Spatial Caughron

```r
library(nlme)
```

```
## Warning: package 'nlme' was built under R version 3.5.2
```

```r
library(vegan)
```

```
## Warning: package 'vegan' was built under R version 3.5.1
```

```
## Loading required package: permute
```

```
## Warning: package 'permute' was built under R version 3.5.1
```
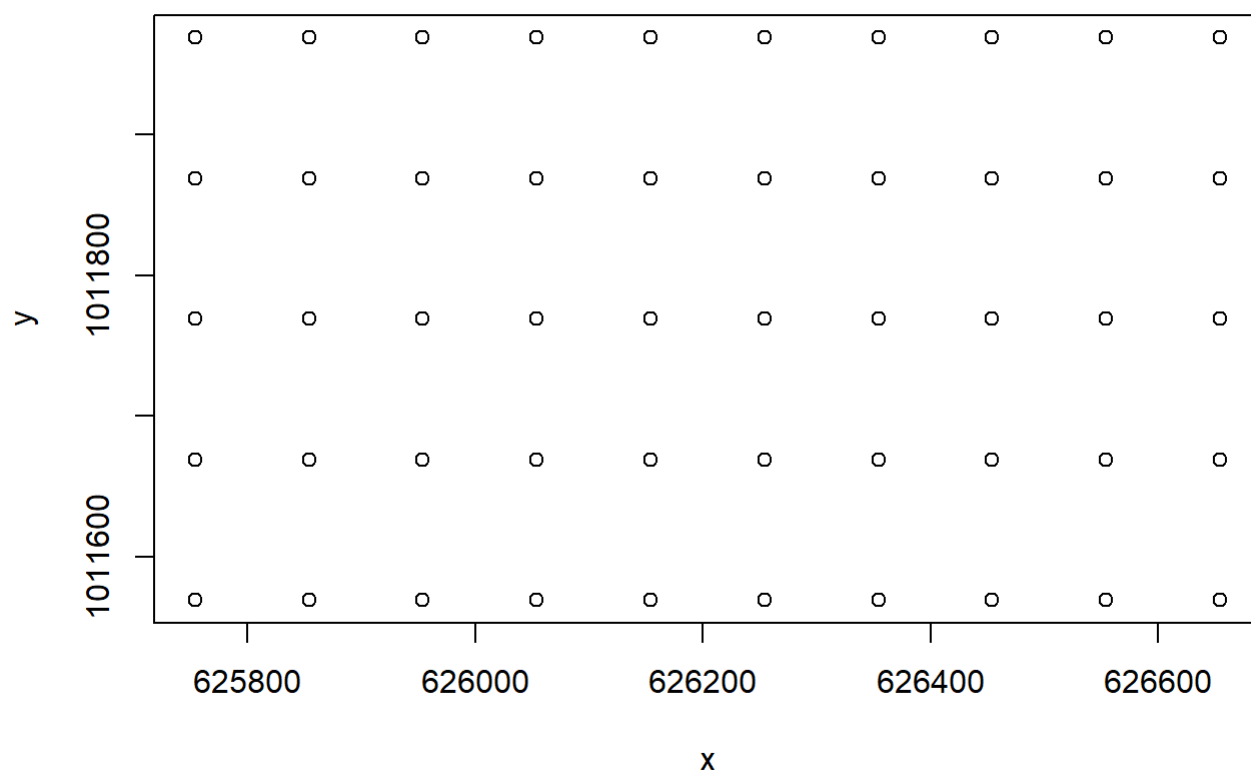
```
## Loading required package: lattice
```
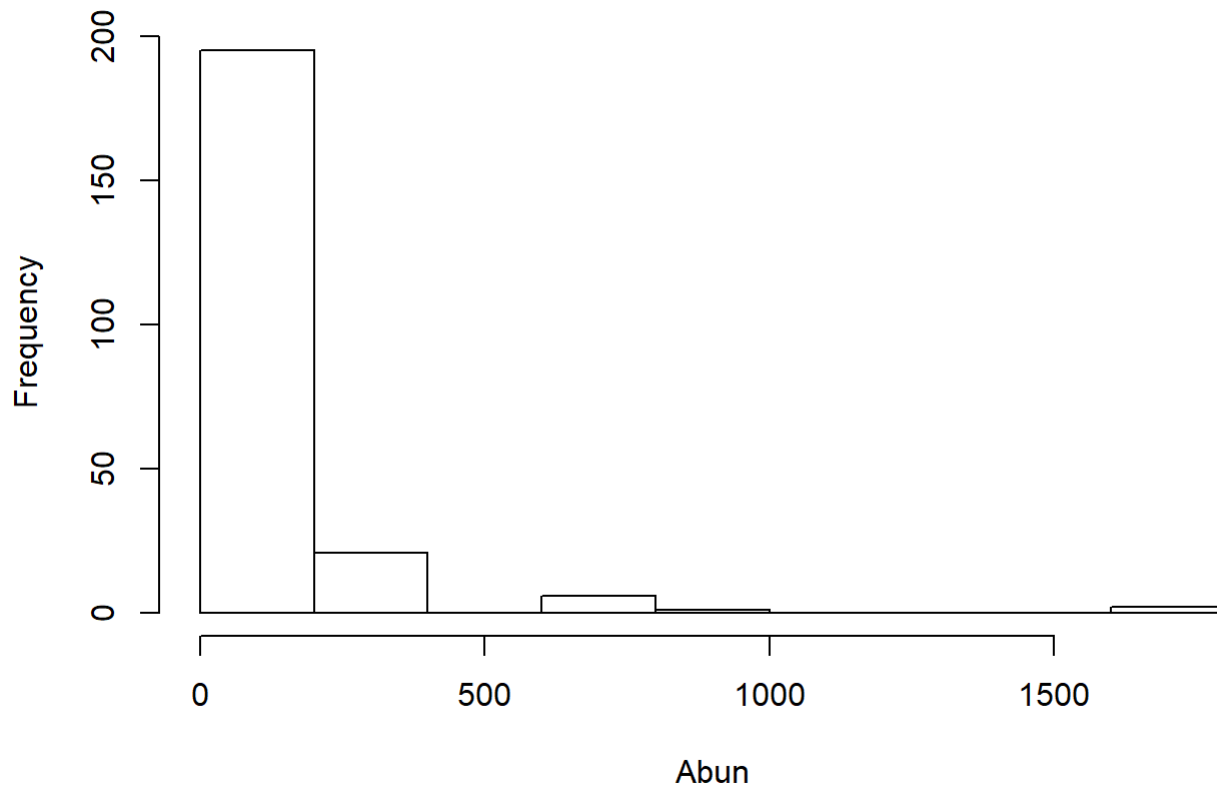
```
## This is vegan 2.5-2
```

```r
data(BCI)
```

```r
BCI_xy<-data.frame(x = rep(seq(625754, 626654, by=100), each=5), y = rep(seq(1011569,  1011969, by=100), len=50))
```
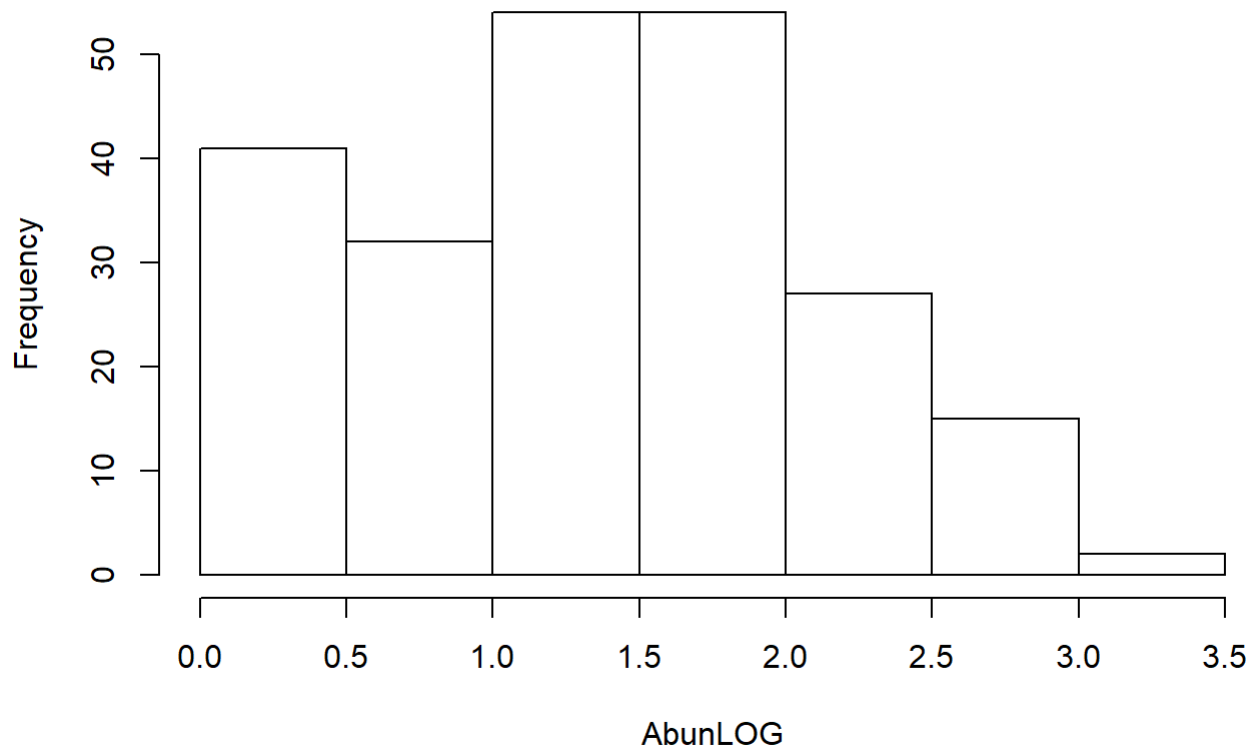
```r
plot(BCI_xy)
```

```
Abun <- colSums(BCI, na.rm = TRUE, dims = 1)
hist(Abun)
```
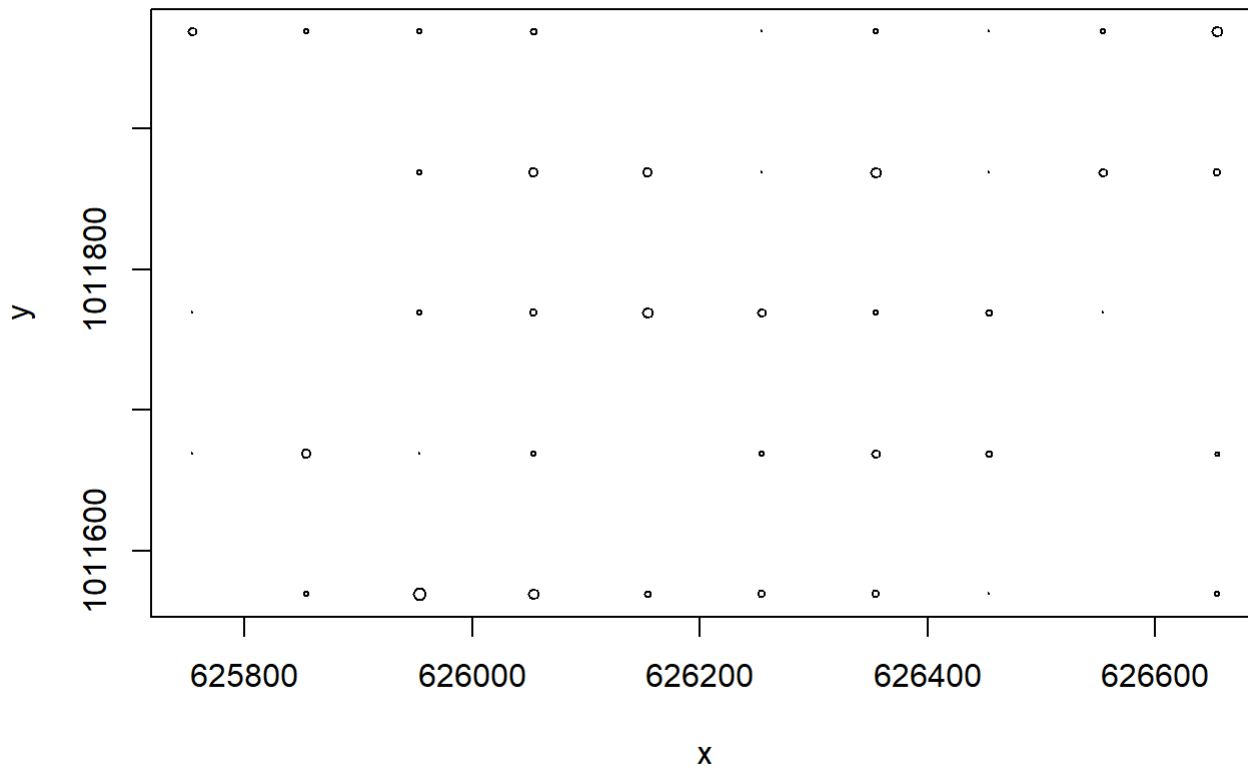
Histogram of Abun


```
AbunLOG <- log10(colSums(BCI, na.rm = TRUE, dims = 1))
hist(AbunLOG)
```
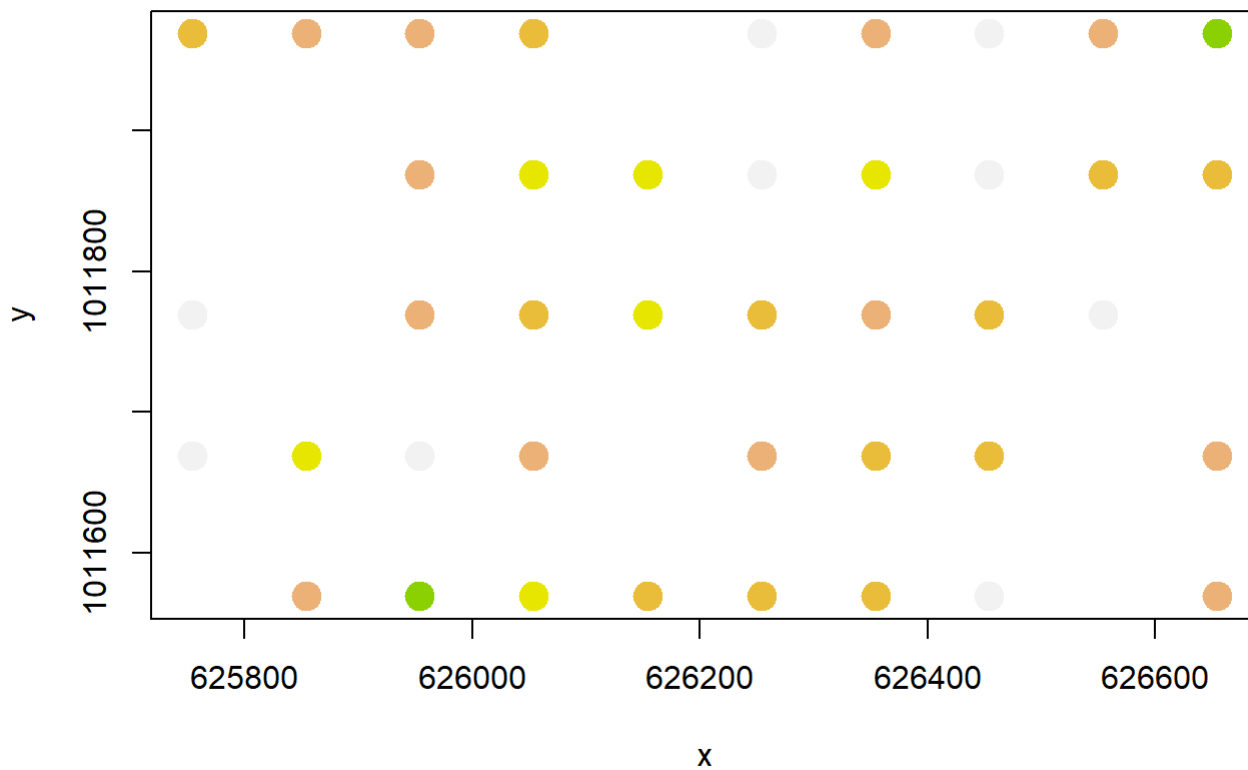
Histogram of AbunLOG


```
plot(BCI_xy, cex=AbunLOG/max(AbunLOG))
```

```
col_brks = hist(AbunLOG, plot=F)$breaks
col_indices = as.numeric(cut(AbunLOG, col_brks))
cols = rev(terrain.colors(length(col_brks)))
plot(BCI_xy, cex=2, pch=19, col=cols[col_indices])
```

```
for (i in seq_along(Abun)){
  if (Abun[i] > 1000) {
        print(names(BCI)[i])
    }
}
```

```
## [1] "Faramea.occidentalis"
## [1] "Trichilia.tuberculata"
```

```
names(BCI)[Abun > 1000]
```

```
## [1] "Faramea.occidentalis"  "Trichilia.tuberculata"
```

```
Common <- BCI$Faramea.occidentalis
```

```
names(BCI)[Abun > 150 & Abun < 200]
```

```
## [1] "Alchornea.costaricensis"      "Brosimum.alicastrum"
## [3] "Eugenia.oerstediana"          "Maquira.guianensis.costaricana"
## [5] "Ocotea.whitei"                "Unonopsis.pittieri"
## [7] "Virola.surinamensis"
```

```
Rare <- BCI$Unonopsis.pittieri
```

```
Common_dist = dist(Common)

xy_dist = dist(BCI_xy)
```

```
max_dist = max(xy_dist) / 2
# plot result
plot(xy_dist, Common_dist)
abline(lm(Common_dist ~ xy_dist), lwd=3, col='red')
lines(lowess(xy_dist, Common_dist), lwd=3, col='pink')
abline(v = max_dist, col='red', lwd=3, lty=2)
```
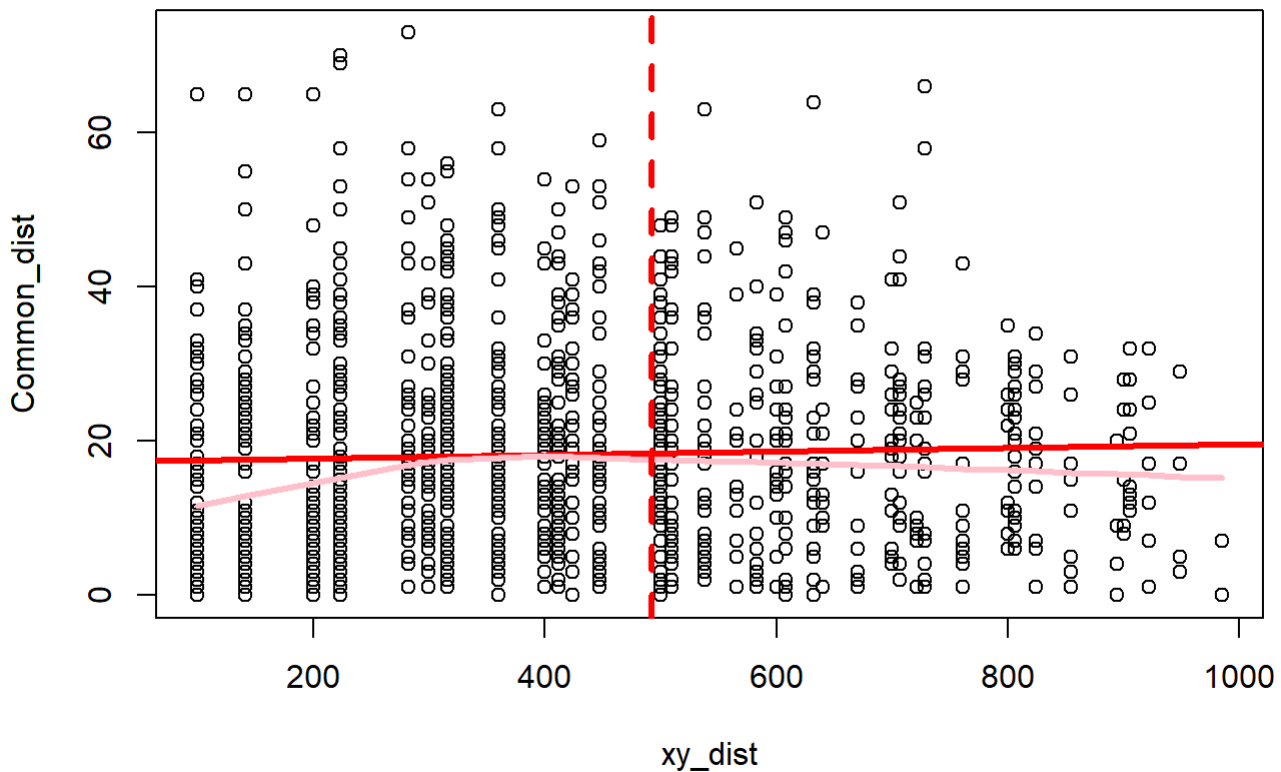


```
Rare_dist = dist(Rare)

xy_dist = dist(BCI_xy)
```
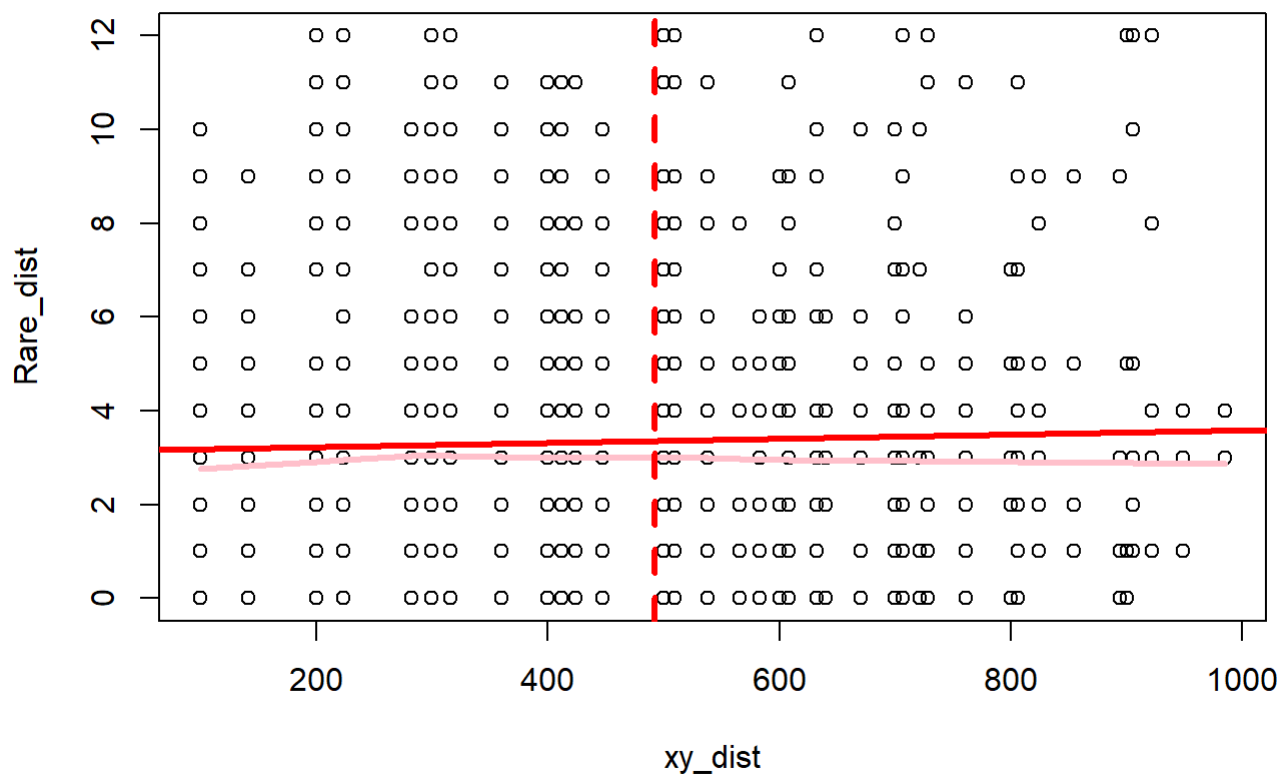
```
max_dist = max(xy_dist) / 2
# plot result
plot(xy_dist, Rare_dist)
abline(lm(Rare_dist ~ xy_dist), lwd=3, col='red')
lines(lowess(xy_dist, Rare_dist), lwd=3, col='pink')
abline(v = max_dist, col='red', lwd=3, lty=2)
```

```
obs_corCom = cor(xy_dist, Common_dist)
obs_corCom
```

```
## [1] 0.0355889
```

```
obs_corRare = cor(xy_dist, Rare_dist)
obs_corRare
```

```
## [1] 0.03295625
```

```
nperm = 1000
null_cor = obs_corCom
for (i in 2:nperm) {
# shuffle the rows of the spatial coordinates
tmp_xy = BCI_xy[sample(nrow(BCI_xy)), ]
# correlation between the shuffled spatial coordinates and sr_dist
null_cor[i] = cor(dist(tmp_xy), Common_dist)
}
# compute the p-value
sum(null_cor >= obs_corCom) / nperm
```

```
## [1] 0.236
```

```
nperm = 1000
null_cor = obs_corRare
for (i in 2:nperm) {
# shuffle the rows of the spatial coordinates
tmp_xy = BCI_xy[sample(nrow(BCI_xy)), ]
# correlation between the shuffled spatial coordinates and sr_dist
null_cor[i] = cor(dist(tmp_xy), Rare_dist)
}
# compute the p-value
sum(null_cor >= obs_corRare) / nperm
```

```
## [1] 0.268
```

```
sr_mantelCommon = mantel(xy_dist, Common_dist)
sr_mantelCommon
```

```
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = xy_dist, ydis = Common_dist)
##
## Mantel statistic r: 0.03559
##       Significance: 0.25
##
## Upper quantiles of permutations (null model):
##     90%    95%  97.5%    99%
## 0.0662 0.0830 0.0996 0.1371
## Permutation: free
## Number of permutations: 999
```

```
sr_mantelRare = mantel(xy_dist, Rare_dist)
sr_mantelRare
```

```
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = xy_dist, ydis = Rare_dist)
##
## Mantel statistic r: 0.03296
##       Significance: 0.234
##
## Upper quantiles of permutations (null model):
##     90%    95%  97.5%    99%
## 0.0624 0.0877 0.1031 0.1261
## Permutation: free
## Number of permutations: 999
```

```
boxplot(list(null_cor, sr_mantelCommon$perm), horizontal = T, boxwex = 0.5,
names = c('mine', 'theirs'), xlab='Correlation', main="Common")
abline(v=obs_corCom, col='red')
```
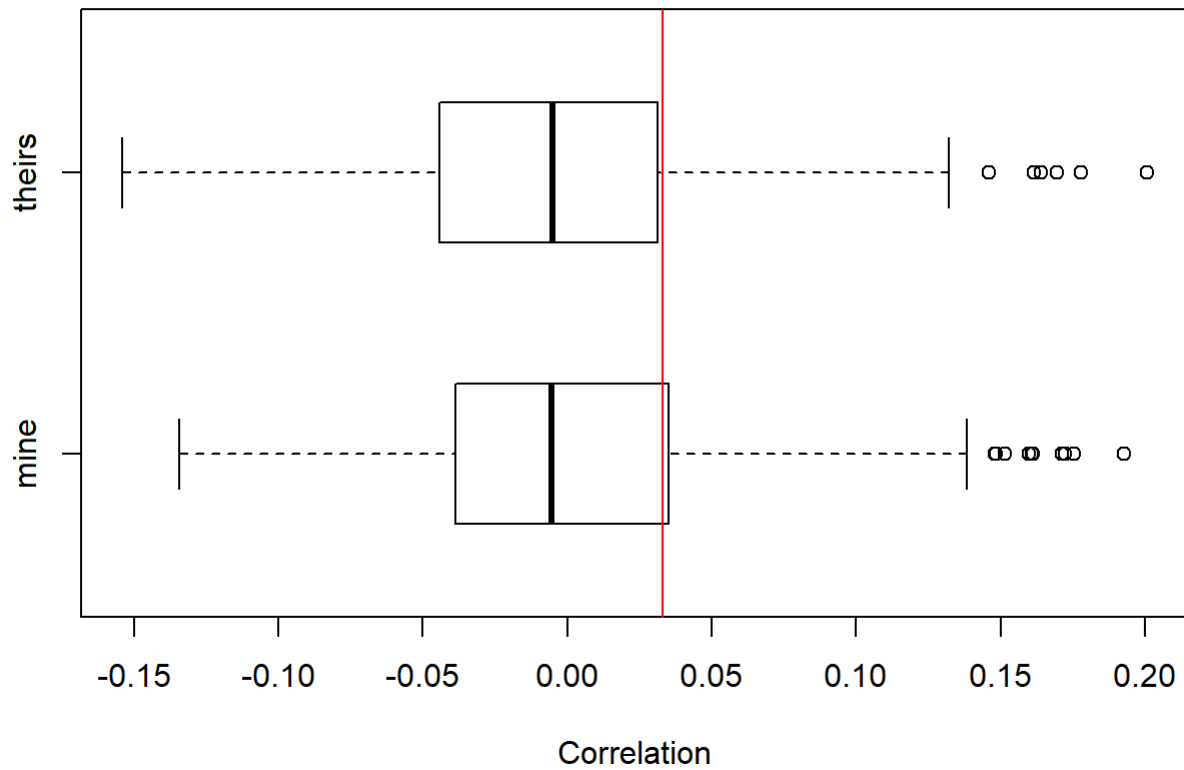

Common
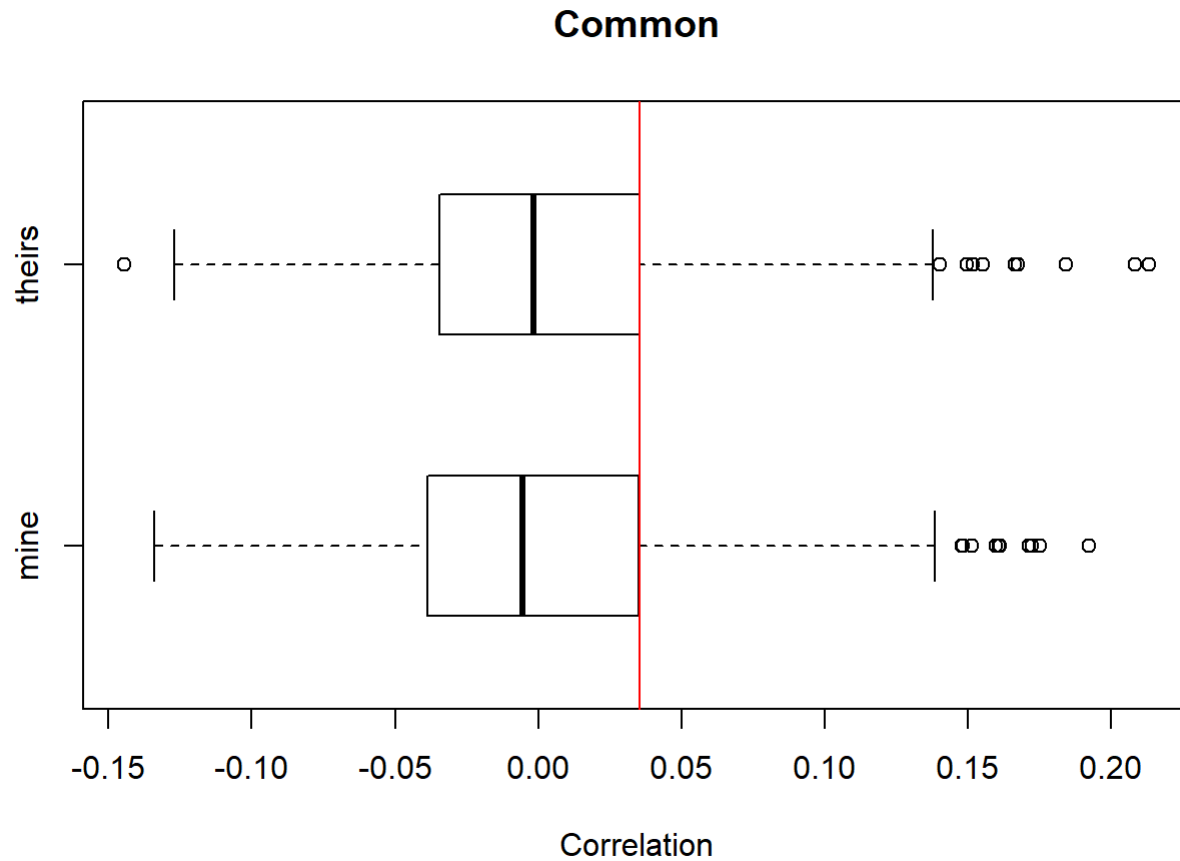
Correlation

```
boxplot(list(null_cor, sr_mantelRare$perm), horizontal = T, boxwex = 0.5,
names = c('mine', 'theirs'), xlab='Correlation', main= "Rare")
abline(v=obs_corRare, col='red')
```

Rare

Neither the rare or common species seems to be spatially dependent. Neither the permutation or mantel test indicated significant results. Preliminary results suggest that there is no significant evidence to conclude that the distance between two points has an impact on the species at those points.

```
comm_dist = vegdist(BCI)
plot(xy_dist, comm_dist)
abline(lm(comm_dist ~ xy_dist), lwd=3, col='red')
lines(lowess(xy_dist, comm_dist), lwd=3, col='pink')
abline(v = max_dist, col='red', lwd=3, lty=2)
```
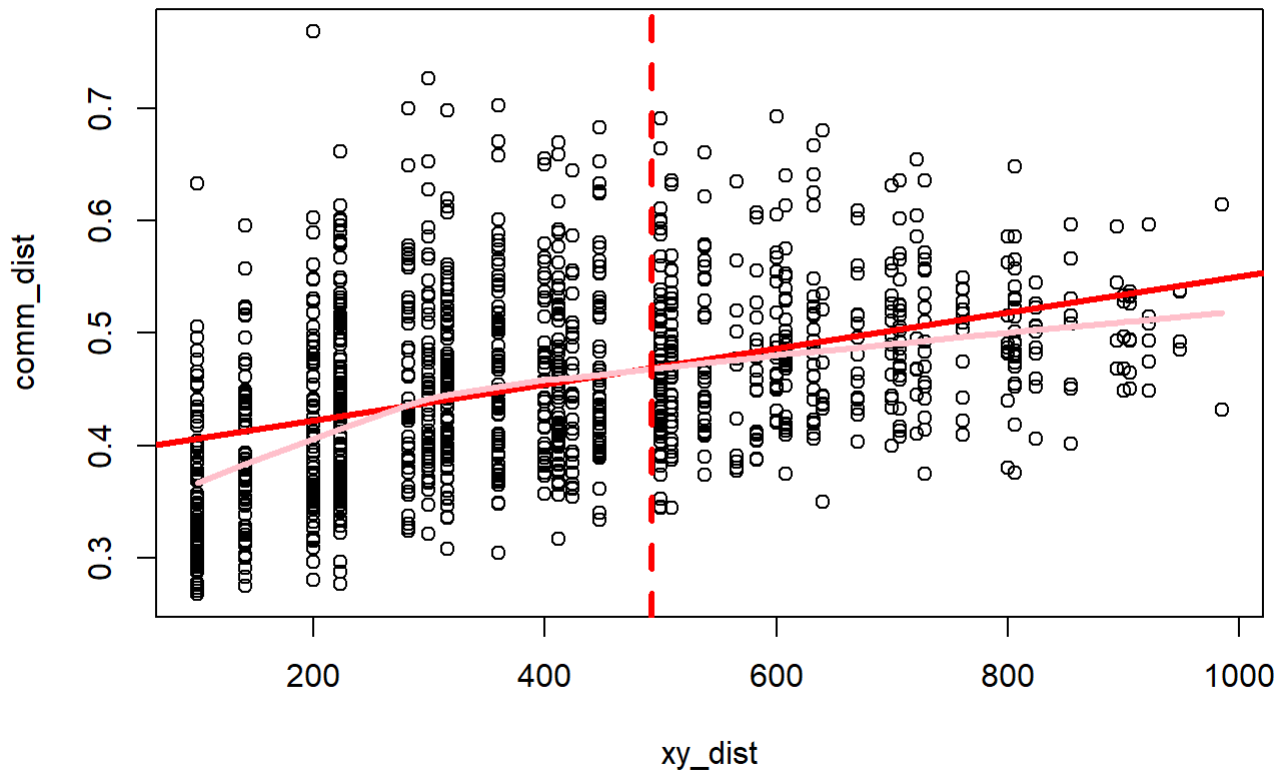
```
comm_mantel = mantel(xy_dist, comm_dist)
comm_mantel
```

```
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = xy_dist, ydis = comm_dist)
##
## Mantel statistic r: 0.4078
##       Significance: 0.001
##
## Upper quantiles of permutations (null model):
##    90%    95%  97.5%     99%
## 0.0667 0.0828 0.0987 0.1140
## Permutation: free
## Number of permutations: 999
```

```
sr_corlogCom = mantel.correlog(Common_dist, xy_dist)
comm_corlogCom = mantel.correlog(comm_dist, xy_dist)
sr_corlogCom
```

```
## 
## Mantel Correlogram Analysis
## 
## Call:
## 
## mantel.correlog(D.eco = Common_dist, D.geo = xy_dist)
## 
##          class.index     n.dist Mantel.cor Pr(Mantel) Pr(corrected)
## D.cl.1    136.870241 144.000000   0.041368      0.047        0.047 *
## D.cl.2    210.610723 376.000000   0.009563      0.374        0.374
## D.cl.3    284.351204 390.000000  -0.054005      0.027        0.081 .
## D.cl.4    358.091686 148.000000  -0.056782      0.012        0.048 *
## D.cl.5    431.832168 372.000000  -0.039064      0.077        0.154
## D.cl.6    505.572649 266.000000  -0.023481      0.139        0.278
## D.cl.7    579.313131 168.000000         NA         NA           NA
## D.cl.8    653.053613 100.000000         NA         NA           NA
## D.cl.9    726.794094 154.000000         NA         NA           NA
## D.cl.10   800.534576  88.000000         NA         NA           NA
## D.cl.11   874.275058  50.000000         NA         NA           NA
## D.cl.12   948.015539  24.000000         NA         NA           NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
sr_corlogRare = mantel.correlog(Rare_dist, xy_dist)
comm_corlogRare = mantel.correlog(comm_dist, xy_dist)
sr_corlogRare
```

```
## 
## Mantel Correlogram Analysis
## 
## Call:
## 
## mantel.correlog(D.eco = Rare_dist, D.geo = xy_dist)
## 
##          class.index      n.dist  Mantel.cor Pr(Mantel) Pr(corrected)
## D.cl.1   136.8702408 144.0000000   0.0201235      0.189         0.189
## D.cl.2   210.6107225 376.0000000  -0.0251947      0.174         0.348
## D.cl.3   284.3512042 390.0000000  -0.0158692      0.267         0.522
## D.cl.4   358.0916859 148.0000000   0.0108906      0.317         0.696
## D.cl.5   431.8321676 372.0000000  -0.0161046      0.285         0.870
## D.cl.6   505.5726492 266.0000000  -0.0056142      0.415         1.000
## D.cl.7   579.3131309 168.0000000          NA         NA            NA
## D.cl.8   653.0536126 100.0000000          NA         NA            NA
## D.cl.9   726.7940943 154.0000000          NA         NA            NA
## D.cl.10  800.5345760  88.0000000          NA         NA            NA
## D.cl.11  874.2750577  50.0000000          NA         NA            NA
## D.cl.12  948.0155393  24.0000000          NA         NA            NA
```

```
par(mfrow=c(1,2))
plot(sr_corlogCom)
mtext(side=3, 'Species Richness')
abline(v = max_dist, col='red', lwd=3, lty=2)
plot(comm_corlogCom)
mtext(side=3, 'Community Composition')
abline(v = max_dist, col='red', lwd=3, lty=2)
```
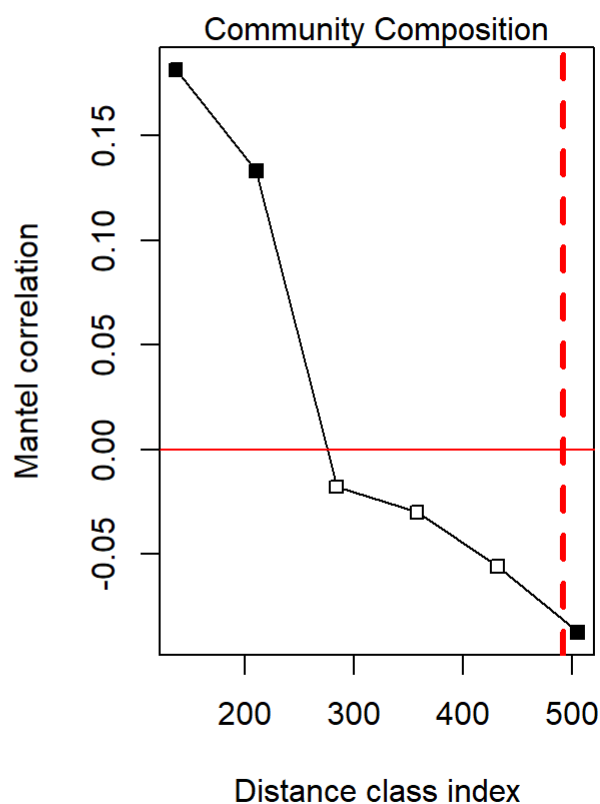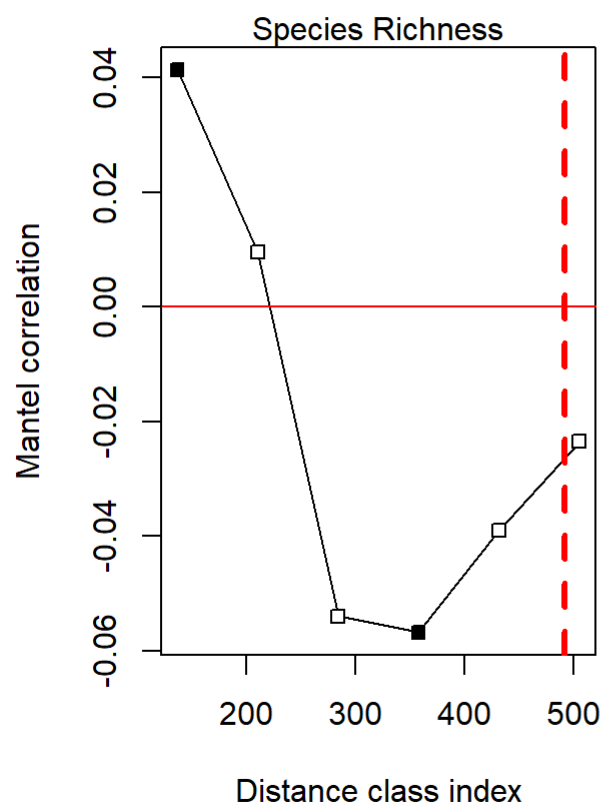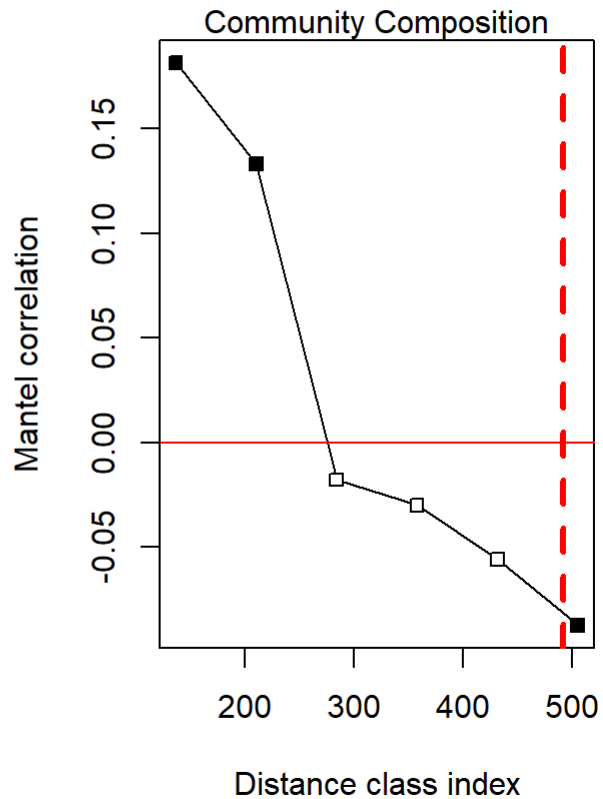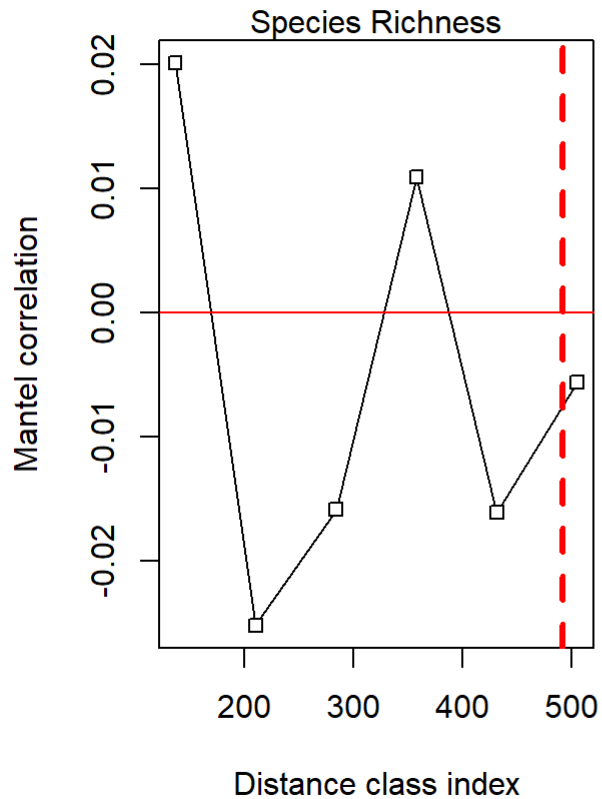


```
par(mfrow=c(1,2))
plot(sr_corlogRare)
mtext(side=3, 'Species Richness')
abline(v = max_dist, col='red', lwd=3, lty=2)
plot(comm_corlogRare)
mtext(side=3, 'Community Composition')
abline(v = max_dist, col='red', lwd=3, lty=2)
```

Modeling

```
BCI_dat = data.frame(BCI, BCI_xy)
BCI_lmQA = gls(Drypetes.standleyi ~ Quassia.amara, data = BCI_dat)
BCI_lmQA
```

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Quassia.amara
##   Data: BCI_dat
##   Log-restricted-likelihood: -165.7644
##
## Coefficients:
##   (Intercept) Quassia.amara
##      4.962810      9.214876
##
## Degrees of freedom: 50 total; 48 residual
## Residual standard error: 7.171316
```

```
BCI_lmALL = gls(Drypetes.standleyi ~ Cordia.alliodora + Hirtella.triandra + Picramnia.latifolia
+ Quassia.amara + Tabernaemontana.arborea + Trattinnickia.aspera + Xylopia.macrantha, data = BCI
_dat)
BCI_lmALL
```

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Cordia.alliodora + Hirtella.triandra + Picramnia.latifolia +
Quassia.amara + Tabernaemontana.arborea + Trattinnickia.aspera +      Xylopia.macrantha
##   Data: BCI_dat
##   Log-restricted-likelihood: -145.8624
##
## Coefficients:
##          (Intercept)        Cordia.alliodora        Hirtella.triandra
##           1.76123327             -0.04854765               0.18114700
##     Picramnia.latifolia           Quassia.amara Tabernaemontana.arborea
##           0.68606540              6.00651776              -0.32533763
##     Trattinnickia.aspera       Xylopia.macrantha
##           1.06489538              0.58671062
##
## Degrees of freedom: 50 total; 42 residual
## Residual standard error: 4.772207
```
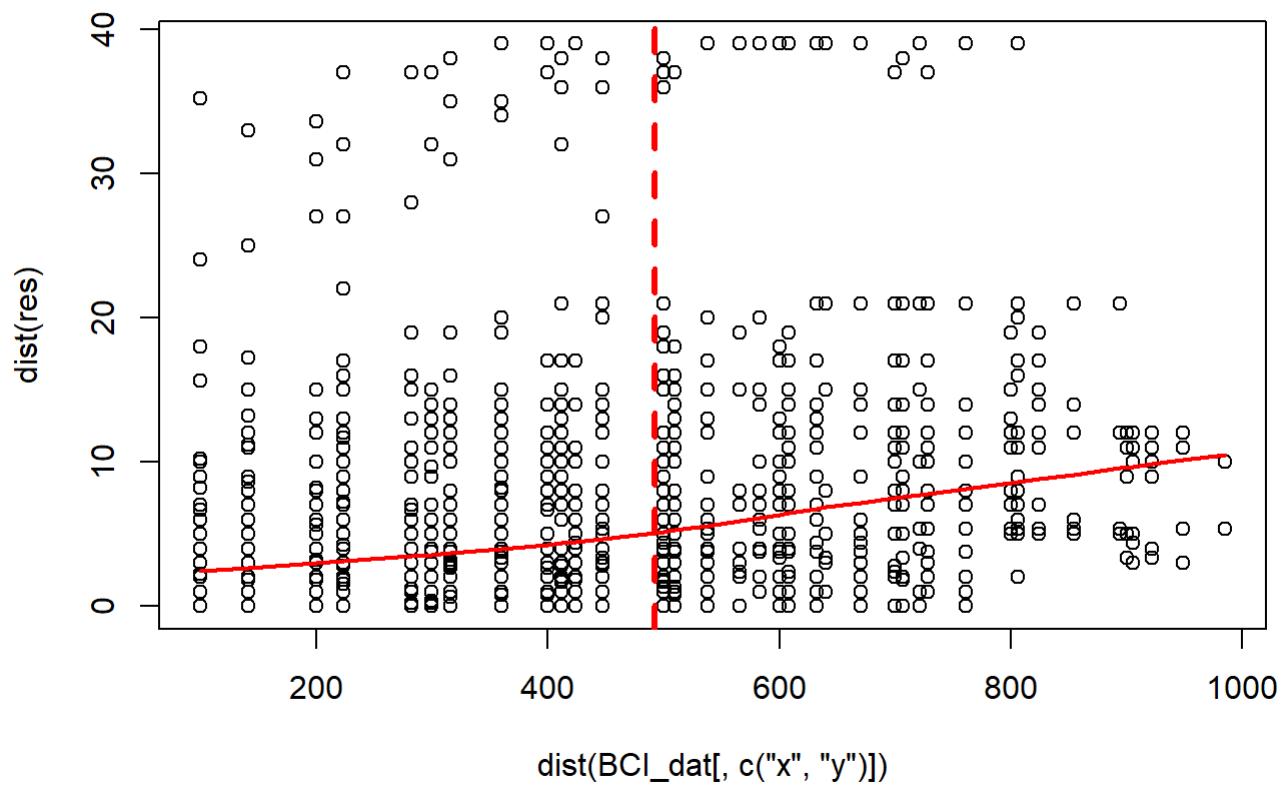
```
par(mfrow=c(1,1))
plot(Variogram(BCI_lmQA, form = ~ x + y))
```
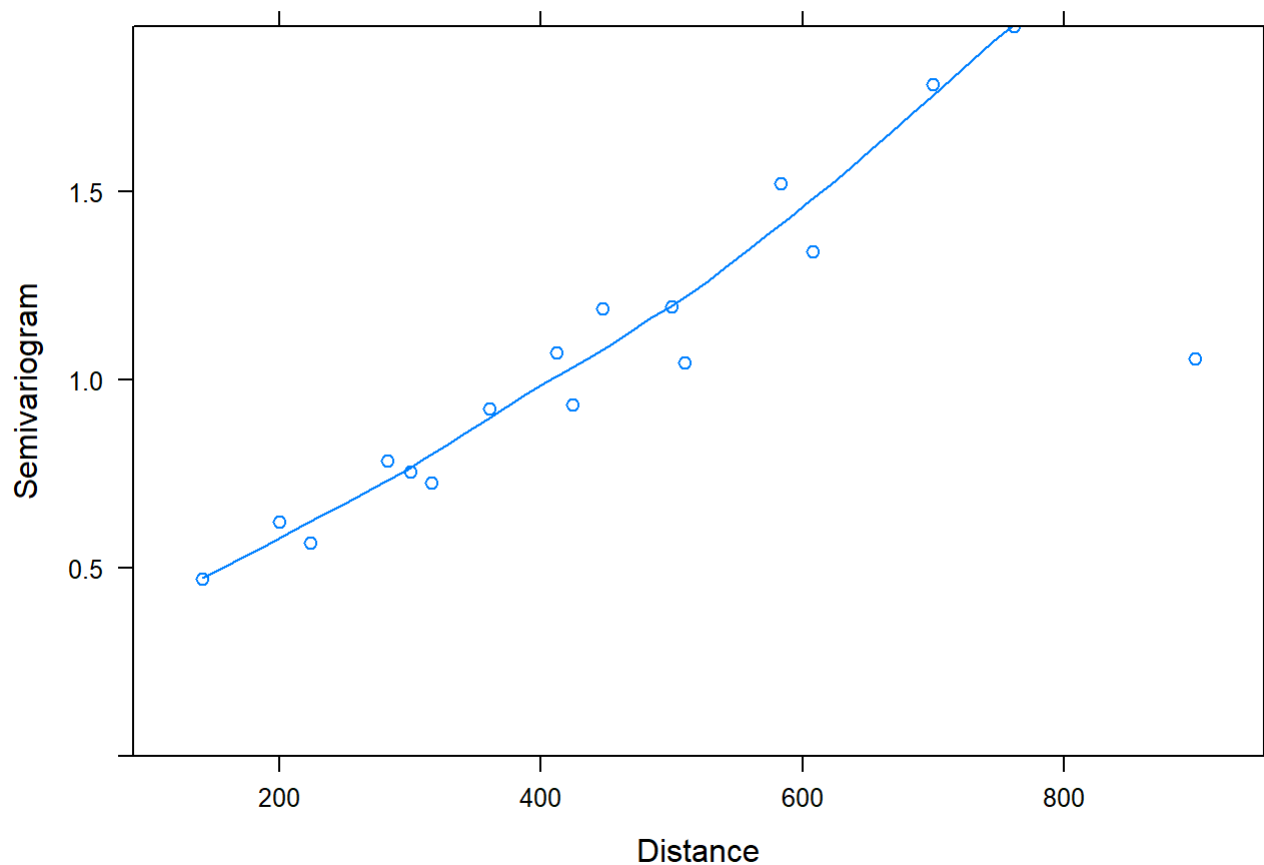


```
par(mfrow=c(1,1))
plot(Variogram(BCI_lmALL, form= ~ x + y))
```
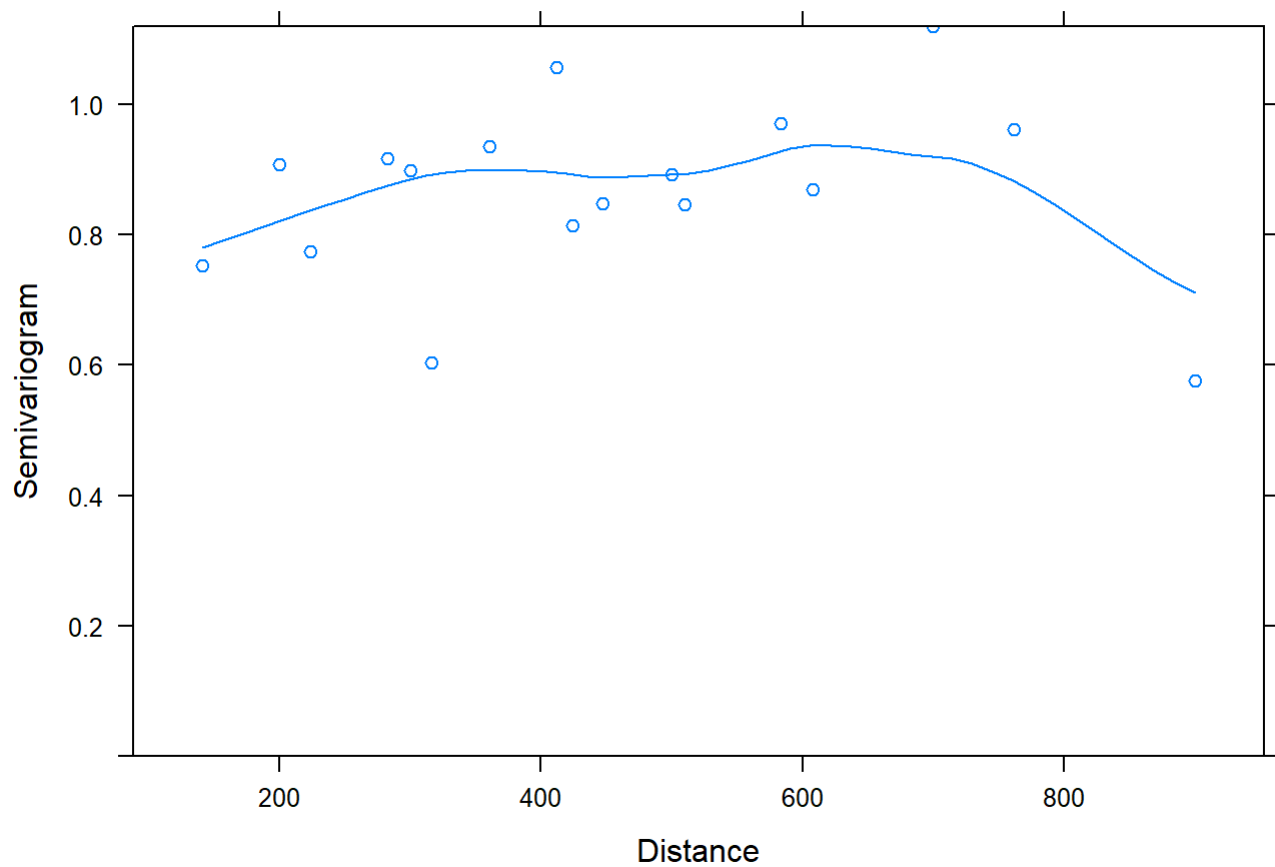
```
res = residuals(BCI_lmQA)
plot(dist(BCI_dat[, c('x', 'y')]), dist(res))
lines(lowess(dist(BCI_dat[, c('x', 'y')]), dist(res)), col='red', lwd=2)
abline(v = max_dist, col='red', lwd=3, lty=2)
```

```
res = residuals(BCI_lmALL)
plot(dist(BCI_dat[, c('x', 'y')]), dist(res))
lines(lowess(dist(BCI_dat[, c('x', 'y')]), dist(res)), col='red', lwd=2)
abline(v = max_dist, col='red', lwd=3, lty=2)
```
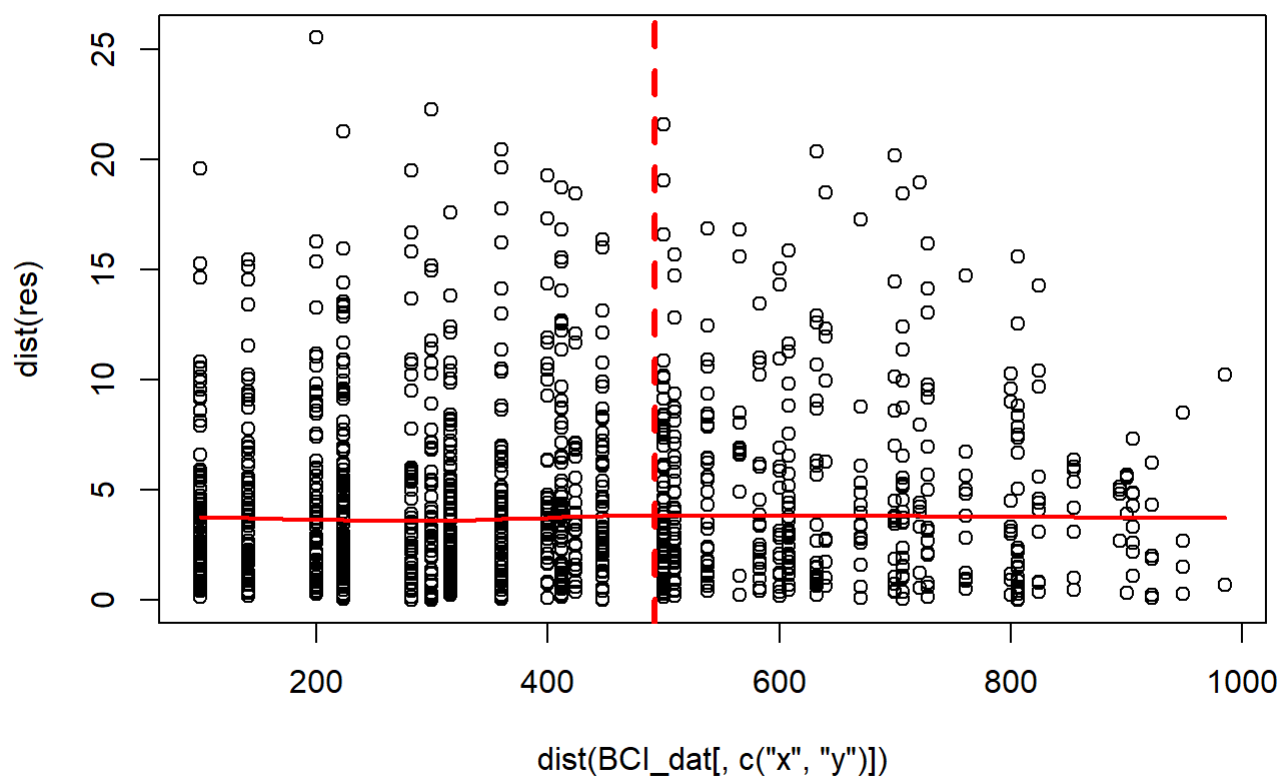
```
BCI_expQA = update(BCI_lmQA, corr=corExp(form=~x + y))
plot(Variogram(BCI_expQA, maxDist = max_dist))
```
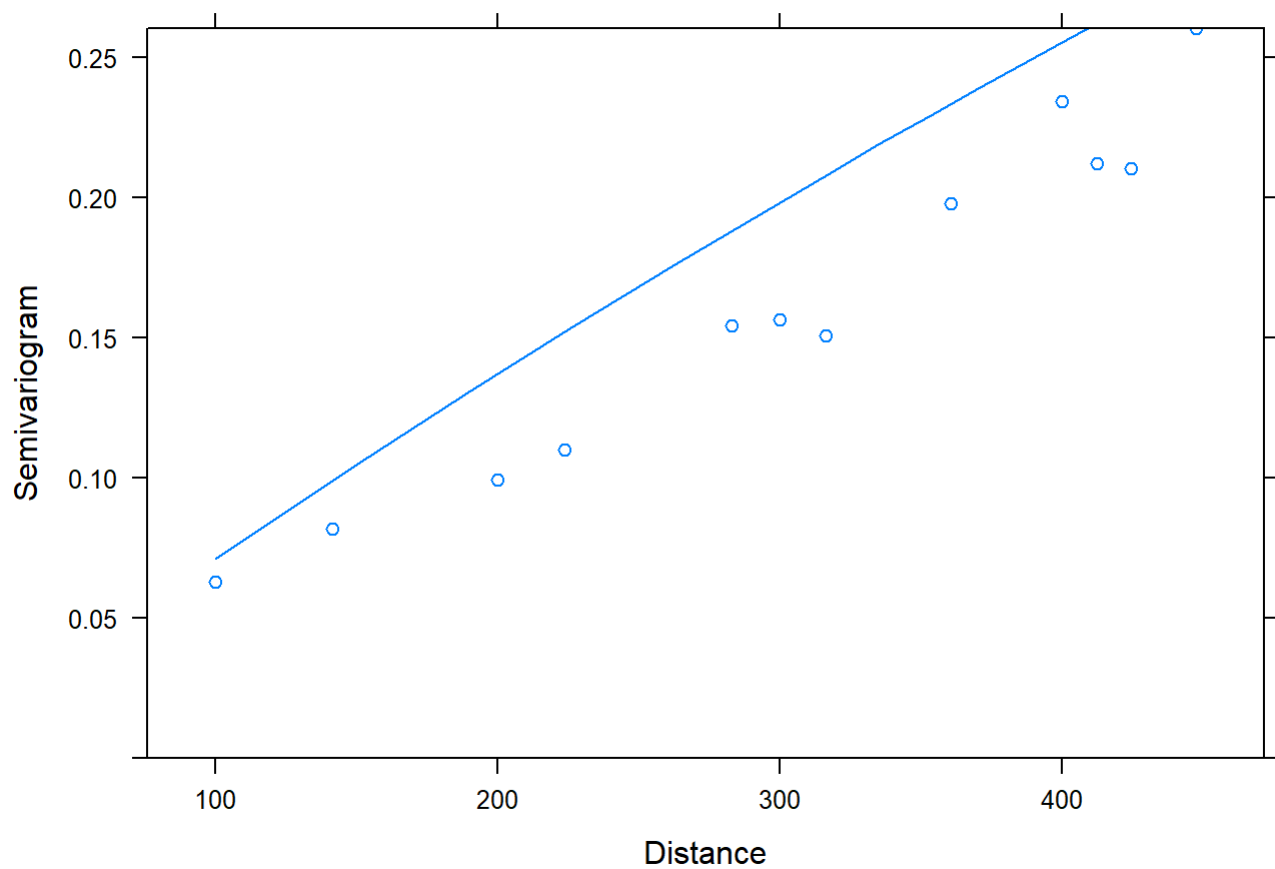
```
plot(Variogram(BCI_expQA, resType='normalized', maxDist = max_dist))
```
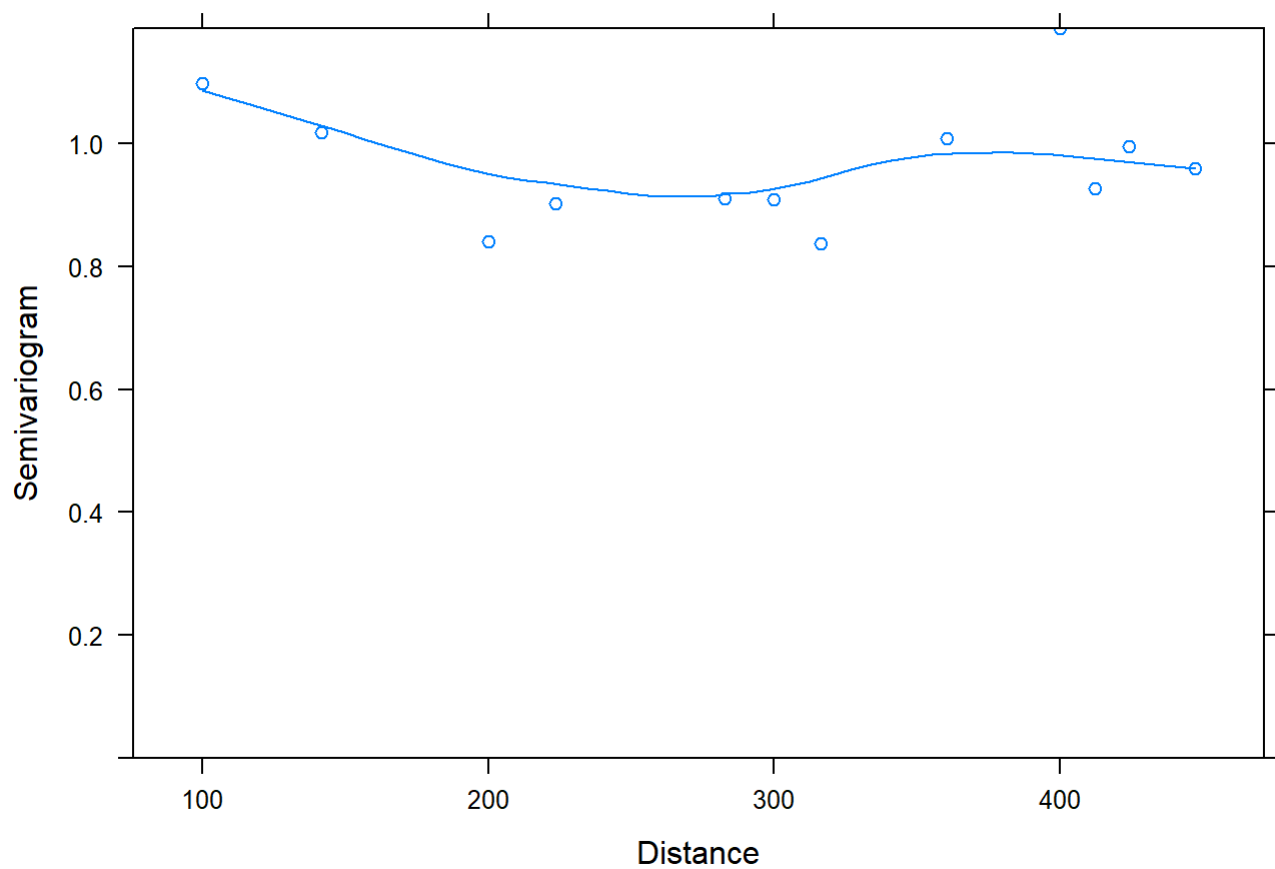
```
BCI_expALL = update(BCI_lmALL, corr=corExp(form=~x + y))
plot(Variogram(BCI_expALL, maxDist = max_dist))
```

```
plot(Variogram(BCI_expALL, resType='normalized', maxDist = max_dist))
```
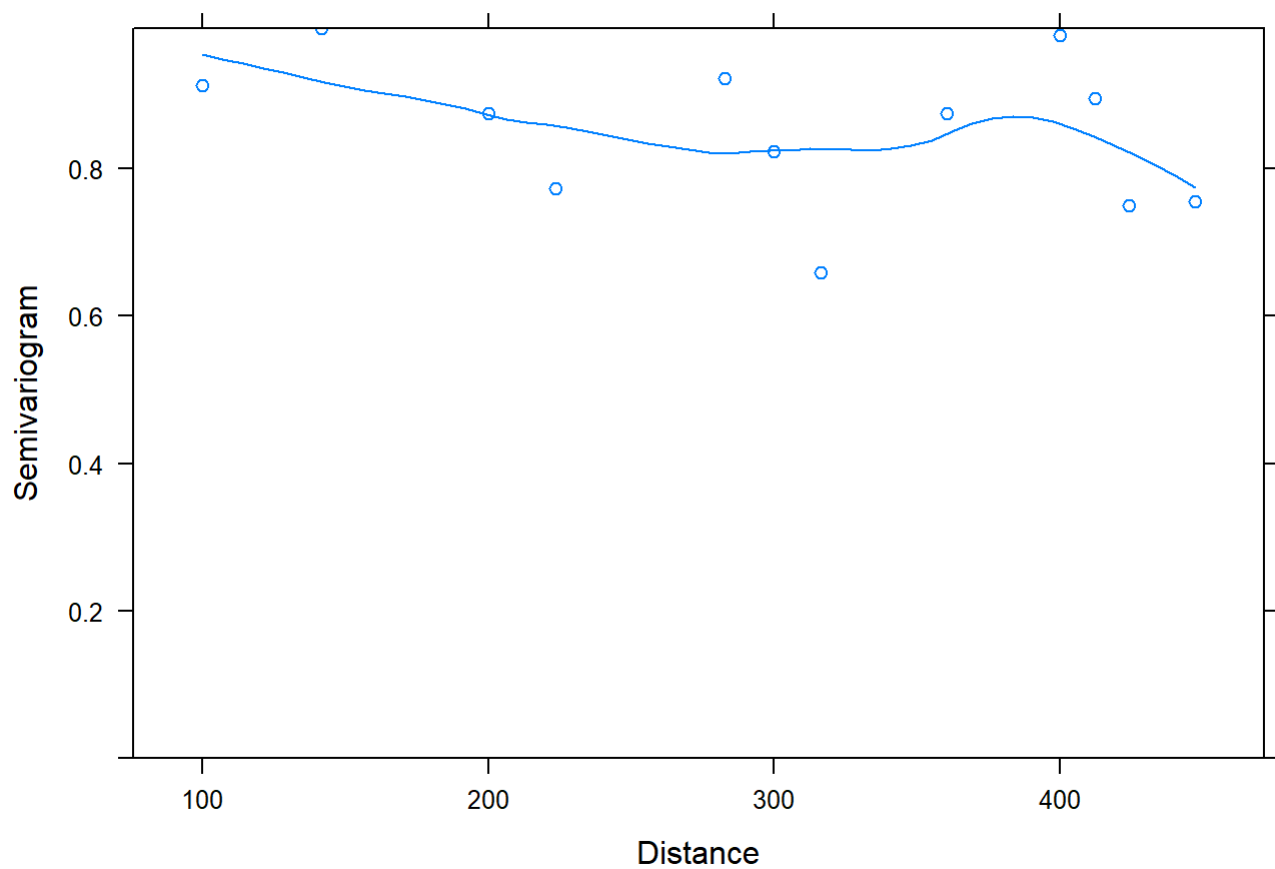
```
anova(BCI_lmQA, BCI_expQA, test=F)
```

```
##            Model df      AIC      BIC    logLik
## BCI_lmQA       1  3 337.5287 343.1423 -165.7644
## BCI_expQA      2  4 301.4029 308.8877 -146.7014
```

```
summary(BCI_lmQA)
```

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Quassia.amara
##   Data: BCI_dat
##        AIC      BIC    logLik
##   337.5287 343.1423 -165.7644
##
## Coefficients:
##                  Value Std.Error  t-value p-value
## (Intercept)   4.962810  1.030804 4.814503   0e+00
## Quassia.amara 9.214876  2.304948 3.997867   2e-04
##
##  Correlation:
##               (Intr)
## Quassia.amara -0.179
##
## Standardized residuals:
##        Min         Q1        Med        Q3        Max
## -0.6920362 -0.6920362 -0.4131473  0.2840748  4.7462963
##
## Residual standard error: 7.171316
## Degrees of freedom: 50 total; 48 residual
```
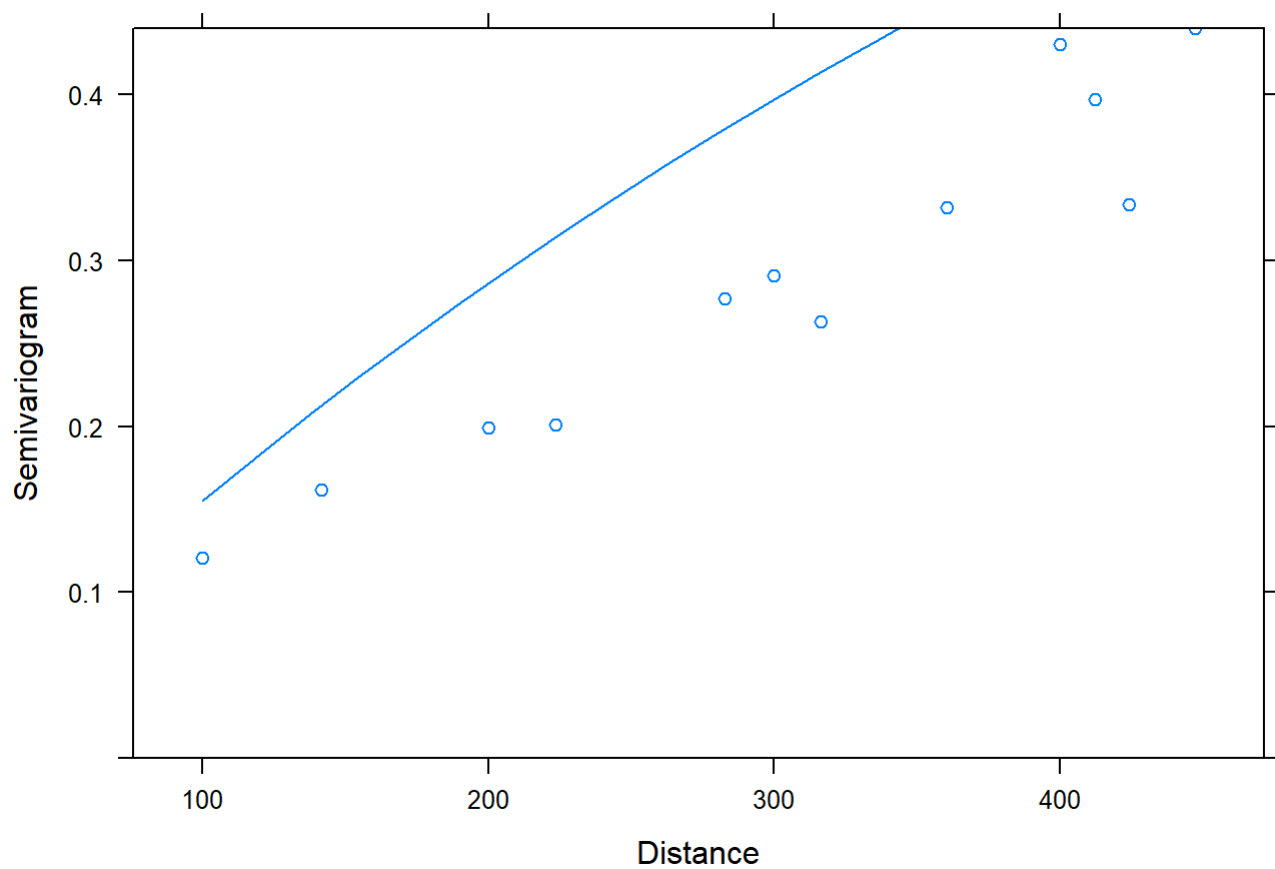
```
summary(BCI_expQA)
```

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Quassia.amara
##   Data: BCI_dat
##        AIC      BIC    logLik
##   301.4029 308.8877 -146.7015
##
## Correlation Structure: Exponential spatial correlation
##  Formula: ~x + y
##  Parameter estimate(s):
##    range
## 1356.62
##
## Coefficients:
##                  Value  Std.Error   t-value p-value
## (Intercept)   9.794547 13.486551 0.7262455  0.4712
## Quassia.amara 3.763073  1.495159 2.5168384  0.0152
##
##  Correlation:
##               (Intr)
## Quassia.amara -0.069
##
## Standardized residuals:
##        Min         Q1        Med         Q3        Max
## -0.5991027 -0.5991027 -0.4767688 -0.1250587  1.7864089
##
## Residual standard error: 16.34869
## Degrees of freedom: 50 total; 48 residual
```

```
anova(BCI_lmALL, BCI_expALL,test=F)
```

```
##             Model df      AIC      BIC    logLik
## BCI_lmALL      1  9 309.7247 325.3637 -145.8623
## BCI_expALL     2 10 300.4918 317.8685 -140.2459
```

```
summary(BCI_lmALL)
```

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Cordia.alliodora + Hirtella.triandra + Picramnia.latifolia +
Quassia.amara + Tabernaemontana.arborea + Trattinnickia.aspera +     Xylopia.macrantha
##   Data: BCI_dat
##        AIC      BIC    logLik
##   309.7247 325.3637 -145.8624
##
## Coefficients:
##                             Value Std.Error    t-value p-value
## (Intercept)              1.761233 1.8539508   0.949989  0.3476
## Cordia.alliodora        -0.048548 0.4740191  -0.102417  0.9189
## Hirtella.triandra        0.181147 0.0793977   2.281514  0.0277
## Picramnia.latifolia      0.686065 0.6684548   1.026345  0.3106
## Quassia.amara            6.006518 2.4524663   2.449174  0.0186
## Tabernaemontana.arborea -0.325338 0.1524922  -2.133470  0.0388
## Trattinnickia.aspera     1.064895 0.7387103   1.441560  0.1568
## Xylopia.macrantha        0.586711 0.1533651   3.825581  0.0004
##
##   Correlation:
##                         (Intr) Crd.ll Hrtll. Pcrmn. Qss.mr Tbrnm. Trttn.
## Cordia.alliodora        -0.329
## Hirtella.triandra       -0.586  0.111
## Picramnia.latifolia      0.010  0.019 -0.410
## Quassia.amara            0.056 -0.422  0.134 -0.310
## Tabernaemontana.arborea -0.660 -0.083  0.263 -0.113  0.277
## Trattinnickia.aspera    -0.042  0.041 -0.260  0.318 -0.652 -0.202
## Xylopia.macrantha       -0.279  0.048  0.125 -0.467  0.242  0.316 -0.275
##
## Standardized residuals:
##          Min          Q1         Med          Q3         Max
## -2.02755548 -0.55498924 -0.05149574  0.25159720  3.32145086
##
## Residual standard error: 4.772207
## Degrees of freedom: 50 total; 42 residual
```

```
summary(BCI_expALL)
```

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Cordia.alliodora + Hirtella.triandra + Picramnia.latifolia +
## Quassia.amara + Tabernaemontana.arborea + Trattinnickia.aspera +    Xylopia.macrantha
##   Data: BCI_dat
##        AIC      BIC    logLik
##   300.4918 317.8685 -140.2459
##
## Correlation Structure: Exponential spatial correlation
##  Formula: ~x + y
##  Parameter estimate(s):
##    range
## 592.6932
##
## Coefficients:
##                             Value Std.Error  t-value p-value
## (Intercept)              3.298228  7.006827 0.470716  0.6403
## Cordia.alliodora         0.121536  0.371801 0.326885  0.7454
## Hirtella.triandra        0.015672  0.099020 0.158273  0.8750
## Picramnia.latifolia      0.209909  0.508071 0.413150  0.6816
## Quassia.amara            1.227442  2.023911 0.606470  0.5475
## Tabernaemontana.arborea  0.075357  0.134237 0.561375  0.5775
## Trattinnickia.aspera     1.791856  0.526848 3.401089  0.0015
## Xylopia.macrantha        0.351386  0.156980 2.238408  0.0306
##
##  Correlation:
##                          (Intr) Crd.ll Hrtll. Pcrmn. Qss.mr Tbrnm. Trttn.
## Cordia.alliodora         -0.100
## Hirtella.triandra        -0.286 -0.021
## Picramnia.latifolia       0.028 -0.001 -0.370
## Quassia.amara            -0.062 -0.489  0.302 -0.145
## Tabernaemontana.arborea  -0.228  0.094  0.285 -0.223  0.051
## Trattinnickia.aspera     -0.050  0.195 -0.236  0.221 -0.623 -0.019
## Xylopia.macrantha        -0.087  0.107 -0.068  0.107  0.178  0.107 -0.141
##
## Standardized residuals:
##        Min         Q1        Med         Q3        Max
## -1.0141086 -0.5281348 -0.3288399  0.2264860  2.1602154
##
## Residual standard error: 9.552439
## Degrees of freedom: 50 total; 42 residual
```

In the case of the single species predictor the exponential fit model did match the data better with an AIC of about 37 lower. However, when all the predictor species were included the AIC didn't change much at all.

I don't think there was a large influence of adding the error term because there didn't seem to be a large spatial dependence earlier on when analyzing a common and rare species. For this reason it would make sense that adding a spatial dependent term might not considerably improve model fit.