

Assignment #5

Sarah Kate Shore

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```
library(vegan)
```

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

```
## Loading required package: lattice
```

```
## This is vegan 2.3-3
```

```
data(BCI)
```

```
## UTM Coordinates (in metres)
```

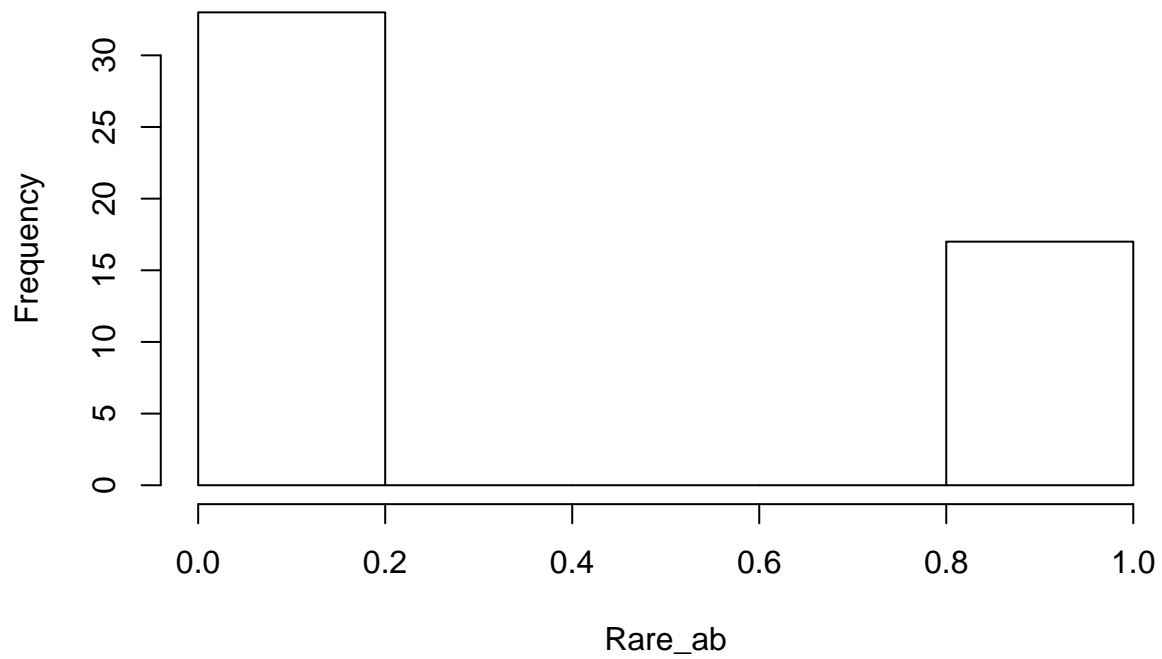
```
BCI_xy = data.frame(x = rep(seq(625754, 626654, by=100), each=5),  
                    y = rep(seq(1011569, 1011969, by=100), len=50))
```

Use Mantel to look at correlation between species richness and spatial distance

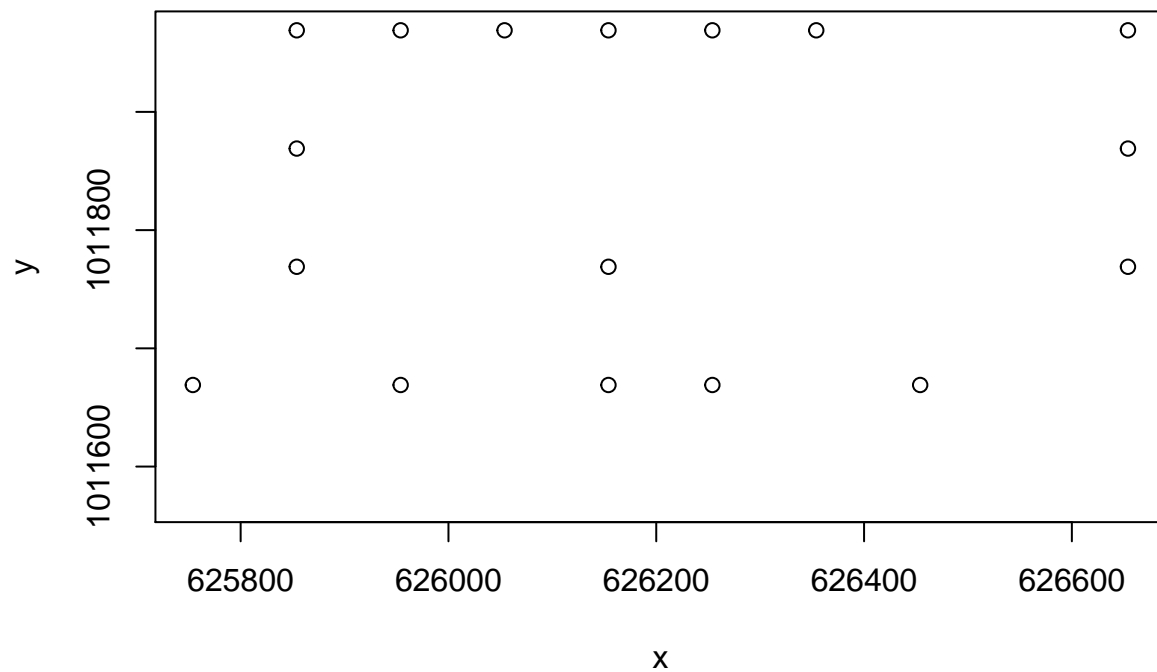
Rare Species

```
BCI_rare = subset(BCI, select = c('Erythroxylum.macrophyllum'))  
Rare_ab = apply(BCI_rare, 1, function(x) sum(x > 0))  
hist(Rare_ab)
```

Histogram of Rare_ab

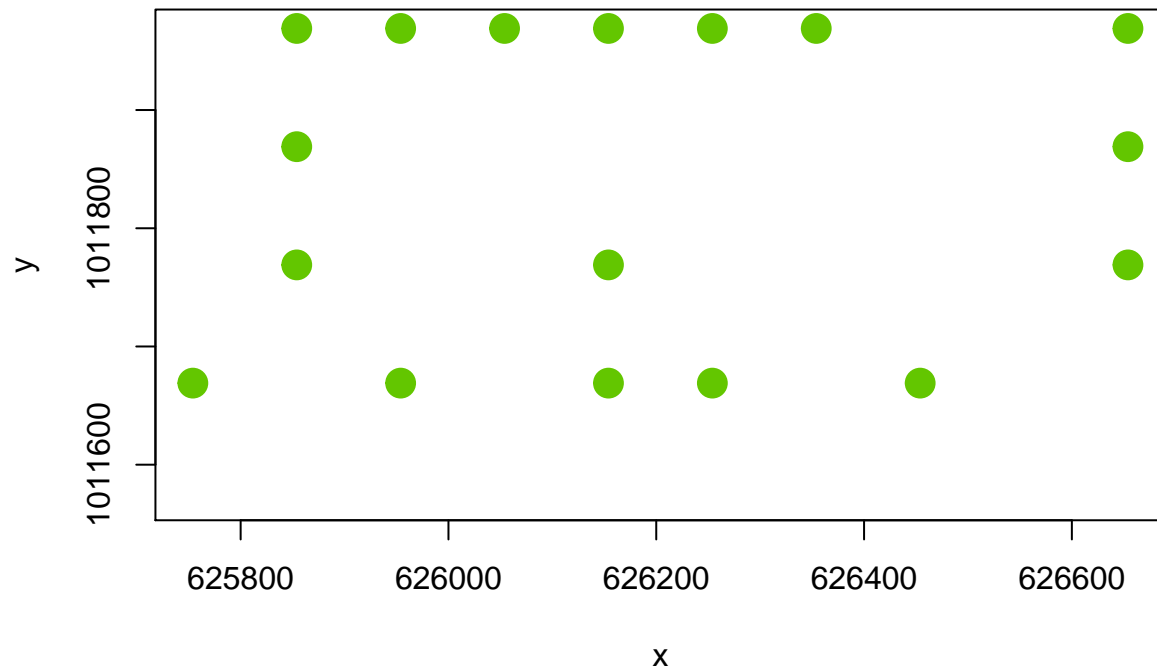


```
plot(BCI_xy, cex=Rare_ab/max(Rare_ab))
```



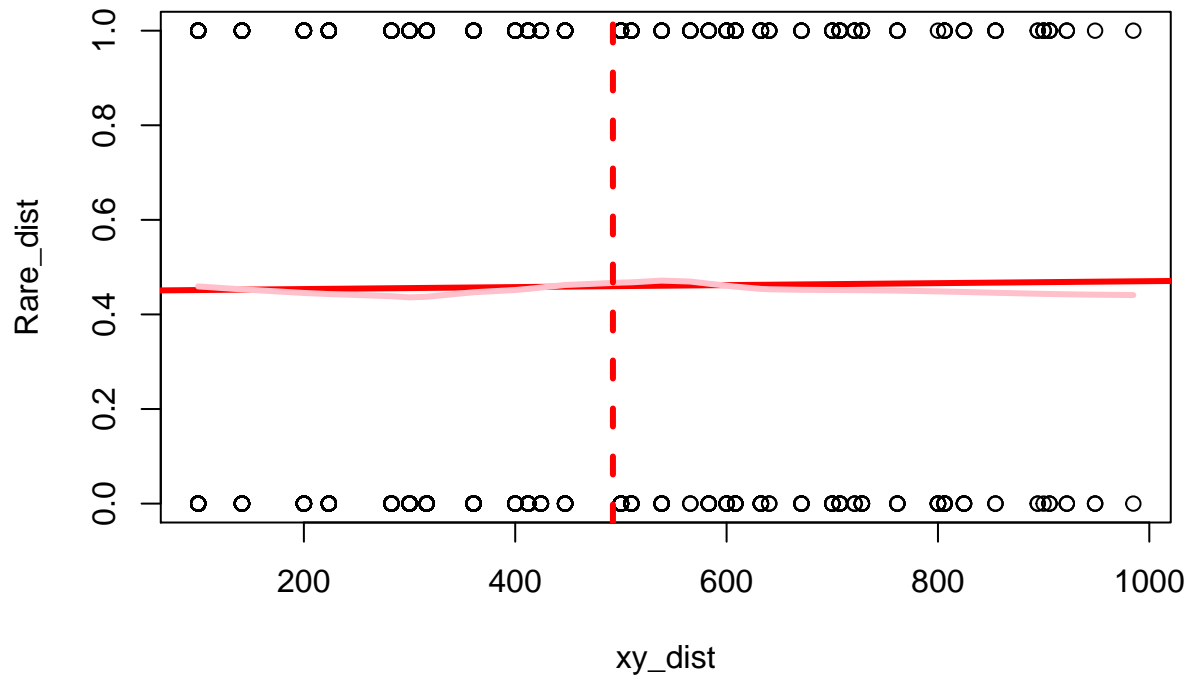
```
col_brks = hist(Rare_ab, plot=F)$breaks
col_indices = as.numeric(cut(Rare_ab, col_brks))
cols = rev(terrain.colors(length(col_brks)))
```

```
plot(BCI_xy, cex=2, pch=19, col=cols[col_indices])
```



#Visually, this plot shows that there may be some spatial dependence due to the linear aggregation of points at the top left of the plot.

```
#Euclidean distance between abundances and spatial coordinates
Rare_dist = dist(Rare_ab)
xy_dist = dist(BCI_xy)
max_dist = max(xy_dist) / 2
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)
```



```
#Observed Correlation
obs_cor = cor(xy_dist, Rare_dist)
obs_cor
```

```
## [1] 0.008761204
```

The correlation is 0.009, which does not indicate much spatial dependence.

```
#mantel statistics
library('vegan')
Rare_mantel = mantel(xy_dist, Rare_dist)
Rare_mantel
```

```
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = xy_dist, ydis = Rare_dist)
##
## Mantel statistic r: 0.008761
##      Significance: 0.384
##
## Upper quantiles of permutations (null model):
##   90%   95%  97.5%   99%
## 0.0513 0.0690 0.0864 0.1070
## Permutation: free
## Number of permutations: 999
```

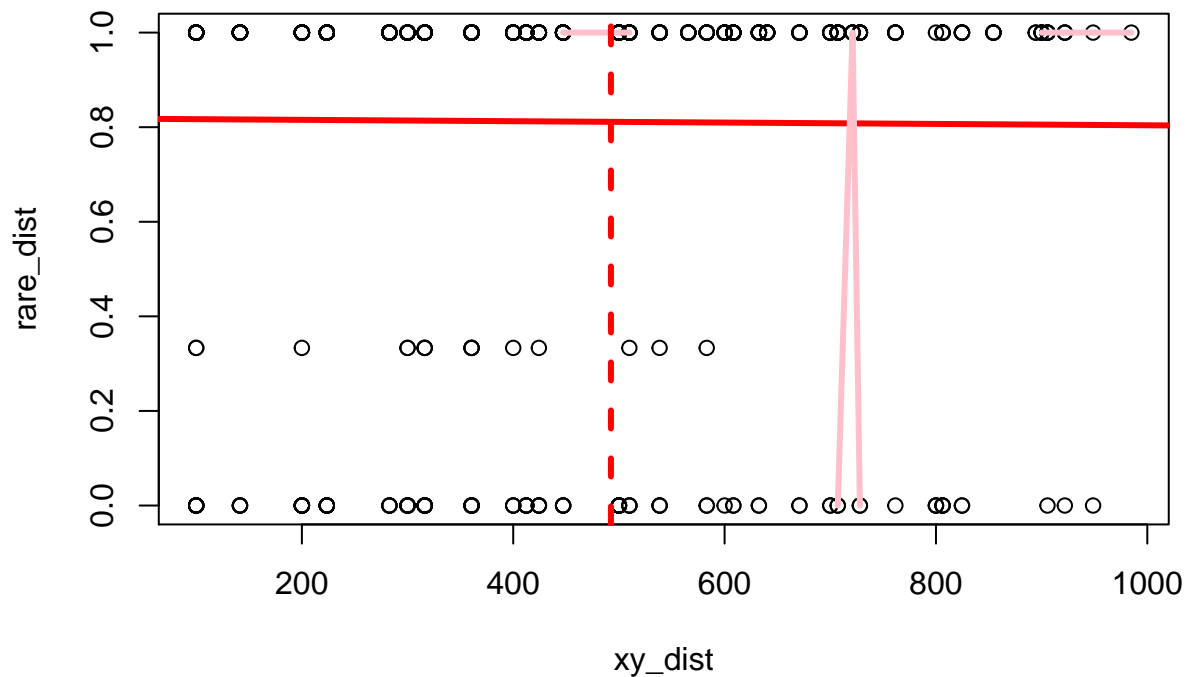
Significance value for mantel is 0.397, so this does not seem to be a spatially dependent species.

```
rare_dist = vegdist(BCI_rare)
```

```
## Warning in vegdist(BCI_rare): you have empty rows: their dissimilarities  
## may be meaningless in method "bray"
```

```
## Warning in vegdist(BCI_rare): missing values in results
```

```
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)
```

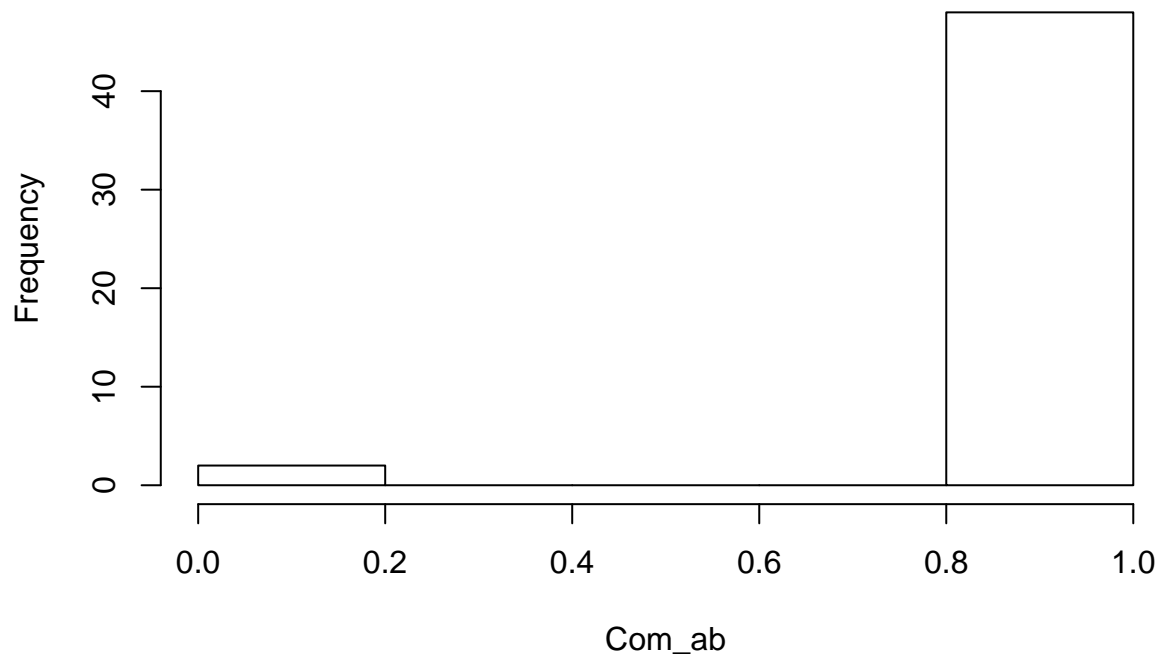


```
#Lowess line is really odd, definitely not linear.
```

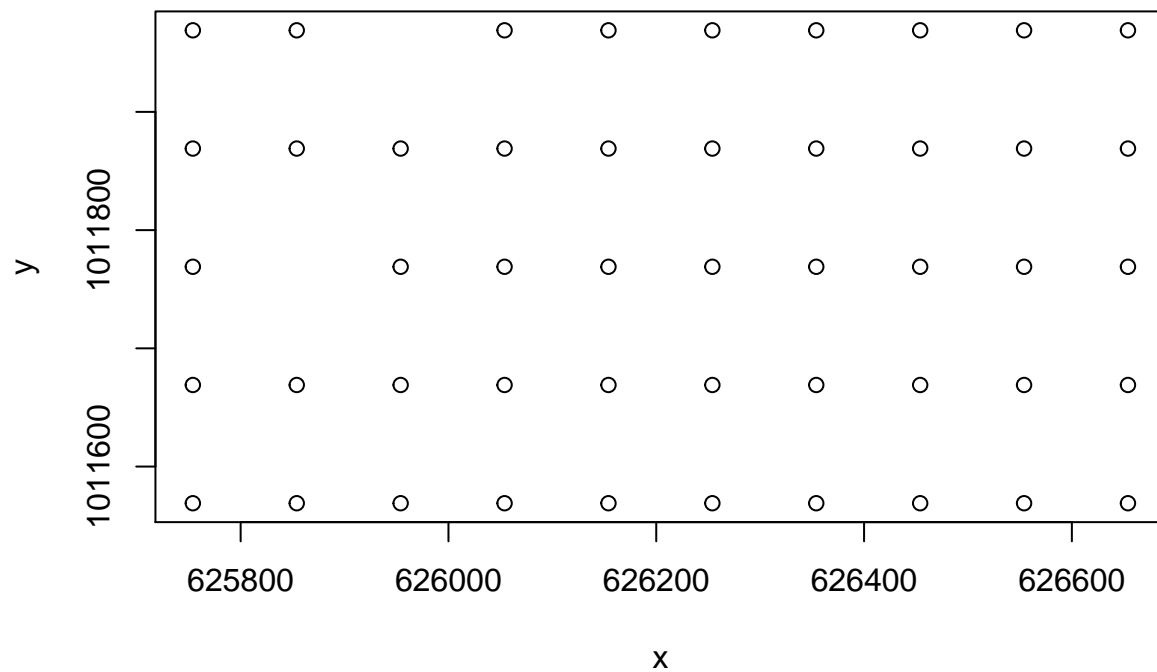
Common Species Spatial Distribution

```
BCI_common = subset(BCI, select = 'Guarea.guidonia')  
Com_ab = apply(BCI_common, 1, function(x) sum(x > 0))  
hist(Com_ab)
```

Histogram of Com_ab

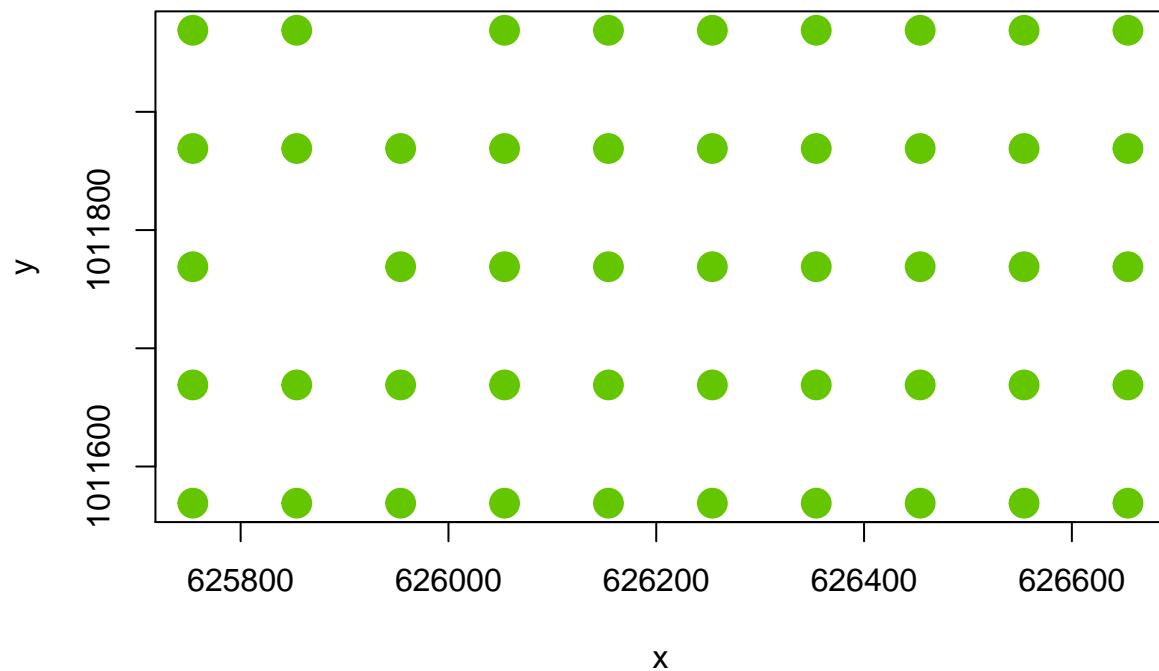


```
plot(BCI_xy, cex = Com_ab/max(Com_ab))
```



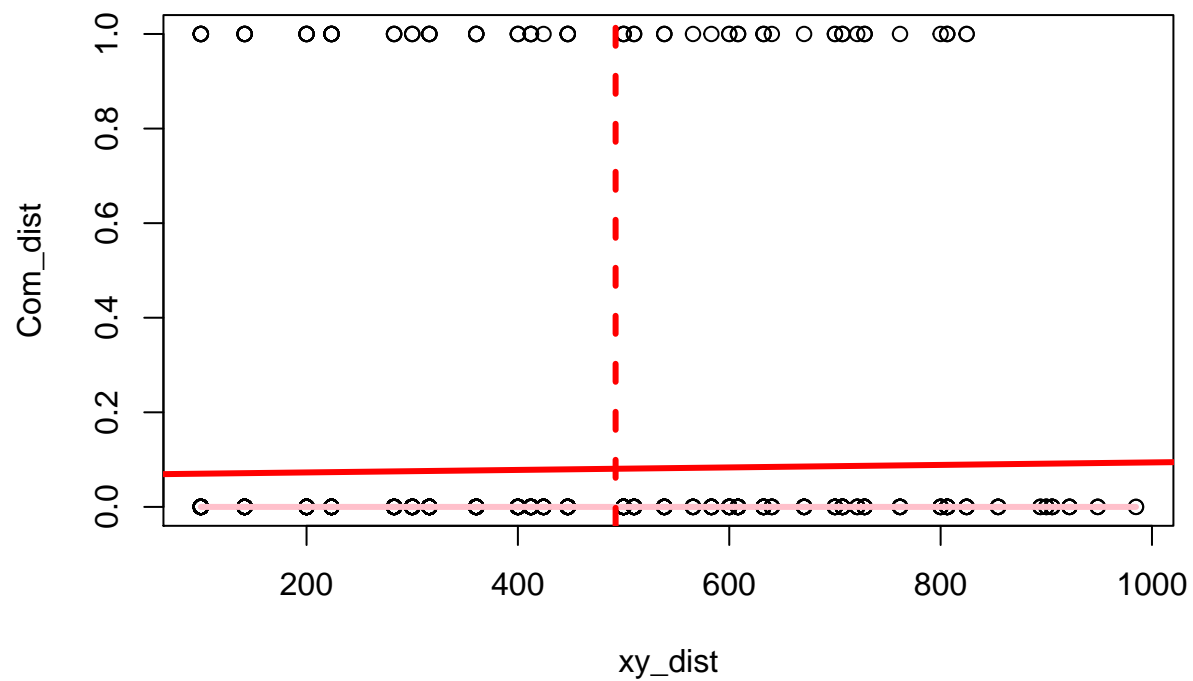
```
col_brks = hist(Com_ab, plot=F)$breaks
col_indices = as.numeric(cut(Com_ab, col_brks))
cols = rev(terrain.colors(length(col_brks)))
```

```
plot(BCI_xy, cex = 2, pch=19, col=cols[col_indices])
```



#Different color classes not showing up, however does not appear aggregated at all.

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



```
obs_cor = cor(xy_dist, Com_dist)
obs_cor
```

```
## [1] 0.02062747
```

Correlation value is 0.02, better than that of rare species but still not high at all.

```
library('vegan')
Com_mantel = mantel(xy_dist, Com_dist)
Com_mantel
```

```
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = xy_dist, ydis = Com_dist)
##
## Mantel statistic r: 0.02063
##      Significance: 0.368
##
## Upper quantiles of permutations (null model):
##      90%    95%  97.5%   99%
## 0.0891 0.1188 0.1434 0.1735
## Permutation: free
## Number of permutations: 999
```

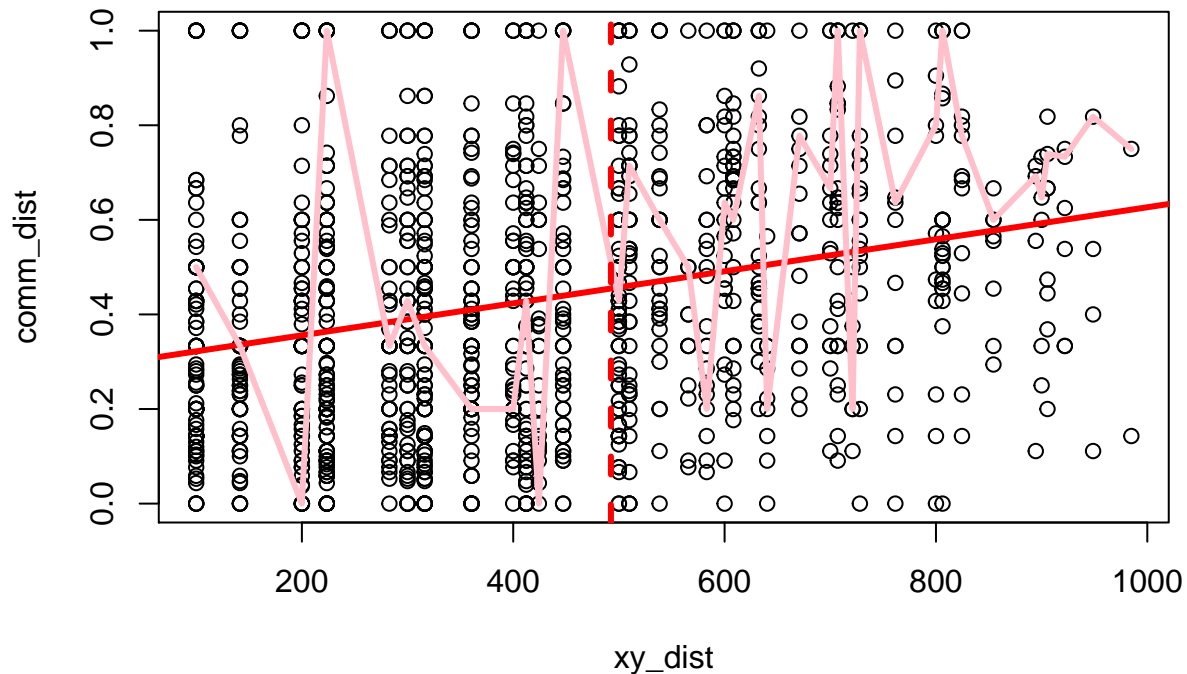
Mantel significance at 0.376, not significant, so no spatial correlation detected.

```
comm_dist = vegdist(BCI_common)
```

```
## Warning in vegdist(BCI_common): you have empty rows: their dissimilarities
## may be meaningless in method "bray"
```

```
## Warning in vegdist(BCI_common): missing values in results
```

```
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)
```

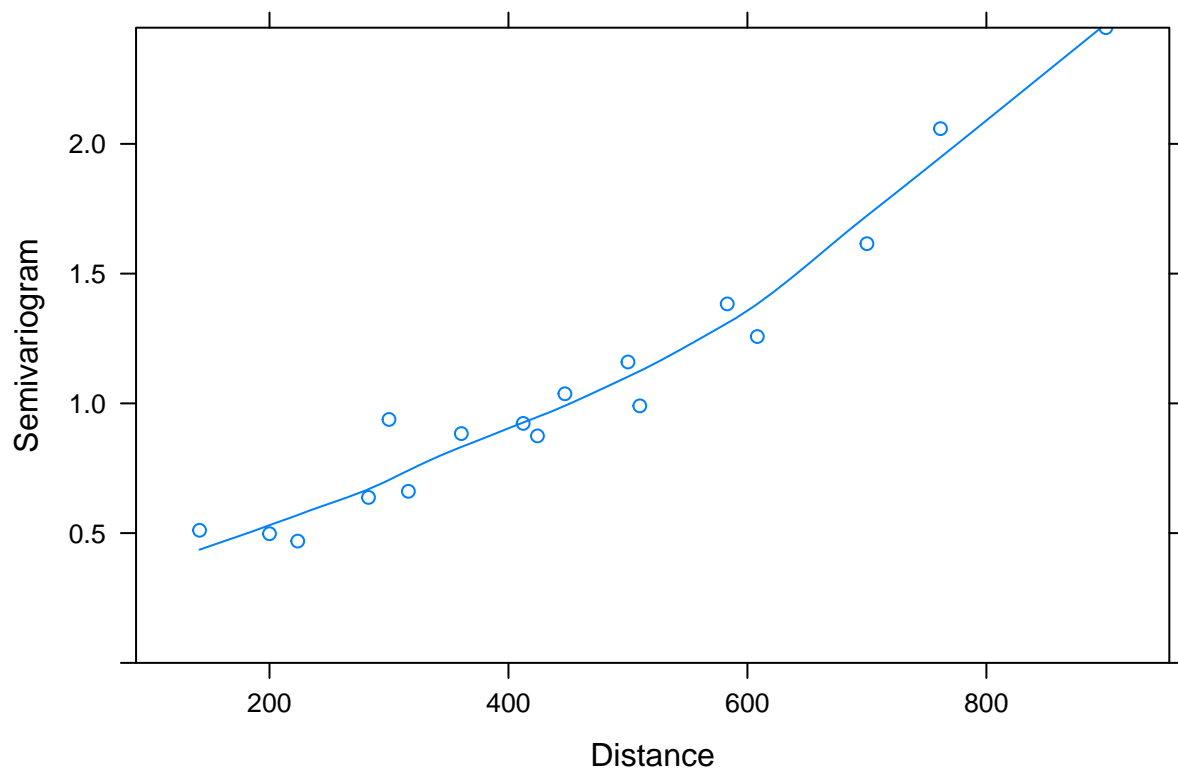



#Crazy lowess line, the regular linear fit line does have an upward trend, but still I don't see any evidence for spatial correlations.

Question 2 Univariate Modeling

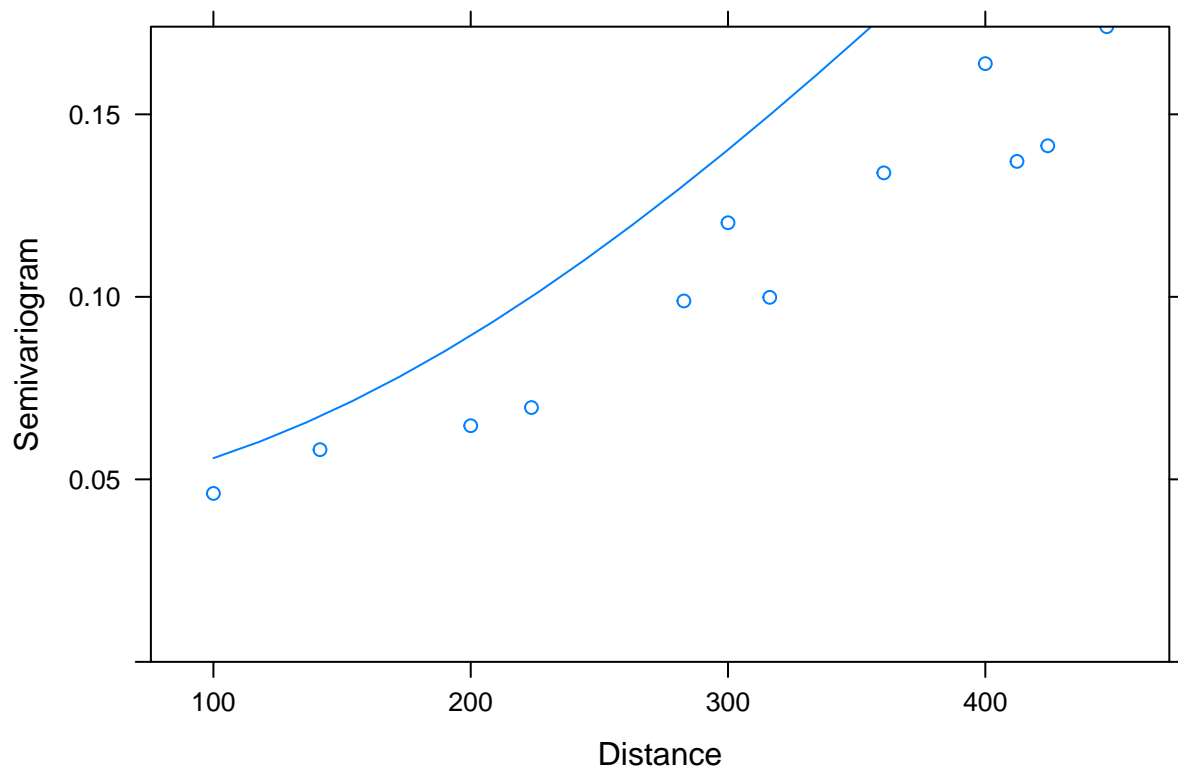
Single Predictor Variable

```
library(nlme)
library(vegan)
#Define what data is used
sp_ids = c("Drypetes.standleyi", "Cordia.lasiocalyx", "Hirtella.triandra",
           "Picramnia.latifolia", "Quassia.amara",
           "Tabernaemontana.arborea", "Trattinnickia.aspera",
           "Xylopia.macrantha")
sp_dat = data.frame(BCI, BCI_xy)
BCI_sp = subset(sp_dat, select=sp_ids)
x = BCI_xy$x
y = BCI_xy$y
#Model plotting one predictor variable for Drypetes.standleyi
One_sp_mod = gls(Drypetes.standleyi ~ Xylopia.macrantha, data = BCI_sp)
par(mfrow=c(1,1))
plot(Variogram(One_sp_mod, form = ~ x + y))
```

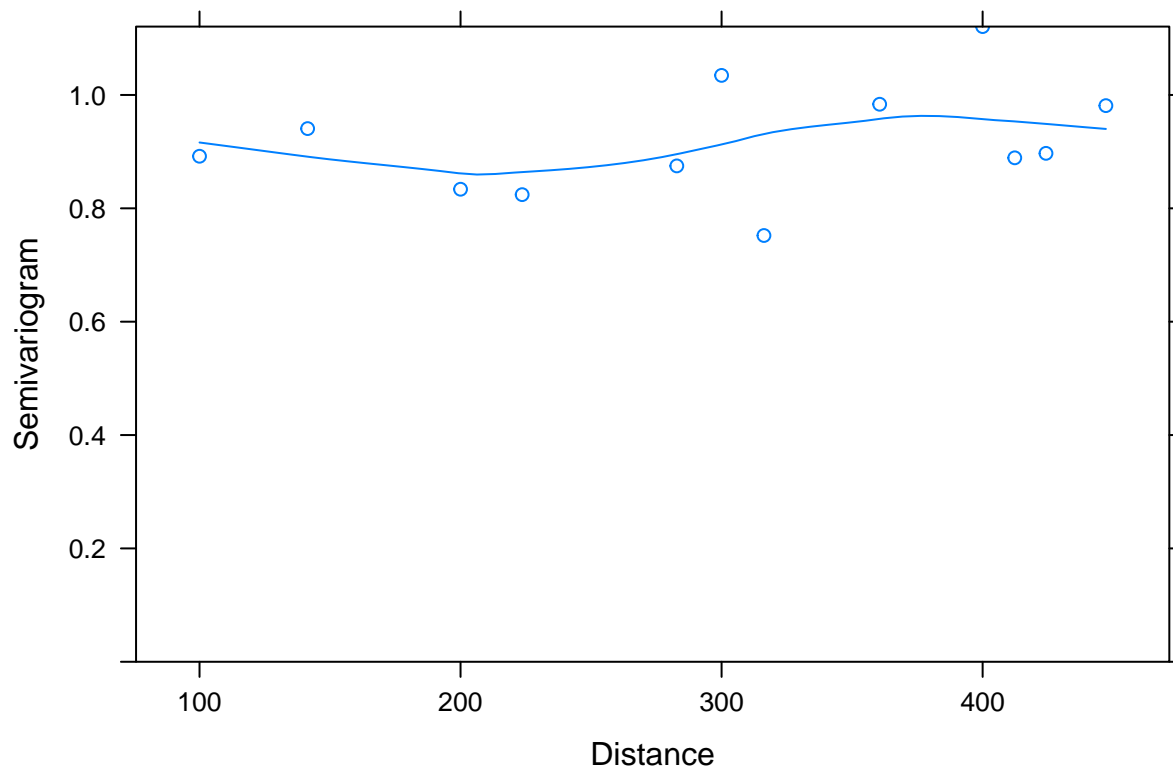


#Model with nugget

```
One_sp_nug = update(One_sp_mod, corr=corRatio(form= ~ x + y, nugget=T))
plot(Variogram(One_sp_nug, maxDist = max_dist))
```



```
plot(Variogram(One_sp_nug, resType='n', maxDist = max_dist))
```



```
One_sp_mod
```

```
## Generalized least squares fit by REML
## Model: Drypetes.standleyi ~ Xylopia.macrantha
## Data: BCI_sp
## Log-restricted-likelihood: -166.1459
##
## Coefficients:
## (Intercept) Xylopia.macrantha
## 3.2852519 0.8443175
##
## Degrees of freedom: 50 total; 48 residual
## Residual standard error: 6.861233
```

```
One_sp_nug
```

```
## Generalized least squares fit by REML
## Model: Drypetes.standleyi ~ Xylopia.macrantha
## Data: BCI_sp
## Log-restricted-likelihood: -148.3015
##
## Coefficients:
```

```
##      (Intercept) Xylopia.macrantha
##      13.8827731      0.2983731
##
## Correlation Structure: Rational quadratic spatial correlation
## Formula: ~x + y
## Parameter estimate(s):
##      range      nugget
## 896.58487625  0.04405078
## Degrees of freedom: 50 total; 48 residual
## Residual standard error: 18.93017
```

```
#Anova to compare
```

```
anova(One_sp_mod, One_sp_nug)
```

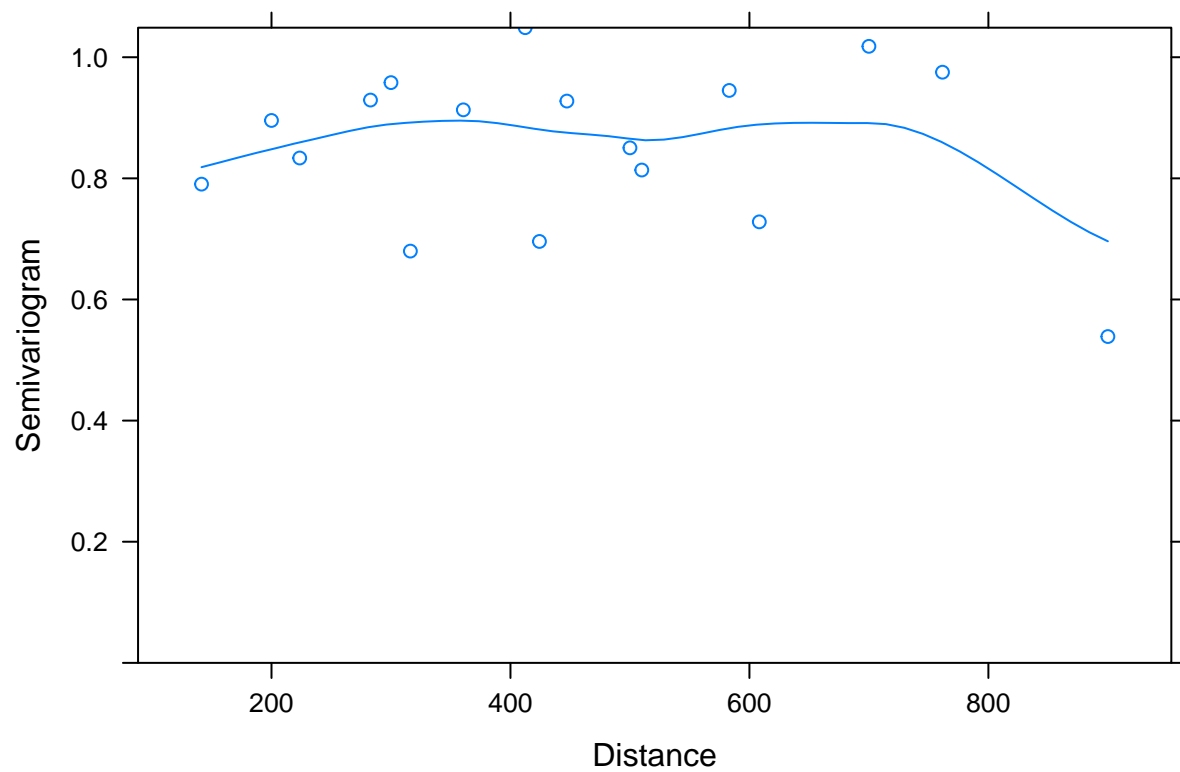
```
##      Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## One_sp_mod    1  3 338.2919 343.9055 -166.1459
## One_sp_nug    2  5 306.6030 315.9590 -148.3015 1 vs 2 35.68886 <.0001
```

Coefficients for one species predictor model reduced by over 0.5 (50%) when spatial error term added.

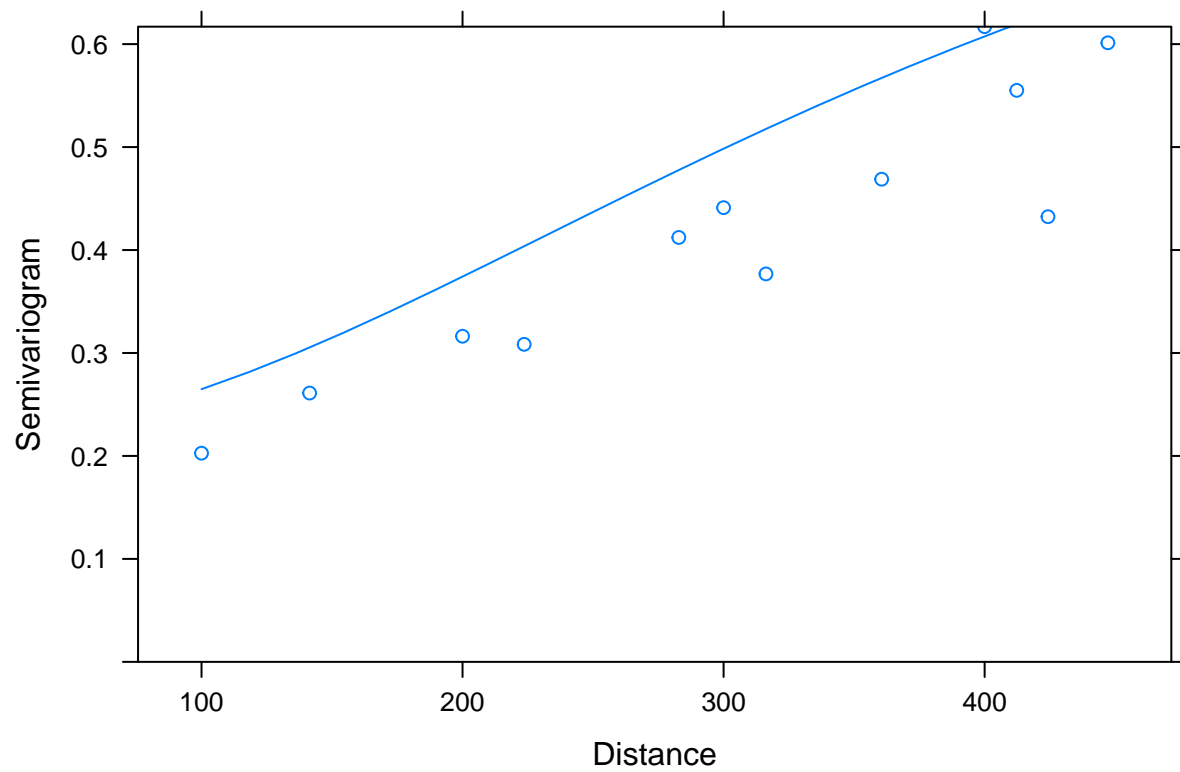
The anova shows that the influence of the nugget causes a >10 change in the AIC between the two models.

Multiple Predictor Variables

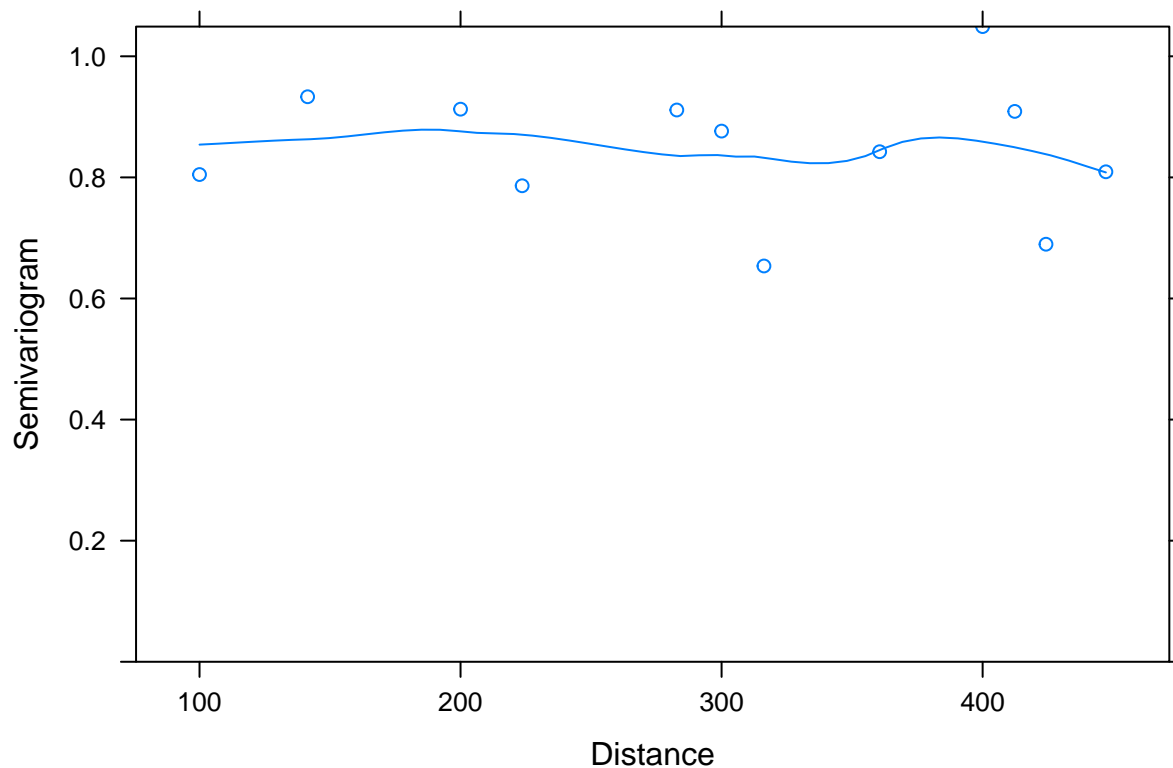
```
library(nlme)
#Define data
sp_ids = c("Drypetes.standleyi", "Cordia.lasiocalyx", "Hirtella.triandra", "Picramnia.latifolia", "Quas")
sp_dat = data.frame(BCI, BCI_xy)
BCI_sp = subset(sp_dat, select=sp_ids)
x = BCI_xy$x
y = BCI_xy$y
#Model plotting multiple predictor variables for Drypetes.standleyi
Mult_sp_mod = gls(Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra + Picramnia.latifolia + Q
par(mfrow=c(1,1))
plot(Variogram(Mult_sp_mod, form = ~ x + y))
```



```
#Model with nugget
Mult_sp_nug = update(Mult_sp_mod, corr=corRatio(form= ~ x + y, nugget=T))
plot(Variogram(Mult_sp_nug, maxDist = max_dist))
```



```
plot(Variogram(Mult_sp_nug, resType='n', maxDist = max_dist))
```



```
Mult_sp_mod
```

```
## Generalized least squares fit by REML
## Model: Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra + Picramnia.latifolia + Qua
## Data: BCI_sp
## Log-restricted-likelihood: -144.5582
##
## Coefficients:
## (Intercept) Cordia.lasiocalyx Hirtella.triandra
## -1.0517523 0.4289202 0.1222789
## Picramnia.latifolia Quassia.amara Tabernaemontana.arborea
## 0.6622595 4.0856614 -0.2497250
## Trattinnickia.aspera Xylopia.macrantha
## 1.3493226 0.5488320
##
## Degrees of freedom: 50 total; 42 residual
## Residual standard error: 4.539713
```

```
Mult_sp_nug
```

```
## Generalized least squares fit by REML
## Model: Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra + Picramnia.latifolia + Qua
```

```
## Data: BCI_sp
## Log-restricted-likelihood: -140.5743
##
## Coefficients:
##           (Intercept)      Cordia.lasiocalyx      Hirtella.triandra
##           2.030692025          0.150809941          0.007669167
##      Picramnia.latifolia      Quassia.amara Tabernaemontana.arborea
##           0.250928914          1.504942337          0.032221941
##      Trattinnickia.aspera      Xylopia.macrantha
##           1.769893578          0.405806125
##
## Correlation Structure: Rational quadratic spatial correlation
## Formula: ~x + y
## Parameter estimate(s):
##      range      nugget
## 402.2077831  0.2194023
## Degrees of freedom: 50 total; 42 residual
## Residual standard error: 7.348772

#Anova to compare models
anova(Mult_sp_mod, Mult_sp_nug)
```

```
##           Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## Mult_sp_mod     1  9 307.1163 322.7554 -144.5582
## Mult_sp_nug     2 11 303.1486 322.2630 -140.5743 1 vs 2 7.967705 0.0186
```

Coefficients decreased for all variables except for *Tabernaemontana.arborea*, which went from a negative value to a positive value.

When the models were compared with anova, the AIC did not change by 10, but instead by 4.

For the most part, both the single predictor value model and the multiple predictor value model are improved by adding a nugget. This is because the nugget accounts for spatial error. Trees in sites such as BCI tend to be at least somewhat aggregated, especially in common species with many instances. Adding the nugget changes the y intercept and allows the Semivariograms to have a better fit.