

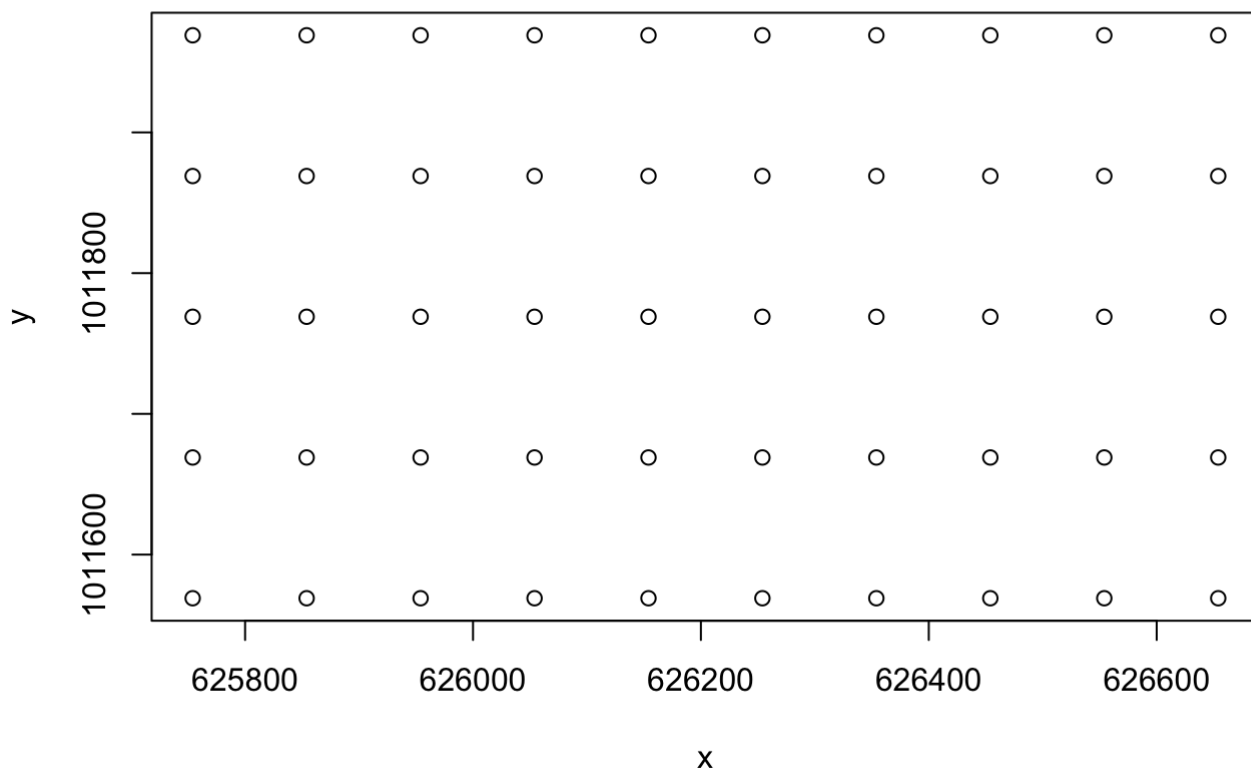
```
library(vegan)
```

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

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

```
## This is vegan 2.5-6
```

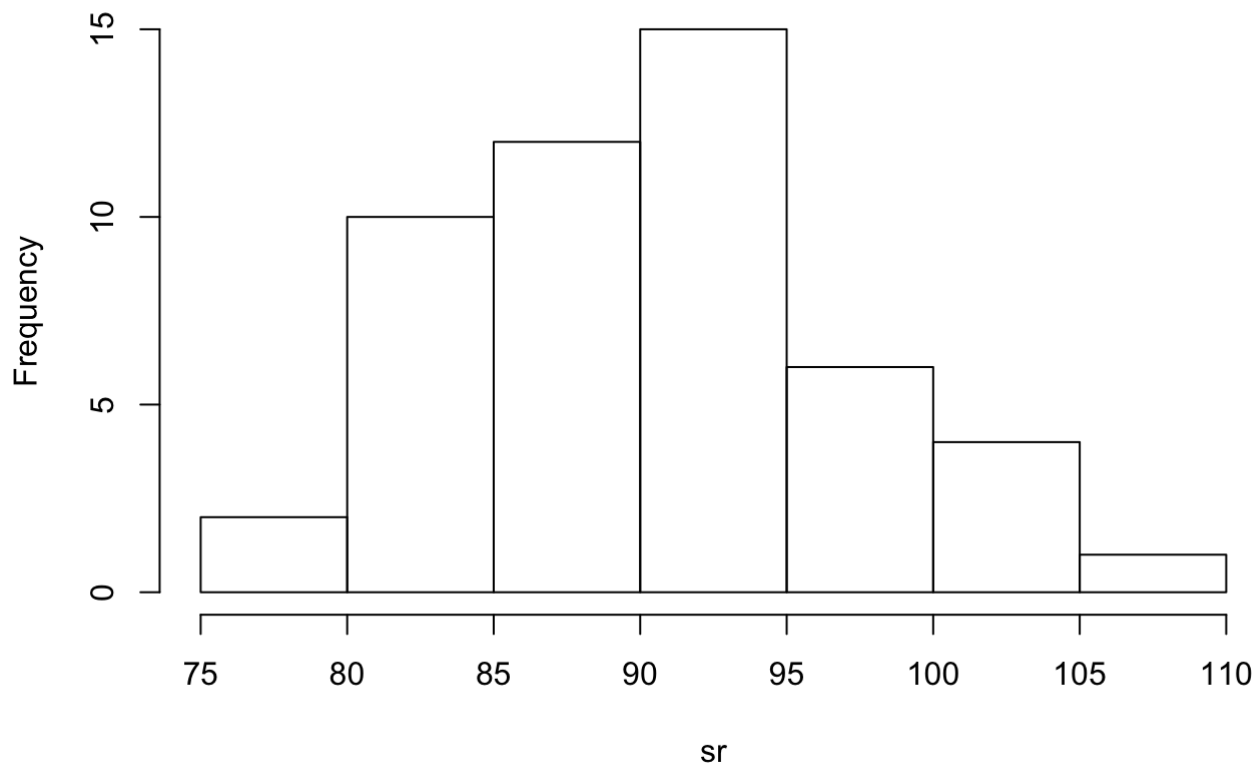
```
library(lattice)
data(BCI)
?BCI
## UTM Coordinates (in metres)
BCI_xy = data.frame(x = rep(seq(625754, 626654, by=100), each=5),
                    y = rep(seq(1011569, 1011969, by=100), len=50))
plot(BCI_xy)
```



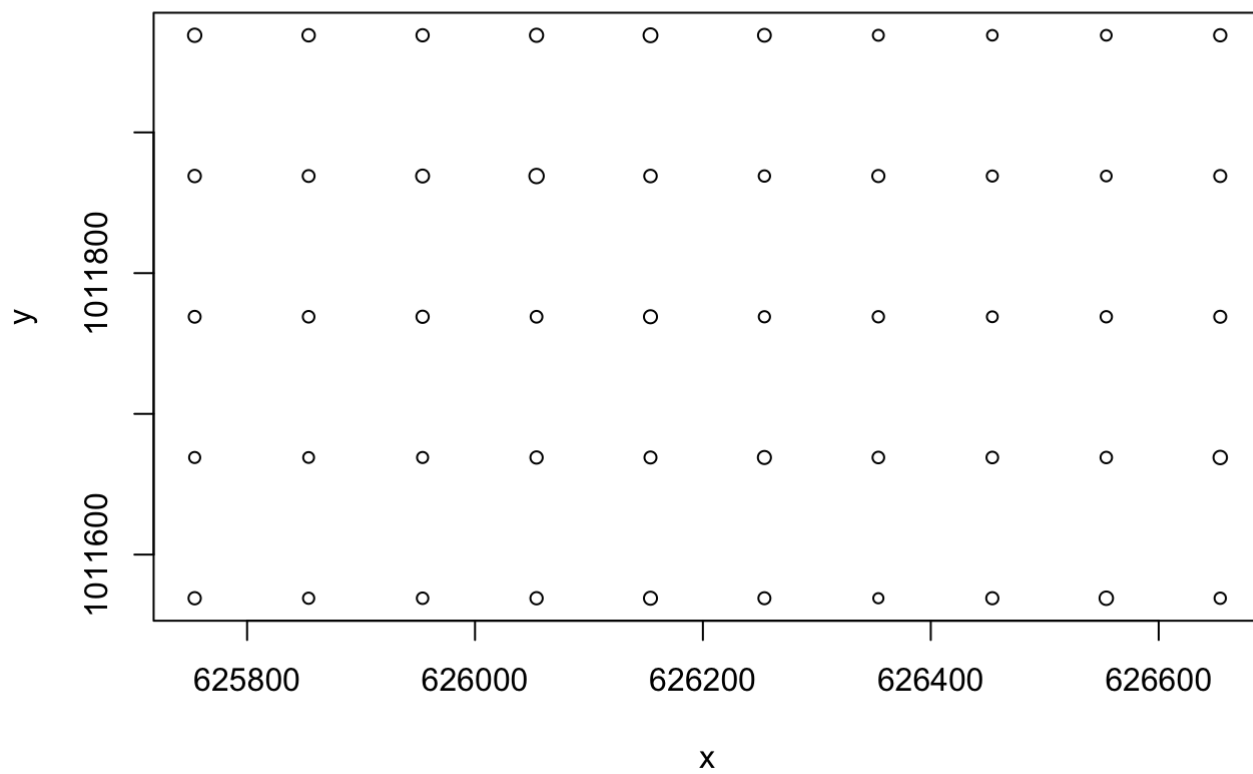
Overall Data (just wanted to see)

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

**Histogram of sr**

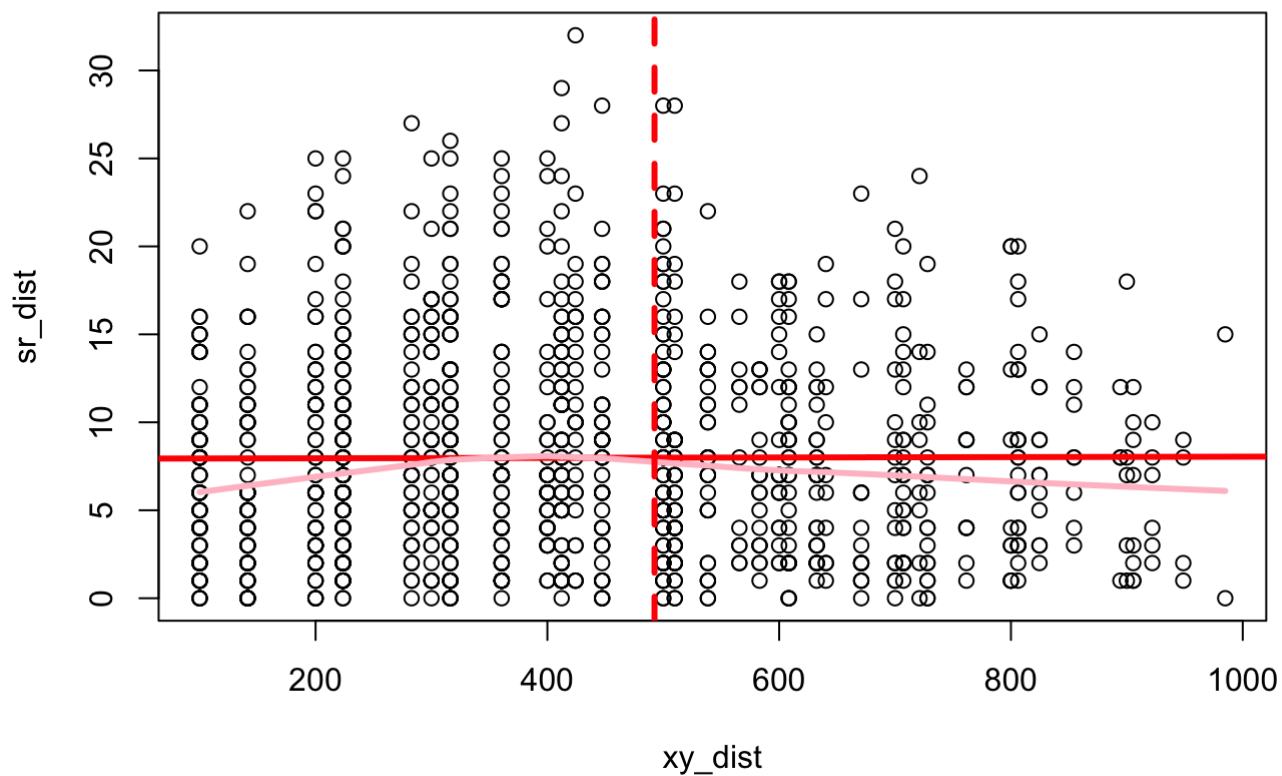


```
plot(BCI_xy, cex = sr/max(sr))
```



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





```
# compute correlation
obs_cor = cor(xy_dist, sr_dist)
obs_cor
```

```
## [1] 0.004339913
```

```
# carry out a permutation test for significance:
nperm = 1000
null_cor = obs_cor
for (i in 2:nperm) {
  # shuffle the rows of the spatial coordinates
  tmp_xy = BCI_xy[sample(nrow(BCI_xy)), ]
  # correlation between the shuffled spatial coordinates and sr_dist
  null_cor[i] = cor(dist(tmp_xy), sr_dist)
}
# compute the p-value
sum(null_cor >= obs_cor) / nperm
```

```
## [1] 0.48
```

```
# carry out the same analysis
sr_mantel = mantel(xy_dist, sr_dist)
sr_mantel
```

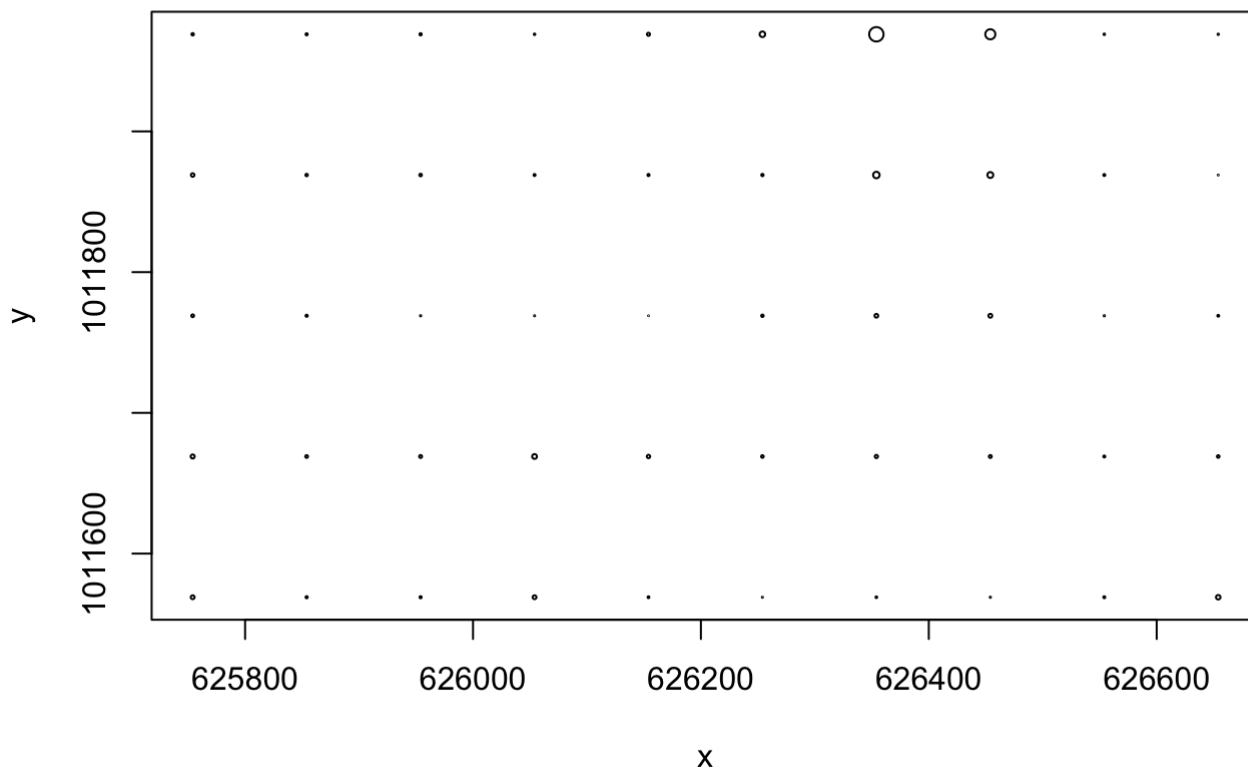
```
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = xy_dist, ydis = sr_dist)
##
## Mantel statistic r: 0.00434
##      Significance: 0.434
##
## Upper quantiles of permutations (null model):
##      90%      95%    97.5%     99%
## 0.0678 0.0883 0.1087 0.1290
## Permutation: free
## Number of permutations: 999
```

## 1. Common

```
alseis = BCI[, "Alseis.blackiana"]
alseis
```

```
## [1] 25 26 18 23 16 14 18 14 16 14 14 19  8 17 15 25 31  7 13 10 12 22  5 14 20
## [26]  7 17 16 15 36 11 21 24 42 93  8 19 25 38 65 13 13  8 13 10 29 17 12  6  9
```

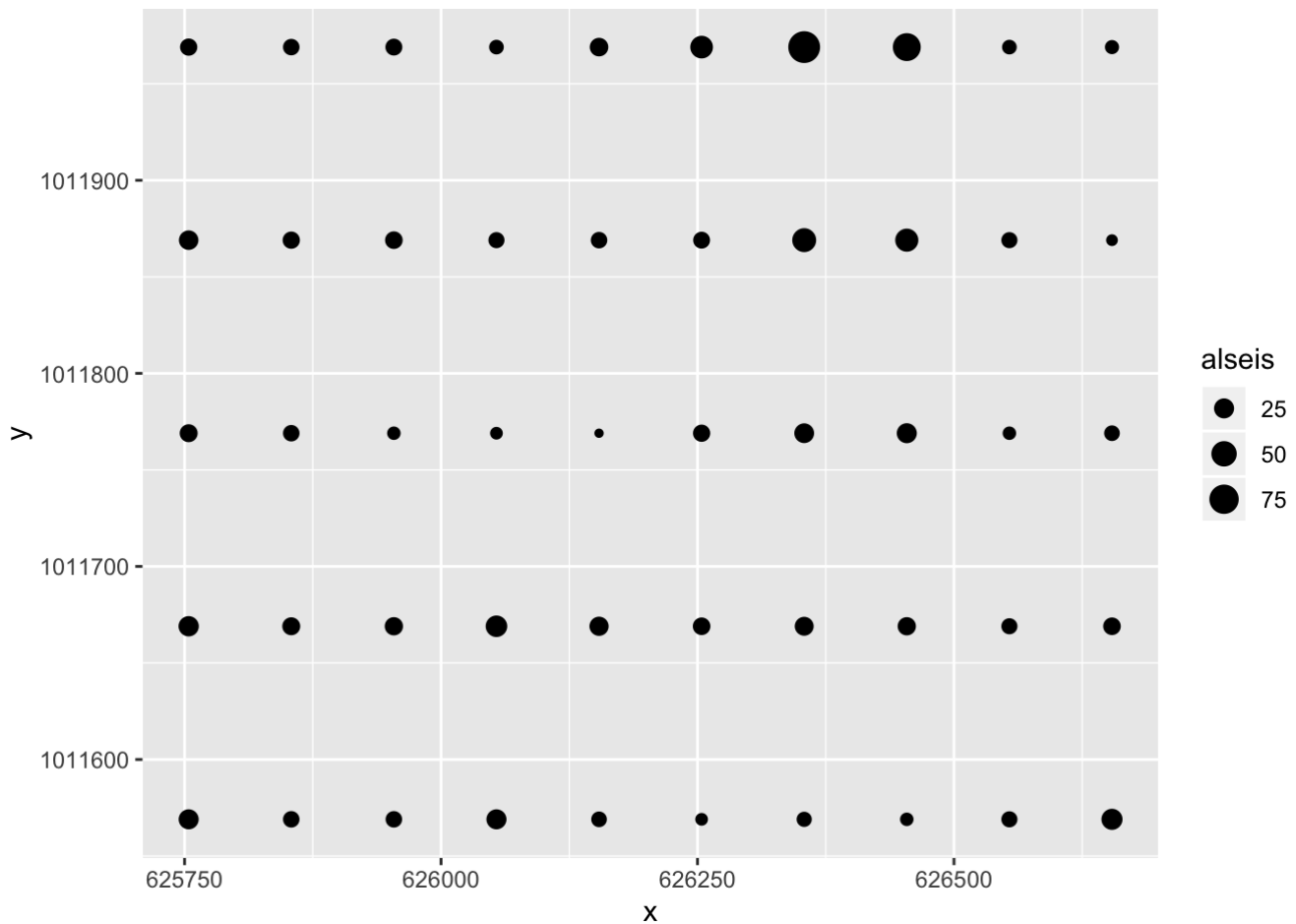
```
plot(BCI_xy, cex = alseis/max(alseis))
```



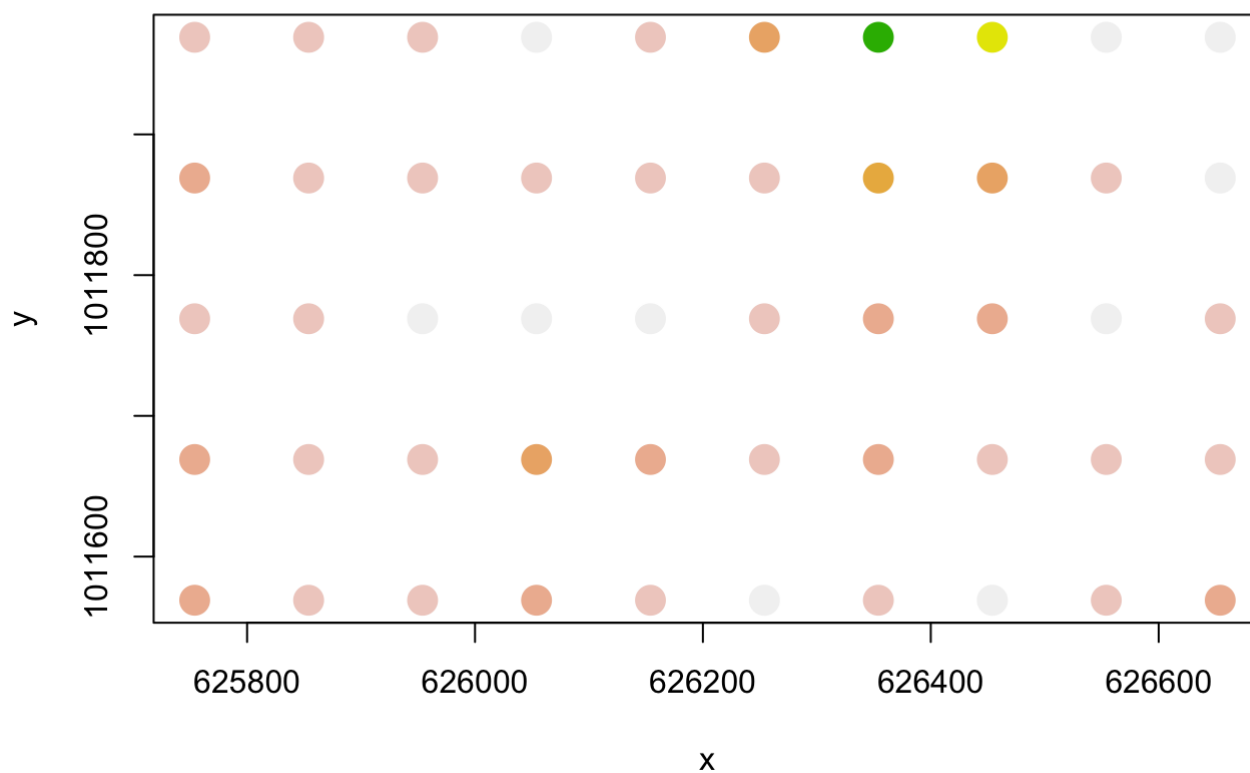
```
##ggplot solution
```

```
library(ggplot2)
```

```
ggplot(BCI_xy, aes(x=x, y=y, size=alseis)) + geom_point() + scale_size_continuous(range  
= c(1,5))
```



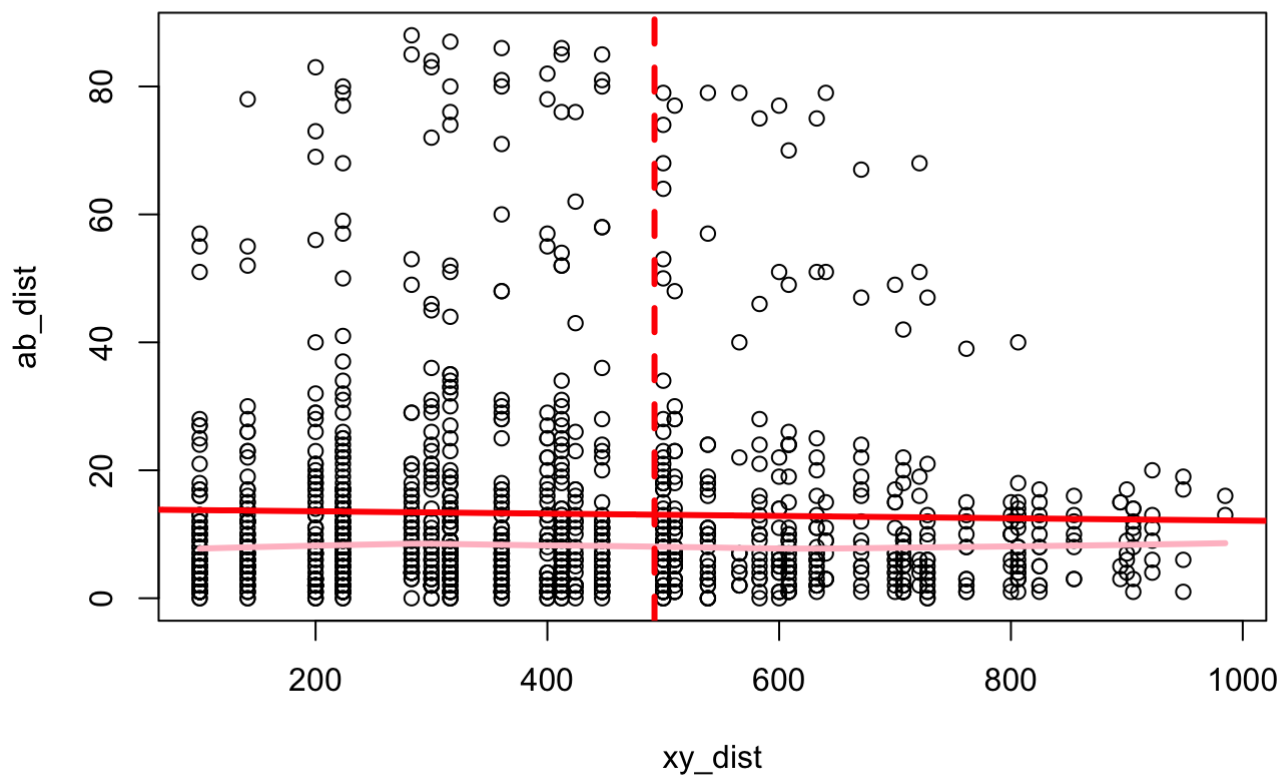
```
col_brks = hist(alseis, plot=F)$breaks  
col_indices = as.numeric(cut(alseis, col_brks))  
cols = rev(terrain.colors(length(col_brks)))  
plot(BCI_xy, cex=2, pch=19, col=cols[col_indices])
```



```
# calculate Euclidean distance between abundance and spatial coordinates
ab_dist = dist(alseis)
xy_dist = dist(BCI_xy)
max_dist = max(xy_dist) / 2
```

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





```
# compute correlation
obs_cor = cor(xy_dist, ab_dist)
obs_cor
```

```
## [1] -0.02348007
```

```
# carry out a permutation test for significance:
nperm = 1000
null_cor = obs_cor
for (i in 2:nperm) {
  # shuffle the rows of the spatial coordinates
  tmp_xy = BCI_xy[sample(nrow(BCI_xy)), ]
  # correlation between the shuffled spatial coordinates and ab_dist
  null_cor[i] = cor(dist(tmp_xy), ab_dist)
}
# compute the p-value
sum(null_cor >= obs_cor) / nperm
```

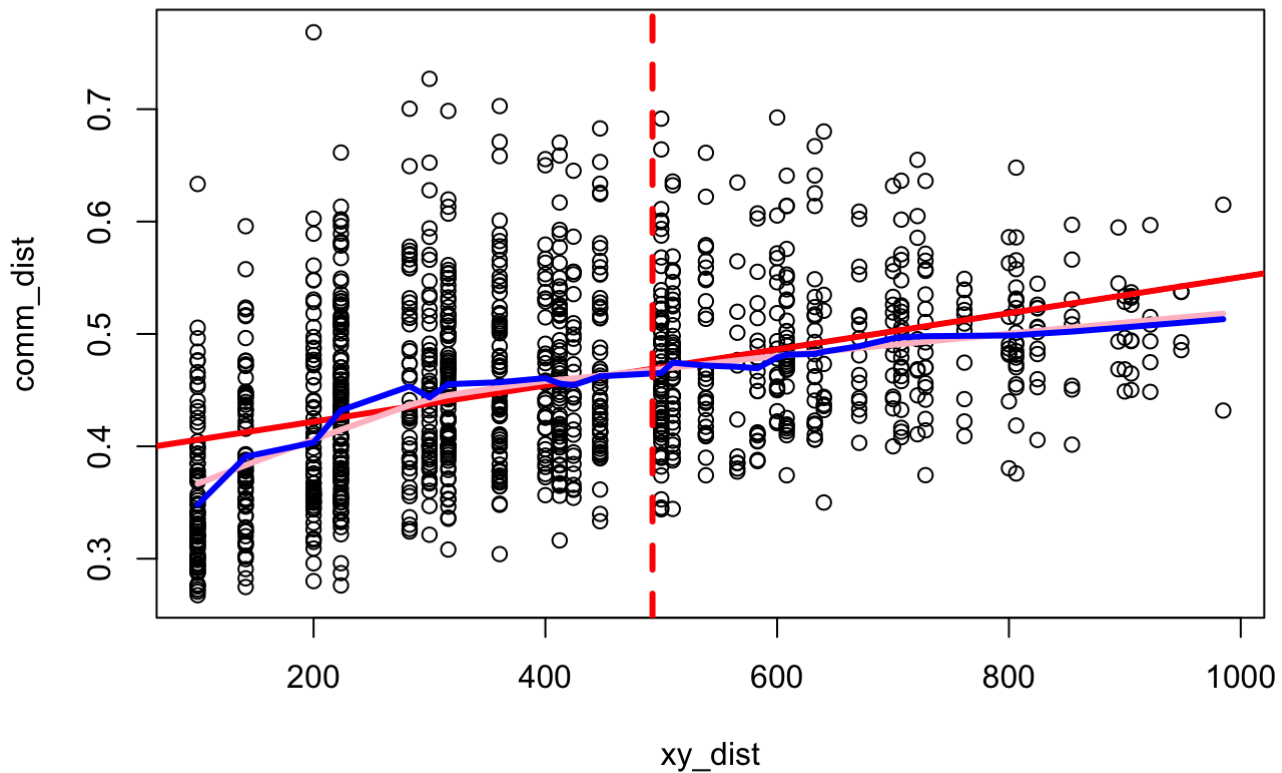
```
## [1] 0.593
```

```
ab_mantel = mantel(xy_dist, ab_dist)
ab_mantel
```

```
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = xy_dist, ydis = ab_dist)
##
## Mantel statistic r: -0.02348
##      Significance: 0.603
##
## Upper quantiles of permutations (null model):
##      90%      95%    97.5%     99%
## 0.0818 0.1057 0.1210 0.1390
## Permutation: free
## Number of permutations: 999
```

```
##examine community
## compute bray curtis distance for the community matrix
comm_dist = vegdist(BCI)
plot(xy_dist, comm_dist)
abline(lm(comm_dist ~ xy_dist), lwd=3, col='red')
lines(lowess(xy_dist, comm_dist), lwd=3, col='pink')
lines(lowess(xy_dist, comm_dist, f=0.1), lwd=3, col='blue')

abline(v = max_dist, col='red', lwd=3, lty=2)
```



```
comm_mantel = mantel(xy_dist, comm_dist)
comm_mantel
```

```
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = xy_dist, ydis = comm_dist)
##
## Mantel statistic r: 0.4078
##      Significance: 0.001
##
## Upper quantiles of permutations (null model):
##      90%      95%  97.5%   99%
## 0.0642 0.0878 0.1019 0.1130
## Permutation: free
## Number of permutations: 999
```

```
ab_corlog = mantel.correlog(ab_dist, xy_dist)
comm_corlog = mantel.correlog(comm_dist, xy_dist)
ab_corlog
```

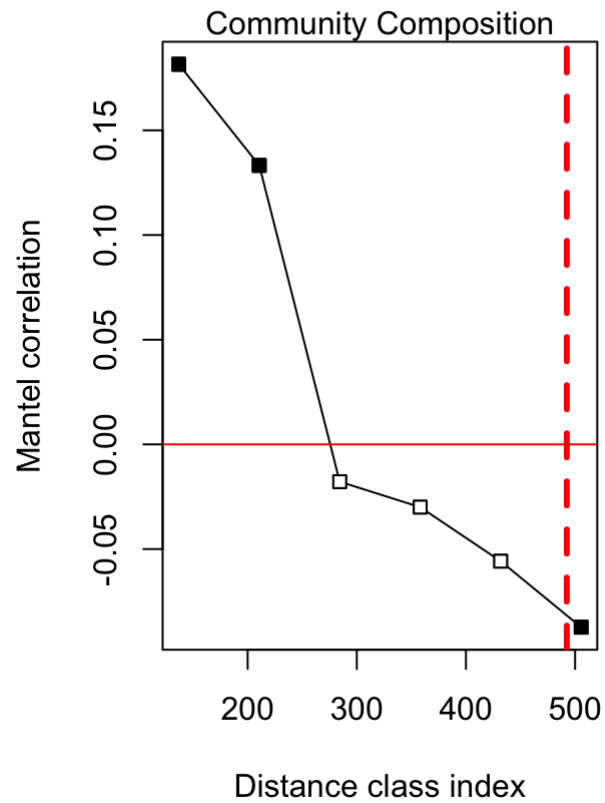
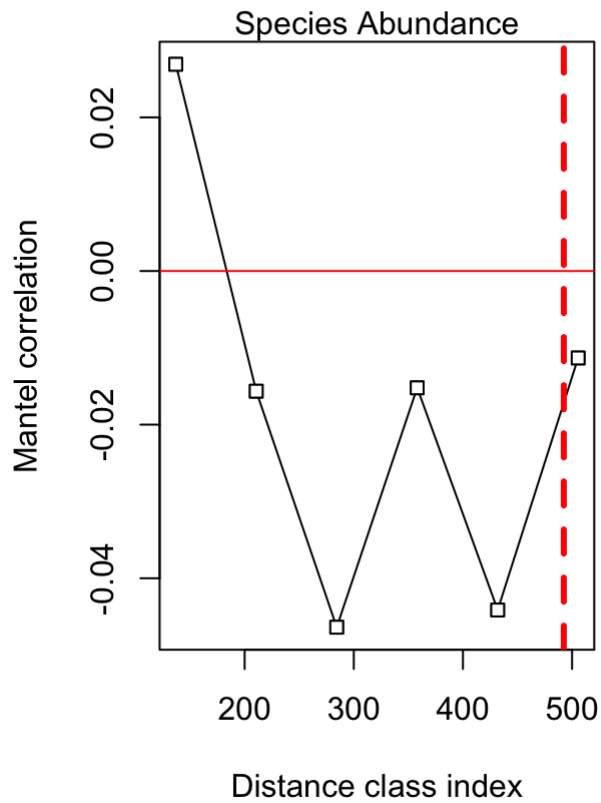
```
##
## Mantel Correlogram Analysis
##
## Call:
##
## mantel.correlog(D.eco = ab_dist, D.geo = xy_dist)
##
##      class.index      n.dist Mantel.cor Pr(Mantel) Pr(corrected)
## D.cl.1      136.870241 144.000000   0.026911     0.105     0.105
## D.cl.2      210.610723 376.000000  -0.015646     0.282     0.282
## D.cl.3      284.351204 390.000000  -0.046374     0.028     0.084 .
## D.cl.4      358.091686 148.000000  -0.015208     0.230     0.460
## D.cl.5      431.832168 372.000000  -0.044131     0.074     0.296
## D.cl.6      505.572649 266.000000  -0.011319     0.179     0.537
## D.cl.7      579.313131 168.000000         NA         NA         NA
## D.cl.8      653.053613 100.000000         NA         NA         NA
## D.cl.9      726.794094 154.000000         NA         NA         NA
## D.cl.10     800.534576  88.000000         NA         NA         NA
## D.cl.11     874.275058  50.000000         NA         NA         NA
## D.cl.12     948.015539  24.000000         NA         NA         NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
comm_corlog
```

```
##
## Mantel Correlogram Analysis
##
## Call:
## mantel.correlog(D.eco = comm_dist, D.geo = xy_dist)
##
##      class.index      n.dist Mantel.cor Pr(Mantel) Pr(corrected)
## D.cl.1      136.870241 144.000000   0.181547     0.001     0.001 ***
## D.cl.2      210.610723 376.000000   0.133245     0.001     0.002 **
## D.cl.3      284.351204 390.000000  -0.017807     0.253     0.253
## D.cl.4      358.091686 148.000000  -0.029965     0.091     0.182
## D.cl.5      431.832168 372.000000  -0.055778     0.039     0.117
## D.cl.6      505.572649 266.000000  -0.087321     0.001     0.006 **
## D.cl.7      579.313131 168.000000         NA         NA         NA
## D.cl.8      653.053613 100.000000         NA         NA         NA
## D.cl.9      726.794094 154.000000         NA         NA         NA
## D.cl.10     800.534576  88.000000         NA         NA         NA
## D.cl.11     874.275058  50.000000         NA         NA         NA
## D.cl.12     948.015539  24.000000         NA         NA         NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

*##no significance in the abundance of Alseis but there is significant in the community structure (non linear)*

```
par(mfrow=c(1,2))
plot(ab_corlog)
mtext(side=3, 'Species Abundance')
abline(v = max_dist, col='red', lwd=3, lty=2)
plot(comm_corlog)
mtext(side=3, 'Community Composition')
abline(v = max_dist, col='red', lwd=3, lty=2)
```

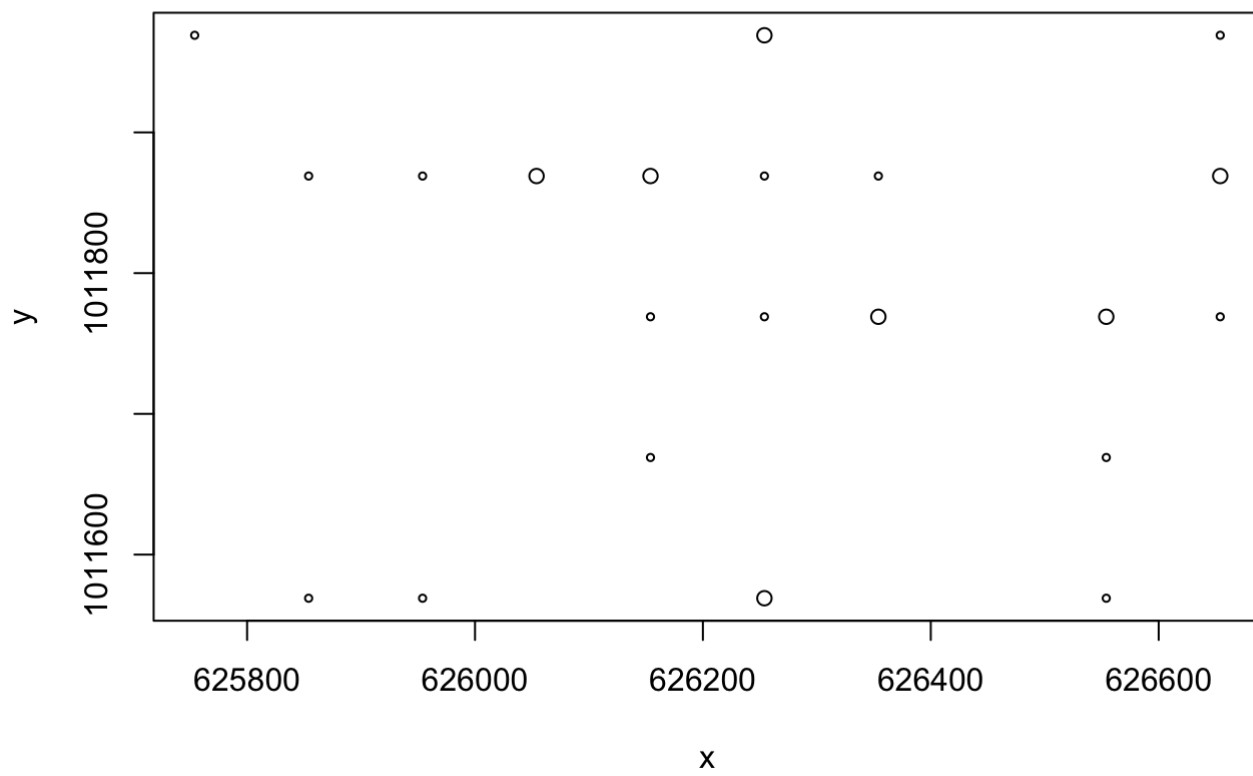


Rare

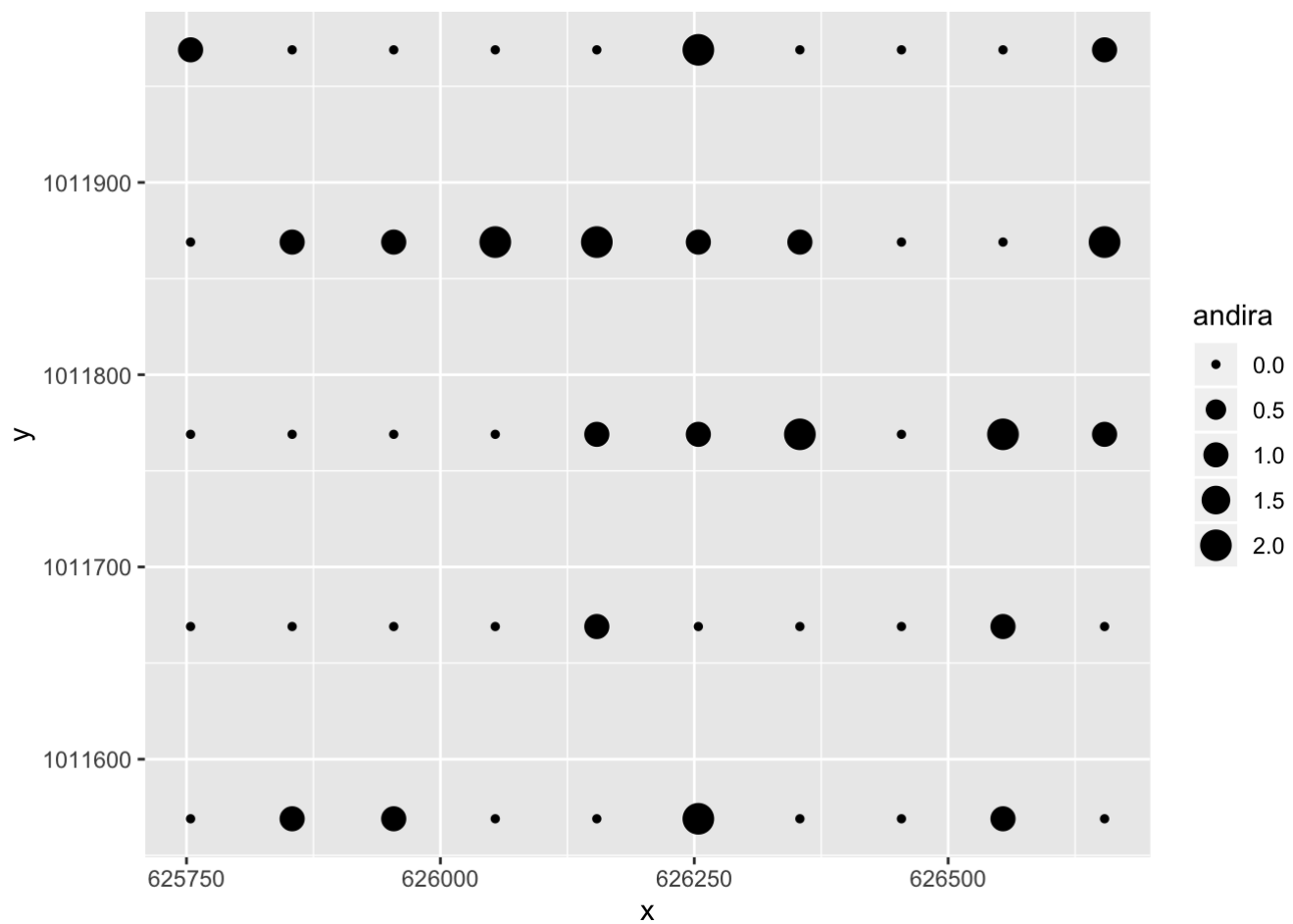
```
andira = BCI[,"Andira.inermis"]
andira
```

```
## [1] 0 0 0 0 1 1 0 0 1 0 1 0 0 1 0 0 0 0 2 0 0 1 1 2 0 2 0 1 1 2 0 0 2 1 0 0 0 0
## [39] 0 0 1 1 2 0 0 0 0 1 2 1
```

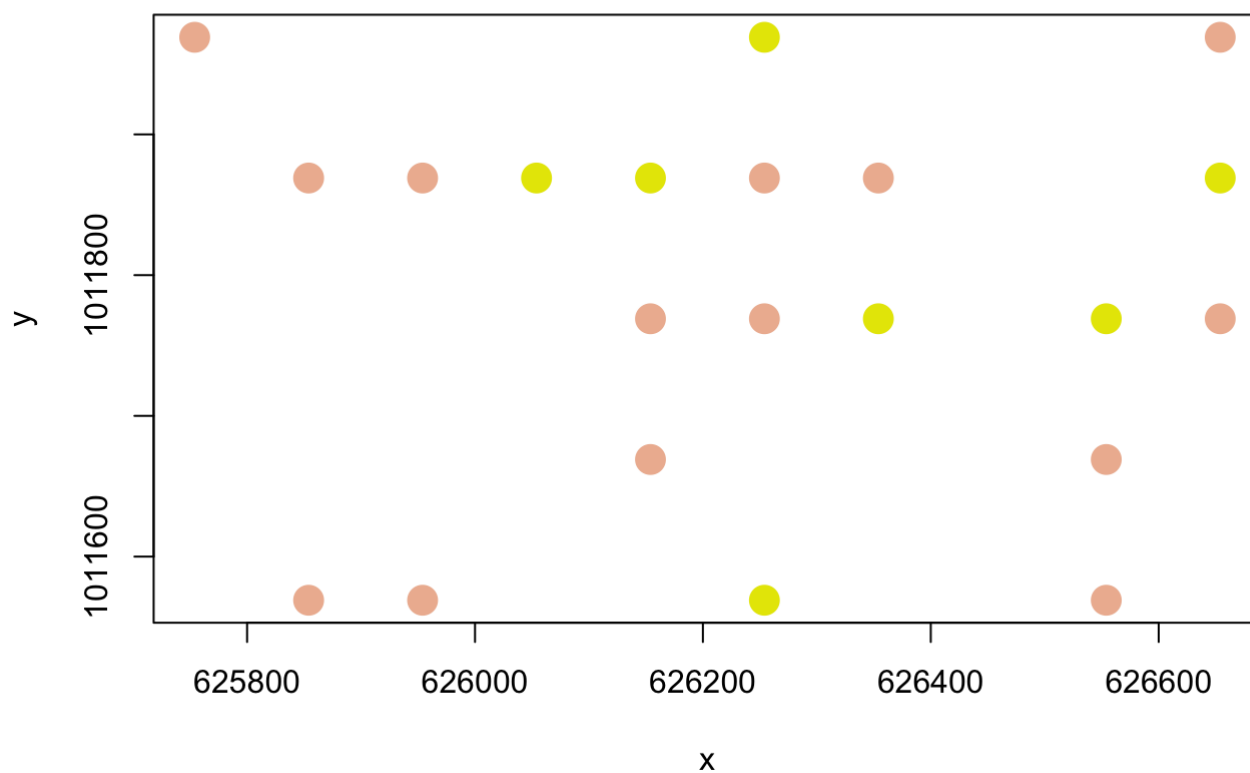
```
plot(BCI_xy, cex = andira/max(andira))
```



```
##ggplot
ggplot(BCI_xy, aes(x=x, y=y, size=andira)) + geom_point() + scale_size_continuous(range
= c(1,5))
```



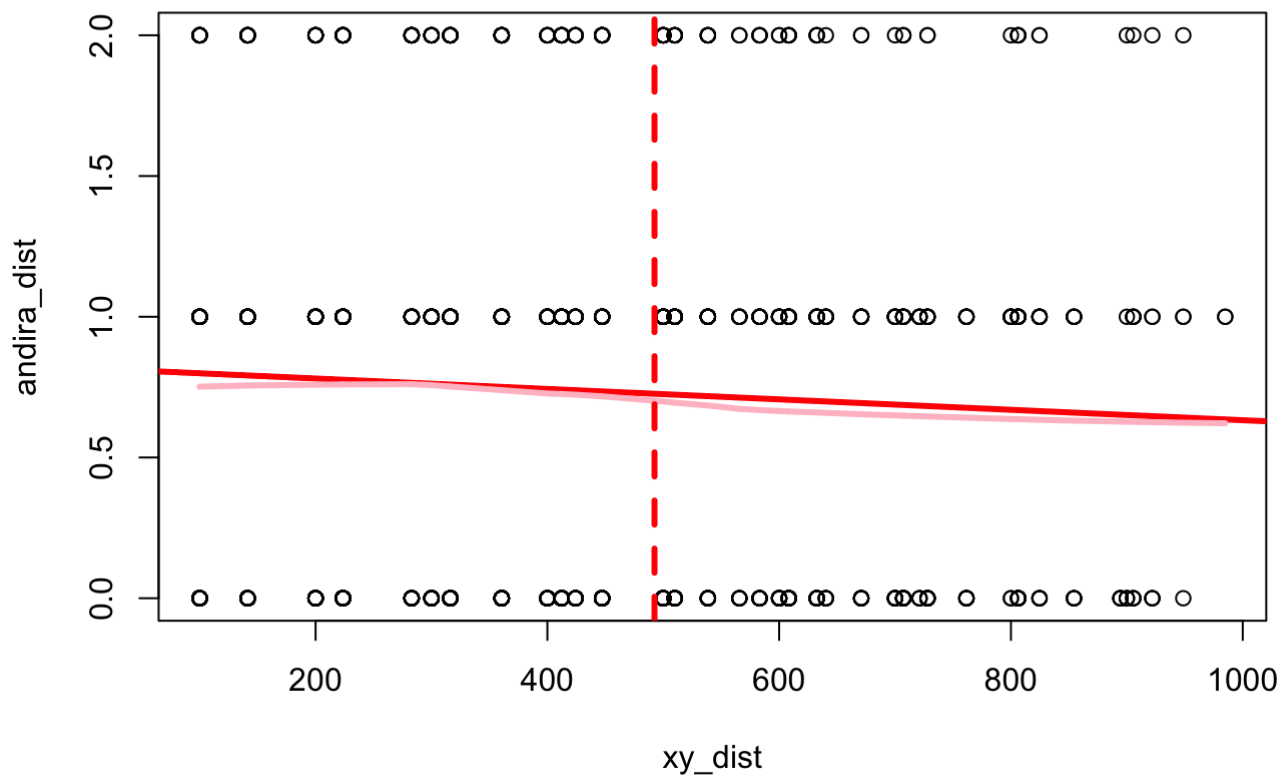
```
col_brks = hist(andira, plot=F)$breaks
col_indices = as.numeric(cut(andira, col_brks))
cols = rev(terrain.colors(length(col_brks)))
plot(BCI_xy, cex=2, pch=19, col=cols[col_indices])
```



```
andira_dist = dist(andira)
xy_dist = dist(BCI_xy)
max_dist = max(xy_dist) / 2
```

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





```
andira_mantel = mantel(xy_dist, andira_dist)
andira_mantel
```

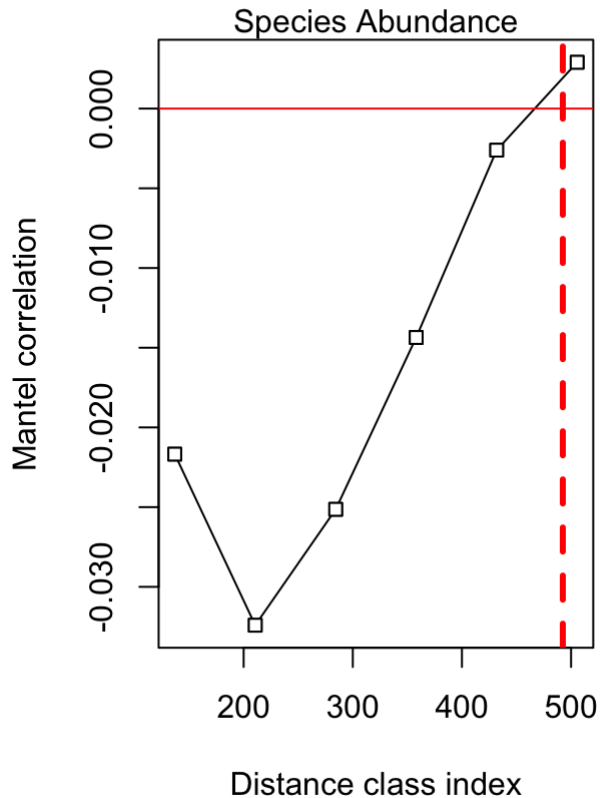
```
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = xy_dist, ydis = andira_dist)
##
## Mantel statistic r: -0.05389
##      Significance: 0.889
##
## Upper quantiles of permutations (null model):
##      90%      95%     97.5%     99%
## 0.0640 0.0845 0.0982 0.1199
## Permutation: free
## Number of permutations: 999
```

```
andira_corlog = mantel.correlog(andira_dist, xy_dist)
andira_corlog
```

```
##
## Mantel Correlogram Analysis
##
## Call:
## mantel.correlog(D.eco = andira_dist, D.geo = xy_dist)
##
```

	class.index	n.dist	Mantel.cor	Pr(Mantel)	Pr(corrected)
## D.cl.1	136.8702408	144.0000000	-0.0216764	0.233	0.233
## D.cl.2	210.6107225	376.0000000	-0.0324079	0.138	0.276
## D.cl.3	284.3512042	390.0000000	-0.0251373	0.201	0.414
## D.cl.4	358.0916859	148.0000000	-0.0143570	0.314	0.603
## D.cl.5	431.8321676	372.0000000	-0.0026076	0.486	0.804
## D.cl.6	505.5726492	266.0000000	0.0029042	0.499	1.000
## D.cl.7	579.3131309	168.0000000	NA	NA	NA
## D.cl.8	653.0536126	100.0000000	NA	NA	NA
## D.cl.9	726.7940943	154.0000000	NA	NA	NA
## D.cl.10	800.5345760	88.0000000	NA	NA	NA
## D.cl.11	874.2750577	50.0000000	NA	NA	NA
## D.cl.12	948.0155393	24.0000000	NA	NA	NA

```
par(mfrow=c(1,2))
plot(andira_corlog)
mtext(side=3, 'Species Abundance')
abline(v = max_dist, col='red', lwd=3, lty=2)
```



There

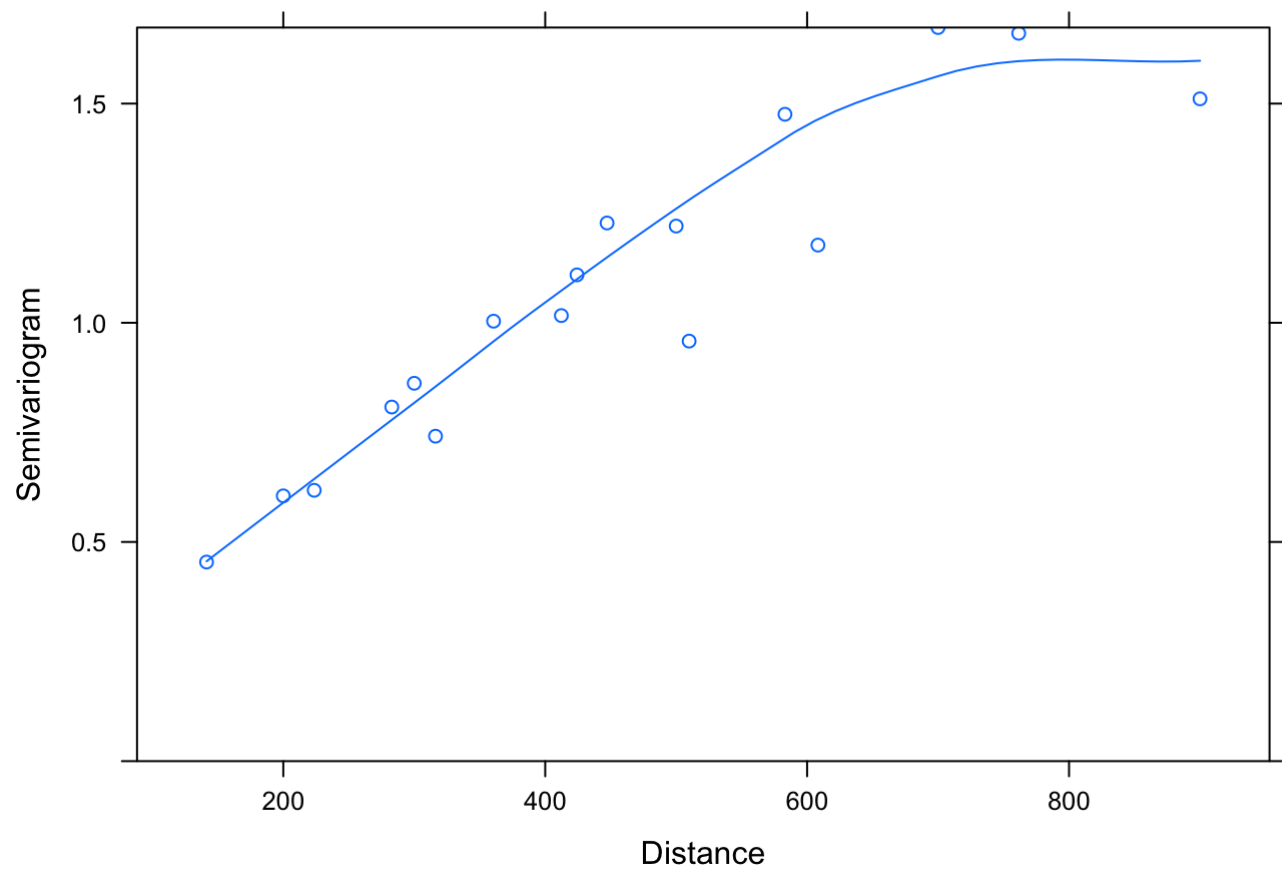
is no evidence of spatial dependence in both the common (Alseis) and rare (Andira) species.

2.one species

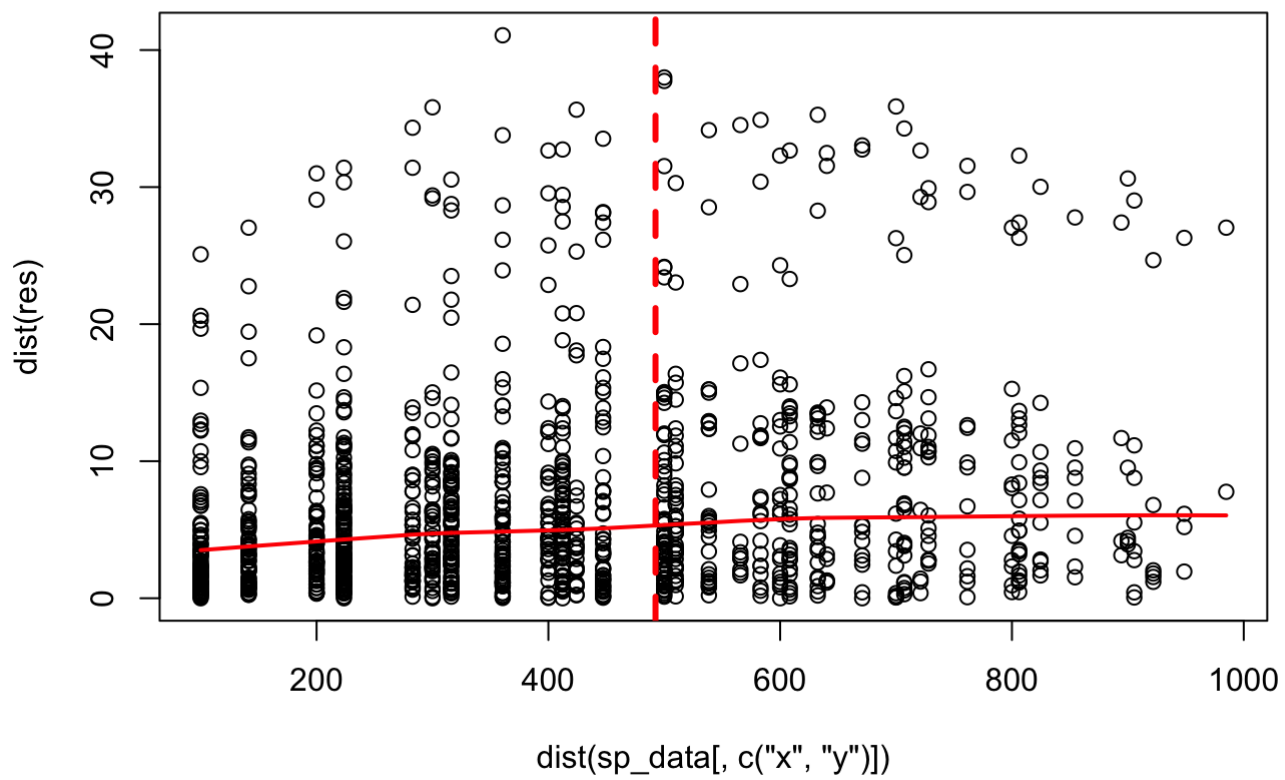
```
sp_ids = c("Cordia.lasiocalyx", "Hirtella.triandra",
           "Picramnia.latifolia", "Quassia.amara",
           "Tabernaemontana.arborea", "Trattinnickia.aspera",
           "Xylopia.macrantha")
BCI_ids = cbind("Drypetes.standleyi", "Cordia.lasiocalyx", "Hirtella.triandra",
               "Picramnia.latifolia",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

```
sp_a <- apply(BCI_ids, 1, function(x) sum(x > 0))
sp_data = data.frame(sp_a, BCI, BCI_xy)
BCI_sub = subset(sp_data, select = BCI_ids)
```

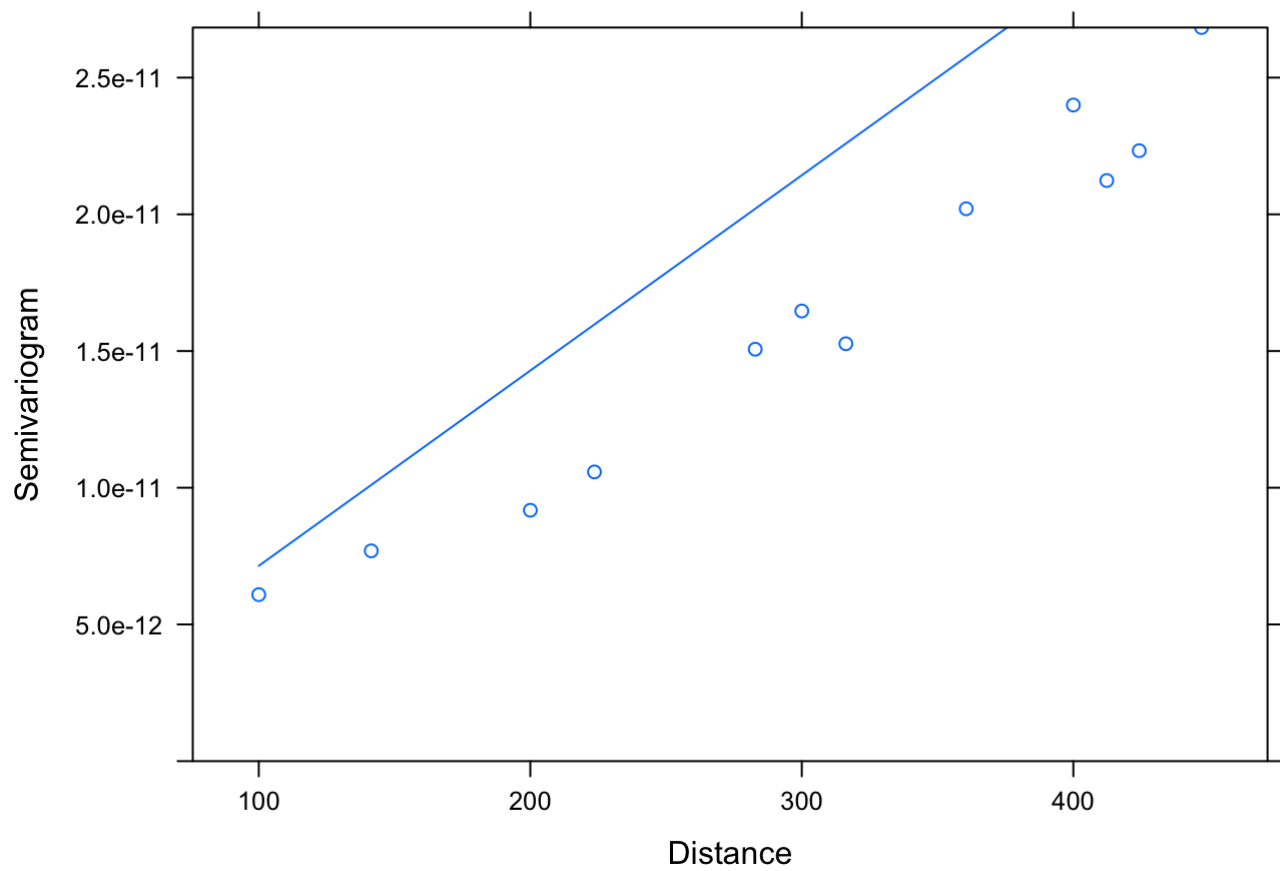
```
library(nlme)
sp_lm = gls(Drypetes.standleyi ~ Hirtella.triandra, data=BCI_sub)
var_sp = Variogram(sp_lm, form= ~ BCI_xy$x + BCI_xy$y)
plot(var_sp)
```



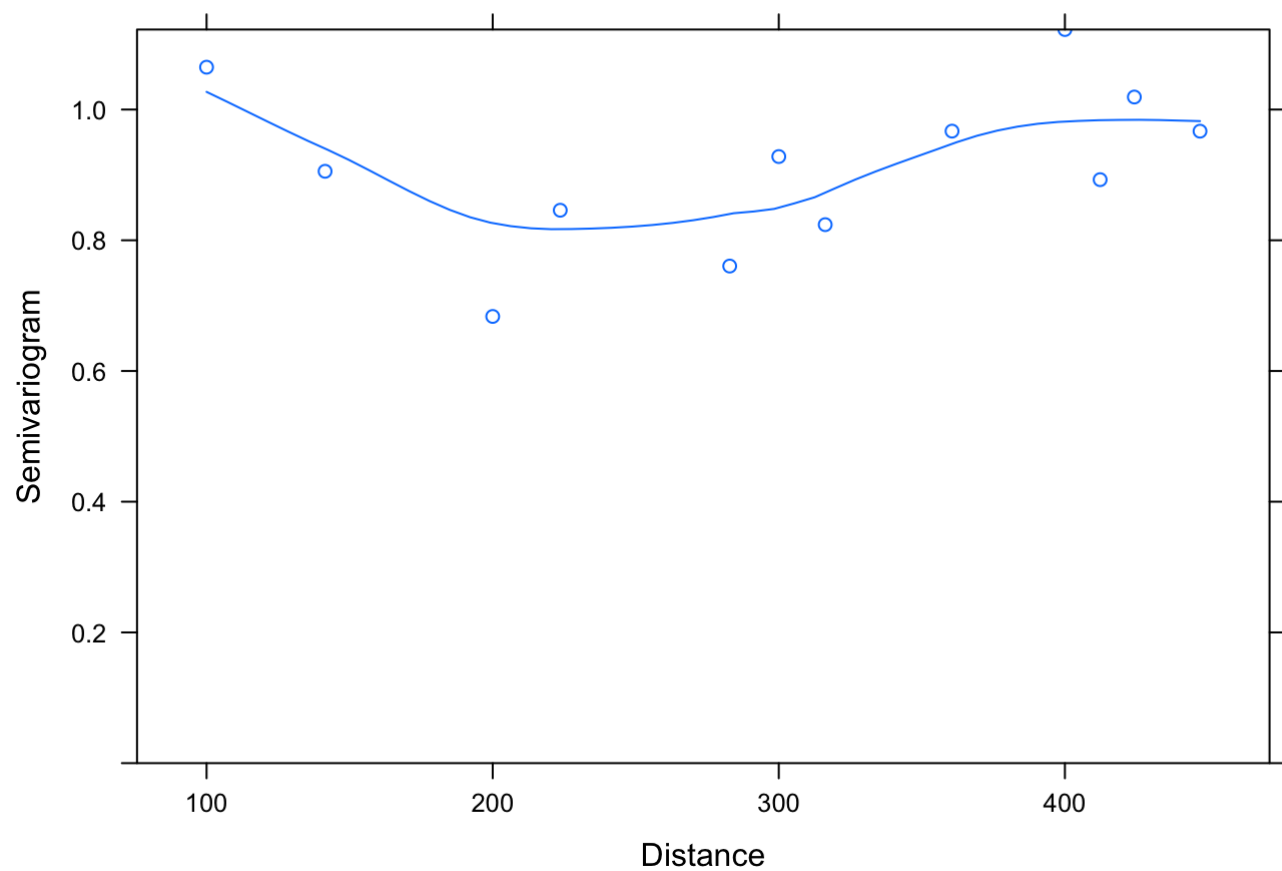
```
res = residuals(sp_lm)
plot(dist(sp_data[, c('x', 'y')]), dist(res))
lines(lowess(dist(sp_data[, c('x', 'y')]), dist(res)), col='red', lwd=2)
abline(v = max_dist, col='red', lwd=3, lty=2)
```



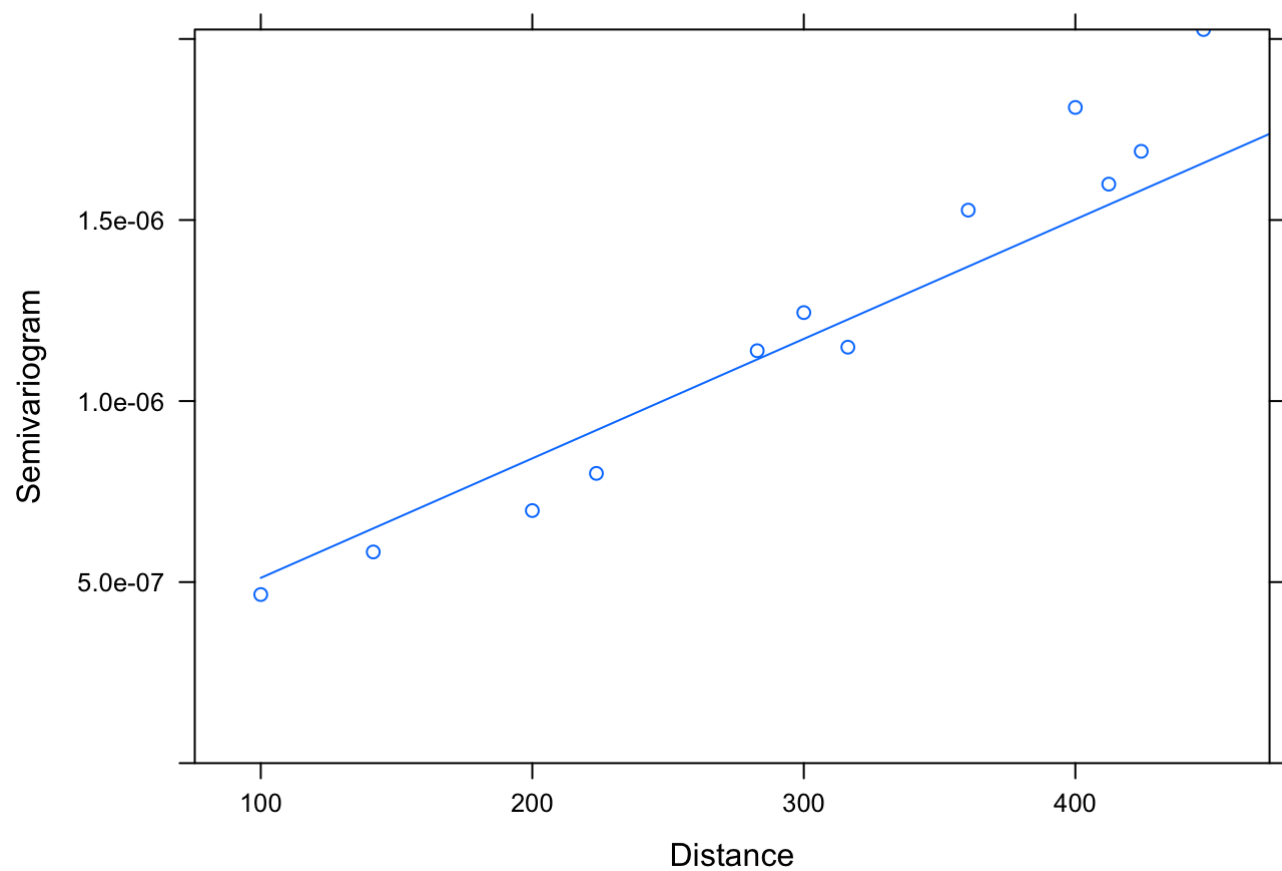
```
x = BCI_xy$x
y = BCI_xy$y
sp_exp = update(sp_lm, corr=corExp(form=~x + y))
plot(Variogram(sp_exp, maxDist = max_dist))
```



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

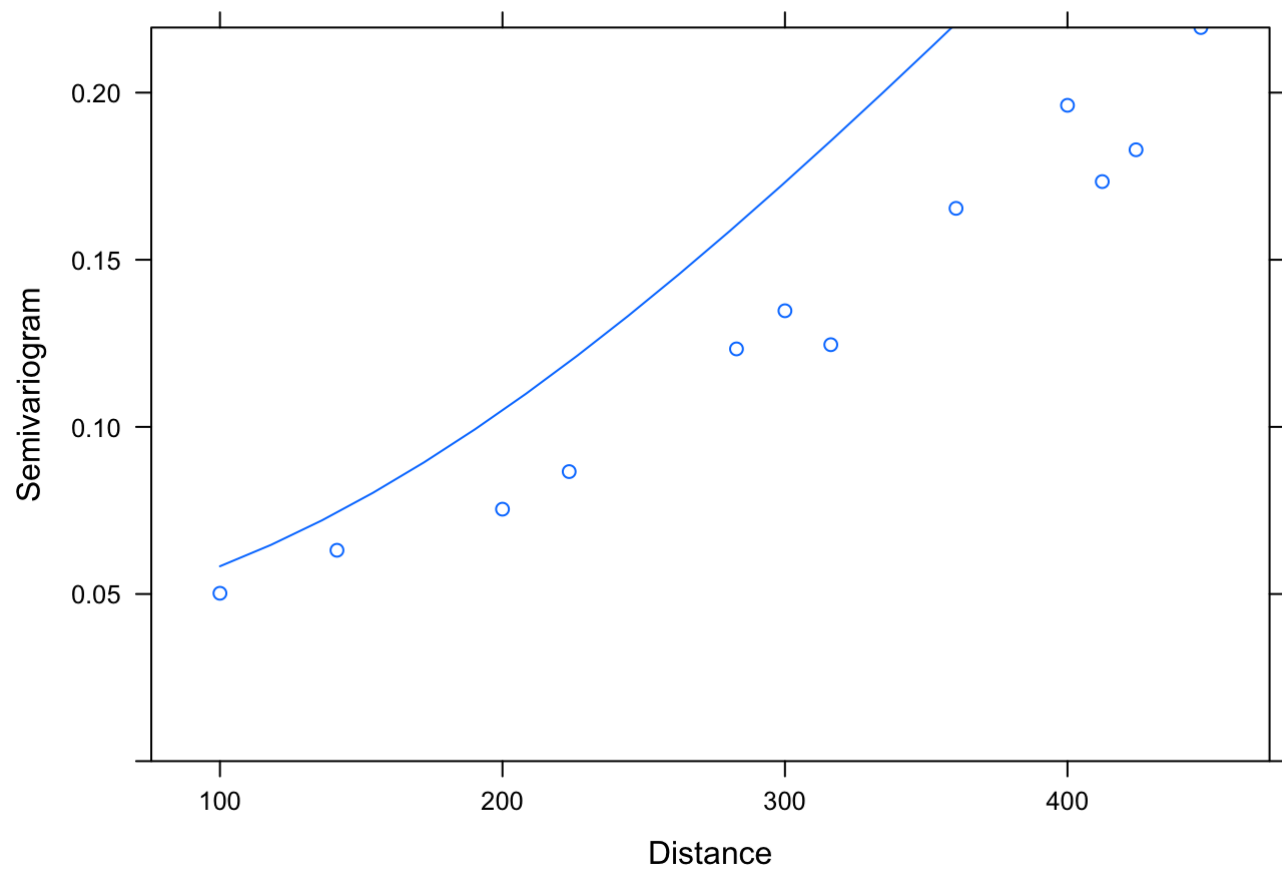


```
sp_exp_nug = update(sp_exp, corr=corExp(form = ~x +y , nugget=T))  
plot(Variogram(sp_exp_nug, maxDist = max_dist))
```

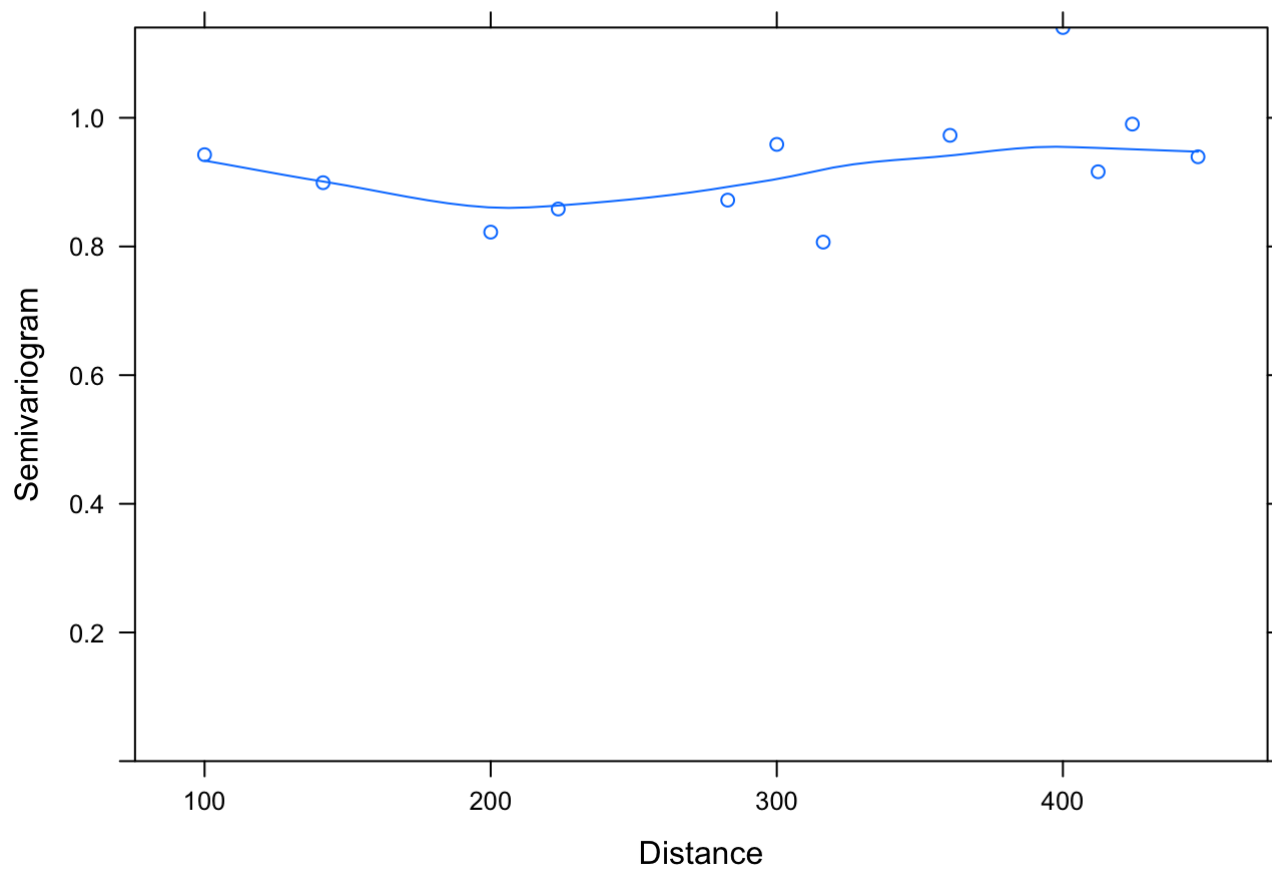


```
sp_rat_nug = update(sp_lm, corr=corRatio(form = ~x + y, nugget=T))  
plot(Variogram(sp_rat_nug, maxDist = max_dist))
```

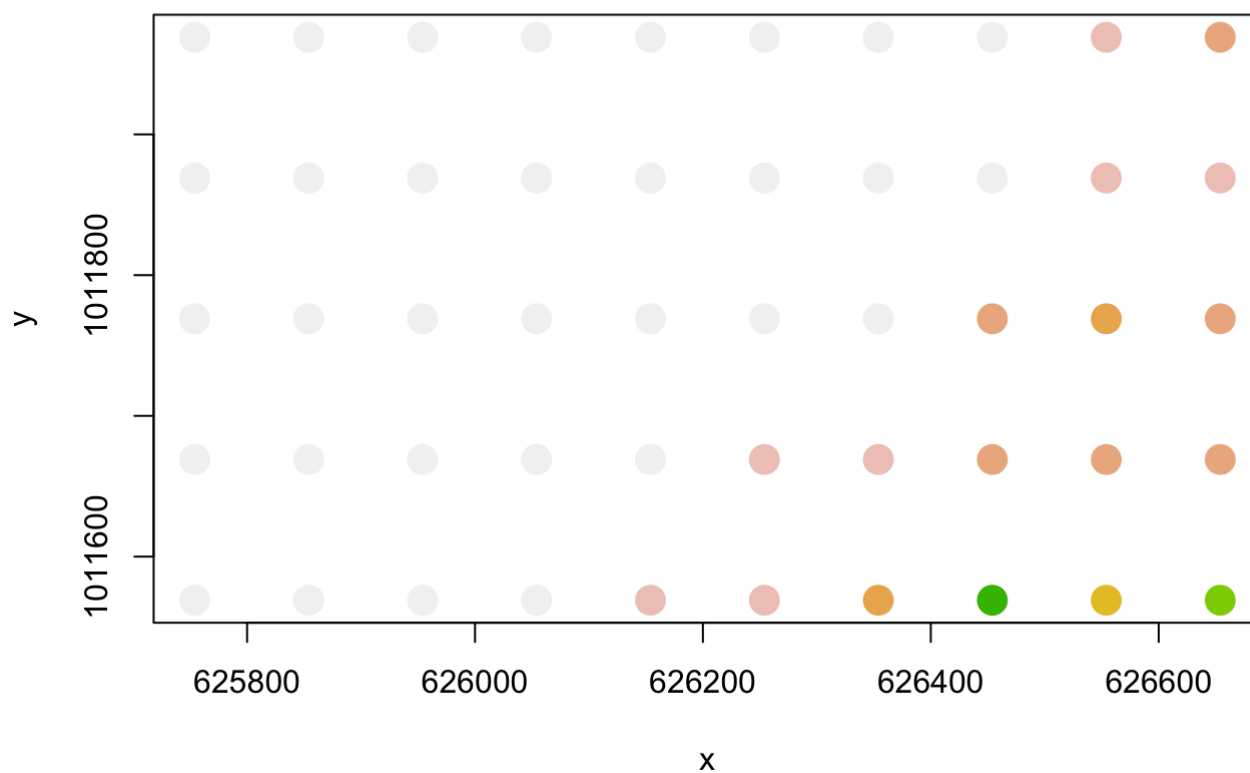




```
plot(Variogram(sp_rat_nug, resType='n', maxDist = max_dist))
```



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



```
anova(sp_lm, sp_exp, sp_exp_nug, sp_rat_nug, test=F)
```

##	Model	df	AIC	BIC	logLik
##	sp_lm	1 3	346.1696	351.7832	-170.0848
##	sp_exp	2 4	312.5365	320.0213	-152.2682
##	sp_exp_nug	3 5	313.2119	322.5679	-151.6059
##	sp_rat_nug	4 5	310.6244	319.9804	-150.3122

```
summary(sp_lm)
```

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Hirtella.triandra
##   Data: BCI_sub
##           AIC      BIC    logLik
##   346.1696 351.7832 -170.0848
##
## Coefficients:
##               Value Std.Error  t-value p-value
## (Intercept)    0.6267619 1.7550545 0.357118 0.7226
## Hirtella.triandra 0.3724844 0.1038112 3.588094 0.0008
##
## Correlation:
##               (Intr)
## Hirtella.triandra -0.806
##
## Standardized residuals:
##           Min      Q1      Med      Q3      Max
## -1.5837021 -0.5405355 -0.2411211 0.1461580 4.0034096
##
## Residual standard error: 7.352136
## Degrees of freedom: 50 total; 48 residual
```

```
summary(sp_exp)
```

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Hirtella.triandra
##   Data: BCI_sub
##           AIC      BIC    logLik
##   312.5365 320.0213 -152.2682
##
## Correlation Structure: Exponential spatial correlation
## Formula: ~x + y
## Parameter estimate(s):
##           range
## 1.399944e+13
##
## Coefficients:
##               Value Std.Error  t-value p-value
## (Intercept)    14.473746 1746021.3 0.000008290 1.000
## Hirtella.triandra -0.000646      0.1 -0.006275689 0.995
##
## Correlation:
##               (Intr)
## Hirtella.triandra 0
##
## Standardized residuals:
##           Min      Q1      Med      Q3      Max
## -8.288079e-06 -8.284289e-06 -7.138550e-06 -3.843500e-06 1.405581e-05
##
## Residual standard error: 1746021
## Degrees of freedom: 50 total; 48 residual
```

```
summary(sp_exp_nug)
```

```
## Generalized least squares fit by REML
## Model: Drypetes.standleyi ~ Hirtella.triandra
## Data: BCI_sub
##      AIC      BIC    logLik
## 313.2119 322.5679 -151.6059
##
## Correlation Structure: Exponential spatial correlation
## Formula: ~x + y
## Parameter estimate(s):
##      range      nugget
## 3.029648e+08 1.815151e-07
##
## Coefficients:
##              Value Std.Error   t-value p-value
## (Intercept)  12.254798  6300.289  0.00194512  0.9985
## Hirtella.triandra  0.017615    0.099  0.17747775  0.8599
##
## Correlation:
##              (Intr)
## Hirtella.triandra 0
##
## Standardized residuals:
##      Min      Q1      Med      Q3      Max
## -0.0019870533 -0.0019562986 -0.0016402511 -0.0007709315  0.0041779703
##
## Residual standard error: 6300.295
## Degrees of freedom: 50 total; 48 residual
```

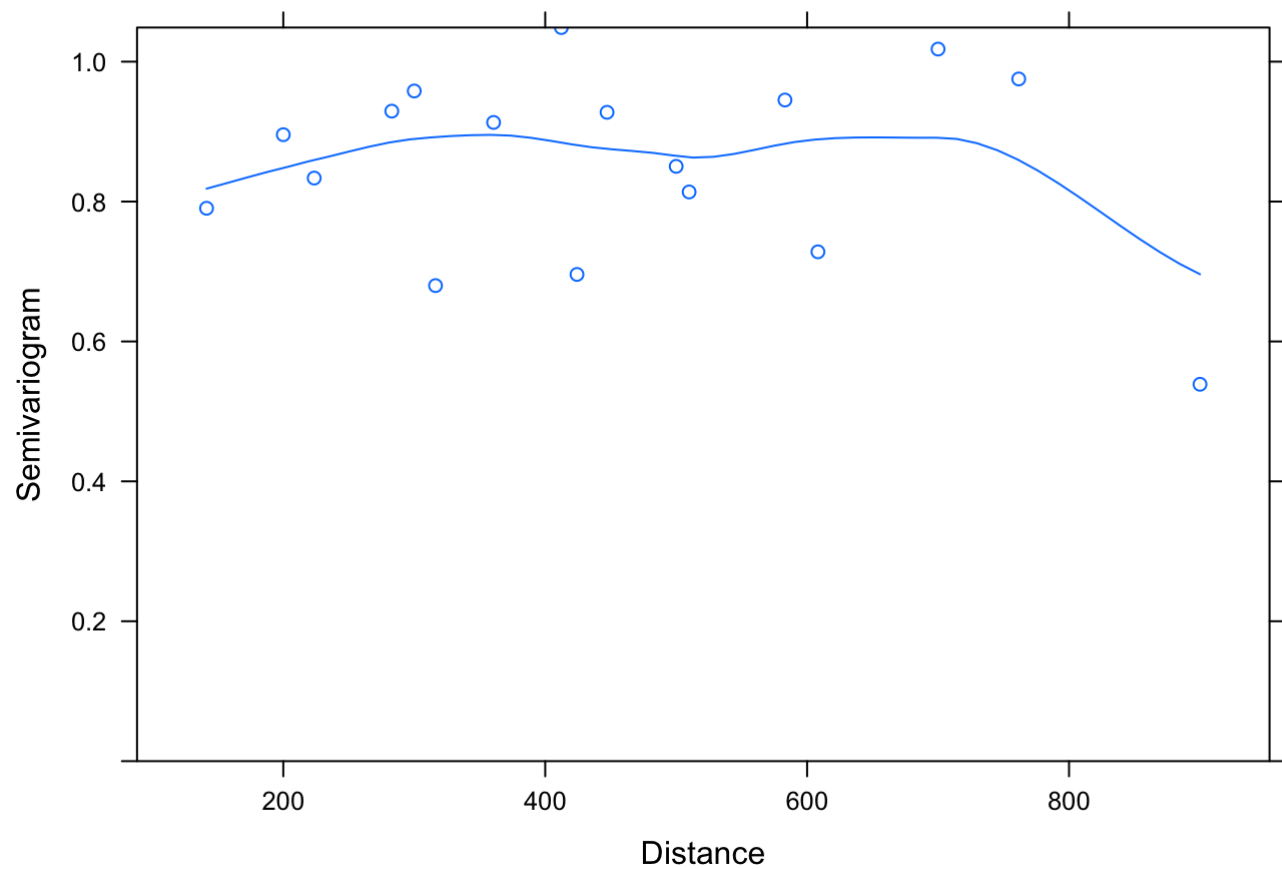
```
summary(sp_rat_nug)
```

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Hirtella.triandra
##   Data: BCI_sub
##           AIC       BIC      logLik
##   310.6244 319.9804 -150.3122
##
## Correlation Structure: Rational quadratic spatial correlation
## Formula: ~x + y
## Parameter estimate(s):
##           range      nugget
## 752.28335795    0.04166127
##
## Coefficients:
##                               Value Std.Error   t-value p-value
## (Intercept)          14.088134 14.874137  0.9471564  0.3483
## Hirtella.triandra   0.011441  0.087993  0.1300210  0.8971
##
## Correlation:
##              (Intr)
## Hirtella.triandra -0.167
##
## Standardized residuals:
##           Min      Q1      Med      Q3      Max
## -0.7428201 -0.7362643 -0.6323781 -0.3420863  1.2834076
##
## Residual standard error: 19.19677
## Degrees of freedom: 50 total; 48 residual
```

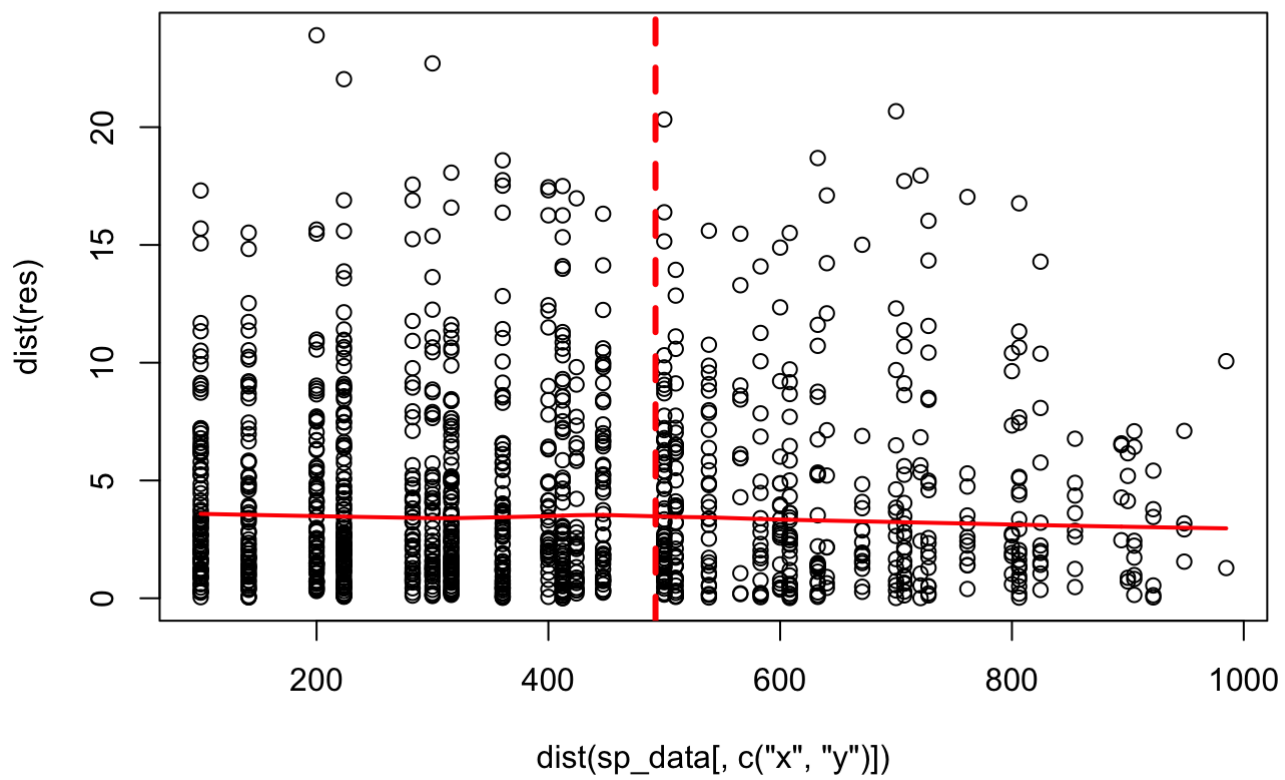
Rational model with the nugget fit better than without spatial error terms

all species

```
sp_all_lm = gls(Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra + Picramnia.l
atifolia + Quassia.amara + Tabernaemontana.arborea + Trattinnickia.aspera + Xylopia.macra
antha , data=sp_data)
plot(Variogram(sp_all_lm, form= ~ BCI_xy$x + BCI_xy$y))
```

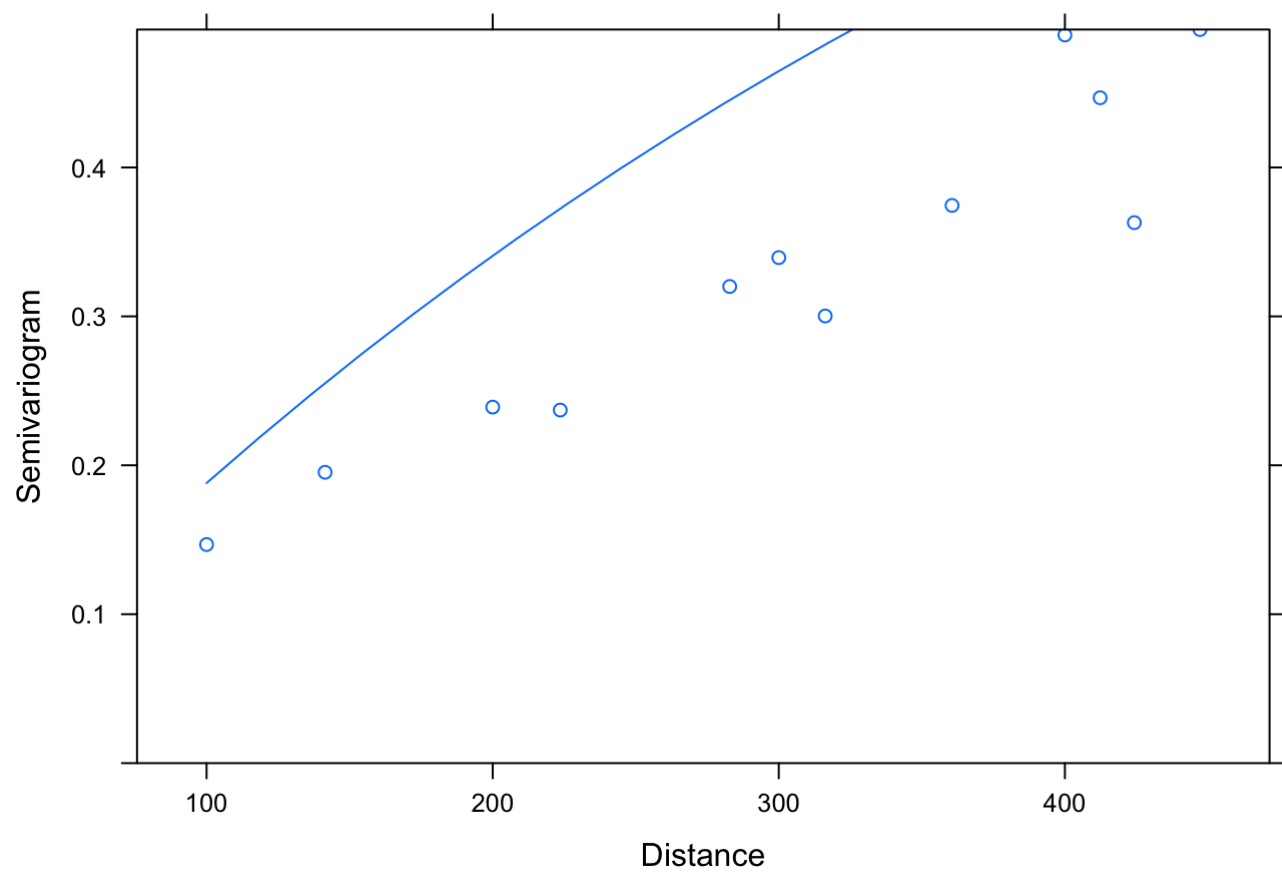


```
res = residuals(sp_all_lm)
plot(dist(sp_data[, c('x', 'y')]), dist(res))
lines(lowess(dist(sp_data[, c('x', 'y')]), dist(res)), col='red', lwd=2)
abline(v = max_dist, col='red', lwd=3, lty=2)
```

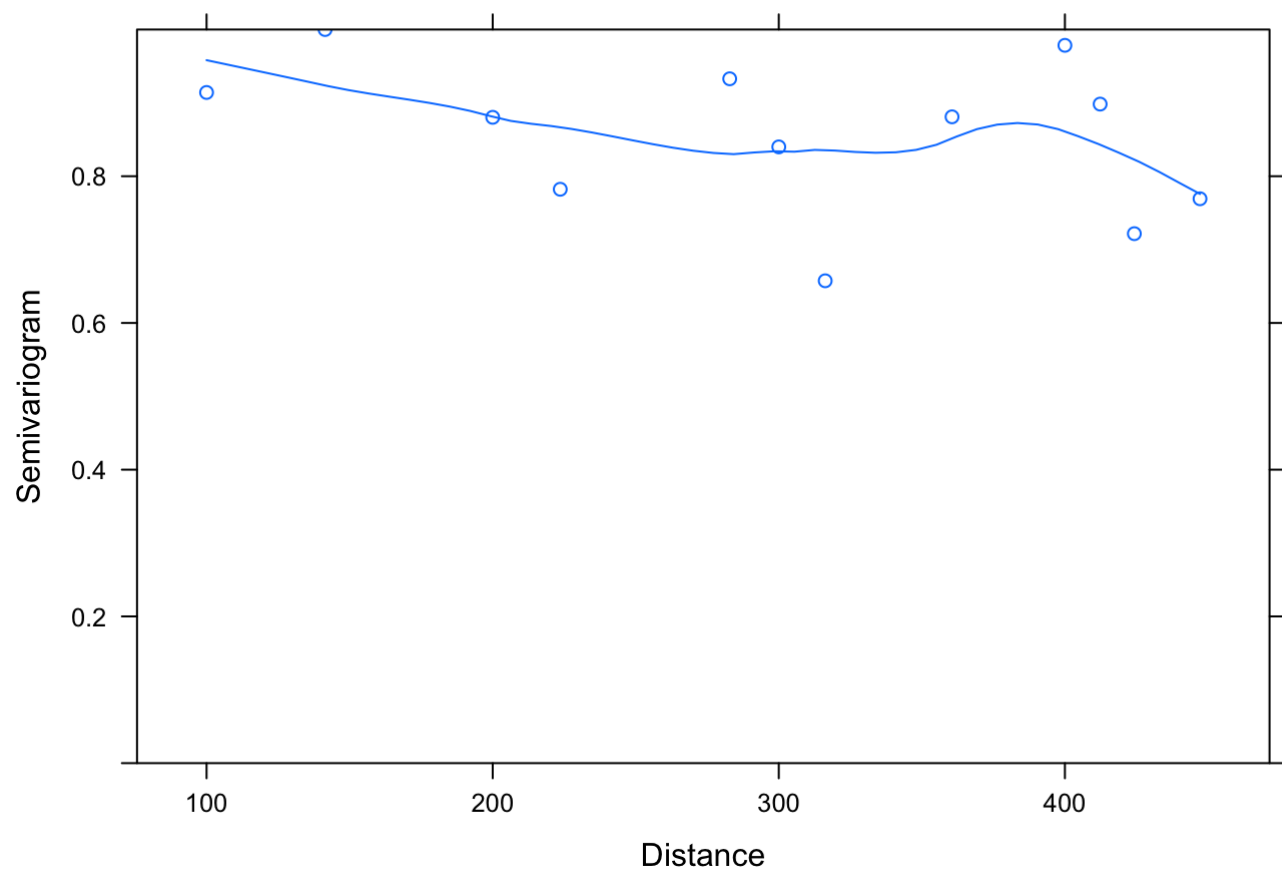


```
sp_all_exp = update(sp_all_lm, corr=corExp(form=~x + y))
plot(Variogram(sp_all_exp, maxDist = max_dist))
```

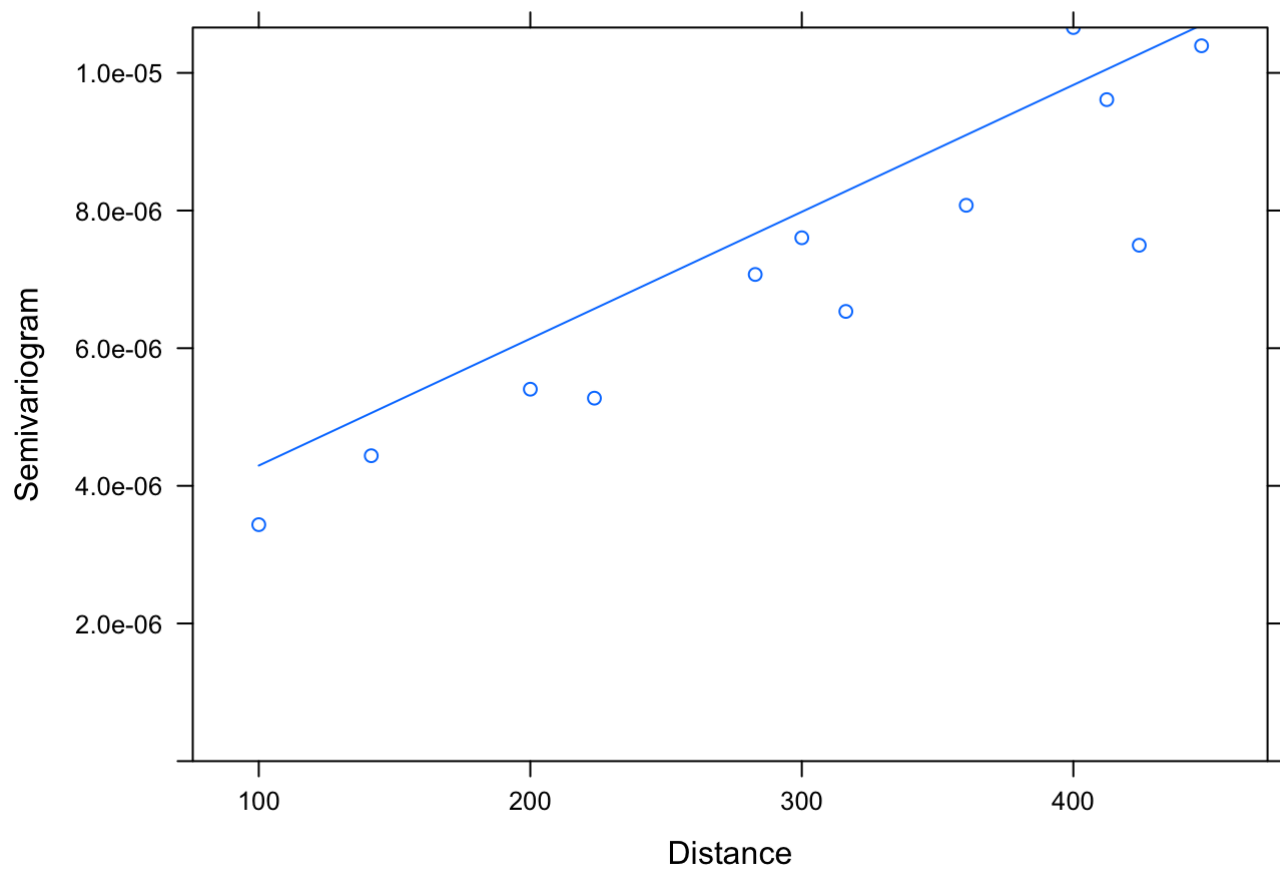




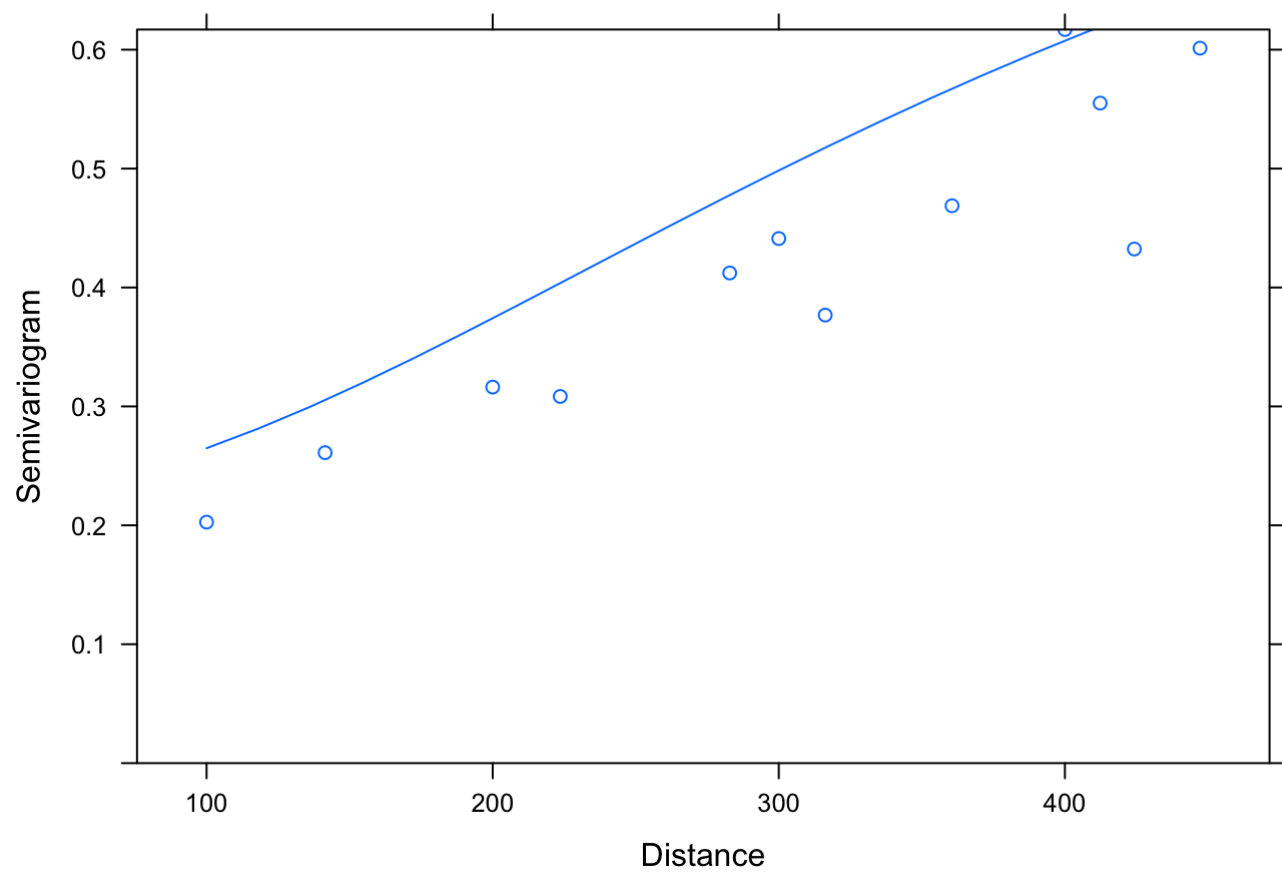
```
plot(Variogram(sp_all_exp, resType='normalized', maxDist = max_dist))
```



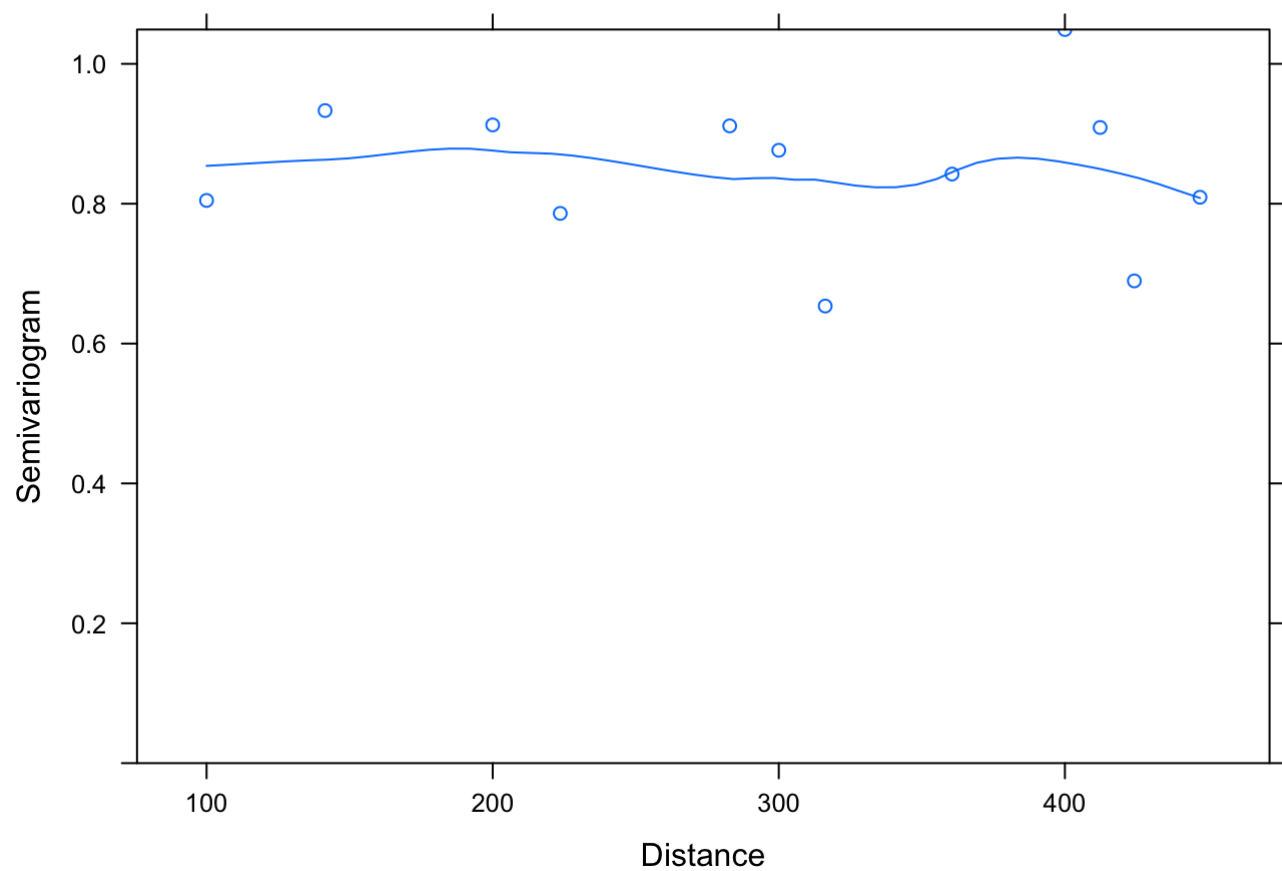
```
sp_all_exp_nug = update(sp_all_exp, corr=corExp(form=~x + y, nugget=T))  
plot(Variogram(sp_all_exp_nug, maxDist = max_dist))
```



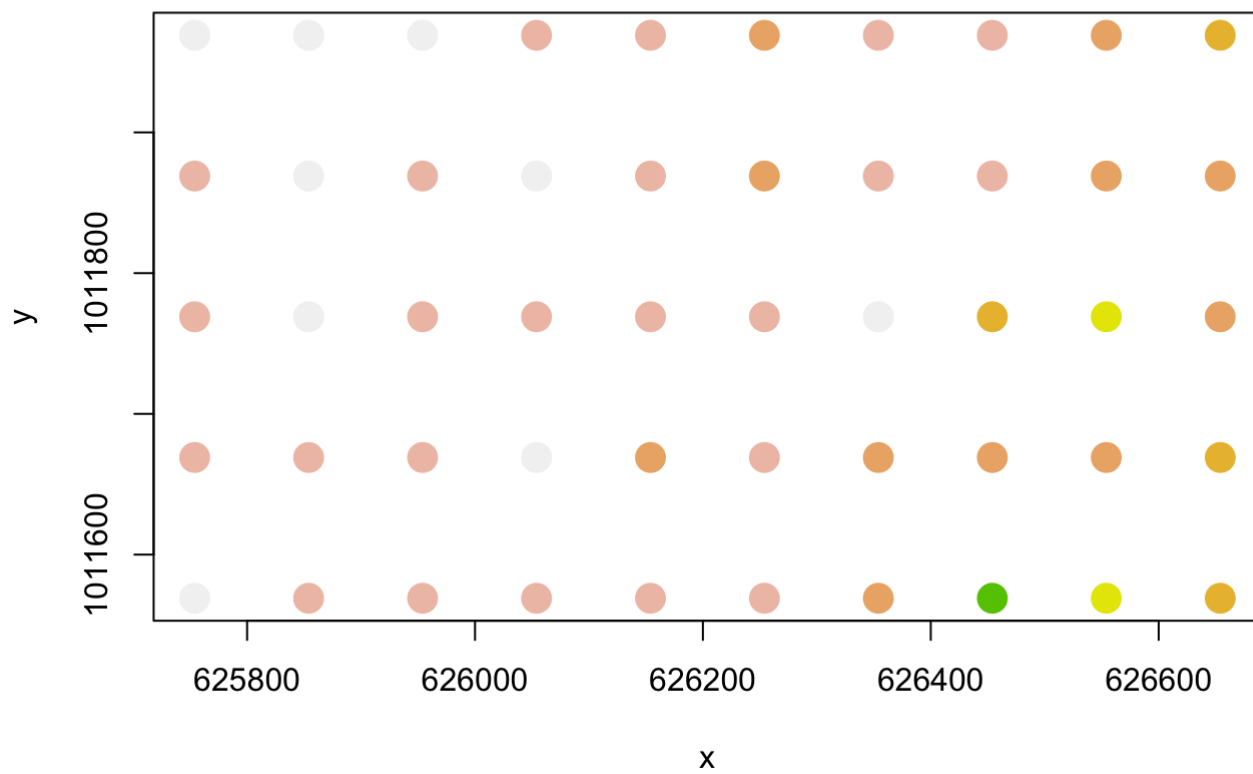
```
sp_all_rat_nug = update(sp_all_lm, corr=corRatio(form=~x + y, nugget=T))  
plot(Variogram(sp_all_rat_nug, maxDist = max_dist))
```



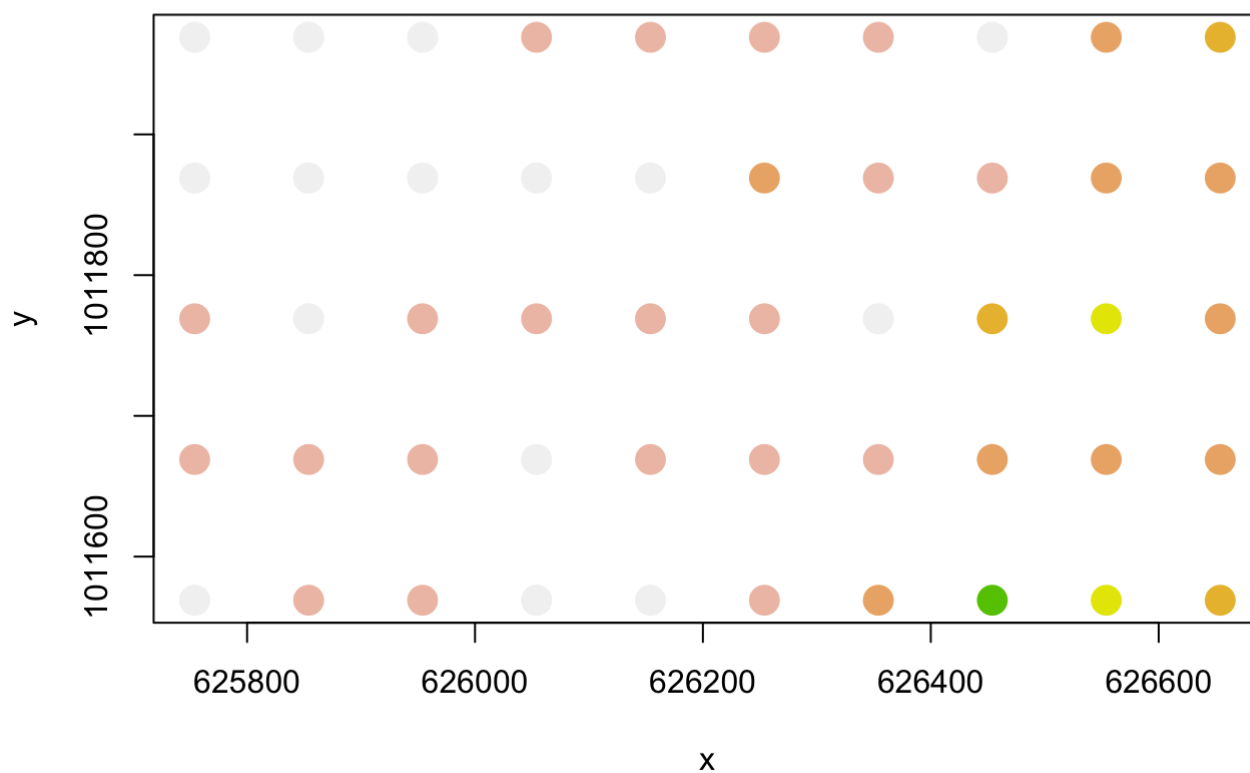
```
plot(Variogram(sp_all_rat_nug, resType='n', maxDist = max_dist))
```



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



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



```
anova(sp_all_lm, sp_all_exp, sp_all_exp_nug, sp_all_rat_nug, test=F)
```

```
##           Model df      AIC      BIC    logLik
## sp_all_lm      1   9 307.1163 322.7554 -144.5582
## sp_all_exp      2  10 301.6062 318.9829 -140.8031
## sp_all_exp_nug   3  11 301.9592 321.0735 -139.9796
## sp_all_rat_nug   4  11 303.1486 322.2630 -140.5743
```

```
summary(sp_all_lm)
```

```
## Generalized least squares fit by REML
## Model: Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra + Picramnia.
latifolia + Quassia.amara + Tabernaemontana.arborea + Trattinnickia.aspera + Xylopi
a.macrantha
## Data: sp_data
## 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
## Xylopi.a.macrantha 0.548832 0.1468772 3.736672 0.0006
##
## Correlation:
## (Intr) Crd.ls Hrtll. Pcrmn. Qss.mr Tbrnm. Trtttn.
## 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
## Xylopi.a.macrantha -0.140 -0.125 0.156 -0.463 0.314 0.279 -0.294
##
## Standardized residuals:
## Min Q1 Med Q3 Max
## -1.87708765 -0.42701500 -0.04032793 0.23615609 3.38768871
##
## Residual standard error: 4.539713
## Degrees of freedom: 50 total; 42 residual
```

```
summary(sp_all_exp)
```



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

```
summary(sp_all_exp_nug)
```

```
## Generalized least squares fit by REML
## Model: Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra + Picramnia.
latifolia + Quassia.amara + Tabernaemontana.arborea + Trattinnickia.aspera + Xylopi
a.macrantha
## Data: sp_data
## AIC BIC logLik
## 301.9592 321.0735 -139.9796
##
## Correlation Structure: Exponential spatial correlation
## Formula: ~x + y
## Parameter estimate(s):
## range nugget
## 5.424635e+07 2.451077e-06
##
## Coefficients:
## Value Std.Error t-value p-value
## (Intercept) 3.0501045 1785.0597 0.001709 0.9986
## Cordia.lasiocalyx 0.1426666 0.1895 0.752752 0.4558
## Hirtella.triandra -0.0017714 0.0904 -0.019600 0.9845
## Picramnia.latifolia 0.2863335 0.5274 0.542880 0.5901
## Quassia.amara 1.3263643 1.9368 0.684818 0.4972
## Tabernaemontana.arborea 0.0407530 0.1395 0.292085 0.7717
## Trattinnickia.aspera 1.8170749 0.5730 3.171303 0.0028
## Xylopi.a.macrantha 0.4086700 0.1537 2.659324 0.0110
##
## Correlation:
## (Intr) Crd.ls Hrtll. Pcrmn. Qss.mr Tbrnm. Trtttn.
## Cordia.lasiocalyx -0.001
## 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 -0.001 -0.020 0.160 -0.197 0.088
## Trattinnickia.aspera 0.000 0.165 -0.276 0.255 -0.655 -0.036
## Xylopi.a.macrantha 0.000 -0.066 -0.037 -0.048 0.306 0.140 -0.183
##
## Standardized residuals:
## Min Q1 Med Q3 Max
## -0.0049325435 -0.0029088009 -0.0020671675 0.0005570041 0.0103697005
##
## Residual standard error: 1785.068
## Degrees of freedom: 50 total; 42 residual
```

```
summary(sp_all_rat_nug)
```

```

## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra + Picramnia.
latifolia + Quassia.amara + Tabernaemontana.arborea + Trattinnickia.aspera + Xylopi
a.macrantha
##   Data: sp_data
##           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
## Xylopi.a.macrantha    0.4058061   0.161181  2.5177087  0.0157
##
## Correlation:
##
##      (Intr) Crd.ls Hrtll. Pcrmn. Qss.mr Tbrnm. Trttn.
## Cordia.lasiocalyx    -0.273
## Hirtella.triandra    -0.272 -0.122
## Picramnia.latifolia    0.017  0.038 -0.387
## Quassia.amara      -0.039 -0.304  0.337 -0.213
## Tabernaemontana.arborea -0.242 -0.029  0.166 -0.201  0.106
## Trattinnickia.aspera  -0.090  0.163 -0.272  0.271 -0.646 -0.036
## Xylopi.a.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

```

Spatial error terms did not effect the model

Adding spatial error terms (rational nugget) for the model with one species improved the model. Fitting error to the model that included all species improved the model, but adding nuggets had no effect. Overall, coefficients for both models had an impact, but this was larger for the model with only one species. Spatial error terms can control for spatial dependence between neighbors and therefore improve our model.