Supplementary Rmarkdown for Davis et al. ‘The integration of lidar and legacy datasets provides improved explanations for the spatial patterning of shell rings in the American Southeast’

Robert J. DiNapoli

3/1/2020

INTRODUCTION

This document provides a reproducible spatial analysis for shell ring features in Beaufort County, S.C.

LOAD PACKAGES

```r
library(spatstat)
library(maptools)
library(raster)
library(rgdal)
library(rgeos) library(sp)
library(MuMIn)
library(here)
```

LOAD WORKSPACE

```r
setwd(here())
```

LOAD DATA

```r
rings_shp <- readOGR(".", "rings_WGS84") #Load all shell rings data set
c_rings_shp <- readOGR(".", "confirmed_rings_WGS84") #Load confirmed shell rings data set
l_rings_shp <- readOGR(".", "LiDAR_rings_WGS") #read in shapefile b_win_shp <- readOGR(".", "Beaufort_Boundary_WGS84_17N") #load boundary window
elev <- mask(raster("DEM_fill_WGS_3m_x3.tif"),b_win_shp) #clip raster to be within survey area
elev[elev < 0] <- 0 #change negative values to 0
water_shp <- readOGR(".", "water_clip_WGS84") #Load water dataset
water_shp_clip <- gIntersection(water_shp, b_win_shp, byid=T) #clip water to boundary window
soils <- raster("soils_perm_rank.tif") #Load soils dataset
```
**CONVERT TO SPATSTAT FORMAT**

```r
b_win <- as.owin(b_win_shp)  # convert to window object
rings_pp <- ppp(rings_shp$POINT_X, rings_shp$POINT_Y, window=b_win)  # convert to pp object
c_rings_pp <- ppp(c_rings_shp$POINT_X, c_rings_shp$POINT_Y, window=b_win)  # convert to pp object
l_rings_pp <- ppp(l_rings_shp$POINT_X, l_rings_shp$POINT_Y, window=b_win)
elev <- as.im(elev)  # convert to pixel image
water <- as.owin(water_shp_clip)  # convert to window object
function water_dist <- distfun(water)  # convert to Euclidean distance function
soils <- as.im(soils)  # convert to pixel image
soils_quad <- as.tess(soils)  # convert to tessellation
```

---

**EXPLORATORY DATA ANALYSIS**

**Kernel density estimates**

Compute kernel density estimates for shell rings using likelihood cross-validation to select a smoothing bandwidth.

```r
KDE_c_rings <- density(c_rings_pp, bw.ppl)  # confirmed rings
KDE_l_rings <- density(l_rings_pp, bw.ppl)  # lidar rings
KDE_rings <- density(rings_pp, bw.ppl)  # all features
```

**Nearest neighbors**

Compute nearest neighbor distances between points.

```r
c_rings_nn <- nndist(c_rings_pp)  # confirmed rings
l_rings_nn <- nndist(l_rings_pp)  # lidar rings
rings_nn <- nndist(rings_pp)  # all features
```

**Pair correlation function**

Compute the pair-correlation function with 999 Monte Carlo simulations of CSR (p=0.002). Because point pattern is likely not isotropic and interaction occurs at large distances, the translation edge correction is used (Baddeley et al. 2015:218,528). This method also implements a distance divisor following Baddeley et al. (2015:229).

```r
rings_pcf <- envelope(rings_pp, fun=pcf, divisor="d", fit.n=T, correction="translation", nsim=999)
c_rings_pcf <- envelope(c_rings_pp, fun=pcf, divisor="d", fit.n=T, correction="translation", nsim=999)
l_rings_pcf <- envelope(l_rings_pp, fun=pcf, divisor="d", fit.n=T, correction="translation", nsim=999)
```
Dependence of point pattern on spatial covariates

This code chunk creates Figure 5

```r
par(mfrow=c(2,2)) par(mai=c(0,0,0.2,0))
plot(KDE_rings, main="Shell rings KDE", col=gray.colors(5, start = 0.3, end = 0.9, gamma = 2.2, rev = FALSE), riblab="Density") plot(c_rings_pp, pch=15, cex=1, col='red', add=T) plot(l_rings_pp, pch=16, cex=1, col='blue', add=T) par(mai=c(0,0,0.2,0.2))
plot(elev, main="Elevation", col=gray.colors(5, start = 0.3, end = 0.9, gamma = 2.2, rev = FALSE), riblab="MASL") plot(b_win, add=T) plot(c_rings_pp, pch=15, cex=1, col='red', add=T) plot(l_rings_pp, pch=16, cex=1, col='blue', add=T) par(mai=c(0,0,0.2,0))
plot(water_dist, main="Distance to water", col=gray.colors(8, start = 0.3, end = 0.9, gamma = 2.2, rev = FALSE), riblab="Meters") plot(b_win, add=T) plot(c_rings_pp, pch=15, cex=1, col='red', add=T) plot(l_rings_pp, pch=16, cex=1, col='blue', add=T) par(mai=c(0,0,0.2,0))
plot(soils_quad, main="Soil Permeability", col=gray.colors(4, start = 0.3, end = 0.9, gamma = 2.2, rev = FALSE), riblab="Class") plot(b_win, add=T) plot(c_rings_pp, pch=15, cex=1, col='red', add=T) plot(l_rings_pp, pch=16, cex=1, col='blue', add=T) par(mfrow=c(1,1)) dev.off()
```

Use nonparametric regression (rhohat) to examine the intensity relative to elevation and distance from water (See Baddeley et al. 2015:180-183 for details). As soils are factor valued, we simply calculated the count of shell rings within each soil permeability class.

```r
c_elev_rh <- rhohat(c_rings_pp, elev)#intensity as a function of elevation, with 95% confidence bands
c_water_rh <- rhohat(c_rings_pp, water_dist)#intensity as a function of water, with 95% confidence bands
c_soils_quad_count <- quadratcount(c_rings_pp, tess=soils_quad)#compute the number of shell rings within each soil permeability ranking 1_elev_rh <- rhohat(l_rings_pp, elev) 1_water_rh <- rhohat(l_rings_pp, water_dist) 1_soils_quad_count <- quadratcount(l_rings_pp, tess=soils_quad)
elev_rh <- rhohat(rings_pp, elev) water_rh <- rhohat(rings_pp, water_dist)
soils_quad_count <- quadratcount(rings_pp, tess=soils_quad)
```

This code chunk creates Figure 6.
Here we fit a series of point process models to the total shell rings point pattern to assess which variables and parameters best account for the patterns. We begin with a null model (ppm0), in this case that the underlying process is complete spatial randomness (CSR), aka a homogeneous Poisson process. We then fit a series of models that contain different combinations of the variables of interest (ppm1 through ppm7). The default edge correction for ppm is 'border', but here we use 'translation' given interaction distances and anisotropy.

```r
par(mfrow=c(5,3))
hist(c_rings_nn, xlab="Confirmed Rings", main="(a) Histogram of nearest neighbors")
mtext(side=3, line=-0.25, at=-0.07, adj=0, cex=0.9, "(a) Histogram of nearest neighbors")
hist(l_rings_nn, xlab="LiDAR Rings", main="(b) Pair correlation function")
plot(c_rings_pcf, main="", ylim=c(0,15), xlim=c(0,8000), legend=F, xlab="r (meters)")
mtext(side=3, line=1, at=-0.07, adj=0, cex=0.9, "(b) Pair correlation function")
plot(l_rings_pcf, main="", ylim=c(0,6), xlim=c(0,8000), legend=F, xlab="r (meters)")
plot(rings_pcf, main="", ylim=c(0,6), xlim=c(0,8000), legend=F, xlab="r (meters)")
plot(c_elev_rh, legend=F, xlab="Elevation (masl)", main="")
mtext(side=3, line=1, at=-0.07, adj=0, cex=0.9, "(c) Rings as a function of elevation")
plot(l_elev_rh, legend=F, xlab="Elevation (masl)", main="")
plot(elev_rh, legend=F, xlab="Elevation (masl)", main="")
plot(c_water_rh, legend=F, main="", xlab="Distance to water (m)", xlim=c(0,4000))
mtext(side=3, line=1, at=-0.07, adj=0, cex=0.9, "(d) Rings as a function of water")
plot(l_water_rh, legend=F, main="", xlab="Distance to water (m)", xlim=c(0,40000))
plot(water_rh, legend=F, main="", xlab="Distance to water (m)", xlim=c(0,4000))
barplot(c_soils_quad_count, ylab="Count")
barplot(c, c_soils_quad_count, ylab="Count")
barplot(c, soils_quad_count, ylab="Count")
par(mfrow=c(1,1)) dev.off()
```

**POINT PROCESS MODELING**

Here we fit a series of point process models to the total shell rings point pattern to assess which variables and parameters best account for the patterns. We begin with a null model (ppm0), in this case that the underlying process is complete spatial randomness (CSR), aka a homogeneous Poisson process. We then fit a series of models that contain different combinations of the variables of interest (ppm1 through ppm7). The default edge correction for ppm is 'border', but here we use 'translation' given interaction distances and anisotropy.
We then use AICc and BIC to compare each model.

```r
MS1_AIC <- model.sel(ppm0, ppm1, ppm2, ppm3, ppm4, ppm5, ppm6, ppm7, rank=AICc)
MS1_BIC <- model.sel(ppm0, ppm1, ppm2, ppm3, ppm4, ppm5, ppm6, ppm7, rank=BIC)
```

This code chunk yields the results in Table 3

### MS1_AIC

<table>
<thead>
<tr>
<th>sls_qud</th>
<th>trend</th>
<th>df</th>
<th>logLik</th>
<th>AICc</th>
<th>delta</th>
<th>weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>ppm2</td>
<td>e</td>
<td>2</td>
<td>-946.931</td>
<td>1898.1</td>
<td>0.00</td>
<td>0.635</td>
</tr>
<tr>
<td>ppm6</td>
<td>e+w_d</td>
<td>3</td>
<td>-946.854</td>
<td>1900.2</td>
<td>2.10</td>
<td>0.222</td>
</tr>
<tr>
<td>ppm4</td>
<td>s_q+e+w_d</td>
<td>5</td>
<td>-951.858</td>
<td>1910.7</td>
<td>3.57</td>
<td>0.107</td>
</tr>
<tr>
<td>ppm7</td>
<td>s_q+e+w_d</td>
<td>6</td>
<td>-956.060</td>
<td>1914.0</td>
<td>5.88</td>
<td>0.034</td>
</tr>
<tr>
<td>ppm1</td>
<td>s_q</td>
<td>4</td>
<td>-950.700</td>
<td>1910.3</td>
<td>12.15</td>
<td>0.001</td>
</tr>
<tr>
<td>ppm5</td>
<td>s_q+w_d</td>
<td>5</td>
<td>-950.305</td>
<td>1911.9</td>
<td>13.81</td>
<td>0.001</td>
</tr>
<tr>
<td>ppm3</td>
<td>w_d</td>
<td>2</td>
<td>-959.384</td>
<td>1923.0</td>
<td>24.91</td>
<td>0.000</td>
</tr>
<tr>
<td>ppm0</td>
<td></td>
<td>1</td>
<td>-961.858</td>
<td>1925.8</td>
<td>27.69</td>
<td>0.000</td>
</tr>
</tbody>
</table>

Abbreviations:  
- trend: = '~1', e = '~elev', e+w_d = '~elev+water_dist',  
- s_q = '~soils_quad', s_q+e = '~soils_quad+elev',  
- s_q+e+w_d = '~soils_quad+elev+water_dist',  
- s_q+w_d = '~soils_quad+water_dist', w_d = '~water_dist'

### MS1_BIC

<table>
<thead>
<tr>
<th>sls_qud</th>
<th>trend</th>
<th>df</th>
<th>logLik</th>
<th>BIC</th>
<th>delta</th>
<th>weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>ppm2</td>
<td>e</td>
<td>2</td>
<td>-946.931</td>
<td>1901.8</td>
<td>0.00</td>
<td>0.856</td>
</tr>
<tr>
<td>ppm6</td>
<td>e+w_d</td>
<td>3</td>
<td>-946.854</td>
<td>1905.6</td>
<td>3.80</td>
<td>0.128</td>
</tr>
<tr>
<td>ppm4</td>
<td>s_q+e+w_d</td>
<td>5</td>
<td>-951.858</td>
<td>1910.1</td>
<td>8.36</td>
<td>0.013</td>
</tr>
<tr>
<td>ppm7</td>
<td>s_q+e+w_d</td>
<td>6</td>
<td>-956.060</td>
<td>1913.8</td>
<td>12.06</td>
<td>0.002</td>
</tr>
<tr>
<td>ppm1</td>
<td>s_q</td>
<td>4</td>
<td>-950.700</td>
<td>1917.2</td>
<td>15.44</td>
<td>0.000</td>
</tr>
<tr>
<td>ppm5</td>
<td>s_q+w_d</td>
<td>5</td>
<td>-950.305</td>
<td>1920.4</td>
<td>18.60</td>
<td>0.000</td>
</tr>
<tr>
<td>ppm3</td>
<td>w_d</td>
<td>2</td>
<td>-959.384</td>
<td>1926.7</td>
<td>24.91</td>
<td>0.000</td>
</tr>
<tr>
<td>ppm0</td>
<td></td>
<td>1</td>
<td>-961.858</td>
<td>1927.7</td>
<td>25.90</td>
<td>0.000</td>
</tr>
</tbody>
</table>

Abbreviations:  
- trend: = '~1', e = '~elev', e+w_d = '~elev+water_dist',
Both model selection criteria suggest that the inhomogeneous model ppm2 that models shell rings as a log-linear function of elevation fits best. To assess the fit between this model and the data, in particular to check for a second-order interaction component, we compare the empirical pattern to expectations from the model by generating 99 simulated realizations of the residual K- and G- functions.

```
K_sim1 <- envelope(ppm2, Kres, nsim=99, fix.n=T, correction="translation")
G_sim1 <- envelope(ppm2, Gres, nsim=99, fix.n=T, correction="best")
```

This code chunk creates Figure 7

```
par(mfrow=c(1,2)) plot(K_sim1, xlim=c(0,4000), main="", legend=F) plot(G_sim1, xlim=c(0,4000), main="",legend=F) par(mfrow=c(1,1))
```

Both tests indicate that the empirical point pattern is more clustered than is accounted for by model ppm2. We then add an interaction term to the model to account for interpoint clustering. Here we use a Gibbs Area Interaction process with irregular parameter r=2000 based on nearest neighbor distances and the pair correlation function. The first model (ppm8) only includes the clustering parameter to test the hypothesis that the point pattern is simply explained by inter-point clustering and not elevation. The second model (ppm9) includes Area Interaction and elevation.

```
ppm8 <- ppm(rings_pp, ~1, AreaInter(2000))
ppm9 <- ppm(rings_pp, ~elev, AreaInter(2000))
```

We then use AICc and BIC to select the best-fitting model.

```
MS2_AIC <- model.sel(ppm2, ppm8, ppm9, rank=AICc)
MS2_BIC <- model.sel(ppm2, ppm8, ppm9, rank=BIC)
```

This code chunk yields the results in Table 4. Both model selection criteria indicate that the model with Area Interaction and elevation (ppm9) fits best.

```
## Model selection table
##   trend correction interaction df logLik AICc delta weight
## ppm9 elev            AreIntr(2000) 3 -676.613 1359.7  0.00  0.969
## ppm8                  AreIntr(2000) 2 -681.170 1366.6  6.86  0.031
## ppm2 elev translatin                2 -946.931 1898.1 538.38  0.000
```

Abbreviations:
Models ranked by AICc(x)

<table>
<thead>
<tr>
<th>Model</th>
<th>trend</th>
<th>correction</th>
<th>interaction</th>
<th>df</th>
<th>logLik</th>
<th>BIC</th>
<th>delta</th>
<th>weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>ppm9</td>
<td>elev</td>
<td></td>
<td>AreIntr(2000)</td>
<td>3</td>
<td>-676.613</td>
<td>1365.1</td>
<td>0.00</td>
<td>0.93</td>
</tr>
<tr>
<td>ppm8</td>
<td></td>
<td></td>
<td>AreIntr(2000)</td>
<td>2</td>
<td>-681.170</td>
<td>1370.2</td>
<td>5.16</td>
<td>0.07</td>
</tr>
<tr>
<td>ppm2</td>
<td>elev</td>
<td>translatin</td>
<td></td>
<td>2</td>
<td>-946.931</td>
<td>1901.8</td>
<td>536.68</td>
<td>0.00</td>
</tr>
</tbody>
</table>

This code chunk yields the results in Table 5 - the parameter estimates for ppm9 and standard errors with 95% confidence intervals.

```r
coef(summary(ppm9))
```

<table>
<thead>
<tr>
<th></th>
<th>Estimate</th>
<th>S.E.</th>
<th>CI95.lo</th>
<th>CI95.hi</th>
<th>Ztest</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>-18.56894494</td>
<td>0.32812007</td>
<td>-19.21208845</td>
<td>-17.92588143</td>
<td>***</td>
</tr>
<tr>
<td>elev</td>
<td>0.04497521</td>
<td>0.01274398</td>
<td>0.01999747</td>
<td>0.06995294</td>
<td>***</td>
</tr>
</tbody>
</table>

Interaction 2.03385337 0.54333298 0.96894029 3.09876645 ***

Zval  
(Intercept) -56.592043
elev 3.529134
Interaction 3.743291

To assess the fit between the interaction component of this model and the data we generate 99 simulated realizations of the residual K- and G- functions. We also compute the lurking variable and partial-residual plots to assess any deviations between the empirical intensity of shell rings and their fitted intensity as a function of elevation. The lurking variable plot shows the relationship between the residuals and elevation, and the partial residual plot shows the relationship between the estimated intensity as a function of elevation and a smoothed estimate of its empirical effect.

```r
K_sim2 <- envelope(ppm9, Kres, nsim=99, fix.n=T, correction="translation")
G_sim2 <- envelope(ppm9, Gres, nsim=99, fix.n=T, correction="best")
lurk1 <- lurking(ppm9, elev, type="Pearson", cumulative=F, envelope=T)
par_res <- parres(ppm9, "elev")
```

This code chunk creates Figure 8.

```r
par(mfrow=c(2,2))
plot(K_sim2, xlim=c(0,4000), legend=F, main="")
plot(G_sim2, xlim=c(0,4000), legend=F, main="")
```
Point process modeling of confirmed shell rings

Here we conduct the same analysis as above but on confirmed (i.e., ground-truthed) shell rings. Here we fit a series of point process models to the confirmed shell rings point pattern to assess which variables and parameters best account for the pattern. We begin with a null model (c_ppm0), in this case that the underlying process is complete spatial randomness (CSR), aka a homogeneous Poisson process. We then fit a series of models that contain different combinations of the variables of interest (c_ppm1 through c_ppm7). The default edge correction for ppm is ‘border’, but here we use ‘translation’ given interaction distances and anisotropy.

```r
c_ppm0 <- ppm(c_rings_pp, ~1, correction="translation")
c_ppm1 <- ppm(c_rings_pp, ~soils_quad, correction="translation")
c_ppm2 <- ppm(c_rings_pp, ~elev, correction="translation")
c_ppm3 <- ppm(c_rings_pp, ~water_dist, correction="translation")
c_ppm4 <- ppm(c_rings_pp, ~soils_quad+elev, correction="translation")
c_ppm5 <- ppm(c_rings_pp, ~soils_quad+water_dist, correction="translation")
c_ppm6 <- ppm(c_rings_pp, ~elev+water_dist, correction="translation")
c_ppm7 <- ppm(c_rings_pp, ~soils_quad+elev+water_dist, correction="translation")
```

We then use AICc and BIC to compare each model.

```r
c_MS1_AIC <- model.sel(c_ppm0, c_ppm1, c_ppm2, c_ppm3, c_ppm4, c_ppm5, c_ppm6, c_ppm7, rank=AICc)
c_MS1_BIC <- model.sel(c_ppm0, c_ppm1, c_ppm2, c_ppm3, c_ppm4, c_ppm5, c_ppm6, c_ppm7, rank=BIC)
```

Print the model selection results.

```r
c_MS1_AIC
## Model selection table
##        sls_qud     trend df   logLik  AICc delta weight
## c_ppm0                    1 -201.459 405.4  0.00  0.586
## c_ppm2                 e  2 -201.027 407.8  2.35  0.181
## c_ppm3               w_d  2 -201.187 408.1  2.67  0.154
## c_ppm6             e+w_d  3 -199.748 409.5  4.08  0.076
## c_ppm1           s_q  4 -200.381 416.8 11.34  0.002
## c_ppm5       +   s_q+w_d  5 -199.382 423.8 18.34  0.000
## c_ppm4         +     s_q+e  5 -200.377 425.8 20.33  0.000
## c_ppm7       + s_q+e+w_d  6 -198.959 437.9 32.50  0.000
```

Abbreviations:
```
## trend:  = '~1', e = '~elev', e+w_d = '~elev+water_dist',
## s_q = '~soils_quad', s_q+e = '~soils_quad+elev',
##```

## Model selection table
##        sls_qud     trend df   logLik  AICc delta weight
## c_ppm0                    1 -201.459 405.4  0.00  0.586
## c_ppm2                 e  2 -201.027 407.8  2.35  0.181
## c_ppm3               w_d  2 -201.187 408.1  2.67  0.154
## c_ppm6             e+w_d  3 -199.748 409.5  4.08  0.076
## c_ppm1           s_q  4 -200.381 416.8 11.34  0.002
## c_ppm5       +   s_q+w_d  5 -199.382 423.8 18.34  0.000
## c_ppm4         +     s_q+e  5 -200.377 425.8 20.33  0.000
## c_ppm7       + s_q+e+w_d  6 -198.959 437.9 32.50  0.000
```
Both model selection criteria suggest that the homogeneous Poisson model ppm0 that models the confirmed shell rings as complete spatial randomness (CSR) fits best. However, in both cases the results suggest that models that include elevation have a relatively high ranking, similar to the analysis for all shell rings above. To assess the fit between c_ppm0 and the data, in particular to check for a second-order interaction component, we compare the empirical pattern to expectations from the model by generating 99 simulated realizations of the residual K-function.

c_K_sim1 <- envelope(c_ppm0, Kres, nsim=99, fix.n=T, correction="translation")

Plot the residual K-function.

plot(c_K_sim1, xlim=c(0,4000), main="", legend=F)
The test indicates that the empirical point pattern is more clustered than is accounted for by model \( c_{ppm0} \). These results are similar to the analysis on all shell rings presented above that show shell rings exhibit a clustered pattern. We then add an interaction term to the model to account for interpoint clustering (\( c_{ppm8} \)). In addition, we also run a model with interpoint clustering and elevation (\( c_{ppm9} \)). Here we use a Gibbs Area Interaction process with irregular parameter \( r=2000 \). \( c_{ppm8} \) only includes the clustering parameter to test the hypothesis that the point pattern is distributed as a series of first-order random clusters, and \( c_{ppm9} \) evaluates whether the confirmed rings are similar to the total shell rings dataset in being clustered and related to elevation.

\[
\begin{align*}
c_{ppm8} &< ppm(c_{rings_pp}, \sim 1, \text{AreaInter}(2000)) \ c_{ppm9} \\
&< ppm(c_{rings_pp}, \sim \text{elev}, \text{AreaInter}(2000))
\end{align*}
\]

We then use \( \text{AICc} \) and \( \text{BIC} \) to compare the Area Interaction models (\( c_{ppm8}, c_{ppm9} \)) with the best-fitting Poisson model (\( c_{ppm0} \)).

\[
\begin{align*}
c_{MS2\_AIC} &< \text{model.sel}(c_{ppm0}, c_{ppm8}, c_{ppm9}, \text{rank=}\text{AICc}) \ c_{MS2\_BIC} \\
&< \text{model.sel}(c_{ppm0}, c_{ppm8}, c_{ppm9}, \text{rank=}\text{BIC})
\end{align*}
\]

Print model selection results. Both model selection criteria indicate that the Area Interaction model (\( c_{ppm8} \)) fits best. Results suggest that a model with Area Interaction and elevation (\( c_{ppm9} \)) fits better than a model based on complete spatial randomness (\( c_{ppm0} \)).
## Model selection table

<table>
<thead>
<tr>
<th>Model</th>
<th>Trend correction</th>
<th>Interaction</th>
<th>df</th>
<th>logLik</th>
<th>AICc</th>
<th>delta</th>
<th>weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>c_ppm8</td>
<td>AreIntr(2000)</td>
<td></td>
<td>2</td>
<td>-153.625</td>
<td>313.0</td>
<td>0.00</td>
<td>0.824</td>
</tr>
<tr>
<td>c_ppm9</td>
<td>elev</td>
<td>AreIntr(2000)</td>
<td>3</td>
<td>-153.026</td>
<td>316.1</td>
<td>3.09</td>
<td>0.176</td>
</tr>
<tr>
<td>c_ppm0</td>
<td>translatin</td>
<td></td>
<td>1</td>
<td>-201.459</td>
<td>405.4</td>
<td>92.46</td>
<td>0.000</td>
</tr>
</tbody>
</table>

### Abbreviations:
- **trend**: `~1`, **elev** = `~elev`
- **correction**: translatin = 'translation'
- **interaction**: AreIntr(2000) = 'AreaInter(2000)'

Models ranked by AICc(x)

## Model selection table

<table>
<thead>
<tr>
<th>Model</th>
<th>Trend correction</th>
<th>Interaction</th>
<th>df</th>
<th>logLik</th>
<th>BIC</th>
<th>delta</th>
<th>weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>c_ppm8</td>
<td>AreIntr(2000)</td>
<td></td>
<td>2</td>
<td>-153.625</td>
<td>311.9</td>
<td>0.00</td>
<td>0.635</td>
</tr>
<tr>
<td>c_ppm9</td>
<td>elev</td>
<td>AreIntr(2000)</td>
<td>3</td>
<td>-153.026</td>
<td>313.0</td>
<td>1.11</td>
<td>0.365</td>
</tr>
<tr>
<td>c_ppm0</td>
<td>translatin</td>
<td></td>
<td>1</td>
<td>-201.459</td>
<td>405.2</td>
<td>93.37</td>
<td>0.000</td>
</tr>
</tbody>
</table>

### Abbreviations:
- **trend**: `~1`, **elev** = `~elev`
- **correction**: translatin = 'translation'
- **interaction**: AreIntr(2000) = 'AreaInter(2000)'

Models ranked by BIC(x)

Print the parameter estimates for c_ppm8 and standard errors with 95% confidence intervals.

```r
cppm8 <- c_ppm8
dv <- summary(cppm8)
dv
```

<table>
<thead>
<tr>
<th>Term</th>
<th>Estimate</th>
<th>S.E.</th>
<th>CI95.lo</th>
<th>CI95.hi</th>
<th>Ztest</th>
<th>Zval</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>-19.49867</td>
<td>0.4526883</td>
<td>-20.385820</td>
<td>-18.611314</td>
<td>***</td>
<td>-43.072828</td>
</tr>
<tr>
<td>Interaction</td>
<td>4.187808</td>
<td>0.9439384</td>
<td>2.337723</td>
<td>6.037893</td>
<td>***</td>
<td>4.436527</td>
</tr>
</tbody>
</table>

To assess the fit between the interaction component of this model and the data we generate 99 simulated realizations of the residual K-function.

```r
c_K_sim2 <- envelope(cppm8, Kres, nsim=99, fix.n=T, correction="translation", global=F)
```

Plot residual K-function results. Results indicate a good fit between the model (c_ppm8) and the data, suggesting that the confirmed rings are best accounted for as a series of randomly located clusters.

```r
plot(c_K_sim2, xlim=c(0,4000), main="", legend=F)
```
Point process modeling of LiDAR rings

The following code executes the same analyses as above but only for those features identified as 'highly likely' of being shell rings by OBIA of the LiDAR dataset. The results are essentially identical to that of the total dataset.

Run inhomogeneous Poisson models.

```r
l_ppm0 <- ppm(l_rings_pp, ~1, correction="translation")
l_ppm1 <- ppm(l_rings_pp, ~soils_quad, correction="translation")
l_ppm2 <- ppm(l_rings_pp, ~elev, correction="translation")
l_ppm3 <- ppm(l_rings_pp, ~water_dist, correction="translation")
l_ppm4 <- ppm(l_rings_pp, ~soils_quad+elev, correction="translation")
l_ppm5 <- ppm(l_rings_pp, ~soils_quad+water_dist, correction="translation")
l_ppm6 <- ppm(l_rings_pp, ~elev+water_dist, correction="translation")
l_ppm7 <- ppm(l_rings_pp, ~soils_quad+elev+water_dist, correction="translation")
```

Execute model selection.

```r
l_MS1_AIC <- model.sel(l_ppm0, l_ppm1, l_ppm2, l_ppm3, l_ppm4, l_ppm5, l_ppm6, l_ppm7, rank=AICc)
l_MS1_BIC <- model.sel(l_ppm0, l_ppm1, l_ppm2, l_ppm3, l_ppm4, l_ppm5,
```

![Graph showing the point process modeling of LiDAR rings](image)
## Model selection table

<table>
<thead>
<tr>
<th>Model</th>
<th>sls_qud</th>
<th>trend</th>
<th>df</th>
<th>logLik</th>
<th>AICc</th>
<th>delta</th>
<th>weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>l_ppm2</td>
<td>e</td>
<td>~1</td>
<td>2</td>
<td>-770.214</td>
<td>1544.7</td>
<td>0.00</td>
<td>0.696</td>
</tr>
<tr>
<td>l_ppm6</td>
<td>e+w_d</td>
<td>~elev</td>
<td>3</td>
<td>-770.202</td>
<td>1547.0</td>
<td>2.30</td>
<td>0.220</td>
</tr>
<tr>
<td>l_ppm4</td>
<td>+ s_q+e</td>
<td>~soils_quad+elev</td>
<td>5</td>
<td>-768.898</td>
<td>1549.5</td>
<td>4.73</td>
<td>0.066</td>
</tr>
<tr>
<td>l_ppm7</td>
<td>+ s_q+e+w_d</td>
<td>~soils_quad+elev+water_dist</td>
<td>6</td>
<td>-768.893</td>
<td>1552.2</td>
<td>7.45</td>
<td>0.017</td>
</tr>
<tr>
<td>l_ppm1</td>
<td>+ s_q</td>
<td>~soils_quad</td>
<td>4</td>
<td>-775.271</td>
<td>1559.6</td>
<td>14.89</td>
<td>0.000</td>
</tr>
<tr>
<td>l_ppm5</td>
<td>+ s_q+w_d</td>
<td>~soils_quad+water_dist</td>
<td>5</td>
<td>-774.201</td>
<td>1560.1</td>
<td>15.33</td>
<td>0.000</td>
</tr>
<tr>
<td>l_ppm3</td>
<td>w_d</td>
<td>~water_dist</td>
<td>2</td>
<td>-782.319</td>
<td>1568.9</td>
<td>24.21</td>
<td>0.000</td>
</tr>
<tr>
<td>l_ppm0</td>
<td>~1</td>
<td>~1</td>
<td>1</td>
<td>-785.855</td>
<td>1573.8</td>
<td>29.07</td>
<td>0.000</td>
</tr>
</tbody>
</table>

Abbreviations:
- trend: = '~1', e = '~elev', e+w_d = '~elev+water_dist',
- s_q = '~soils_quad', s_q+e = '~soils_quad+elev',
- s_q+e+w_d = '~soils_quad+elev+water_dist',
- s_q+w_d = '~soils_quad+water_dist', w_d = '~water_dist'

## Model selection table

<table>
<thead>
<tr>
<th>Model</th>
<th>sls_qud</th>
<th>trend</th>
<th>df</th>
<th>logLik</th>
<th>BIC</th>
<th>delta</th>
<th>weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>l_ppm2</td>
<td>e</td>
<td>~1</td>
<td>2</td>
<td>-770.214</td>
<td>1547.9</td>
<td>0.00</td>
<td>0.853</td>
</tr>
<tr>
<td>l_ppm6</td>
<td>e+w_d</td>
<td>~elev</td>
<td>3</td>
<td>-770.202</td>
<td>1551.6</td>
<td>3.71</td>
<td>0.133</td>
</tr>
<tr>
<td>l_ppm4</td>
<td>+ s_q+e</td>
<td>~soils_quad+elev</td>
<td>5</td>
<td>-768.898</td>
<td>1556.5</td>
<td>8.58</td>
<td>0.012</td>
</tr>
<tr>
<td>l_ppm7</td>
<td>+ s_q+e+w_d</td>
<td>~soils_quad+elev+water_dist</td>
<td>6</td>
<td>-768.893</td>
<td>1560.2</td>
<td>12.31</td>
<td>0.002</td>
</tr>
<tr>
<td>l_ppm1</td>
<td>+ s_q</td>
<td>~soils_quad</td>
<td>4</td>
<td>-775.271</td>
<td>1565.5</td>
<td>17.59</td>
<td>0.000</td>
</tr>
<tr>
<td>l_ppm5</td>
<td>+ s_q+w_d</td>
<td>~soils_quad+water_dist</td>
<td>5</td>
<td>-774.201</td>
<td>1567.1</td>
<td>19.19</td>
<td>0.000</td>
</tr>
<tr>
<td>l_ppm3</td>
<td>w_d</td>
<td>~water_dist</td>
<td>2</td>
<td>-782.319</td>
<td>1572.1</td>
<td>24.21</td>
<td>0.000</td>
</tr>
<tr>
<td>l_ppm0</td>
<td>~1</td>
<td>~1</td>
<td>1</td>
<td>-785.855</td>
<td>1575.4</td>
<td>27.54</td>
<td>0.000</td>
</tr>
</tbody>
</table>

Abbreviations:
- trend: = '~1', e = '~elev', e+w_d = '~elev+water_dist',
- s_q = '~soils_quad', s_q+e = '~soils_quad+elev',
- s_q+e+w_d = '~soils_quad+elev+water_dist',
- s_q+w_d = '~soils_quad+water_dist', w_d = '~water_dist'

Models ranked by AICc(x) l_MS1_AIC

### Run and plot residual K- and G-functions.

```r
l_K_sim1 <- envelope(l_ppm2, Kres, nsim=99, fix.n=T, correction="translation")

l_G_sim1 <- envelope(l_ppm2, Gres, nsim=99, fix.n=T, correction="best")

par(mfrow=c(1,2)) plot(l_K_sim1, xlab='', main='', legend=F)
plot(l_G_sim1, xlab='', xlab='', main='', legend=F)
```
Run Area Interaction models.

\[
\begin{align*}
l_{ppm8} & \leftarrow ppm(l\text{\_rings\_pp, } \sim 1, \text{AreaInter}(2000)) \quad l_{ppm9} \\
& \leftarrow ppm(l\text{\_rings\_pp, } \sim \text{elev, AreaInter}(2000))
\end{align*}
\]

Run model selection for Area Interaction models

\[
\begin{align*}
l_{MS2\_AIC} & \leftarrow \text{model.sel}(l_{ppm0}, l_{ppm8}, l_{ppm9}, \text{rank=AICc}) \\
l_{MS2\_BIC} & \leftarrow \text{model.sel}(l_{ppm0}, l_{ppm8}, l_{ppm9}, \text{rank=BIC})
\end{align*}
\]

\#
## Model selection table
## trend correction interaction df logLik AICc delta weight
## l_ppm9 elev AreIntr(2000) 3 540.699 1088.0 0.00 0.993
## l_ppm8 AreIntr(2000) 2 546.747 1097.8 9.77 0.007
## l_ppm0 translatin 1 785.855 1573.8 485.78 0.000
## Abbreviations:
## trend: = '1', elev = 'elev'
## correction: translatin = 'translation'
## interaction: AreIntr(2000) = 'AreaInter(2000)'
## Models ranked by AICc(x) l_MS2_BIC
Print the parameter estimates for `l_ppm9` and standard errors with 95% confidence intervals.

```
coef(summary(l_ppm9))
```

```
#                  Estimate       S.E.      CI95.lo      CI95.hi Ztest
# (Intercept) -18.75437448 0.34197235 -19.42462797 -18.08412100 ***
# elev          0.05952516 0.01969005   0.02093338   0.09811694    **
# Interaction   1.53361726 0.94050911   0.30974672   3.37698124 ##

Zval
# (Intercept) -54.841786
# elev          3.023109
# Interaction   1.630625
```

Plot residual K-function results.

```
l_K_sim2 <- envelope(l_ppm9, Kres, nsim=99, fix.n=T, correction="translation", global=F)
```

```
## Generating 99 simulated realisations of fitted Gibbs model with fixed number of points ...
## 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99.
## Done. plot(l_K_sim2, xlim=c(0,4000), main="", legend=F)
```