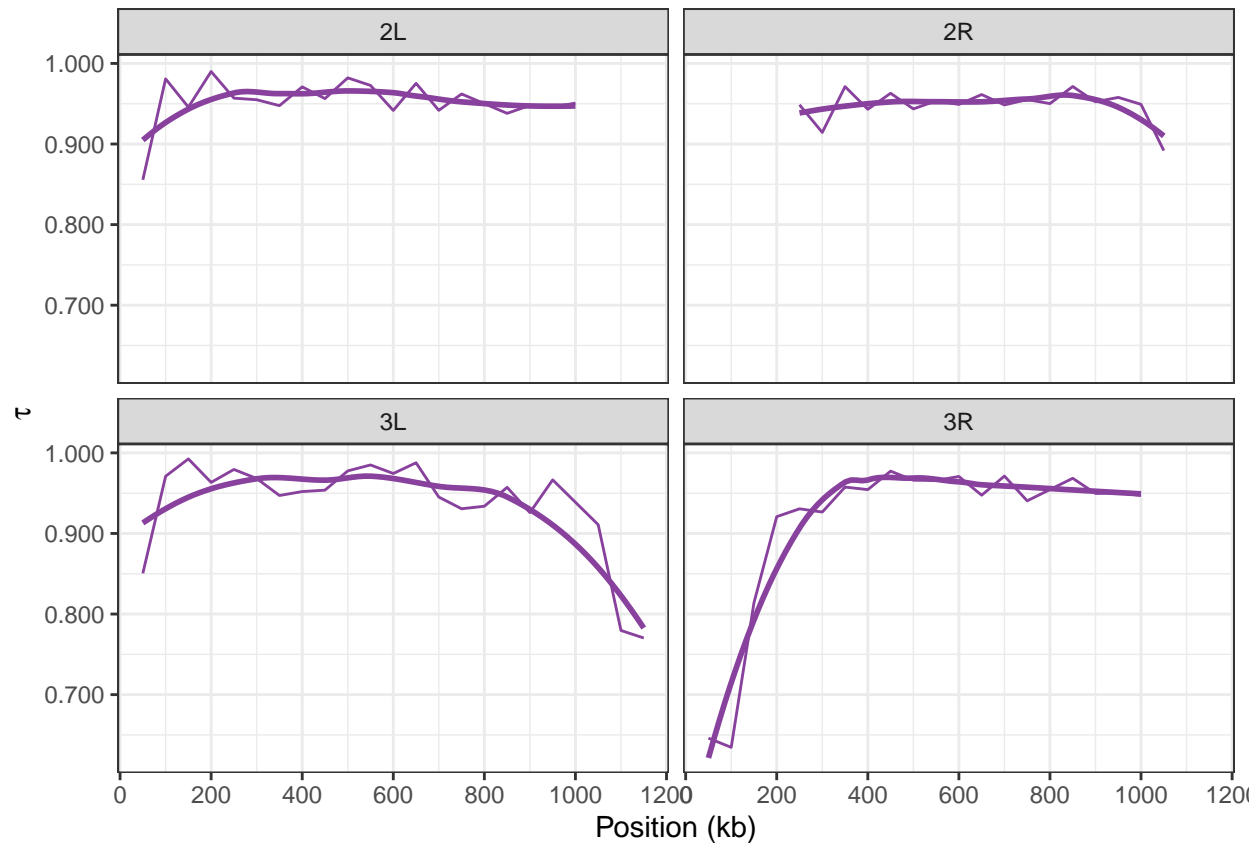
```

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

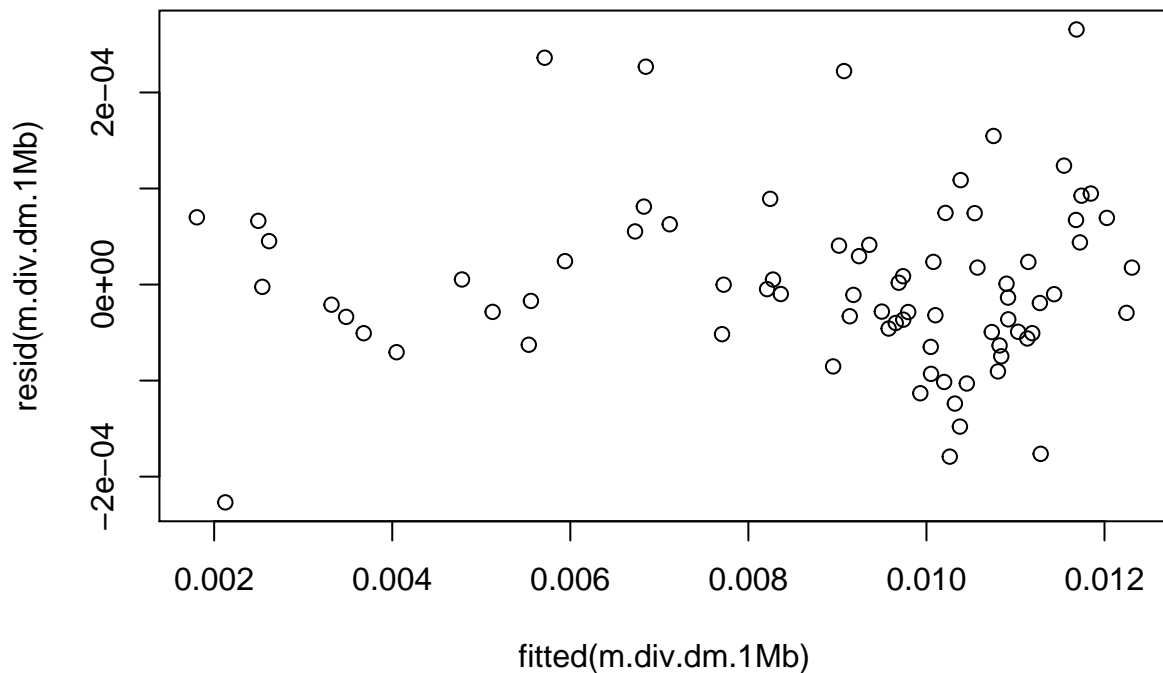
# Linear models
# centering
dm.lands.1Mb$thetaC <- dm.lands.1Mb$theta - mean(dm.lands.1Mb$theta)
dm.lands.1Mb$tmrcaC <- dm.lands.1Mb$tmrca - mean(dm.lands.1Mb$tmrca)
dm.lands.1Mb$rhoC <- dm.lands.1Mb$rho - mean(dm.lands.1Mb$rho)

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

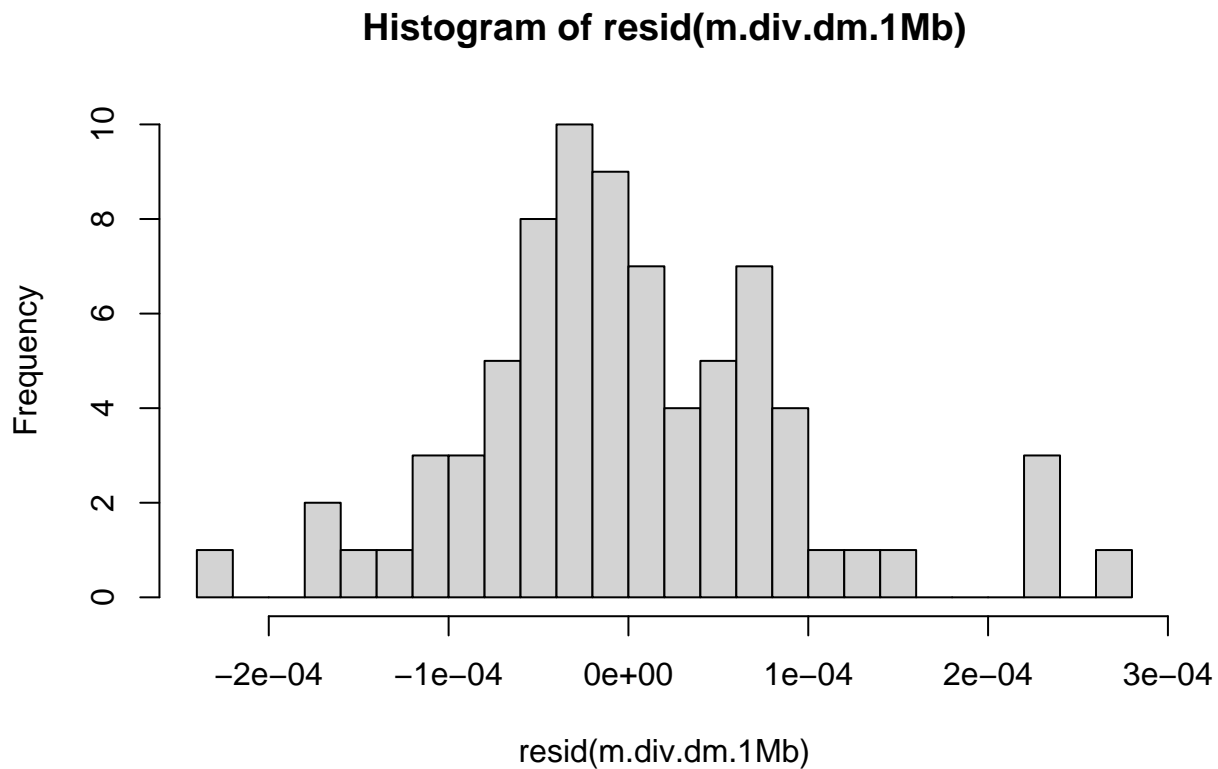
m.div.dm.1Mb <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC), data = dm.lands.1Mb)

plot(resid(m.div.dm.1Mb)~fitted(m.div.dm.1Mb))

```




```
hist(resid(m.div.dm.1Mb), nclass = 30)
```



```
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
```

```
hmcetest(m.div.dm.1Mb, nsim = 10000)
```

```
##
## Harrison-McCabe test
##
## data: m.div.dm.1Mb
## HMC = 0.72492, p-value = 0.9989
```

```
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), cor = corAR1(0, ~bin), method = "ML")
g.div.dm.1Mb.2 <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                      data = dm.lands.1Mb, weights = varPower(0, ~theta), cor = corAR1(0, ~bin), method = "ML")
g.div.dm.1Mb.3 <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                      data = dm.lands.1Mb, weights = varPower(0, ~theta), method = "ML")
g.div.dm.1Mb.4 <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC),
                      data = dm.lands.1Mb, weights = varPower(0, ~tmrcaC), 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 8 -1217.301
## g.div.dm.1Mb.2 8 -1201.998
## g.div.dm.1Mb.3 7 -1202.666
## g.div.dm.1Mb.4 7 -1212.858
```

```
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
## -1217.301 -1198.55 616.6504
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.329231
## Variance function:
## Structure: Power of variance covariate
## Formula: ~tmrcaC
## Parameter estimates:
##      power
## 0.3397723
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept)  0.0087767 0.00001307 671.7413 0.0000
## thetaC       0.9802560 0.00621327 157.7682 0.0000
## rhoC         0.0011873 0.00289132   0.4106 0.6826
## tmrcaC       0.0104410 0.00061019  17.1110 0.0000
## thetaC:tmrcaC 0.6526937 0.13373906   4.8804 0.0000
##
## Correlation:
##              (Intr) thetaC rhoC   tmrcaC
## thetaC       0.103
## rhoC         0.445 0.443
## tmrcaC       -0.420 -0.548 -0.612
## thetaC:tmrcaC -0.380 -0.263 -0.344 0.648
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -2.0750069 -0.4573721 0.0584087 0.6288927 3.3539991
##
## Residual standard error: 0.000319641
## Degrees of freedom: 77 total; 72 residual
```

```
vif(g.div.dm.1Mb.1)
```

```
##      thetaC      rhoC      tmrcaC thetaC:tmrcaC
##      1.495499      1.648966      2.893035      1.769719
```

```
# Linear model without TMRCA --> rho becomes significant
g.div.dm.1Mb.5 <- gls(diversity ~ (thetaC + rhoC),
                      data = dm.lands.1Mb, weights = varPower(0, ~thetaC), cor = corAR1(0, ~bin), method = "REML")
summary(g.div.dm.1Mb.5)
```

```
## Generalized least squares fit by maximum likelihood
## Model: diversity ~ (thetaC + rhoC)
## Data: dm.lands.1Mb
##      AIC      BIC    logLik
## -1057.094 -1043.031 534.5471
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.5269524
## Variance function:
## Structure: Power of variance covariate
## Formula: ~thetaC
## Parameter estimates:
##      power
## 0.2848498
##
## Coefficients:
##              Value   Std.Error   t-value p-value
## (Intercept) 0.0089322 0.000043593 204.90100      0
## thetaC      1.0791361 0.020716292  52.09118      0
## rhoC        0.0391251 0.007136742   5.48221      0
##
## Correlation:
##      (Intr) thetaC
## thetaC -0.120
## rhoC    0.015 -0.254
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -4.40808231 -0.66442792 -0.06662625  0.47302409  1.50444256
##
## Residual standard error: 0.001760621
## Degrees of freedom: 77 total; 74 residual
```

3.4 Divergence with *Drosophila yakuba*

This is how we generated the table from raw data:

```
# divergence data from D. melanogaster and D. yakuba
divergence.2L.5kb <- read.table("dm_data/dm_misc/Droso2L_divergence.statistics5kb.csv", header = T)
divergence.2R.5kb <- read.table("dm_data/dm_misc/Droso2R_divergence.statistics5kb.csv", header = T)
divergence.3L.5kb <- read.table("dm_data/dm_misc/Droso3L_divergence.statistics5kb.csv", header = T)
divergence.3R.5kb <- read.table("dm_data/dm_misc/Droso3R_divergence.statistics5kb.csv", header = T)
```

```

divergence <- rbind.data.frame(divergence.2L.5kb, divergence.2R.5kb, divergence.3L.5kb, divergence.3R.5kb)
divergence <- divergence[,c(1:3, 6)]
divergence$Chr <- as.character(divergence$Chr)

# reorder maps to use GR
dm.maps.50kb <- dm.lands.50kb[,c(8,1:6)]

# converts objects to GenomicRanges
dm.gr <- makeGRangesFromDataFrame(dm.maps.50kb)
values(dm.gr) <- dm.maps.50kb[, (4:7)]
divergence.gr <- makeGRangesFromDataFrame(divergence)
values(divergence.gr) <- DataFrame(score = divergence$MLModelFit.BrLen0)

hits <- findOverlaps(query = divergence.gr, subject = dm.gr, type = "within")
ranges(divergence.gr)[queryHits(hits)] = ranges(dm.gr)[subjectHits(hits)]

lands.gr.df <- as.data.frame(dm.gr)
divergence.gr.df <- as.data.frame(divergence.gr)
# deletes non-matching windows
divergence.gr.df <- divergence.gr.df[-which(((divergence.gr.df$width - 1) %% 50000) != 0),]

# compute mean divergence within 50kb windows
dummy.tbl <- divergence.gr.df[, -c(4, 5)]
dummy.tbl$seqnames <- as.character(dummy.tbl$seqnames)
dummy.tbl$seqnames[which(dummy.tbl$seqnames == "2L")] <- 2
dummy.tbl$seqnames[which(dummy.tbl$seqnames == "2R")] <- 3
dummy.tbl$seqnames[which(dummy.tbl$seqnames == "3L")] <- 4
dummy.tbl$seqnames[which(dummy.tbl$seqnames == "3R")] <- 5
dummy.tbl$seqnames <- as.numeric(dummy.tbl$seqnames)

tmp <- ddply(.data = dummy.tbl, .variables = c("seqnames", "start"), .fun = colMeans)

divergence.gr.df.2L <- divergence.gr.df[divergence.gr.df$seqnames == "2L",]
divergence.gr.df.2L <- divergence.gr.df.2L[!duplicated(divergence.gr.df.2L$start),]
divergence.gr.df.2R <- divergence.gr.df[divergence.gr.df$seqnames == "2R",]
divergence.gr.df.2R <- divergence.gr.df.2R[!duplicated(divergence.gr.df.2R$start),]
divergence.gr.df.3L <- divergence.gr.df[divergence.gr.df$seqnames == "3L",]
divergence.gr.df.3L <- divergence.gr.df.3L[!duplicated(divergence.gr.df.3L$start),]
divergence.gr.df.3R <- divergence.gr.df[divergence.gr.df$seqnames == "3R",]
divergence.gr.df.3R <- divergence.gr.df.3R[!duplicated(divergence.gr.df.3R$start),]

divergence.gr.df.chr <- rbind.data.frame(divergence.gr.df.2L, divergence.gr.df.2R, divergence.gr.df.3L,
divergence.gr.df.chr$score <- tmp$score

lands.gr.df.2L <- lands.gr.df[which(lands.gr.df$seqnames == "2L"),]
lands.gr.df.2L <- lands.gr.df.2L[which(lands.gr.df.2L$start %in% divergence.gr.df.2L$start),]
lands.gr.df.2R <- lands.gr.df[which(lands.gr.df$seqnames == "2R"),]
lands.gr.df.2R <- lands.gr.df.2R[which(lands.gr.df.2R$start %in% divergence.gr.df.2R$start),]
lands.gr.df.3L <- lands.gr.df[which(lands.gr.df$seqnames == "3L"),]
lands.gr.df.3L <- lands.gr.df.3L[which(lands.gr.df.3L$start %in% divergence.gr.df.3L$start),]
lands.gr.df.3R <- lands.gr.df[which(lands.gr.df$seqnames == "3R"),]
lands.gr.df.3R <- lands.gr.df.3R[which(lands.gr.df.3R$start %in% divergence.gr.df.3R$start),]

```

```
lands.gr.df.chr <- rbind.data.frame(lands.gr.df.2L, lands.gr.df.2R, lands.gr.df.3L, lands.gr.df.3R)

lands.divergence.dm <- cbind.data.frame(lands.gr.df.chr[, -(which(names(lands.gr.df.chr) == "strand"))],
names(lands.divergence.dm)[ncol(lands.divergence.dm)] <- "divergence"

write.table(lands.divergence.dm, "dm_data/dm_chr_maps/dm_maps_50kb_divergence.tsv",
            quote = F, sep = "\t", col.names = T, row.names = F)
```

We can read the table provided and move on with the analyses:

```
lands.divergence.dm <- read.table("dm_data/dm_chr_maps/dm_maps_50kb_divergence.tsv", header = T, sep =
cor.test(x = lands.divergence.dm$divergence, y = lands.divergence.dm$diversity, method = "spearman")
```

```
##
## Spearman's rank correlation rho
##
## data: lands.divergence.dm$divergence and lands.divergence.dm$diversity
## S = 96430038, p-value = 4.547e-10
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.2063362
```

```
cor.test(lands.divergence.dm$divergence, lands.divergence.dm$theta, method = "spearman")
```

```
##
## Spearman's rank correlation rho
##
## data: lands.divergence.dm$divergence and lands.divergence.dm$theta
## S = 97624952, p-value = 2.989e-09
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.1965015
```

```
cor.test(x = lands.divergence.dm$divergence, y = lands.divergence.dm$rho, method = "spearman")
```

```
##
## Spearman's rank correlation rho
##
## data: lands.divergence.dm$divergence and lands.divergence.dm$rho
## S = 121823318, p-value = 0.9364
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.002662291
```

```
pcor.test(x = lands.divergence.dm$divergence, y = lands.divergence.dm$diversity,
          z = lands.divergence.dm$theta, method = "spearman")
```

```
##      estimate    p.value statistic    n gp    Method
## 1 0.06663225 0.04579294  2.000078 900  1 spearman
```

3.5 Evolutionary (Protein) Rates

This is how we generated the table from raw data:

```
# loads
dm.raw <- read.table("dm_data/dm_misc/dpgp3_Dyak_bpp.all.csv", header = T, fill = T, stringsAsFactors=
dm.tbl <- na.omit(dm.raw)

# gets ratios
dm.tbl$PiS <- dm.tbl$PiS / dm.tbl$MeanNumberSynPos
dm.tbl$PiN <- dm.tbl$PiN / (3 - dm.tbl$MeanNumberSynPos)
dm.tbl$dS <- as.numeric(dm.tbl$dS) / dm.tbl$MeanNumberSynPosDiv
dm.tbl$dN <- dm.tbl$dN / (3 - dm.tbl$MeanNumberSynPosDiv)
# cleans
dm.tbl.popgen <- as.data.frame(cbind(dm.tbl$PiN, dm.tbl$PiS, dm.tbl$dN, dm.tbl$dS, dm.tbl$GeneID))
dm.tbl.popgen <- na.omit(dm.tbl.popgen)
names(dm.tbl.popgen) <- c("PiN", "PiS", "dN", "dS", "geneID")

# for each gene, sums ratios of each codon
dm.tbl.genes <- ddply(.data = dm.tbl.popgen, .variables = "geneID", .fun = colSums, na.rm = T)
# substitutes gene id and computes ratios
dm.tbl.genes$geneID <- unique(dm.tbl$GeneID)
dm.tbl.genes$dNdS <- dm.tbl.genes$dN / dm.tbl.genes$dS
dm.tbl.genes$PiNPiS <- dm.tbl.genes$PiN / dm.tbl.genes$PiS
dm.tbl.popstats <- cbind.data.frame(as.character(dm.tbl.genes$geneID), dm.tbl.genes$PiN, dm.tbl.genes$P
dm.tbl.genes$dN, dm.tbl.genes$dS, dm.tbl.genes$dNdS)
names(dm.tbl.popstats) <- c("geneID", "PiN", "PiS", "PiNPiS", "dN", "dS", "dNdS")
dm.tbl.popstats$PiS <- as.numeric(dm.tbl.popstats$PiS)
dm.tbl.popstats$dS <- as.numeric(dm.tbl.popstats$dS)
dm.tbl.popstats$PiN <- as.numeric(dm.tbl.popstats$PiN)
dm.tbl.popstats$dN <- as.numeric(dm.tbl.popstats$dN)
dm.tbl.popstats$PiNPiS <- as.numeric(dm.tbl.popstats$PiNPiS)
dm.tbl.popstats$dNdS <- as.numeric(dm.tbl.popstats$dNdS)

dm.tbl.popstats.clean <- dm.tbl.popstats[which(dm.tbl.popstats$PiNPiS > 0),]
dm.tbl.popstats.clean <- dm.tbl.popstats.clean[which(dm.tbl.popstats.clean$dNdS > 0),]

dm.genes.coord <- read.table("dm_data/dm_misc/Dmel_trans_nooverlaps-final.txt", header = F)
names(dm.genes.coord) <- c("chr", "start", "end", "x", "geneID", "length")
dm.genes.coord <- dm.genes.coord[,-4]

dm.evol <- merge(dm.genes.coord, dm.tbl.popstats.clean, by = "geneID")
dm.evol <- dm.evol[order(dm.evol$chr),]

# reorder maps to use GR
dm.maps.50kb <- dm.lands.50kb[,c(8,1:6)]

# grouping per gene coordinate
dm.lands.gr <- makeGRangesFromDataFrame(dm.maps.50kb)
values(dm.lands.gr) <- dm.maps.50kb[, (4:7)]
evolrate.gr <- makeGRangesFromDataFrame(dm.evol)
values(evolrate.gr) <- dm.evol[, (5:11)]

hits <- findOverlaps(query = evolrate.gr, subject = dm.lands.gr, type = "within")
```

```

evolrate.gr.df <- as.data.frame(evolverate.gr[queryHits(hits)], row.names = NULL)
dm.lands.gr.df <- as.data.frame(dm.lands.gr[subjectHits(hits)], row.names = NULL)

dm.lands.evolrate <- cbind.data.frame(dm.lands.gr.df[,c(1:3,6:9)], evolrate.gr.df[,c(2,3,6:12)])
dm.lands.evolrate <- dm.lands.evolrate[which(dm.lands.evolrate$PiNPiS < 1),]
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"

# NOTE: must sort rows of dm.lands.evolrate by chr and start coords

write.table(dm.lands.evolrate, "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 provided and move on with the analyses:

```

dm.lands.evolrate <- read.table("dm_data/dm_chr_maps/dm_maps_50kb_protein_rates.tsv", header = T, sep =

# linear model in coding regions

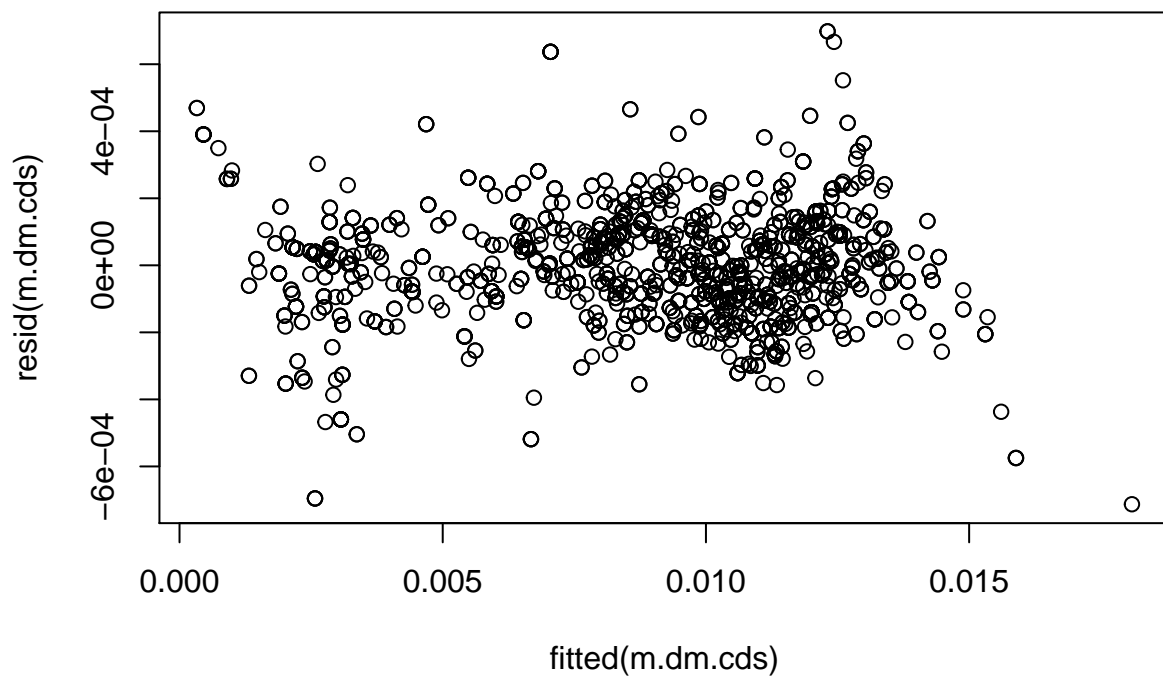
# centering
dm.lands.evolrate$thetaC <- dm.lands.evolrate$theta - mean(dm.lands.evolrate$theta)
dm.lands.evolrate$tmrcaC <- dm.lands.evolrate$tmrca - mean(dm.lands.evolrate$tmrca)
dm.lands.evolrate$rhoC <- dm.lands.evolrate$rho - mean(dm.lands.evolrate$rho)

dm.lands.evolrate$bin <- 1:nrow(dm.lands.evolrate)

m.dm.cds <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC*tmrcaC) * chr, data = dm.lands.evolrate)

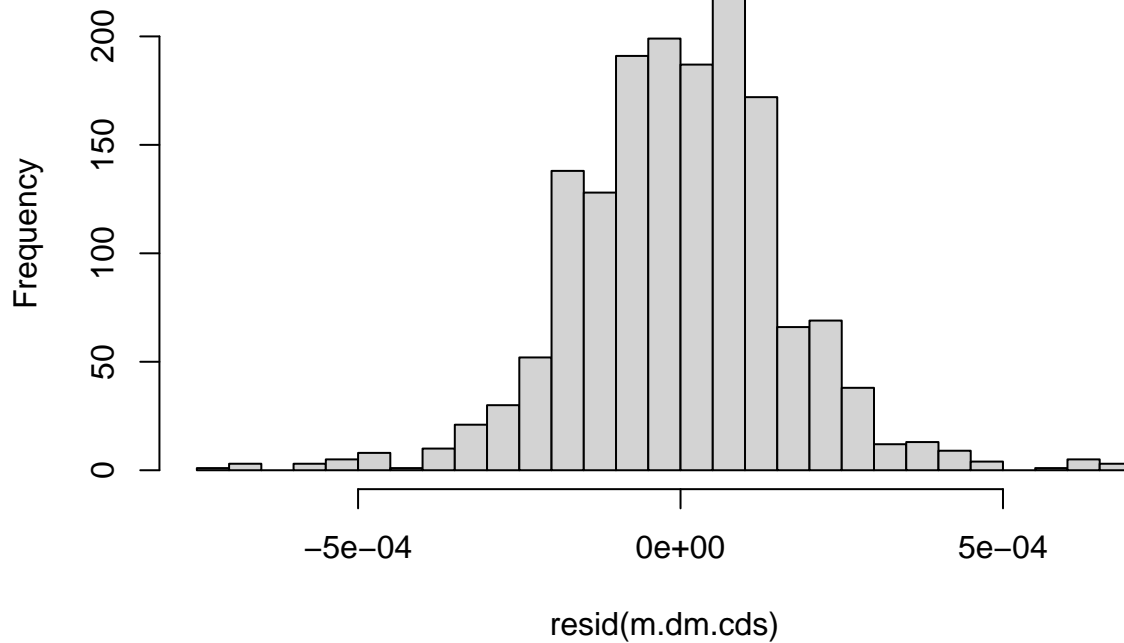
plot(resid(m.dm.cds)~fitted(m.dm.cds))

```

```
hist(resid(m.dm.cds), nclass = 30)
```

Histogram of resid(m.dm.cds)



```
dwtest(m.dm.cds)
```

```
##
## Durbin-Watson test
##
## data: m.dm.cds
## DW = 1.5993, p-value < 2.2e-16
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmcetest(m.dm.cds, nsim = 10000)
```

```
##
## Harrison-McCabe test
##
## data: m.dm.cds
## HMC = 0.49262, p-value = 0.3497
```

```
summary(m.dm.cds)
```

```
##
## Call:
## lm(formula = diversity ~ (thetaC + rhoC + tmrcaC + thetaC * tmrcaC) *
##     chr, data = dm.lands.evolrate)
##
```

```
## Residuals:
##      Min       1Q   Median       3Q      Max
## -7.128e-04 -1.001e-04  1.390e-06  9.878e-05  6.981e-04
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      8.676e-03  1.524e-05  569.308 < 2e-16 ***
## thetaC           9.645e-01  6.083e-03  158.546 < 2e-16 ***
## rhoC             2.041e-03  1.592e-03   1.282  0.19998
## tmrcaC           1.152e-02  1.980e-04  58.174 < 2e-16 ***
## chr2R            -1.026e-04  1.853e-05  -5.538 3.59e-08 ***
## chr3L            -1.193e-04  1.793e-05  -6.655 3.92e-11 ***
## chr3R            -7.623e-05  1.837e-05  -4.151 3.49e-05 ***
## thetaC:tmrcaC     1.157e+00  4.060e-02  28.489 < 2e-16 ***
## thetaC:chr2R     -1.051e-02  7.513e-03  -1.399  0.16189
## thetaC:chr3L      1.895e-03  6.809e-03   0.278  0.78084
## thetaC:chr3R      1.794e-03  6.875e-03   0.261  0.79417
## rhoC:chr2R       -1.540e-03  2.232e-03  -0.690  0.49023
## rhoC:chr3L       1.806e-03  2.026e-03   0.892  0.37279
## rhoC:chr3R       -2.798e-03  2.100e-03  -1.332  0.18300
## tmrcaC:chr2R      5.183e-04  2.713e-04   1.910  0.05629 .
## tmrcaC:chr3L     -1.435e-04  2.470e-04  -0.581  0.56128
## tmrcaC:chr3R     -1.162e-05  2.575e-04  -0.045  0.96403
## thetaC:tmrcaC:chr2R -1.827e-01  5.754e-02  -3.176  0.00152 **
## thetaC:tmrcaC:chr3L -4.053e-03  4.876e-02  -0.083  0.93377
## thetaC:tmrcaC:chr3R -1.500e-01  5.615e-02  -2.672  0.00762 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0001668 on 1567 degrees of freedom
## Multiple R-squared:  0.9976, Adjusted R-squared:  0.9976
## F-statistic: 3.471e+04 on 19 and 1567 DF,  p-value: < 2.2e-16
```

```
# type 2 anova
anova.diversity.cds <- Anova(m.dm.cds)
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          0.0077497    1 2.7861e+05 0.000000 0.92854
## rhoC            0.0000001    1 4.7384e+00 0.029645 0.00002
## tmrcaC          0.0004408    1 1.5846e+04 0.000000 0.05281
## chr            0.0000028    3 3.3004e+01 0.000000 0.00033
## thetaC:tmrcaC   0.0001074    1 3.8597e+03 0.000000 0.01286
## thetaC:chr      0.0000002    3 2.5774e+00 0.052269 0.00003
## rhoC:chr        0.0000002    3 2.2474e+00 0.081029 0.00002
## tmrcaC:chr      0.0000008    3 1.0025e+01 0.000002 0.00010
## thetaC:tmrcaC:chr 0.0000006    3 6.9341e+00 0.000123 0.00007
## Residuals      0.0000436 1567                0.00522
```

```
# GLS
dm.lands.evolrate$bin <- 1:nrow(dm.lands.evolrate)

g.dm.cds <- gls(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC) * chr,
               data = dm.lands.evolrate, weights = varPower(0, ~tmrcaC), cor = corAR1(0, ~bin), method = "REML")

summary(g.dm.cds)
```

```
## Generalized least squares fit by maximum likelihood
## Model: diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC) * chr
## Data: dm.lands.evolrate
##      AIC      BIC    logLik
## -23186.05 -23062.55 11616.02
##
## Correlation Structure: AR(1)
## Formula: ~bin
## Parameter estimate(s):
##      Phi
## 0.2102794
## Variance function:
## Structure: Power of variance covariate
## Formula: ~tmrcaC
## Parameter estimates:
##      power
## 0.08186304
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept)    0.0086636 0.00001607  539.1035  0.0000
## thetaC         0.9653020 0.00587441  164.3233  0.0000
## rhoC           0.0018200 0.00158283   1.1498  0.2504
## tmrcaC         0.0115808 0.00019937  58.0883  0.0000
## chr2R          -0.0000979 0.00001985  -4.9335  0.0000
## chr3L          -0.0001137 0.00001915  -5.9376  0.0000
## chr3R          -0.0000700 0.00001953  -3.5826  0.0004
## thetaC:tmrcaC   1.1967188 0.04328591  27.6468  0.0000
## thetaC:chr2R   -0.0094250 0.00737731  -1.2776  0.2016
## thetaC:chr3L   -0.0043817 0.00663394  -0.6605  0.5090
## thetaC:chr3R    0.0007989 0.00672829   0.1187  0.9055
## rhoC:chr2R     -0.0009199 0.00224851  -0.4091  0.6825
## rhoC:chr3L     0.0017874 0.00202249   0.8838  0.3770
## rhoC:chr3R     -0.0029736 0.00207158  -1.4354  0.1514
## tmrcaC:chr2R    0.0003693 0.00027904   1.3235  0.1858
## tmrcaC:chr3L   -0.0000629 0.00024875  -0.2530  0.8003
## tmrcaC:chr3R   -0.0000114 0.00026351  -0.0433  0.9655
## thetaC:tmrcaC:chr2R -0.1965653 0.06207246  -3.1667  0.0016
## thetaC:tmrcaC:chr3L -0.0189961 0.05164825  -0.3678  0.7131
## thetaC:tmrcaC:chr3R -0.1691567 0.05970810  -2.8331  0.0047
##
## Correlation:
##              (Intr) thetaC rhoC    tmrcaC chr2R  chr3L  chr3R  thtC:C
## thetaC          -0.447
## rhoC            0.053 -0.101
```

```

## tmrcaC          0.026 -0.460 -0.440
## chr2R          -0.809  0.362 -0.043 -0.021
## chr3L          -0.839  0.375 -0.045 -0.022  0.679
## chr3R          -0.823  0.368 -0.044 -0.021  0.666  0.690
## thetaC:tmrcaC  -0.379  0.065 -0.054  0.180  0.307  0.318  0.312
## thetaC:chr2R    0.356 -0.796  0.080  0.367 -0.346 -0.299 -0.293 -0.052
## thetaC:chr3L    0.396 -0.886  0.090  0.408 -0.320 -0.315 -0.326 -0.057
## thetaC:chr3R    0.390 -0.873  0.088  0.402 -0.316 -0.328 -0.216 -0.057
## rhoC:chr2R     -0.036  0.071 -0.706  0.310  0.015  0.030  0.030  0.038
## rhoC:chr3L     -0.042  0.079 -0.783  0.344  0.034  0.145  0.034  0.042
## rhoC:chr3R     -0.041  0.077 -0.764  0.336  0.033  0.034 -0.060  0.041
## tmrcaC:chr2R   -0.018  0.329  0.314 -0.714 -0.032  0.015  0.015 -0.129
## tmrcaC:chr3L   -0.021  0.369  0.352 -0.801  0.017 -0.107  0.017 -0.144
## tmrcaC:chr3R   -0.020  0.348  0.333 -0.757  0.016  0.016 -0.083 -0.136
## thetaC:tmrcaC:chr2R 0.266 -0.045  0.036 -0.125 -0.329 -0.223 -0.219 -0.698
## thetaC:tmrcaC:chr3L 0.318 -0.054  0.045 -0.151 -0.257 -0.399 -0.262 -0.838
## thetaC:tmrcaC:chr3R 0.275 -0.047  0.039 -0.130 -0.223 -0.231 -0.386 -0.725
##               thC:2R thC:3L thC:3R rhC:2R rhC:3L rhC:3R tmC:2R tmC:3L
## thetaC
## rhoC
## tmrcaC
## chr2R
## chr3L
## chr3R
## thetaC:tmrcaC
## thetaC:chr2R
## thetaC:chr3L    0.705
## thetaC:chr3R    0.695  0.773
## rhoC:chr2R     -0.043 -0.063 -0.062
## rhoC:chr3L     -0.062 -0.009 -0.069  0.552
## rhoC:chr3R     -0.061 -0.068 -0.044  0.539  0.598
## tmrcaC:chr2R   -0.452 -0.291 -0.287 -0.403 -0.246 -0.240
## tmrcaC:chr3L   -0.294 -0.469 -0.322 -0.249 -0.485 -0.269  0.573
## tmrcaC:chr3R   -0.278 -0.308 -0.418 -0.235 -0.260 -0.405  0.540  0.606
## thetaC:tmrcaC:chr2R -0.012  0.040  0.039 -0.016 -0.028 -0.027  0.184  0.100
## thetaC:tmrcaC:chr3L  0.044  0.003  0.048 -0.032 -0.090 -0.035  0.108  0.343
## thetaC:tmrcaC:chr3R  0.038  0.042 -0.014 -0.027 -0.031  0.034  0.093  0.104
##               tmC:3R tC:C:2 tC:C:3L
## thetaC
## rhoC
## tmrcaC
## chr2R
## chr3L
## chr3R
## thetaC:tmrcaC
## thetaC:chr2R
## thetaC:chr3L
## thetaC:chr3R
## rhoC:chr2R
## rhoC:chr3L
## rhoC:chr3R
## tmrcaC:chr2R
## tmrcaC:chr3L
## tmrcaC:chr3R

```

```
## thetaC:tmrcaC:chr2R 0.094
## thetaC:tmrcaC:chr3L 0.114 0.585
## thetaC:tmrcaC:chr3R 0.412 0.506 0.608
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -4.00891254 -0.61065163 0.01328723 0.61217794 4.00913774
##
## Residual standard error: 0.0002143828
## Degrees of freedom: 1587 total; 1567 residual
```

```
# correlations
```

```
cor.test(dm.lands.evolrate$PiN, dm.lands.evolrate$theta, method = "spearman")
```

```
##
## Spearman's rank correlation rho
##
## data: dm.lands.evolrate$PiN and dm.lands.evolrate$theta
## S = 556084020, p-value = 3.517e-11
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.1652411
```

```
cor.test(dm.lands.evolrate$PiS, dm.lands.evolrate$theta, method = "spearman")
```

```
##
## Spearman's rank correlation rho
##
## data: dm.lands.evolrate$PiS and dm.lands.evolrate$theta
## S = 400587864, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.3986623
```

```
cor.test(dm.lands.evolrate$dS, dm.lands.evolrate$PiS, method = "spearman")
```

```
##
## Spearman's rank correlation rho
##
## data: dm.lands.evolrate$dS and dm.lands.evolrate$PiS
## S = 277666666, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.583184
```

```
pcor.test(dm.lands.evolrate$dS, dm.lands.evolrate$PiS, dm.lands.evolrate$theta, method = "spearman")
```

```
##      estimate      p.value statistic      n gp      Method
## 1 0.6572142 9.3304e-197 34.70434 1587 1 spearman
```

```
cor.test(dm.lands.evolrate$dS, dm.lands.evolrate$theta, method = "spearman")
```

```
##  
## Spearman's rank correlation rho  
##  
## data: dm.lands.evolrate$dS and dm.lands.evolrate$theta  
## S = 697693032, p-value = 0.0594  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## -0.04733358
```

```
pcor.test(dm.lands.evolrate$dS, dm.lands.evolrate$theta, dm.lands.evolrate$tmrca, method = "spearman")
```

```
## estimate p.value statistic n gp Method  
## 1 -0.02711326 0.2805332 -1.079491 1587 1 spearman
```

```
# checking about rec rate
```

```
cor.test(dm.lands.evolrate$PiS, dm.lands.evolrate$rho, method = "spearman")
```

```
##  
## Spearman's rank correlation rho  
##  
## data: dm.lands.evolrate$PiS and dm.lands.evolrate$rho  
## S = 553913829, p-value = 1.423e-11  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## 0.1684989
```

```
pcor.test(dm.lands.evolrate$PiS, dm.lands.evolrate$rho, dm.lands.evolrate$tmrca, method = "spearman")
```

```
## estimate p.value statistic n gp Method  
## 1 0.02471291 0.3253336 0.983862 1587 1 spearman
```

```
cor.test(dm.lands.evolrate$dS, dm.lands.evolrate$rho, method = "spearman")
```

```
##  
## Spearman's rank correlation rho  
##  
## data: dm.lands.evolrate$dS and dm.lands.evolrate$rho  
## S = 679701757, p-value = 0.4184  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## -0.02032619
```

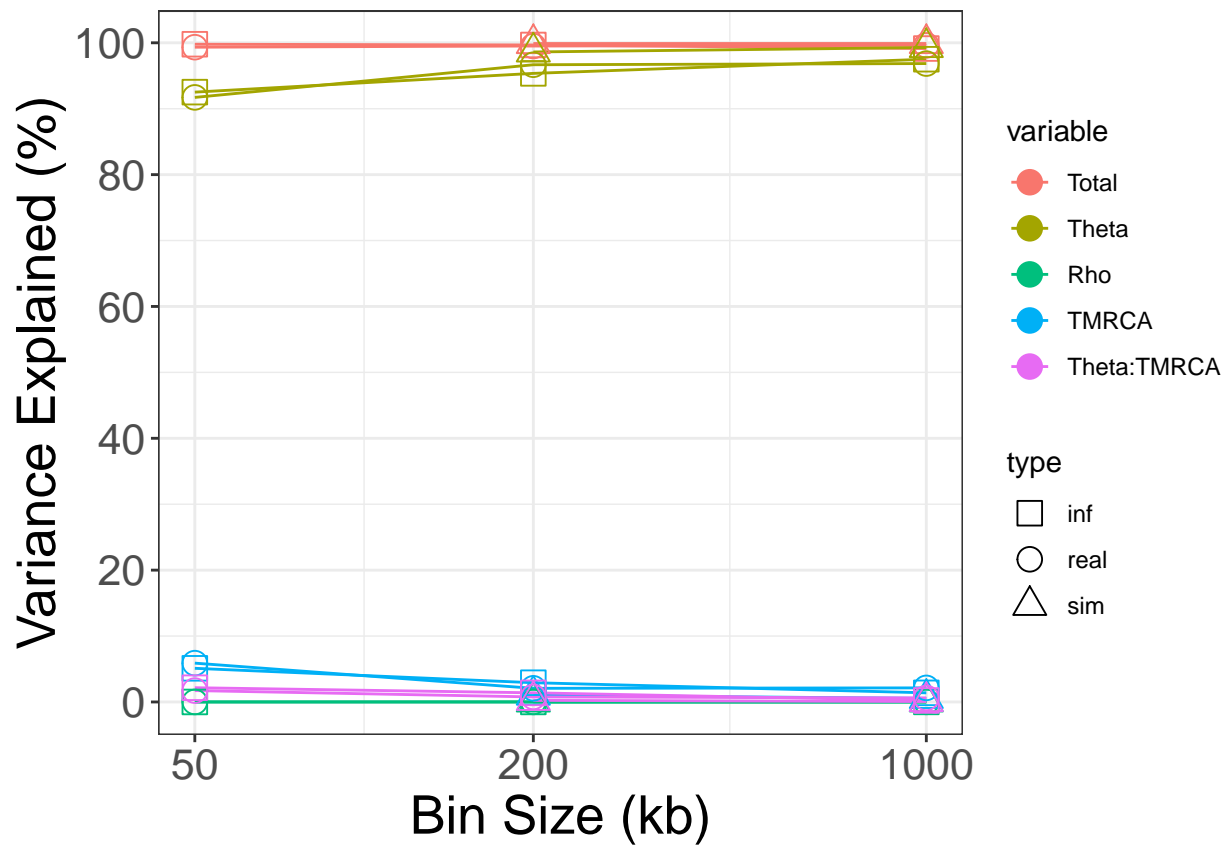
4 R² plot with real, simulated (true) and simulated (inferred) data.

```
# true landscapes
r2.sim.avg <- rbind.data.frame(r2.sim.50kb$average, r2.sim.200kb$average, r2.sim.1Mb$average, make.row.names = 1:3)
colnames(r2.sim.avg) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
r2.sim.avg$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$average, make.row.names = 1:3)
colnames(r2.inf.avg) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
r2.inf.avg$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("Fig4.pdf", r2.plot, device = "pdf", )
```