DATA589_Project

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1. Introduction

1.1 Ascomycota as a phylum of the kingdom Fungi

Ascomycota is a phylum (or category) of the kingdom Fungi. In fact, it is the largest phylum of Fungi. Its members are also commonly known as sac fungi.

Among many other Fungi phylum, Ascomycota is of particularly useful to humans. As it can be used as sources of medicinally important compounds (e.g. antibiotics), and fermentation for various food products such as alcoholic beverages, bread and cheese. One famous example of its members is Penicillium, which has been widely used and utilized in natural environment, in food spoilage, and food and drug production.

The Ascomycota also plays an important role in most land-based ecosystems, because they are efficient decomposers, breaking down organic materials (e.g. dead leaves and animals) and completing the nutrient cycle.

1.2 Data Source

Data is downloaded from GBIF with the download link below : URL: https://www.gbif.org/occurrence/download/0165170-230224095556074

1.3 Research Questions

Due to the potential medically and various practical values of Ascomycota, we would be interested in exploring and investigating its growth distribution, patterns and population density in terms of spatial analysis.

During this project, we hope to answer the following questions :

- Are there any spatial patterns?
- Is the distribution homogeneous and inhomogeneous?
- Are there any significant correlation with the available covariate data such as Elevation, Forest, and Distance to Water?
- Are there evidence to support any occurrence clustering, independence or avoidance? Are these affected by the homogeneity and inhomogeneity assumption of the data?
- What are the possible prediction models? Does complicated model outperform simple model? Is the complicated model worth it?
- Can higher-degree polynomial model further improve the prediction model?

1.4 References

- https://www.britannica.com/science/fungus/Outline-of-classification-of-fungi
- https://en.wikipedia.org/wiki/Penicillium
- https://en.wikipedia.org/wiki/Ascomycota

2. Methods and Results

2.1 Dataset Variables and Selection

A total of about 69,000 occurrences records are available in BC, which are consolidated from a total of 109 datasets. However, the following three major parties constitute about 85% of the total occurrences records :

- UBC Herbarium - Licen Collection
- iNaturalist Research-grade Observations
- Assembly and activity of microbial communities in the Pacific temperate rainforest

```
# install.packages("rgbif")
library(rgbif)
#?rgbif

species <- c("Ascomycota")

# Get number of occurrence records from rgbif
#occ_count(scientificName = species) #16069587 in the dataset

#Filter Ascomycota data to only in BC
asc_count <- occ_count(scientificName = species,
                           hasCoordinate = TRUE,
                           country = "CA",
                           stateProvince = "British Columbia")

asc_bc_data <- occ_data(scientificName = species,
                            hasCoordinate = TRUE,
                            country = "CA",
                            stateProvince = "British Columbia") #* 102 illegal points stored in attr(,"r

# class(asc_bc_data) #gbif_data
asc_bc_data <- asc_bc_data$data #gbif_data to data.frame
## head(asc_bc_data) #contain "Ascomycota" data only in BC
```

2.1.1 Data Records

Firstly, screen through some sample records of the dataset to see what information it contains and which attributes would and would not be useful and valuable in our analysis.

A total of 75 data columnns are available. These columns can be broadly divided into the following three main categories :

- Scientific Classification and Taxonomy Details : Scientific Name, Hierarchy of Biological classification and taxonomic ranks, etc
- Point and Location Details : Continent, State/Province, Coordinates, Coordinates Uncertainty Meters, etc
- Data Collection Details : Collector, Date and Timestamp

2.1.2 Data Cleaning

As the dataset contains too much information, including many detailed timestamps, internal key/identifiers information and dataset/records identifiers which should not be valuable in our analysis and complicate our

subsequent analysis, we have performed preliminary cleaning procedure and performed attributes selection, in order to only retain those few potentially useful attributes, speeding up our subsequent analysis and making it more focused. The cleaned list is shown below.

```
# View(data.frame(names(asc_bc_data)))
cleaned_asc_bc <- asc_bc_data[ , c("decimalLongitude", "decimalLatitude", "order", "family", "genus", "s
                                   "year", "month", "day", "eventDate", "occurrenceStatus", "class", "cou
                                   "verbatimEventDate", "collectionCode", "gbifID", "verbatimLocality"
                                   )]
```

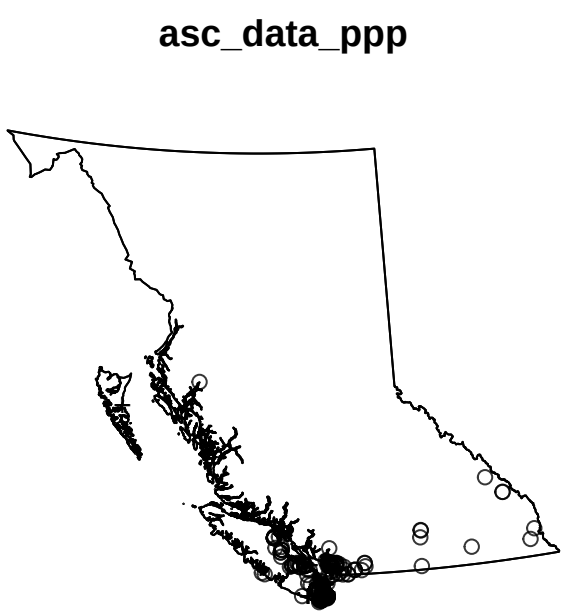
```
names(cleaned_asc_bc)
```

```
##  [1] "decimalLongitude"              "decimalLatitude"
##  [3] "order"                         "family"
##  [5] "genus"                         "species"
##  [7] "genericName"                   "specificEpithet"
##  [9] "coordinateUncertaintyInMeters" "stateProvince"
## [11] "year"                          "month"
## [13] "day"                           "eventDate"
## [15] "occurrenceStatus"              "class"
## [17] "countryCode"                   "country"
## [19] "verbatimLocality"              "taxonID"
## [21] "catalogNumber"                 "institutionCode"
## [23] "eventTime"                     "verbatimEventDate"
## [25] "collectionCode"                "gbifID"
## [27] "verbatimLocality.1"
```

2.1.3 Spatial Dataset Object Conversion and Preparation

As the current format of the fungi data is not in a PPP class object, to facilitate subsequent analysis and plots, we would firstly convert it to the PPP, which would make subsequent plotting and analysis library much more accessible.

```
plot(asc_data_ppp)
```



2.2 Statistical Packages

The following packages are used to perform the analysis :

- rgbif : allow searching and retrieving data from GBIF, access various dataset metadata, species names, and occurences details
- sp, rgdal : process, manipulate and transform the data source longitude and latitude information
- spstat : provides many statistical tests, analysis and plots
- maptools : provides utilities to handle and analyze spatial objects
- Others supporting libraries include kdensity and splines

2.3 Analytical Workflow

The report will start with some basic Exploratory Data Analysis and basic data plottings to have an initial understanding of the overall data points pattern.

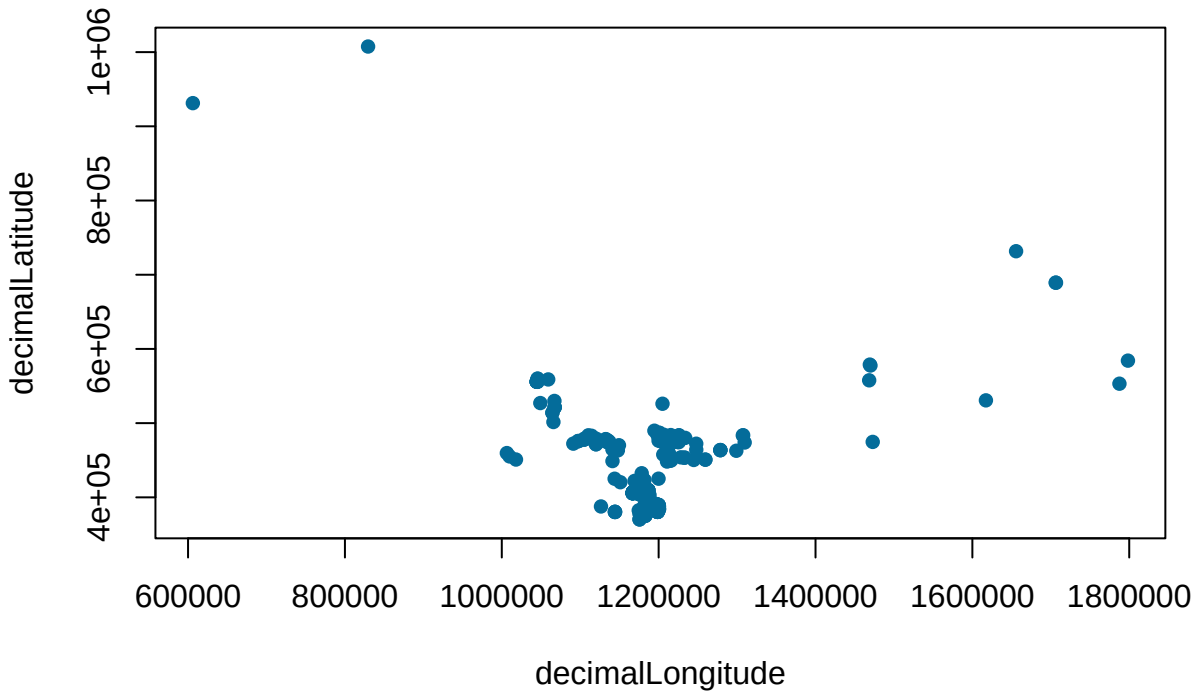
We will then conduct First Moment Analysis which will include homogeneity analysis and covariates study on some variables. Afterwards, we will perform Second Moment analysis where popular tools such as K-function and Pair Correlation Function will be deployed to investigate any clustering.

The report will then conduct model fitting and selection with both lower and higher polynomial variable terms and evaluate the fitness and its costs with AIC values. The report is concluded by a final model validation process for the resulted model to assess the wellness of the model fitting.

2.3.1 EDA : Initial Coordinates Plotting

First, we have a coordinate plot to observe the general pattern in terms of the coordinates.

```
#Visualise the data
plot(decimalLatitude ~ decimalLongitude,
     pch = 16,
     col = "#046C9A",
     data = cleaned_asc_bc)
```



From the initial coordinate plot, we have identified the following very preliminary observation :

- Points clustering is highly likely as a large group of data points is spotted at the decimal Longitude between 1000K and 1300K and Latitude between 4e+5 and 5e+5.

- Therefore is only a single major and significant large clustering only. Although there are some other scattered points observed near the Longitude range 1500K-1800K, they are simply incomparable to the large clustering.

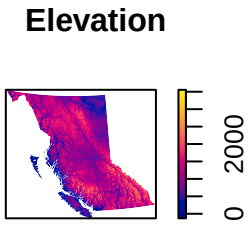
2.3.2 EDA : BC Windows and Covariates Data Walkthough

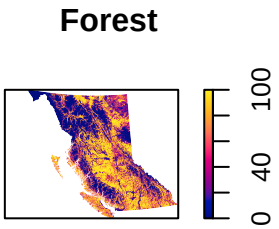
Let's see what the BC_Covariates.Rda file provide us which may help us to identify and choose appropriate fields to be used in the covariates analysis in the later part of this analysis. It should contain the information on the BC province :

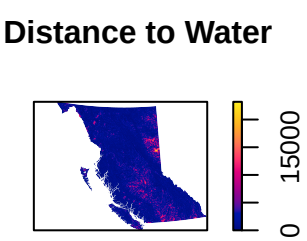
- Windows
- Elevation
- Forest
- Dist Water

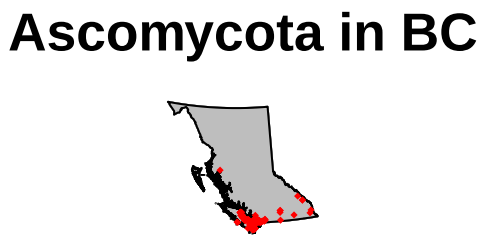
```
#plot(BC_win, pch = 16, cols = "red", main = "BC windows data")
```

```
par(mfrow=c(2,2))

#Elevation
plot(BC$Elevation, main = "Elevation")
#Forest
plot(BC$Forest, main = "Forest")
#Dist_Water
plot(BC$Dist_Water, main = "Distance to Water")
plot(asc_data_ppp,
     which.marks = "species", # Which mark to use
     col = "grey", #The colour of the window
     cols = 'red', #The colours of the points
     cex = 0.6,
     pch = 18, # The plotting symbol
     main = "Ascomycota in BC", # The title
     par(bg="grey40", cex.main = 2),
     cex = 0.6,
     legend = T) # Turn off the legend depending on needs
```









Next, We try to pick Elevation to divide its values into 5 levels, and see if there are any patterns for the distribution of the fungi points in the different elevation level.

```
cut <- cut(BC$Elevation,5,
labels = c("low","low-medium","medium","medium-high","high"))
table(cut[asc_data_ppp]) #most in low elevation
```

```
##
##         low  low-medium      medium medium-high        high
##         315           8           1           0           0
```

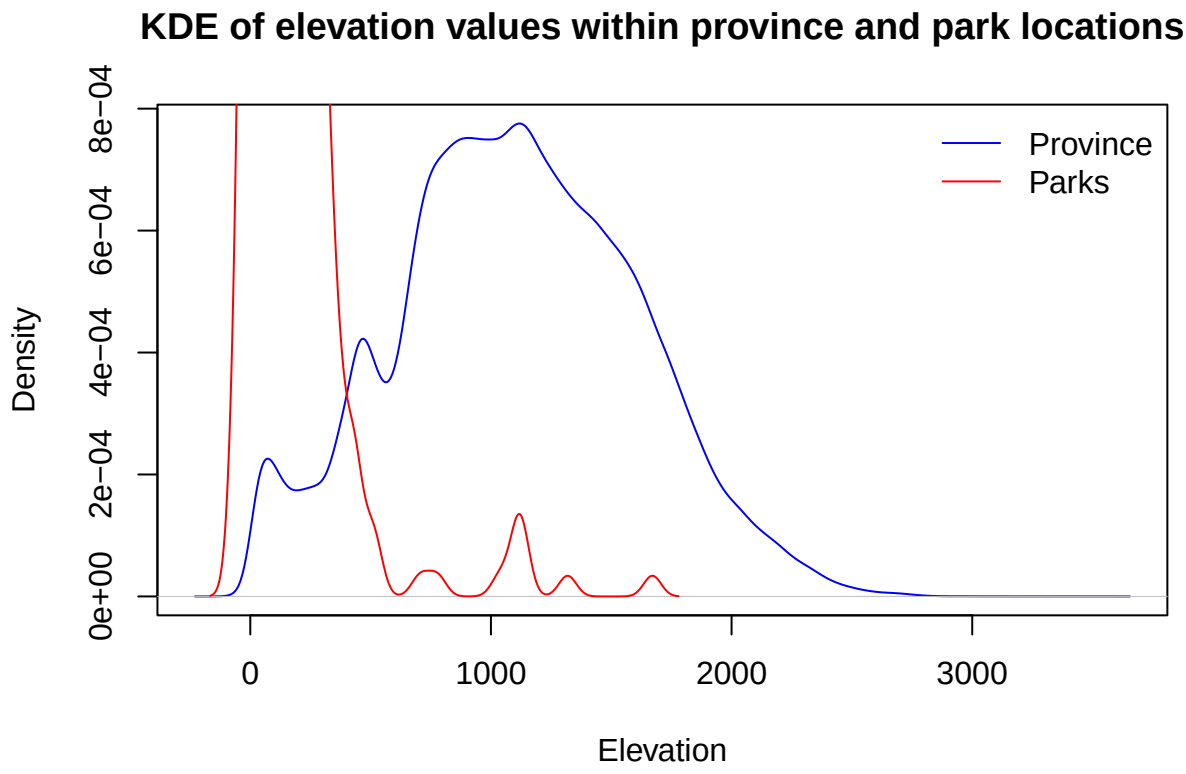
Finding :

- Overwhelming majority of the fungi points are found in the low elevation region

2.3.3 KDE Analysis (?? should this part be skipped, don't know its interpretation/purpose??)

```
# nn_dist <- nndist(asc_data_ppp)
# marks(asc_data_ppp) <- nn_dist
# plot(asc_data_ppp, main = "Ascomycota Distance",which.marks = "Dist", pch = 16)
# BC$Elevation[asc_data_ppp]

library("kdensity")
```

```r
asc_density <- density(BC$Elevation[asc_data_ppp])
province_density <- density(BC$Elevation$v, na.rm=T)


plot(province_density, main = "KDE of elevation values within province and park locations", xlab = "Ele
lines(asc_density, col = "red")
legend("topright", legend = c("Province", "Parks"), lty = 1, col = c("blue", "red"), bty = "n")
```




```r
#
# plot(province_density, main = "KDE of elevation values within province and park locations", xlab = "E
# lines(park_density, col = "red")
# legend("topright", legend = c("Province", "Parks"), lty = 1, col = c("blue", "red"), bty = "n")
```

2.3.4 First Moment Descriptive Statistics

After preliminary EDA and high level plot, we will study various first moment descriptive statistical measures.

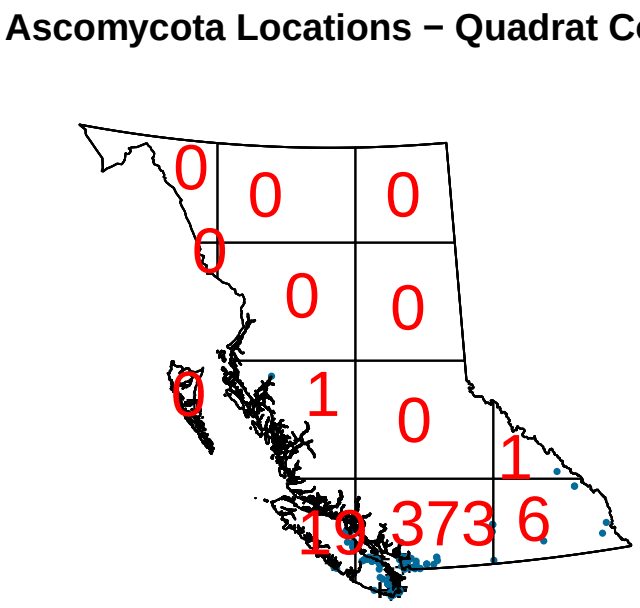
```r
intensity(asc_data_ppp)
```

2.3.5.a Intensity

```
## [1] 4.218242e-10
```

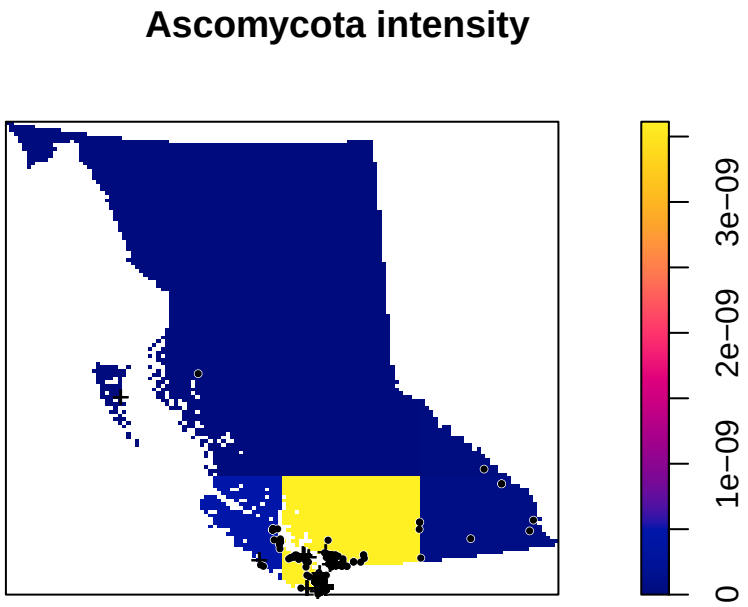
2.3.5.b Homogeneity Studies, Quadrat Test and Hotspot Analysis Note that the intensity is a very small number. This is consistent with our plots above. There are not many points in the whole BC windows. Overwhelming majority of the points are sparesely located in the BC. Let's verify this with the Quadrat Count Plot.

```
Q <- quadratcount(asc_data_ppp,
                  nx = 4,
                  ny = 4)

#Plot the output
plot(asc_data_ppp,
     pch = 16,
     cex = 0.5,
     cols = "#046C9A",
     main = " Ascomycota Locations - Quadrat Count")

plot(Q, cex = 2, col = "red", add = T)
```




```
plot(intensity(Q, image = T),
     main = "Ascomycota intensity")

plot(asc_data_ppp,
     pch = 16,
     cex = 0.6,
     cols = "white",
```

```
     add = T)

plot(asc_data_ppp,
     pch = 16,
     cex = 0.5,
     cols = "black",
     add = T)
```



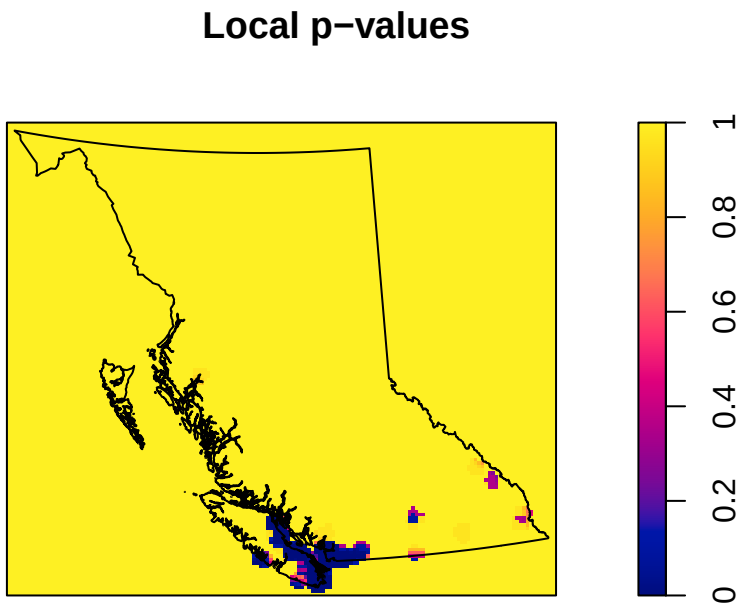
Next, we perform a Qudart test of homogeneity

```
#Quadrat test of homogeneity
quadrat.test(Q)
```

```
##
##  Chi-squared test of CSR using quadrat counts
##
## data:
## X2 = 2818.1, df = 12, p-value < 2.2e-16
## alternative hypothesis: two.sided
##
## Quadrats: 13 tiles (irregular windows)
```

In addition, We also perform a Likelihood Ratio Test to evaluate the degree of homogeneity as cross reference.

```
R <- bw.ppl(asc_data_ppp)
LR <- scanLRTS(asc_data_ppp,r=R)

#plot(LR,"Likelihood Ratio Test")
#plot(asc_data_ppp$window,"Likelihood Ratio Test")

pvals <- eval.im(pchisq(LR,
                        df = 1,
                        lower.tail = FALSE))


#Plot the output
plot(pvals, main = "Local p-values")
plot(asc_data_ppp$window,add=T)
```



Once again, these plots have strongly verified the spatial inhomogeneity nature of the fungi distribution :

- Overwhelming majority of the regions have zero or near zero points.
- Quadrat Test and Likelihood Ratio Test indicates portions of certain significant deviation from homogeneity.

- Hot spot analysis shows only a very few prominent hot spots/areas with low p-values. Most regions (in yellow, p to close 1) show no deviation from Poisson distribution. These deviations are mainly concentrated in the southern part of the province.

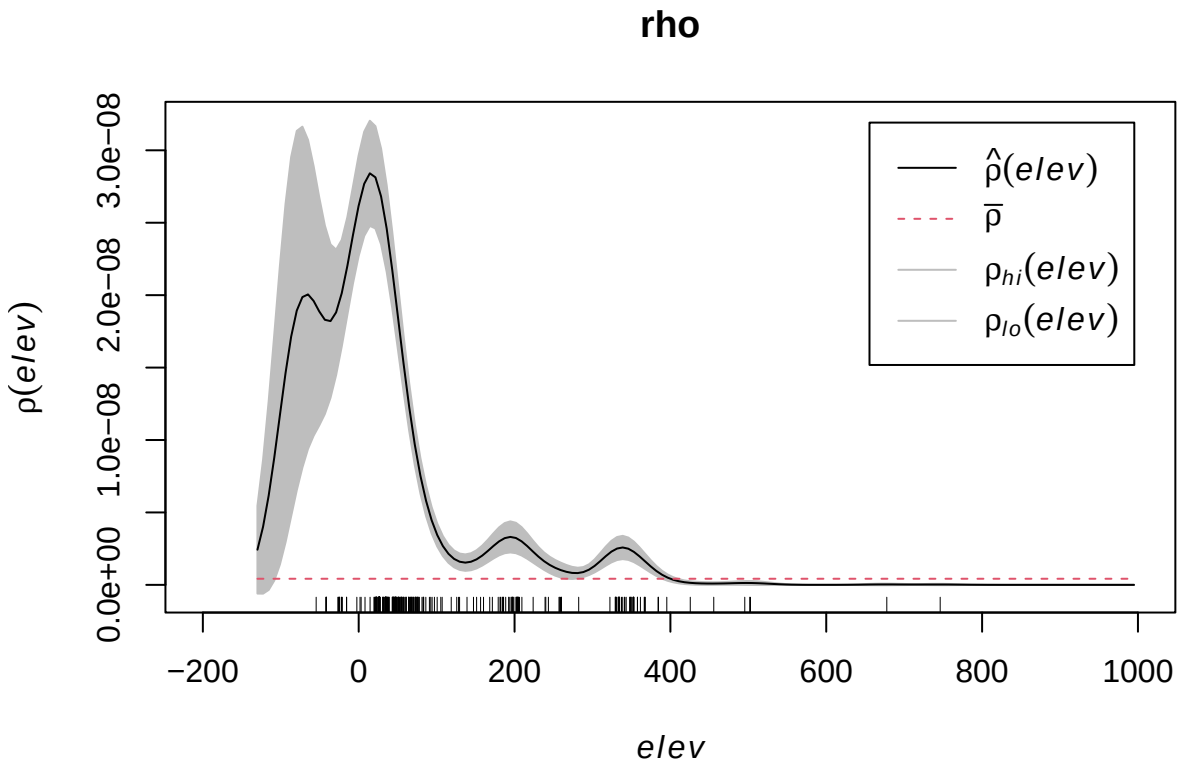
2.3.6 Covariate Study

Now, we will study the covariate behaviour individually, and see whether there are strong support or observable patterns. We will conduct quantile split into 4 sections for each of the covariates.

2.3.6.a Covariate Variable : Elevation Let's start with Elevation.

```
elev <- BC$Elevation
b <- quantile(elev,probs=(0:4)/4,type=2)
Zcut <- cut(elev,breaks=b)
V <- tess(image=Zcut)
quadratcount(asc_data_ppp,tess=V)
```

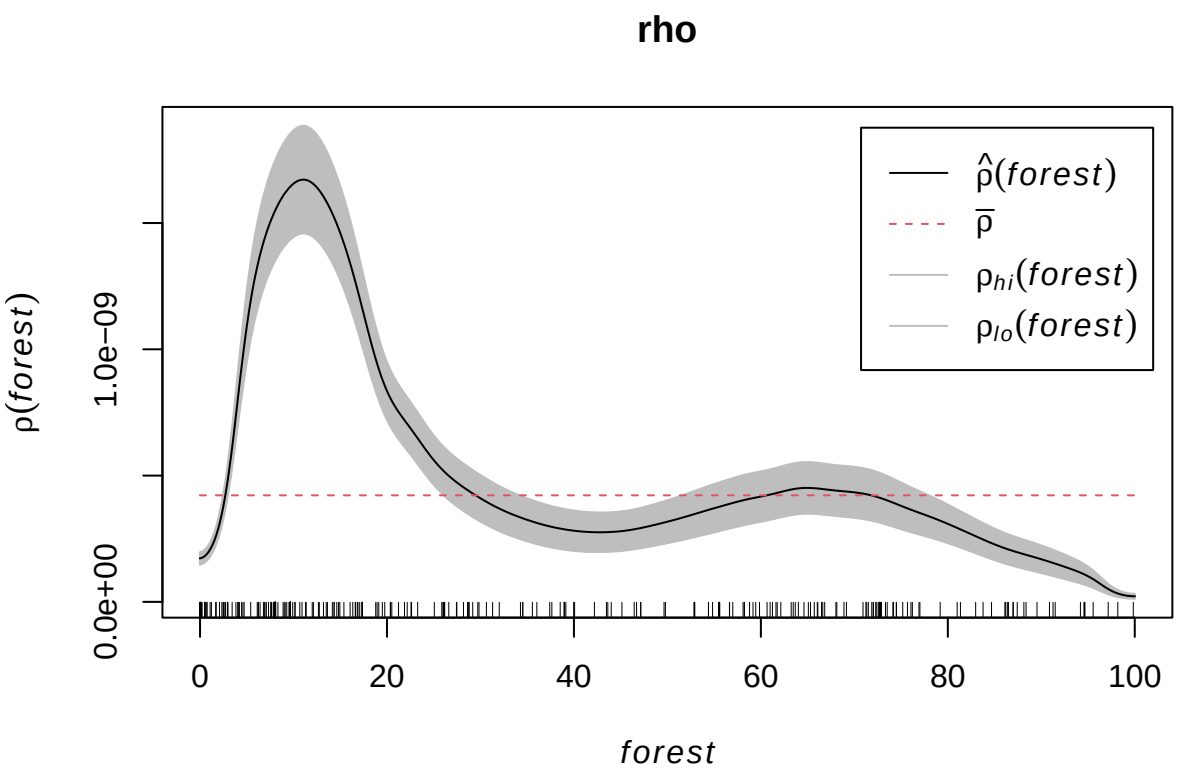
```
## tile
##          (-130,761]       (761,1.1e+03]  (1.1e+03,1.46e+03] (1.46e+03,3.56e+03]
##                 392                   2                   5                   1
```



2.3.6.b Covariate Variable : Forest Then, let's the check Forest as covariate.

```
forest <- BC$Forest
b <- quantile(forest,probs=(0:4)/4,type=2)
Zcut <- cut(forest,breaks=b)
V <- tess(image=Zcut)
quadratcount(asc_data_ppp,tess=V)
```

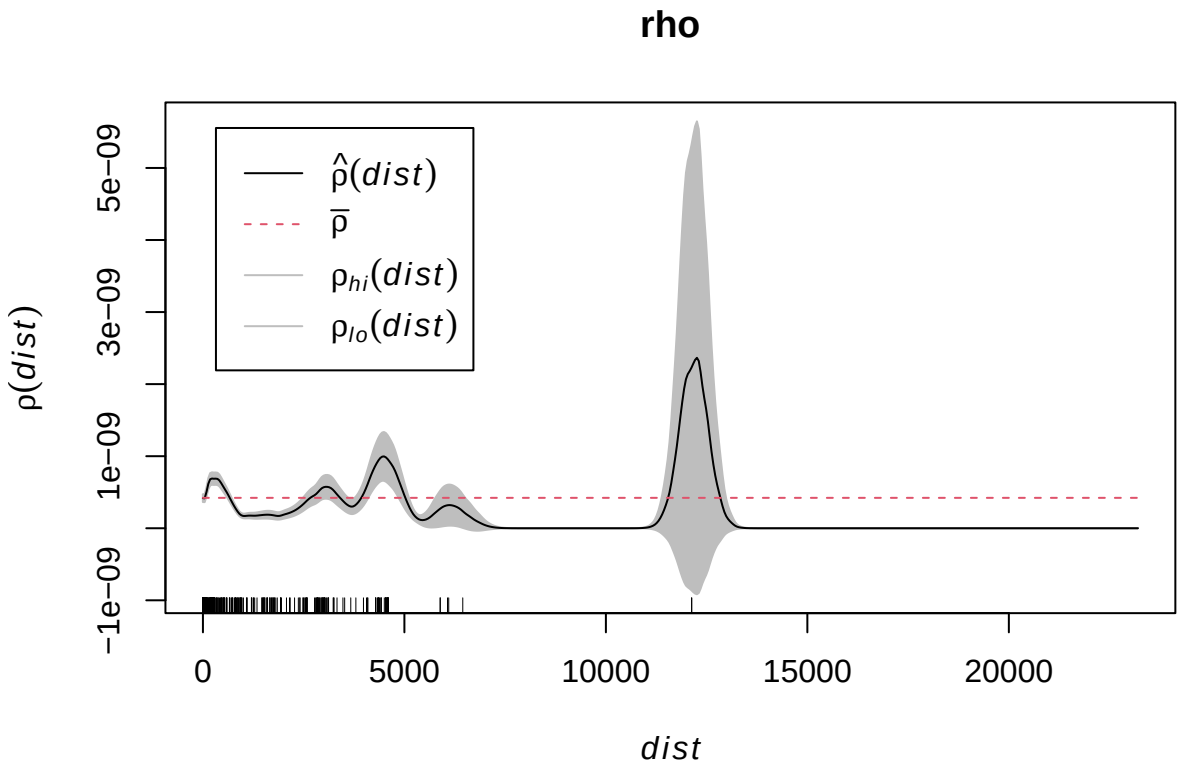
```
## tile
##    (0,11.6] (11.6,50.2] (50.2,86.9]  (86.9,100]
##         197          93          81          29
```



2.3.6.c Covariate Variable : Distance to Water Then, we look into "Distance to Water".

```
dist <- BC$Dist_Water
b <- quantile(dist,probs=(0:4)/4,type=2)
Zcut <- cut(dist,breaks=b)
V <- tess(image=Zcut)
quadratcount(asc_data_ppp,tess=V)
```

```
## tile
##             (0,483]       (483,1.1e+03]  (1.1e+03,2.18e+03] (2.18e+03,2.32e+04]
##                 213                  47                  38                  96
```



2.3.6.d Covariates Section Conclusion The observation is made from the above plots :

- For Elevation Level :
  - It is obvious that the fungi is overwhelmingly clustered in the low elevation level region.
  - The proportion of occurrence that appears in the lowest elevation sector accounts for more than 97% of the identified points.
- For Forest and Distance to Water :
  - It is observed that the fungi is correlated to both Forest and distance .
  - The proportion of occurrence that appears in the respective smallest sectors account for about 50% of the identified points.

2.3.7 Second Moment Descriptives

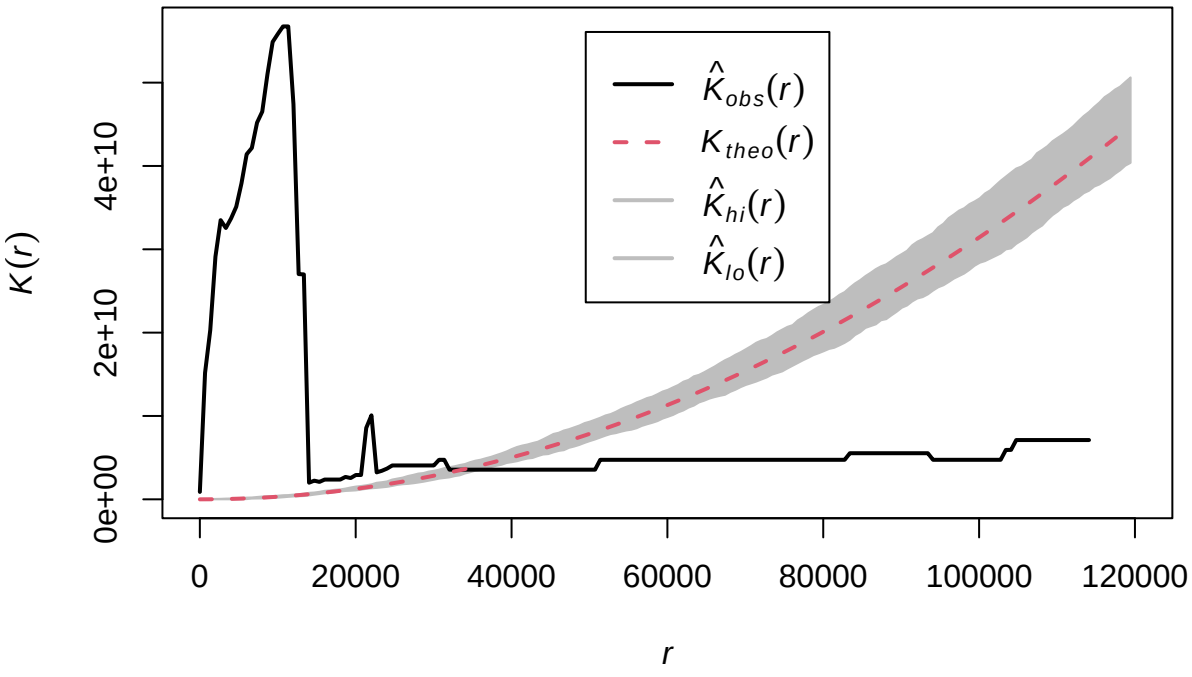
To continue the analysis, we will explore the second moment descriptives to uncover any variances and correlation characteristics of the data.

2.3.7.a Ripley's K-function ??? why K goes down??? We firstly use the typical K-function to measure the spatial clustering and point pattern.

```r
# Bootstrapped CIs
# rank = 1 means the max and min
# Border correction is to correct for edges around the window
# values will be used for CI
E_asc <- envelope(asc_data_ppp,
                  Kest,
                  correction="border",
                  rank = 1,
                  nsim = 19,
                  fix.n = T)
```

```
## Generating 19 simulations of CSR with fixed number of points  ...
## 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18,  19.
##
## Done.
```

```r
# visualise the results
plot(E_asc,
     main = "",
     lwd = 2,
     xlim=c(0,120000))
```

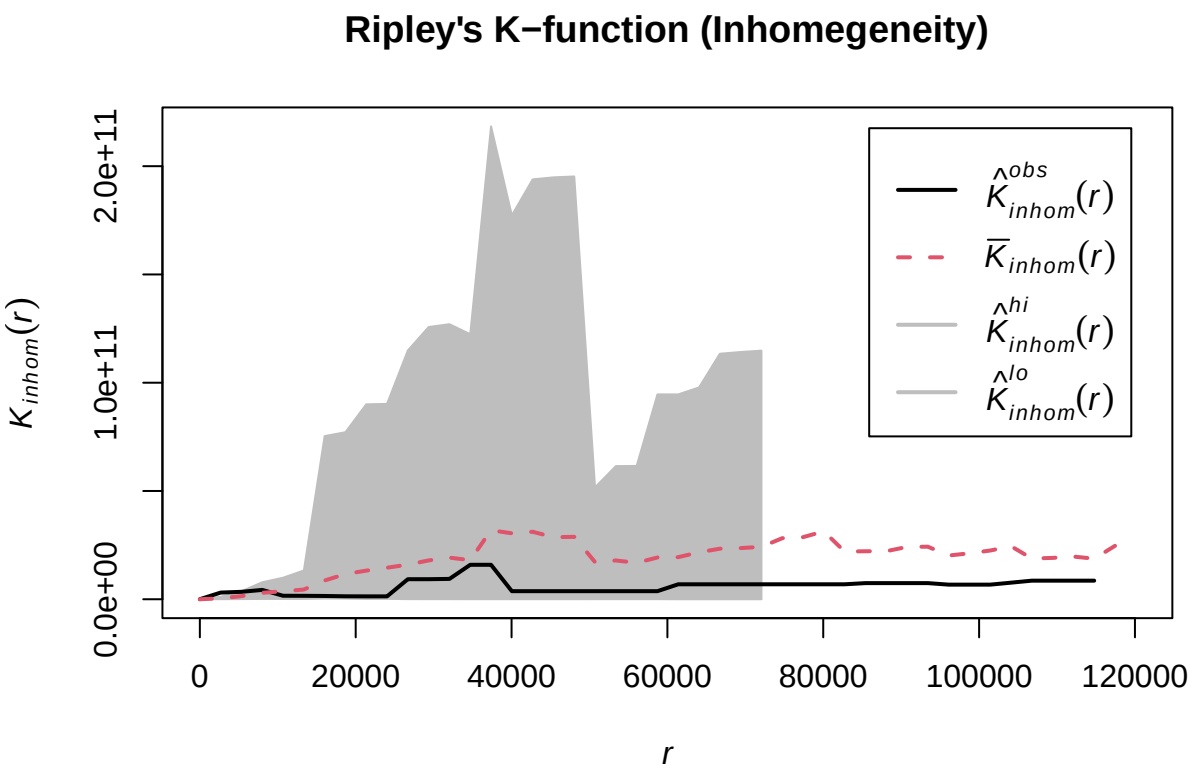


As inhomogeneity has been observed, we are going to correct for inhomogeneity and reperform the test for a more accurate result.

```
lambda_asc <- density(asc_data_ppp, bw.ppl)
Kinhom_asc <- Kinhom(asc_data_ppp, lambda_asc)

#Estimate a strictly positive density
lambda_asc_pos <- density(asc_data_ppp,
                          sigma=bw.ppl,
                          positive=TRUE)

#Simulation envelope (with points drawn from the estimated intensity)
E_asc_inhom <- envelope(asc_data_ppp,
                        Kinhom,
                        simulate = expression(rpoispp(lambda_asc_pos)),
                        correction="border",
                        rank = 1,
                        nsim = 19,
                        fix.n = TRUE)
```

```
## Generating 19 simulations by evaluating expression  ...
## 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18,  19.
##
## Done.
```

```
# visualise the results
# par(mfrow = c(1,2))
plot(E_asc_inhom,
     main = "Ripley's K-function (Inhomegeneity)",
     lwd = 2,
     xlim=c(0,120000))
```



Finding :

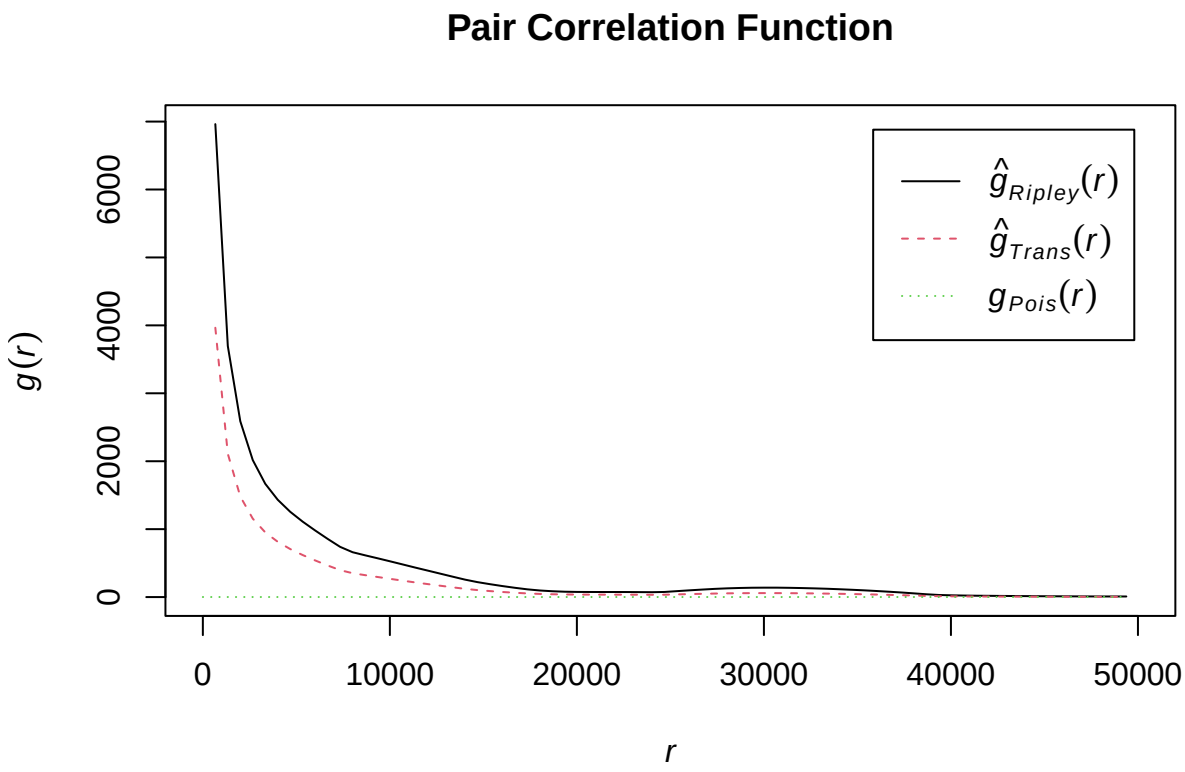
- When assumed homogeneity, the observed data show a strong clustering at small r value range.
- When corrected for inhomogeneity, such clustering pattern is no longer observed.

2.3.7.b Pair Correlation Function We are also interested in checking the points relation using pair correlation function.

```
# Estimate the g function
pcf_asc <- pcf(asc_data_ppp)

pcf_asc
```

```
## Function value object (class 'fv')
## for the function r -> g(r)
## ....................................................................
##       Math.label        Description
## r     r                 distance argument r
## theo  g[Pois](r)        theoretical Poisson g(r)
## trans hat(g)[Trans](r)  translation-corrected estimate of g(r)
## iso   hat(g)[Ripley](r) isotropic-corrected estimate of g(r)
## ....................................................................
## Default plot formula:  .~r
## where "." stands for 'iso', 'trans', 'theo'
## Recommended range of argument r: [0, 341660]
## Available range of argument r: [0, 341660]
```

```
plot(pcf_asc,xlim=c(0,50000),main="Pair Correlation Function")
```

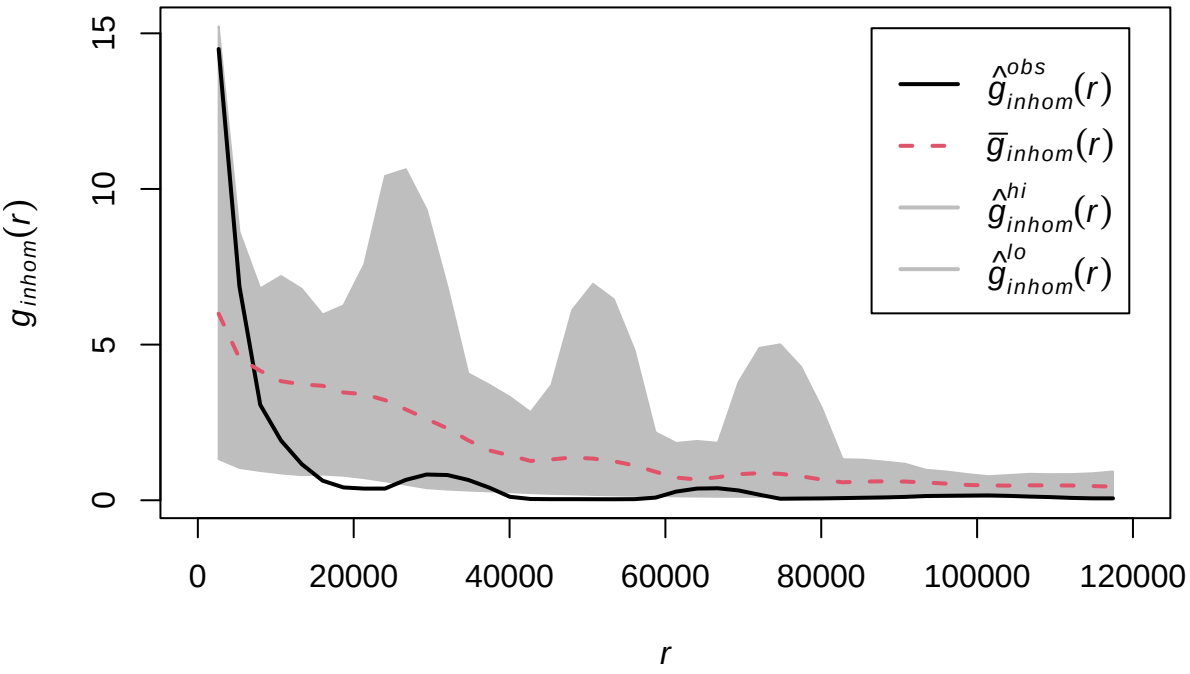


The above estimator also assumes homogeneity. Let's relax this assumption to produce a more accurate analysis.

```
#Simulation envelope (with points drawn from the estimated intensity)
pcf_asc_inhom <- envelope(asc_data_ppp,
                          pcfinhom,
                          simulate = expression(rpoispp(lambda_asc_pos)),
                          rank = 1,
                          nsim = 19)
```

```
## Generating 19 simulations by evaluating expression  ...
## 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18,  19.
##
## Done.
```

```
plot(pcf_asc_inhom,
     xlim = c(0,120000),
     main = "",
     lwd = 2)
```



Finding :

- When corrected for homogeneity, the locations of the fungi appear not to have any significant correlations.

2.3.8 Model Fitting and Selection with AIC

In this section, we will proceed with model fitting and selection, in order to achieve a reasonably effective model, while following the rule of parisomny as much as possible. To do this, we will try to fit model with different polynomial degree terms and then assess for the performance gains versus the cost of the extra complexity.

```
fit <- ppm(asc_data_ppp ~ Elevation + Dist_Water + Forest, data = BC)
fit
```

```
## Nonstationary Poisson process
## Fitted to point pattern dataset 'asc_data_ppp'
##
## Log intensity:  ~Elevation + Dist_Water + Forest
##
## Fitted trend coefficients:
##   (Intercept)     Elevation    Dist_Water        Forest
## -1.649783e+01 -9.746289e-03  5.074702e-05 -2.772079e-02
##
##                  Estimate         S.E.       CI95.lo       CI95.hi Ztest
```

```
## (Intercept) -1.649783e+01 8.719049e-02 -1.666872e+01 -1.632694e+01   ***
## Elevation   -9.746289e-03 3.872771e-04 -1.050534e-02 -8.987240e-03   ***
## Dist_Water   5.074702e-05 2.503222e-05  1.684771e-06  9.980928e-05     *
## Forest      -2.772079e-02 1.803605e-03 -3.125579e-02 -2.418579e-02   ***
##                     Zval
## (Intercept) -189.215943
## Elevation    -25.166190
## Dist_Water     2.027268
## Forest       -15.369657
## *** Fitting algorithm for 'glm' did not converge ***
```

Elevation and Forest are significant but Distance to Water isn't. OK, then try one higher order.

```
fit <- ppm(asc_data_ppp ~ Elevation + I(Elevation^2) + Dist_Water + I(Dist_Water^2), data = BC)
fit
```

```
## Nonstationary Poisson process
## Fitted to point pattern dataset 'asc_data_ppp'
##
## Log intensity:  ~Elevation + I(Elevation^2) + Dist_Water + I(Dist_Water^2)
##
## Fitted trend coefficients:
##     (Intercept)       Elevation  I(Elevation^2)      Dist_Water I(Dist_Water^2)
##   -1.751444e+01   -1.298691e-02    3.757783e-06    2.313973e-04   -2.416955e-08
##
##                      Estimate         S.E.       CI95.lo       CI95.hi Ztest
## (Intercept)     -1.751444e+01 8.075694e-02 -1.767272e+01 -1.735616e+01   ***
## Elevation       -1.298691e-02 5.148358e-04 -1.399597e-02 -1.197785e-02   ***
## I(Elevation^2)   3.757783e-06 1.849431e-07  3.395301e-06  4.120264e-06   ***
## Dist_Water       2.313973e-04 7.552735e-05  8.336647e-05  3.794282e-04    **
## I(Dist_Water^2) -2.416955e-08 1.138818e-08 -4.648997e-08 -1.849130e-09     *
##                       Zval
## (Intercept)     -216.878412
## Elevation        -25.225346
## I(Elevation^2)    20.318594
## Dist_Water         3.063756
## I(Dist_Water^2)   -2.122337
## *** Fitting algorithm for 'glm' did not converge ***
```

Similarly, after several rounds of tuning (the details are not shown here due to repetitive and routine nature), the following seems to be a improved fit :

```
fit_simple <- ppm(asc_data_ppp ~ Elevation + Forest, data = BC)
fit_simple
```

```
## Nonstationary Poisson process
## Fitted to point pattern dataset 'asc_data_ppp'
##
## Log intensity:  ~Elevation + Forest
##
## Fitted trend coefficients:
##   (Intercept)     Elevation        Forest
## -16.449678447  -0.009601581  -0.027922868
```

```
##
##                  Estimate         S.E.      CI95.lo       CI95.hi Ztest
## (Intercept) -16.449678447 0.0831309100 -16.61261204 -16.286744858   ***
## Elevation    -0.009601581 0.0003758118  -0.01033816  -0.008865003   ***
## Forest       -0.027922868 0.0018099253  -0.03147026  -0.024375480   ***
##                    Zval
## (Intercept) -197.87680
## Elevation    -25.54891
## Forest       -15.42764
## *** Fitting algorithm for 'glm' did not converge ***
```

```
fit <- ppm(asc_data_ppp ~ Elevation + I(Elevation^2) + Forest + I(Forest^2), data = BC)
fit
```

```
## Nonstationary Poisson process
## Fitted to point pattern dataset 'asc_data_ppp'
##
## Log intensity:  ~Elevation + I(Elevation^2) + Forest + I(Forest^2)
##
## Fitted trend coefficients:
##    (Intercept)      Elevation I(Elevation^2)         Forest    I(Forest^2)
##  -1.621033e+01  -1.173001e-02   3.259440e-06  -4.196879e-02   1.826759e-04
##
##                     Estimate         S.E.       CI95.lo       CI95.hi Ztest
## (Intercept)    -1.621033e+01 9.367906e-02 -1.639394e+01 -1.602673e+01   ***
## Elevation      -1.173001e-02 4.272309e-04 -1.256736e-02 -1.089265e-02   ***
## I(Elevation^2)  3.259440e-06 1.877594e-07  2.891438e-06  3.627441e-06   ***
## Forest         -4.196879e-02 5.890907e-03 -5.351476e-02 -3.042283e-02   ***
## I(Forest^2)     1.826759e-04 6.812603e-05  4.915130e-05  3.162004e-04    **
##                       Zval
## (Intercept)    -173.041168
## Elevation       -27.455891
## I(Elevation^2)   17.359658
## Forest           -7.124334
## I(Forest^2)       2.681440
## *** Fitting algorithm for 'glm' did not converge ***
```

Now, the model gets more complicated. We will evaluate if the additional cost overhead of adopting such a more complicated model is well justified by benchmarking with the AIC values.

```
#AIC values
AIC(fit); AIC(fit_simple)
```

```
## [1] 15464.31
```

```
## [1] 15508.45
```

```
#Delta AIC
AIC(fit_simple) - AIC(fit)
```

```
## [1] 44.14666
```

We will also like to conduct a anova LRT test as an additional objective measurement to compare the two models :

```
anova(fit_simple, fit, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: ~Elevation + Forest      Poisson
## Model 2: ~Elevation + I(Elevation^2) + Forest + I(Forest^2)   Poisson
##   Npar Df Deviance  Pr(>Chi)
## 1    3
## 2    5  2   48.147 3.508e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The following conclusion is drawn :

- The model with quadratic terms provides a better fit to the data
- A delta AIC value of 44 indicates a significant fitting improvement, the extra complexity is therefore well justified.
- So, a possible model should be

$$\lambda_{ASC}(u) = e^{-16.2 \ - \ 0.017 \text{ elevation}(u) \ - \ 0.000003 \text{ elevation}(u)^2 \ - \ 0.042 \text{ forest}(u) \ + \ 0.00018 \text{ forest}(u)^2}$$

2.3.9 Model Validation

Now, given the following fitted model, we will finally evaluate the overall model performance again with Quadrat Test and PPP Residuals.

$$\lambda_{ASC}(u) = e^{-16.2 \ - \ 0.017 \text{ elevation}(u) \ - \ 0.000003 \text{ elevation}(u)^2 \ - \ 0.042 \text{ forest}(u) \ + \ 0.00018 \text{ forest}(u)^2}$$

2.3.9.a Quadrat Test Let's see the quadrat test result of the higher degree polynomial model.

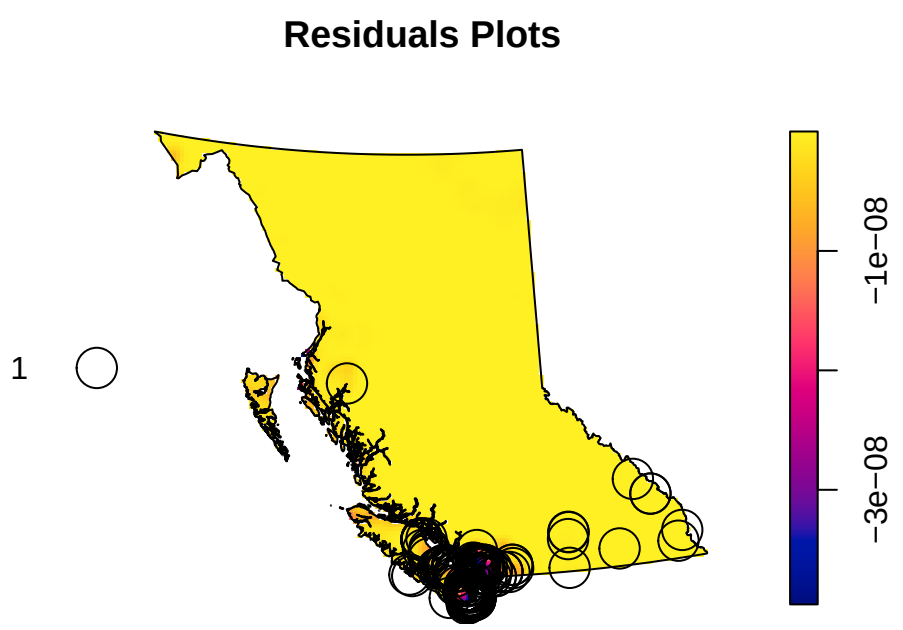
```
#Run the quadrat test
quadrat.test(fit, nx = 4, ny = 4)
```

```
##
##  Chi-squared test of fitted Poisson model 'fit' using quadrat counts
##
## data:  data from fit
## X2 = 585.05, df = 8, p-value < 2.2e-16
## alternative hypothesis: two.sided
##
## Quadrats: 13 tiles (irregular windows)
```

This has small p value, suggesting significant deviation from our model's prediction. Room for further improvement is therefore expected, but it does not provide hint for how to achieve any improvement.

2.3.9.b PPP Residuals We will also check the distribution of residuals value of the model.

```r
#Calculate the residuals
res <- residuals(fit)

#Visualise
plot(res,
#     cols = "transparent",
     main="Residuals Plots")
```



From the plot, it's observed that :

- The residuals are small in magnitude (e^-8).

- The negative residual values suggest over-prediction of the model.
- There is room for improvement for the model

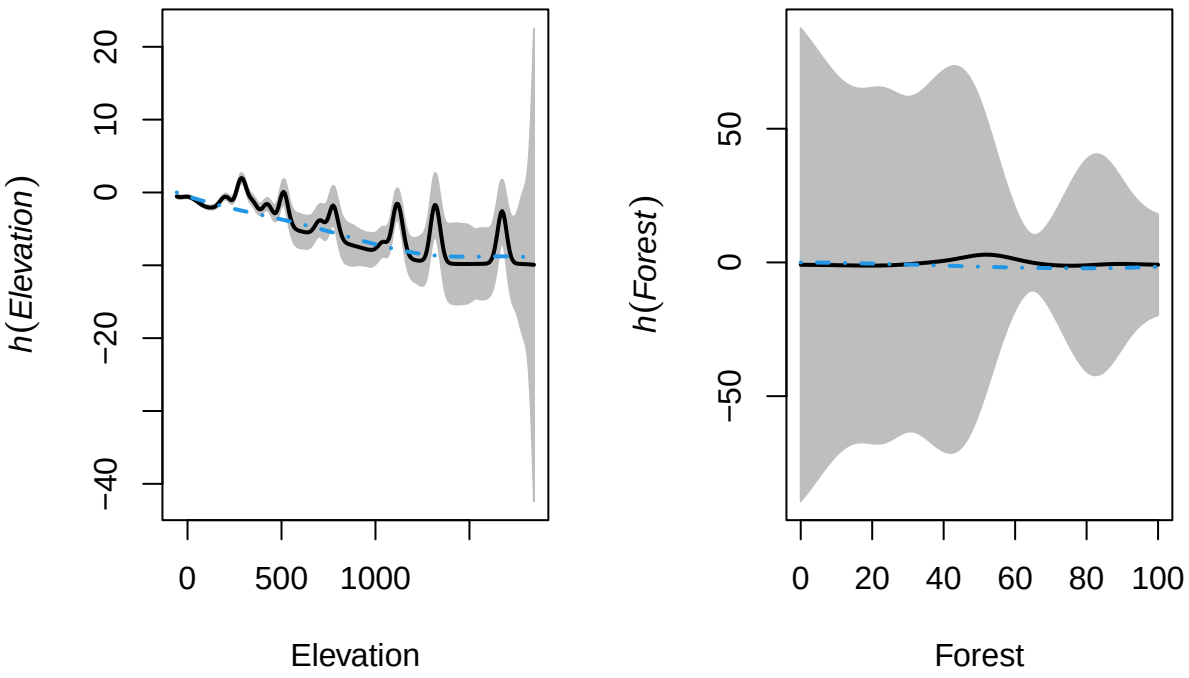
2.3.10 Higher Order Polynomial Fitting with Spline and Validation

As the above analysis indicated a room for improvement, we will finally try to add higher-order polynomials with the spline packages.

```r
library(splines)

#Fit the PPP model
fit_smooth <- ppm(asc_data_ppp ~ bs(Elevation,7) + bs(Forest, 3), data = BC, use.gam = TRUE)

fit_smooth
```

```
## Nonstationary Poisson process
## Fitted to point pattern dataset 'asc_data_ppp'
##
## Log intensity:  ~bs(Elevation, 7) + bs(Forest, 3)
##
## Fitted trend coefficients:
##       (Intercept) bs(Elevation, 7)1 bs(Elevation, 7)2 bs(Elevation, 7)3
##       -15.1837101        -2.1215999        -3.9107238       -10.2916364
## bs(Elevation, 7)4 bs(Elevation, 7)5 bs(Elevation, 7)6 bs(Elevation, 7)7
##        -6.9600818       -20.1516125        49.1493840     -1129.0583122
##    bs(Forest, 3)1    bs(Forest, 3)2    bs(Forest, 3)3
##        -0.2110034        -3.4557922        -1.6215046
##
## For standard errors, type coef(summary(x))
```

```
#Calculate the partial residuals as a function of elevation
par_res_elev <- parres(fit_smooth, "Elevation")

#Calculate the relative intensity as a function of gradient
par_res_forest <- parres(fit_smooth, "Forest")

#Side by side plotting
par(mfrow = c(1,2))
plot(par_res_elev,
     legend = FALSE,
     lwd = 2,
     main = "",
     xlab = "Elevation")
plot(par_res_forest,
     legend = FALSE,
     lwd = 2,
     main = "",
     xlab = "Forest")
```



Now, compare the AIC values for both the simpler and higher polynomial degree models.

```
#AIC values
AIC(fit); AIC(fit_smooth)
```

```
## [1] 15464.31
```

```
## [1] 15440.68
```

```
#Delta AIC
AIC(fit) - AIC(fit_smooth)
```

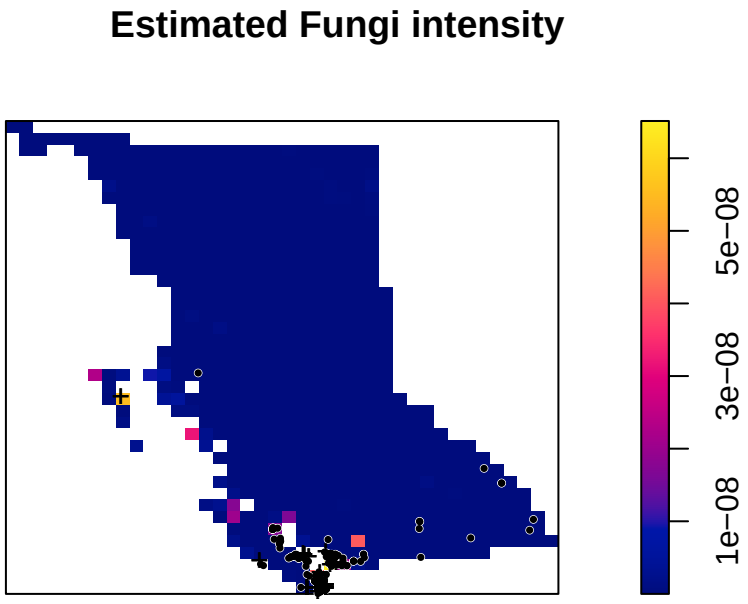
```
## [1] 23.62747
```

```
#Likelihood ratio test
anova(fit, fit_smooth, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: ~Elevation + I(Elevation^2) + Forest + I(Forest^2)   Poisson
## Model 2: ~bs(Elevation, 7) + bs(Forest, 3)    Poisson
##   Npar Df Deviance  Pr(>Chi)
## 1    5
## 2   11  6   35.622 3.264e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

All these suggest that this complex models provides a better fit to the data. Let's finally visualize the predictions as before.

```
#Plot the model predictions
plot(fit_smooth,
     se = FALSE,
     superimpose = FALSE,
     main = "Estimated Fungi intensity")

#Overlay the ocations
plot(asc_data_ppp,
     pch = 16,
     cex = 0.6,
     cols = "white",
     add = TRUE)
plot(asc_data_ppp,
     pch = 16,
     cex = 0.5,
     cols = "black",
     add = TRUE)
```



From this visualisation, the following is observed :

- Although the model is not yet perfect, it is progressively having improvement after rounds of variables selection process.

- Considering the fact that we are predicting the locations of one species of fungi in a biodiverse continent based only on Elevation and Forest, and have no information on all of the many other factors that would significantly influence fungi growth (e.g. humidity, moisture level, temperature, pH value, oxygen content, etc.)

3. Discussion:

Provide a brief summary of your findings. Length: ca. 1 page.

4. References:

Include references to all necessary literature.