Spatial Modeling Homework

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```r
library(vegan)
```

```
## Loading required package: permute

## Loading required package: lattice

## This is vegan 2.3-3
```

```r
data(BCI)
data(BCI.env)

## 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))

#Common Species that i chose: Alseis blackiana
#Rare Species I chose is: Casearia sylvestris



#Subset Species for common and rare species

common <- BCI$Alseis.blackiana

rare <- BCI[ , "Casearia.sylvestris"]


#Histogram shows frequency of trees counts for rare and common species
```
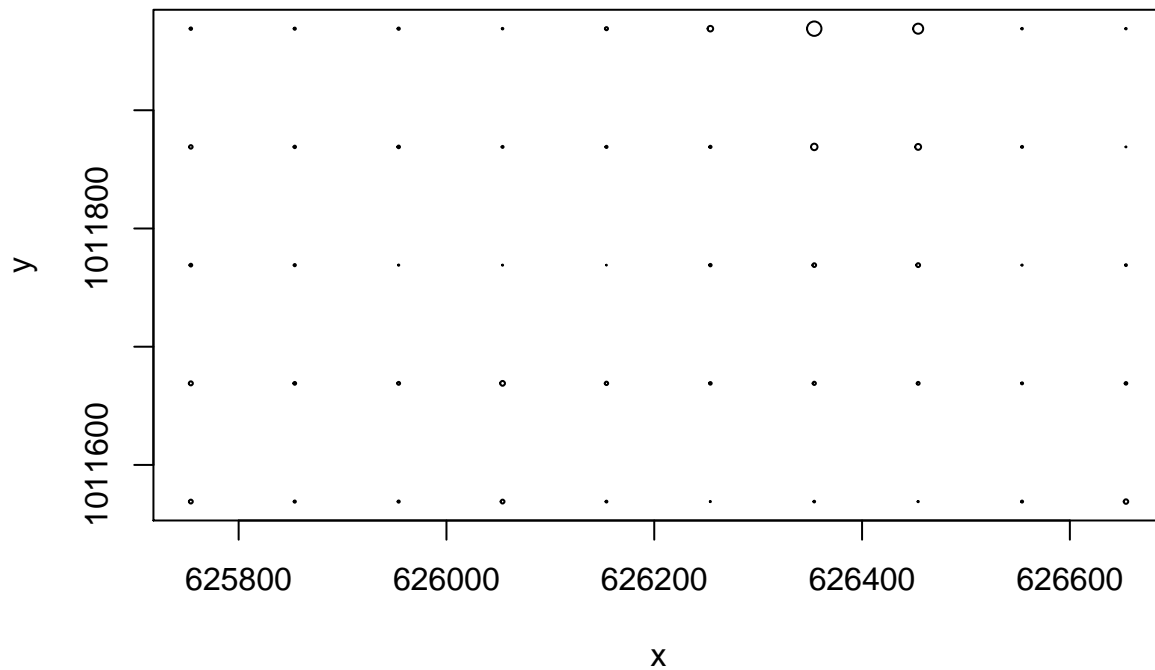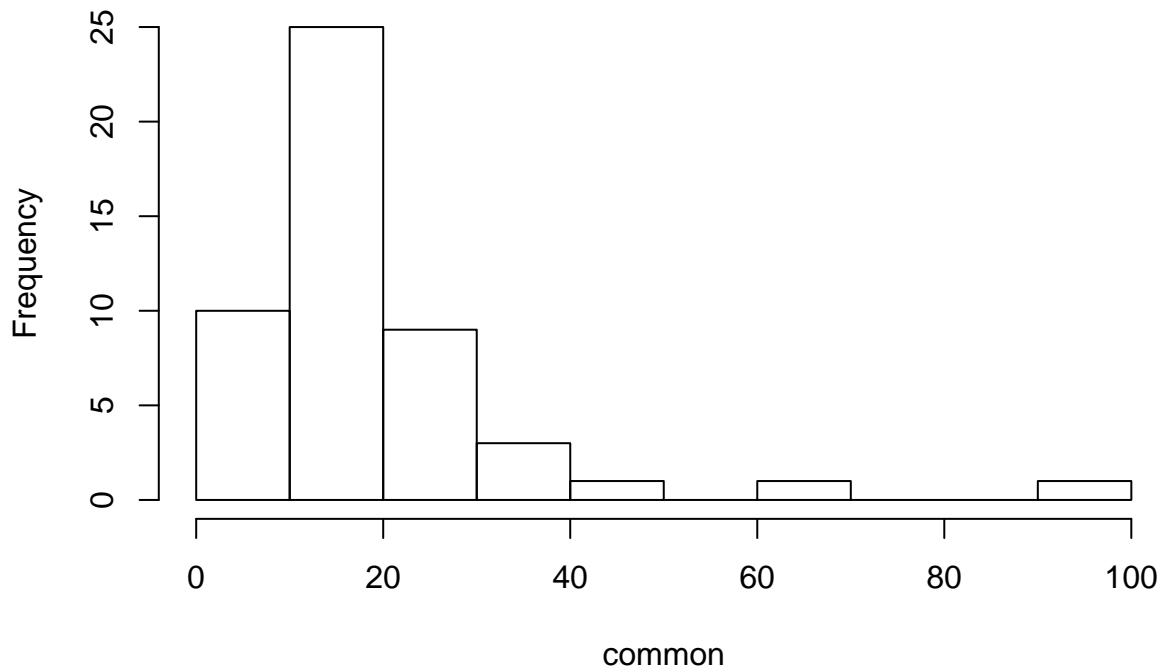
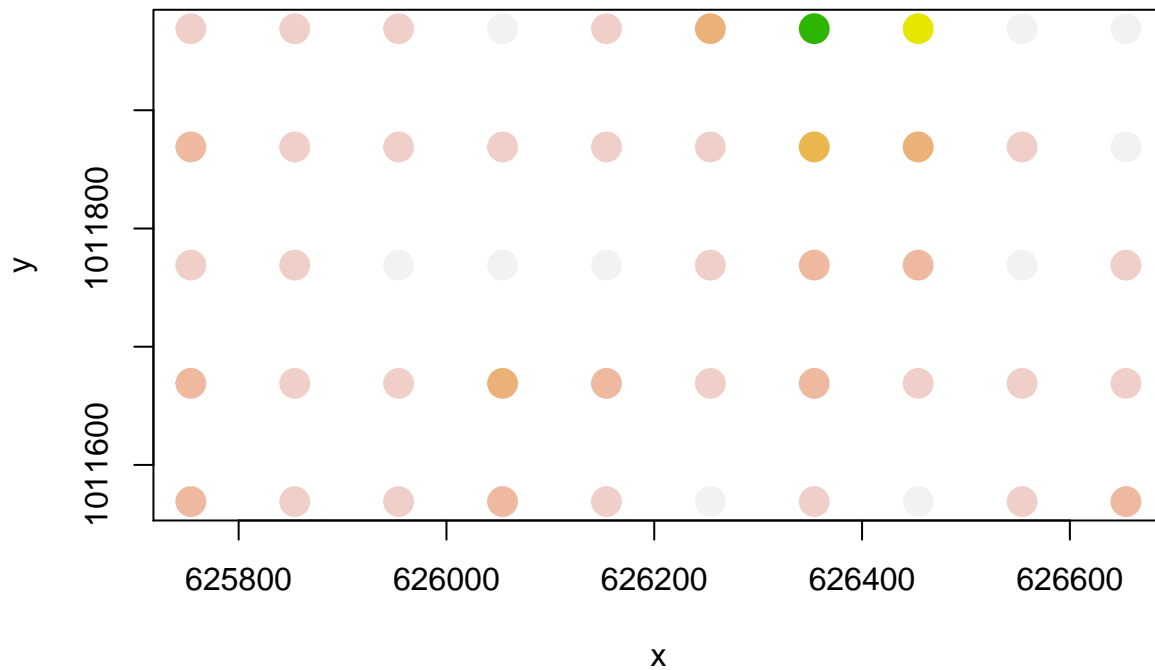Common Species

```r
plot(BCI_xy, cex=common/max(common))
```

```
col_brks = hist(common, plot=T)$breaks
```

Histogram of common


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

```
#These are all mixed together and do not appear to be spatially dependent
#on one another. There is no clear association dependent on space.
# The green and yellow are closer together, and it is
#possible that those points are spatially dependent, but I cannot come to this
#conclusion based on 3 points. For now, I am going to say that this common
#species is not spatially dependent.


common_dist = dist(common)
xy_dist = dist(BCI_xy)

max_dist = max(xy_dist) / 2

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)
```
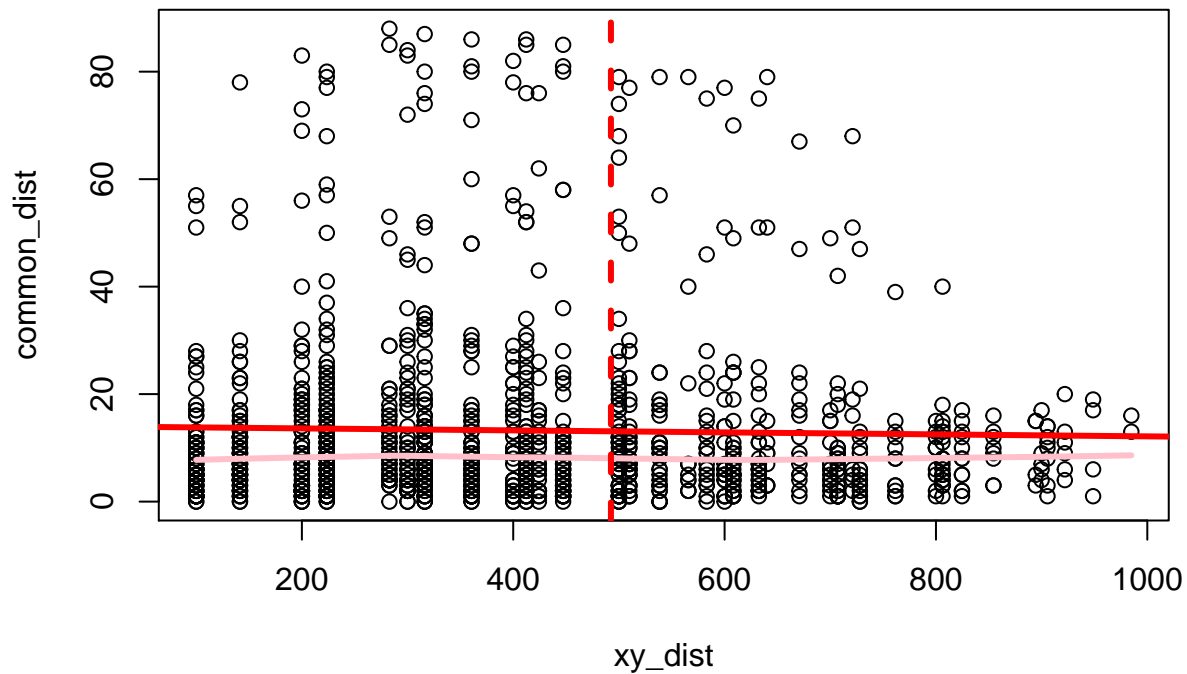
```
#This looks like the the larger xy_dist become, the less distributed they get.
#It appears that the common species have a greater distribution
#when xy_dist is small. We can see a slightly negative slope as well.


#correlation
common_cor = cor(xy_dist, common_dist)
#-0.02348007

#The spearman's rho is saying that one variable is increasing while the
#other variable is decreasing. This confirms my previous statement, but
#this coefficient is a pretty small correlation so the variables vary together,
#but not by much to indicate they are significant.
```
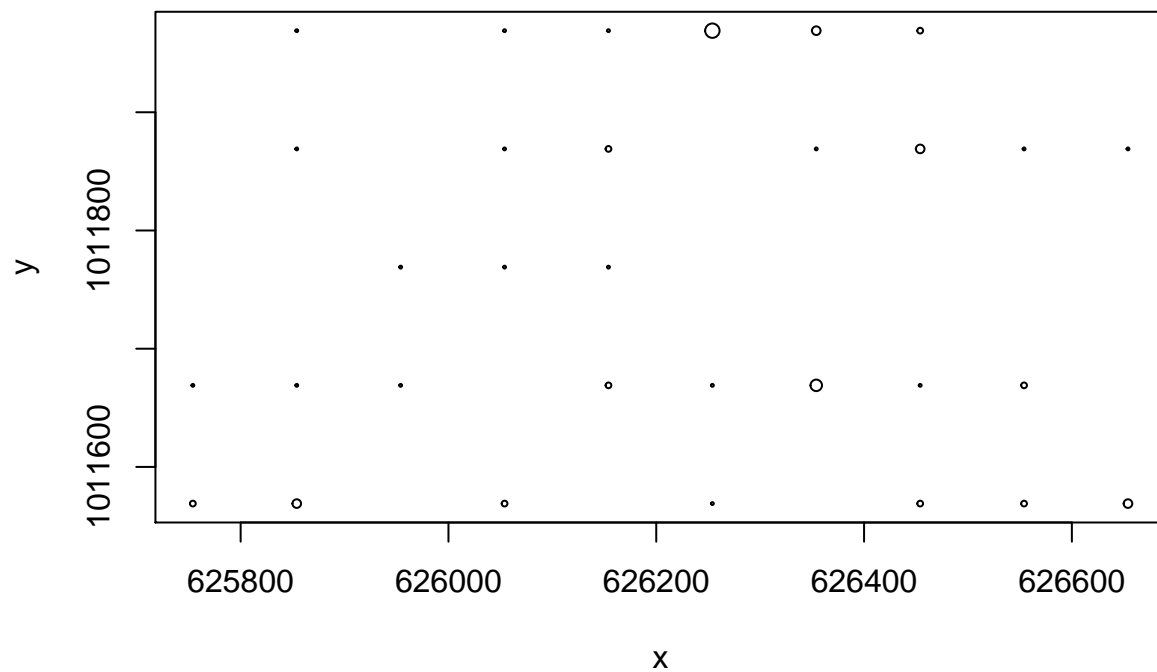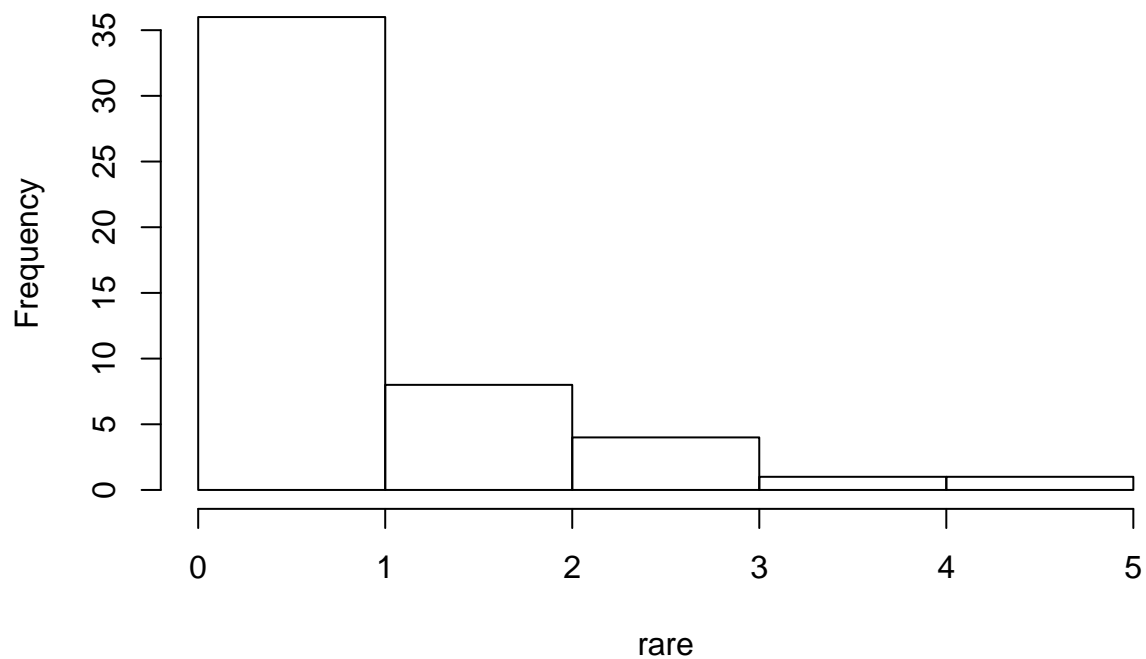
Rare Species
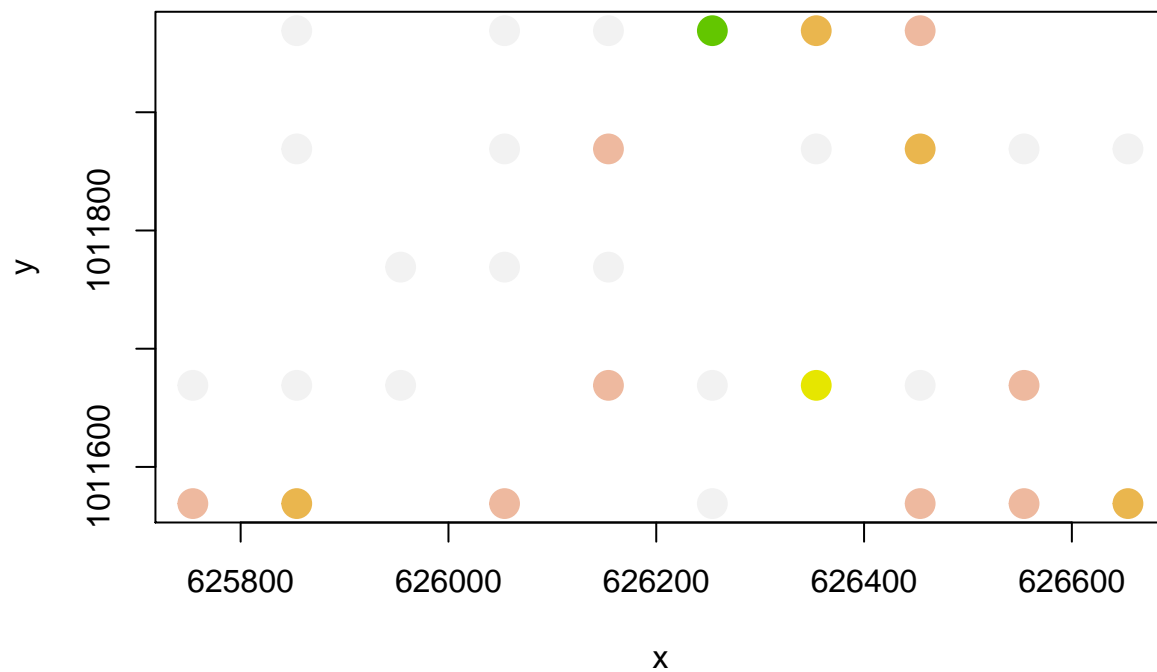
```
#rare

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

```
col_brks = hist(rare, plot=T)$breaks
```

Histogram of rare


```
col_indices = as.numeric(cut(rare, col_brks))
cols = rev(terrain.colors(length(col_brks)))
plot(BCI_xy, cex=2, pch=19, col=cols[col_indices])
```
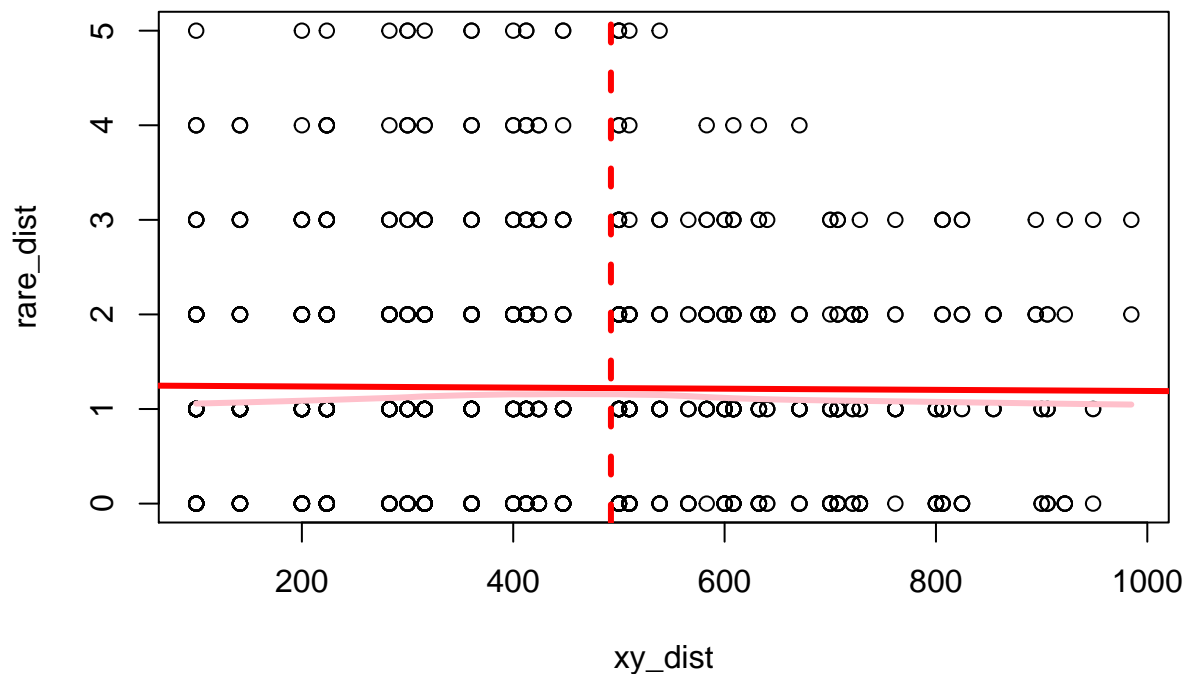
```
#Does not indicate any visual relationship of spatial dependence.

rare_dist = dist(rare)
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)
```

```
#Interpretation:
#It appears that the greater the xy_dist, the closer the points get together.
#Likewise, the lower the xy_distribution, the further apart they are distributed
#from one another. Also, rare distribution at 5 individuals can only be found
#close together and at a lower xy_distribution. Similarily, there is a greater
#abundance in the range of 1-3 at a greater xy_distribution. Again,
#slight negative slope indicating a negative correlation, but one very close to
#0 which indicates no significant relationship.

#compute rare correlation
rare_cor = cor(xy_dist, rare_dist)
#-0.01116346

#This is a very small (negative) corrleation. It is very close to 0 indicating
#no relationship
```

Using the mantel function

```
com = mantel(xy_dist, common_dist)
com
```

```
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = xy_dist, ydis = common_dist)
##
## Mantel statistic r: -0.02348
##       Significance: 0.6
##
## Upper quantiles of permutations (null model):
```

```
##     90%    95%  97.5%    99%
## 0.0857 0.1137 0.1318 0.1513
## Permutation: free
## Number of permutations: 999
```

```
ra= mantel(xy_dist, rare_dist)
ra
```

```
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = xy_dist, ydis = rare_dist)
##
## Mantel statistic r: -0.01116
##       Significance: 0.527
##
## Upper quantiles of permutations (null model):
##     90%    95%  97.5%    99%
## 0.0697 0.0893 0.1052 0.1204
## Permutation: free
## Number of permutations: 999
```

Common

```
boxplot(list(com$perm), horizontal = T, boxwex = 0.5,
        names = c( 'mantel'), xlab='Correlation')
abline(v=common_cor, col='red')
```
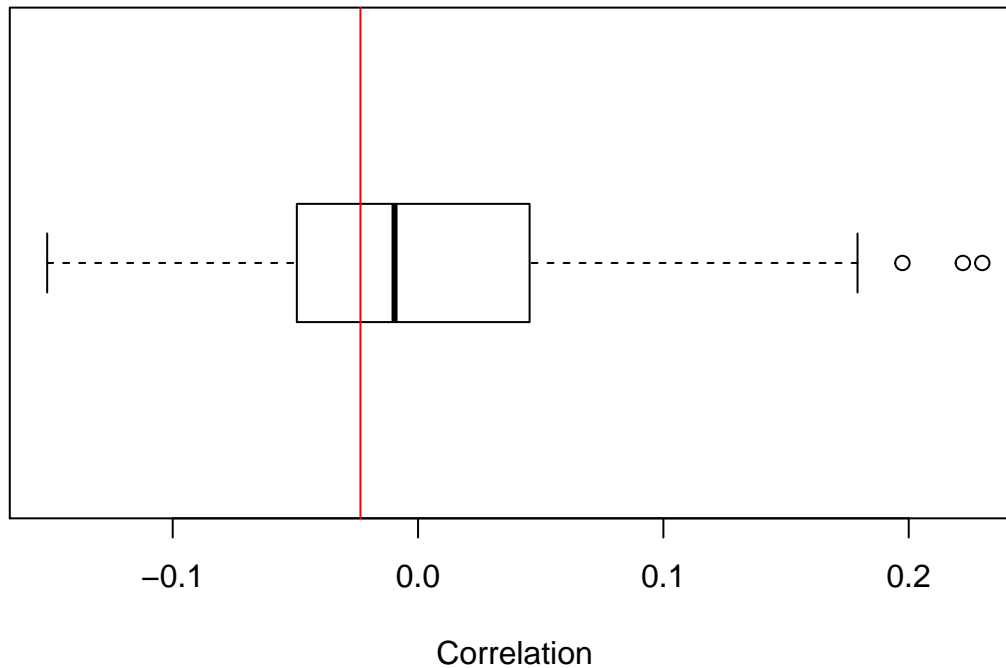

Correlation

```
#For common speices, Alseis blackiana, the observed value is smaller
#than the null realizations, but not significantly smaller. This indicates
#no significant relationship between spatial distance and the abundance
#of individuals for the common species.
```

Rare

```
boxplot(list(ra$perm), horizontal = T, boxwex = 0.5,
        names = c( 'mantel'), xlab='Correlation')
abline(v=rare_cor, col='red')
```
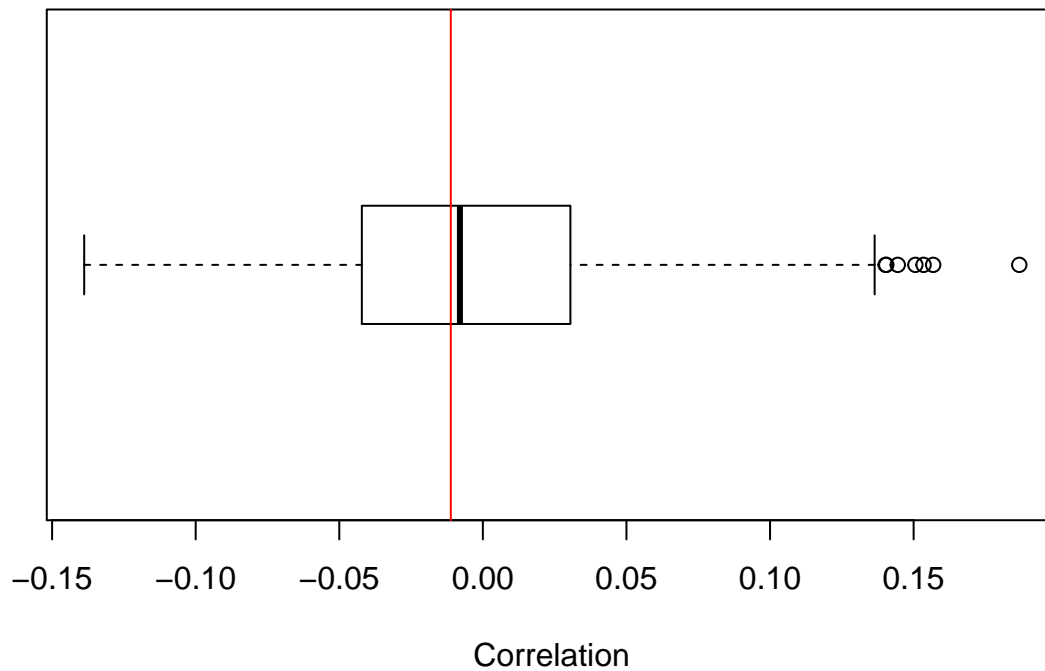


```
#For rare species, Casearia sylvestris, the observed value is
#slightly smaller than the null realizations, indicating that there is not a #significant difference fr
#spatial distance and the difference in number of individuals for the rare
#species.
```

2. Model 1: only include a single species as a predictor variable

```
library(permute)
library(lattice)
library(vegan)
library(nlme)

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

#This is the single predictor species that I chose
```

```
sp_predictor <- BCI[ , "Cordia.lasiocalyx"]
sp_response <- BCI$Drypetes.standleyi

#GLS Model

single_sp_mod <- data.frame(sp_response, sp_predictor, BCI_xy)

mod1_lm = gls(sp_response ~ sp_predictor, data=single_sp_mod)


#Plotting and examining the residuals

par(mfrow=c(1,1))
plot(Variogram(mod1_lm, form= ~ x + y))
```
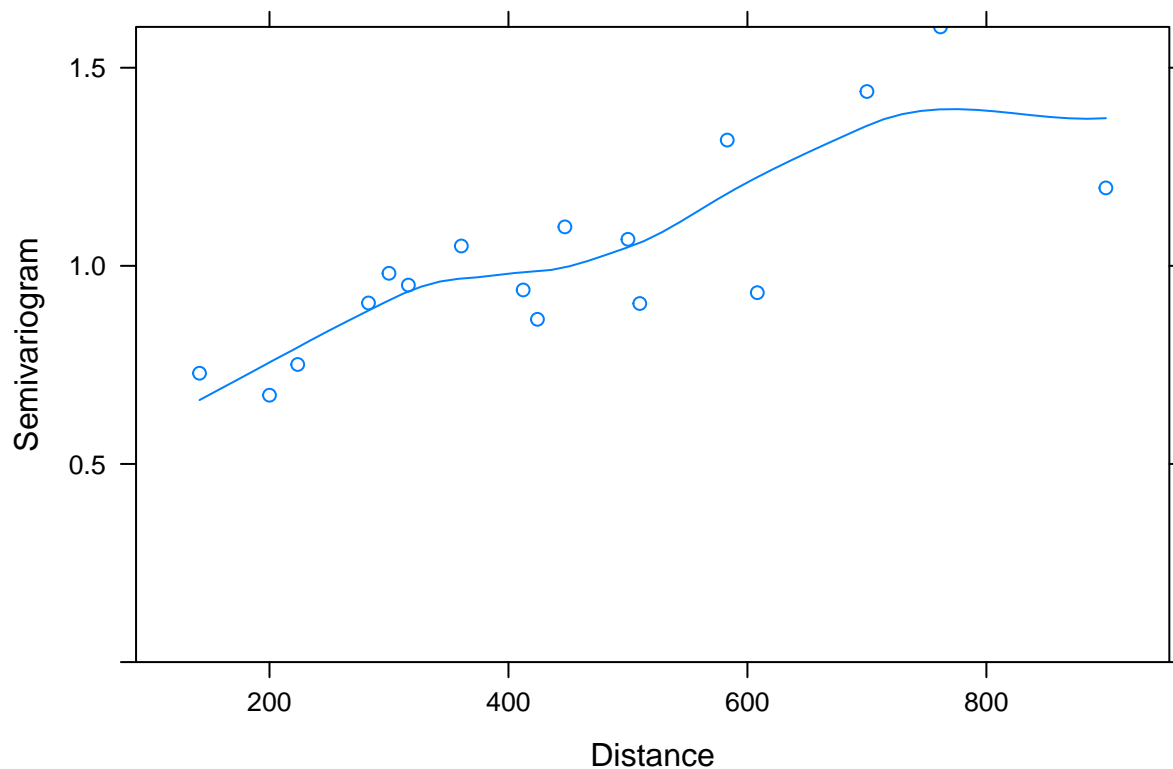


```
#This isn't terrible, and appears to fit our data well. Our
#residuals appear to be getting larger as distance increases.
#We can see that the variogram increases with distance, illustrating
#that there is a spatial correlation. There also appears to be a nugget.
#(see nugget GLS below)

res = residuals(mod1_lm)
plot(dist(single_sp_mod [, c('x', 'y')]), dist(res))
lines(lowess(dist(single_sp_mod [, c('x', 'y')]), dist(res)), col='red', lwd=2)
abline(v = max_dist, col='red', lwd=3, lty=2)
```
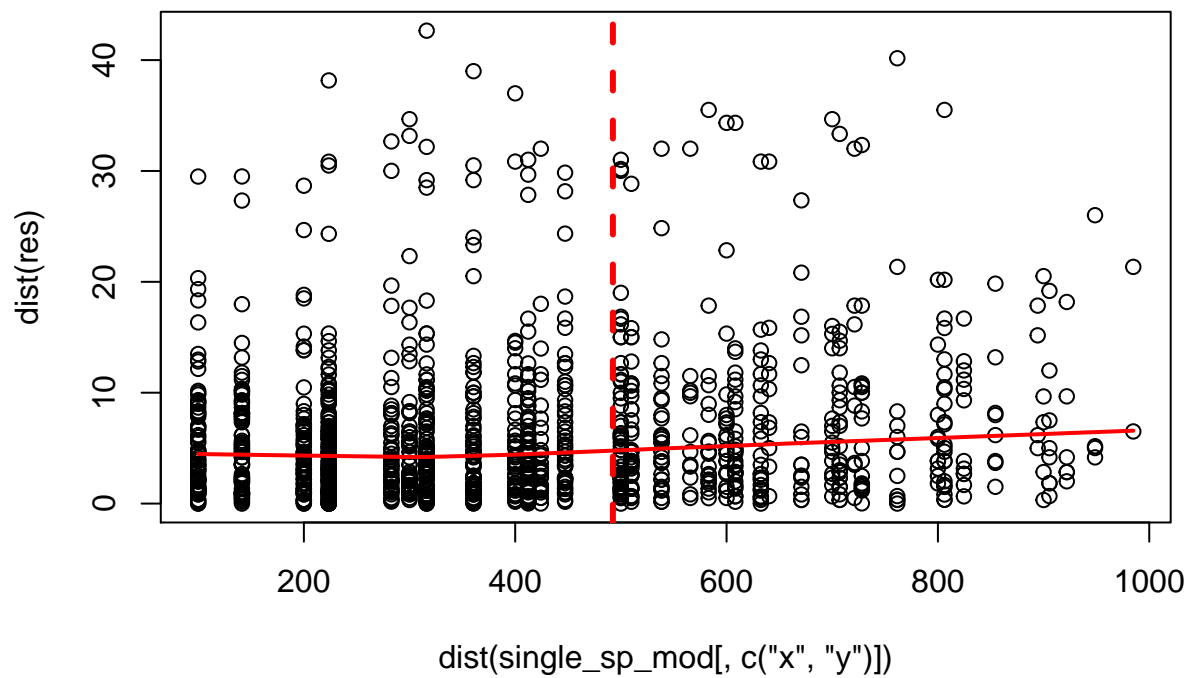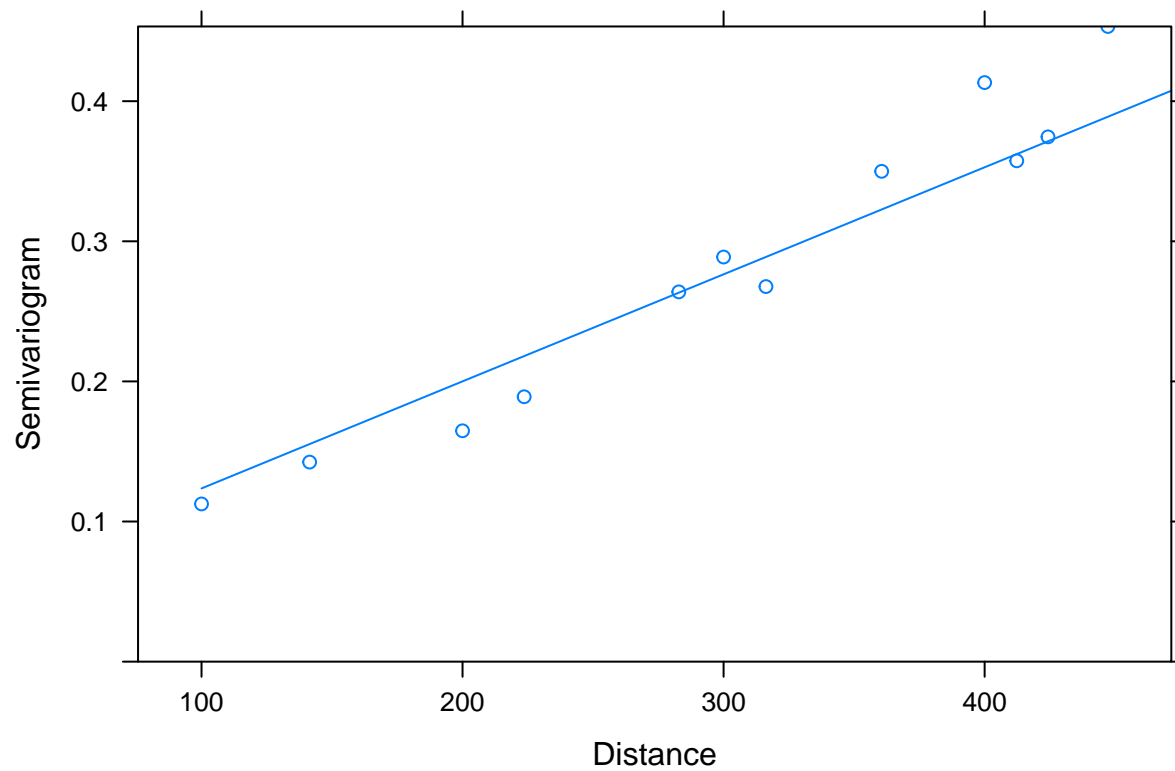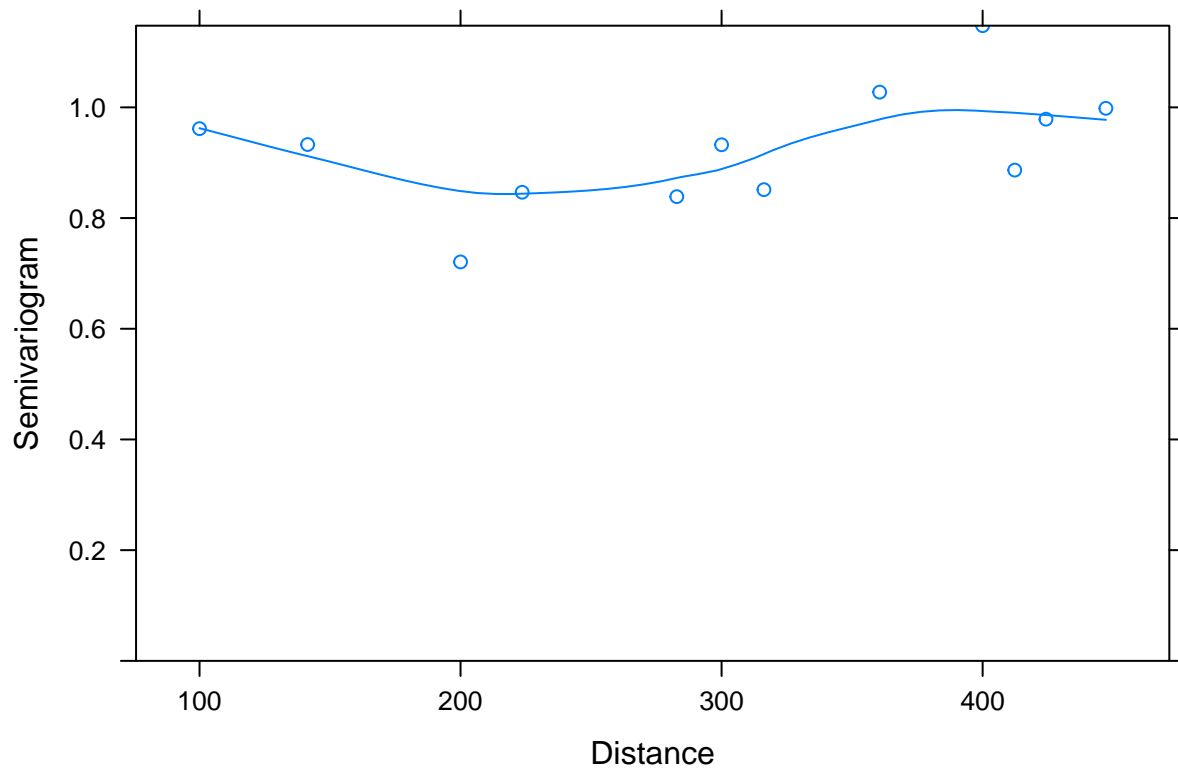
```
#GLS with Nugget

gls_nug <- update(mod1_lm, corr=corLin(form=~x + y, nugget=T))
plot(Variogram(gls_nug, maxDist = max_dist))
```

```
#This fits extremely well, and illustrates the expected spatial correlation.

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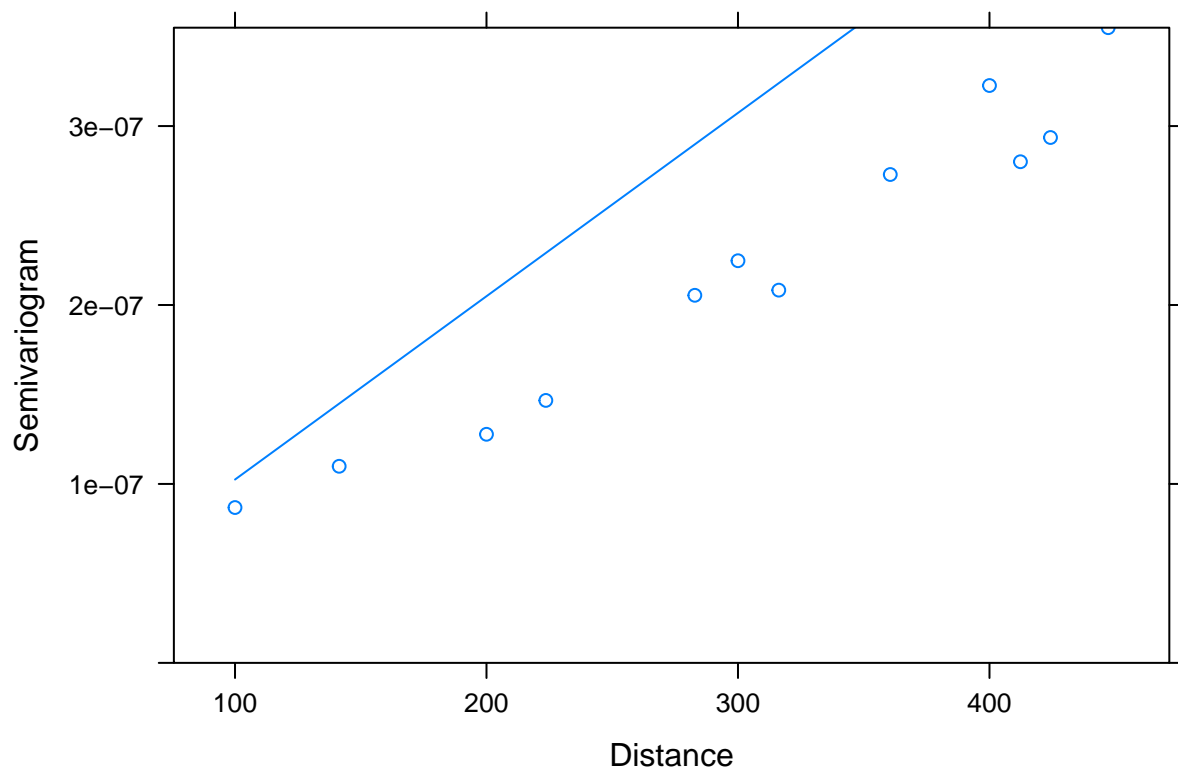


```
#This model fits very well, our residuals are normally distributed

#Exponential Variogram

mod1_exp = update(mod1_lm, corr=corExp(form=~x + y))
plot(Variogram(mod1_exp, maxDist = max_dist))
```
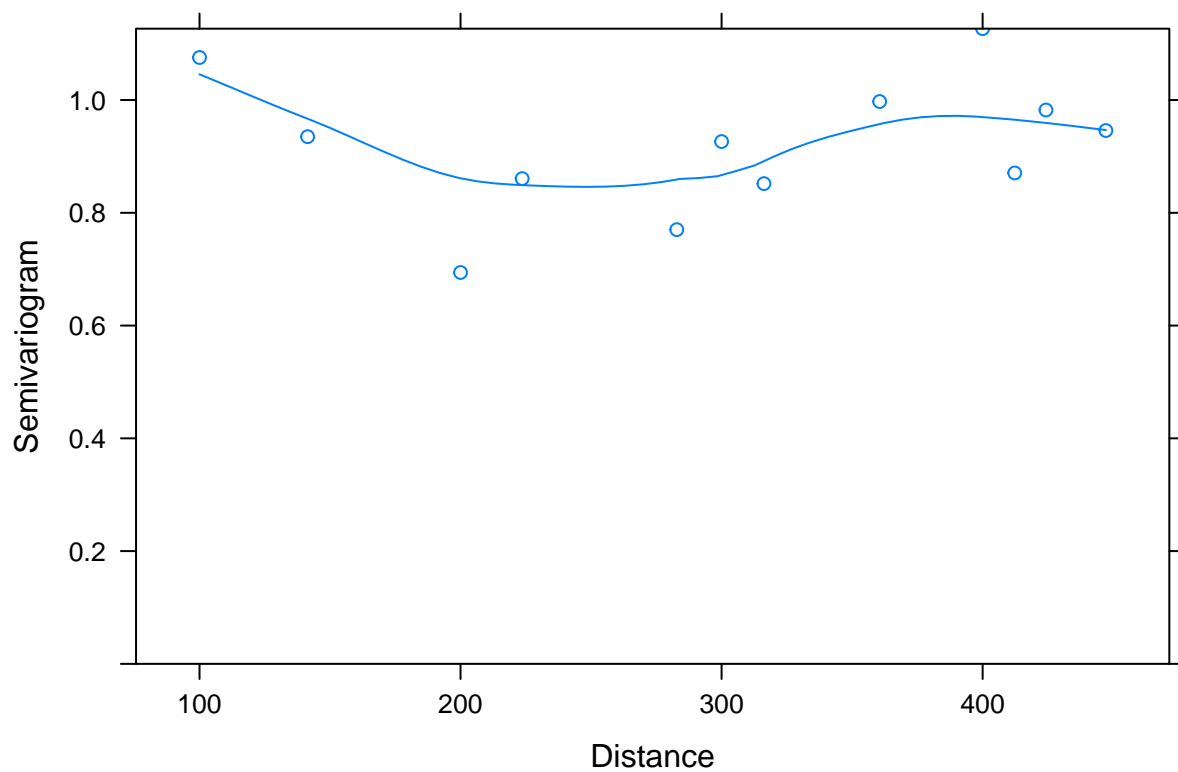
```
#This looks awful, and does not fit error at all.
#Does not appear to have a nugget.

plot(Variogram(mod1_exp, resType='normalized', maxDist = max_dist))
```

```
#Looking at the normalized residuals, this model doesn't do too bad
#because they look normally distributed.


#Exponential Model with a Nugget

#exp_nug <- update(mod1_exp, corr=corExp(form=~x + y, nugget=T))

#false convergence, confirmed above. Just showing that this model
#will not work.



#Rational Quadratic Model Spatial Correlation

rat_mod1 = update(mod1_lm, corr=corRatio(form=~x + y))
plot(Variogram(rat_mod1, maxDist = max_dist))
```
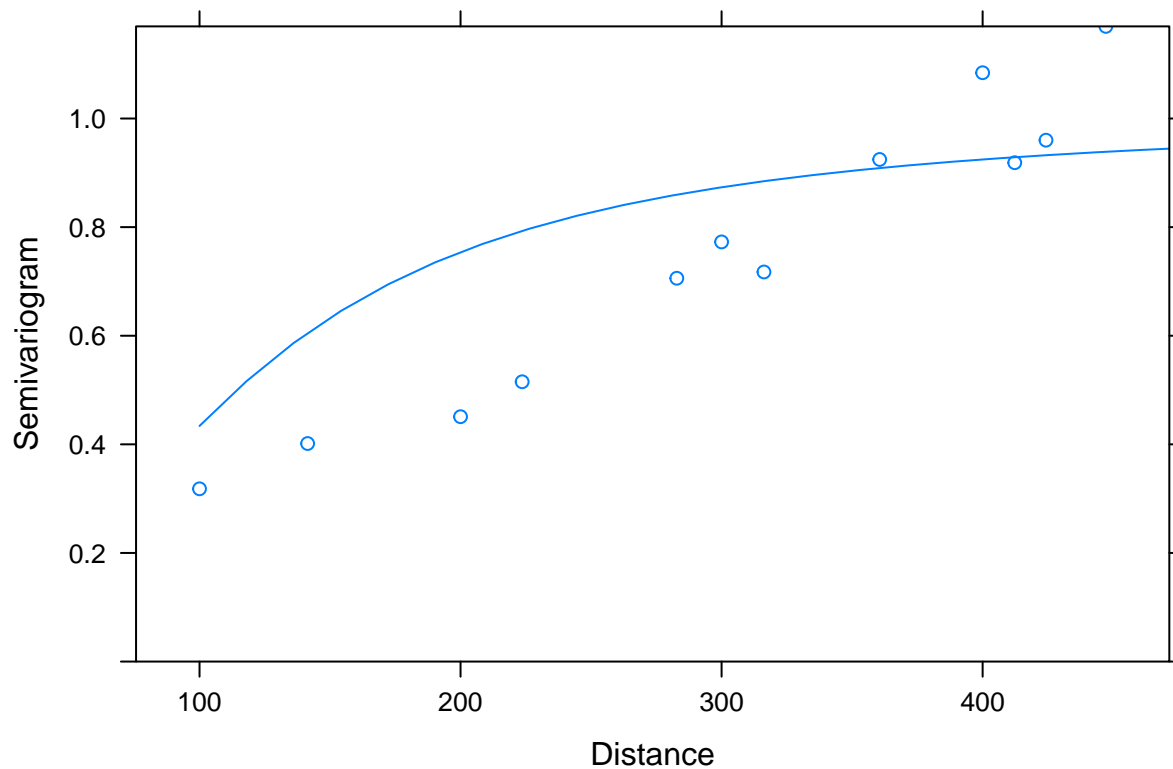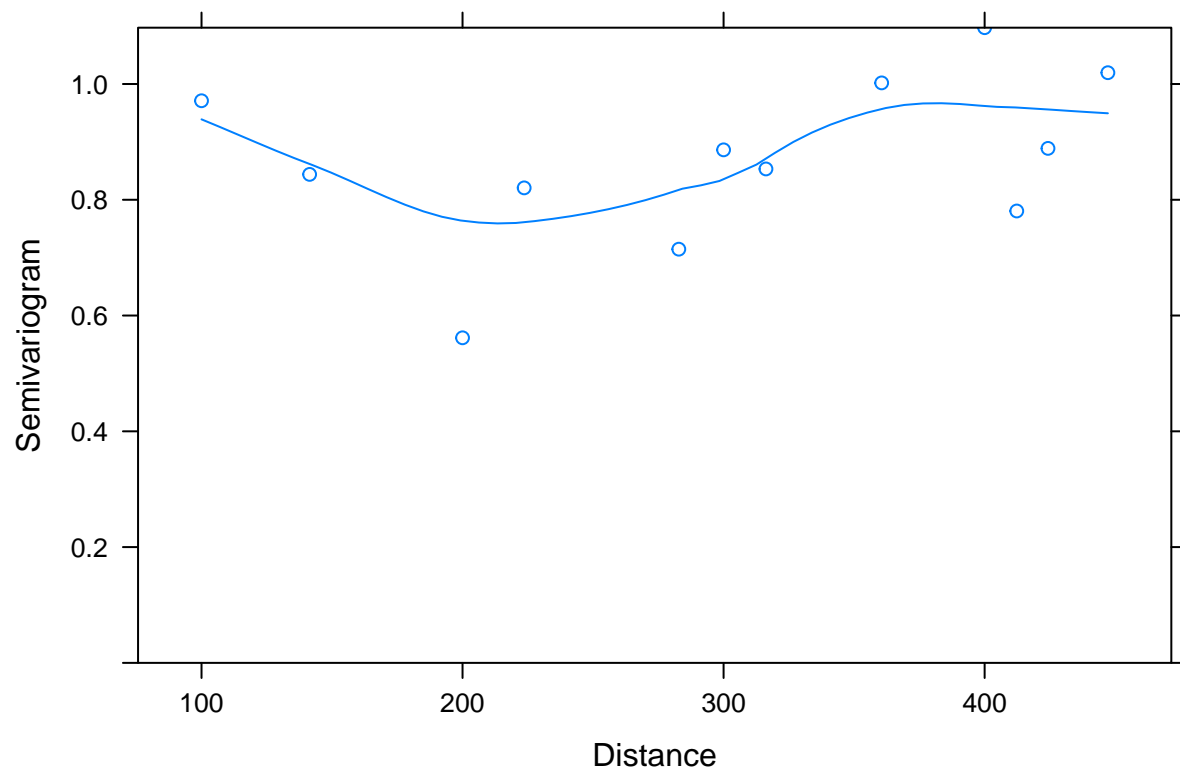


```
#This is not a good fit either to the raw data.

plot(Variogram(rat_mod1, resType='normalized', maxDist = max_dist))
```

```
#This is not too bad, looks very similar to the exponential model


#Rational Quadratic Model With Nugget

rat_nug_mod1 = update(mod1_lm, corr=corRatio(form=~x + y, nugget=T))

plot(Variogram(rat_nug_mod1, maxDist = max_dist))
```
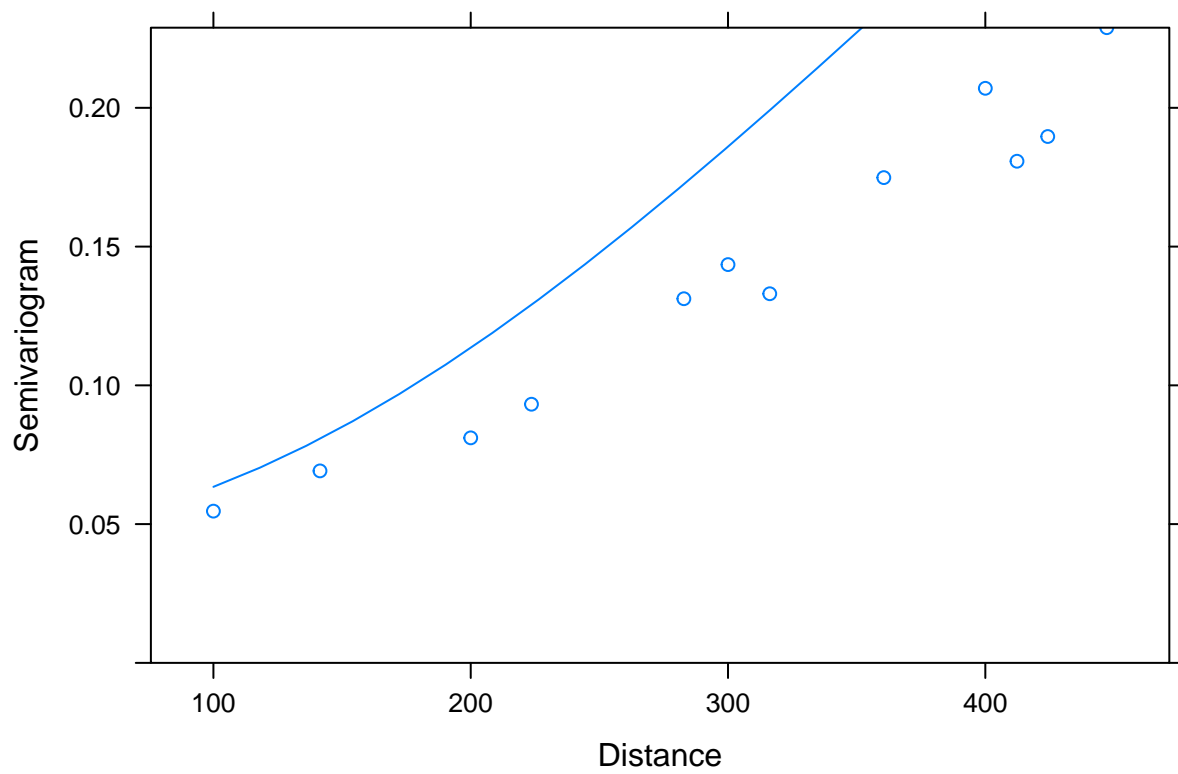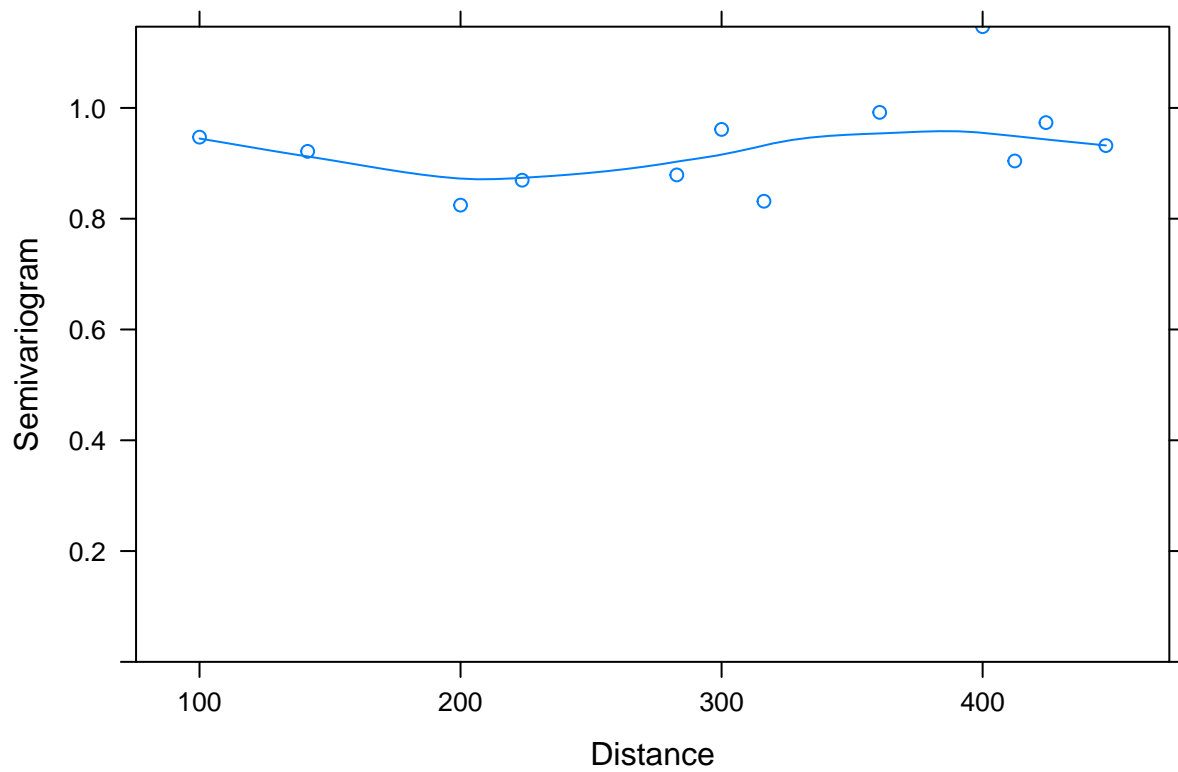
```
#This looks like it is getting closer to explaining our error, but this
#model still is not doing that.

plot(Variogram(rat_nug_mod1, resType='n', maxDist = max_dist))
```

```
#There is no pattern in the variogram (of our residuals),
#so we can conclude that the rational quadratic model is a
#good model to use.


#Gaussian Spatial Model

gaus_mod1 = update(mod1_lm, corr=corGaus(form=~x + y))

plot(Variogram(gaus_mod1, maxDist = max_dist))
```
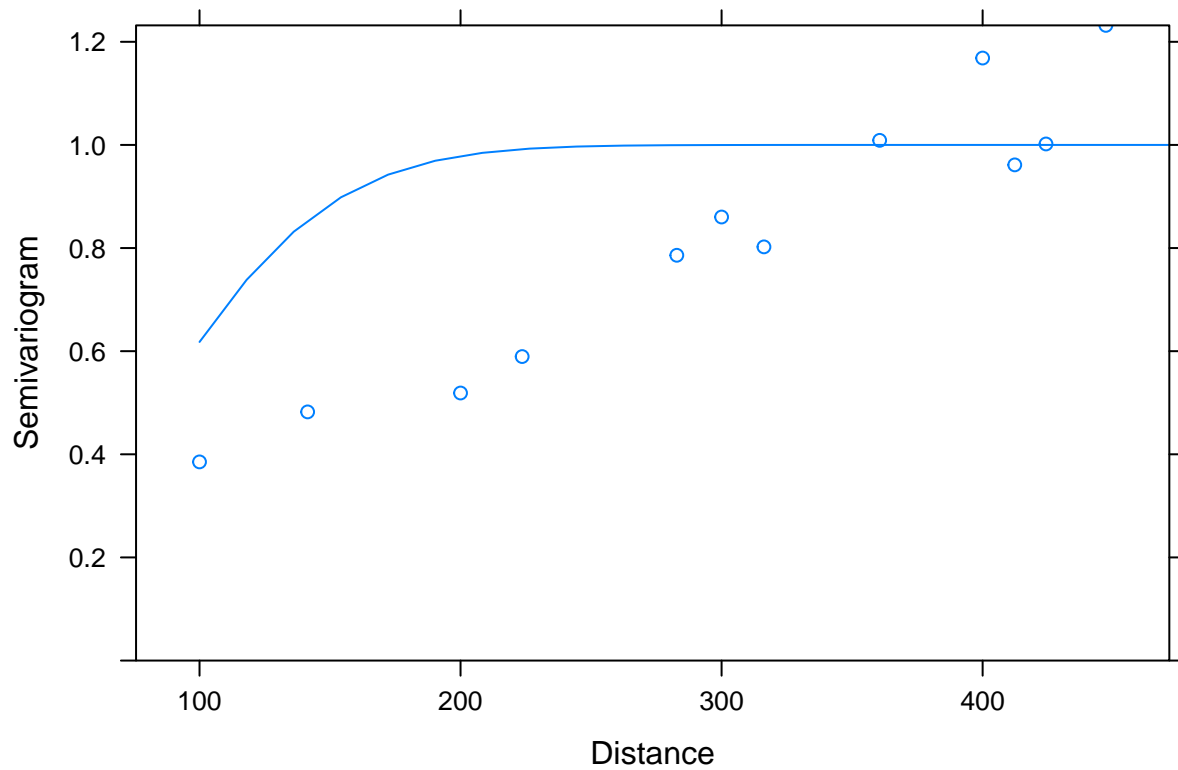


```
#This does not do a good job either.

plot(Variogram(gaus_mod1, resType='n', maxDist = max_dist))
```
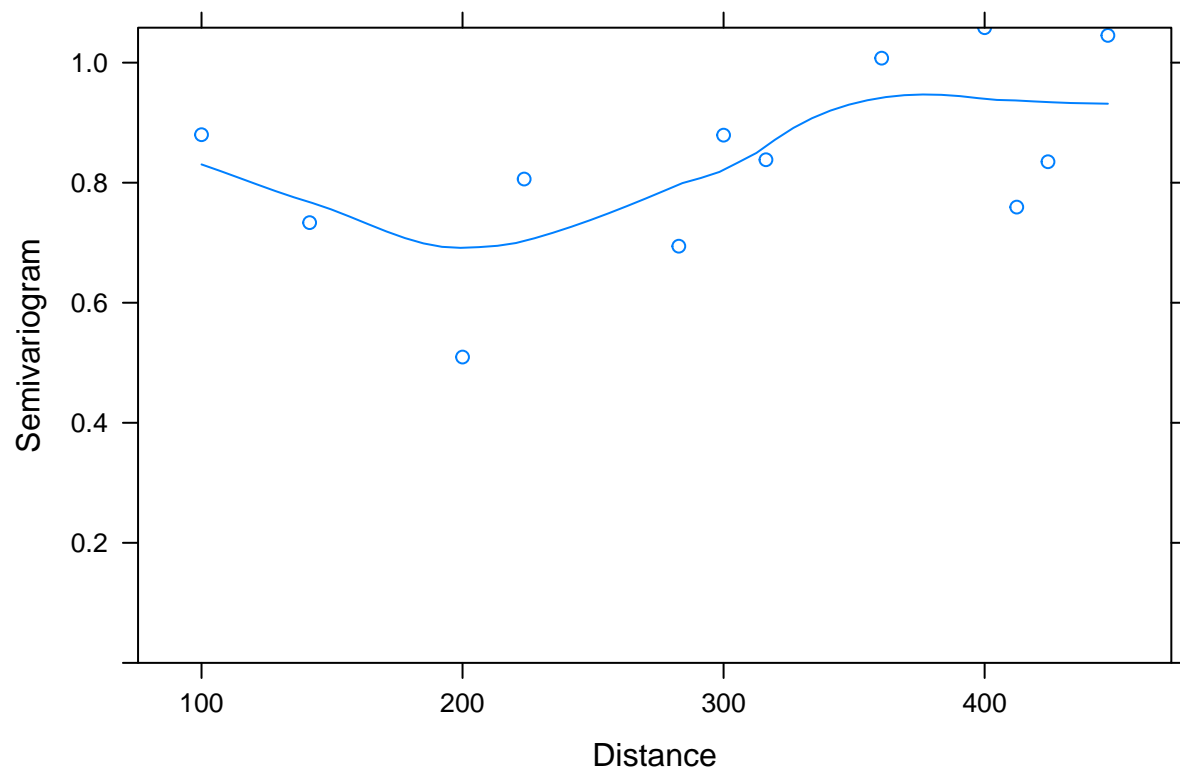
```
#I can see a small trend but this isn't bad.


#Gaussian Spatial Model with Nugget

gaus_nug_mod1 = update(gaus_mod1, corr=corGaus(form=~x + y, nugget=T))

plot(Variogram(gaus_nug_mod1, maxDist = max_dist))
```

```
#This does not fit the data very well, but we can see that the variogram
#increases with distance, suggesting a spatial correlation.

plot(Variogram(gaus_nug_mod1, resType='n', maxDist = max_dist))
```
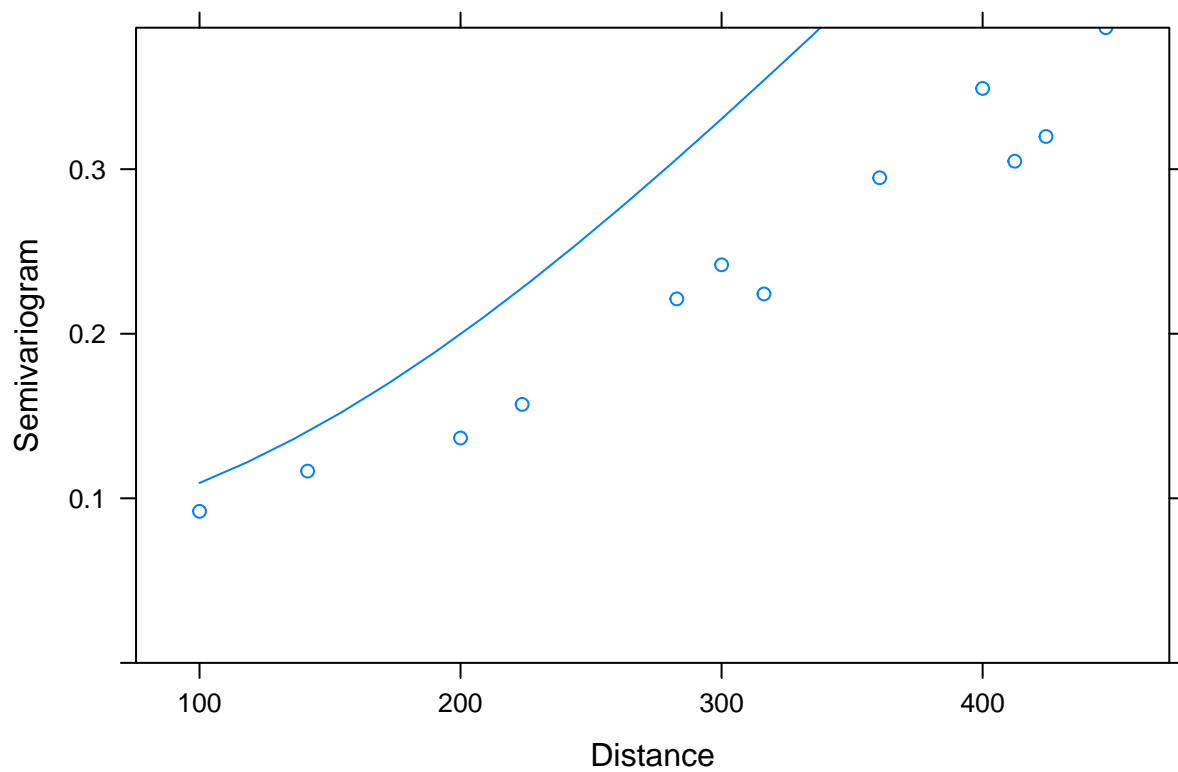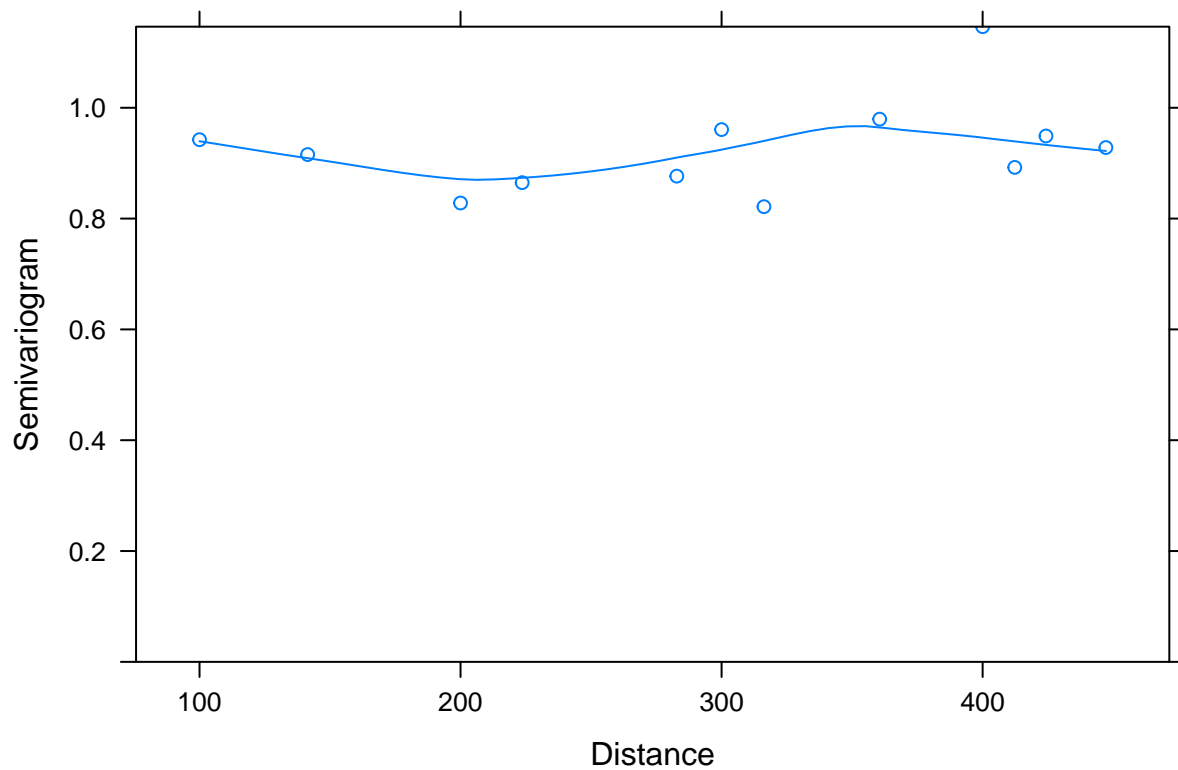
```r
#pretty good fit, similar to the rational quadratic with a nugget model

anova(mod1_lm, gls_nug, mod1_exp, rat_mod1, rat_nug_mod1, gaus_mod1, gaus_nug_mod1, test=T)
```

```
##               Model df      AIC      BIC    logLik   Test   L.Ratio
## mod1_lm           1  3 335.1246 340.7382 -164.5623
## gls_nug           2  5 311.0547 320.4107 -150.5274 1 vs 2 28.069888
## mod1_exp          3  4 310.6438 318.1286 -151.3219 2 vs 3  1.589082
## rat_mod1          4  4 318.9170 326.4018 -155.4585
## rat_nug_mod1      5  5 308.6589 318.0149 -149.3295 4 vs 5 12.258056
## gaus_mod1         6  4 326.5514 334.0362 -159.2757 5 vs 6 19.892433
## gaus_nug_mod1     7  5 308.8879 318.2440 -149.4440 6 vs 7 19.663411
##              p-value
## mod1_lm
## gls_nug       <.0001
## mod1_exp      0.2075
## rat_mod1
## rat_nug_mod1  0.0005
## gaus_mod1     <.0001
## gaus_nug_mod1 <.0001
```

```r
#The rational quadratic model with the nugget and the gaussian model with the #nugget are almost identi
#gaussian model. When a nugget was included for the gls, rational quadratic, and #gaussian models, it i
#is a significant difference between a model with and without a nugget.
#I was not able to get
#the model to work for the exponential model with a nugget. Including
#the spatial error term for both of these models improved it significantly.


summary(rat_nug_mod1)
```

```
## Generalized least squares fit by REML
##   Model: sp_response ~ sp_predictor
##   Data: single_sp_mod
##        AIC      BIC    logLik
##   308.6589 318.0149 -149.3295
##
## Correlation Structure: Rational quadratic spatial correlation
##  Formula: ~x + y
##  Parameter estimate(s):
##        range        nugget
## 721.93442068    0.04545983
##
## Coefficients:
##                 Value Std.Error    t-value p-value
## (Intercept)  12.879120 14.012990 0.9190843  0.3626
## sp_predictor  0.104606  0.211529 0.4945249  0.6232
##
##  Correlation:
##              (Intr)
## sp_predictor -0.157
##
## Standardized residuals:
```

20

```
##          Min          Q1         Med          Q3         Max
## -0.7668581 -0.7168281 -0.6175156 -0.3685195   1.3705711
##
## Residual standard error: 18.29516
## Degrees of freedom: 50 total; 48 residual
```

```
summary(gaus_nug_mod1)
```

```
## Generalized least squares fit by REML
##   Model: sp_response ~ sp_predictor
##   Data: single_sp_mod
##        AIC      BIC    logLik
##   308.8879 318.244 -149.444
##
## Correlation Structure: Gaussian spatial correlation
##  Formula: ~x + y
##  Parameter estimate(s):
##        range       nugget
## 529.28590917   0.07696144
##
## Coefficients:
##                 Value Std.Error   t-value p-value
## (Intercept)  11.390225  8.549499 1.3322681  0.1891
## sp_predictor  0.102479  0.210639 0.4865159  0.6288
##
##  Correlation:
##            (Intr)
## sp_predictor -0.232
##
## Standardized residuals:
##          Min          Q1         Med          Q3         Max
## -0.8879327 -0.8243254 -0.6951762 -0.3713946   1.8858142
##
## Residual standard error: 14.09735
## Degrees of freedom: 50 total; 48 residual
```
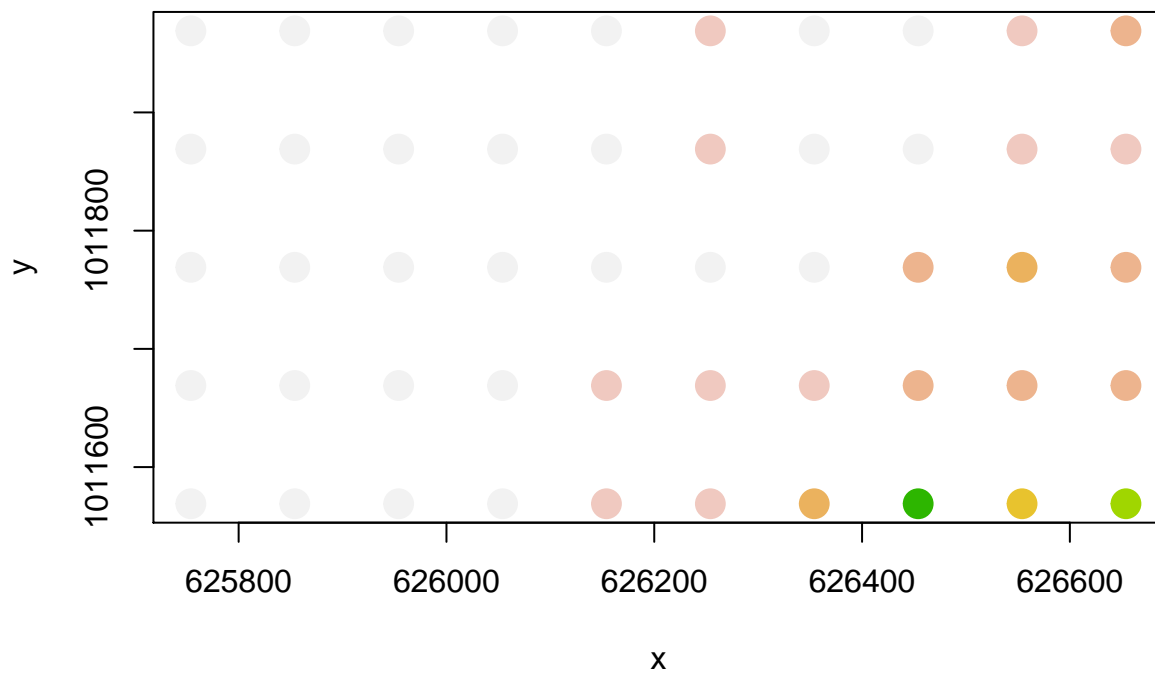
```
#We want a smaller t value and a large p value because that means there is less #difference of the resi
#This is observed in the rat_nug_mod1.
```

```
col_brks = hist(residuals(rat_nug_mod1), plot=T)$breaks
```

Histogram of residuals(rat_nug_mod1)
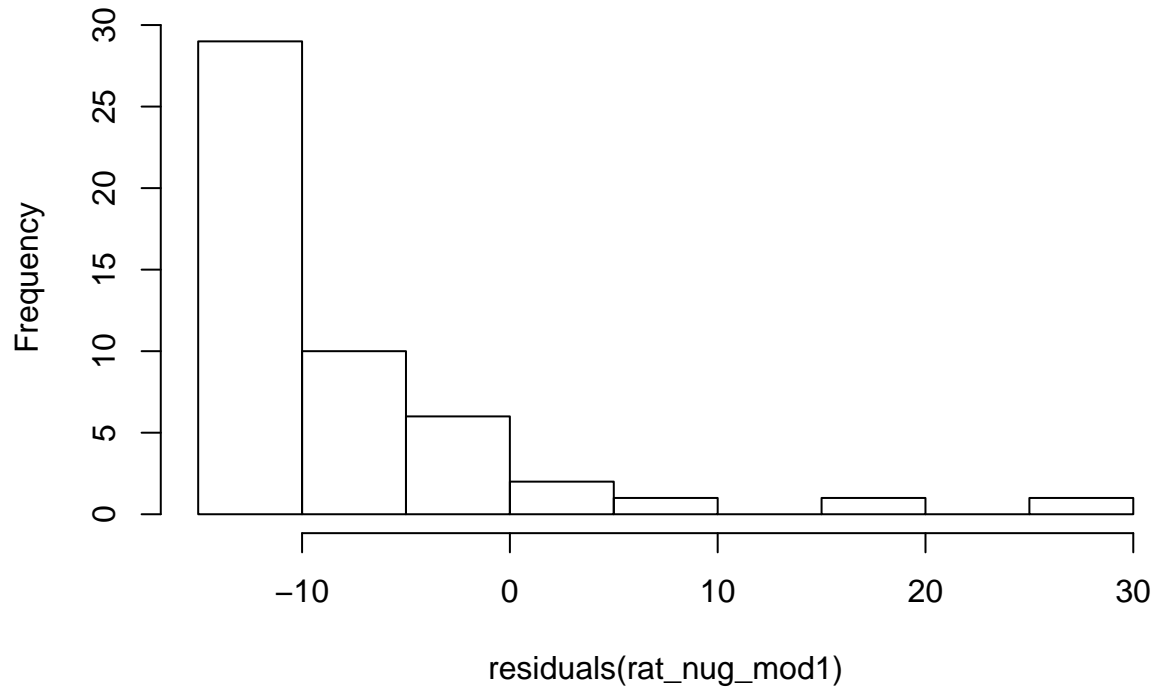

```
col_indices = as.numeric(cut(residuals(rat_nug_mod1), col_brks))
cols = rev(terrain.colors(length(col_brks)))
plot(BCI_xy, cex=2, pch=19, col=cols[col_indices])
```



```
#By looking at a spatial map of our residuals, we can see they do look
#spatially structured, especially at large distances for x. This suggests
#that the x spatial paramater might have more of an effect on the abundance
```

```
#of species. We can see this at high values for x, but not for high values of
#y. When we included the models with a nugget, the models were significantly
#improved. This is because there is a large spatial influence on tree abundance.
#By examining the residuals, we can see that
#there is spatial dependence, which is concurrent with the rest of our data.
```

Model 2: include all species as predictor variables: Full Model

```
#Our response species


Drypetes_response <- BCI$Drypetes.standleyi

#make our predictor species (I originally tried it through
#different ways posted via Github, but kept resulting in error messages
#when I got to the updated models; resorted to the longer route)

c_las <- BCI$Cordia.lasiocalyx
h_tri <- BCI$Hirtella.triandra
p_lat <- BCI$Picramnia.latifolia
q_ama <- BCI$Quassia.amara
t_arb <- BCI$Tabernaemontana.arborea
t_asp <- BCI$Trattinnickia.aspera
x_mac <- BCI$Xylopia.macrantha


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

#make our data frame with our response species, our multiple predictor
#species, and our x/y coordinates.

bci_sp <- data.frame(Drypetes_response, c_las, h_tri, p_lat, q_ama, t_arb, t_asp, x_mac, BCI_xy)

x = BCI_xy$x
y = BCI_xy$y


#Linear Model using all Species as a Predictor

full_gls <- gls( Drypetes_response ~ c_las + h_tri + p_lat + q_ama + t_arb
+ t_asp + x_mac , data=bci_sp)

par(mfrow=c(1,1))
plot(Variogram(full_gls, form= ~ x + y))
```
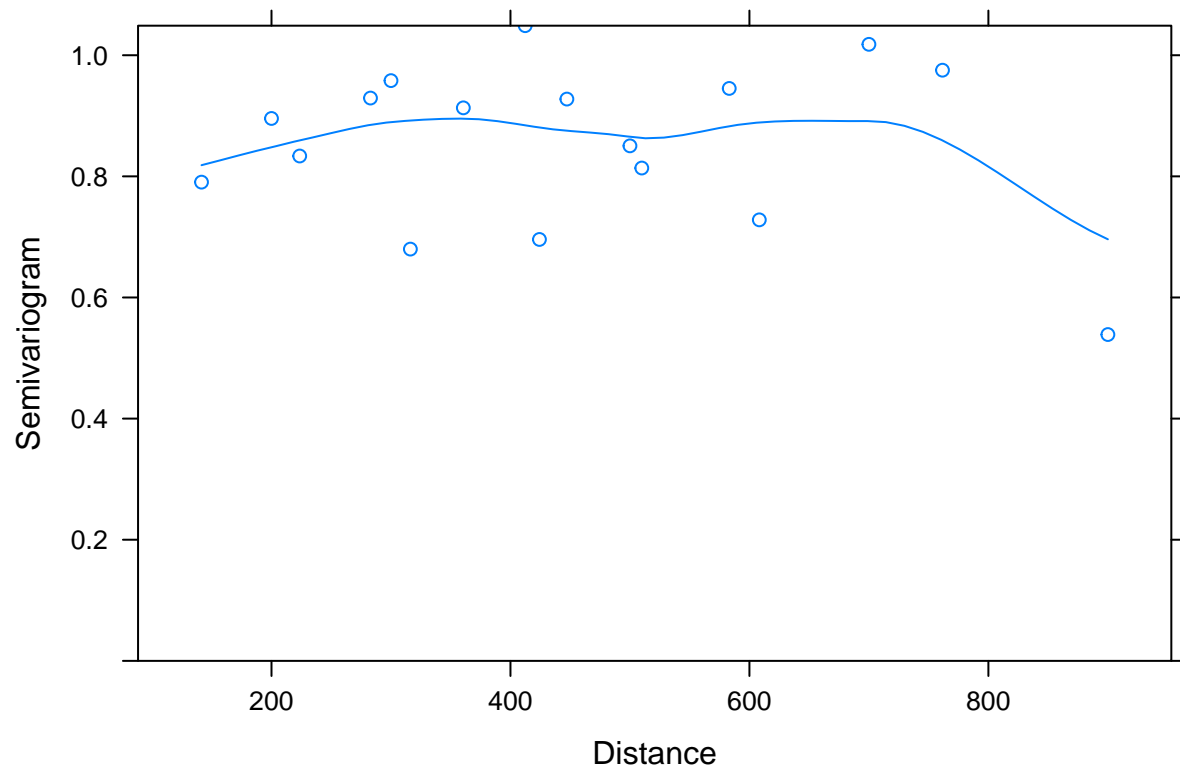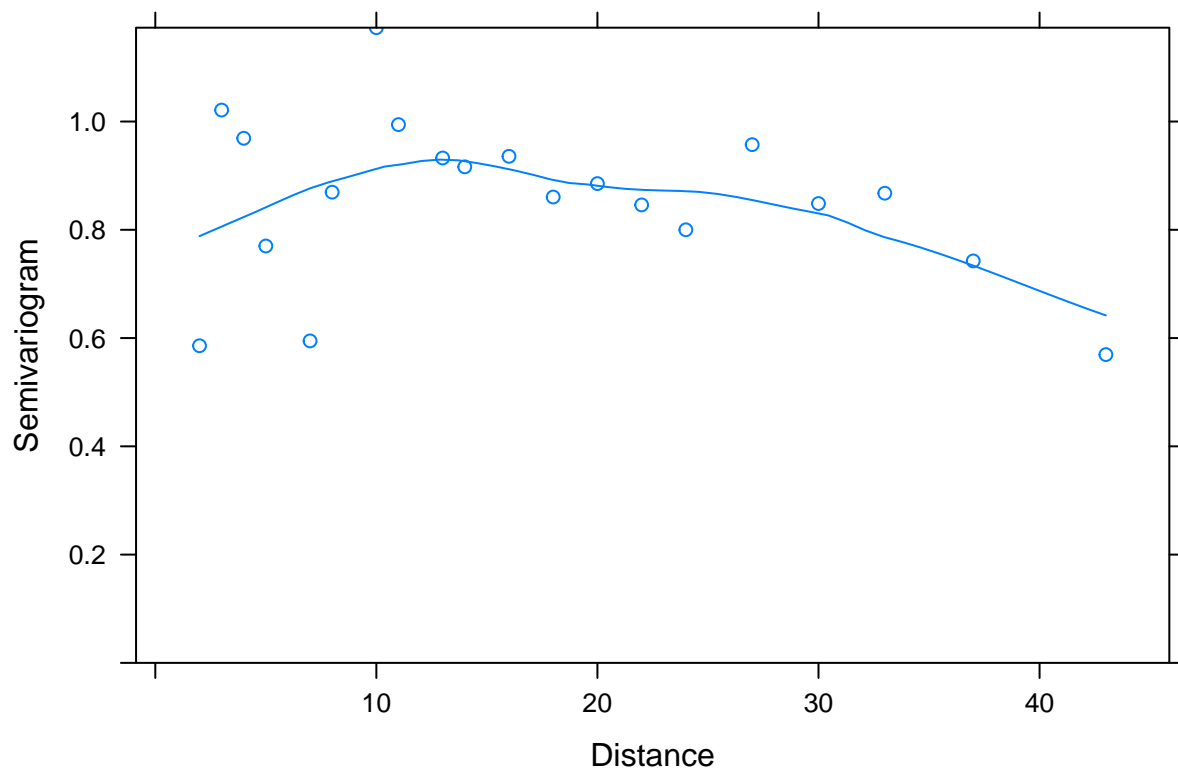
```
#This looks like a pretty good fit and looks like residuals are
#normally distributed. It appears that the variogram is decreasing
#with distance, possilby indicating that there is no spatial correlation.
#It appears there is a nugget of .8

plot(Variogram(full_gls, resType='normalized', maxDist = max_dist))
```
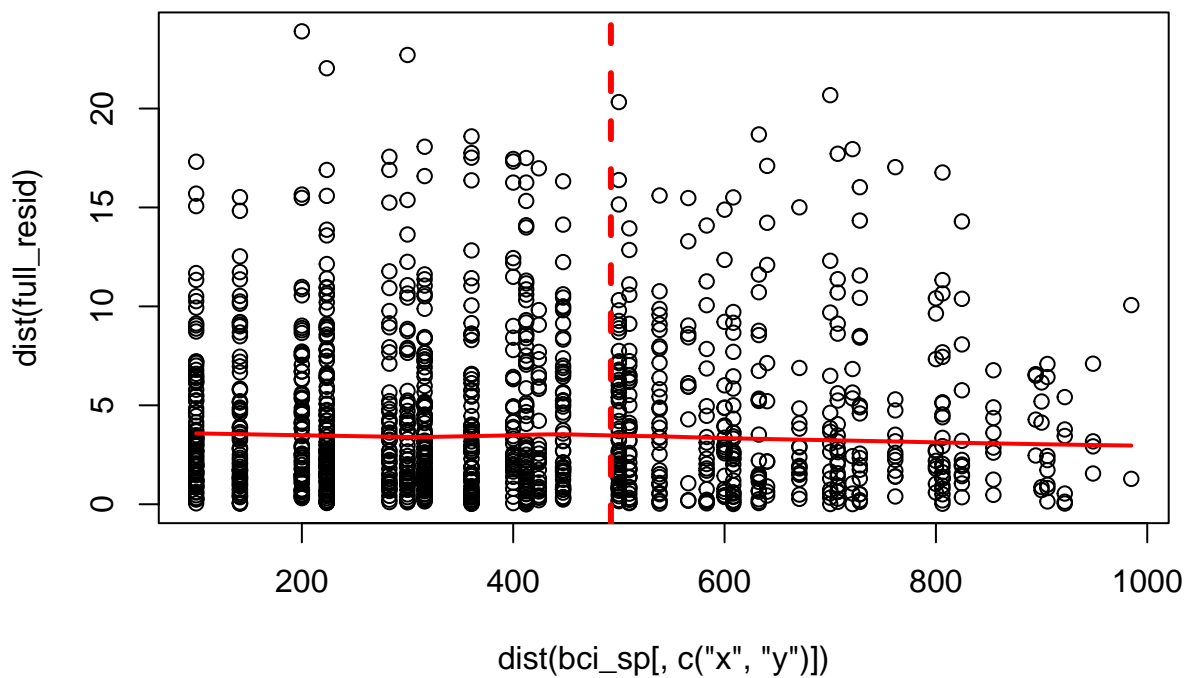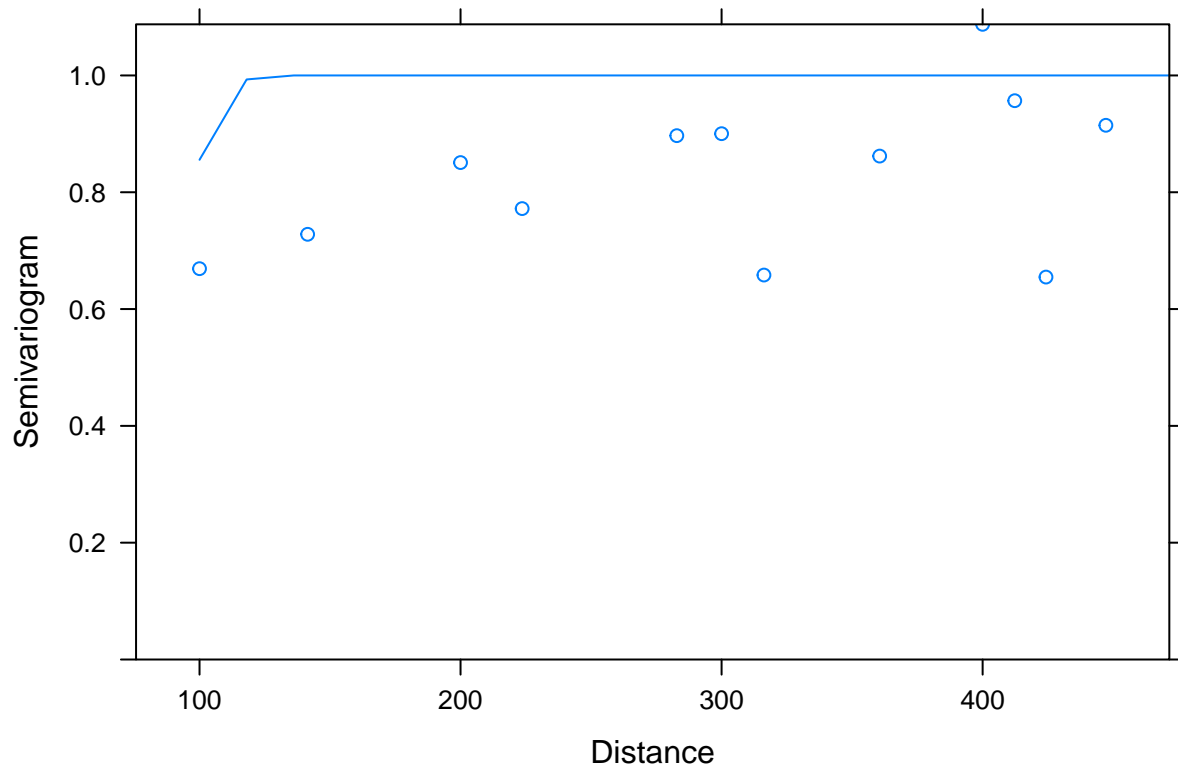
```
#This provides a pretty good fit to the data


full_resid <- residuals(full_gls)
plot(dist(bci_sp [, c('x', 'y')]), dist(full_resid))
lines(lowess(dist(bci_sp [, c('x', 'y')]), dist(full_resid)), col='red', lwd=2)
abline(v = max_dist, col='red', lwd=3, lty=2)
```
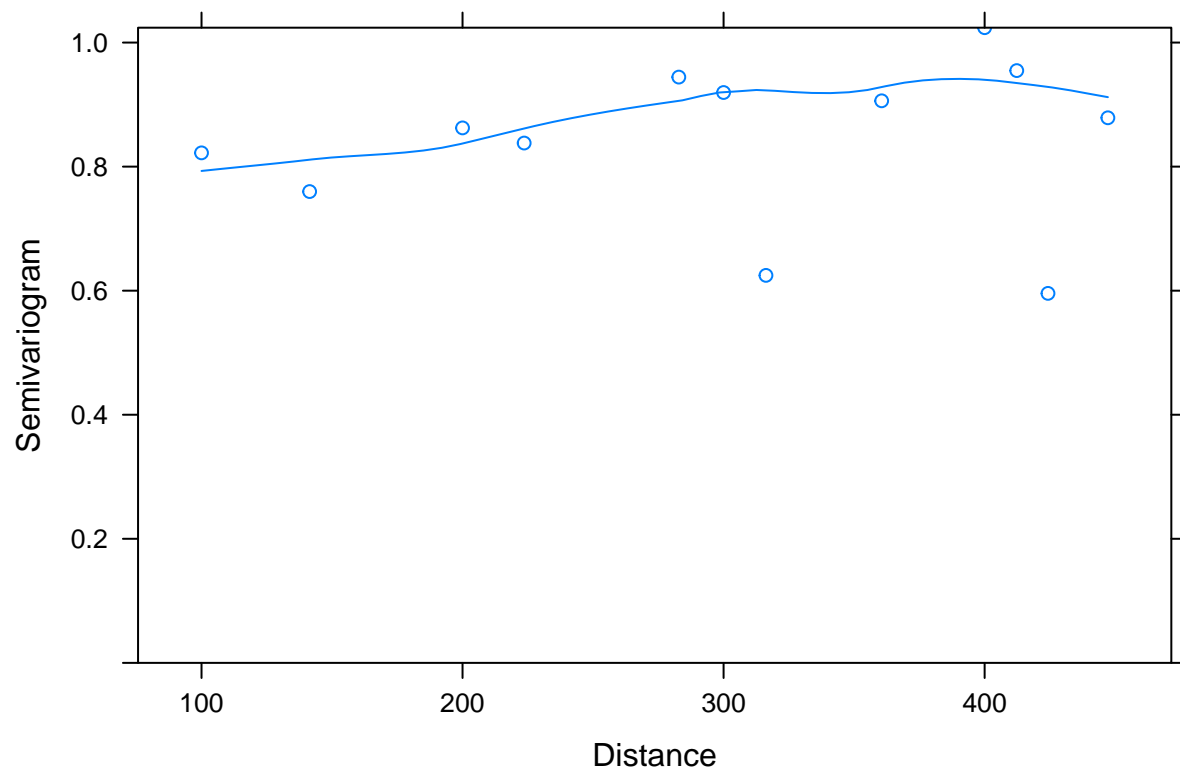
```
#negative slope

#GLS with Nugget

full_gls_nug <- update(full_gls, corr=corLin(form=~x + y, nugget=T))
plot(Variogram(full_gls_nug, maxDist = max_dist))
```

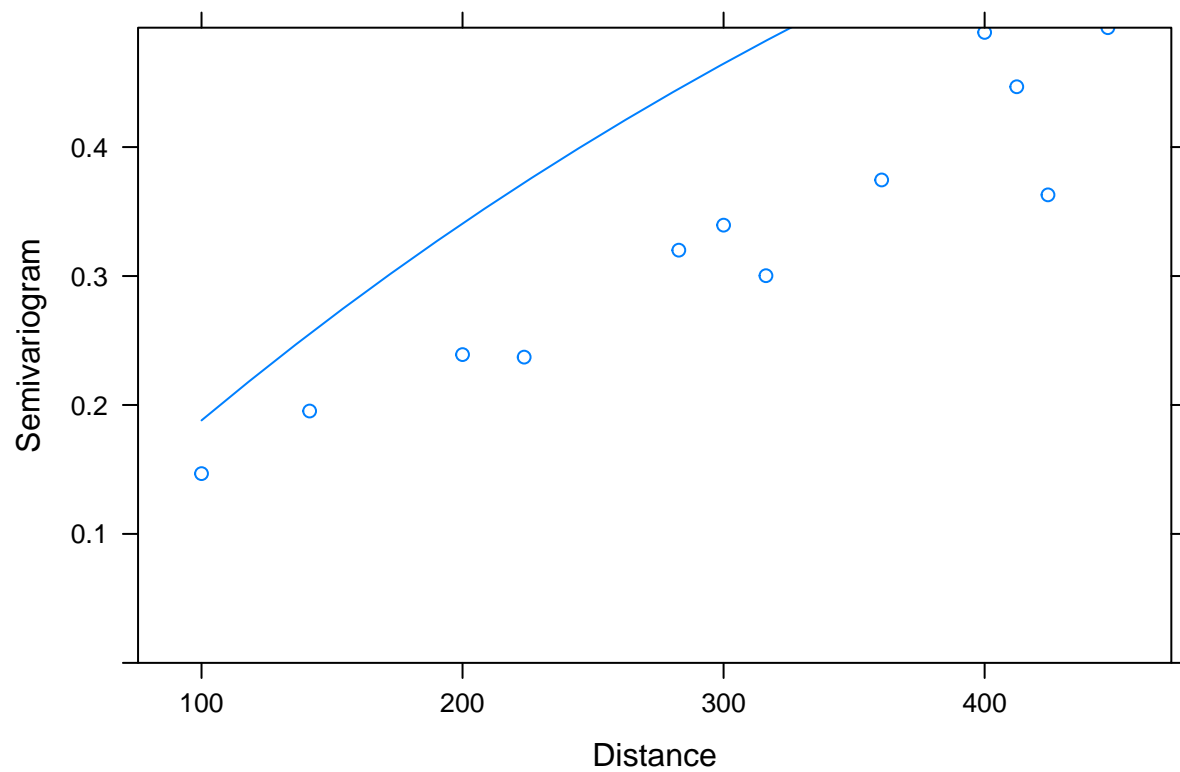

```
#This does not fit the data at all; the slope is 0, indicating no correlation.

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

```r
#Exponential Variogram

full_exp <- update(full_gls, corr = corExp(form=~x + y))
#This is a good fit of our residuals.

plot(Variogram(full_exp, maxDist = max_dist))
```
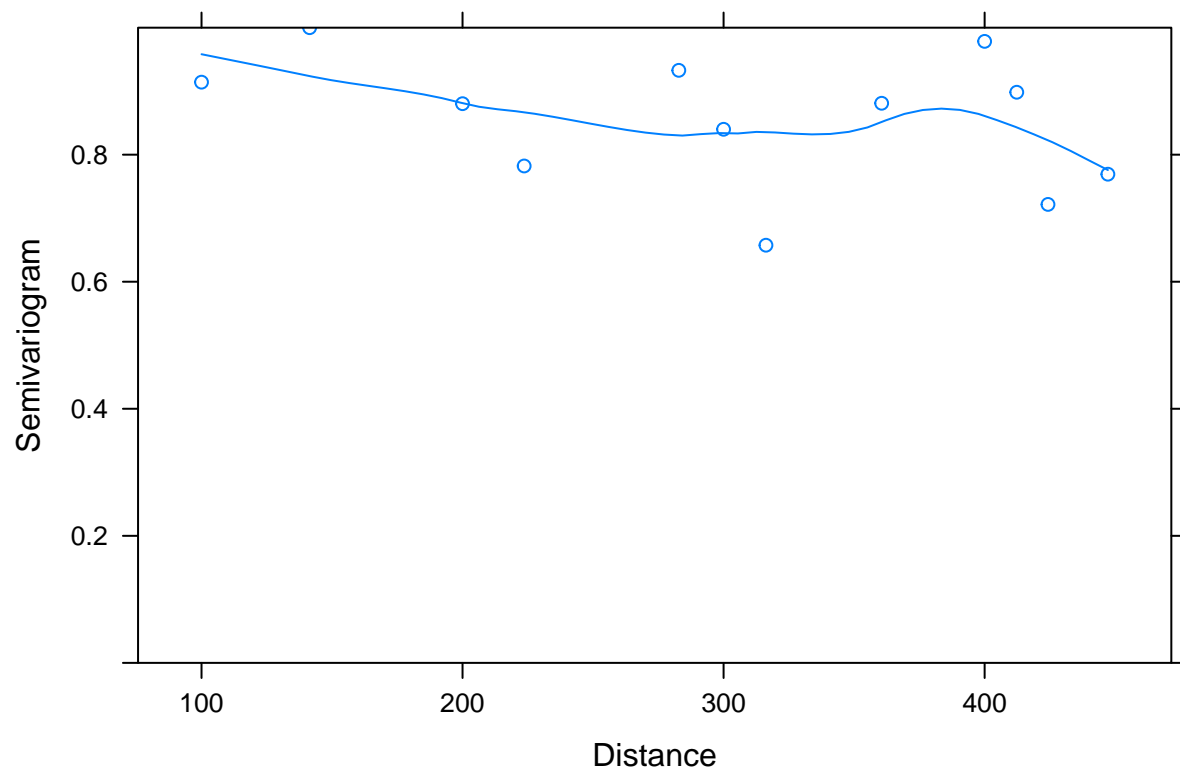
```
#This doesn't look good because the model does not fit the error at all.
#Does not appear to have a y intercept. Does not have a nugget,
#or a non-0 y intercept.

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

```
#Rational Quadratic Model Spatial Correlation

full_rat = update(full_gls, corr=corRatio(form=~x + y))

plot(Variogram(full_rat, maxDist = max_dist))
```
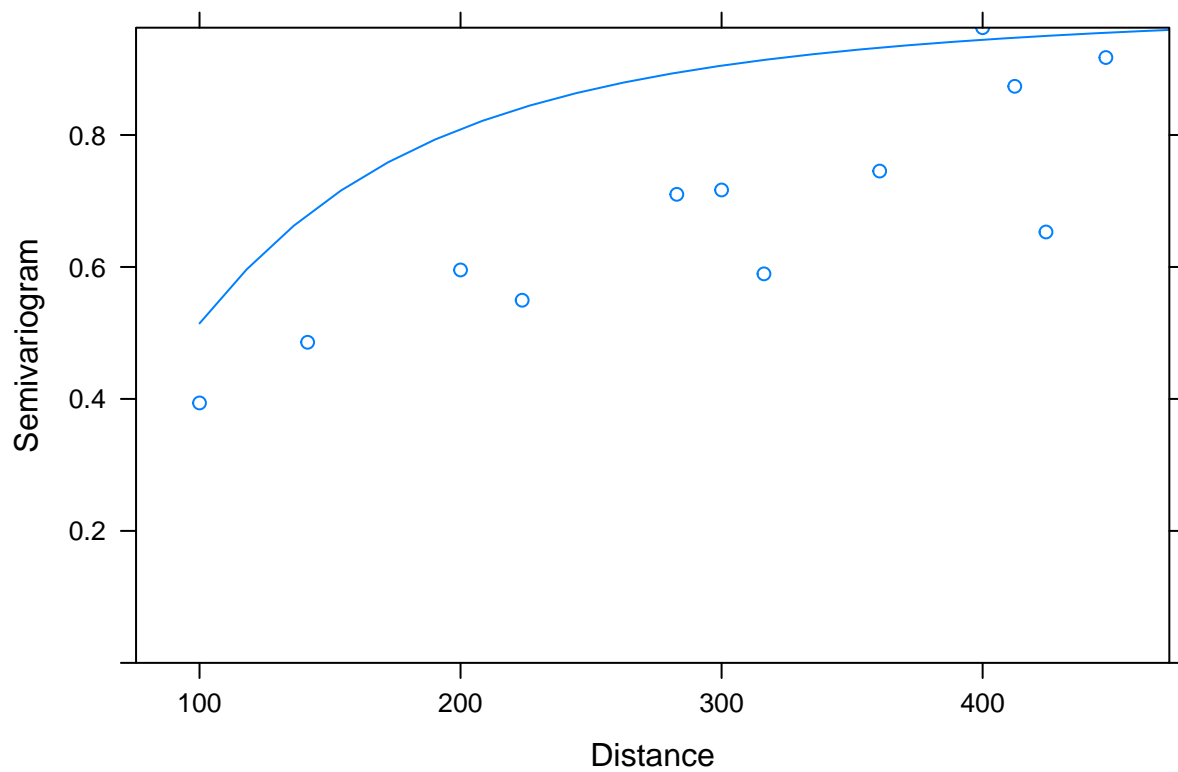
```
#this still does not fit the model, as the model does not fit the
#error. Still does not have a nugget.

plot(Variogram(full_rat, resType='normalized', maxDist = max_dist))
```
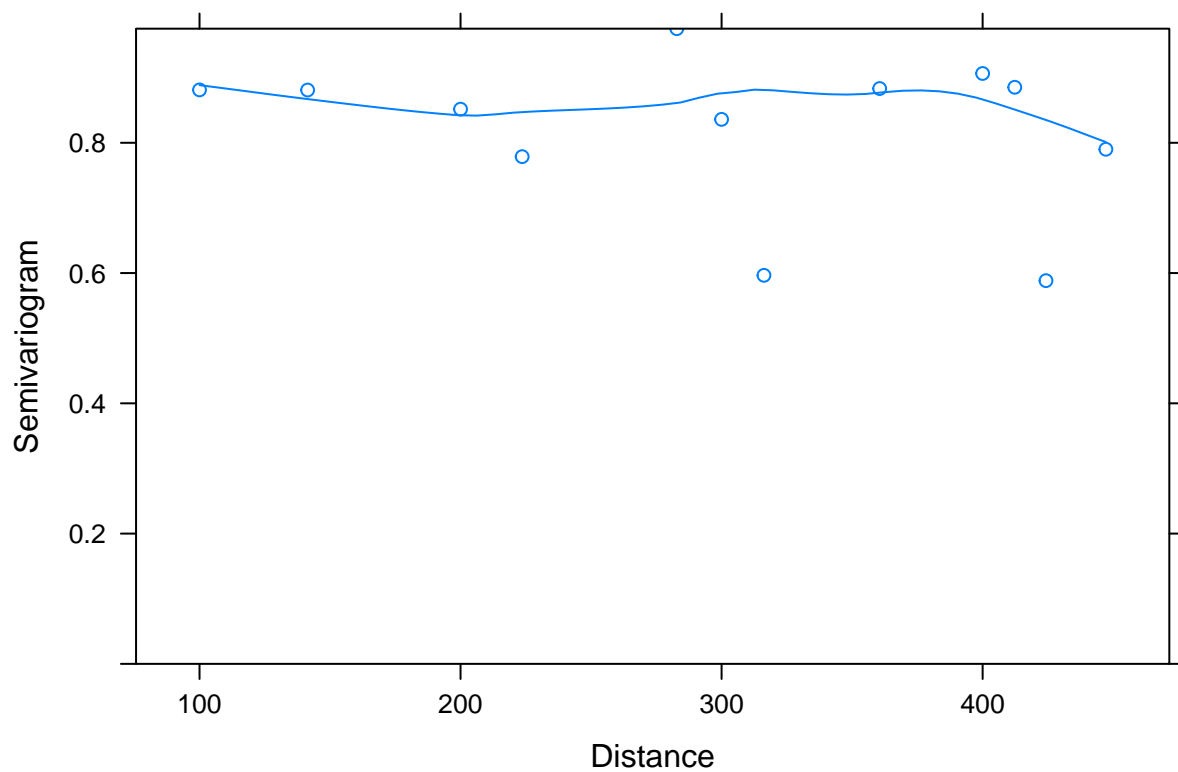
```
#Rational Quadratic Model With Nugget

full_rat_nug = update(full_gls, corr=corRatio(form=~x + y, nugget=T))

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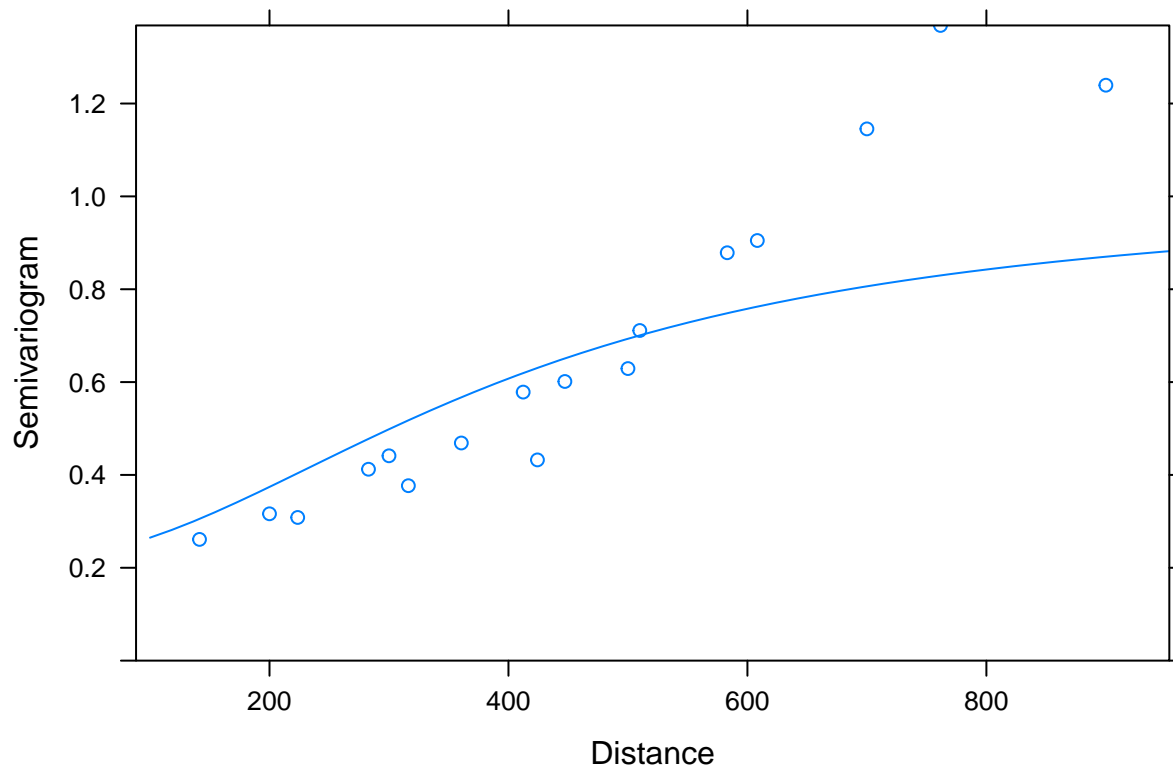


```
#This looks bad too. The trend of the raw residuals
#appears to be gaussian.

plot(Variogram(rat_nug_mod1, resType='n', maxDist = max_dist))
```
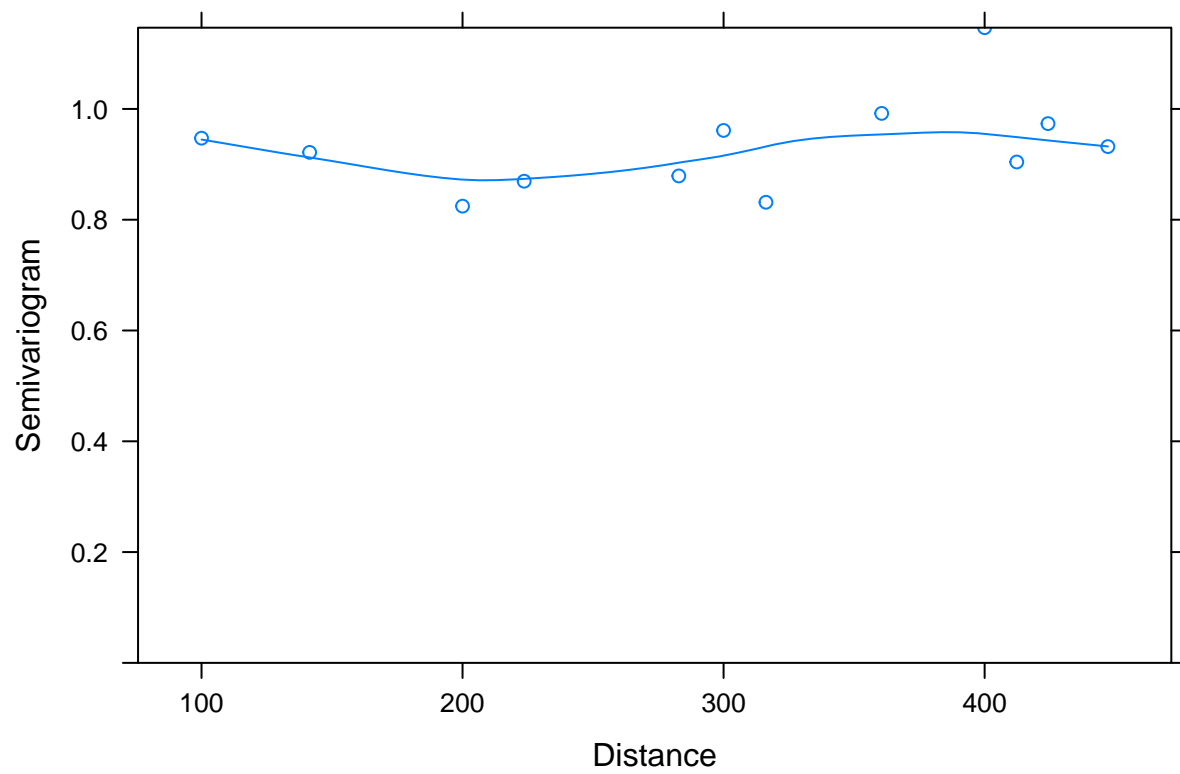
```r
#Gaussian Spatial Model

full_gaus = update(full_gls, corr=corGaus(form=~x + y))

plot(Variogram(full_gaus, maxDist = max_dist))
```
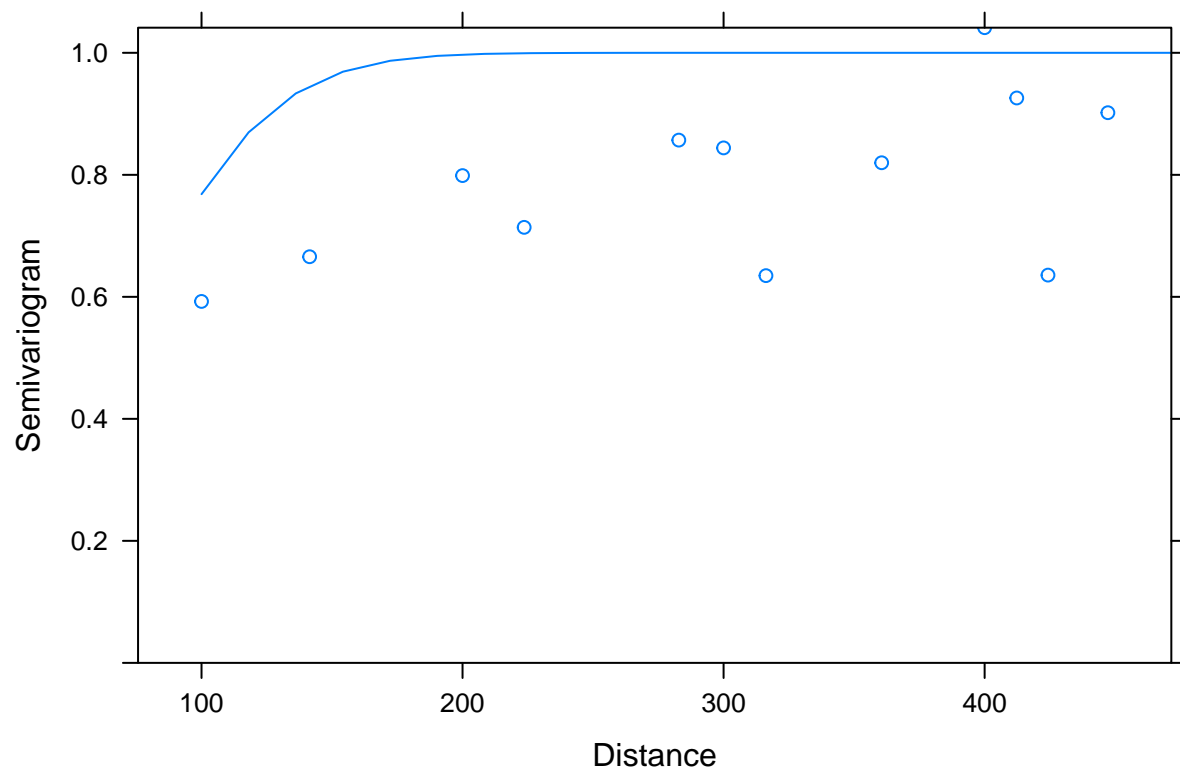
```
#Not as good as I had hoped.

plot(Variogram(full_gaus, resType='n', maxDist = max_dist))
```
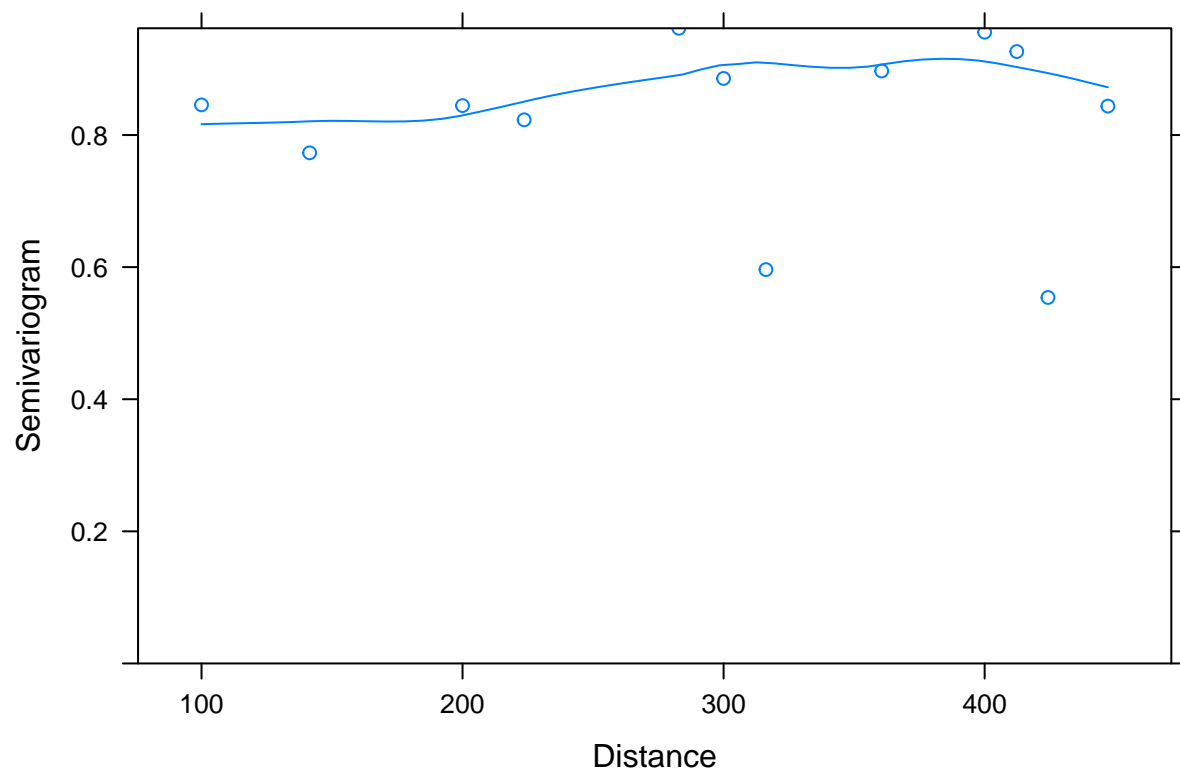
```
#Gaussian Spatial Model with Nugget

full_gaus_nug = update(full_gaus, corr=corGaus(form=~x + y, nugget=T))

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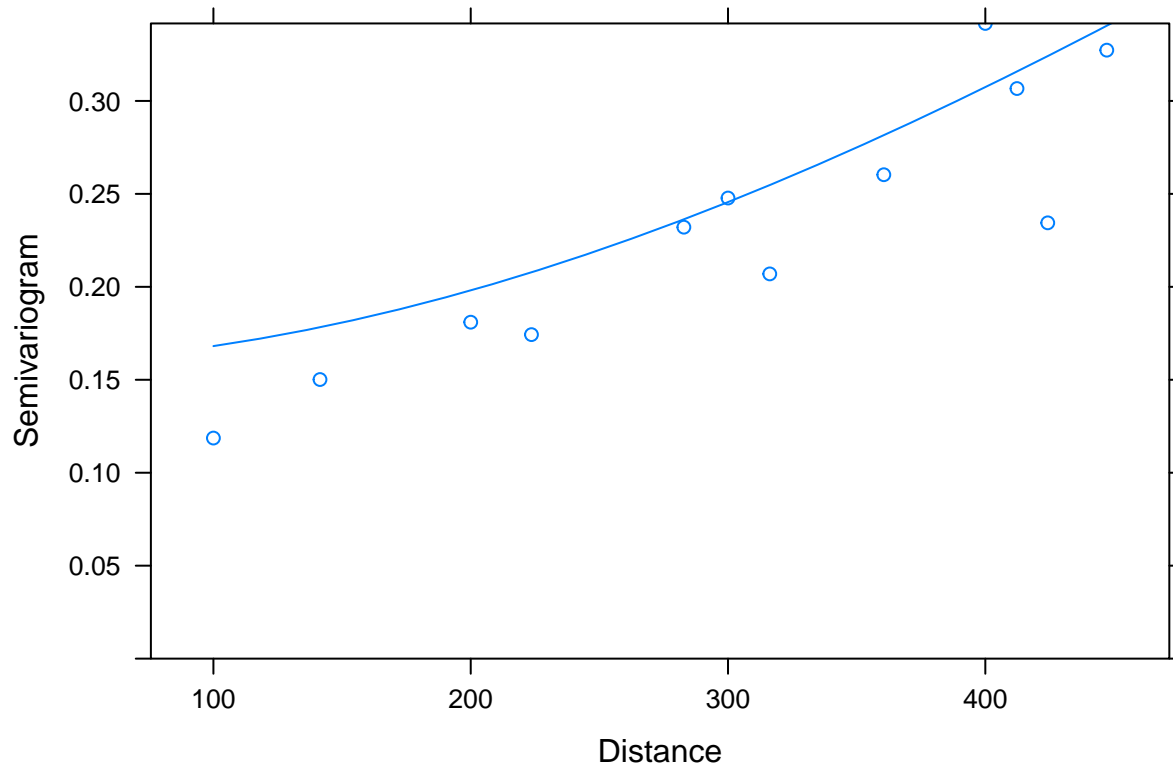


```
#This looks better than what we have seen, but the model still
#does not fit the error as well.

plot(Variogram(full_gaus_nug, resType='n', maxDist = max_dist))
```
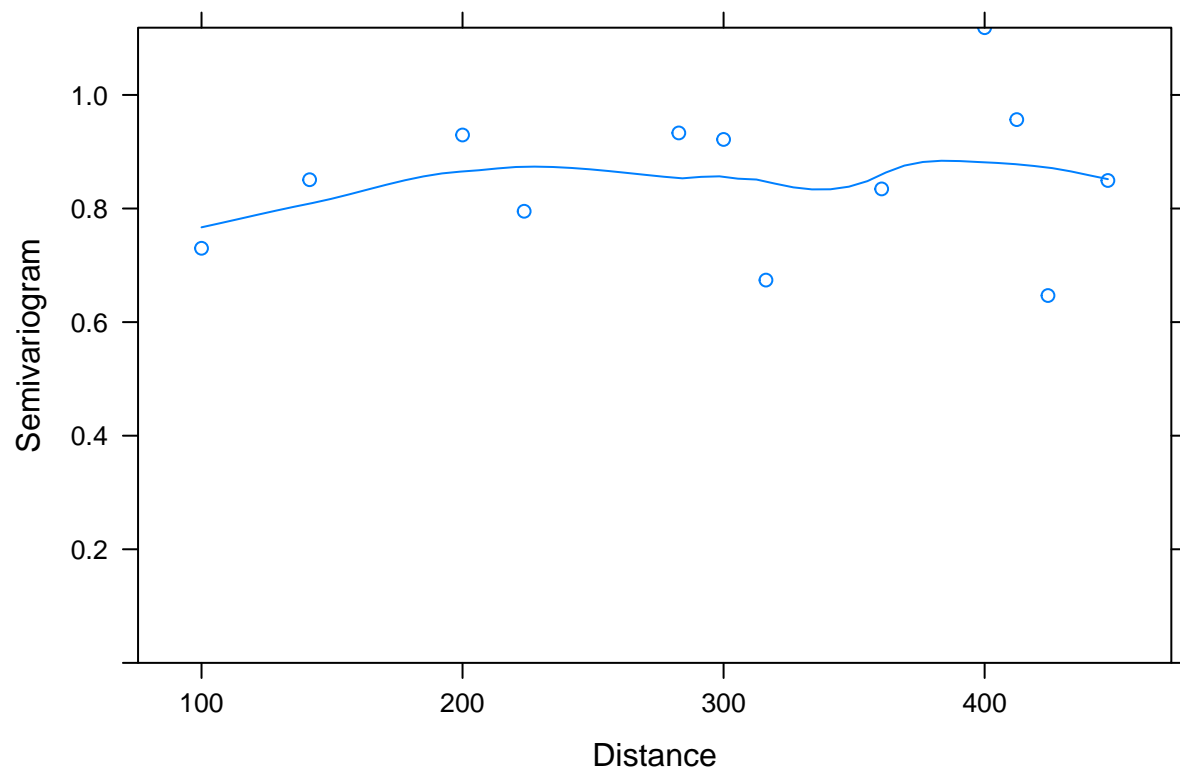
```r
#Sperical Spatial Model

sphere_full = update(full_gls, corr=corSpher(form=~x + y))

plot(Variogram(sphere_full, maxDist = max_dist))
```
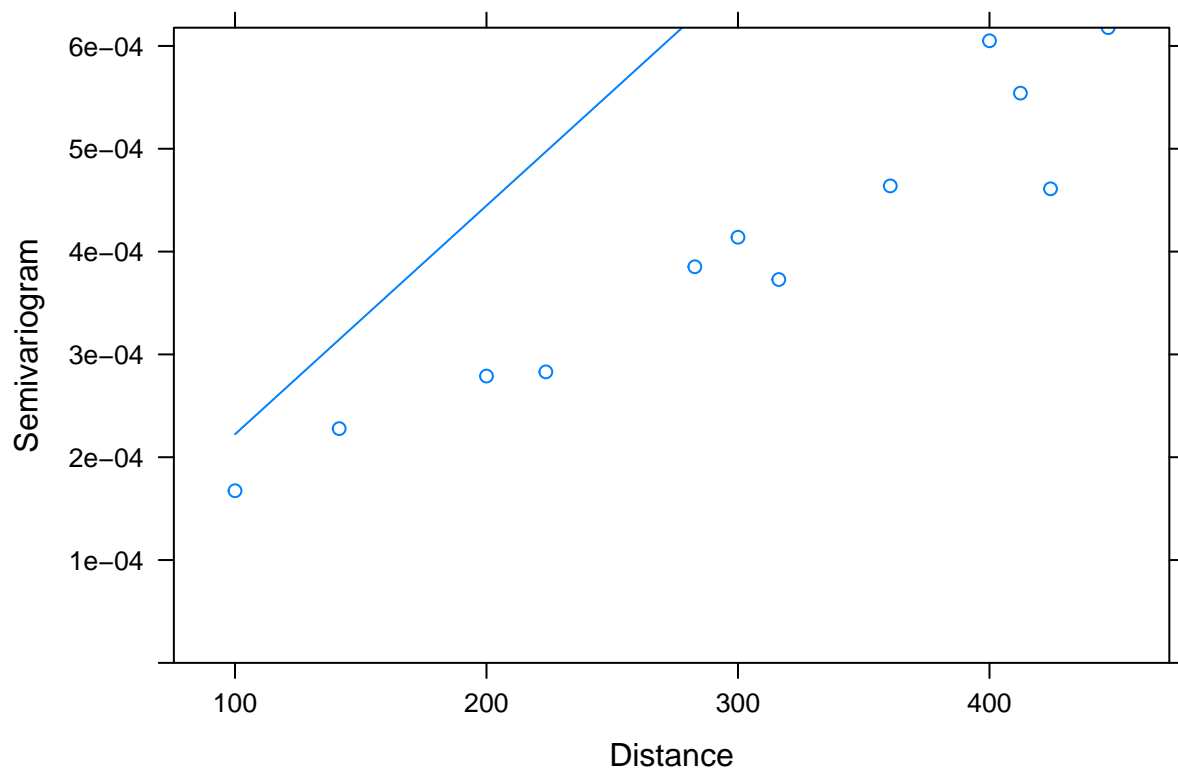
```
#This doesn't look good either.

plot(Variogram(sphere_full, resType='n', maxDist = max_dist))
```
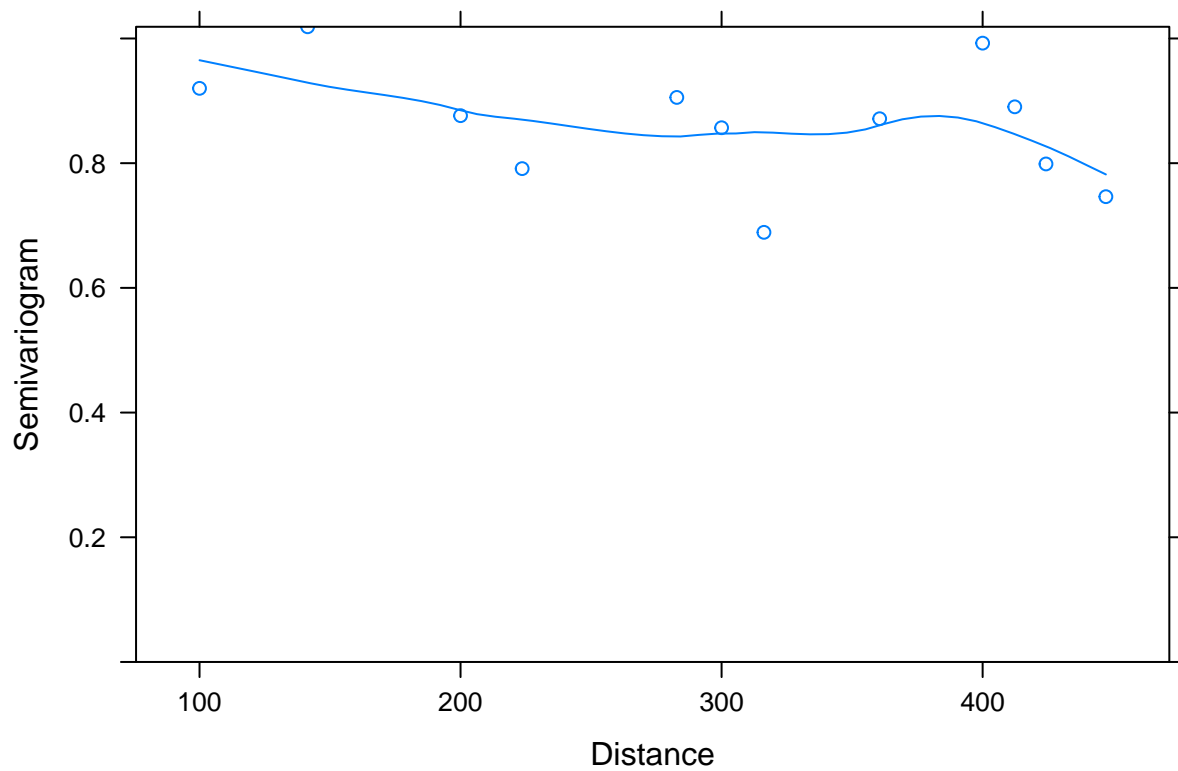
```
#Spherical Spatial Model with Nugget
sphere_full_nug = update(sphere_full, corr=corSpher(form=~x + y, nugget=T))

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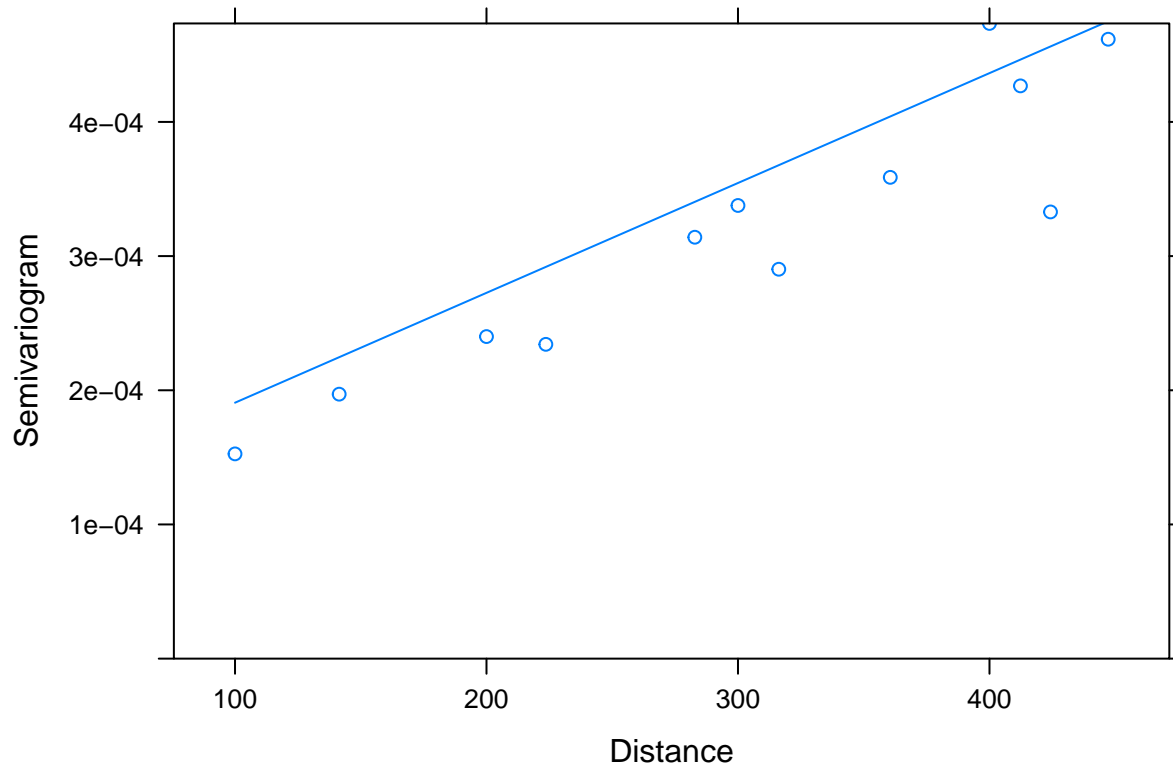


```
#This actually does not look too bad.
plot(Variogram(sphere_full_nug, resType='n', maxDist = max_dist))
```
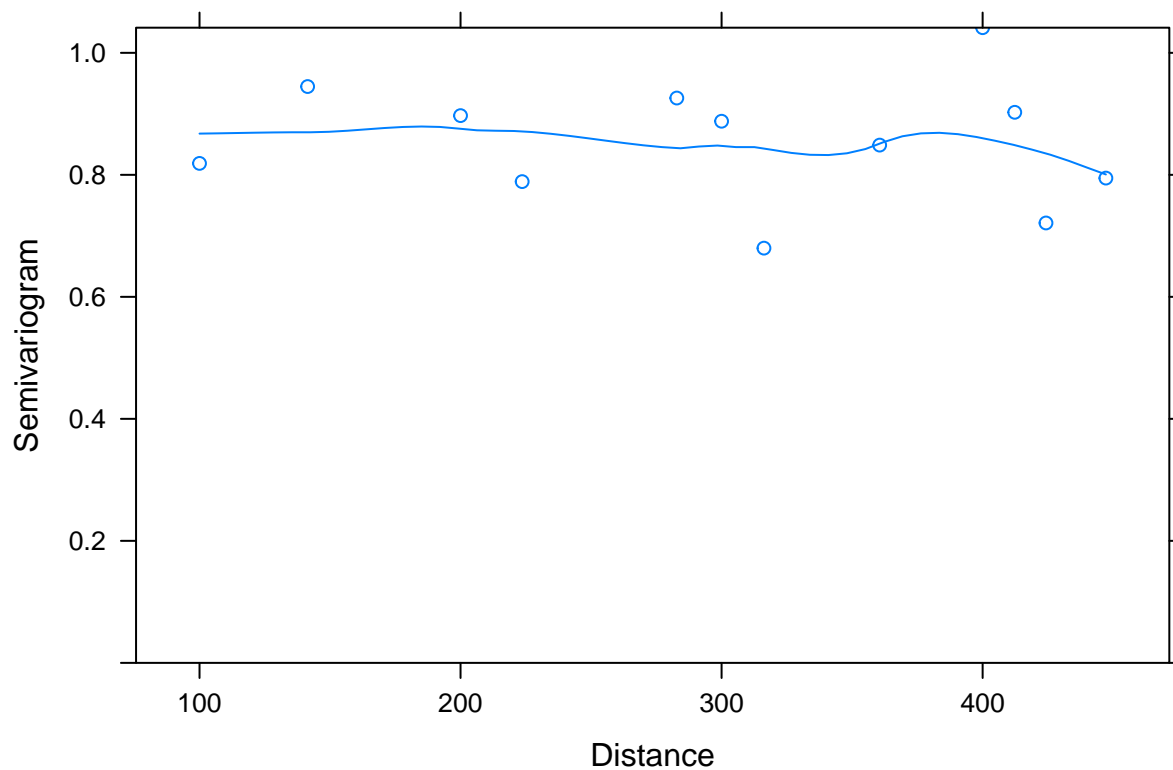
```
#There is not pattern in the plot of the sample variogram, so this is a
#good model to use.




#Compare the Models for the Full Data Set


anova(full_gls, full_gls_nug, full_exp, full_rat, full_rat_nug, full_gaus, full_gaus_nug, sphere_full, s
```

```
##                Model df      AIC      BIC    logLik   Test   L.Ratio
## full_gls           1  9 307.1163 322.7554 -144.5582
## full_gls_nug       2 11 309.7308 328.8452 -143.8654 1 vs 2 1.385539
## full_exp           3 10 301.6062 318.9829 -140.8031 2 vs 3 6.124637
## full_rat           4 10 303.8542 321.2309 -141.9271
## full_rat_nug       5 11 303.1486 322.2630 -140.5743 4 vs 5 2.705548
## full_gaus          6 10 307.2070 324.5837 -143.6035 5 vs 6 6.058355
## full_gaus_nug      7 11 303.8653 322.9797 -140.9327 6 vs 7 5.341637
## sphere_full        8 10 301.9254 319.3021 -140.9627 7 vs 8 0.060069
## sphere_full_nug    9 11 301.9592 321.0735 -139.9796 8 vs 9 1.966257
##               p-value
## full_gls
## full_gls_nug    0.5002
## full_exp        0.0133
## full_rat
## full_rat_nug    0.1000
## full_gaus       0.0138
## full_gaus_nug   0.0208
## sphere_full     0.8064
```

```
## sphere_full_nug  0.1608
```

```
#When using multiple models, we can see that the exponential model
#and both spherical models fit equally as well and much better than
#the other models. All of the models with a nugget have a lower AIC
#than the same spatial model without a spatial error term, so by including
#the nugget in each of the models, this improved the fit of each model.
#Including the nugget did lower the AIC values, but not by much. So this
#may indicate there there is a small spatial dependence overall for the data.
#(The exponential model could not fit a nugget due to false convergence, and
#was an argument not interpretable as logical *this is the error message that
#I received. ).

summary(full_exp)
```

```
## Generalized least squares fit by REML
##   Model: Drypetes_response ~ c_las + h_tri + p_lat + q_ama + t_arb + t_asp +     x_mac
##   Data: bci_sp
##        AIC      BIC    logLik
##   301.6062 318.9829 -140.8031
##
## Correlation Structure: Exponential spatial correlation
##  Formula: ~x + y
##  Parameter estimate(s):
##     range
## 480.0567
##
## Coefficients:
##                 Value Std.Error  t-value p-value
## (Intercept) 2.3485197 6.154919 0.381568  0.7047
## c_las       0.1208390 0.179811 0.672033  0.5052
## h_tri       0.0191759 0.098501 0.194677  0.8466
## p_lat       0.2014516 0.509196 0.395627  0.6944
## q_ama       1.2792289 1.847570 0.692385  0.4925
## t_arb       0.0674943 0.133782 0.504511  0.6165
## t_asp       1.8115374 0.525147 3.449582  0.0013
## x_mac       0.3388574 0.156874 2.160064  0.0365
##
##  Correlation:
##       (Intr) c_las  h_tri  p_lat  q_ama  t_arb  t_asp
## c_las -0.226
## h_tri -0.309 -0.022
## p_lat  0.045 -0.066 -0.369
## q_ama -0.059 -0.304  0.321 -0.142
## t_arb -0.240 -0.016  0.288 -0.221  0.112
## t_asp -0.069  0.168 -0.237  0.212 -0.633 -0.041
## x_mac -0.056 -0.137 -0.063  0.109  0.290  0.102 -0.186
##
## Standardized residuals:
##        Min         Q1        Med         Q3        Max
## -1.0051632 -0.5235683 -0.3176178  0.2208753  2.3746027
##
## Residual standard error: 8.628464
## Degrees of freedom: 50 total; 42 residual
```

```
summary(sphere_full)
```

```
## Generalized least squares fit by REML
##   Model: Drypetes_response ~ c_las + h_tri + p_lat + q_ama + t_arb + t_asp +      x_mac
##   Data: bci_sp
##        AIC      BIC    logLik
##   301.9254 319.3021 -140.9627
##
## Correlation Structure: Spherical spatial correlation
##  Formula: ~x + y
##  Parameter estimate(s):
##     range
## 674629.1
##
## Coefficients:
##                Value Std.Error   t-value p-value
## (Intercept)  3.988119 256.16657  0.015568  0.9877
## c_las        0.111421   0.17643  0.631546  0.5311
## h_tri       -0.001071   0.09890 -0.010832  0.9914
## p_lat        0.149191   0.50026  0.298227  0.7670
## q_ama        0.813048   1.83774  0.442417  0.6605
## t_arb        0.075313   0.13096  0.575101  0.5683
## t_asp        1.834240   0.51295  3.575877  0.0009
## x_mac        0.309959   0.15670  1.978002  0.0545
##
##  Correlation:
##       (Intr) c_las  h_tri  p_lat  q_ama  t_arb  t_asp
## c_las -0.007
## h_tri -0.010 -0.007
## p_lat  0.002 -0.066 -0.361
## q_ama -0.003 -0.290  0.339 -0.127
## t_arb -0.007 -0.017  0.287 -0.227  0.108
## t_asp -0.003  0.171 -0.232  0.207 -0.623 -0.039
## x_mac -0.001 -0.133 -0.061  0.134  0.298  0.089 -0.183
##
## Standardized residuals:
##          Min           Q1          Med           Q3          Max
## -0.038619444 -0.023162234 -0.015811190  0.003689907  0.078083046
##
## Residual standard error: 256.311
## Degrees of freedom: 50 total; 42 residual
```

```
summary(sphere_full_nug)
```

```
## Generalized least squares fit by REML
##   Model: Drypetes_response ~ c_las + h_tri + p_lat + q_ama + t_arb + t_asp +      x_mac
##   Data: bci_sp
##        AIC      BIC    logLik
##   301.9592 321.0735 -139.9796
##
## Correlation Structure: Spherical spatial correlation
##  Formula: ~x + y
```

```
##   Parameter estimate(s):
##        range         nugget
## 1.831904e+06 1.088636e-04
##
## Coefficients:
##                 Value Std.Error    t-value p-value
## (Intercept)  3.0501051 267.79376  0.011390  0.9910
## c_las        0.1426672   0.18953  0.752754  0.4558
## h_tri       -0.0017713   0.09038 -0.019599  0.9845
## p_lat        0.2863351   0.52743  0.542882  0.5901
## q_ama        1.3263713   1.93681  0.684821  0.4972
## t_arb        0.0407524   0.13952  0.292080  0.7717
## t_asp        1.8170748   0.57298  3.171298  0.0028
## x_mac        0.4086712   0.15367  2.659334  0.0110
##
##   Correlation:
##        (Intr) c_las  h_tri  p_lat  q_ama  t_arb  t_asp
## c_las -0.006
## h_tri -0.007 -0.098
## p_lat  0.001  0.017 -0.360
## q_ama -0.001 -0.292  0.344 -0.193
## t_arb -0.005 -0.020  0.160 -0.197  0.088
## t_asp -0.002  0.165 -0.276  0.255 -0.655 -0.036
## x_mac -0.001 -0.066 -0.037 -0.048  0.306  0.140 -0.183
##
## Standardized residuals:
##          Min           Q1          Med          Q3          Max
## -0.032872366 -0.019385351 -0.013776425  0.003711977  0.069107528
##
## Residual standard error: 267.852
## Degrees of freedom: 50 total; 42 residual
```

```
#After looking at the t values associated with each model, we can see that
#the spherical spatial model is a better fit than the exponential model,
#but the spherical model with a nugget has even a better fit than that.
#So the Spherical spatial model with a spatial error term is a much
#better fit to our data than the other models.

col_brks = hist(residuals(sphere_full_nug), plot=T)$breaks
```

Histogram of residuals(sphere_full_nug)
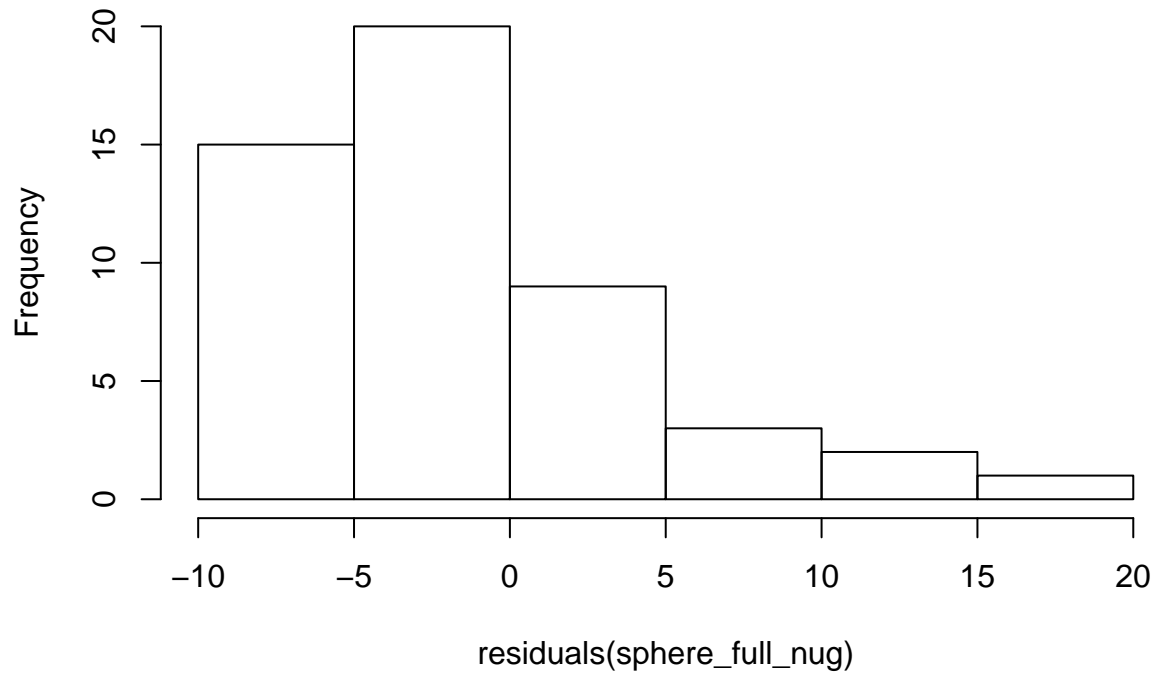

```
col_indices = as.numeric(cut(residuals(sphere_full_nug), col_brks))
cols = rev(terrain.colors(length(col_brks)))
plot(BCI_xy, cex=2, pch=19, col=cols[col_indices])
```
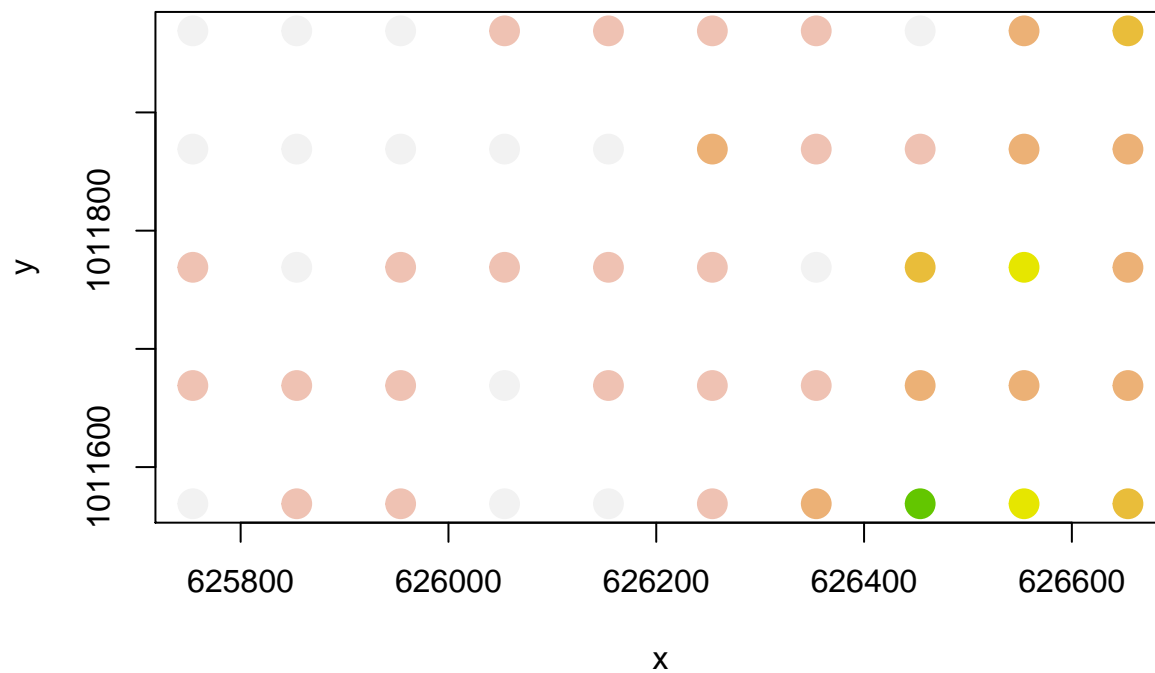


```
#It appears that at low distances, we have clumping of trees abundance
#indicated with the pink dots. We can also see clumping of larger
#tree abundances at larger xy distances, indicating spatial dependence
```

```
#in our residuals. This pattern is concurrent with the full data set;
#this is why we saw a difference (lower AIC) when we included the spatial
#error term.
```