

# spatial modeling assignment

Merry Andersen

February 17, 2016

```
library(vegan)

## Loading required package: permute
## Loading required package: lattice
## This is vegan 2.3-3

library(nlme)
data(BCI)
?BCI

## starting httpd help server ...

## done

dim(BCI)

## [1] 50 225

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

spsubset = subset(BCI, select=sp_ids)
head(spsubset)

## Cordia.lasiocalyx Hirtella.triandra Picramnia.latifolia Quassia.amara
## 1 8 21 0 0
## 2 6 14 0 0
## 3 6 5 1 0
## 4 11 4 0 0
## 5 7 6 0 0
## 6 6 6 0 0
## Tabernaemontana.arborea Trattinnickia.aspera Xylopia.macrantha
## 1 9 3 1
## 2 5 1 0
## 3 6 1 0
## 4 10 0 0
## 5 16 2 0
## 6 11 0 0
## Drypetes.standleyi
## 1 2
## 2 1
## 3 2
## 4 0
```

```
## 5          0
## 6          0

BCI_sub = data.frame(BCI_xy, ssubset)
head(BCI_sub)

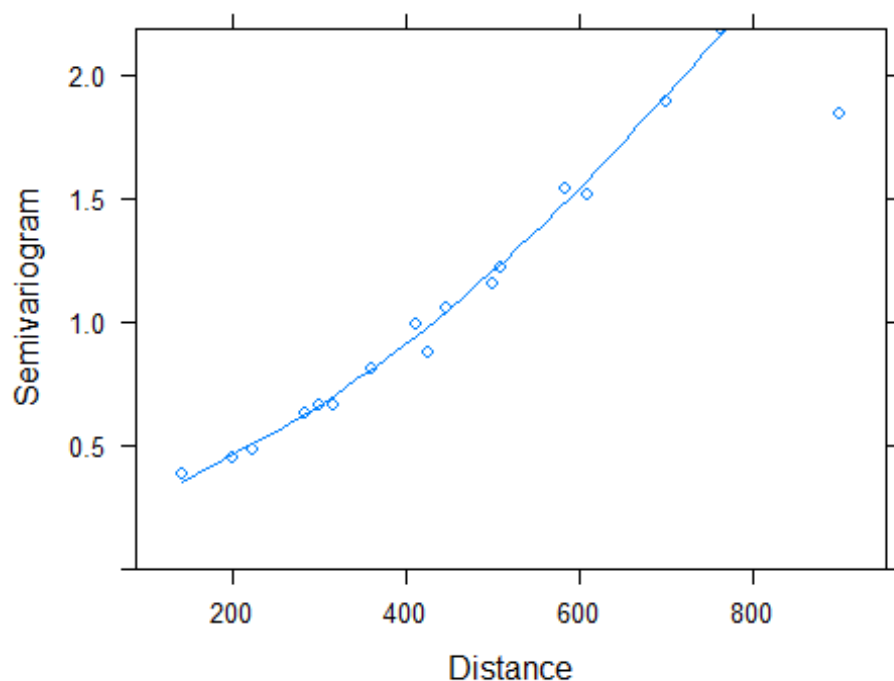
##           x           y Cordia.lasiocalyx Hirtella.triandra Picramnia.latifolia
## 1 625754 1011569           8           21              0
## 2 625754 1011669           6           14              0
## 3 625754 1011769           6            5              1
## 4 625754 1011869          11            4              0
## 5 625754 1011969           7            6              0
## 6 625854 1011569           6            6              0
##  Quassia.amara Tabernaemontana.arborea Trattinnickia.aspera
## 1           0           9              3
## 2           0           5              1
## 3           0           6              1
## 4           0          10              0
## 5           0          16              2
## 6           0          11              0
##  Xylopia.macrantha Drypetes.standleyi
## 1           1           2
## 2           0           1
## 3           0           2
## 4           0           0
## 5           0           0
## 6           0           0
```

Model 1: general least squares with *Trattinnickia aspera* as the predictive variable and *Drypetes standleyi* as the response variable

```
#gls ~ Trattinnickia.aspera
modtratt = gls(Drypetes.standleyi ~ Trattinnickia.aspera, data=BCI_sub)
summary(modtratt)

## Generalized least squares fit by REML
## Model: Drypetes.standleyi ~ Trattinnickia.aspera
## Data: BCI_sub
##      AIC      BIC    logLik
## 341.9598 347.5734 -167.9799
##
## Coefficients:
##              Value Std.Error  t-value p-value
## (Intercept)   3.411628 1.2161012  2.805381  0.0072
## Trattinnickia.aspera 2.860465 0.7916145  3.613457  0.0007
##
## Correlation:
##              (Intr)
## Trattinnickia.aspera -0.521
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -1.4974564 -0.5819394 -0.1922903  0.5909678  3.2892088
##
## Residual standard error: 7.341131
## Degrees of freedom: 50 total; 48 residual
```

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



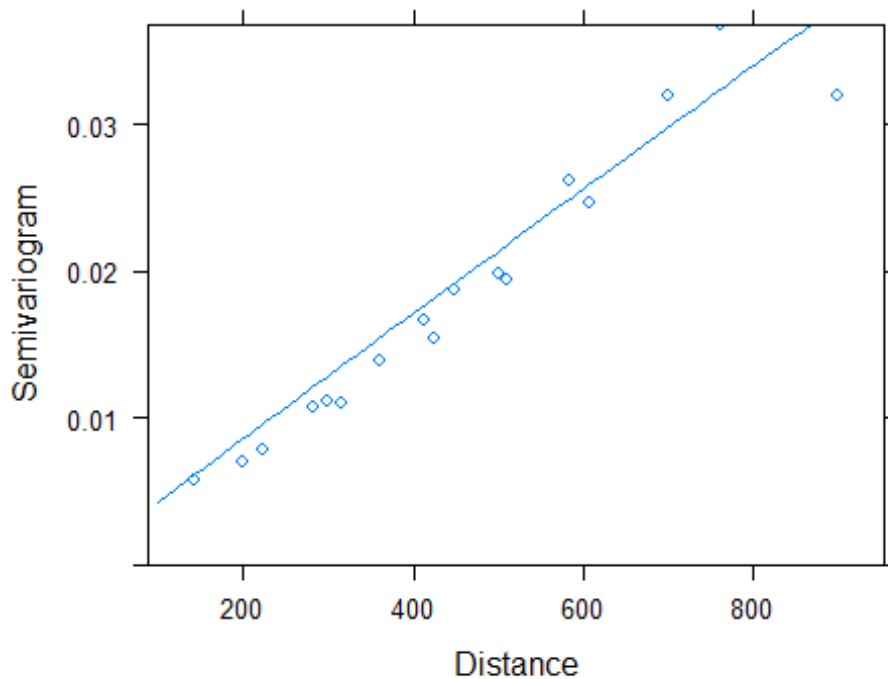
```
#modtratt with exponential error
```

```
modtratt1 = gls(Drypetes.standleyi ~ Trattinnickia.aspera, data= BCI_sub, corr=
corExp(form= ~ x + y))
summary(modtratt1)
```

```
## Generalized least squares fit by REML
## Model: Drypetes.standleyi ~ Trattinnickia.aspera
## Data: BCI_sub
##      AIC      BIC    logLik
## 289.2043 296.6891 -140.6022
##
## Correlation Structure: Exponential spatial correlation
## Formula: ~x + y
## Parameter estimate(s):
##   range
## 23112.03
##
## Coefficients:
##              Value Std.Error  t-value p-value
## (Intercept)    6.912837  56.75482  0.121802  0.9036
## Trattinnickia.aspera 1.958851   0.39021  5.019993  0.0000
##
## Correlation:
##              (Intr)
## Trattinnickia.aspera -0.026
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -0.20510401 -0.12026497 -0.08547029  0.01456441  0.42191609
##
```

```
## Residual standard error: 57.48005
## Degrees of freedom: 50 total; 48 residual

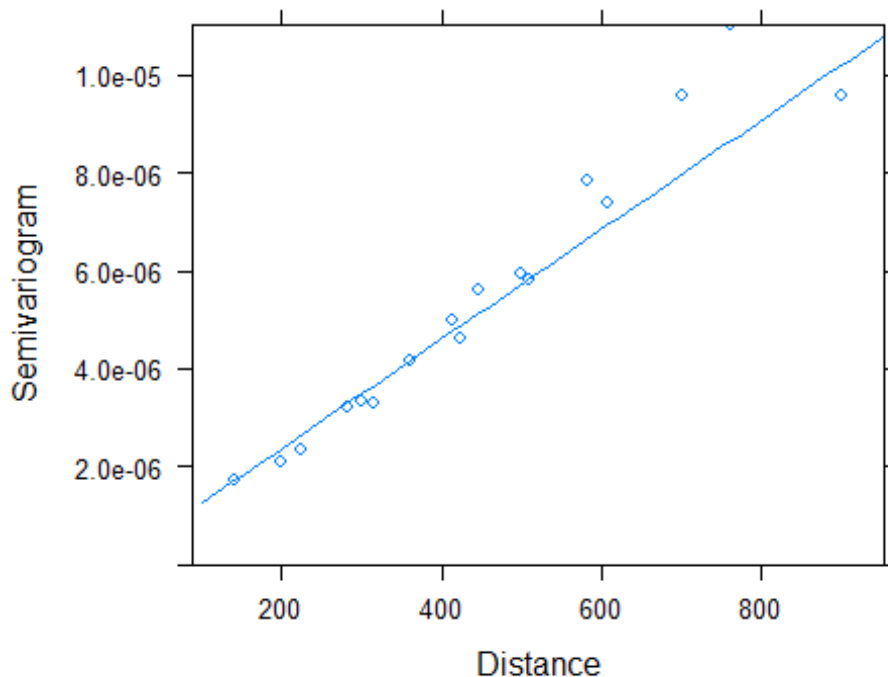
plot(Variogram(modtratt1, form= ~ x + y))
```



```
#modtratt with exponential error and nugget
modtratt1nug = gls(Drypetes.standleyi ~ Trattinnickia.aspera, data= BCI_sub, corr=
corExp(form= ~ x + y, nugget = T))
summary(modtratt1nug)

## Generalized least squares fit by REML
## Model: Drypetes.standleyi ~ Trattinnickia.aspera
## Data: BCI_sub
##      AIC      BIC    logLik
## 291.1105 300.4665 -140.5553
##
## Correlation Structure: Exponential spatial correlation
## Formula: ~x + y
## Parameter estimate(s):
##      range      nugget
## 8.960024e+07 1.501151e-07
##
## Coefficients:
##              Value Std.Error t-value p-value
## (Intercept)    6.828988  3322.563  0.002055  0.9984
## Trattinnickia.aspera 1.958035    0.398  4.917613  0.0000
##
## Correlation:
##              (Intr)
## Trattinnickia.aspera 0
##
## Standardized residuals:
```

```
##           Min           Q1           Med           Q3           Max
## -0.0035222969 -0.0020553305 -0.0014533876  0.0002771983  0.0073253060
##
## Residual standard error: 3322.574
## Degrees of freedom: 50 total; 48 residual
plot(Variogram(modtratt1nug, form= ~ x + y))
```



```
#anova of models
anova(modtratt, modtratt1, modtratt1nug, test = F)

##           Model df          AIC          BIC        logLik
## modtratt         1  3 341.9598 347.5734 -167.9799
## modtratt1         2  4 289.2043 296.6891 -140.6021
## modtratt1nug       3  5 291.1105 300.4665 -140.5553
```

Both models show strong correlation between *D. standleyi* and *T. aspera*. Including the exponential error decreased the regression coefficient and the p-value for *T. aspera*. In the ANOVA the AIC and BIC were reduced by including the error, indicating a better fit for the model, but the graph shows an exponential trend along the data points. This means a different regression model is probably needed. Adding a nugget did not improve the model fit.

Model 2: *D. standleyi* as response variable, all other species as predictive variables

```
#gls ~ all species
modall = gls(Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra +
Picramnia.latifolia + Quassia.amara + Tabernaemontana.arborea + Trattinnickia.aspera +
Xylopia.macrantha, data=BCI_sub)
summary(modall)

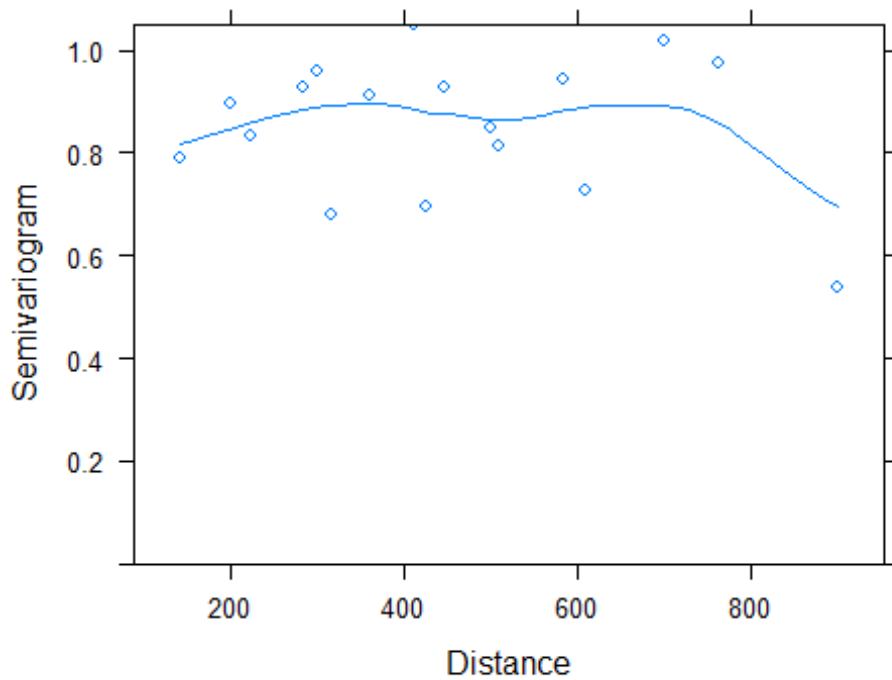
## Generalized least squares fit by REML
## Model: Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra +
Picramnia.latifolia + Quassia.amara + Tabernaemontana.arborea + Trattinnickia.aspera
```

```

+ Xylophia.macrantha
## Data: BCI_sub
## 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
## Xylophia.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
## Xylophia.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(modall, form= ~ x + y))

```



*#modall with exponential error*

```
modall1 = gls(Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra +
Picramnia.latifolia + Quassia.amara + Tabernaemontana.arborea + Trattinnickia.aspera +
Xylopiamacrantha, data= BCI_sub, corr= corExp(form= ~ x + y))
summary(modall1)
```

## Generalized least squares fit by REML

## Model: Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra +  
Picramnia.latifolia + Quassia.amara + Tabernaemontana.arborea + Trattinnickia.aspera  
+ Xylopiamacrantha

## Data: BCI\_sub

## AIC BIC logLik  
## 301.6062 318.9829 -140.8031

##

## Correlation Structure: Exponential spatial correlation

## Formula: ~x + y

## Parameter estimate(s):

## range

## 480.0567

##

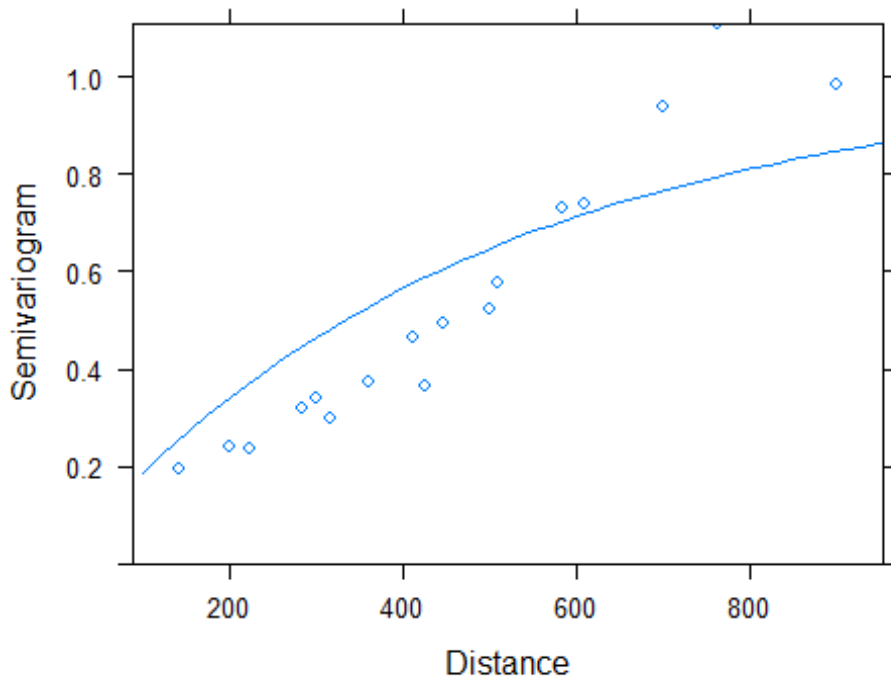
## Coefficients:

	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
## Xylopiamacrantha	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(modall1, form= ~ x + y))
```

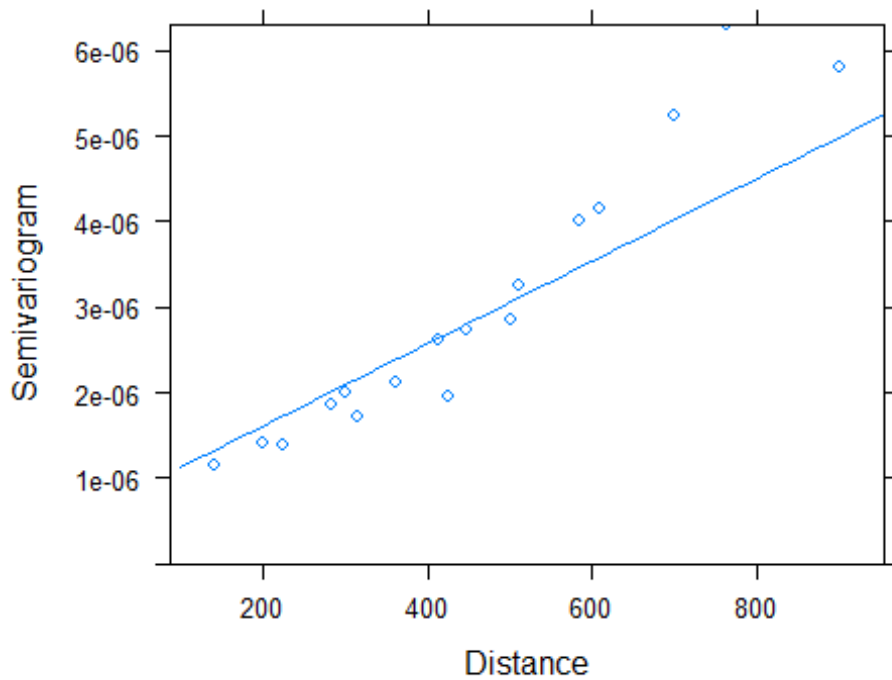


```
#try exponential error with nugget
modall1nug = gls(Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra +
  Picramnia.latifolia + Quassia.amara + Tabernaemontana.arborea + Trattinnickia.aspera +
  Xylopia.macrantha, data= BCI_sub, corr= corExp(form= ~ x + y, nugget = T))
summary(modall1nug)

## Generalized least squares fit by REML
## Model: Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra +
  Picramnia.latifolia + Quassia.amara + Tabernaemontana.arborea + Trattinnickia.aspera
  + Xylopia.macrantha
## Data: BCI_sub
##      AIC      BIC    logLik
##  301.9592 321.0735 -139.9796
```

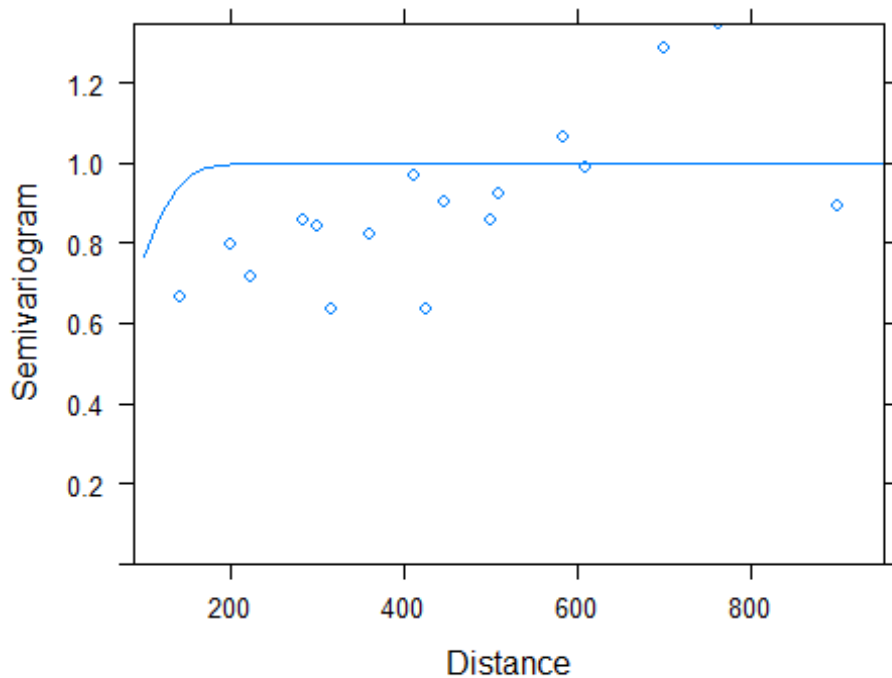


```
##
## Correlation Structure: Exponential spatial correlation
## Formula: ~x + y
## Parameter estimate(s):
##      range      nugget
## 2.069876e+08 6.423682e-07
##
## Coefficients:
##              Value Std.Error   t-value p-value
## (Intercept)   3.0501207  3486.910   0.000875  0.9993
## Cordia.lasiocalyx  0.1426665    0.190   0.752751  0.4558
## Hirtella.triandra -0.0017716    0.090  -0.019602  0.9845
## Picramnia.latifolia  0.2863333    0.527   0.542880  0.5901
## Quassia.amara    1.3263608    1.937   0.684817  0.4972
## Tabernaemontana.arborea  0.0407531    0.140   0.292086  0.7717
## Trattinnickia.aspera  1.8170752    0.573   3.171304  0.0028
## Xylopia.macrantha   0.4086698    0.154   2.659323  0.0110
##
## Correlation:
##              (Intr) Crd.ls Hrtll. Pcrmn. Qss.mr Tbrnm. Trttn.
## Cordia.lasiocalyx    0.000
## Hirtella.triandra  -0.001 -0.098
## Picramnia.latifolia  0.000  0.017 -0.360
## Quassia.amara        0.000 -0.292  0.344 -0.193
## Tabernaemontana.arborea  0.000 -0.020  0.160 -0.197  0.088
## Trattinnickia.aspera  0.000  0.165 -0.276  0.255 -0.655 -0.036
## Xylopia.macrantha    0.000 -0.066 -0.037 -0.048  0.306  0.140 -0.183
##
## Standardized residuals:
##              Min      Q1      Med      Q3      Max
## -0.0025251382 -0.0014891171 -0.0010582565  0.0002851465  0.0053085949
##
## Residual standard error: 3486.914
## Degrees of freedom: 50 total; 42 residual
plot(Variogram(modall1nug, form= ~ x + y))
```



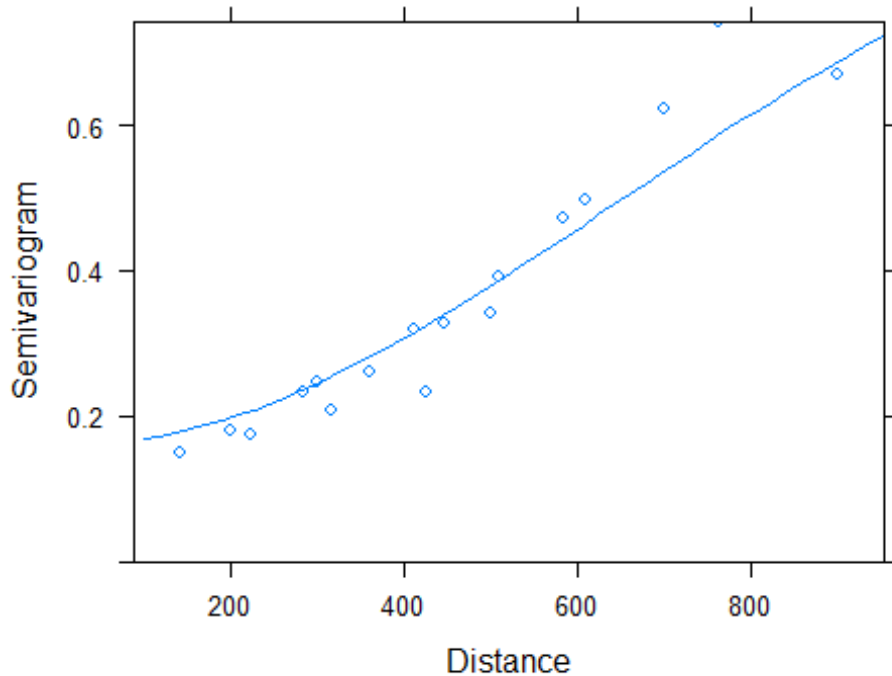
*#There seems to be systematic error with the exponential correlation so try Gaussian instead*

```
modallG = gls(Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra +
Picramnia.latifolia + Quassia.amara + Tabernaemontana.arborea + Trattinnickia.aspera +
Xylopia.macrantha, data= BCI_sub, corr= corGaus(form= ~ x + y))
plot(Variogram(modallG, form= ~ x + y))
```



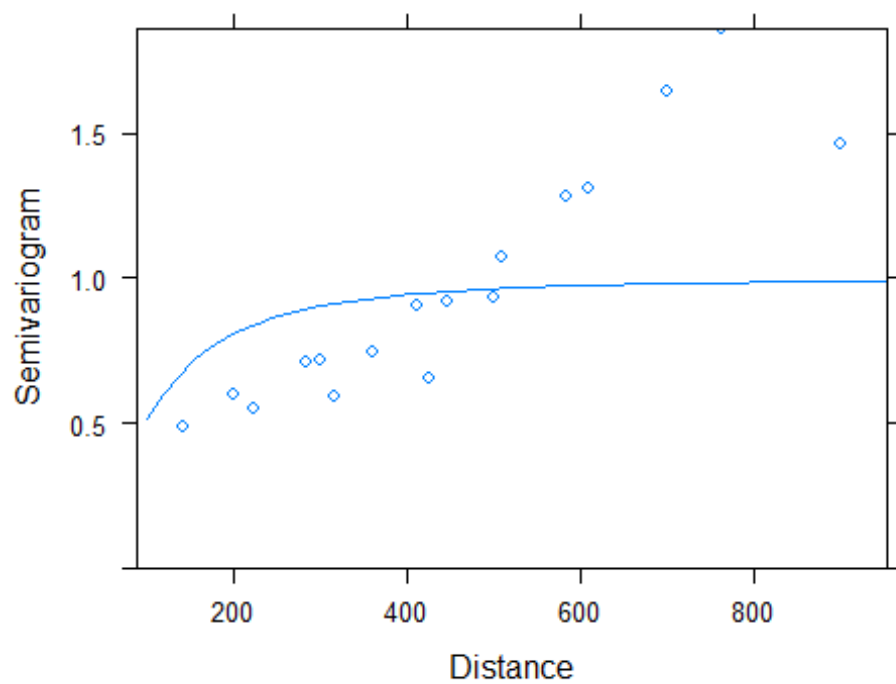
*#Try Gaussian with nugget*

```
modallGnug = gls(Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra +  
Picramnia.latifolia + Quassia.amara + Tabernaemontana.arborea + Trattinnickia.aspera +  
Xylopia.macrantha, data= BCI_sub, corr= corGaus(form= ~ x + y, nugget = T))  
plot(Variogram(modallGnug, form= ~ x + y))
```



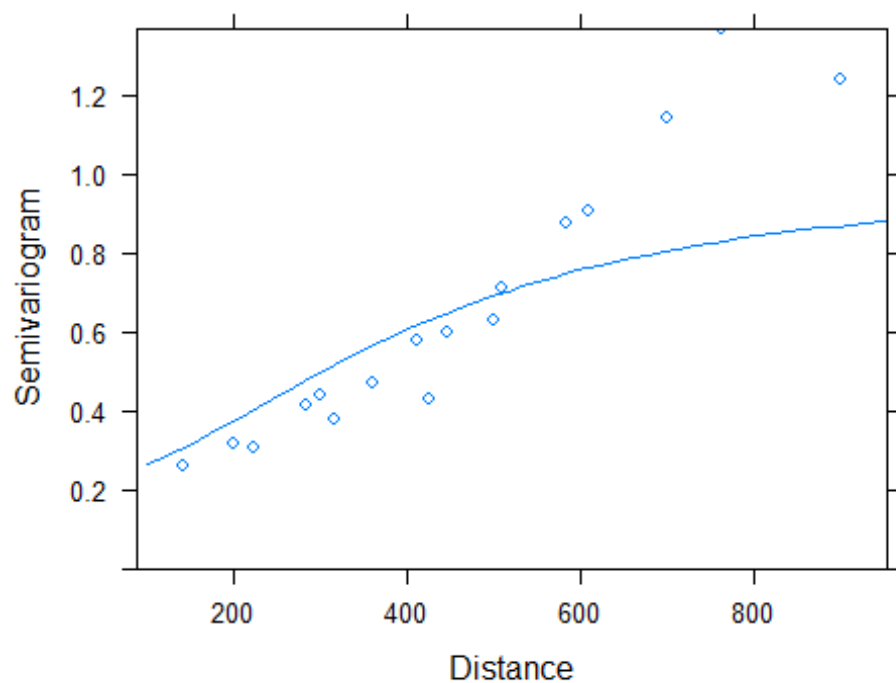
*#Try rational quadratic*

```
modallR = gls(Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra +  
Picramnia.latifolia + Quassia.amara + Tabernaemontana.arborea + Trattinnickia.aspera +  
Xylopia.macrantha, data= BCI_sub, corr= corRatio(form= ~ x + y))  
plot(Variogram(modallR, form= ~ x + y))
```



*#Try rational quadratic with nugget*

```
modallRnug = gls(Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra +
  Picramnia.latifolia + Quassia.amara + Tabernaemontana.arborea + Trattinnickia.aspera +
  Xylopia.macrantha, data= BCI_sub, corr= corRatio(form=~x + y, nugget = T))
plot(Variogram(modallRnug, form=~x + y))
```



#### *#Anova of all models*

```
anova(modall, modall1, modall1nug, modallG, modallGnug, modallR, modallRnug, test = F)
```

##	Model	df	AIC	BIC	logLik
## modall	1	9	307.1163	322.7554	-144.5582
## modall1	2	10	301.6062	318.9829	-140.8031
## modall1nug	3	11	301.9592	321.0735	-139.9796
## modallG	4	10	307.2070	324.5837	-143.6035
## modallGnug	5	11	303.8653	322.9797	-140.9327
## modallR	6	10	303.8542	321.2309	-141.9271
## modallRnug	7	11	303.1486	322.2630	-140.5743

Including exponential error in the model changed the coefficients of each variable, decreasing some while increasing others. The exponential error model had the best fit according to the ANOVA. Including a nugget or trying other types of error did not improve the fit. As with the first model, there seems to be systematic error in the variogram including exponential error. However, other types of error did not provide a better fit.

While adding error improved both models, the improvement was much more noticeable in the model with only one explanatory variable. This is most likely because there is no apparent correlation between *D. standleyi* and the other species as a whole, but there is between *D. standleyi* and *T. aspera* alone.