

# Spatial Modeling Homework

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```
library(vegan)
```

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

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

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

```
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
```

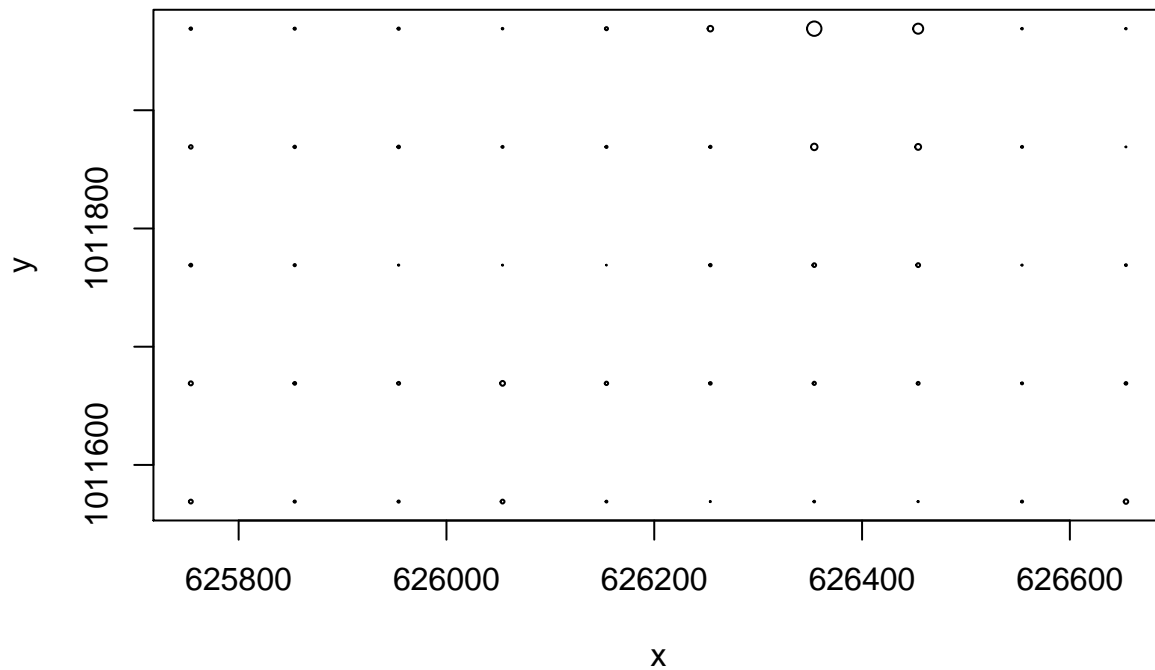
```
common <- BCI$Alseis.blackiana
```

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

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

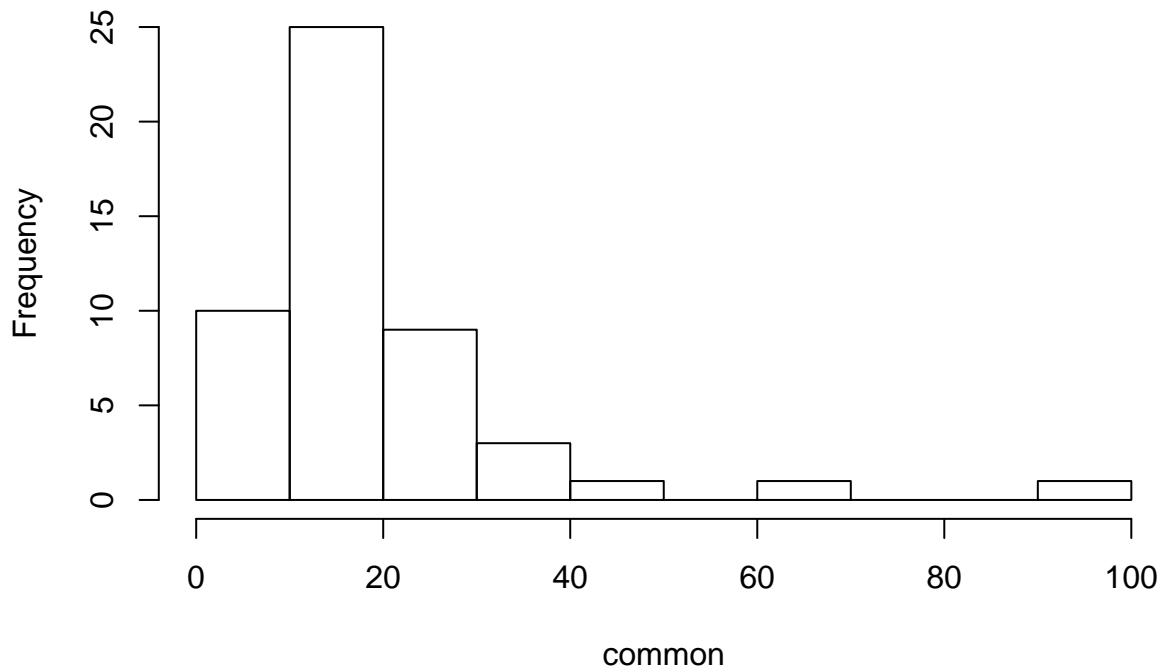
Common Species

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

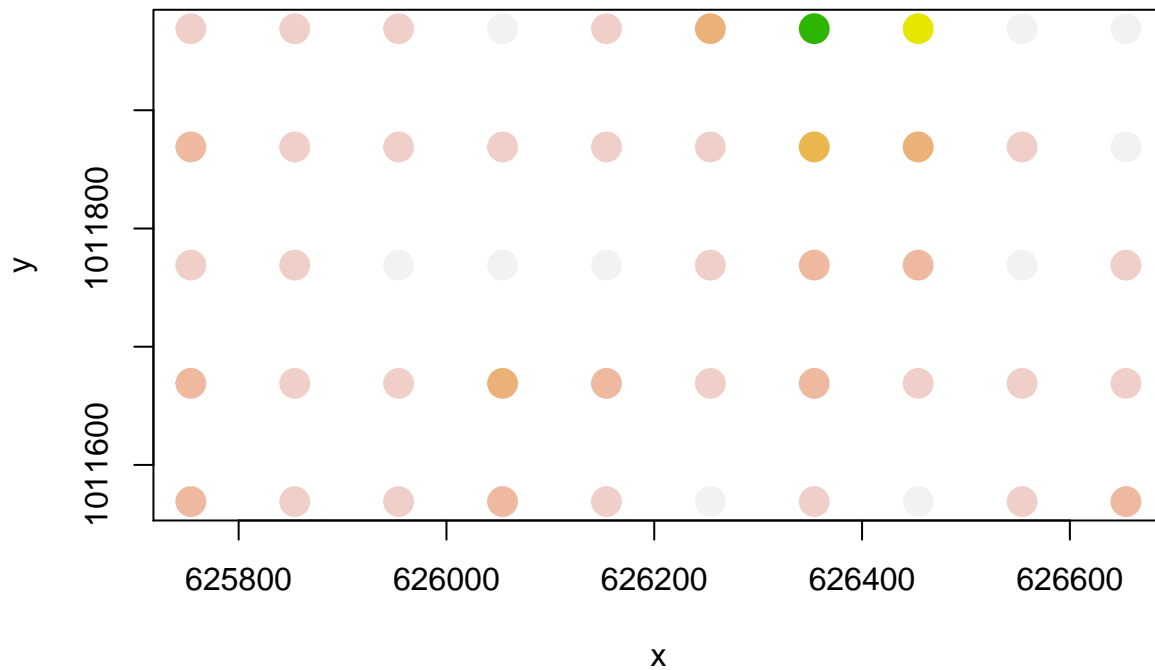


```
col_brks = hist(common, plot=T)$breaks
```

### 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])
```

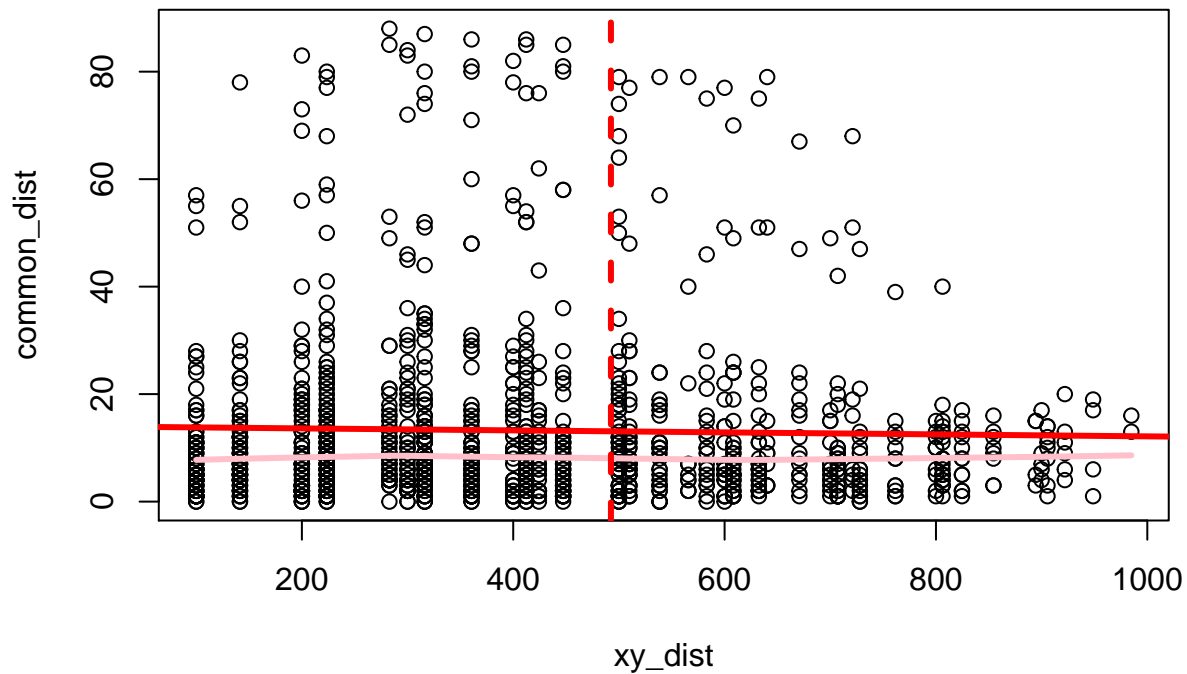


*#These are all mixed together and do not appear to be spatially dependent  
#on one another. There is no clear association dependent on space.  
# The green and yellow are closer together, and it is  
#possible that those points are spatially dependent, but I cannot come to this  
#conclusion based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

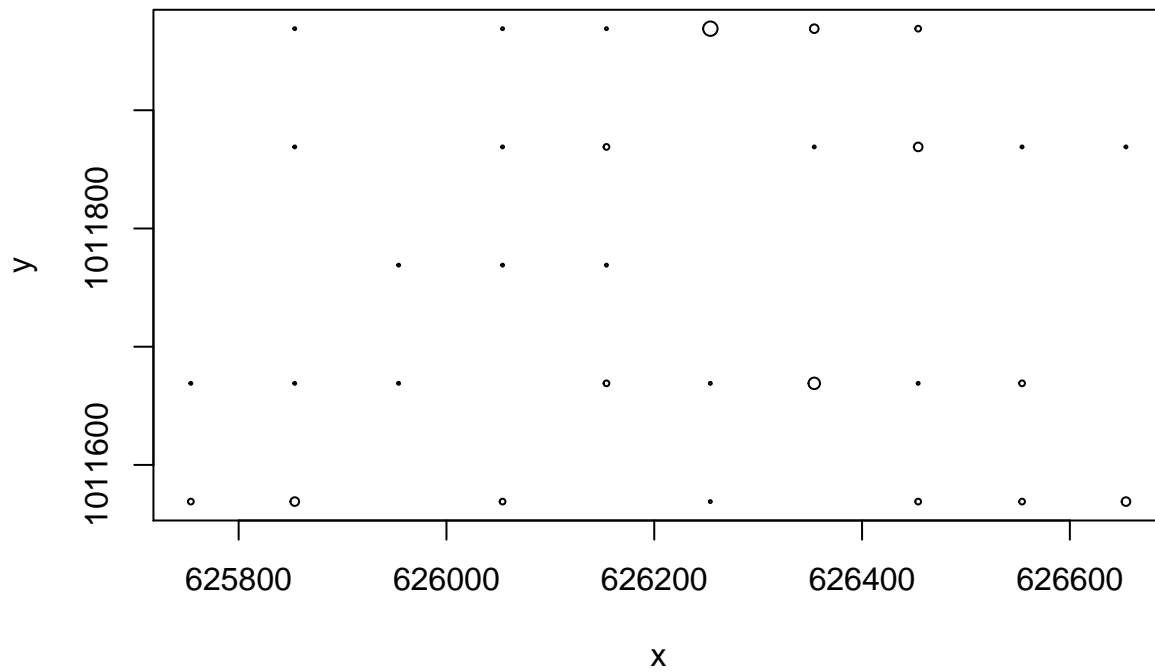
```
#correlation
common_cor = cor(xy_dist, common_dist)
#-0.02348007
```

*#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

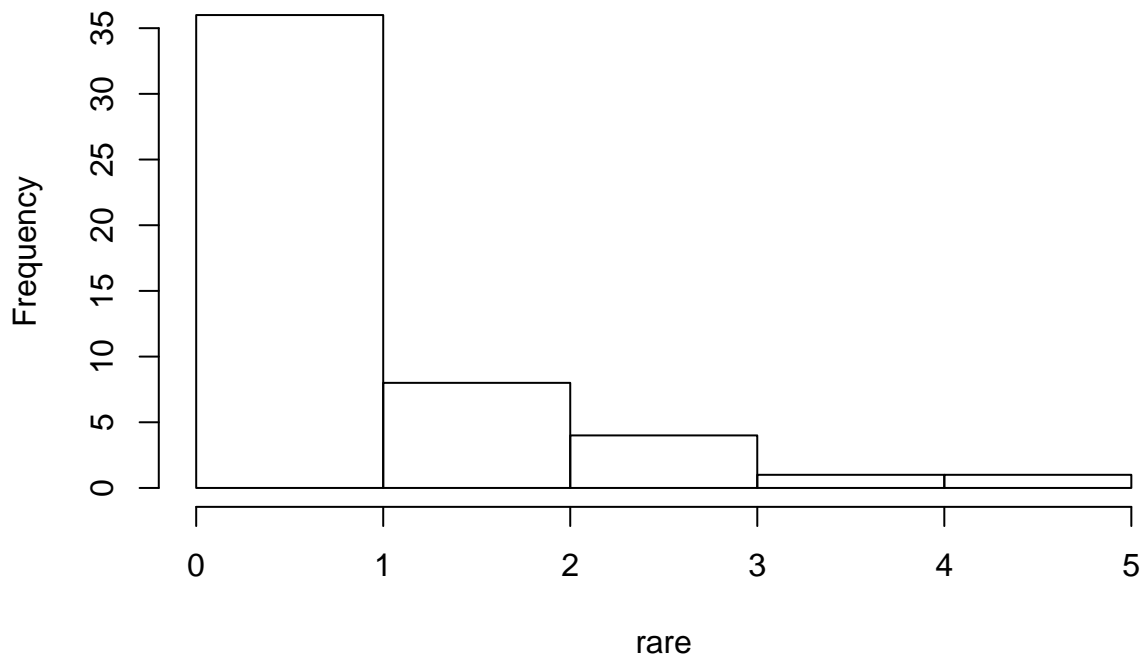
```
#rare

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

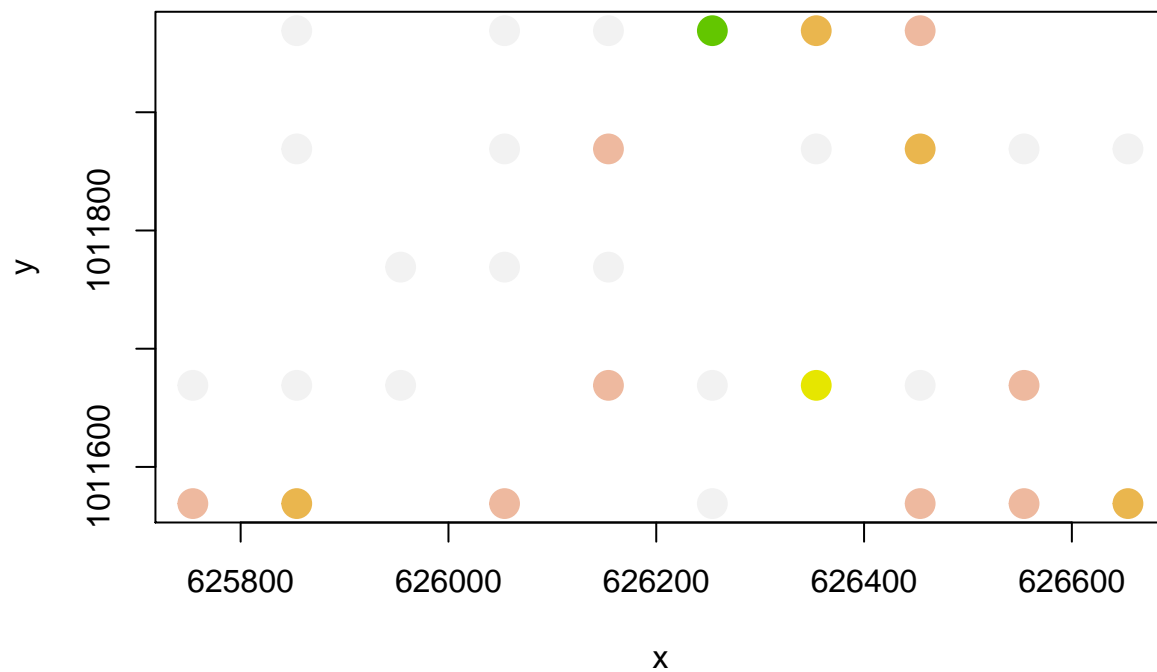


```
col_brks = hist(rare, plot=T)$breaks
```

### 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])
```

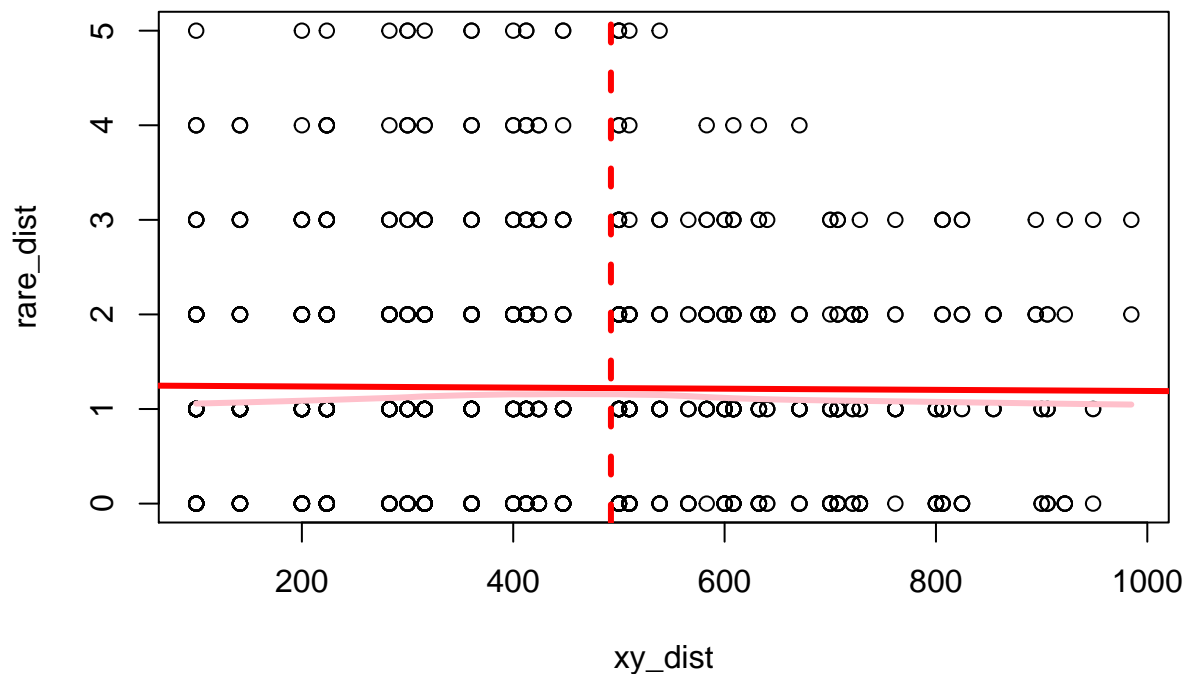


*#Does not indicate any visual relationship of spatial dependence.*

```
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. Similarly, 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)
#-0.0116346

#This is a very small (negative) correlation. 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: 0.613
##
## Upper quantiles of permutations (null model):
```

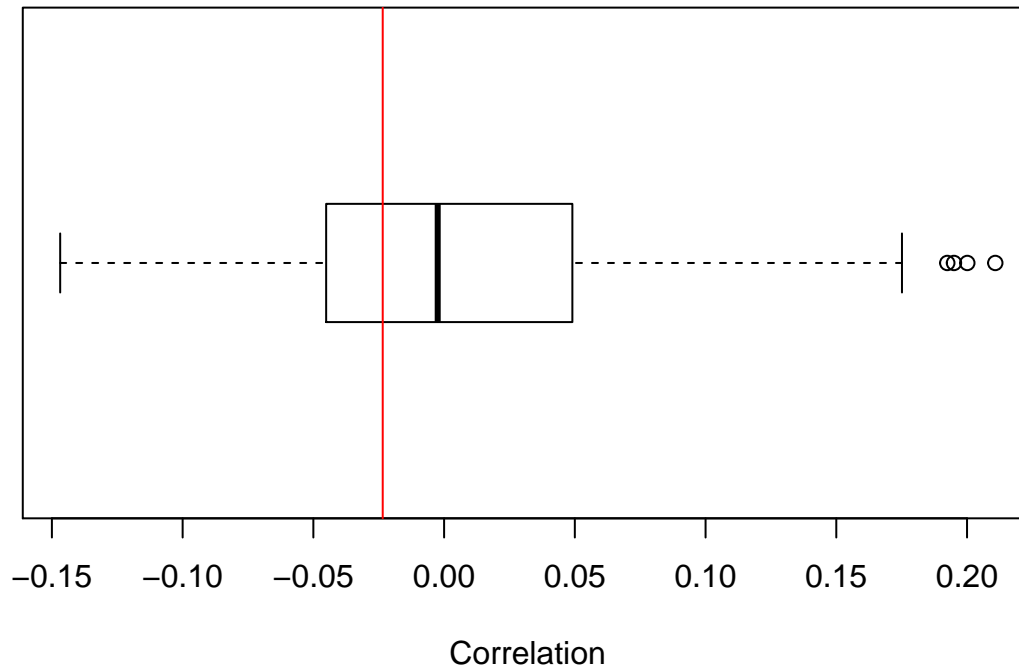
```
##      90%      95%  97.5%   99%
## 0.0955 0.1176 0.1418 0.1580
## Permutation: free
## Number of permutations: 999
```

```
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: 0.553
##
## Upper quantiles of permutations (null model):
##      90%      95%  97.5%   99%
## 0.0726 0.0977 0.1137 0.1374
## 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')
```

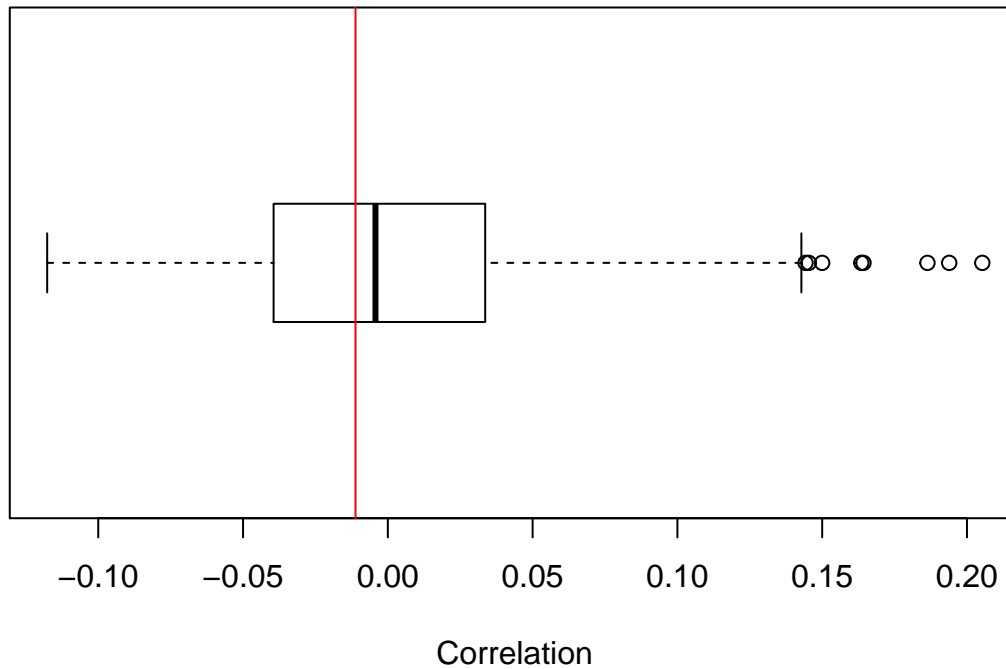




```
#For common speices, Alseis blackiana, the observed value is smaller
#than the null realizations, but not significantly smaller. This indicates
#no significant relationship between spatial distance and the abundance
#of individuals for the common species.
```

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

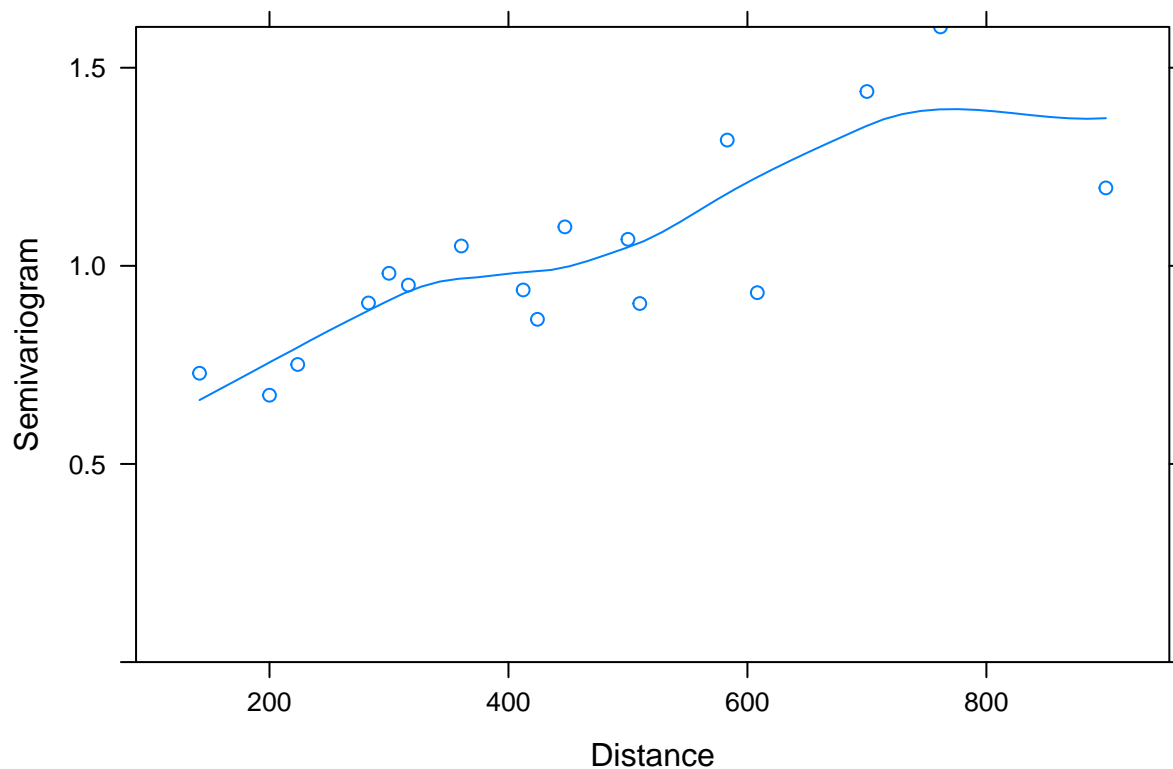
single_sp_mod <- data.frame(sp_response, sp_predictor, BCI_xy)

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))

```

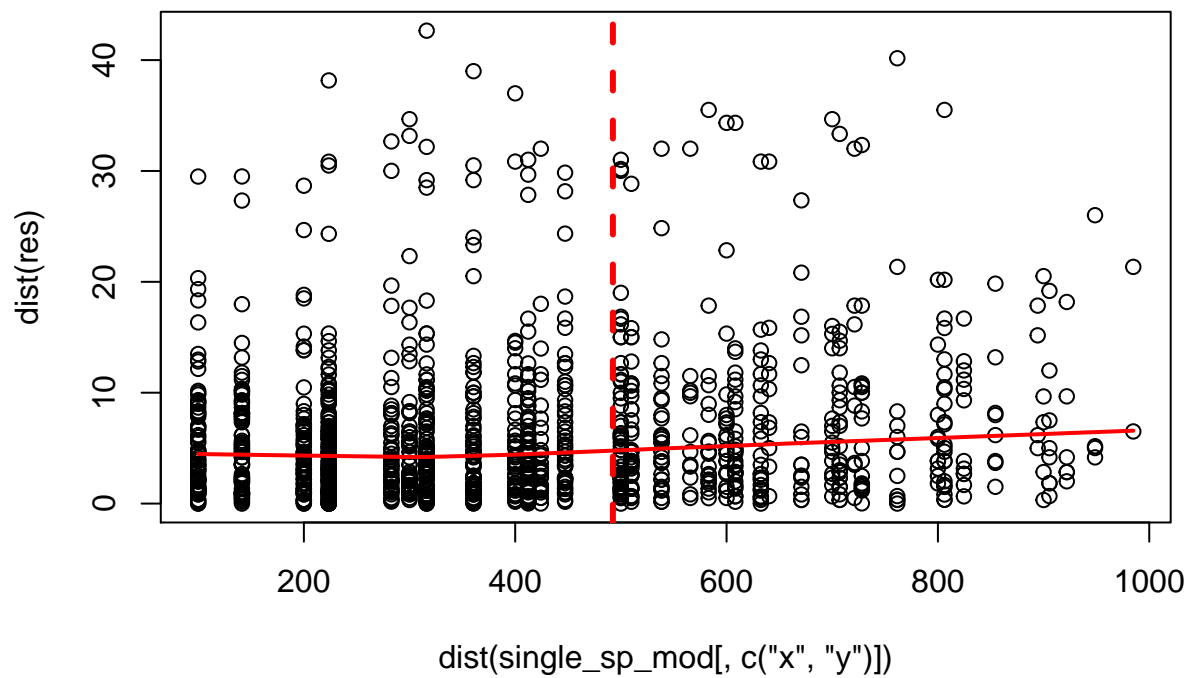


```

#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)

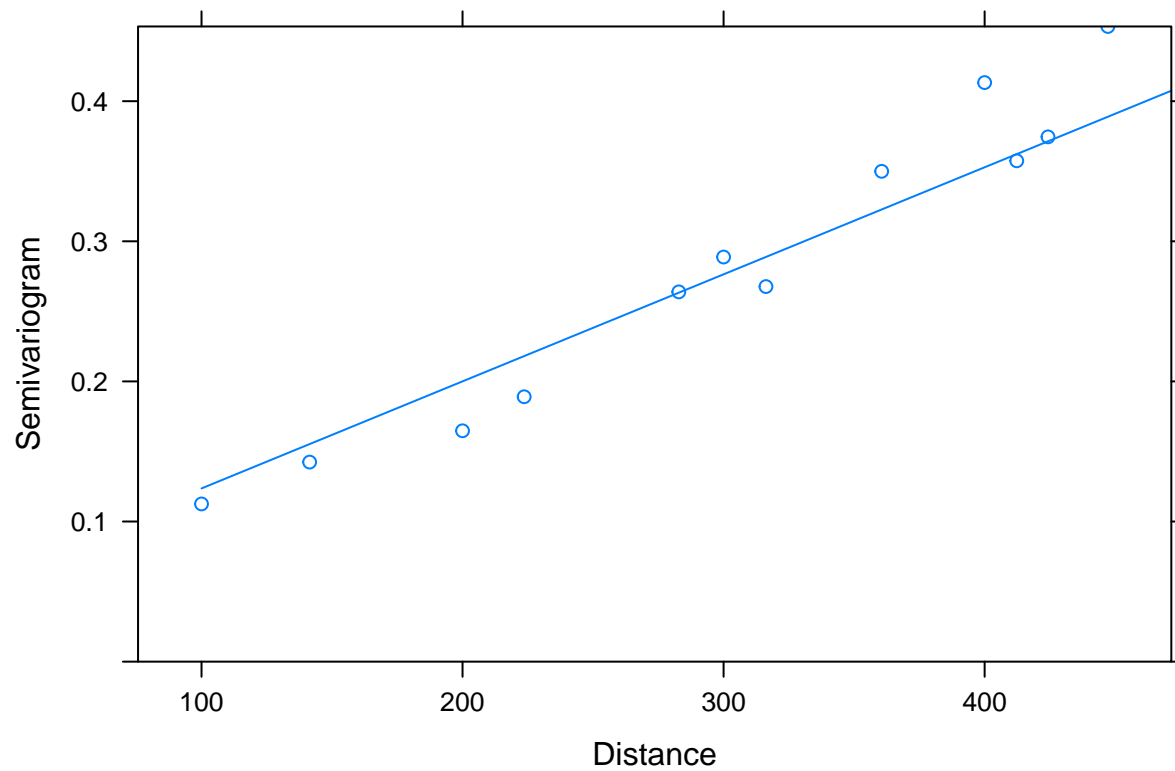
res = residuals(mod1_lm)
plot(dist(single_sp_mod [, c('x', 'y')]), dist(res))
lines(lowess(dist(single_sp_mod [, c('x', 'y')]), dist(res)), col='red', lwd=2)
abline(v = max_dist, col='red', lwd=3, lty=2)

```



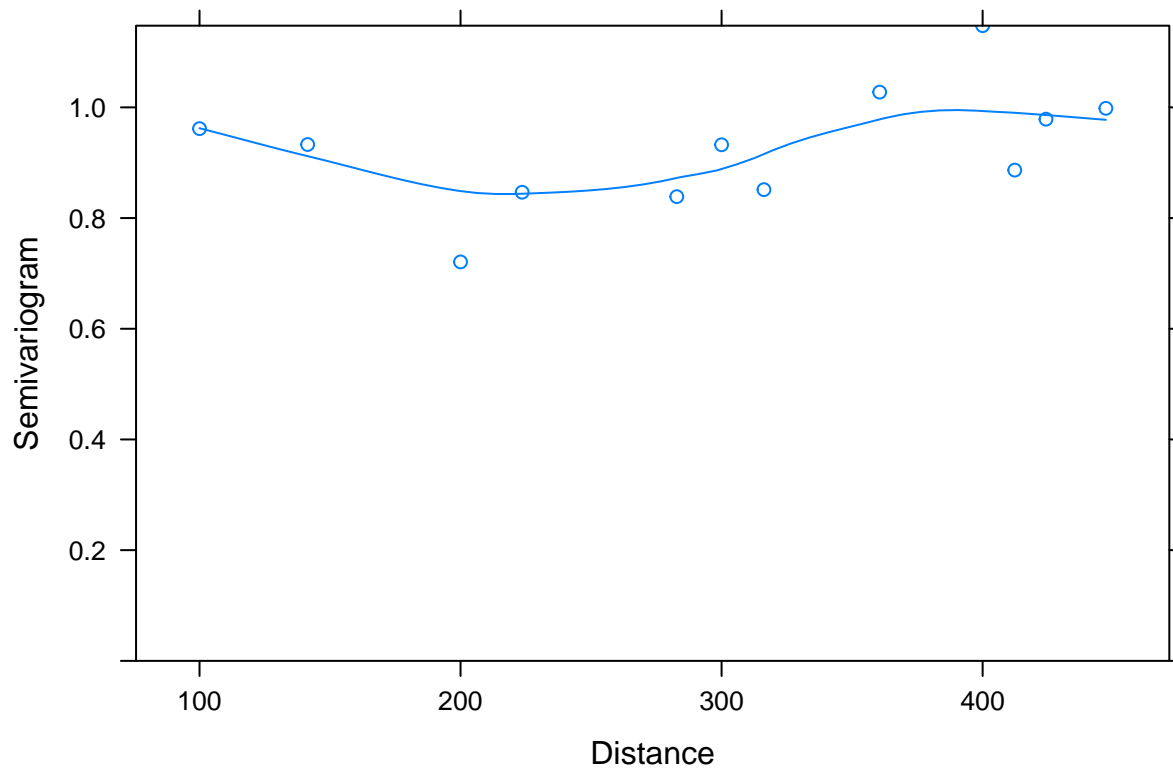
*#GLS with Nugget*

```
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))
```

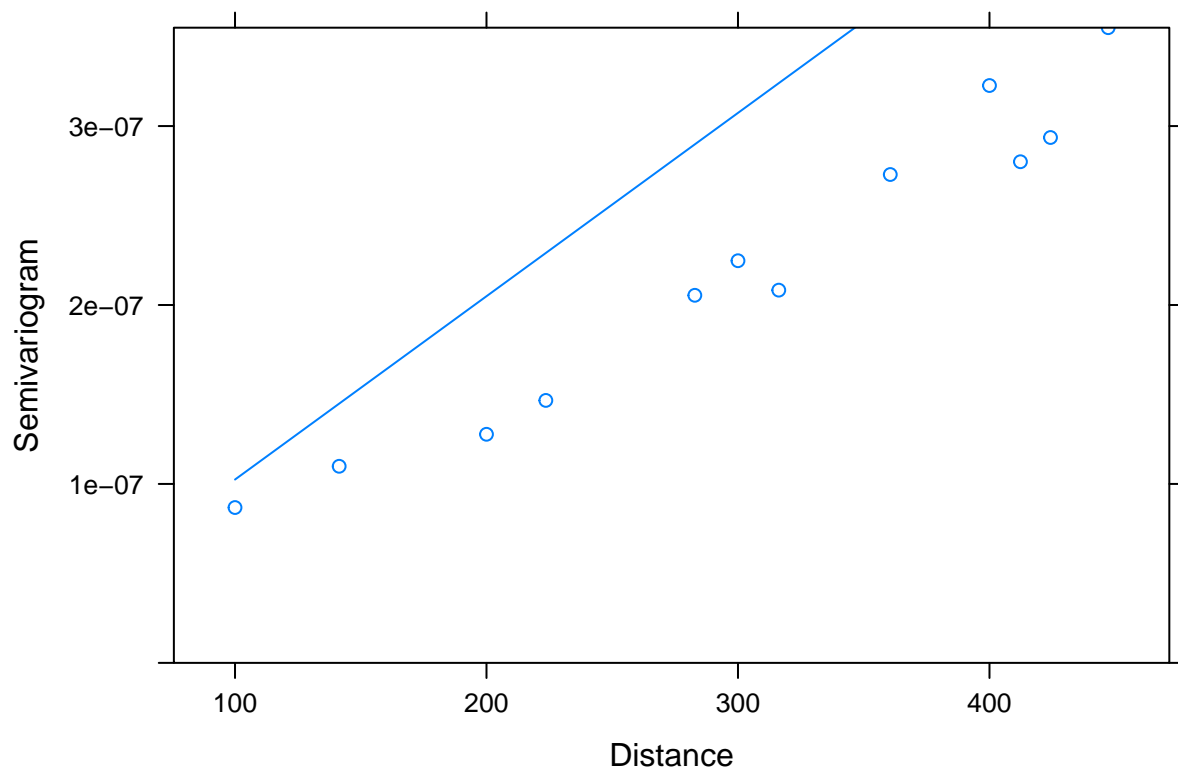


```
#This model fits very well, our residuals are normally distributed
```

```
#Exponential Variogram
```

```
mod1_exp = update(mod1_lm, corr=corExp(form=~x + y))
```

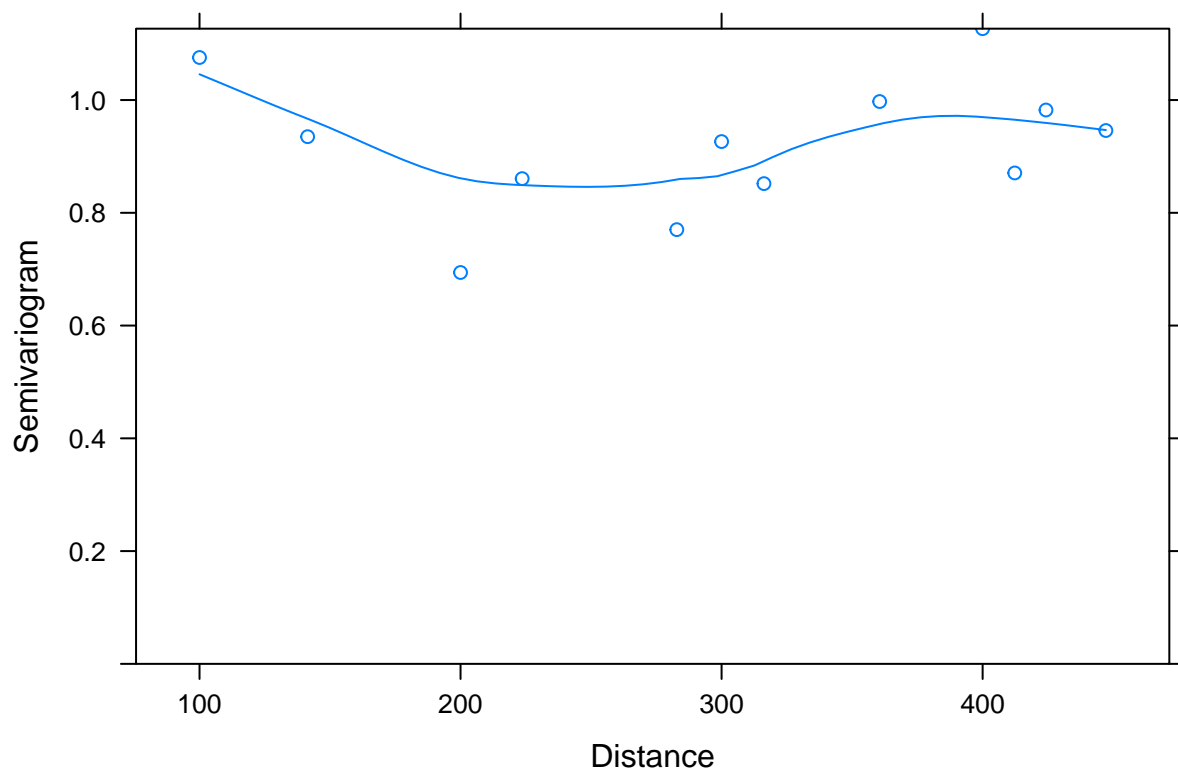
```
plot(Variogram(mod1_exp, maxDist = max_dist))
```



*#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.
```

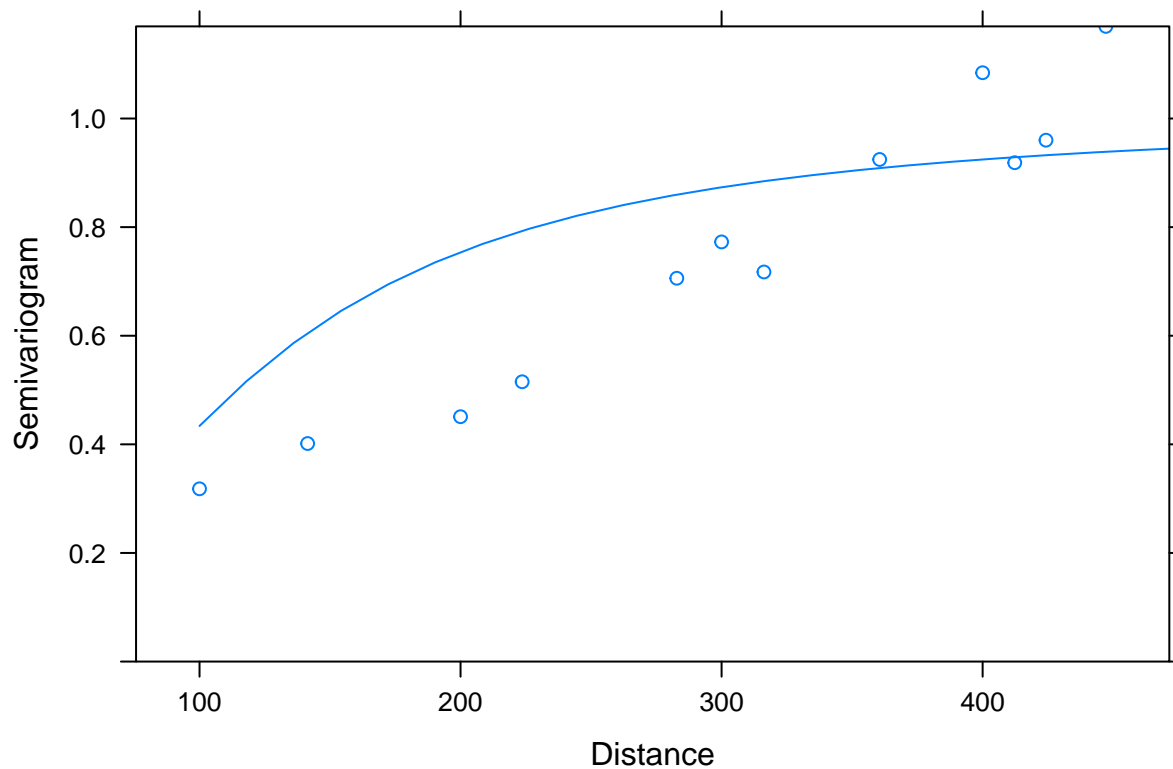
```
#Exponential Model with a Nugget
```

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

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

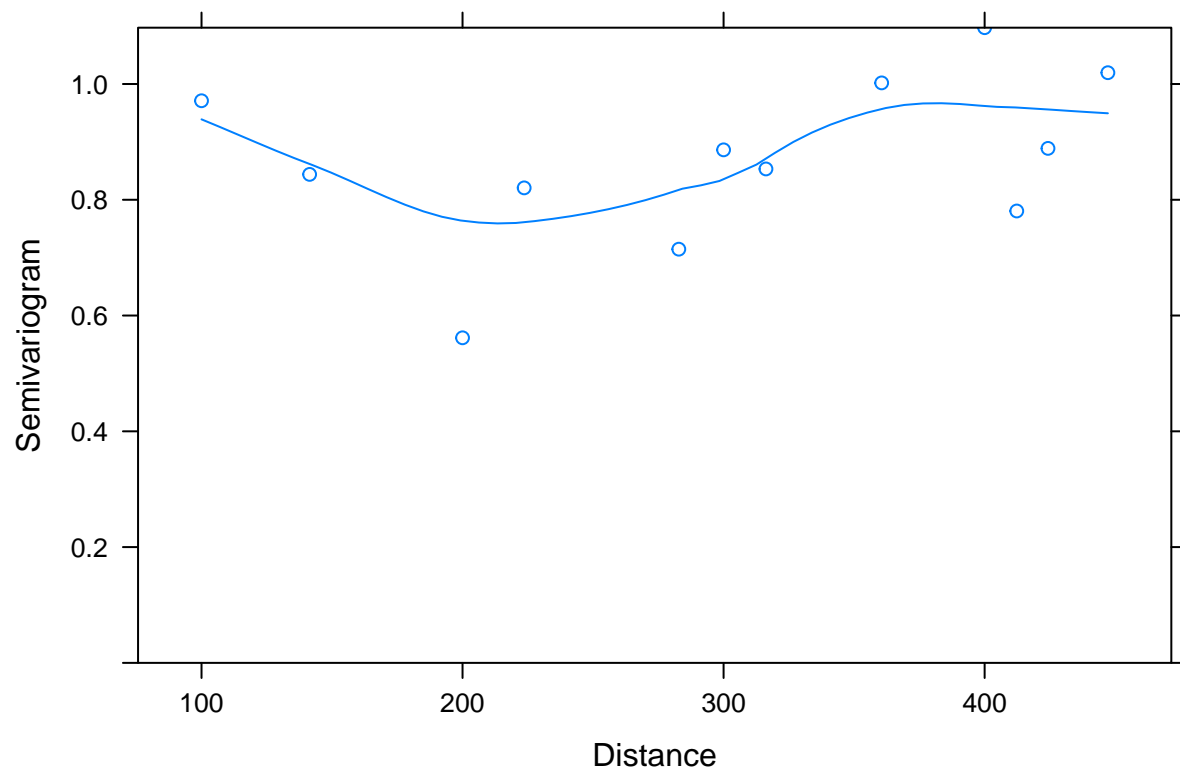
```
#Rational Quadratic Model Spatial Correlation
```

```
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))
```

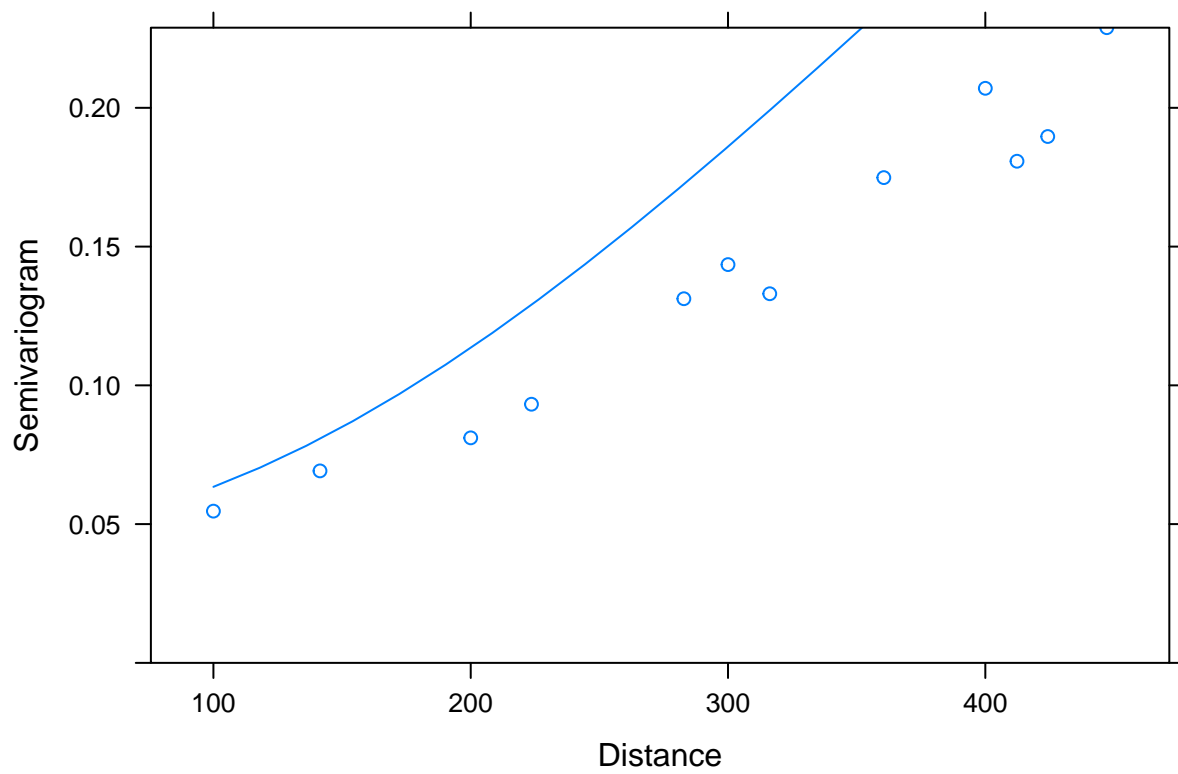


*#This is not too bad, looks very similar to the exponential model*

*#Rational Quadratic Model With Nugget*

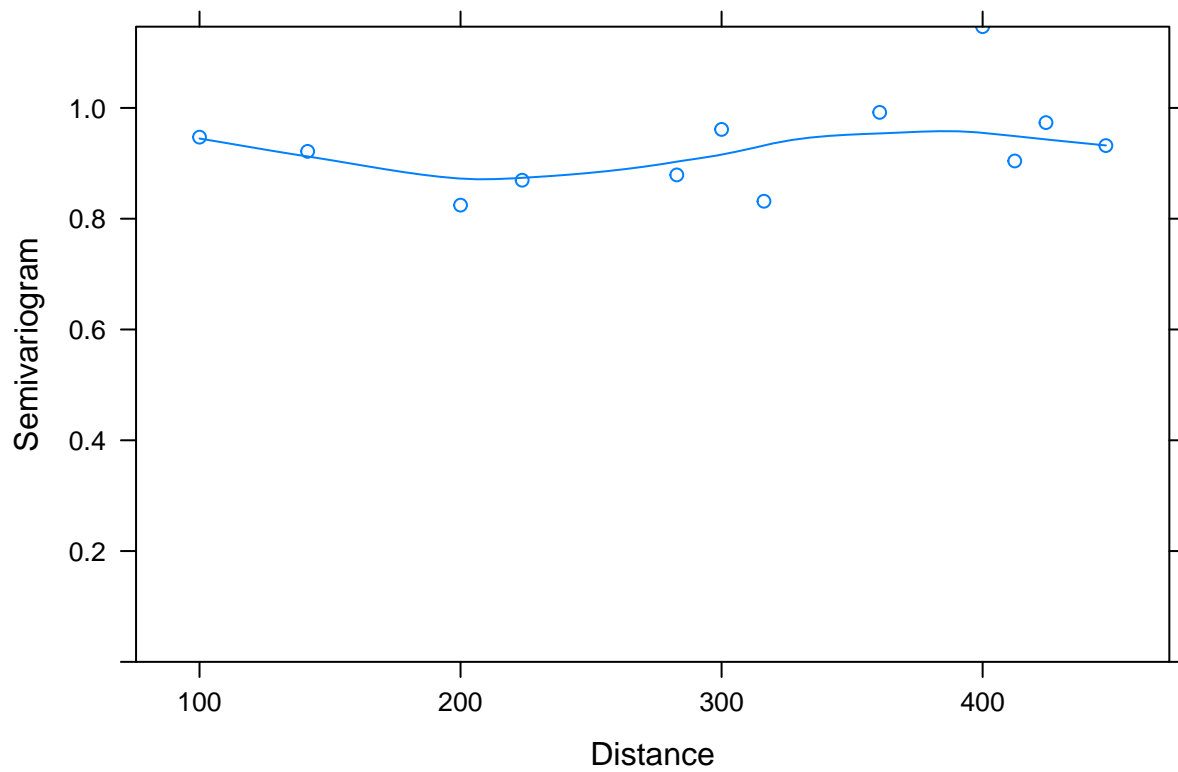
```
rat_nug_mod1 = update(mod1_lm, corr=corRatio(form=-x + y, nugget=T))
```

```
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))
```



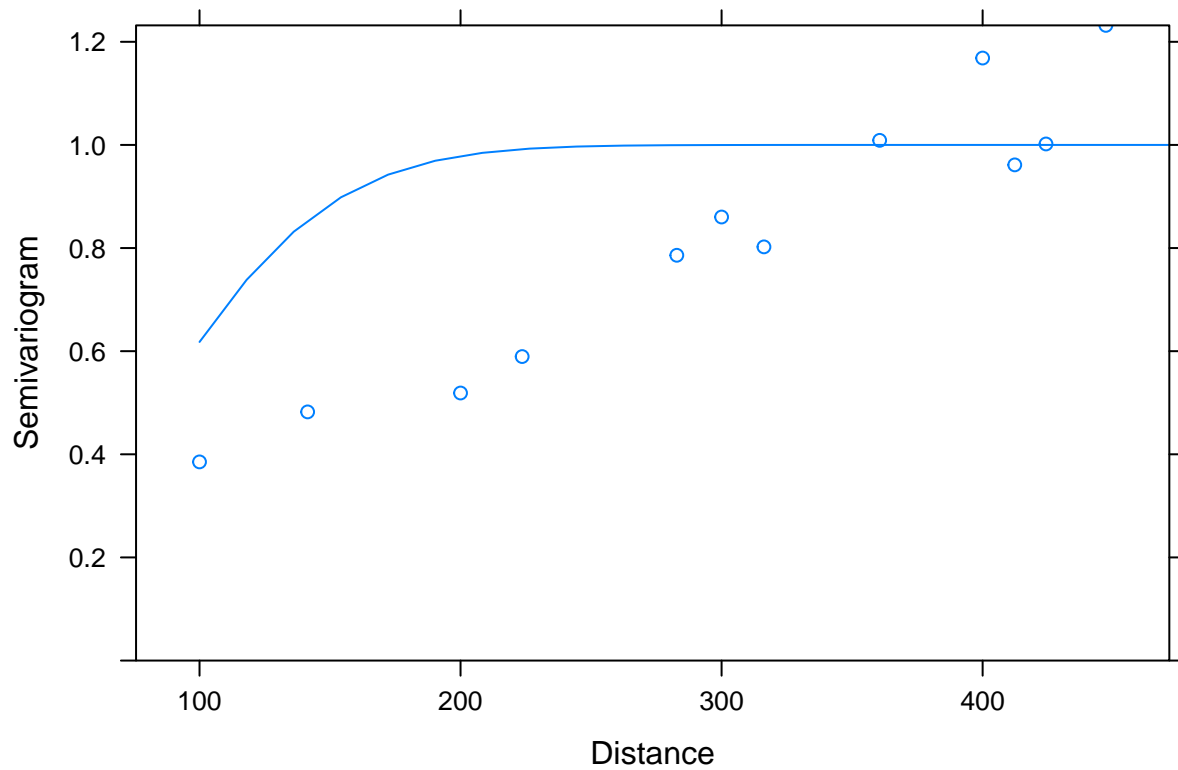


```
#There is no pattern in the variogram (of our residuals),  
#so we can conclude that the rational quadratic model is a  
#good model to use.
```

```
#Gaussian Spatial Model
```

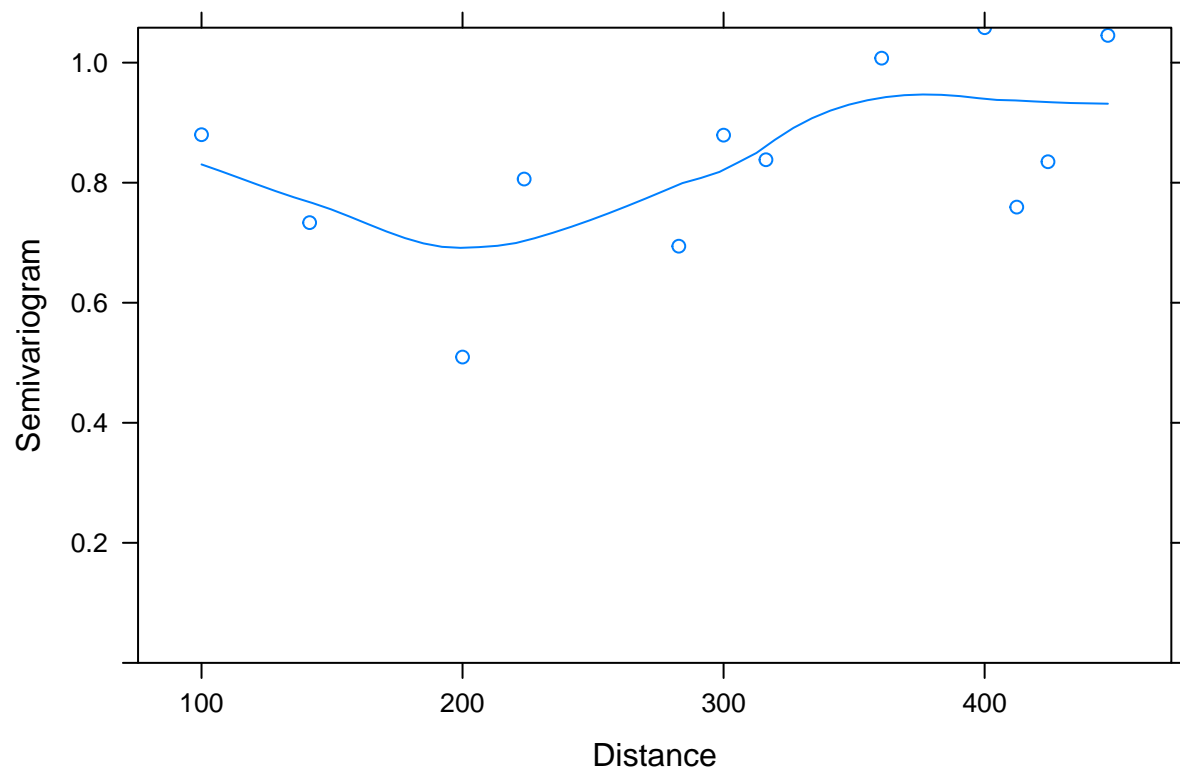
```
gaus_mod1 = update(mod1_lm, corr=corGaus(form=~x + y))
```

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



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

```
plot(Variogram(gaus_mod1, resType='n', maxDist = max_dist))
```

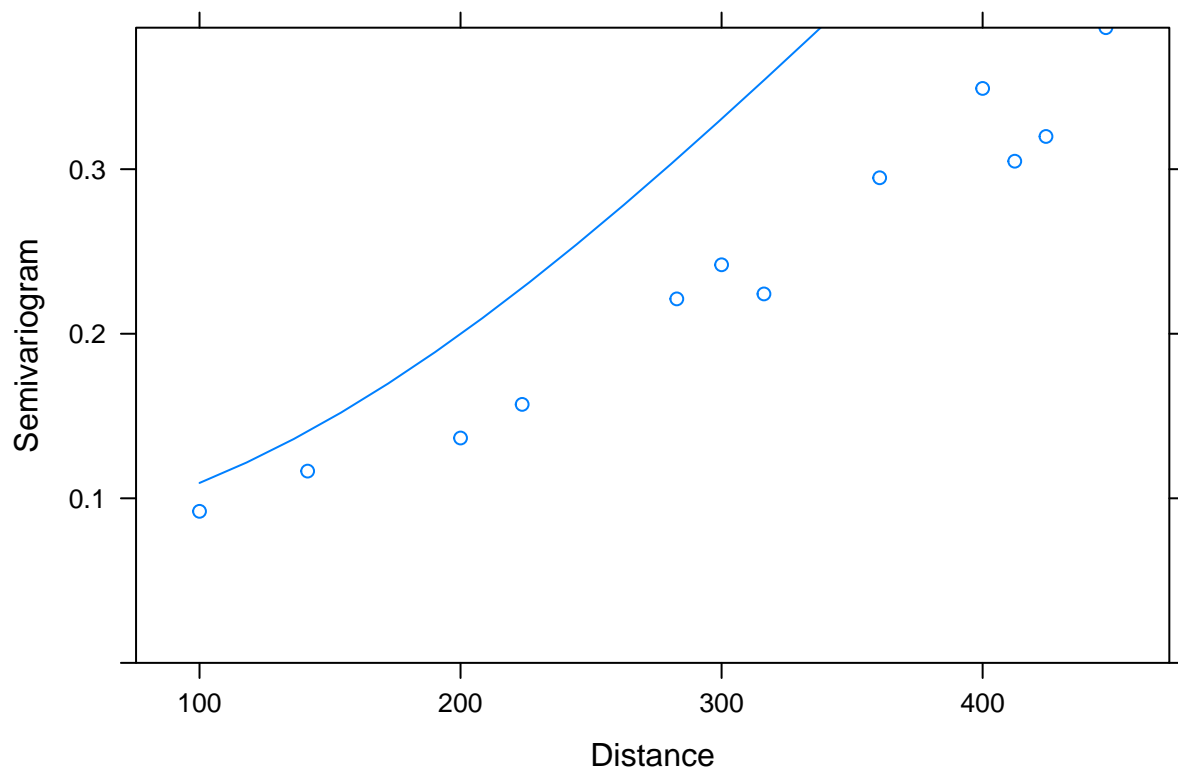


*#I can see a small trend but this isn't bad.*

*#Gaussian Spatial Model with Nugget*

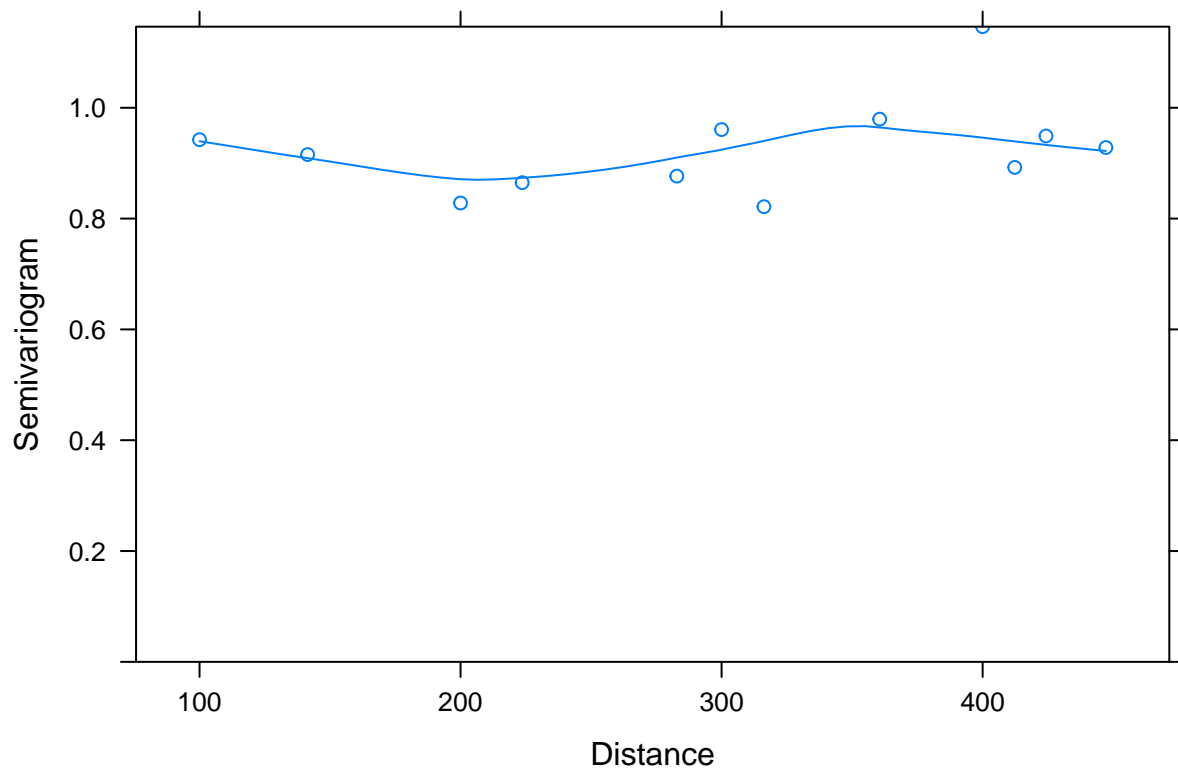
```
gaus_nug_mod1 = update(gaus_mod1, corr=corGaus(form=~x + y, nugget=T))
```

```
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))
```



*#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
```

*#The rational quadratic model with the nugget and the gaussian model with the #nugget are almost identical to the #gaussian model. When a nugget was included for the gls, rational quadratic, and #gaussian models, it is not 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:
```

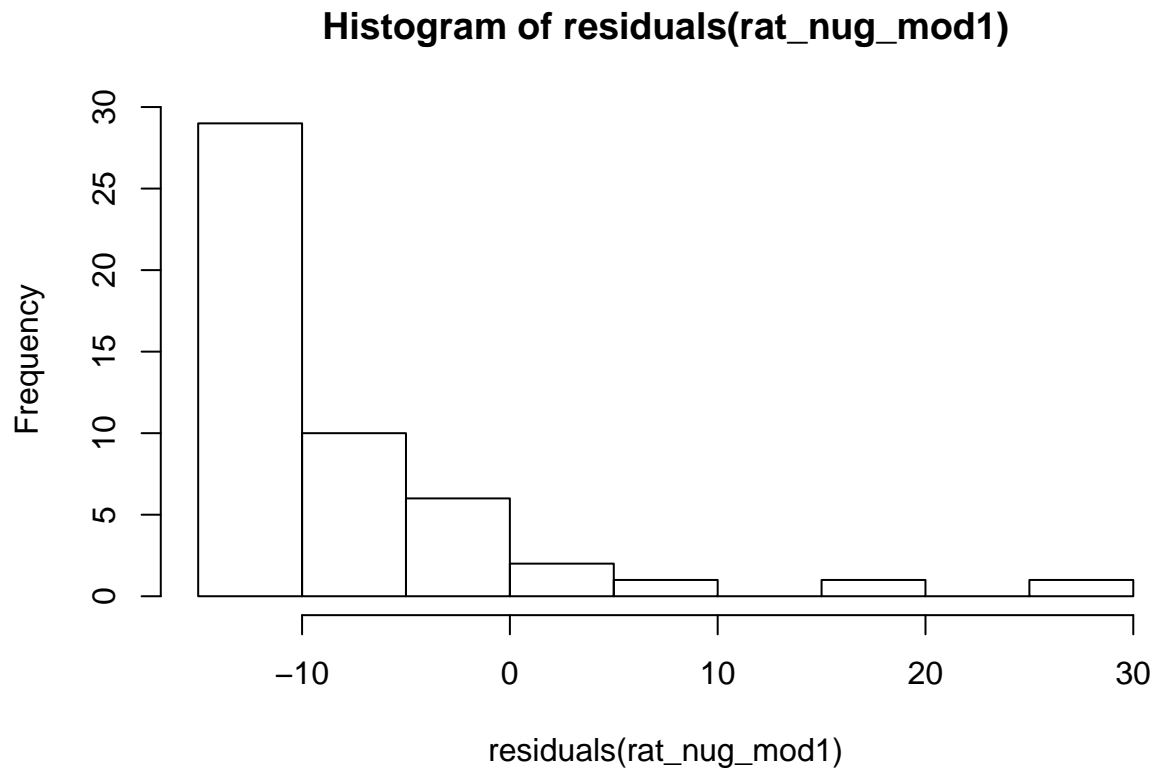
```
##           Min           Q1           Med           Q3           Max
## -0.7668581 -0.7168281 -0.6175156 -0.3685195  1.3705711
##
## Residual standard error: 18.29516
## Degrees of freedom: 50 total; 48 residual
```

```
summary(gaus_nug_mod1)
```

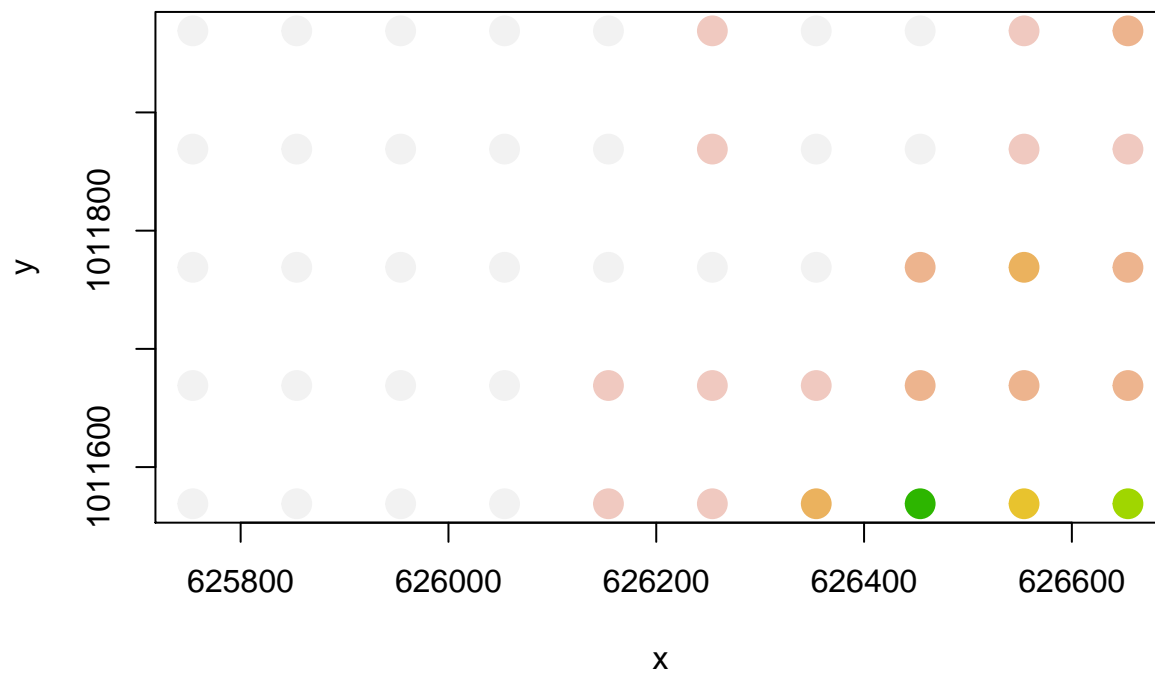
```
## Generalized least squares fit by REML
## Model: sp_response ~ sp_predictor
## Data: single_sp_mod
##      AIC      BIC    logLik
## 308.8879 318.244 -149.444
##
## Correlation Structure: Gaussian spatial correlation
## Formula: ~x + y
## Parameter estimate(s):
##      range      nugget
## 529.28590917  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 residuals  
#This is observed in the rat\_nug\_mod1.*

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



```
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 parameter 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.

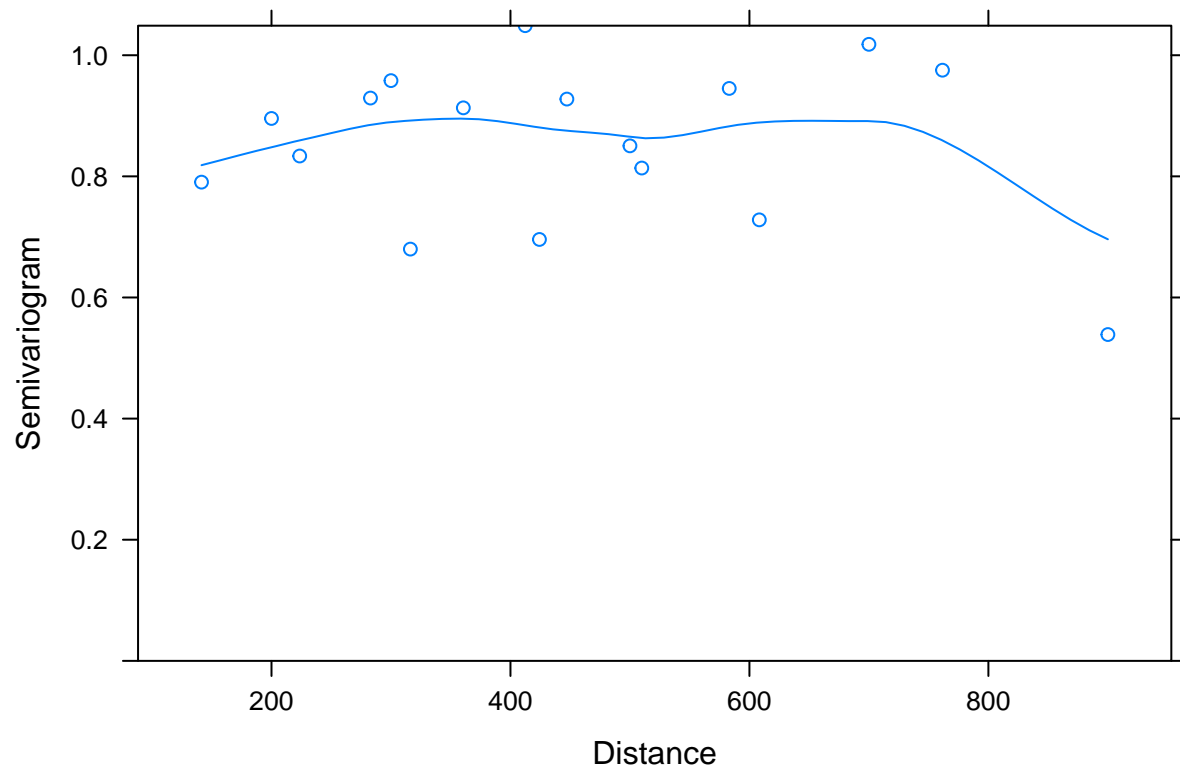
bci_sp <- data.frame(Drypetes_response, c_las, h_tri, p_lat, q_ama, t_arb, t_asp, x_mac, BCI_xy)

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)

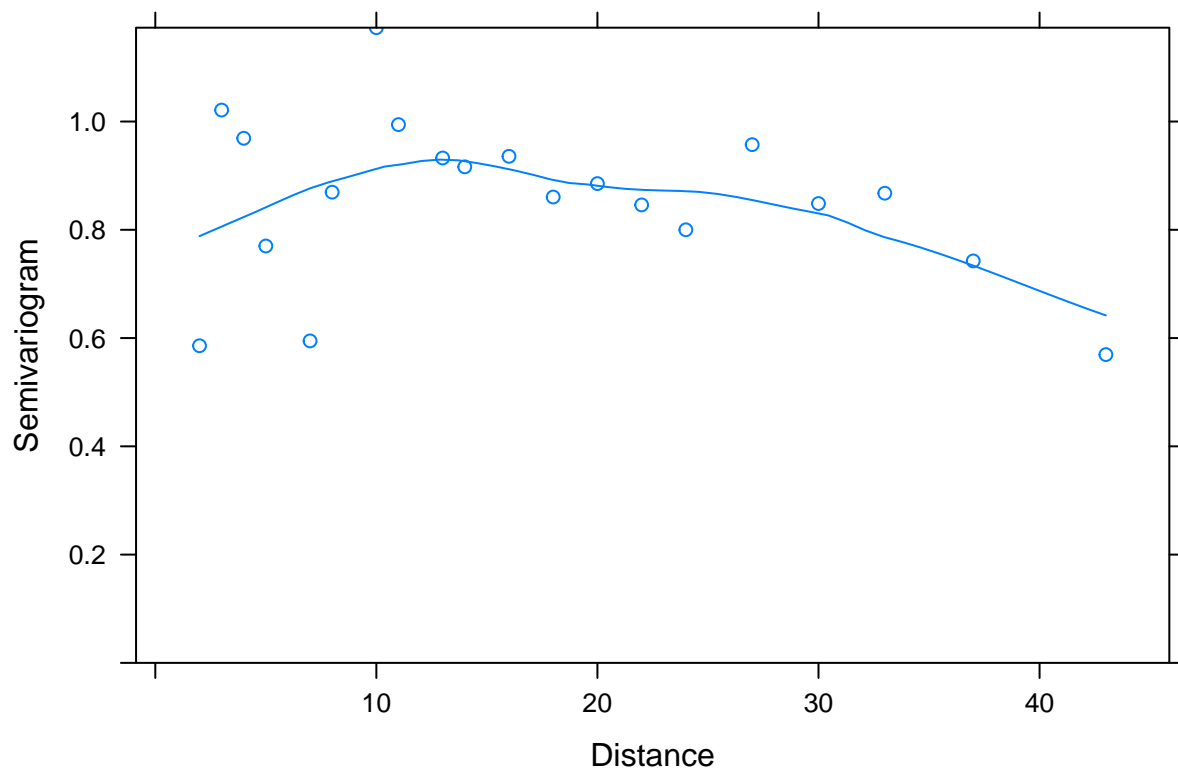
par(mfrow=c(1,1))
plot(Variogram(full_gls, form= ~ x + y))
```



*#This looks like a pretty good fit and looks like residuals are  
#normally distributed. It appears that the variogram is decreasing  
#with distance, possibly indicating that there is no spatial correlation.  
#It appears there is a nugget of .8*

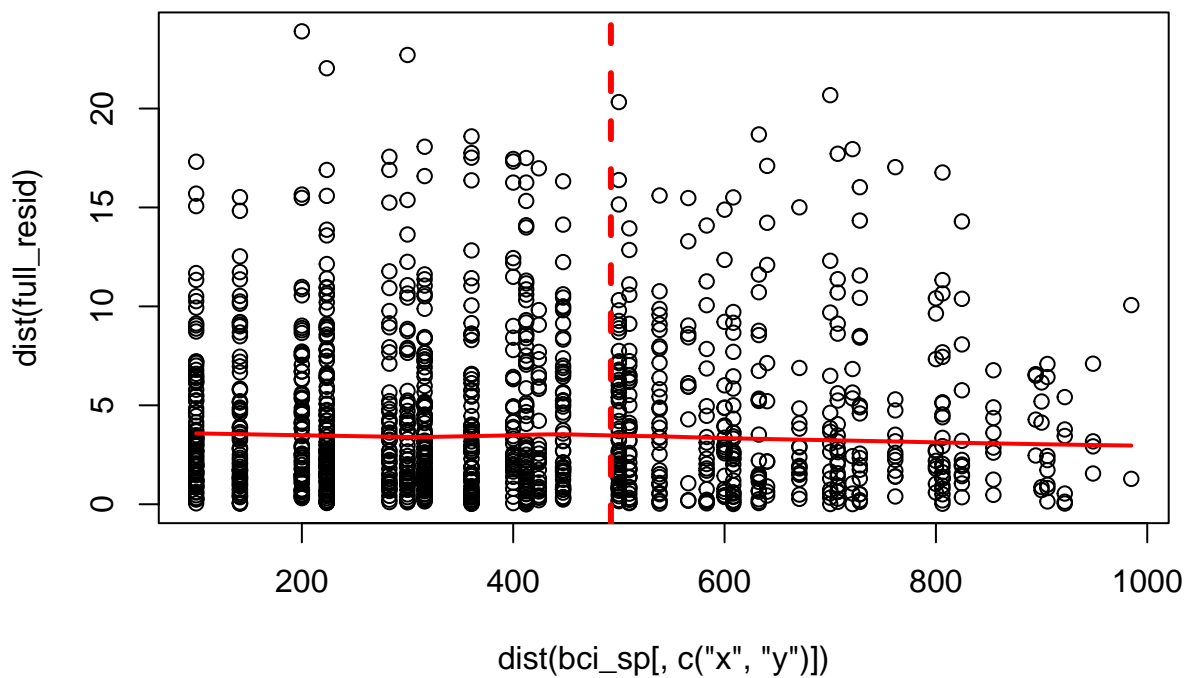
```
plot(Variogram(full_gls, resType='normalized', maxDist = max_dist))
```





*#This provides a pretty good fit to the data*

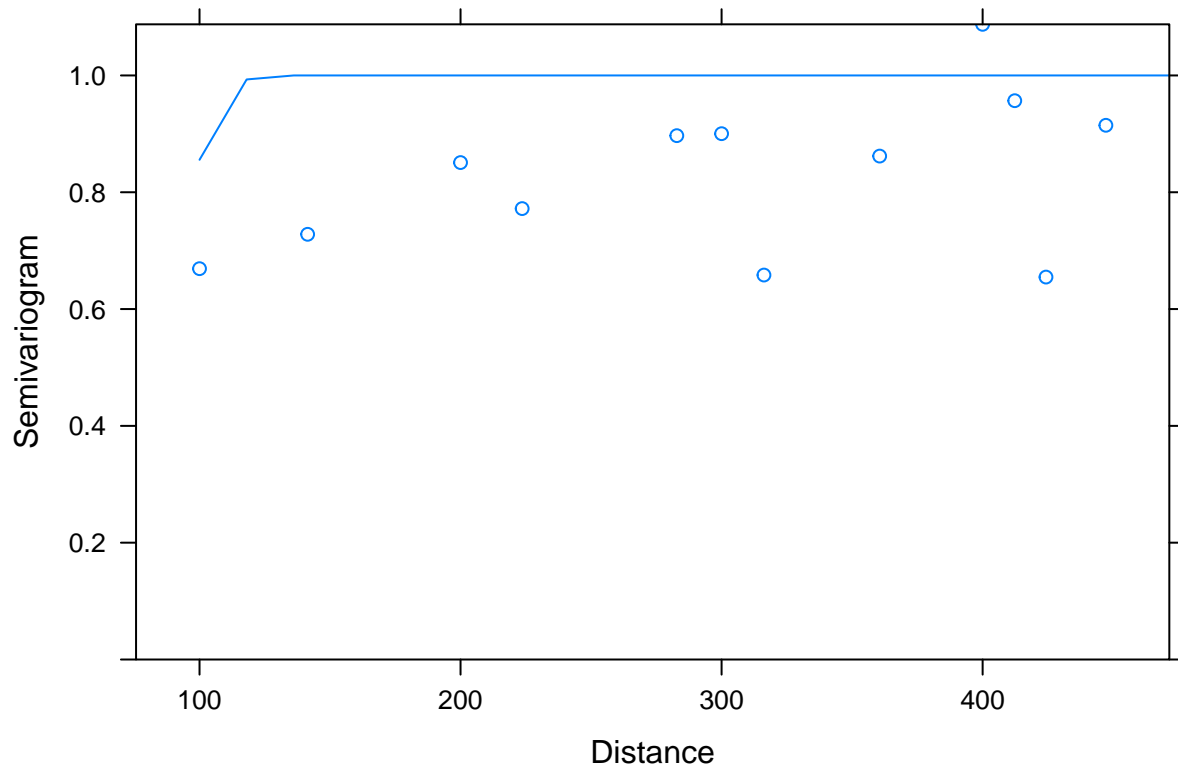
```
full_resid <- residuals(full_gls)
plot(dist(bci_sp[, c('x', 'y')]), dist(full_resid))
lines(lowess(dist(bci_sp[, c('x', 'y')])), dist(full_resid), col='red', lwd=2)
abline(v = max_dist, col='red', lwd=3, lty=2)
```



```
#negative slope
```

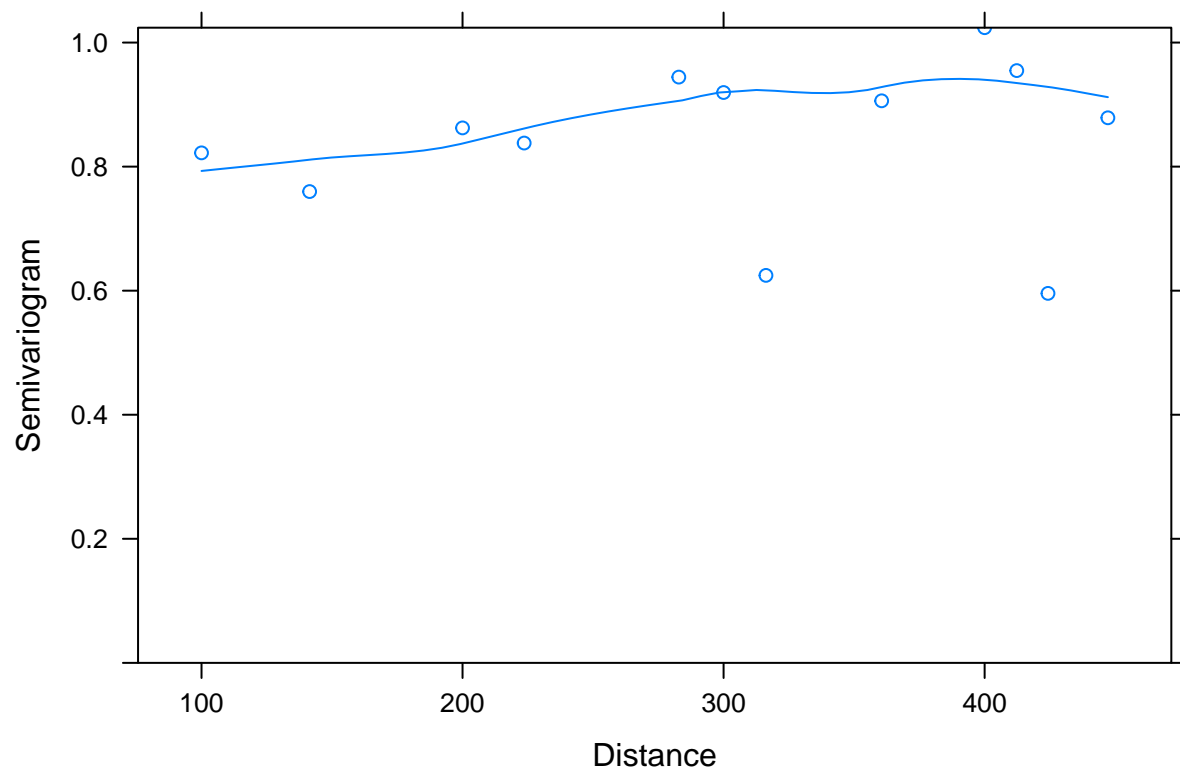
```
#GLS with Nugget
```

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

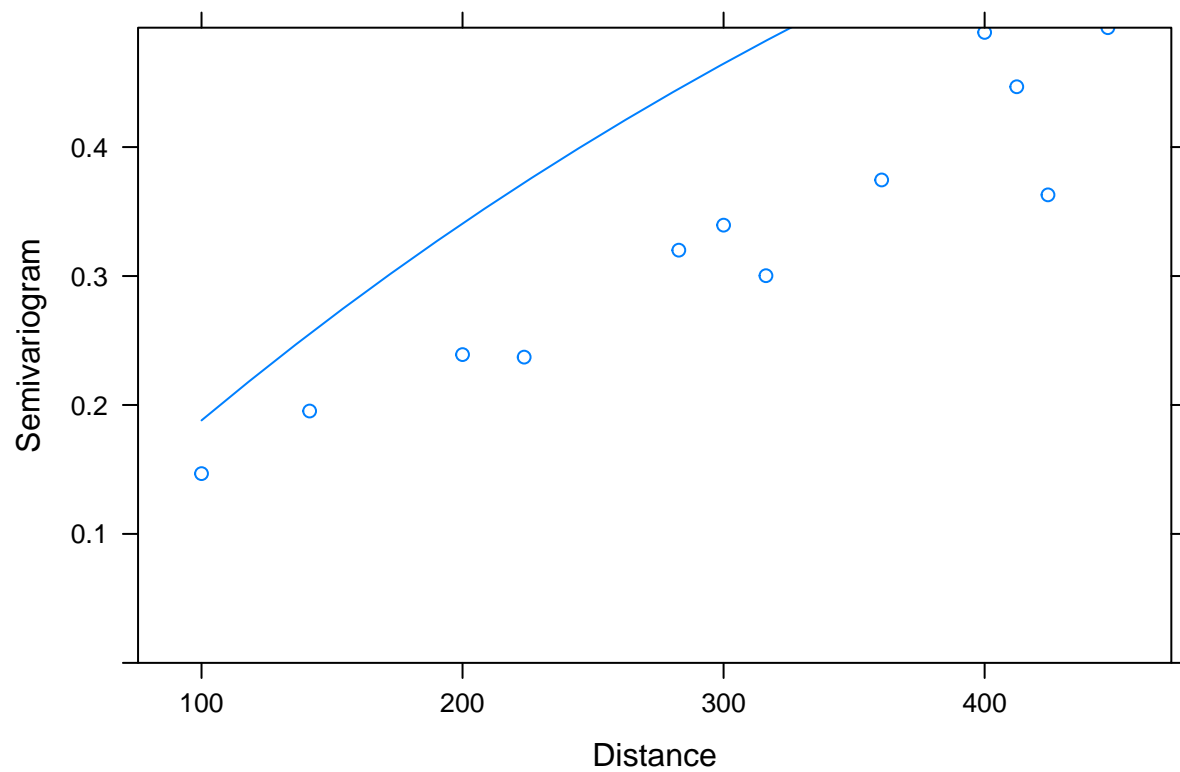


```
#This does not fit the data at all; the slope is 0, indicating no correlation.
```

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

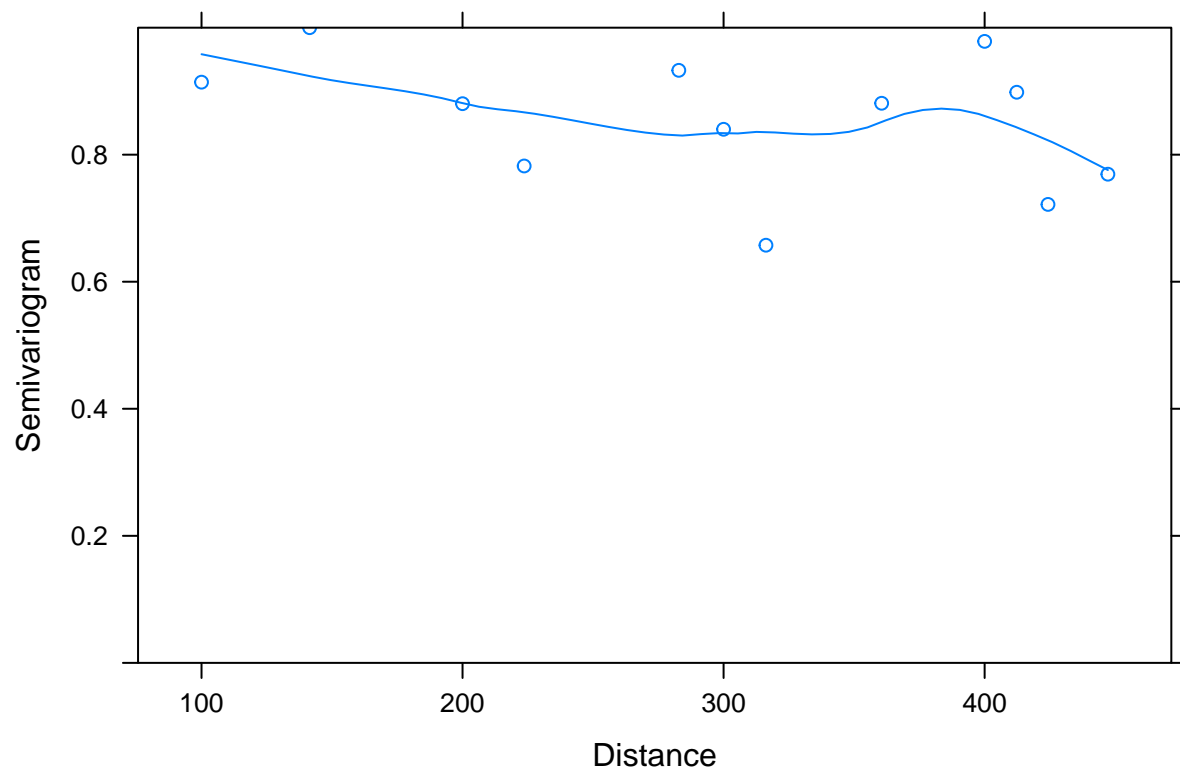


```
#Exponential Variogram  
  
full_exp <- update(full_gls, corr = corExp(form=~x + y))  
#This is a good fit of our residuals.  
  
plot(Variogram(full_exp, maxDist = max_dist))
```

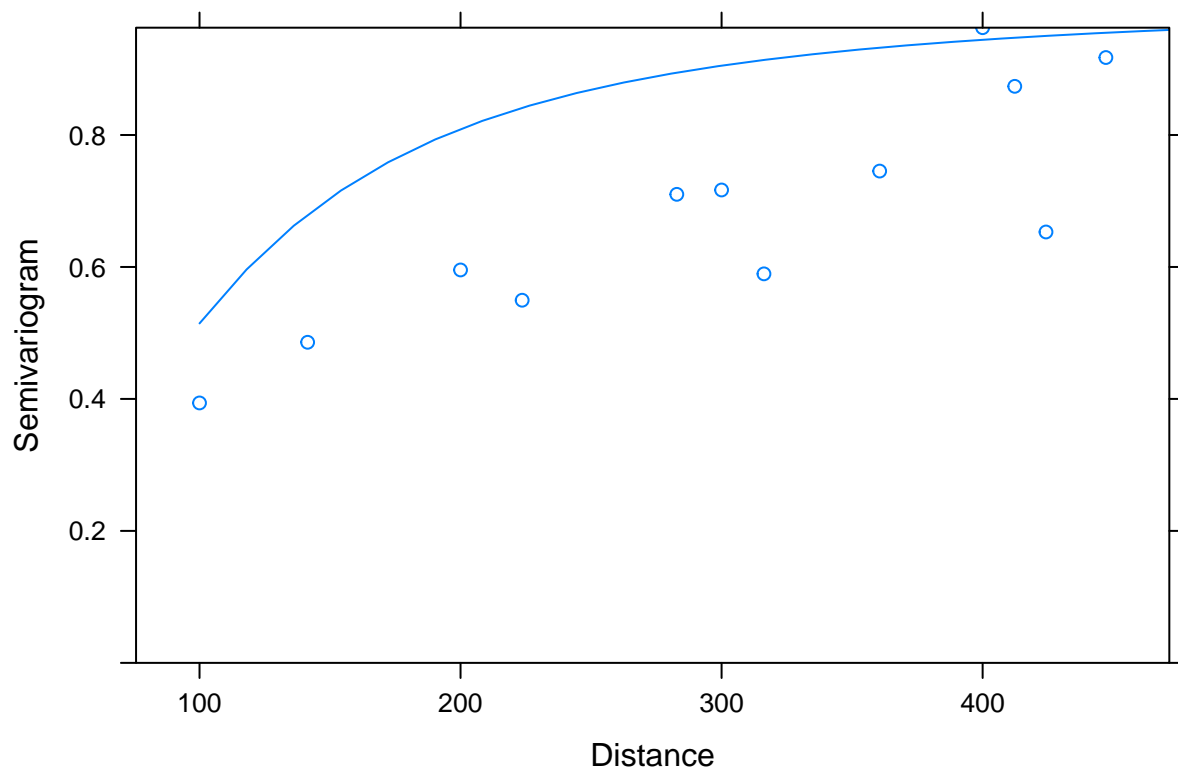


*#This doesn't look good because the model does not fit the error at all.  
#Does not appear to have a y intercept. Does not have a nugget,  
#or a non-0 y intercept.*

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

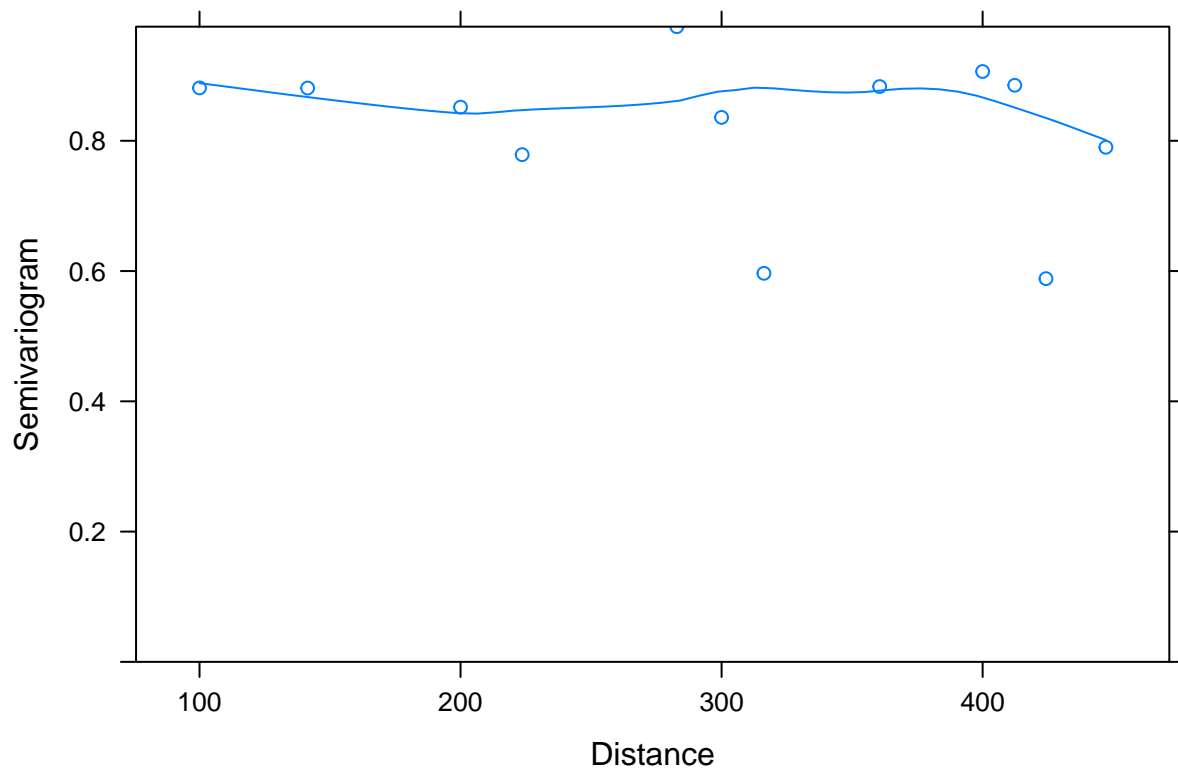


```
#Rational Quadratic Model Spatial Correlation  
  
full_rat = update(full_gls, corr=corRatio(form=~x + y))  
  
plot(Variogram(full_rat, maxDist = max_dist))
```



*#this still does not fit the model, as the model does not fit the  
#error. Still does not have a nugget.*

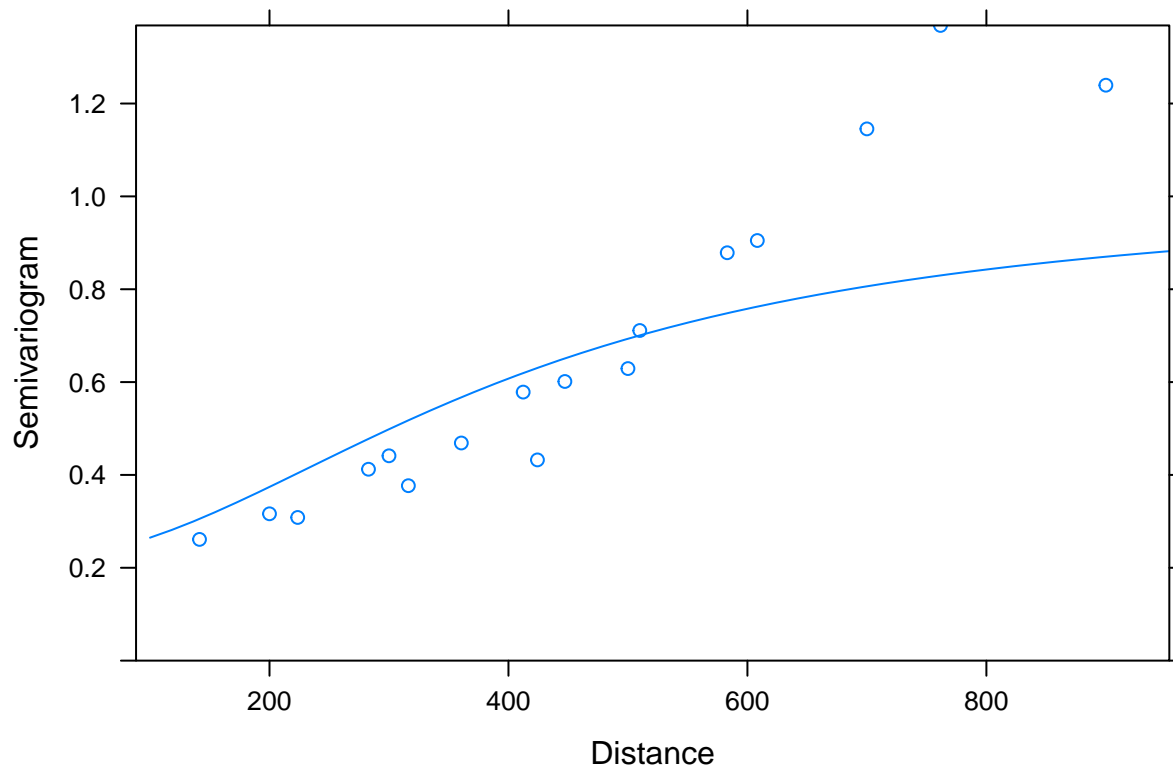
```
plot(Variogram(full_rat, resType='normalized', maxDist = max_dist))
```



```
#Rational Quadratic Model With Nugget
```

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

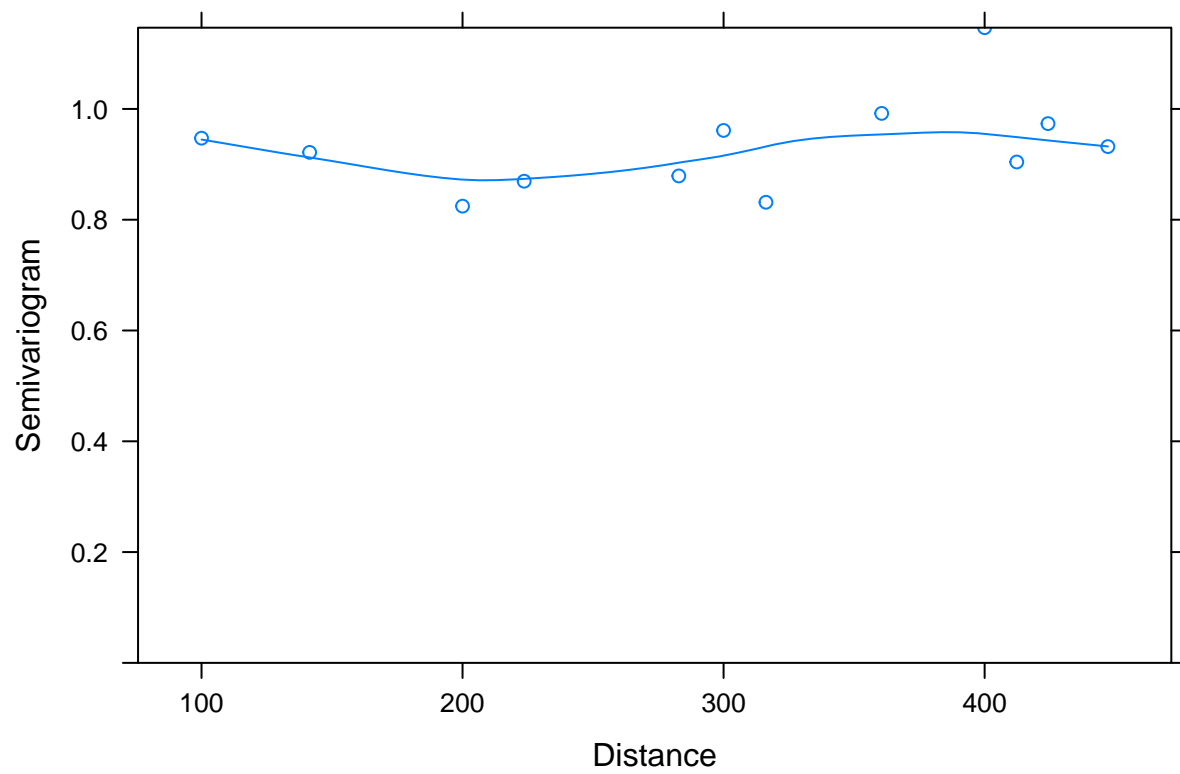
```
plot(Variogram(full_rat_nug), maxDist = max_dist)
```



```
#This looks bad too. The trend of the raw residuals
```

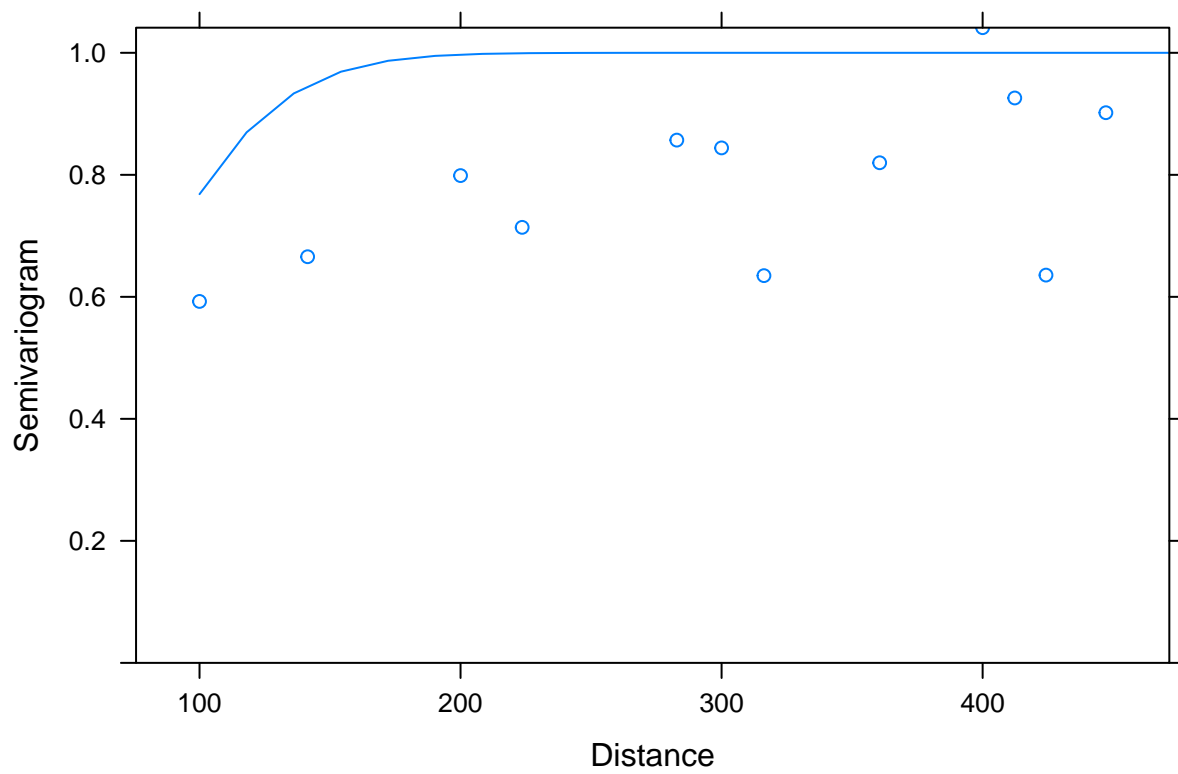
```
#appears to be gaussian.
```

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



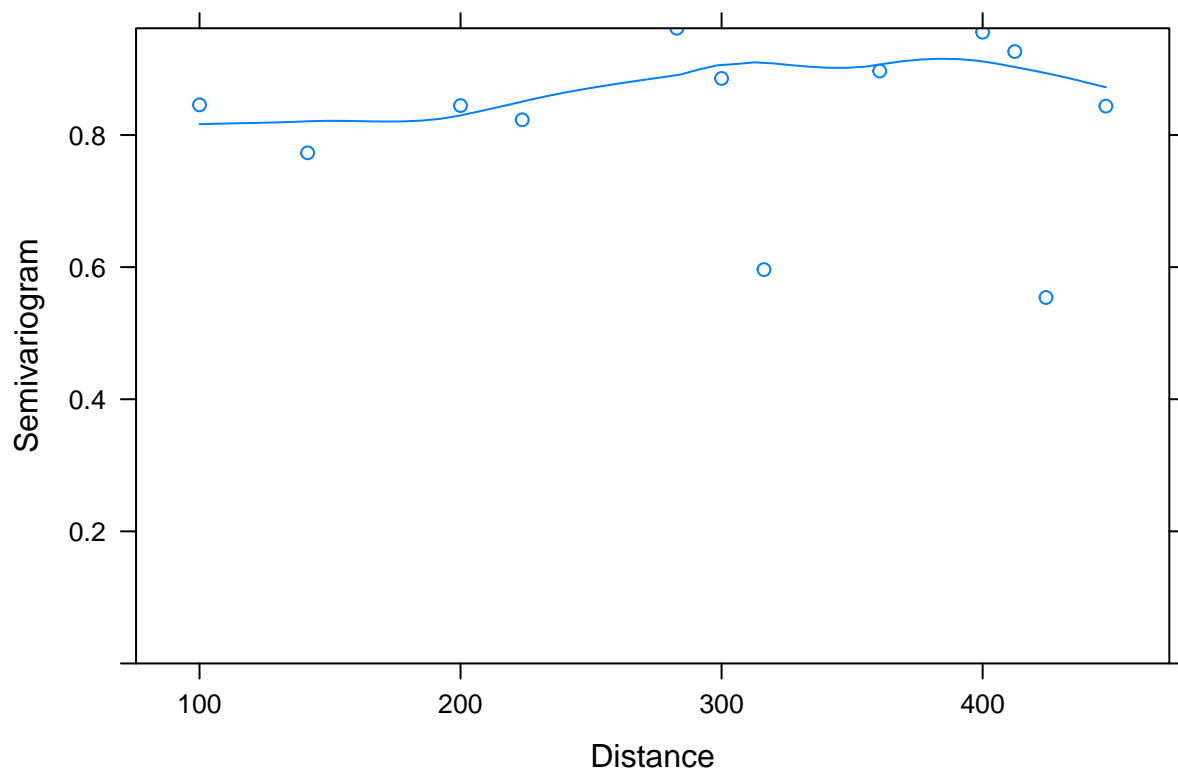
```
#Gaussian Spatial Model  
  
full_gaus = update(full_gls, corr=corGaus(form=~x + y))  
  
plot(Variogram(full_gaus, maxDist = max_dist))
```





*#Not as good as I had hoped.*

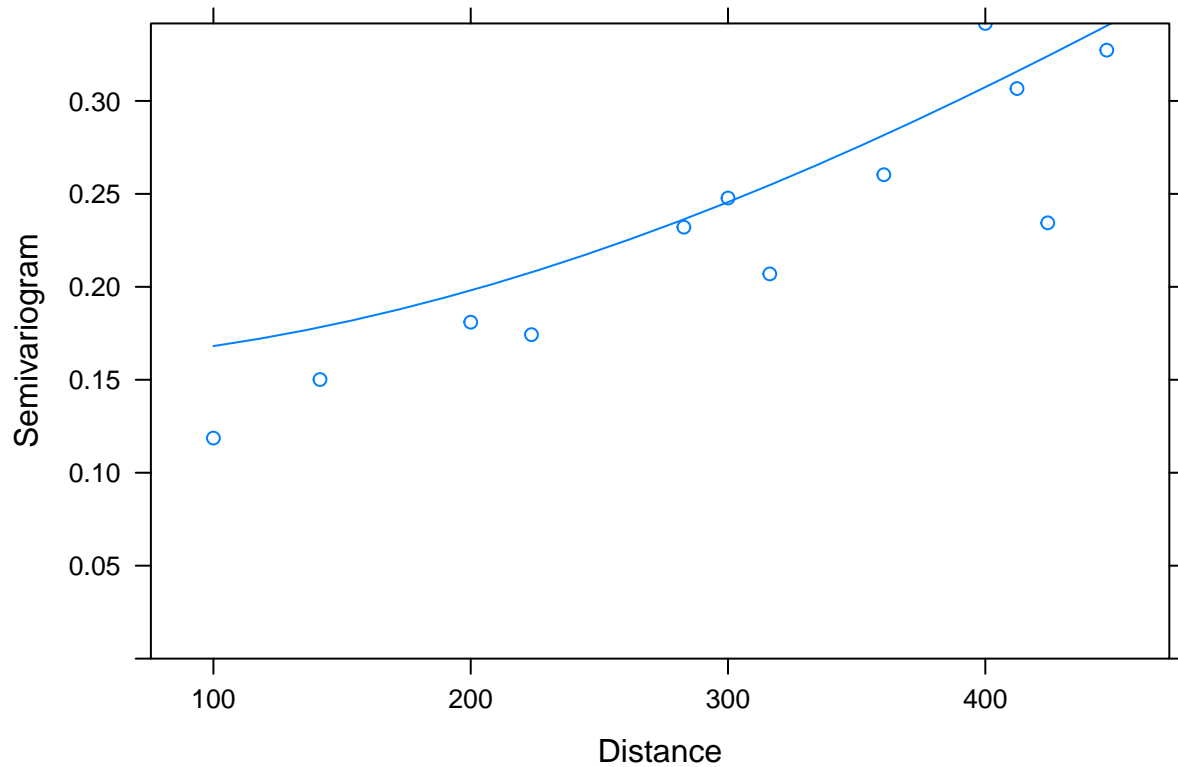
```
plot(Variogram(full_gaus, resType='n', maxDist = max_dist))
```



```
#Gaussian Spatial Model with Nugget
```

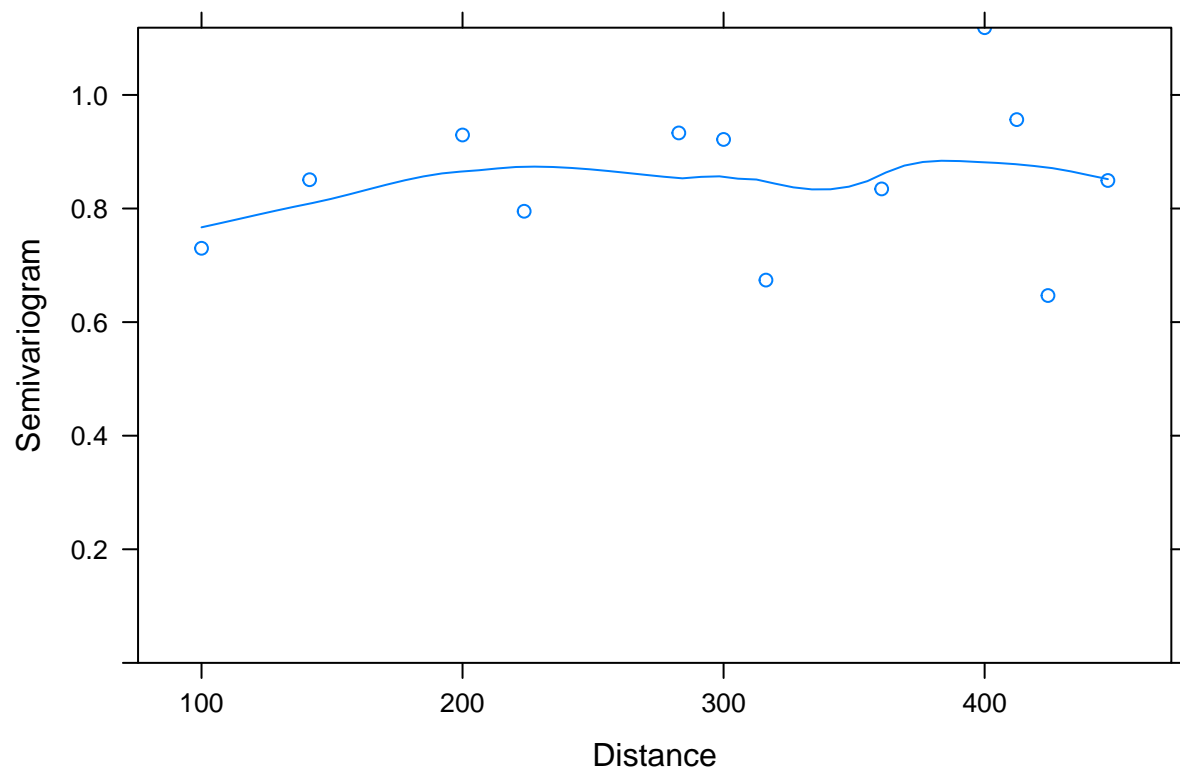
```
full_gaus_nug = update(full_gaus, corr=corGaus(form=~x + y, nugget=T))
```

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

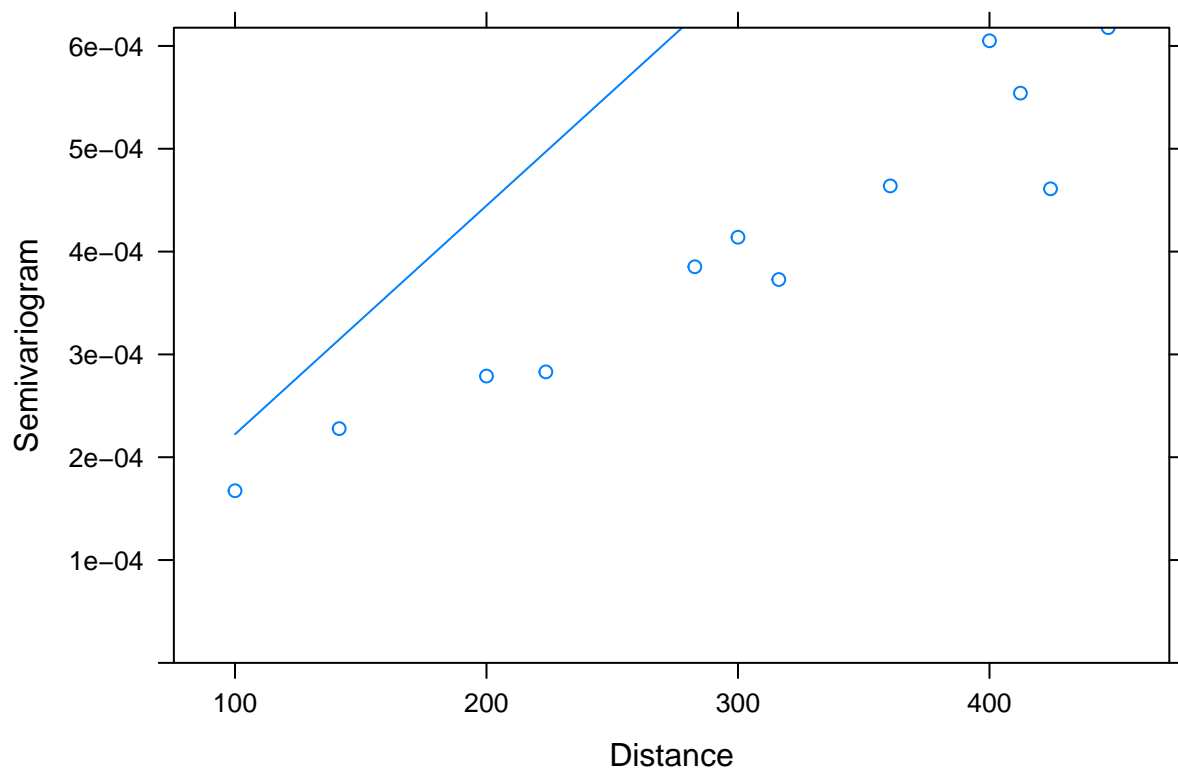


```
#This looks better than what we have seen, but the model still  
#does not fit the error as well.
```

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

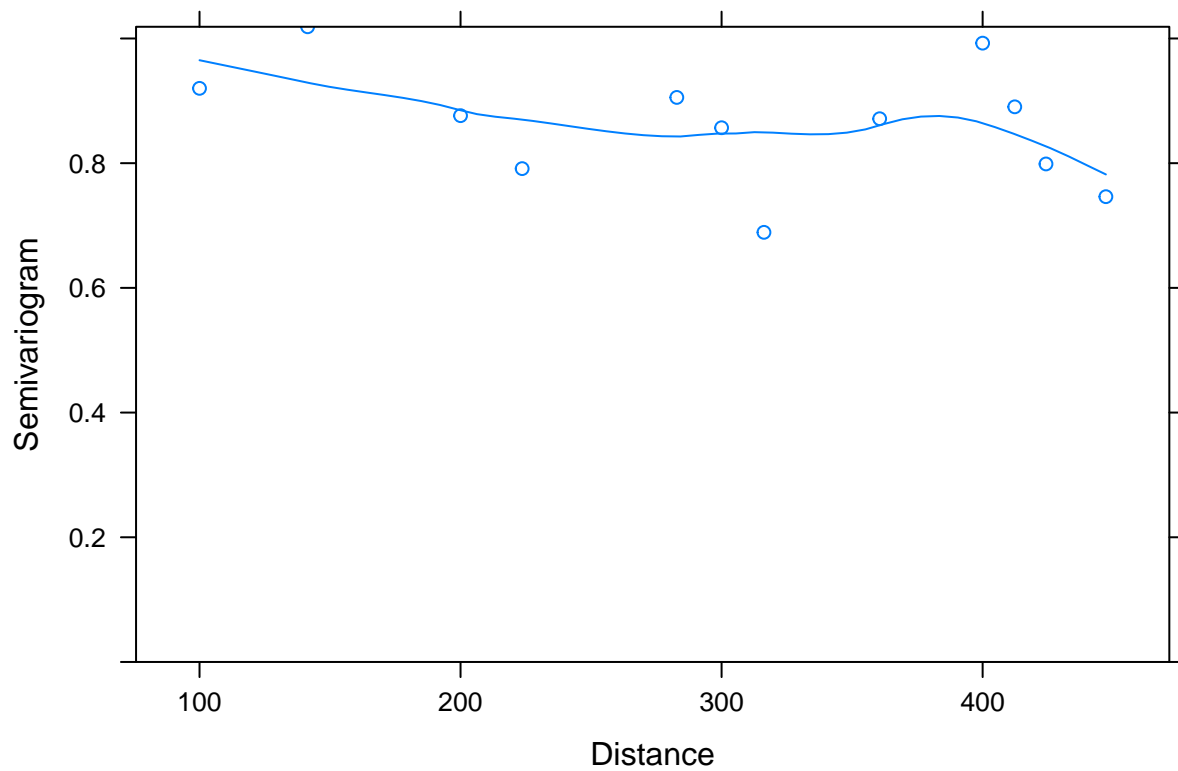


```
#Spherical Spatial Model  
sphere_full = update(full_gls, corr=corSpher(form=~x + y))  
plot(Variogram(sphere_full, maxDist = max_dist))
```



*#This doesn't look good either.*

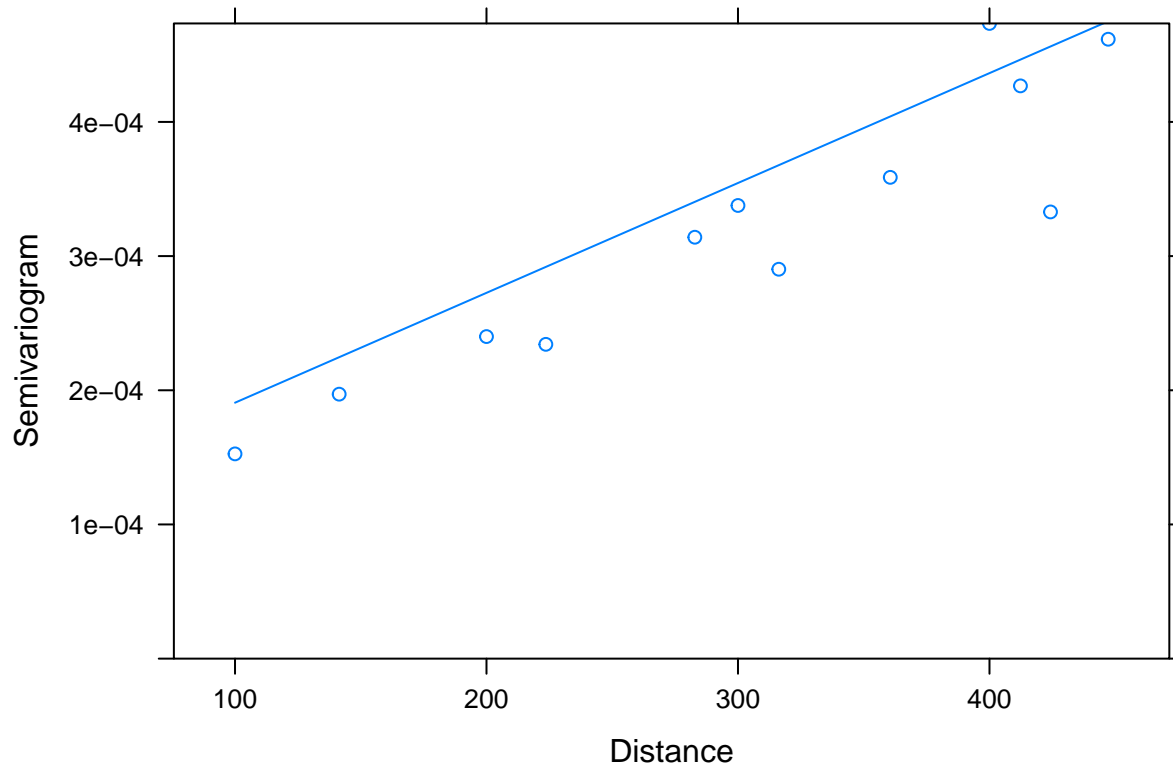
```
plot(Variogram(sphere_full, resType='n', maxDist = max_dist))
```



```
#Spherical Spatial Model with Nugget
```

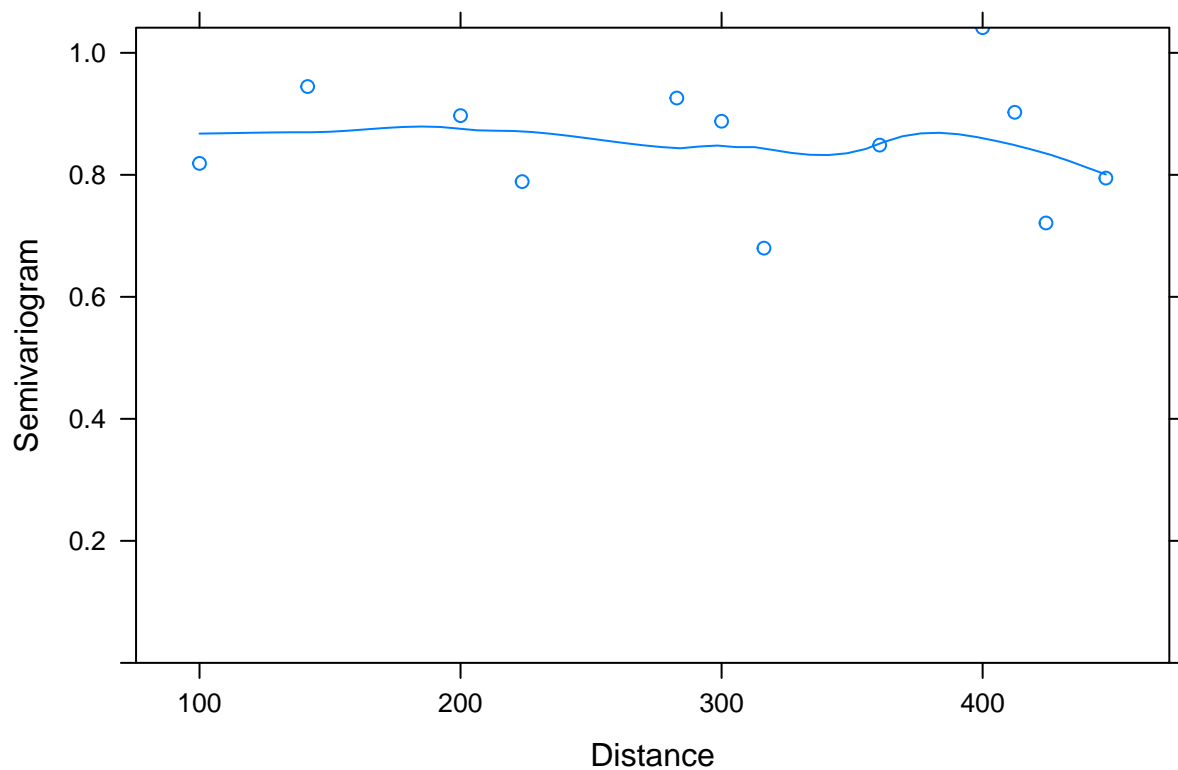
```
sphere_full_nug = update(sphere_full, corr=corSpher(form=~x + y, nugget=T))
```

```
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, sphere_full_nug)
```

##	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 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
```

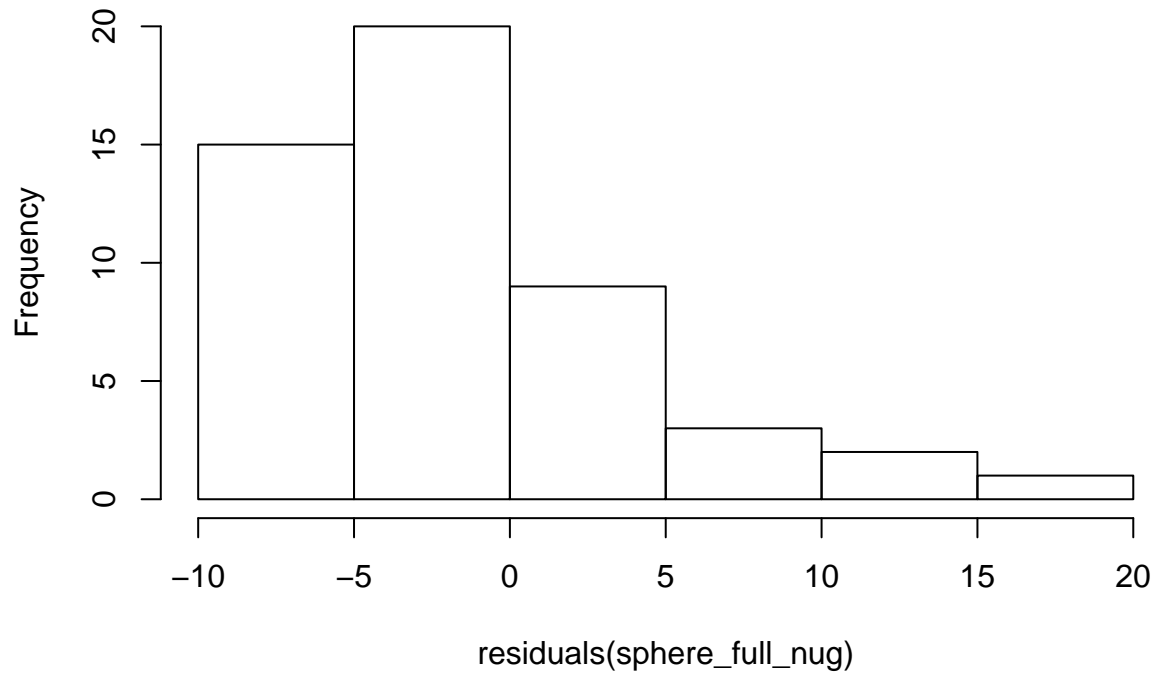


```
## Parameter estimate(s):
##      range      nugget
## 1.831904e+06 1.088636e-04
##
## Coefficients:
##           Value Std.Error   t-value p-value
## (Intercept)  3.0501051 267.79376   0.011390  0.9910
## c_las        0.1426672   0.18953   0.752754  0.4558
## h_tri       -0.0017713   0.09038  -0.019599  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
```

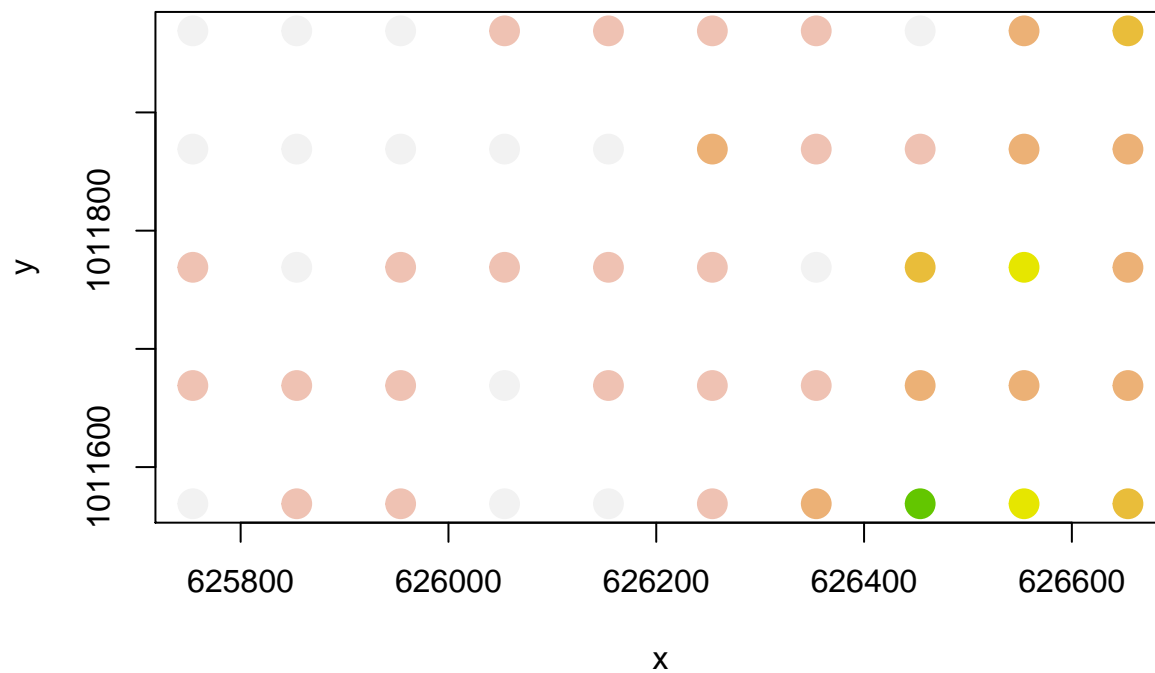
*#After looking at the t values associated with each model, we can see that  
#the spherical spatial model is a better fit than the exponential model,  
#but the spherical model with a nugget has even a better fit than that.  
#So the Spherical spatial model with a spatial error term is a much  
#better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