

# HW5

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## Question 1:

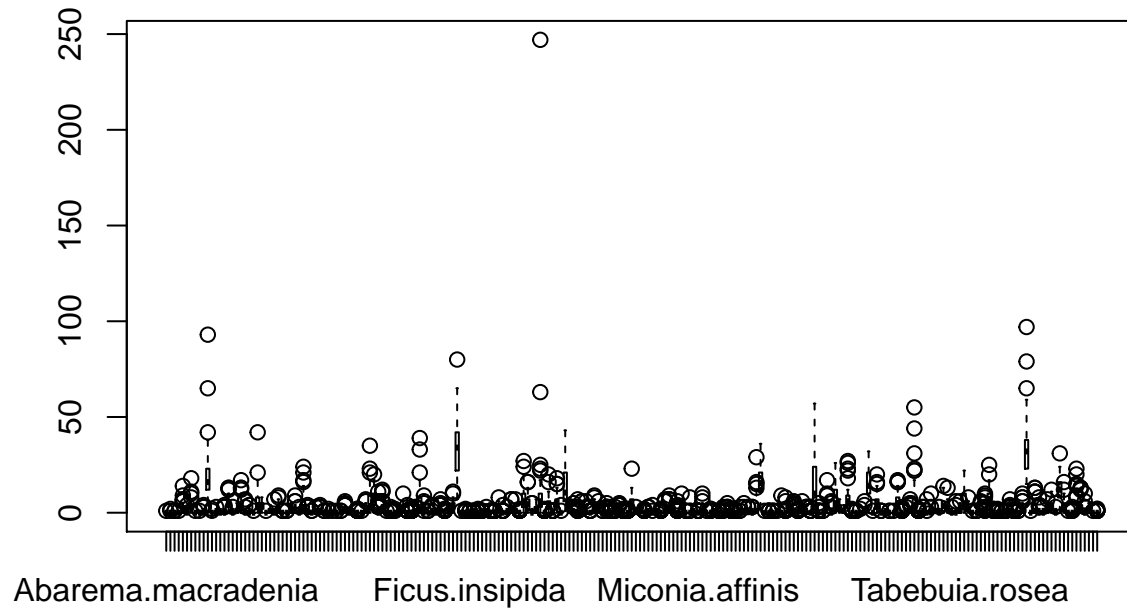
I examined the dataset and selected a relatively common species, *T. tuberculata* and a relatively rare species, *P. elegans*. I examined the relationship between the abundance of each species and space based on the BCI dataset.

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

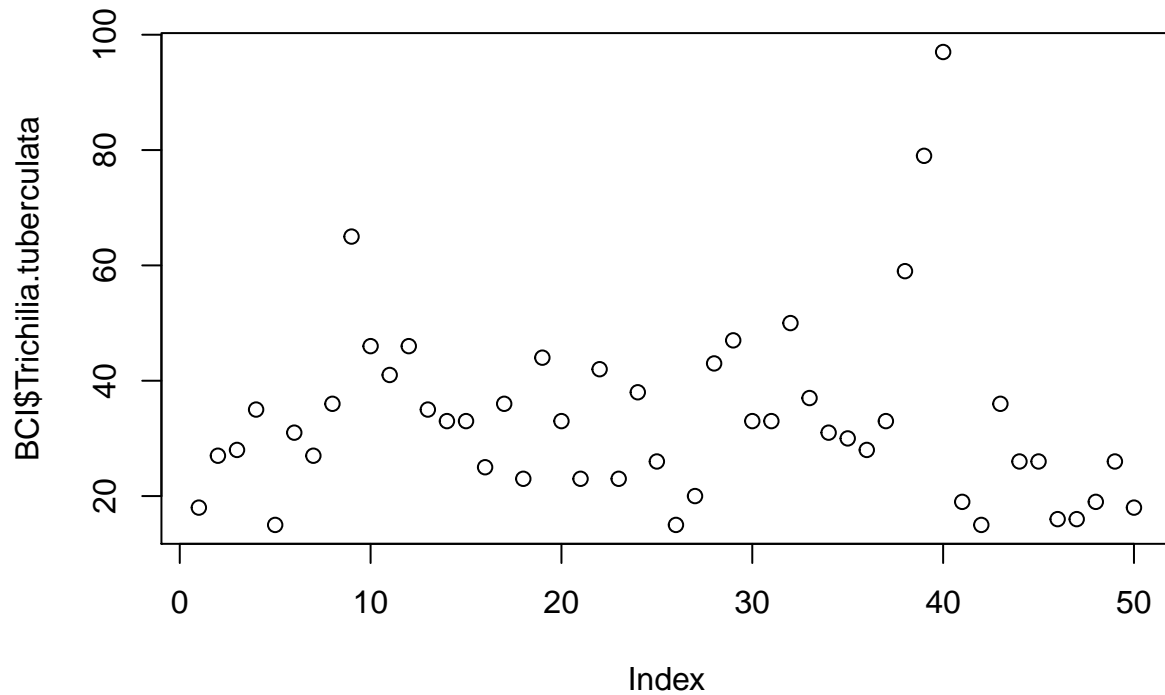
```
## Loading required package: lattice
```

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

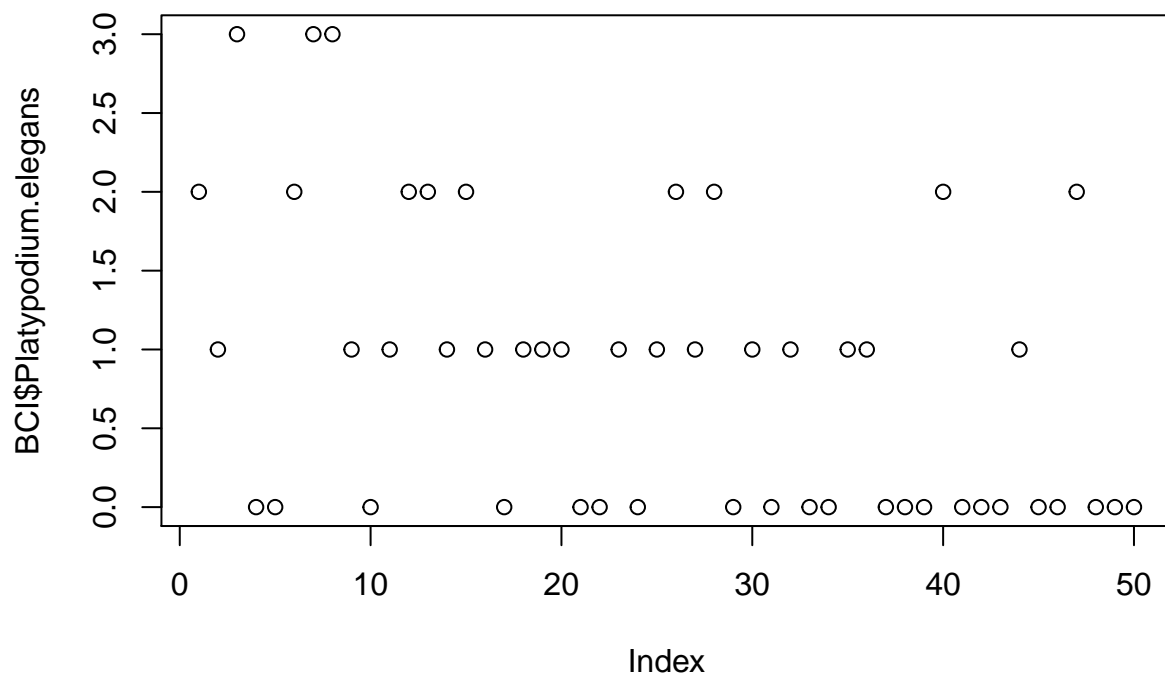
```
boxplot(BCI)
```



```
plot(BCI$Trichilia.tuberculata)# abundant
```

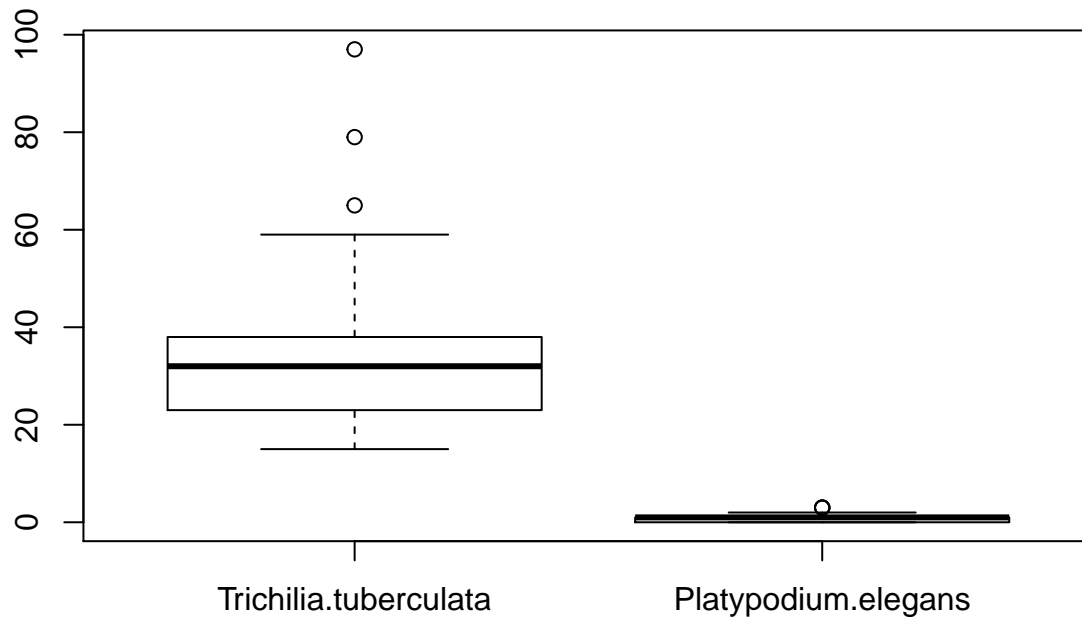


```
plot(BCI$Platypodium.elegans) # rare, but enough for me to work with
```



```
BCI_sub=subset(BCI, select= c(Trichilia.tuberculata, Platypodium.elegans))
BCI_lots=BCI$Trichilia.tuberculata
BCI_few=BCI$Platypodium.elegans

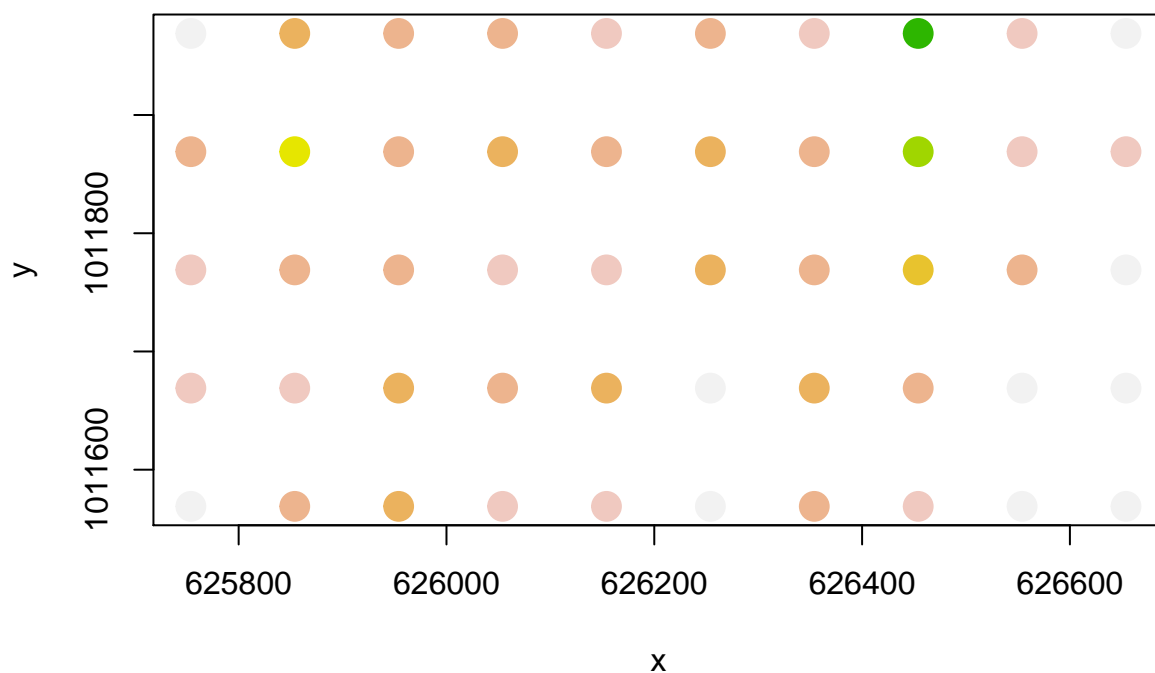
boxplot(BCI_sub)
```



Common Species: *T. tuberculata* is abundant and widely distributed. This species does not exhibit any form of spatial dependence. Biologically, this makes sense, a species that occurs commonly and in high abundance in a given habitat is not likely to be dependent on any specific environmental variables within that habitat

```
#visual summary of abundance
col_brks = hist(BCI_lots, plot=F)$breaks
col_indices = as.numeric(cut(BCI_lots, col_brks))
cols = rev(terrain.colors(length(col_brks)))
plot(BCI_xy, cex=2, pch=19, col=cols[col_indices], main="Spatial Distribution of T. tuberculata ")
```

### Spatial Distribution of *T. tuberculata*

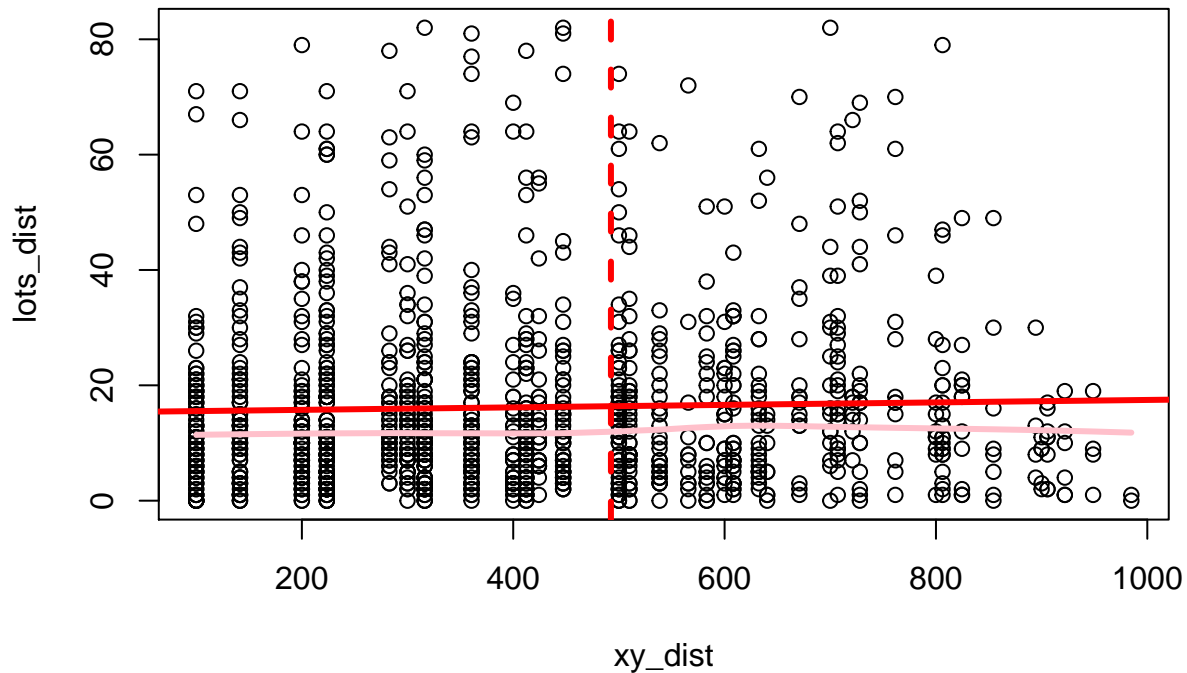


```

#Determine distances
lots_dist = dist(BCI_lots)
xy_dist = dist(BCI_xy)
max_dist = max(xy_dist) / 2

# plot result
plot(xy_dist, lots_dist)
abline(lm(lots_dist ~ xy_dist), lwd=3, col='red') #positive line is pretty level
lines(lowess(xy_dist, lots_dist), lwd=3, col='pink')
abline(v = max_dist, col='red', lwd=3, lty=2) #line is fairly level, certainly levels off with distance

```



```

#Compute Correlation
lots_cor = cor(xy_dist, lots_dist)
lots_cor # weakly correlated

```

```
## [1] 0.02876206
```

```

#mantel test
lots_mantel = mantel(xy_dist, lots_dist)
lots_mantel # observed spatial patterns not significantly different from random.

```

```

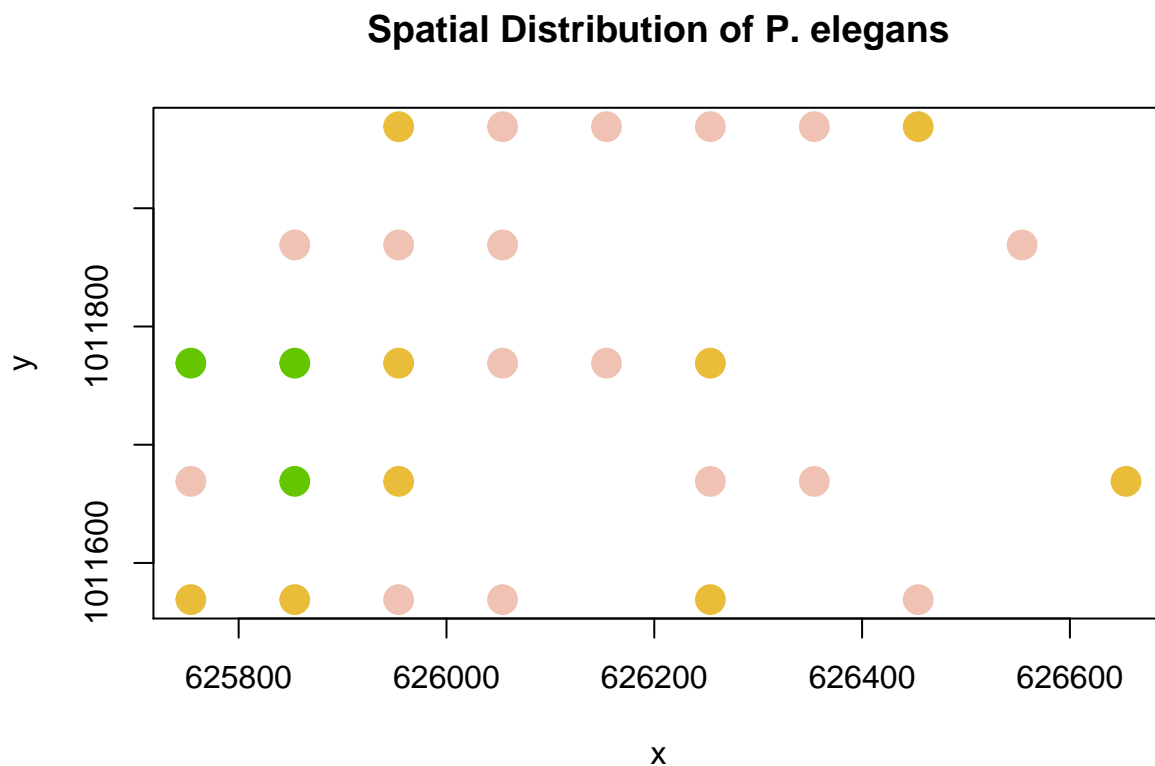
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = xy_dist, ydis = lots_dist)
##
## Mantel statistic r: 0.02876
##      Significance: 0.328

```

```
##
## Upper quantiles of permutations (null model):
##   90%   95%  97.5%   99%
## 0.0814 0.1063 0.1212 0.1471
## Permutation: free
## Number of permutations: 999
```

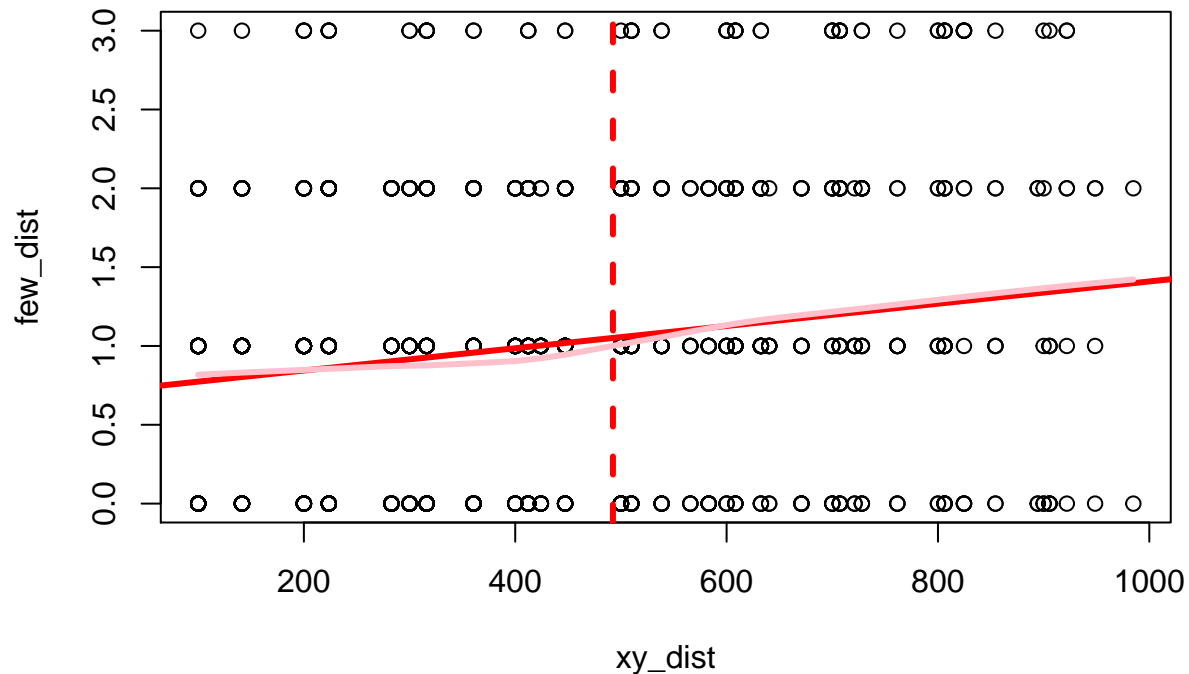
Rare Species: *P. elegans* is patchy in distribution and more abundant in some patches than others. This species does appear to be spatially dependent, as its distribution pattern is significantly different from random ( $p < 0.01$ ). *P. elegans* is a large tree whose spatial distribution is likely dependent on its ability to out compete other trees for sunlight, potentially explaining its patchy, spatially dependent distribution.

```
#visual summary of abundance
col_brks = hist(BCI_few, plot=F)$breaks
col_indices = as.numeric(cut(BCI_few, col_brks))
cols = rev(terrain.colors(length(col_brks)))
plot(BCI_xy, cex=2, pch=19, col=cols[col_indices], main="Spatial Distribution of P. elegans")
```



```
#Determine distances
few_dist = dist(BCI_few)

# plot result
plot(xy_dist, few_dist)
abline(lm(few_dist ~ xy_dist), lwd=3, col='red') #positive line is pretty level
lines(lowess(xy_dist, few_dist), lwd=3, col='pink')
abline(v = max_dist, col='red', lwd=3, lty=2) #line has distinct positive slope which does not appear t
```



```
#Compute Correlation
few_cor = cor(xy_dist, few_dist)
few_cor # correlated
```

```
## [1] 0.1725242
```

```
#mantel test
few_mantel = mantel(xy_dist, few_dist)
few_mantel # observed spatial patterns are significantly different from random.
```

```
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = xy_dist, ydis = few_dist)
##
## Mantel statistic r: 0.1725
##      Significance: 0.001
##
## Upper quantiles of permutations (null model):
##      90%      95%    97.5%    99%
## 0.0575 0.0826 0.1036 0.1188
## Permutation: free
## Number of permutations: 999
```

## Question2 :

I developed two GLMs to predict the abundance of a species of interest, *D. standleyi* as a function of the abundance of other species.

```
#Structuring data for the models
#thanks to Tom for this workaround
```

```
sp_ids = c("Cordia.lasiocalyx", "Hirtella.triandra", "Picramnia.latifolia", "Quassia.amara",
response = BCI$Drypetes.standleyi
```

```
modeling_dat = data.frame(response,BCI[,which(colnames(BCI) %in% sp_ids)],BCI_xy)
```

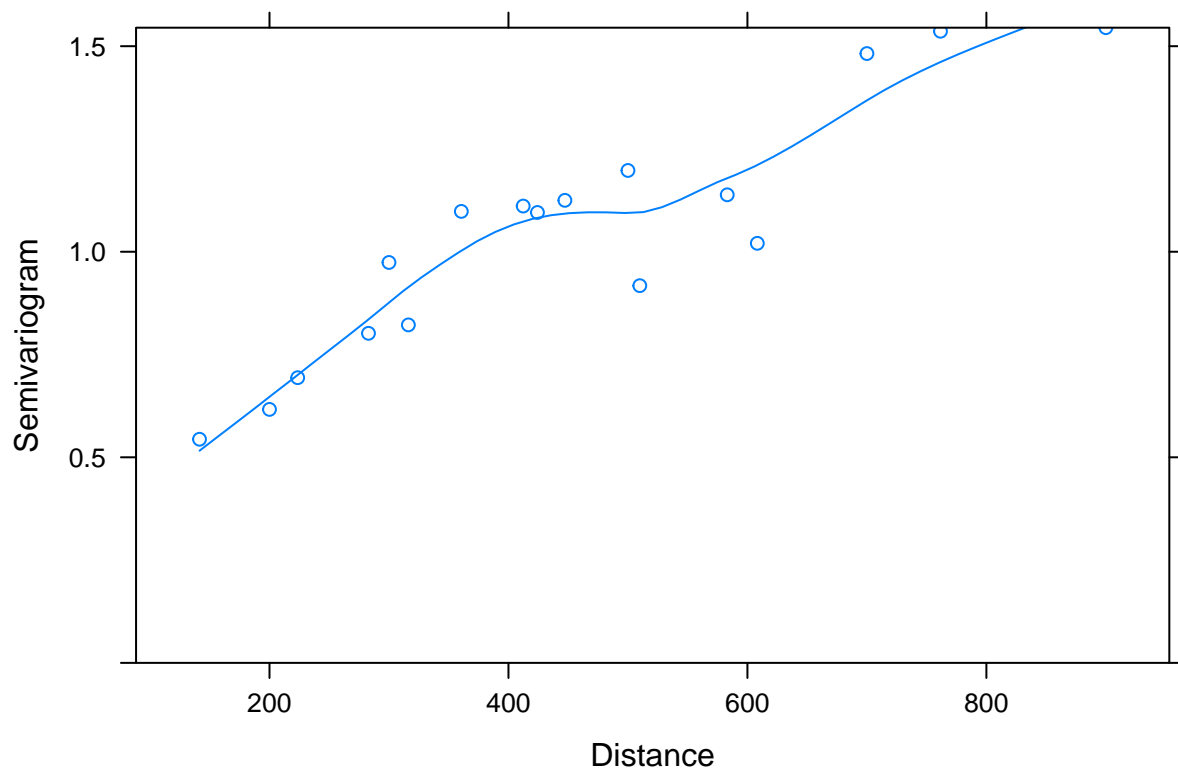
Model 1: Picking the species *T. arborea*, I constructed a general linear model to predict the abundance of our species of interest, *D. standleyi*. I also examined spatial dependence of the model residuals. The model. Using only a single species and without accounting for spatial dependence, does not do a very adequate job of explaining abundance of the species of interest. Adding a spatial error term (in the form of Variograms) altered the model coefficients and generally improved the fit. Of the spatial error terms applied the rational quadratic model provided the best fit.

```
sp_e = modeling_dat$Tabernaemontana.arborea #cause I dont want to type out Tabernaemontana.arborea a ba
```

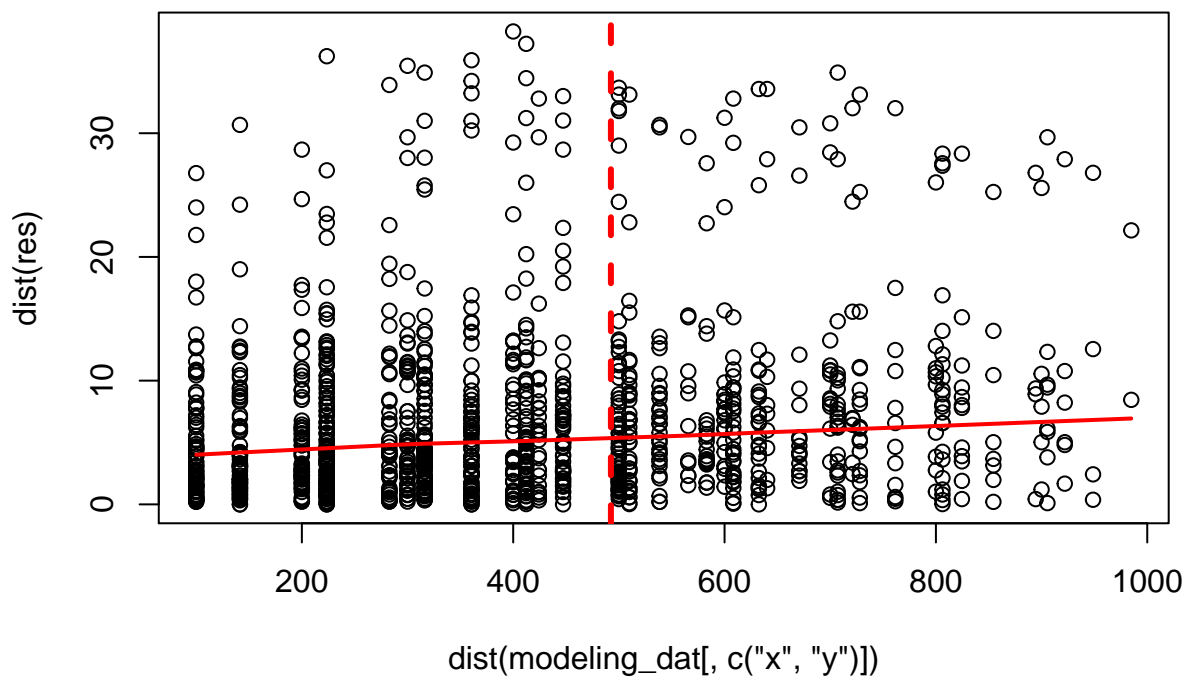
```
mod1 = gls(response~sp_e, data=modeling_dat)
summary(mod1)
```

```
## Generalized least squares fit by REML
## Model: response ~ sp_e
## Data: modeling_dat
##      AIC      BIC    logLik
## 343.6604 349.274 -168.8302
##
## Coefficients:
##              Value Std.Error   t-value p-value
## (Intercept) 10.692034 1.6722054   6.393972   0e+00
## sp_e         -0.775161 0.2048435  -3.784160   4e-04
##
## Correlation:
##      (Intr)
## sp_e -0.789
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -1.2580847 -0.6060094 -0.2654214  0.3098872  4.0024269
##
## Residual standard error: 7.266373
## Degrees of freedom: 50 total; 48 residual
```

```
plot(Variogram(mod1, form= ~ x + y, nugget=T)) #dat nugget
```



```
#residuals
res = residuals(mod1)
plot(dist(modeling_dat[, c('x', 'y')]), dist(res))
lines(lowess(dist(modeling_dat[, c('x', 'y')])), dist(res)), col='red', lwd=2)
abline(v = max_dist, col='red', lwd=3, lty=2)
```



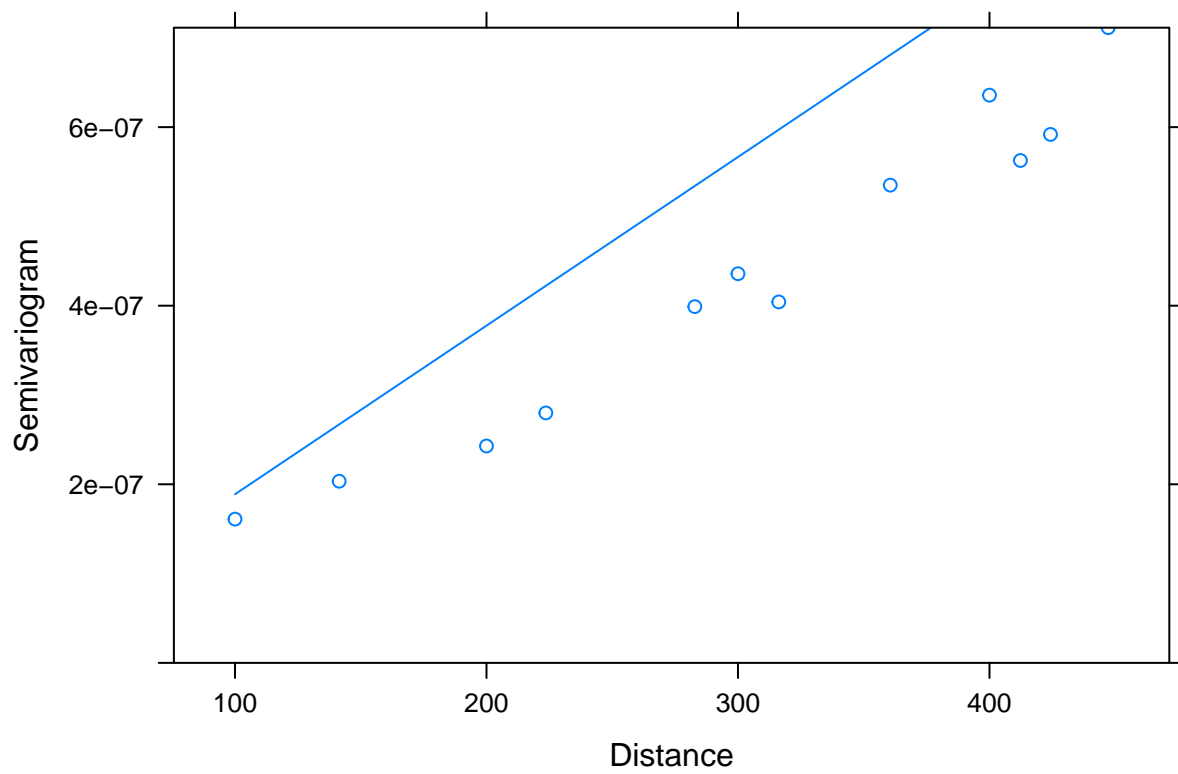


```
#fit of error model: expodential
```

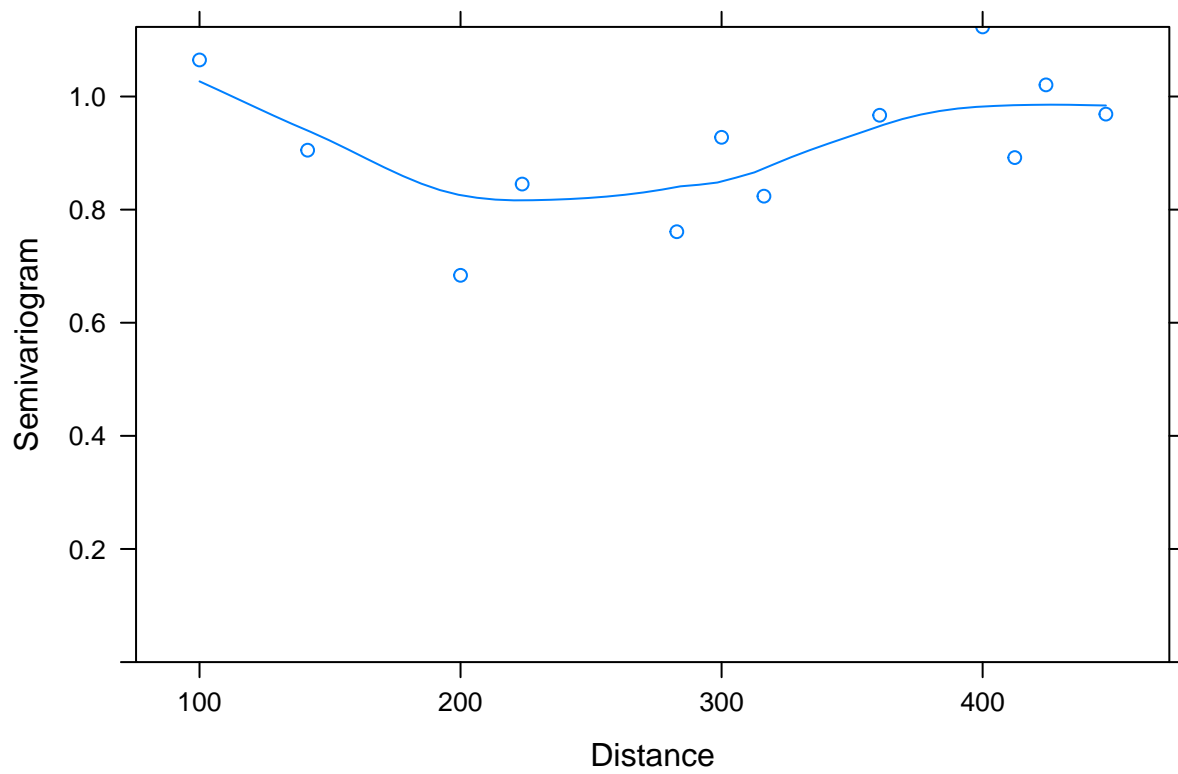
```
mod1_exp = update(mod1, corr=corExp(form=~x + y))  
summary(mod1_exp)
```

```
## Generalized least squares fit by REML  
##   Model: response ~ sp_e  
##   Data: modeling_dat  
##       AIC      BIC    logLik  
##  311.7838 319.2686 -151.8919  
##  
## Correlation Structure: Exponential spatial correlation  
## Formula: ~x + y  
## Parameter estimate(s):  
##   range  
## 529559931  
##  
## Coefficients:  
##           Value Std.Error   t-value p-value  
## (Intercept) 14.40840  10738.70  0.00134173  0.9989  
## sp_e         0.00579    0.15  0.03863059  0.9693  
##  
## Correlation:  
##   (Intr)  
## sp_e 0  
##  
## Standardized residuals:  
##           Min           Q1           Med           Q3           Max  
## -0.0013535864 -0.0013440167 -0.0011576398 -0.0006219242  0.0022894562  
##  
## Residual standard error: 10738.71  
## Degrees of freedom: 50 total; 48 residual
```

```
plot(Variogram(mod1_exp, maxDist = max_dist)) #yeah, this is bad
```



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



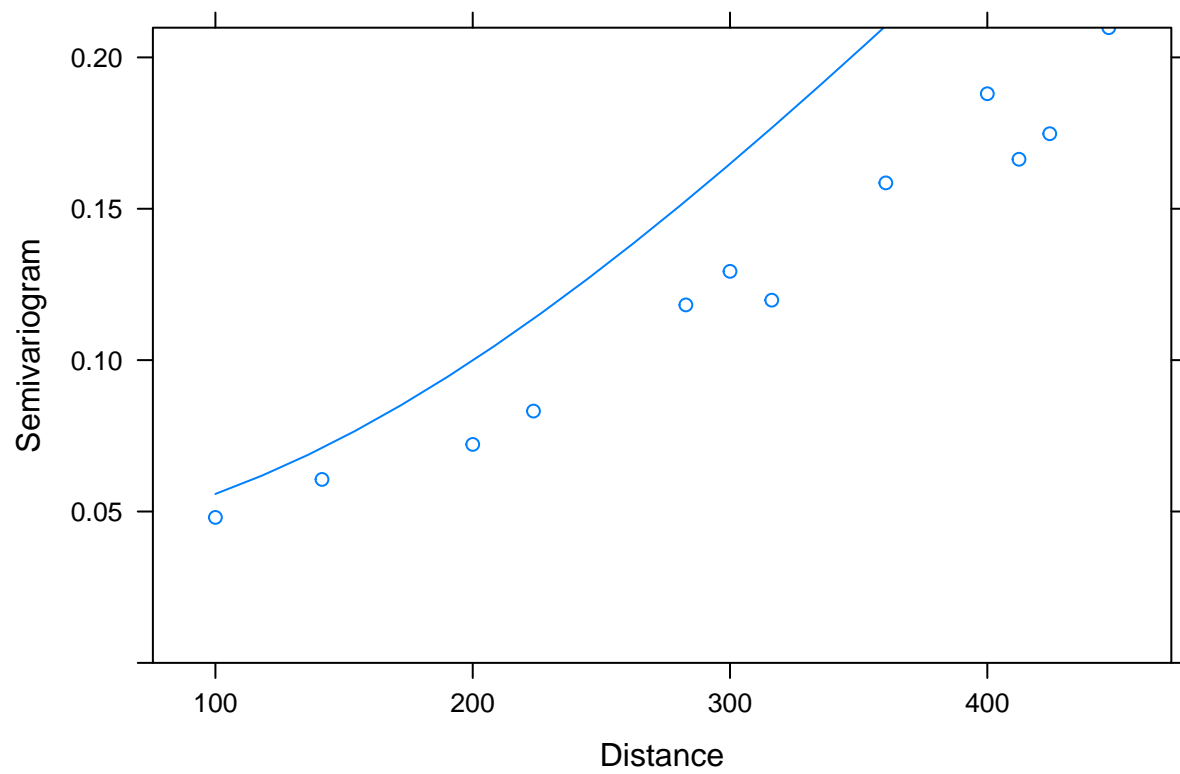
```

#fit of error model: rational quadratic
mod1_rat = update(mod1_exp, corr=corRatio(form=~x+y, nugget=T))
summary(mod1_rat)

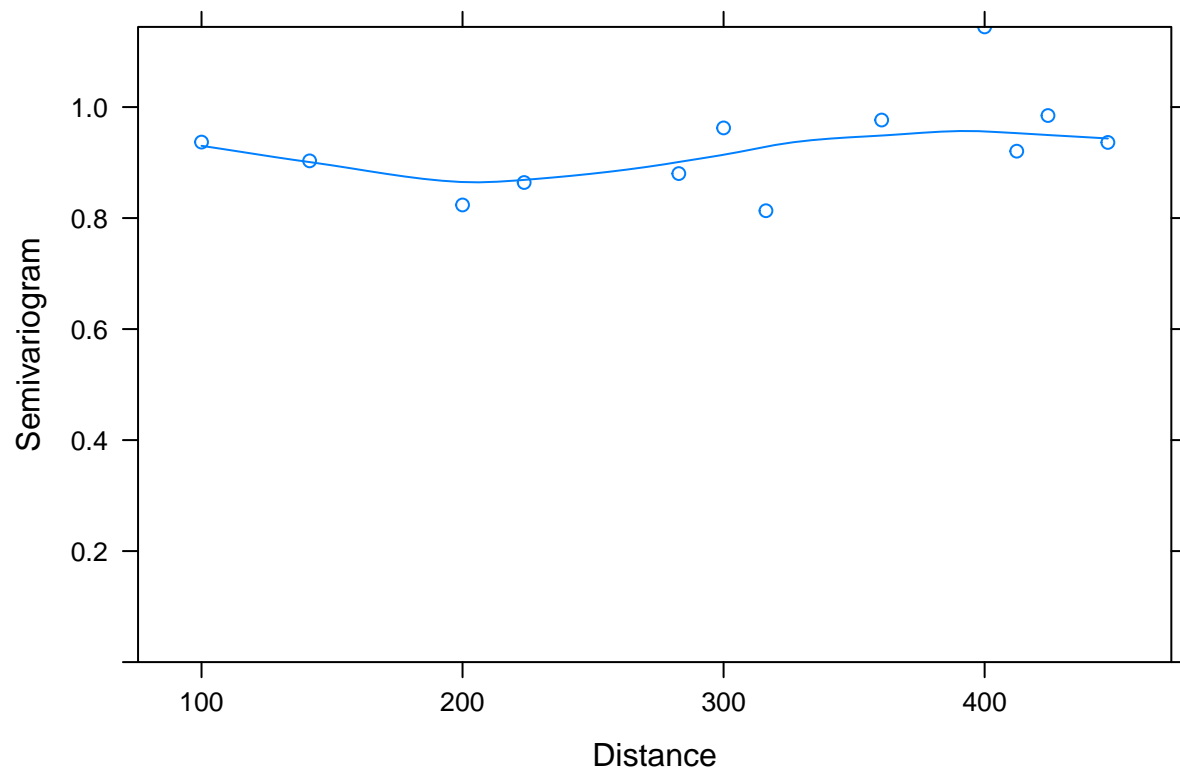
## Generalized least squares fit by REML
##   Model: response ~ sp_e
##   Data: modeling_dat
##       AIC      BIC    logLik
##  309.4934 318.8494 -149.7467
##
## Correlation Structure: Rational quadratic spatial correlation
## Formula: ~x + y
## Parameter estimate(s):
##      range      nugget
## 776.37893006  0.04013737
##
## Coefficients:
##              Value Std.Error   t-value p-value
## (Intercept) 14.860430 15.180613  0.9789084  0.3325
## sp_e        -0.016207  0.155317 -0.1043500  0.9173
##
## Correlation:
##      (Intr)
## sp_e -0.092
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -0.7548583 -0.7420696 -0.6485052 -0.3588807  1.2297120
##
## Residual standard error: 19.64344
## Degrees of freedom: 50 total; 48 residual

plot(Variogram(mod1_rat, maxDist = max_dist))

```



```
plot(Variogram(mod1_rat, resType = 'n', maxDist = max_dist)) #much better
```

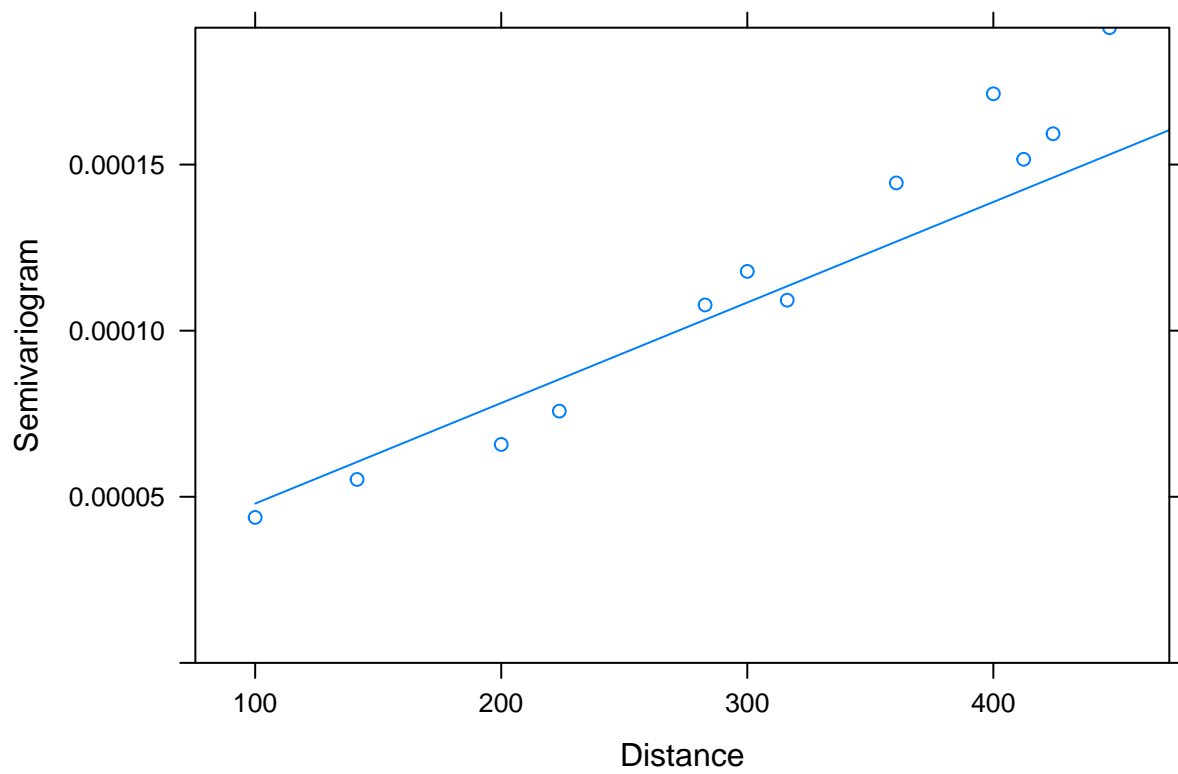


```
#fit of error model: Spherical
```

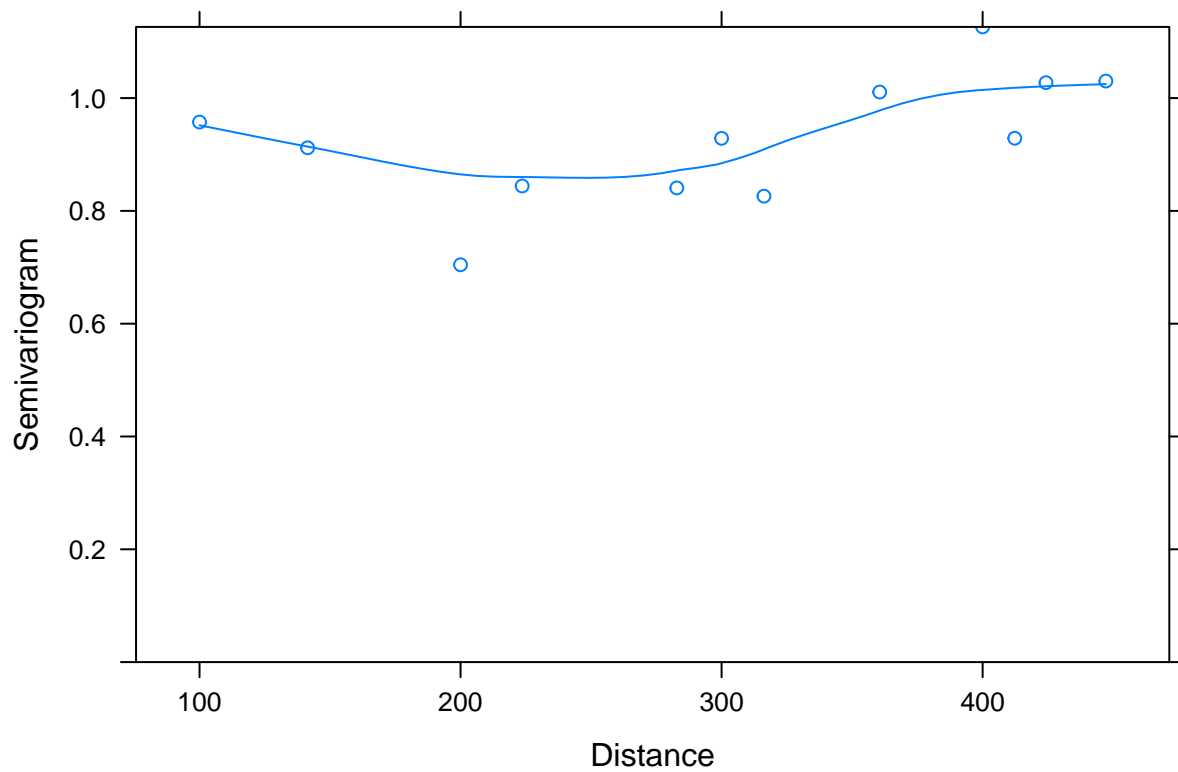
```
mod1_spher = update(mod1_rat, corr=corSpher(form=~x+y, nugget = T))  
summary(mod1_spher)
```

```
## Generalized least squares fit by REML  
##   Model: response ~ sp_e  
##   Data: modeling_dat  
##       AIC      BIC    logLik  
##  312.2971 321.6531 -151.1486  
##  
## Correlation Structure: Spherical spatial correlation  
## Formula: ~x + y  
## Parameter estimate(s):  
##      range      nugget  
## 4.956499e+06 1.769119e-05  
##  
## Coefficients:  
##              Value Std.Error   t-value p-value  
## (Intercept) 12.75215   650.7233  0.01959689  0.9844  
## sp_e        -0.01576    0.1588 -0.09921663  0.9214  
##  
## Correlation:  
##      (Intr)  
## sp_e -0.002  
##  
## Standardized residuals:  
##      Min      Q1      Med      Q3      Max  
## -0.019546577 -0.019171226 -0.016340179 -0.007595515  0.040356775  
##  
## Residual standard error: 650.7856  
## Degrees of freedom: 50 total; 48 residual
```

```
plot(Variogram(mod1_spher, maxDist = max_dist))
```



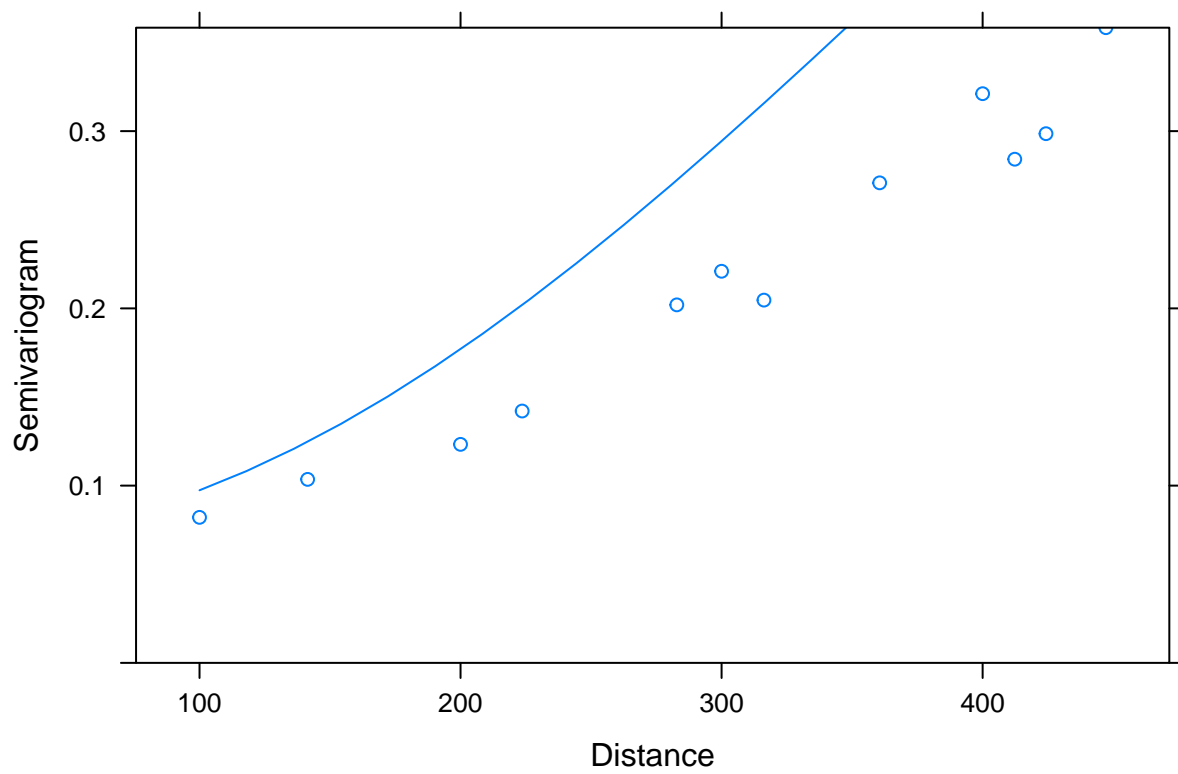
```
plot(Variogram(mod1_spher, resType = 'n', maxDist = max_dist)) #rational quadratic better
```



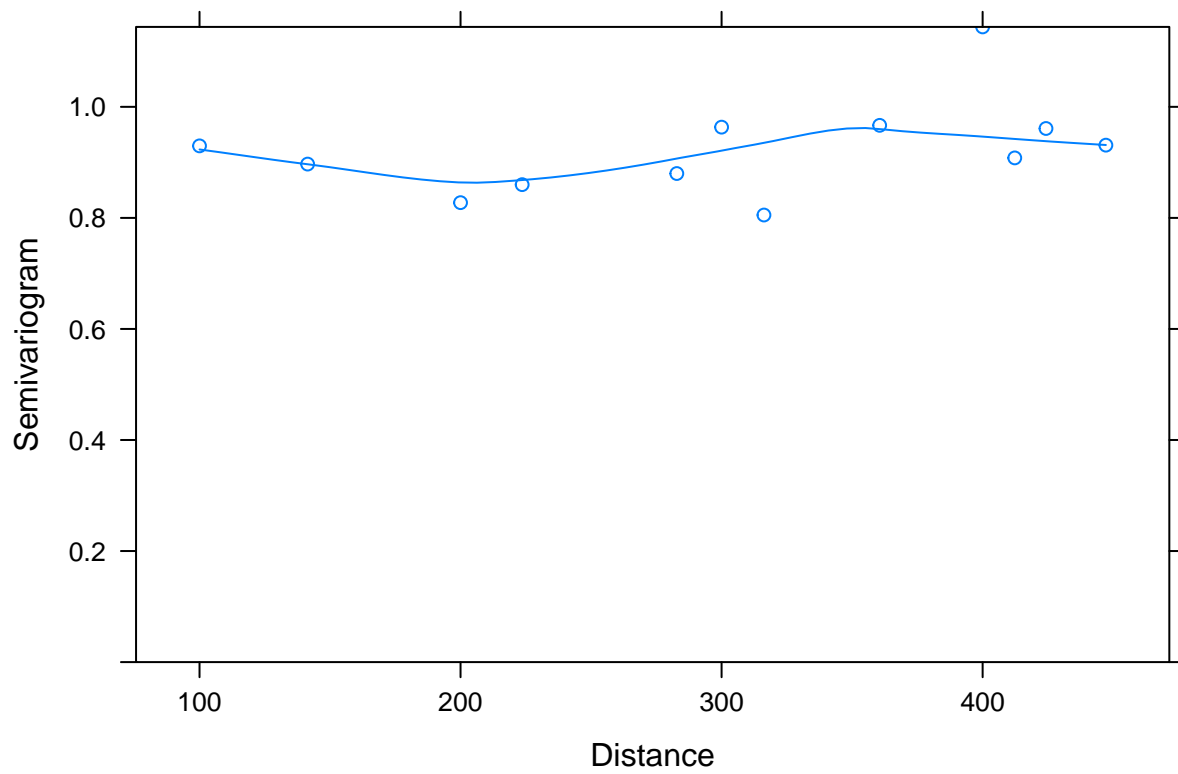
```
#fit of error model: Gaussian
mod1_gaus = update(mod1_spher, corr=corGaus(form=~x+y, nugget=T))
summary(mod1_gaus)
```

```
## Generalized least squares fit by REML
##   Model: response ~ sp_e
##   Data: modeling_dat
##       AIC       BIC    logLik
##  309.6905 319.0465 -149.8453
##
## Correlation Structure: Gaussian spatial correlation
## Formula: ~x + y
## Parameter estimate(s):
##      range      nugget
## 570.00120543  0.06915011
##
## Coefficients:
##              Value Std.Error   t-value p-value
## (Intercept) 13.32397  9.237273  1.4424137  0.1557
## sp_e        -0.01681  0.155782 -0.1079053  0.9145
##
## Correlation:
##      (Intr)
## sp_e -0.146
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -0.8843877 -0.8670497 -0.7451483 -0.3667173  1.7096940
##
## Residual standard error: 15.02774
## Degrees of freedom: 50 total; 48 residual
```

```
plot(Variogram(mod1_gaus, maxDist = max_dist))
```



```
plot(Variogram(mod1_gaus, resType = 'n', maxDist = max_dist)) #also pretty good
```





```
anova(mod1, mod1_exp, mod1_rat, mod1_spher, mod1_gaus)
```

```
##           Model df      AIC      BIC    logLik    Test  L.Ratio p-value
## mod1          1  3 343.6604 349.2740 -168.8302
## mod1_exp       2  4 311.7838 319.2686 -151.8919 1 vs 2 33.87651 <.0001
## mod1_rat       3  5 309.4934 318.8494 -149.7467 2 vs 3  4.29048  0.0383
## mod1_spher     4  5 312.2971 321.6531 -151.1486
## mod1_gaus      5  5 309.6905 319.0465 -149.8453
```

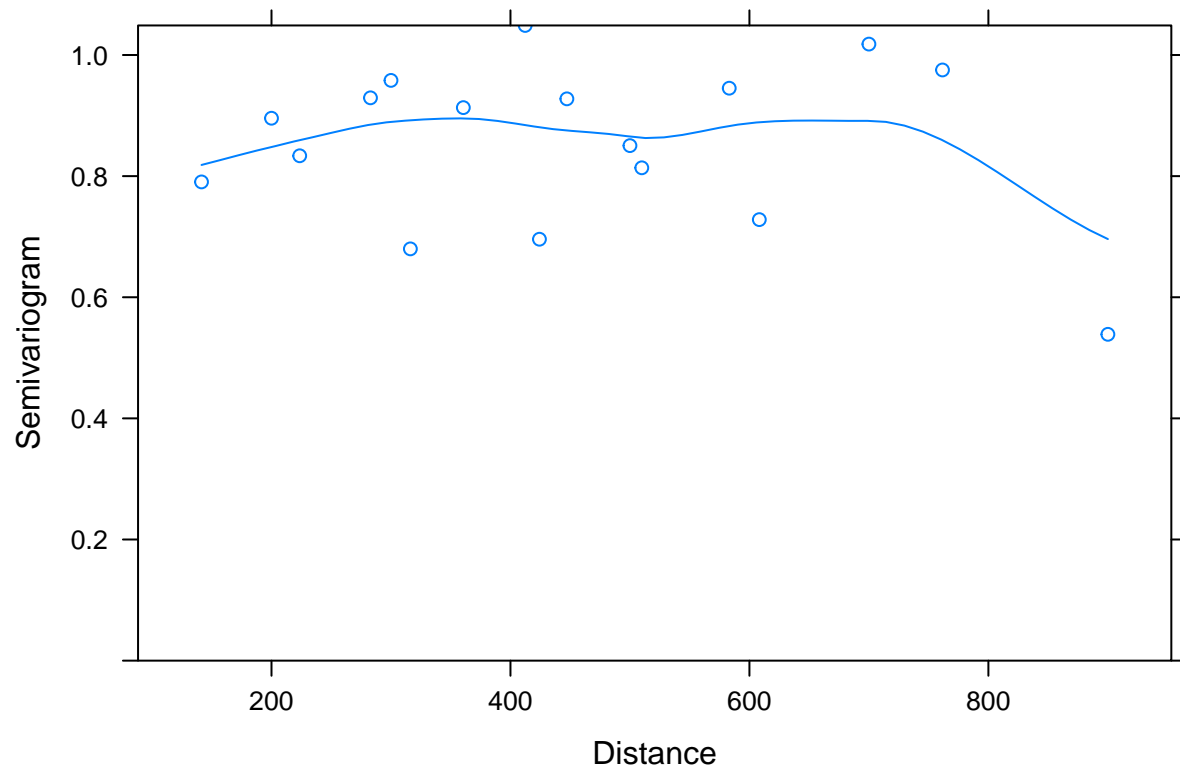
```
#rational quadratic model has lowest AIC, barely
```

Model 2: To develop a model to better predict the abundance of our species of interest, additional predictor species were included in a second GLM. This model better predicts the abundance of our species of interest. Again, the addition of an spatial error term was able to provide some improvement of the fit. In this instance, exponential spatial error term provided the best fit.

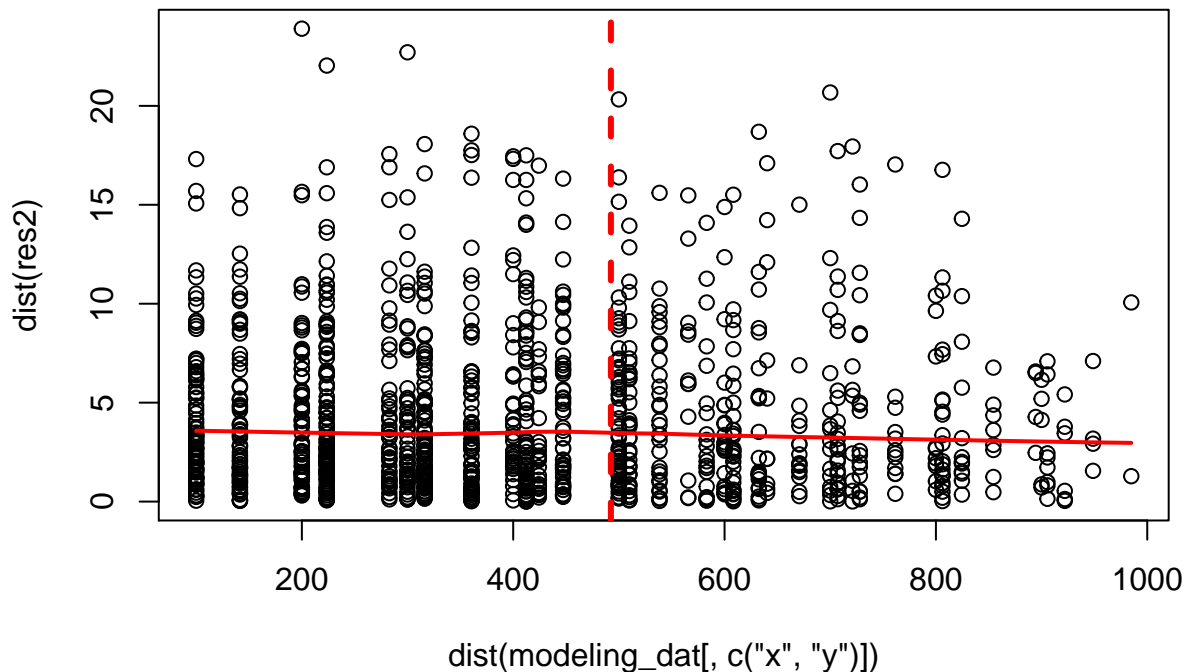
```
mod2=glms(response~Cordia.lasiocalyx+Hirtella.triandra+Picramnia.latifolia+Quassia.amara+Tabernaemontana
summary(mod2)
```

```
## Generalized least squares fit by REML
## Model: response ~ Cordia.lasiocalyx + Hirtella.triandra + Picramnia.latifolia +      Quassia.amara
## Data: modeling_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(mod2, form=~x+y))
```



```
#residuals  
res2 = residuals(mod2)  
plot(dist(modeling_dat[, c('x', 'y')]), dist(res2))  
lines(lowess(dist(modeling_dat[, c('x', 'y')]), dist(res2)), col='red', lwd=2)  
abline(v = max_dist, col='red', lwd=3, lty=2)
```



```
#fit of error model: expodential
```

```
mod2_exp = update(mod2, corr=corExp(form=~x + y))
```

```
summary(mod2_exp)
```

```
## Generalized least squares fit by REML
```

```
## Model: response ~ Cordia.lasiocalyx + Hirtella.triandra + Picramnia.latifolia +
```

```
Quassia.amara
```

```
## Data: modeling_dat
```

```
## 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
```

```
## Cordia.lasiocalyx 0.1208390 0.179811 0.672033 0.5052
```

```
## Hirtella.triandra 0.0191759 0.098501 0.194677 0.8466
```

```
## Picramnia.latifolia 0.2014516 0.509196 0.395627 0.6944
```

```
## Quassia.amara 1.2792289 1.847570 0.692385 0.4925
```

```
## Tabernaemontana.arborea 0.0674943 0.133782 0.504511 0.6165
```

```
## Trattinnickia.aspera 1.8115374 0.525147 3.449582 0.0013
```

```
## Xylopia.macrantha 0.3388574 0.156874 2.160064 0.0365
```

```
##
```

```
## Correlation:
```

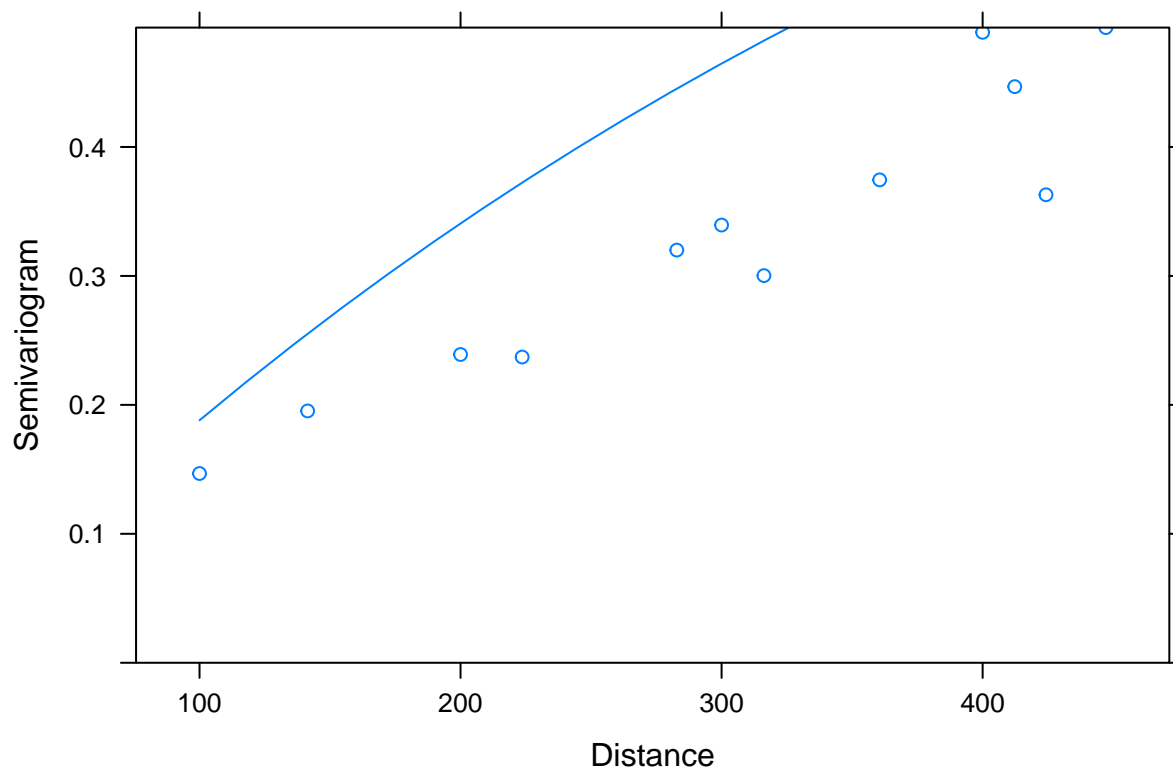
```
## (Intr) Crd.ls Hrtll. Pcrmn. Qss.mr Tbrnm. Trttn.
```

```
## Cordia.lasiocalyx -0.226
```

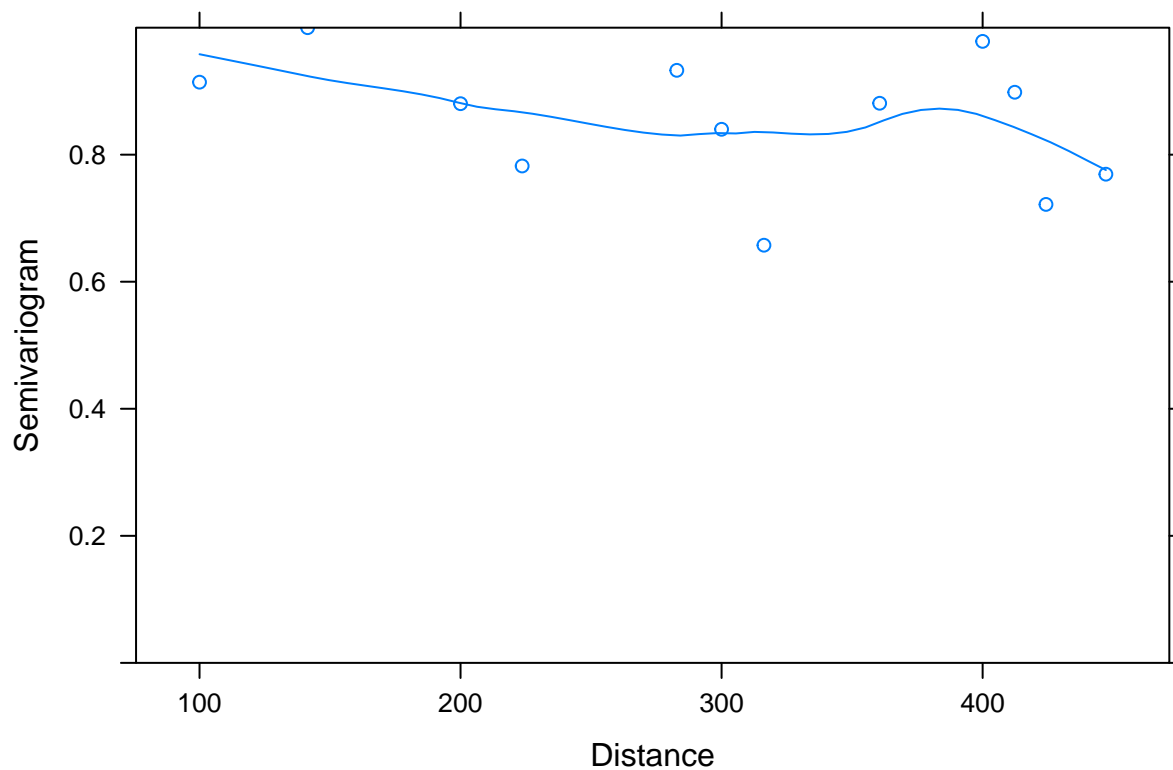
```
## Hirtella.triandra -0.309 -0.022
```

```
## Picramnia.latifolia      0.045 -0.066 -0.369
## Quassia.amara           -0.059 -0.304  0.321 -0.142
## Tabernaemontana.arborea -0.240 -0.016  0.288 -0.221  0.112
## Trattinnickia.aspera    -0.069  0.168 -0.237  0.212 -0.633 -0.041
## Xylopia.macrantha       -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
```

```
plot(Variogram(mod2_exp, maxDist = max_dist, data=modeling_dat)) #yeah, this is bad
```



```
plot(Variogram(mod2_exp, resType = 'normalized', maxDist = max_dist, data=modeling_dat))
```



```
#fit of error model: rational quadratic
```

```
mod2_rat = update(mod2_exp, corr=corRatio(form=~x+y, nugget=T))
summary(mod2_rat)
```

```
## Generalized least squares fit by REML
```

```
## Model: response ~ Cordia.lasiocalyx + Hirtella.triandra + Picramnia.latifolia +
```

```
Quassia.amara
```

```
## Data: modeling_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
```

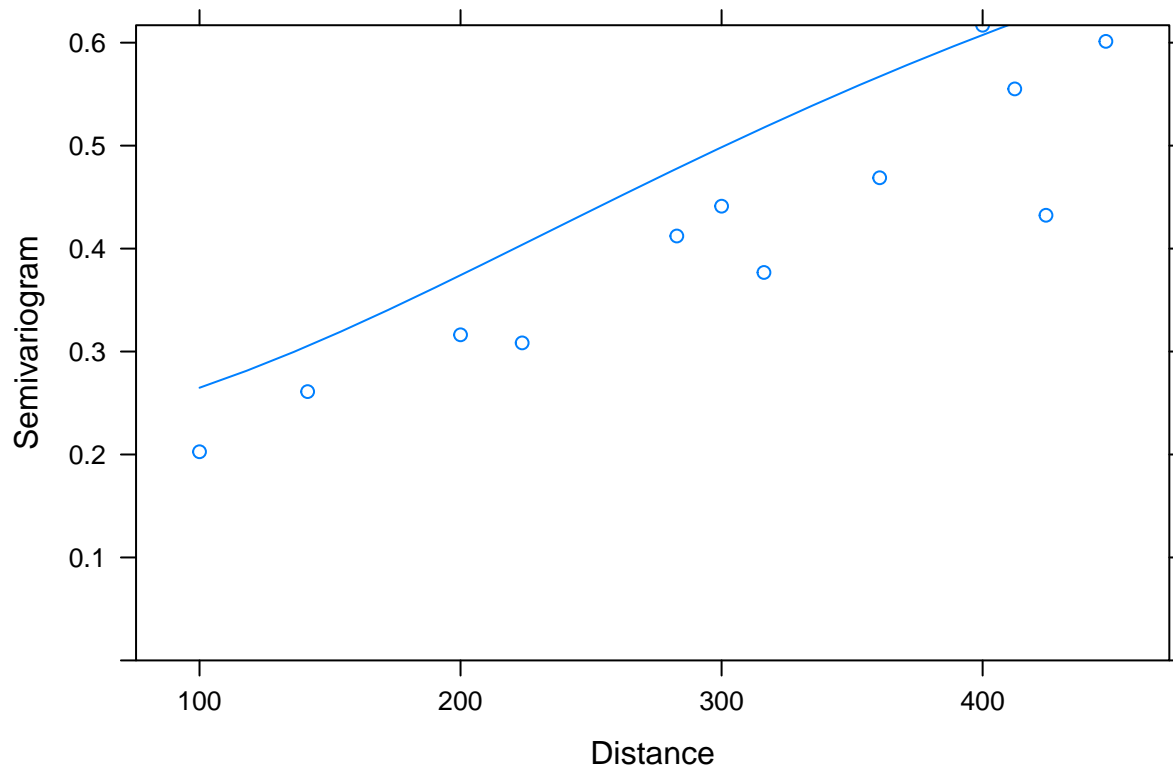
```
## Xylopia.macrantha 0.4058061 0.161181 2.5177087 0.0157
```

```
##
```

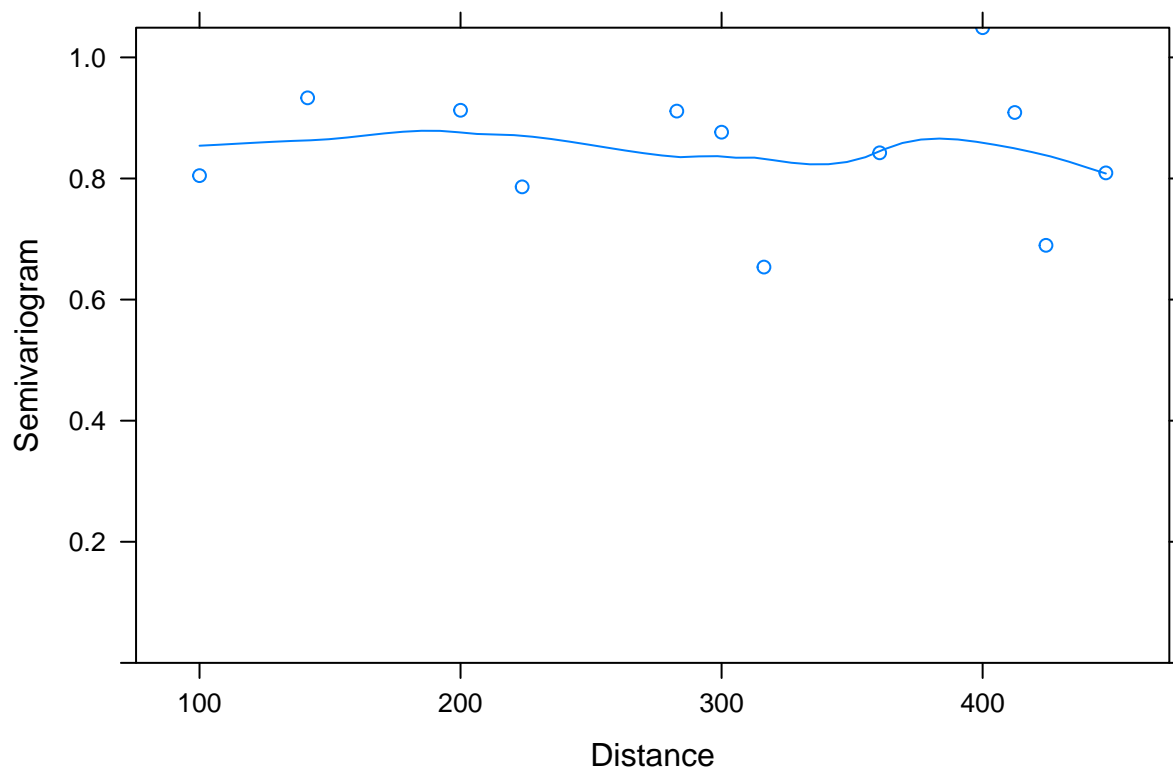
```
## Correlation:
```

```
##              (Intr) Crd.l.s 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
```

```
plot(Variogram(mod2_rat, maxDist = max_dist, data=modeling_dat))
```



```
plot(Variogram(mod2_rat, resType = 'n', maxDist = max_dist, data=modeling_dat))
```



```
#fit of error model: Spherical
```

```
mod2_spher = update(mod2_rat, corr=corSpher(form=~x+y, nugget = T))
summary(mod2_spher)
```

```
## Generalized least squares fit by REML
```

```
## Model: response ~ Cordia.lasiocalyx + Hirtella.triandra + Picramnia.latifolia +
```

```
Quassia.amara
```

```
## Data: modeling_dat
```

```
## 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
```

```
## Cordia.lasiocalyx 0.1426672 0.18953 0.752754 0.4558
```

```
## Hirtella.triandra -0.0017713 0.09038 -0.019599 0.9845
```

```
## Picramnia.latifolia 0.2863351 0.52743 0.542882 0.5901
```

```
## Quassia.amara 1.3263713 1.93681 0.684821 0.4972
```

```
## Tabernaemontana.arborea 0.0407524 0.13952 0.292080 0.7717
```

```
## Trattinnickia.aspera 1.8170748 0.57298 3.171298 0.0028
```

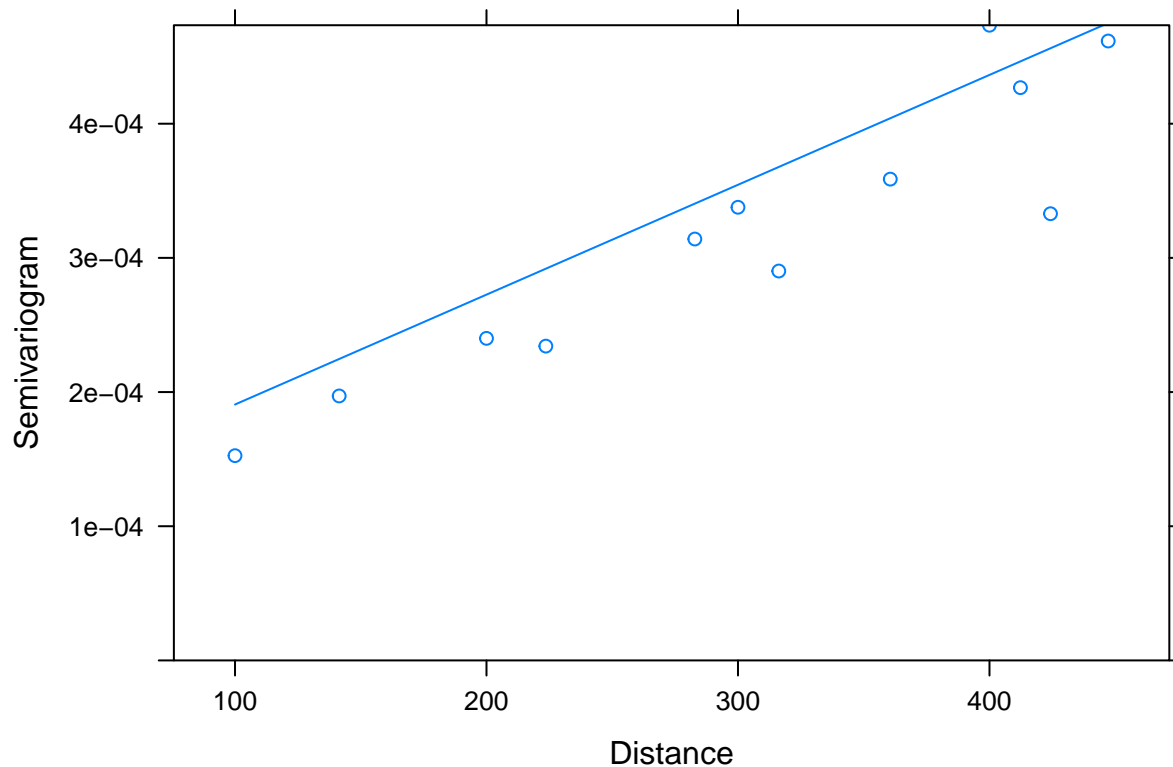
```
## Xylopia.macrantha 0.4086712 0.15367 2.659334 0.0110
```

```
##
```

```
## Correlation:
```

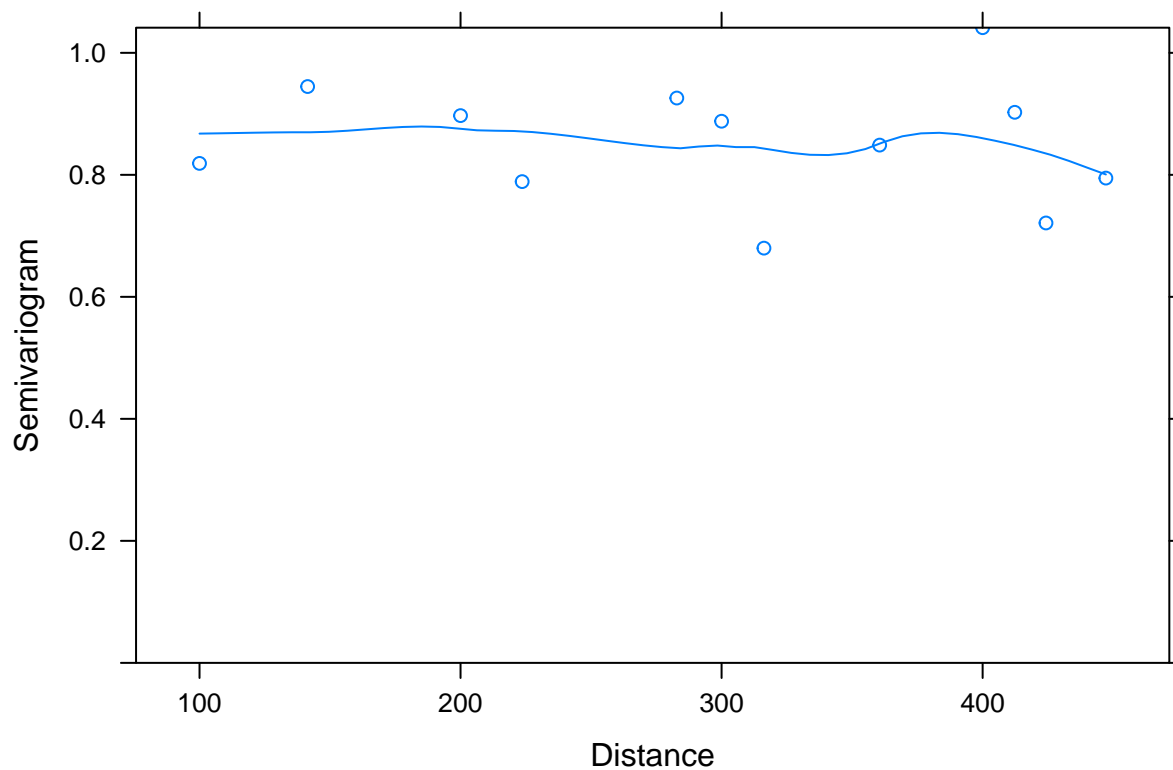
```
##          (Intr) Crd.l.s Hrtll. Pcrmn. Qss.mr Tbrnm. Trttn.
## Cordia.lasiocalyx      -0.006
## Hirtella.triandra      -0.007 -0.098
## Picramnia.latifolia     0.001  0.017 -0.360
## Quassia.amara          -0.001 -0.292  0.344 -0.193
## Tabernaemontana.arborea -0.005 -0.020  0.160 -0.197  0.088
## Trattinnickia.aspera    -0.002  0.165 -0.276  0.255 -0.655 -0.036
## Xylopia.macrantha      -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
```

```
plot(Variogram(mod2_spher, maxDist = max_dist, data=modeling_datt))
```



```
plot(Variogram(mod2_spher, resType = 'n', maxDist = max_dist, data=modeling_dat))
```





```
#fit of error model: Gaussian
```

```
mod2_gaus = update(mod2_spher, corr=corGaus(form=~x+y, nugget=T))
summary(mod2_gaus)
```

```
## Generalized least squares fit by REML
```

```
## Model: response ~ Cordia.lasiocalyx + Hirtella.triandra + Picramnia.latifolia +
```

```
Quassia.amara
```

```
## Data: modeling_dat
```

```
## AIC BIC logLik
```

```
## 303.8654 322.9797 -140.9327
```

```
##
```

```
## Correlation Structure: Gaussian spatial correlation
```

```
## Formula: ~x + y
```

```
## Parameter estimate(s):
```

```
## range nugget
```

```
## 904.7631566 0.1578976
```

```
##
```

```
## Coefficients:
```

```
## Value Std.Error t-value p-value
```

```
## (Intercept) 4.958338 7.584282 0.6537650 0.5168
```

```
## Cordia.lasiocalyx 0.121133 0.198583 0.6099867 0.5452
```

```
## Hirtella.triandra 0.014383 0.077806 0.1848564 0.8542
```

```
## Picramnia.latifolia 0.266221 0.556581 0.4783142 0.6349
```

```
## Quassia.amara 1.852602 2.046397 0.9052997 0.3705
```

```
## Tabernaemontana.arborea 0.010043 0.147242 0.0682063 0.9459
```

```
## Trattinnickia.aspera 1.741247 0.633528 2.7484923 0.0088
```

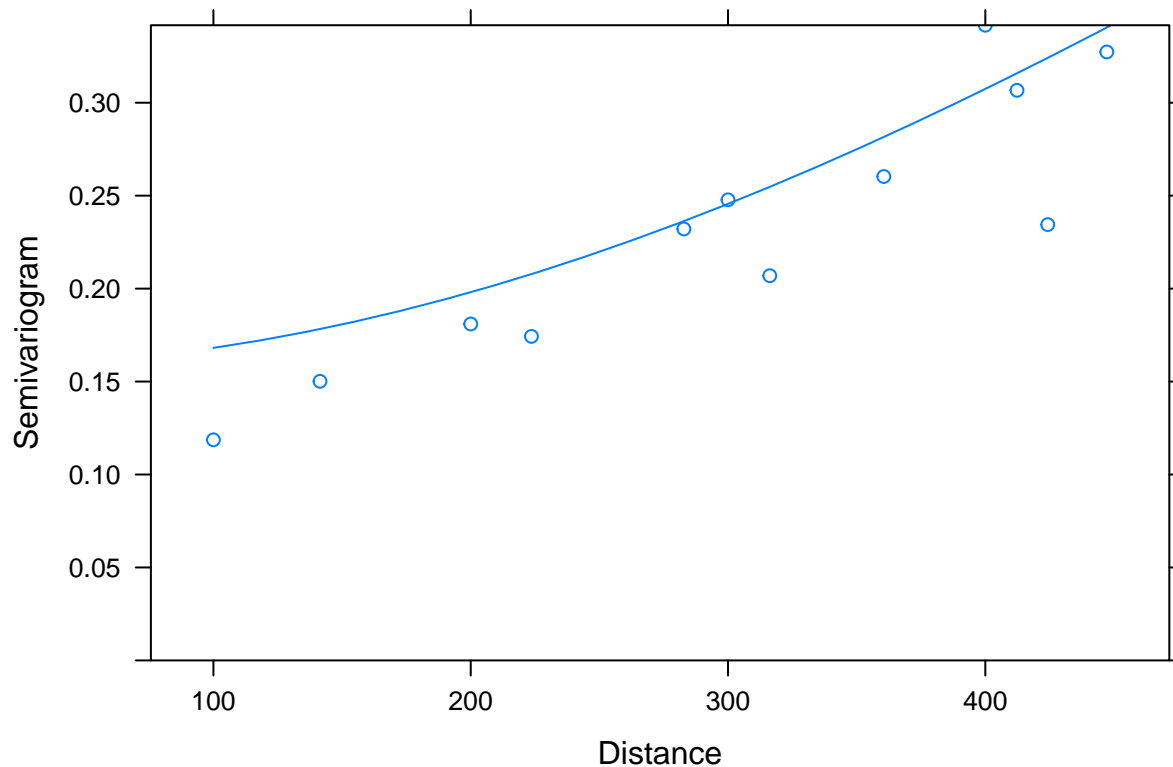
```
## Xylopia.macrantha 0.453893 0.148331 3.0600007 0.0038
```

```
##
```

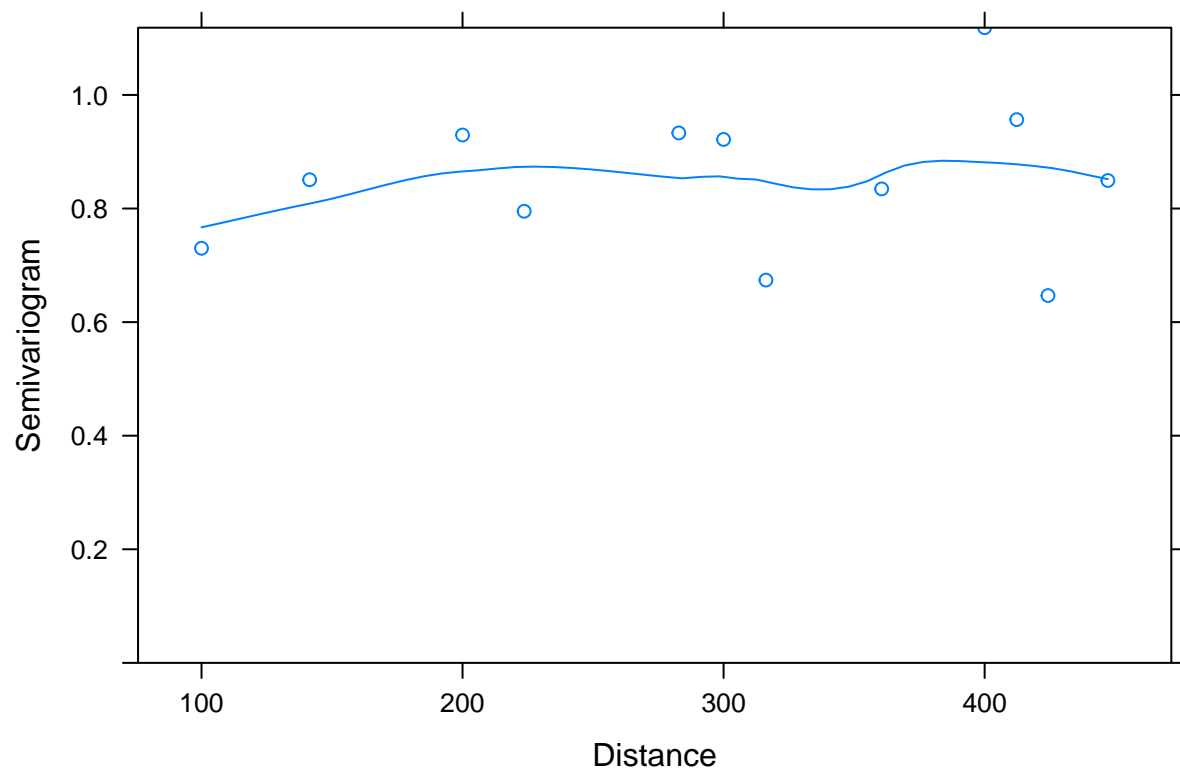
```
## Correlation:
```

```
##                               (Intr) Crd.l.s Hrtll. Pcrmn. Qss.mr Tbrnm. Trttn.
## Cordia.lasiocalyx           -0.271
## Hirtella.triandra           -0.200 -0.113
## Picramnia.latifolia         -0.011  0.055 -0.322
## Quassia.amara               -0.018 -0.246  0.323 -0.218
## Tabernaemontana.arborea     -0.123  0.012 -0.007 -0.177  0.036
## Trattinnickia.aspera        -0.091  0.164 -0.300  0.267 -0.683 -0.022
## Xylopia.macrantha           -0.059 -0.043  0.026 -0.252  0.351  0.156 -0.233
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -1.0940060 -0.6952369 -0.5606242 -0.1752861  1.6478169
##
## Residual standard error: 9.649015
## Degrees of freedom: 50 total; 42 residual
```

```
plot(Variogram(mod2_gaus, maxDist = max_dist))
```



```
plot(Variogram(mod2_gaus, resType = 'n', maxDist = max_dist))
```



```
anova(mod2, mod2_exp, mod2_rat, mod2_spher, mod2_gaus)
```

##	Model	df	AIC	BIC	logLik	Test	L.Ratio	p-value
##	mod2	1	9	307.1163	322.7554	-144.5582		
##	mod2_exp	2	10	301.6062	318.9829	-140.8031	1 vs 2	7.510175 0.0061
##	mod2_rat	3	11	303.1486	322.2630	-140.5743	2 vs 3	0.457530 0.4988
##	mod2_spher	4	11	301.9592	321.0735	-139.9796		
##	mod2_gaus	5	11	303.8653	322.9797	-140.9327		

*#exponential model has lowest AIC, barely.*