```
library(vegan)
```

```
## Warning: package 'vegan' was built under R version 3.5.3
```

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

```
## Warning: package 'permute' was built under R version 3.5.3
```

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

```
## Warning: package 'lattice' was built under R version 3.5.3
```

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

```
data(BCI)
BCI_xy <- data.frame(x = rep(seq(625754, 626654, by=100), each=5),
                     y = rep(seq(1011569,  1011969, by=100), len=50))
?BCI
```
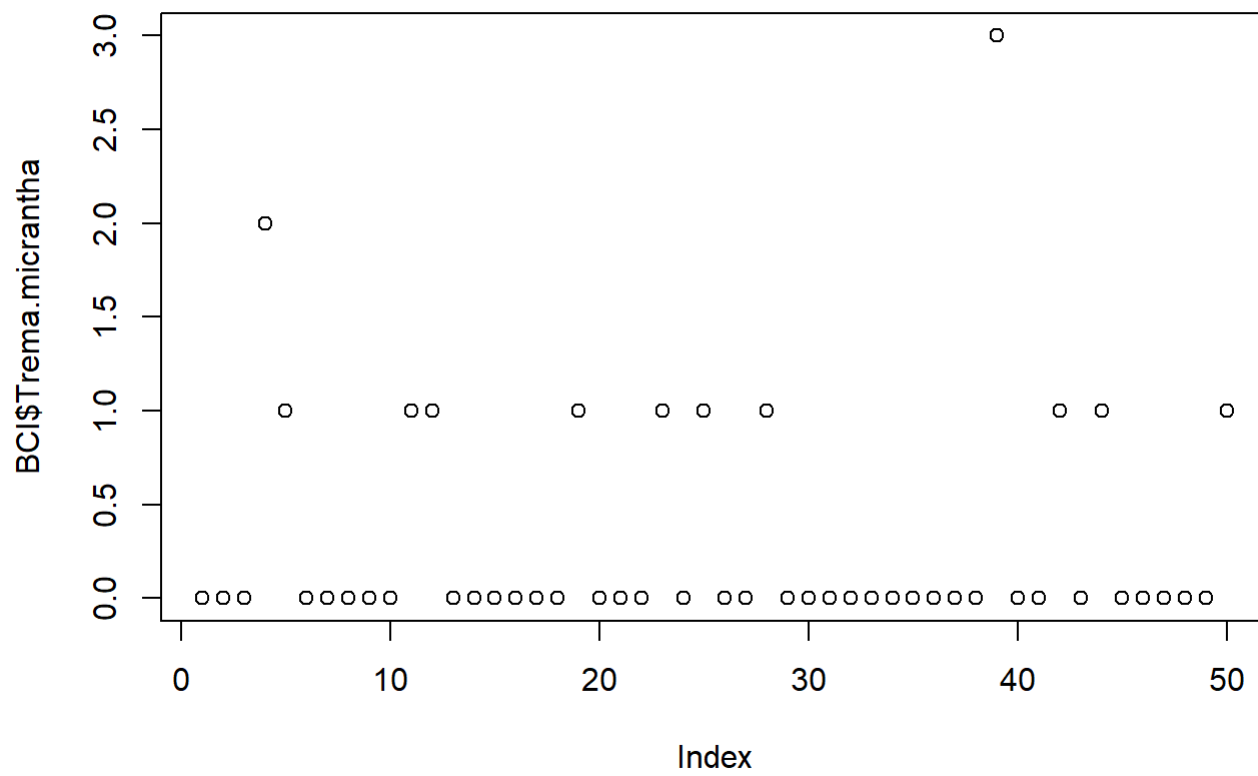
```
## starting httpd help server ...
```
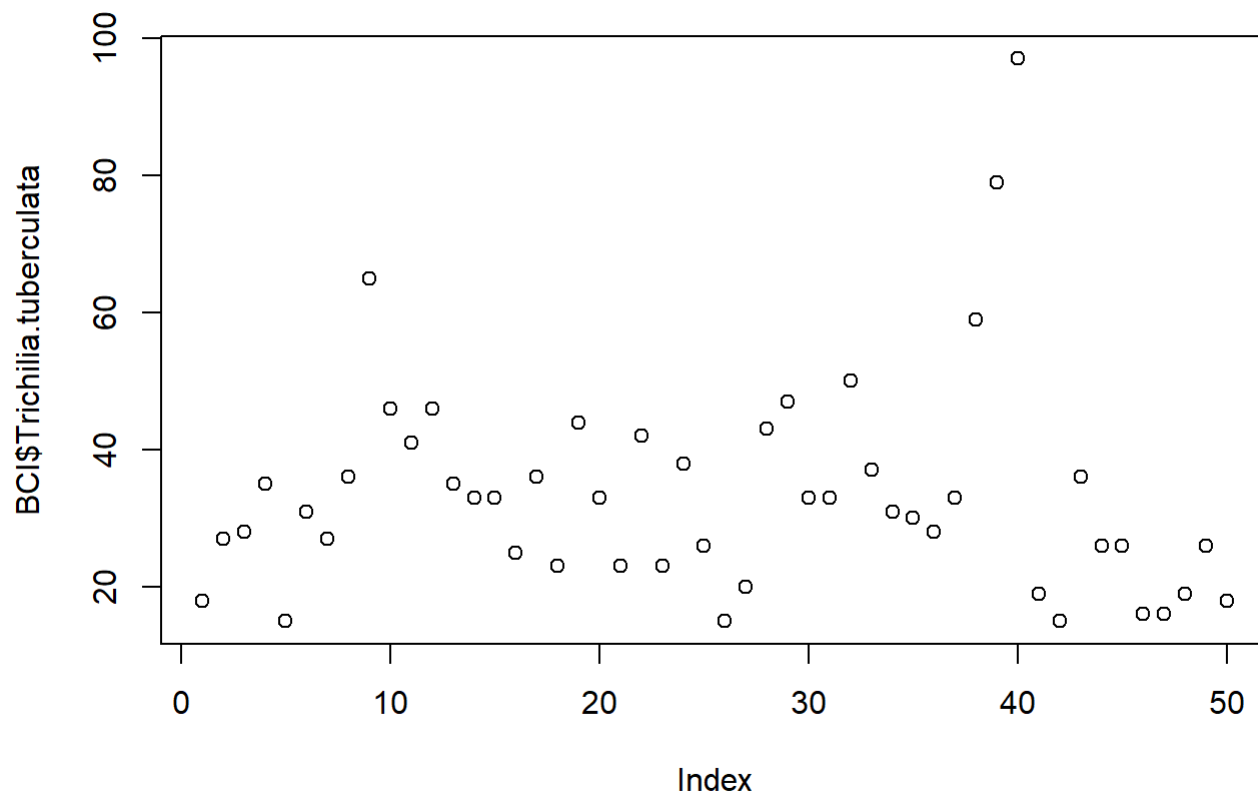
```
##  done
```

Trichilia.tuberculata-common Trema.micrantha-rare

```
rare <- data.frame(BCI$Trema.micrantha)
com <- data.frame(BCI$Trichilia.tuberculata)
```

```
plot(BCI$Trema.micrantha)
```

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

For

Trichilia tuberculata, there doesn't seem to be any sort of spatial dependence.

For Trema micrantha, I don't see any sort of spatial dependence, but it has a more spotty distribution.

```
c_dist <- dist(com)
r_dist <- dist(rare)
xy_dist <- dist(BCI_xy)
max_dist <- max(xy_dist)/2

plot(xy_dist, c_dist)
abline(lm(c_dist ~ xy_dist), lwd=3, col='red')
lines(lowess(xy_dist, c_dist), lwd=3, col='pink')
abline(v = max_dist, col='red', lwd=3, lty=2)
```
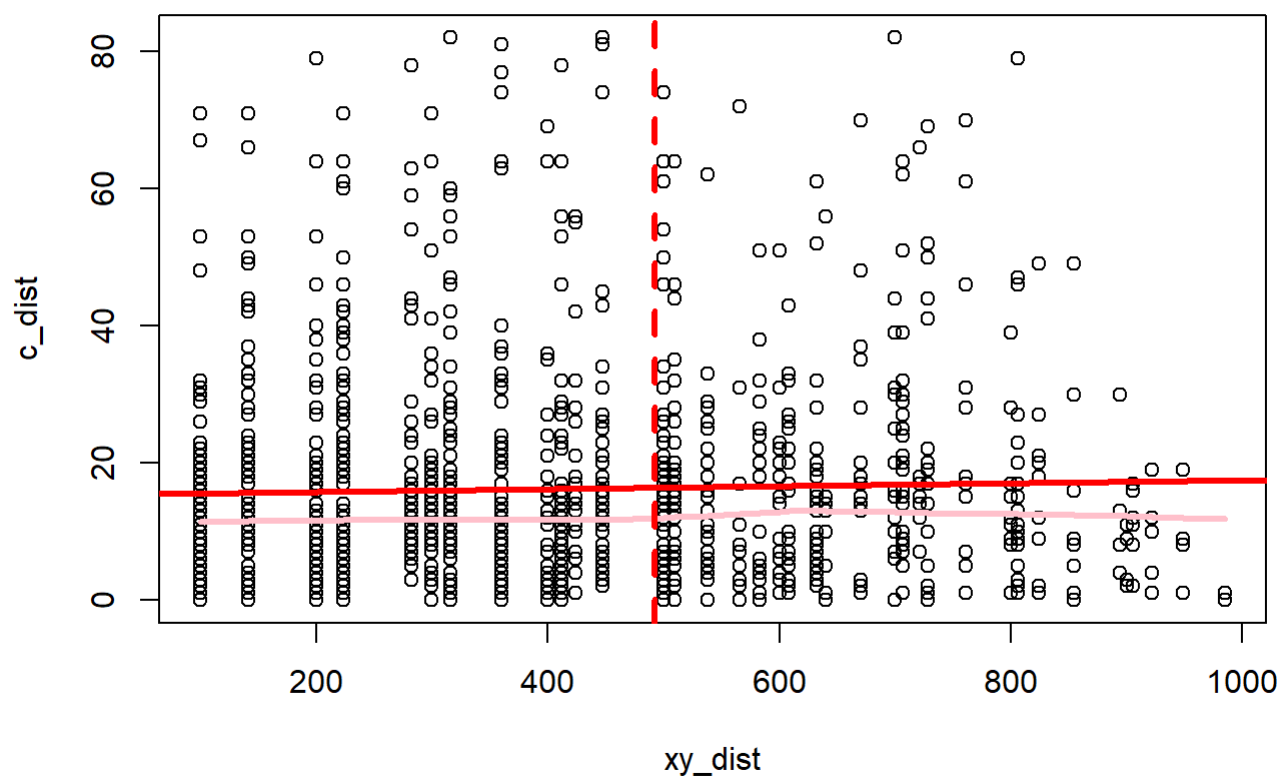
```
plot(xy_dist, r_dist)
abline(lm(r_dist ~ xy_dist), lwd=3, col='red')
lines(lowess(xy_dist, r_dist), lwd=3, col='pink')
abline(v = max_dist, col='red', lwd=3, lty=2)
```
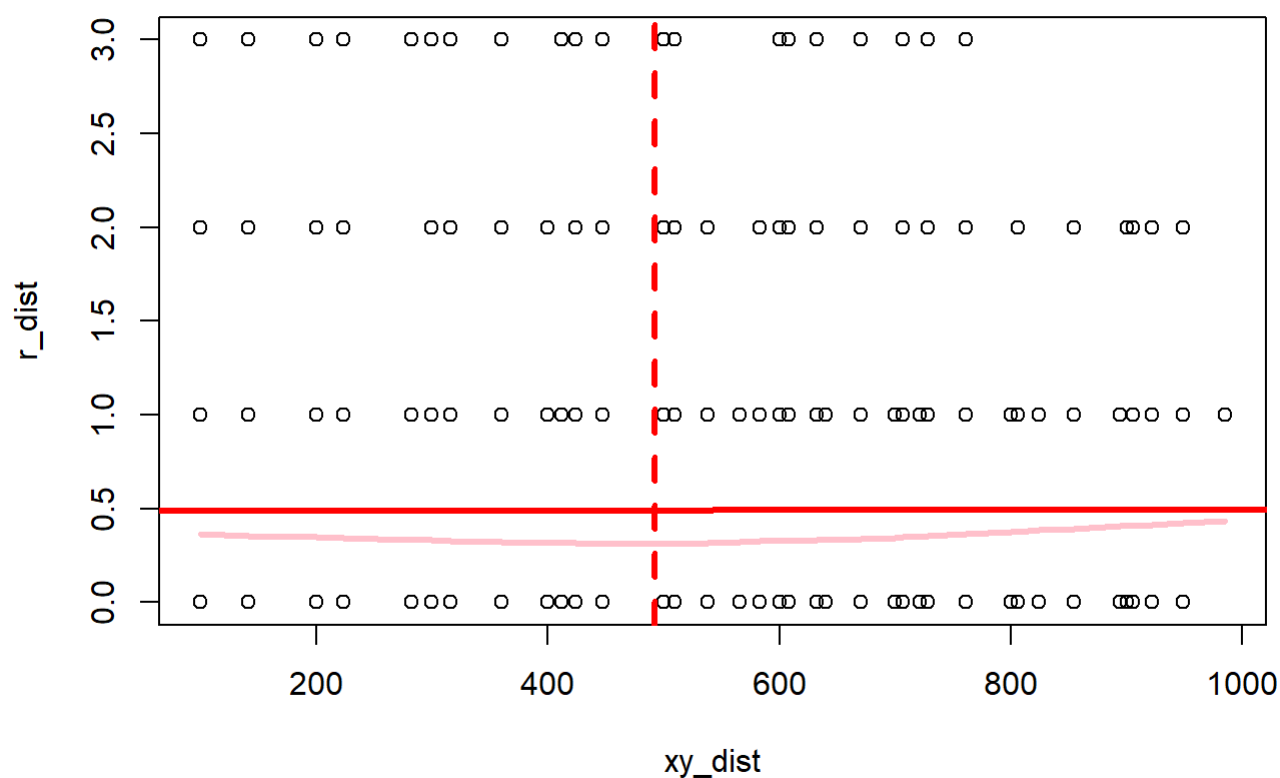
```
c_mantel <- mantel(xy_dist, c_dist)
c_mantel
```

```
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = xy_dist, ydis = c_dist)
##
## Mantel statistic r: 0.02876
##       Significance: 0.311
##
## Upper quantiles of permutations (null model):
##    90%    95%  97.5%    99%
## 0.0826 0.1040 0.1242 0.1493
## Permutation: free
## Number of permutations: 999
```

```
r_mantel <- mantel(xy_dist, r_dist)
r_mantel
```

```
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = xy_dist, ydis = r_dist)
##
## Mantel statistic r: 0.002549
##       Significance: 0.49
##
## Upper quantiles of permutations (null model):
##    90%   95% 97.5%   99%
## 0.086 0.107 0.125 0.163
## Permutation: free
## Number of permutations: 999
```

From these mantel test, there still doesn't appear to be any type of spatial relationship

```
sp_a <- c("Cordia.lasiocalyx", "Hirtella.triandra",
          "Picramnia.latifolia", "Quassia.amara",
          "Tabernaemontana.arborea", "Trattinnickia.aspera",
          "Xylopia.macrantha")
```

```
library(nlme)
dstand <- BCI[ , c('Drypetes.standleyi', sp_a)]
dat <- data.frame(dstand, BCI_xy)
model1 <- gls(Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra +
          Picramnia.latifolia + Quassia.amara +
          Tabernaemontana.arborea + Trattinnickia.aspera +
          Xylopia.macrantha, data = dat)
model2 <- gls(Drypetes.standleyi ~ Cordia.lasiocalyx , data = dat)
model1
```

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra +     Picramnia.latifoli
a + Quassia.amara + Tabernaemontana.arborea +     Trattinnickia.aspera + Xylopia.macrantha
##   Data: dat
##   Log-restricted-likelihood: -144.5582
##
## Coefficients:
##           (Intercept)       Cordia.lasiocalyx       Hirtella.triandra
##            -1.0517523               0.4289202               0.1222789
##     Picramnia.latifolia          Quassia.amara Tabernaemontana.arborea
##             0.6622595               4.0856614              -0.2497250
##     Trattinnickia.aspera       Xylopia.macrantha
##             1.3493226               0.5488320
##
## Degrees of freedom: 50 total; 42 residual
## Residual standard error: 4.539713
```
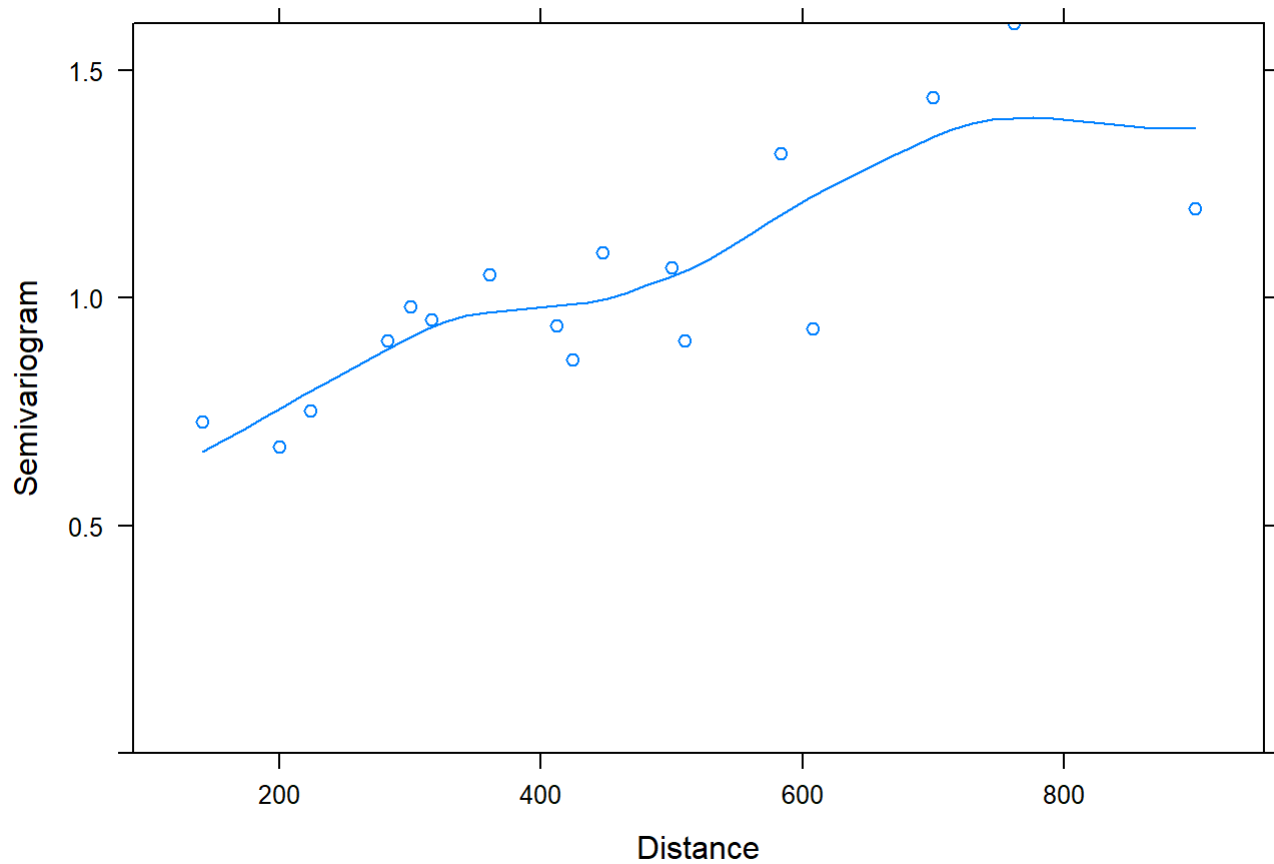
```
model2
```

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Cordia.lasiocalyx
##   Data: dat
##   Log-restricted-likelihood: -164.5623
##
## Coefficients:
##       (Intercept) Cordia.lasiocalyx
##         -2.782804          1.165220
##
## Degrees of freedom: 50 total; 48 residual
## Residual standard error: 6.675561
```
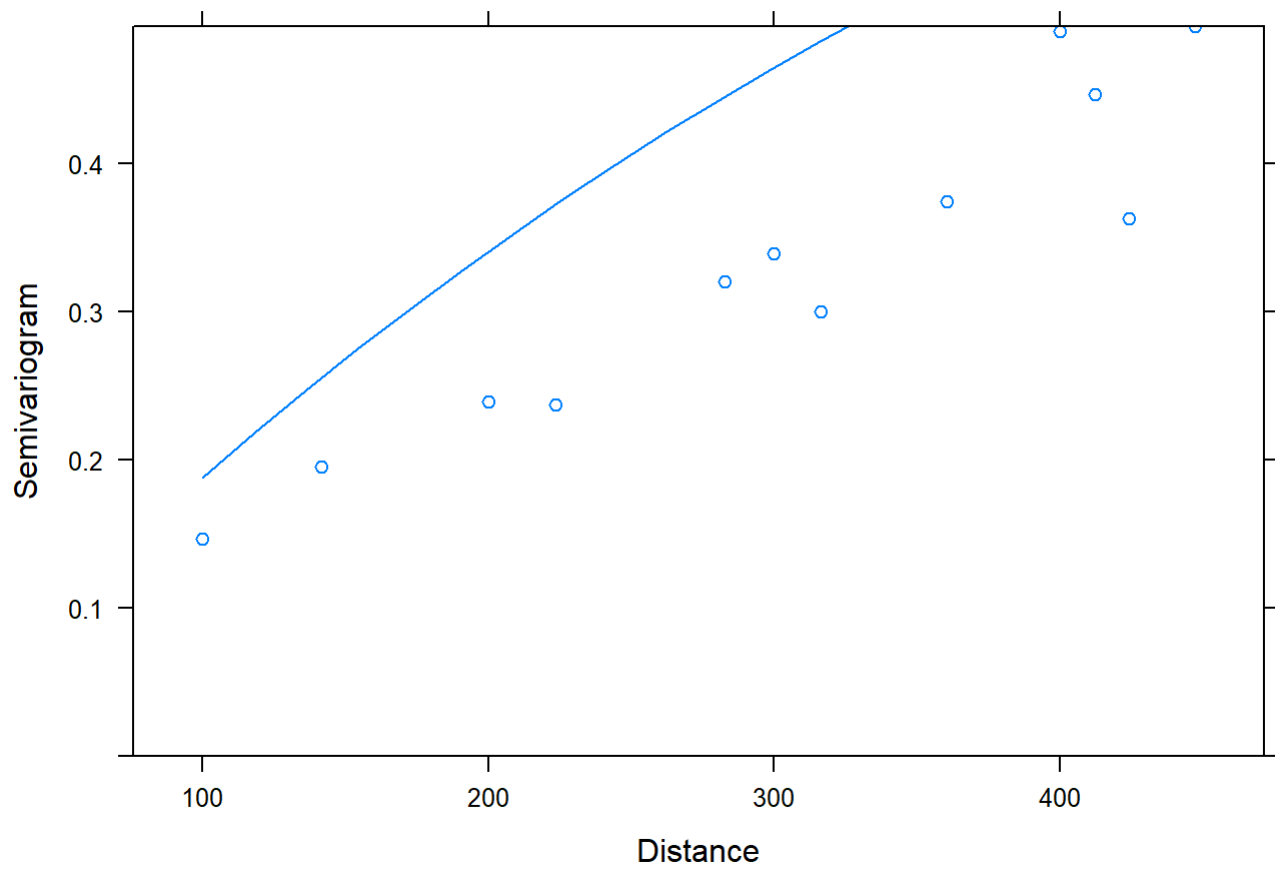
```
?Variogram
library(nlme)
plot(Variogram(model1, form = ~ x + y))
```
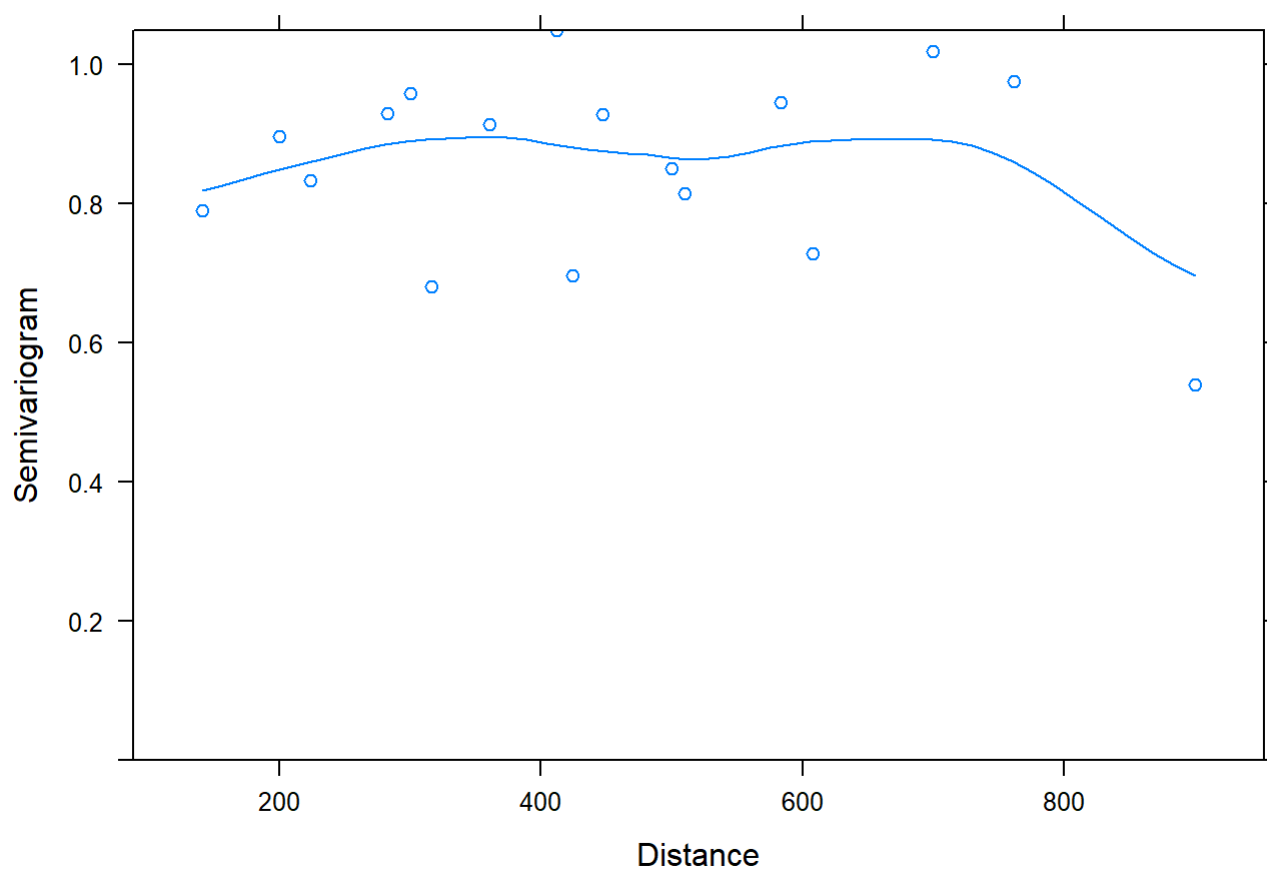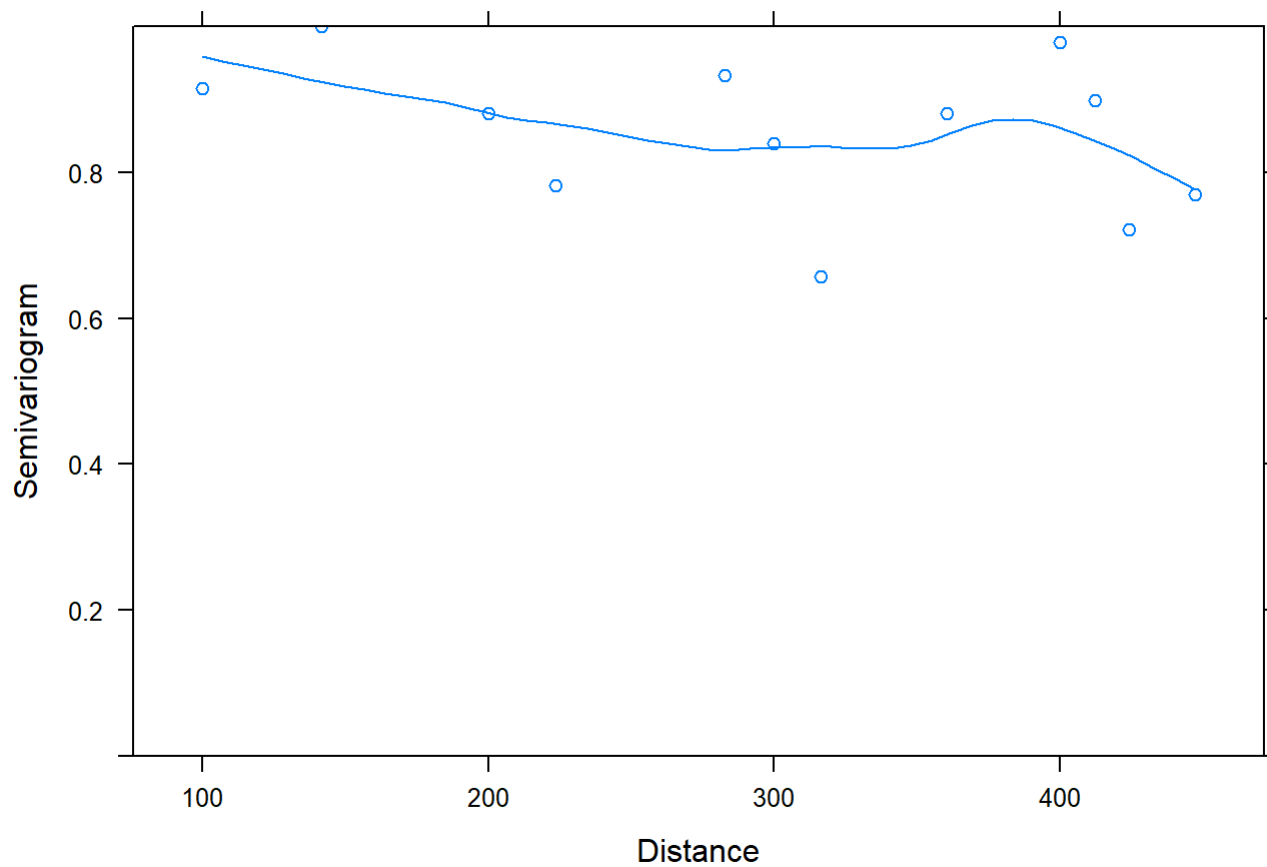


```
plot(Variogram(model2, form = ~ x + y))
```
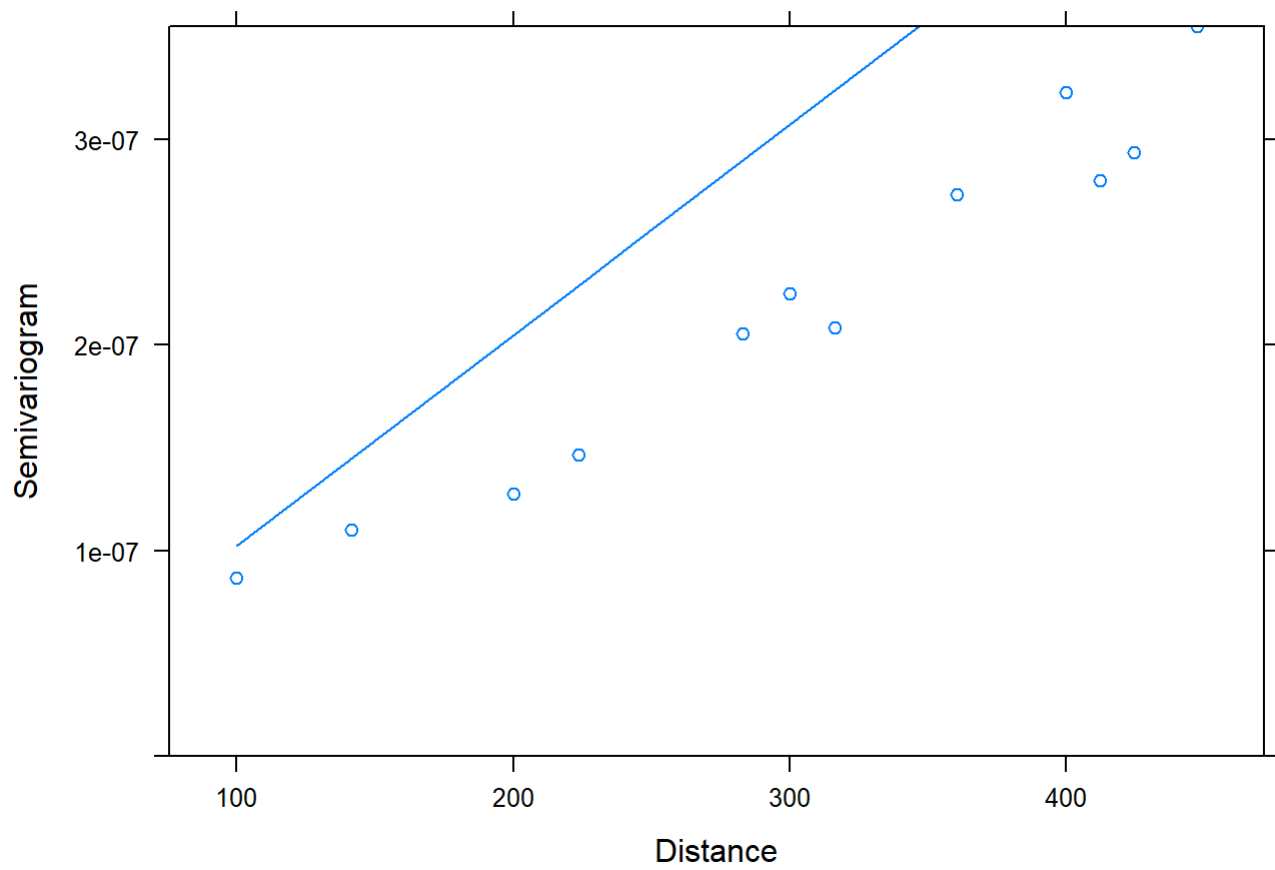
```
model1_exp = update(model1, corr=corExp(form=~x + y))
model2_exp = update(model2, corr=corExp(form=~x + y))
plot(Variogram(model1_exp, maxDist = max_dist))
```

```
plot(Variogram(model1_exp, resType='normalized', maxDist = max_dist))
```

```
plot(Variogram(model2_exp, maxDist = max_dist))
```

```
plot(Variogram(model2_exp, resType='normalized', maxDist = max_dist))
```

```
mod1_exp_nug = update(model1_exp, corr=corExp(form=~x + y, nugget=T))
mod2_exp_nug = update(model2_exp, corr=corExp(form=~x + y, nugget=T))
plot(Variogram(mod1_exp_nug, maxDist = max_dist))
```

```
plot(Variogram(mod1_exp_nug, resType='n', maxDist = max_dist))
```

```
plot(Variogram(mod2_exp_nug, maxDist = max_dist))
```

```
plot(Variogram(mod2_exp_nug, resType='n', maxDist = max_dist))
```

```
mod1_rat_nug = update(model1, corr=corRatio(form=~x + y, nugget=T))
mod2_rat_nug = update(model2, corr=corRatio(form=~x + y, nugget=T))
plot(Variogram(mod1_rat_nug, maxDist = max_dist))
```
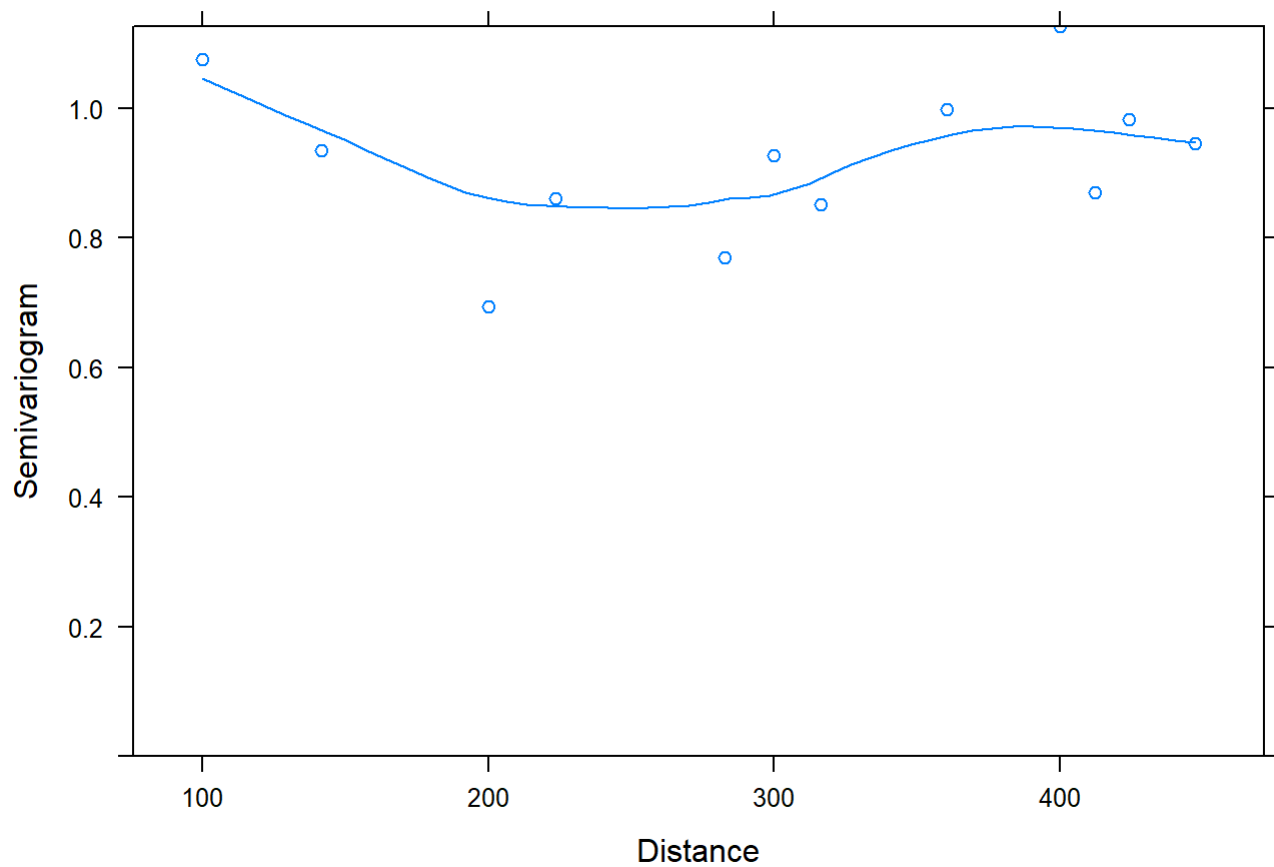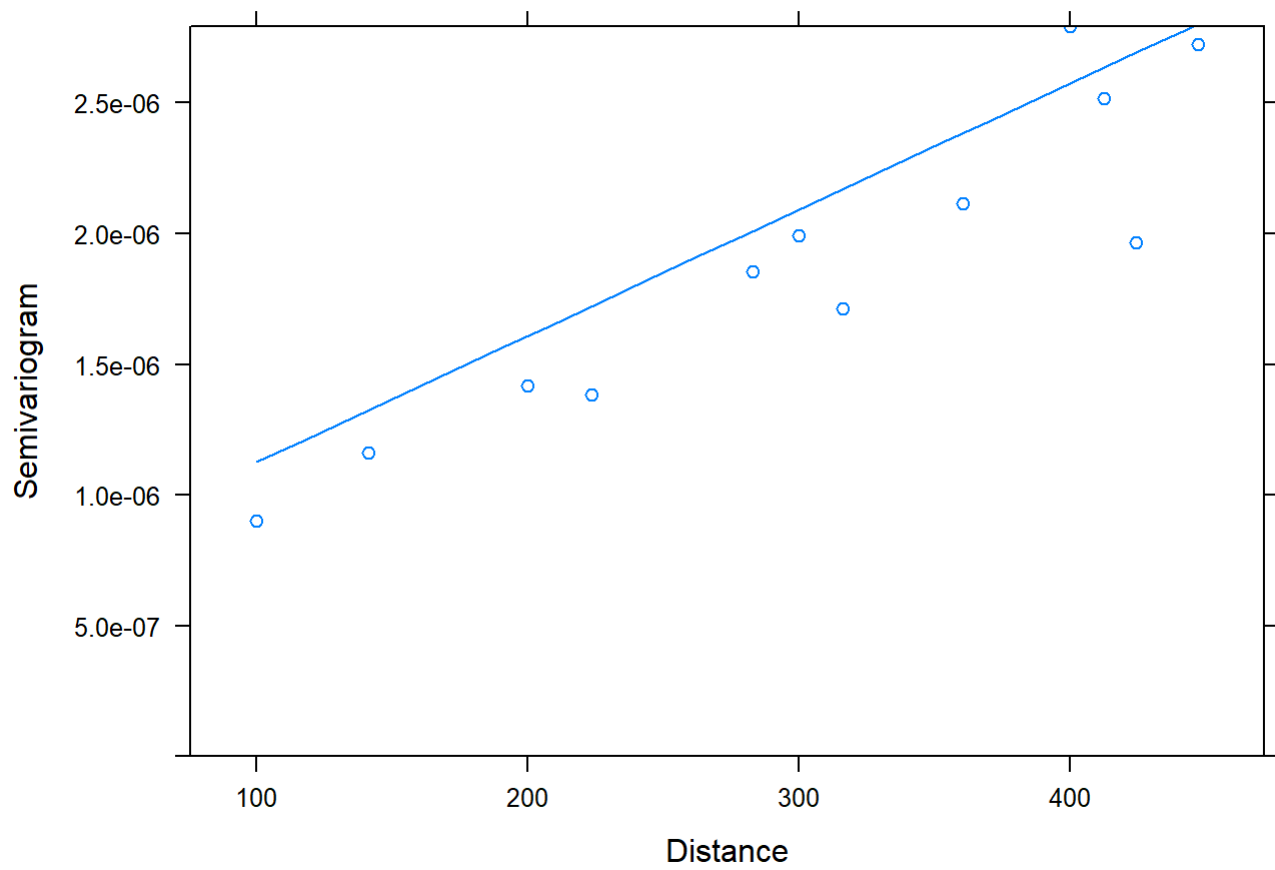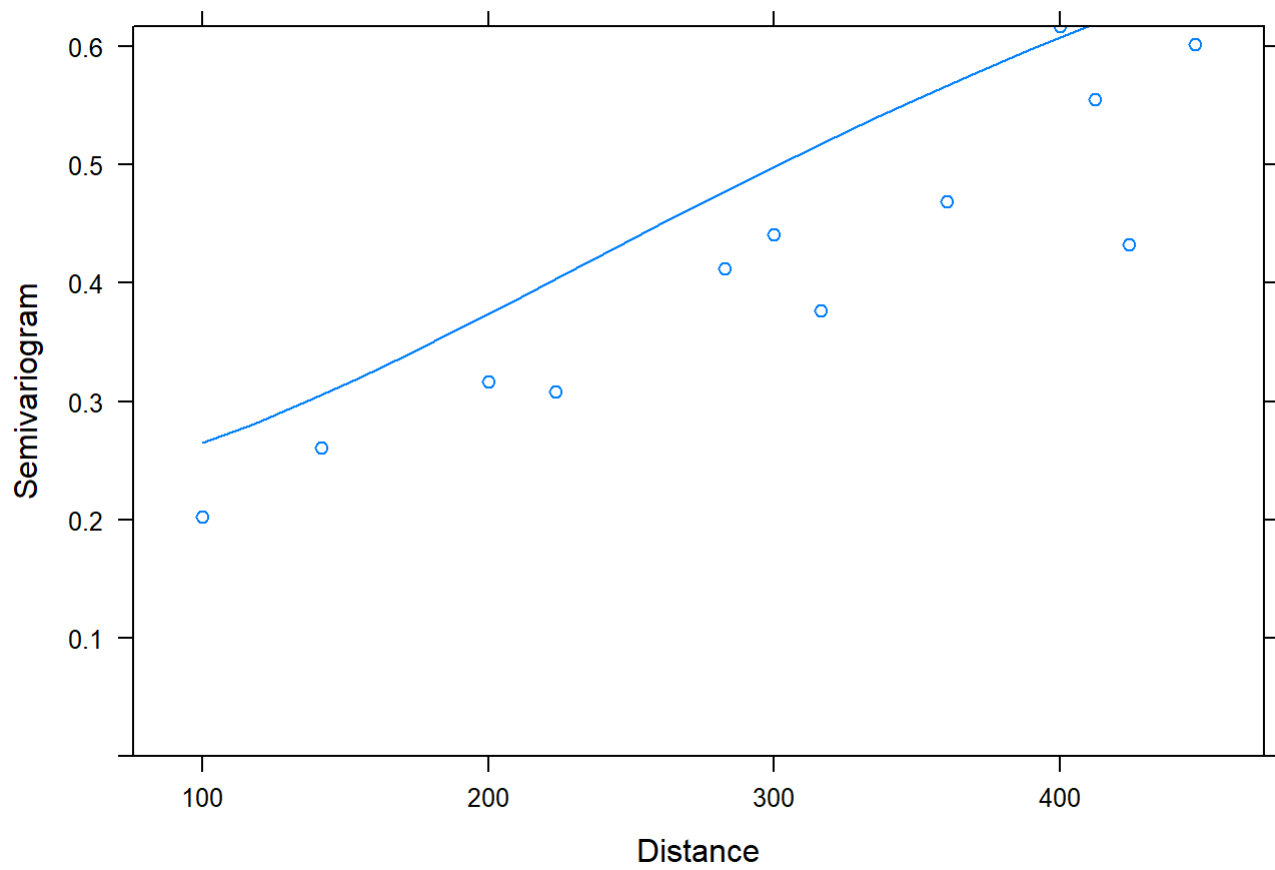
```
plot(Variogram(mod1_rat_nug, resType='n', maxDist = max_dist))
```
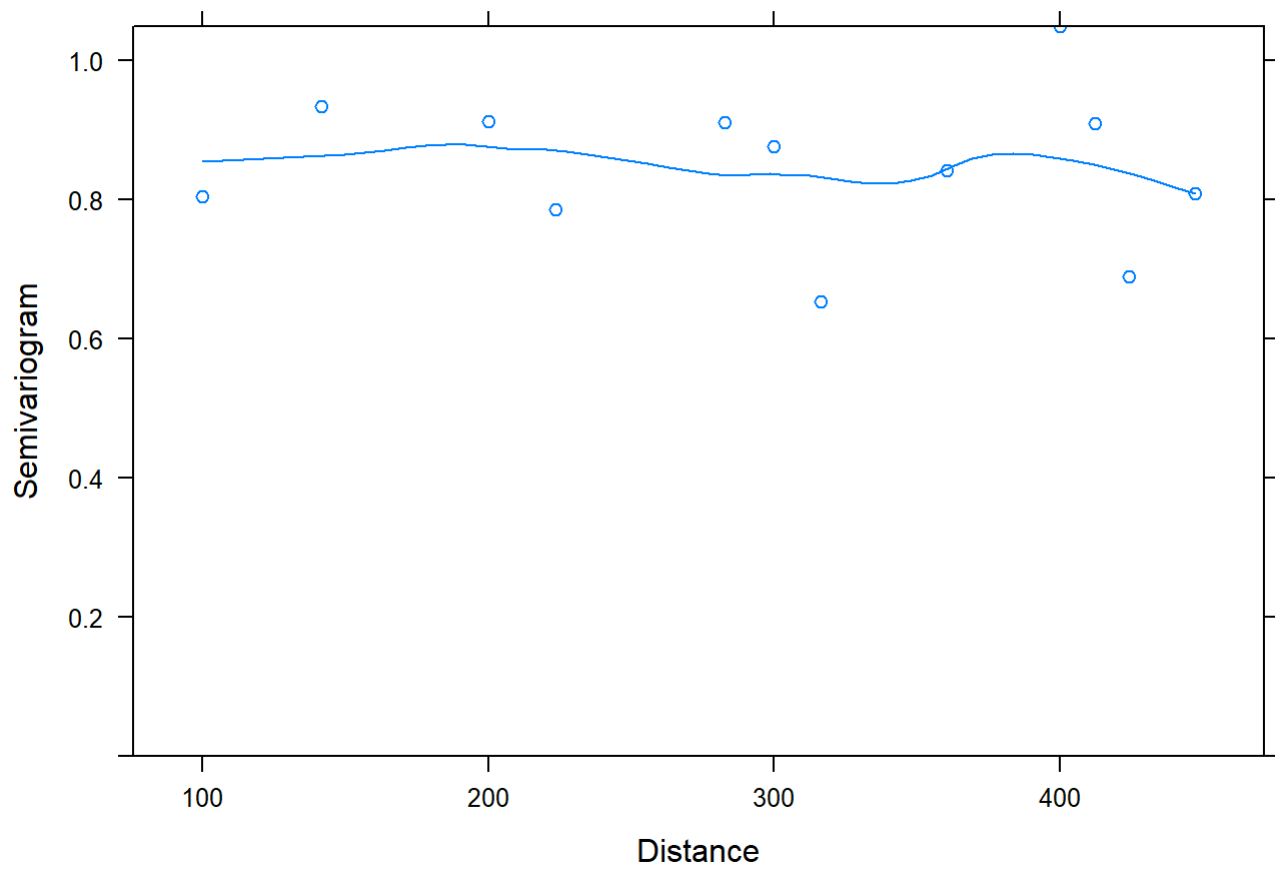
```
plot(Variogram(mod2_rat_nug, maxDist = max_dist))
```
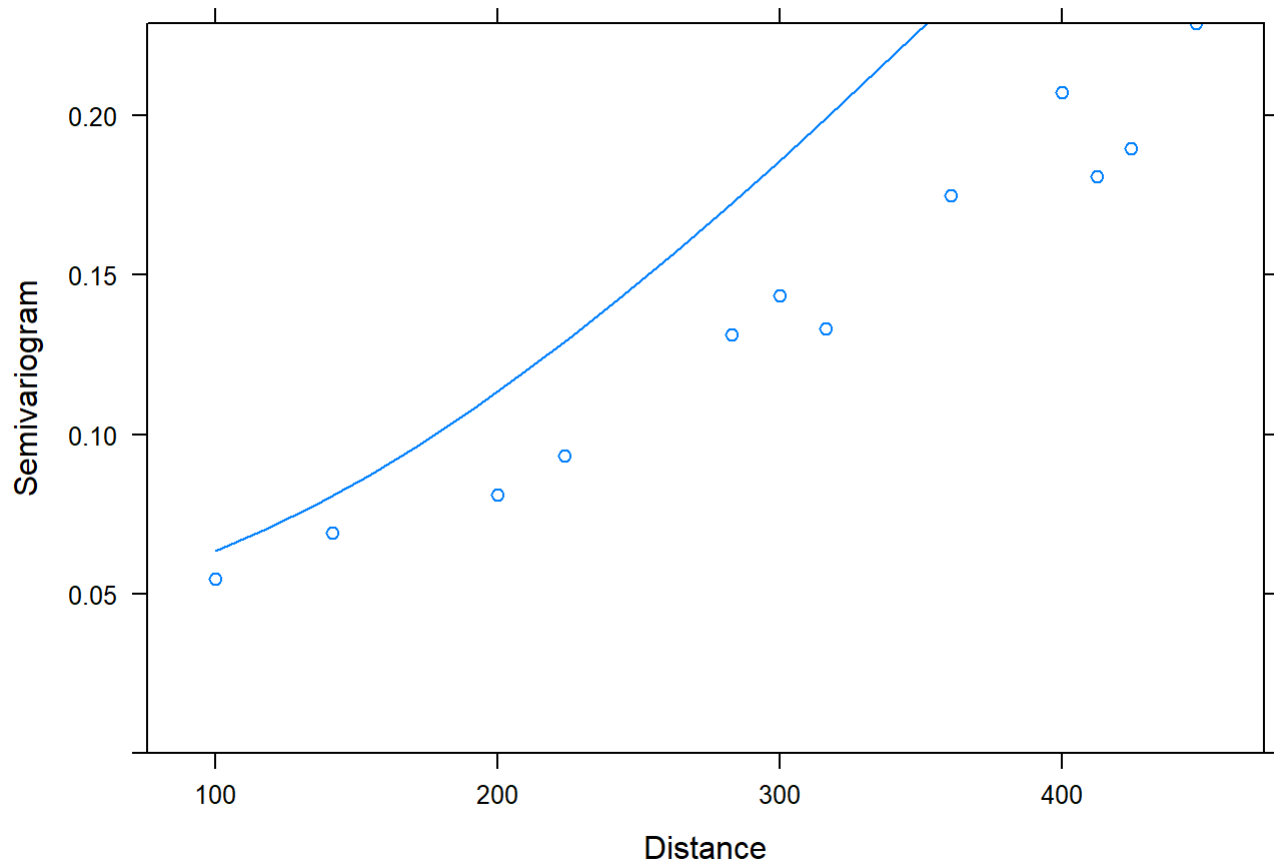
```
plot(Variogram(mod2_rat_nug, resType='n', maxDist = max_dist))
```
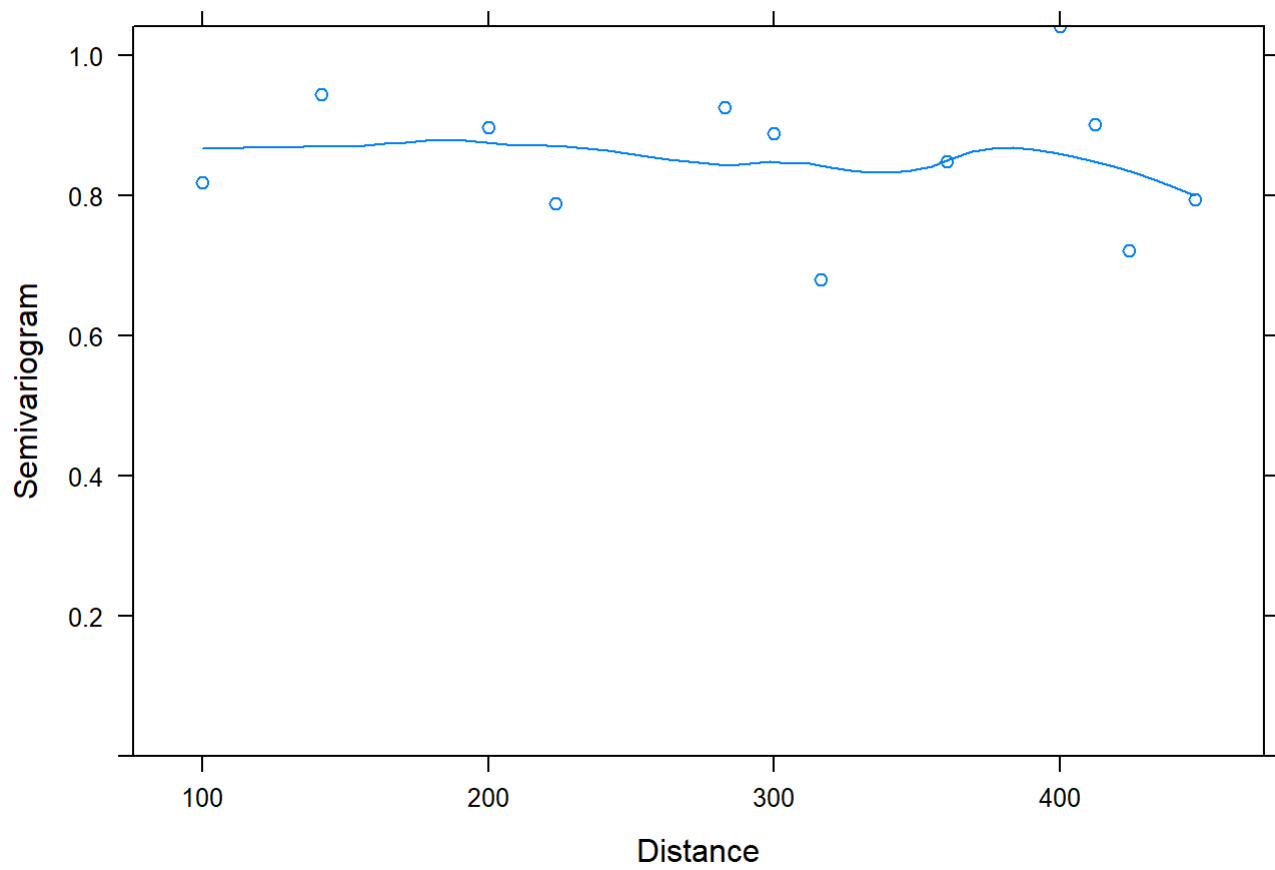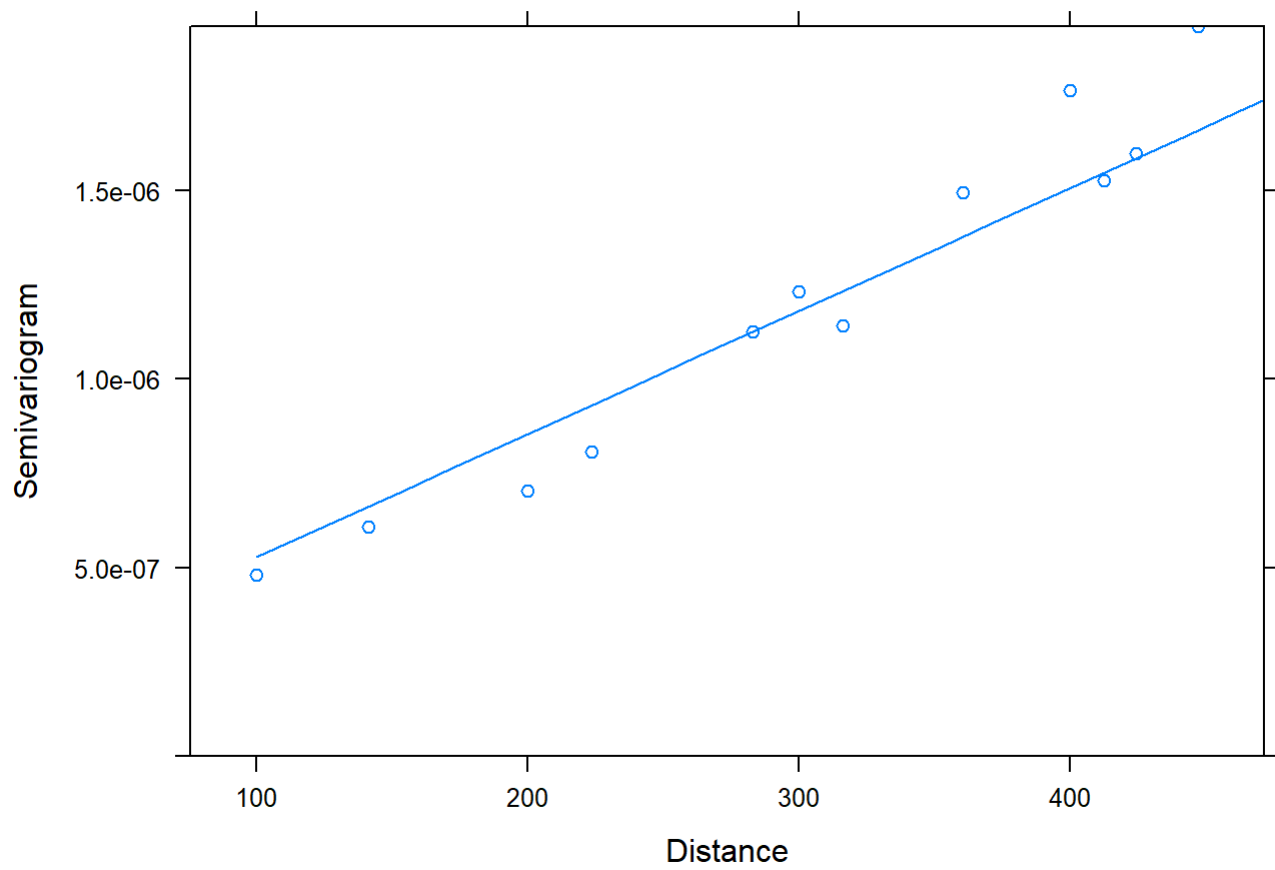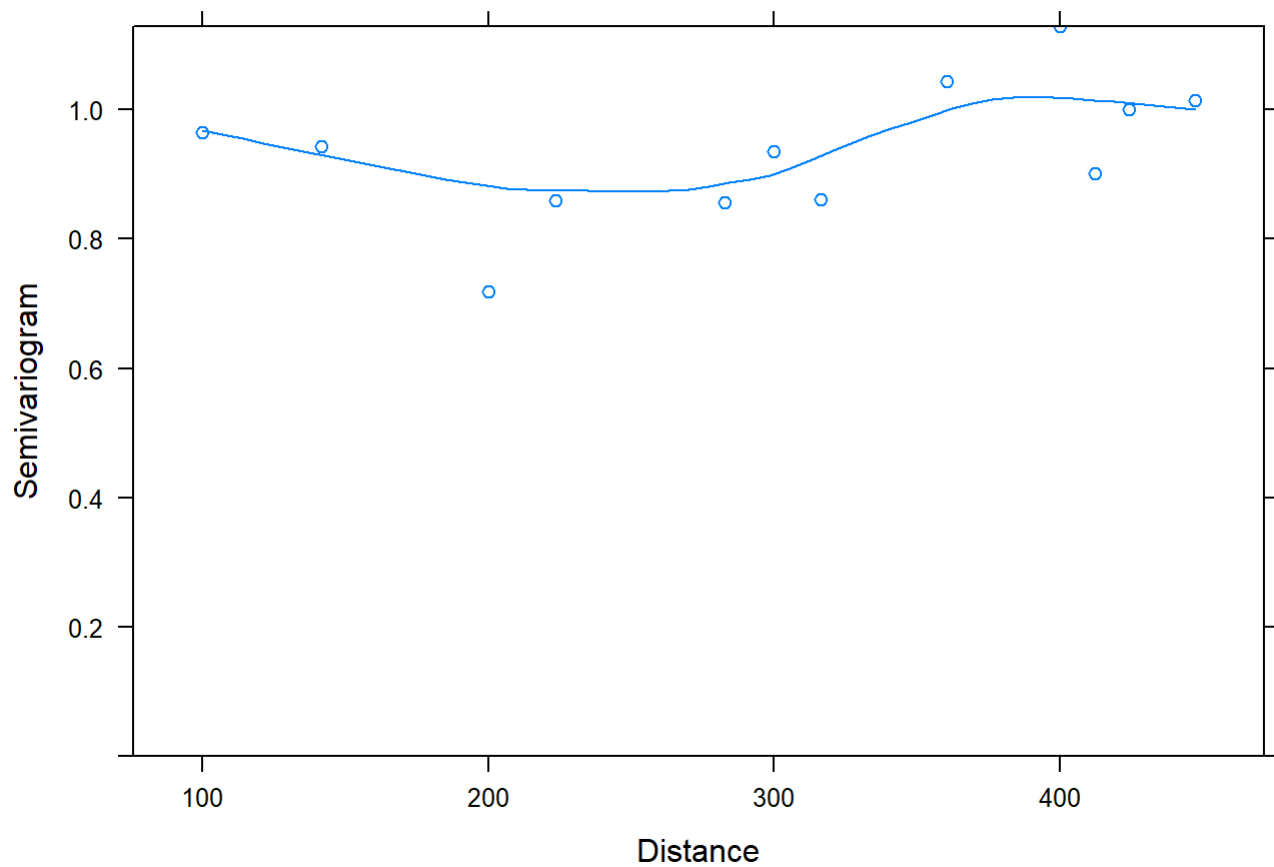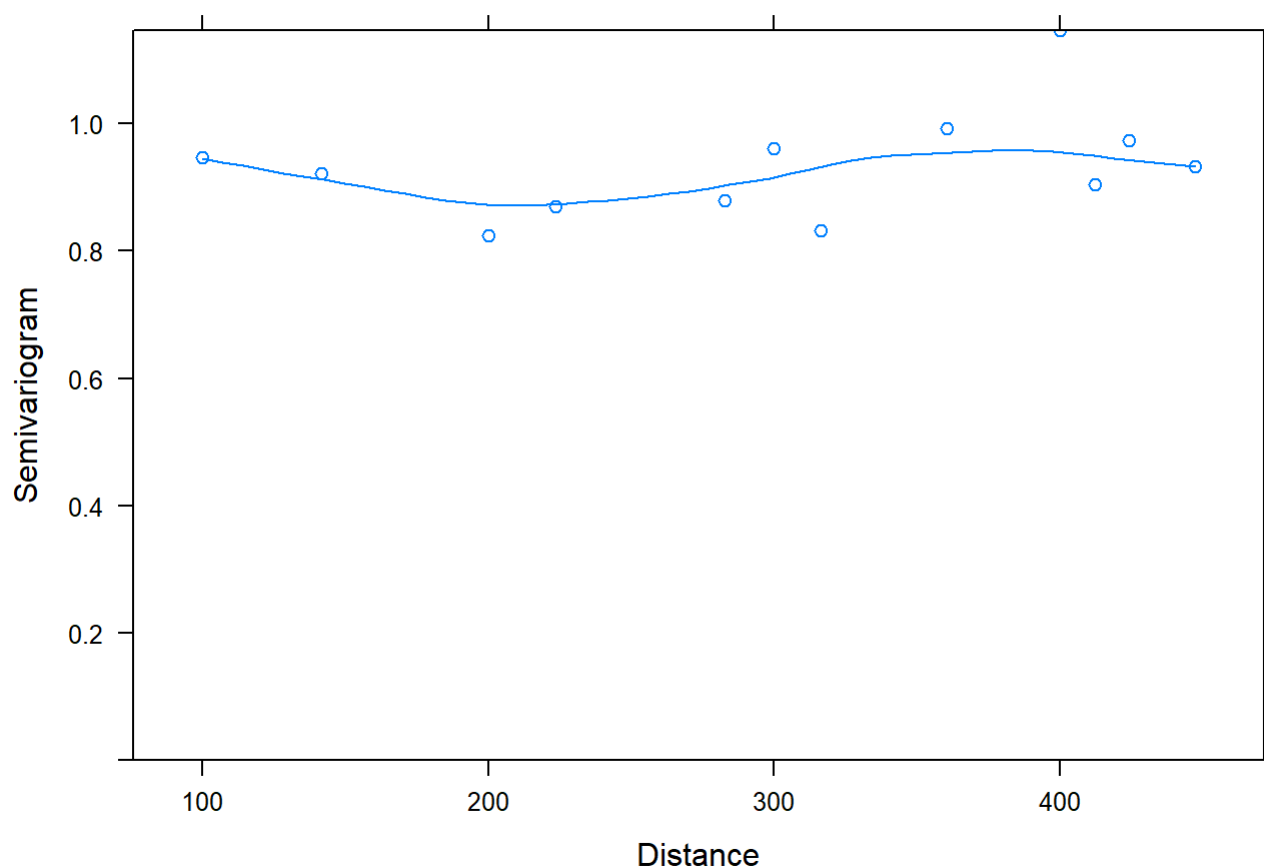
model1

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra +     Picramnia.latifoli
a + Quassia.amara + Tabernaemontana.arborea +     Trattinnickia.aspera + Xylopia.macrantha
##   Data: dat
##   Log-restricted-likelihood: -144.5582
##
## Coefficients:
##           (Intercept)        Cordia.lasiocalyx       Hirtella.triandra
##            -1.0517523               0.4289202               0.1222789
##     Picramnia.latifolia              Quassia.amara Tabernaemontana.arborea
##             0.6622595               4.0856614              -0.2497250
##     Trattinnickia.aspera       Xylopia.macrantha
##             1.3493226               0.5488320
##
## Degrees of freedom: 50 total; 42 residual
## Residual standard error: 4.539713
```

model1_exp

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra +     Picramnia.latifoli
a + Quassia.amara + Tabernaemontana.arborea +     Trattinnickia.aspera + Xylopia.macrantha
##   Data: dat
##   Log-restricted-likelihood: -140.8031
##
## Coefficients:
##          (Intercept)      Cordia.lasiocalyx       Hirtella.triandra
##           2.34851969             0.12083904              0.01917586
##     Picramnia.latifolia          Quassia.amara Tabernaemontana.arborea
##           0.20145161             1.27922893              0.06749426
##    Trattinnickia.aspera     Xylopia.macrantha
##           1.81153745             0.33885742
##
## Correlation Structure: Exponential spatial correlation
##  Formula: ~x + y
##  Parameter estimate(s):
##     range
## 480.0567
## Degrees of freedom: 50 total; 42 residual
## Residual standard error: 8.628464
```

mod1_exp_nug

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra +     Picramnia.latifoli
a + Quassia.amara + Tabernaemontana.arborea +     Trattinnickia.aspera + Xylopia.macrantha
##   Data: dat
##   Log-restricted-likelihood: -139.9796
##
## Coefficients:
##          (Intercept)      Cordia.lasiocalyx       Hirtella.triandra
##           3.05012074             0.14266650             -0.00177162
##     Picramnia.latifolia          Quassia.amara Tabernaemontana.arborea
##           0.28633329             1.32636077              0.04075306
##    Trattinnickia.aspera     Xylopia.macrantha
##           1.81707519             0.40866983
##
## Correlation Structure: Exponential spatial correlation
##  Formula: ~x + y
##  Parameter estimate(s):
##       range        nugget
## 2.069876e+08 6.423682e-07
## Degrees of freedom: 50 total; 42 residual
## Residual standard error: 3486.914
```

mod1_rat_nug

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Cordia.lasiocalyx + Hirtella.triandra +     Picramnia.latifoli
a + Quassia.amara + Tabernaemontana.arborea +     Trattinnickia.aspera + Xylopia.macrantha
##   Data: dat
##   Log-restricted-likelihood: -140.5743
##
## Coefficients:
##           (Intercept)        Cordia.lasiocalyx        Hirtella.triandra
##            2.030692025              0.150809941              0.007669167
##      Picramnia.latifolia              Quassia.amara Tabernaemontana.arborea
##            0.250928914              1.504942337              0.032221941
##      Trattinnickia.aspera        Xylopia.macrantha
##            1.769893578              0.405806125
##
## Correlation Structure: Rational quadratic spatial correlation
##   Formula: ~x + y
##   Parameter estimate(s):
##        range        nugget
## 402.2077831    0.2194023
## Degrees of freedom: 50 total; 42 residual
## Residual standard error: 7.348772
```

Adding the error terms affected the coefficients for model 1. The best looking model was the orginial model too, based off the plots.

```
model2
```

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Cordia.lasiocalyx
##   Data: dat
##   Log-restricted-likelihood: -164.5623
##
## Coefficients:
##       (Intercept) Cordia.lasiocalyx
##         -2.782804          1.165220
##
## Degrees of freedom: 50 total; 48 residual
## Residual standard error: 6.675561
```

```
model2_exp
```

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Cordia.lasiocalyx
##   Data: dat
##   Log-restricted-likelihood: -151.3219
##
## Coefficients:
##        (Intercept) Cordia.lasiocalyx
##         12.8115337         0.1471799
##
## Correlation Structure: Exponential spatial correlation
##  Formula: ~x + y
##  Parameter estimate(s):
##      range
## 976086327
## Degrees of freedom: 50 total; 48 residual
## Residual standard error: 14500.58
```

mod2_exp_nug

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Cordia.lasiocalyx
##   Data: dat
##   Log-restricted-likelihood: -150.5274
##
## Coefficients:
##        (Intercept) Cordia.lasiocalyx
##         10.7064068         0.1730591
##
## Correlation Structure: Exponential spatial correlation
##  Formula: ~x + y
##  Parameter estimate(s):
##         range        nugget
## 3.065585e+08 2.017074e-07
## Degrees of freedom: 50 total; 48 residual
## Residual standard error: 6161.285
```

mod2_rat_nug

```
## Generalized least squares fit by REML
##   Model: Drypetes.standleyi ~ Cordia.lasiocalyx
##   Data: dat
##   Log-restricted-likelihood: -149.3295
##
## Coefficients:
##       (Intercept) Cordia.lasiocalyx
##        12.8791201         0.1046064
##
## Correlation Structure: Rational quadratic spatial correlation
##  Formula: ~x + y
##  Parameter estimate(s):
##        range         nugget
## 721.93442068     0.04545983
## Degrees of freedom: 50 total; 48 residual
## Residual standard error: 18.29516
```

The error terms changed the coefficients slightly with model 2. Based off the plots, the exponential model with a nugget was the best model 2.

```
anova(model1, model1_exp, mod1_exp_nug, mod1_rat_nug)
```

```
##                Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## model1            1  9 307.1163 322.7554 -144.5582
## model1_exp        2 10 301.6062 318.9829 -140.8031 1 vs 2 7.510175  0.0061
## mod1_exp_nug      3 11 301.9592 321.0735 -139.9796 2 vs 3 1.646998  0.1994
## mod1_rat_nug      4 11 303.1486 322.2630 -140.5743
```

```
anova(model2, model2_exp, mod2_exp_nug, mod2_rat_nug)
```

```
##                Model df      AIC      BIC    logLik   Test  L.Ratio p-value
## model2            1  3 335.1246 340.7382 -164.5623
## model2_exp        2  4 310.6438 318.1286 -151.3219 1 vs 2 26.48081  <.0001
## mod2_exp_nug      3  5 311.0547 320.4107 -150.5274 2 vs 3  1.58908  0.2075
## mod2_rat_nug      4  5 308.6589 318.0149 -149.3295
```

So the spatial error terms did not really improve the models fit for model 1. It improved the model when compared to the orginal, but the best model was the exponential one. I would assume this is because the model is looking at the effect of multiple species on the species of interest so the error term had less of an effect on the model.

The error term did improve the model for model 2. The best model was the rational quadratic model. The error terms improved model 2 more than they did in model 1. I would assume this is because there was only one species being examined in the model in so error term had more of an effect.

I'm not sure I'm understanding why the error terms influence the models correctly…