

Determinants of the genome-wide diversity in *Drosophila*

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```
knitr::opts_chunk$set(echo = TRUE)

library(ppcor)
library(MASS)
library(reshape2)
library(tidyverse)
library(cowplot)
library(lmtest)
library(nlme)
library(car)
library(plyr)
library(tidyverse)
library(GenomicRanges)
library(RColorBrewer)
library(scales)
library(interactions)

knitr::opts_knit$set(root.dir = "~/Data/iSMC/theta_paper/root")

nreps <- 10
reps <- character(length = nreps)
for(i in 1:nreps) {
  reps[i] <- paste("rep_", i, sep = "")
}
```

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

First batch of 10 replicate simulations using parameters as inferred from real *Drosophila* data.

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")
```

rep_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$sample_mean, tmrca.50k$sample_mean))
names(inf.lands.50k.rep_1) <- c("diversity", "theta", "rho", "tmrca")

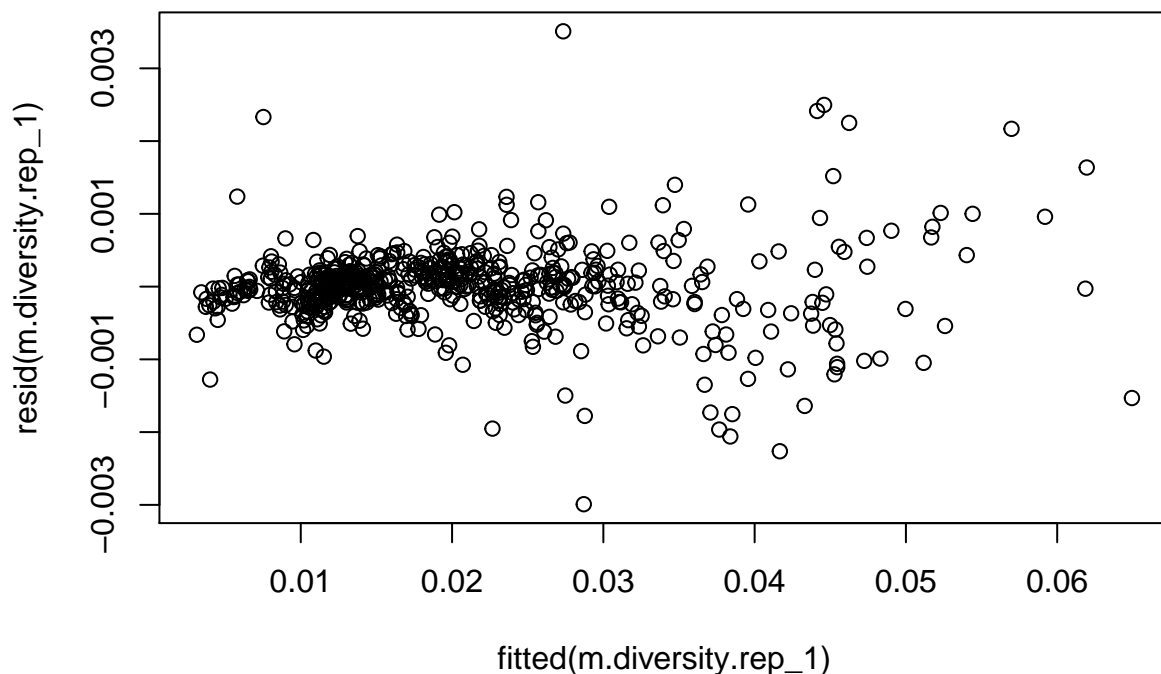
# centering
inf.lands.50k.rep_1$thetaC <- inf.lands.50k.rep_1$theta - mean(inf.lands.50k.rep_1$theta)
inf.lands.50k.rep_1$tmrcaC <- inf.lands.50k.rep_1$tmrca - mean(inf.lands.50k.rep_1$tmrca)
inf.lands.50k.rep_1$rhoC <- inf.lands.50k.rep_1$rho - mean(inf.lands.50k.rep_1$rho)

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)
```

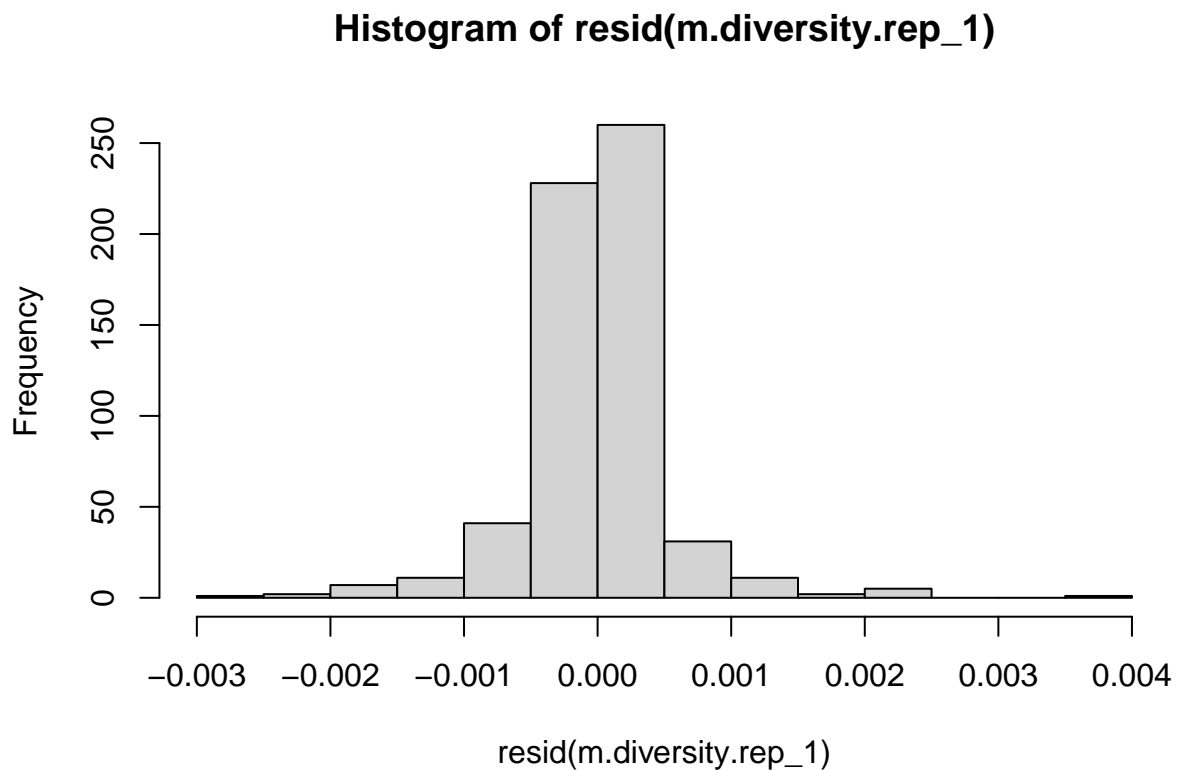
```
##
```

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

```
hmctest(m.diversity.rep_1)
```

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

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

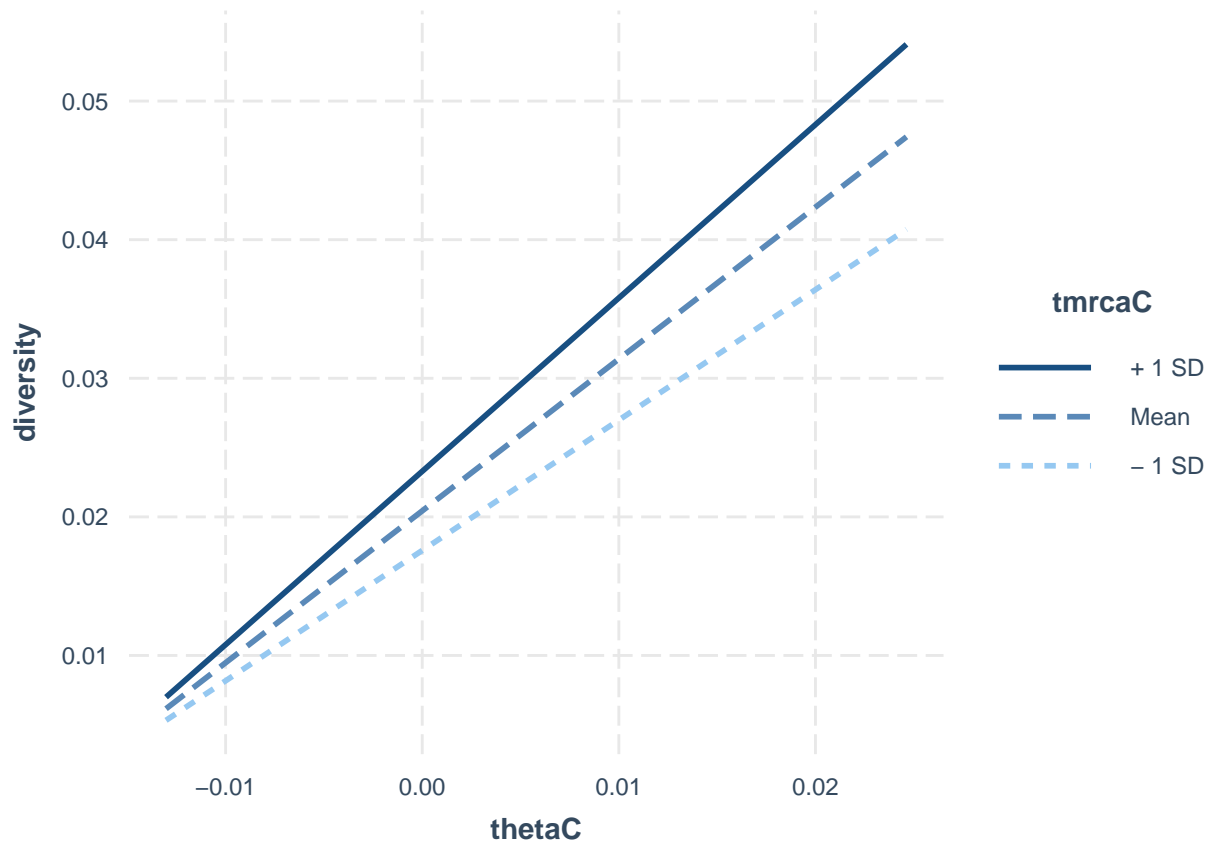


```
summary(m.diversity.rep_1)
```

```
##
## 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
```

rep_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)

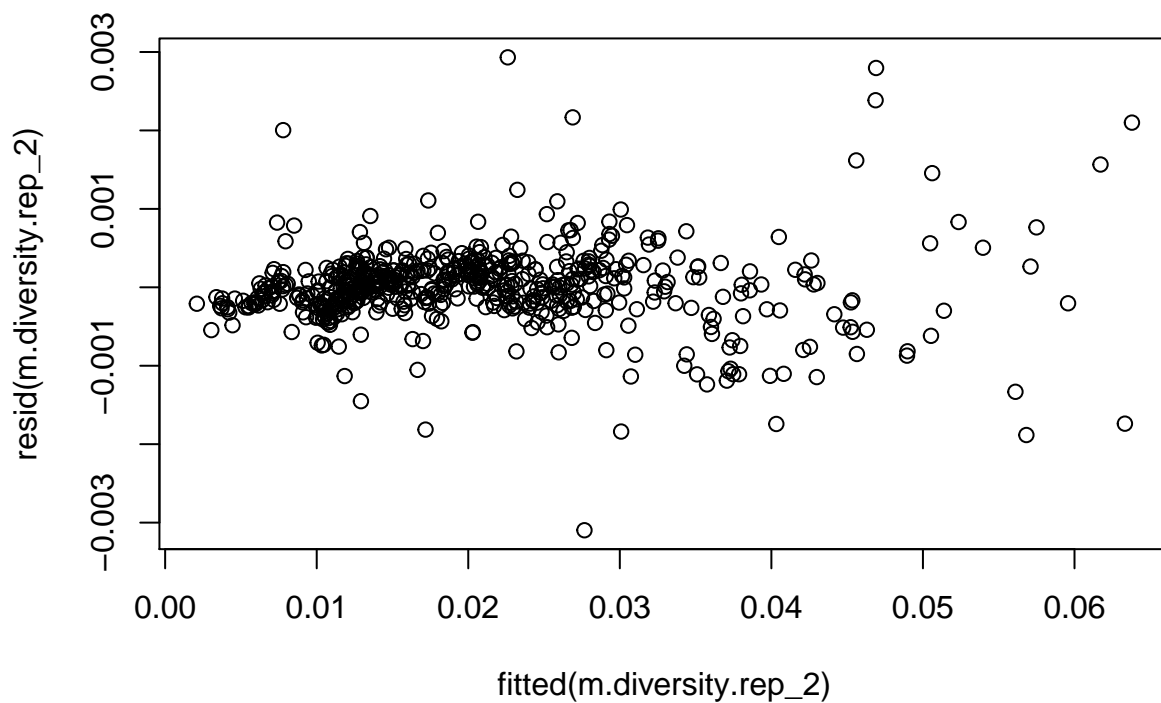
inf.lands.50k.rep_2 <- as.data.frame(cbind(pi.50k$avg, theta.50k$sample_mean, rho.50k$sample_mean, tmrca.50k$sample_mean))
names(inf.lands.50k.rep_2) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

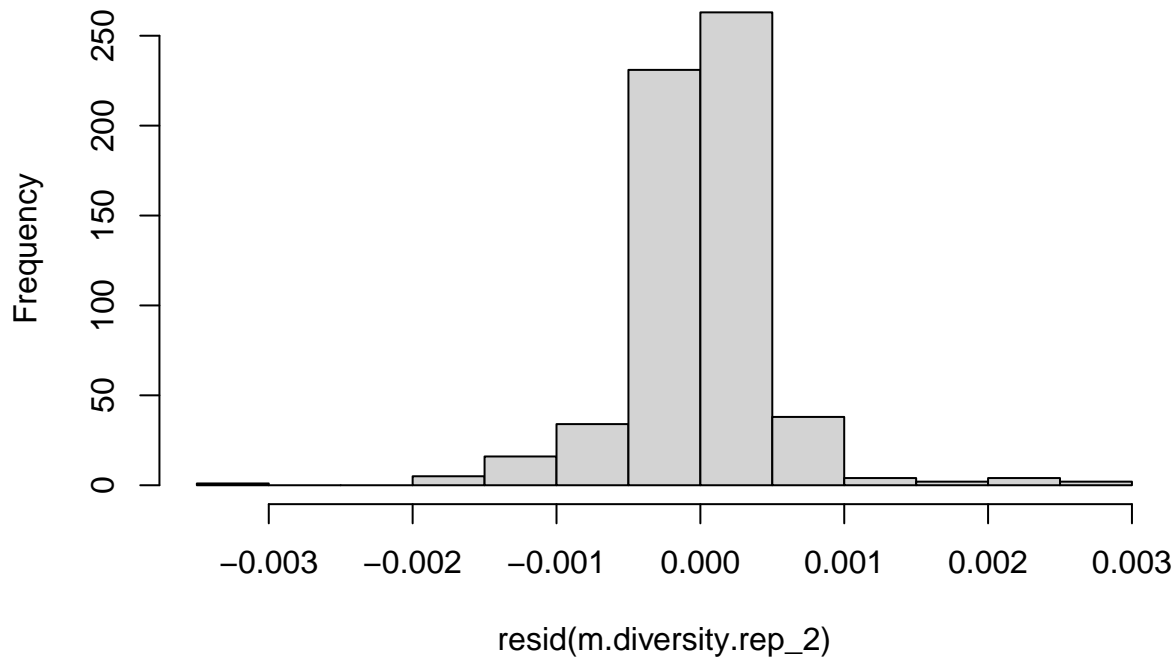
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_2  
## DW = 1.3609, p-value = 1.173e-15  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
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)

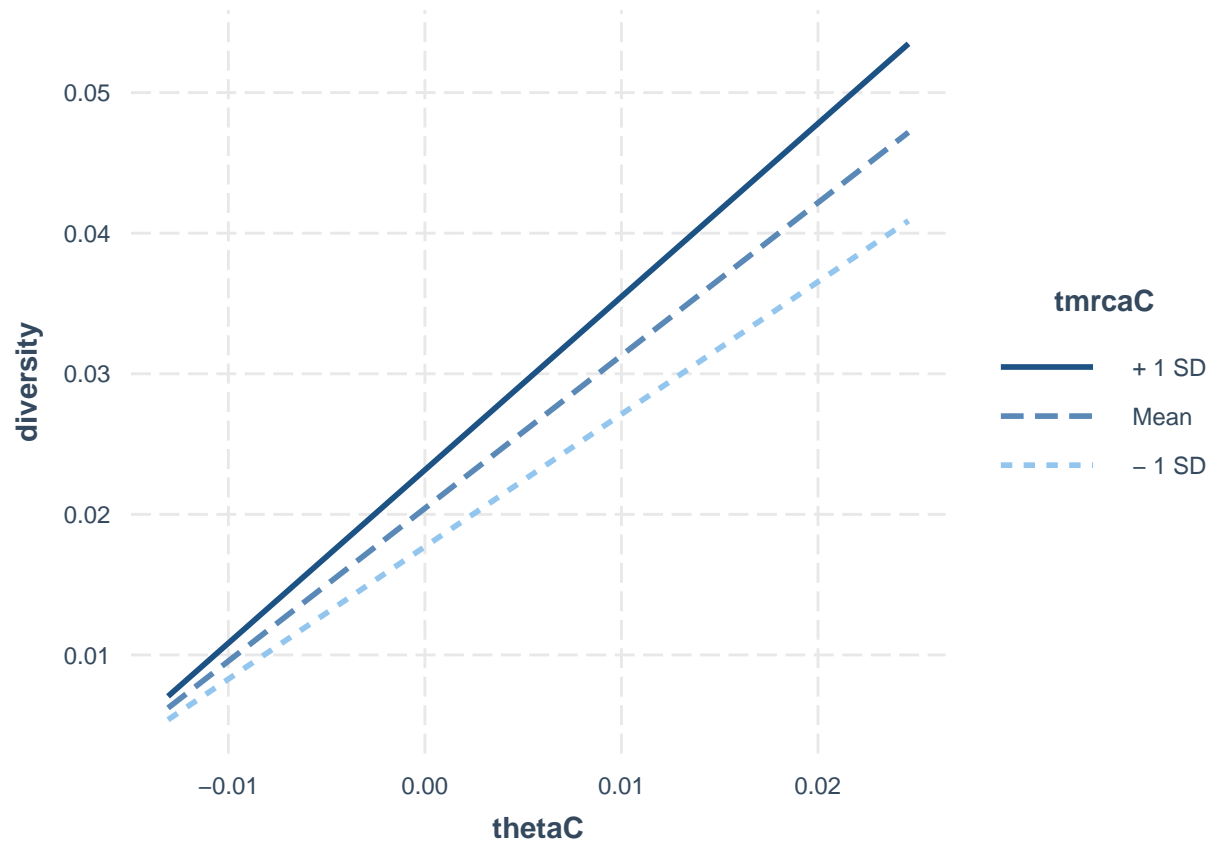


```
summary(m.diversity.rep_2)
```

```
##
## 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
```

rep_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)

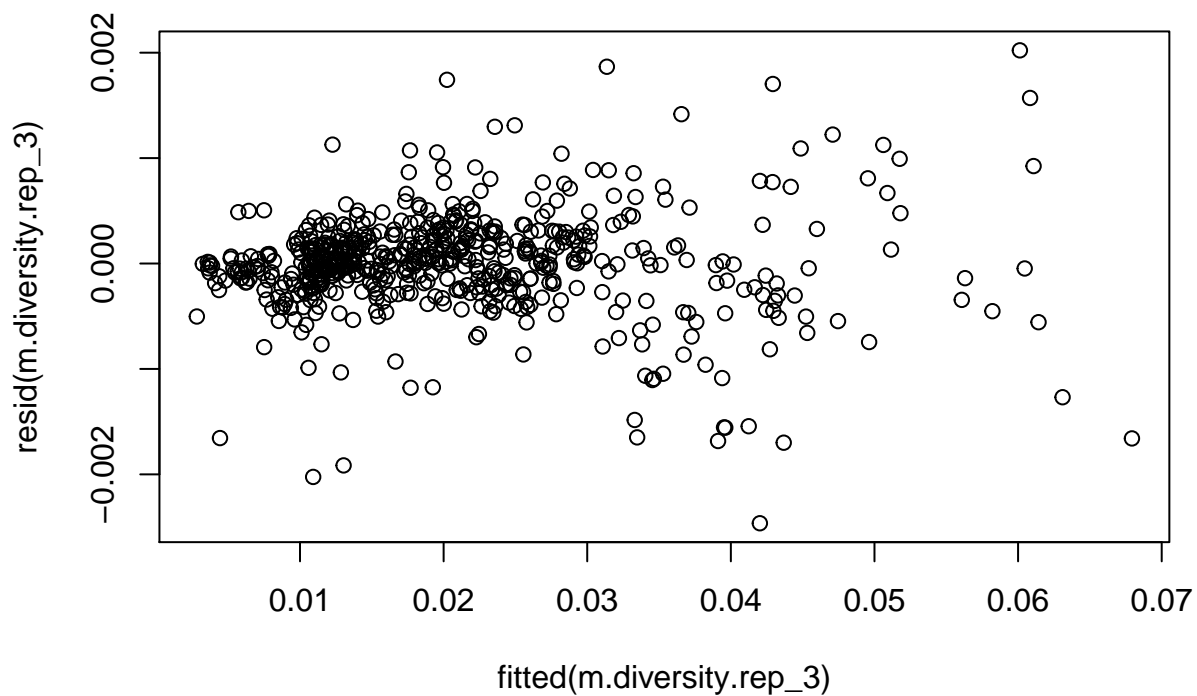
inf.lands.50k.rep_3 <- as.data.frame(cbind(pi.50k$avg, theta.50k$sample_mean, rho.50k$sample_mean, tmrca.50k$avg))
names(inf.lands.50k.rep_3) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

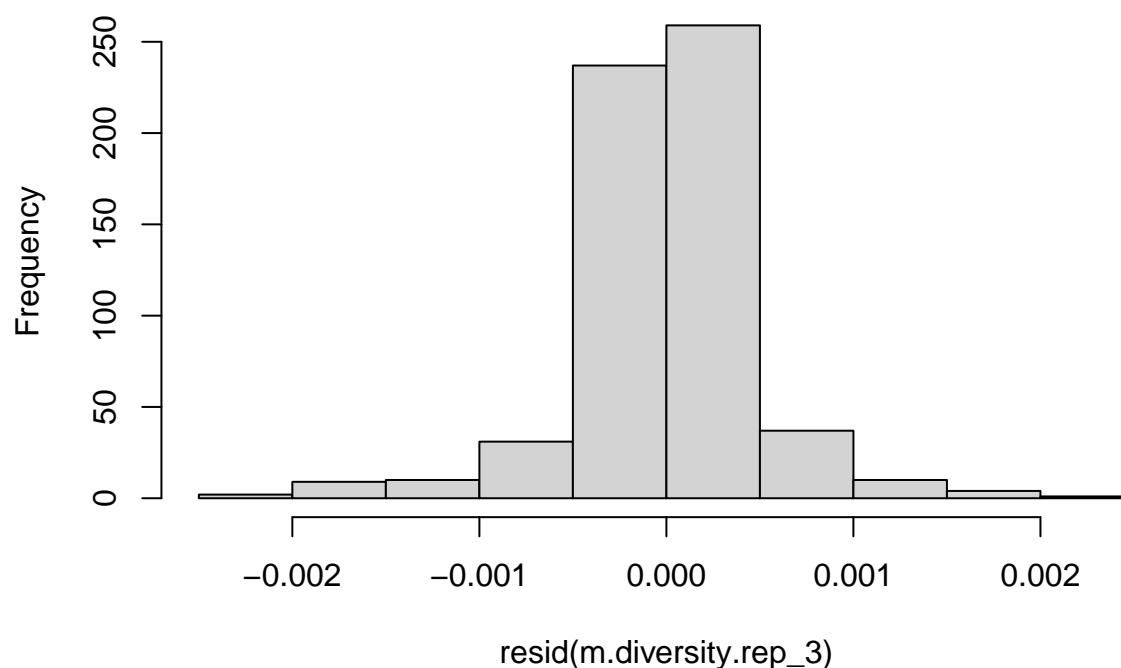
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_3  
## DW = 1.4619, p-value = 1.133e-11  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_3  
## HMC = 0.52153, p-value = 0.763
```

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

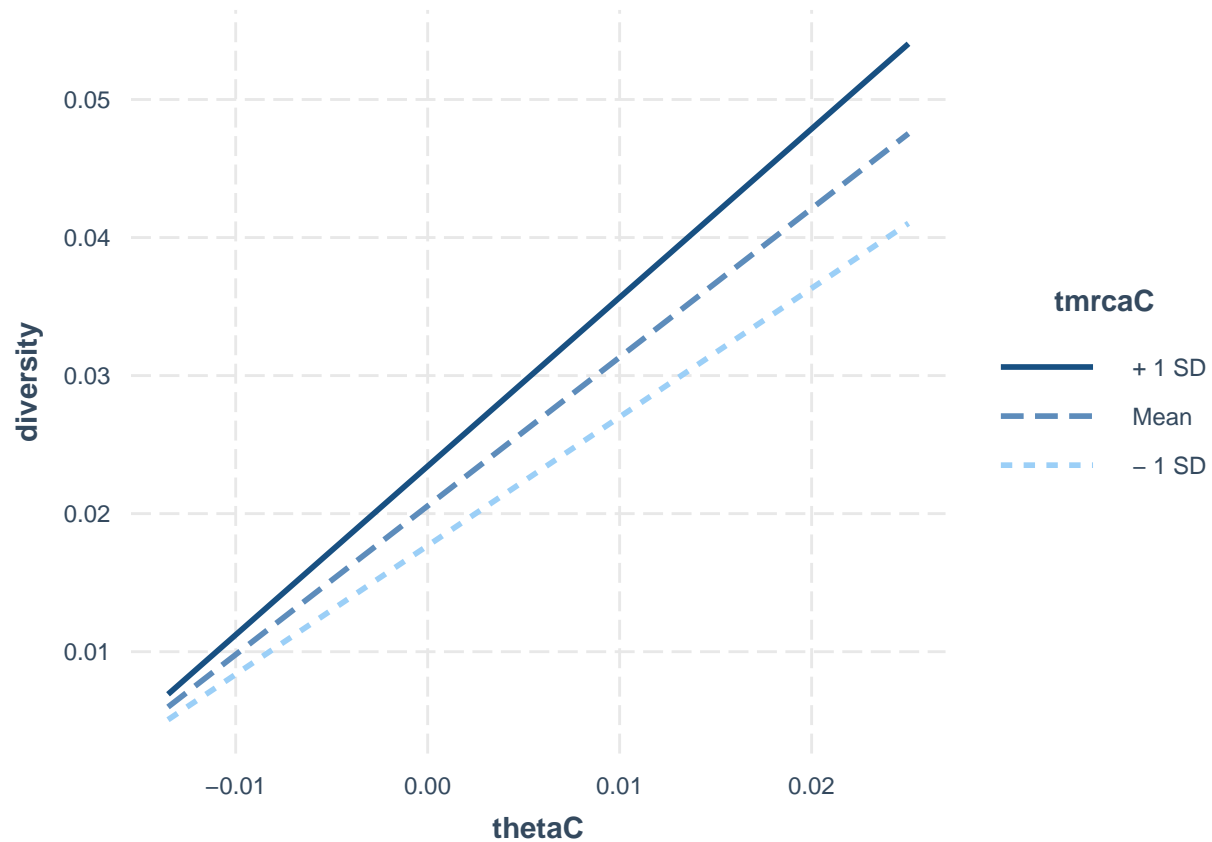
Histogram of resid(m.diversity.rep_3)



```
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
```

rep_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)

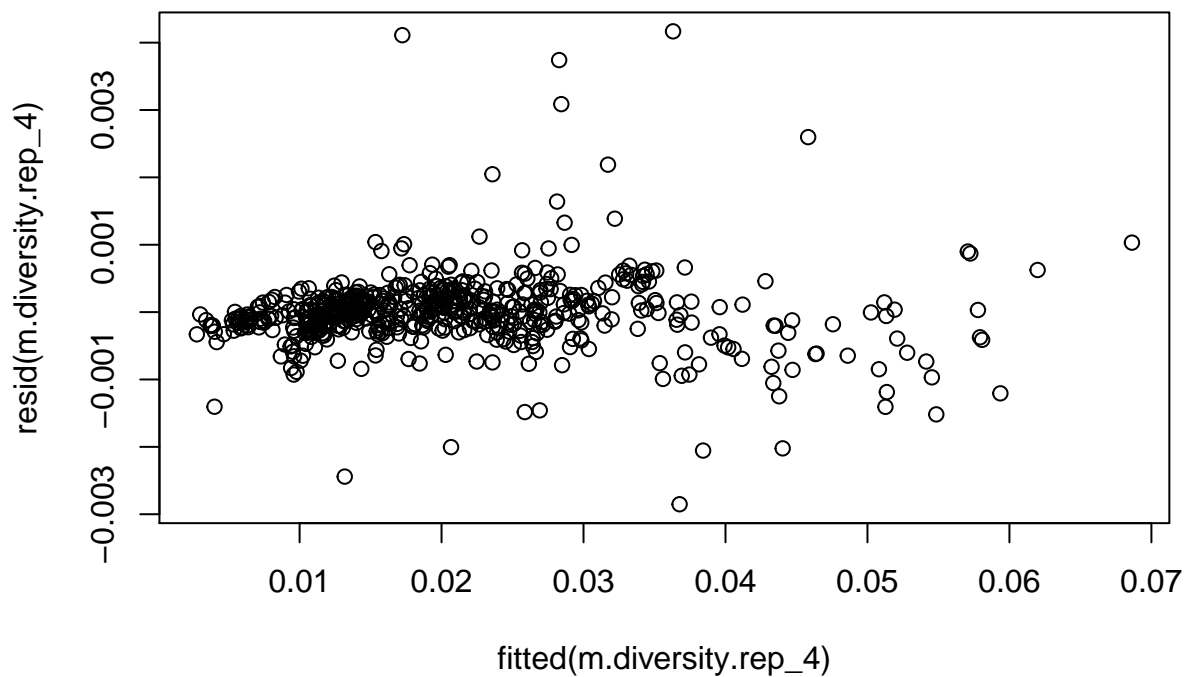
inf.lands.50k.rep_4 <- as.data.frame(cbind(pi.50k$avg, theta.50k$sample_mean, rho.50k$sample_mean, tmrca.50k$sample_mean))
names(inf.lands.50k.rep_4) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

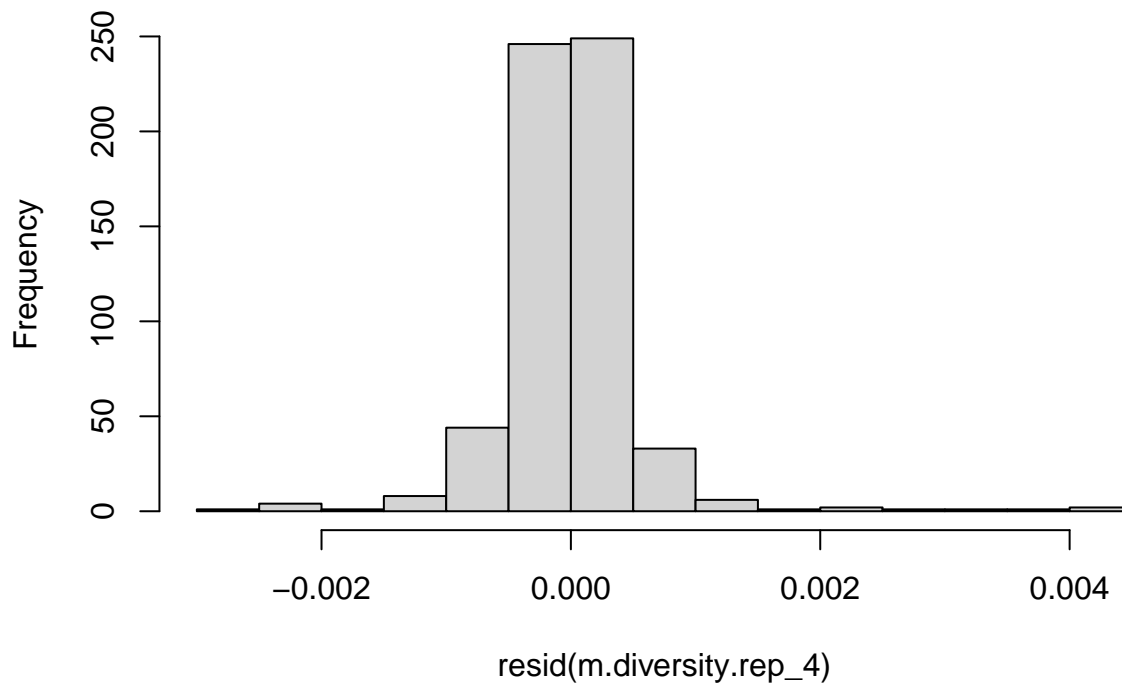
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_4  
## DW = 0.96213, p-value < 2.2e-16  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
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))
```

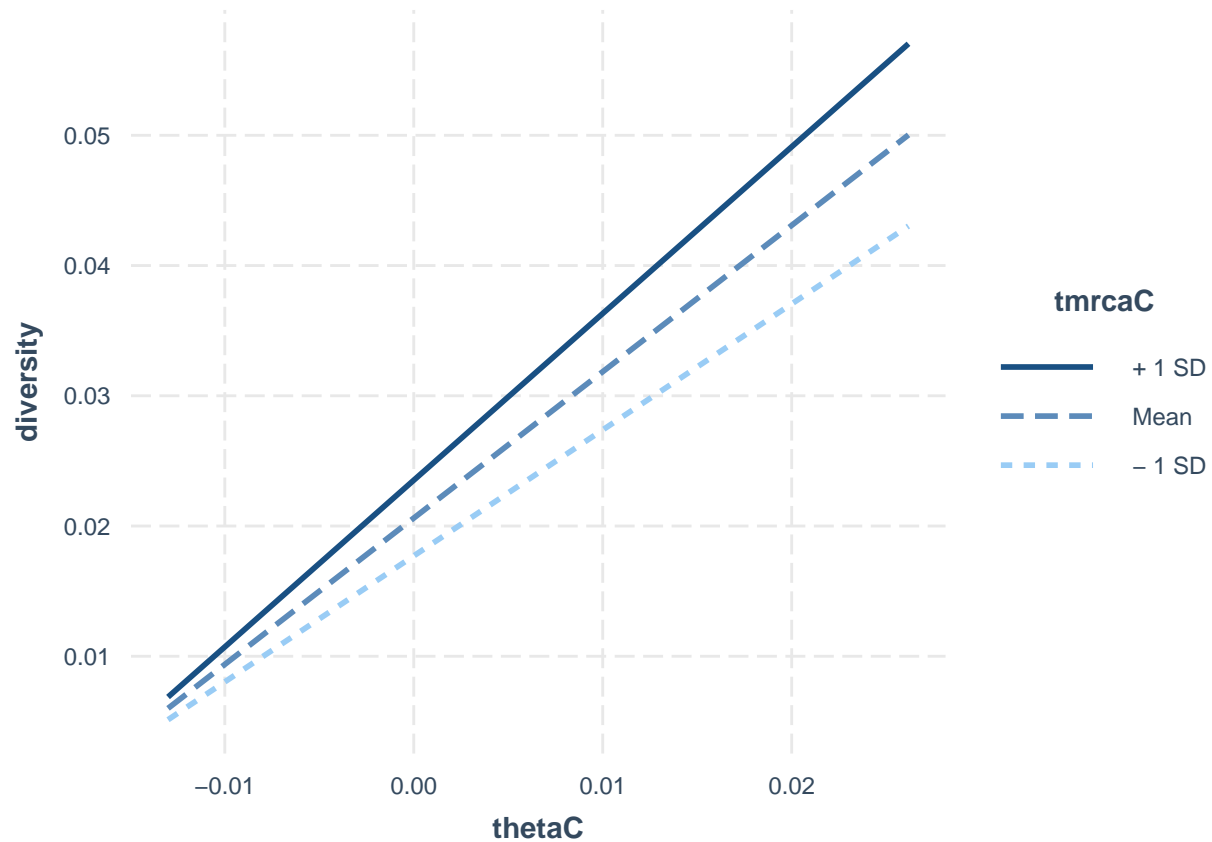
Histogram of resid(m.diversity.rep_4)



```
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
```

rep_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)

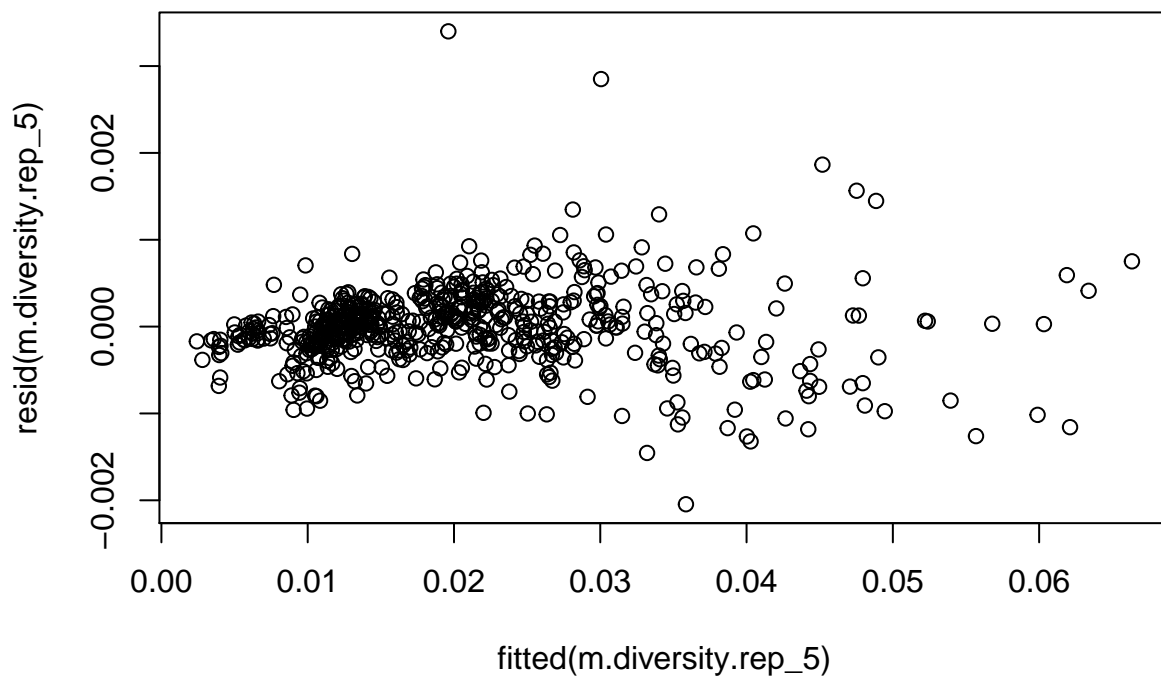
inf.lands.50k.rep_5 <- as.data.frame(cbind(pi.50k$avg, theta.50k$sample_mean, rho.50k$sample_mean, tmrca.50k$sample_mean))
names(inf.lands.50k.rep_5) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

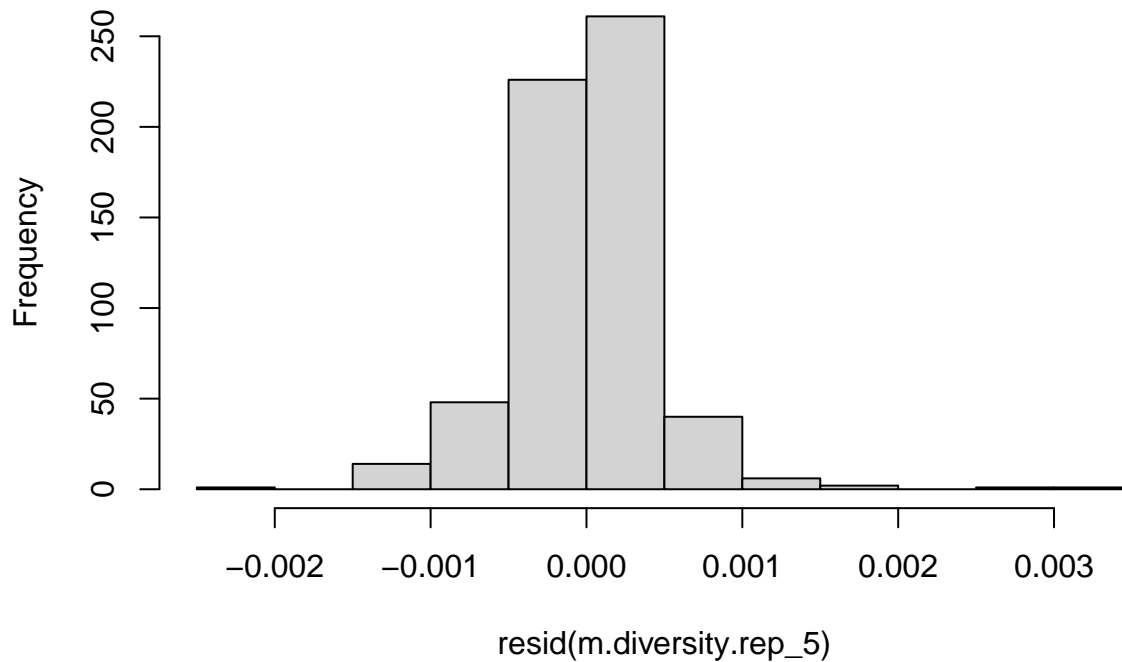
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_5  
## DW = 1.4275, p-value = 5.886e-13  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_5  
## HMC = 0.55418, p-value = 0.964
```

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

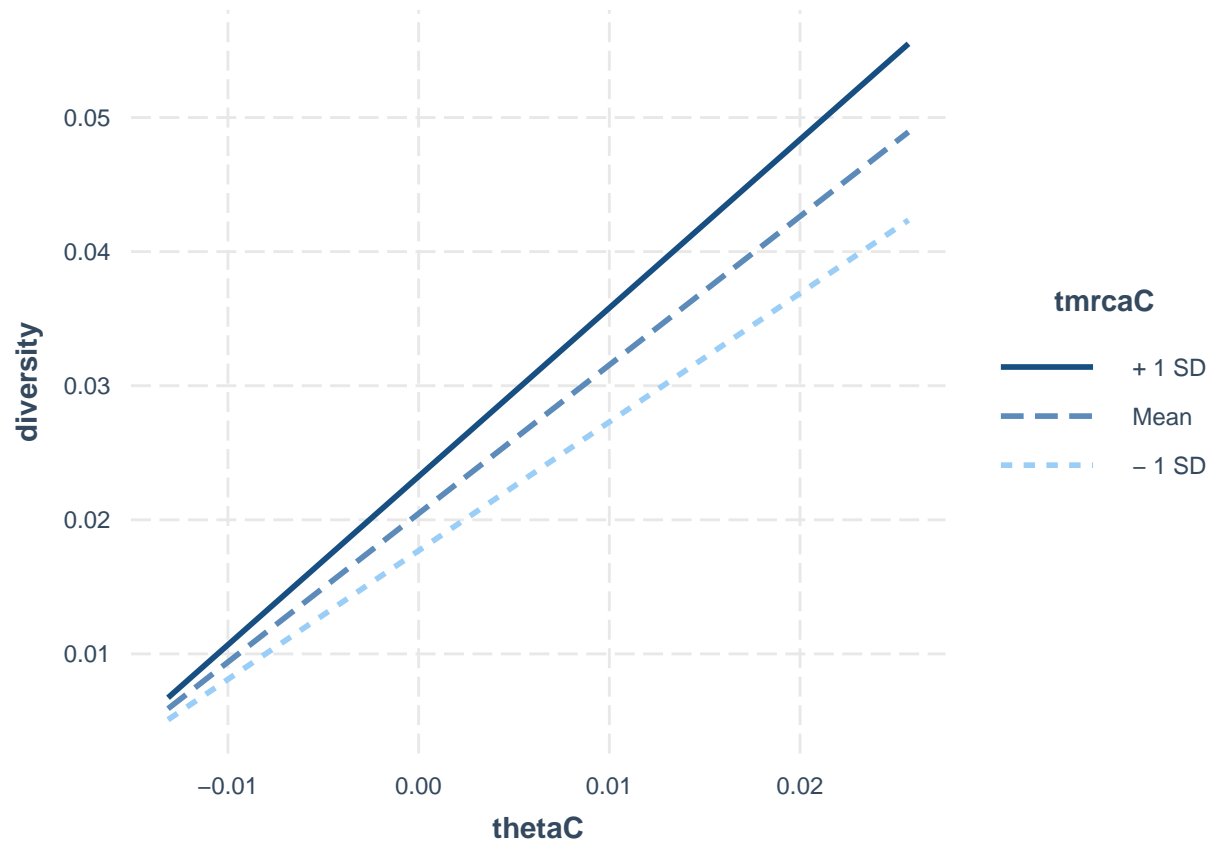
Histogram of resid(m.diversity.rep_5)



```
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
```

rep_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)

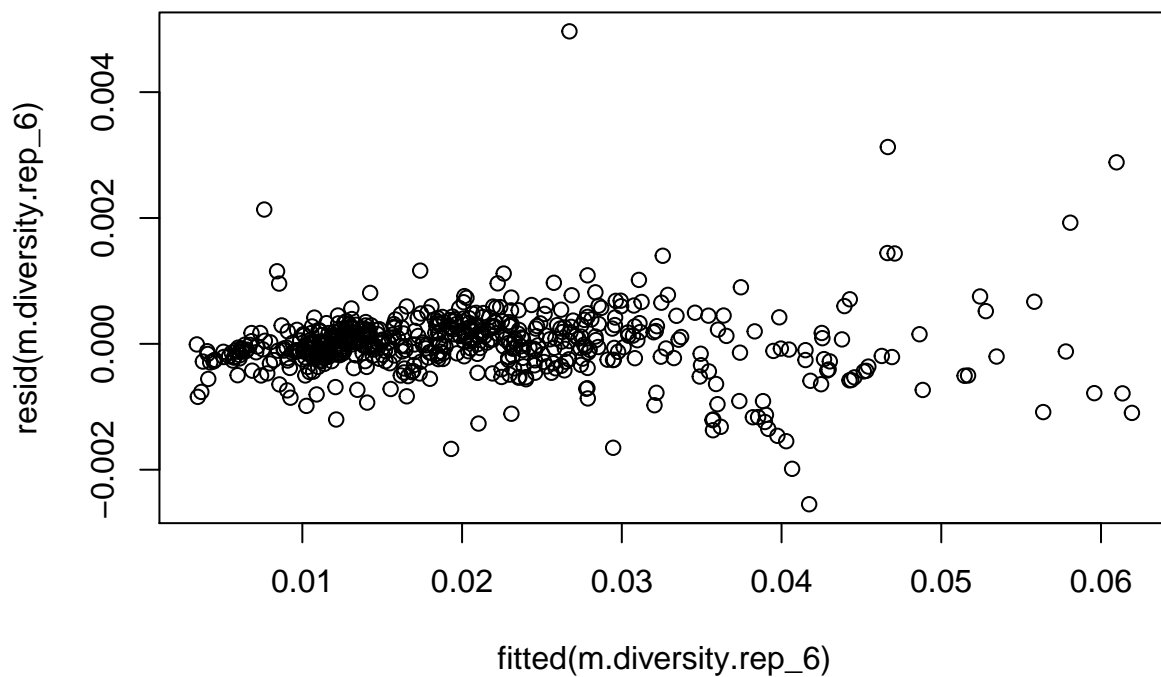
inf.lands.50k.rep_6 <- as.data.frame(cbind(pi.50k$avg, theta.50k$sample_mean, rho.50k$sample_mean, tmrca.50k$avg))
names(inf.lands.50k.rep_6) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

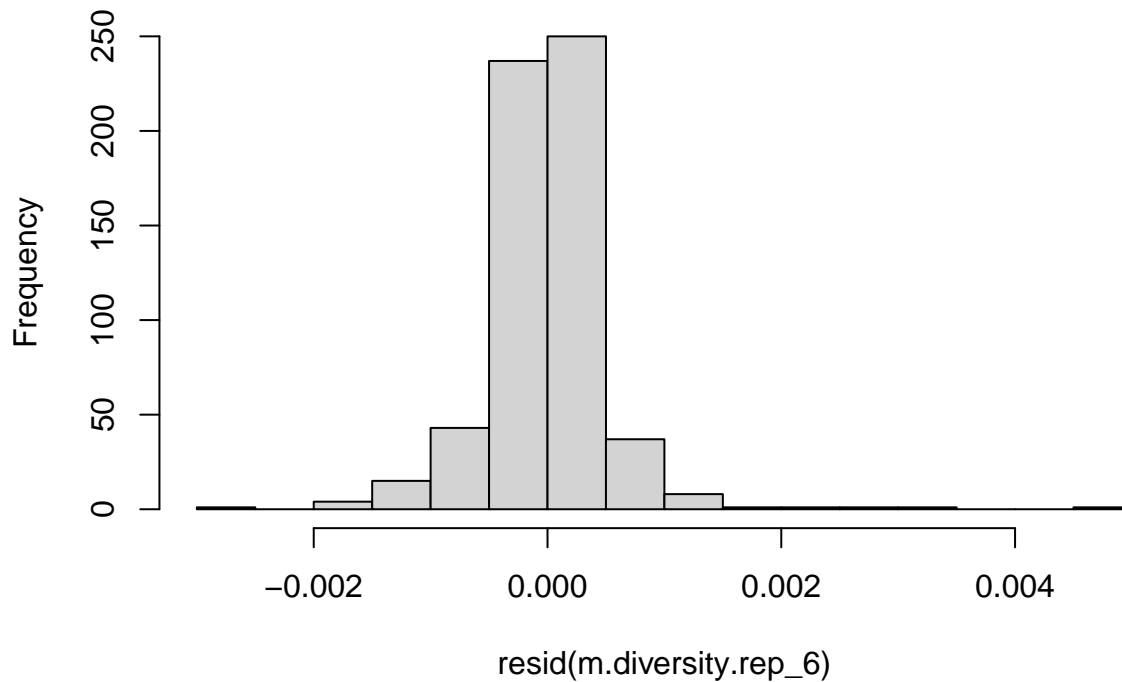
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_6  
## DW = 1.4152, p-value = 1.956e-13  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_6  
## HMC = 0.5501, p-value = 0.965
```

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

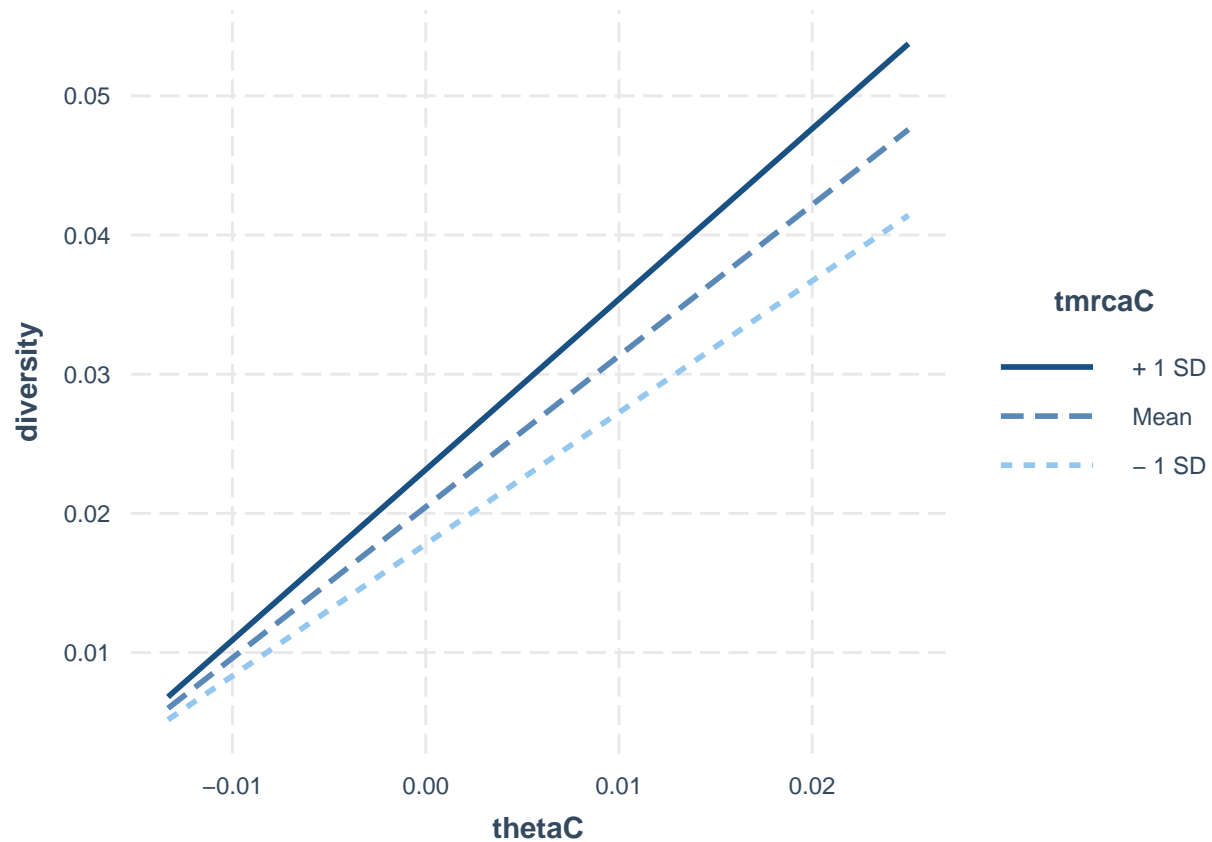
Histogram of resid(m.diversity.rep_6)



```
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
```

rep_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)

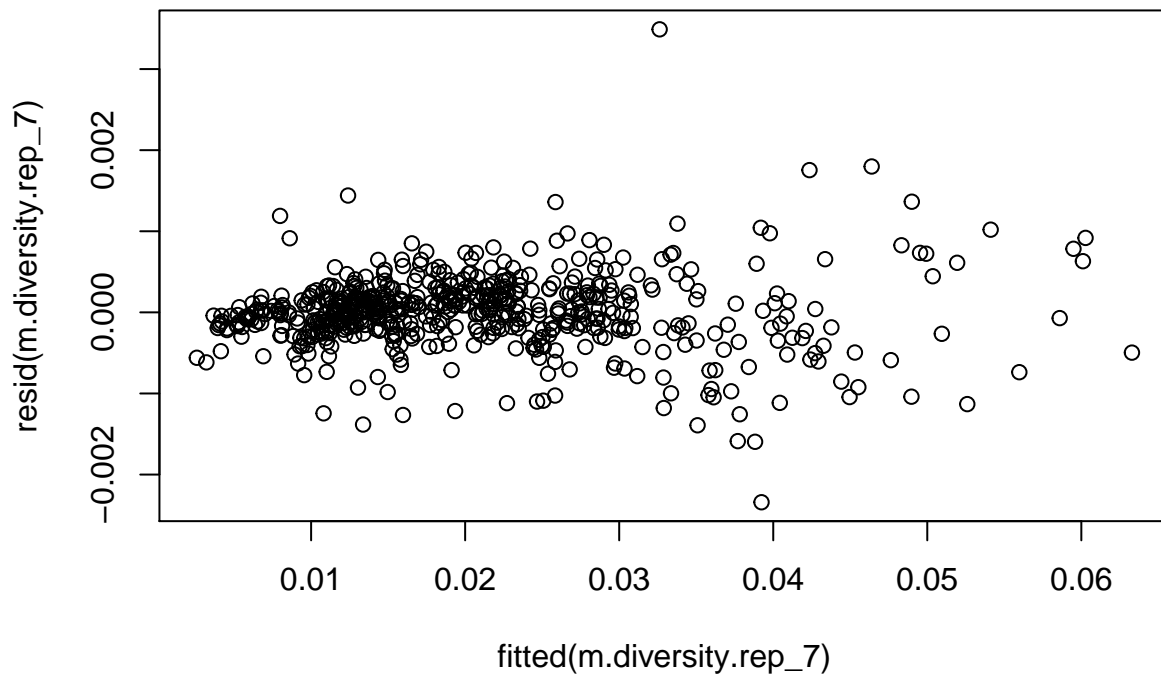
inf.lands.50k.rep_7 <- as.data.frame(cbind(pi.50k$avg, theta.50k$sample_mean, rho.50k$sample_mean, tmrca.50k$avg))
names(inf.lands.50k.rep_7) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

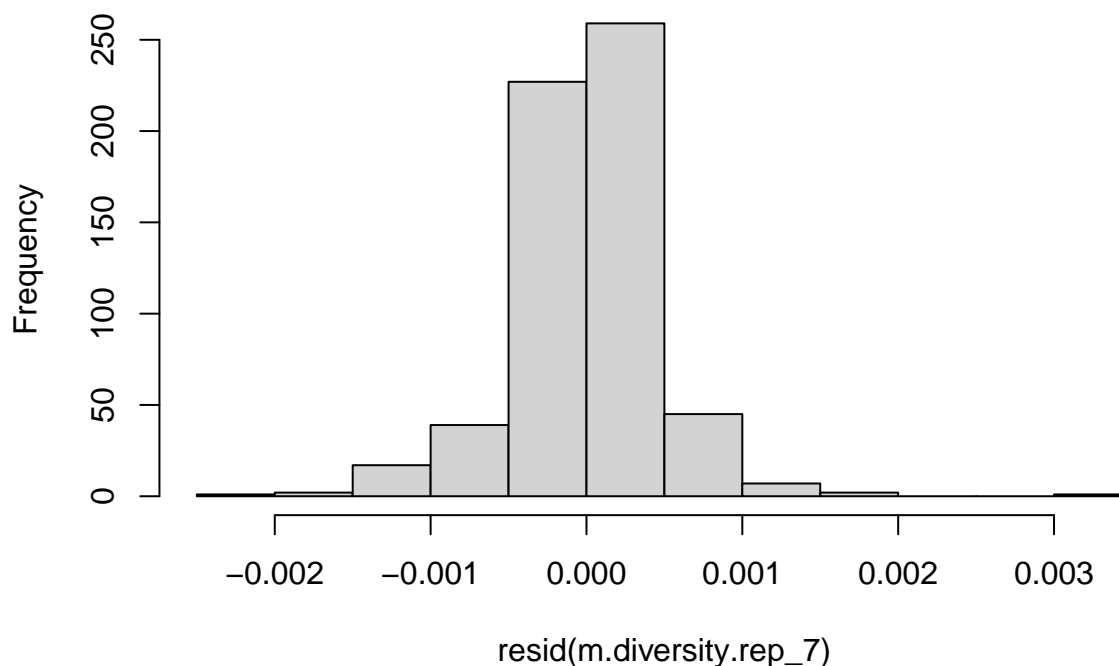
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_7  
## DW = 1.2084, p-value < 2.2e-16  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
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))
```

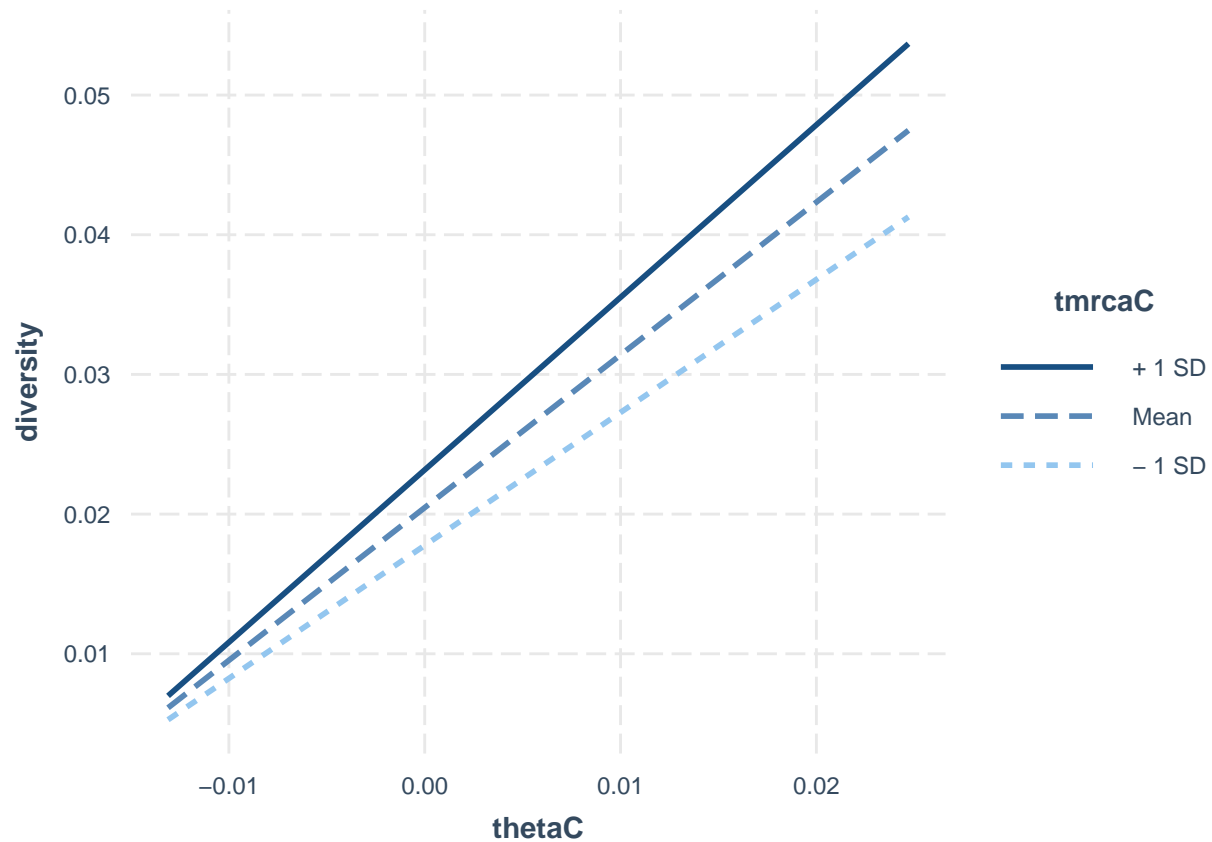

Histogram of resid(m.diversity.rep_7)



```
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
```

rep_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)

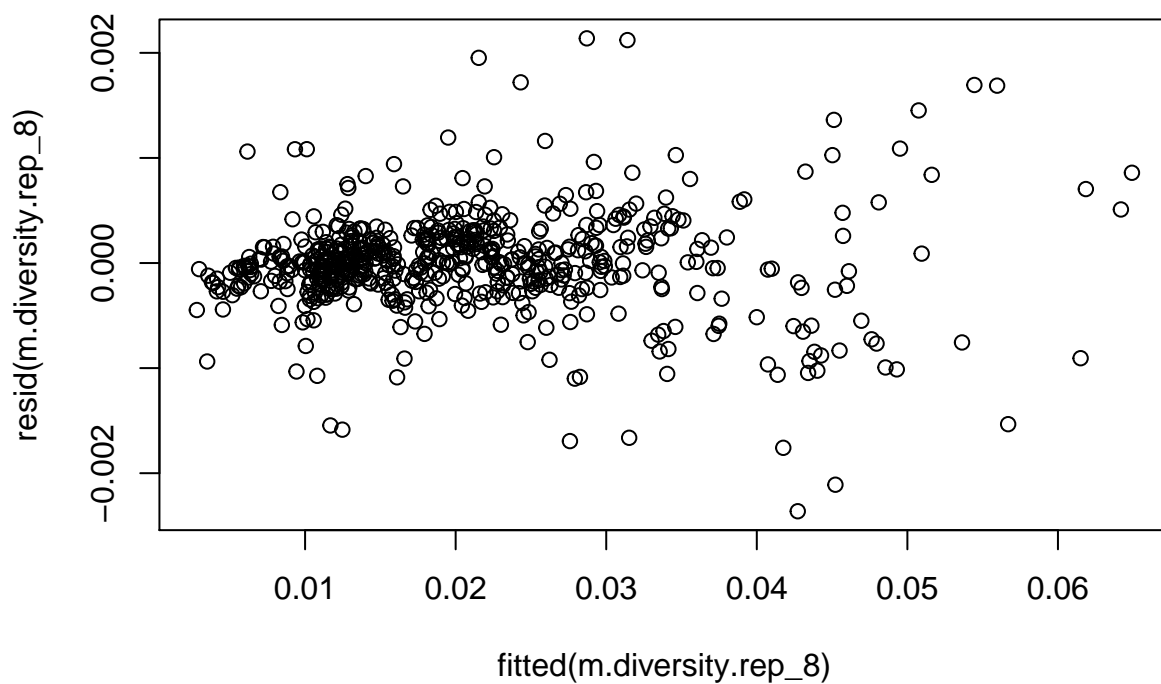
inf.lands.50k.rep_8 <- as.data.frame(cbind(pi.50k$avg, theta.50k$sample_mean, rho.50k$sample_mean, tmrca.50k$sample_mean))
names(inf.lands.50k.rep_8) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

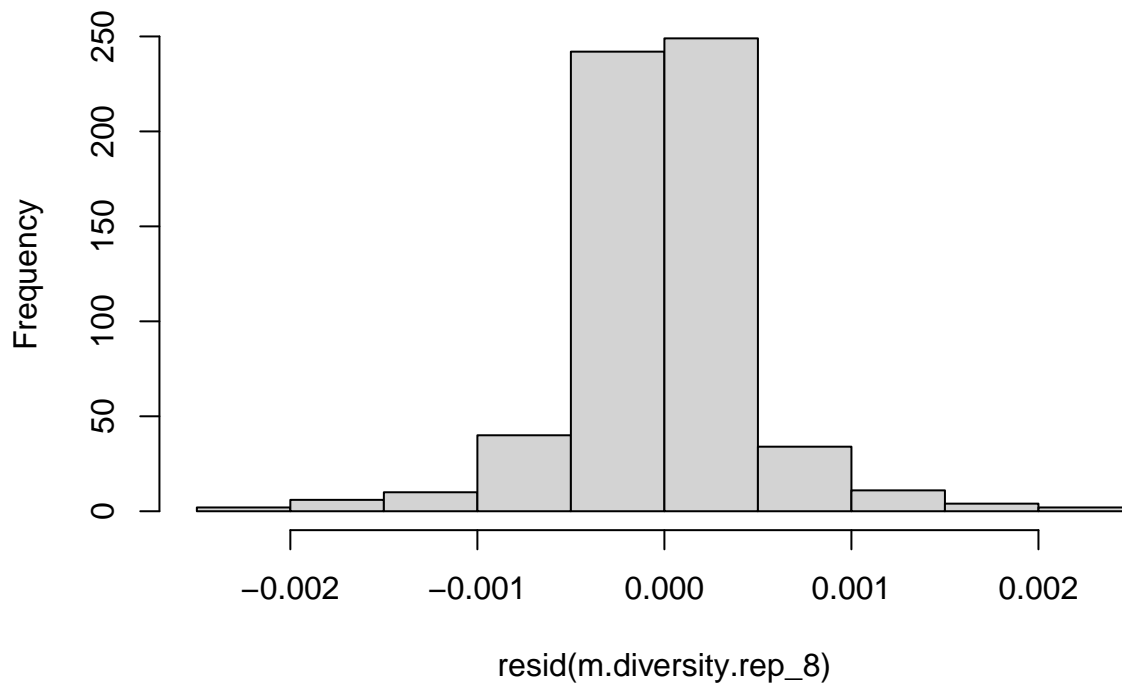
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_8  
## DW = 1.3796, p-value = 6.877e-15  
## alternative hypothesis: true autocorrelation is greater than 0
```

```
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))
```

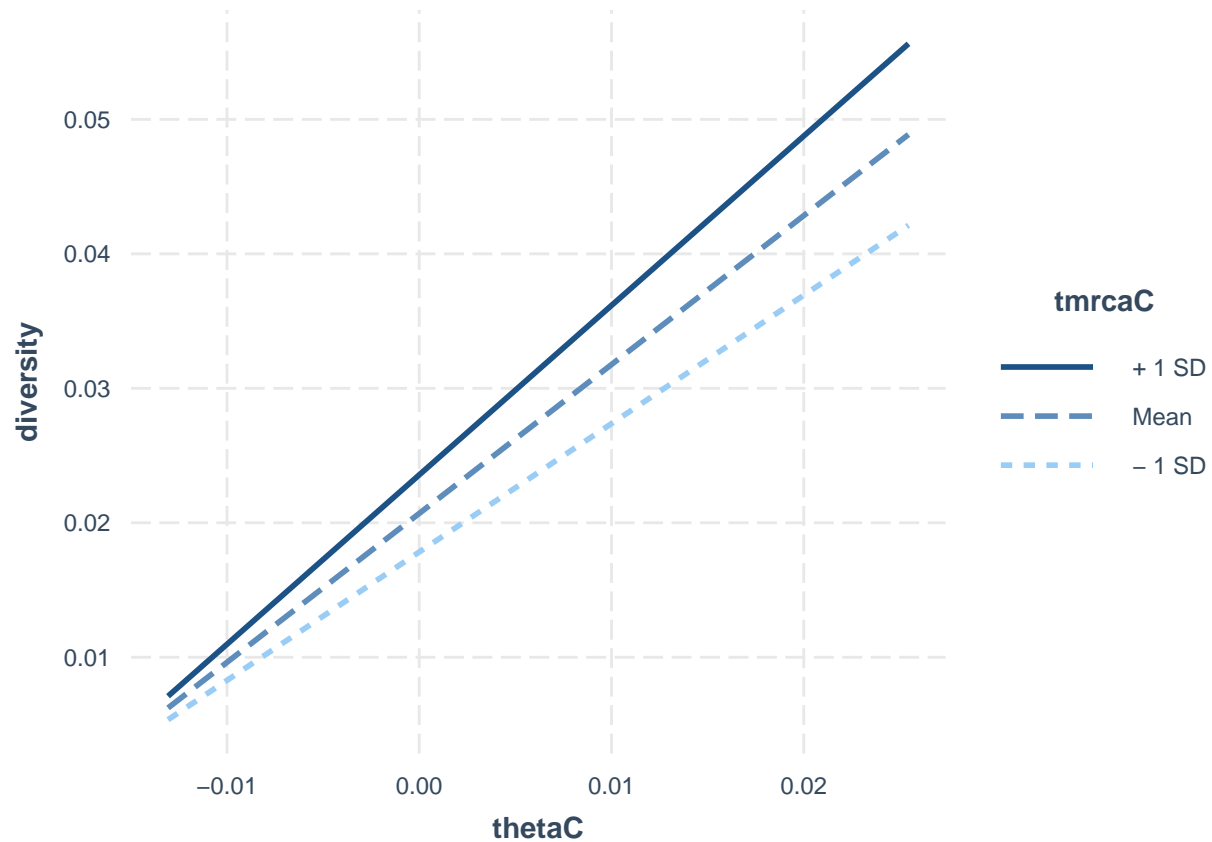
Histogram of resid(m.diversity.rep_8)



```
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
```

rep_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)

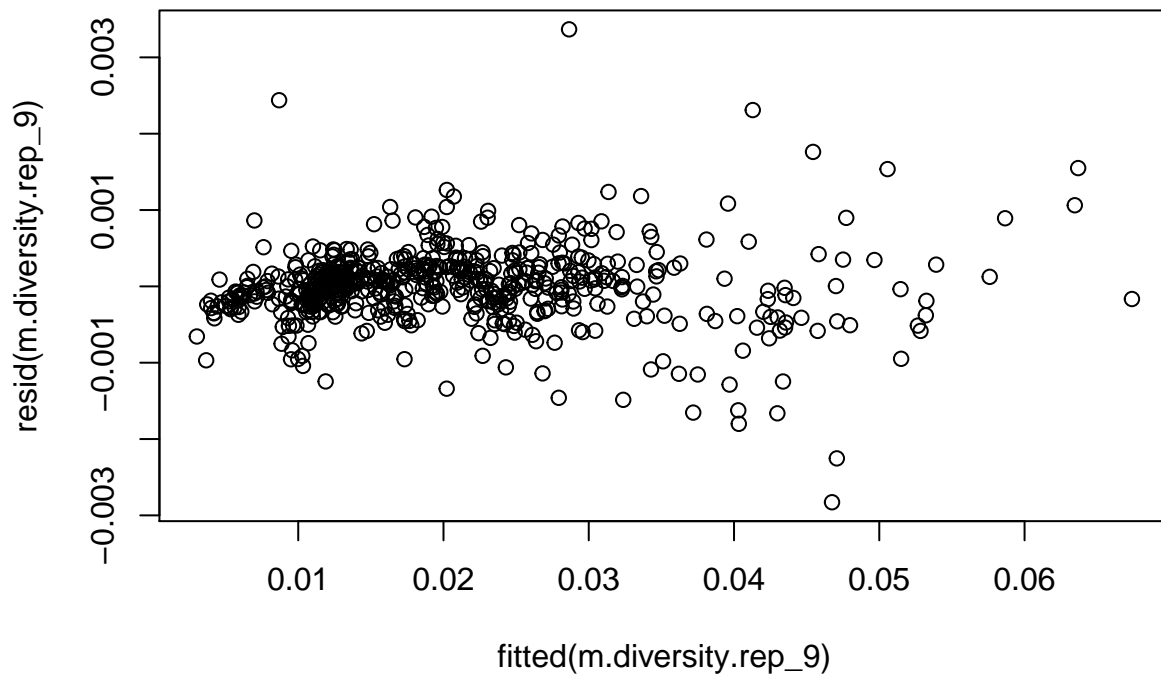
inf.lands.50k.rep_9 <- as.data.frame(cbind(pi.50k$avg, theta.50k$sample_mean, rho.50k$sample_mean, tmrca.50k$sample_mean))
names(inf.lands.50k.rep_9) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

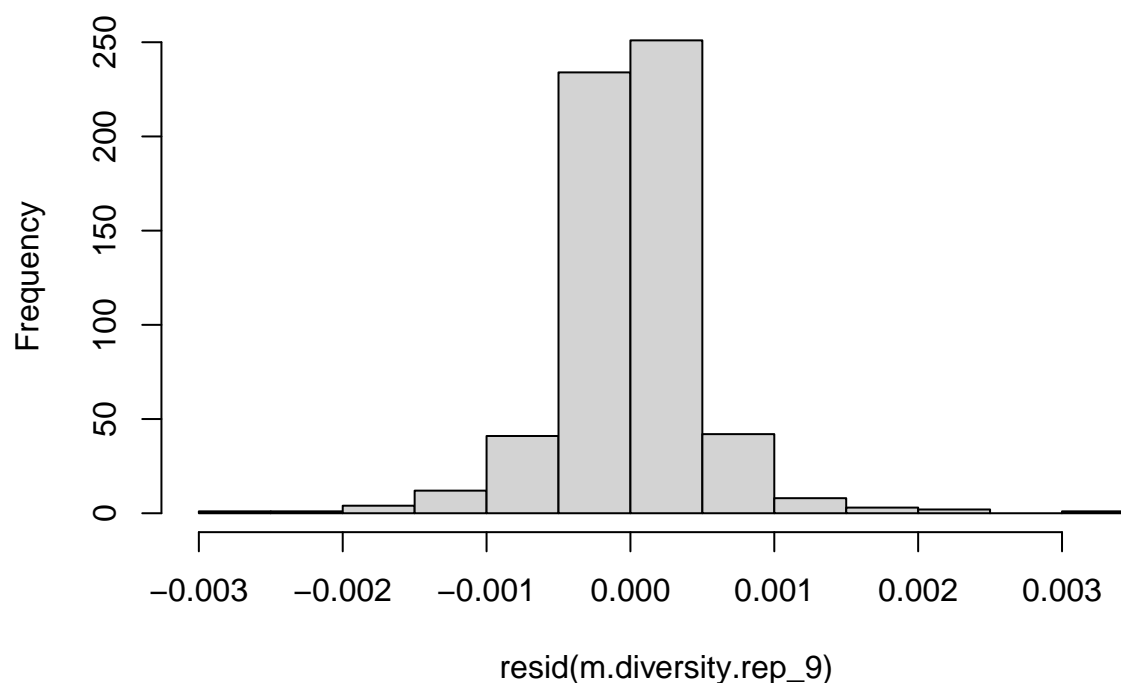
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_9  
## DW = 1.3455, p-value = 2.541e-16  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_9  
## HMC = 0.52947, p-value = 0.85
```

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

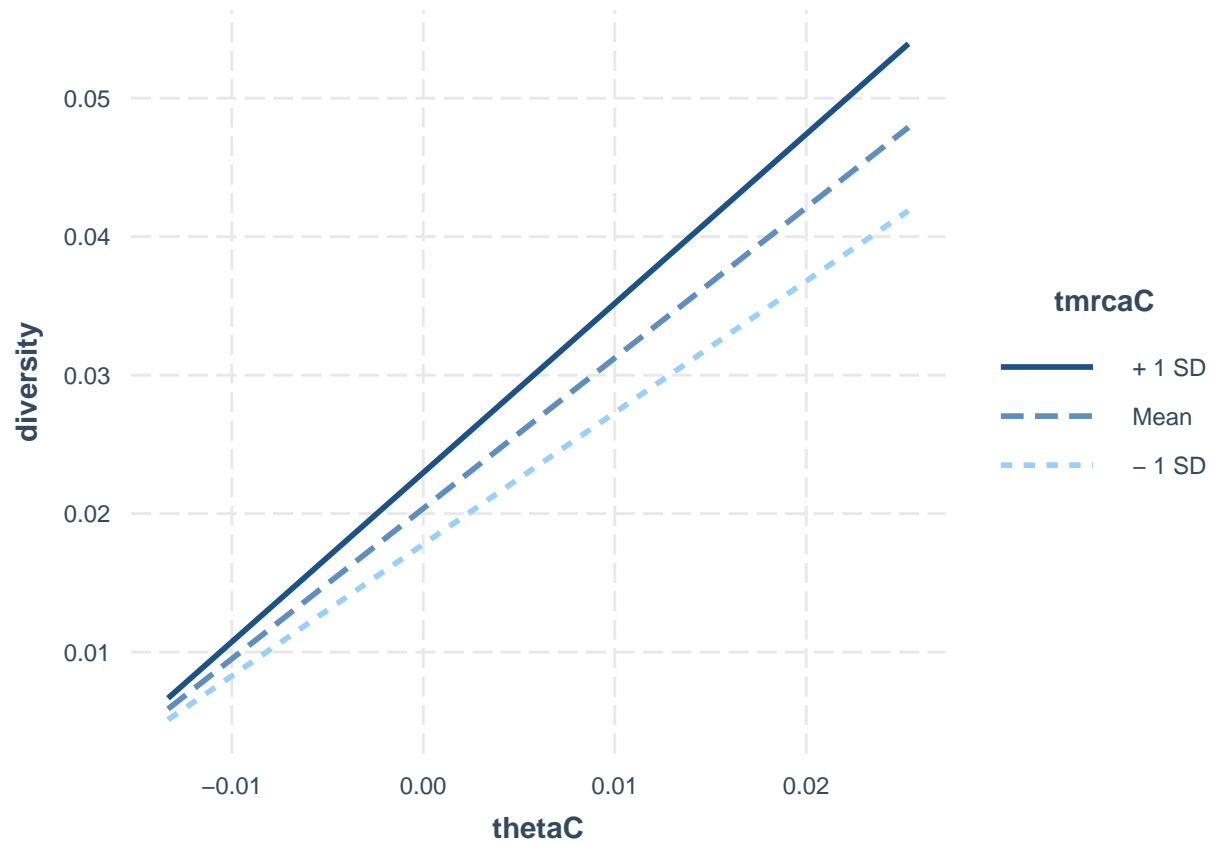
Histogram of resid(m.diversity.rep_9)



```
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
```

rep_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)

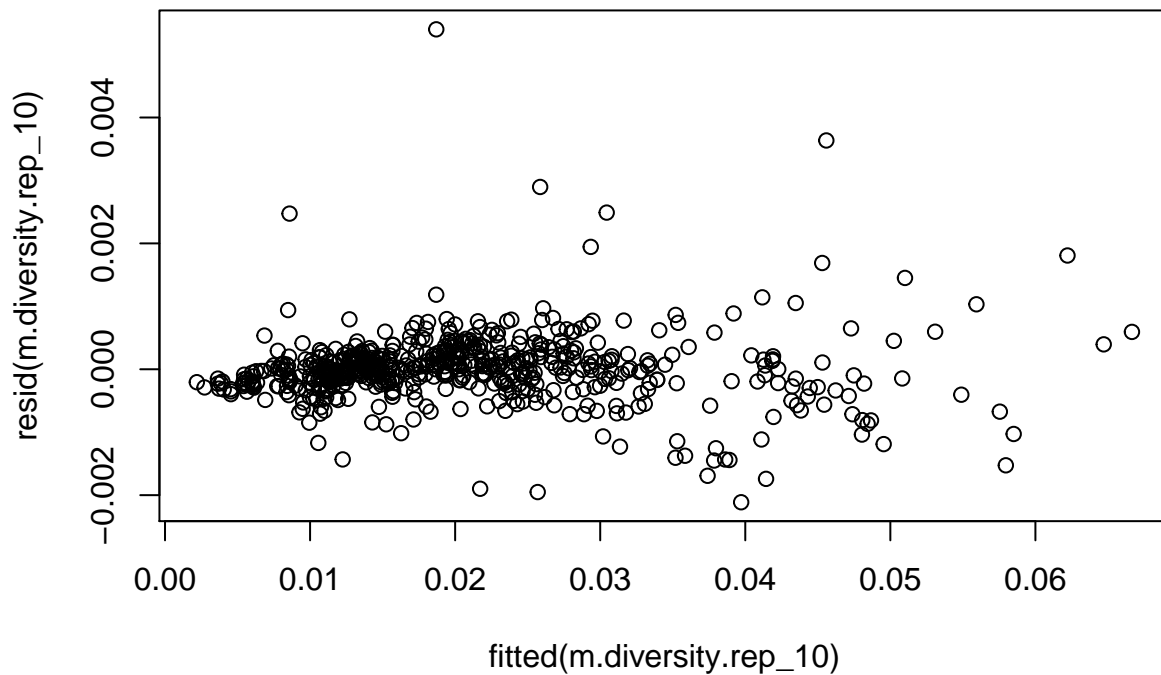
inf.lands.50k.rep_10 <- as.data.frame(cbind(pi.50k$avg, theta.50k$sample_mean, rho.50k$sample_mean, tmr
names(inf.lands.50k.rep_10) <- c("diversity", "theta", "rho", "tmrca")

# 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))
```



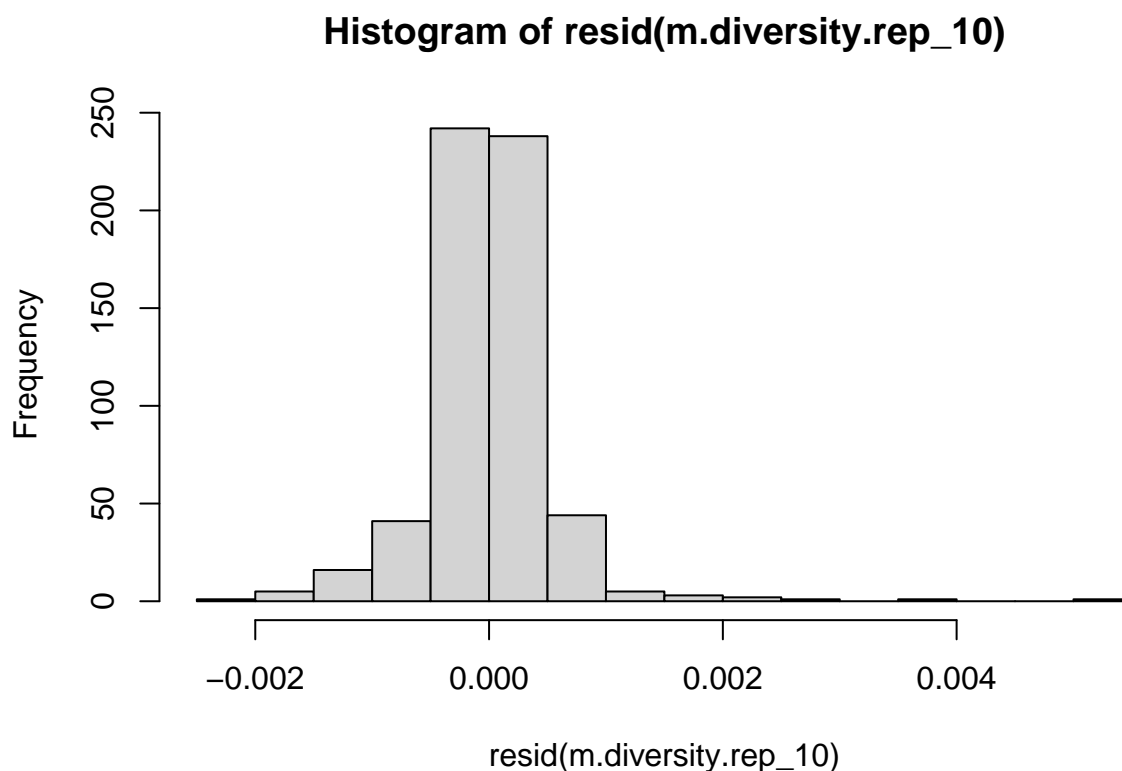
```
dwtest(m.diversity.rep_10)
```

```
##  
## 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))
```

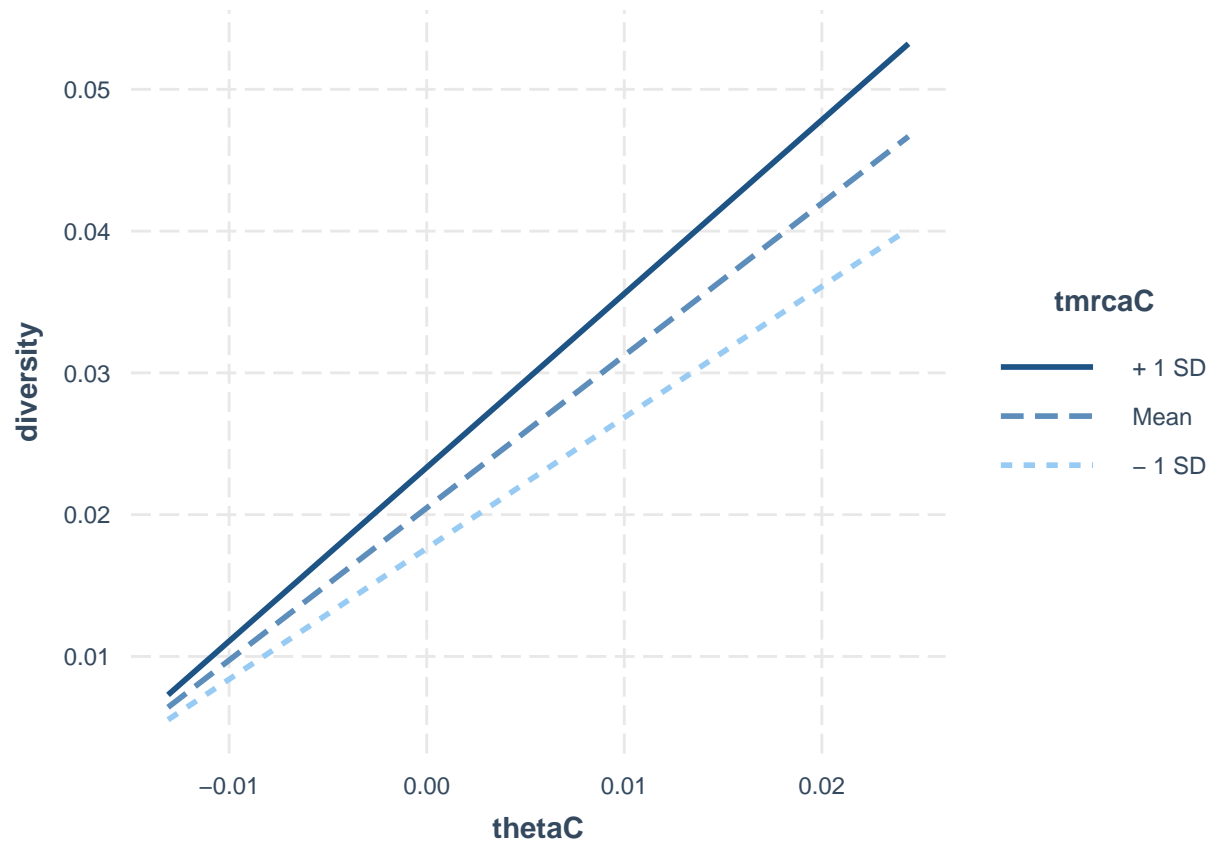


```
summary(m.diversity.rep_10)
```

```
##
## 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$VarExp[3]
r2.inf.50kb[2, 10] <- anova.diversity$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))
```

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(v
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
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 =

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,
```

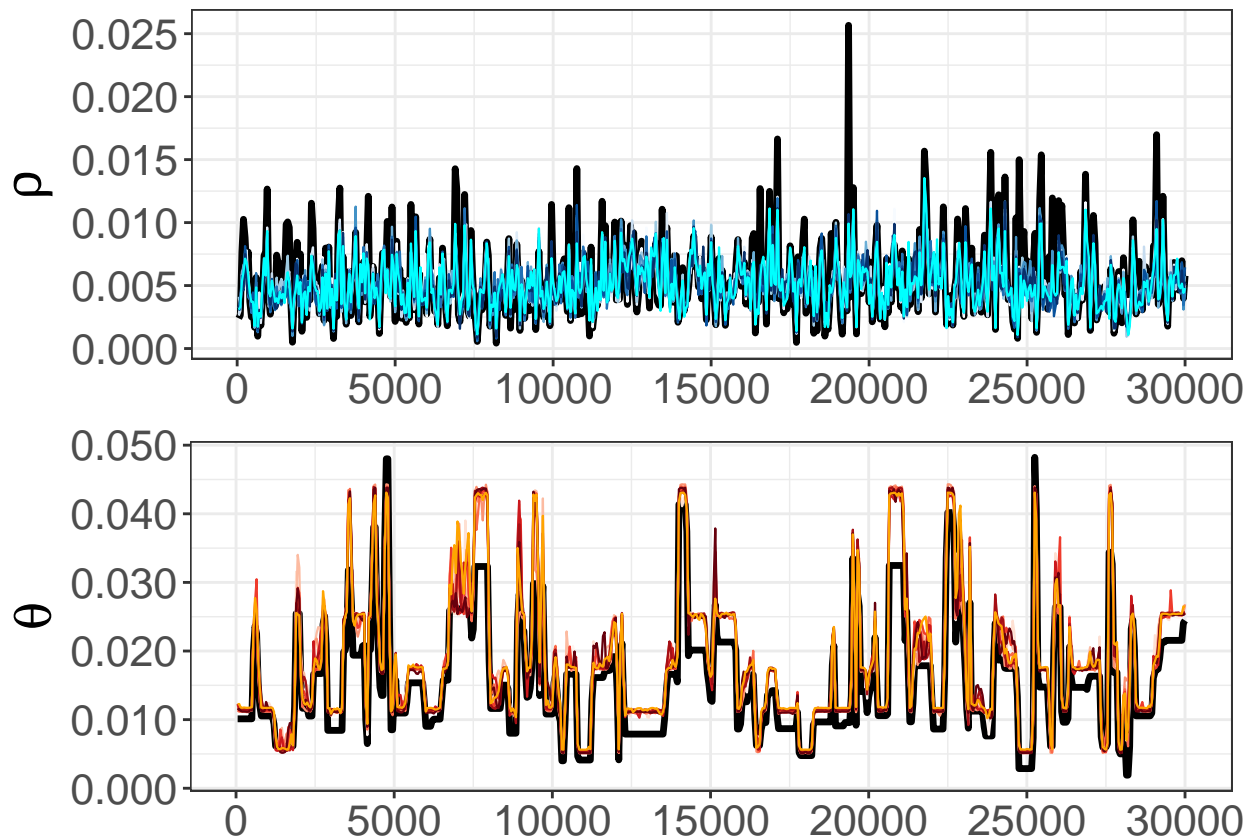
```

      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(si

plot_grid(rho.map.50kb, theta.map.50kb, nrow = 2, ncol = 1)

```



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")
```

rep_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")
```

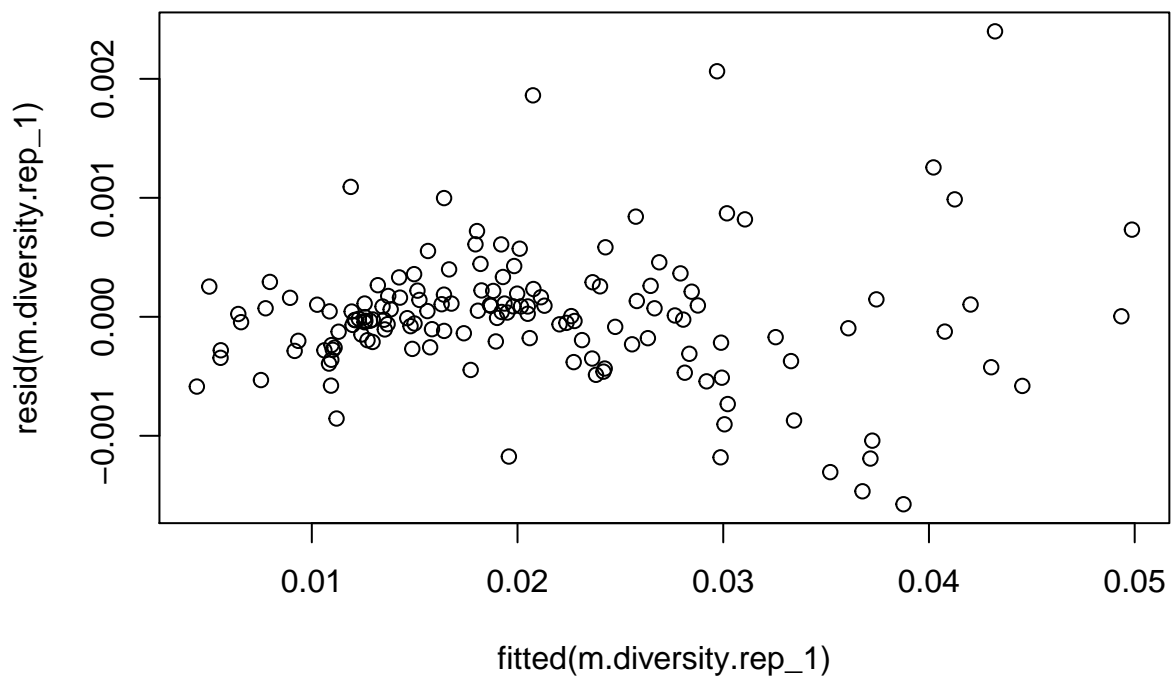
centering

```
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)
```

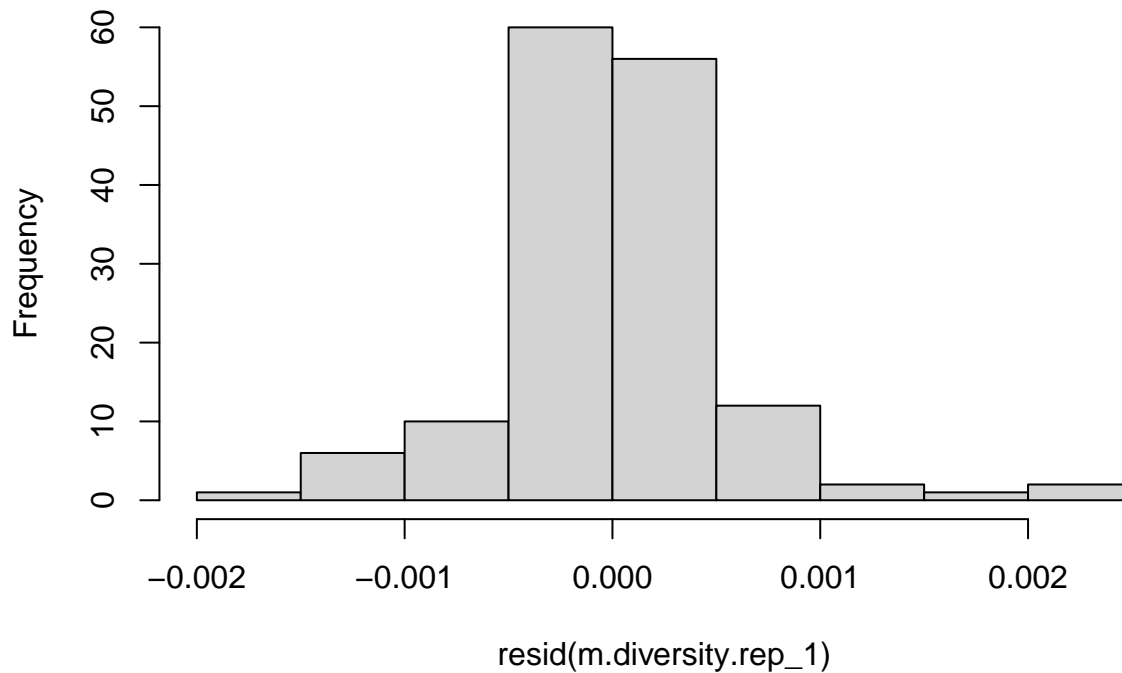
```
##
## Durbin-Watson test
##
## data:  m.diversity.rep_1
## DW = 1.8429, p-value = 0.1407
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##
## Harrison-McCabe test
##
## data:  m.diversity.rep_1
## HMC = 0.49224, p-value = 0.443
```

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

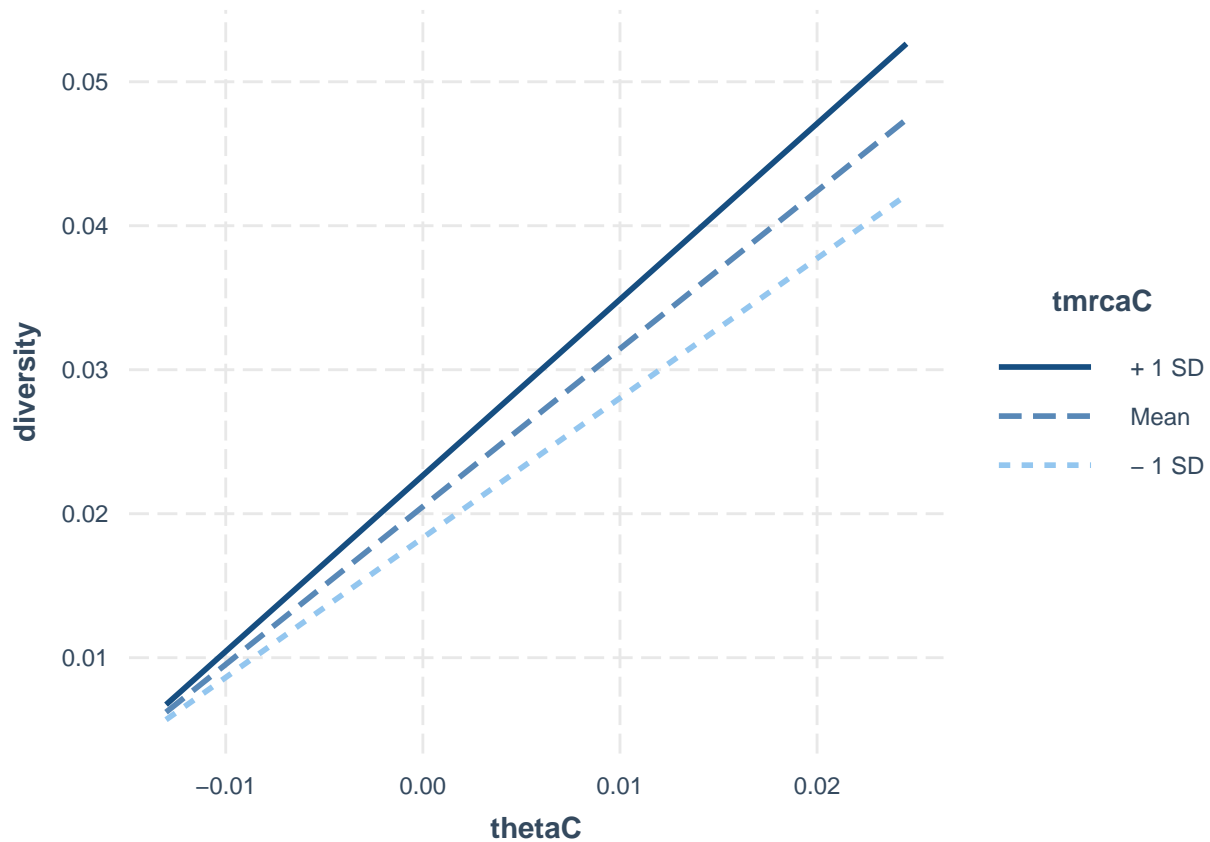
Histogram of resid(m.diversity.rep_1)



```
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
```

rep_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)

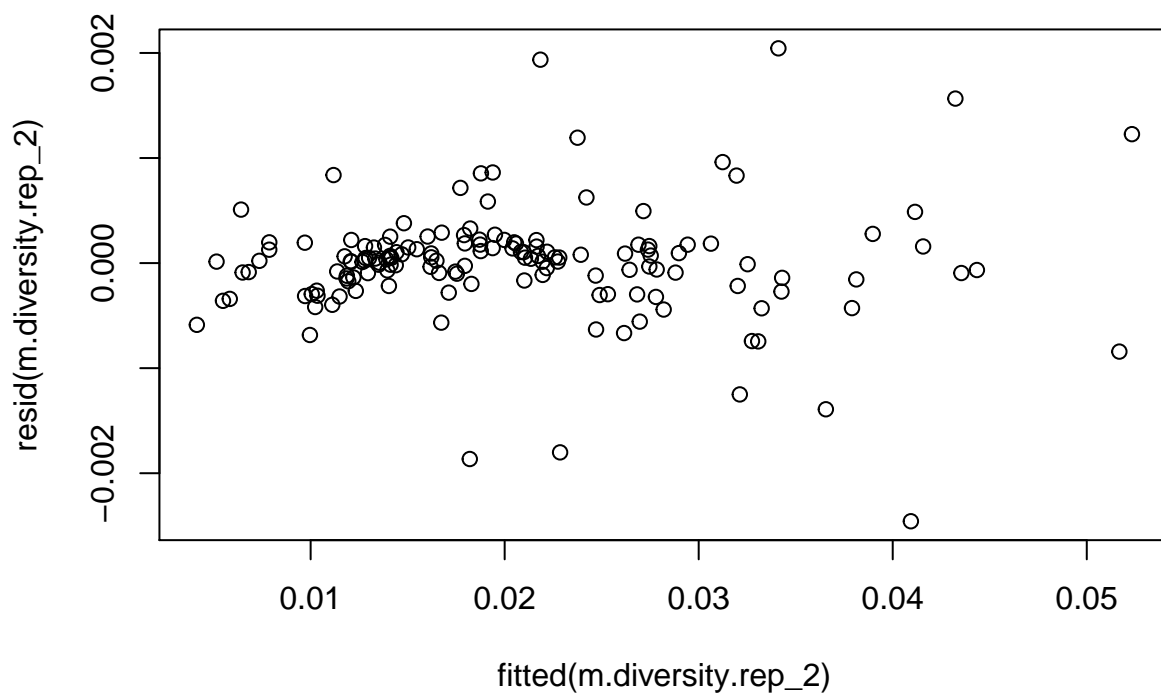
inf.lands.200k.rep_2 <- as.data.frame(cbind(pi.200k$avg, theta.200k$sample_mean, rho.200k$sample_mean, tmrca.200k$avg))
names(inf.lands.200k.rep_2) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

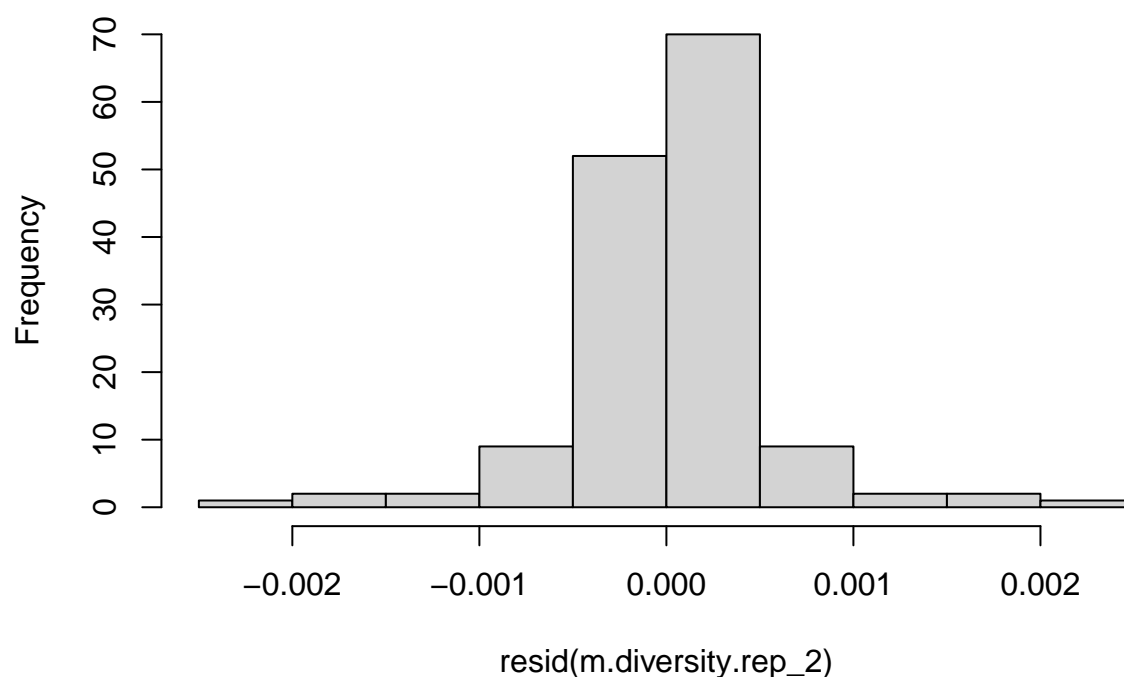
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_2  
## DW = 1.7156, p-value = 0.03159  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_2  
## HMC = 0.50531, p-value = 0.557
```

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

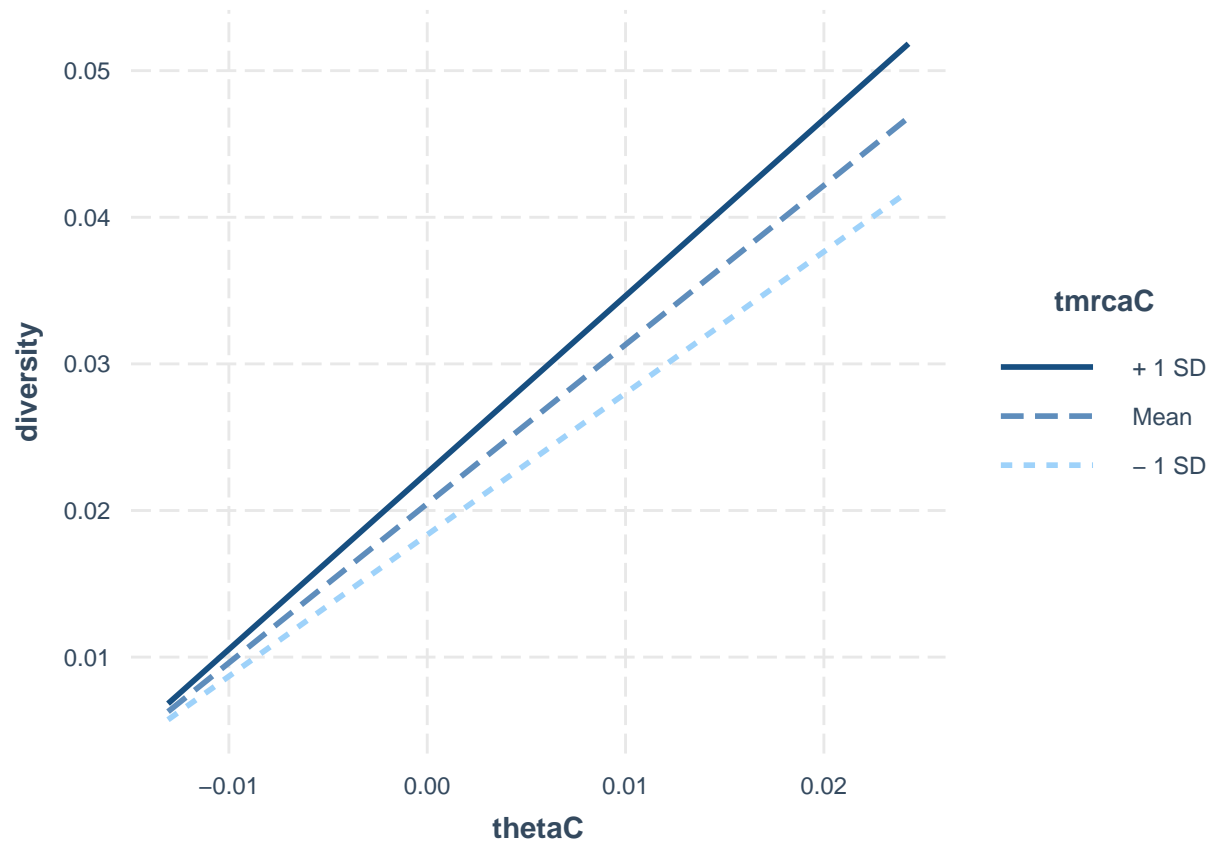
Histogram of resid(m.diversity.rep_2)



```
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
```

rep_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)

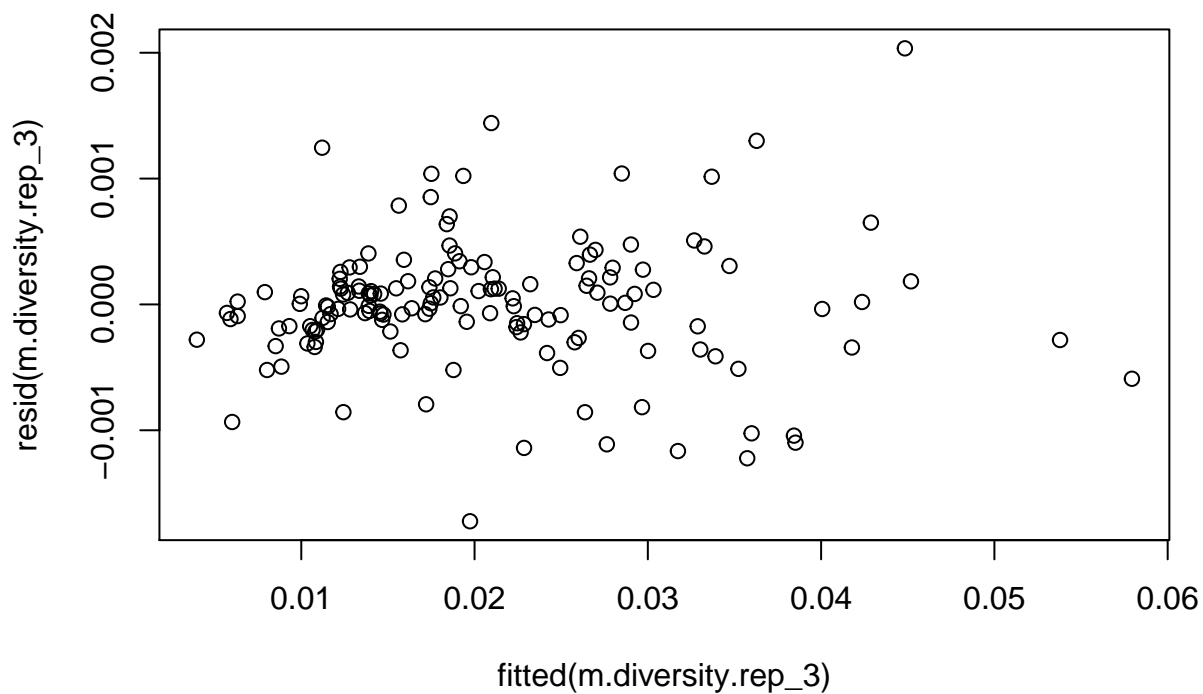
inf.lands.200k.rep_3 <- as.data.frame(cbind(pi.200k$avg, theta.200k$sample_mean, rho.200k$sample_mean, tmrca.200k$avg))
names(inf.lands.200k.rep_3) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

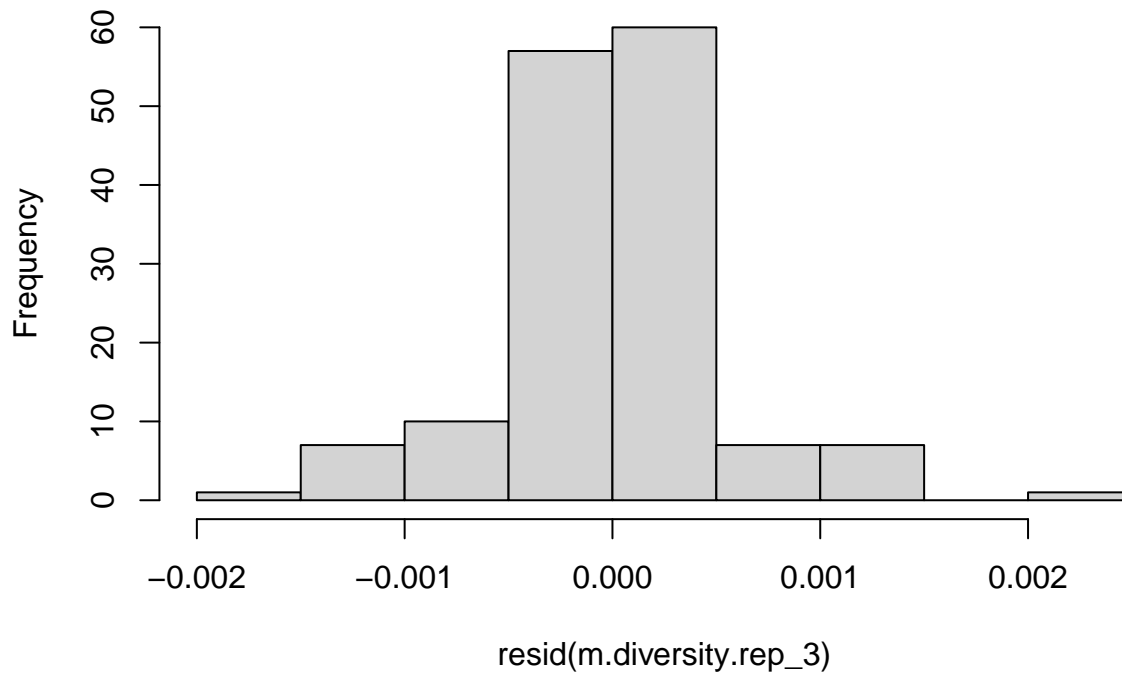
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_3  
## DW = 1.7271, p-value = 0.03626  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_3  
## HMC = 0.49269, p-value = 0.466
```

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

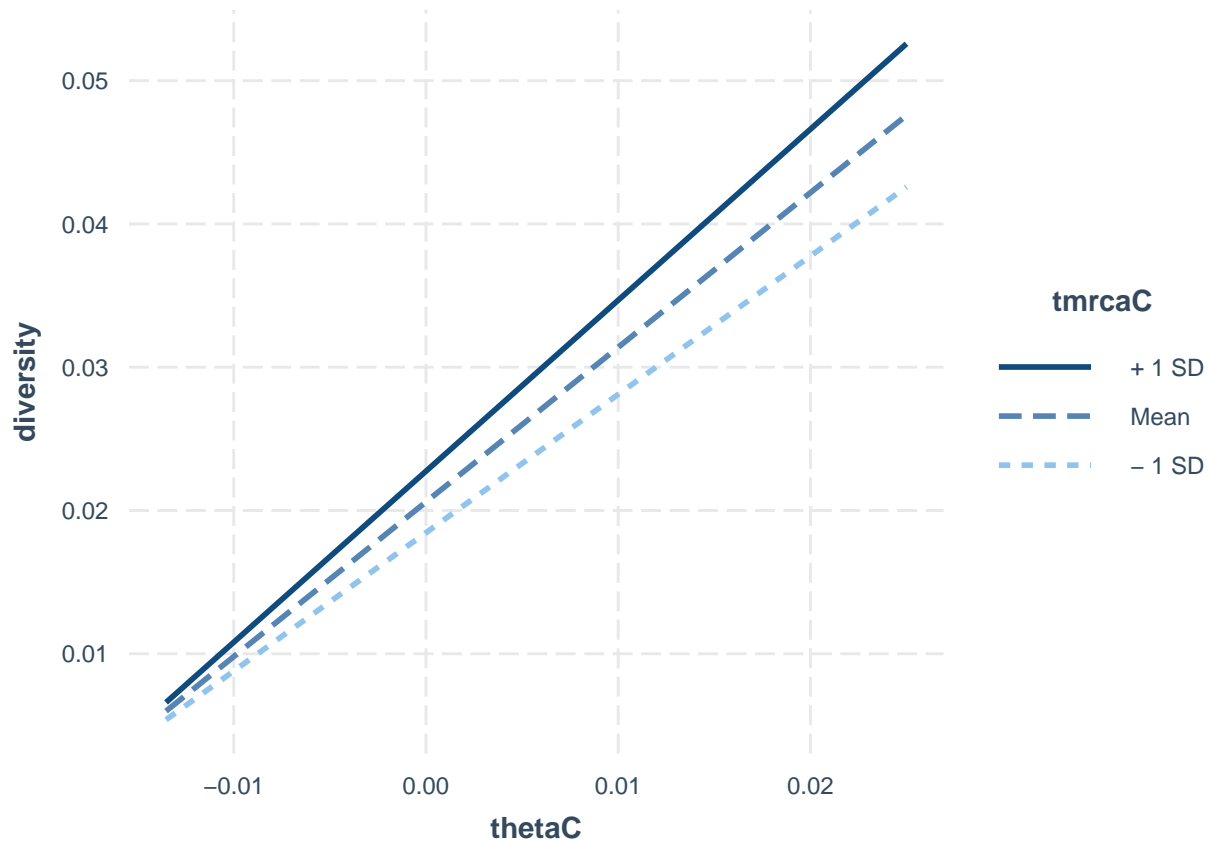

Histogram of resid(m.diversity.rep_3)



```
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
```

rep_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)

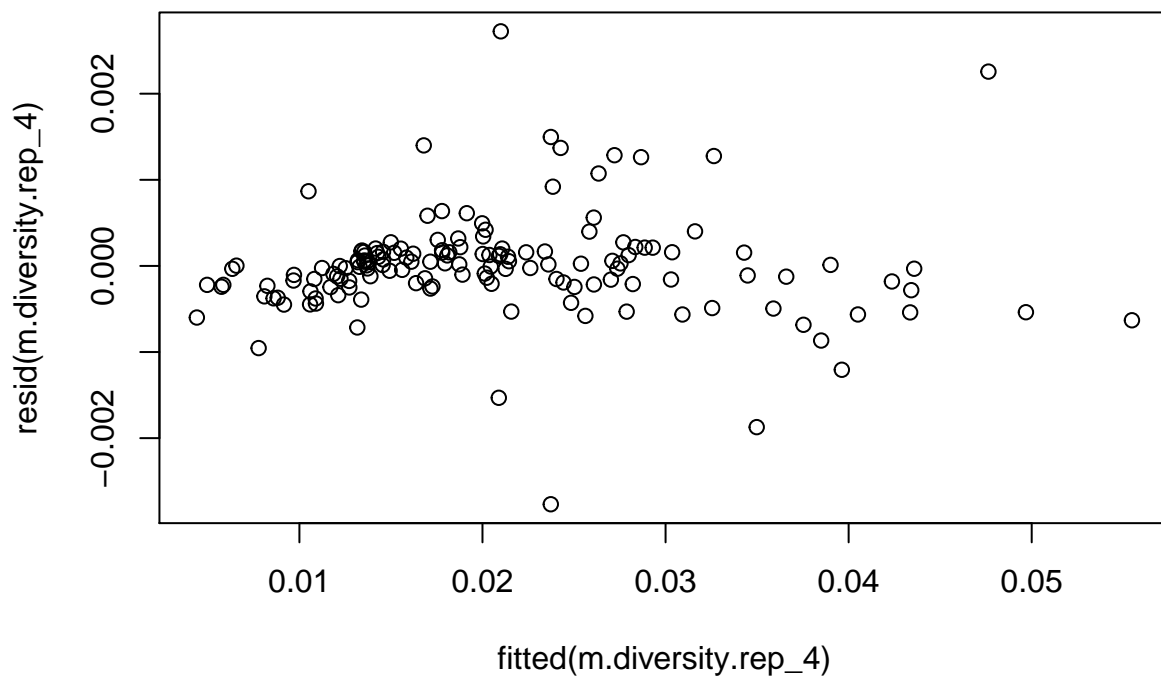
inf.lands.200k.rep_4 <- as.data.frame(cbind(pi.200k$avg, theta.200k$sample_mean, rho.200k$sample_mean,
names(inf.lands.200k.rep_4) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

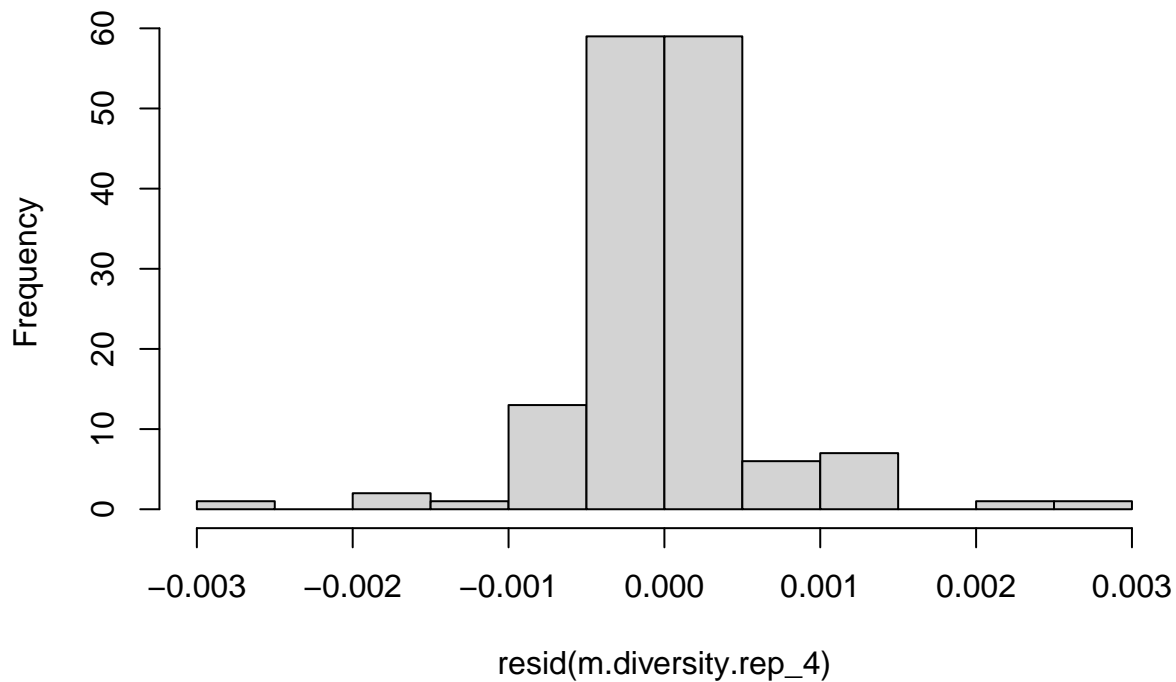
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_4  
## DW = 1.6283, p-value = 0.00823  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_4  
## HMC = 0.54628, p-value = 0.813
```

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

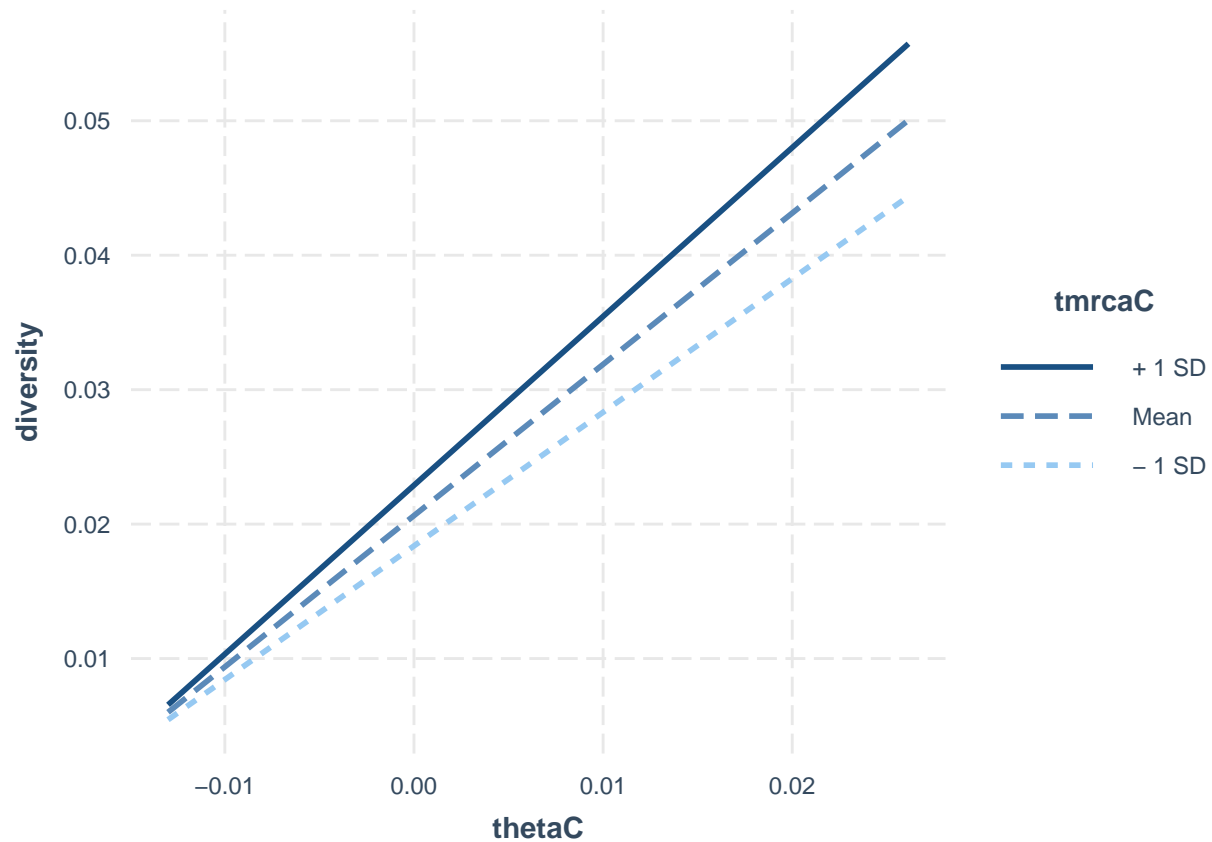
Histogram of resid(m.diversity.rep_4)



```
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
```

rep_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)

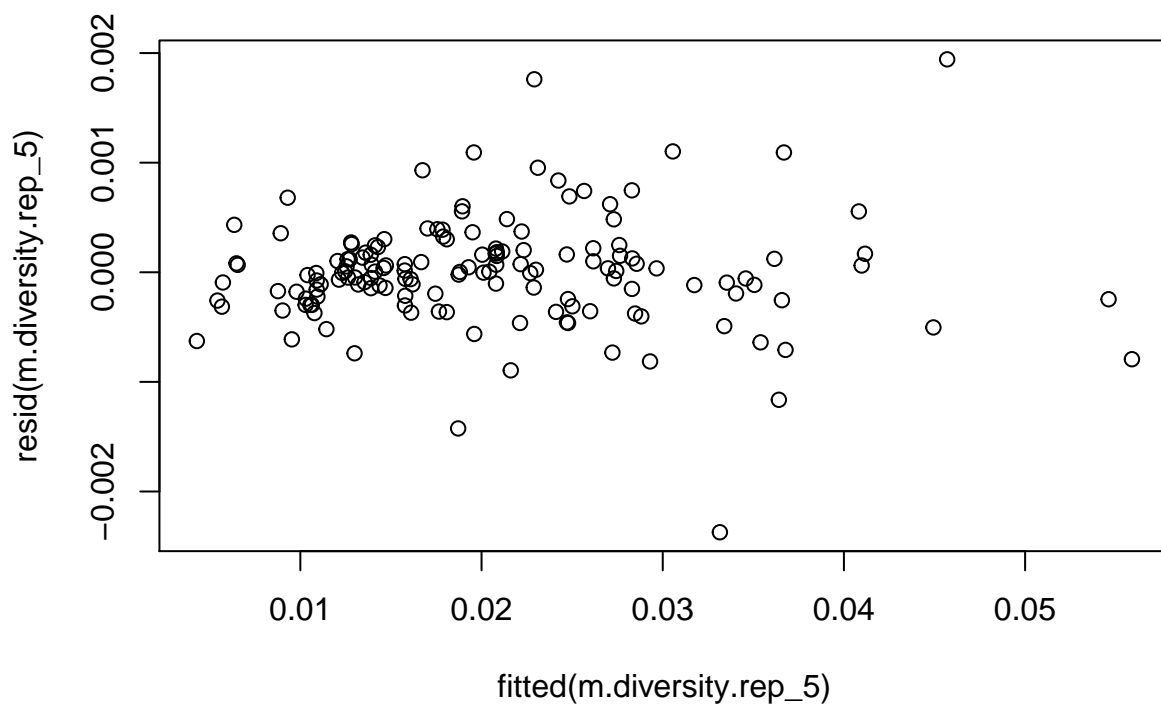
inf.lands.200k.rep_5 <- as.data.frame(cbind(pi.200k$avg, theta.200k$sample_mean, rho.200k$sample_mean, tmrca.200k$avg))
names(inf.lands.200k.rep_5) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

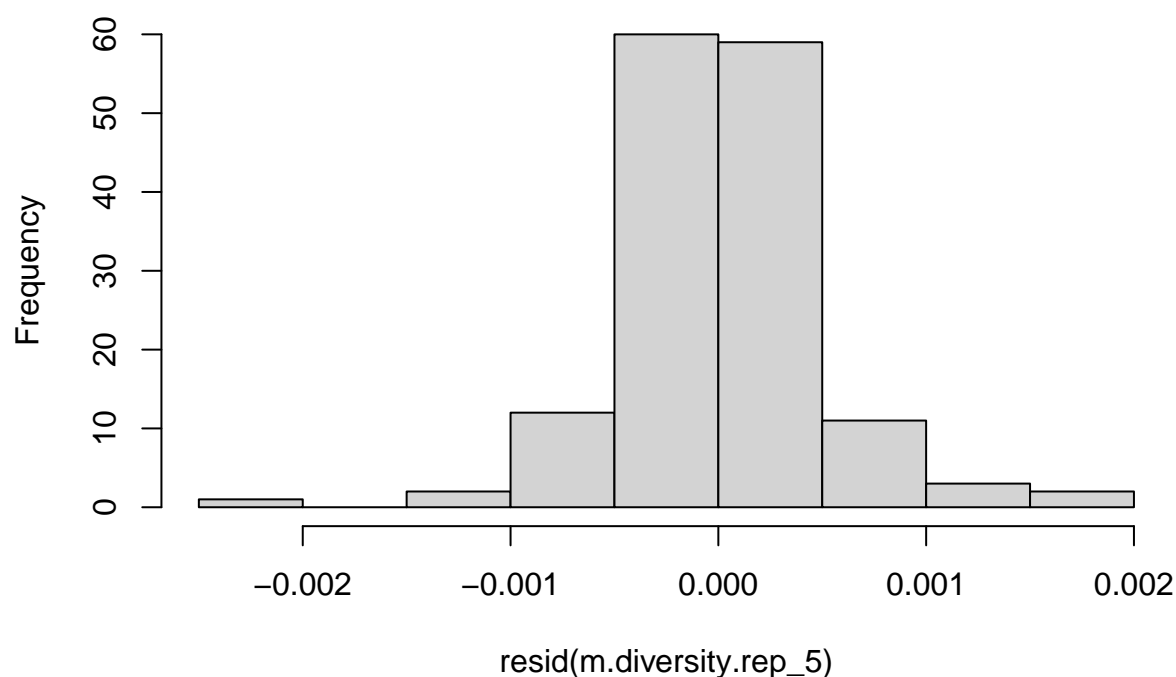
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_5  
## DW = 1.473, p-value = 0.0003904  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_5  
## HMC = 0.42356, p-value = 0.097
```

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

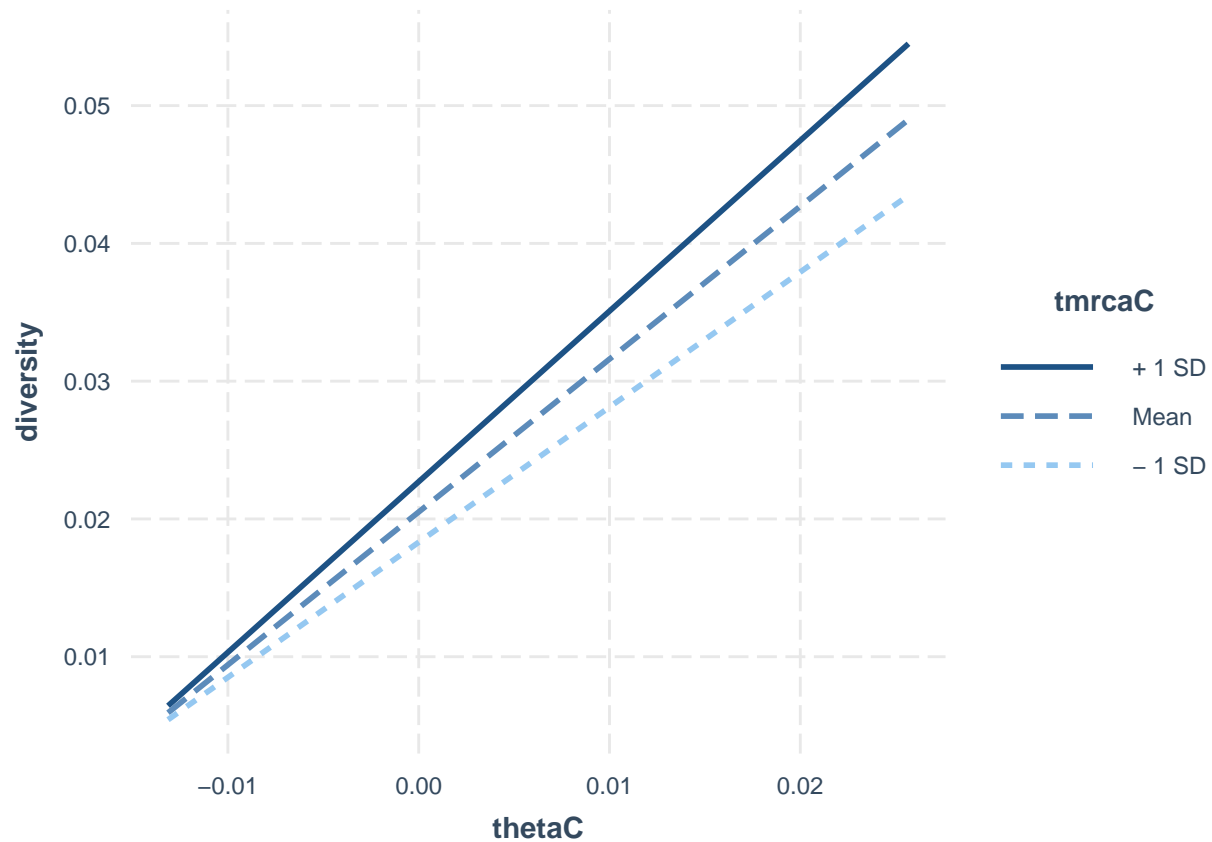
Histogram of resid(m.diversity.rep_5)



```
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$VarExp[5]
r2.inf.200kb[2, 5] <- anova.diversity$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
```

rep_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)

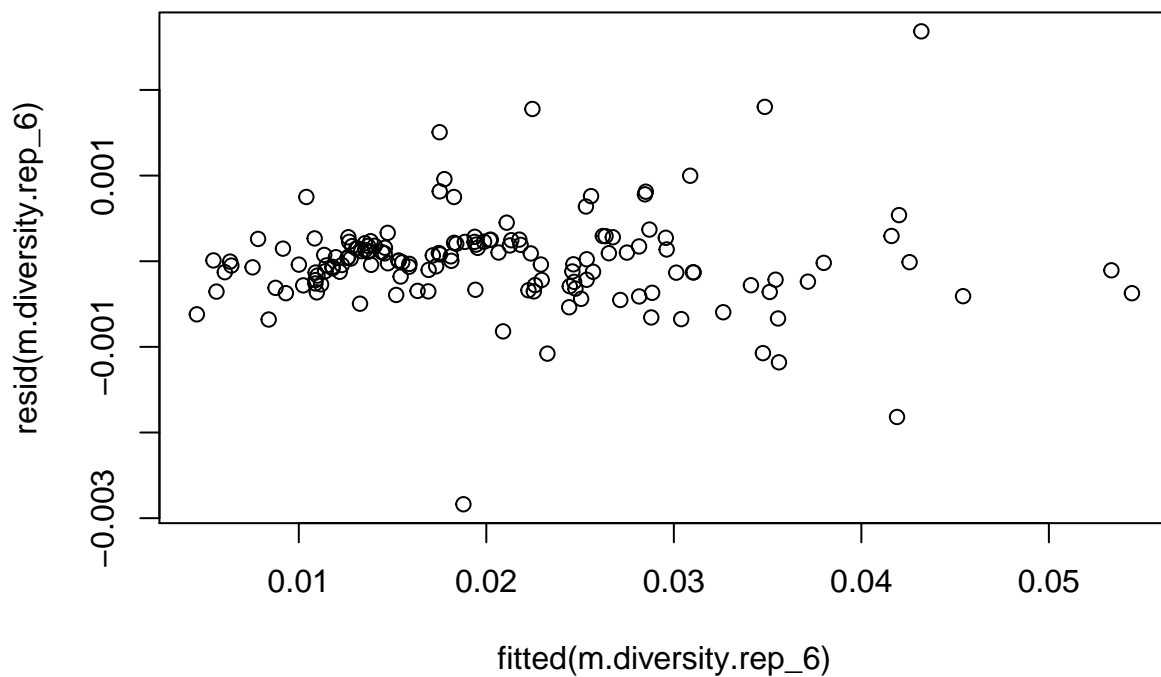
inf.lands.200k.rep_6 <- as.data.frame(cbind(pi.200k$avg, theta.200k$sample_mean, rho.200k$sample_mean, tmrca.200k$avg))
names(inf.lands.200k.rep_6) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

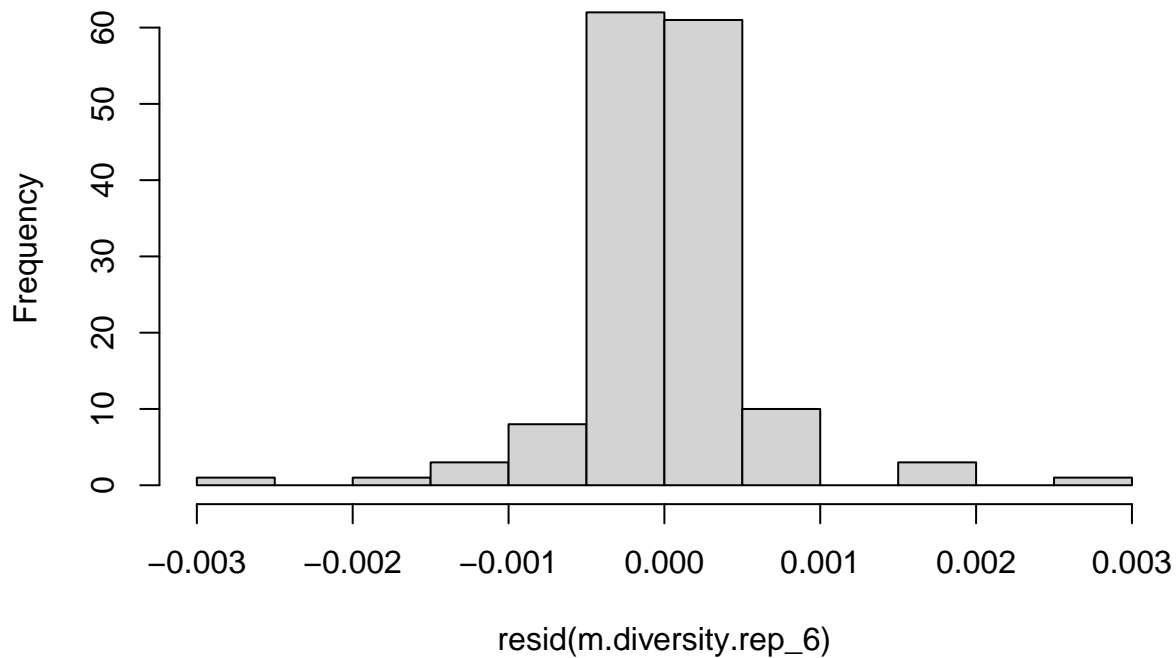
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_6  
## DW = 1.6828, p-value = 0.01928  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_6  
## HMC = 0.48734, p-value = 0.417
```

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

Histogram of resid(m.diversity.rep_6)

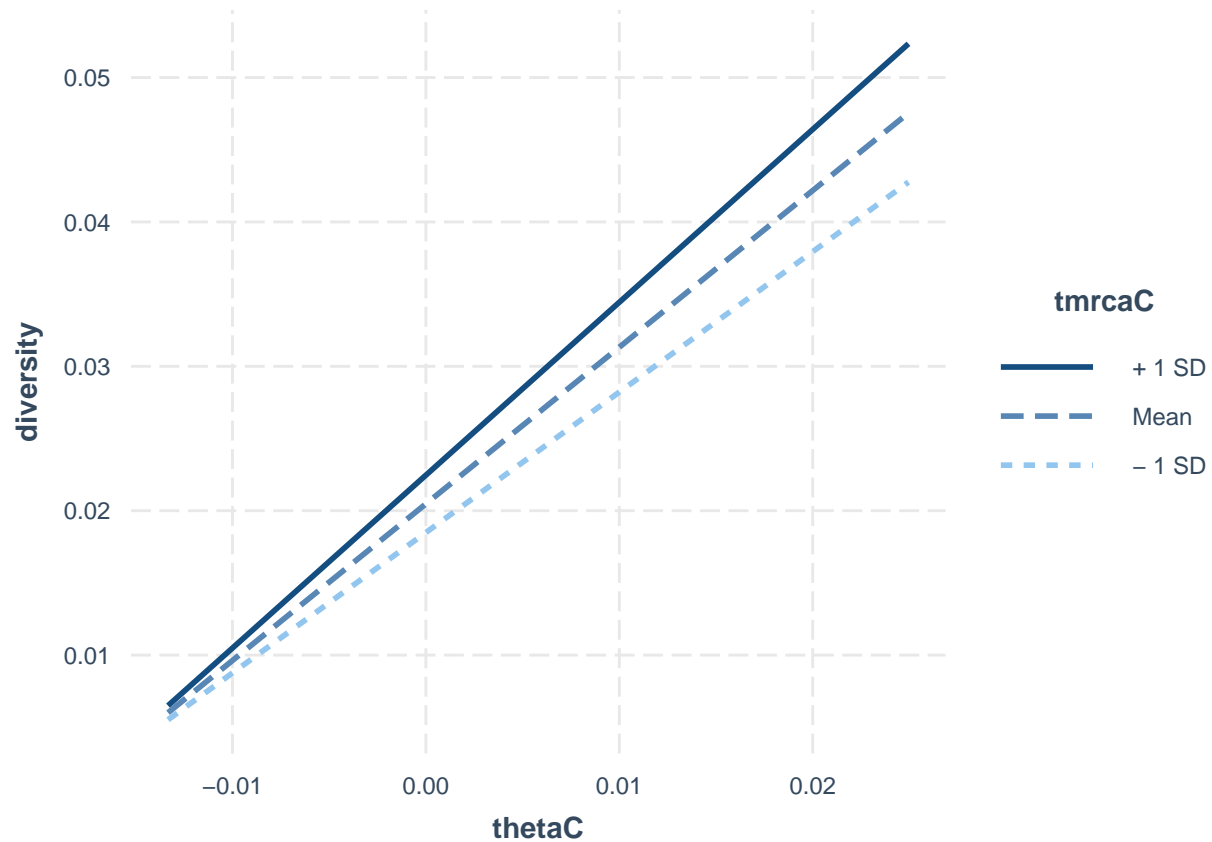


```
summary(m.diversity.rep_6)
```

```
##
## 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$VarExp[3] + anova.diversity$VarExp[4] + anova.diversity$VarExp[5]) / anova.diversity$VarExp[6]
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
```

rep_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)

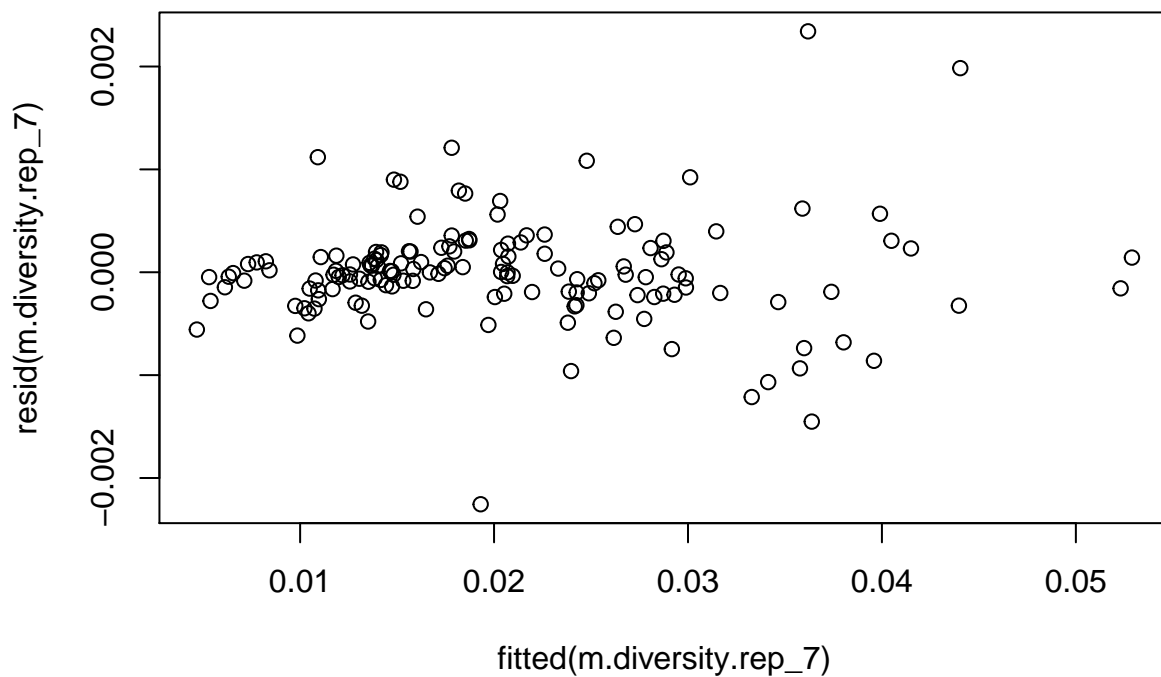
inf.lands.200k.rep_7 <- as.data.frame(cbind(pi.200k$avg, theta.200k$sample_mean, rho.200k$sample_mean, tmrca.200k$avg))
names(inf.lands.200k.rep_7) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

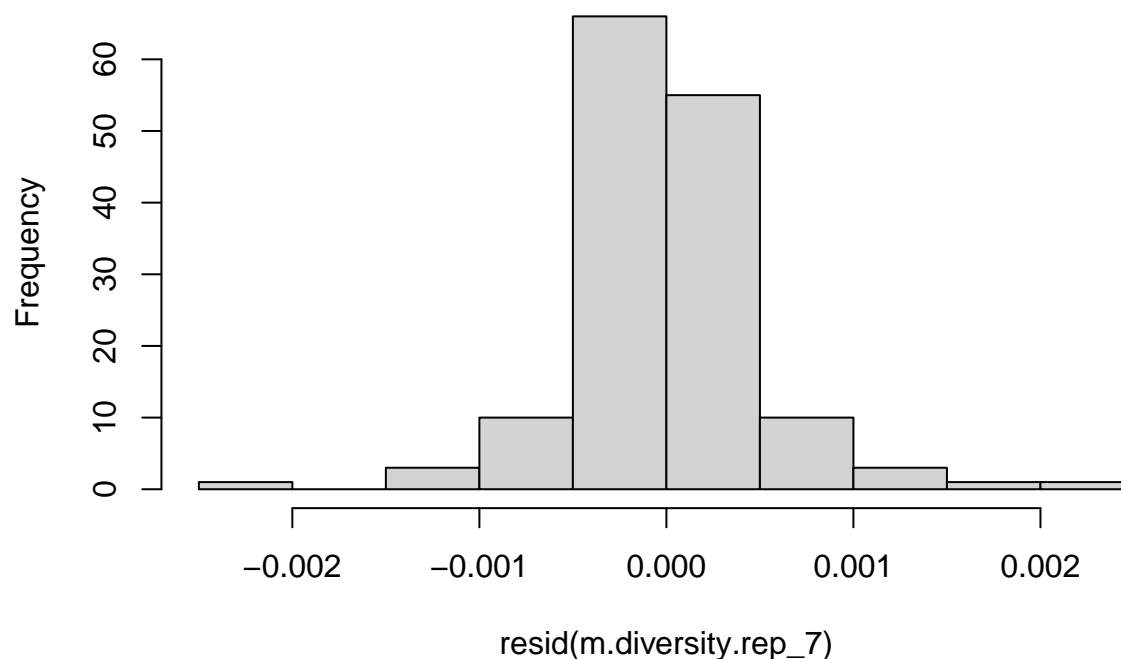
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_7  
## DW = 1.6673, p-value = 0.01553  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_7  
## HMC = 0.43605, p-value = 0.14
```

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

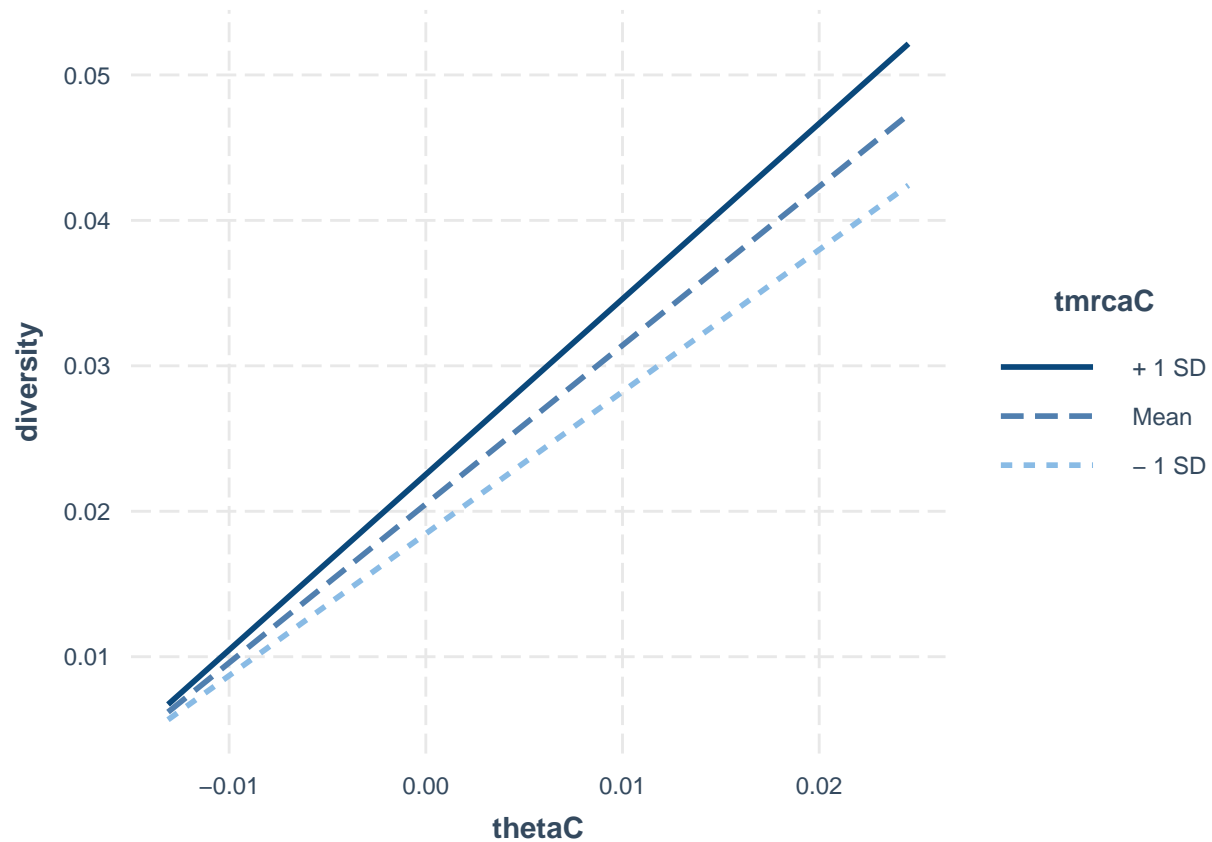
Histogram of resid(m.diversity.rep_7)



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

rep_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)

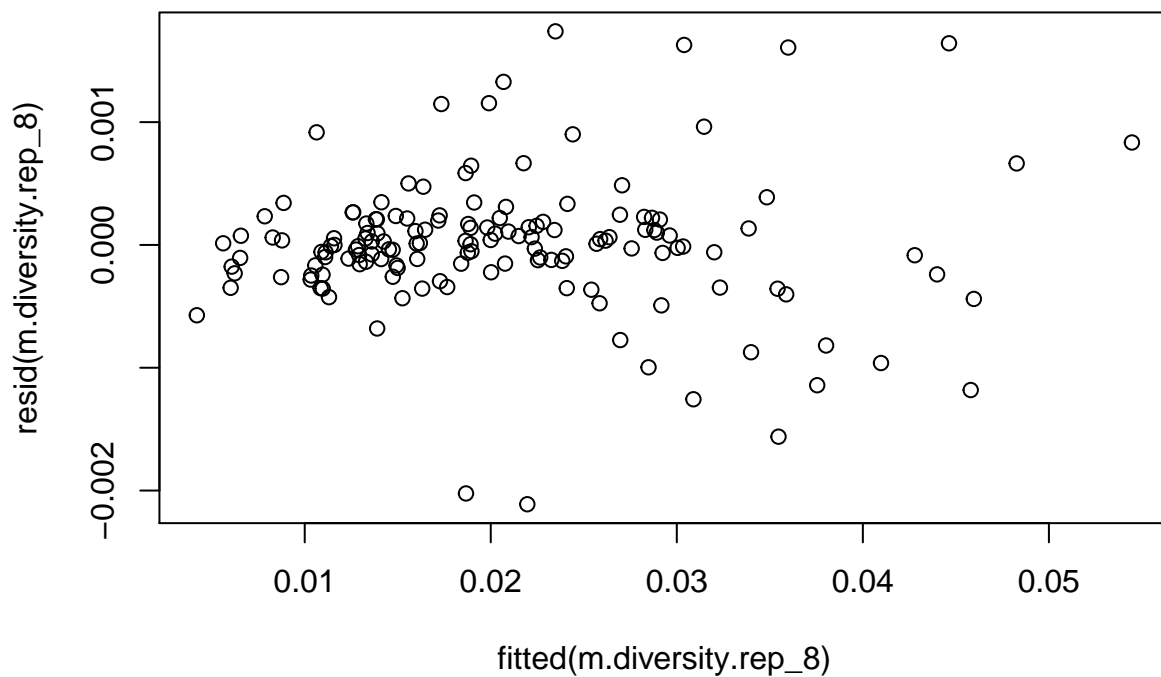
inf.lands.200k.rep_8 <- as.data.frame(cbind(pi.200k$avg, theta.200k$sample_mean, rho.200k$sample_mean, tmrca.200k$avg))
names(inf.lands.200k.rep_8) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

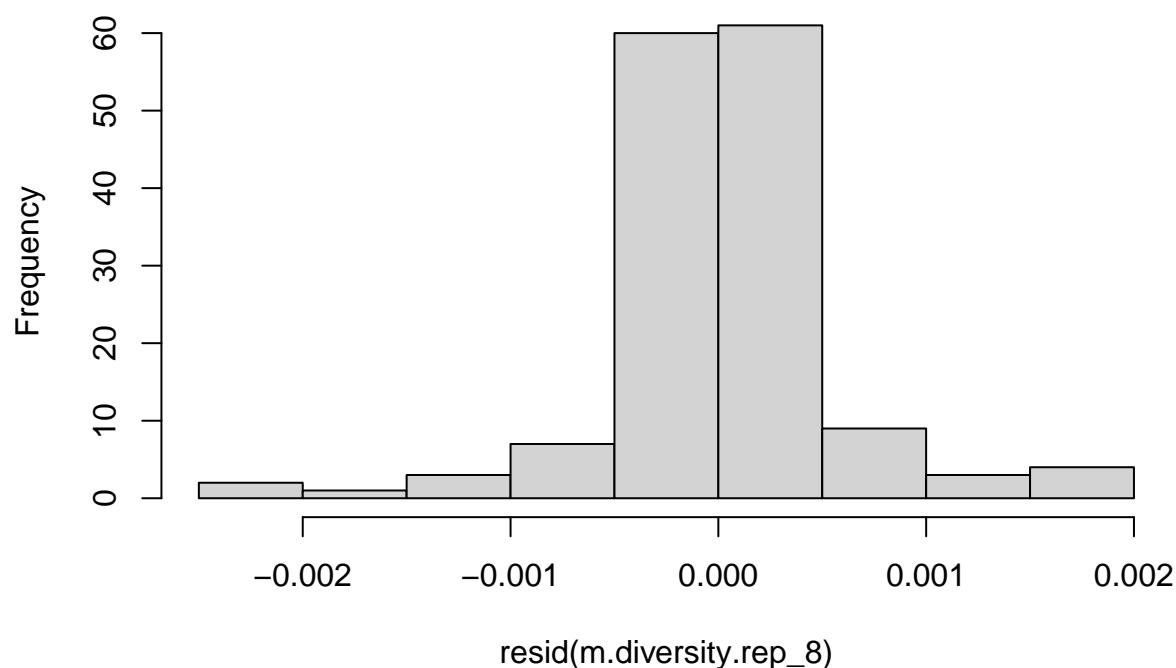
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_8  
## DW = 1.5909, p-value = 0.004238  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_8  
## HMC = 0.45552, p-value = 0.237
```

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

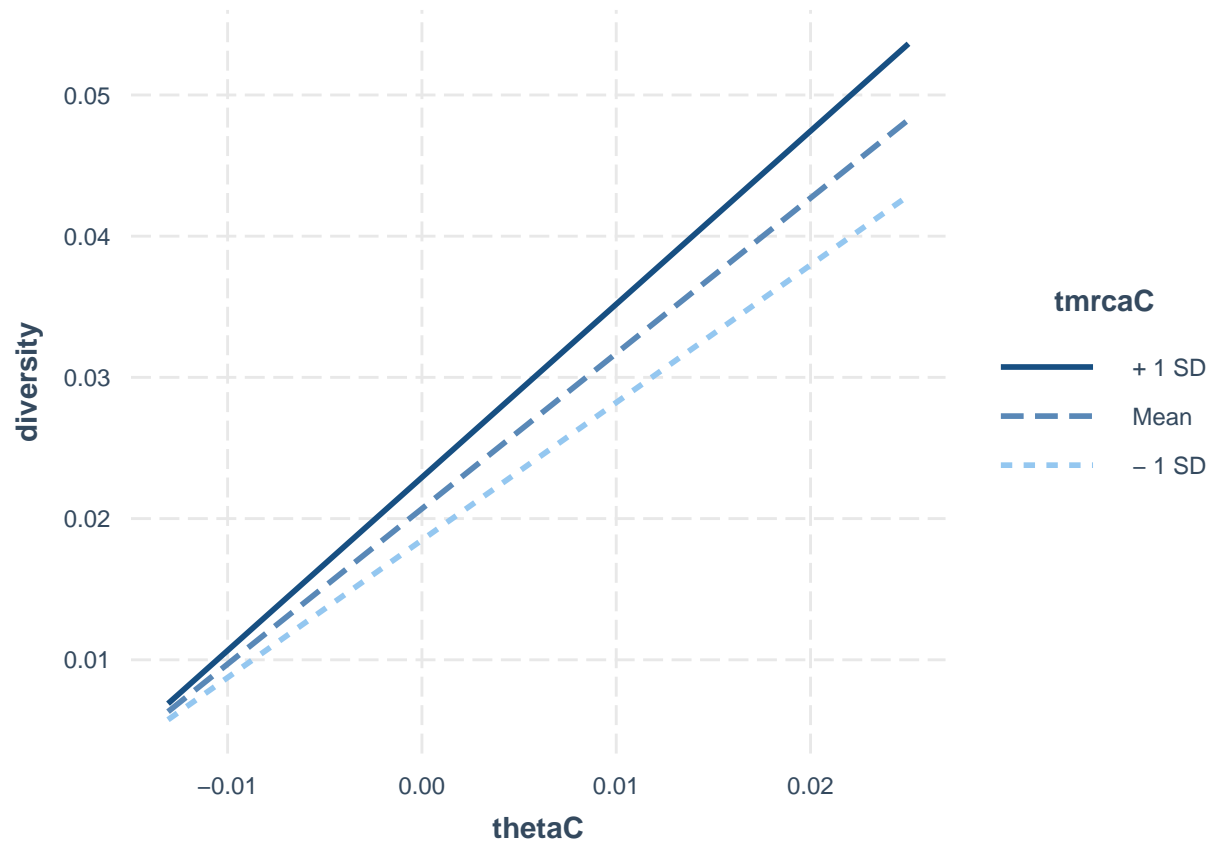
Histogram of resid(m.diversity.rep_8)



```
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$VarExp[1]
r2.inf.200kb[2, 8] <- anova.diversity$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
```

rep_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)

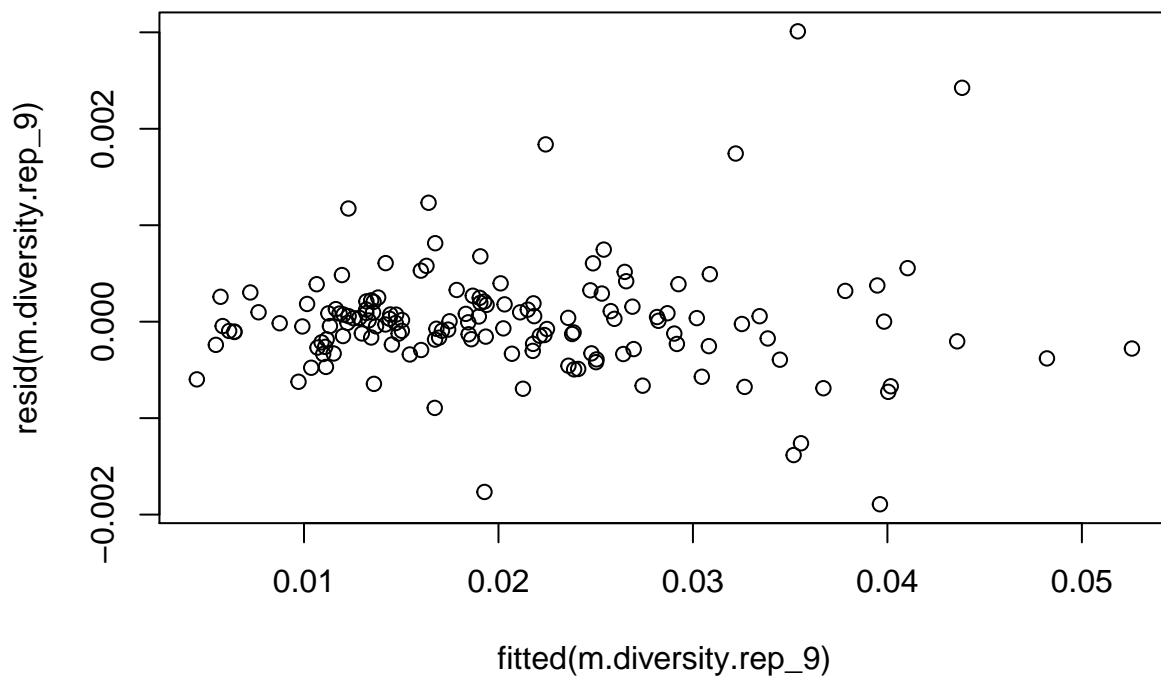
inf.lands.200k.rep_9 <- as.data.frame(cbind(pi.200k$avg, theta.200k$sample_mean, rho.200k$sample_mean, tmrca.200k$avg))
names(inf.lands.200k.rep_9) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

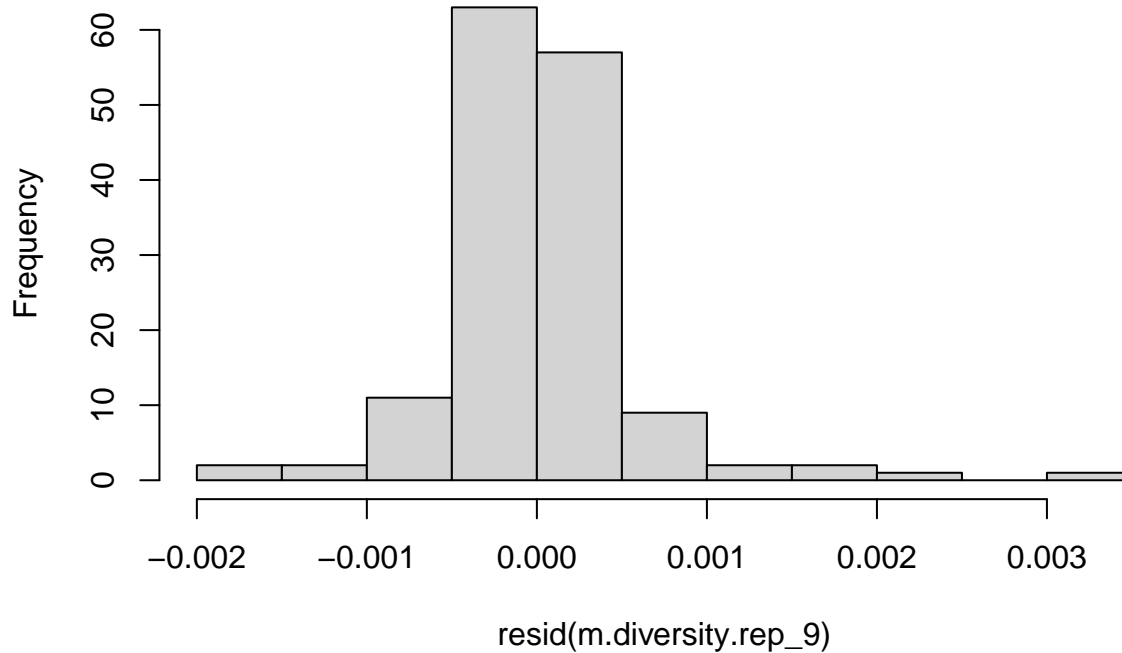
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_9  
## DW = 1.6772, p-value = 0.01787  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_9  
## HMC = 0.38369, p-value = 0.026
```

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

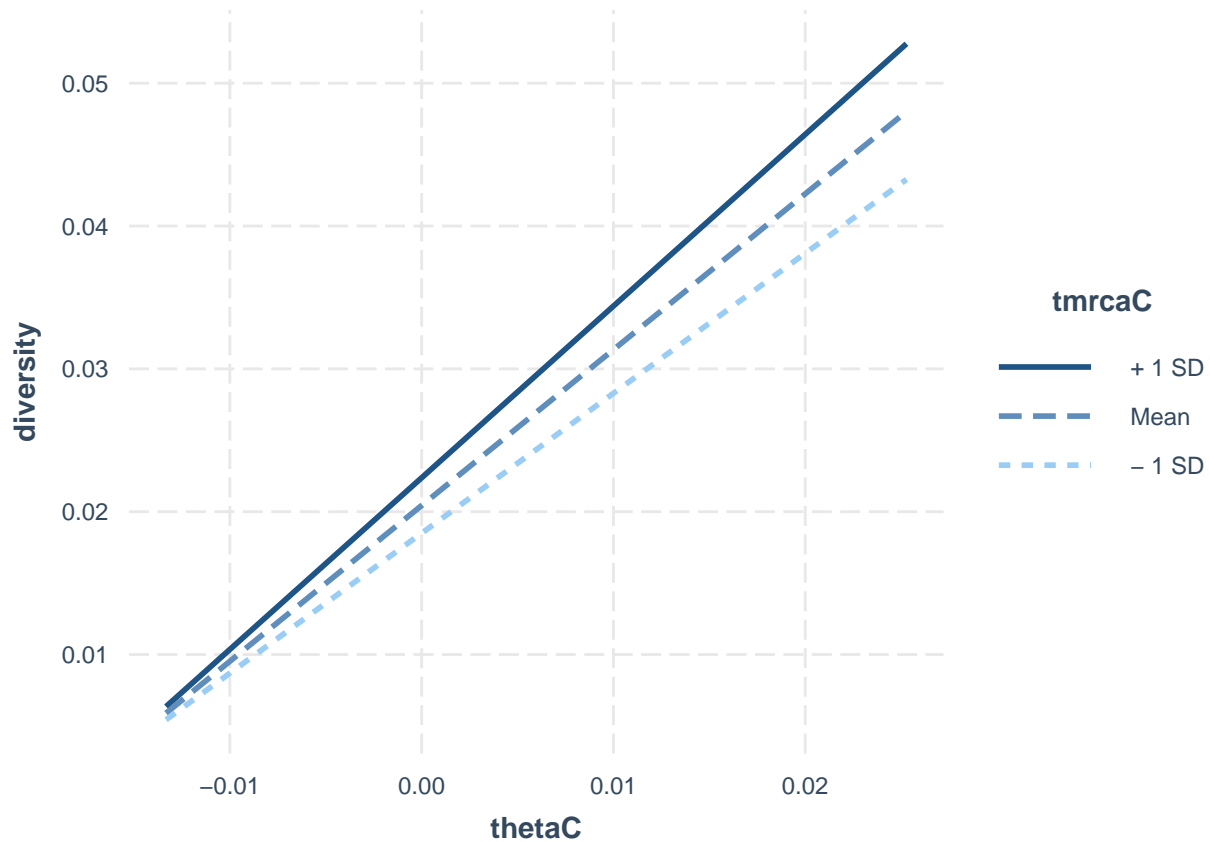
Histogram of resid(m.diversity.rep_9)



```
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
```

rep_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)

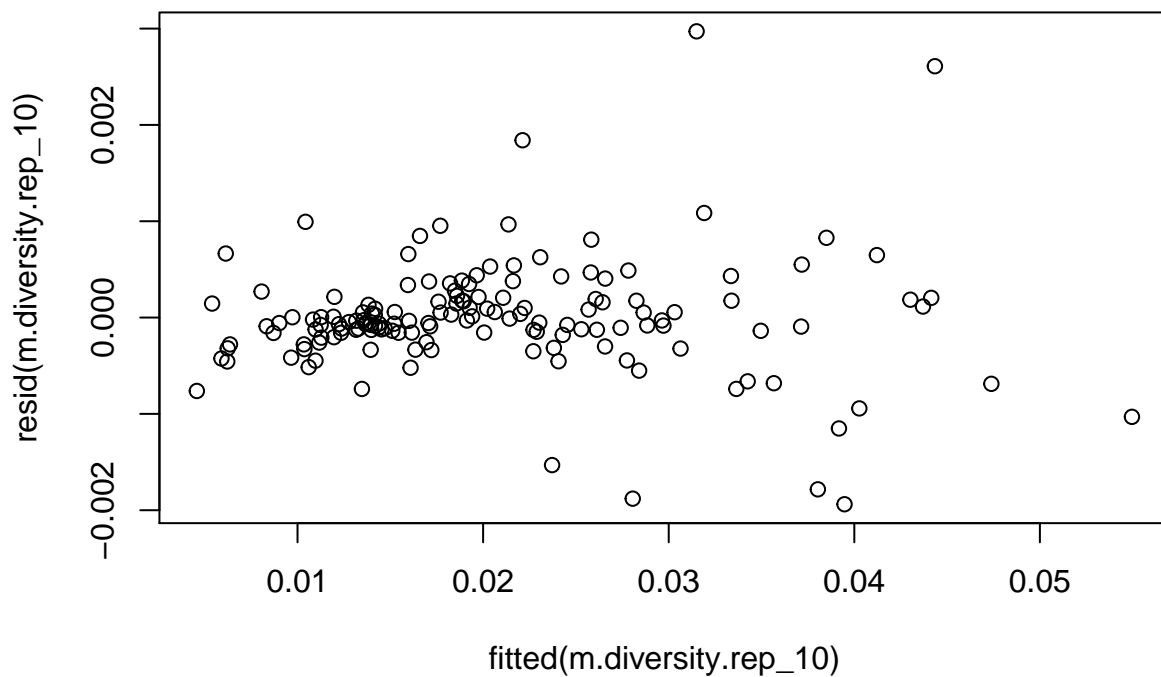
inf.lands.200k.rep_10 <- as.data.frame(cbind(pi.200k$avg, theta.200k$sample_mean, rho.200k$sample_mean,
names(inf.lands.200k.rep_10) <- c("diversity", "theta", "rho", "tmrca")

# 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_10)

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



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

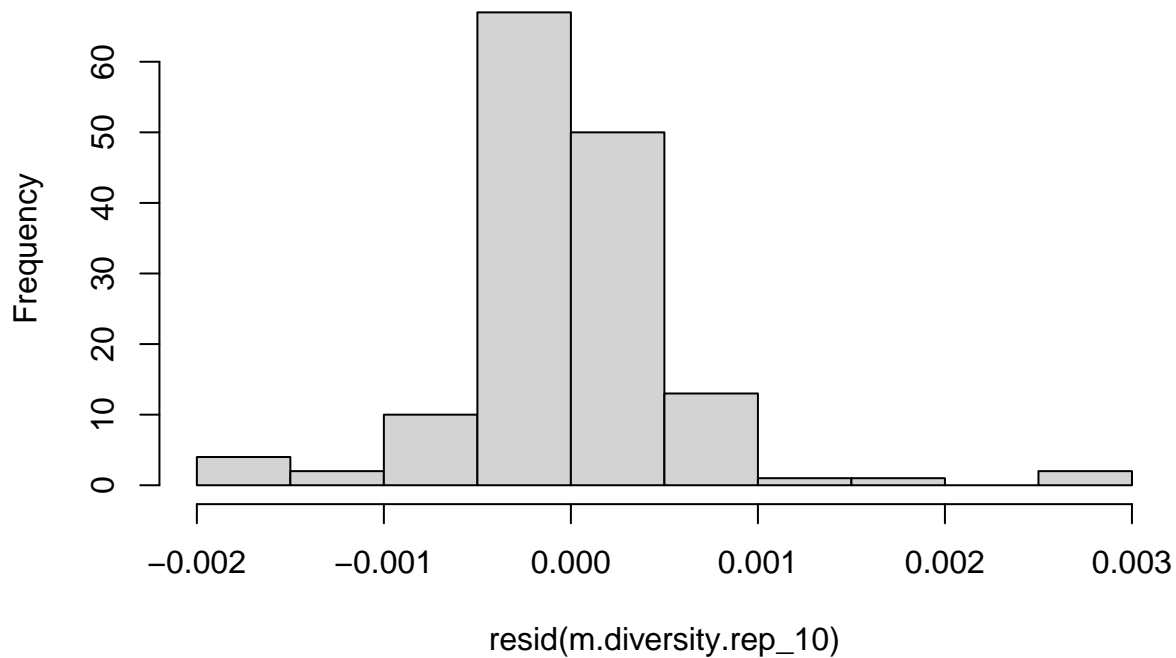
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_10  
## DW = 1.777, p-value = 0.06912  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_10  
## HMC = 0.6193, p-value = 0.978
```

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

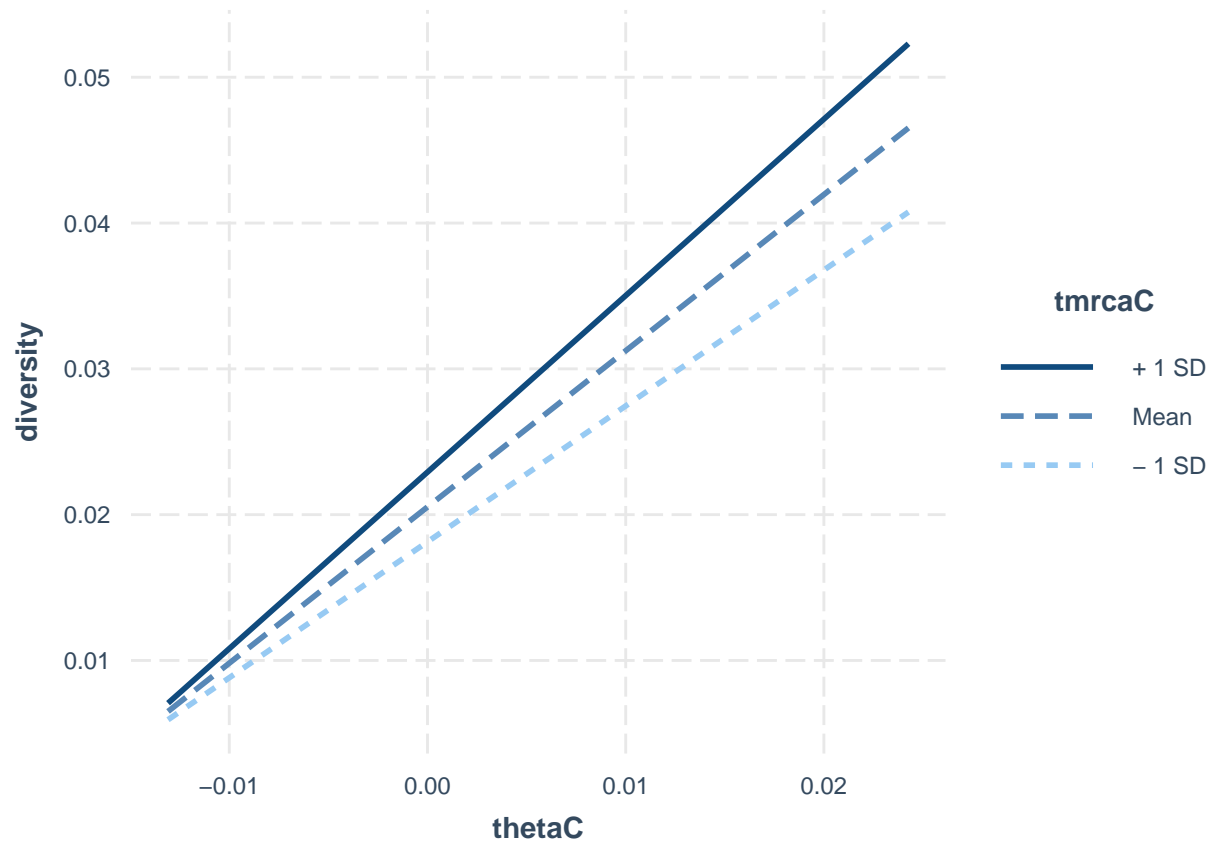
Histogram of resid(m.diversity.rep_10)



```
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))
```

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 * 50, 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))
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,
```

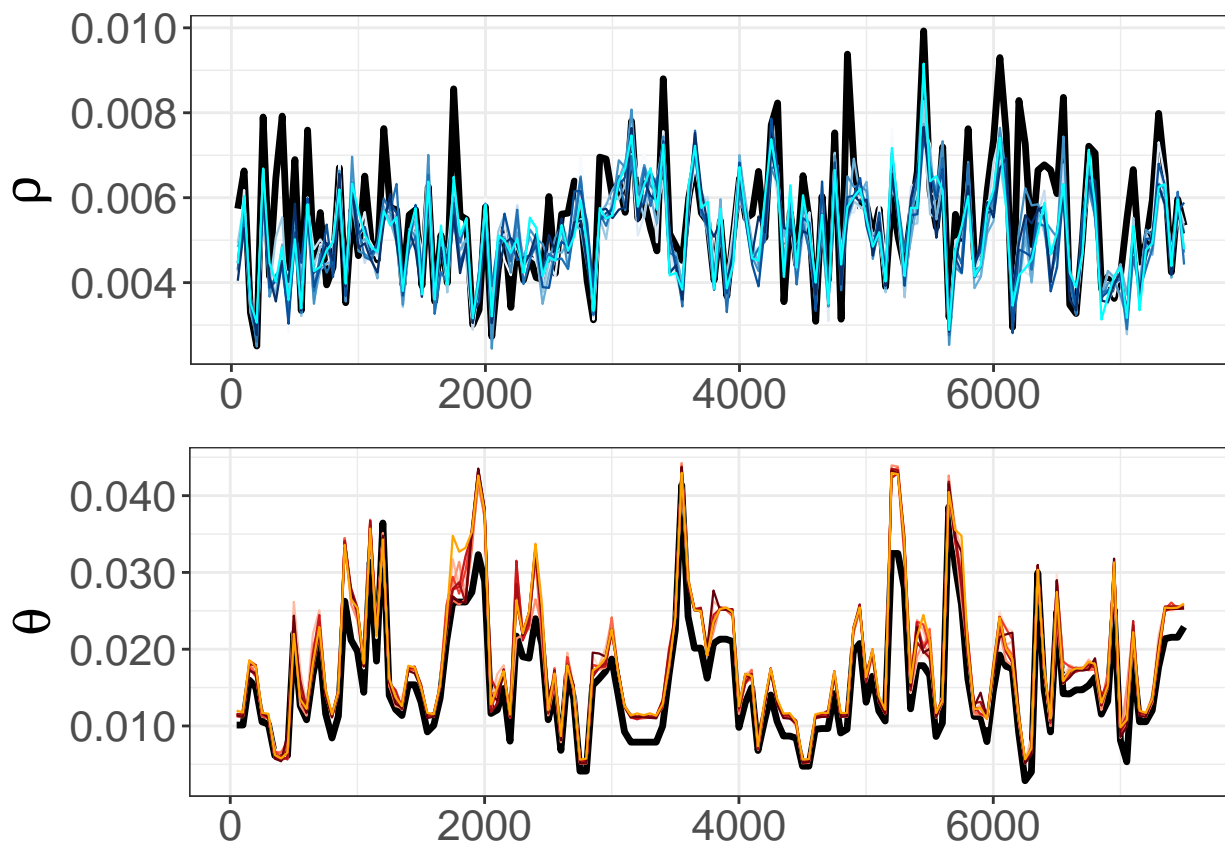
```

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 * 50, y = value, colour = variable)) + theme_minimal()
theta.map.200kb <- theta.map.200kb + geom_line(data = molten.theta, aes(size = variable)) + scale_size_rel(1)
theta.map.200kb <- theta.map.200kb + scale_color_manual(values = c("black", brewer.pal(n = 9, name = "RdYlGn")))
theta.map.200kb <- theta.map.200kb + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_breaks())
theta.map.200kb <- theta.map.200kb + labs(title = NULL, x = NULL, y = expression(theta))
theta.map.200kb <- theta.map.200kb + theme(text = element_text(size = 20), axis.title.x = element_text(size = 20))

plot_grid(rho.map.200kb, theta.map.200kb, nrow = 2, ncol = 1)

```



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")

```


rep_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)

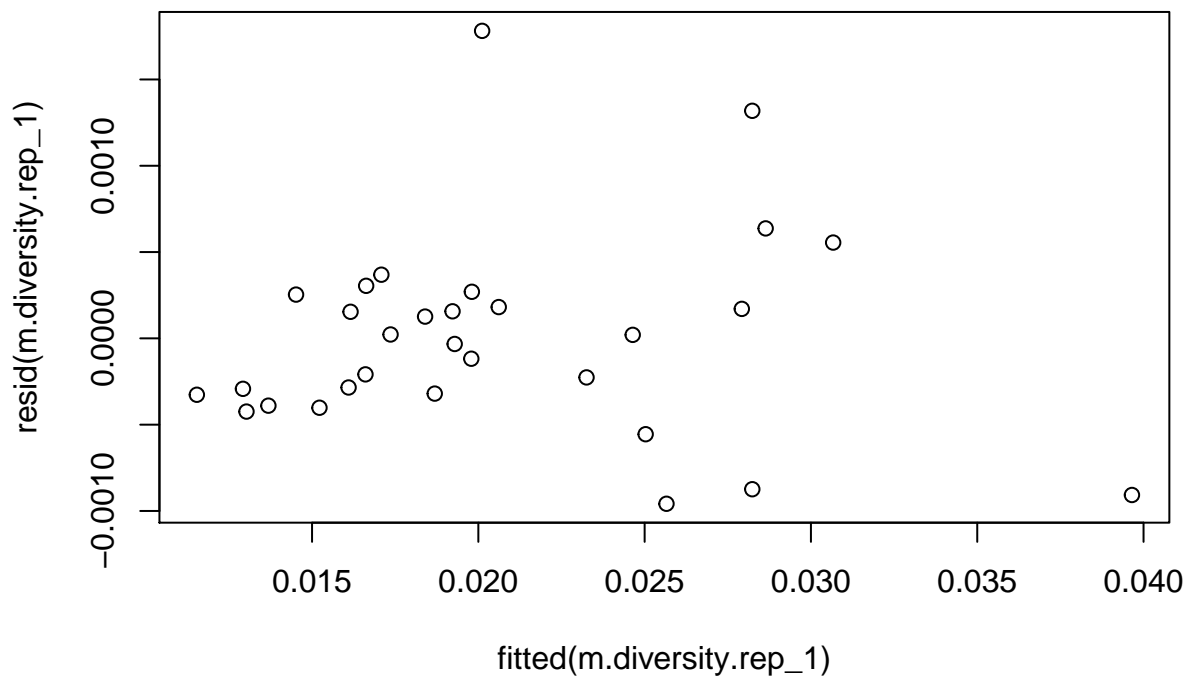
inf.lands.1M.rep_1 <- as.data.frame(cbind(pi.1M$avg, theta.1M$sample_mean, rho.1M$sample_mean, tmrca.1M$sample_mean))
names(inf.lands.1M.rep_1) <- c("diversity", "theta", "rho", "tmrca")

# 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))
```



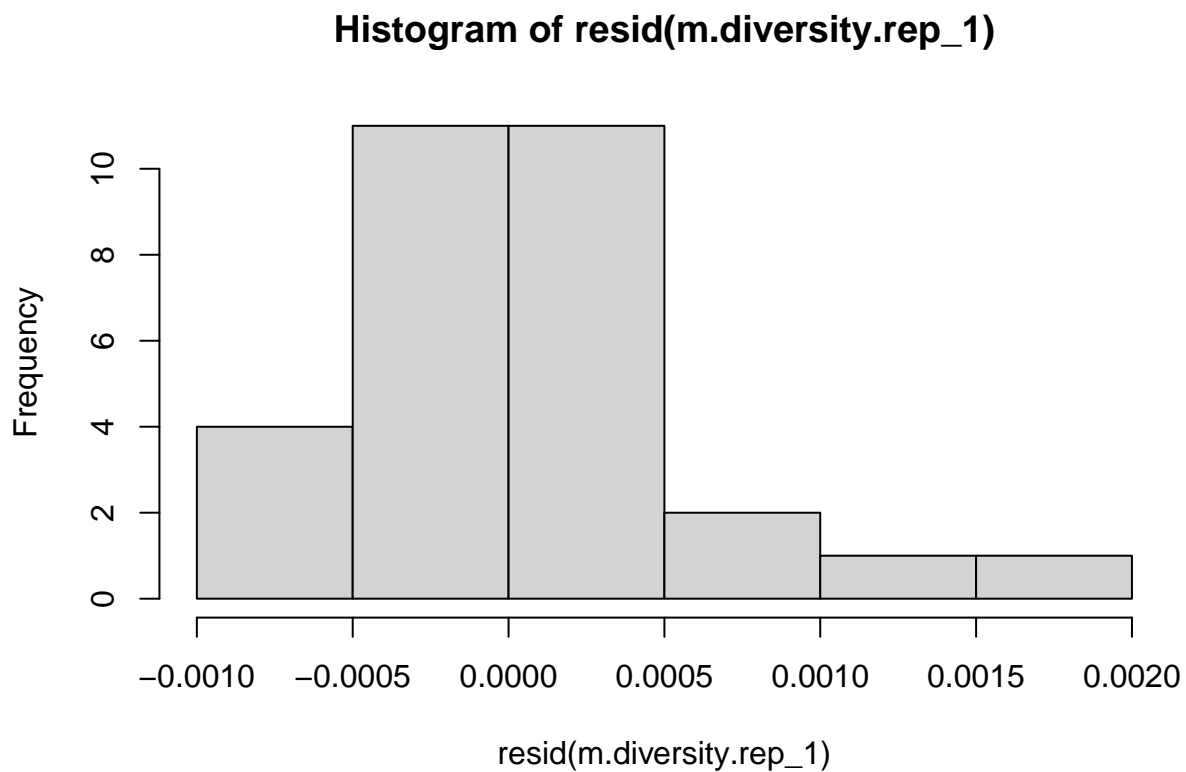
```
dwtest(m.diversity.rep_1)
```

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

```
hmctest(m.diversity.rep_1)
```

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_1  
## HMC = 0.46606, p-value = 0.391
```

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

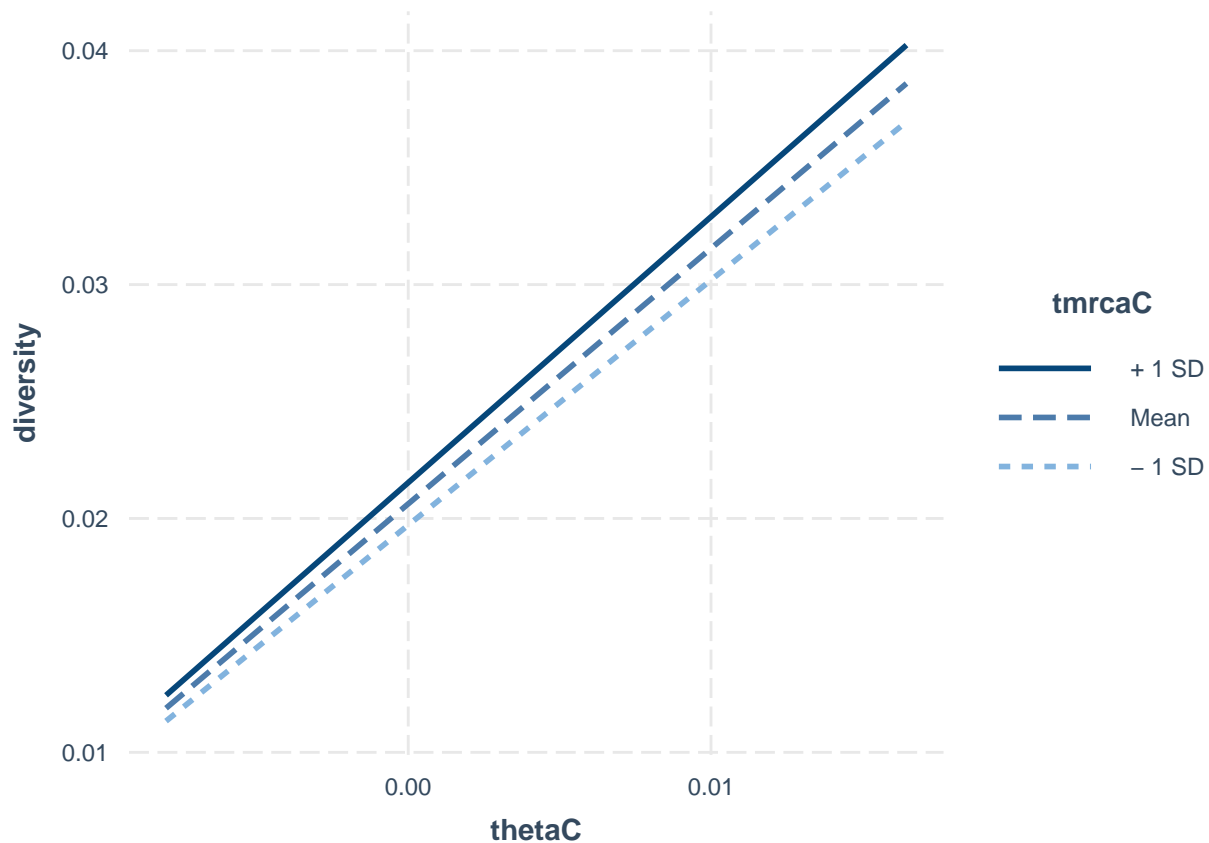


```
summary(m.diversity.rep_1)
```

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

rep_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)
```

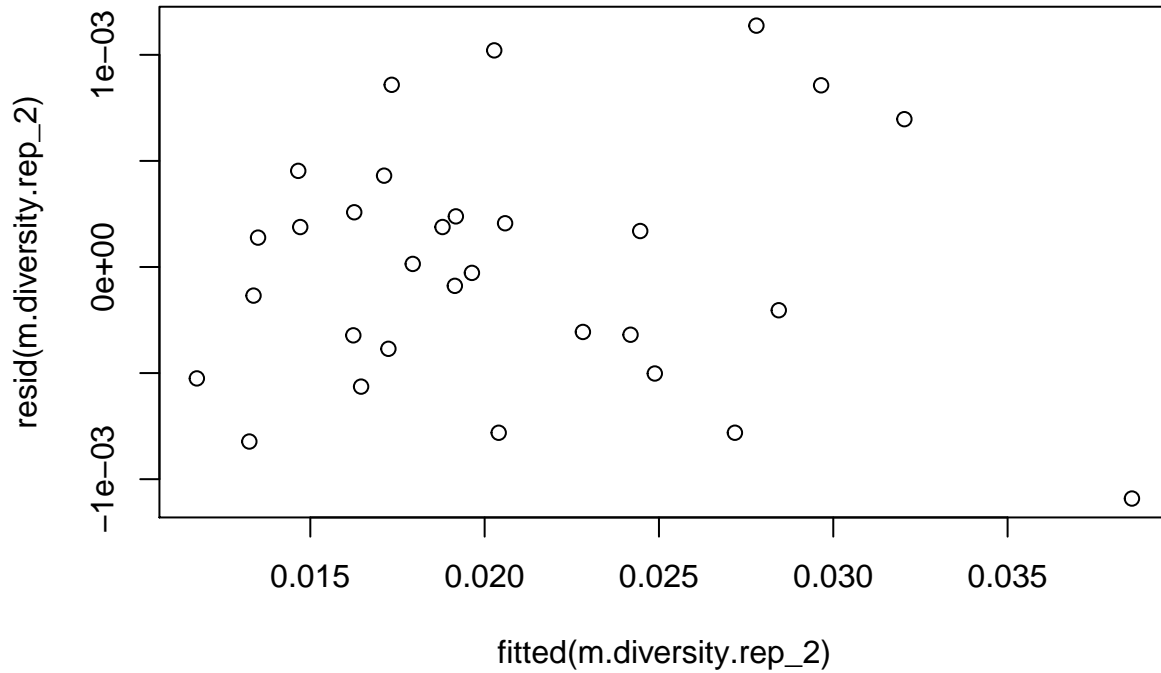
```

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

m.diversity.rep_2 <- lm(多样性 ~ 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

```

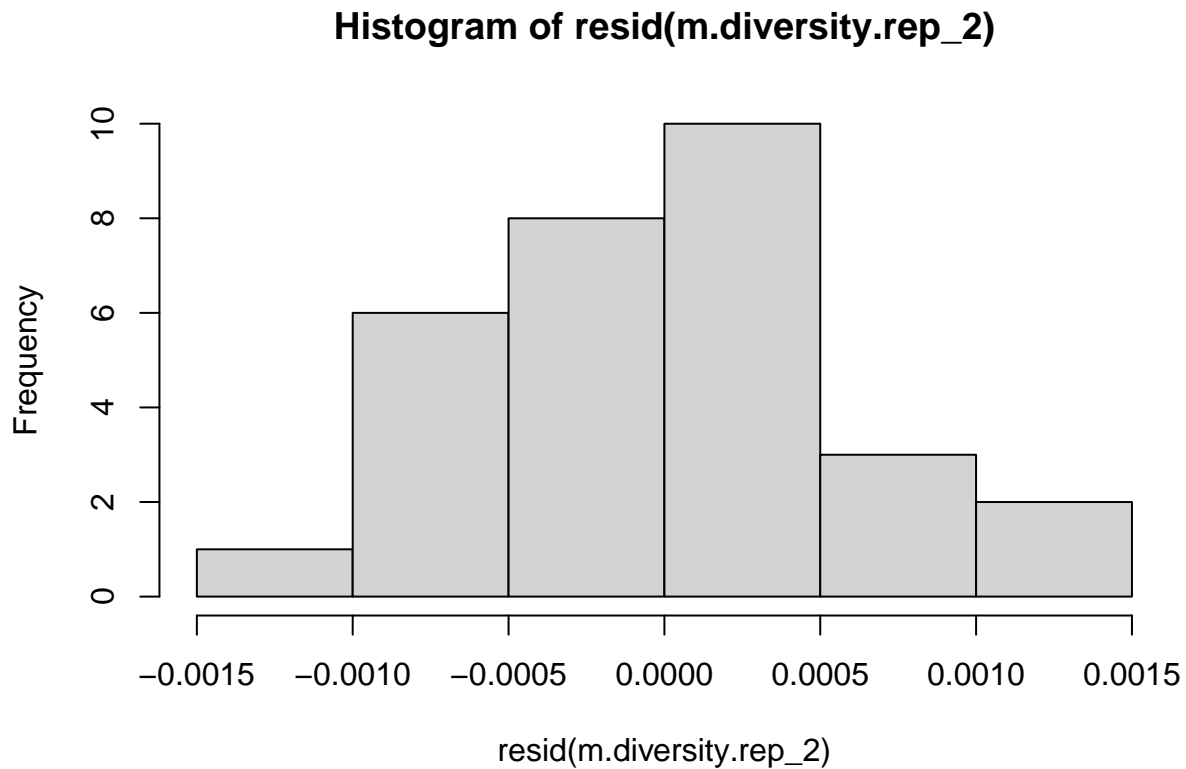
```
hmcetest(m.diversity.rep_2)
```

```

##
## Harrison-McCabe test
##
## data: m.diversity.rep_2
## HMC = 0.4866, p-value = 0.468

```

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

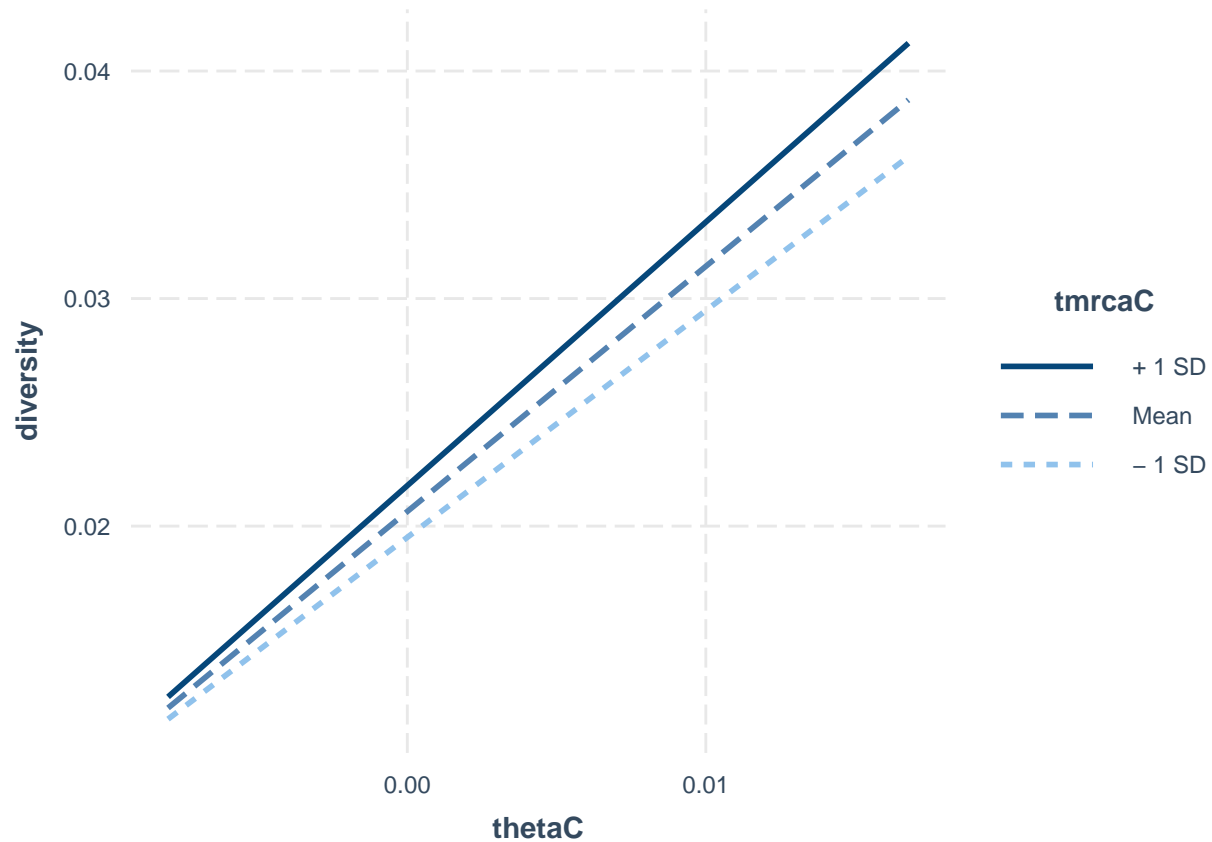


```
summary(m.diversity.rep_2)
```

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

rep_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)

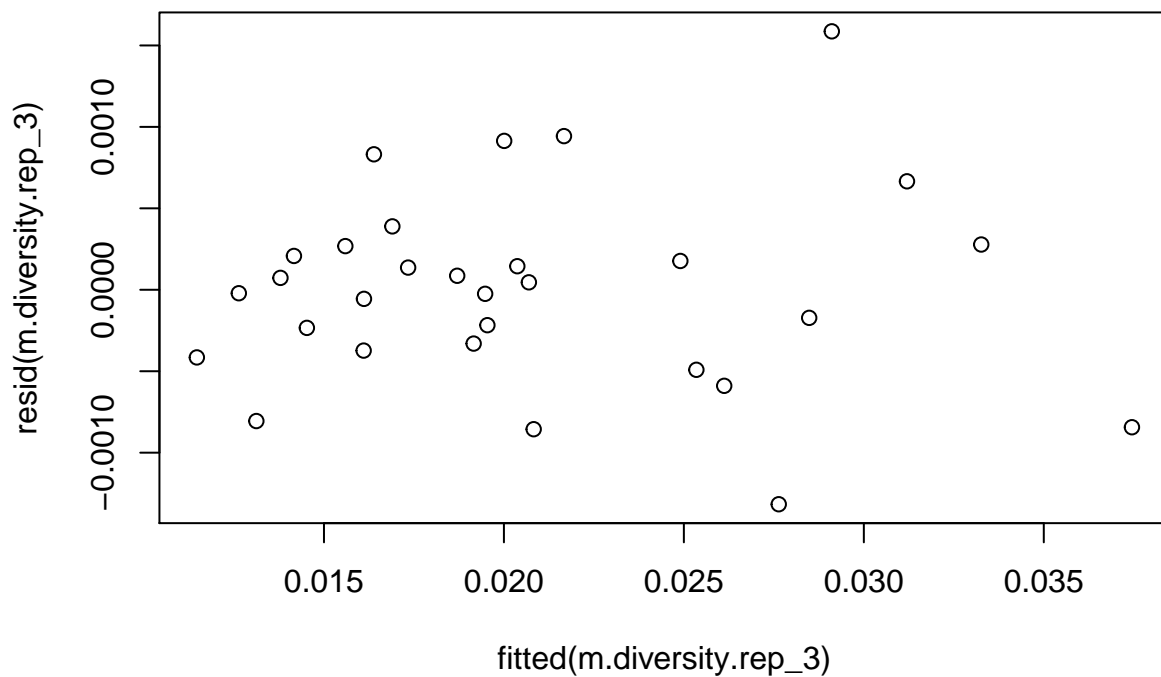
inf.lands.1M.rep_3 <- as.data.frame(cbind(pi.1M$avg, theta.1M$sample_mean, rho.1M$sample_mean, tmrca.1M$sample_mean))
names(inf.lands.1M.rep_3) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

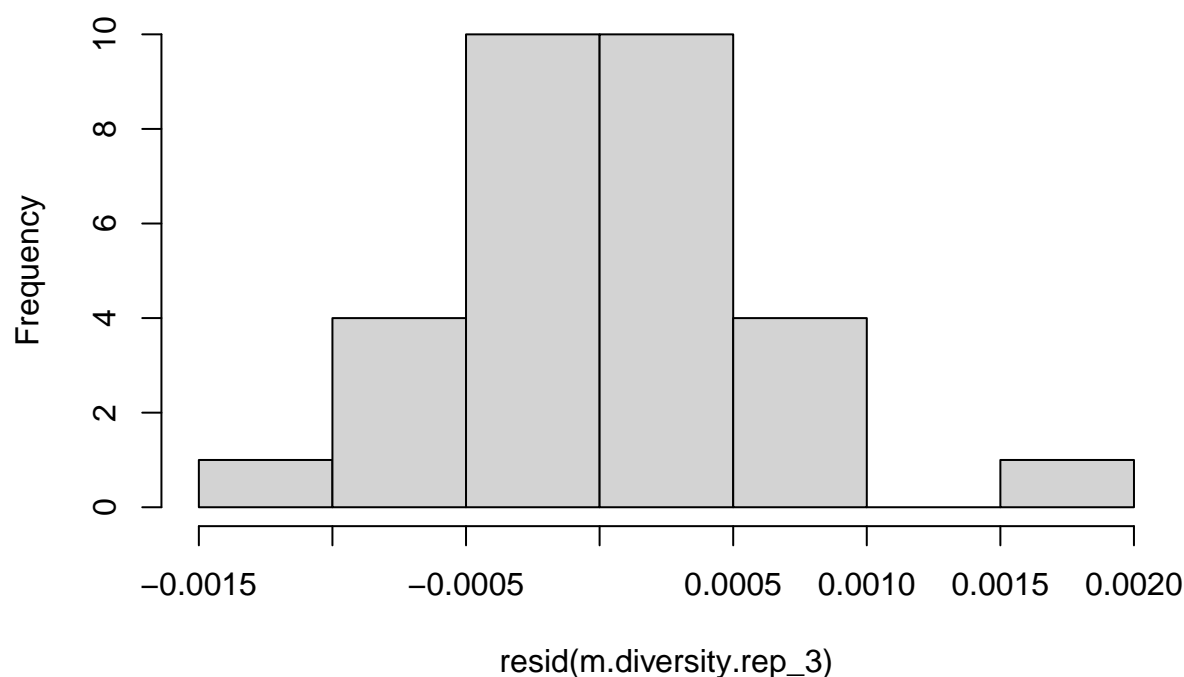
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_3  
## DW = 1.3502, p-value = 0.02515  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_3  
## HMC = 0.51975, p-value = 0.573
```

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

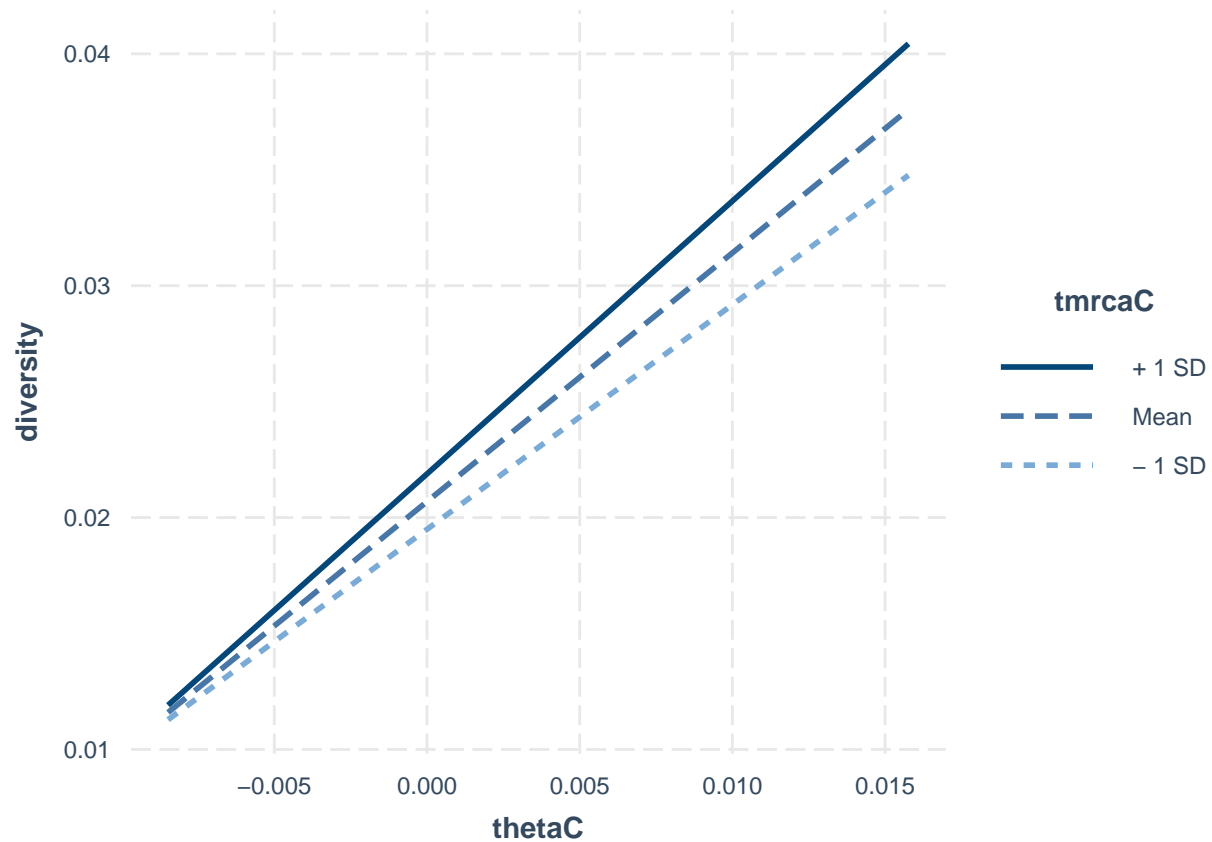
Histogram of resid(m.diversity.rep_3)



```
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]
```

rep_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)

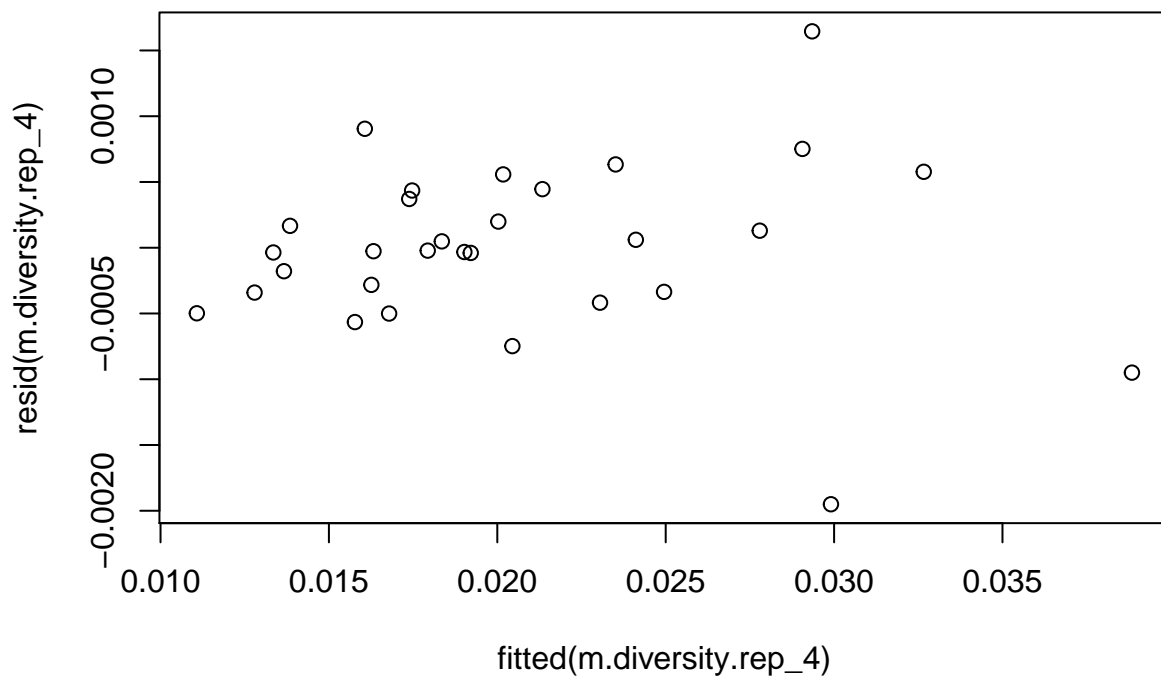
inf.lands.1M.rep_4 <- as.data.frame(cbind(pi.1M$avg, theta.1M$sample_mean, rho.1M$sample_mean, tmrca.1M$avg))
names(inf.lands.1M.rep_4) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

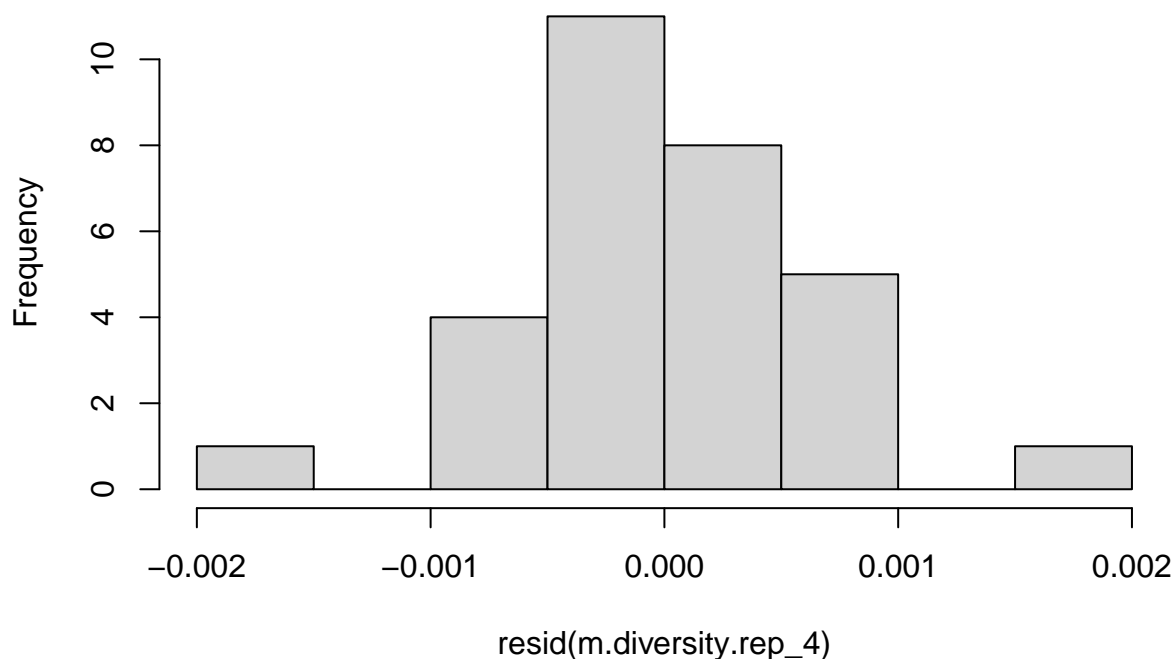
```
##
## Durbin-Watson test
##
## data: m.diversity.rep_4
## DW = 2.0871, p-value = 0.5863
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##
## Harrison-McCabe test
##
## data: m.diversity.rep_4
## HMC = 0.42593, p-value = 0.269
```

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

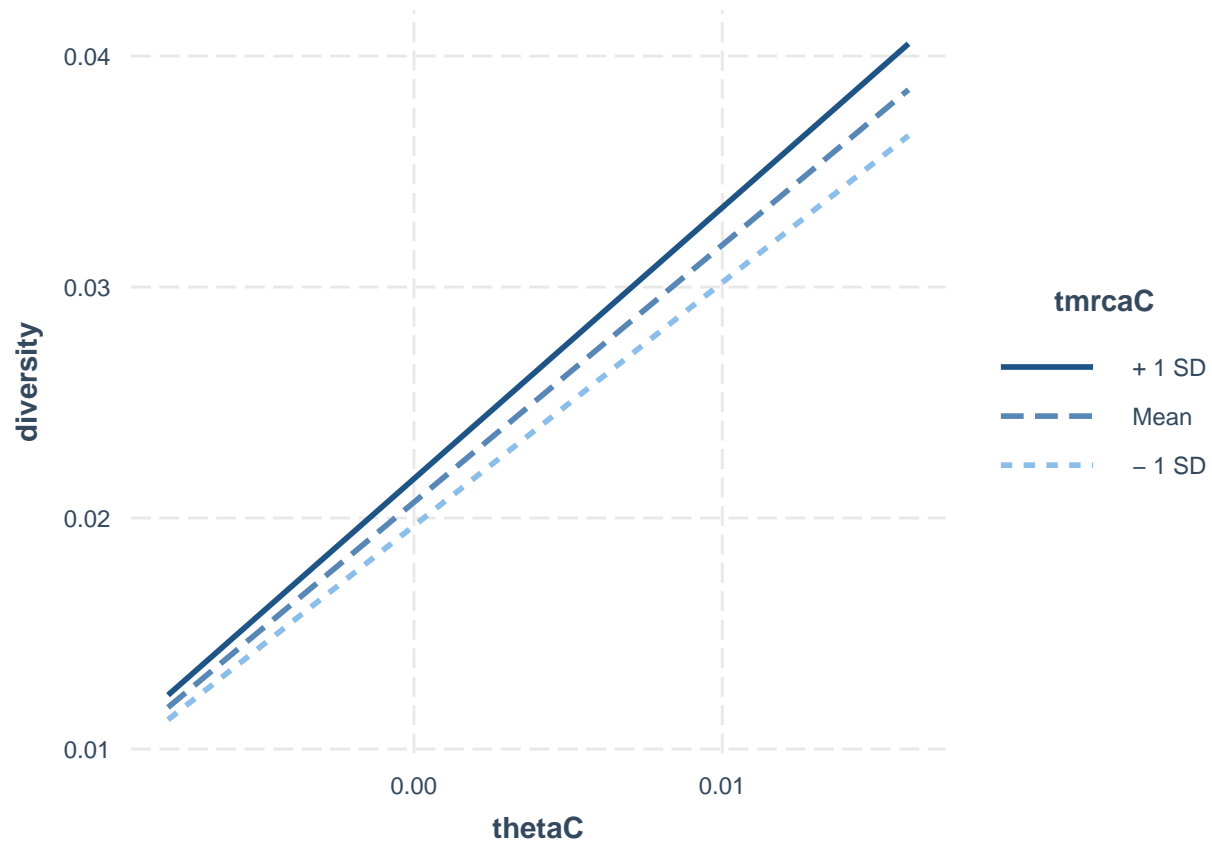

Histogram of resid(m.diversity.rep_4)



```
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]
```

rep_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)

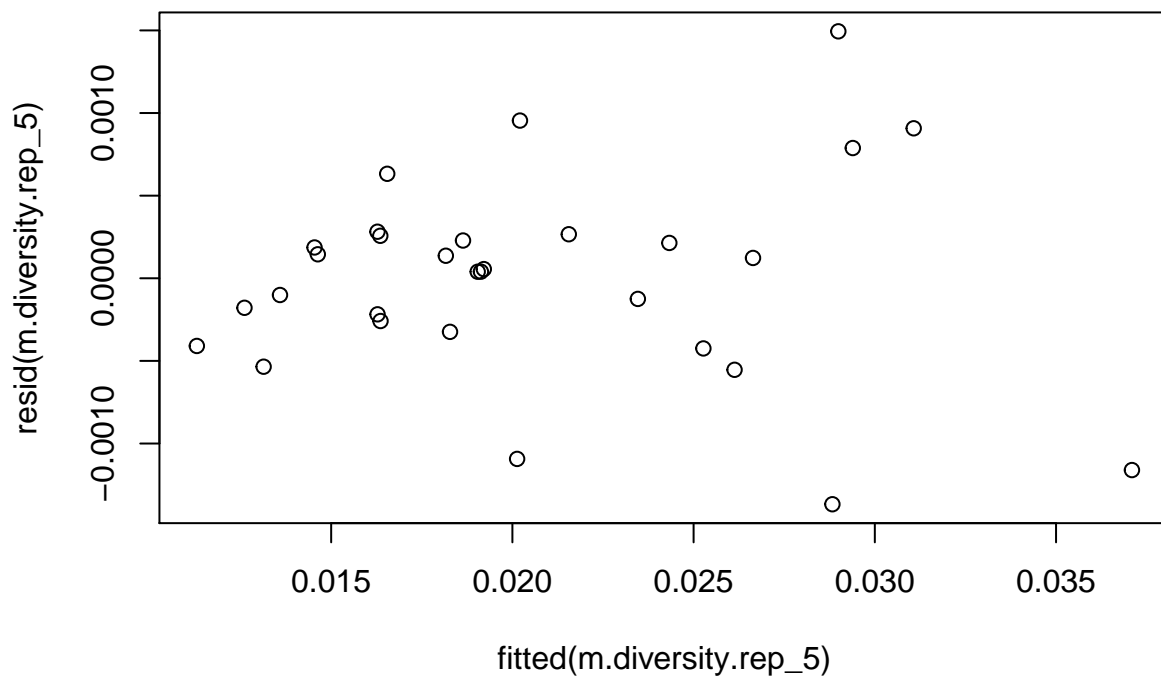
inf.lands.1M.rep_5 <- as.data.frame(cbind(pi.1M$avg, theta.1M$sample_mean, rho.1M$sample_mean, tmrca.1M$sample_mean))
names(inf.lands.1M.rep_5) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

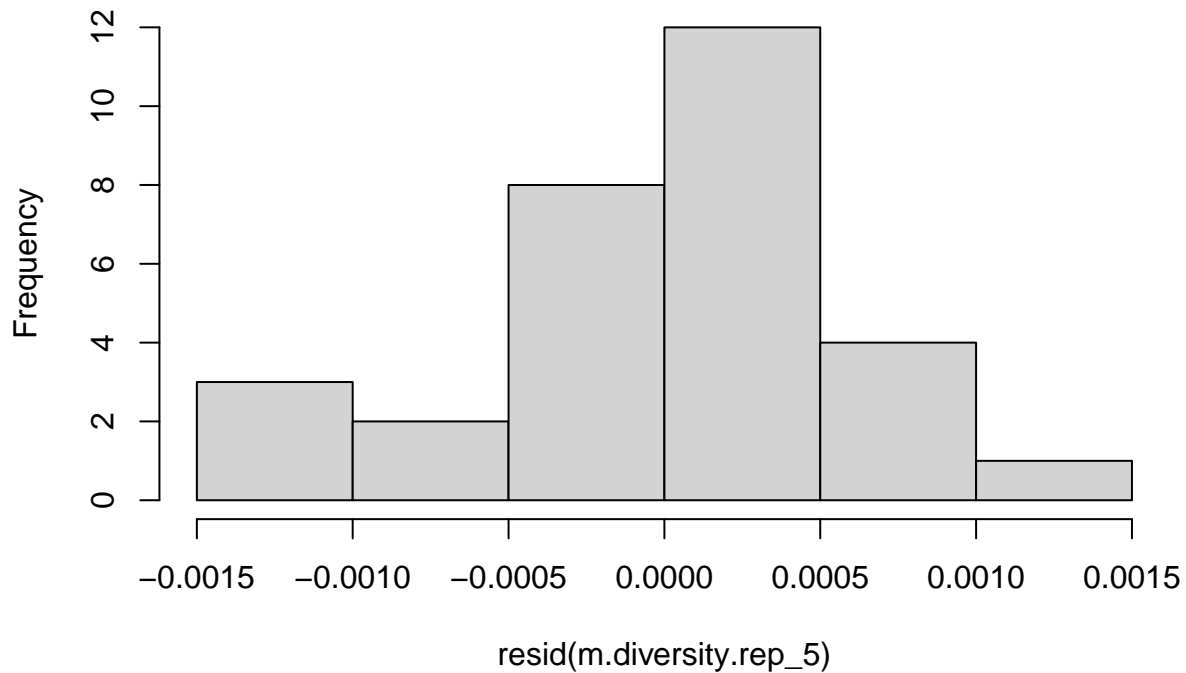
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_5  
## DW = 1.8381, p-value = 0.2796  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_5  
## HMC = 0.49429, p-value = 0.503
```

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

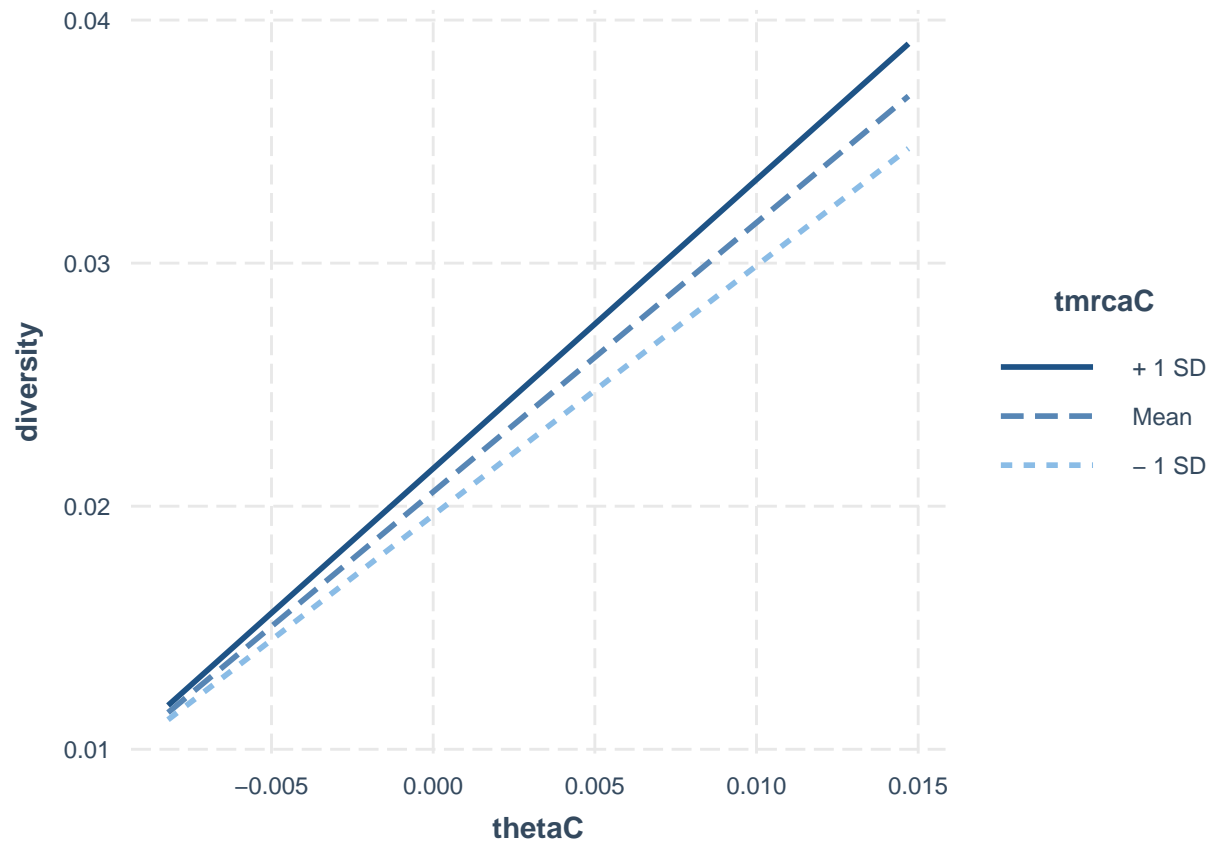
Histogram of resid(m.diversity.rep_5)



```
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$VarExp[1]
r2.inf.1Mb[2, 5] <- anova.diversity$VarExp[1] / anova.diversity$VarExp[1]
r2.inf.1Mb[3, 5] <- anova.diversity$VarExp[2] / anova.diversity$VarExp[1]
r2.inf.1Mb[4, 5] <- anova.diversity$VarExp[3] / anova.diversity$VarExp[1]
r2.inf.1Mb[5, 5] <- anova.diversity$VarExp[4] / anova.diversity$VarExp[1]
```

rep_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)

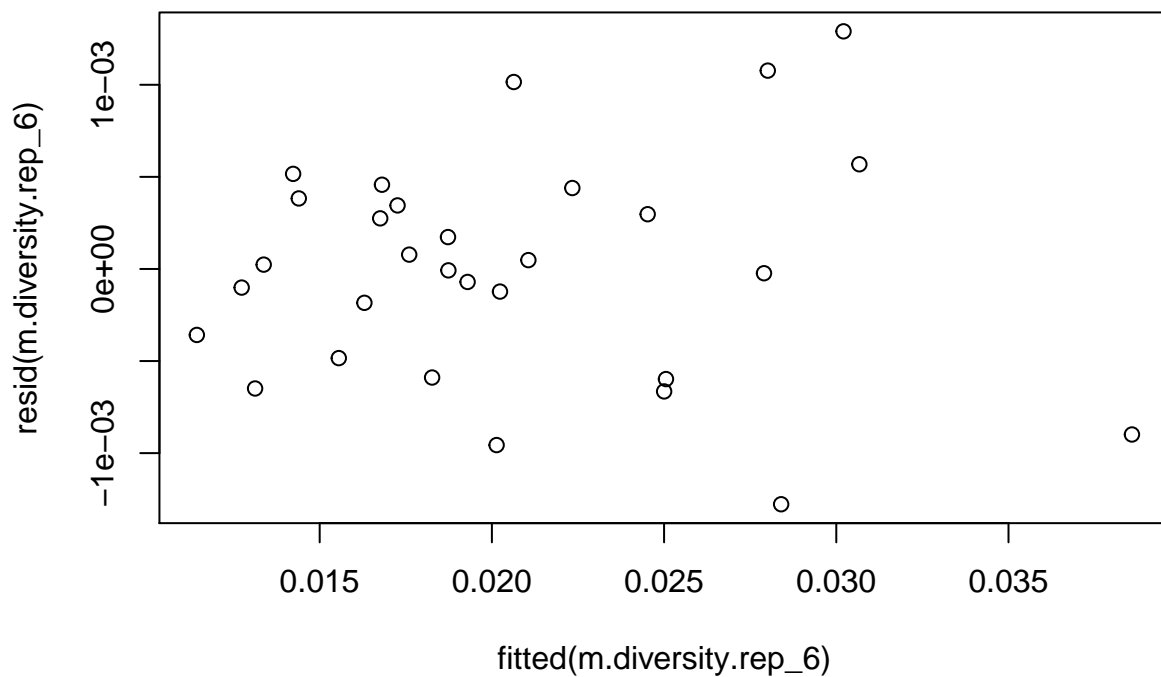
inf.lands.1M.rep_6 <- as.data.frame(cbind(pi.1M$avg, theta.1M$sample_mean, rho.1M$sample_mean, tmrca.1M$avg))
names(inf.lands.1M.rep_6) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

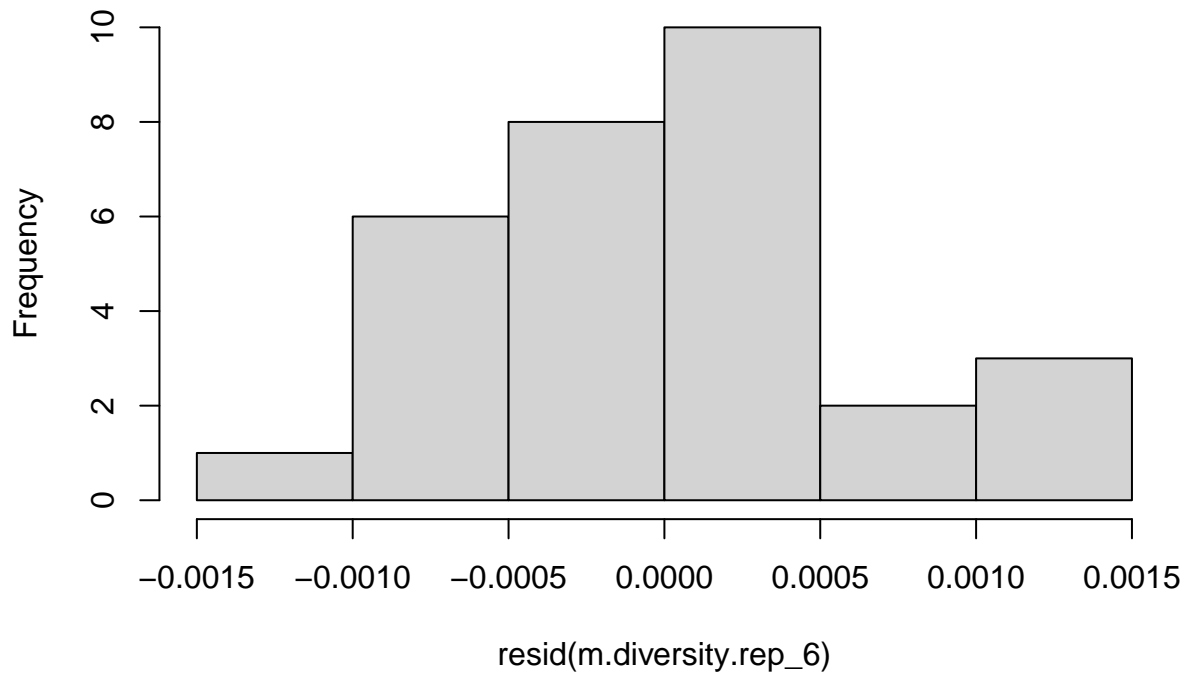
```
##
## Durbin-Watson test
##
## data: m.diversity.rep_6
## DW = 1.7678, p-value = 0.2162
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmctest(m.diversity.rep_6)
```

```
##
## Harrison-McCabe test
##
## data: m.diversity.rep_6
## HMC = 0.38206, p-value = 0.195
```

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

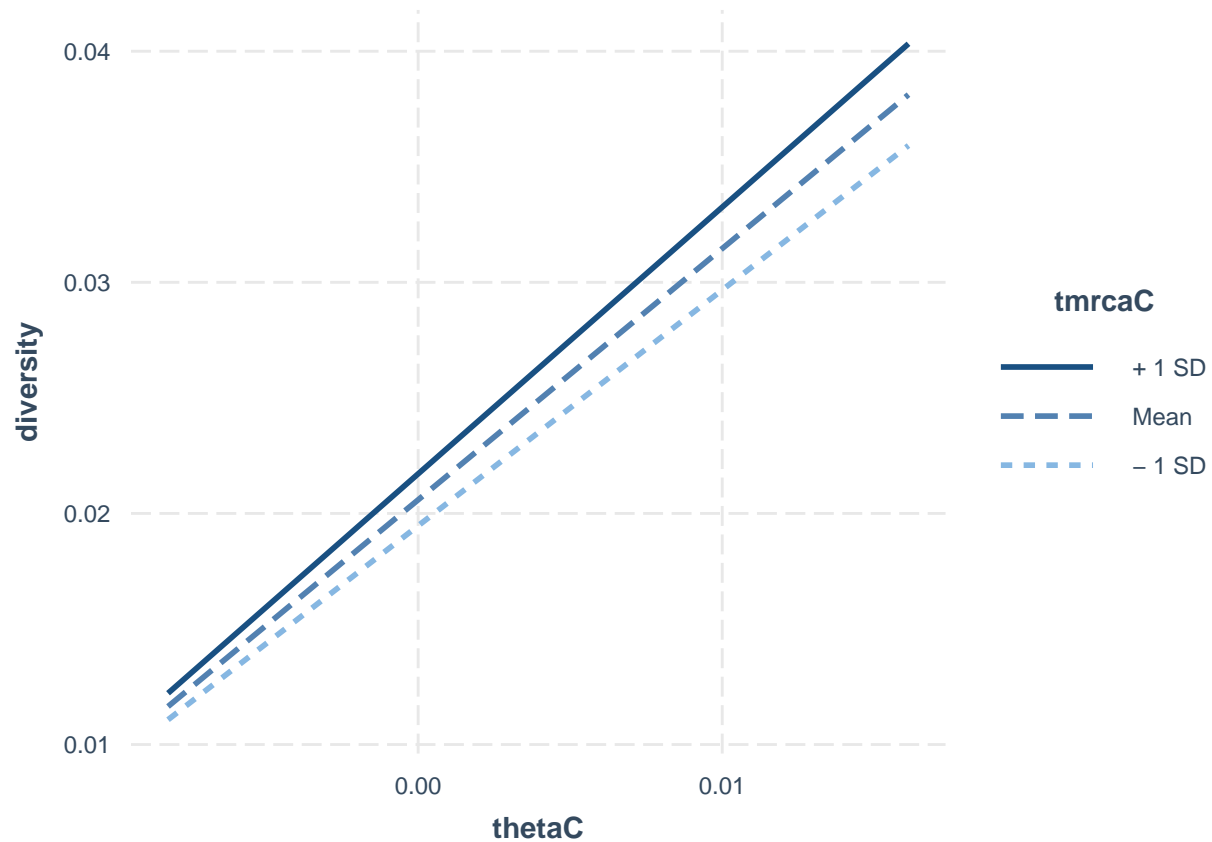
Histogram of resid(m.diversity.rep_6)



```
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$VarExp[3] + anova.diversity$VarExp[4]) / anova.diversity$VarExp[1]
r2.inf.1Mb[2, 6] <- anova.diversity$VarExp[1] / anova.diversity$VarExp[1]
r2.inf.1Mb[3, 6] <- anova.diversity$VarExp[2] / anova.diversity$VarExp[1]
r2.inf.1Mb[4, 6] <- anova.diversity$VarExp[3] / anova.diversity$VarExp[1]
r2.inf.1Mb[5, 6] <- anova.diversity$VarExp[4] / anova.diversity$VarExp[1]
```

rep_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)

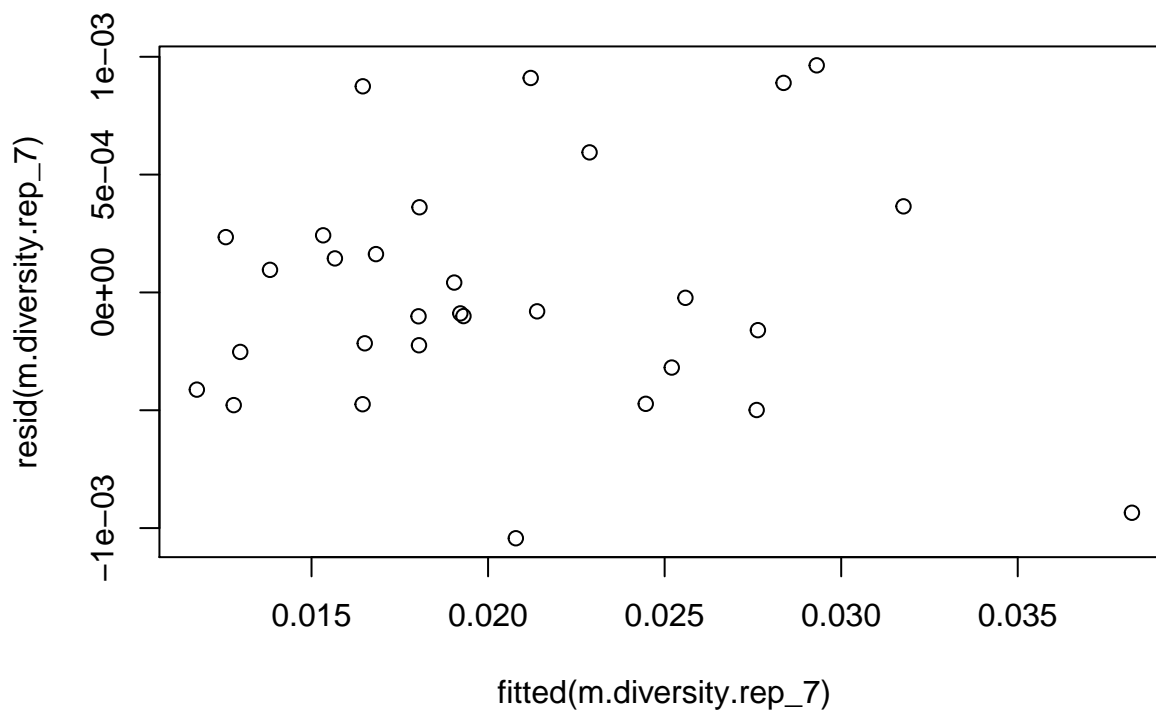
inf.lands.1M.rep_7 <- as.data.frame(cbind(pi.1M$avg, theta.1M$sample_mean, rho.1M$sample_mean, tmrca.1M$avg))
names(inf.lands.1M.rep_7) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

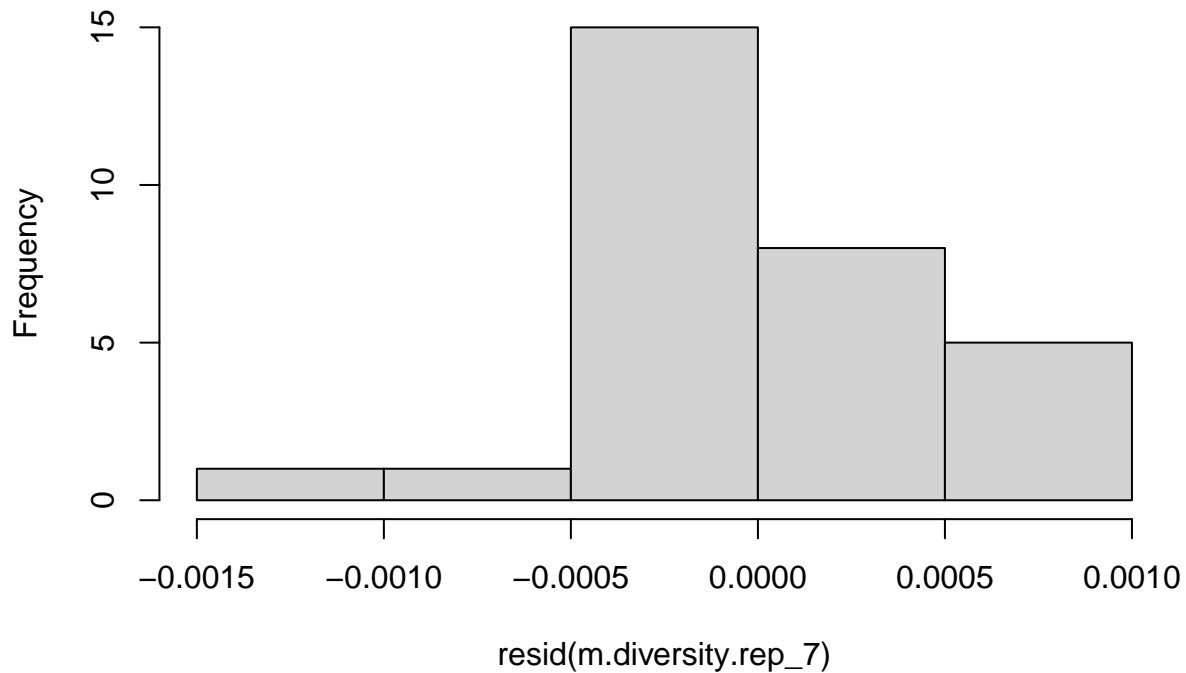
```
##
## Durbin-Watson test
##
## data: m.diversity.rep_7
## DW = 1.6938, p-value = 0.1634
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##
## Harrison-McCabe test
##
## data: m.diversity.rep_7
## HMC = 0.40789, p-value = 0.258
```

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

Histogram of resid(m.diversity.rep_7)

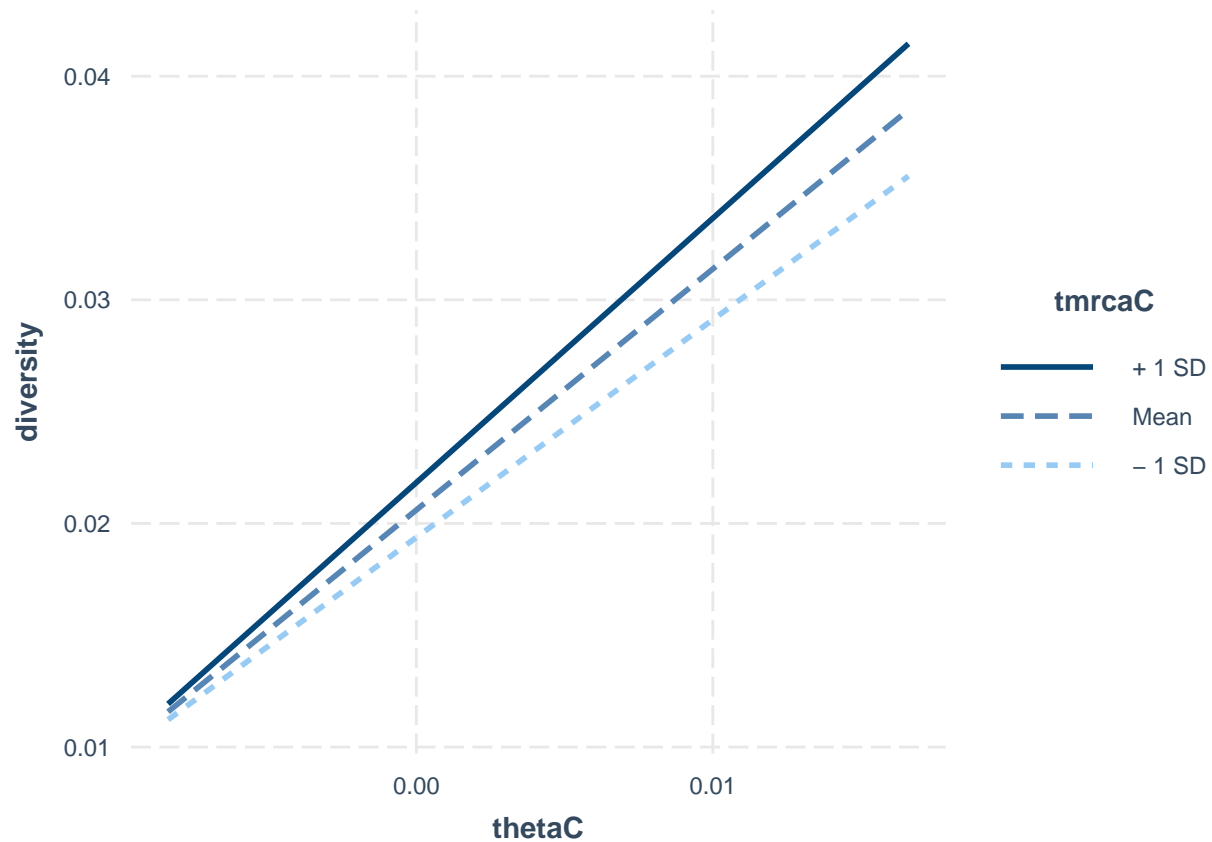


```
summary(m.diversity.rep_7)
```

```
##
## 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
```

rep_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)

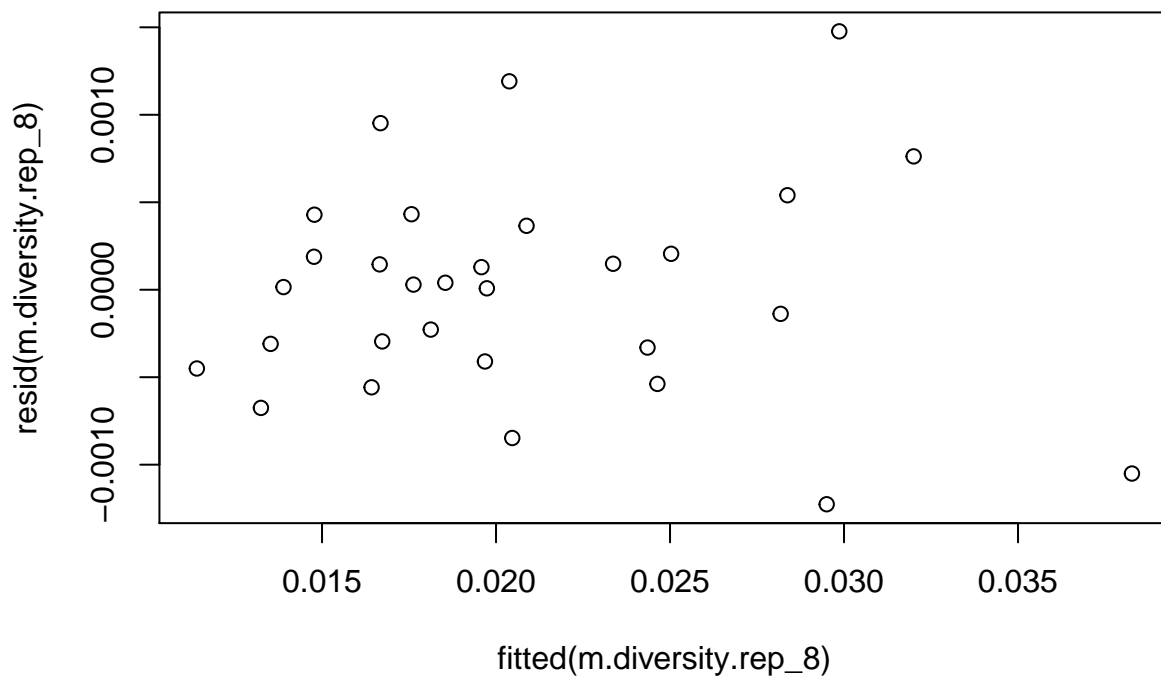
inf.lands.1M.rep_8 <- as.data.frame(cbind(pi.1M$avg, theta.1M$sample_mean, rho.1M$sample_mean, tmrca.1M$sample_mean))
names(inf.lands.1M.rep_8) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

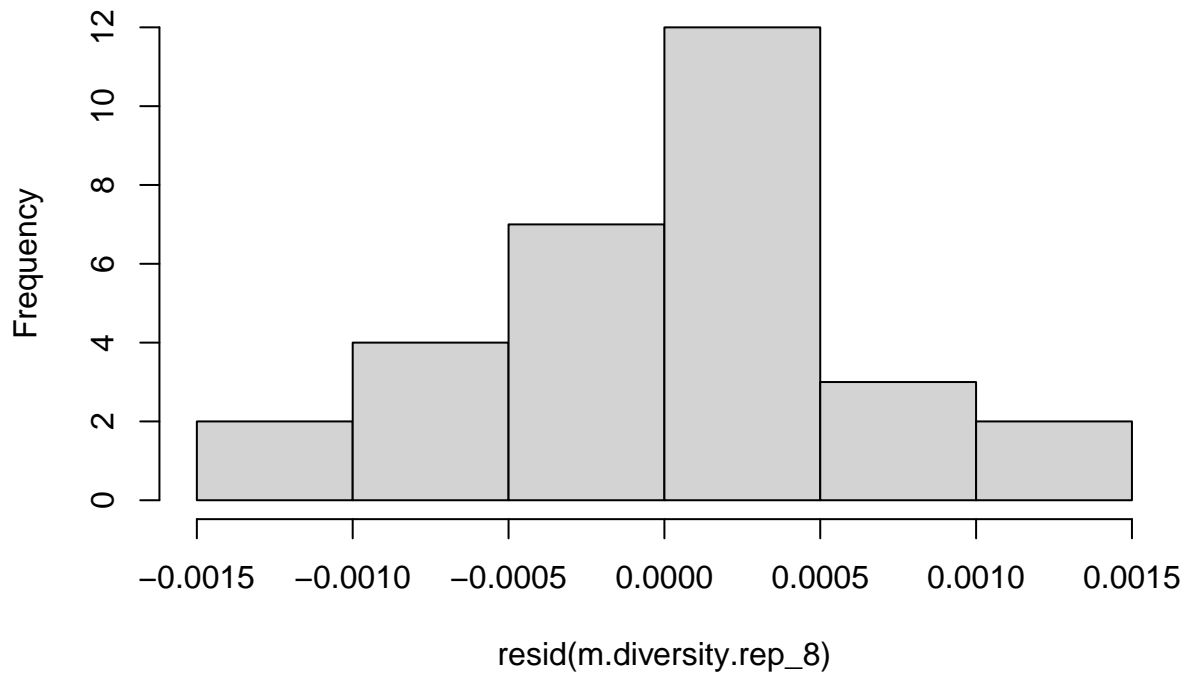
```
##
## Durbin-Watson test
##
## data: m.diversity.rep_8
## DW = 1.6816, p-value = 0.17
## alternative hypothesis: true autocorrelation is greater than 0
```

```
hmctest(m.diversity.rep_8)
```

```
##
## Harrison-McCabe test
##
## data: m.diversity.rep_8
## HMC = 0.45613, p-value = 0.35
```

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

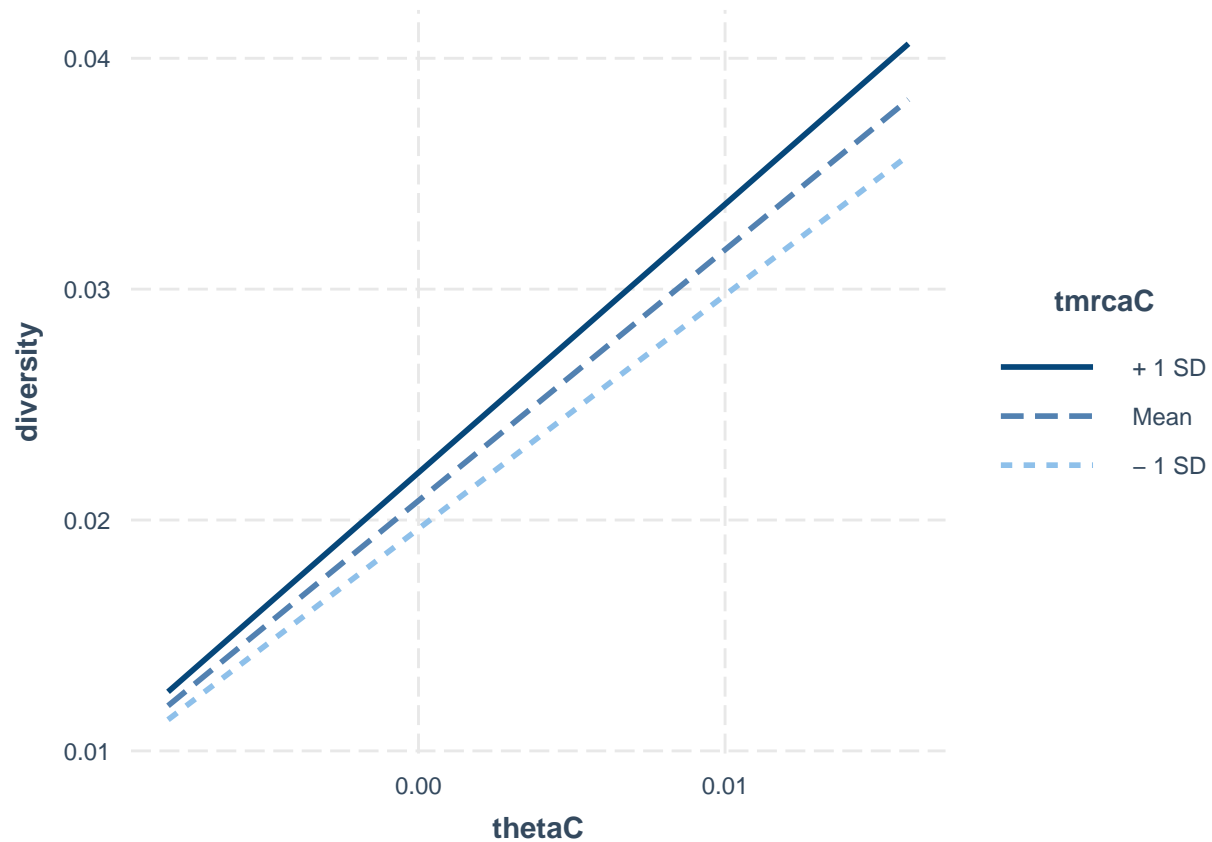
Histogram of resid(m.diversity.rep_8)



```
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$VarExp[3] + anova.diversity$VarExp[4]) / anova.diversity$VarExp[1]
r2.inf.1Mb[2, 8] <- anova.diversity$VarExp[1] / anova.diversity$VarExp[1]
r2.inf.1Mb[3, 8] <- anova.diversity$VarExp[2] / anova.diversity$VarExp[1]
r2.inf.1Mb[4, 8] <- anova.diversity$VarExp[3] / anova.diversity$VarExp[1]
r2.inf.1Mb[5, 8] <- anova.diversity$VarExp[4] / anova.diversity$VarExp[1]
```

rep_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)

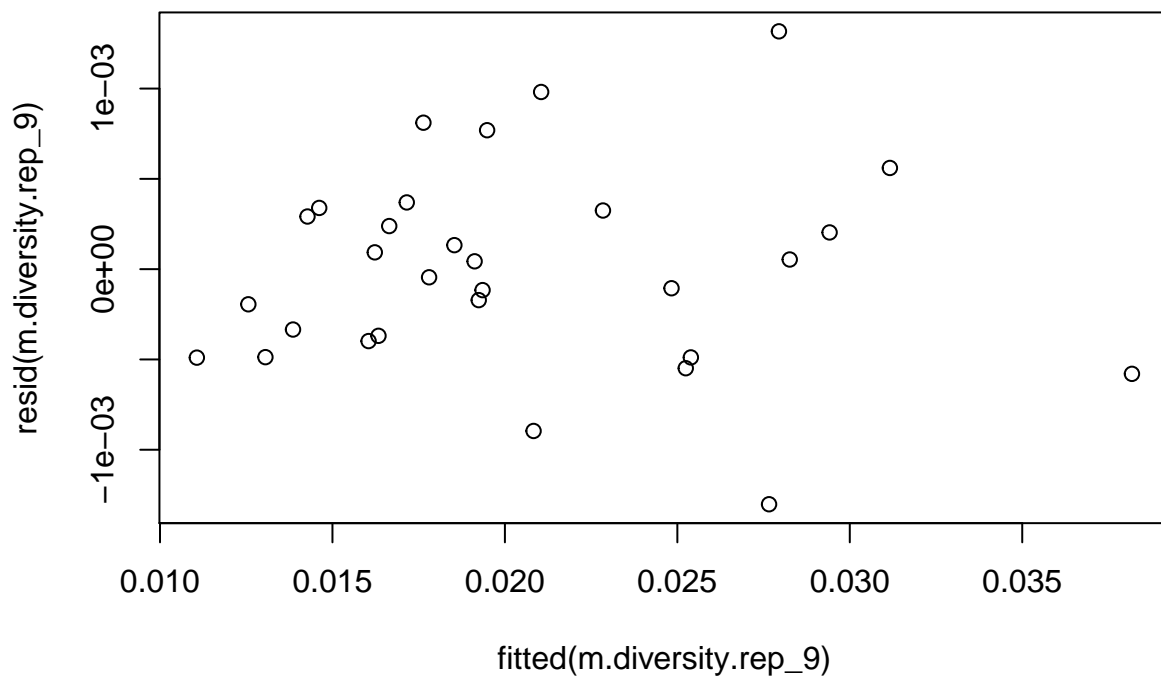
inf.lands.1M.rep_9 <- as.data.frame(cbind(pi.1M$avg, theta.1M$sample_mean, rho.1M$sample_mean, tmrca.1M$sample_mean))
names(inf.lands.1M.rep_9) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

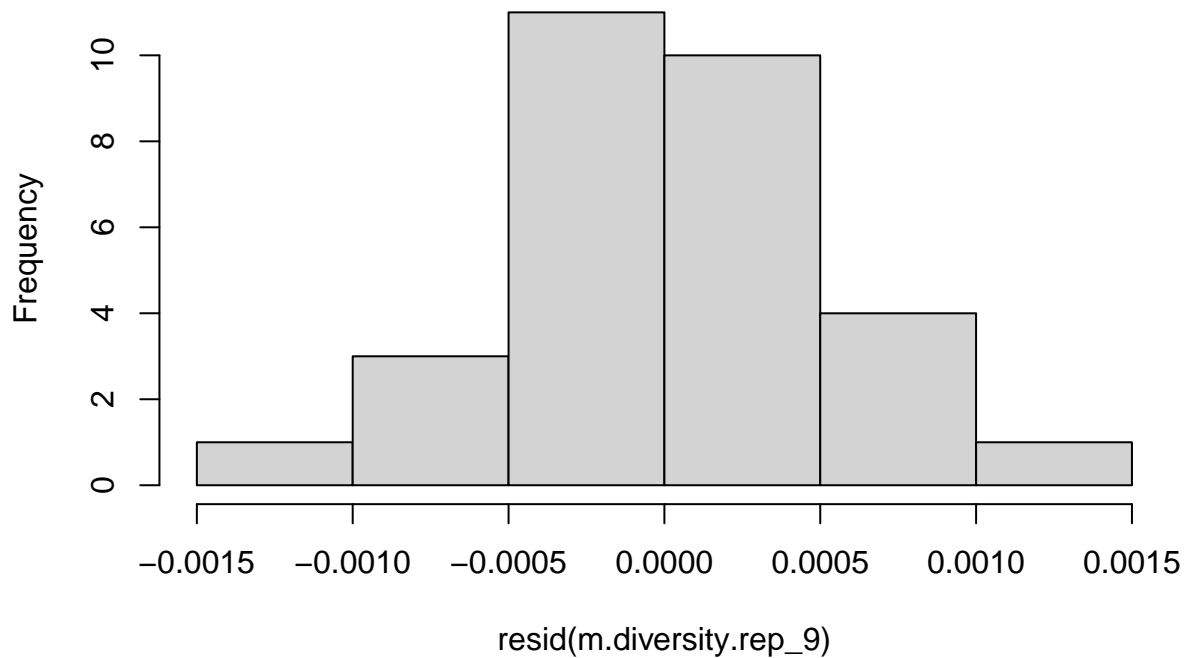
```
##  
## Durbin-Watson test  
##  
## data: m.diversity.rep_9  
## DW = 1.686, p-value = 0.1501  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.diversity.rep_9  
## HMC = 0.49123, p-value = 0.449
```

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

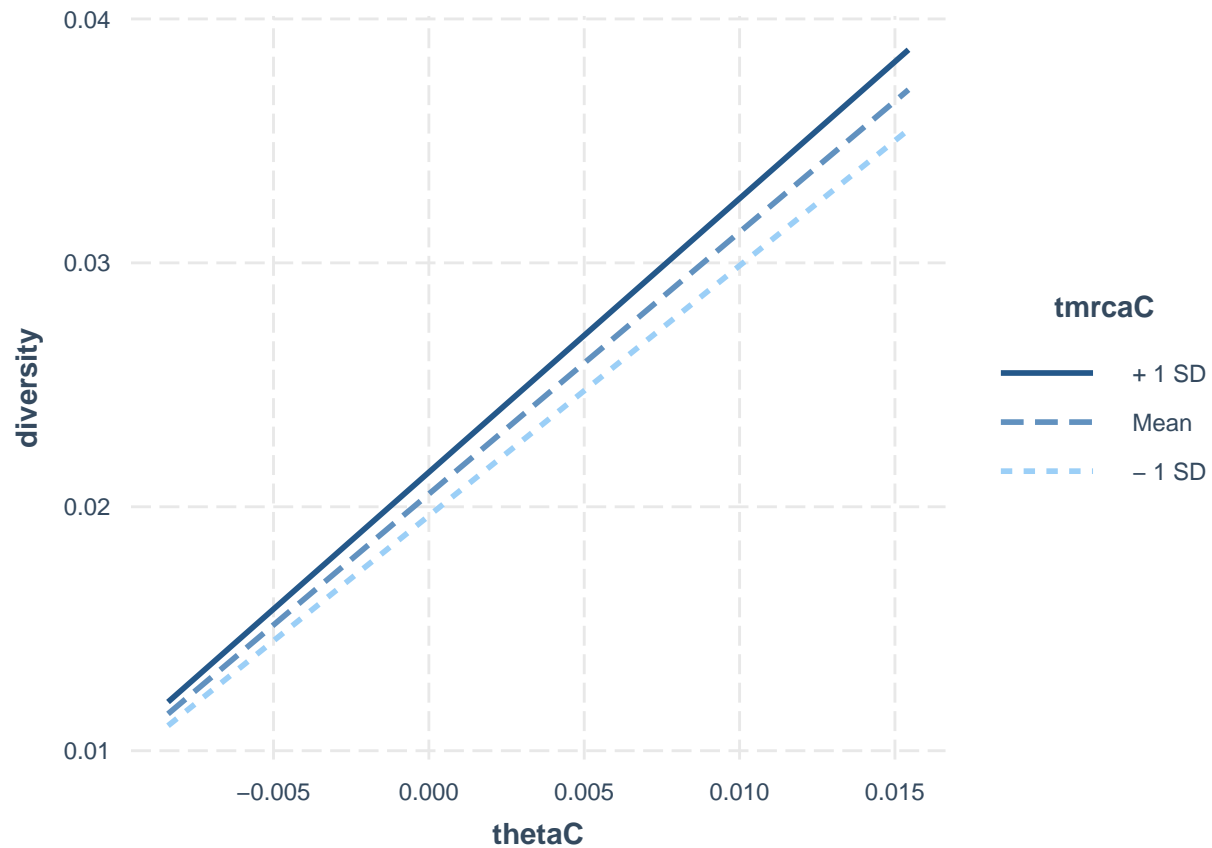
Histogram of resid(m.diversity.rep_9)



```
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]
```

```
rep_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)

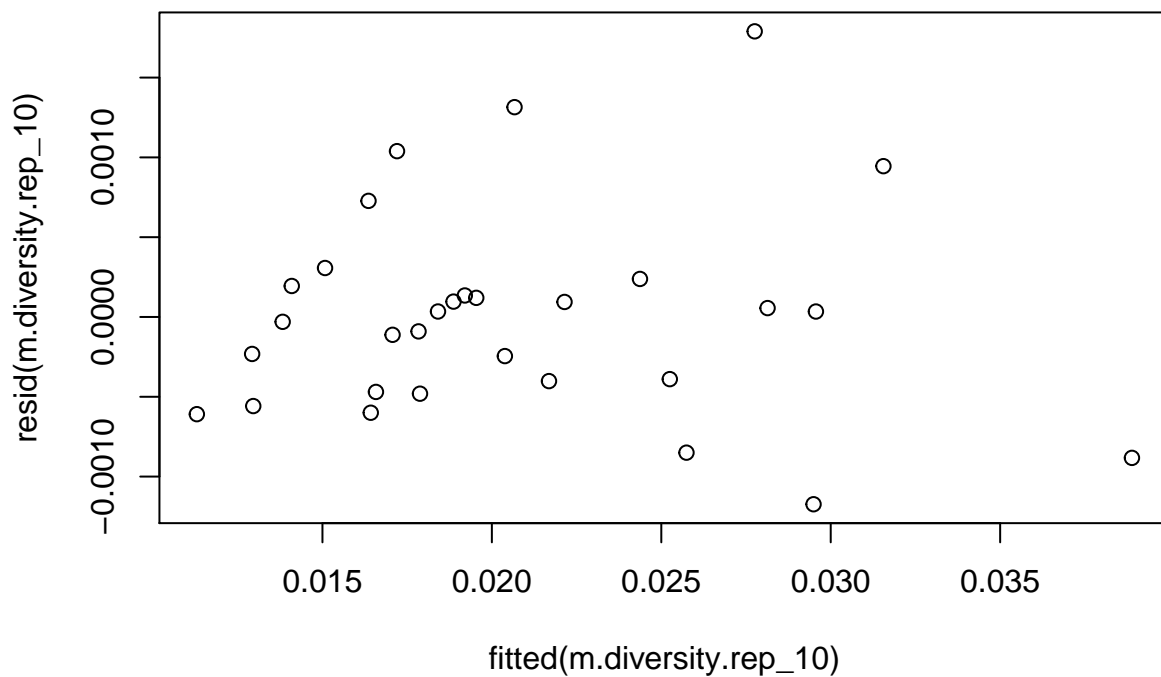
inf.lands.1M.rep_10 <- as.data.frame(cbind(pi.1M$avg, theta.1M$sample_mean, rho.1M$sample_mean, tmrca.1M$avg))
names(inf.lands.1M.rep_10) <- c("diversity", "theta", "rho", "tmrca")

# 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)
```

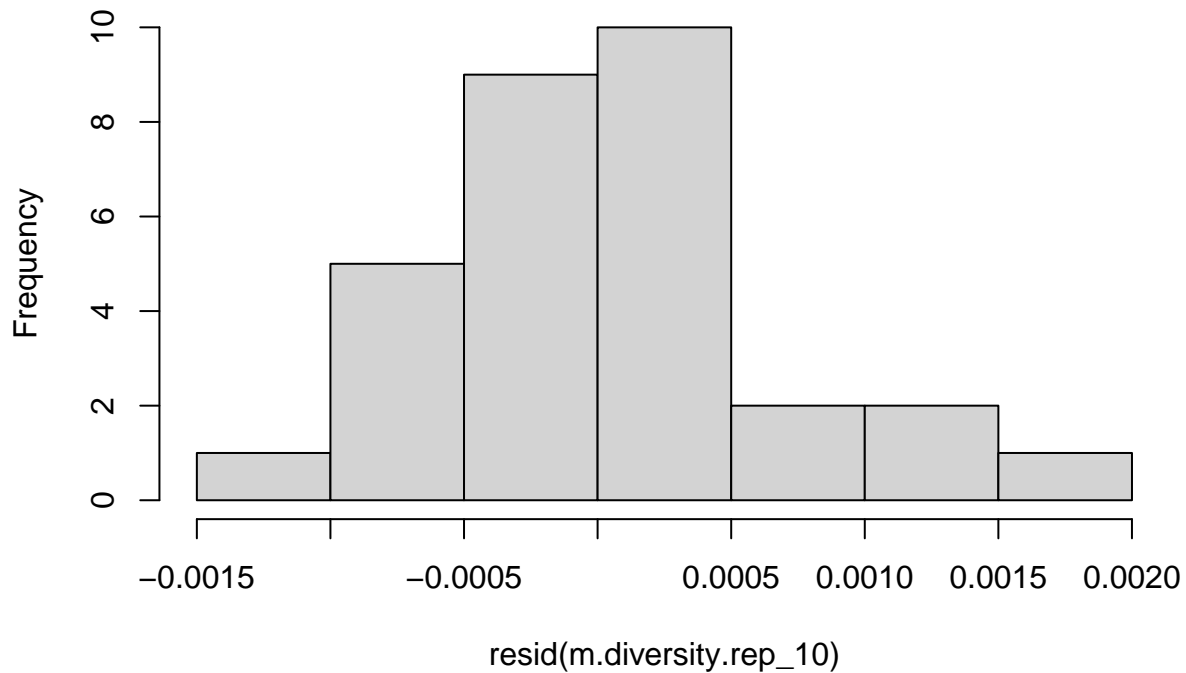
```
##
## Durbin-Watson test
##
## data: m.diversity.rep_10
## DW = 1.5209, p-value = 0.06939
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##
## Harrison-McCabe test
##
## data: m.diversity.rep_10
## HMC = 0.59687, p-value = 0.758
```

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

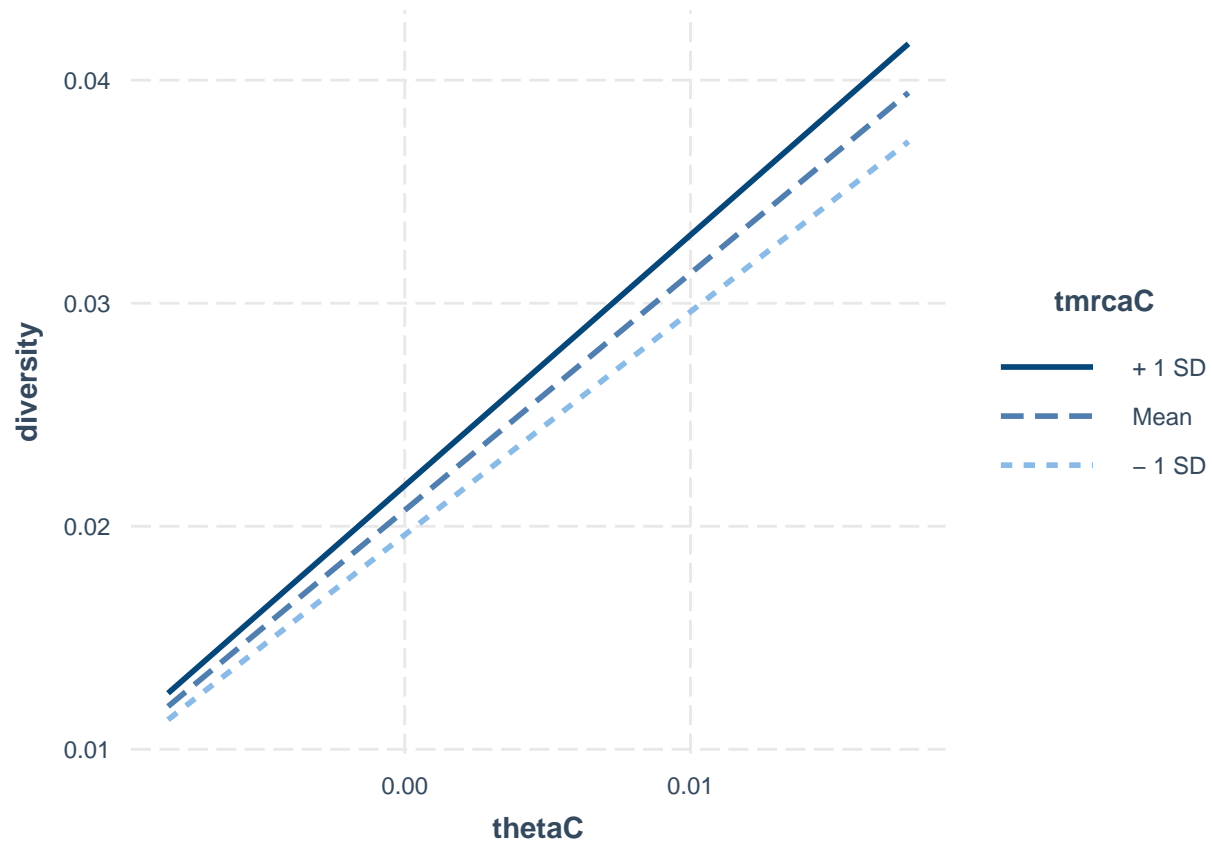
Histogram of resid(m.diversity.rep_10)



```
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))
```

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 * 50, y = value, colour = variable)) + theme_bw()
rho.map.1Mb <- rho.map.1Mb + geom_line(data = molten.rho, aes(size = variable)) + scale_size_manual(values =
rho.map.1Mb <- rho.map.1Mb + scale_color_manual(values = c("black", brewer.pal(n = 9, name = "Blues")),
rho.map.1Mb <- rho.map.1Mb + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks =
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,
```

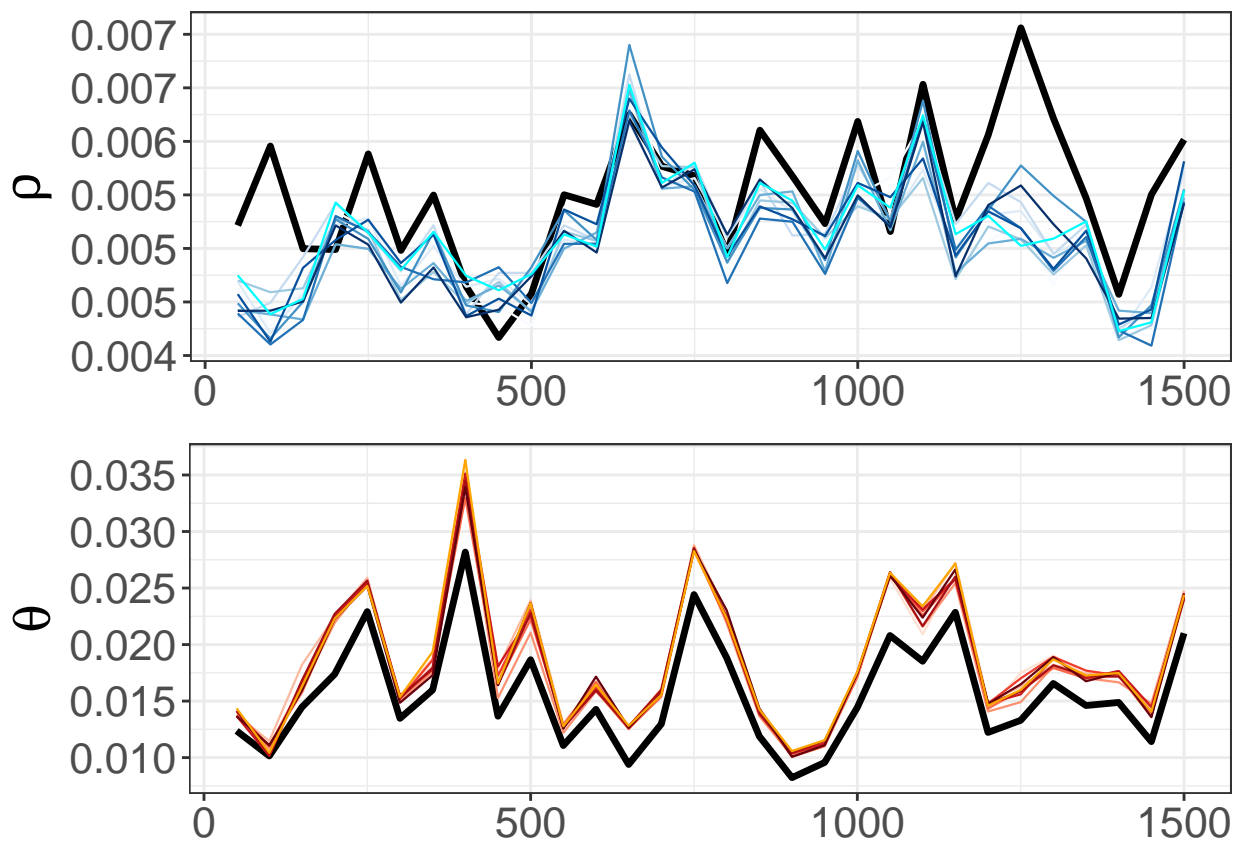
```

      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 * 50, y = value, colour = variable)) + theme_bw()
theta.map.1Mb <- theta.map.1Mb + geom_line(data = molten.theta, aes(size = variable)) + scale_size_manual(values = c(1, 2, 3, 4, 5, 6, 7, 8, 9))
theta.map.1Mb <- theta.map.1Mb + scale_color_manual(values = c("black", brewer.pal(n = 9, name = "Reds")))
theta.map.1Mb <- theta.map.1Mb + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_breaks())
theta.map.1Mb <- theta.map.1Mb + labs(title = NULL, x = NULL, y = expression(theta))
theta.map.1Mb <- theta.map.1Mb + theme(text = element_text(size = 20), axis.title.x = element_text(size = 20))

plot_grid(rho.map.1Mb, theta.map.1Mb, nrow = 2, ncol = 1)

```



Real *Drosophila* data. We 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)

```

Real Drosophila data – whole-genome analyses

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=TRUE)
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):
##      Phil
## 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 =
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

```

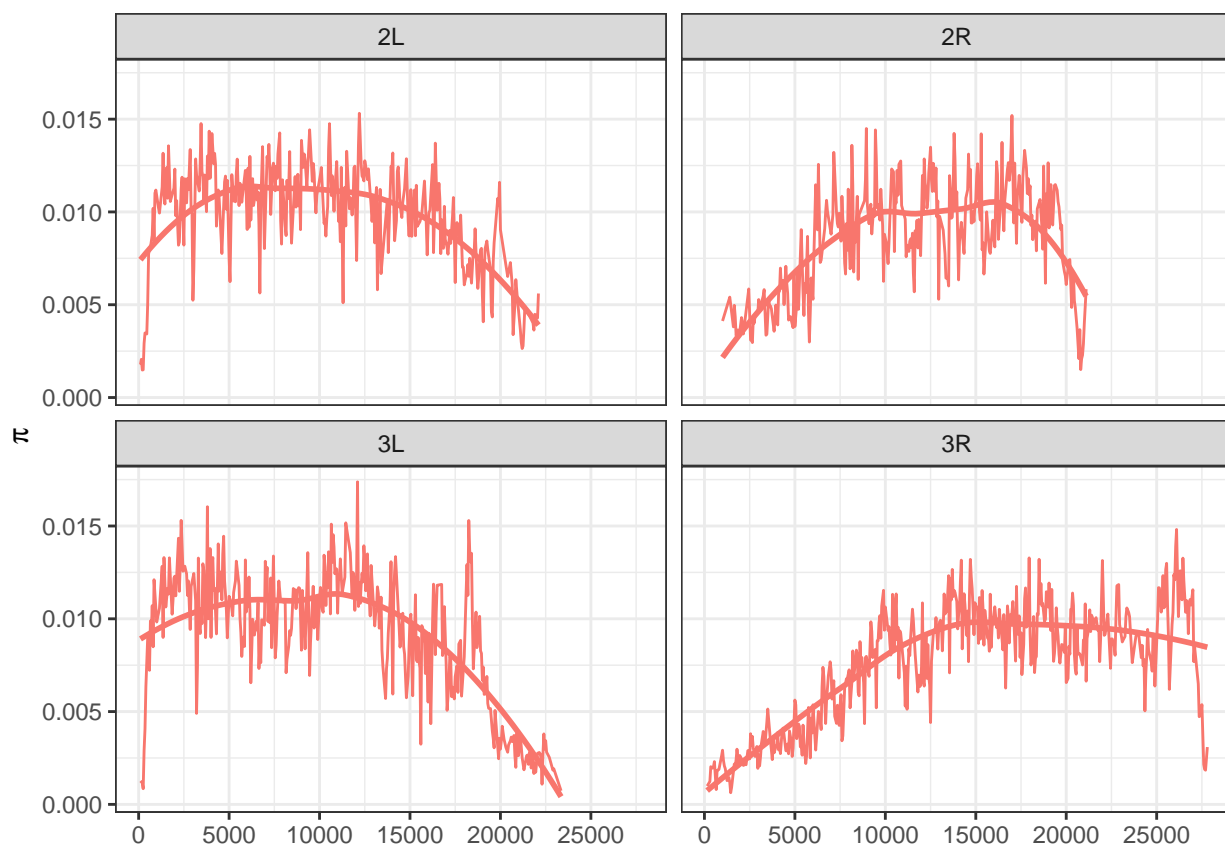
```

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 = pretty_breaks())
diversity.map <- diversity.map + labs(title = NULL, x = NULL, y = expression(pi))
diversity.map <- diversity.map + theme(axis.title.x = element_text(size = 20), axis.title.y = element_text(size = 20))
diversity.map

```

'geom_smooth()' using formula 'y ~ x'

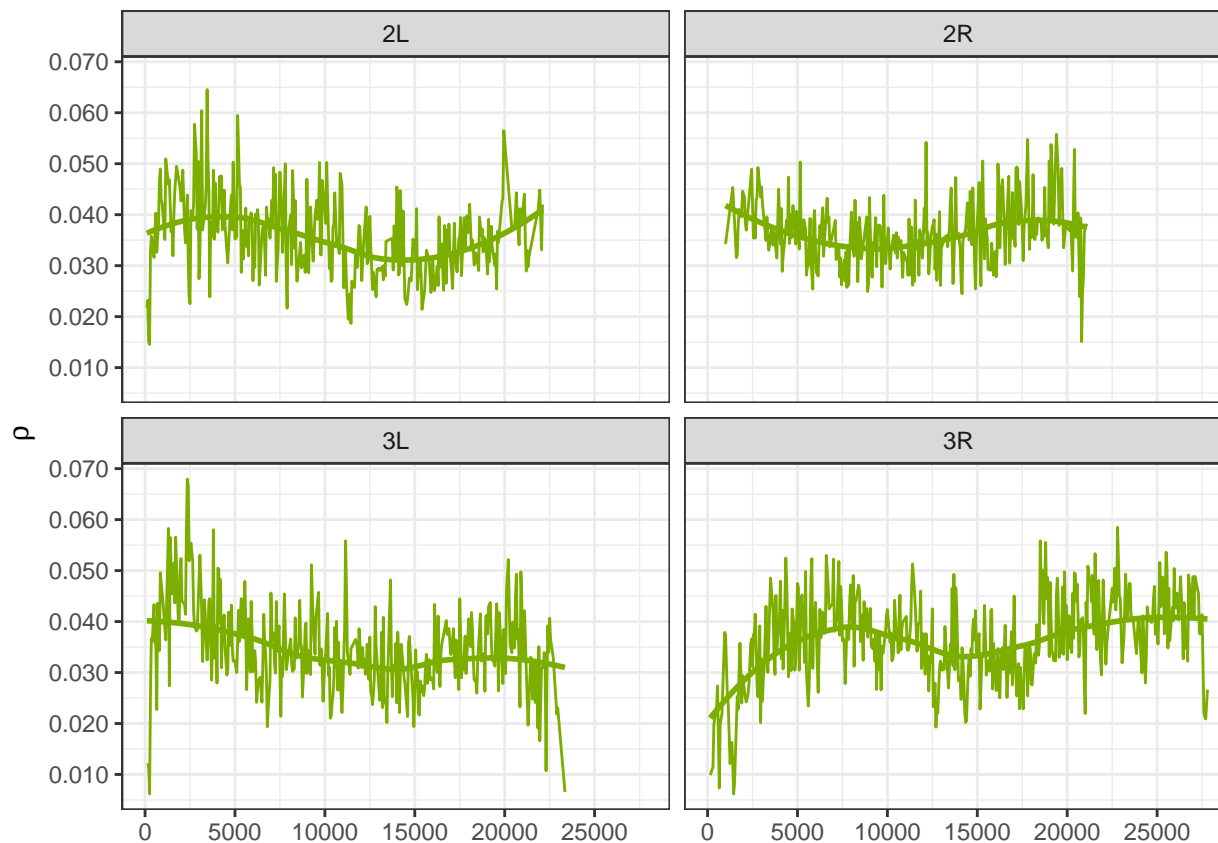


```

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

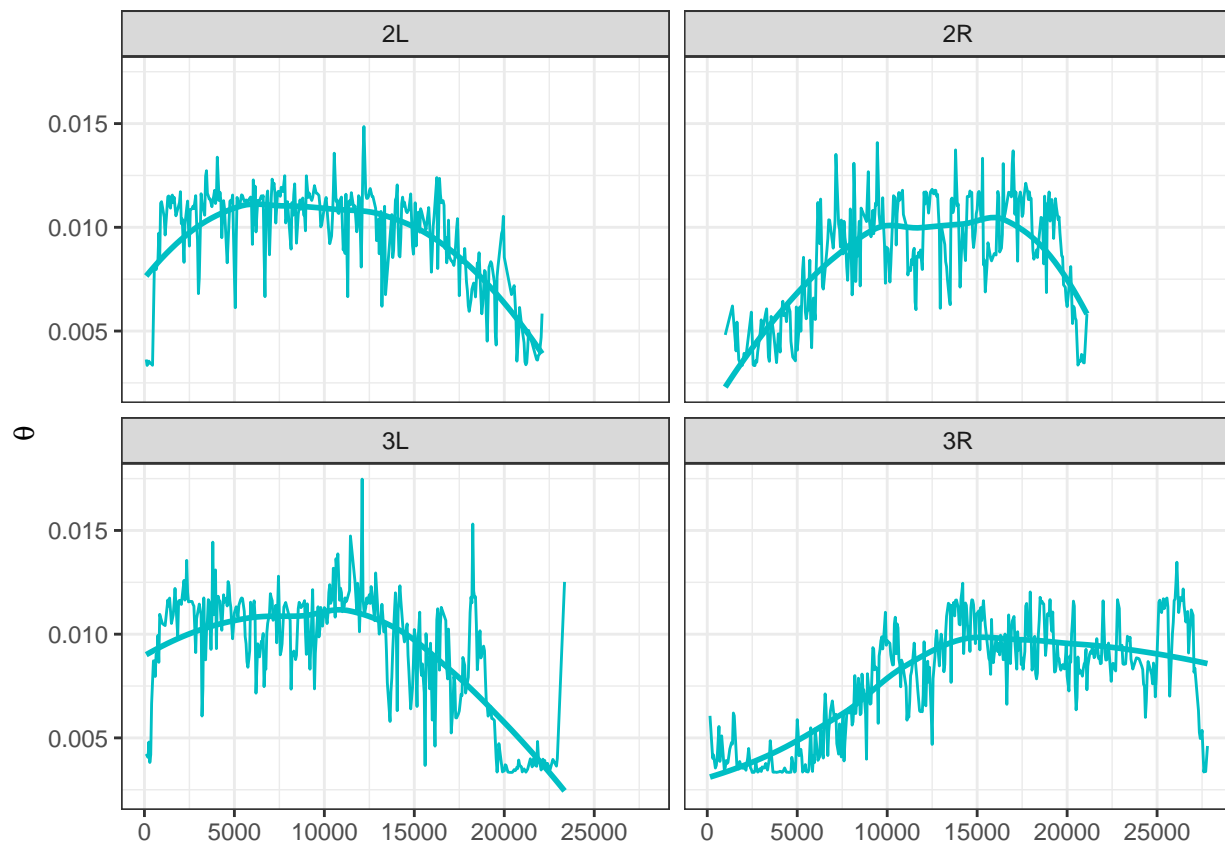
```

'geom_smooth()' using formula 'y ~ x'



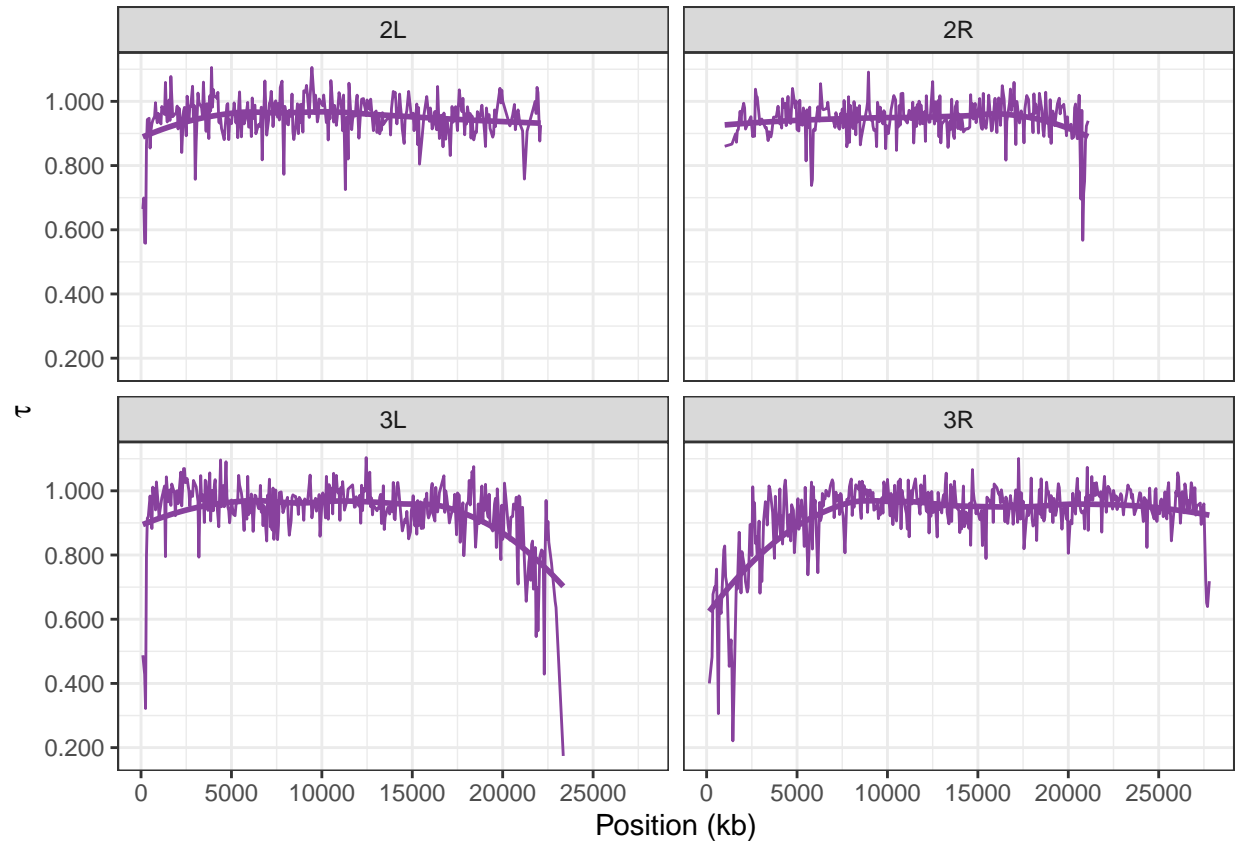
```
molten.theta <- melt(dm.lands.50kb[c(4,7,8)], id.vars = c("bin", "chr"))
theta.map <- ggplot(data = molten.theta, aes(x = bin * 50, y = value)) + facet_wrap(~chr)
theta.map <- theta.map + geom_line(data = molten.theta, colour = "#00BFC4")
theta.map <- theta.map + geom_smooth(method = "loess", se = 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
```

```
## 'geom_smooth()' using formula 'y ~ x'
```



```
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
```

```
## 'geom_smooth()' using formula 'y ~ x'
```



```
# 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

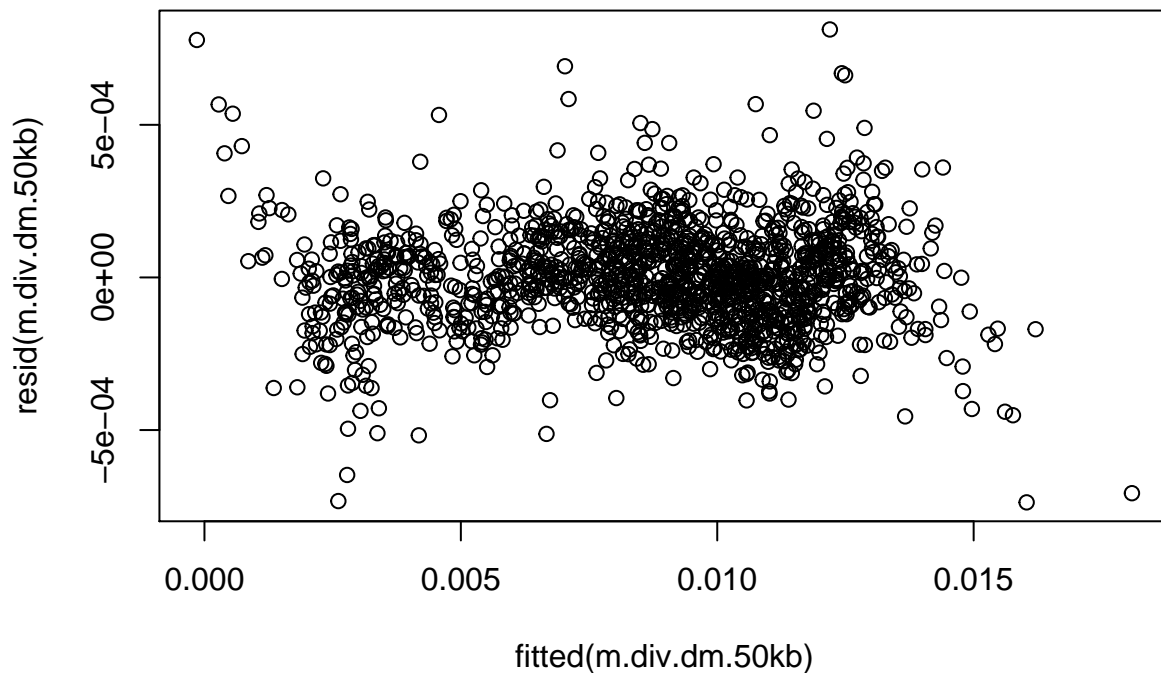
# Linear models
# centering
dm.lands.50kb$thetaC <- dm.lands.50kb$theta - mean(dm.lands.50kb$theta)
dm.lands.50kb$tmrcaC <- dm.lands.50kb$tmrca - mean(dm.lands.50kb$tmrca)
dm.lands.50kb$rhoC <- dm.lands.50kb$rho - mean(dm.lands.50kb$rho)

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

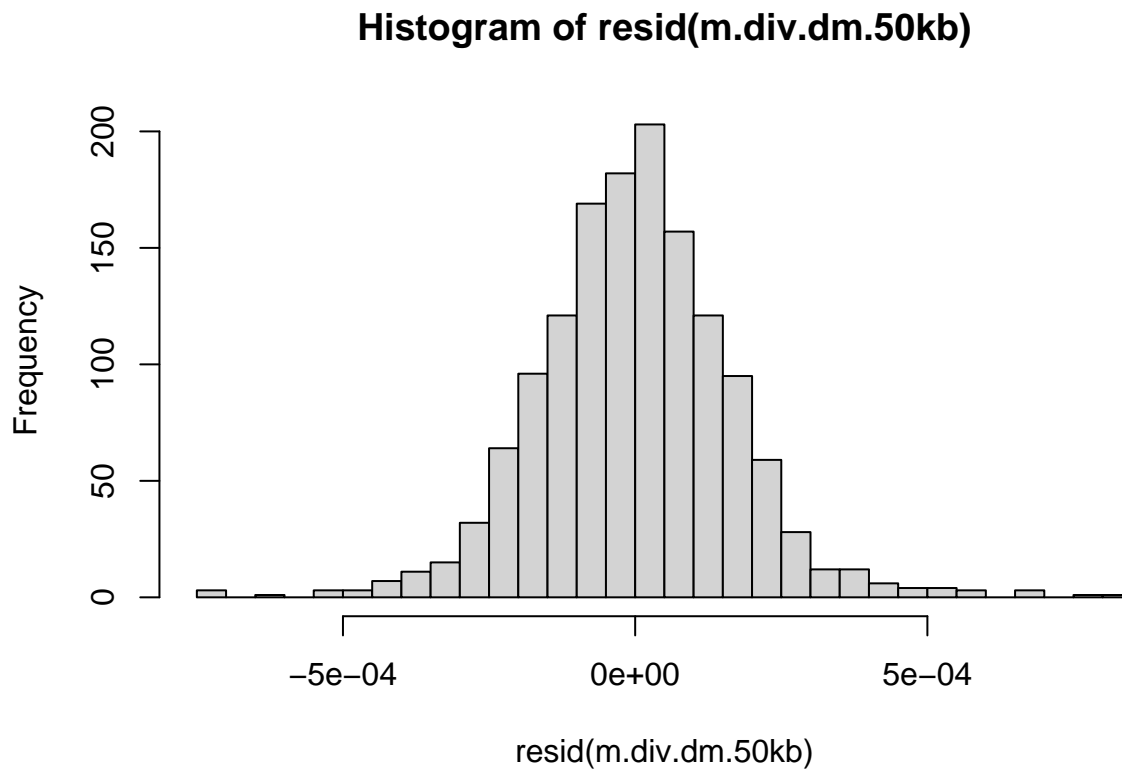
m.div.dm.50kb <- lm( diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC), data = dm.lands.50kb)

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 = 0.6116
```

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

Real data 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

```

'geom_smooth()' using formula 'y ~ x'



```

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)

```

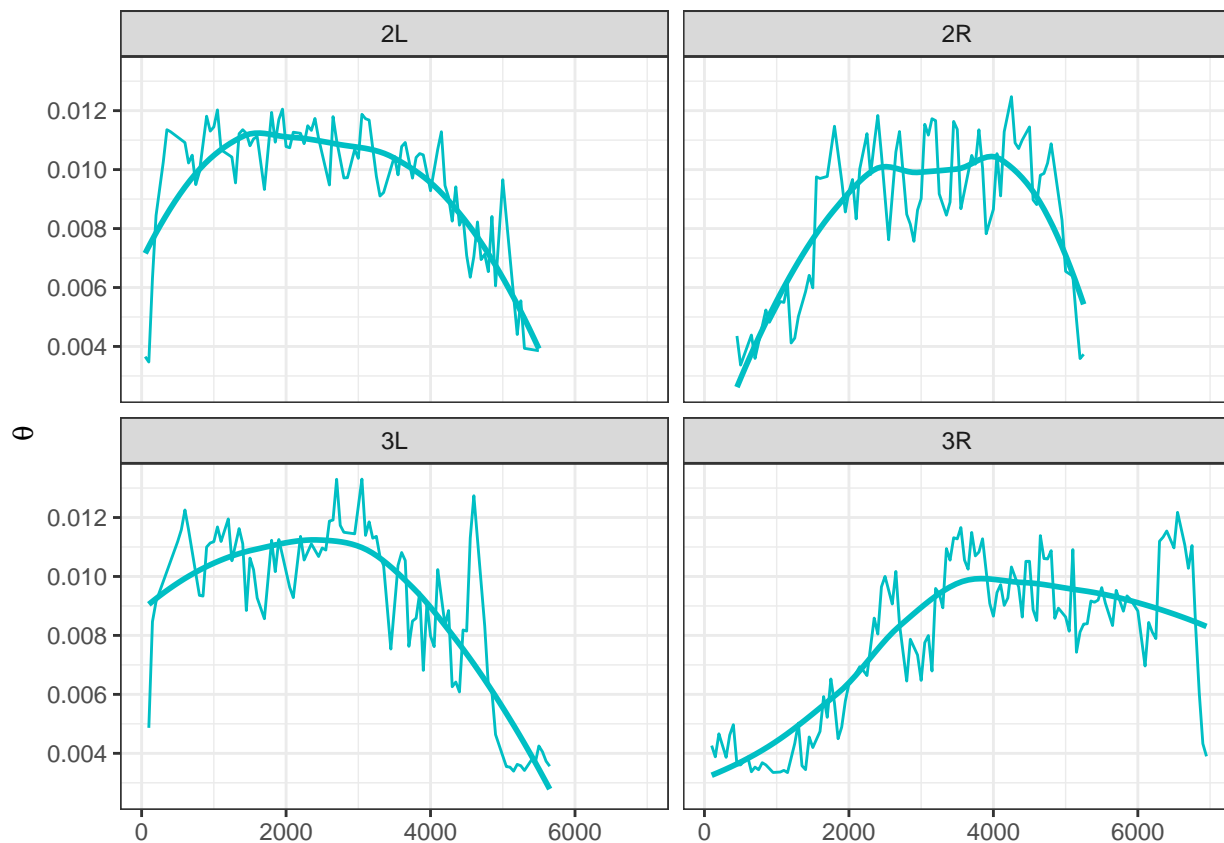
```
rho.map <- rho.map + geom_line(data = molten.rho, colour = "#7CAE00")
rho.map <- rho.map + geom_smooth(method = "loess", se = F, colour = "#7CAE00")
rho.map <- rho.map + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_breaks())
rho.map <- rho.map + labs(title = NULL, 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
```

```
## 'geom_smooth()' using formula 'y ~ x'
```



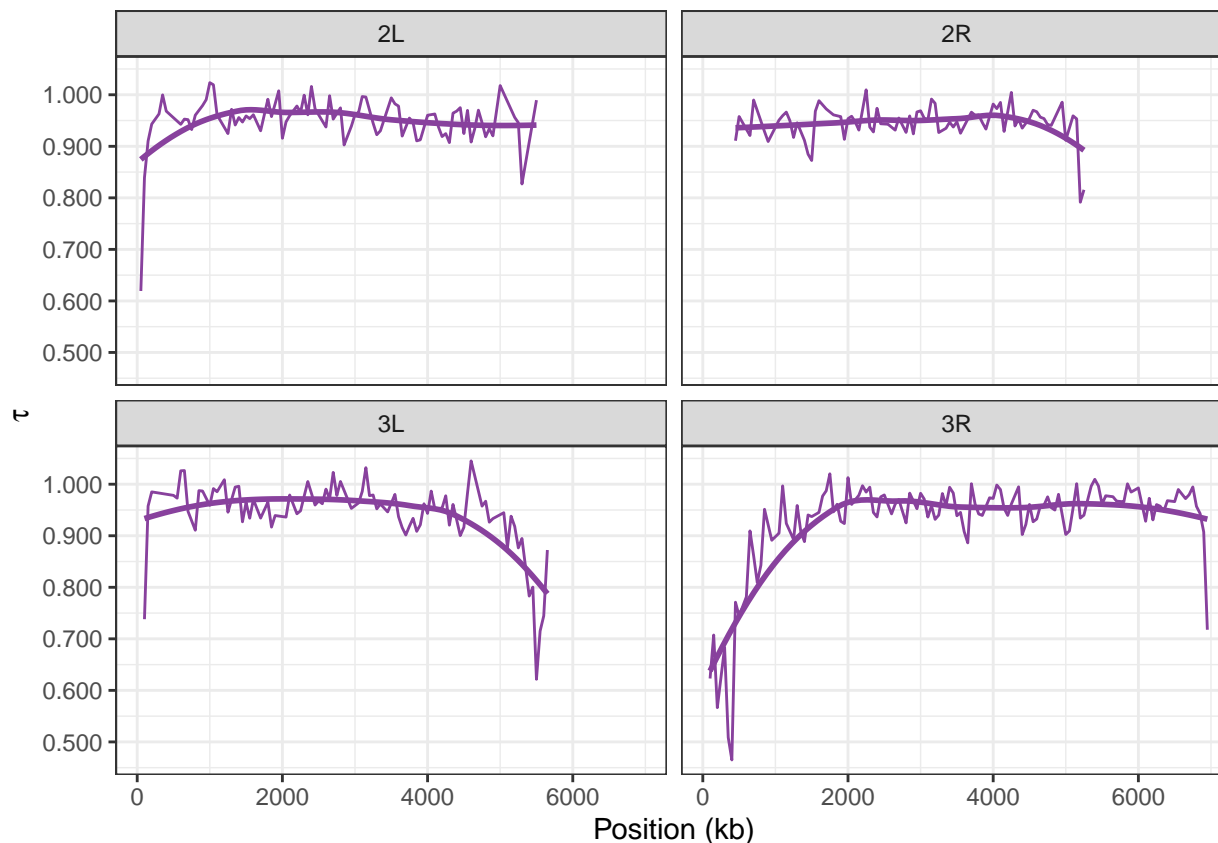
```
molten.theta <- melt(dm.lands.200kb[c(4,7,8)], id.vars = c("bin", "chr"))
theta.map <- ggplot(data = molten.theta, aes(x = bin * 50, y = value)) + facet_wrap(~chr)
theta.map <- theta.map + geom_line(data = molten.theta, colour = "#00BFC4")
theta.map <- theta.map + geom_smooth(method = "loess", se = 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
```

```
## 'geom_smooth()' using formula 'y ~ x'
```



```
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
```

```
## 'geom_smooth()' using formula 'y ~ x'
```



```
# 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

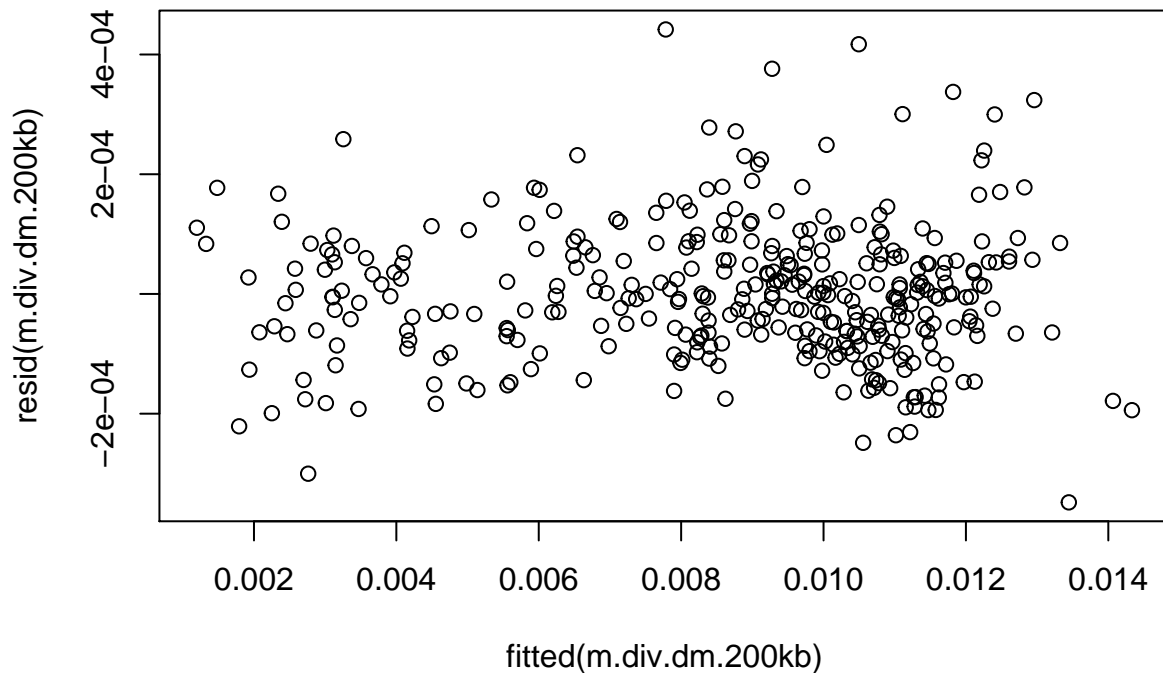
# Linear models
# centering
dm.lands.200kb$thetaC <- dm.lands.200kb$theta - mean(dm.lands.200kb$theta)
dm.lands.200kb$tmrcaC <- dm.lands.200kb$tmrca - mean(dm.lands.200kb$tmrca)
dm.lands.200kb$rhoC <- dm.lands.200kb$rho - mean(dm.lands.200kb$rho)

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

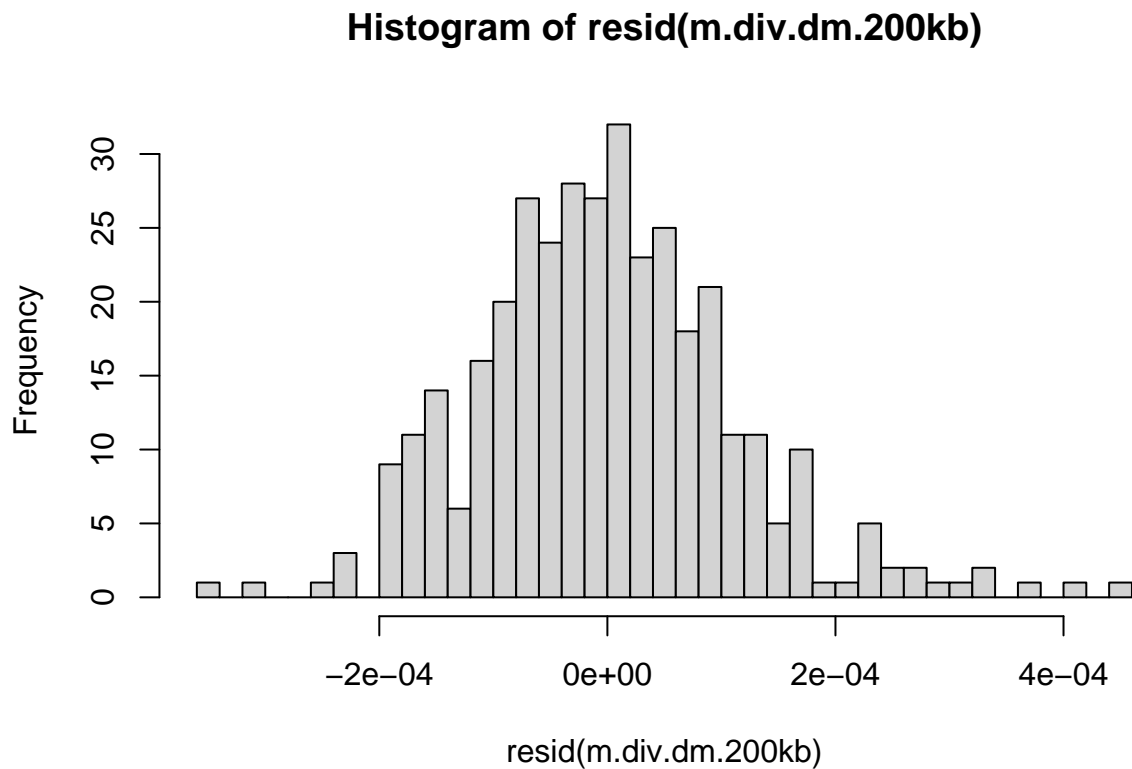
m.div.dm.200kb <- lm(community ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC), data = dm.lands.200kb)

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 = 0.9684
```

```
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
```

Real data 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), n

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), method = "REML")

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, col.names = F)

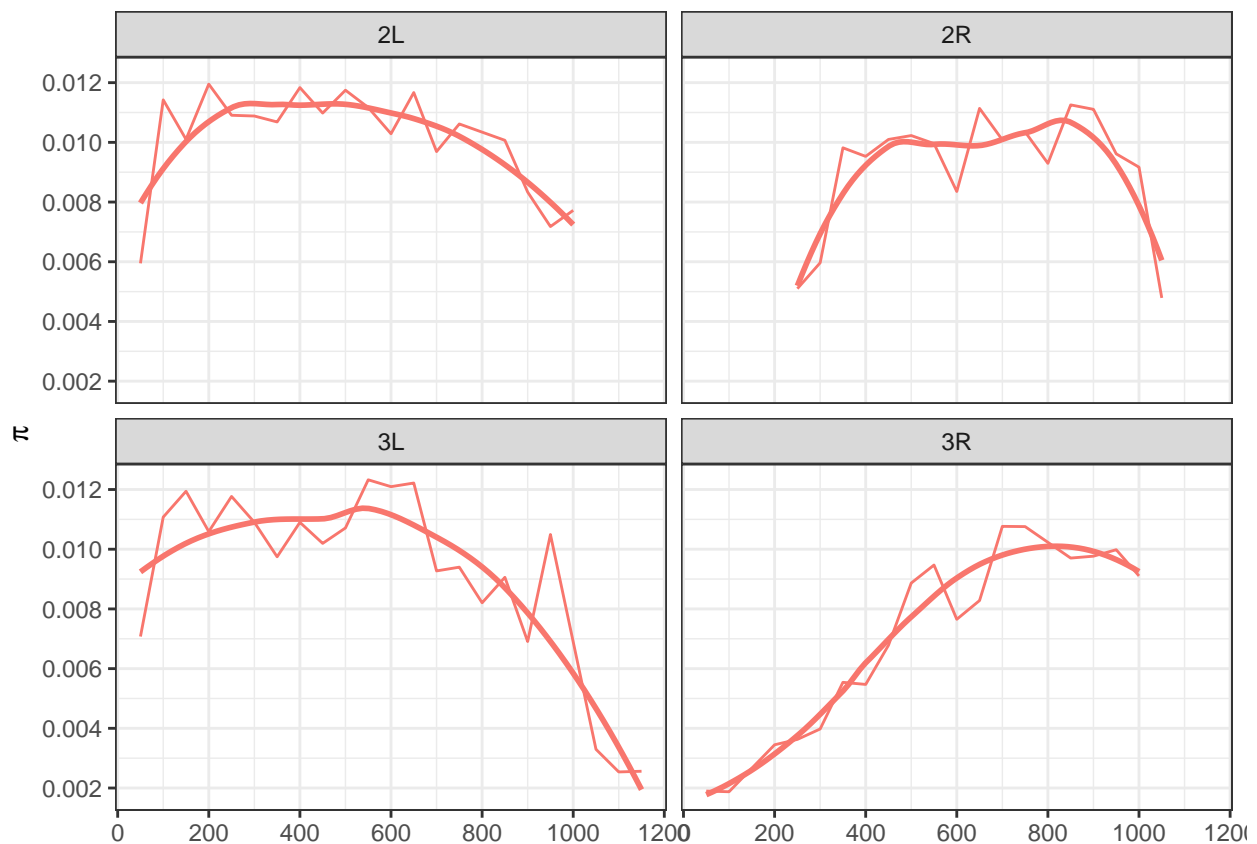
# Plots
scale.3d <- function(x) sprintf("%.3f", x) # digits shown in y axis

setTimeLimit(cpu = Inf, elapsed = Inf, transient = F)

molten.diversity <- melt(dm.lands.1Mb[c(3,7,8)], id.vars = c("bin", "chr"))
diversity.map <- ggplot(data = molten.diversity, aes(x = bin * 50, y = value)) + facet_wrap(~chr)
diversity.map <- diversity.map + geom_line(data = molten.diversity, colour = "#F8766D")
diversity.map <- diversity.map + geom_smooth(method = "loess", se = F, colour = "#F8766D")
diversity.map <- diversity.map + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = 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

```

'geom_smooth()' using formula 'y ~ x'



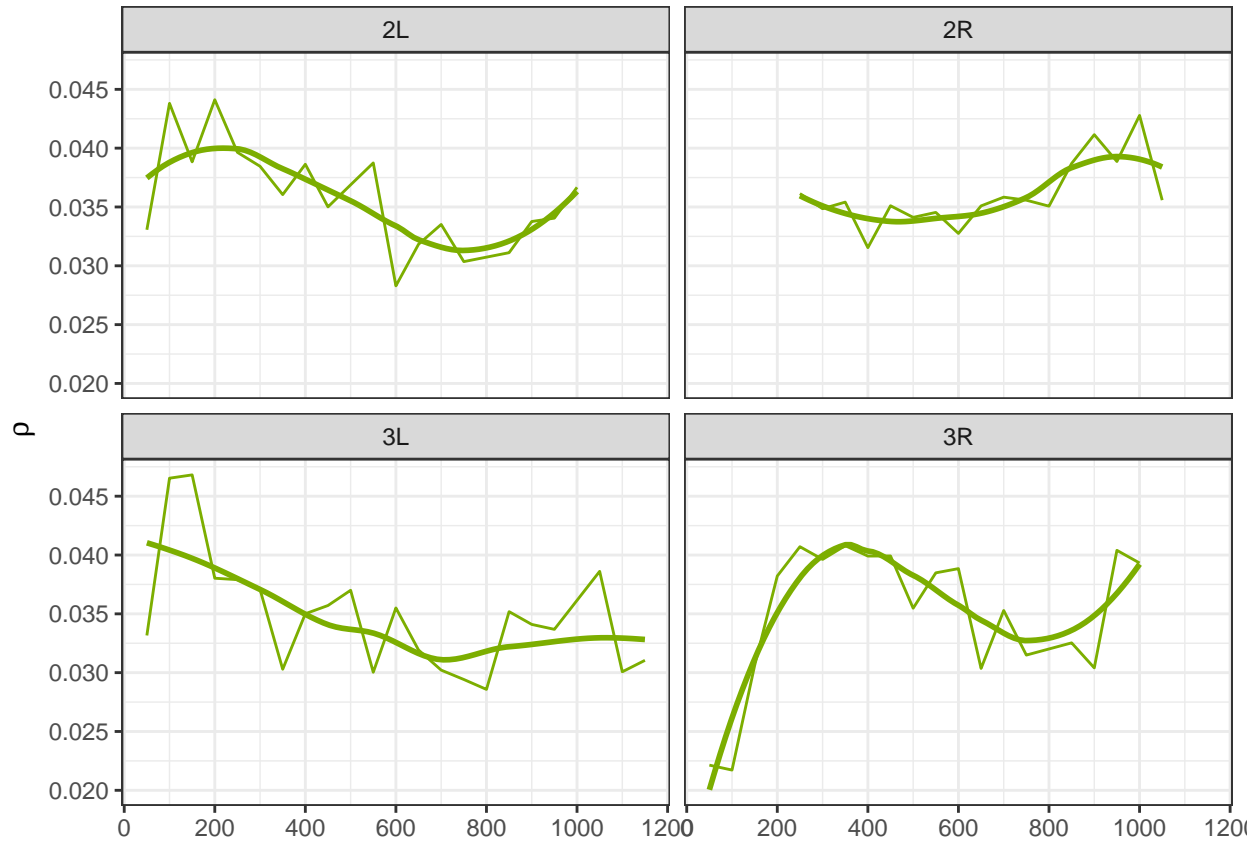
```

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)

```

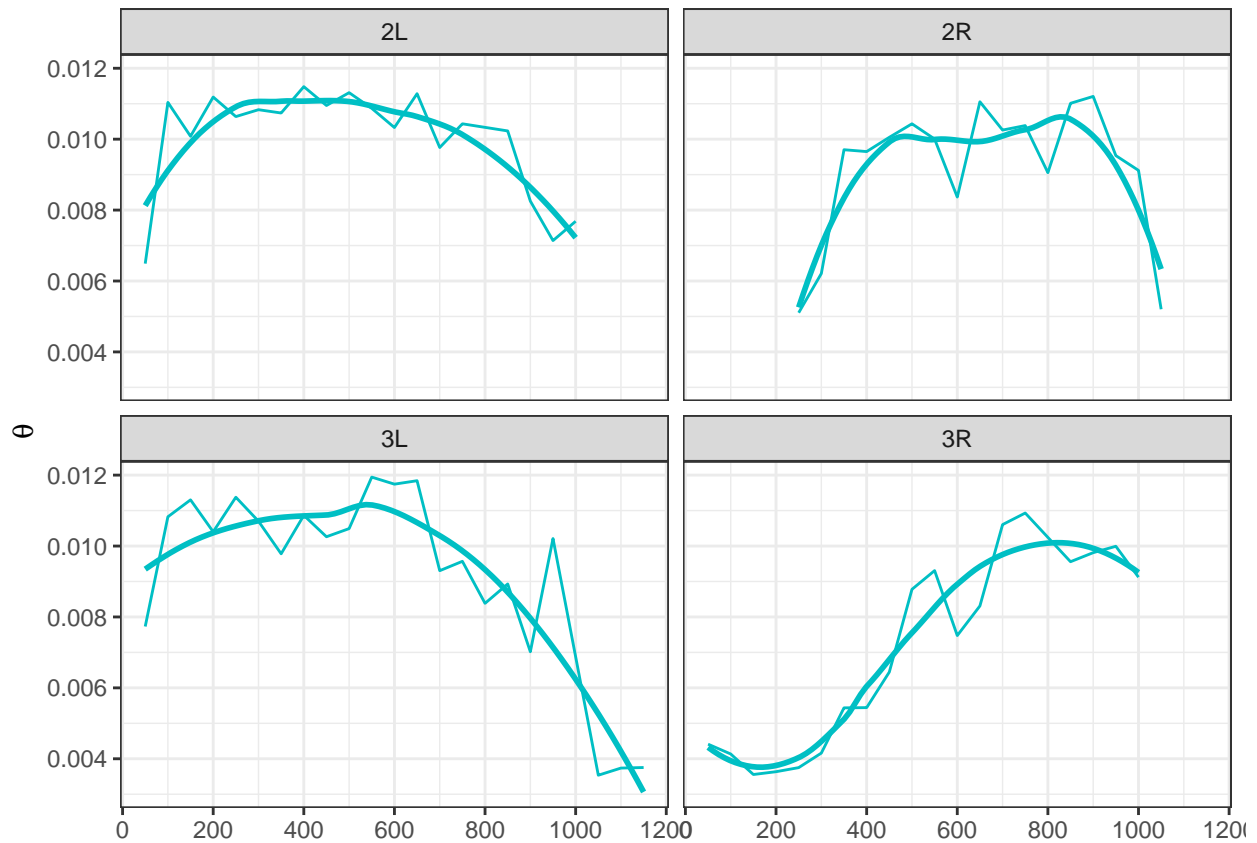
```
rho.map <- rho.map + geom_line(data = molten.rho, colour = "#7CAE00")
rho.map <- rho.map + geom_smooth(method = "loess", se = F, colour = "#7CAE00")
rho.map <- rho.map + scale_x_continuous(breaks = pretty_breaks()) + scale_y_continuous(breaks = pretty_breaks())
rho.map <- rho.map + labs(title = NULL, 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
```

'geom_smooth()' using formula 'y ~ x'



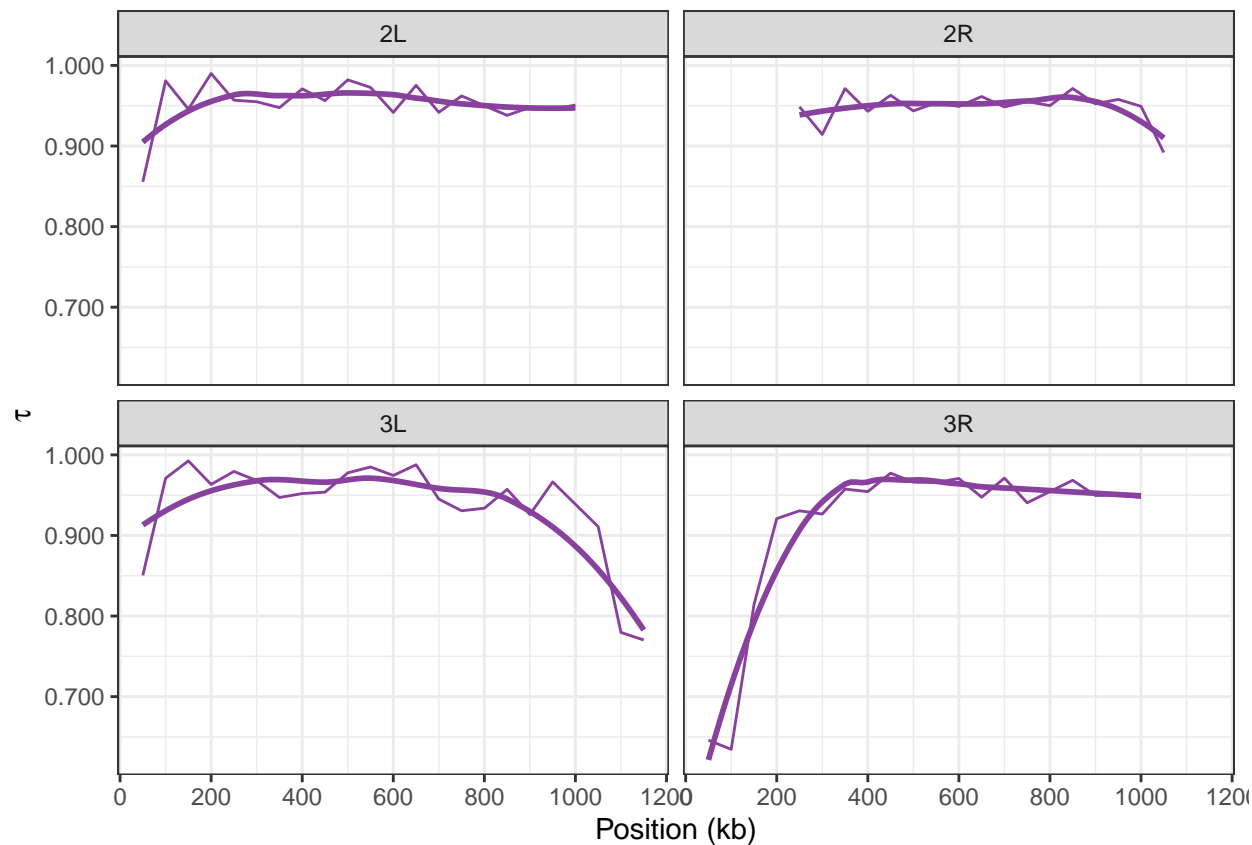
```
molten.theta <- melt(dm.lands.1Mb[c(4,7,8)], id.vars = c("bin", "chr"))
theta.map <- ggplot(data = molten.theta, aes(x = bin * 50, y = value)) + facet_wrap(~chr)
theta.map <- theta.map + geom_line(data = molten.theta, colour = "#00BFC4")
theta.map <- theta.map + geom_smooth(method = "loess", se = 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
```

'geom_smooth()' using formula 'y ~ x'



```
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
```

```
## 'geom_smooth()' using formula 'y ~ x'
```



```
# 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

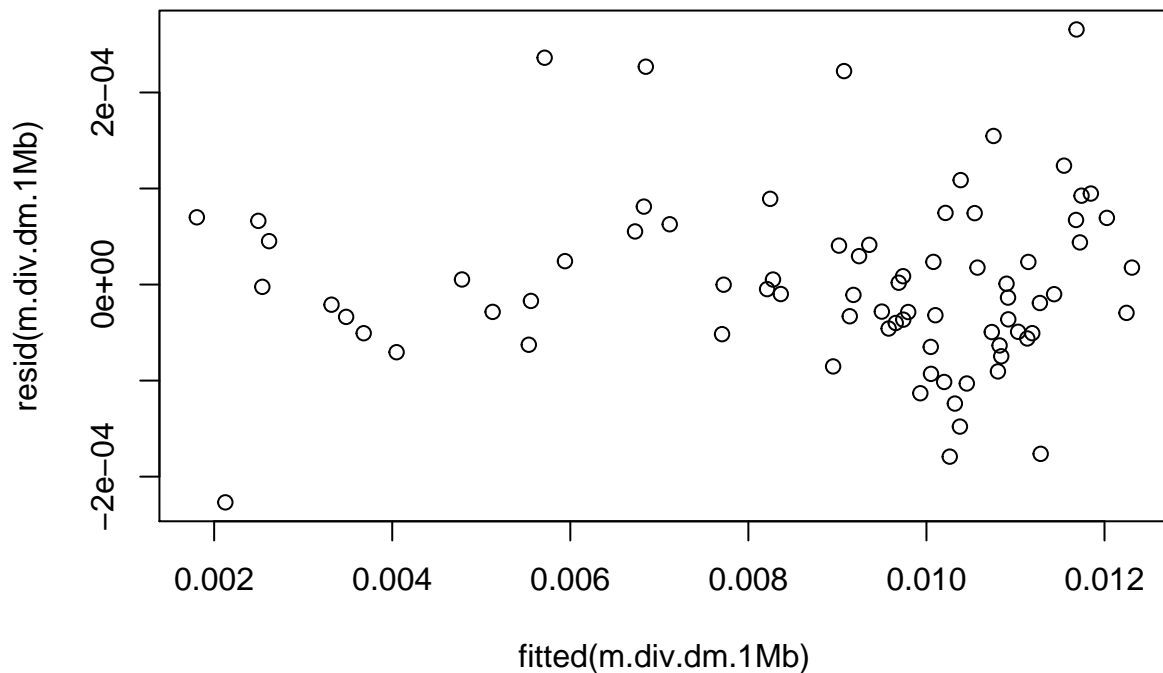
# Linear models
# centering
dm.lands.1Mb$thetaC <- dm.lands.1Mb$theta - mean(dm.lands.1Mb$theta)
dm.lands.1Mb$tmrcaC <- dm.lands.1Mb$tmrca - mean(dm.lands.1Mb$tmrca)
dm.lands.1Mb$rhoC <- dm.lands.1Mb$rho - mean(dm.lands.1Mb$rho)

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

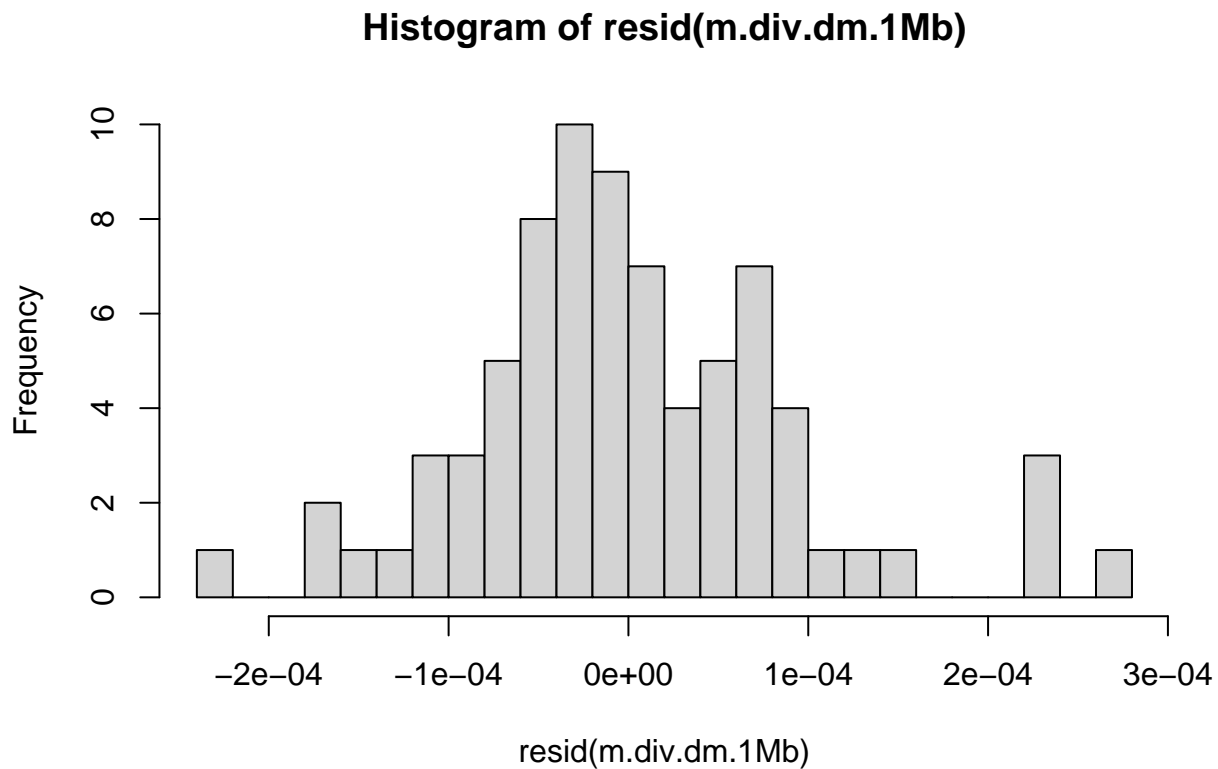
m.div.dm.1Mb <- lm(diversity ~ (thetaC + rhoC + tmrcaC + thetaC:tmrcaC), data = dm.lands.1Mb)

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 = "REML")

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 = "REML")

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), metho

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
```

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:

```
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
```

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 <- ddpby(.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(evolve.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)], evolve.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:

```

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

# linear model in coding regions

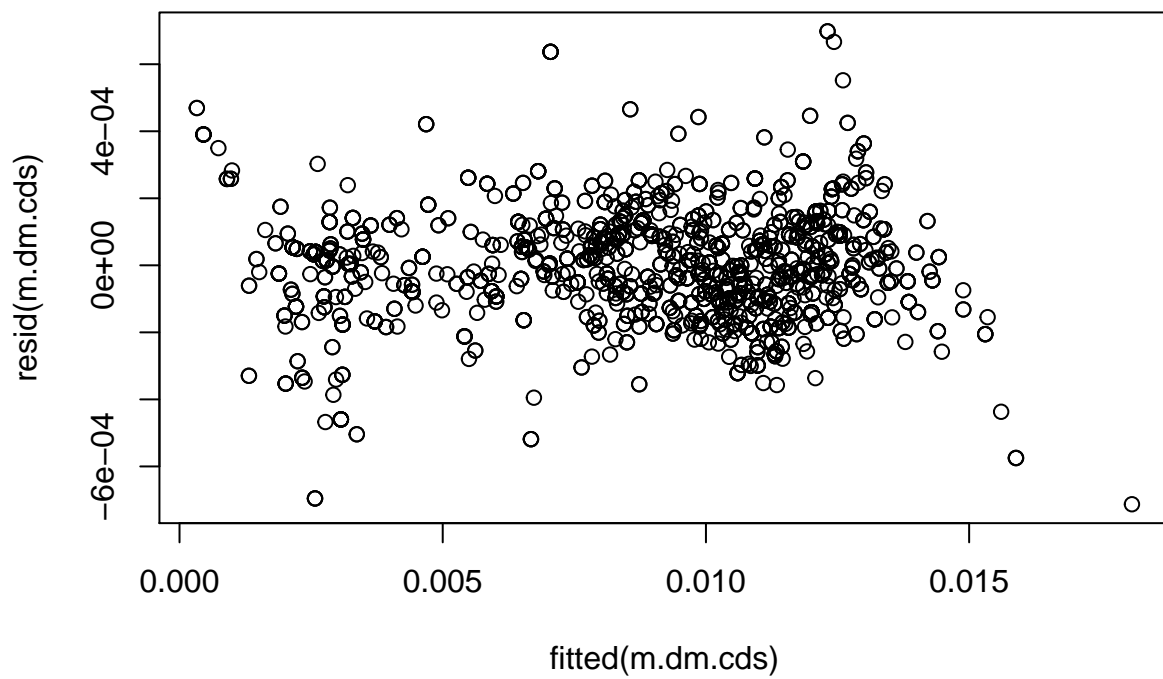
# centering
dm.lands.evolrate$thetaC <- dm.lands.evolrate$theta - mean(dm.lands.evolrate$theta)
dm.lands.evolrate$tmrcaC <- dm.lands.evolrate$tmrca - mean(dm.lands.evolrate$tmrca)
dm.lands.evolrate$rhoC <- dm.lands.evolrate$rho - mean(dm.lands.evolrate$rho)

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

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

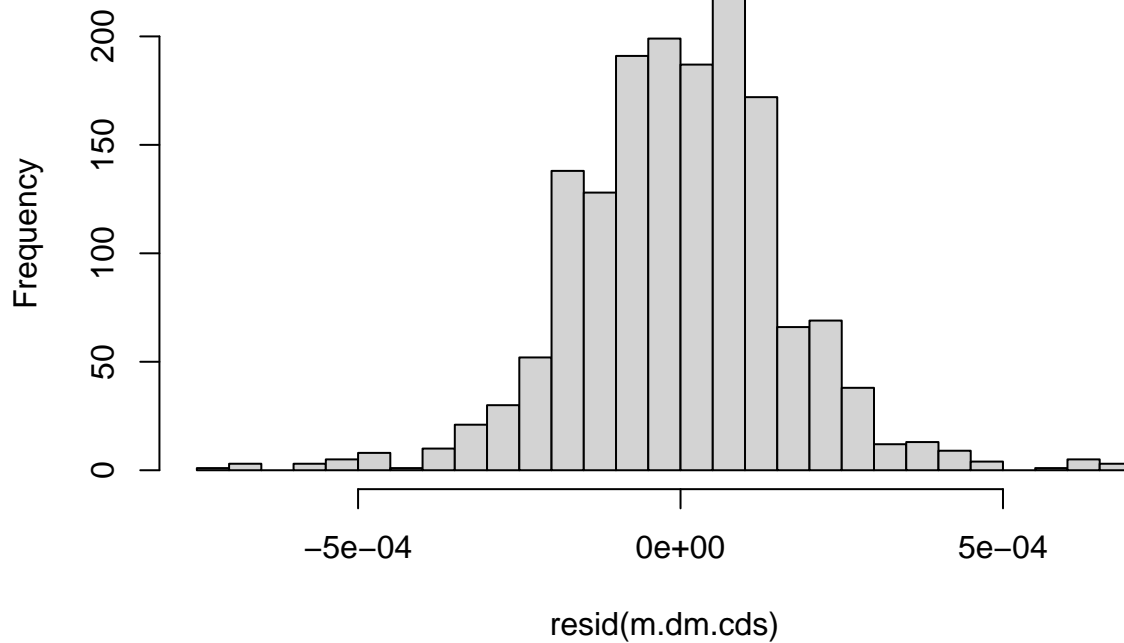
plot(resid(m.dm.cds)~fitted(m.dm.cds))

```



```
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 = 0.338
```

```
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")

## Warning in cor.test.default(dm.lands.evolrate$PiN, dm.lands.evolrate$theta, :
## Cannot compute exact p-value with ties

##
## 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")

## Warning in cor.test.default(dm.lands.evolrate$PiS, dm.lands.evolrate$theta, :
## Cannot compute exact p-value with ties

##
## 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")
```

```
## Warning in cor.test.default(dm.lands.evolrate$dS, dm.lands.evolrate$theta, :
## Cannot compute exact p-value with ties
```

```
##
## 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")
```

```
## Warning in cor.test.default(dm.lands.evolrate$PiS, dm.lands.evolrate$rho, :
## Cannot compute exact p-value with ties
```

```
##
## 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")
```

```
## Warning in cor.test.default(dm.lands.evolrate$dS, dm.lands.evolrate$rho, :
## Cannot compute exact p-value with ties
```

```
##
## 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
```

Drosophila-like neutral simulations of 2L (True landscapes for plotting)

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)

# rep 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")
```

```
## 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 = 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")
```

```
## 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 = 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)

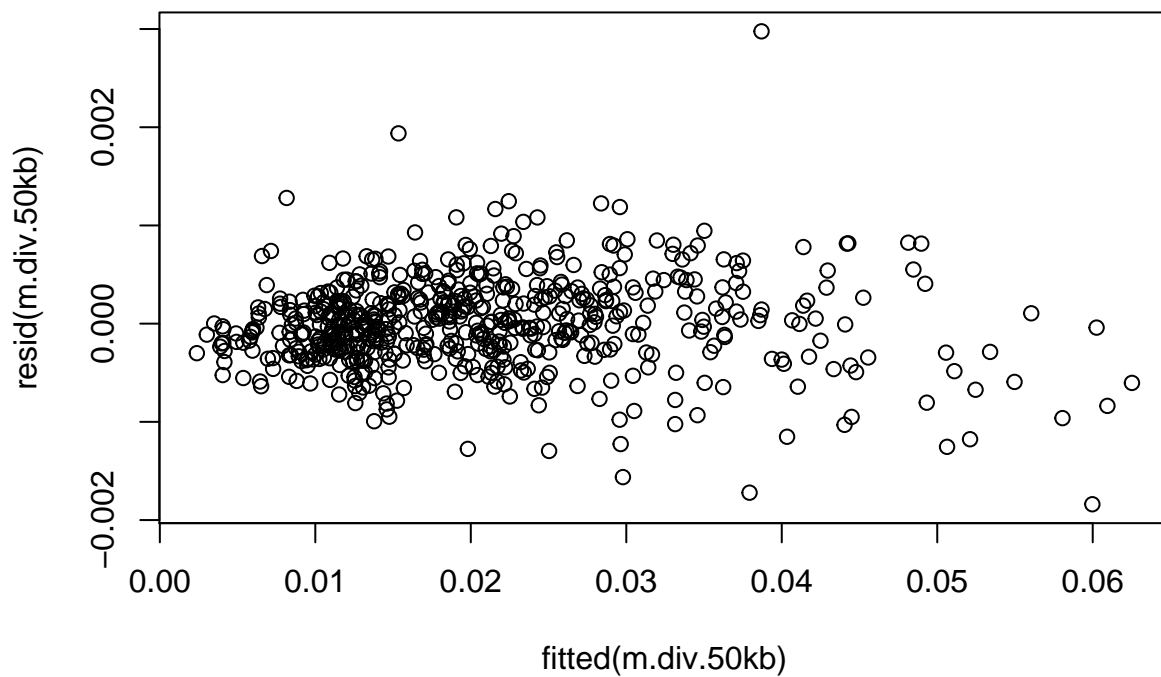
sim.lands.50kb$bin <- 1:nrow(sim.lands.50kb)

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)
```

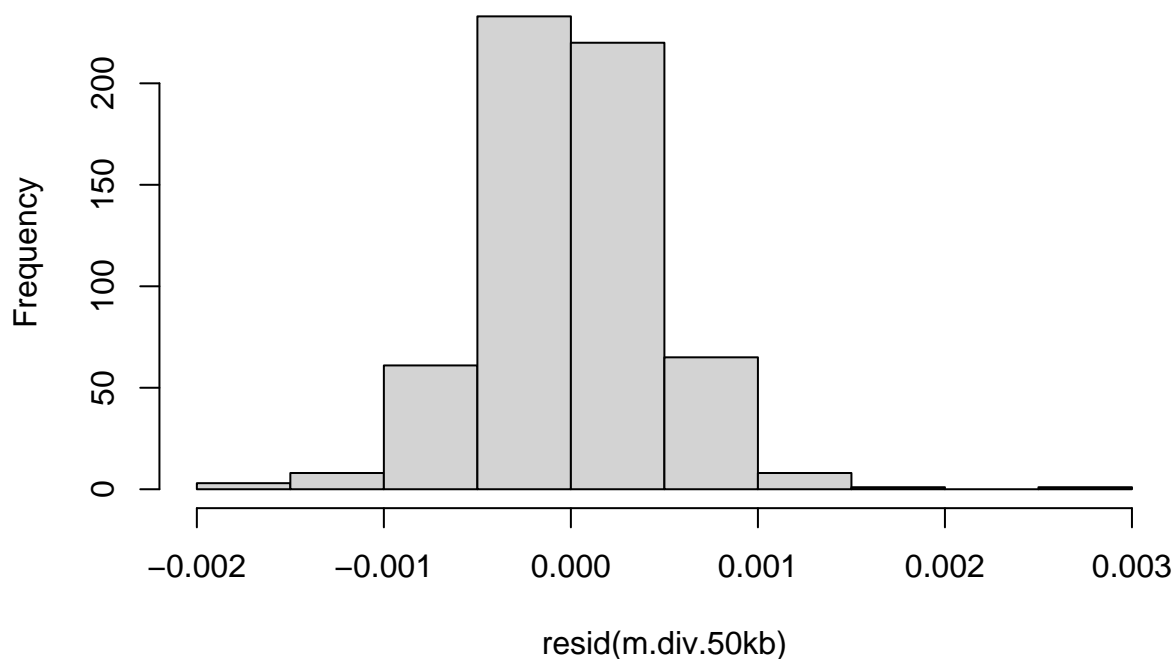
```
##  
## Durbin-Watson test  
##  
## data: m.div.50kb  
## DW = 2.1111, p-value = 0.9056  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

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

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

Histogram of resid(m.div.50kb)



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

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

```

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

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

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

```
# rep_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")
```

```
## 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 = 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")
```

```
## 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 = 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)
```

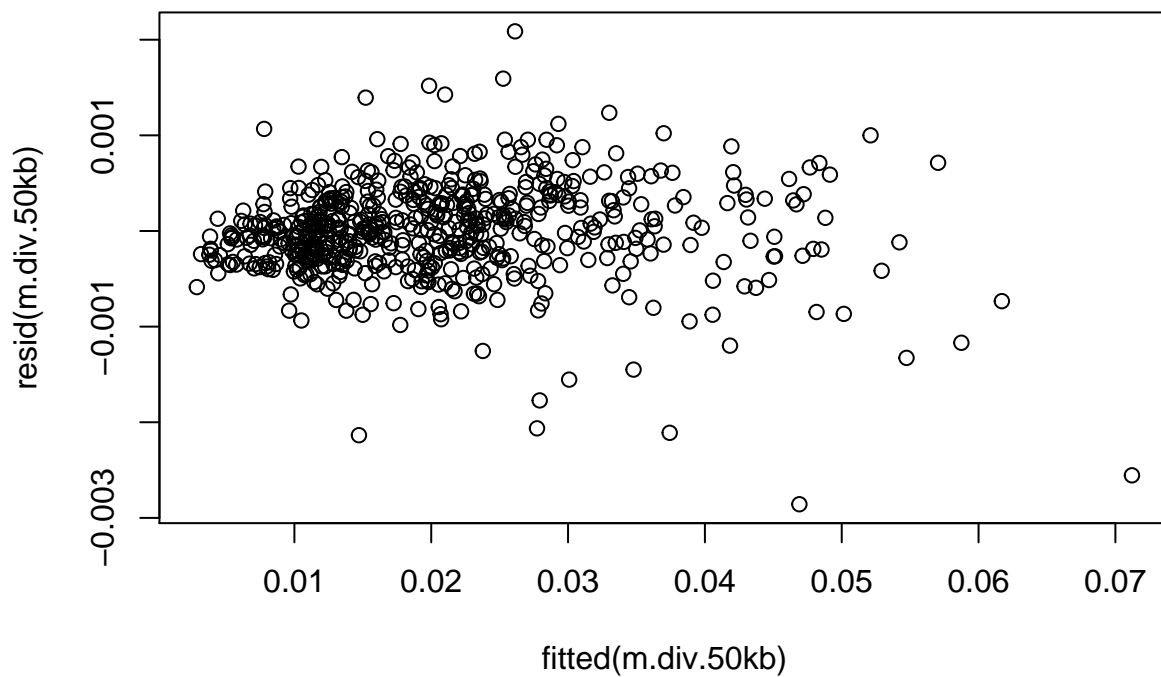
```
sim.lands.50kb$bin <- 1:nrow(sim.lands.50kb)
```

```
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)
```

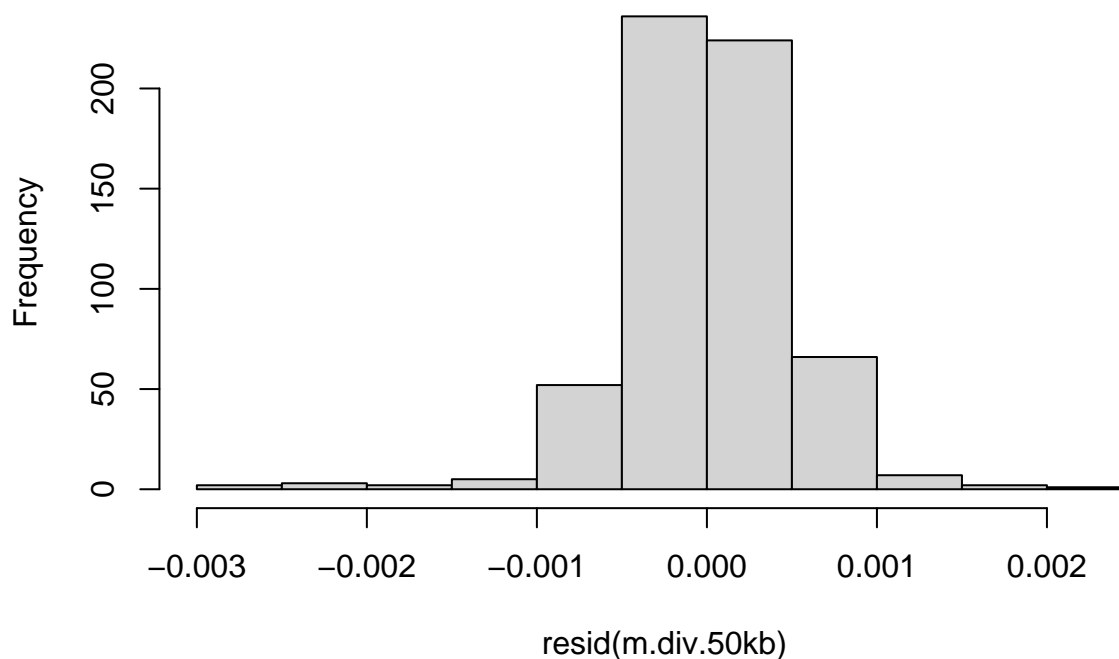
```
##  
## Durbin-Watson test  
##  
## data: m.div.50kb  
## DW = 1.9715, p-value = 0.3445  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.div.50kb  
## HMC = 0.51438, p-value = 0.678
```

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

Histogram of resid(m.div.50kb)



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

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##     data = sim.lands.50kb)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.857e-03 -2.640e-04  1.830e-06  2.990e-04  2.087e-03
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.057e-02  2.047e-05 1005.301  <2e-16 ***
## thetaC       1.299e+00  2.448e-03  530.815  <2e-16 ***
## rhoC        -1.009e-02  6.919e-03   -1.459    0.145
## tmrcaC       2.385e-02  2.831e-04  84.273   <2e-16 ***
## thetaC:tmrcaC 1.515e+00  3.222e-02  47.015   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0005011 on 595 degrees of freedom
## Multiple R-squared:  0.9979, Adjusted R-squared:  0.9979
## F-statistic: 7.16e+04 on 4 and 595 DF, p-value: < 2.2e-16
```

```

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

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

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

```

```

## 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 = 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")

```

```

## 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

```

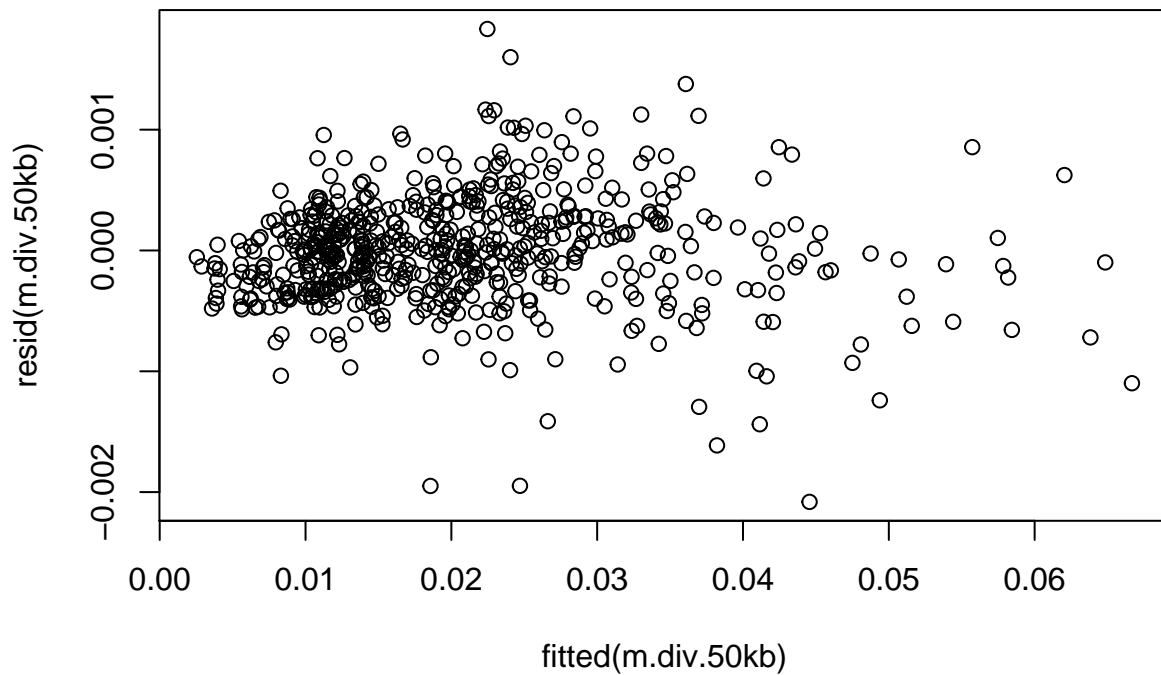


```
##
## data: rho and tmrca
## S = 35383984, p-value = 0.6757
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.01710883

# 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))
```



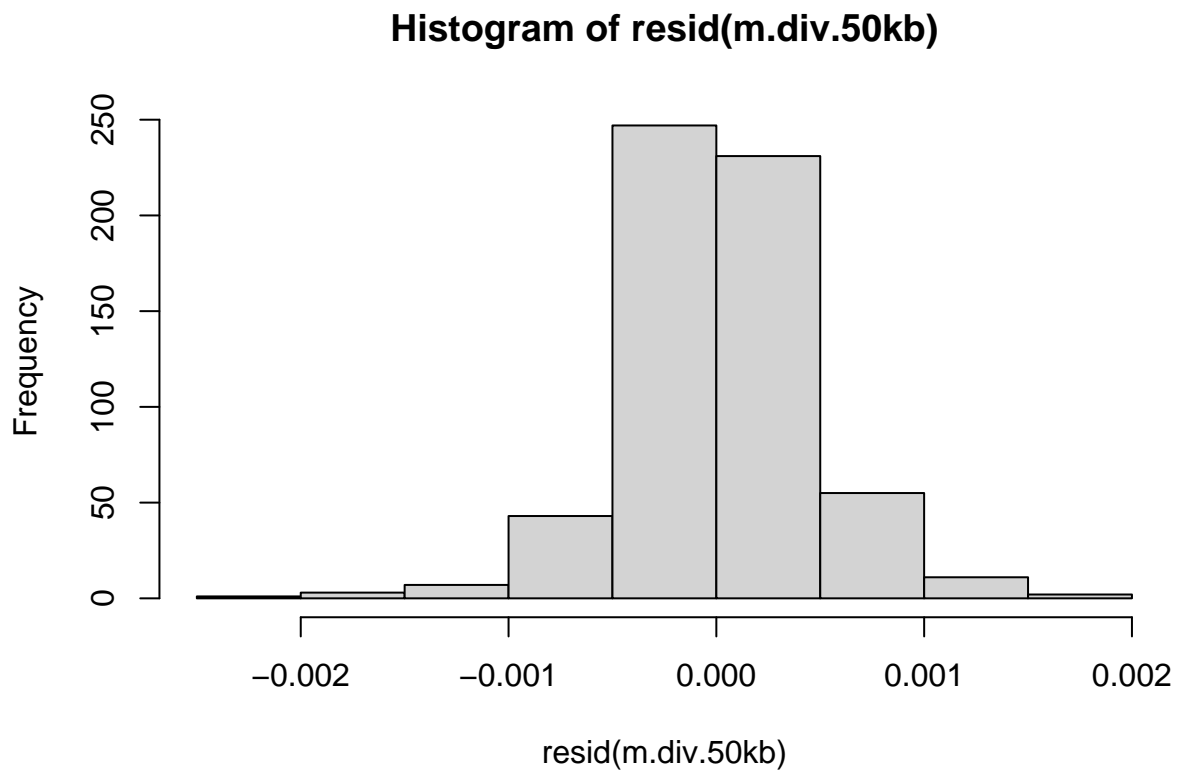
```
dwtest(m.div.50kb)
```

```
##
## 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 = 0.561
```

```
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

# rep_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")
```

```
## 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 = 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")
```

```
## 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
```

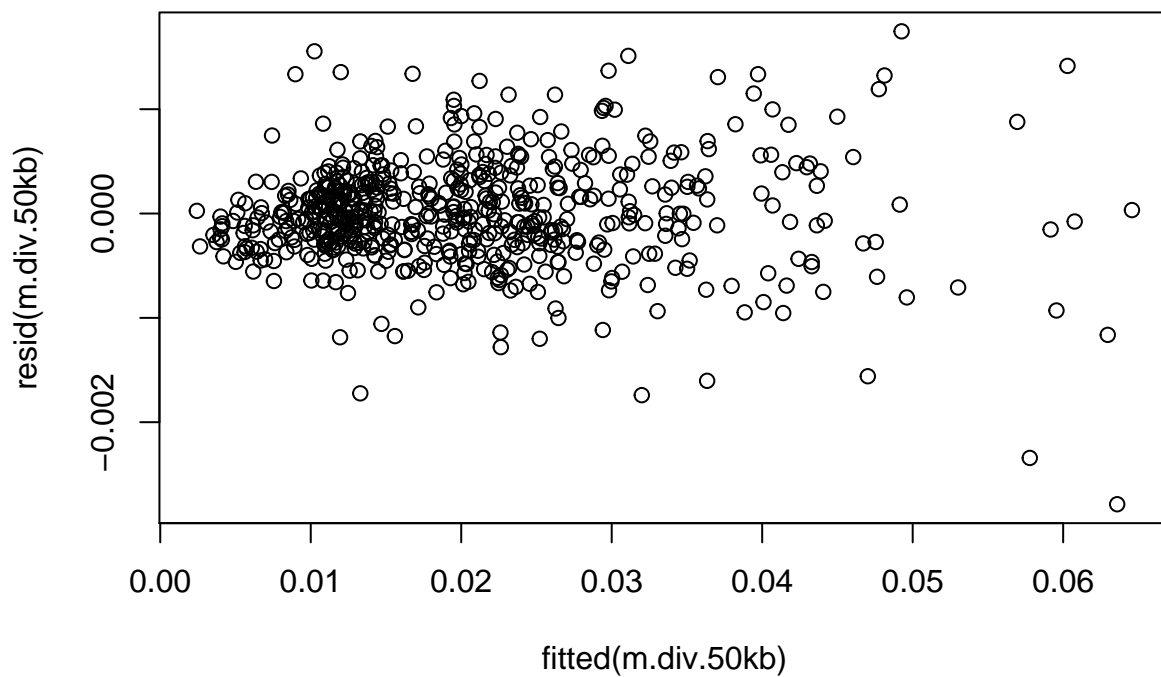
```
cor.test(~rho+tmrca, data = sim.lands.50kb, method = "spearman")
```

```
##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 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)
```

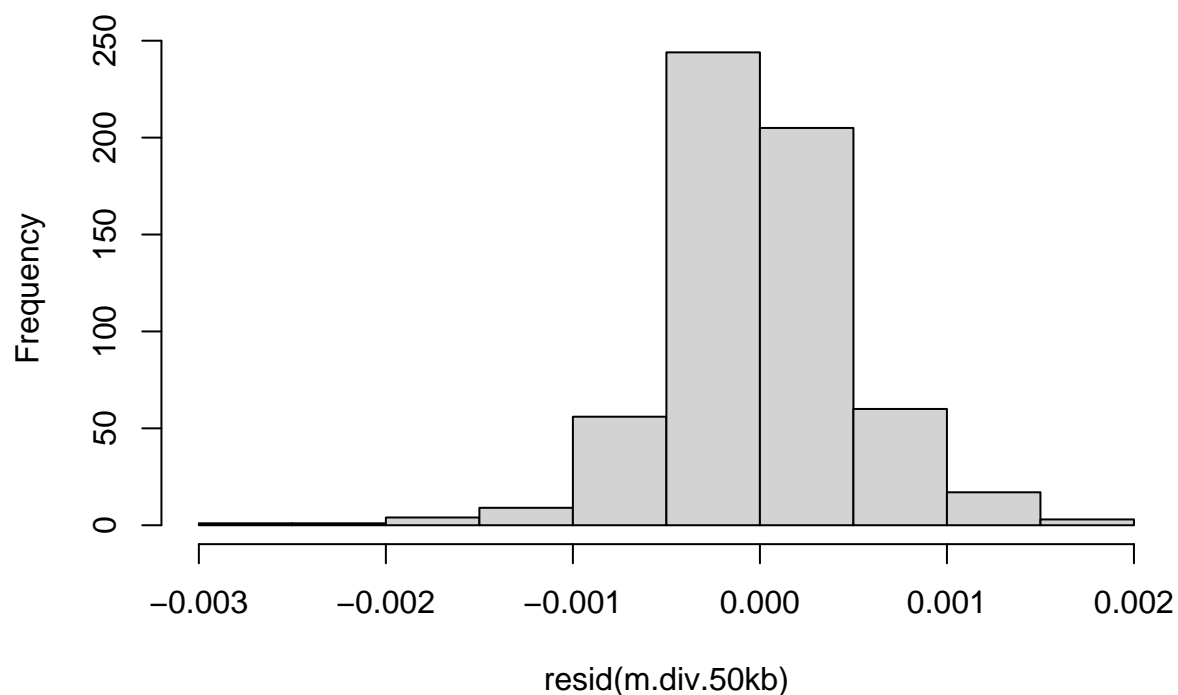
```
##  
## Durbin-Watson test  
##  
## data: m.div.50kb  
## DW = 2.0985, p-value = 0.8779  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.div.50kb  
## HMC = 0.53836, p-value = 0.899
```

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

Histogram of resid(m.div.50kb)



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

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

```

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

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

# rep_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")

```

```

## 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 = 35425520, p-value = 0.6965
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## 0.01595505

```

```

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

```

```

## 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

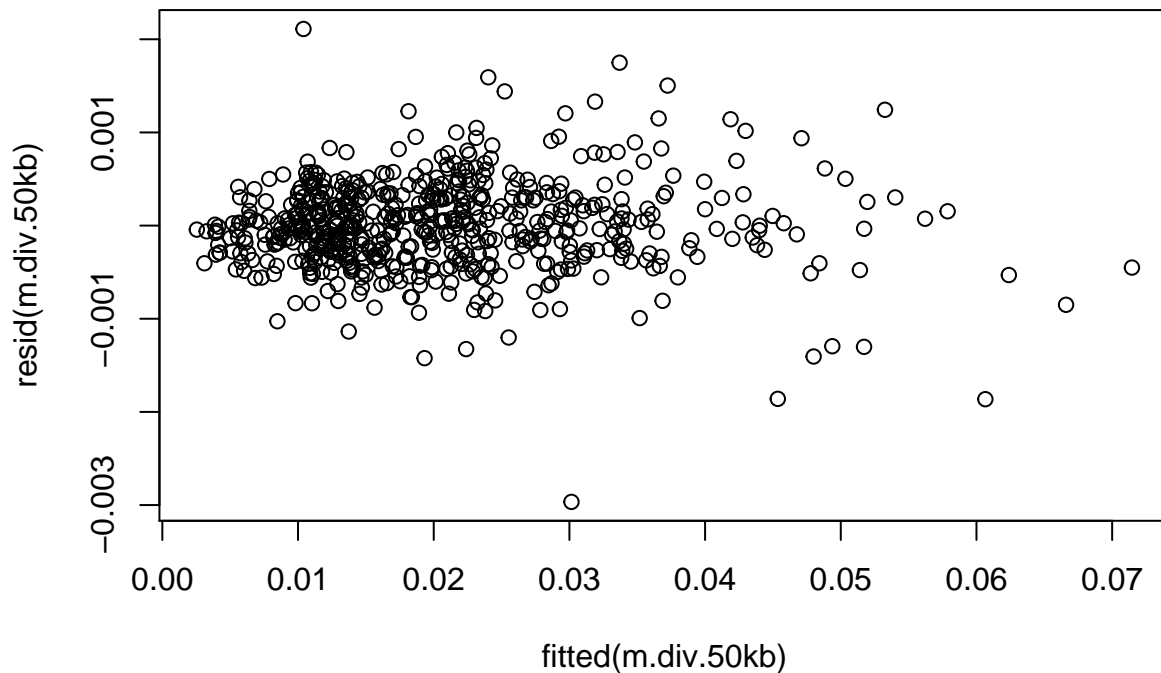
```

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

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

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

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



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

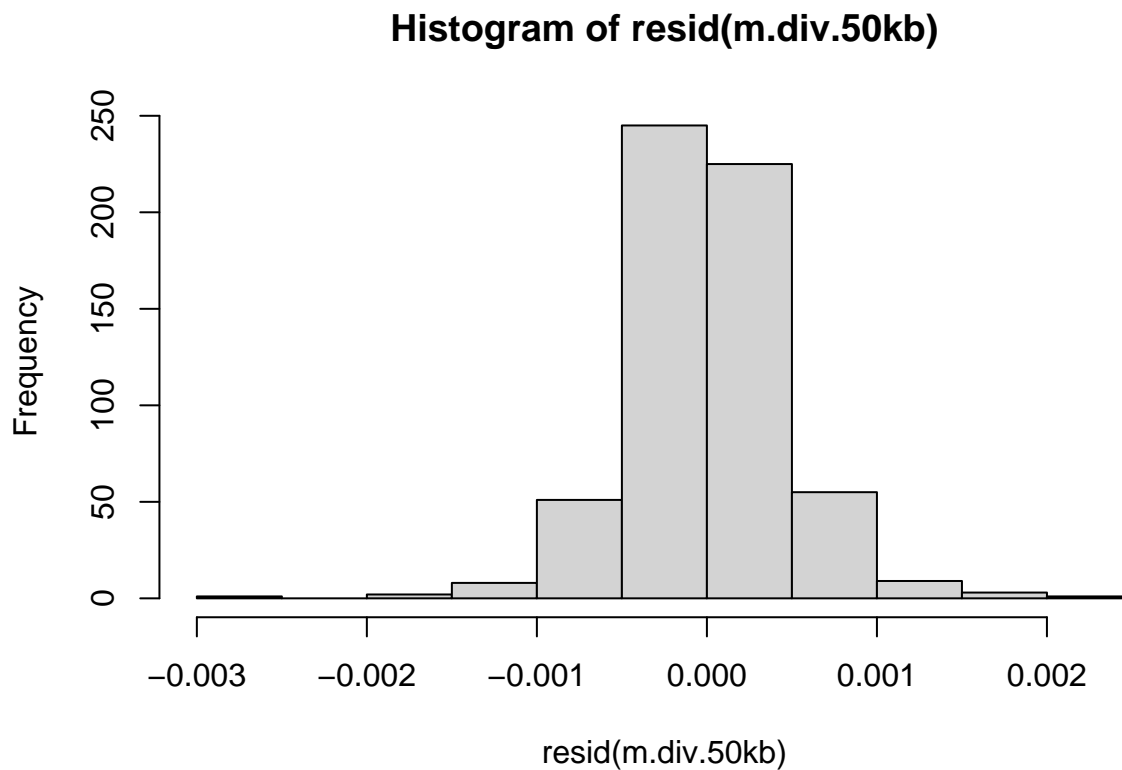
```
##
## Durbin-Watson test
##
## data: m.div.50kb
## DW = 2.0931, p-value = 0.864
## alternative hypothesis: true autocorrelation is greater than 0
```



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

```
##  
## Harrison-McCabe test  
##  
## data: m.div.50kb  
## HMC = 0.45962, p-value = 0.086
```

```
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   
## -2.966e-03 -2.902e-04 -1.674e-05  2.879e-04  2.110e-03   
##  
## Coefficients:  
##              Estimate Std. Error t value Pr(>|t|)      
## (Intercept)  2.062e-02  1.967e-05 1048.31  <2e-16 ***
```

```
## thetaC      1.308e+00  2.348e-03  557.06   <2e-16 ***
## rhoC        1.528e-03  6.645e-03    0.23    0.818
## tmrcaC      2.374e-02  2.674e-04   88.80   <2e-16 ***
## thetaC:tmrcaC 1.471e+00  3.126e-02   47.05   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0004816 on 595 degrees of freedom
## Multiple R-squared:  0.9981, Adjusted R-squared:  0.9981
## F-statistic: 7.932e+04 on 4 and 595 DF,  p-value: < 2.2e-16
```

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

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

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

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

```
## 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
```

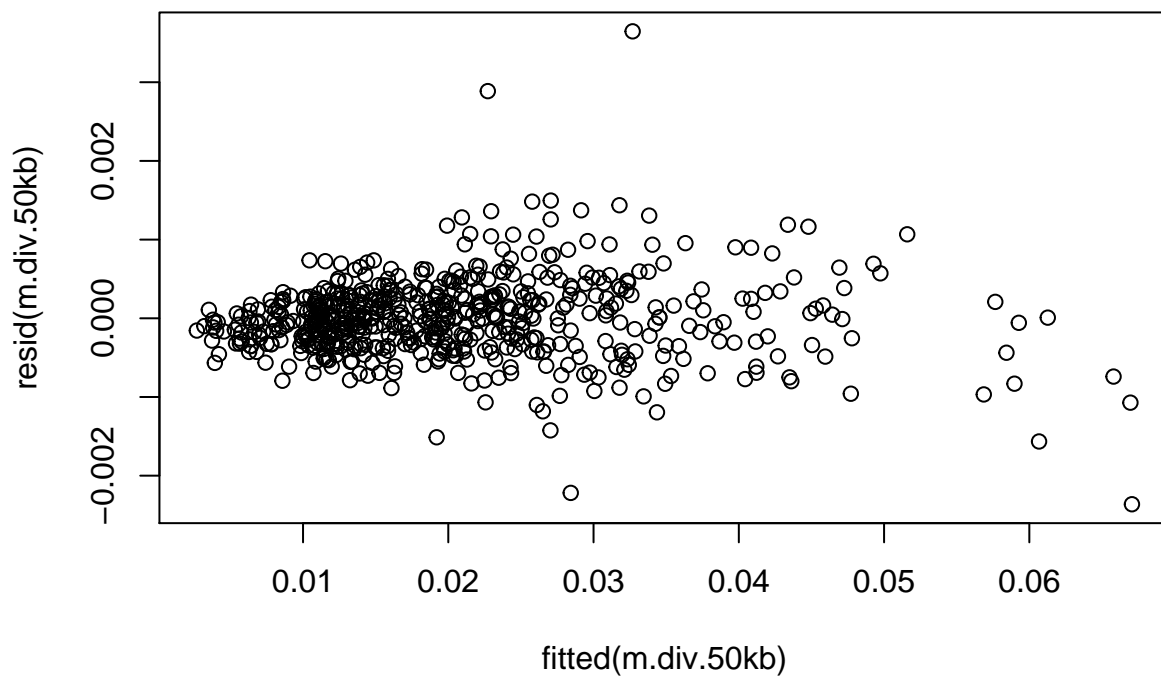
```
cor.test(~rho+tmrca, data = sim.lands.50kb, method = "spearman")
```

```
##
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 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)
```

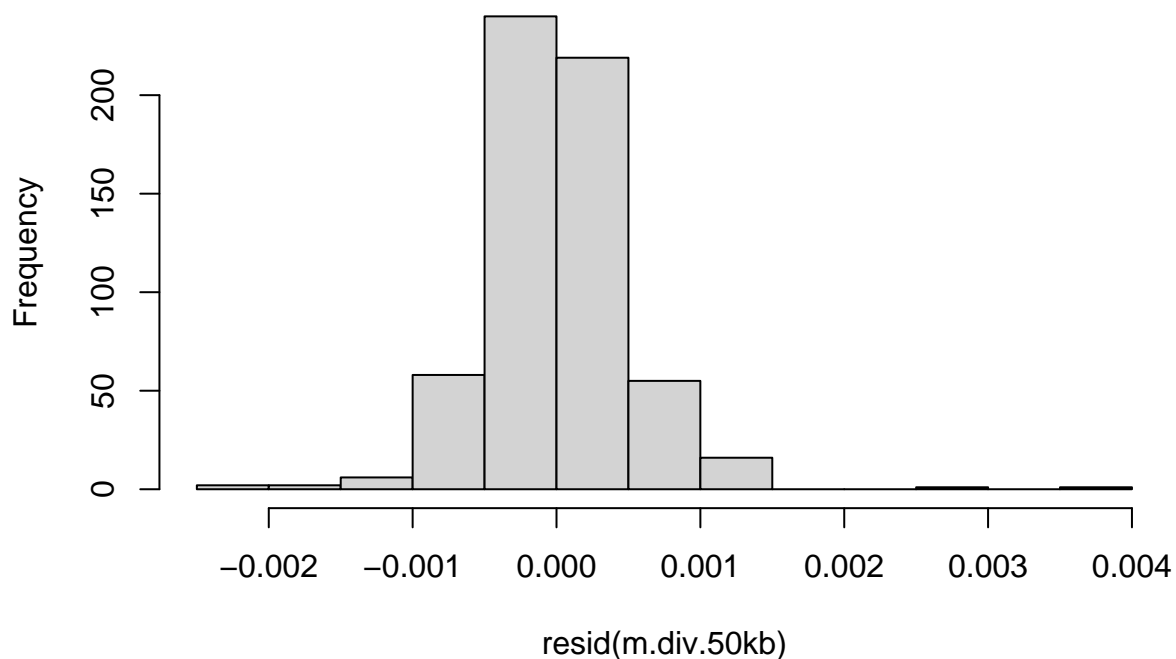
```
##  
## Durbin-Watson test  
##  
## data: m.div.50kb  
## DW = 2.1478, p-value = 0.9618  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.div.50kb  
## HMC = 0.46094, p-value = 0.092
```

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

Histogram of resid(m.div.50kb)



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

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

```

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

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

# rep_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")

```

```

## 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 = 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")

```

```

## 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

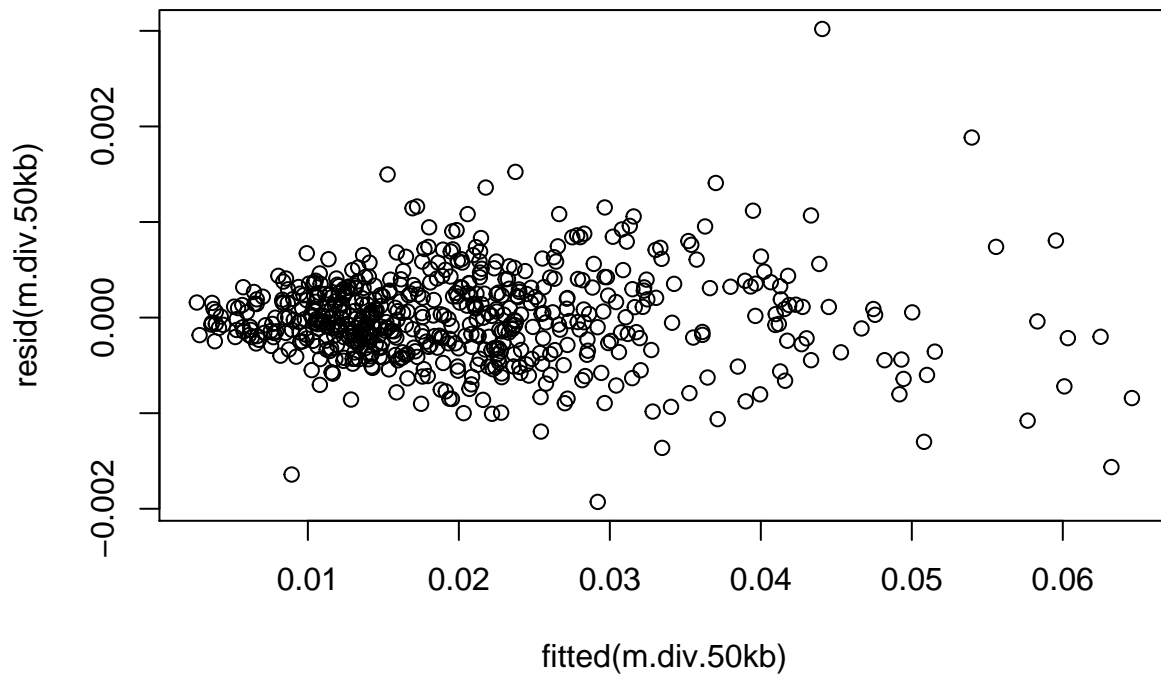
```

```
##
## data: rho and tmrca
## S = 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))
```



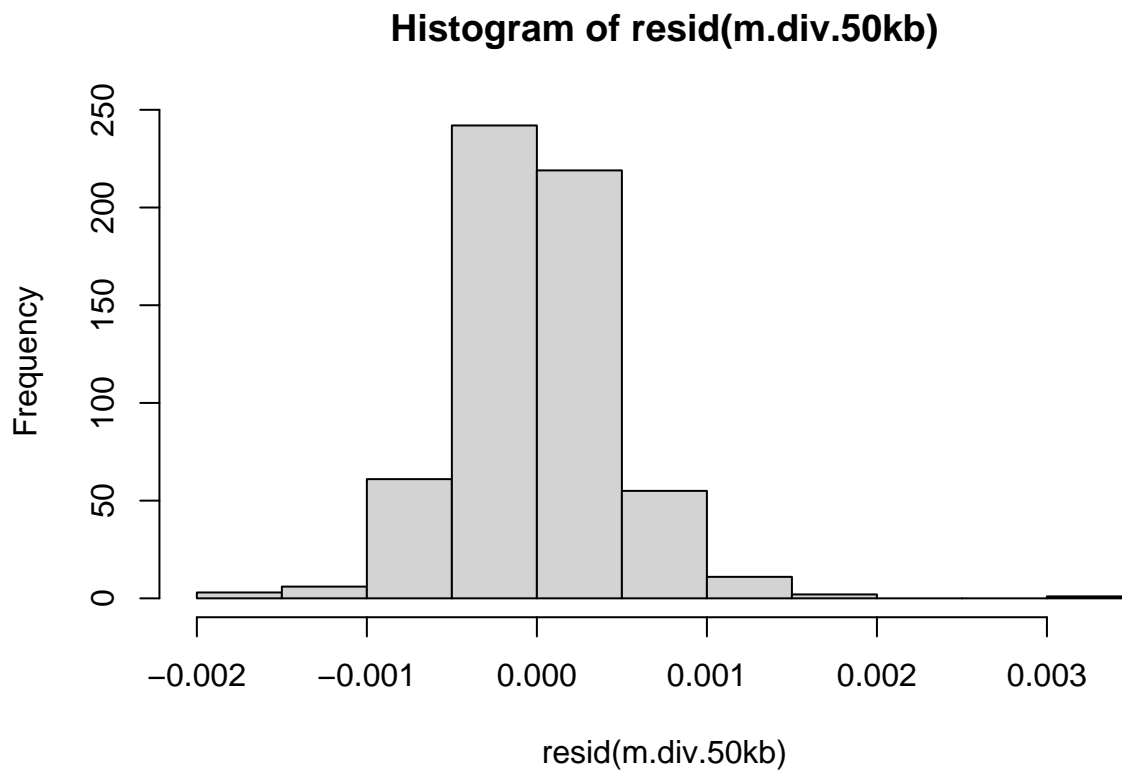
```
dwtest(m.div.50kb)
```

```
##
## 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 = 0.239
```

```
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

# rep_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
```

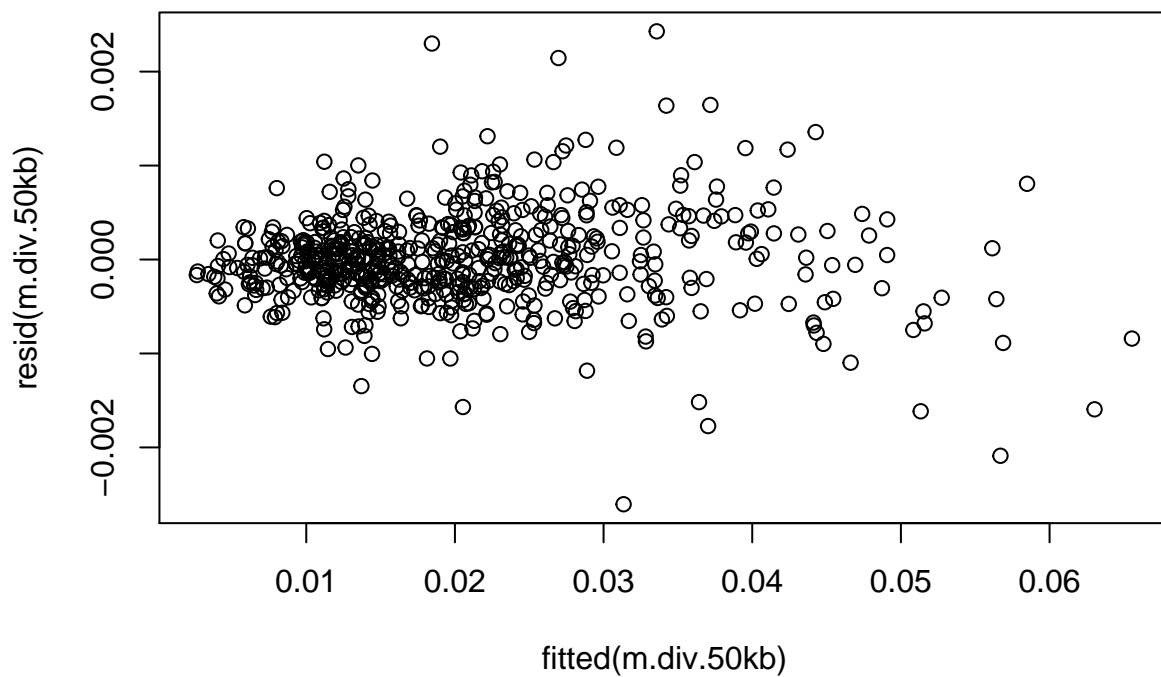
```
cor.test(~rho+tmrca, data = sim.lands.50kb, method = "spearman")
```

```
##
## 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)
```

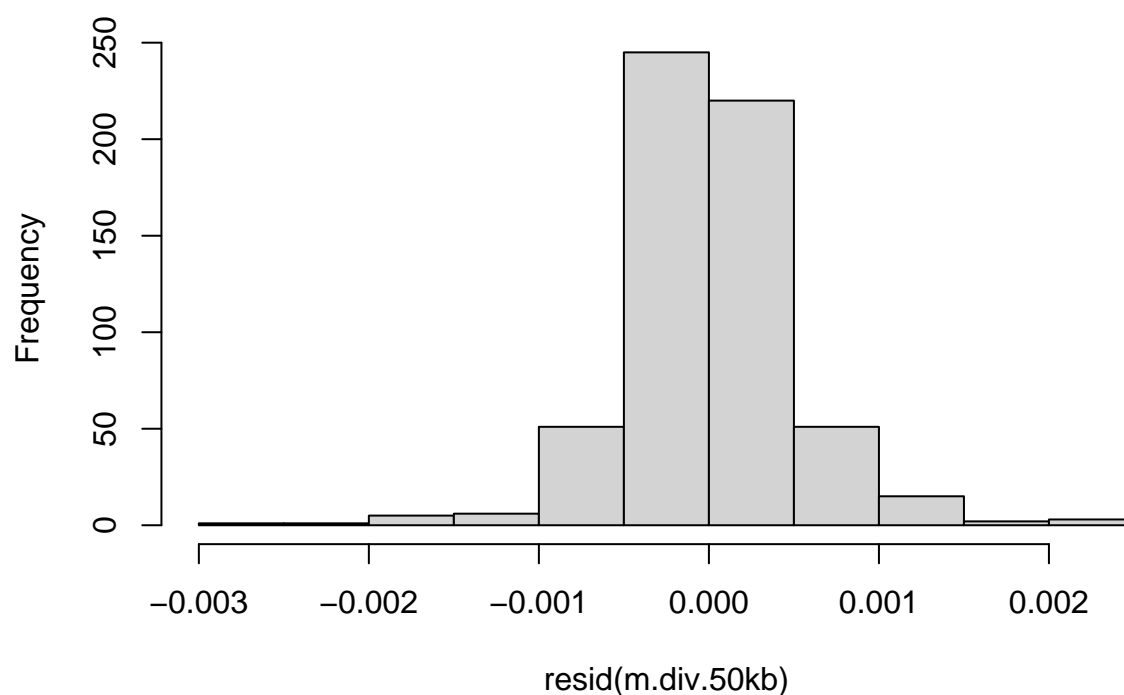
```
##  
## Durbin-Watson test  
##  
## data: m.div.50kb  
## DW = 2.0323, p-value = 0.6384  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.div.50kb  
## HMC = 0.48525, p-value = 0.296
```

```
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

# rep_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")

```

```

## 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 = 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")

```

```

## 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

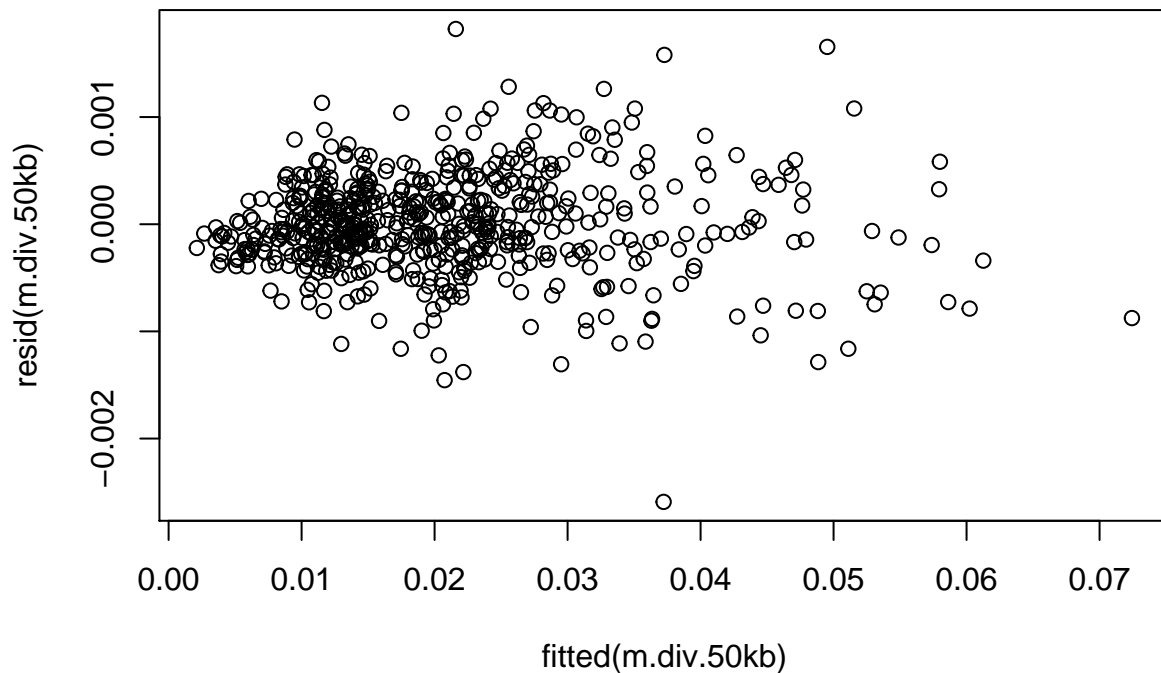
```

```
##
## data: rho and tmrca
## S = 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))
```



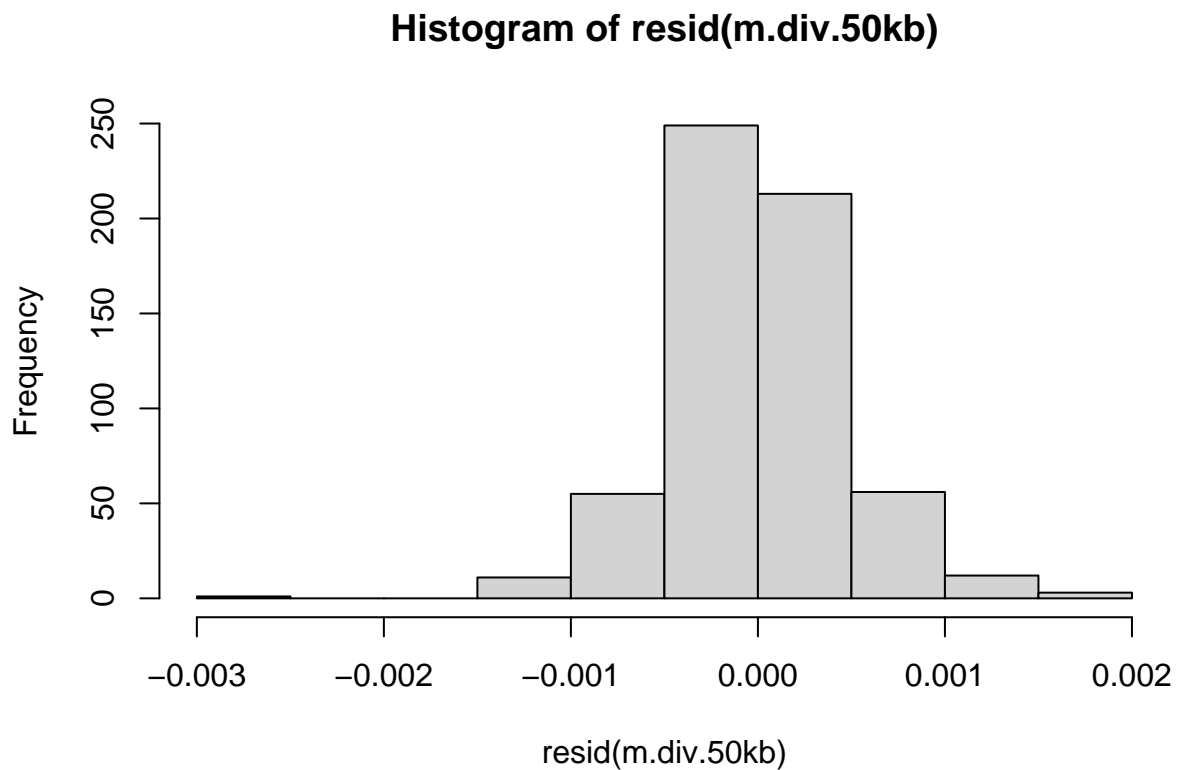
```
dwtest(m.div.50kb)
```

```
##
## 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 = 0.972
```

```
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

# rep_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")
```

```
## 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 = 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")
```

```
## 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
```

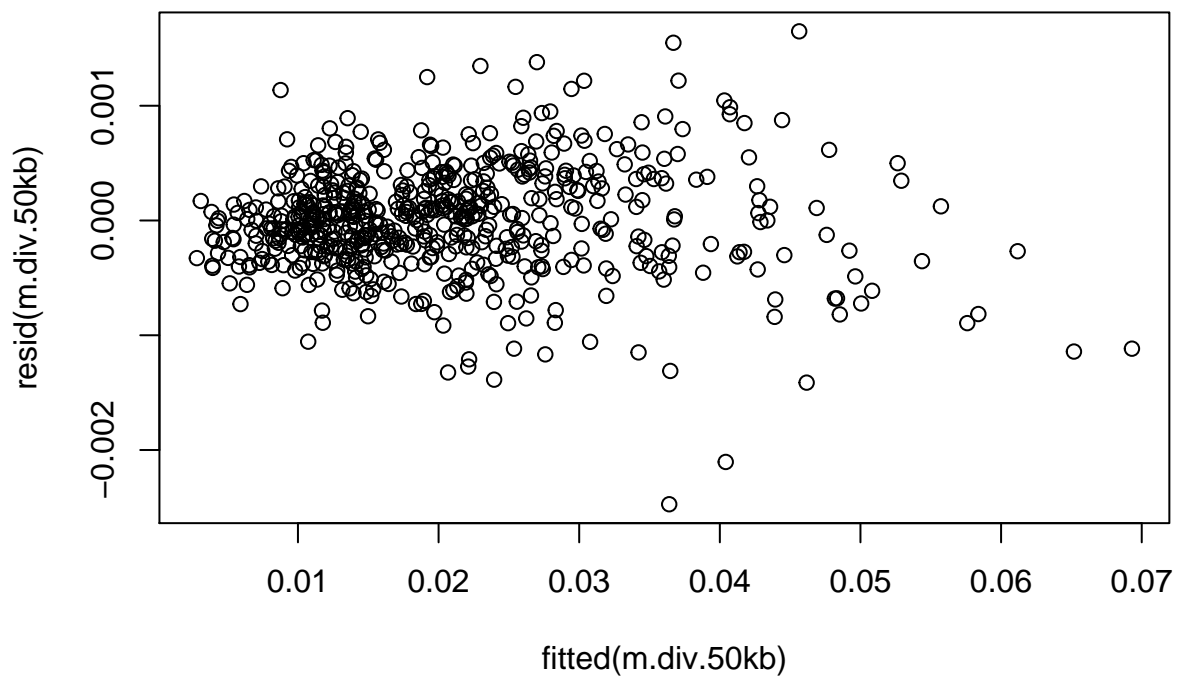
```
cor.test(~rho+tmrca, data = sim.lands.50kb, method = "spearman")
```

```
##
## Spearman's rank correlation rho
##
## data:  rho and tmrca
## S = 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)
```

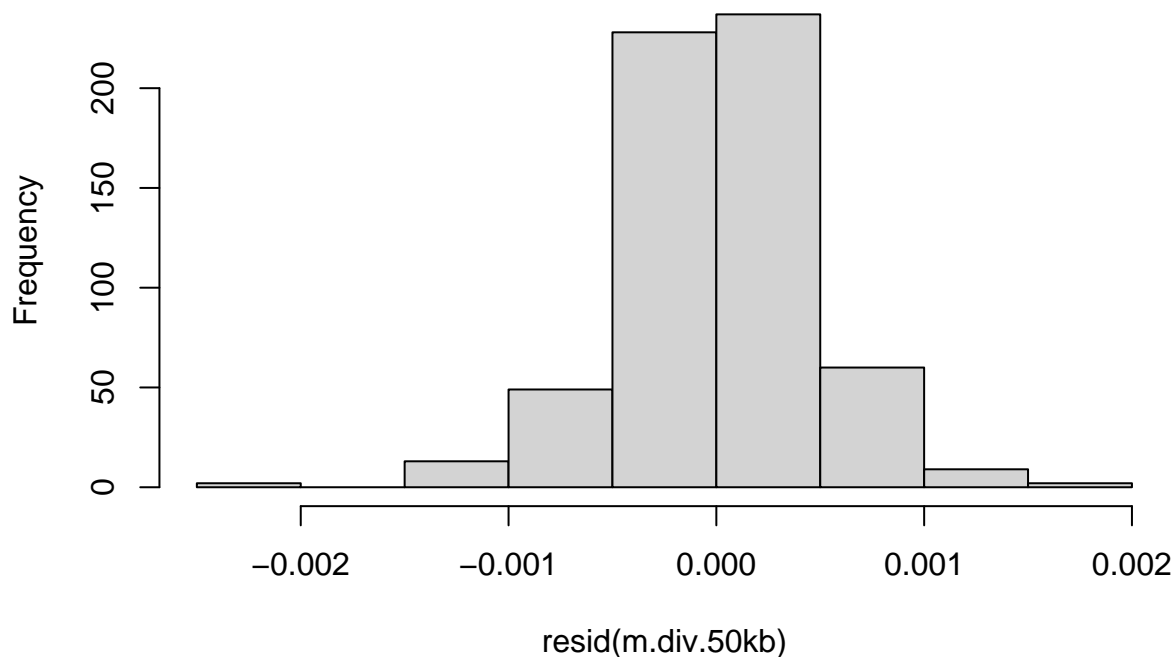
```
##  
## Durbin-Watson test  
##  
## data: m.div.50kb  
## DW = 1.9775, p-value = 0.3738  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.div.50kb  
## HMC = 0.43153, p-value = 0.008
```

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

Histogram of resid(m.div.50kb)



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

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

```

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

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

```

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)

# rep 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")

```

```

## 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 = 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")

```

```

## 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 = 593676, p-value = 0.5002
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.0554712
```

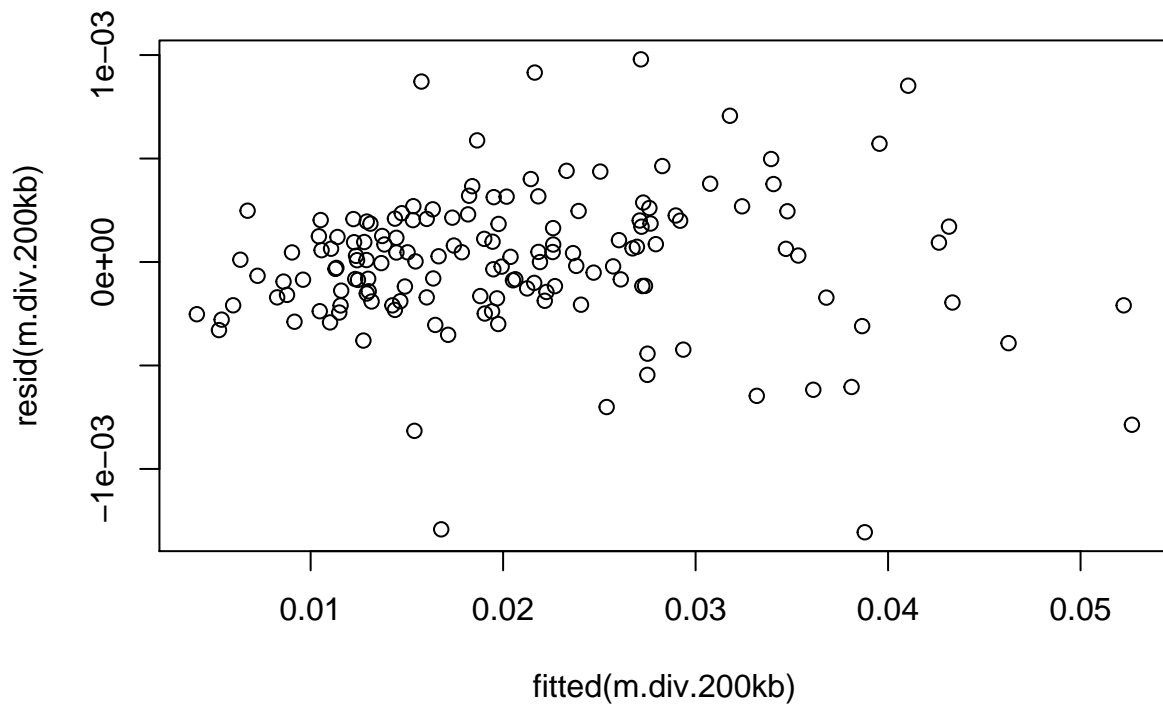
```
cor.test(~rho+tmrca, data = sim.lands.200kb, method = "spearman")
```

```
##
## 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)
```

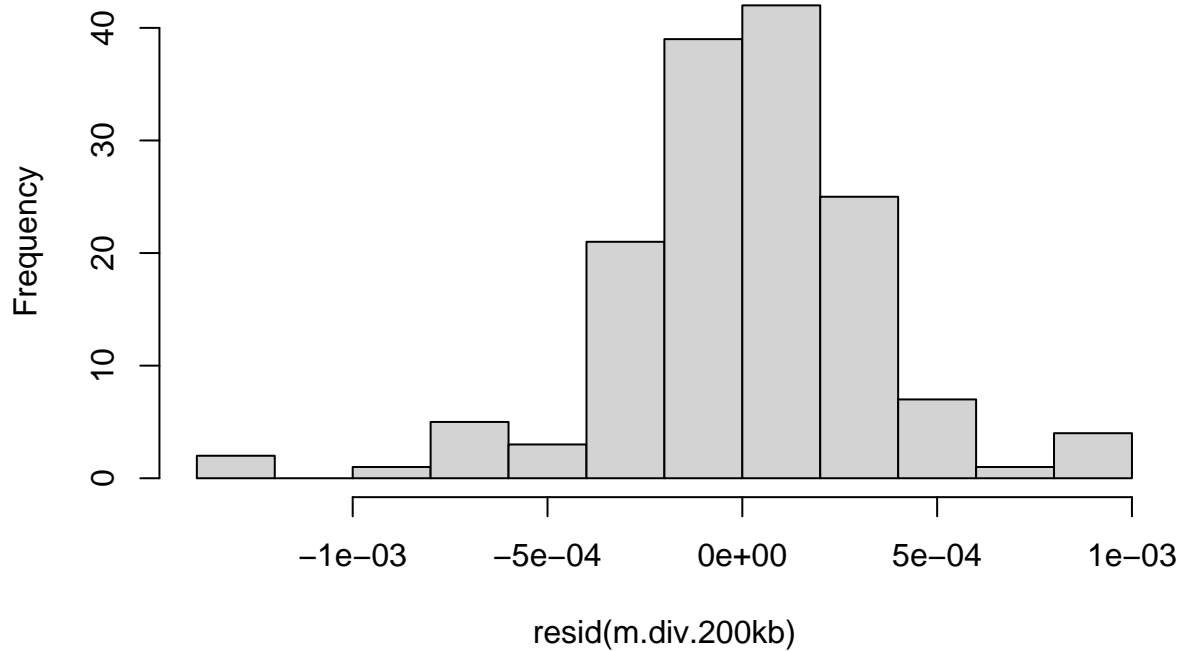
```
##  
## Durbin-Watson test  
##  
## data: m.div.200kb  
## DW = 1.9751, p-value = 0.4234  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.div.200kb  
## HMC = 0.49982, p-value = 0.493
```

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

# rep_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, as.is = 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, as.is = 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")

```

```

## 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 = 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")

```

```

## 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 = 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")

```

```

##

```

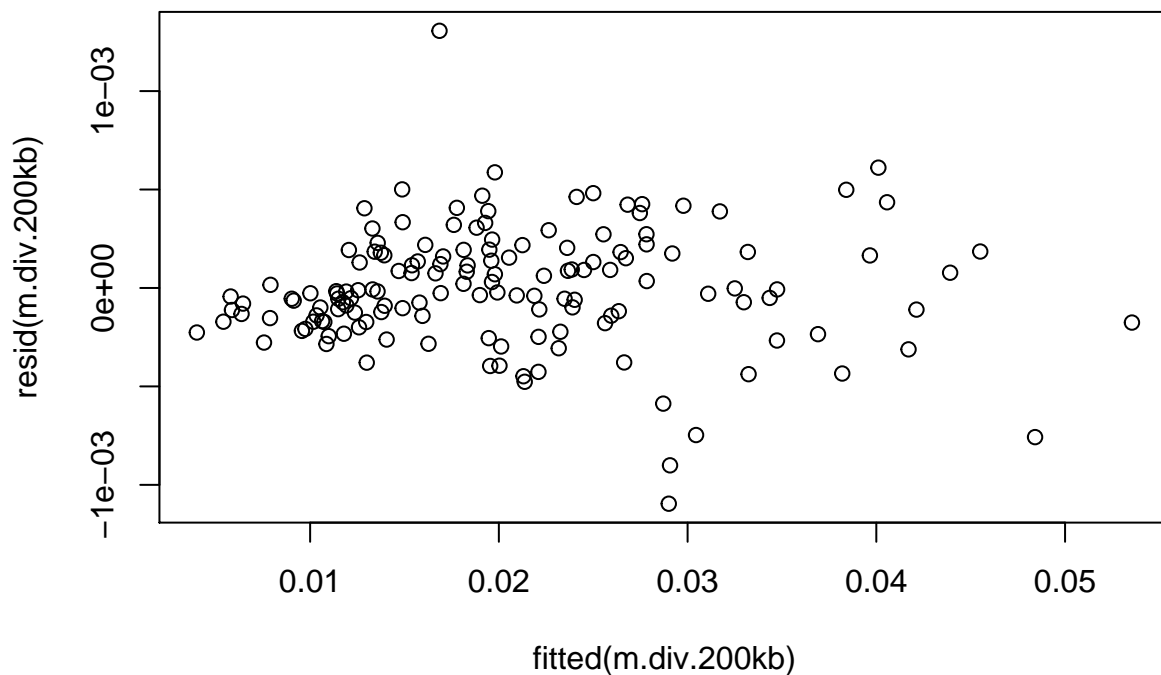


```
## Spearman's rank correlation rho
##
## data: rho and tmrca
## S = 533372, p-value = 0.529
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## 0.05174097
```

```
# 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)
```

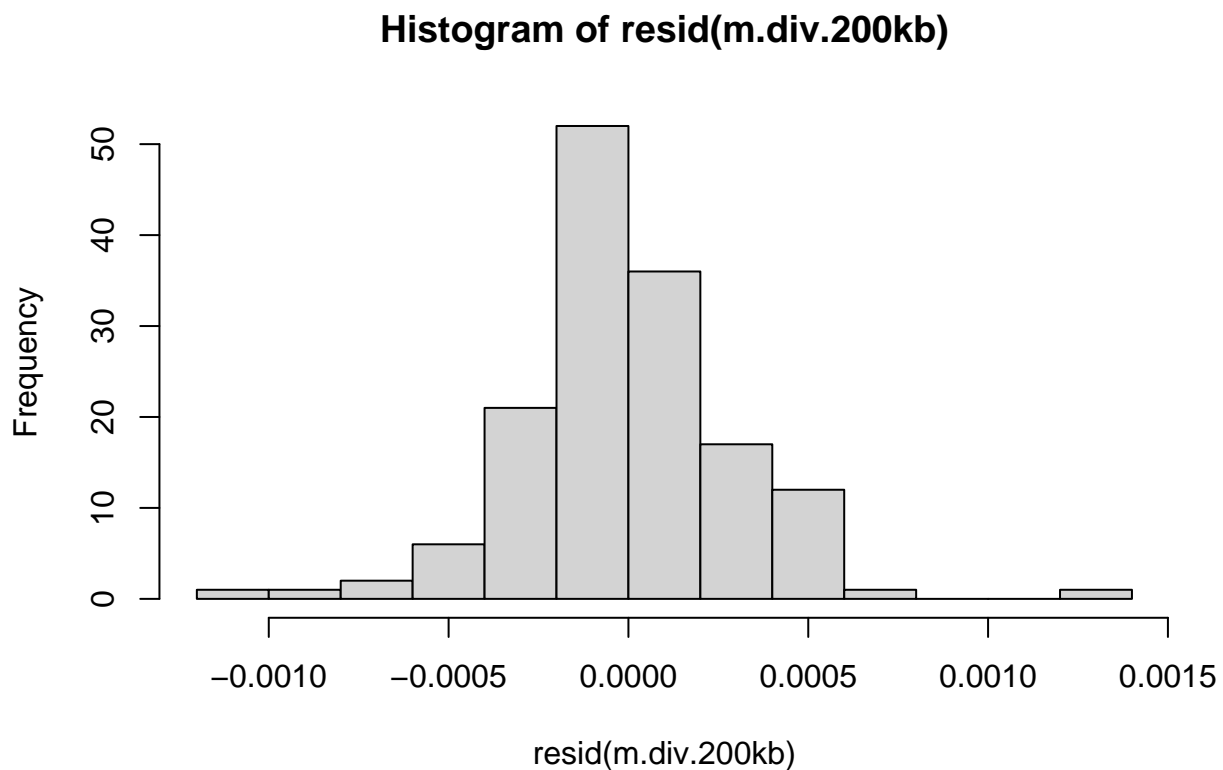
```
##
## Durbin-Watson test
##
## data: m.div.200kb
```

```
## 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 = 0.937
```

```
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

# rep_3
rep_3.pi.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_3/rep_3.pi.200kb.bedgraph", header=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")
```

```
## 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 = 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")
```

```
## 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 = 593676, p-value = 0.5002
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.0554712
```

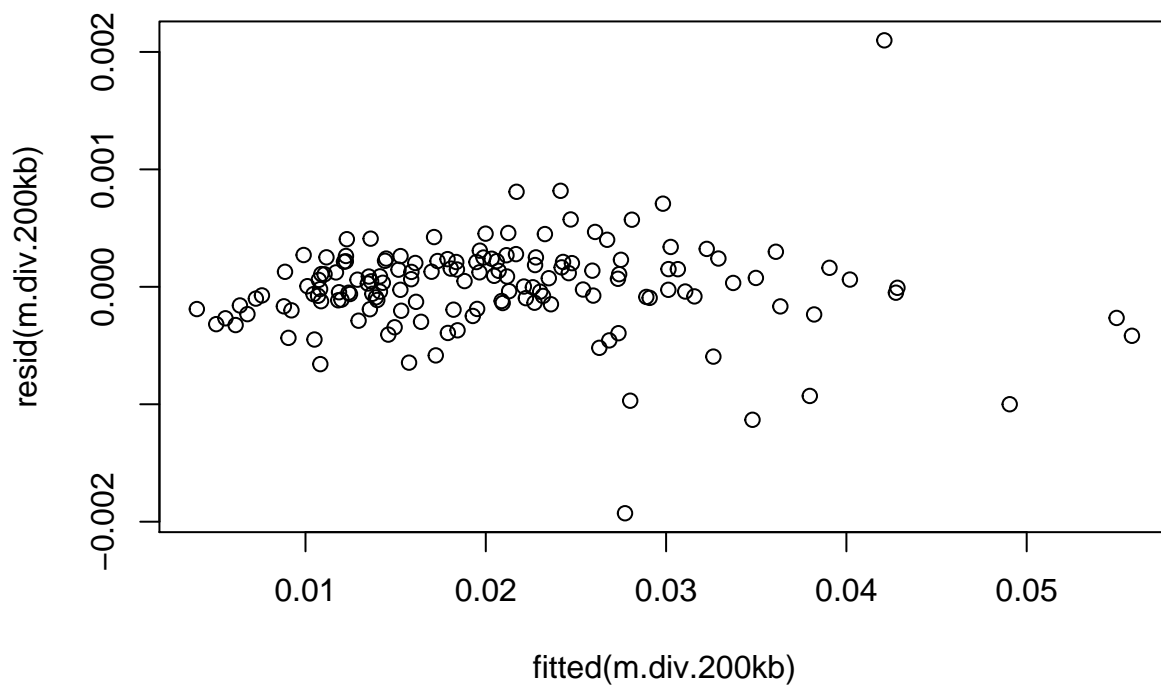
```
cor.test(~rho+tmrca, data = sim.lands.200kb, method = "spearman")
```

```
##
## 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)
```

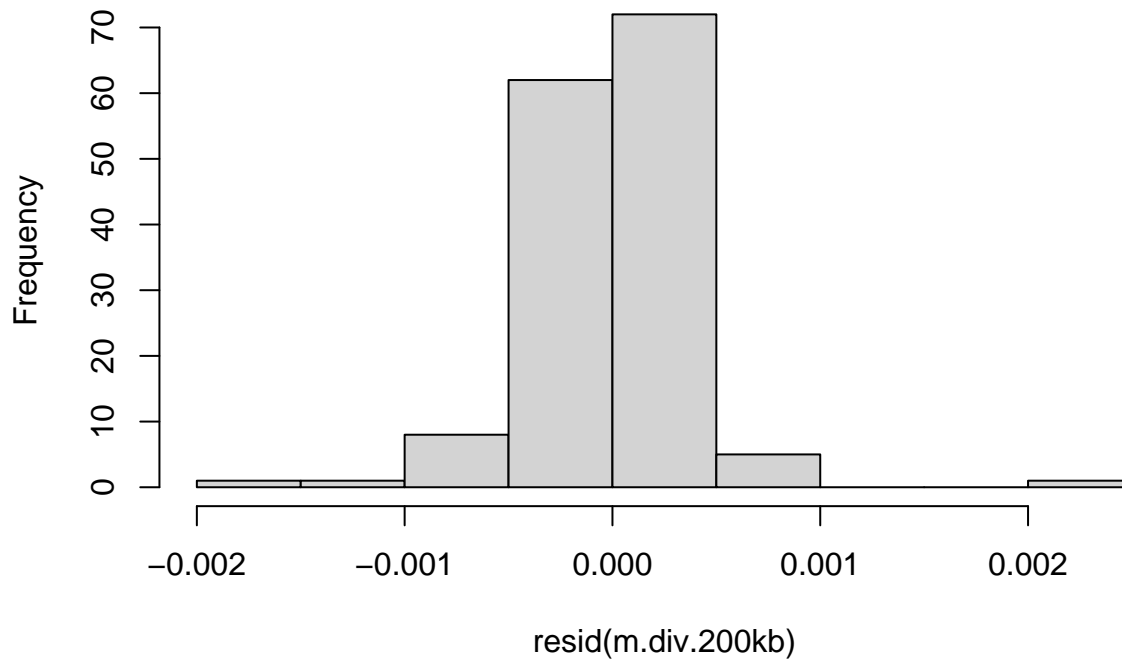
```
##  
## Durbin-Watson test  
##  
## data: m.div.200kb  
## DW = 1.9205, p-value = 0.2965  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.div.200kb  
## HMC = 0.45845, p-value = 0.235
```

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

Histogram of resid(m.div.200kb)



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

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

```

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

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

# rep_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")

```

```

## 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 = 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")

```

```

## 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 = 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

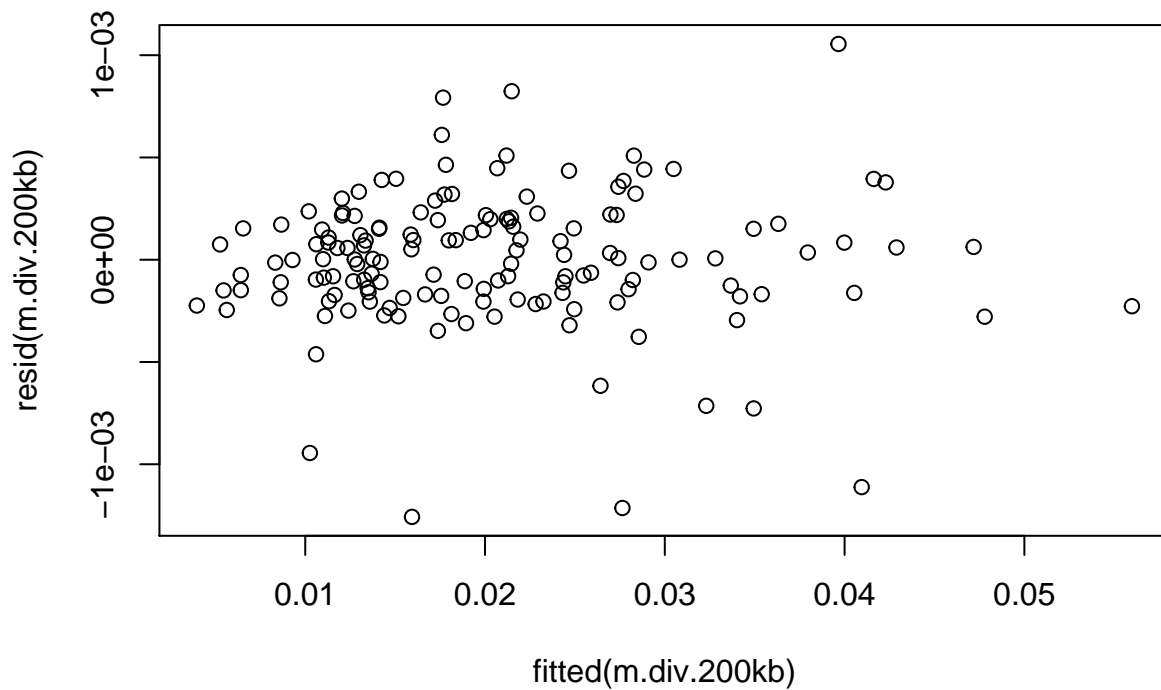
```

```
##
## 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(多样性 ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC, data = sim.lands.200kb)
plot(resid(m.div.200kb)~fitted(m.div.200kb))
```



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

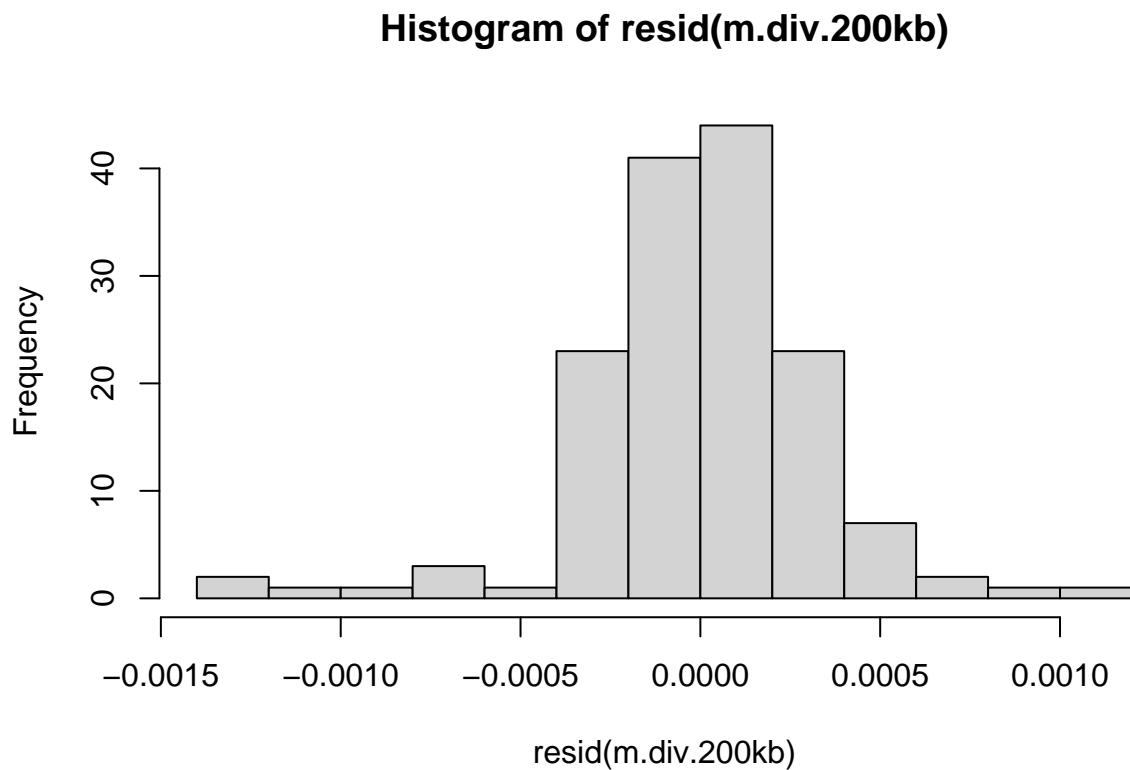
```
##
## Durbin-Watson test
##
## data: m.div.200kb
## DW = 1.9887, p-value = 0.4477
## alternative hypothesis: true autocorrelation is greater than 0
```



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

```
##  
## Harrison-McCabe test  
##  
## data: m.div.200kb  
## HMC = 0.4058, p-value = 0.043
```

```
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   
## -1.257e-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

# rep_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=1)
rep_5.tmrca.200kb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_5/sim.tmrca.200k.map", header=1)

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")
```

```
## 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 = 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")
```

```
## 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 = 593676, p-value = 0.5002
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.0554712
```

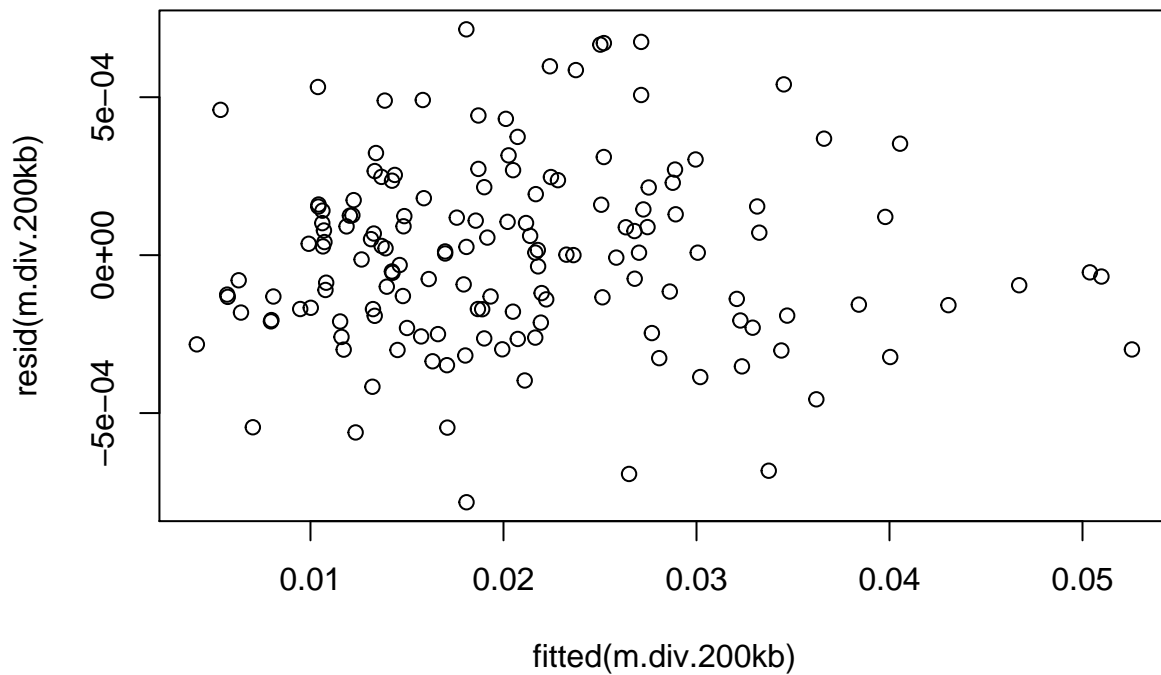
```
cor.test(~rho+tmrca, data = sim.lands.200kb, method = "spearman")
```

```
##
## 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)
```

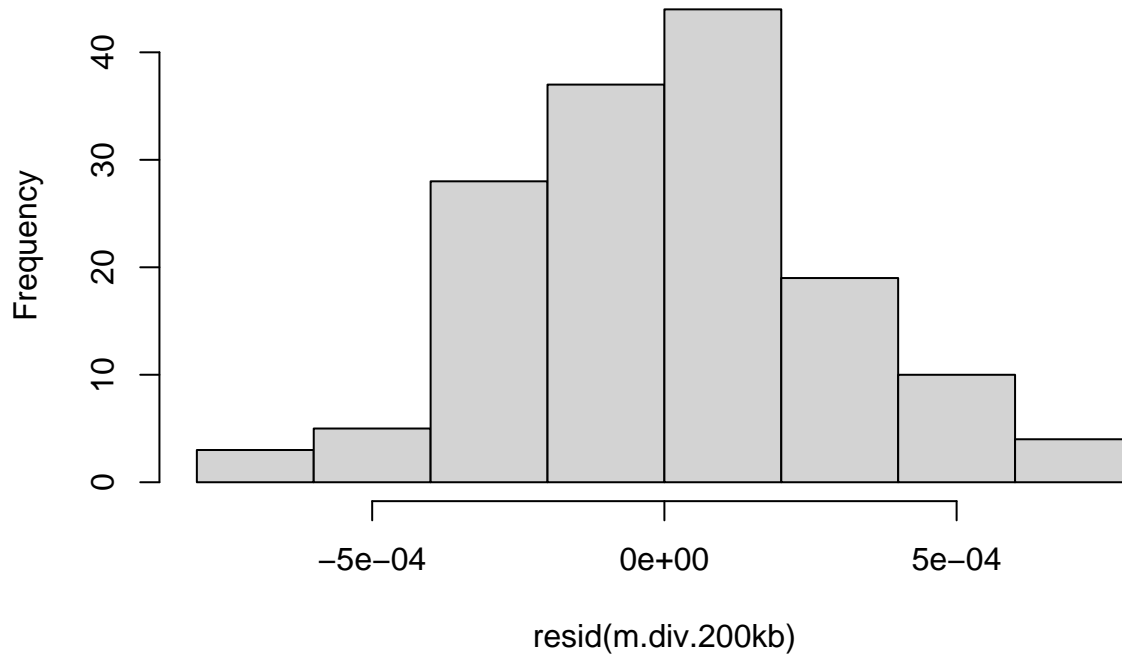
```
##
## Durbin-Watson test
##
## data:  m.div.200kb
## DW = 1.9065, p-value = 0.2691
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##
## Harrison-McCabe test
##
## data:  m.div.200kb
## HMC = 0.42468, p-value = 0.1
```

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

Histogram of resid(m.div.200kb)



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

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

```

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

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

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

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

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

```

```

## 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 = 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

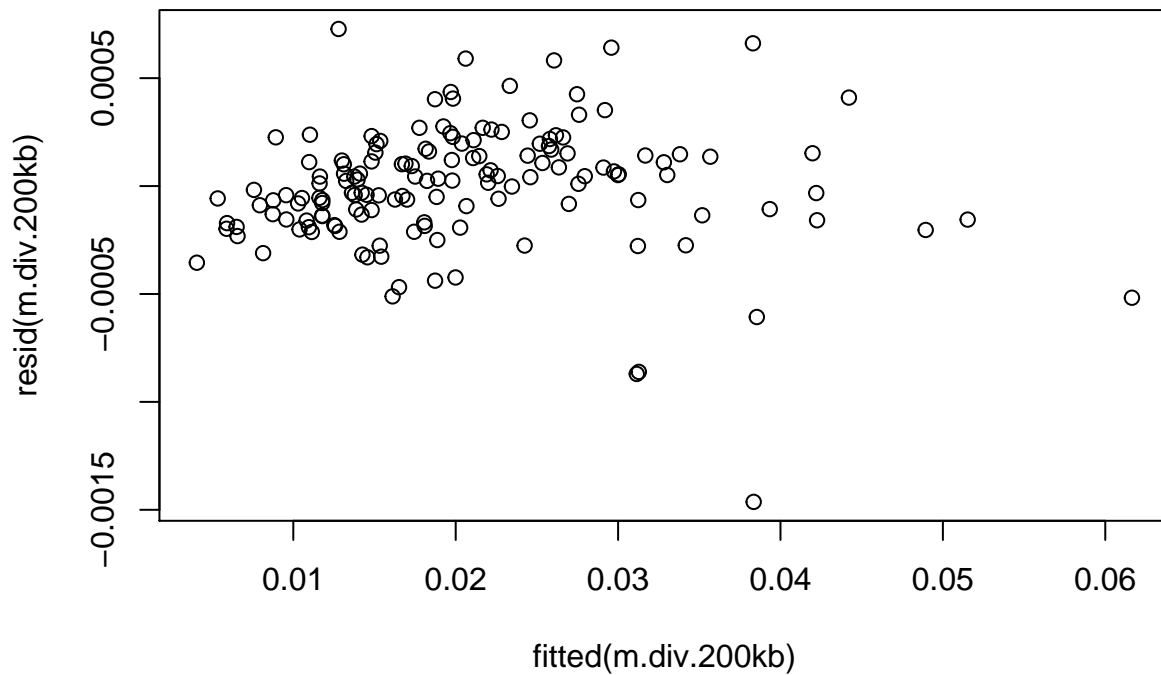
```

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



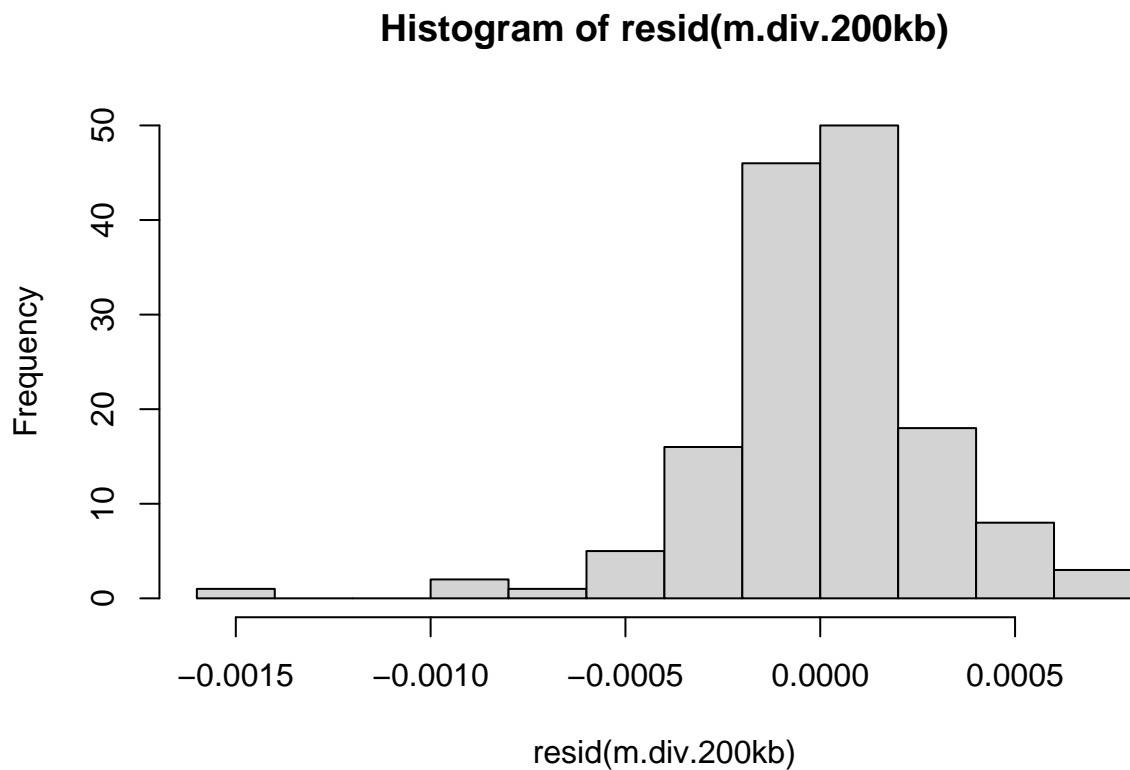
```
dwtest(m.div.200kb)
```

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

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

```
##  
## Harrison-McCabe test  
##  
## data: m.div.200kb  
## HMC = 0.59616, p-value = 0.939
```

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

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

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

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

```
## 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 = 593676, p-value = 0.5002
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.0554712
```

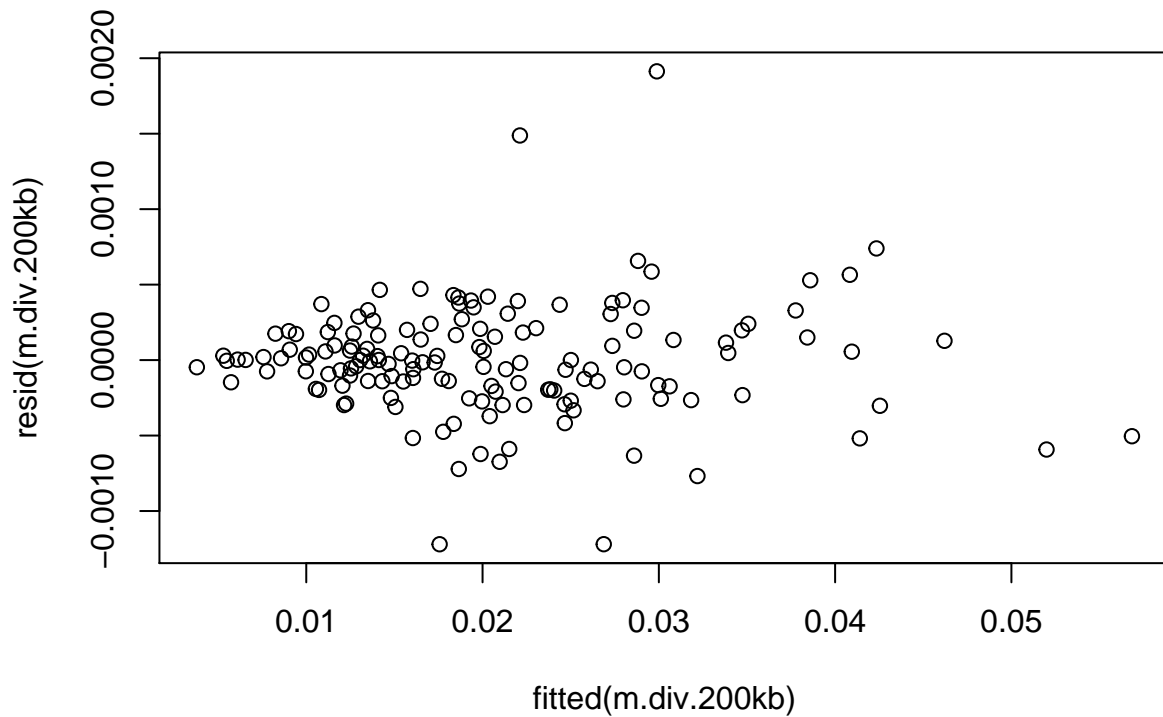
```
cor.test(~rho+tmrca, data = sim.lands.200kb, method = "spearman")
```

```
##
## 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)
```

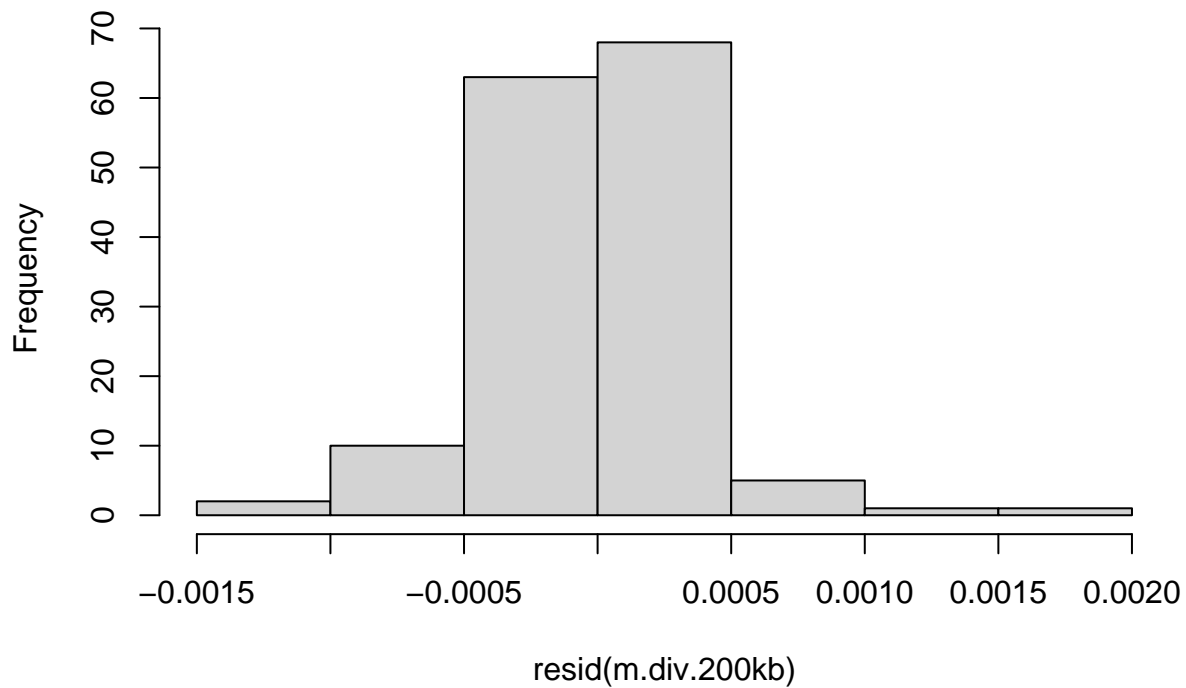
```
##  
## Durbin-Watson test  
##  
## data: m.div.200kb  
## DW = 1.9801, p-value = 0.4361  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.div.200kb  
## HMC = 0.40495, p-value = 0.063
```

```
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

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

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

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

```

```

## 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 = 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")

```

```

##

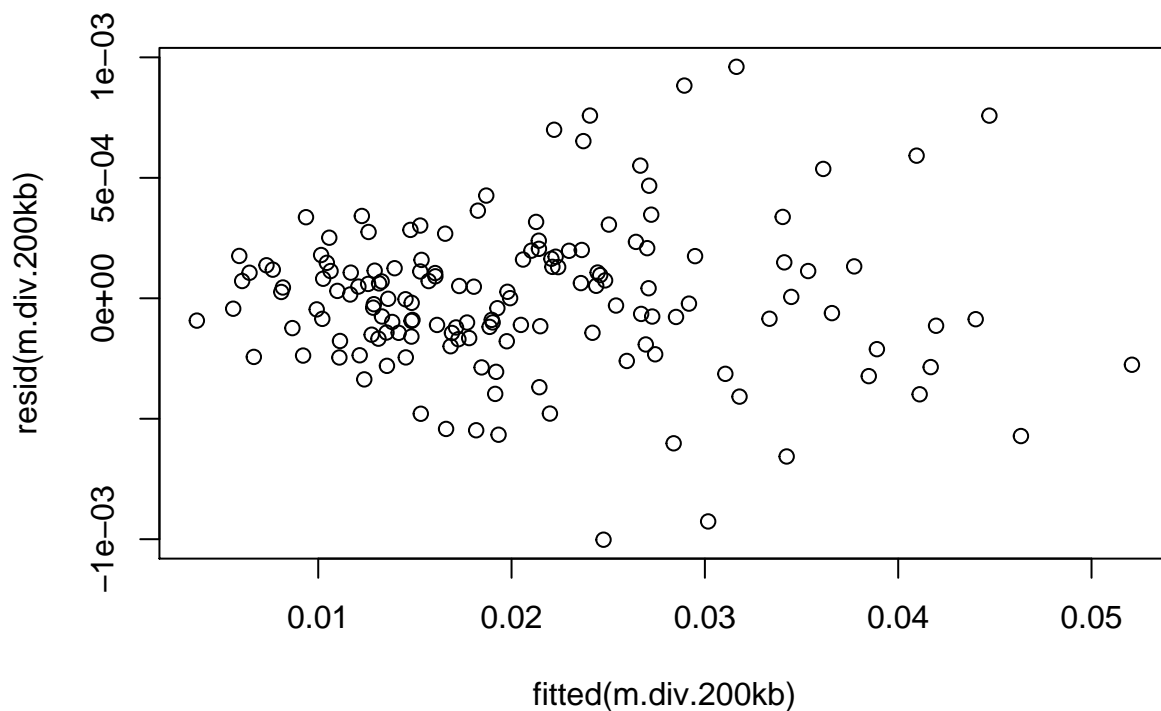
```

```
## 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)
```

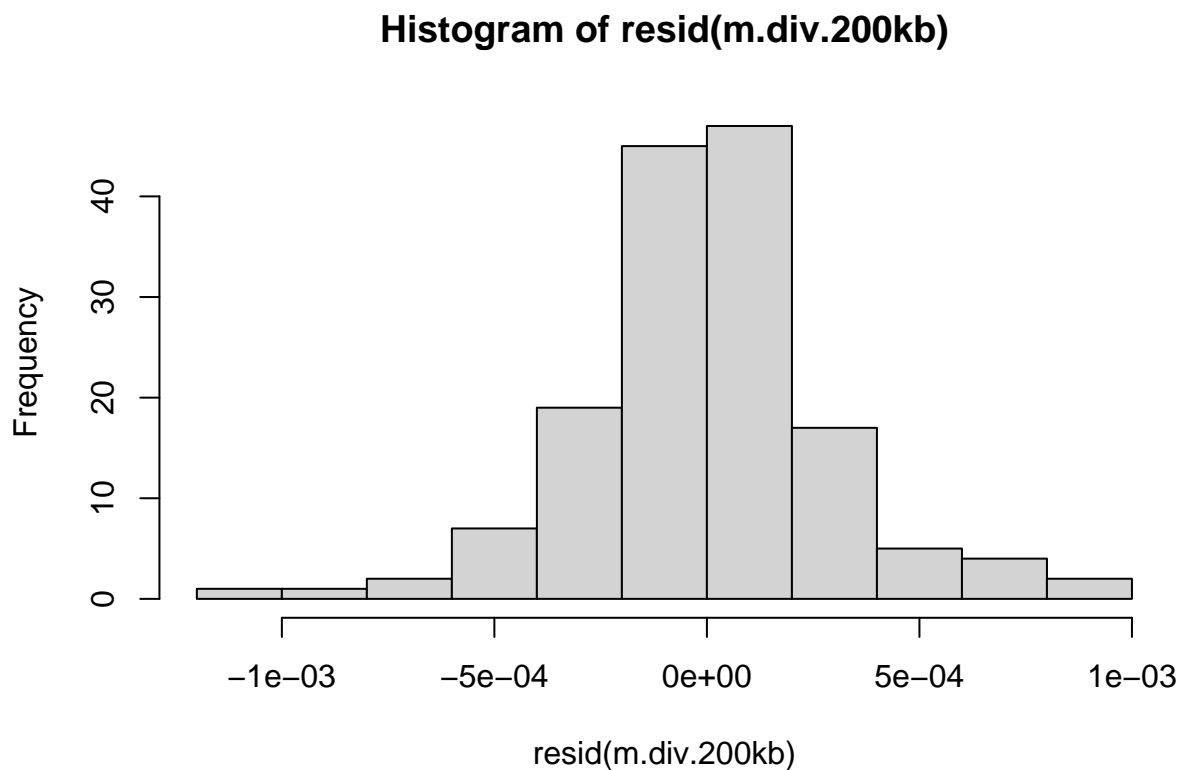
```
##
## Durbin-Watson test
##
## data: m.div.200kb
```

```
## 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 = 0.777
```

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

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

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

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

```
## 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 = 593676, p-value = 0.5002
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##      rho
## -0.0554712
```

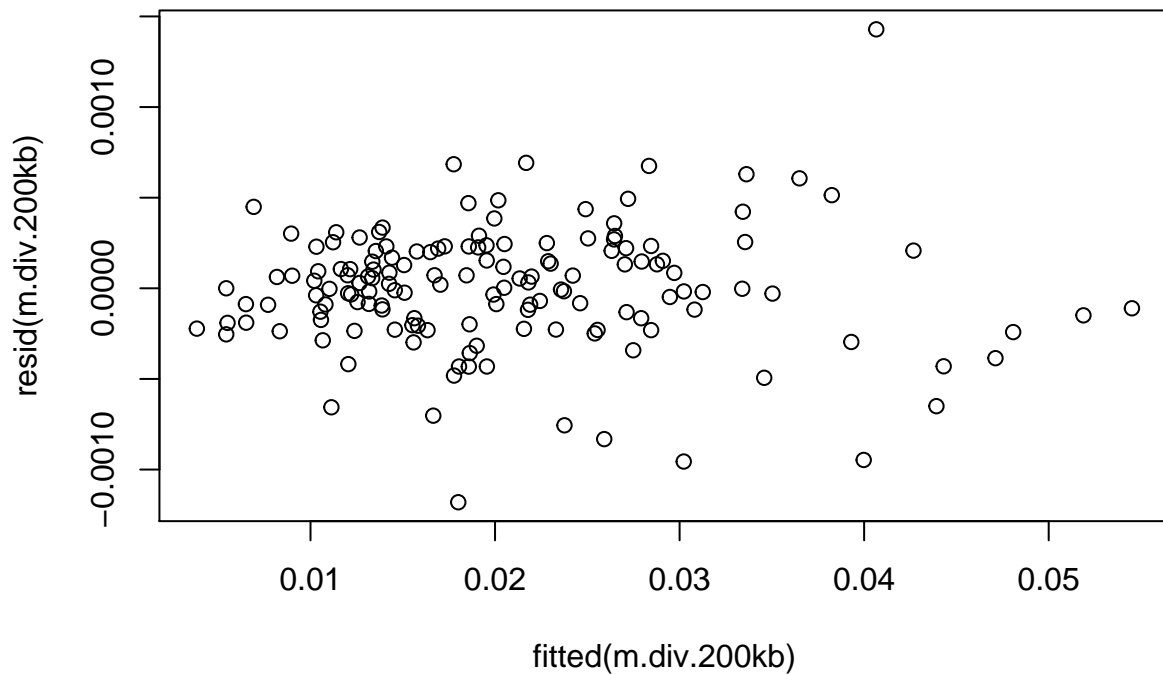
```
cor.test(~rho+tmrca, data = sim.lands.200kb, method = "spearman")
```

```
##
## 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)
```

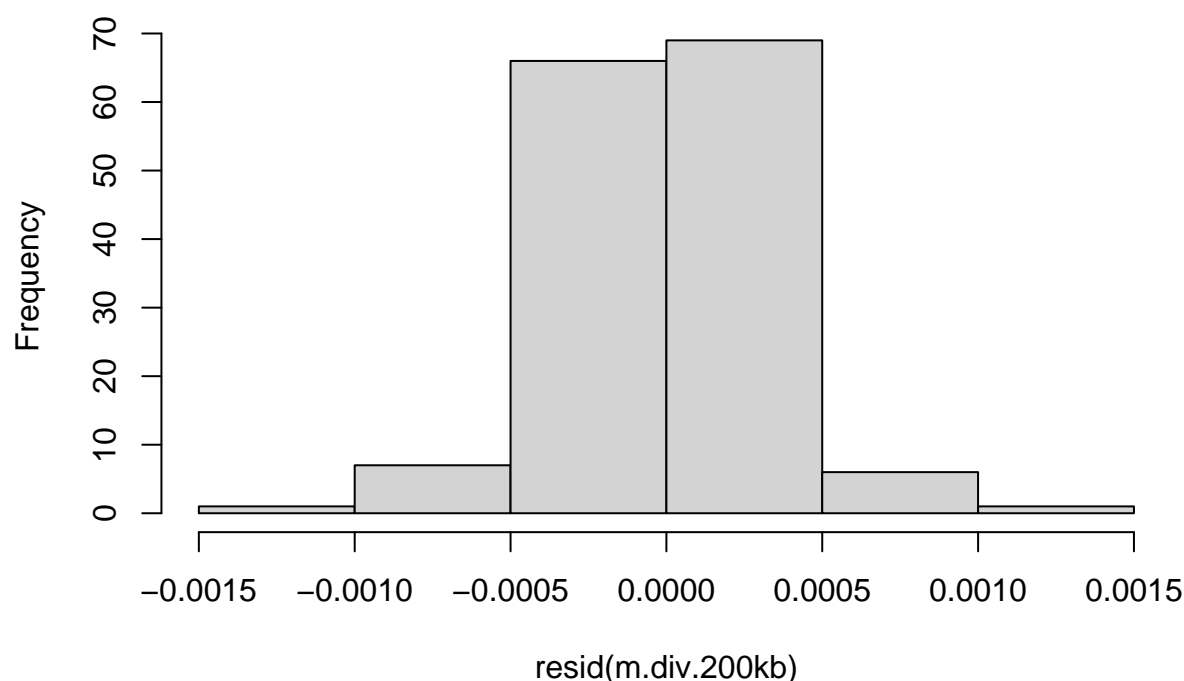
```
##  
## Durbin-Watson test  
##  
## data: m.div.200kb  
## DW = 1.6818, p-value = 0.022  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.div.200kb  
## HMC = 0.42403, p-value = 0.105
```

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

Histogram of resid(m.div.200kb)



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

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

```

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

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

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

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

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

```

```

## 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 = 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

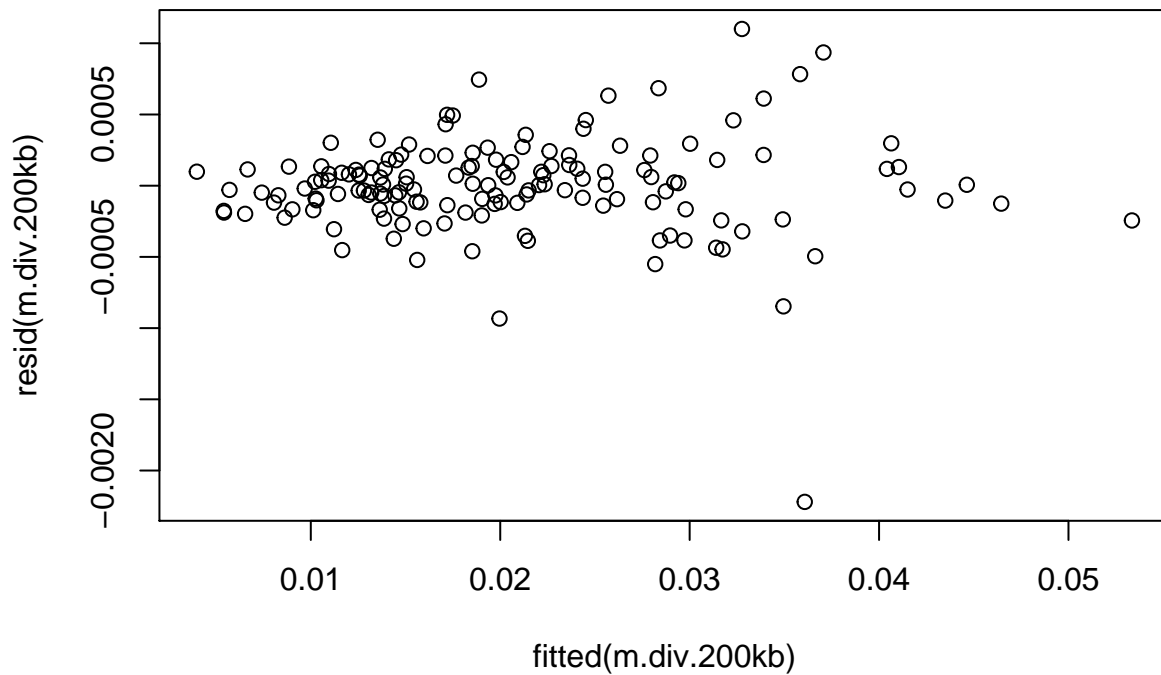
```

```
##
## 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))
```



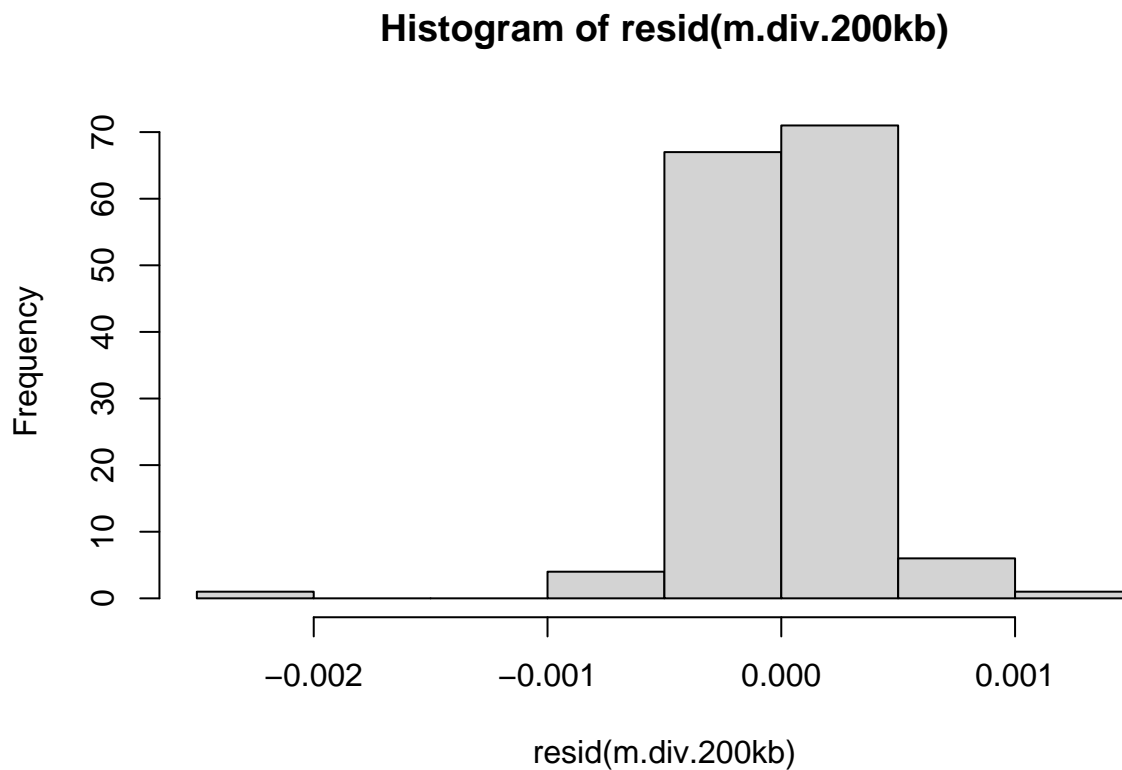
```
dwtest(m.div.200kb)
```

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

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

```
##  
## Harrison-McCabe test  
##  
## data: m.div.200kb  
## HMC = 0.41358, p-value = 0.073
```

```
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   
## -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])
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 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)

# rep 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")
```

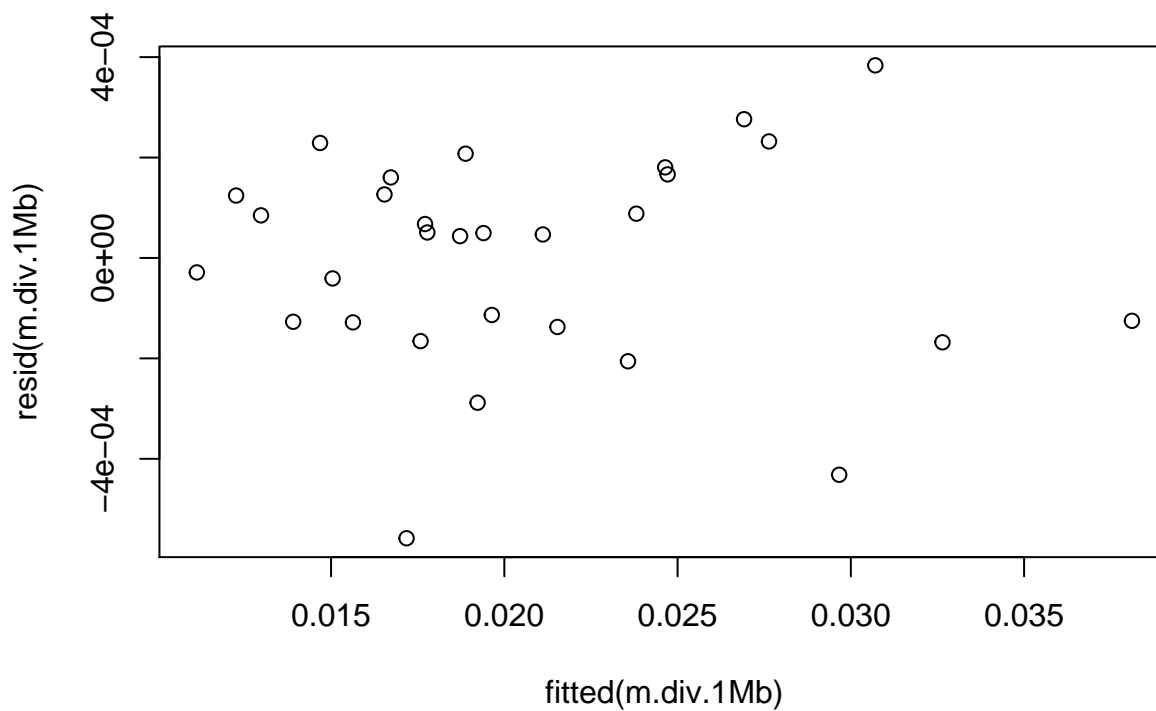
```
##  
## Spearman's rank correlation rho  
##  
## data: rho and tmrca  
## S = 4576, p-value = 0.9251  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## -0.01802002
```

```
# 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)
```

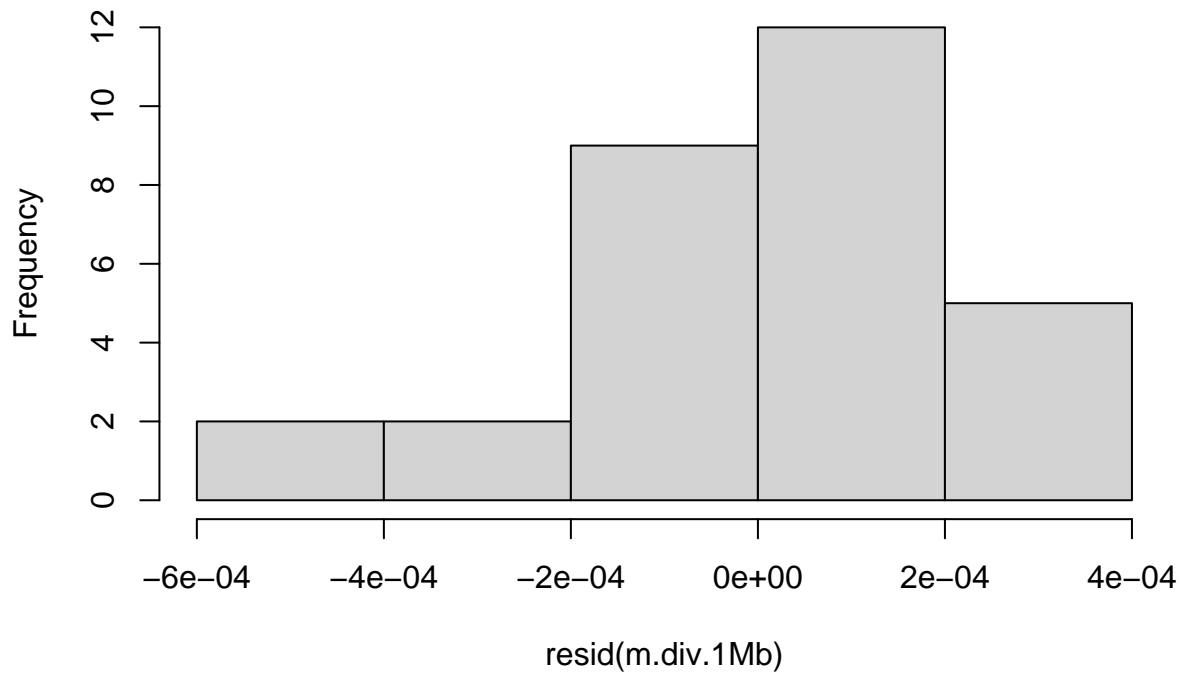
```
##
## Durbin-Watson test
##
## data: m.div.1Mb
## DW = 1.5295, p-value = 0.09374
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##
## Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.59412, p-value = 0.75
```

```
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

# rep_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")
```

```
## Warning in cor.test.default(x = c(0.0145114444444444, 0.0138530418459019, :  
## Cannot compute exact p-value with ties
```

```
##  
## 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")
```

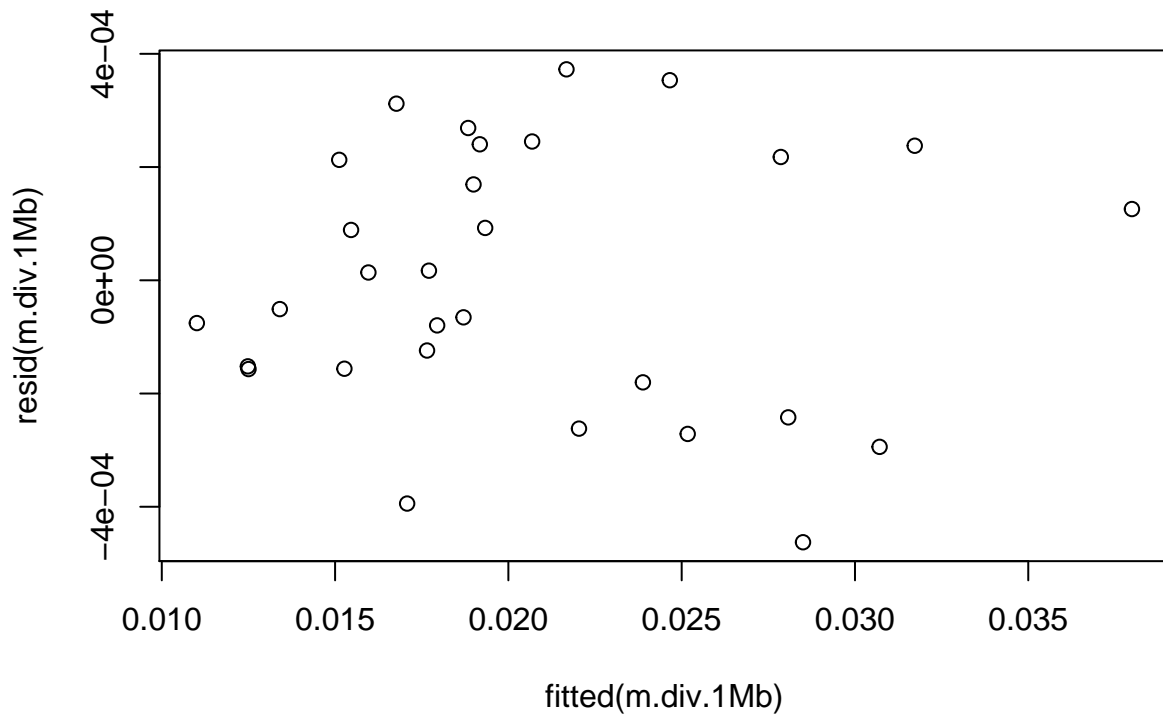
```
##  
## Spearman's rank correlation rho  
##  
## data: diversity and rho  
## S = 596694, p-value = 0.4591  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## -0.06083648
```

```
# 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)
```

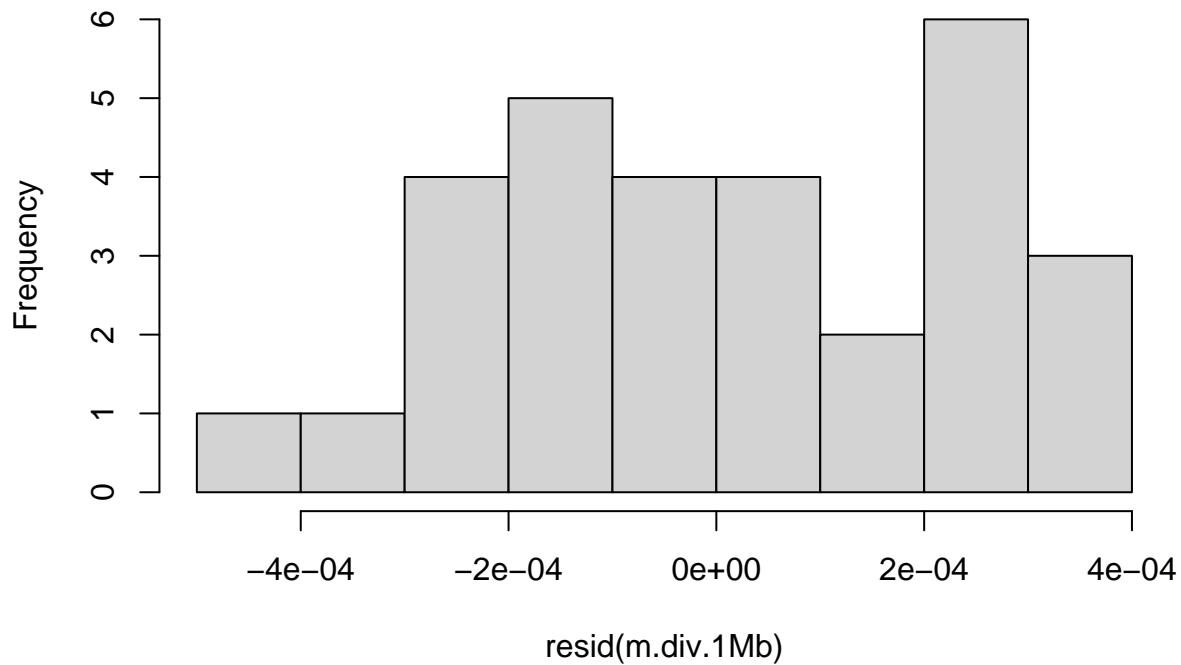
```
##  
## Durbin-Watson test  
##  
## data: m.div.1Mb  
## DW = 2.6531, p-value = 0.9631  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.div.1Mb  
## HMC = 0.51119, p-value = 0.53
```

```
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

# rep_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")
```

```
## Warning in cor.test.default(x = c(0.0145114444444444, 0.0138530418459019, :  
## Cannot compute exact p-value with ties
```

```
##  
## 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")
```

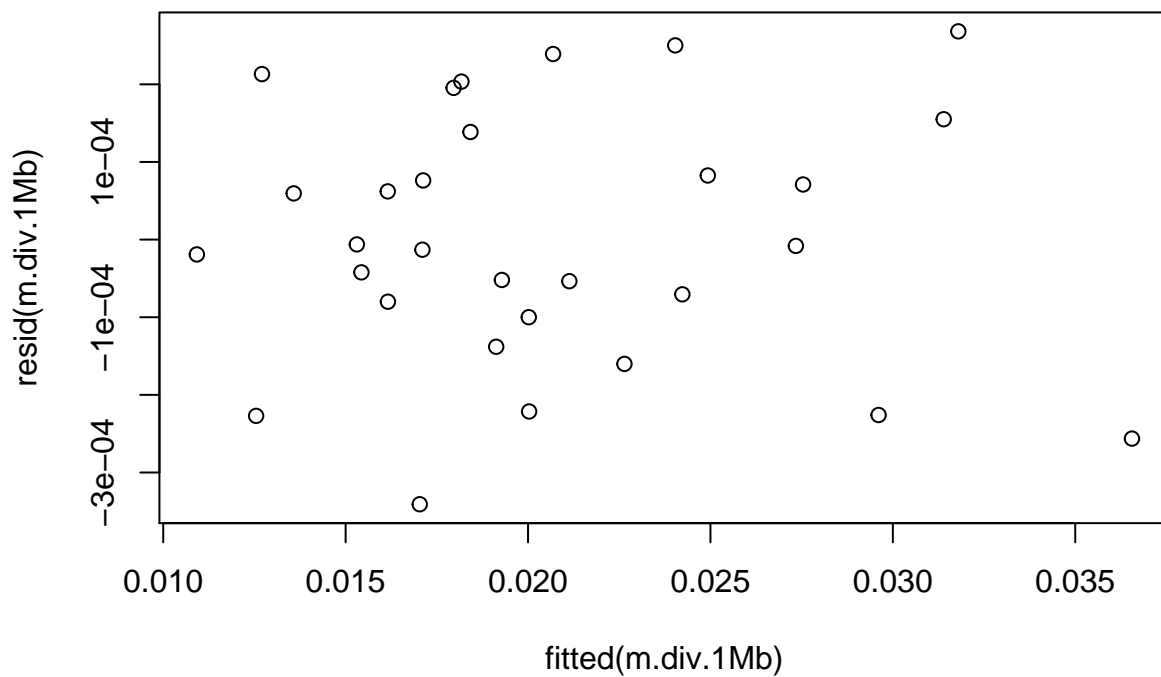
```
##  
## Spearman's rank correlation rho  
##  
## data: diversity and rho  
## S = 596694, p-value = 0.4591  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## -0.06083648
```

```
# 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)
```

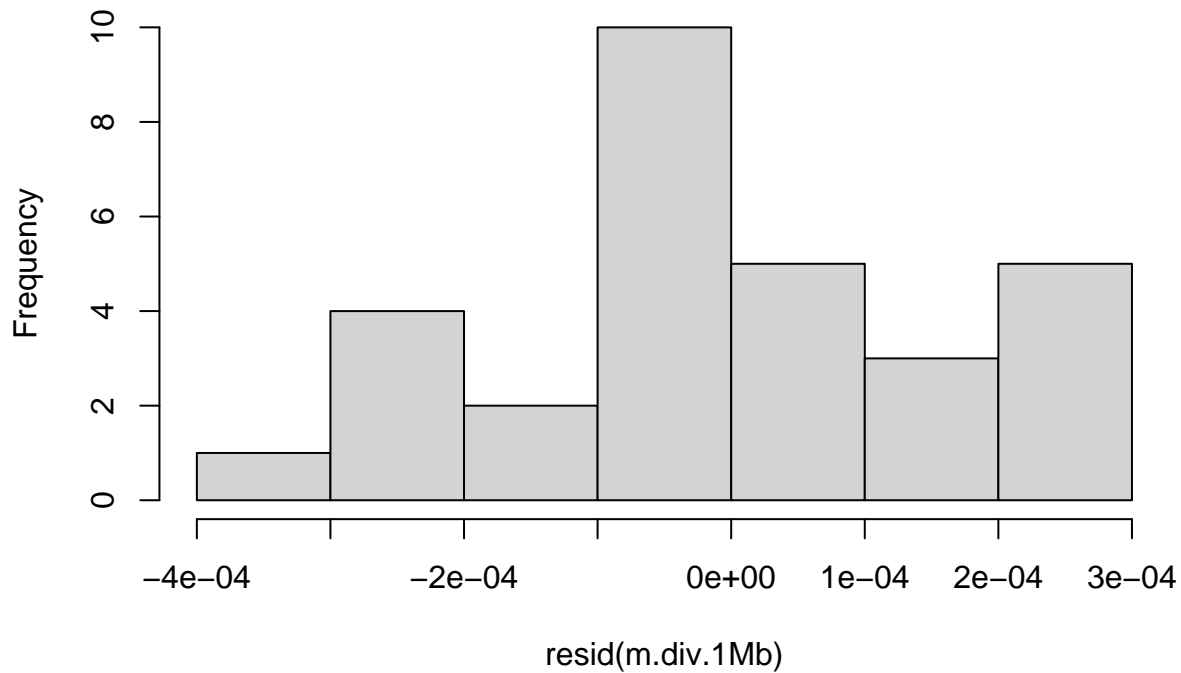
```
##
## Durbin-Watson test
##
## data: m.div.1Mb
## DW = 2.3611, p-value = 0.8304
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##
## Harrison-McCabe test
##
## data: m.div.1Mb
## HMC = 0.69982, p-value = 0.934
```

```
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

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

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

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

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

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

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

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

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

```

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

```
## Warning in cor.test.default(x = c(0.0145114444444444, 0.0138530418459019, :  
## Cannot compute exact p-value with ties
```

```
##  
## 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")
```

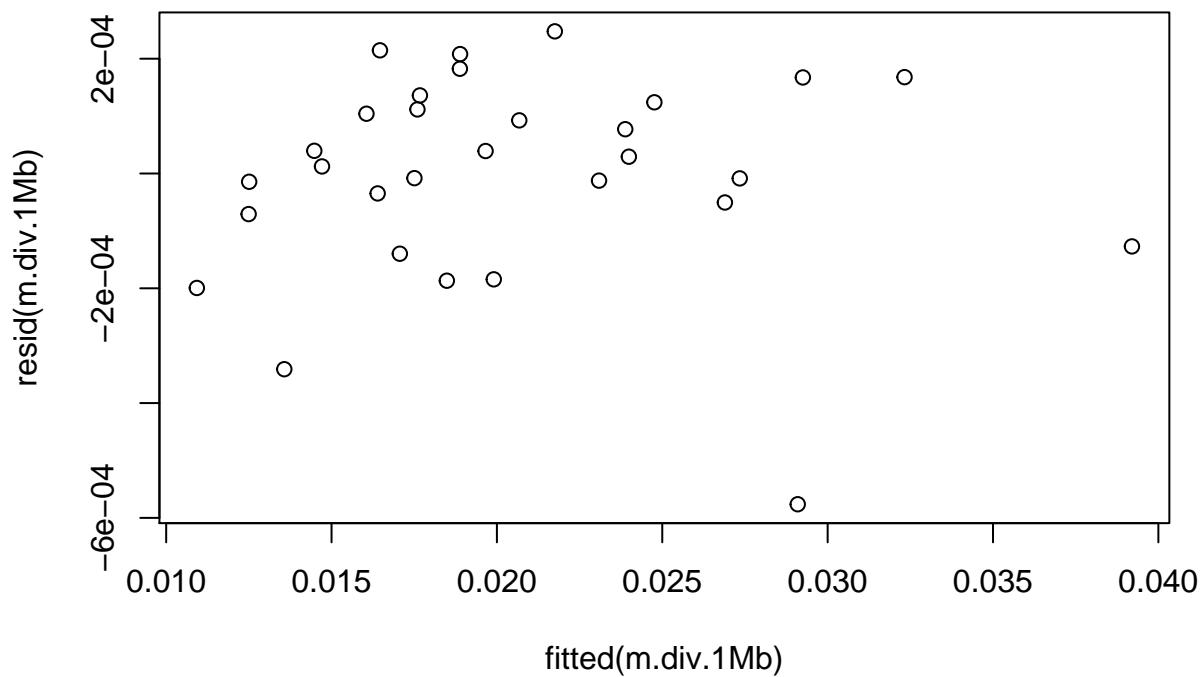
```
##  
## Spearman's rank correlation rho  
##  
## data: diversity and rho  
## S = 596694, p-value = 0.4591  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## -0.06083648
```

```
# 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)
```

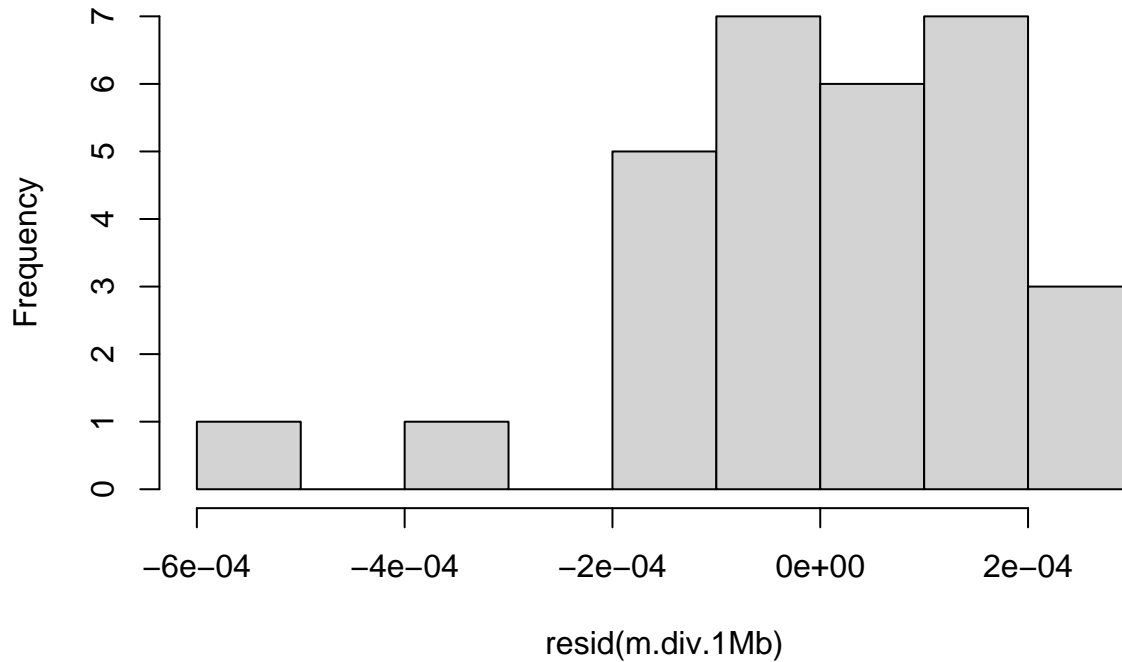
```
##  
## Durbin-Watson test  
##  
## data: m.div.1Mb  
## DW = 2.4044, p-value = 0.8773  
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##  
## Harrison-McCabe test  
##  
## data: m.div.1Mb  
## HMC = 0.39065, p-value = 0.2
```

```
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

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

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

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

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

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

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

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

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

```

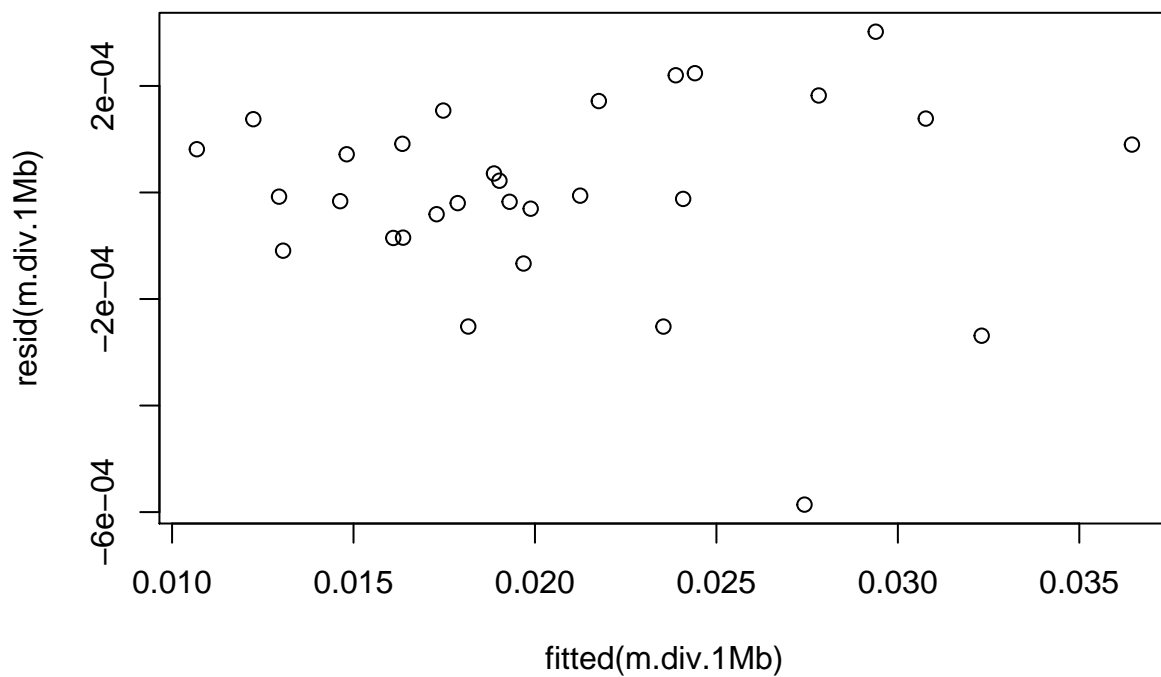
```

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

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

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

```



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

```

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

```

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

```

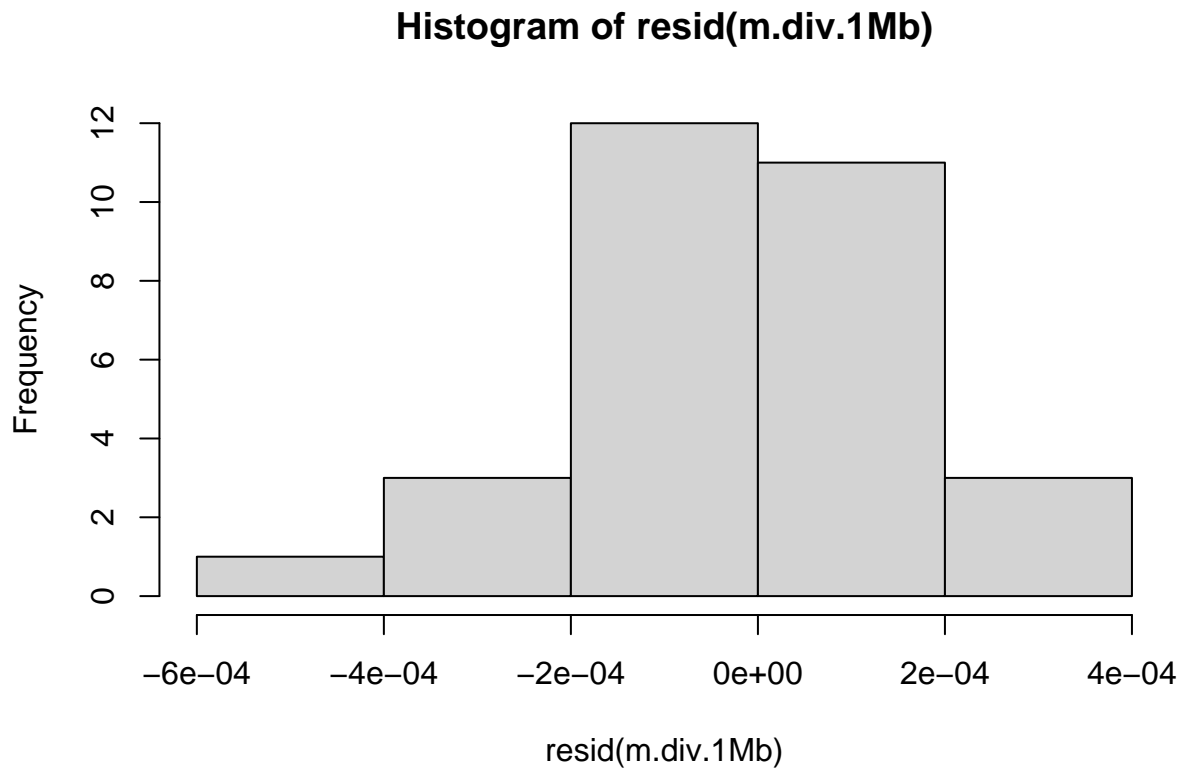
##
## Harrison-McCabe test
##

```



```
## data:  m.div.1Mb
## HMC = 0.35533, p-value = 0.128
```

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



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

```
##
## Call:
## lm(formula = diversity ~ thetaC + rhoC + tmrcaC + thetaC:tmrcaC,
##     data = sim.lands.1Mb)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.859e-04 -7.379e-05 -6.890e-06  1.260e-04  3.018e-04
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.060e-02  3.534e-05  582.791  < 2e-16 ***
## thetaC       1.306e+00  7.849e-03  166.389  < 2e-16 ***
## rhoC        -3.495e-02  5.720e-02  -0.611   0.5467
## tmrcaC       2.514e-02  2.157e-03  11.655  1.34e-11 ***
## thetaC:tmrcaC 1.135e+00  5.053e-01   2.246   0.0338 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 0.0001933 on 25 degrees of freedom
## Multiple R-squared: 0.9992, Adjusted R-squared: 0.9991
## F-statistic: 7809 on 4 and 25 DF, p-value: < 2.2e-16

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

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

# rep_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 =
rep_6.tmrca.1Mb <- read.table("dm_data/dm_chr_maps/2L/dm_coal_sims_2/rep_6/sim.tmrca.1M.map", header =

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

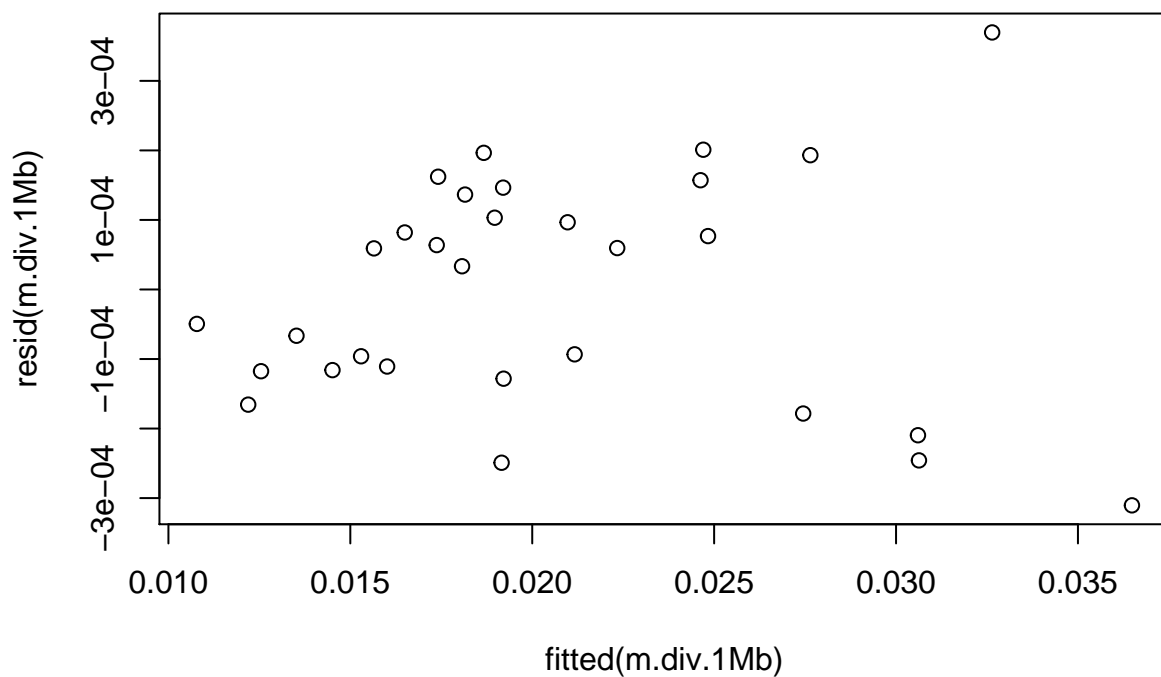
##
## Spearman's rank correlation rho
##
## data: rho and tmrca
```

```
## 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))
```



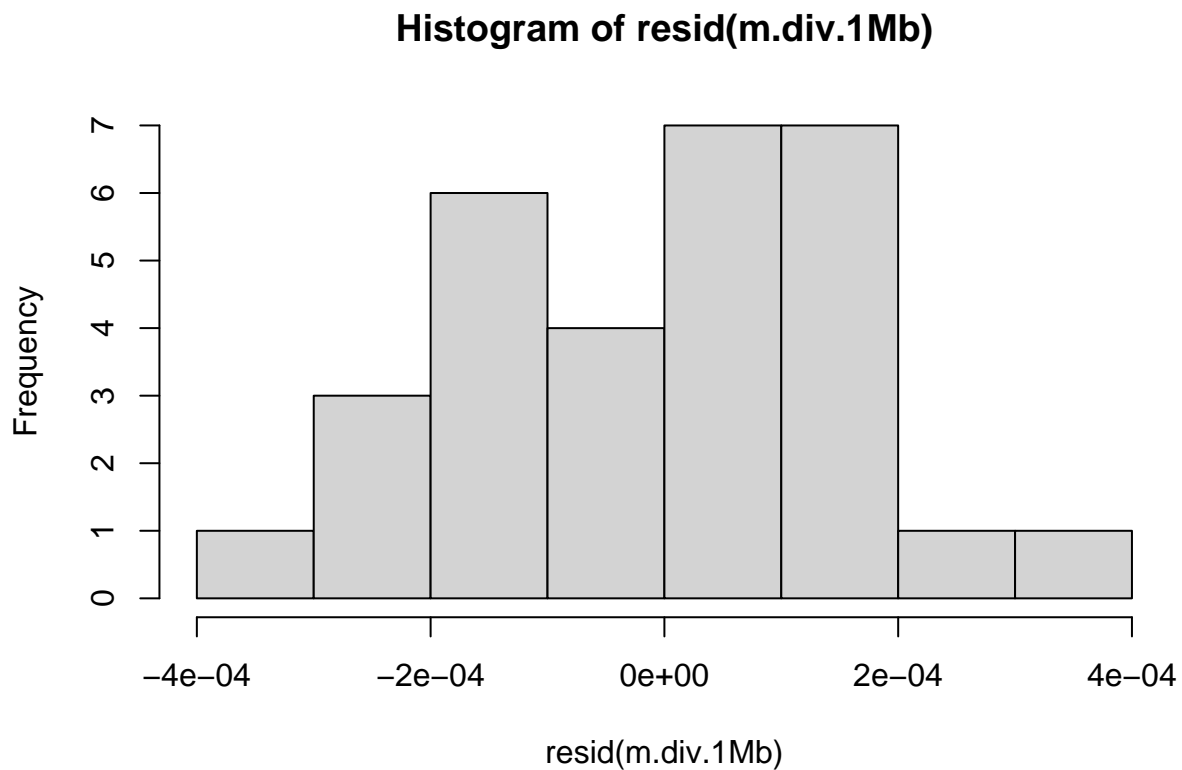
```
dwtest(m.div.1Mb)
```

```
##
## 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 = 0.808
```

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

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

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

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

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

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

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

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

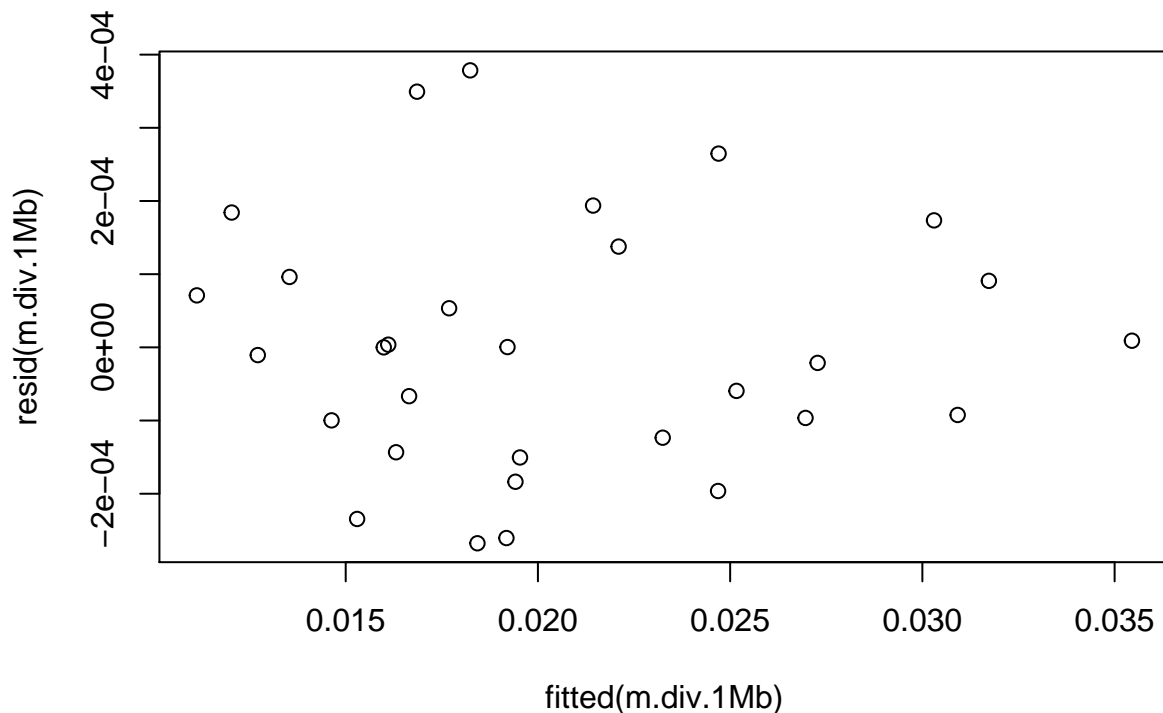
```
##  
## Spearman's rank correlation rho  
##  
## data: rho and tmrca  
## S = 3620, p-value = 0.3013  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
##      rho  
## 0.1946607
```

```
# centering
```

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

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

```
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)
```

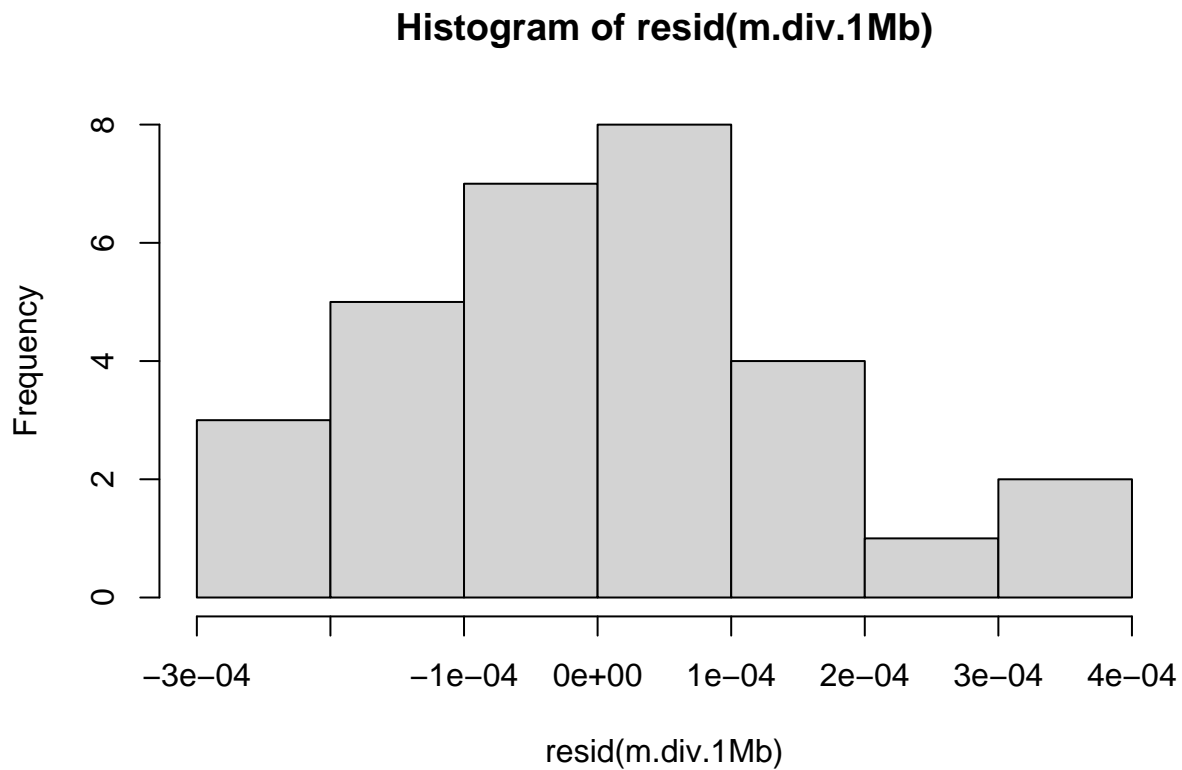
```
##
```

```
## 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 = 0.891
```

```
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
## -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

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

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
```

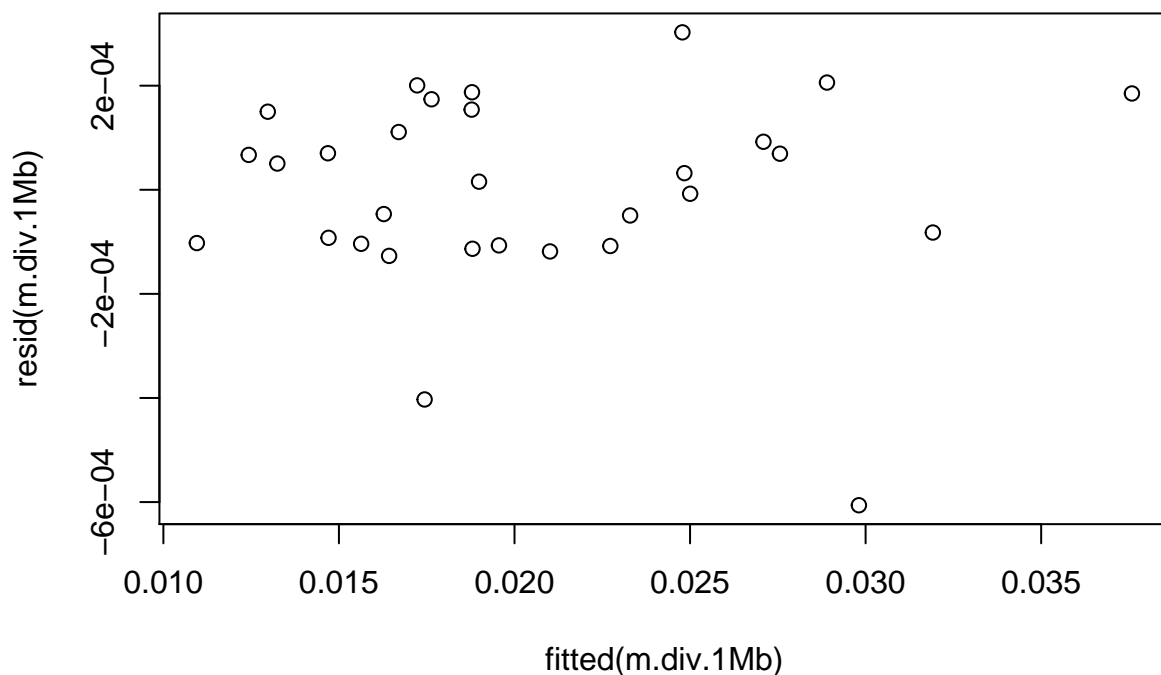
```
cor.test(~rho+tmrca, data = sim.lands.1Mb, method = "spearman")
```

```
##
## 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))
```



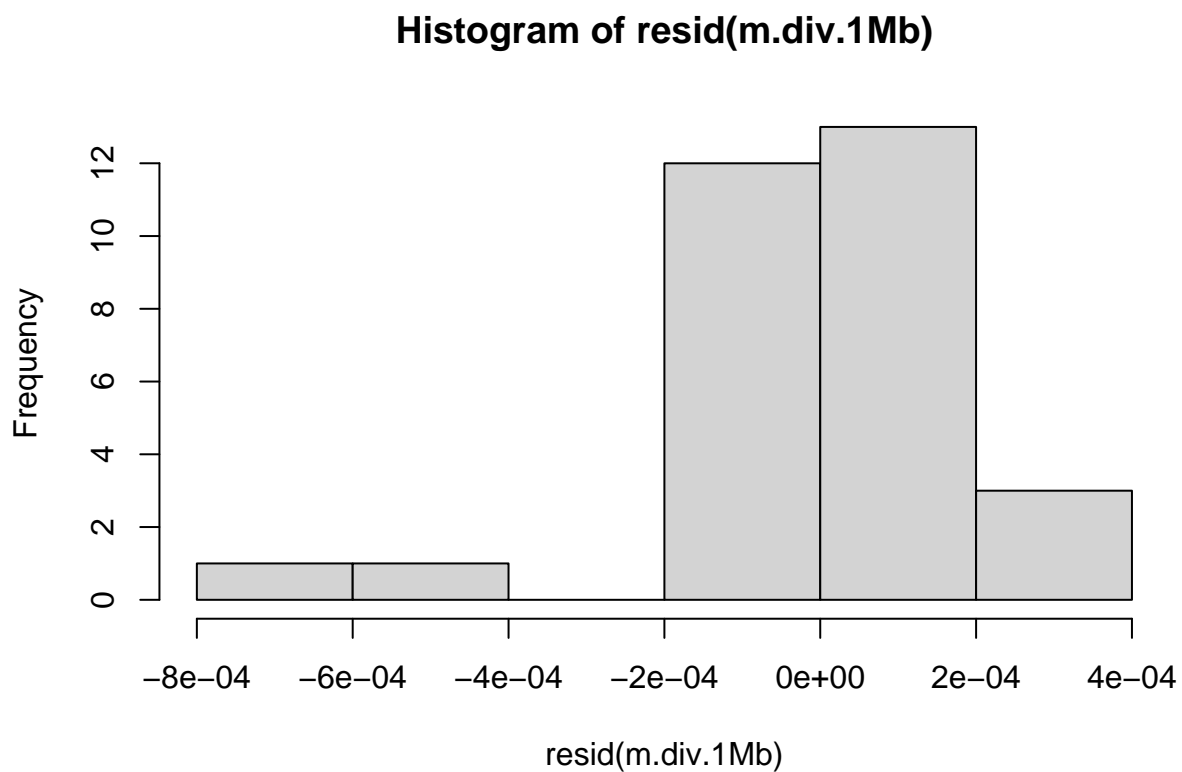
```
dwtest(m.div.1Mb)
```

```
##  
## 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 = 0.933
```

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

```
# rep_9
```

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

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

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

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

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

```
##
```

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

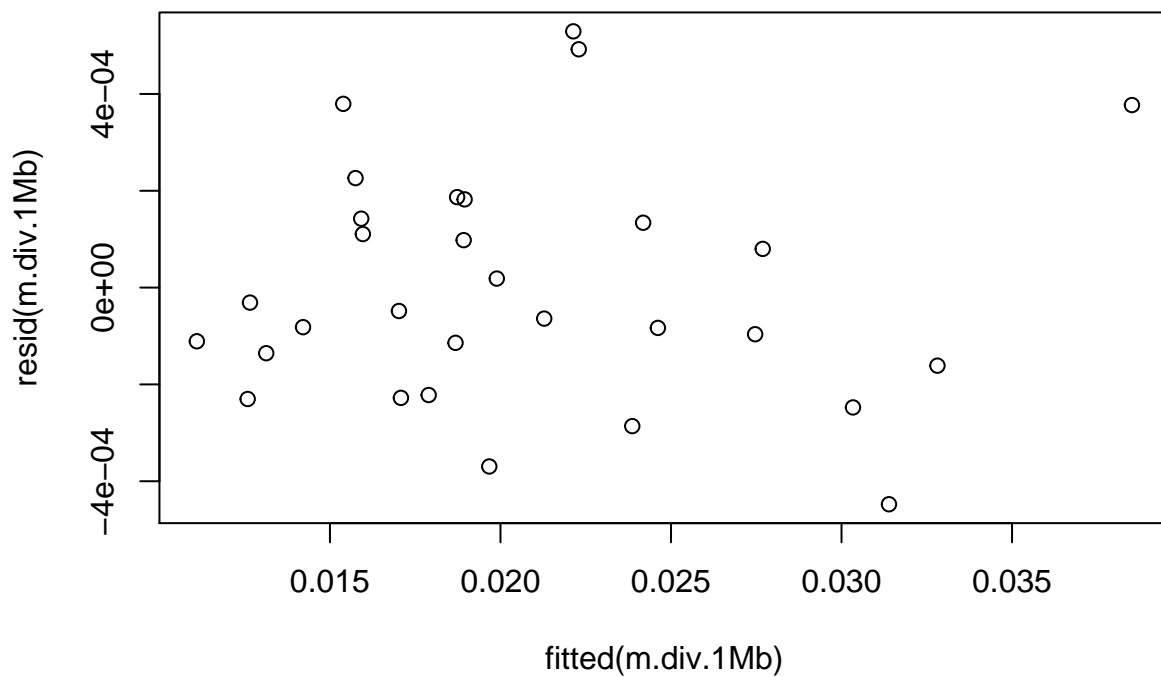
```
cor.test(~rho+tmrca, data = sim.lands.1Mb, method = "spearman")
```

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

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

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

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)
```

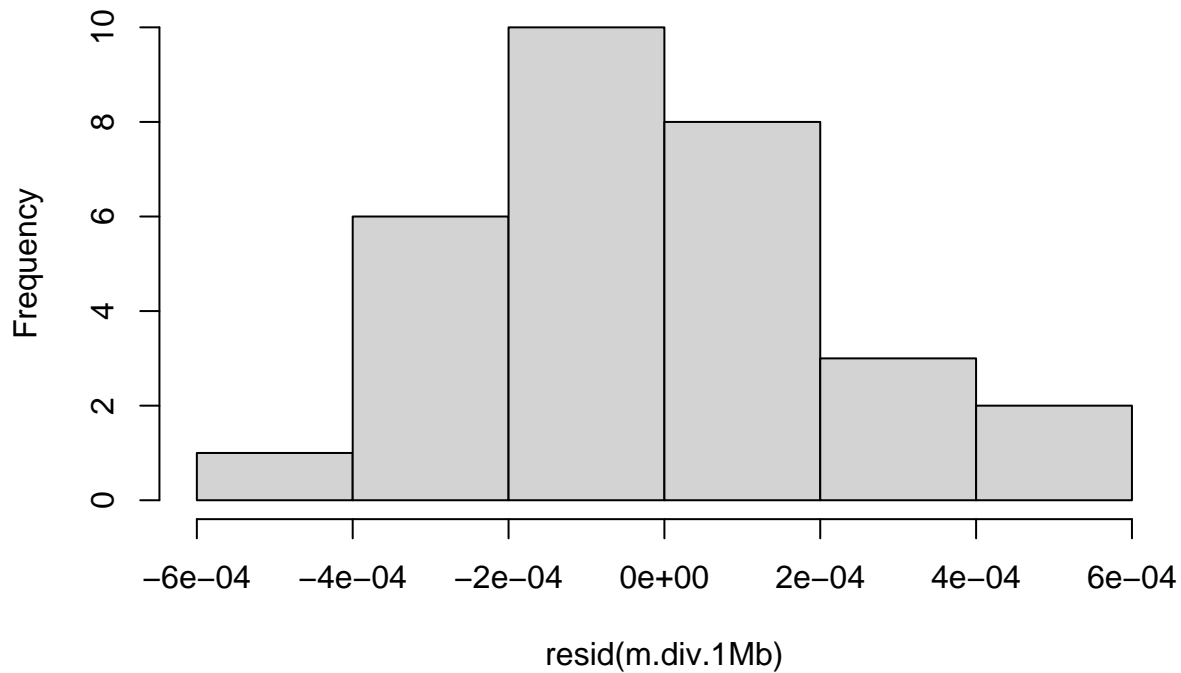
```
##
## Durbin-Watson test
##
## data:  m.div.1Mb
## DW = 2.2409, p-value = 0.7322
## alternative hypothesis: true autocorrelation is greater than 0
```

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

```
##
## Harrison-McCabe test
##
## data:  m.div.1Mb
## HMC = 0.5612, p-value = 0.688
```

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

Histogram of resid(m.div.1Mb)



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

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

```

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

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

# rep_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

```

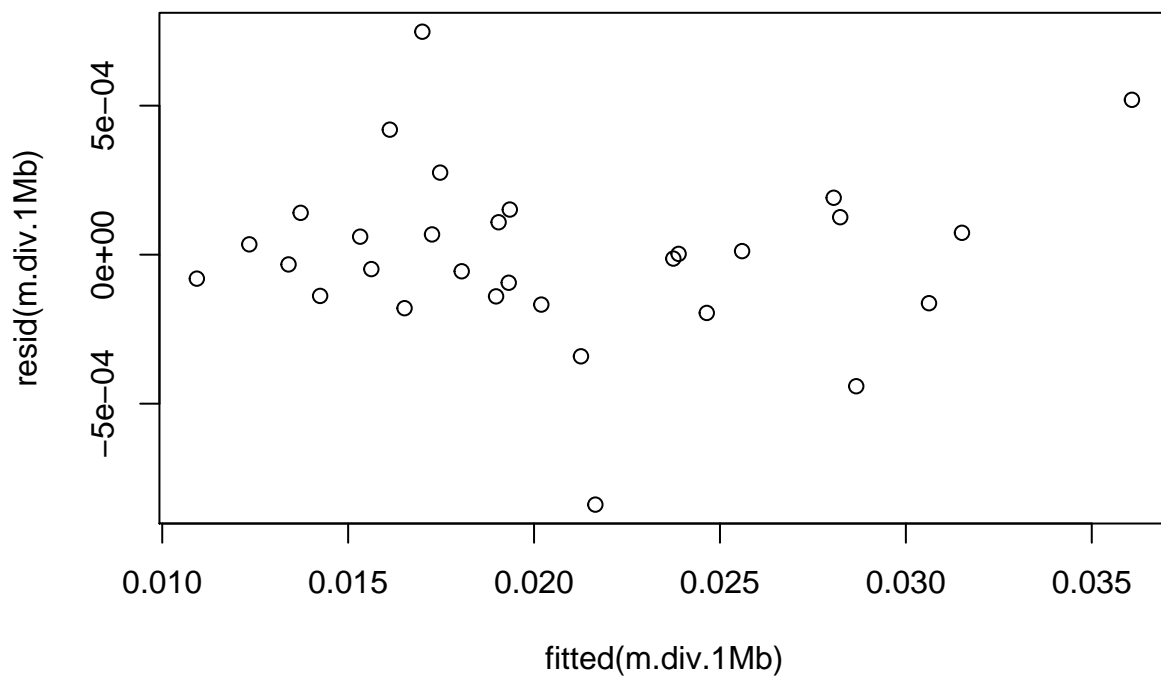
```

# 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(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 = 2.2351, p-value = 0.7114
## alternative hypothesis: true autocorrelation is greater than 0

```

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

```

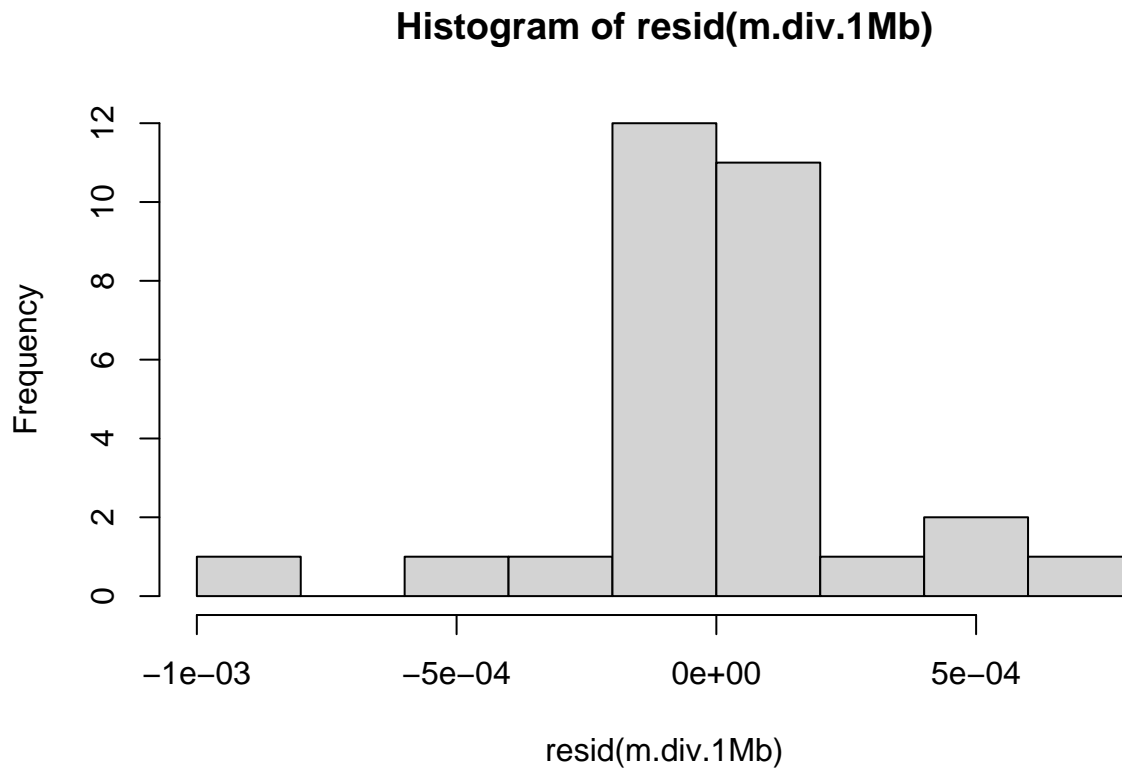
##
## Harrison-McCabe test
##

```



```
## data:  m.div.1Mb
## HMC = 0.50343, p-value = 0.507
```

```
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
## -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))
```

R² plot

```
# true landscapes
r2.sim.avg <- rbind.data.frame(r2.sim.50kb$average, r2.sim.200kb$average, r2.sim.1Mb$average, make.row.names = FALSE)
colnames(r2.sim.avg) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
r2.sim.avg$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$average, make.row.names = FALSE)
colnames(r2.inf.avg) <- c("Total", "Theta", "Rho", "TMRCA", "Theta:TMRCA")
r2.inf.avg$bin.size <- c(50, 200, 1000)

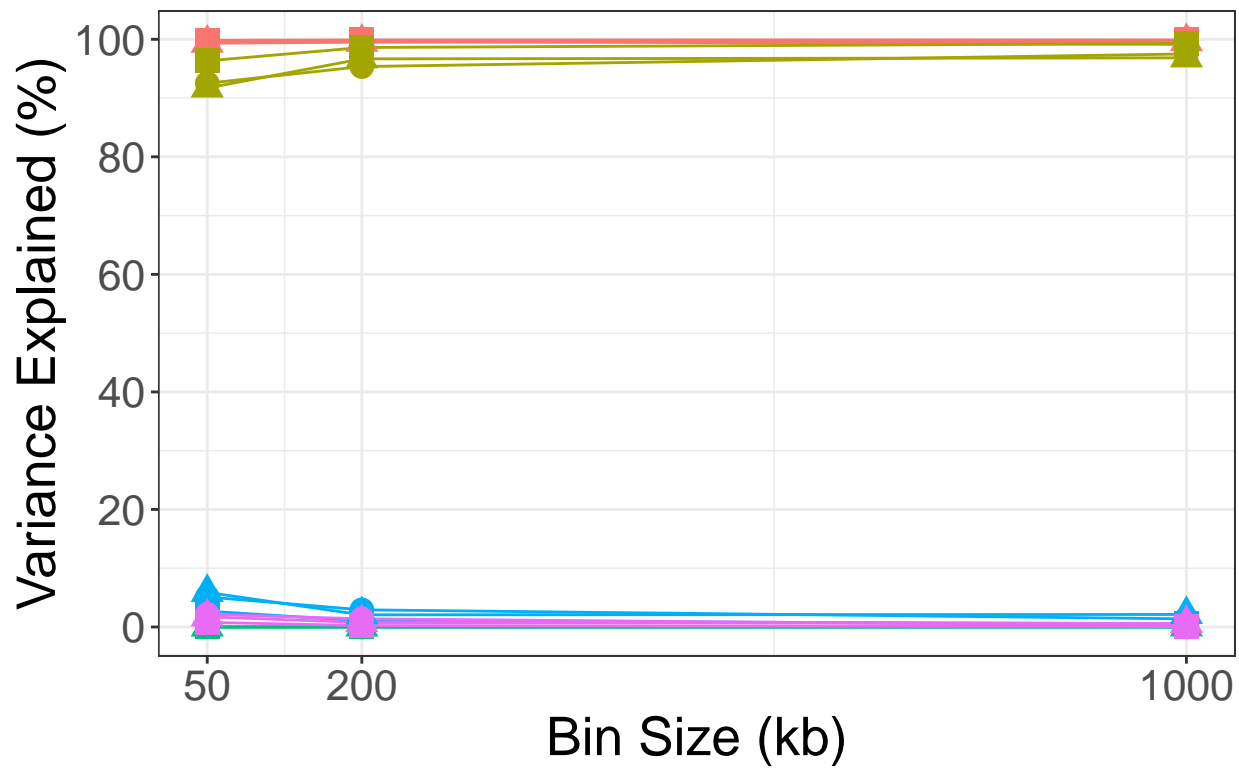
r2.dm.tab.2 <- as.data.frame(cbind(apply(r2.dm.tab, 2, as.numeric)))

r2.tab.comb <- rbind.data.frame(r2.dm.tab.2, 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))
r2.plot <- r2.plot + scale_y_continuous(breaks = pretty_breaks())
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))

leg <- get_legend(r2.plot + theme(legend.position="bottom"))

fig4 <- plot_grid(r2.plot + theme(legend.position = "none", legend.title = NULL),
                  leg, nrow = 2, labels = NULL, rel_heights = c(1, 0.1), scale = c(1, 0.2))
fig4
```



riable Total Theta Rho TMRCA Theta:TMRCA type ● inf ▲ real ■ s