

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 directly from GBIF with the gbif R package. According to the GBIF classification system, Ascomycota comprises of about 20 Classes as immediate children species. The whole phylum makes up a total of 16 million occurrences records across the globe.

The detail will be discussed in the later sections.

1.3 Research Questions

Due to the potential medical and various practical values of Ascomycota mentioned above, 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 - Lichen Collection
- iNaturalist Research-grade Observations
- Assembly and activity of microbial communities in the Pacific temperate rainforest

We tried to load the complete 69K occurrences set into our computer, we found that loading the whole dataset takes a tremendous amount of time for most processes and operation. For example, it took about 4 hours just to load the complete set of data from gbif api! Running operations like scanLRTS(), rhohat(), envelope() took even longer! After consulting the course instructor, we have set the limit to 2000 records when we retrieve the data with the gbif api to make it ‘computing-resources affordable’.

```
# 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",
                        limit=2000) ## 102 illegal points stored in attr(),"rejects" ***

# 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 columns 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 many 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.

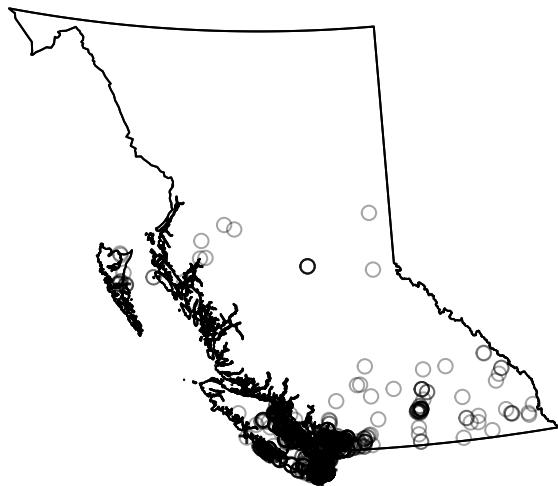
```
# View(data.frame(names(asc_bc_data)))
cleaned_asc_bc <- asc_bc_data[, c("decimalLongitude", "decimalLatitude", "order", "family", "genus", "year", "month", "day", "eventDate", "occurrenceStatus", "class", "verbatimEventDate", "collectionCode", "gbifID", "verbatimLocality")]
])
```

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)
```

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 occurrences 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.

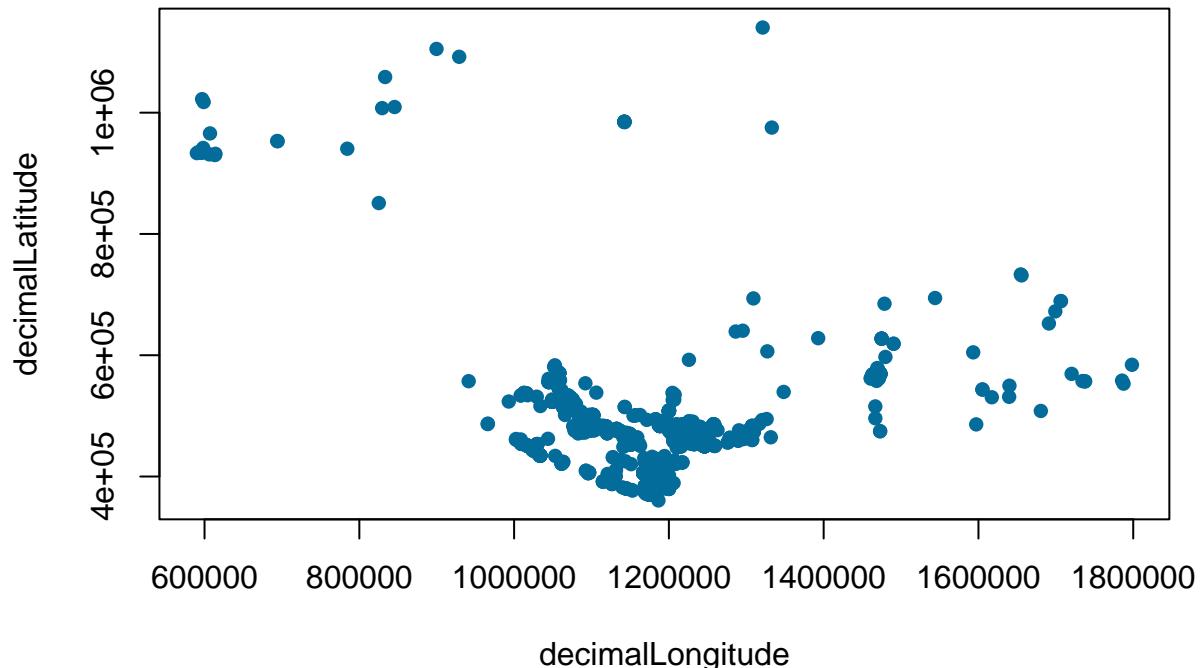
We will then conduct First Moment Analysis including homogeneity analysis and covariates study on some variables. Afterwards, we will perform Second Moment analysis where popular tools such as K-function and Pair Correlation Function will be deployed to investigate any clustering.

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.

- There is only a single major and significantly 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 in terms of the scale.

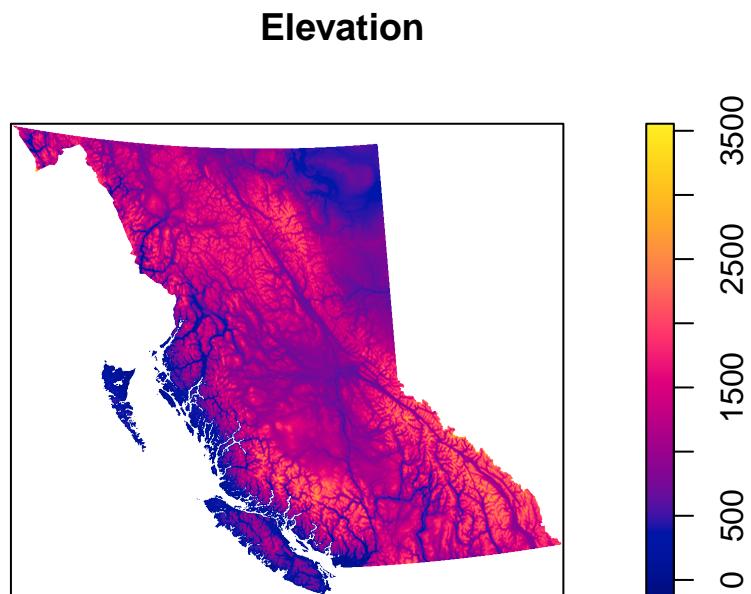
2.3.2 EDA : BC Windows and Covariates Data Walkthrough

Let's see what the BC_Covariates.Rda file provides 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

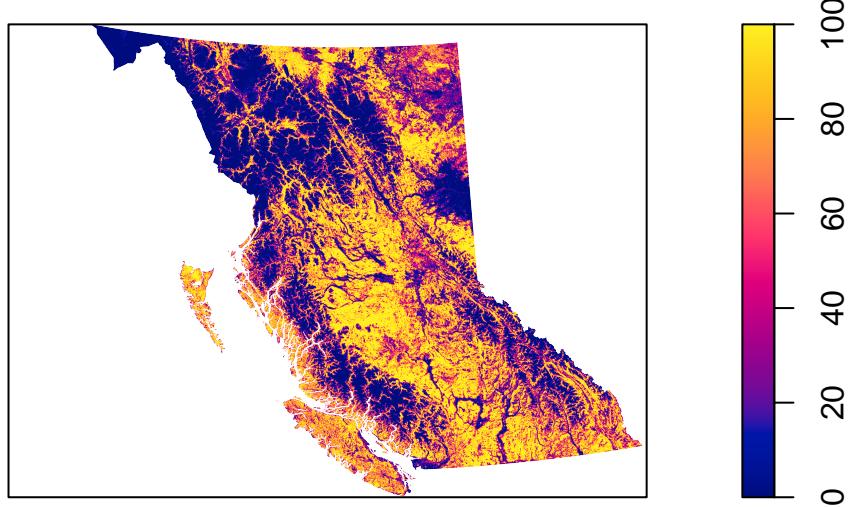
```
#par(mfrow=c(2,2))

#Elevation
plot(BC$Elevation, main = "Elevation")
```



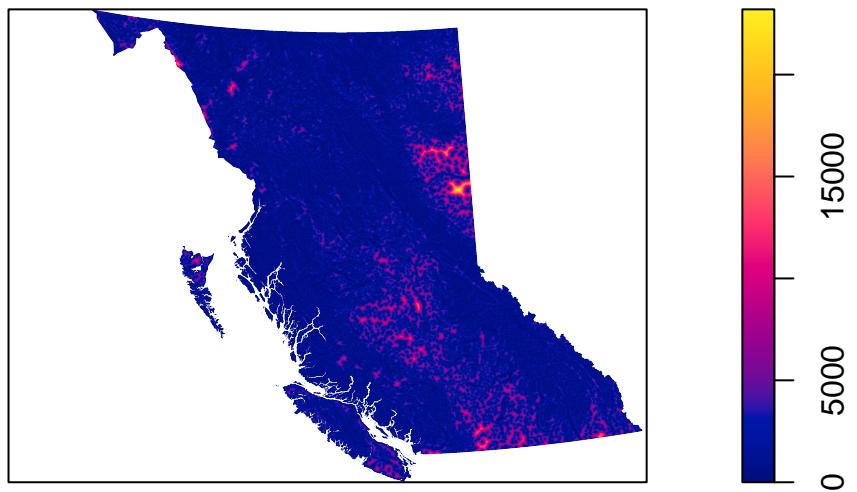
```
#Forest
plot(BC$Forest, main = "Forest")
```

Forest



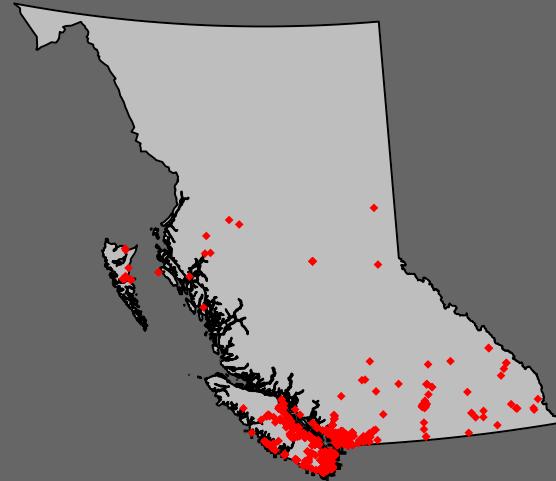
```
#Dist_Water  
plot(BC$Dist_Water, main = "Distance to Water")
```

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
```

Ascomycota in BC



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 levels.

```
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
##      1481           67            8            0            0
```

Finding :

- Overwhelming majority of the fungi points are found in the low elevation region.
- There is a trend : the higher the elevation region is, the less occurrences of the fungi is observed.
- The change is like ‘exponentially declined’.

2.3.3 First Moment Descriptive Statistics

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

```
intensity(asc_data_ppp)
```

2.3.3.a Intensity

```
## [1] 1.843372e-09
```

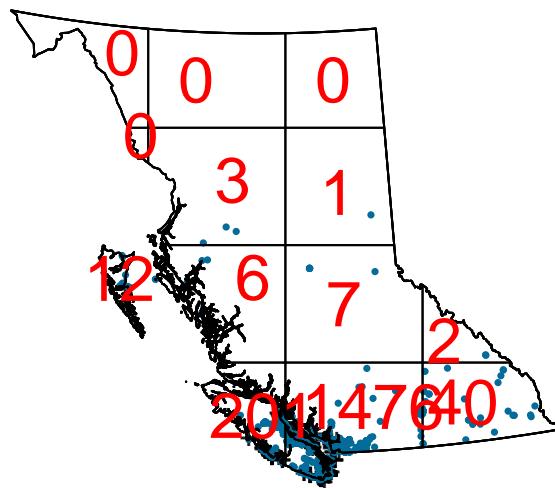
2.3.3.b Homogeneity Studies, Quadrat Test and Hotspot Analysis Note that the intensity is a very small number. This is consistent with our plots above. There are not many points in the whole BC windows. Overwhelming majority of the points are sparsely located in the BC. Let's verify this with the Quadrat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

Ascomycota Locations – Quadrat Count



```

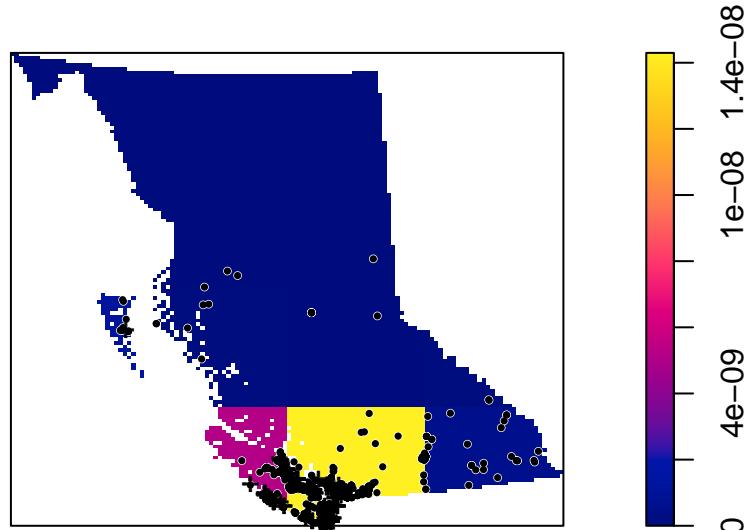
plot(intensity(Q, image = T),
     main = "Ascomycota intensity")

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)

```

Ascomycota intensity



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 = 10279, 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)

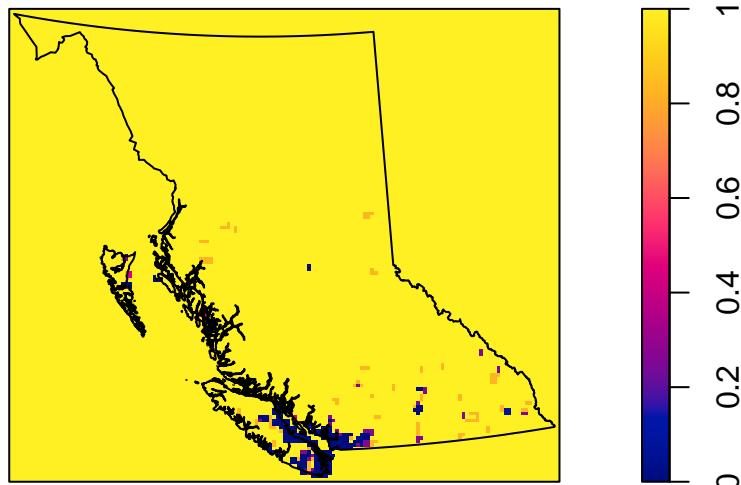
#plot(LR, "Likelihood Ratio Test")
#plot(asc_data_ppp$window, "Likelihood Ratio Test")

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)

```

Local p-values



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. The quadrat count plot has shown drastic difference between the quadrats.

- From the intensity plot, The points are observed being clustered in the south-east region of BC
- Quadrat Test and Likelihood Ratio Test indicates a significant deviation from homogeneity for the points.
- Hot spot analysis shows only a very few prominent hot spot with low p-values. Most regions rarely have significant distribution, and therefore are shown in purely yellow (i.e. $p=1$).

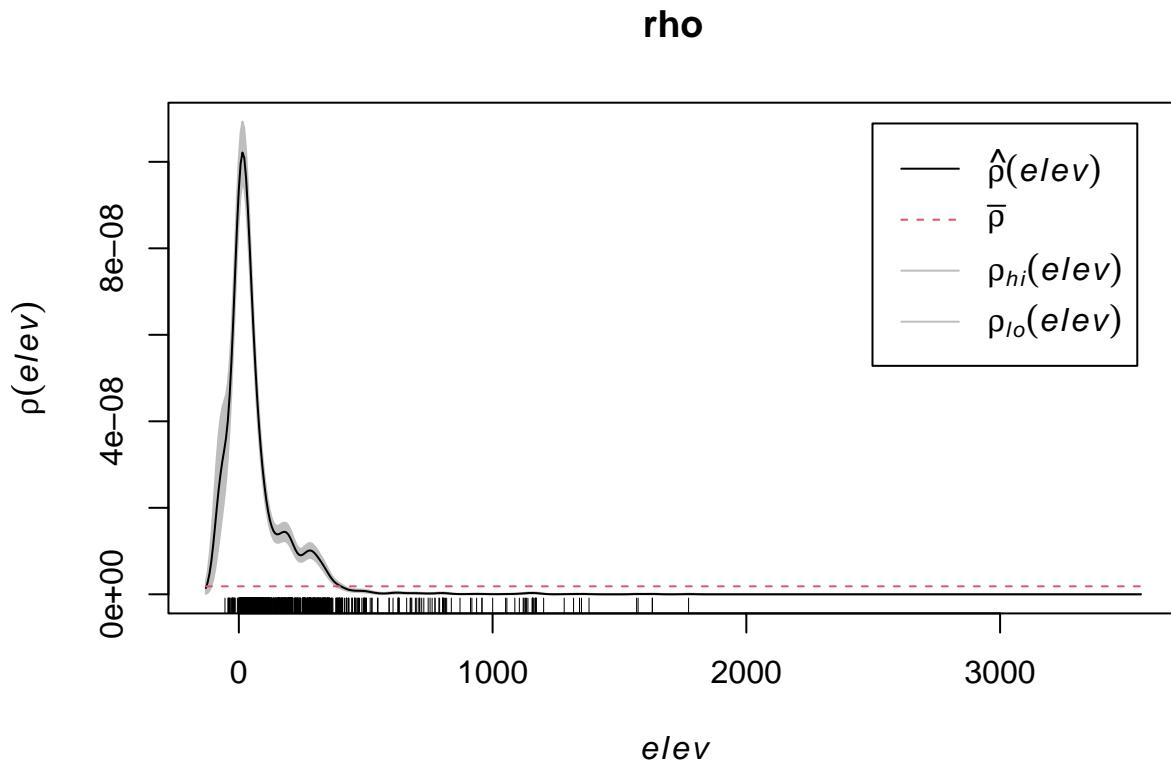
2.3.4 Covariate Study

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.

2.3.4.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)
```

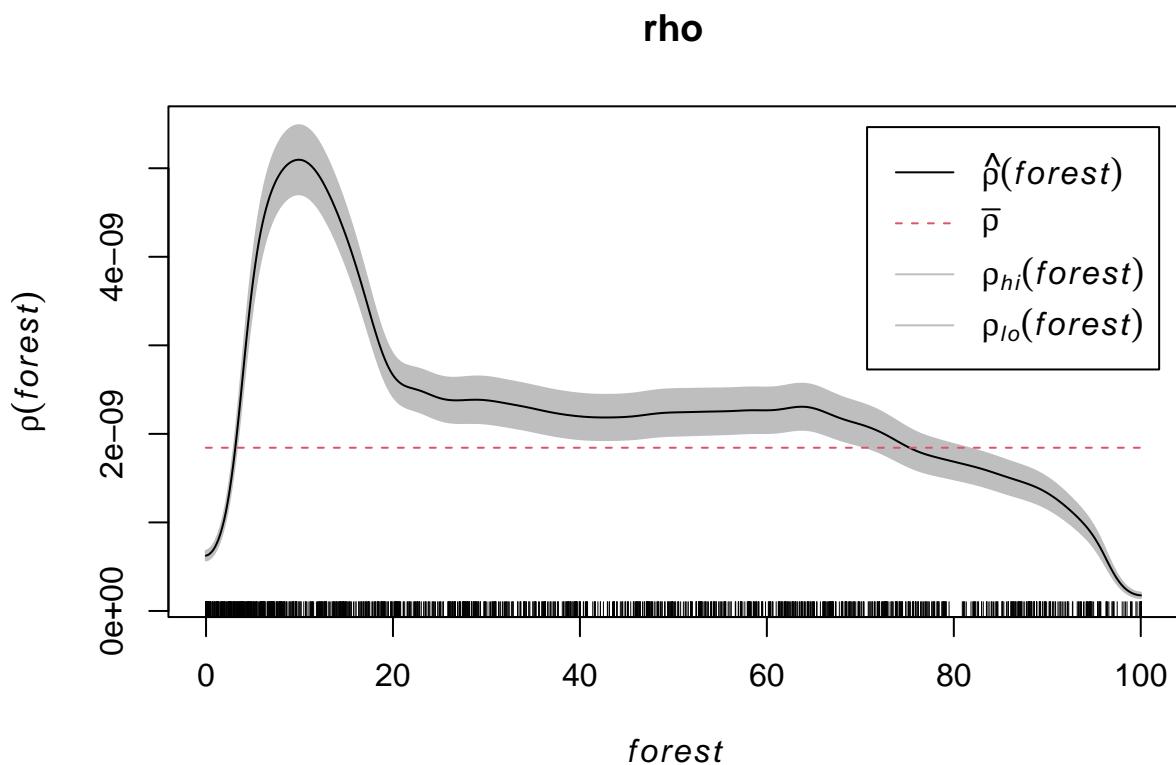
```
## tile
## (-130,761]      (761,1.1e+03]  (1.1e+03,1.46e+03] (1.46e+03,3.56e+03]
##          1694           24            25             5
```



2.3.4.b Covariate Variable : Forest Then, let's see Forest.

```
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)
```

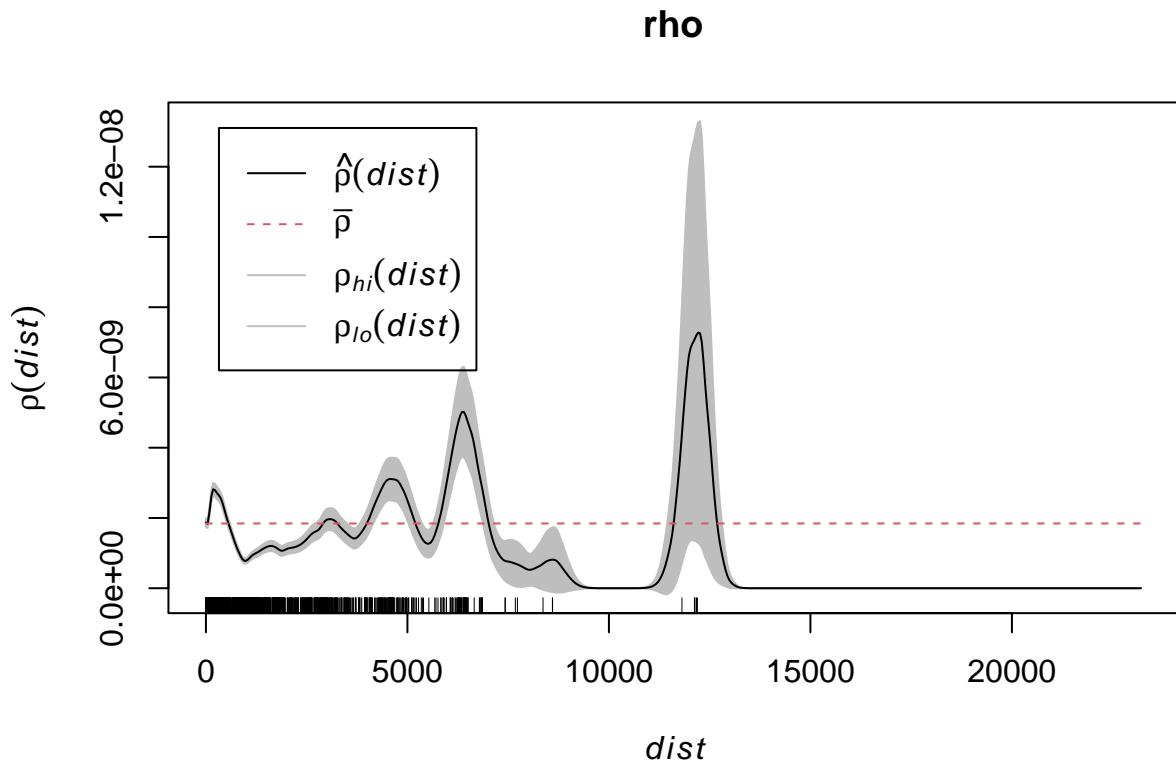
```
## tile
##      (0,11.6] (11.6,50.2] (50.2,86.9] (86.9,100]
##      582          533          455          177
```



2.3.4.c Covariate Variable : Distance to Water Followed by 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]
##      785           220                  267                 424
```



2.3.4.d Section Conclusion Observation :

- For Elevation Level :
 - It is obvious that the fungi is overwhelmingly correlated to the low elevation level.
 - The proportion of occurrence that appears in the lowest elevation sector accounts for about 95% of the identified points.
 - A significant clustering is observed at the low elevation.
 - There are basically a very few (if any) occurrence for elevation higher than around 400m.
- For Forest and Distance to Water :
 - It is observed that the fungi is correlated to both Forest and distance .
 - Clustering of observed at the low forest value range and at middle distance to water level.
 - For the highest forest value region, the intensity has been decreasing to near-zero intensity.

2.3.5 Second Moment Descriptives

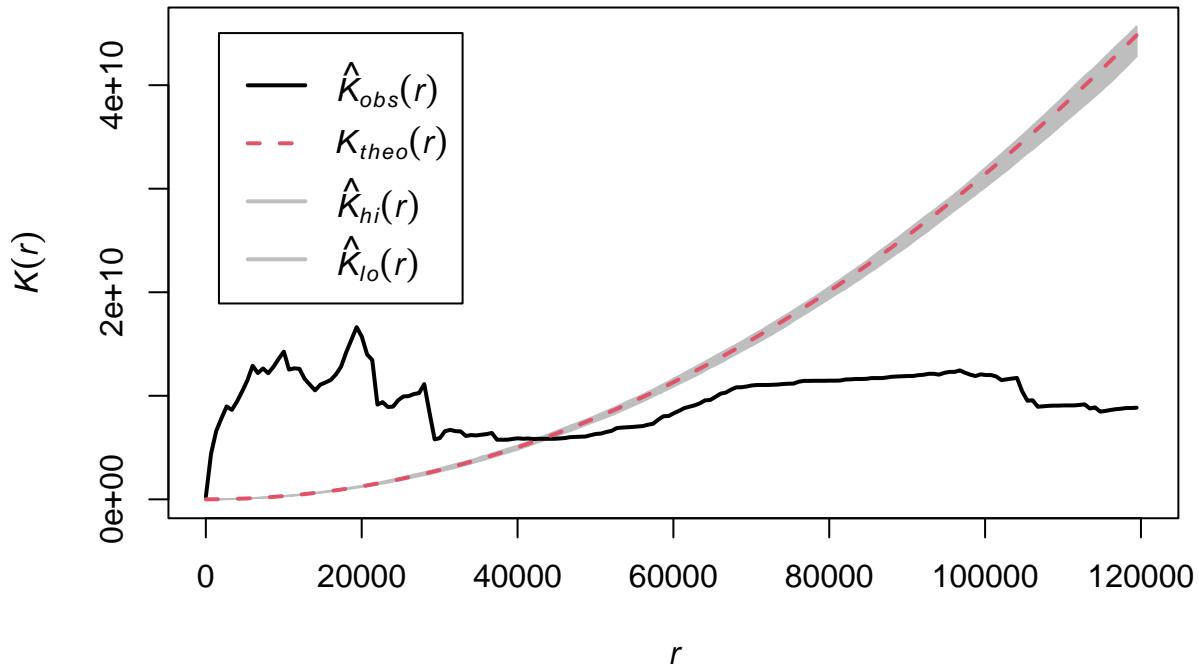
To continue the analysis, we will explore the second moment descriptives to uncover any variances and correlation characteristics of the data.

2.3.5.a Ripley's K-function We firstly use the typical K-function to measure the spatial clustering and point pattern.

```
# 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.

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



However, note that the above analysis assumed homogeneity. In our case, as previous analysis reveals that there is inhomogeneity in our data, 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)

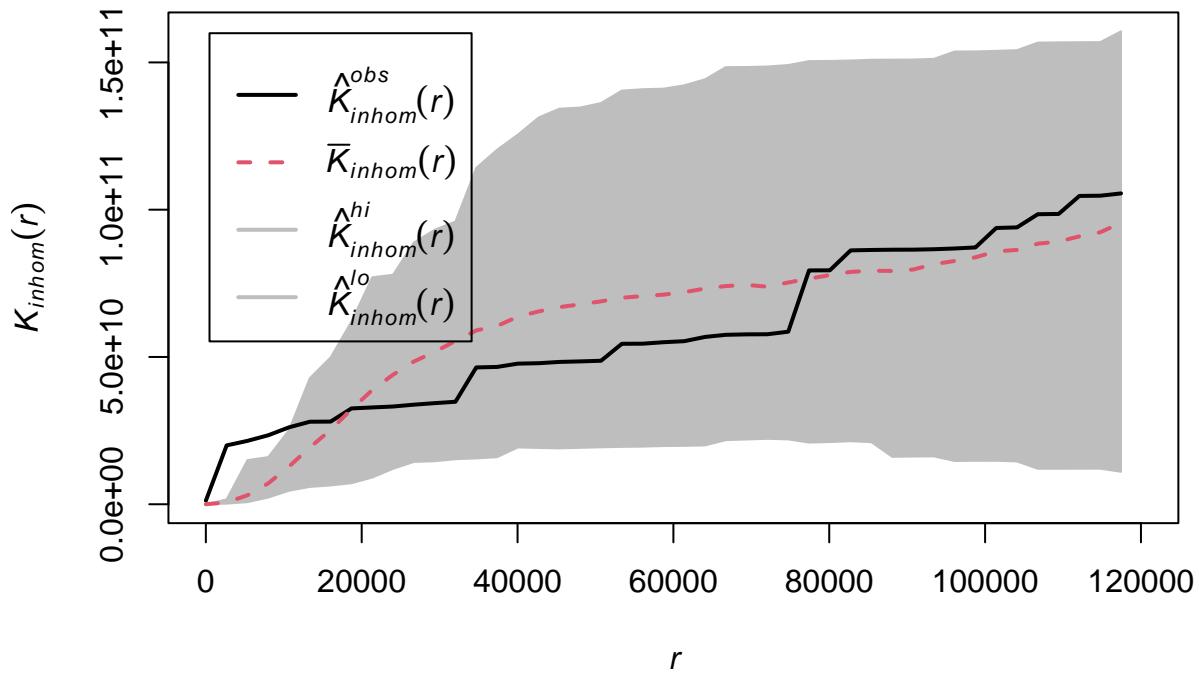
#Estimate a strictly positive density
lambda_asc_pos <- density(asc_data_ppp,
                           sigma=bw.ppl,
                           positive=TRUE)

#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))
```

Ripley's K-function (Inhomogeneity)



Finding :

- When assumed homogeneity, the observed data shows a strong clustering at small r value range.
- When corrected for inhomogeneity, except that there is some evidence pointing to clustering at the starting region r (0-10,000), obvious clustering pattern is no longer observed.

2.3.5.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

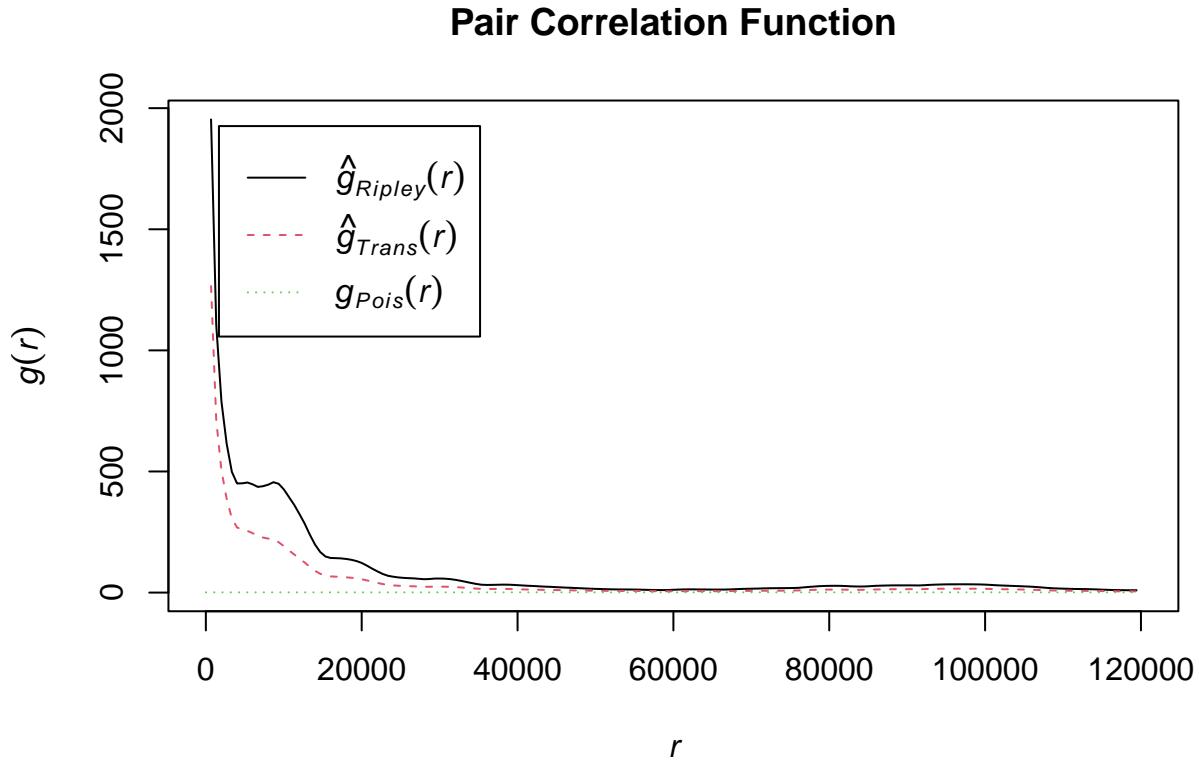
## Function value object (class 'fv')
## for the function r -> g(r)
##
##          Math.label      Description
## r           r             distance argument r
## theo     g[Pois](r)    theoretical Poisson g(r)
## trans   hat(g)[Trans](r) translation-corrected estimate of g(r)
## iso     hat(g)[Ripley](r) 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(0,120000),main="Pair Correlation Function")

```



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

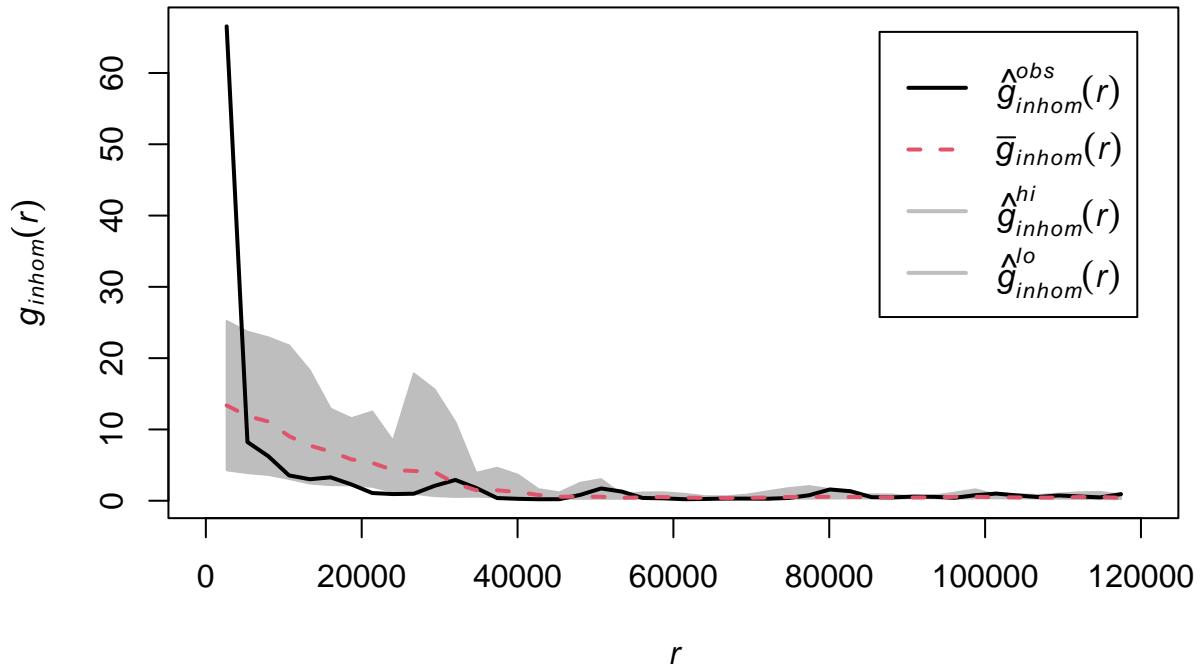
```

#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.

2.3.6 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 parsimony as much as possible. We will try to start with the simplest linear models. Then we will adjust the model according to the data behaviour and increase the model complexity if situation warranted.

OK, as the above covariate analysis shows possibility of relation with Elevation, Dist_Water and Forest, we will start with a simple model comprising of all these three variables as below.

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

```
## 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
```

```

## -1.554979e+01 -8.296173e-03 7.447185e-05 -1.888729e-02
##
##             Estimate      S.E.      CI95.lo      CI95.hi Ztest
## (Intercept) -1.554979e+01 4.578366e-02 -1.563952e+01 -1.546006e+01 *** 
## Elevation    -8.296173e-03 1.475849e-04 -8.585434e-03 -8.006912e-03 *** 
## Dist_Water   7.447185e-05 1.070499e-05  5.349046e-05  9.545325e-05 *** 
## Forest       -1.888729e-02 8.248117e-04 -2.050390e-02 -1.727069e-02 *** 
##             Zval
## (Intercept) -339.636224
## Elevation    -56.212900
## Dist_Water   6.956742
## Forest       -22.898918
## Problem:
## Values of the covariate 'Elevation' were NA or undefined at 0.02% (1 out of
## 5445) of the quadrature points

```

From this table, all three variables are found to be significant.

In addition, from the rhohat plots above, all three variables have not shown linear relation with the points. So, we proceed to increment from linear to quadratic relation to increase the model complexity to see the performance.

```

fit <- ppm(asc_data_ppp ~ Elevation + I(Elevation^2) + Dist_Water + I(Dist_Water^2) + Forest + I(Forest^2)
fit

```

```

## Nonstationary Poisson process
## Fitted to point pattern dataset 'asc_data_ppp'
##
## Log intensity: ~Elevation + I(Elevation^2) + Dist_Water + I(Dist_Water^2) +
## Forest + I(Forest^2)
##
## Fitted trend coefficients:
##     (Intercept)      Elevation  I(Elevation^2)      Dist_Water I(Dist_Water^2)
## -1.531795e+01 -1.070888e-02  2.920187e-06   3.475518e-04 -3.611186e-08
##           Forest      I(Forest^2)
## -3.601118e-02   1.916898e-04
##
##             Estimate      S.E.      CI95.lo      CI95.hi Ztest
## (Intercept) -1.531795e+01 5.621098e-02 -1.542812e+01 -1.520778e+01 *** 
## Elevation    -1.070888e-02 1.825758e-04 -1.106672e-02 -1.035104e-02 *** 
## I(Elevation^2) 2.920187e-06 9.220401e-08  2.739471e-06  3.100904e-06 *** 
## Dist_Water   3.475518e-04 3.210804e-05  2.846212e-04  4.104824e-04 *** 
## I(Dist_Water^2) -3.611186e-08 4.437988e-09 -4.481015e-08 -2.741356e-08 *** 
## Forest      -3.601118e-02 2.752538e-03 -4.140606e-02 -3.061631e-02 *** 
## I(Forest^2)  1.916898e-04 2.926991e-05  1.343218e-04  2.490577e-04 *** 
##             Zval
## (Intercept) -272.508190
## Elevation    -58.654426
## I(Elevation^2) 31.670933
## Dist_Water   10.824447
## I(Dist_Water^2) -8.136989
## Forest      -13.082902
## I(Forest^2)  6.549040
## Problem:
## Values of the covariate 'Elevation' were NA or undefined at 0.02% (1 out of

```

```

## 5445) of the quadrature points
##
## *** 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] 63903.24

```

```

## [1] 64198.62

```

```

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

```

```

## [1] 295.3815

```

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 + Dist_Water + Forest      Poisson
## Model 2: ~Elevation + I(Elevation^2) + Dist_Water + I(Dist_Water^2) + Forest + I(Forest^2)    Poisson
##   Npar Df Deviance  Pr(>Chi)
## 1     4
## 2     7  3   301.38 < 2.2e-16 ***
## ---
## 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
- With such a significant delta AIC value, the extra complexity is well supported.
- So, a possible model should be [model to be changed.....parameters to be updated.....]

$$\lambda_{ASC}(u) = e^{-15.3 - 0.011 \text{ elevation}(u) - 0.0000029 \text{ elevation}(u)^2 - 0.00035 \text{ forest}(u) - 0.000000036 \text{ forest}(u)^2}$$

2.3.7 Model Validation

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

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

2.3.7.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 = 2257.6, df = 6, 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.

2.3.8 Higher Order Polynomial Fitting with Spline and Validation

As the above analysis indicated a room for improvement, we would also like to try GAMs. However, as mentioned in the lab material, GAMs should allow more flexible covariate effects, but it has not been covered in course. So, we would just have a very brief test using some dummy parameters given in the lab materials to have an initial impression of its potential performance.

```

library(splines)

#Fit the PPP model
fit_smooth <- ppm(asc_data_ppp ~ bs(Elevation,5) + bs(Forest, 5) + bs(Dist_Water,5) , data = BC, use.gam=TRUE)

fit_smooth

## Nonstationary Poisson process
## Fitted to point pattern dataset 'asc_data_ppp'
##
## Log intensity: ~bs(Elevation, 5) + bs(Forest, 5) + bs(Dist_Water, 5)
##
## Fitted trend coefficients:
##          (Intercept) bs(Elevation, 5)1 bs(Elevation, 5)2 bs(Elevation, 5)3
## -14.9174536      -1.8084055     -5.4654103    -13.8896499
## bs(Elevation, 5)4 bs(Elevation, 5)5 bs(Forest, 5)1 bs(Forest, 5)2
##       6.3545167     -222.8213032      1.5998639     -2.1591734
## bs(Forest, 5)3   bs(Forest, 5)4   bs(Forest, 5)5 bs(Dist_Water, 5)1
##      0.2557491      -1.5366760      -1.0190291      0.2393593
## bs(Dist_Water, 5)2 bs(Dist_Water, 5)3 bs(Dist_Water, 5)4 bs(Dist_Water, 5)5
##      -0.1967620      3.0902045     -3.0348470     -5.9810698
##
## For standard errors, type coef(summary(x))
## Problem:
## Values of the covariate 'Elevation' were NA or undefined at 0.02% (1 out of
## 5445) of the quadrature points

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

```

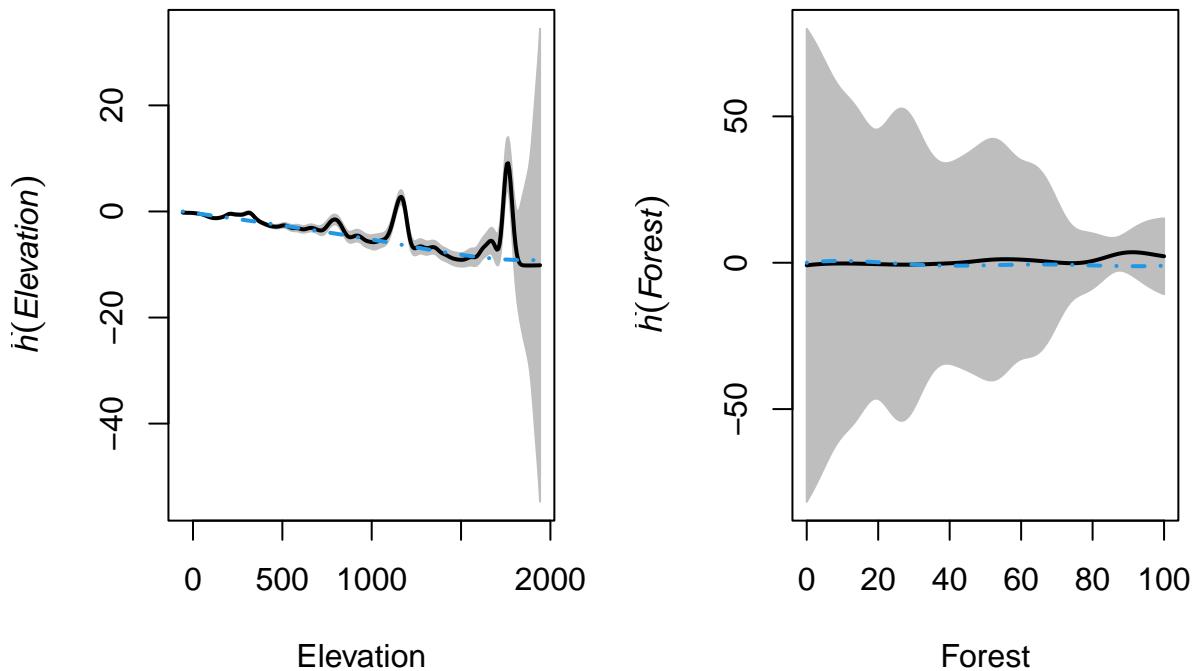
```

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

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

#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")

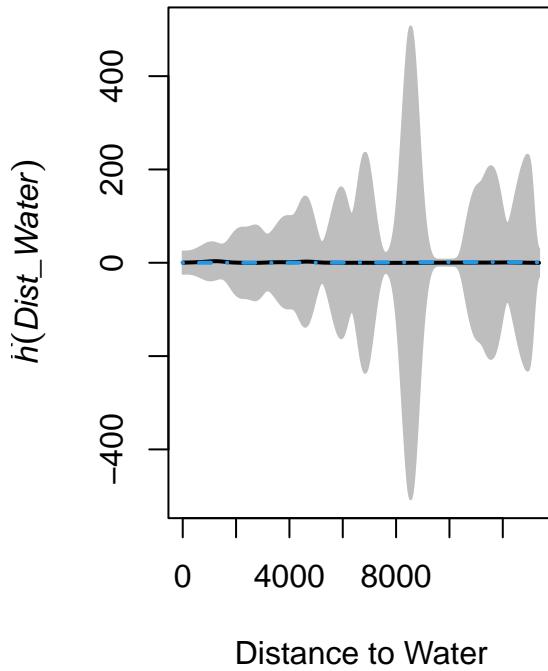
```



```

plot(par_res_water,
      legend = FALSE,
      lwd = 2,
      main = "",
      xlab = "Distance to Water")

```



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

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

## [1] 63903.24

## [1] 63671.42

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

## [1] 231.8208

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

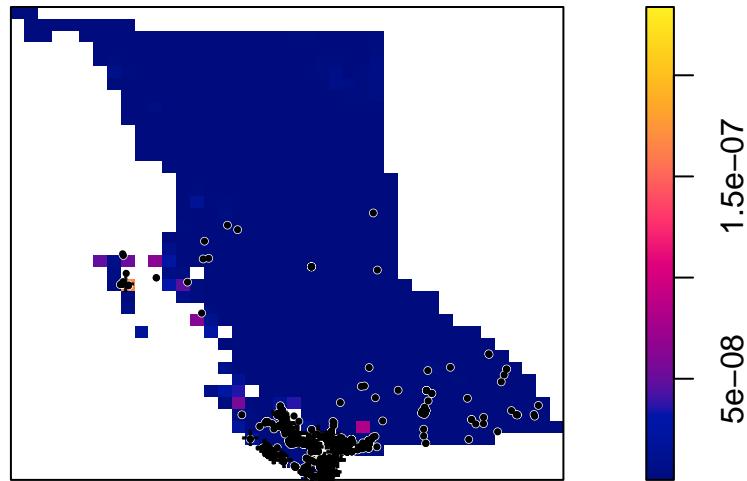
## Analysis of Deviance Table
##
## Model 1: ~Elevation + I(Elevation^2) + Dist_Water + I(Dist_Water^2) + Forest + I(Forest^2) Poisson
## Model 2: ~bs(Elevation, 5) + bs(Forest, 5) + bs(Dist_Water, 5) Poisson
##   Npar Df Deviance Pr(>Chi)
## 1     7
## 2    16  9  249.82 < 2.2e-16 ***
## ---
## Signif. 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 locations
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)
```

Estimated Fungi intensity



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.