Spatial Modeling

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```
library(vegan)
```

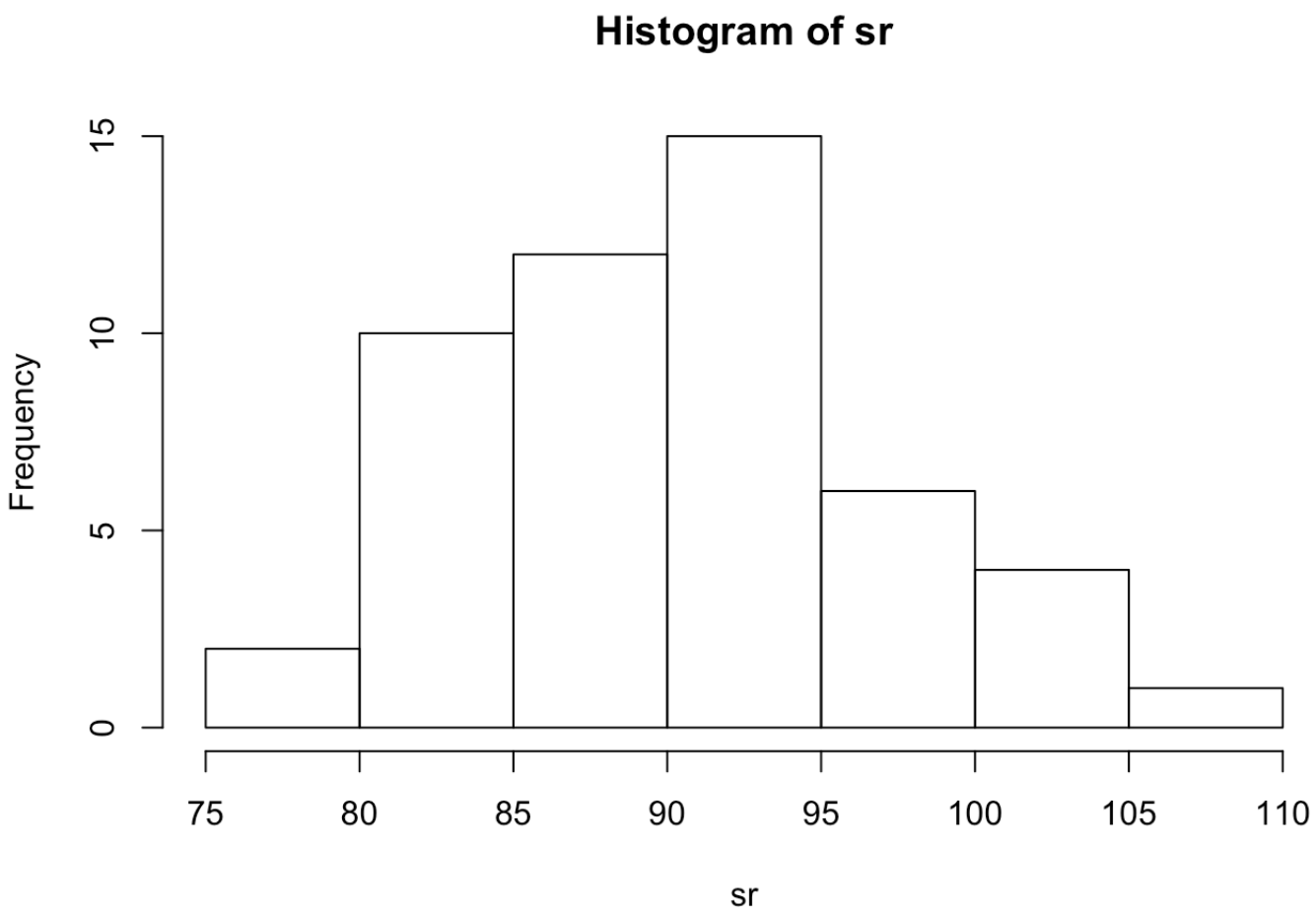
```
## Loading required package: permute
```

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

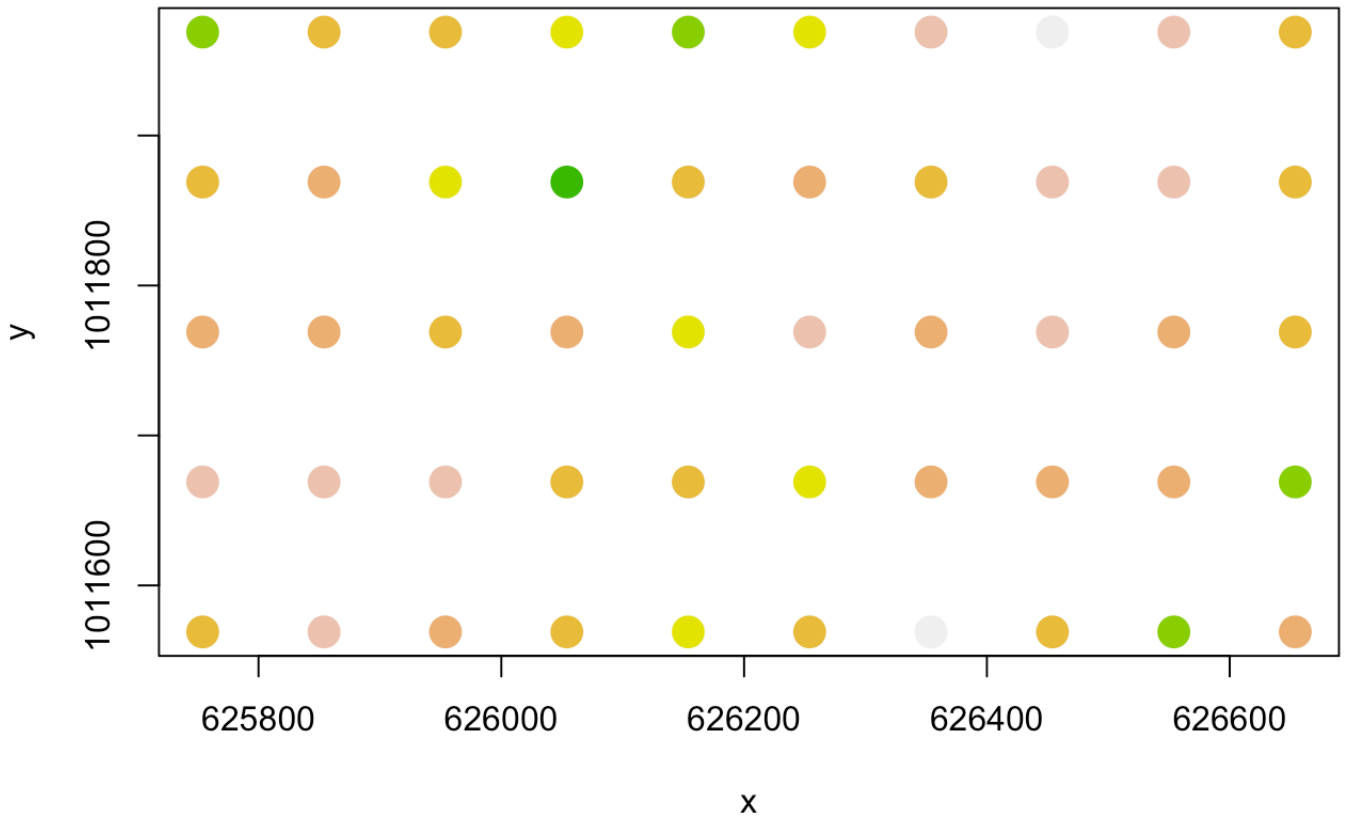
```
## This is vegan 2.4-6
```

```
library(nlme)
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))
```

```
#Question 1. Examine if there is evidence of spatial dependence...

sr = apply(BCI, 1, function(x) sum(x > 0))
hist(sr)
```



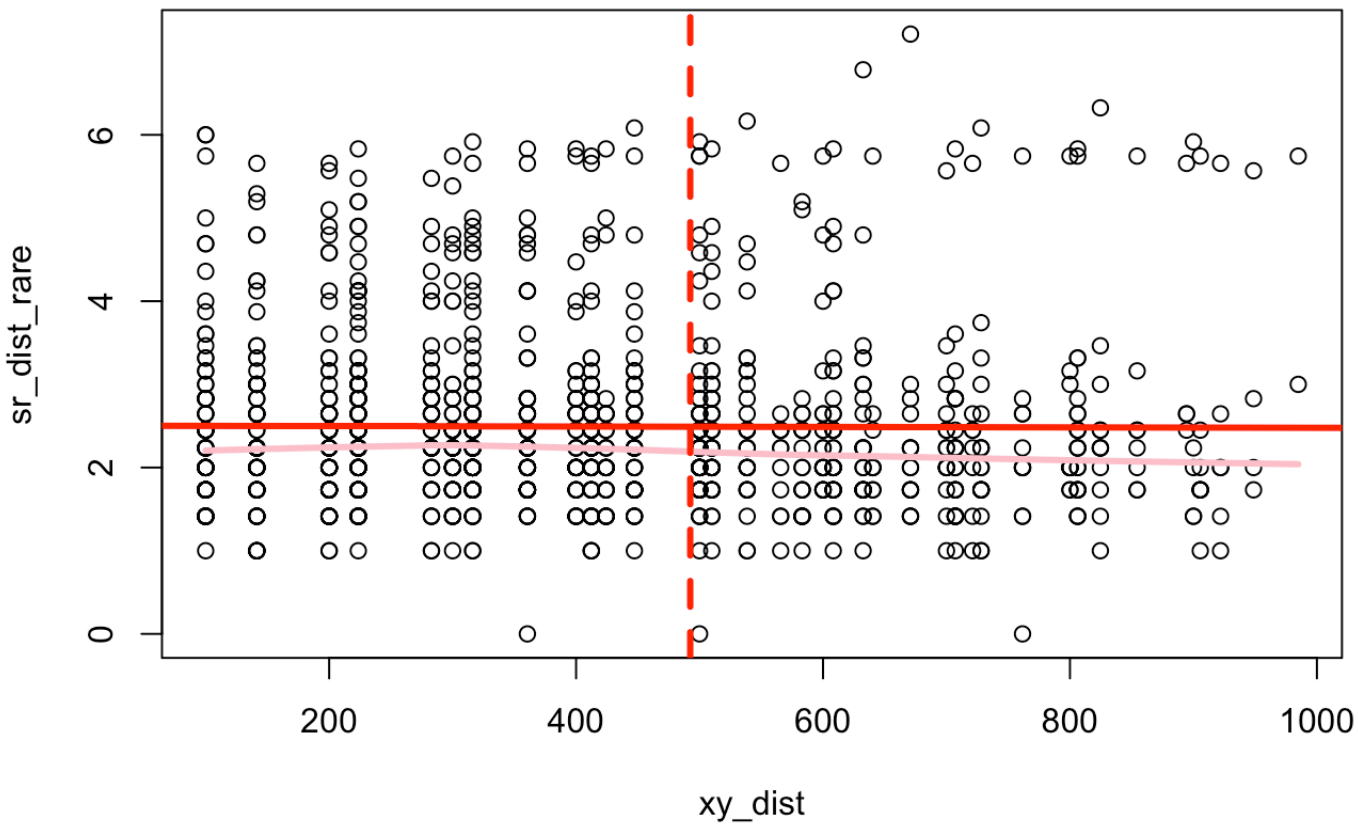

```
col_brks = hist(sr, plot=F)$breaks
col_indices = as.numeric(cut(sr, col_brks))
cols = rev(terrain.colors(length(col_brks)))
plot(BCI_xy, cex=2, pch=19, col=cols[col_indices])
```




```
abu <- colSums(BCI)

quantile(abu, c(0.25, 0.75))
```

```
## 25% 75%
##   7  82
```

```
sp_ids_rare <- BCI[ , abu < 7]

sp_ids_common <- BCI[ , abu > 82]

#Examining if there is evidence of spatial dependence in rare species...
sr_dist_rare <- dist(sp_ids_rare)
xy_dist <- dist(BCI_xy)

max_dist <- max(xy_dist) / 2

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




```
obs_cor <- cor(xy_dist, sr_dist_rare)
obs_cor
```

```
## [1] -0.005664822
```

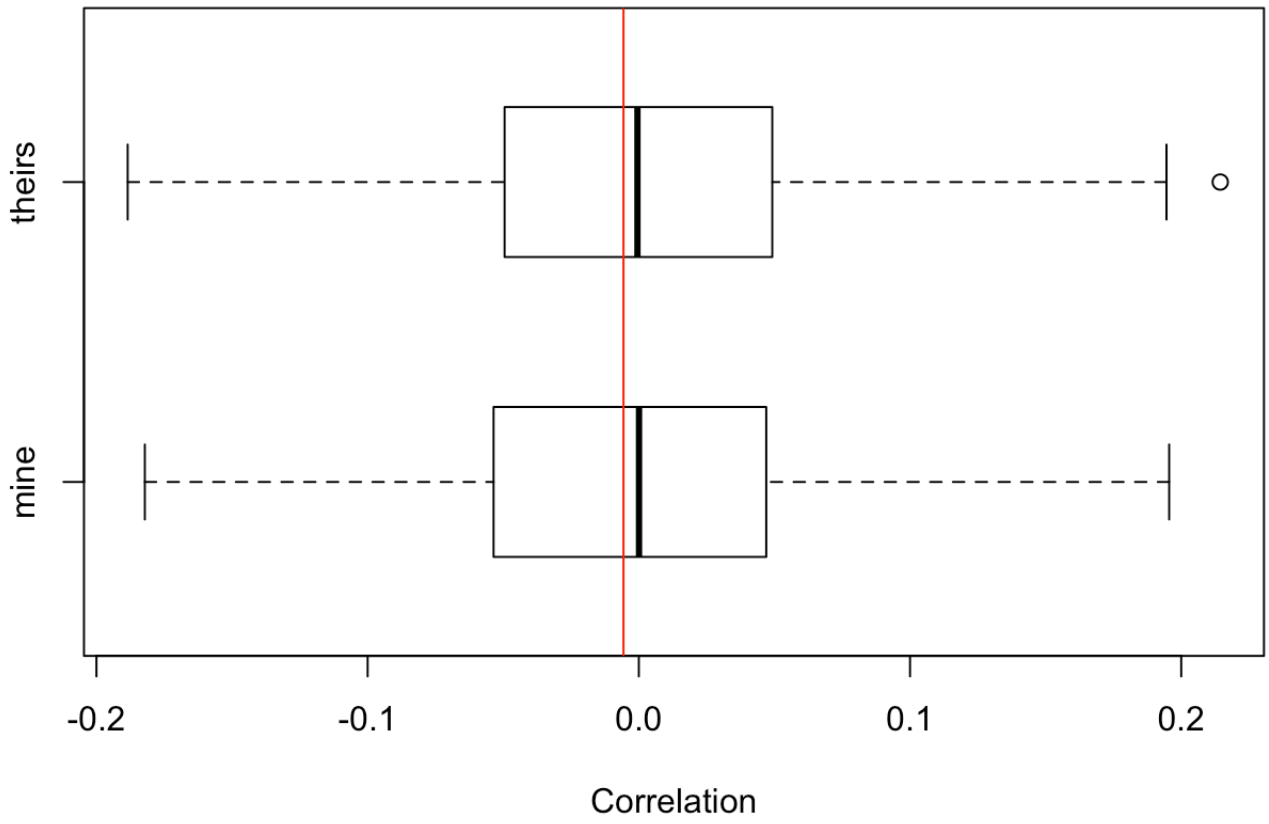
```
nperm = 1000
null_cor = obs_cor
for (i in 2:nperm) {
    tmp_xy = BCI_xy[sample(nrow(BCI_xy)), ]
    null_cor[i] = cor(dist(tmp_xy), sr_dist_rare)
}

sum(null_cor >= obs_cor) / nperm
```

```
## [1] 0.524
```

```
sr_mantel_rare <- mantel(xy_dist, sr_dist_rare)
sr_mantel_rare
```

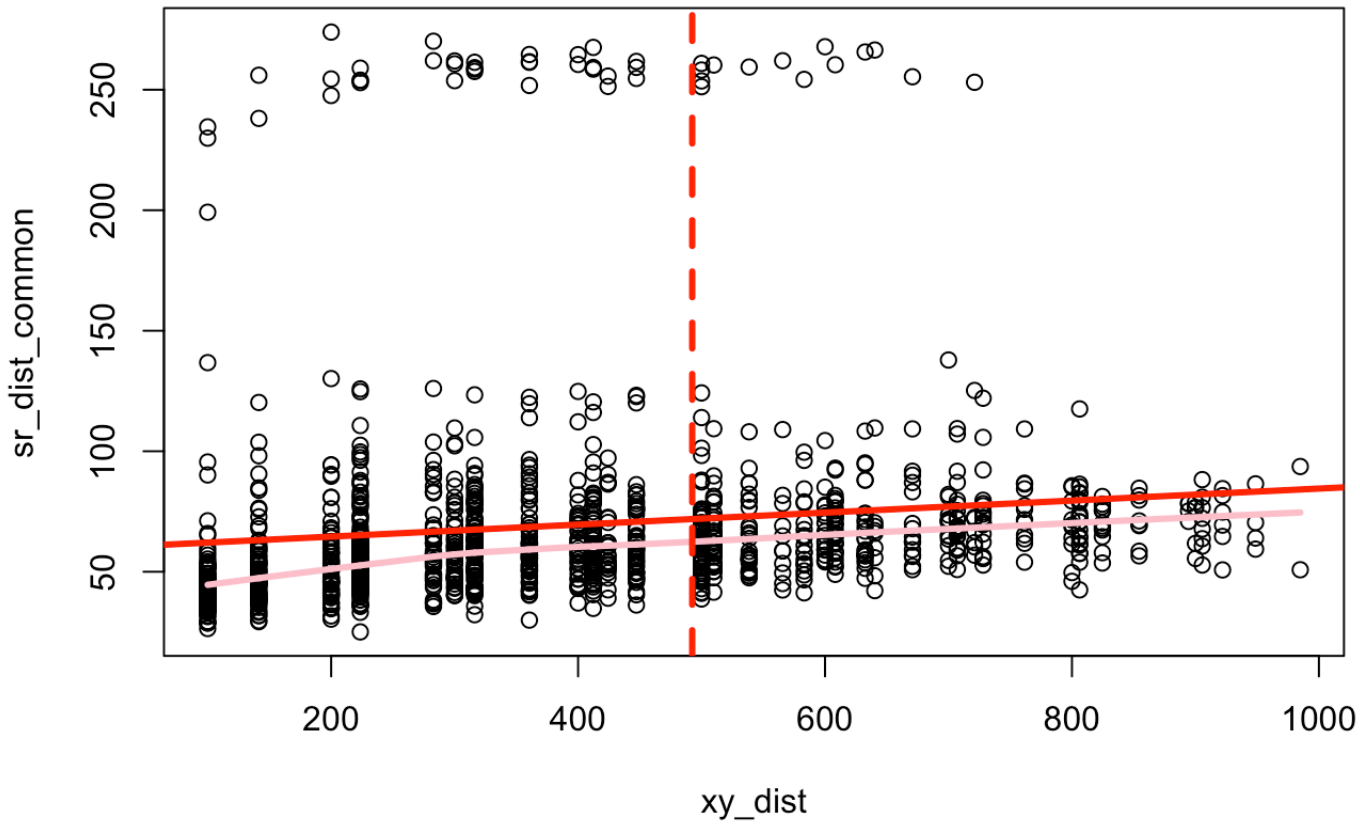
```
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = xy_dist, ydis = sr_dist_rare)
##
## Mantel statistic r: -0.005665
##       Significance: 0.522
##
## Upper quantiles of permutations (null model):
##   90%   95% 97.5%   99%
## 0.096 0.118 0.137 0.165
## Permutation: free
## Number of permutations: 999
```

```
boxplot(list(null_cor, sr_mantel_rare$perm), horizontal = T, boxwex = 0.5,
        names = c('mine', 'theirs'), xlab='Correlation')
abline(v=obs_cor, col='red')
```




```
#The observed value is not larger than the null realizations, indicating that there i
s not a significant difference between the observed spatial pattern and one due to ra
ndom chance.
```

```
#Examining if there is evidence of spatial dependence in common species...
sr_dist_common <- dist(sp_ids_common)
xy_dist <- dist(BCI_xy)

max_dist <- max(xy_dist) / 2

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




```
obs_cor <- cor(xy_dist, sr_dist_common)
obs_cor
```

```
## [1] 0.1242412
```

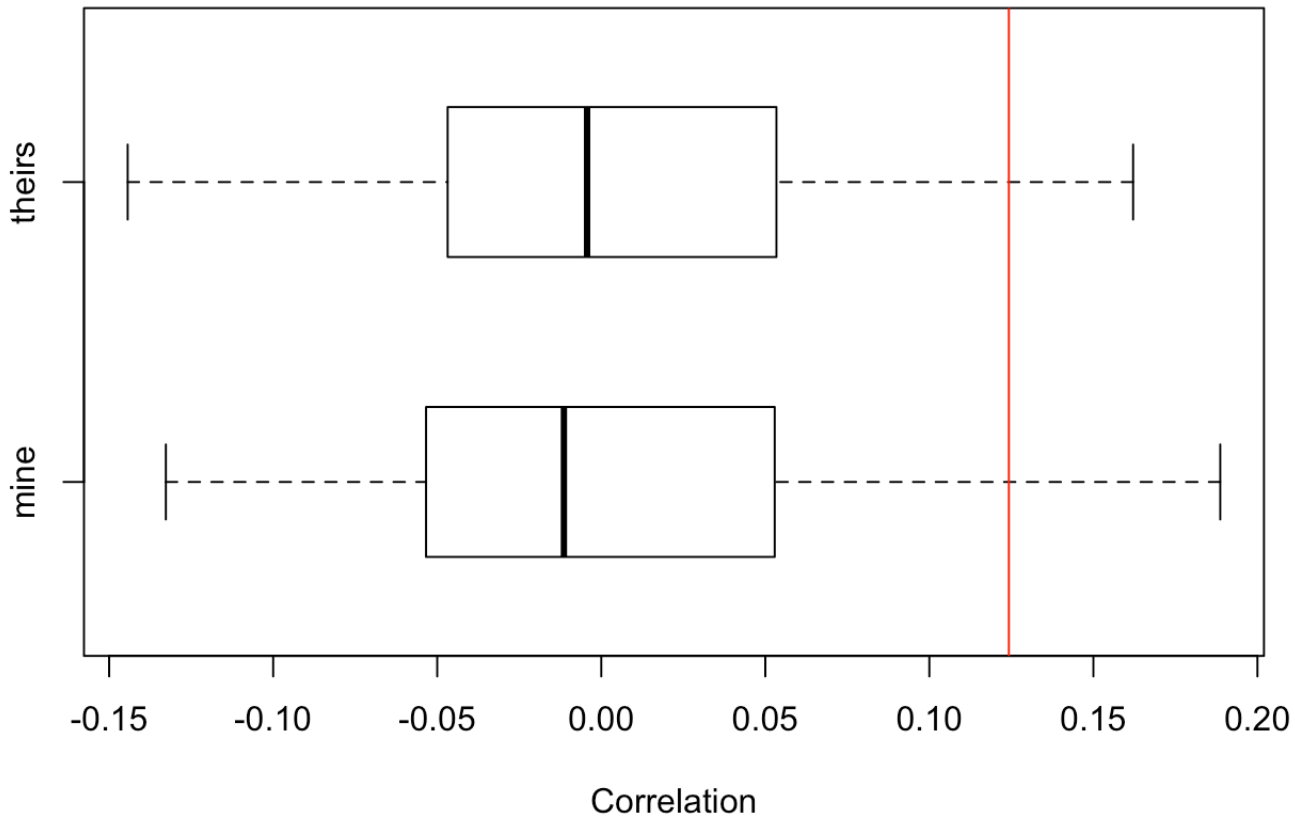
```
nperm = 1000
null_cor = obs_cor
for (i in 2:nperm) {
    tmp_xy = BCI_xy[sample(nrow(BCI_xy)), ]
    null_cor[i] = cor(dist(tmp_xy), sr_dist_common)
}

sum(null_cor >= obs_cor) / nperm
```

```
## [1] 0.035
```

```
sr_mantel_common <- mantel(xy_dist, sr_dist_common)
sr_mantel_common
```

```
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = xy_dist, ydis = sr_dist_common)
##
## Mantel statistic r: 0.1242
##       Significance: 0.034
##
## Upper quantiles of permutations (null model):
##    90%    95%  97.5%    99%
## 0.0982 0.1184 0.1289 0.1395
## Permutation: free
## Number of permutations: 999
```

```
boxplot(list(null_cor, sr_mantel_common$perm), horizontal = T, boxwex = 0.5,
        names = c('mine', 'theirs'), xlab='Correlation')
abline(v=obs_cor, col='red')
```

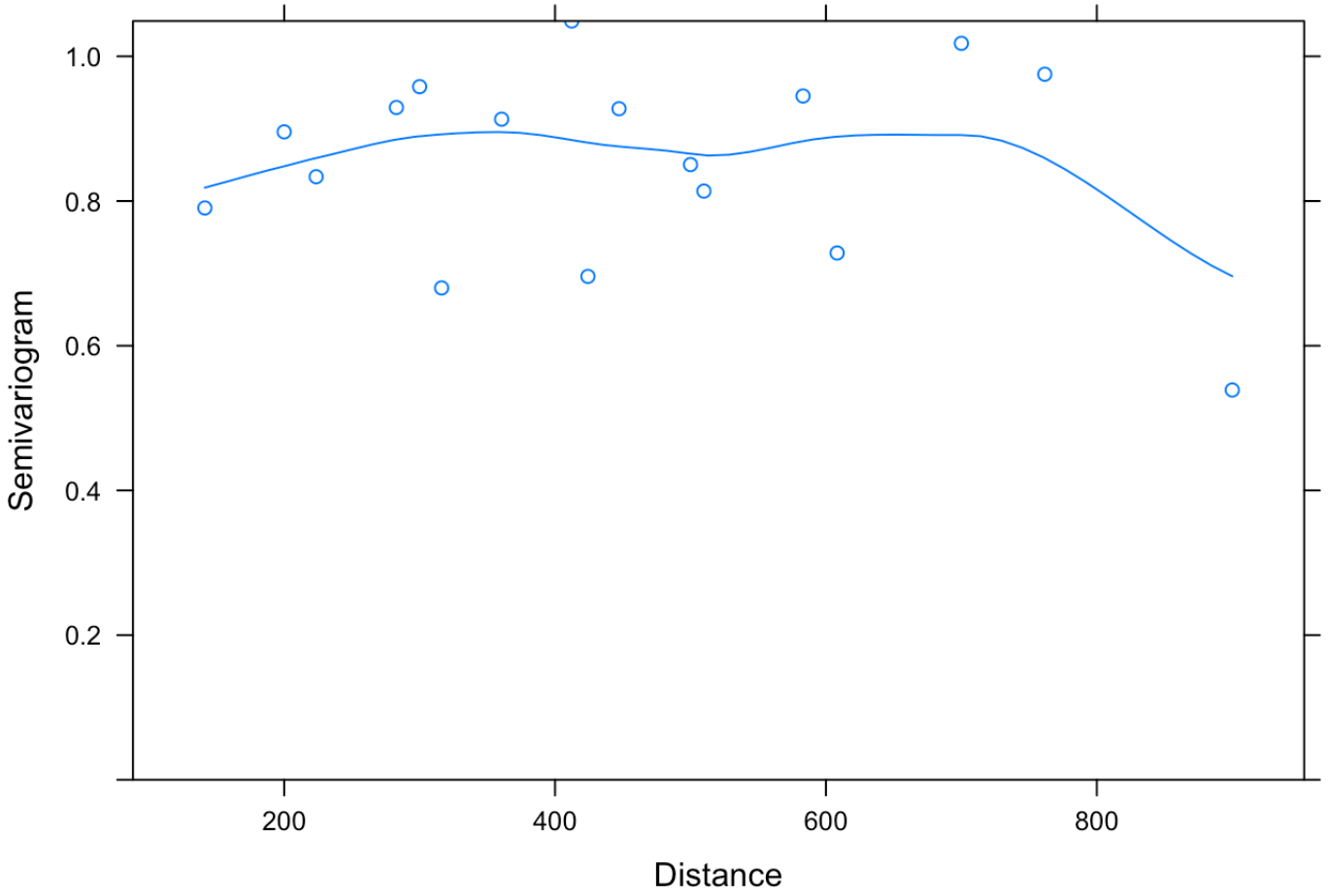



```
#The observed value is larger than the null realizations, indicating that there is a
significant difference between the observed spatial pattern and one due to random cha
nce.
```

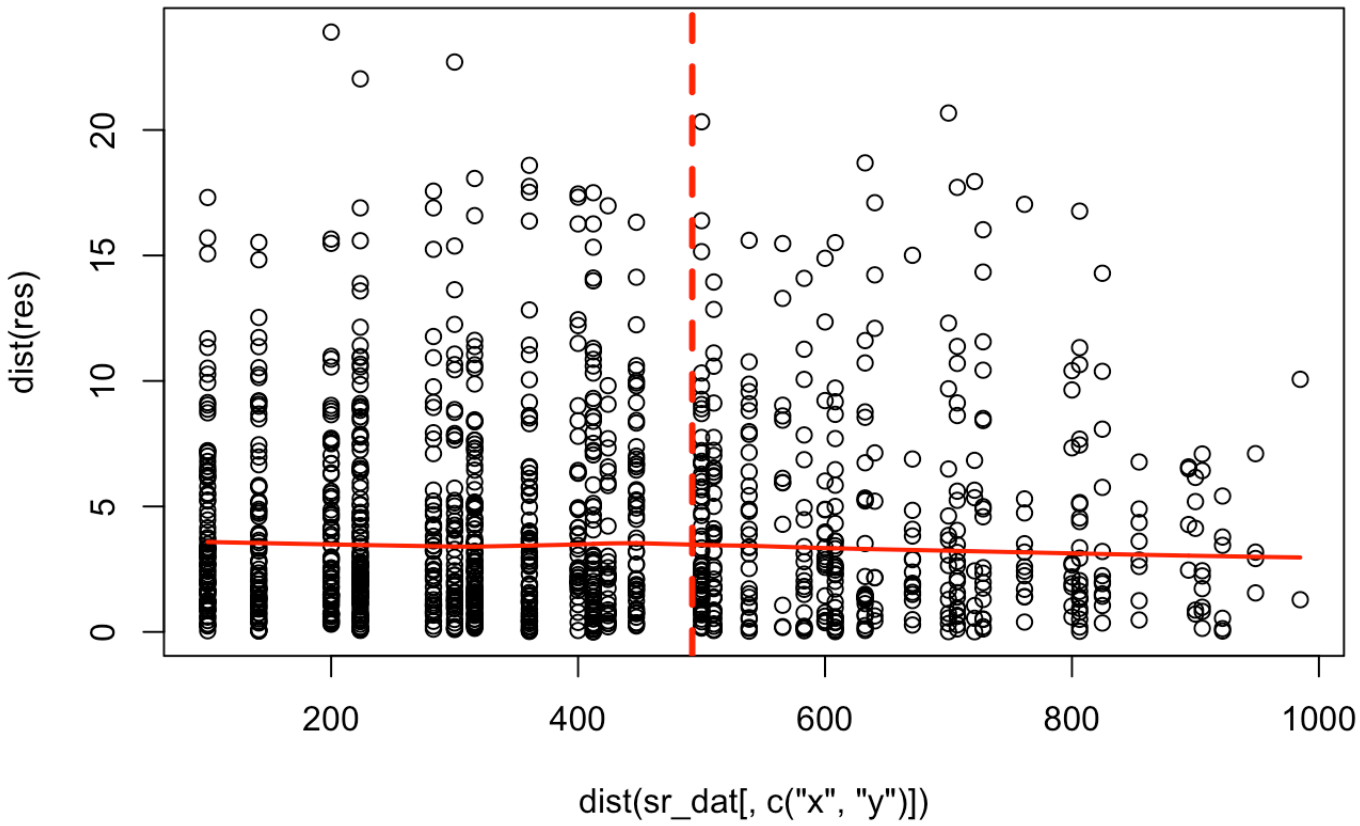
```
#Question 2. Build two generalized linear models...

sp_ids <- c("Cordia.lasiocalyx", "Hirtella.triandra",
            "Picramnia.latifolia", "Quassia.amara",
            "Tabernaemontana.arborea", "Trattinnickia.aspera",
            "Xylopia.macrantha")

sr_dat <- data.frame(sr, BCI, BCI_xy)

#Generalized linear model with all predictor variables...

abu_allpredictors <- gls(Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra +
Picramnia.latifolia + Quassia.amara + Tabernaemontana.arborea + Trattinnickia.aspera
+ Xylopia.macrantha, data=sr_dat)
summary(abu_allpredictors)
```

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra +      Picramn
ia.latifolia + Quassia.amara + Tabernaemontana.arborea +      Trattinnickia.aspera +
Xylopia.macrantha
##   Data: sr_dat
##        AIC      BIC    logLik
##   307.1163 322.7554 -144.5582
##
## Coefficients:
##                             Value Std.Error   t-value p-value
## (Intercept)             -1.051752 2.1175346 -0.496687  0.6220
## Cordia.lasiocalyx        0.428920 0.2039316  2.103255  0.0415
## Hirtella.triandra        0.122279 0.0802638  1.523462  0.1351
## Picramnia.latifolia      0.662259 0.6358905  1.041468  0.3036
## Quassia.amara            4.085661 2.2842770  1.788602  0.0809
## Tabernaemontana.arborea -0.249725 0.1491192 -1.674667  0.1014
## Trattinnickia.aspera     1.349323 0.7147412  1.887848  0.0660
## Xylopia.macrantha        0.548832 0.1468772  3.736672  0.0006
##
##  Correlation:
##                         (Intr) Crd.ls Hrtll. Pcrmn. Qss.mr Tbrnm. Trttn.
## Cordia.lasiocalyx       -0.618
## Hirtella.triandra       -0.212 -0.354
## Picramnia.latifolia      0.025 -0.019 -0.381
## Quassia.amara            0.163 -0.378  0.307 -0.302
## Tabernaemontana.arborea -0.708  0.245  0.163 -0.113  0.148
## Trattinnickia.aspera    -0.139  0.187 -0.311  0.308 -0.708 -0.144
## Xylopia.macrantha       -0.140 -0.125  0.156 -0.463  0.314  0.279 -0.294
##
## Standardized residuals:
##         Min          Q1         Med          Q3         Max
## -1.87708765 -0.42701500 -0.04032793  0.23615609  3.38768871
##
## Residual standard error: 4.539713
## Degrees of freedom: 50 total; 42 residual
```

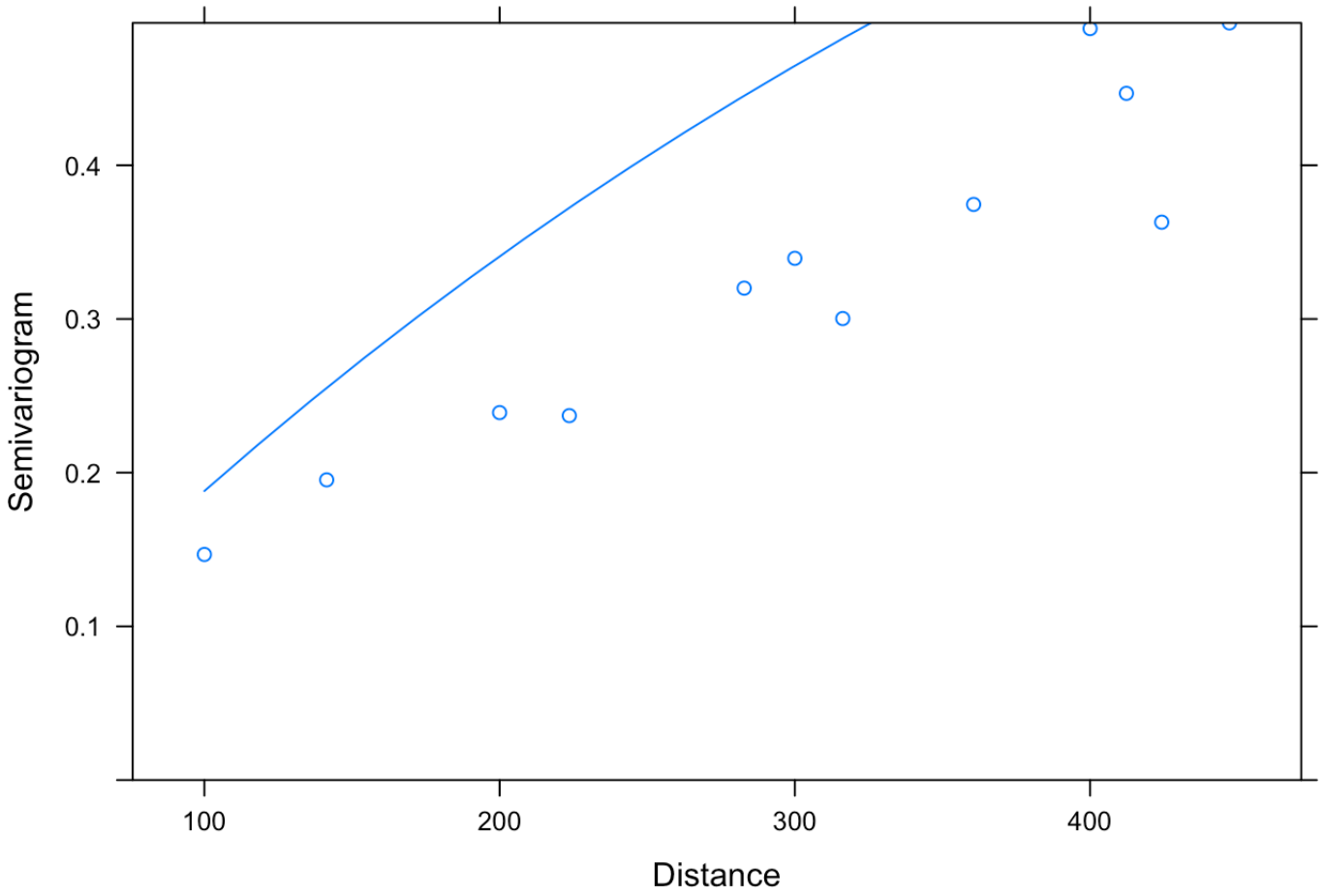
```
plot(Variogram(abu_allpredictors, form= ~ x + y))
```



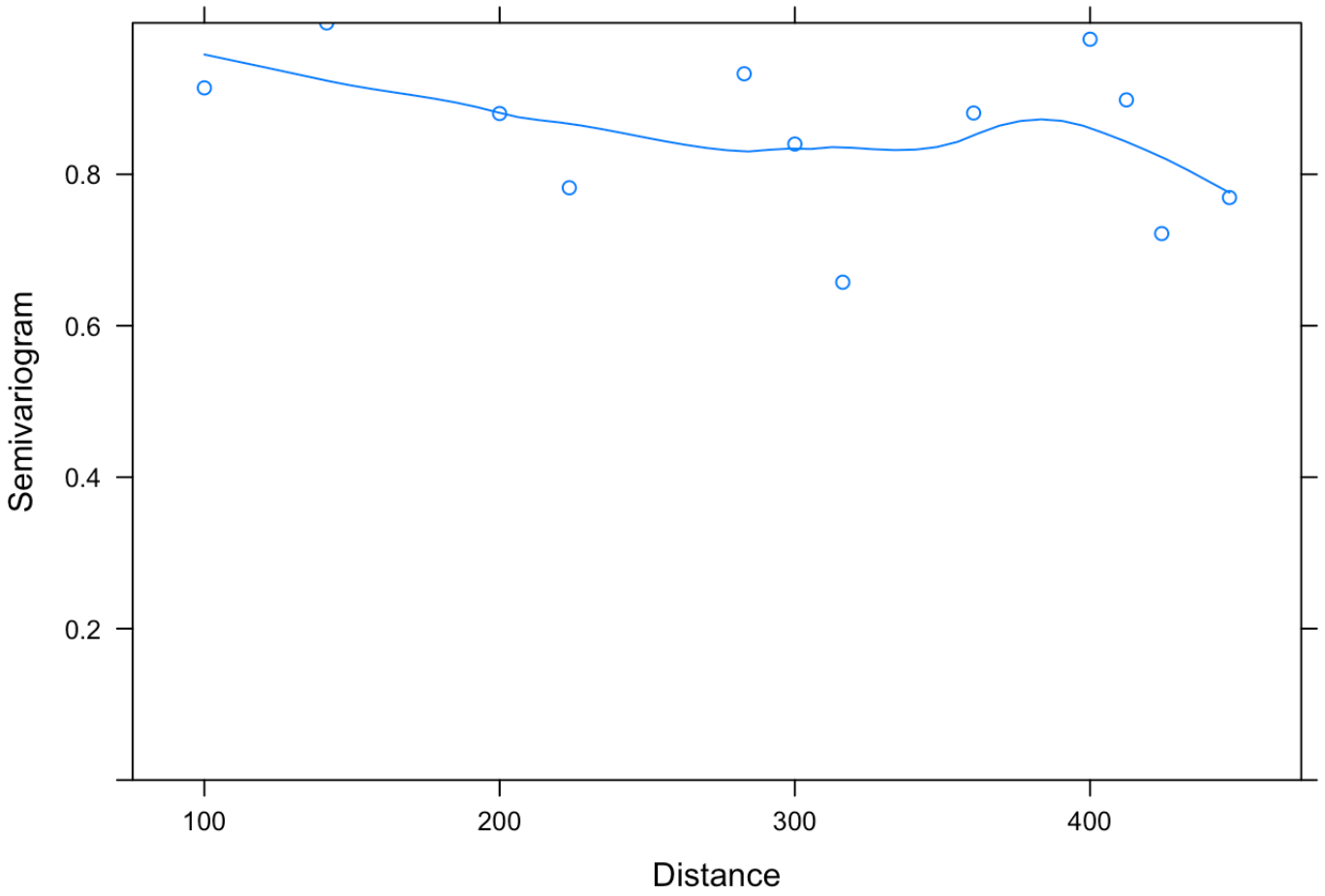

```
res <- residuals(abu_allpredictors)
plot(dist(sr_dat[, c('x', 'y')]), dist(res))
lines(lowess(dist(sr_dat[, c('x', 'y')]), dist(res)), col='red', lwd=2)
abline(v = max_dist, col='red', lwd=3, lty=2)
```



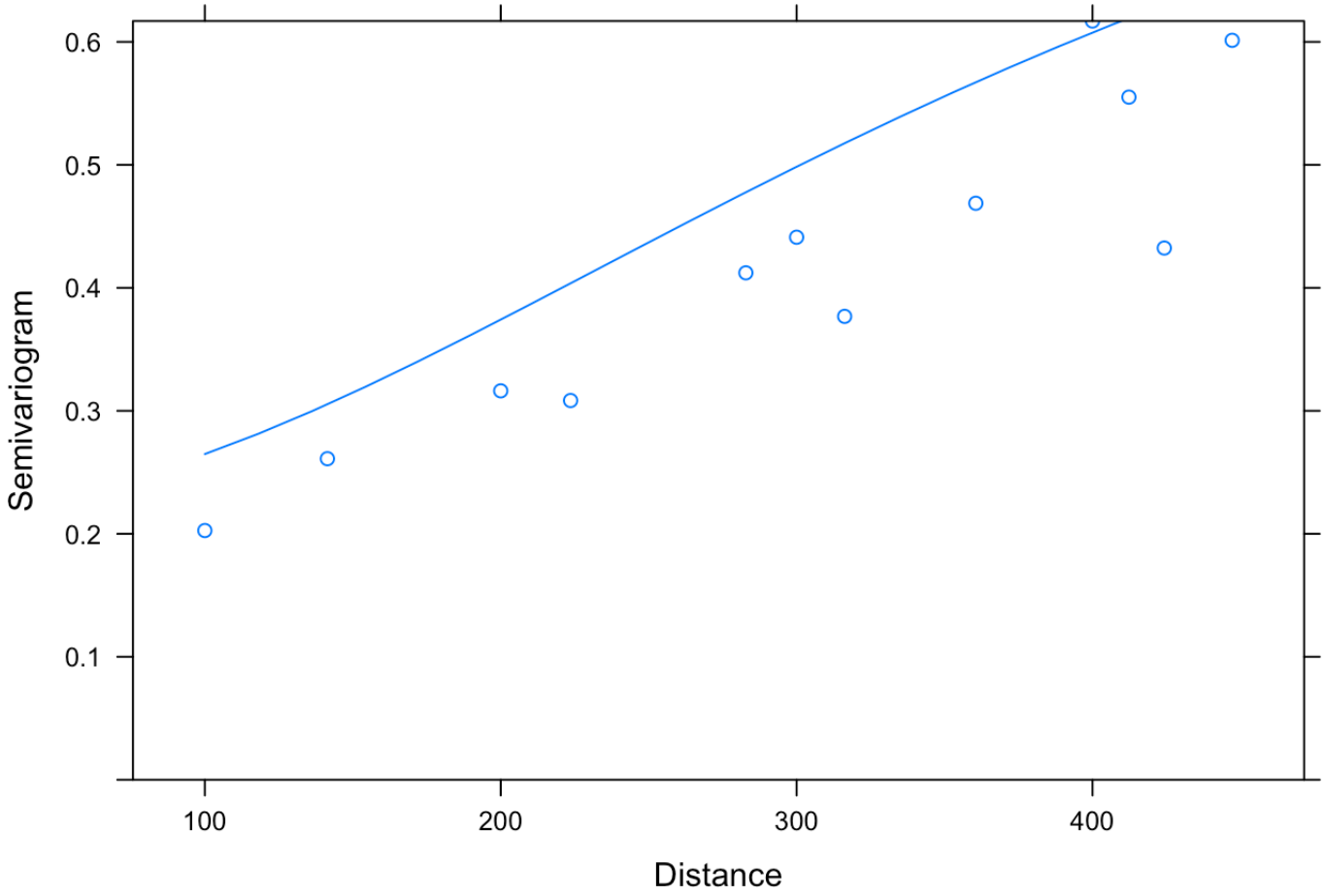

```
abu_all_exp <- update(abu_allpredictors, corr=corExp(form=~x + y))
plot(Variogram(abu_all_exp, maxDist = max_dist))
```



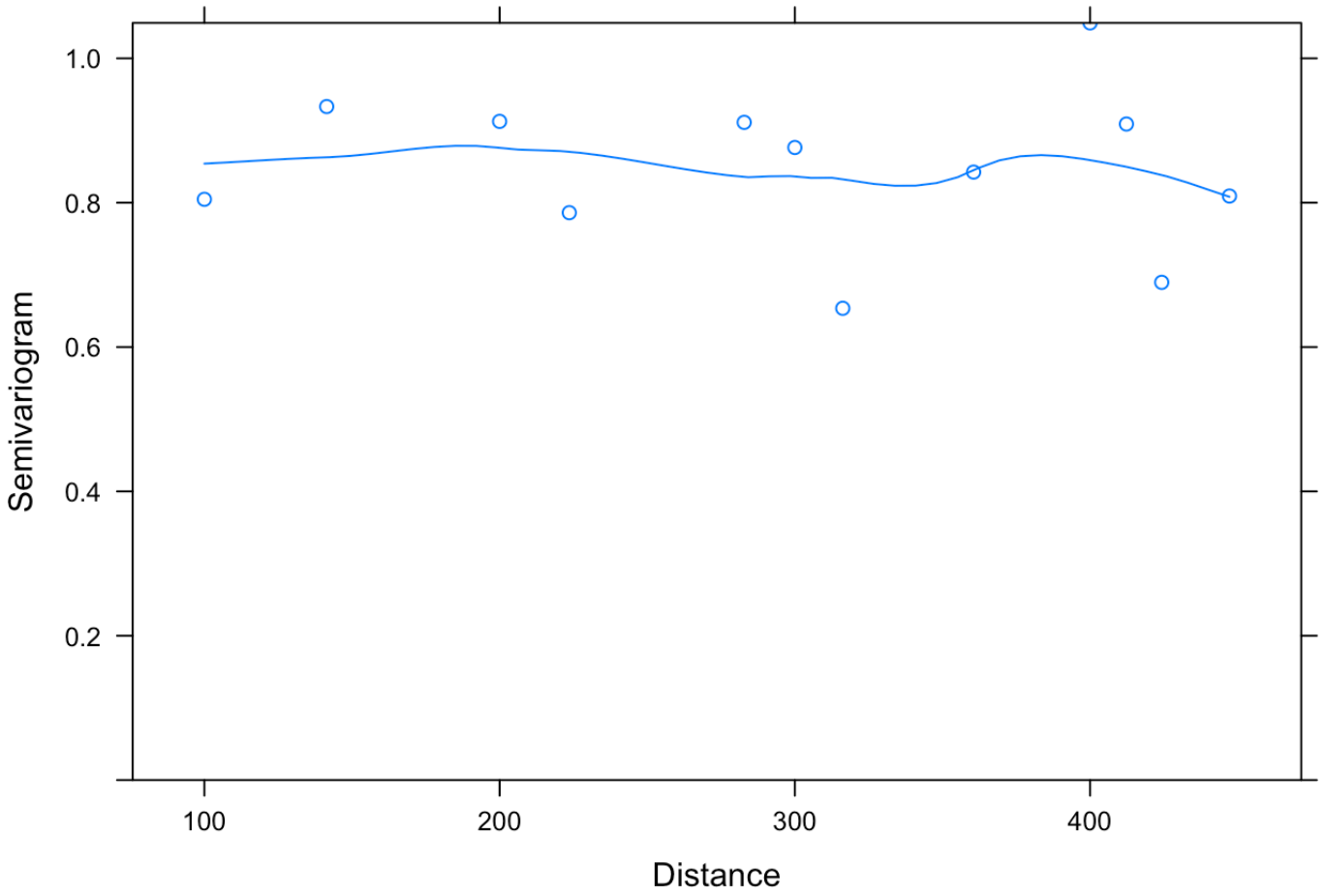

```
plot(Variogram(abu_all_exp, resType='normalized', maxDist = max_dist))
```




```
abu_all_rat_nug <- update(abu_allpredictors, corr=corRatio(form=~x + y, nugget=T))

plot(Variogram(abu_all_rat_nug, maxDist = max_dist))
```




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




```
anova(abu_allpredictors, abu_all_exp, abu_all_rat_nug, test=F)
```

```
##                   Model df      AIC      BIC    logLik
## abu_allpredictors     1  9 307.1163 322.7554 -144.5582
## abu_all_exp           2 10 301.6062 318.9829 -140.8031
## abu_all_rat_nug       3 11 303.1486 322.2630 -140.5743
```

```
summary(abu_allpredictors)
```

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra +      Picramn
ia.latifolia + Quassia.amara + Tabernaemontana.arborea +      Trattinnickia.aspera +
Xylopia.macrantha
##   Data: sr_dat
##        AIC      BIC    logLik
##   307.1163 322.7554 -144.5582
##
## Coefficients:
##                             Value Std.Error   t-value p-value
## (Intercept)             -1.051752 2.1175346 -0.496687  0.6220
## Cordia.lasiocalyx        0.428920 0.2039316  2.103255  0.0415
## Hirtella.triandra        0.122279 0.0802638  1.523462  0.1351
## Picramnia.latifolia      0.662259 0.6358905  1.041468  0.3036
## Quassia.amara            4.085661 2.2842770  1.788602  0.0809
## Tabernaemontana.arborea -0.249725 0.1491192 -1.674667  0.1014
## Trattinnickia.aspera     1.349323 0.7147412  1.887848  0.0660
## Xylopia.macrantha        0.548832 0.1468772  3.736672  0.0006
##
##  Correlation:
##                         (Intr) Crd.ls Hrtll. Pcrmn. Qss.mr Tbrnm. Trttn.
## Cordia.lasiocalyx       -0.618
## Hirtella.triandra       -0.212 -0.354
## Picramnia.latifolia      0.025 -0.019 -0.381
## Quassia.amara            0.163 -0.378  0.307 -0.302
## Tabernaemontana.arborea -0.708  0.245  0.163 -0.113  0.148
## Trattinnickia.aspera    -0.139  0.187 -0.311  0.308 -0.708 -0.144
## Xylopia.macrantha       -0.140 -0.125  0.156 -0.463  0.314  0.279 -0.294
##
## Standardized residuals:
##         Min          Q1         Med          Q3         Max
## -1.87708765 -0.42701500 -0.04032793  0.23615609  3.38768871
##
## Residual standard error: 4.539713
## Degrees of freedom: 50 total; 42 residual
```

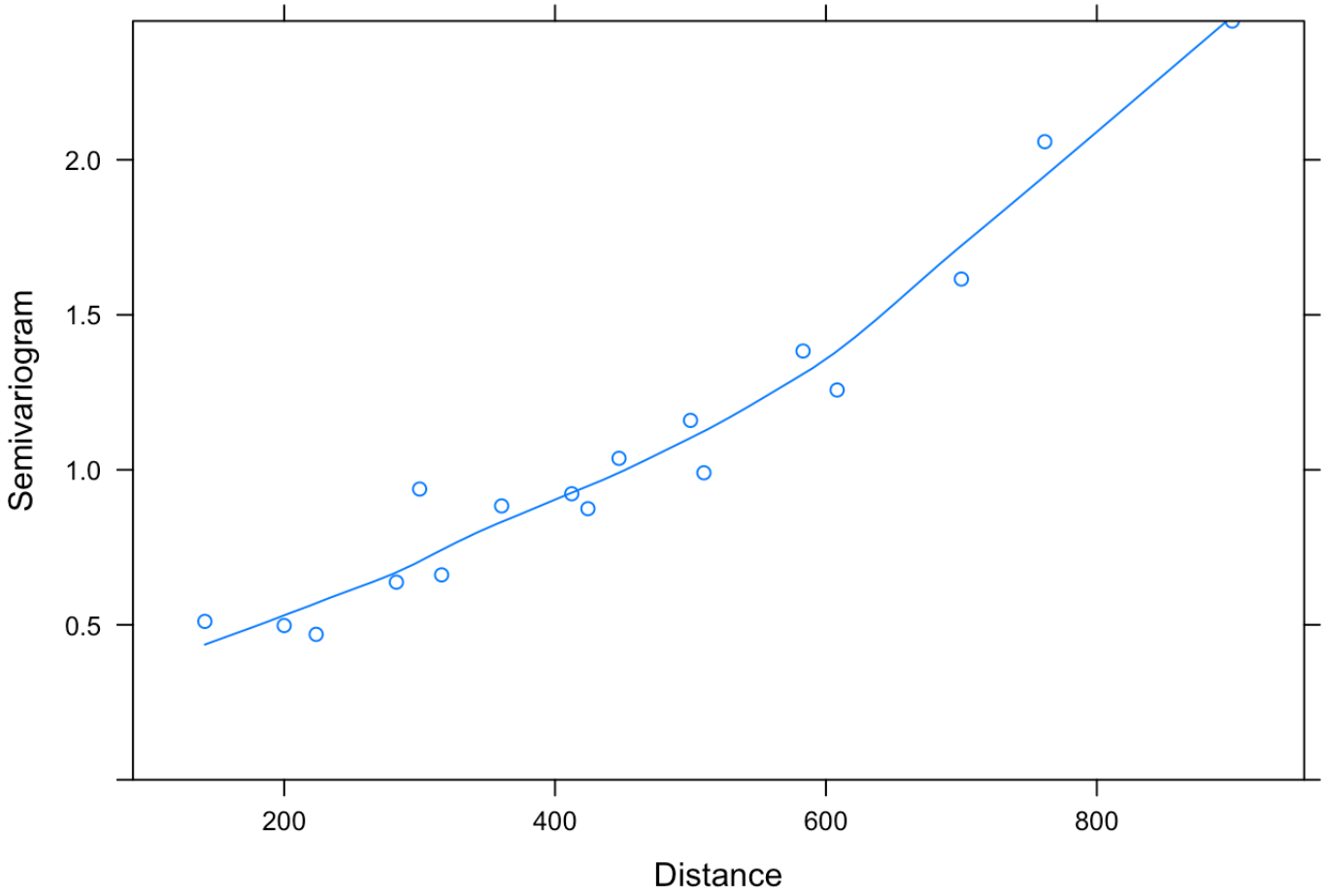
```
summary(abu_all_rat_nug)
```

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra +      Picramn
ia.latifolia + Quassia.amara + Tabernaemontana.arborea +      Trattinnickia.aspera +
Xylopia.macrantha
##   Data: sr_dat
##        AIC     BIC    logLik
##   303.1486 322.263 -140.5743
##
## Correlation Structure: Rational quadratic spatial correlation
##  Formula: ~x + y
##  Parameter estimate(s):
##       range      nugget
## 402.2077831   0.2194023
##
## Coefficients:
##                            Value Std.Error   t-value p-value
## (Intercept)             2.0306920  5.171732 0.3926522  0.6966
## Cordia.lasiocalyx       0.1508099  0.194940 0.7736210  0.4435
## Hirtella.triandra       0.0076692  0.091987 0.0833720  0.9340
## Picramnia.latifolia     0.2509289  0.539635 0.4649976  0.6443
## Quassia.amara           1.5049423  1.960799 0.7675147  0.4471
## Tabernaemontana.arborea 0.0322219  0.142012 0.2268964  0.8216
## Trattinnickia.aspera    1.7698936  0.583930 3.0310015  0.0042
## Xylopia.macrantha       0.4058061  0.161181 2.5177087  0.0157
##
##  Correlation:
##                         (Intr) Crd.ls Hrtll. Pcrmn. Qss.mr Tbrnm. Trttn.
## Cordia.lasiocalyx       -0.273
## Hirtella.triandra       -0.272 -0.122
## Picramnia.latifolia      0.017  0.038 -0.387
## Quassia.amara           -0.039 -0.304  0.337 -0.213
## Tabernaemontana.arborea -0.242 -0.029  0.166 -0.201  0.106
## Trattinnickia.aspera    -0.090  0.163 -0.272  0.271 -0.646 -0.036
## Xylopia.macrantha       -0.095 -0.055 -0.073 -0.035  0.295  0.143 -0.164
##
## Standardized residuals:
##        Min         Q1        Med         Q3        Max
## -1.0645964 -0.5625847 -0.3564599  0.2563989  2.6599508
##
## Residual standard error: 7.348772
## Degrees of freedom: 50 total; 42 residual
```

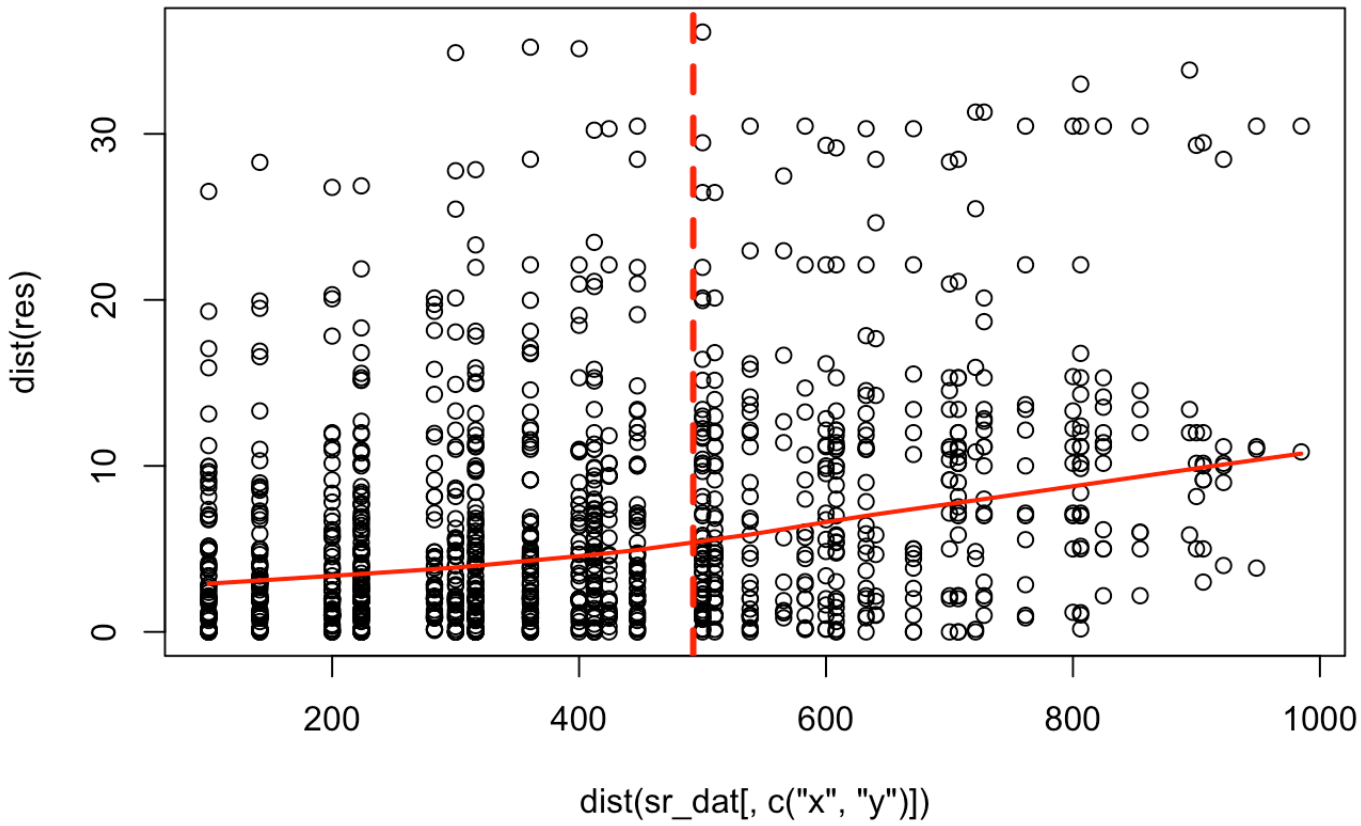
```
#Generalized linear model with single predictor variable...

abu_singlepredictor <- gls(Drypetes.standleyi ~ Xylopia.macrantha, data=sr_dat)
summary(abu_singlepredictor)
```

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Xylopia.macrantha
##   Data: sr_dat
##        AIC      BIC    logLik
##   338.2919 343.9055 -166.1459
##
## Coefficients:
##                       Value Std.Error  t-value p-value
## (Intercept)       3.285252 1.0990108 2.989281  0.0044
## Xylopia.macrantha 0.844318 0.1804326 4.679407  0.0000
##
##  Correlation:
##                   (Intr)
## Xylopia.macrantha -0.47
##
## Standardized residuals:
##        Min         Q1        Med         Q3        Max
## -1.3044324 -0.4788137 -0.3103771  0.1041720  3.9616489
##
## Residual standard error: 6.861233
## Degrees of freedom: 50 total; 48 residual
```

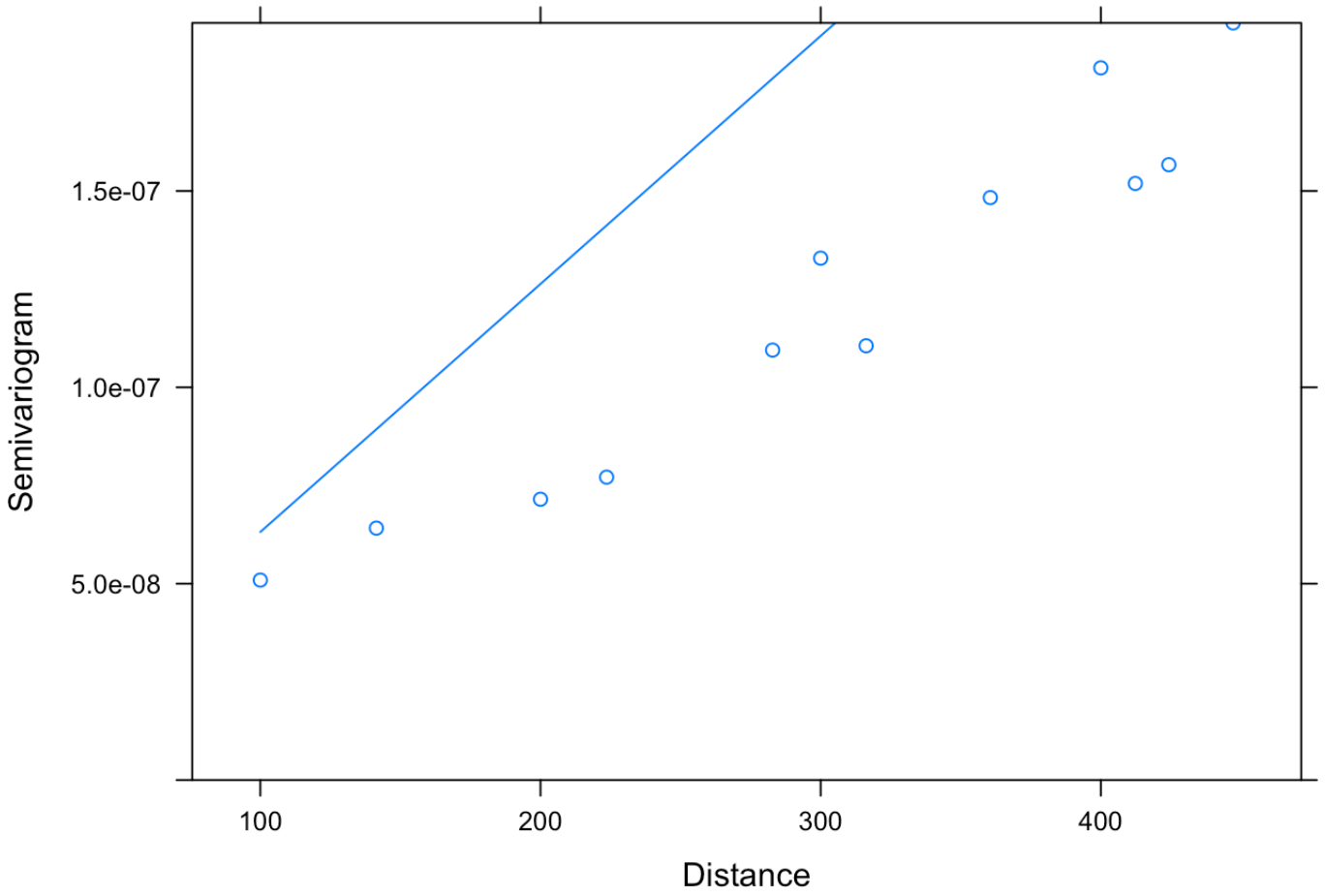
```
plot(Variogram(abu_singlepredictor, form= ~ x + y))
```



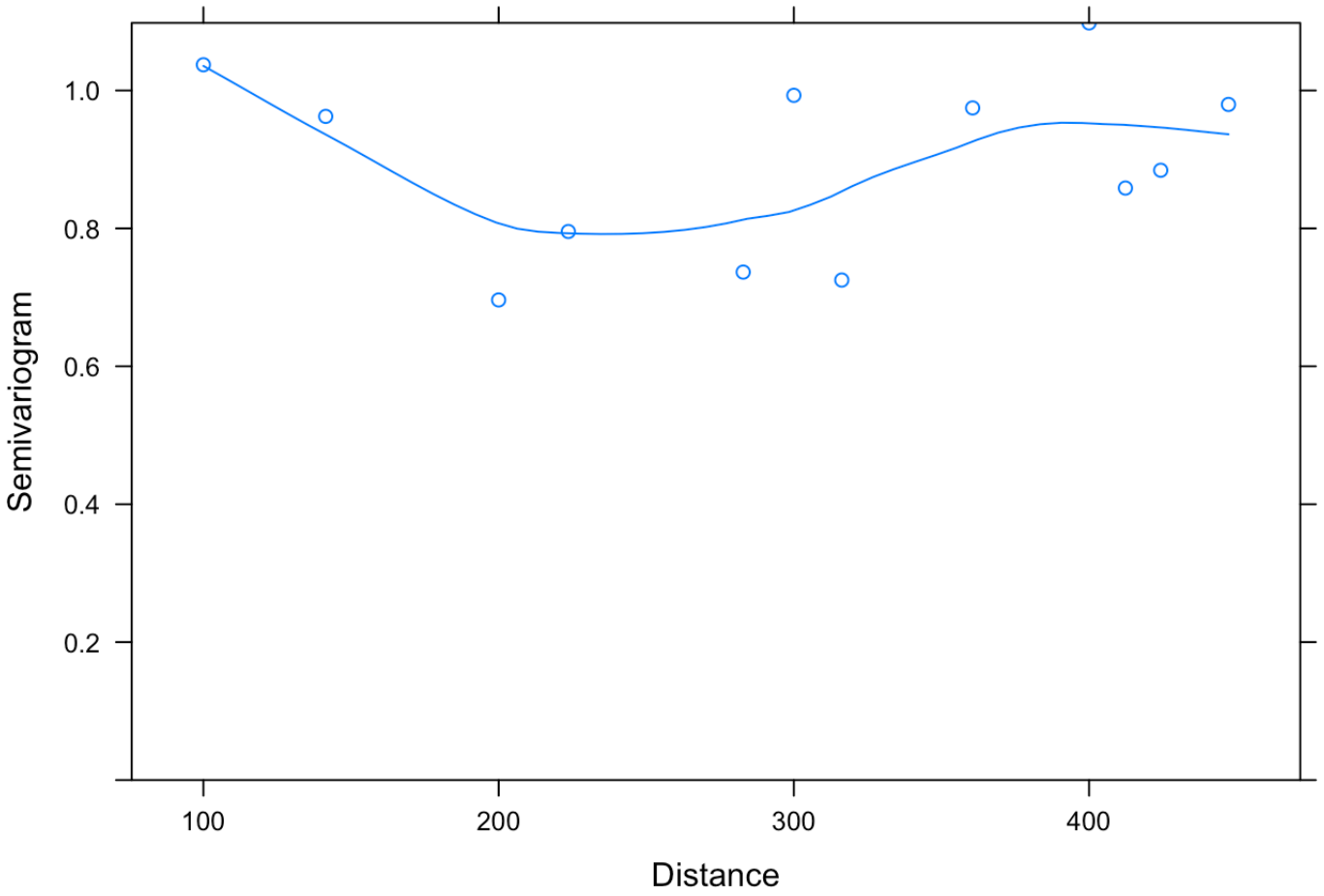

```
res <- residuals(abu_singlepredictor)
plot(dist(sr_dat[, c('x', 'y')]), dist(res))
lines(lowess(dist(sr_dat[, c('x', 'y')]), dist(res)), col='red', lwd=2)
abline(v = max_dist, col='red', lwd=3, lty=2)
```



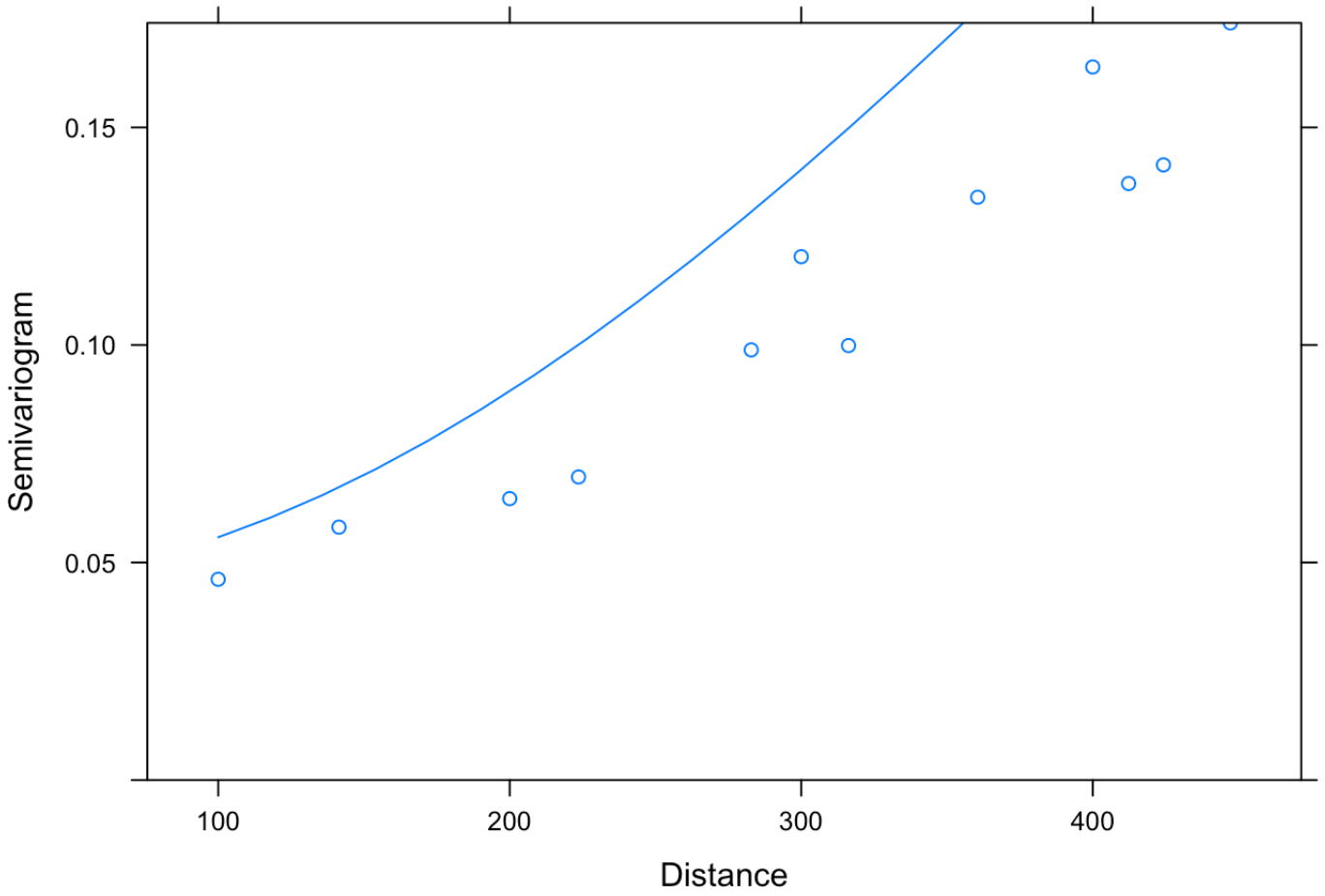

```
abu_single_exp <- update(abu_singlepredictor, corr=corExp(form=~x + y))
plot(Variogram(abu_single_exp, maxDist = max_dist))
```



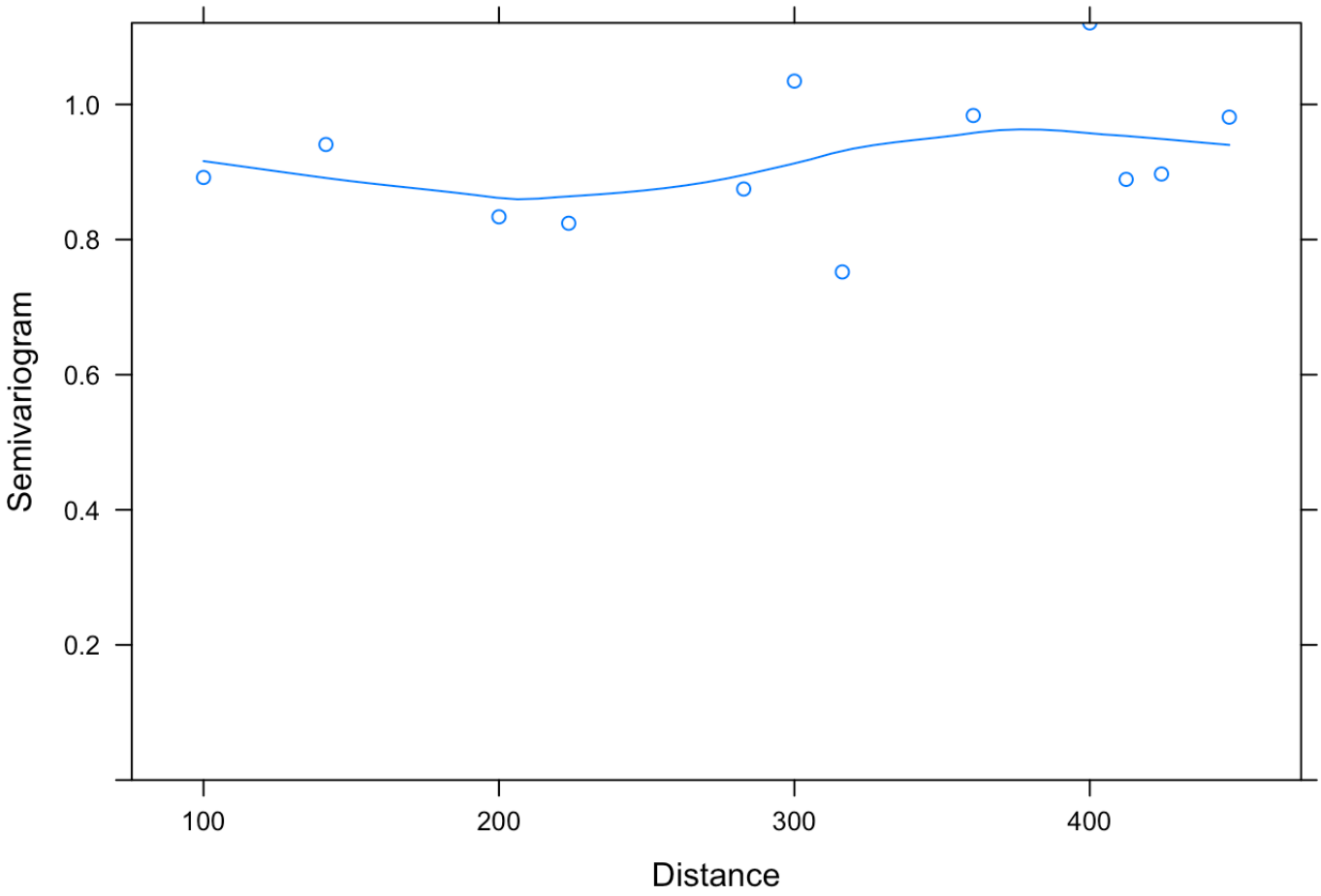

```
plot(Variogram(abu_single_exp, resType='normalized', maxDist = max_dist))
```




```
abu_single_rat_nug <- update(abu_singlepredictor, corr=corRatio(form=~x + y, nugget=T
))

plot(Variogram(abu_single_rat_nug, maxDist = max_dist))
```




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




```
anova(abu_singlepredictor, abu_single_exp, abu_single_rat_nug, test=F)
```

```
##                      Model df      AIC      BIC    logLik
## abu_singlepredictor      1  3 338.2919 343.9055 -166.1459
## abu_single_exp           2  4 308.6325 316.1173 -150.3163
## abu_single_rat_nug       3  5 306.6030 315.9590 -148.3015
```

```
summary(abu_singlepredictor)
```

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Xylopia.macrantha
##   Data: sr_dat
##        AIC      BIC    logLik
##   338.2919 343.9055 -166.1459
##
## Coefficients:
##                      Value Std.Error  t-value p-value
## (Intercept)       3.285252 1.0990108 2.989281  0.0044
## Xylopia.macrantha 0.844318 0.1804326 4.679407  0.0000
##
##  Correlation:
##                   (Intr)
## Xylopia.macrantha -0.47
##
## Standardized residuals:
##        Min         Q1        Med         Q3        Max
## -1.3044324 -0.4788137 -0.3103771  0.1041720  3.9616489
##
## Residual standard error: 6.861233
## Degrees of freedom: 50 total; 48 residual
```

```
summary(abu_single_rat_nug)
```

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Xylopia.macrantha
##   Data: sr_dat
##       AIC     BIC    logLik
##   306.603 315.959 -148.3015
##
## Correlation Structure: Rational quadratic spatial correlation
##  Formula: ~x + y
##  Parameter estimate(s):
##        range       nugget
## 896.58487625   0.04405078
##
## Coefficients:
##                        Value Std.Error   t-value p-value
## (Intercept)       13.882773 15.078391 0.9207065  0.3618
## Xylopia.macrantha  0.298373  0.164721 1.8113836  0.0763
##
##  Correlation:
##                   (Intr)
## Xylopia.macrantha -0.064
##
## Standardized residuals:
##        Min         Q1        Med         Q3        Max
## -0.7964146 -0.7333675 -0.6277160 -0.3900003  1.0116000
##
## Residual standard error: 18.93017
## Degrees of freedom: 50 total; 48 residual
```

##Did including the spatial error term have a large impact on the coefficients of the model?
#Including the spatial error term improved the model fit, and had an impact on the co efficients in the models.

##Did including the spatial error terms significantly improve model fit?
#Comparing the models using the 'anova()' function confirms that including the spatia l error terms significantly improves model fit. Both the exponential and rational qua dratic models have a lower AIC than the GLS with no spatial error.

##Explain why you did or did not observe a difference in the influence of adding the spatial error term between the two models.
#Including the spatial error term influences the models because it takes into account potential relationships between samples that are closer together, for instance. In ot her words, the spatial error term accounts for potential non-independence between sam ples.