IBD and IBR - S. botryophora

Prepare distance matricies

Calulate geographic distance between localities

```r
# load packages
library(geosphere)

# import geographic distance data
sp.geo <- read.csv("../Samples/Syagrus_localities_final.csv")
sp.geo <- subset(sp.geo,sp.geo$Syagrus_sp =='S_botryophora')
#geo <- subset(geo,geo$Syagrus_sp =='S_pseudococos')
#sp.geo <- subset(sp.geo,sp.geo$Code != 'ps13')

# calculate geographic distance
geo <- distm(cbind(sp.geo$Lat_dec,sp.geo$Long_dec))
geo <- geo/1000 #convert from meters to km
Dgeo <- dist(geo)
```

Read in genetic distance between localities (Nei's distance)

```r
gen <- as.matrix(read.csv('gen_bo50.csv'))
Dgen <- dist(gen)
```

Read in the resistance distance matricies created in Circuitscape

```r
curr <- read.csv("../Circuitscape/Curr/bo_resistances.out",
                 sep = " ")
stab <- read.csv("../Circuitscape/Stab/bo_resistances.out",
                 sep = " ")
stab_blind <- read.csv("../Circuitscape/Stab_blind/bo_resistances.out",
                 sep = " ")

# stab <- read.csv("../Circuitscape/Output/ps_MESS_resistances.out",
#                  sep = " ")

curr <- as.matrix(curr[,-1])
stab <- as.matrix(stab[,-1])
stab_blind <- as.matrix(stab_blind[,-1])
Dcurr <- dist(curr)
```

```
Dstab <- dist(stab)
Dstab_blind <- dist(stab_blind)
```
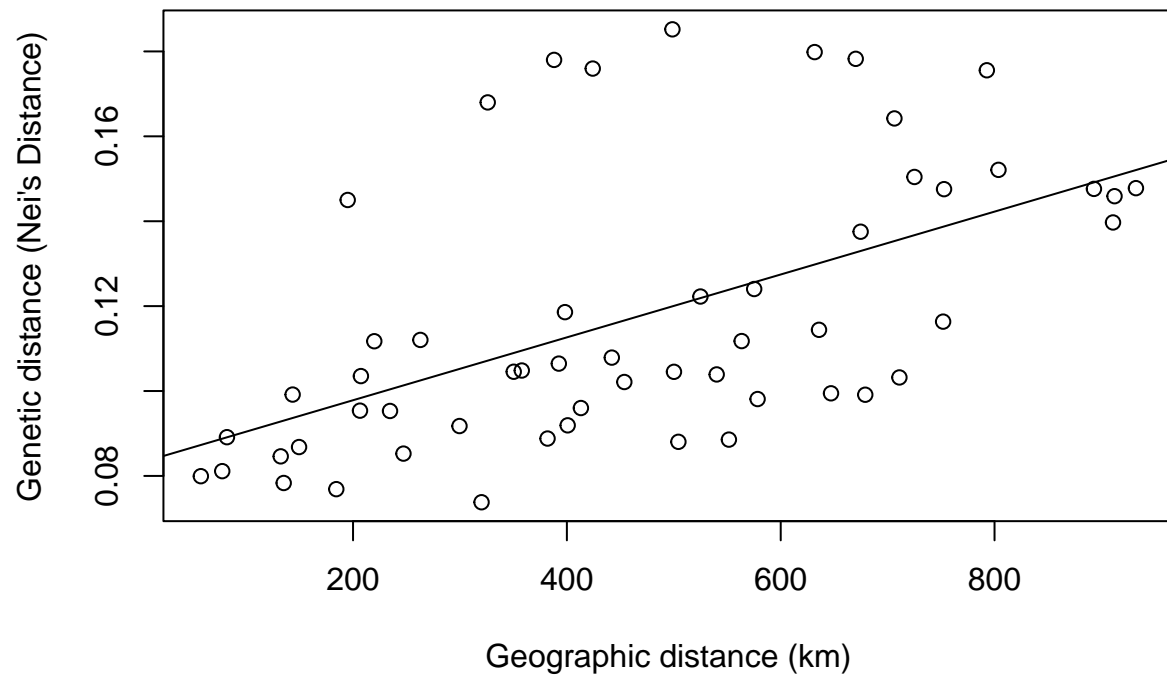
Correlation tests

Correlation genetic - geographic distances (IBD)

```
cor.test(Dgeo, Dgen)
```

```
##
##  Pearson's product-moment correlation
##
## data:  Dgeo and Dgen
## t = 4.9304, df = 53, p-value = 8.48e-06
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.3470839 0.7190719
## sample estimates:
##       cor
## 0.5607472
```

Isolation by distance plot

```
regrIBD <- lm(Dgen ~ Dgeo)
plot(Dgeo,Dgen,xlab="Geographic distance (km)",ylab="Genetic distance (Nei's Distance)")
abline(regrIBD)
```
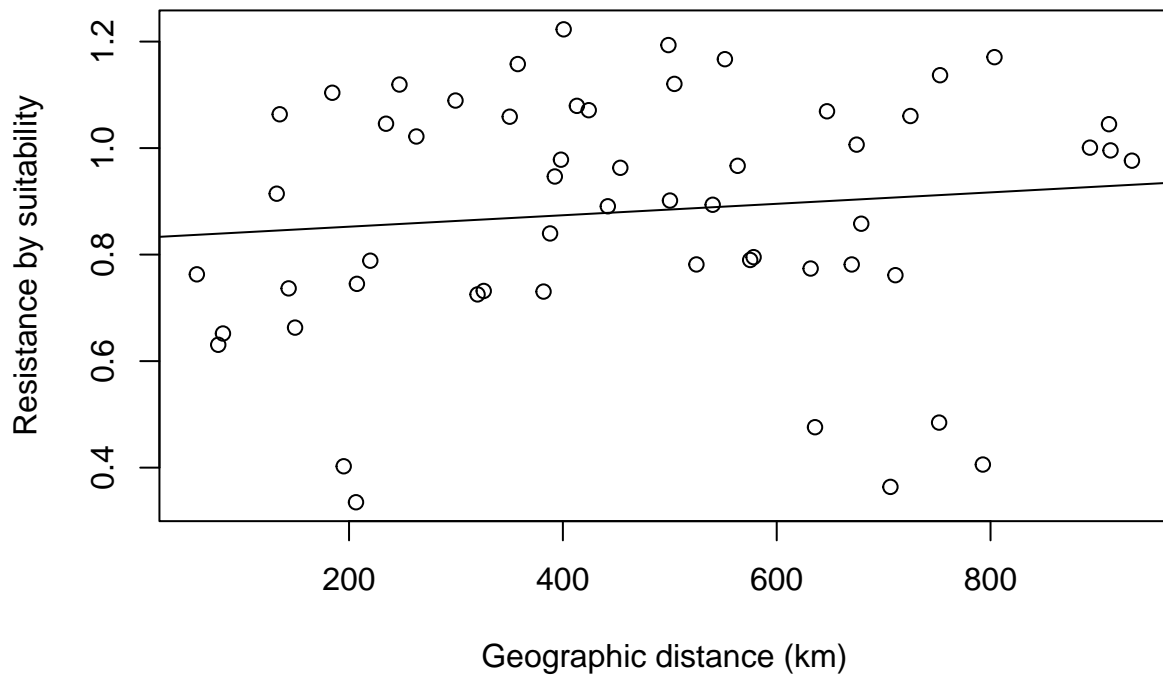
Correlation current suitabliity resistance - distance distances

```
cor.test(Dgeo,Dcurr)
```

```
##
##   Pearson's product-moment correlation
##
## data:  Dgeo and Dcurr
## t = 0.83537, df = 53, p-value = 0.4073
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.1560163  0.3681620
## sample estimates:
##       cor
## 0.1139994
```

Plot geographic-resistance correlation

```
GeoCurr <- lm(Dcurr ~ Dgeo)
plot(Dgeo, Dcurr ,xlab="Geographic distance (km)",ylab="Resistance by suitability")
abline(GeoCurr)
```
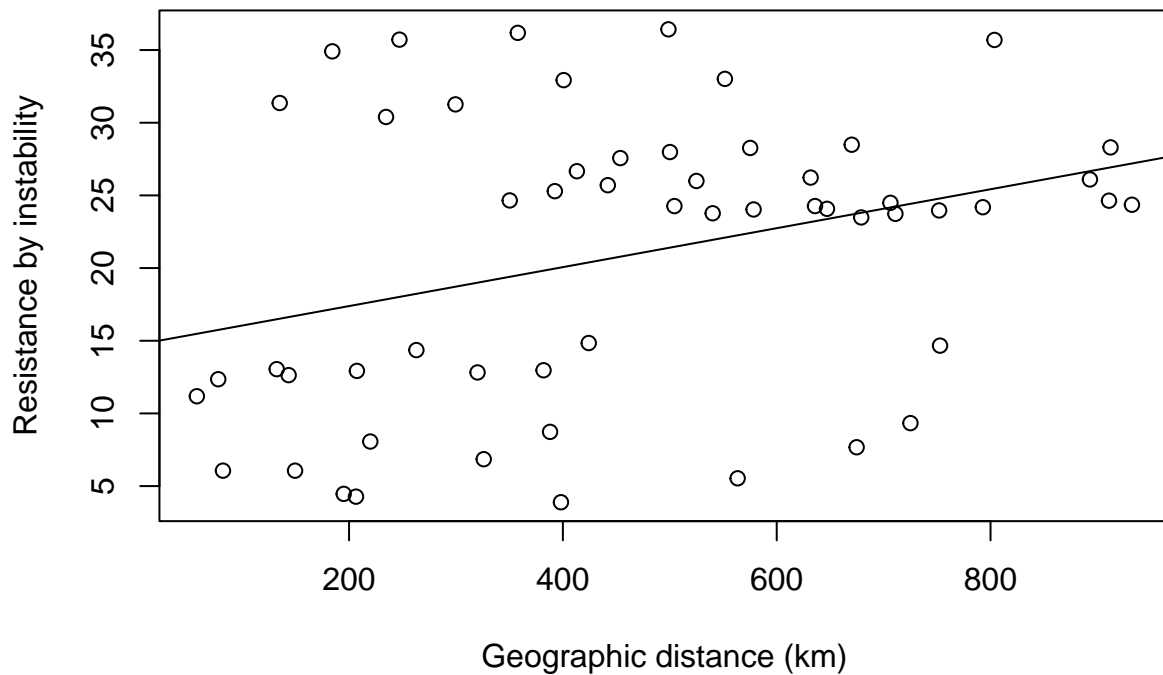
Correlation stability resistance - distance distances

```
cor.test(Dgeo,Dstab)
```

```
##
##   Pearson's product-moment correlation
##
## data:  Dgeo and Dstab
## t = 2.5404, df = 53, p-value = 0.01404
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.07031823 0.54695817
## sample estimates:
##       cor
## 0.3294691
```

Plot geographic-resistance correlation

```
GeoStab <- lm(Dstab ~ Dgeo)
plot(Dgeo, Dstab ,xlab="Geographic distance (km)",ylab="Resistance by instability")
abline(GeoStab)
```
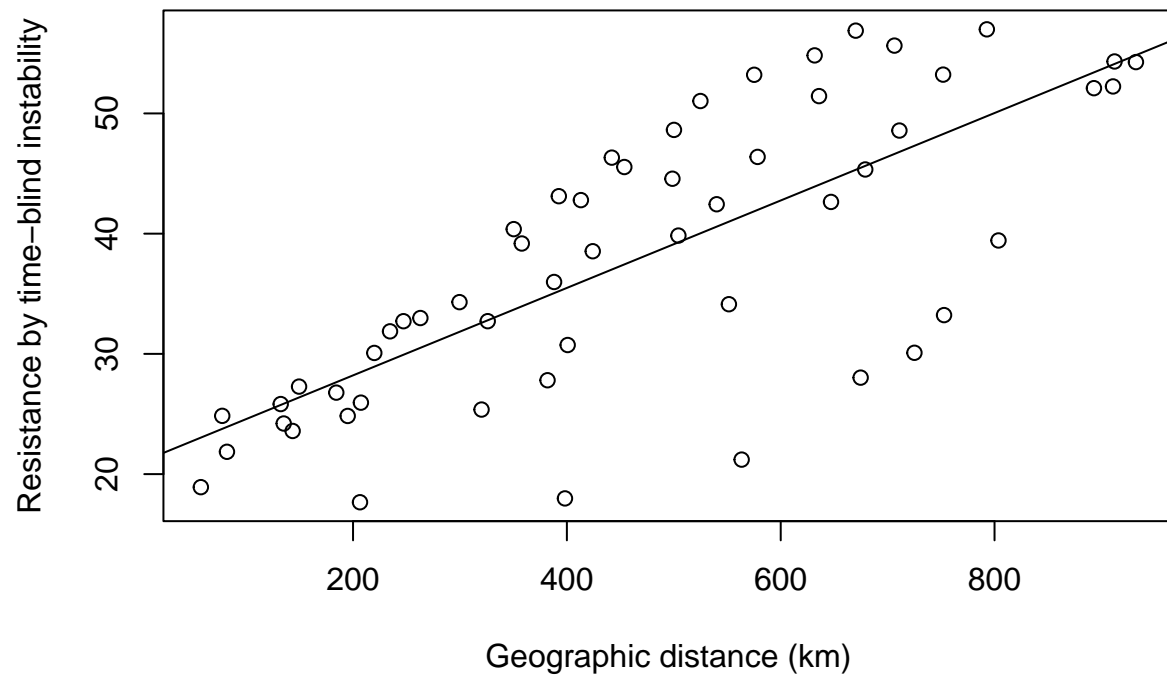
Correlation time-blind stability resistance - distance distances

```
cor.test(Dgeo,Dstab_blind)
```

```
##
##  Pearson's product-moment correlation
##
## data:  Dgeo and Dstab_blind
## t = 8.2605, df = 53, p-value = 4.302e-11
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.6054276 0.8469512
## sample estimates:
##       cor
## 0.7502249
```
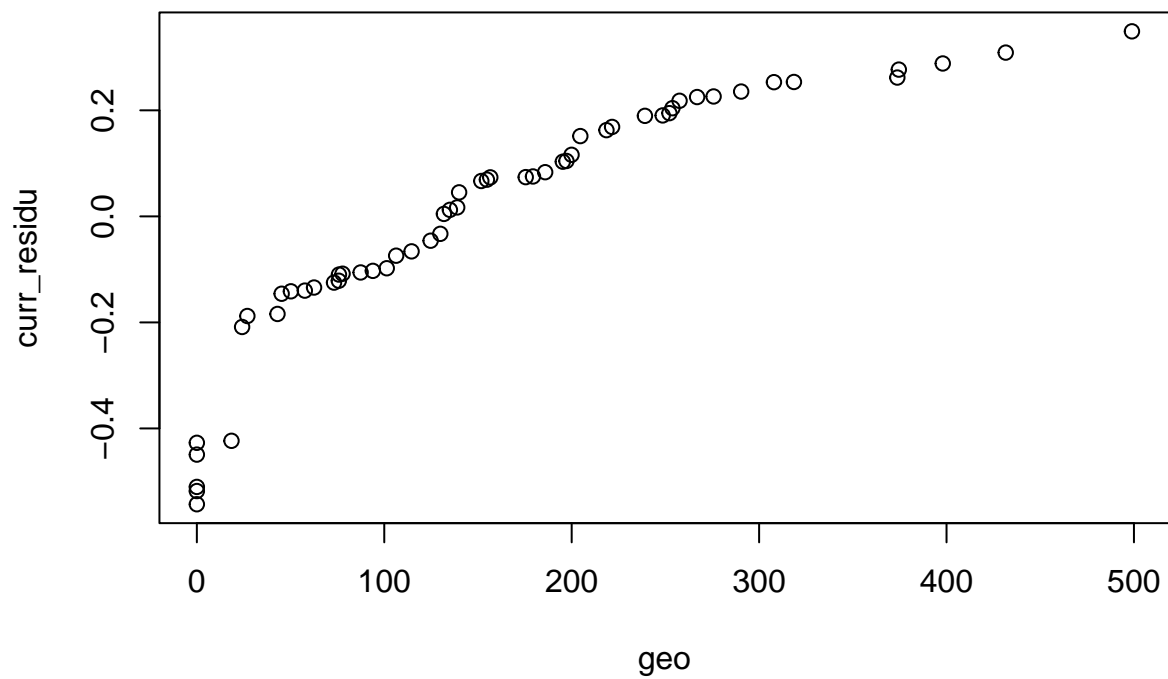
Plot geographic-resistance correlation

```
GeoStab_blind <- lm(Dstab_blind ~ Dgeo)
plot(Dgeo, Dstab_blind ,xlab="Geographic distance (km)",ylab="Resistance by time-blind instability")
abline(GeoStab_blind)
```
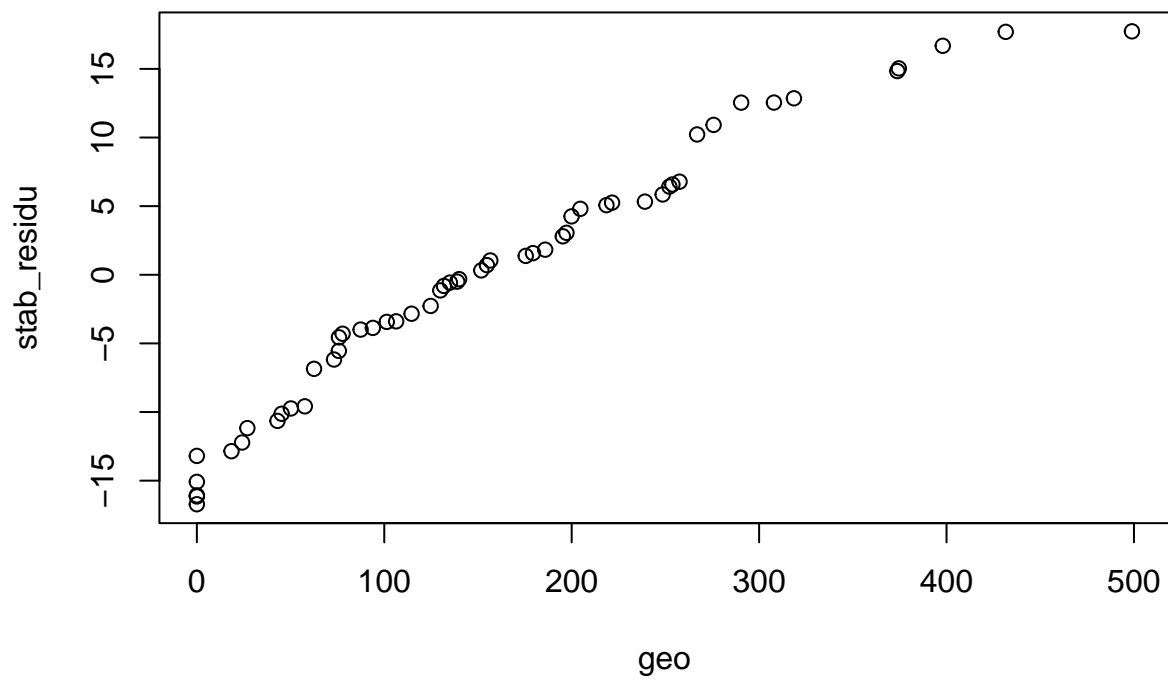
Calculate residuals of current suitability resistance - distance correlation

```
curr_residu <- residuals(GeoCurr)
qqplot(geo,curr_residu)
```
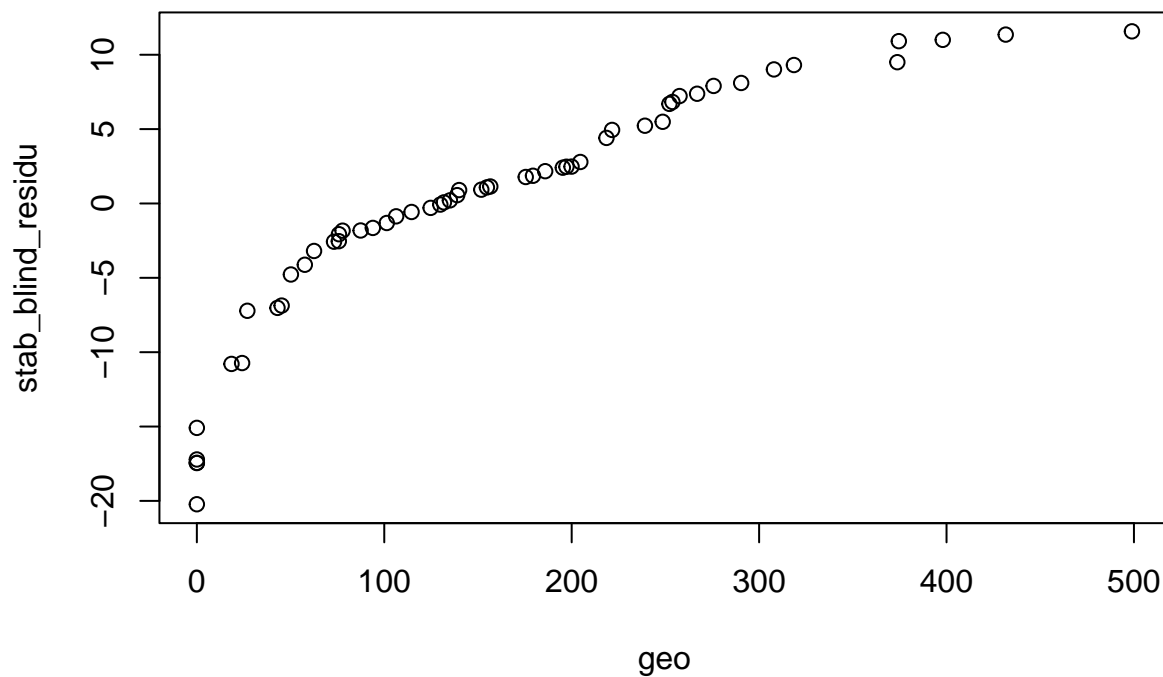
Calculate residuals of stability resistance - distance correlation

```
stab_residu <- residuals(GeoStab)
qqplot(geo,stab_residu)
```

Calculate residuals of time-blind stability resistance - distance correlation

```
stab_blind_residu <- residuals(GeoStab_blind)
qqplot(geo,stab_blind_residu)
```
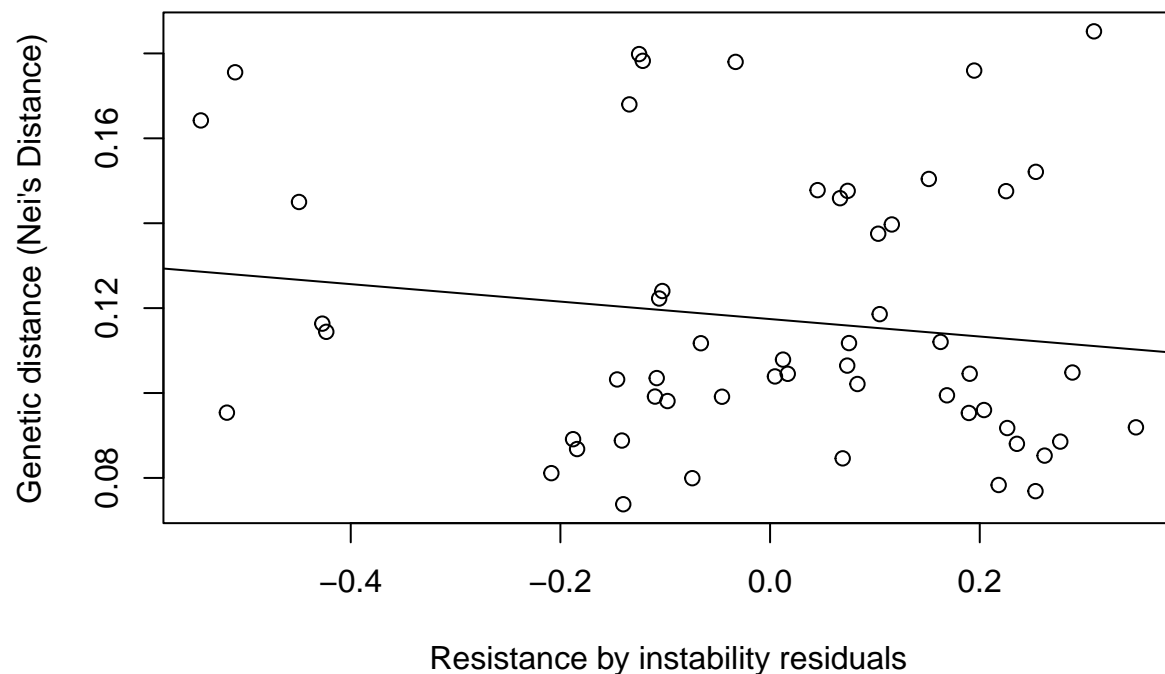
Correlation genetic - current resistance residuals distances (IBR with residuals)

```
cor.test(curr_residu, Dgen)
```

```
##
##  Pearson's product-moment correlation
##
## data:  curr_residu and Dgen
## t = -1.0726, df = 53, p-value = 0.2883
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.3957484  0.1243516
## sample estimates:
##        cor
## -0.145754
```

Isolation by instability plot

```
regrIBR_residu_curr <- lm(Dgen ~ curr_residu)
plot(curr_residu, Dgen, xlab="Resistance by instability residuals", ylab="Genetic distance (Nei's Distan
abline(regrIBR_residu_curr)
```
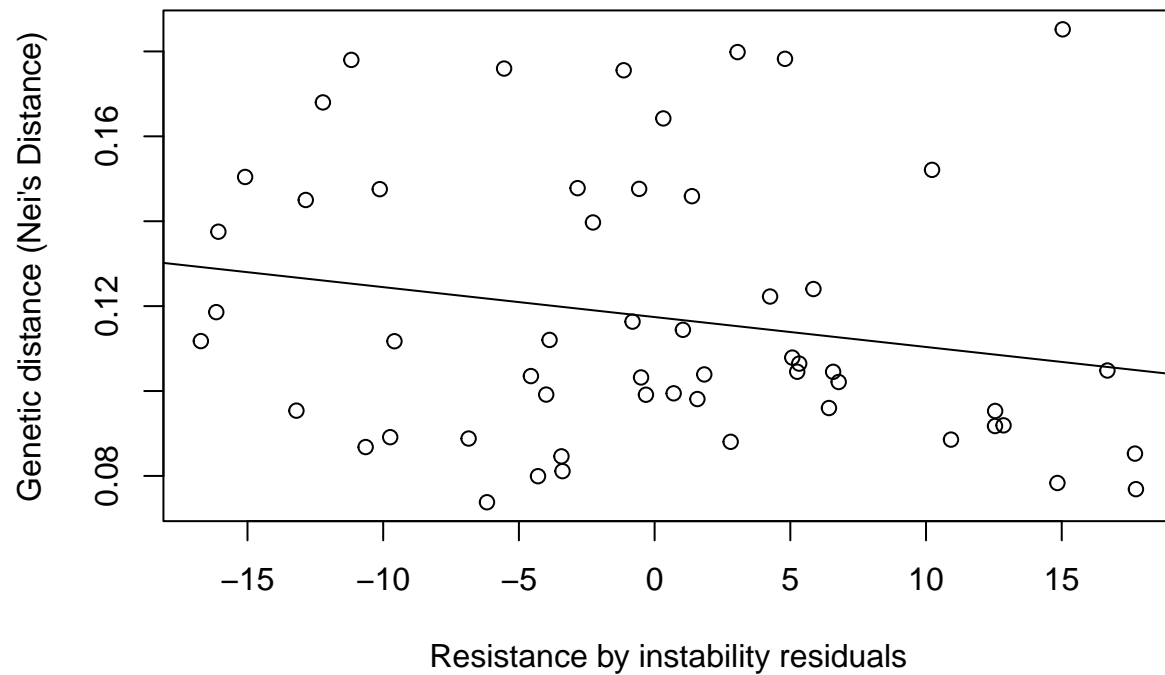
Correlation genetic - stability resistance residuals distances (IBR with residuals)

```
cor.test(stab_residu, Dgen)
```

```
##
##  Pearson's product-moment correlation
##
## data:  stab_residu and Dgen
## t = -1.5242, df = 53, p-value = 0.1334
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.44597273  0.06384742
## sample estimates:
##        cor
## -0.2049208
```

Isolation by instability plot

```
regrIBR_residu <- lm(Dgen ~ stab_residu)
plot(stab_residu, Dgen, xlab="Resistance by instability residuals", ylab="Genetic distance (Nei's Distar
abline(regrIBR_residu)
```

Correlation genetic - time-blind stability resistance residuals distances (IBR with residuals)

```
cor.test(stab_blind_residu, Dgen)
```

```
##
##  Pearson's product-moment correlation
##
## data:  stab_blind_residu and Dgen
## t = 0.76217, df = 53, p-value = 0.4493
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.1657526  0.3594900
## sample estimates:
##       cor
## 0.1041232
```

Isolation by instability plot

```
regrIBR_residu_blind <- lm(Dgen ~ stab_blind_residu)
plot(stab_blind_residu, Dgen, xlab="Resistance by instability residuals", ylab="Genetic distance (Nei's
abline(regrIBR_residu_blind)
```
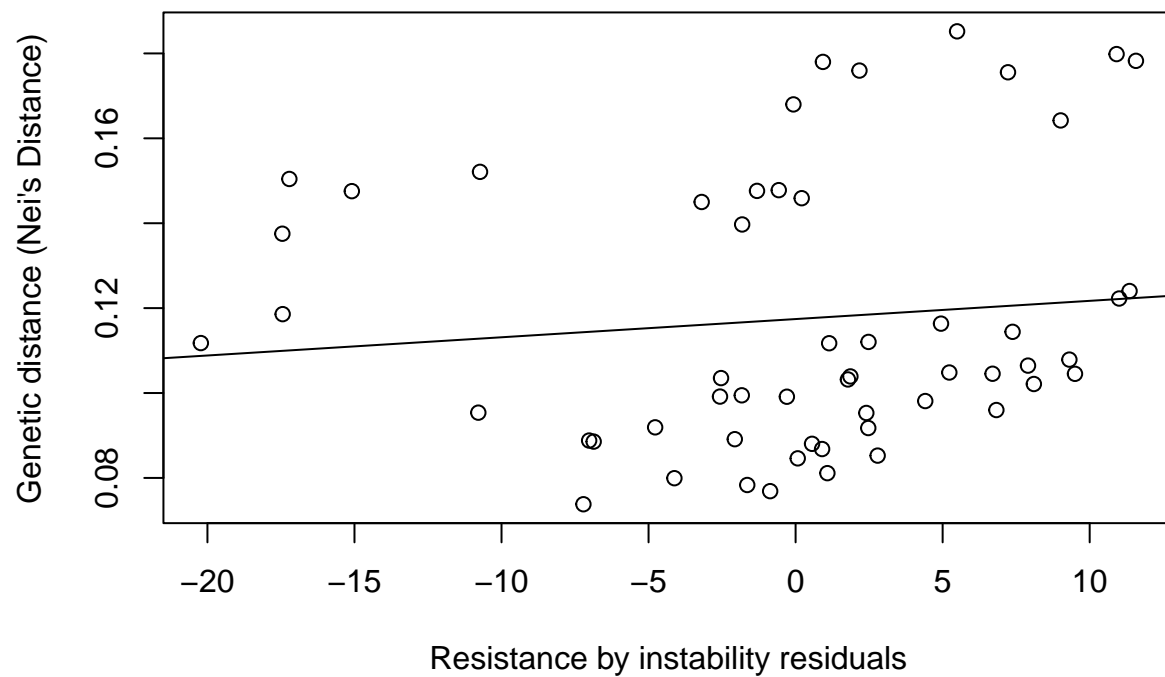
Multiple Regressions

using the method of Legendre et al. 1994

```
library(ecodist)
mr_curr <- MRM(Dgen ~ Dgeo + curr_residu)
mr_curr
```

```
## $coef
##                     Dgen  pval
## Int          8.302185e-02 0.973
## Dgeo         7.405215e-05 0.008
## curr_residu -2.056726e-02 0.533
##
## $r.squared
##        R2       pval
## 0.3356817 0.0340000
##
## $F.test
##        F    F.pval
## 13.13786  0.03400
```

```
mr_stab <- MRM(Dgen ~ Dgeo + stab_residu)
mr_stab
```

```
## $coef
##                     Dgen   pval
## Int          8.302185e-02 0.980
## Dgeo         7.405215e-05 0.011
## stab_residu -7.048570e-04 0.212
##
## $r.squared
##      R2    pval
## 0.35643 0.05000
##
## $F.test
##        F   F.pval
## 14.39965  0.05000
```

```
mr_stab_blind <- MRM(Dgen ~ Dgeo + stab_blind_residu)
mr_stab_blind
```

```
## $coef
##                          Dgen   pval
## Int               8.302185e-02 0.999
## Dgeo              7.405215e-05 0.025
## stab_blind_residu 4.290442e-04 0.423
##
## $r.squared
##        R2      pval
## 0.3252791 0.0810000
##
## $F.test
##        F   F.pval
## 12.53445  0.08100
```