IBD and IBR - S. pseudococos

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$Syagrus_sp =='S_botryophora')
sp.geo <- subset(sp.geo,sp.geo$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_ps50.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 = " ")

curr <- read.csv("../Circuitscape/Curr/ps_resistances.out",
                  sep = " ")
stab <- read.csv("../Circuitscape/Stab/ps_resistances.out",
                  sep = " ")
stab_blind <- read.csv("../Circuitscape/Stab_blind/ps_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)
```
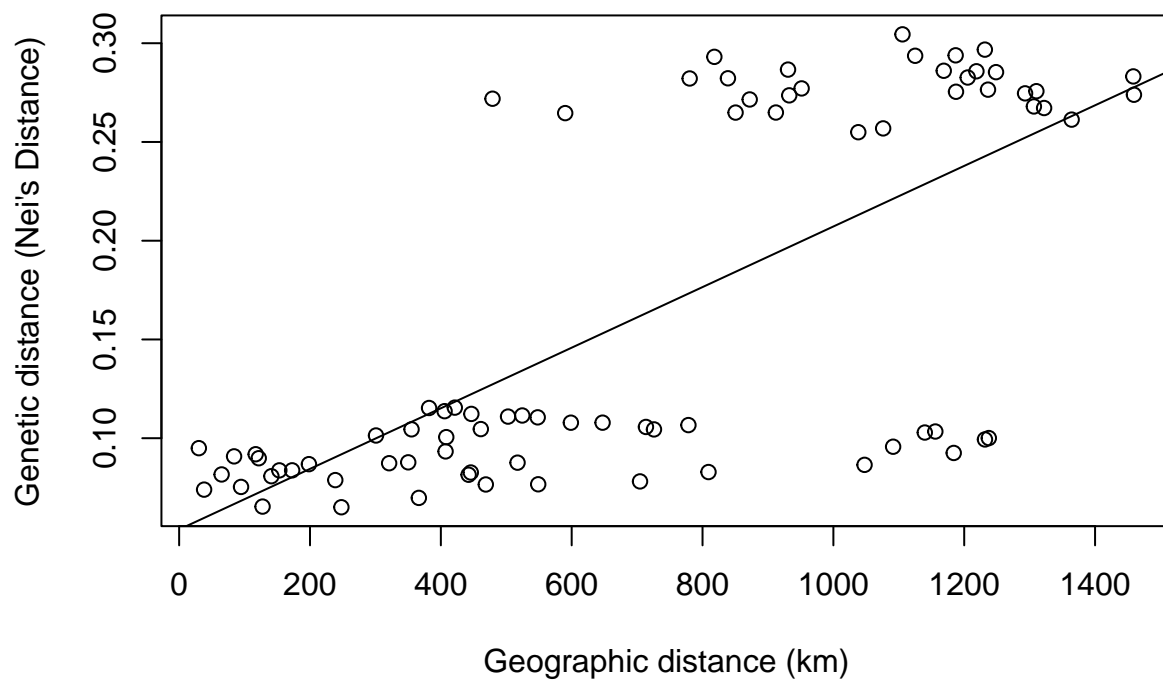
Correlation tests

Correlation genetic - geographic distances (IBD)

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

```
##
##  Pearson's product-moment correlation
##
## data:  Dgeo and Dgen
## t = 8.7808, df = 76, p-value = 3.51e-13
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.5784675 0.8050466
## sample estimates:
##       cor
## 0.7096476
```

Isolation by distance plot

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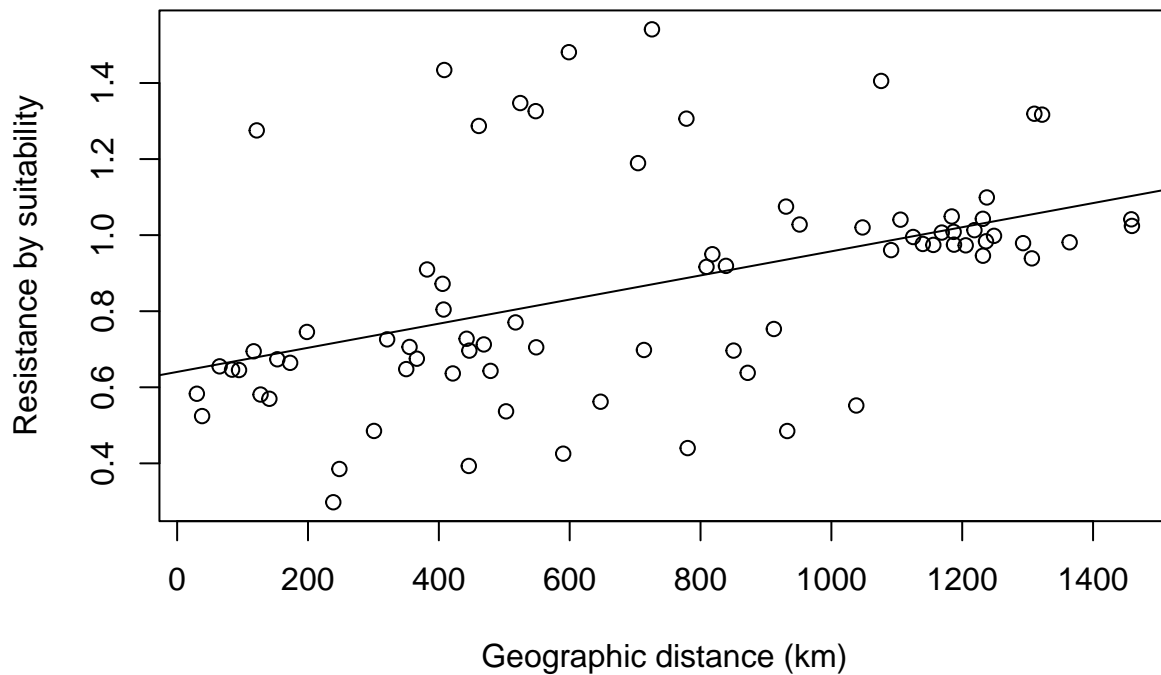
Correlation current suitabliity resistance - distance distances

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

```
##
##  Pearson's product-moment correlation
##
## data:  Dgeo and Dcurr
## t = 4.6267, df = 76, p-value = 1.499e-05
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.2749444 0.6260169
## sample estimates:
##       cor
## 0.4687928
```

Plot geographic-resistance correlation

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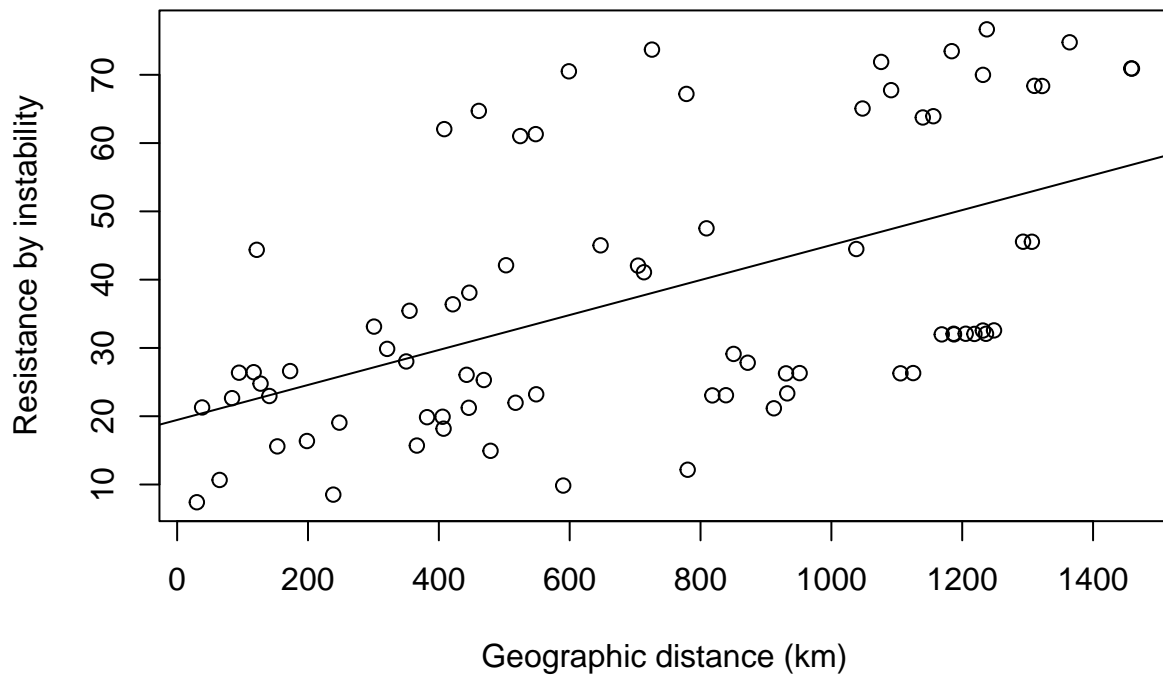
Correlation stability resistance - distance distances

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

```
##
##   Pearson's product-moment correlation
##
## data:  Dgeo and Dstab
## t = 5.5737, df = 76, p-value = 3.633e-07
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.3591879 0.6797168
## sample estimates:
##       cor
## 0.5386632
```

Plot geographic-resistance correlation

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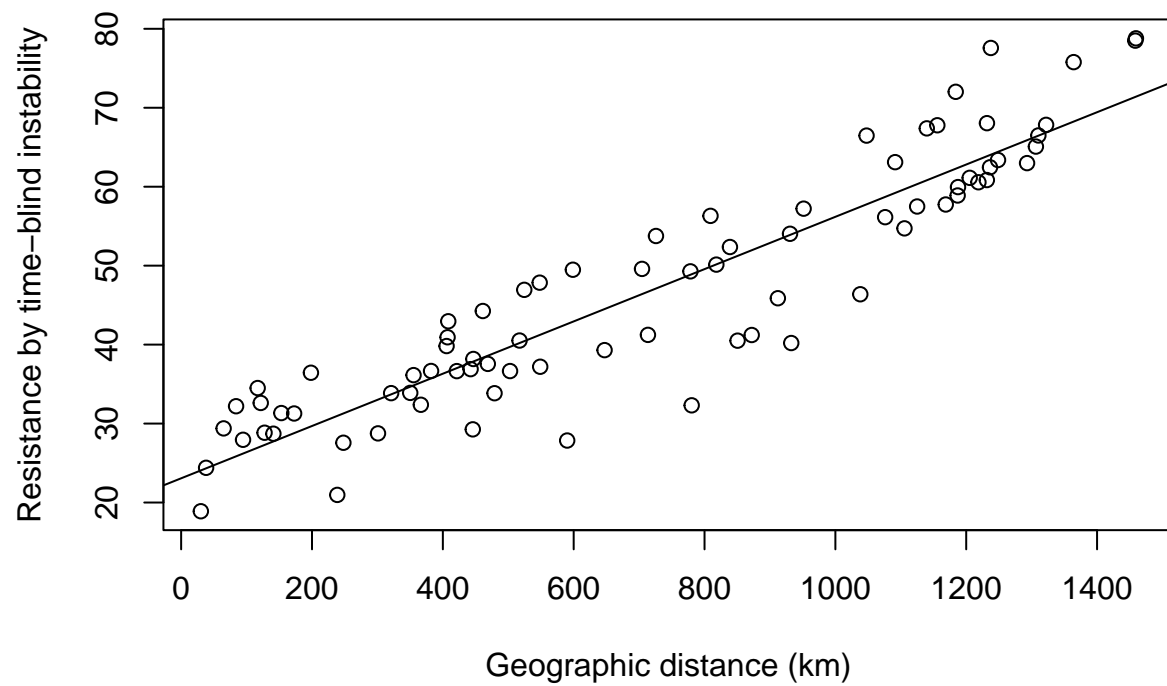
Correlation time-blind stability resistance - distance distances

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

```
##
##  Pearson's product-moment correlation
##
## data:  Dgeo and Dstab_blind
## t = 20.459, df = 76, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.8769627 0.9483472
## sample estimates:
##       cor
## 0.9199619
```
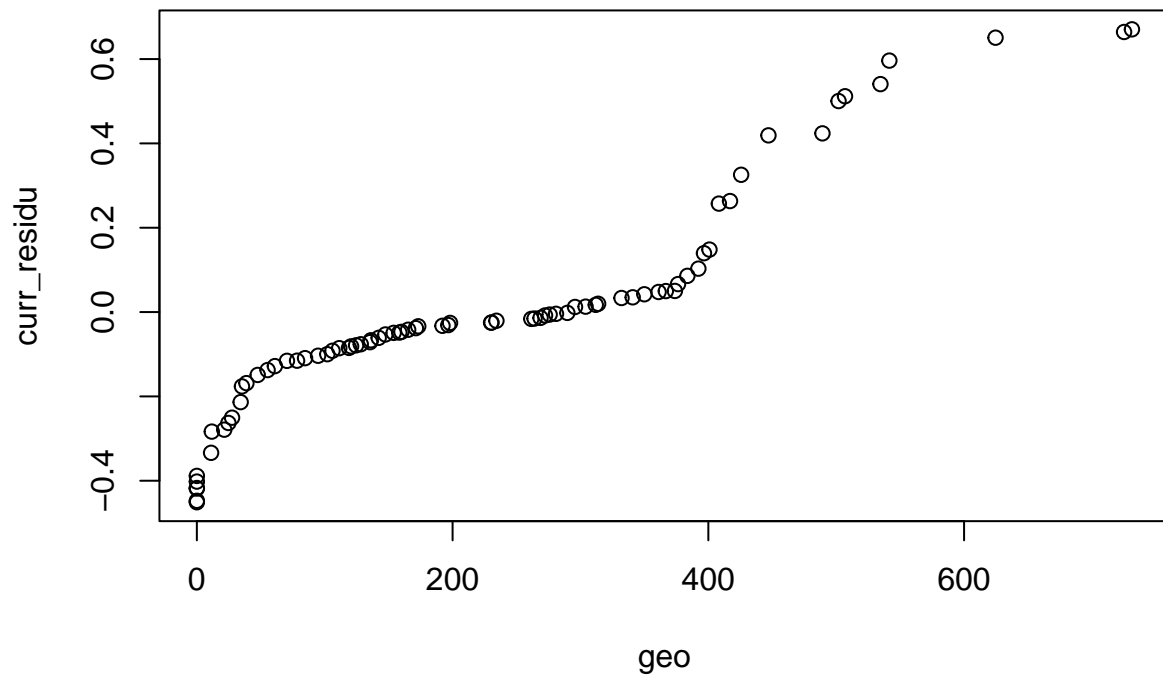
Plot geographic-resistance correlation

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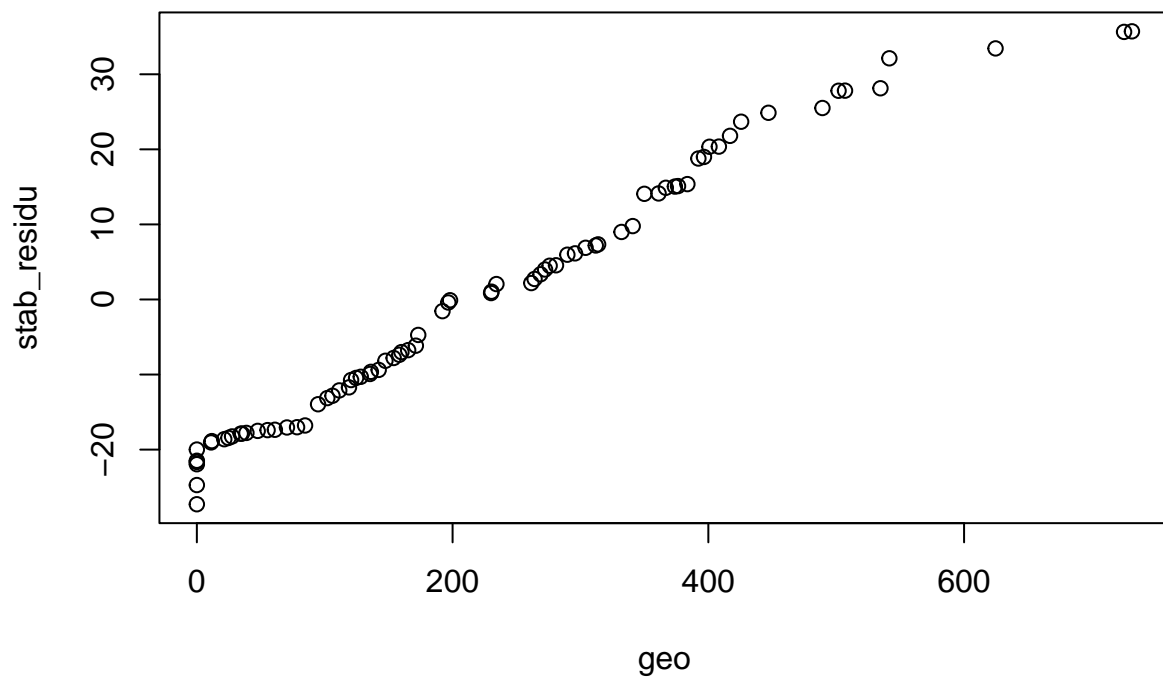
Calculate residuals of current suitability resistance - distance correlation

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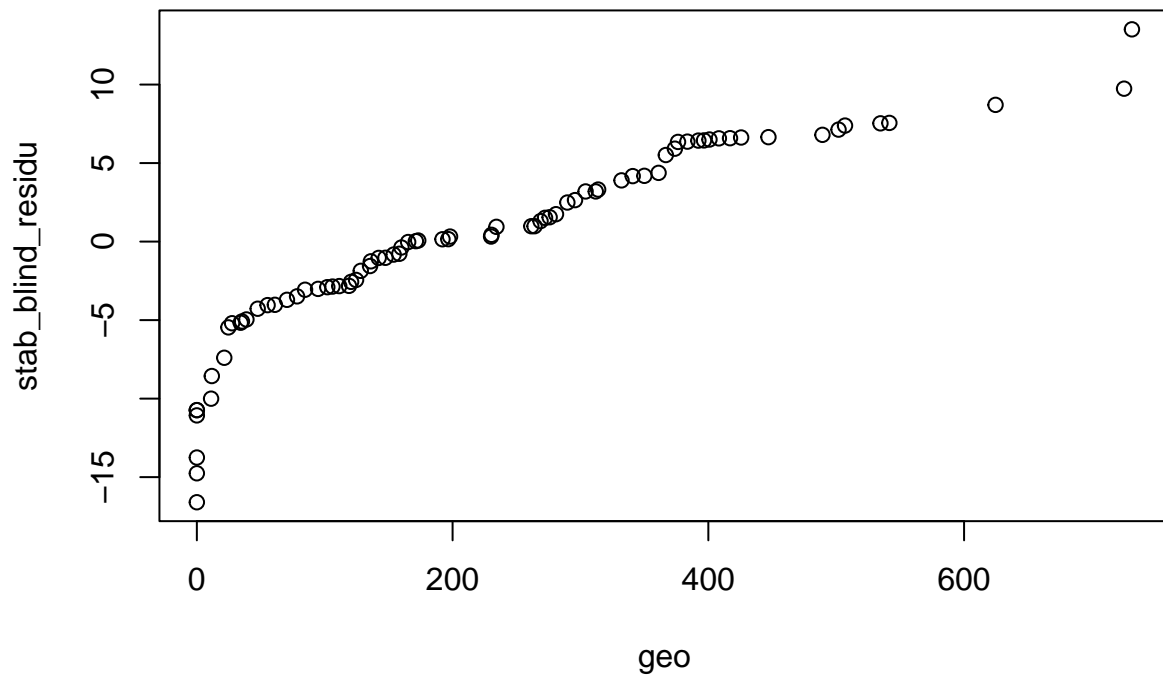
Calculate residuals of stability resistance - distance correlation

```
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)
```
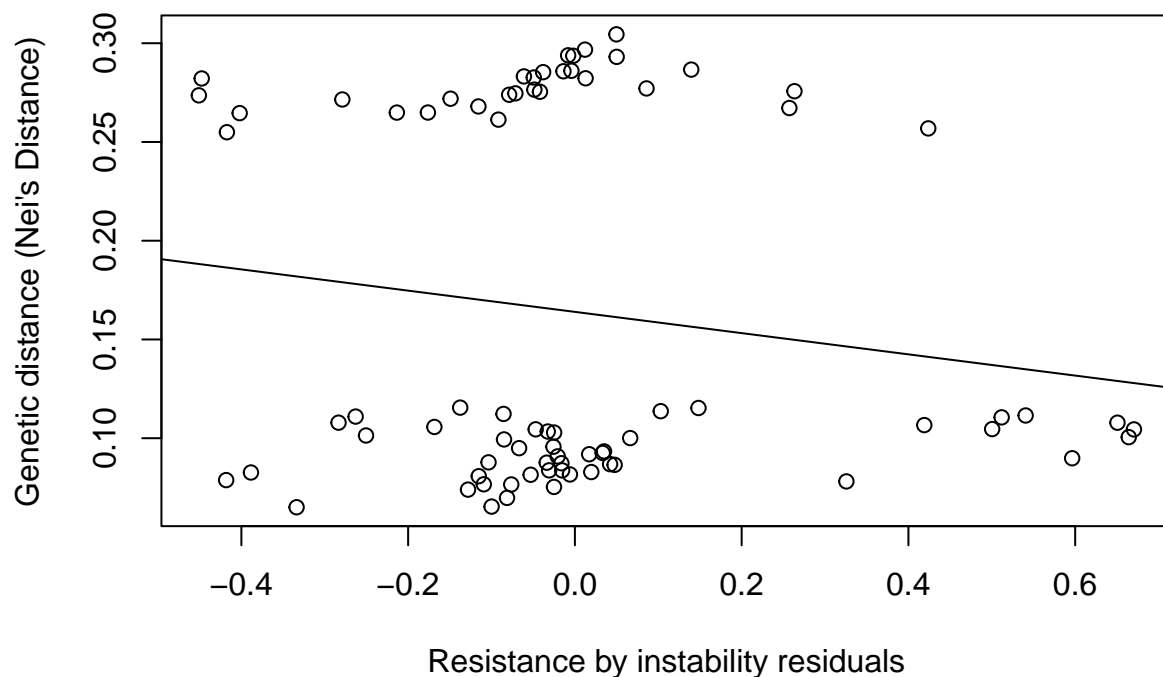
Correlation genetic - current resistance residuals distances (IBR with residuals)

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

```
##
##  Pearson's product-moment correlation
##
## data:  curr_residu and Dgen
## t = -1.3097, df = 76, p-value = 0.1943
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.35921740  0.07649749
## sample estimates:
##        cor
## -0.1485623
```

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)
```
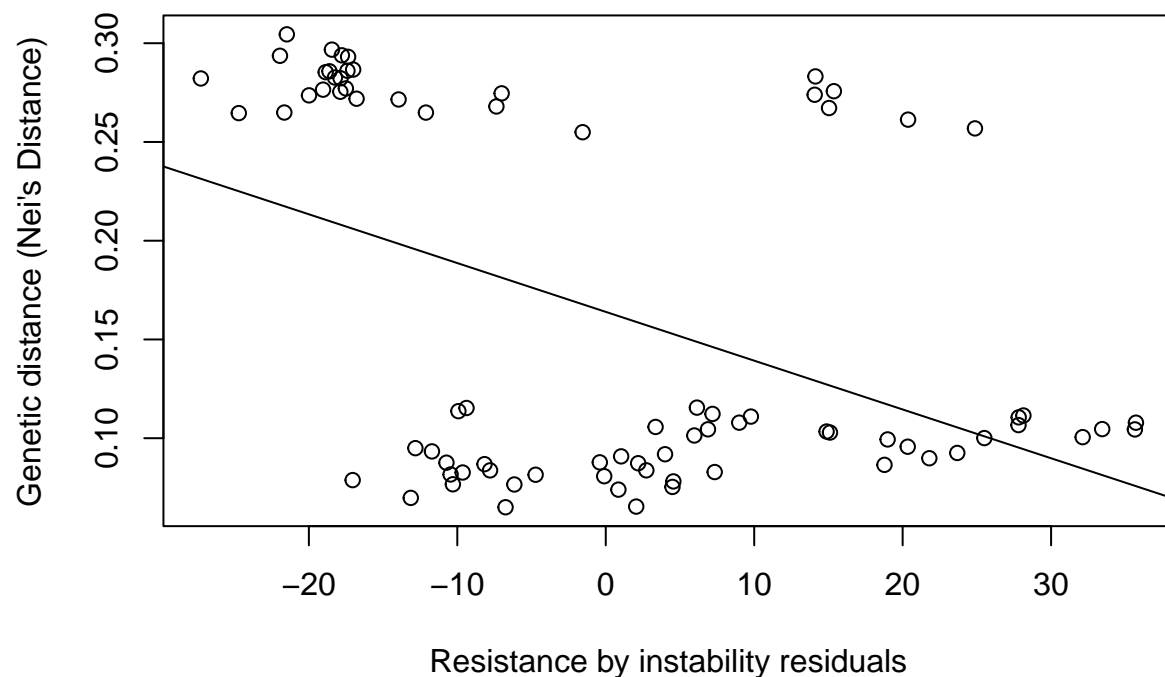
Correlation genetic - stability resistance residuals distances (IBR with residuals)

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

```
##
##  Pearson's product-moment correlation
##
## data:  stab_residu and Dgen
## t = -4.489, df = 76, p-value = 2.507e-05
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.6174276 -0.2619518
## sample estimates:
##        cor
## -0.4577965
```

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 = -3.8514, df = 76, p-value = 0.0002434
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.5749326 -0.1995133
## sample estimates:
##        cor
## -0.4041028
```

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)
```
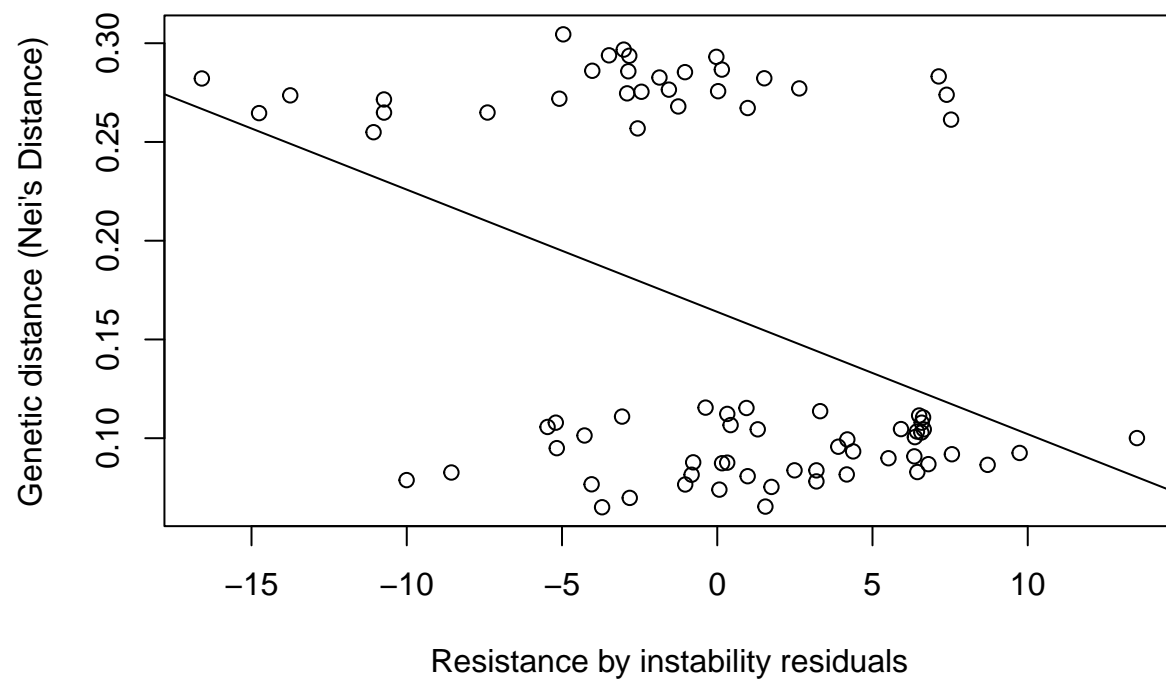
Multiple Regressions

using the method of Legendre et al. 1994

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

```
## $coef
##                     Dgen  pval
## Int            0.0537886152 1.000
## Dgeo           0.0001534119 0.001
## curr_residu   -0.0537652333 0.250
##
## $r.squared
##         R2        pval
## 0.5256704 0.0010000
##
## $F.test
##        F    F.pval
## 41.55895  0.00100
```

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

```
## $coef
##                    Dgen   pval
## Int          0.0537886152 0.995
## Dgeo         0.0001534119 0.001
## stab_residu -0.0024708637 0.011
##
## $r.squared
##        R2       pval
## 0.7131773 0.0030000
##
## $F.test
##        F   F.pval
## 93.24278  0.00300
```

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

```
## $coef
##                         Dgen  pval
## Int                0.0537886152 0.995
## Dgeo               0.0001534119 0.001
## stab_blind_residu -0.0061905853 0.004
##
## $r.squared
##        R2       pval
## 0.6668987 0.0010000
##
## $F.test
##        F   F.pval
## 75.07838  0.00100
```