Honey Bees (Apis mellifera Linnaeus) Spatial Analysis

Alyssa Foote, Noman Mohammad, and Vimaljeet Singh

r format(Sys.time(), '%d %B, %Y')

1 Introduction

Spatial statistics have increasingly become an essential tool in understanding species distribution and habitat preferences, as well as in informing conservation and management decisions. In this report, we will analyze the occurrence data of the western honey bee (Apis mellifera Linnaeus) in the province of British Columbia (BC), Canada.

The western honey bee, a critical pollinator species, plays a vital role in agriculture and ecosystem services. Understanding the distribution patterns and potential drivers of honey bee occurrence can provide valuable insights for the conservation of this species and the ecosystems they support.

The honeybee is a vital pollinator that plays a significant role in both agricultural production and the maintenance of biodiversity in natural ecosystems. These insects contribute to the pollination of a wide range of crops, which directly affects human food supply, as well as sustaining the health and productivity of various plant species within their habitats (Klein et al., 2007).

British Columbia (BC), a province within Canada, encompasses diverse ecosystems that support a rich array of plant and animal species. Honeybees are vital contributors to the pollination processes within these ecosystems and are essential for the productivity of the region's agricultural sector. Understanding the spatial distribution of honeybee populations in British Columbia is crucial for developing effective conservation and management strategies to protect these invaluable pollinators.

In this study, we aim to explore the spatial distribution of honeybee populations (Apis mellifera) in British Columbia using occurrence data obtained from the Global Biodiversity Information Facility (GBIF) database. Our analysis will focus on describing the spatial distribution of Apis mellifera in the region, identifying any clustering or dispersion patterns in the occurrence data, and assessing the relationships between honeybee occurrence and various covariates, such as elevation, forest cover, Human Footprint Index (HFI), and distance to water sources. To achieve our objectives, we will construct a Poisson process model to analyze the spatial distribution of Apis mellifera occurrences in British Columbia. We will explore various statistical techniques, including creating rho plots, and examining the first

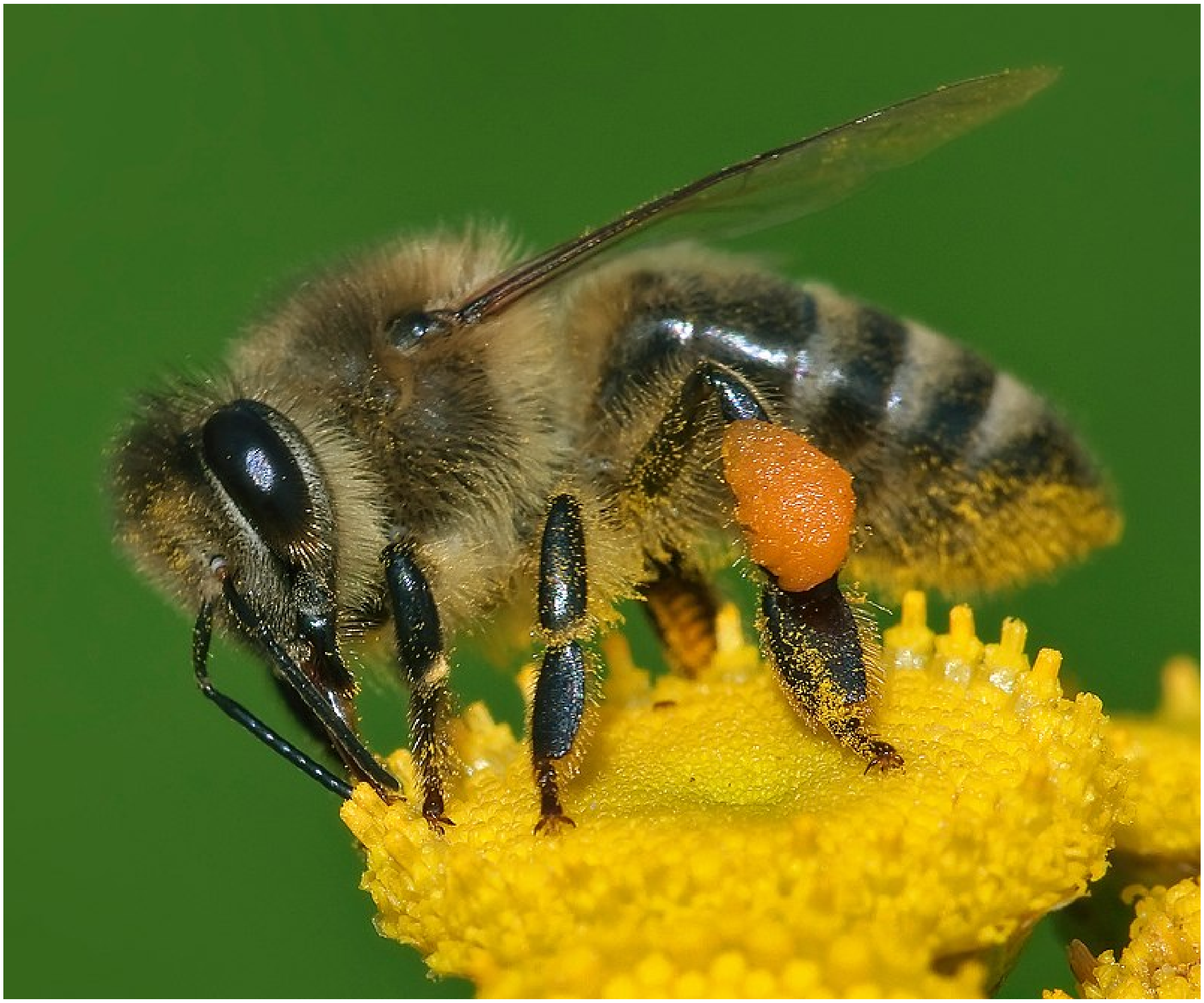


Figure 1: Apis mellifera

and second moment statistics to gain insights into the clustering or dispersion patterns in the data. Furthermore, we will evaluate the relationship between honeybee occurrence and covariates such as elevation, forest cover, HFI, and distance to water sources, using spatial regression analysis. This will enable us to identify significant predictors that influence the spatial distribution of honeybee populations in the region. Additionally, we will explore collinearity between covariates, and use model validation techniques such as chi-squared tests and AIC scores. Overall, our approach will involve a combination of statistical modeling and exploratory data analysis techniques to gain a deeper understanding of the factors that influence honeybee occurrence in British Columbia.

2 Methods - All, see subsections

There should be enough information that anyone can reproduce the workflow if they had access to the data. Length: As long as necessary.

2.1 Data collection and Description

This dataset contains occurrence records of the honey bee species Apis mellifera Linnaeus in the province of British Columbia, Canada. The data was collected using the 'rgbif' package in R, which allows for the retrieval of biodiversity data from the Global Biodiversity Information Facility (GBIF) database. It is important to note that the dataset may be subject to potential biases due to the reliance on self-reporting by the individuals or institutions responsible for collecting the data. This means that the accuracy and completeness of the information provided may vary depending on the quality of the reporting.

The first step involved querying the number of records available for Apis mellifera Linnaeus in British Columbia. The complete dataset was then downloaded by specifying the scientific name, coordinates, country, and stateProvince parameters. After obtaining the data, it was saved as a CSV file.

The dataset contains various variables, including decimalLongitude, decimalLatitude, country, stateProvince, occurrenceStatus, coordinateUncertaintyInMeters, taxonID, catalogNumber, institutionCode, eventTime, verbatimEventDate, collectionCode, gbifID, verbatimLocality, class, isInCluster, year, month, day, eventDate, modified, and lastInterpreted. These variables provide information on the location of each occurrence, the institution responsible for collecting the data, and other details about the occurrence event.

To clean the dataset, records indicating absence or zero-abundance were removed. Furthermore, the dataset's coordinates were adjusted to match the covariate data's format. A SpatialPointsDataFrame object was created using the cleaned dataset, and the WGS84 CRS (EPSG:4326) was assigned to it. The coordinates were then transformed to match the CRS of the BC_win object, which has the Albers Equal Area Conic projection, and the transformed coordinates were added to the original cleaned dataframe.

Finally, the cleaned and transformed data was saved as a new CSV file.

In addition to the occurrence data, covariate data for the province of British Columbia is available. The covariate dataset includes variables such as Elevation, Forest, HFI (Human Footprint Index), and Dist_water (Distance to water). These variables provide information about the environmental conditions of each occurrence site, which can be useful for understanding the factors influencing the distribution and abundance of Apis mellifera Linnaeus in the province.

2.2 Exploratory Analysis - Vimal

Provide a detailed description of the analytical workflow that was applied to the data, citing any relevant literature and statistical packages employed.

2.3 Model Development

The spatstats package, additionally has numerous functions that allow for easy predictive modeling on spatial data. For this study, before any models were built scaling of the elevation and distance to water (dist_water) covariates was required. This is because the scales for these variables have a wider range than the scales for the human footprint index, 0 to 10, and the forest coverage, 0 to 100 percent. Furthermore, as with all modeling building, it was also important to check for collinearity among the covariates. This was done using the package's cor.im function. Then numerous models, in the form of linear, quadratic, and generalize additive (gam), were built using the ppm function. Additionally, a b-spline function was used from the splines package for the gam models. Each of these models were evaluated by reviewing the partial residuals, AIC scores, likelihood ratio test, and diagnostics via the parres, AIC, anova, and diagnose ppm functions. Finally, all the models were tested on their ability to predict the intensity of honey bees in British Columbia using a fitted trend plot and the quadrat.test function.

3 Results

3.1 Exploratory Analysis - Vimal

Describe your statistical findings. Tables and figures should be used throughout. Length: As long as necessary.

3.2 Model Selection

As describe in the Model Development section, above, before developing any predictive models, it is important to review the collinearity among the covariates. Table 1 and Figure 2, show that although there is some correlation between all covariates, the strongest is between elevation and HFI with a negative correlation of -0.266. Since this value is less than the typical threshold of ±0.4, the model building proceeded without taking these correlations into consideration.

Table 1: Covariate Correlation Matrix

	elev	forest	HFI	dist_water
elev	1.0000000	-0.2620472	-0.2662563	-0.0342639
forest	-0.2620472	1.0000000	0.0661554	0.0482544
HFI	-0.2662563	0.0661554	1.0000000	0.1322941
dist_water	-0.0342639	0.0482544	0.1322941	1.0000000

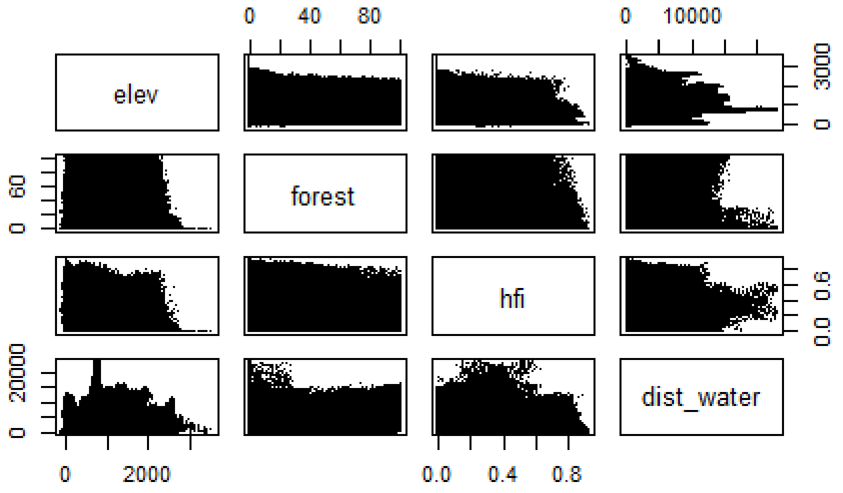
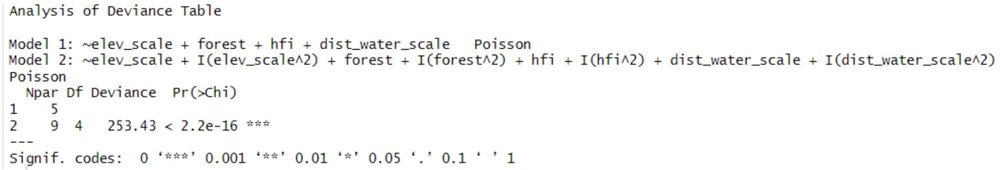


Figure 2: Covariate Correlation Matrix

Based on the results describe in the Exploratory section, the first model taken into consideration was a full quadratic model. This was because of the evidence that the relationship between honey bee intensity and the covariates was at least not linear. Further proven by comparing the AIC values - 8.7043583×10^4 for the linear model versus 8.6798149×10^4 for the full quadratic model - and running a likelihood ratio test that rejected the linear model in favour of this full quadratic model, seen in Figure 3. However, based on the predicted intensity plot in Figure 4, it is clear that this model is not very good. There are many areas of the province that are predicted to have high intensity even though there are few bees located there, which are represented by the black dots. The poor model fit is further exemplified in the quadrat test for deviance as seen in Figure 5. The tiny p-value of 0.001 means that the suitability of this model for predicting the intensity of honey bees should be rejected. Additionally the model summary, in Figure 6, indicates that only the quadratic term of the dist_water covariate is significant.



```
Analysis of Deviance Table

Model 1: ~elev_scale + forest + hfi + dist_water_scale   Poisson
Model 2: ~elev_scale + I(elev_scale^2) + forest + I(forest^2) + hfi + I(hfi^2) + dist_water_scale + I(dist_water_scale^2)
Poisson
  Npar Df Deviance  Pr(>Chi)
1    5
2    9  4   253.43 < 2.2e-16 ***
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Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Figure 3: Likelihood Ratio Test - Full Quadratic Model

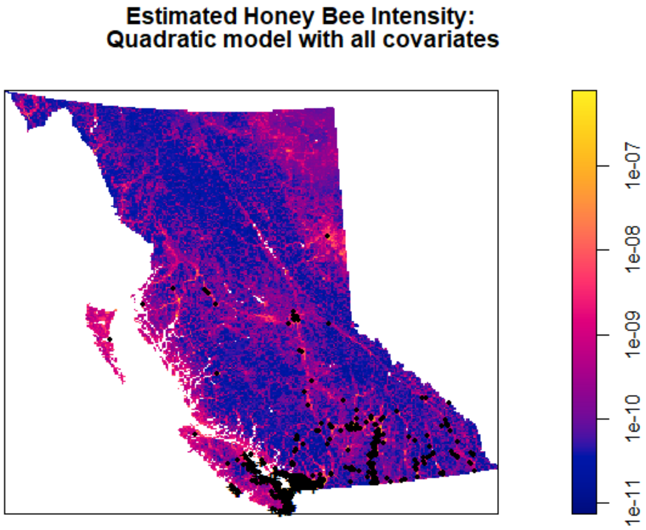
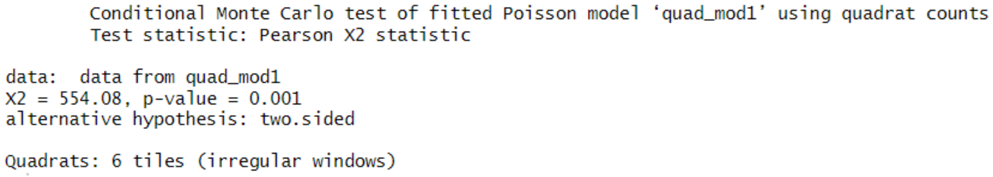

Estimated Honey Bee Intensity:
Quadratic model with all covariates
1e-07
1e-08
1e-09
1e-10
1e-11

Figure 4: Predicted Honey Bee Intensity - Full Quadratic Model



```
        Conditional Monte Carlo test of fitted Poisson model ‘quad_mod1’ using quadrat counts
        Test statistic: Pearson X2 statistic

data:  data from quad_mod1
X2 = 554.08, p-value = 0.001
alternative hypothesis: two.sided

Quadrats: 6 tiles (irregular windows)
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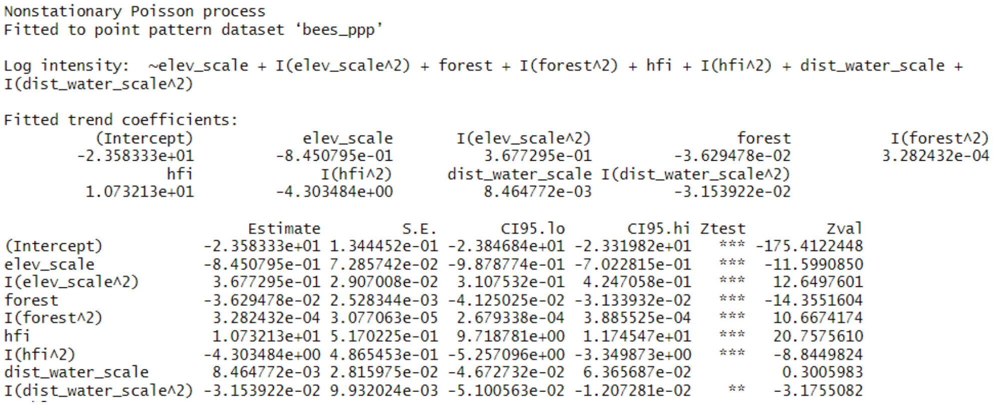
Figure 5: Predicted Deviance - Full Quadratic Model



```
Nonstationary Poisson process
Fitted to point pattern dataset ‘bees_ppp’

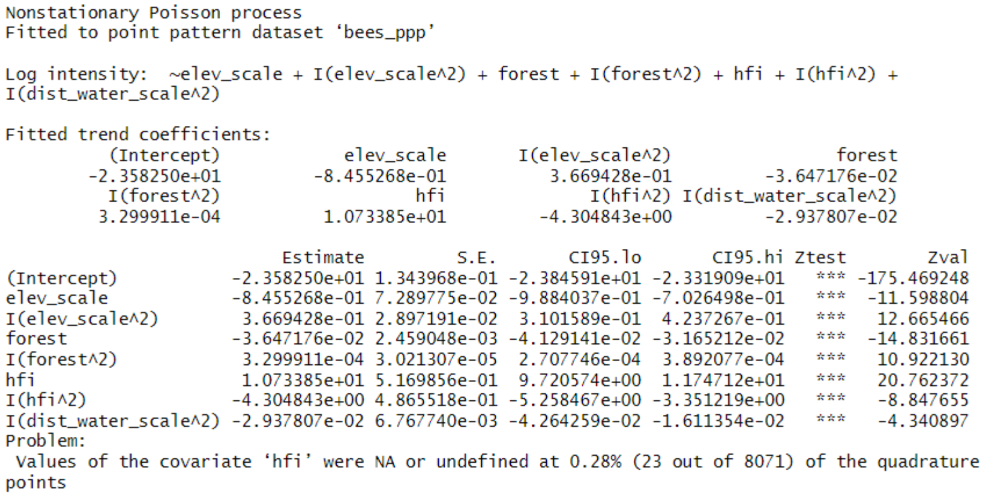
Log intensity:  ~elev_scale + I(elev_scale^2) + forest + I(forest^2) + hfi + I(hfi^2) + dist_water_scale +
I(dist_water_scale^2)

Fitted trend coefficients:
         (Intercept)           elev_scale       I(elev_scale^2)               forest          I(forest^2)
       -2.358333e+01        -8.450795e-01          3.677295e-01        -3.629478e-02         3.282432e-04
                 hfi             I(hfi^2)      dist_water_scale I(dist_water_scale^2)
        1.073213e+01        -4.303484e+00          8.464772e-03        -3.153922e-02

                          Estimate         S.E.       CI95.lo       CI95.hi Ztest         Zval
(Intercept)          -2.358333e+01 1.344452e-01 -2.384684e+01 -2.331982e+01   *** -175.4122448
elev_scale           -8.450795e-01 7.285742e-02 -9.878774e-01 -7.022815e-01   ***  -11.5990850
I(elev_scale^2)       3.677295e-01 2.907008e-02  3.107532e-01  4.247058e-01   ***   12.6497601
forest               -3.629478e-02 2.528344e-03 -4.125025e-02 -3.133932e-02   ***  -14.3551604
I(forest^2)           3.282432e-04 3.077063e-05  2.679338e-04  3.885525e-04   ***   10.6674174
hfi                   1.073213e+01 5.170225e-01  9.718781e+00  1.174547e+01   ***   20.7575610
I(hfi^2)             -4.303484e+00 4.865453e-01 -5.257096e+00 -3.349873e+00   ***   -8.8449824
dist_water_scale      8.464772e-03 2.815975e-02 -4.672732e-02  6.365687e-02          0.3005983
I(dist_water_scale^2) -3.153922e-02 9.932024e-03 -5.100563e-02 -1.207281e-02    **   -3.1755082
```

Figure 6: Full Quadratic Model Summary

Therefore, the next model examined was another quadratic model but without the insignificant ‘dist_water’ term. While all the predictors were seen as significant in this model, as seen in Figure 7, the predicted intensity plot did not change, Figure 8. This model was also only a small improvement in AIC from the full quadratic model, 8.6796239×10^4 from 8.6798149×10^4. However, the likelihood ratio test, as seen in Figure 9, does not support the reduced complexity since the p-value of $0.7636 > 0.05$. Meaning that the full quadratic model cannot be rejected in favour of the quadratic model without the ‘dist_water term’. Furthermore, both models had nearly identical diagnostic plots, seen in Figure 10, that indicate both models do not predicate the y coordinates adequately. That is for all parts of the province, the sum of residuals on the y coordinate fall outside the acceptable confidence band indicated by the dotted line. For the x coordinate, only the western and eastern edges of the province had acceptable residuals. No further diagnostics for either of these models were reviewed as a result.



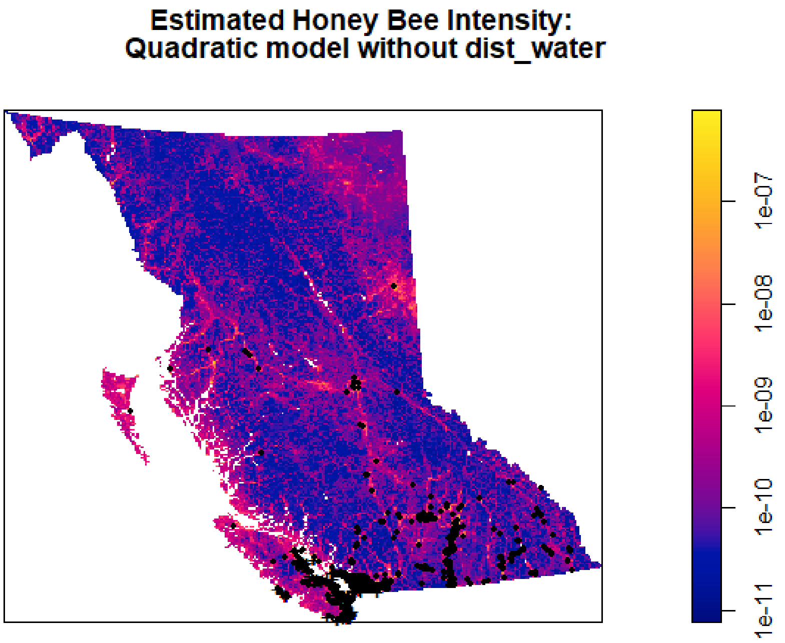
```
Nonstationary Poisson process
Fitted to point pattern dataset ‘bees_ppp’

Log intensity:  ~elev_scale + I(elev_scale^2) + forest + I(forest^2) + hfi + I(hfi^2) +
I(dist_water_scale^2)

Fitted trend coefficients:
          (Intercept)            elev_scale       I(elev_scale^2)                forest
        -2.358250e+01         -8.455268e-01          3.669428e-01         -3.647176e-02
          I(forest^2)                   hfi              I(hfi^2) I(dist_water_scale^2)
         3.299911e-04          1.073385e+01         -4.304843e+00         -2.937807e-02

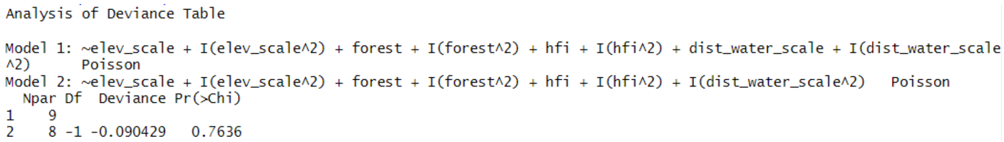
                          Estimate         S.E.       CI95.lo       CI95.hi Ztest        Zval
(Intercept)          -2.358250e+01 1.343968e-01 -2.384591e+01 -2.331909e+01   *** -175.469248
elev_scale           -8.455268e-01 7.289775e-02 -9.884037e-01 -7.026498e-01   ***  -11.598804
I(elev_scale^2)       3.669428e-01 2.897191e-02  3.101589e-01  4.237267e-01   ***   12.665466
forest               -3.647176e-02 2.459048e-03 -4.129141e-02 -3.165212e-02   ***  -14.831661
I(forest^2)           3.299911e-04 3.021307e-05  2.707746e-04  3.892077e-04   ***   10.922130
hfi                   1.073385e+01 5.169856e-01  9.720574e+00  1.174712e+01   ***   20.762372
I(hfi^2)             -4.304843e+00 4.865518e-01 -5.258467e+00 -3.351219e+00   ***   -8.847655
I(dist_water_scale^2) -2.937807e-02 6.767740e-03 -4.264259e-02 -1.611354e-02   ***   -4.340897
Problem:
 Values of the covariate ‘hfi’ were NA or undefined at 0.28% (23 out of 8071) of the quadrature
points
```

Figure 7: Partial Quadratic Model Summary



Estimated Honey Bee Intensity:
Quadratic model without dist_water

Figure 8: Predicted Honey Bee Intensity - Partial Quadratic Model



```
Analysis of Deviance Table

Model 1: ~elev_scale + I(elev_scale^2) + forest + I(forest^2) + hfi + I(hfi^2) + dist_water_scale + I(dist_water_scale
^2)      Poisson
Model 2: ~elev_scale + I(elev_scale^2) + forest + I(forest^2) + hfi + I(hfi^2) + I(dist_water_scale^2)    Poisson
  Npar Df  Deviance Pr(>Chi)
1    9
2    8 -1 -0.090429   0.7636
```

Figure 9: Likelihood Ratio Test - Partial Quadratic Model

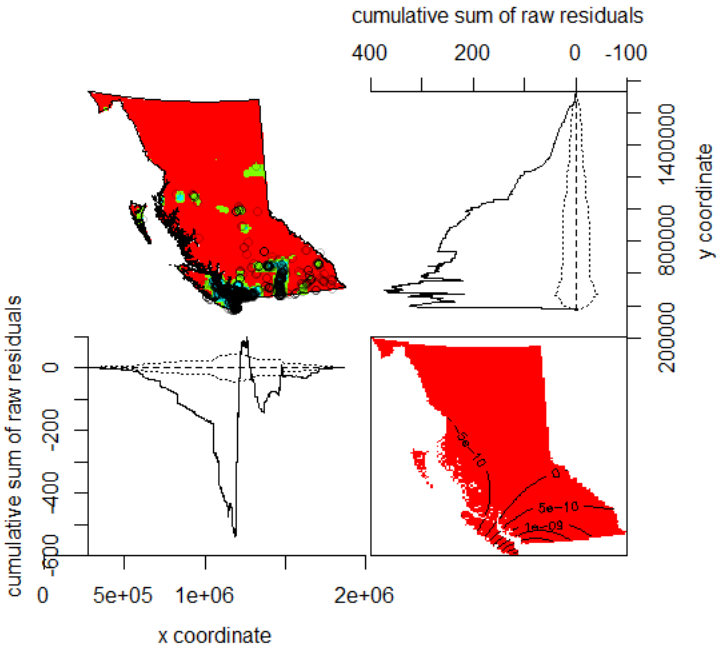
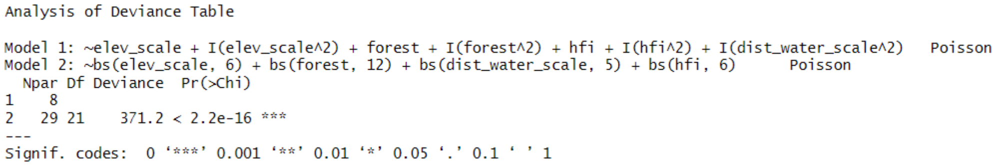


Figure 10: Diagnostics - Quadratic Models

Thus, another type of model, such as a generalized additive model (GAM), seemed appropriate. The first GAM model trialed was a full model with 6 knots on the scaled elevation, 12 knots on the forest coverage, 5 knots on the scaled distance to water, and 6 knots on the HFI. As compared to the quadratic models, this more complex model was supported by the AIC comparison, 8.6469035×10^4 versus 8.6796239×10^4, and the likelihood ratio test, as seen in Figure 11. The tiny p-value means that the quadratic model can be rejected in favour of the current gam model. A review of the partial residuals plot in Figure 12, shows that elevation, distance to water, forest coverage, and human footprint index are all well represented overall. However, as seen in a visualization of the predicted intensity, Figure 13, there are still a lot of low populated areas that have been predicted to have high intensity. The test for deviation between predicted and observed gives evidence, with a p-value of 0.001, to reject the current game model, as seen in Figure 14. The diagnostic plot, seen in Figure 15, shows further evidence that while there was an improvement in the residuals when compared to the quadratic models, there was still room for improvement.



```
Analysis of Deviance Table

Model 1: ~elev_scale + I(elev_scale^2) + forest + I(forest^2) + hfi + I(hfi^2) + I(dist_water_scale^2)   Poisson
Model 2: ~bs(elev_scale, 6) + bs(forest, 12) + bs(dist_water_scale, 5) + bs(hfi, 6)      Poisson
  Npar Df Deviance  Pr(>Chi)
1    8
2   29 21    371.2 < 2.2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Figure 11: Likelihood Ratio Test - GAM Model

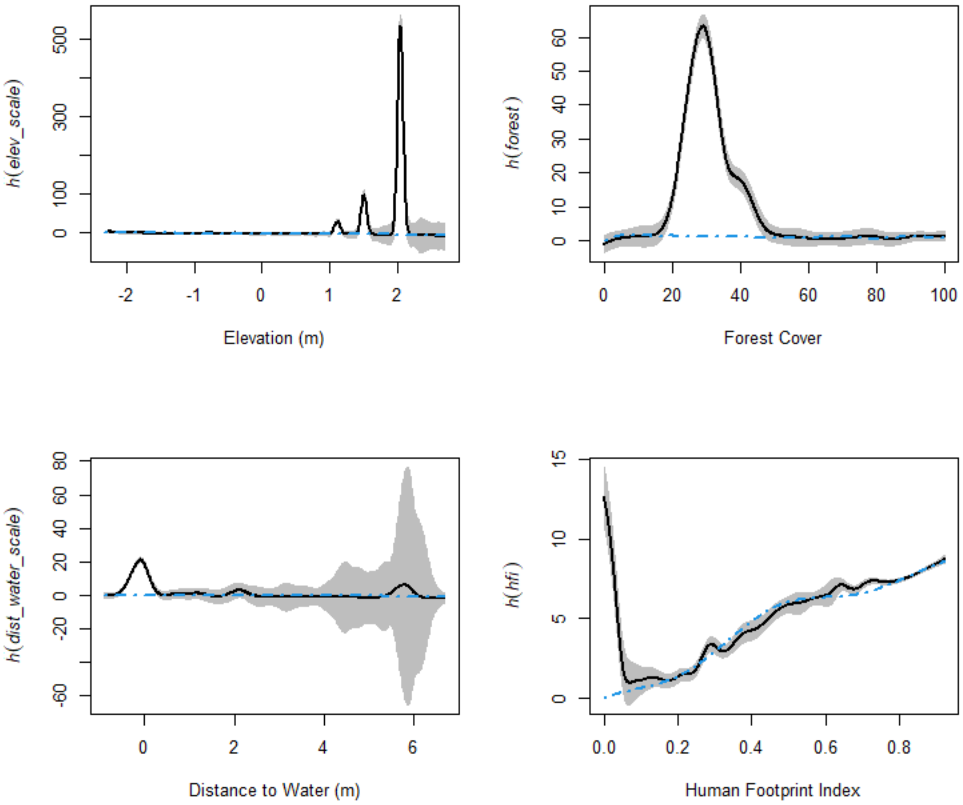


Figure 12: Partial Residuals - GAM Model

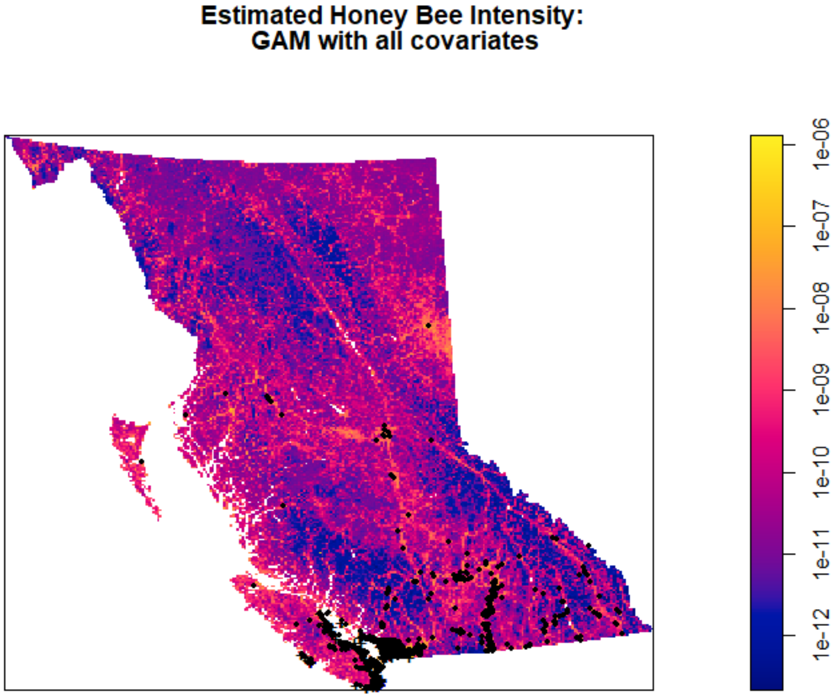
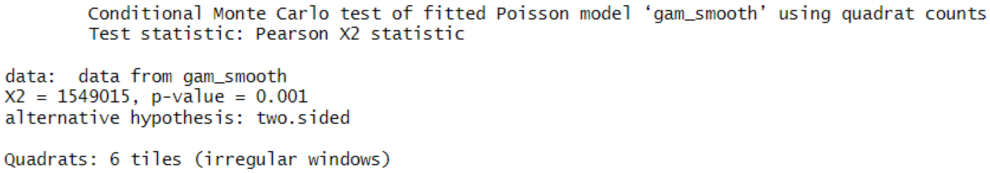


Figure 13: Predicted Honey Bee Intensity - GAM Model



```
        Conditional Monte Carlo test of fitted Poisson model ‘gam_smooth’ using quadrat counts
        Test statistic: Pearson X2 statistic

data:  data from gam_smooth
X2 = 1549015, p-value = 0.001
alternative hypothesis: two.sided

Quadrats: 6 tiles (irregular windows)
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Figure 14: Predicted Deviance - GAM Model

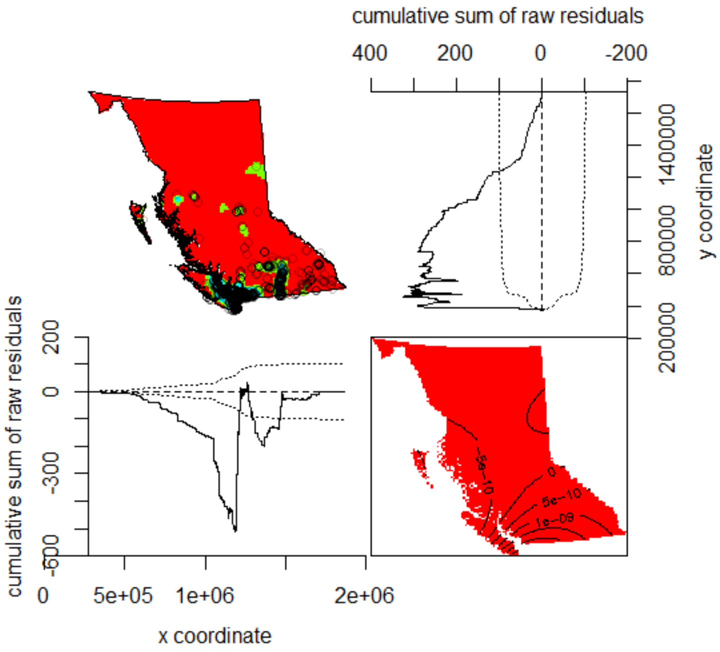
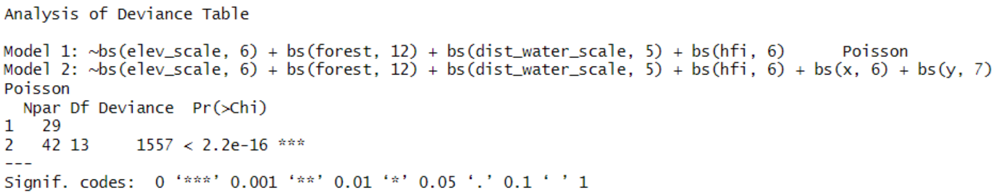


Figure 15: Diagnostics - GAM Model

Since no other covariates were available for consideration, the last gam model was built with the same covariates as the previous model with the addition of the x and y coordinates as proxy covariates. These new predictors had 6 knots on the x coordinate and 7 knots on the y coordinate. When compared to the previous gam model, this new model did better with an AIC of 8.4938034×10^4, as compared to 8.6469035×10^4, and is supported as per the small p-value of $< 2.2e^{-16}$ seen in the likelihood ratio results in Figure 16. The partial residuals plot, in Figure 17, also indicate that all variables are better represented. Although this model should be rejected as per the quadrat test results seen in Figure 18, the resulting p-value of 0.039 is the highest of the 4 models reviewed. Meaning that the deviation between the predicted and observed values was the lowest in this model. Visually, there are some further improvements in the predicted intensity plot, as seen in Figure 19. However, there are still low observation areas that are predicted to have low intensity. This is likely due to the significant amount of residuals in the lower parts of the province as seen in the diagnostics plot in Figure 20.



```
Analysis of Deviance Table

Model 1: ~bs(elev_scale, 6) + bs(forest, 12) + bs(dist_water_scale, 5) + bs(hfi, 6)      Poisson
Model 2: ~bs(elev_scale, 6) + bs(forest, 12) + bs(dist_water_scale, 5) + bs(hfi, 6) + bs(x, 6) + bs(y, 7)
Poisson
  Npar Df Deviance  Pr(>Chi)
1   29
2   42 13     1557 < 2.2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Figure 16: Likelihood Ratio Test - GAM Model with X-Y

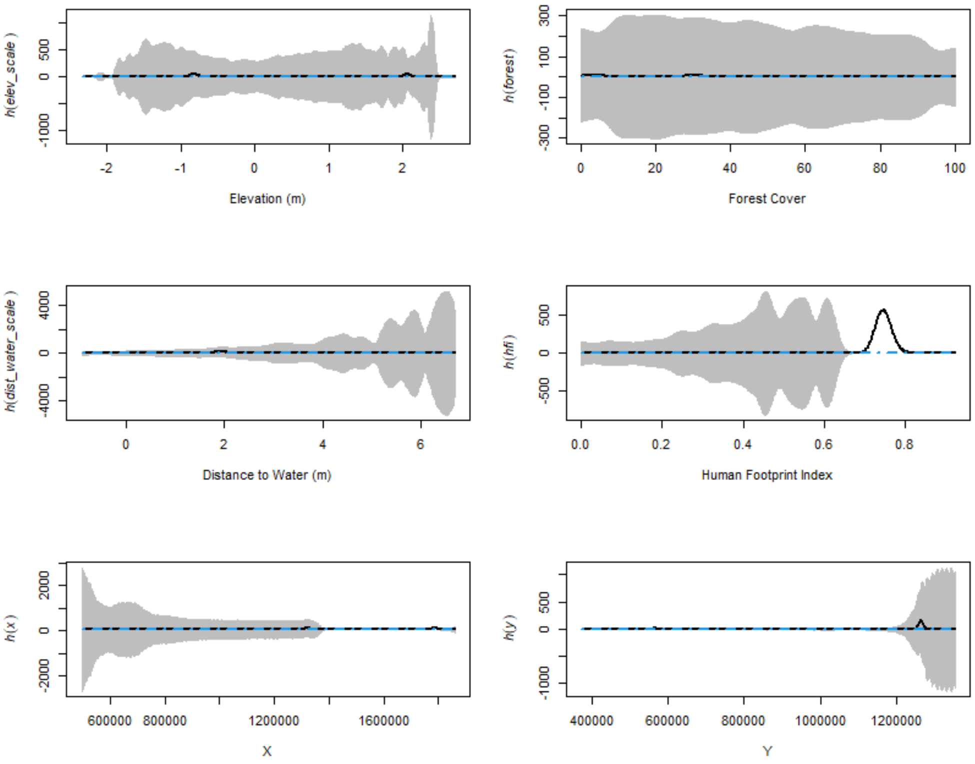
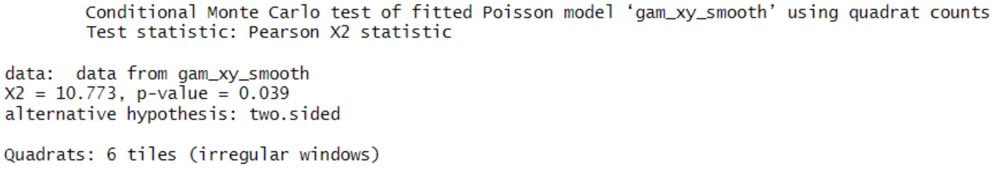


Figure 17: Partial Residuals - GAM Model with X-Y



```
        Conditional Monte Carlo test of fitted Poisson model ‘gam_xy_smooth’ using quadrat counts
        Test statistic: Pearson X2 statistic

data:  data from gam_xy_smooth
X2 = 10.773, p-value = 0.039
alternative hypothesis: two.sided

Quadrats: 6 tiles (irregular windows)
```

Figure 18: Predicted Deviance - GAM Model with X-Y

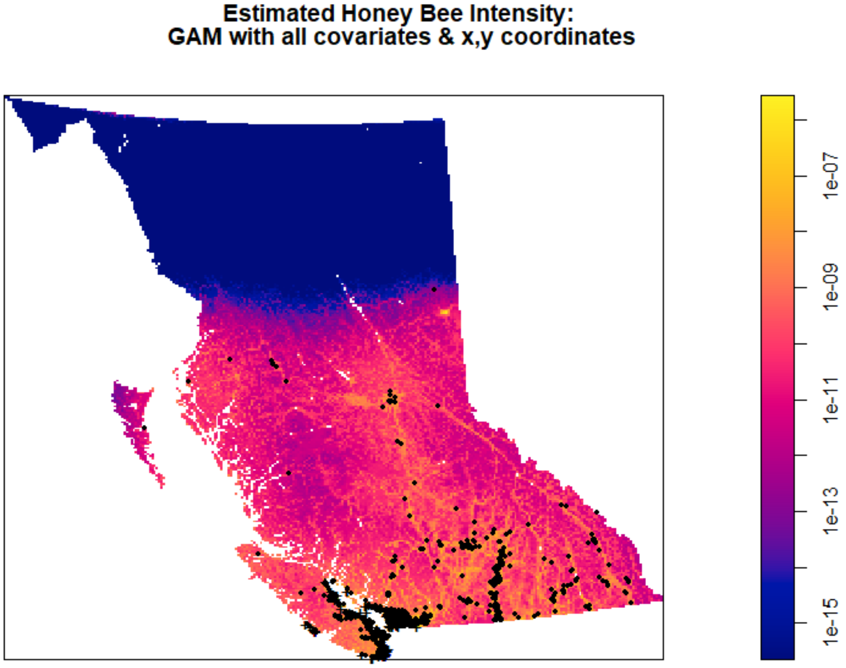

Estimated Honey Bee Intensity:
GAM with all covariates & x,y coordinates
1e-07
1e-09
1e-11
1e-13
1e-15

Figure 19: Predicted Honey Bee Intensity - GAM Model with X-Y

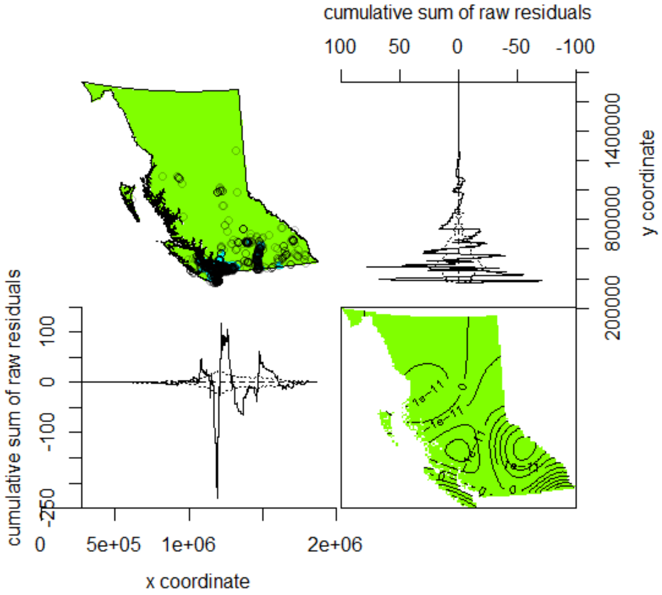


Figure 20: Diagnostics - GAM Model with X-Y

4 Discussion - Vimal and Alyssa

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

5 References - All

Klein, A. M., Vaissiere, B. E., Cane, J. H., Steffan-Dewenter, I., Cunningham, S. A., Kremen, C., & Tscharntke, T. (2007). Importance of pollinators in changing landscapes for world crops. Proceedings of the Royal Society B: Biological Sciences, 274(1608), 303–313. https://doi.org/10.1098/rspb.2006.3721