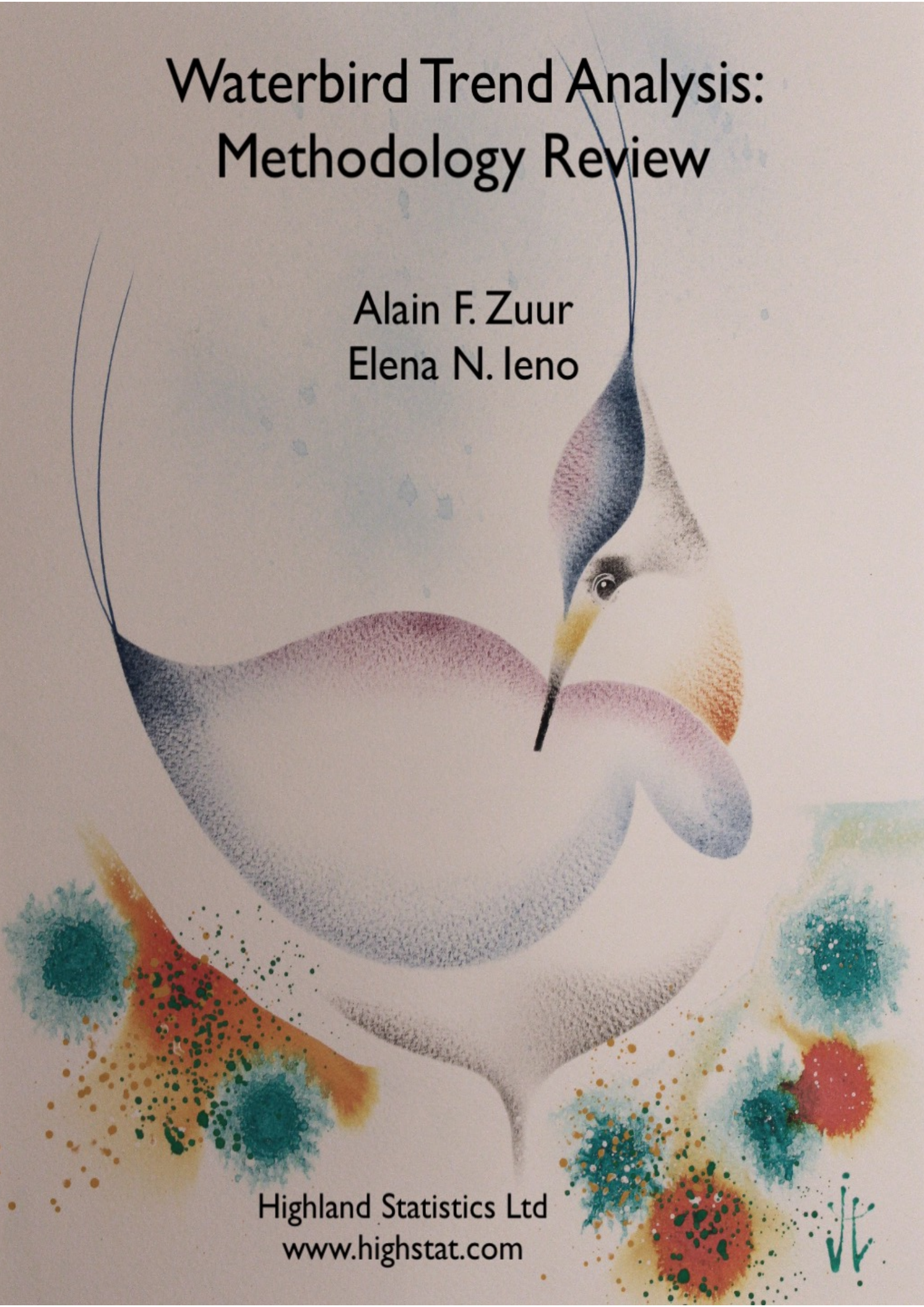
Waterbird Trend Analysis: Methodology Review

Alain F. Zuur
Elena N. Ieno



Highland Statistics Ltd
www.highstat.com

March 2021

Contents

Chapter 1

Executive summary

In this report we will analyse Red knot data from the United Kingdom and Oystercatcher data from South Africa and Namibia. Both data sets contain annual counts that are obtained from a large number of sites. The Red knot data were sampled between 1975 and 2018, and the Oystercatcher data are from 1992 to 2018. Some sites were sampled every year and other sites only once. The counts vary between 0 and 120,000.

From a statistical point of view, these data are challenging. The main problems that we encountered are spatial dependency, zero inflation, non-linear trends, missing covariates and large variation in the bird counts. Ignoring any of these problems is likely to result in statistical models that provide incorrect ecological conclusions. Adopting the *wrong* solution for a specific problem will result in poor models and incorrect conclusions as well. As an example, due to the large variation in the data the initial models were highly overdispersed. The dispersion statistic was around 500. Adopting a quasi-Poisson approach is a popular solution for dealing with overdispersion, but with such a large overdispersion one should not do this. Instead, the source of the overdispersion should be found and modelled accordingly (Hilbe, 2014).

Strong spatial correlation is present in the Red knot data (not only in the UK data but also in the European data). Ignoring spatial dependency is the worst sin that a statistician (or anyone who is analysing data) can commit, and it results in pseudoreplication. As a result the models will produce measures of uncertainty that are too small. It may also result in parameter estimates that are wrong, and this can lead to incorrect ecological conclusions.

We were able to extend the models with spatial and spatial-temporal correlation using a recently developed statistical technique called INLA (Rue et al., 2009; Blangiardo and Cameletti, 2015; Zuur et al., 2017; Zuur and Ieno, 2018). We also dealt with the non-linear temporal patterns using generalised additive models and incorporated statistical distributions especially designed for data with excessive numbers of zeros. The resulting models show trends over time and also indicate which sites are utilised by the birds (where and when).

The methods that we applied in this report are highly sophisticated and require a fair amount of knowledge to work with. This report aims to provide a quasi-layperson's term introduction to Poisson, negative binomial and zero-inflated negative binomial generalised additive models with spatial and spatial-temporal correlation. We assume that the reader is familiar with multiple linear regression, mixed-effects modelling and generalised linear modelling (Zuur et al., 2009).

Chapter 2

Introduction

In this report we will analyse Red knot data from the United Kingdom and Oystercatcher data from South Africa and Namibia. The analysis of these data sets requires statistical techniques that can deal with spatial dependency, temporal dependency, zero inflation, large variation and non-linear trends. We will apply generalised additive models with spatial and spatial-temporal correlation using the software R-INLA.

In Chapter 3 we will apply a detailed data exploration on the Red knot data. These are counts, and the first model that we will apply is a generalised linear mixed-effects model (GLMM) with a Poisson distribution in Chapter 4. The model is highly overdispersed, and a detailed model validation indicates that we definitely need to deal with spatial dependency and also with a non-linear year effect and zero-inflation issues. In Chapter 5 we show how to execute a generalised additive model (GAM) in R-INLA, and the model is extended with spatial dependency in Chapter 6. Here is also where the numerical estimation problems start to appear. We noticed that tweaking initial values, priors and configurations of spatial components sometimes resulted in rather different posterior distributions of the parameters. This indicates model instability. The variation in the Red knot data is extremely large; we have sites with 0 counts and sites with 120,000 birds. We suspect that the numerical problems are partly due to this large variation. We also made an attempt to extend the models towards spatial-temporal dependency, but either the Red knots are not temporally correlated or numerical estimation problems prevented the model from finding the right solution. It should also be noted that computing time for these models is in terms of half day on a modern computer. In Chapter 8 we apply the same methodology on the Oystercatcher data, but our impression is that the spatial GAM does not provide an essential improvement compared to an 'ordinary' GAMM. This is because the spatial correlation is low for this data set.

In Chapter 9 we discuss the statistical approach that is currently being applied on these data, namely TRIM.

All calculations are carried out in the statistical software package R (R Core Team, 2020). This report was written with the add-on package Bookdown (Xie, 2020), which is an extension of the RMarkdown language. This means that the source files that were used to create this report contain all R code required to reproduce the analyses, and it can also be used to repeat the analysis for future data sets. Readers who are not interested in the R code can ignore the parts of text pertaining to the code. As to the statistical methods, we assume familiarity with multiple linear regression, generalised linear models and generalised additive models.

Chapter 3

Data exploration for the Red knot data

A statistical analysis should always start with data exploration. See for example Zuur et al. (2010), who developed an 8-step protocol for this. As part of this protocol we need to look at the presence of outliers, collinearity (i.e. correlation between covariates), the type of relationships that we may expect between covariates and the response variable (e.g. linear versus non-linear), and we also need to visualise spatial and spatial-temporal dependency.

3.1 Import the data and load the packages

Before we start data exploration, we first import the Red knot data with the `read.csv` function. It is assumed that the first row in the csv file contains the names of the variables (`header = TRUE`). Missing values should be coded as `NA` in the data file. The code that we do not show here is setting the working directory with the `setwd()` function as this is computer specific.

```
CC <- read.csv(file = "CALCA.csv",
               header = TRUE,
               na.strings = "NA",
               stringsAsFactors = TRUE)
source("HighstatLibV13.R")
```

The `source` function sources our support file `HighstatLibV13.R`, which is available from www.highstat.com. We load a large number of packages.

```
library(easypackages) #Defines 'libraries' function to load packages.
libraries("sp", "rgdal", "raster", "utils", "colorRamps", "rgdal",
          "raster", "dismo","rasterVis", "RColorBrewer", "lattice",
          "gridExtra", "splancs", "lattice", "INLA", "gstat", "ggplot2",
          "mgcv", "ggmap", "plyr", "rgl", "cowplot", "maps", "maptools",
```

```
          "glmmTMB", "dplyr",
          "mapdata", "worldHiresMapEnv", "fields", "rgeos", "performance",
          "gamm4", "inlabru")
```

3.2 Data preparation

At certain stages of the analyses we need to calculate Euclidean distances between the sampling locations, and we will use UTM coordinates for this. We therefore convert the WGS84 coordinates of the sampling locations into UTM coordinates. We will use the function `LongLatToUTM` from our support file `HighstatLibV13.R`. This function requires the longitude and latitude coordinates of each site, and one value for the UTM zone. The study area covers various UTM zones and in such a case it is recommended to use the UTM value of the center of the study area. We will use UTM zone 31 for this.

```
#' Convert WGS84 to UTM
xy <- LongLatToUTM(x = CC$Long,
                   y = CC$Lat,
                   zone = 31,
                   Hemisphere = "north")
CC$Xkm <- xy[,2] / 1000
CC$Ykm <- xy[,3] / 1000
```

We have data from 44 years, and during the statistical analysis we will use year as a continuous covariate. At various stages of the data exploration and model validation, it is useful to have year also as a categorical covariate.

```
CC$fYear <- factor(CC$Year)
```

The response variable is the number of observed Red knots at a site in a year. In the next chapter we will present the statistical models. In these models we will use the notation RK_{is} for the number of observed knots at site i in year s. The data file uses `Count` for this. To avoid confusion, we will use the same name in the R code. We therefore rename the variable `Count` to `RK`.

```
CC$RK <- CC$Count
#CC <- rename(CC, "RK" = "Count")
```

During the analysis we need a variable that identifies the country. The first two characters of the variable `Site` identify the country. For example, the first element of `Site` is DE01756, and this is an observation from Germany (DE refers to 'Deutschland'). We will create a new variable `Country` that contains these two characters. We do this with the `substr` function, but the input of this functions needs to be of the type 'character' and not a categorical variable. This explains why we first convert `Site` into a vector of characters.

```
Site.Char  <- as.character(CC$Site)
CountryID  <- substr(x = Site.Char, start = 1, stop =  2)
CC$Country <- factor(CountryID)
```

At some stage during the data exploration we will visualise the absence and presence of Red knots. For this we need a variable that contains zeros and ones for the absence and presence of Red knots, respectively. We use the `ifelse` function for this. If `RK` is larger than 0, then `RK01` is 1, and 0 otherwise.

```
CC$RK01 <- ifelse(CC$RK > 0, 1, 0)
```

We now have all the required variables for the data exploration and the analysis.

3.3 Spatial locations

Figure 3.1 shows the spatial locations of all the sites. There are 546 sites in 11 countries. As mentioned in Chapter 2, one of the underlying questions in this report is to estimate one trend for all countries. As it currently stands, this trend will be based on all the sites illustrated in Figure 3.1.

The `get_map` function and some basic ggplot2 code (Wickham et al., 2020) are used to create this graph.

```
glgmap   <- get_map(location = c(-11, 36, 14, 61),
                    zoom = 4,
                    maptype= "terrain",
                    col = "bw")
p <- ggmap(glgmap)
p <- p + geom_point(data = CC,
                    aes(x = Long, y = Lat),
                    col = "red",
                    size = 0.3,
                    shape = 1)
p <- p + xlab("Longitude") + ylab("Latitude")
p
```

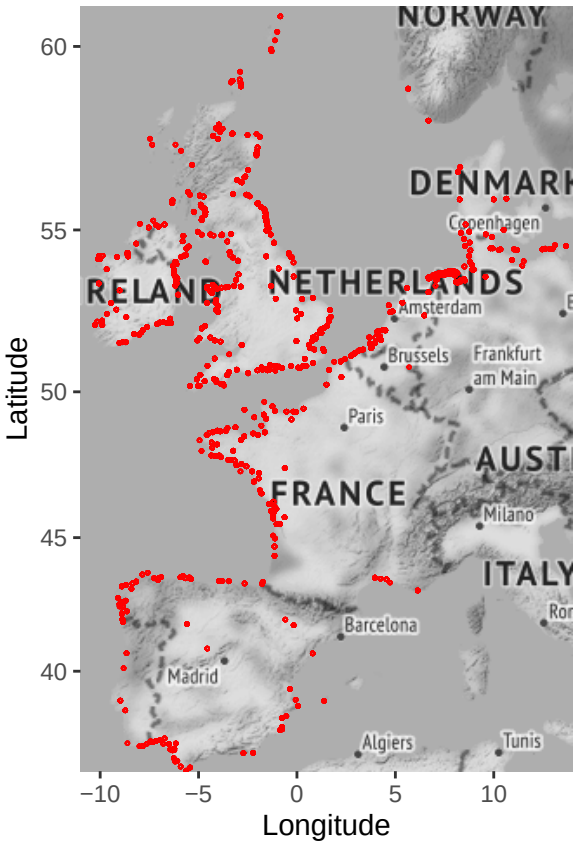


Figure 3.1: Sampling locations for all years.

3.4 Spatial-temporal resolution

The data are from 44 years. Figure 3.2 shows the sampling locations for each year. Note that the sampling resolution is not consistent over time. Some countries were measured throughout the sampling period, whereas other countries were only sampled during the latter years. This is a major problem as it means that changes in the long-term trend may be due to changes in the spatial position of the sampling locations.

We used the `xyplot` function from the `lattice` package (Sarkar, 2020) to create this graph.

```
xyplot(Lat ~ Long | fYear,
       data = CC,
       pch = 16,
       aspect = "iso",
       col = 1,
       cex = 0.3)
```

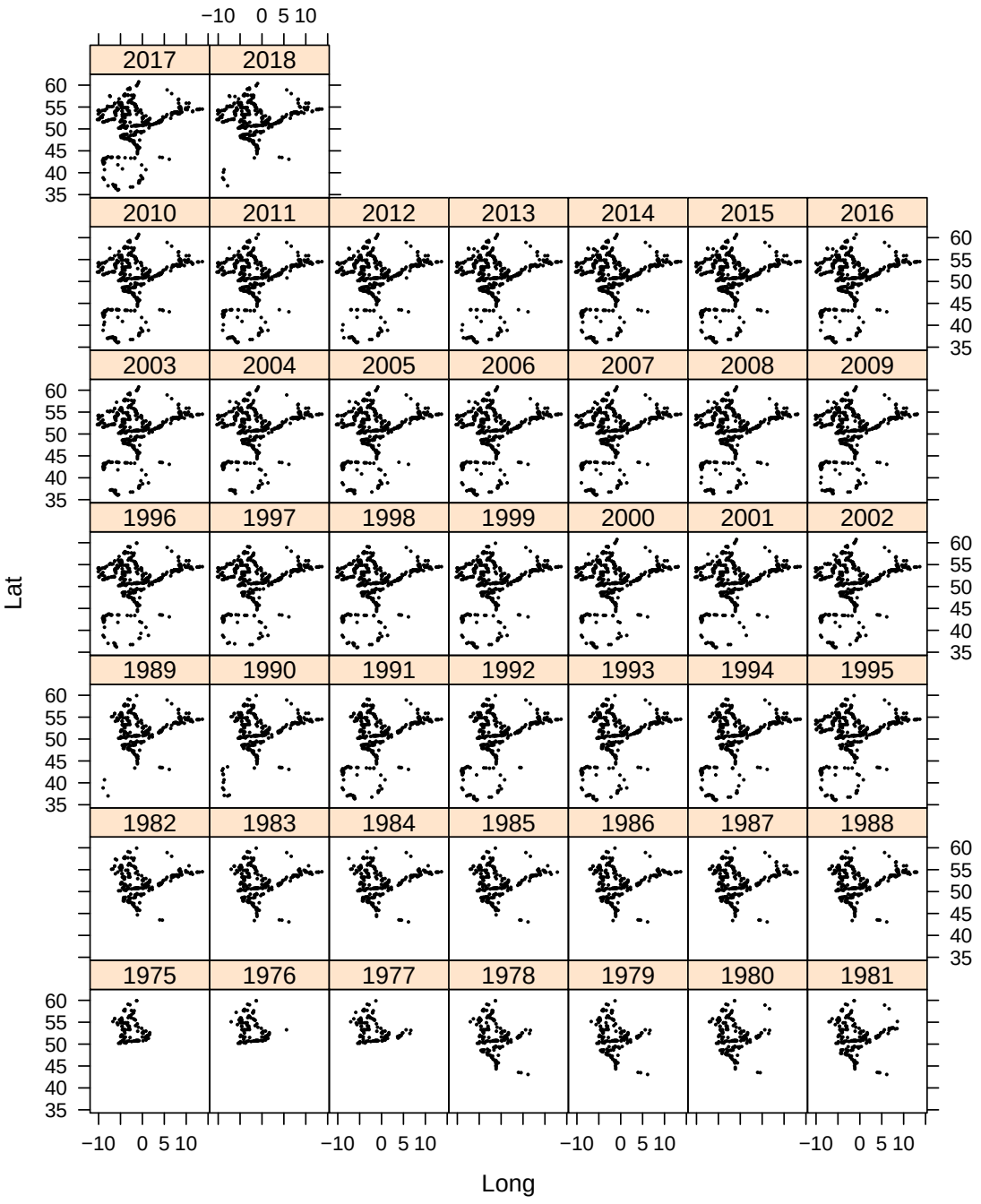


Figure 3.2: Sampling locations for each year.

We further investigate the unbalanced spatial-temporal resolution of the data as this is a rather important aspect of the data. To see which countries were measured in which years, we create a table of the two variables `Country` and `Year`.

```
Z <- table(CC$Country, CC$Year)
```

This table has 11 rows (countries) and 44 columns (years), which makes it too large to print. We will visualise the values in this table using the `ggplot` function. To do this, we need to convert the 11 by 44 matrix `Z` into a vector of length 484 by 1. We also add the year and site names. We use the `as.vector` and `rep` functions to do this. The results are stored in the data frame `DataSiteYear2`.

```
DataSiteYear <- data.frame(NumSites  = as.vector(Z),
                           Years     = rep(colnames(Z), each = nrow(Z)),
                           Countries = rep(rownames(Z), ncol(Z)))
DataSiteYear2 <- subset(DataSiteYear, NumSites > 0)
head(DataSiteYear2, 5) #' Show the first 5 rows
```

```
##    NumSites Years Countries
## 6       119  1975        GB
## 17      115  1976        GB
## 19        1  1976        NL
## 28      114  1977        GB
## 30       16  1977        NL
```

The data frame `MyData2` contains the number of sampled sites per year and country. We have plotted this information in Figure 3.3. A dot means that sampling took place in a specific country and year, whereas if nothing is plotted then no sampling took place for that country and year. The size of the dot is proportional to the number of sampled sites in that year and site. The graph indicates that in various countries, sampling started between 1975 and 1980, but there are also countries where sampling started much later (e.g. Spain, Ireland). Also note that the number of sampling sites differs considerably between the countries. A sensible approach is to use only the data from 1995 onwards.

Basic `ggplot2` code is used to create this graph.

```
DataSiteYear2$MySize <- DataSiteYear2$NumSites / max(DataSiteYear2$NumSites)
DataSiteYear2$Years  <- as.numeric(DataSiteYear2$Years)
p2 <- ggplot(DataSiteYear2,
             aes(x = Years,
                 y = Countries,
                 size = NumSites))
p2 <- p2 + geom_point()
p2 <- p2 + scale_x_continuous(breaks = seq(from = 1975, to = 2020, by = 10))
p2 <- p2 + labs(x = "Year", y = "Country")
p2 <- p2 + theme(text = element_text(size=10))
p2
```

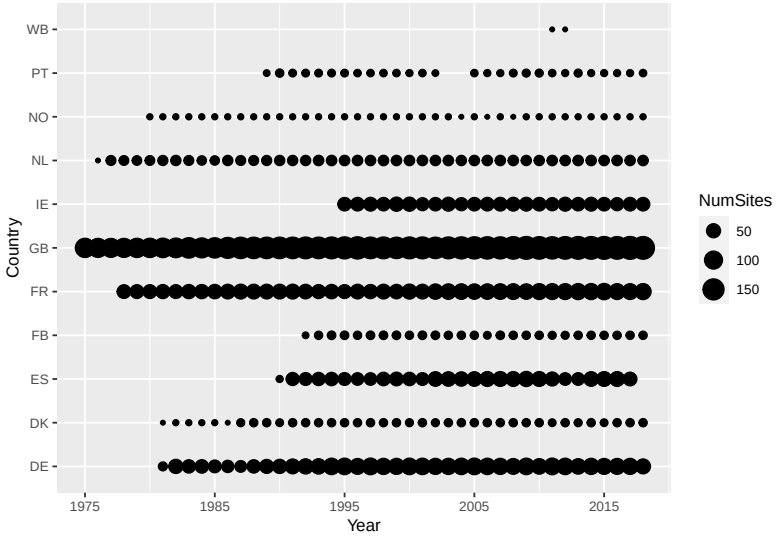


Figure 3.3: Visualisation of the number of sampled sites by country and year. The size of a dot is proportional to the number of sampled sites.

The total number of sampled sites also increase over time within a country; see Figure 3.4. Trends over time in the red Knot abundances per country may be related to the number of sampled sites per country. The overall trend may be influenced by the different starting times of the time series.

```
p2 <- ggplot(DataSiteYear2, aes(x = Years,
                                y = NumSites,
                                Countries = Countries))
p2 <- p2 + geom_point(aes(col = Countries),
                      size = 1)
p2 <- p2 + geom_line(aes(x = Years,
                         y = NumSites,
                         group = Countries,
                         col = Countries))
p2 <- p2 + scale_x_continuous(breaks = seq(from = 1975, to = 2020, by = 10))
p2 <- p2 + labs(x = "Year", y = "Number of sampled sites")
p2 <- p2 + theme(text = element_text(size=10))
p2
```

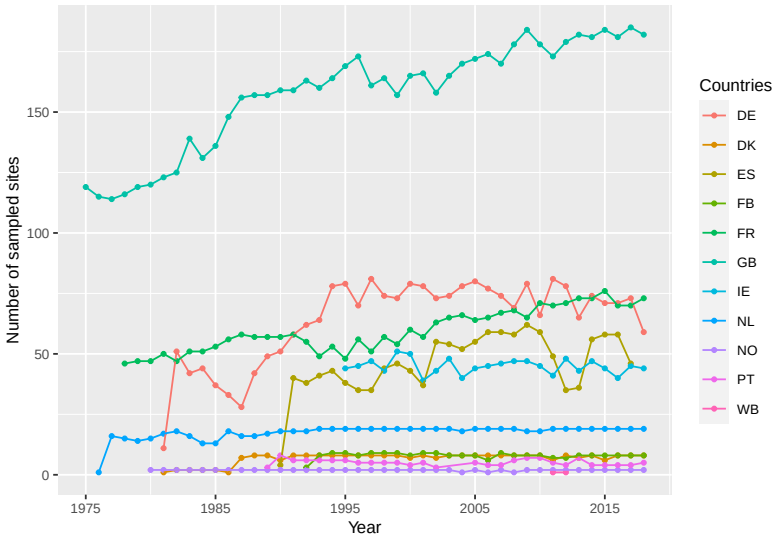


Figure 3.4: Visualisation of the number of sampled sites per country and year.

Figure 3.5 is another graph visualising the potential problems with different sampling effort over time. It shows the total number of sampled sites in the study area. There is a sharp increase in the number of sampled sites from 1975 to 1995, after which the number of sampled sites is roughly constant. It may be interesting to compare this curve with the trend that will come out of the statistical analyses.

The R code to create this graph uses basic `ggplot2` code.

```
MyData <- data.frame(NumYears = as.numeric(table(CC$fYear)),
                     Years    = as.numeric(names(table(CC$fYear))))
p2 <- ggplot(MyData, aes(x = Years,
                         y = NumYears))
p2 <- p2 + geom_line() + geom_point()
p2 <- p2 + scale_x_continuous(breaks =seq(from = 1975, to = 2020, by = 10))
p2 <- p2 + labs(x = "Year", y = "Number of sampled sites")
p2 <- p2 + theme(text = element_text(size=10))
p2
```

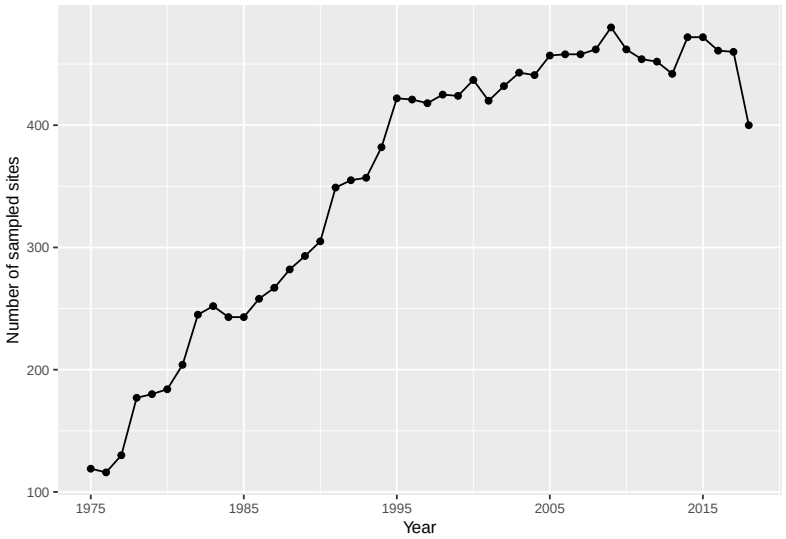


Figure 3.5: Total number of sampled sites per year for the study area.

In the next chapter we will apply a generalised linear mixed-effects model in which we use `Site` as random effect. Figure 3.6 shows one more time the number of observations per site. The number of observations (i.e. years) per site varies between 2 and 44.

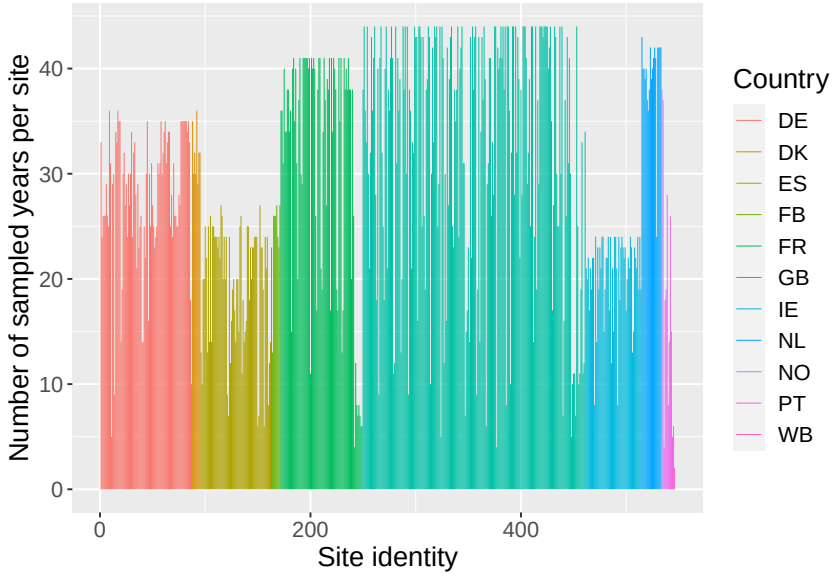


Figure 3.6: Number of sampled years per site. The different colours correspond to different sites.

3.5 Red knot numbers versus year

We will now focus on the temporal trend in the Red knot counts. Figure 3.7 shows the number of Red knots for all sites versus year. A scatterplot smoother was added to aid the visual interpretation. There are no clear patterns, but this may be due to the large number of zeros and the large variation in the data.

```
p <- ggplot(data = CC, aes(x = Year, y = RK))
p <- p + geom_jitter(size = 0.1, height = 0.01, width = 0.1)
p <- p + geom_smooth()
p <- p + xlab("Year") + ylab("Counts of birds")
p <- p + theme(text = element_text(size=15))
p
```

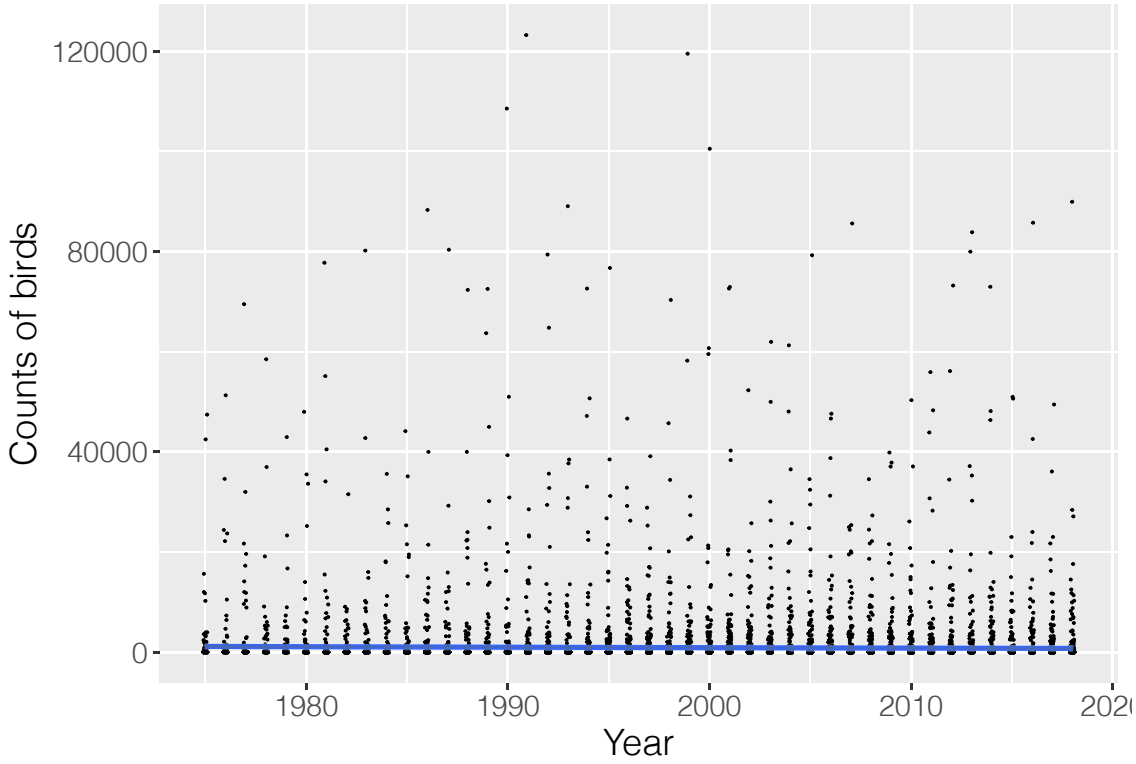


Figure 3.7: Scatterplot of number of birds versus year. A scatterplot smoother was added to aid visual interpretation.

We also created this graph for each country, but the resulting smoothers were similar to the one in Figure 3.7.

3.6 Number of zeros

The number of zeros in the Red knot data is 64.81%, which is relatively large. We also present the number of observations and the number of observations equal (and not equal) to zero by country; see the table below.

```
##    Number of observations Number of zeros Number of non-zeros % of zeros
## DE                   2426            2008                 418         83
## DK                    256             203                  53         79
## ES                   1295            1014                 281         78
## FB                    215             158                  57         73
## FR                   2445            1437                1008         59
## GB                   6931            4194                2737         61
## IE                   1076             424                 652         39
## NL                    750             533                 217         71
## NO                     75              73                   2         97
## PT                    143              74                  69         52
## WB                      2               1                   1         50
```

One of the statistical techniques that we will apply in later chapters is a zero-altered negative binomial GLM. In such a model we analyse the absence/presence data, and also the presence-only data. It is important to know the number of non-zeros as this will determine the complexity of the models that can be applied on the non-zero data. The numbers in the table above show that in some countries the number of non-zeros is relatively small, which means that estimating national trends based on only the data from one country may be impractical. Formulated differently, to estimate national trends we recommend using a model that is applied on all the data, and not on the data from only one country.

Figure 3.8 shows a scatterplot of the 0-1 data versus year. We also added a scatterplot smoother. The pattern of this smoother is non-linear, which indicates that we may need a smoothing function of year in the model. This guides us towards generalised additive modelling techniques.

Basic `ggplot2` coding was used to create this figure.

```
#' Scatterplot of absence-presence data versus year
p1 <- ggplot()
p1 <- p1 + geom_jitter(data = CC,
                       aes(x = Year, y = RK01),
                       size = 0.1, height = 0.01, width = 0.1)
p1 <- p1 + geom_smooth(data = CC,
                       aes(x = Year,
                           y = RK01))
p1 <- p1 + xlab("Year") + ylab("Counts of birds")
p1 <- p1 + theme(text = element_text(size=12))
#' Scatterplot of presence-only data versus year
CCPos <- subset(CC, RK > 0)
p2 <- ggplot()
p2 <- p2 + geom_jitter(data = CCPos,
                       aes(x = Year, y = RK),
                       size = 0.1, height = 0.1, width = 0.1)
p2 <- p2 + geom_smooth(data = CCPos,
                       aes(x = Year,
                           y = RK))
```

```
p2 <- p2 + xlab("Year") + ylab("Counts of birds")
p2 <- p2 + theme(text = element_text(size=12))
#' Plot both graphs
plot_grid(p1, p2, ncol = 2,
          labels = c('A', 'B'),
          rel_widths = c(1, 1))
```

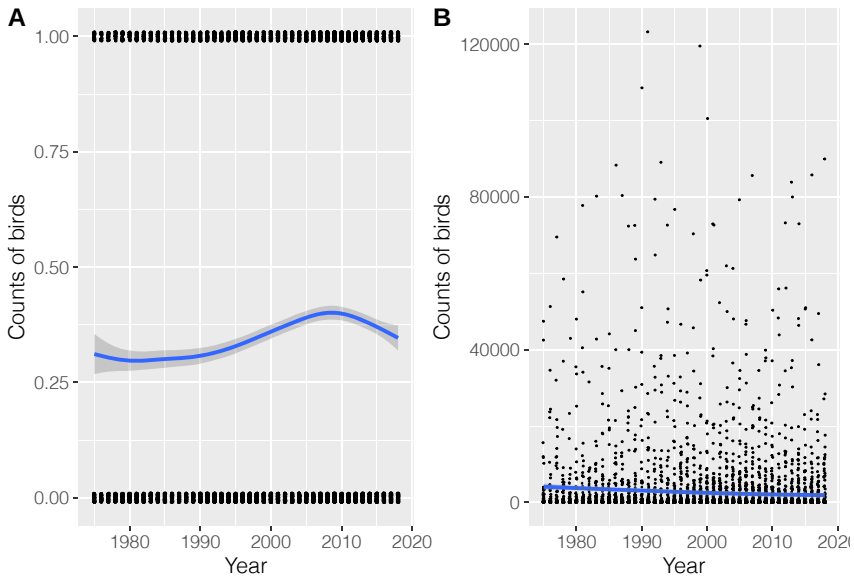


Figure 3.8: A: Scatterplot of absence/presence of Red knots versus year. B: Scatterplot of the presence-only data versus year.

3.7 Country effect

Figure 3.9 shows a boxplot of the Red knot counts conditional on country. One can clearly see the excessive number of zeros for some countries.

```
p <- ggplot(data = CC, aes(x = Country, y = RK))
p <- p + geom_boxplot()
p <- p + xlab("Country") + ylab("Number of Red knots")
p <- p + theme(text = element_text(size=15))
p
```

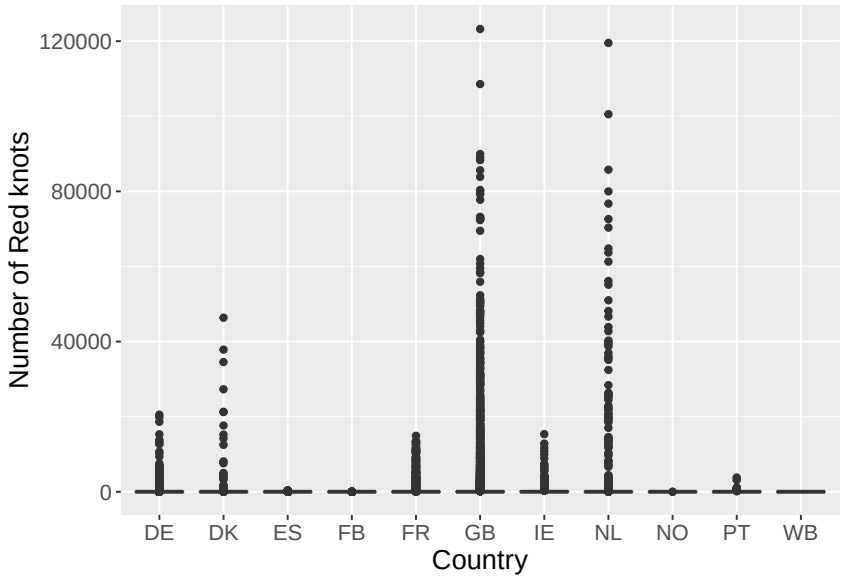


Figure 3.9: Boxplots of the number of Red knots conditional on country.

3.8 Conclusions

Data exploration has indicated that the Red knot counts contain a large number of zero counts. There may be non-linear patterns over time. And most importantly, the spatial resolution has changed over time. With this we mean that not all countries were sampled from start to end. And the number of sampled sites has increase sharply from 1975 to 1995. This means that trends over time may be confounding with the spatial position of the sampling locations.

A large number of imputation methods exist to estimate missing values in time series. However, the number of site-year combinations with no data is 35.01%. This is a rather large percentage of missing values to predict. Furthermore, the majority of these missing values are not 'missing at random', but due to sites and countries where sampling starts much later (e.g. around 1995). Hence these are structured missing values. Prediction of such missing values is a much more hazardous exercise than predicting a missing value for a single year in the middle of a time series (a random missing value). An additional argument not to implement imputation methods is that the scatterplot smoothers indicate that any temporal trend is likely to give a poor fit. So, we do not have a good model to predict missing values. Finally, computing time will also be an issue. In later chapters we will execute models with spatial-temporal dependency. With such models we do not have the luxury of rerunning the model multiple times.

In summary, there are no magical tools that can resolve a situation in which 35.01% of the data are missing due to time series starting in different years. The safe option is to truncate the data and analyse the data from 1995 onwards. It should be noted that the techniques that will be applied later are quite capable of predicting missing values, and they even provide measures of uncertainty (e.g. a posterior distribution and 95% credible intervals for each missing value). For missing values at random, we have no qualms about using these. For non-random missing values we caution against using these for imputation purposes.

In the remaining chapters we will run the models on the 1995+ data. These are in the object `CC2`.

```
CC2 <- subset(CC, Year >= 1995)
CC2 <- droplevels(CC2)
```

Chapter 4

Poisson GLMM applied on the Red knot data

Our strategy to find the optimal model for the Red knot data is to start simple and slowly build up the complexity of the model. We will first apply a Poisson generalised linear mixed-effects model (GLMM) on the Red knot data. Based on the data exploration results in Chapter 3, we expect that such a model will have problems with zero inflation and spatial dependency. A zero-inflated negative binomial (ZINB) generalised additive model (GAM) with a smoother for year and spatial-temporal dependency may solve some of the problems that we are going to encounter in this chapter. However, it is unwise to start with such a model. The excessive number of zeros in the data may be explained by the temporal trend. If the sites with zeros are next to one another, then the spatial correlation component may model the zeros. If sites have zero observations repeatedly over time, then this is auto-correlation. And if all these things happen, then the different components in the ZINB GAM with spatial-temporal dependency may all fight for the same information, potentially resulting in numerical estimation problems. This explains our motivation to start simple.

4.1 Model formulation

The first model that we will apply is a Poisson GLMM of the form

$$\begin{array}{rcl} \mathrm{RK}_{is} & \sim & \mathrm{Poisson}\left(\mu_{is}\right) \\ \mathrm{E}\left[\mathrm{RK}_{is}\right] & = & \mu_{is} \\ \mathrm{var}\left[\mathrm{RK}_{is}\right] & = & \mu_{is} \\ \log\left(\mu_{is}\right) & = & \beta_1 + \beta_2 \times \mathrm{Year}_s + a_i \end{array} \tag{4.1}$$

where RK_{is} is the number of counted Red knots at site i in year s. This expression states that the observed number of Red knots at a specific site i in year s follows a Poisson distribution with parameter μ_{is}. By definition, the expected value of the number of Red knots at site i in year s is μ_{is} and so is its variance. The mean μ_{is} is modelled as an exponential function of the intercept (β_1), covariates and the random effects.

The selected data set contains measurements from 1995 to 2018, hence the subscript s runs from 1 to 24. The total number of sites is 546, and therefore the index i runs from 1 to 546. The total sample size is 10673.

The term a_i is a random intercept and these 546 random intercepts are assumed to be normal and independently distributed with mean 0 and variance σ^2. The random intercepts impose a dependency structure between all Red knots counts from the same site. All observations from different sites are assumed to be independent of one another. We have visualised this dependency structure in Figure 4.1.

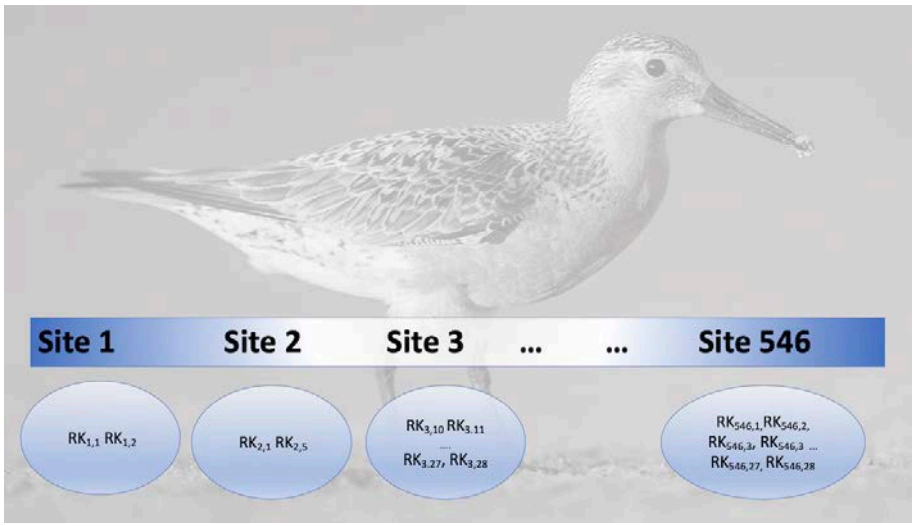


Figure 4.1: Dependency structure imposed by a Poisson GLMM using site as random intercept. All observations from the same site are correlated with a value ϕ. Observations from different sites are assumed to be independent, even if they are close to one another.

At some sites we only have 1 measurement over time, and at other sites we have 24 observations. The dependency structure that is being imposed assumes that the correlation between any two Red knot observations from the same site is the same. Whether the distance in time between these two observations is 1 year or 27 years is not taken into account by this dependency structure.

4.2 Applying the Poisson GLMM

The R code below executes the Poisson GLMM. Due to the logarithmic link function it is crucial to standardise the covariate `Year`; otherwise we get numerical estimation problems. The function `MyStd` subtracts the mean and divides by the standard deviation. It is available in our support file `HighstLibV13.R`. The `glmmTMB` package (Magnusson et al., 2020) is used to execute the Poisson GLMM.

```
CC2$Year.c <- MyStd(CC2$Year)
M1 <- glmmTMB(RK ~ Year.c + (1| Site),
              data = CC2,
              family = poisson)
```

4.3 Overdispersion

The first thing that we should do after executing a Poisson GLM(M) is to check for overdispersion. To do this we obtain the Pearson residuals, square them, add them all up and divide this by the sample size minus the number of parameters. This ratio should be close to 1.

```
E1   <- resid(M1, type = "pearson")
N    <- nrow(CC2)
Npar <- length(fixef(M1)) + 1 #One sigma
Dispersion1 <- sum(E1^2) / (N - Npar)
Dispersion1
```

```
## [1] 503.2121
```

In this case, the dispersion parameter is 503.21, which is considerably larger than 1, and indicates serious overdispersion. This means that the confidence intervals for the regression parameters and the long-term trend are too small, and the estimated regression parameters may be biased.

Several factors can cause overdispersion, namely outliers, missing covariates, missing interactions, zero inflation, wrongly modelled covariate effects (e.g. non-linear instead of linear relationships), wrongly modelled dependency, wrong link function or variation that is larger than the Poisson distribution allows for. Each of these causes has its own solution. For example, if zero inflation is the cause of the overdispersion, then a zero-inflated Poisson GLMM needs to be applied. If there are missing interactions, then these should be added to the model. This whole process of fitting, assessing and modifying models does give the analysis a data phishing element, but this is sometimes unavoidable.

If there is overdispersion we need to figure out the cause of the overdispersion and adjust the model accordingly. If we make the wrong choice, then the estimated parameters may be biased.

To determine why we have overdispersion we continue with model validation. Note that if the dispersion statistic had been 1, we would still have to carry out a complete model validation.

4.4 Model validation

4.4.1 Model validation steps for a regression-type model

After executing the Poisson GLMM model, we need to apply a detailed model validation. Figure 4.2 shows a flowchart of all relevant model validation steps. We need to plot Pearson residuals versus fitted values and assess that there is no violation of heterogeneity. We also need to plot the residuals versus each covariate in the model. In this case the only covariate

is year. If such a graph shows non-linear patterns, then we need to consider allowing for more flexibility by using, for example, a smoother (i.e. allow it to be more non-linear) or allow for interactions. We also need to plot the residuals versus each covariate not in the model. For example, we can plot the residuals versus country identity, or plot residuals versus year for different regions in Europe. If these graphs indicate that there are patterns, then we can conclude that the model with one temporal trend is not good and that model extensions are required. We also need to assess the residuals for temporal dependency and spatial dependency. We must also verify whether the GLMM can cope with the excessive number of zeros. All these steps are part of a systematic approach that should *always* be followed when working with regression-type models.

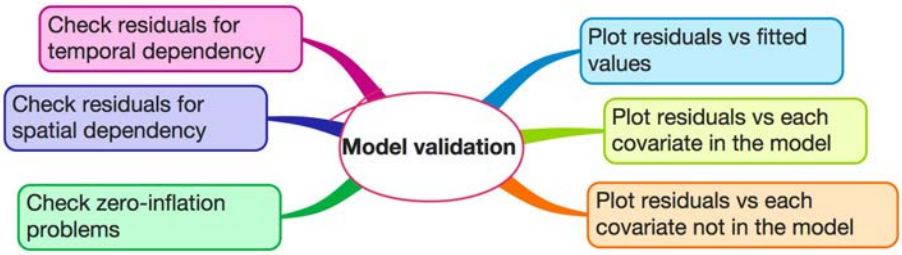


Figure 4.2: Model validation steps for a regression-type analysis (including GLMM).

4.4.2 Residuals versus fitted values

We will plot Pearson residuals versus fitted values and Pearson residuals. To do that, we first extract the fitted values (we already have the Pearson residuals). We call these `mu1` in the code below. They are an estimate of μ_{is} in Equation (4.1).

```
CC2$mu1 <- fitted(M1)
CC2$E1  <- E1
```

Now that we have the Pearson residuals and fitted values we plot them against one another; see Figure 4.3. The graph shows heterogeneity. This may be one of the causes of the overdispersion. It also indicates that the Poisson distribution is probably not appropriate for these data. The following R code was used to generate this figure.

```
p1 <- ggplot(CC2, aes(x = mu1, y = E1))
p1 <- p1 + geom_point(size = 0.5)
p1 <- p1 +geom_hline(yintercept = 0,
                     linetype="dashed",
                     color = "red")
p1 <- p1 + labs(x = "Fitted values", y = "Pearson residuals")
p1 <- p1 + theme(text = element_text(size=10))
p1
```

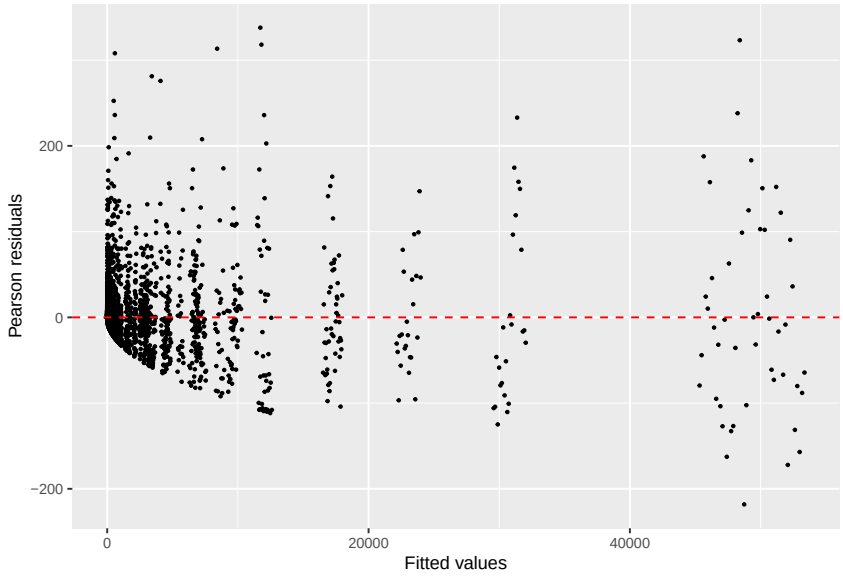


Figure 4.3: Pearson residuals plotted versus fitted values obtained by the Poisson GLMM.

4.4.3 Observed versus fitted Red knot values

We also plot the fitted values of the Poisson GLMM versus the observed Red knot values; see Figure 4.4. We would like to see that the majority of the points are close to the 1-1 line, as this would indicate a good fit. Note that the model is not performing well with respect to the larger observed Red knot counts.

The following R code was used to plot the fitted values versus the observed PIKE values.

```
p3 <- ggplot(CC2, aes(x = mu1, y = RK))
p3 <- p3 + geom_point(size = 0.5, col= grey(0.5))
p3 <- p3 + geom_abline(intercept = 0, slope = 1, color = "red")
p3 <- p3 + labs(x = "Fitted values", y = "Observed counts")
p3 <- p3 + coord_fixed()
p3 <- p3 + xlim(0, max(CC2$RK)) + ylim(0, max(CC2$RK))
p3 <- p3 + theme(text = element_text(size=10))
p3
```

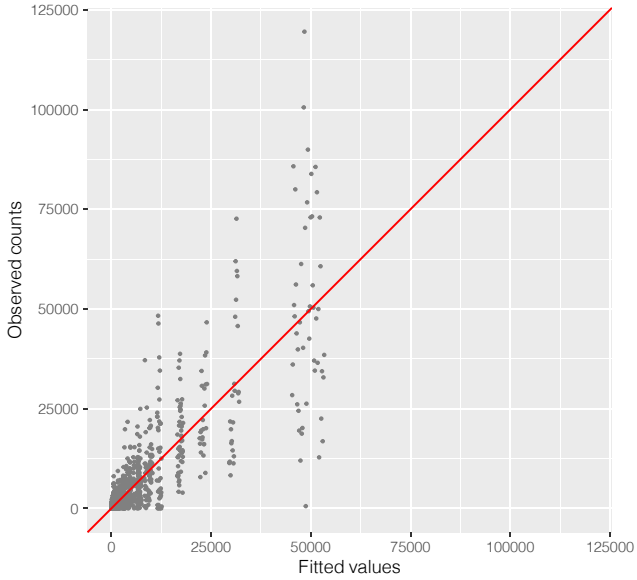


Figure 4.4: Pearson residuals plotted versus fitted values obtained by the Poisson GLMM.

4.4.4 Residuals versus covariates

Figure 4.5 shows a plot of the Pearson residuals versus year. We have added a simple smoother to aid visual interpretation of this graph. If this smoother always contains 0 in its 95% confidence intervals, then there are no important residual patterns. In this case there are no clear residual patterns. However, it is indeed possible that the time effect is non-linear once we improve the model by adding spatial dependency and deal with the zero inflation.

The R code to generate Figure 4.5 is given below.

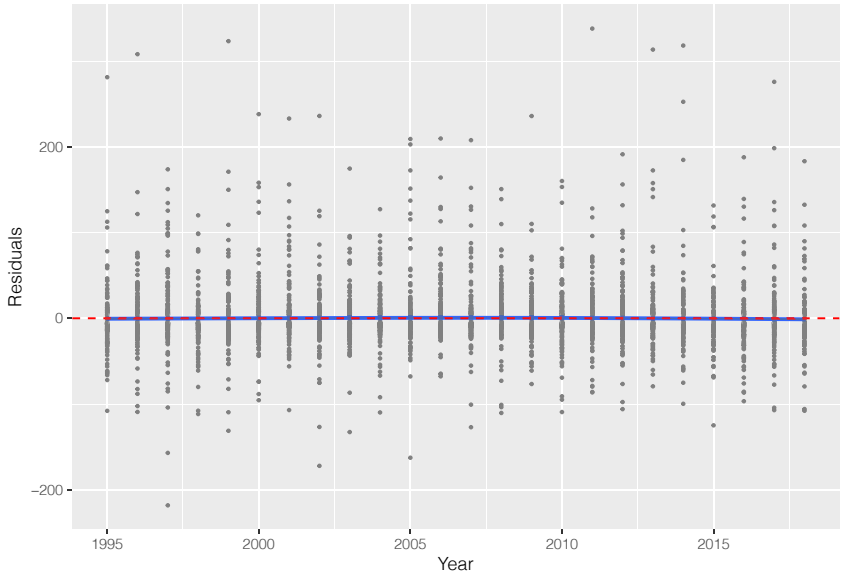


Figure 4.5: Pearson residuals versus the covariate year. A scatterplot smoother is added to aid visual interpretation.

```
p <- ggplot(data = CC2, aes(x = Country, y = E1))
p <- p + geom_boxplot()
p <- p + xlab("Country") + ylab("Pearson residuals")
p <- p + theme(text = element_text(size=15))
p
```

4.4.5 Spartial dependency in the random effects

The next model validation step pertains to spatial correlation. We should check the Pearson residuals and the random effects for spatial dependency. Checking for spatial dependency in the random intercepts is often ignored in the literature. The random effects are assumed to be normal and independently distributed. We will investigate whether the random intercepts are indeed spatially independent.

The first thing we do is visualise the values of the random intercepts with respect to the spatial locations of the sites. For this we first need to obtain the spatial locations of the sites. We do this with the `tapply` function.

```
MyData <- data.frame(Xkm = tapply(CC2$Xkm, FUN = mean, INDEX = CC2$Site),
                     Ykm = tapply(CC2$Ykm, FUN = mean, INDEX = CC2$Site))
```

We now have the spatial location of each site in UTM coordinates. We add the random effects to this data frame.

```
MyData$ai <- ranef(M1)$cond$Site$'(Intercept)'
```

Next we plot the sampling locations. The colour of the points reflects the sign of the random intercepts. If we can see a grouping of dots with the same colour, then this indicates sites close to one another have a similar value for the estimated random effect. And that is a violation of the spatial independence assumption. Figure 4.6 shows that this is indeed the case.

Figure 4.6: Visualisation of values of the random effect site. The colour reflects its sign.

Based on a visual assessment, there seems to be a certain degree of spatial correlation in the random intercepts for `Site`. One may feel uncomfortable with a visual assessment of the presence of spatial dependency in Figure 4.6. To formalise the assessment, we can make a variogram of the random intercepts; see Figure 4.7. If the points in the sample variogram form a horizontal band of points, then we can conclude that there is no (stationary) spatial correlation. If the sample variogram shows a steady increase and then reaches a plateau, then we have spatial dependency in the Pearson residuals. In this case it seems that we have spatial dependency.

```
coordinates(MyData) <- c("Xkm", "Ykm")
V1a <- variogram(ai ~ Xkm + Ykm ,
                 data = MyData,
                 cutoff = 200,
                 cressie = TRUE)
p4 <- ggplot()
p4 <- p4 + geom_point(data = V1a,
                      aes(x = dist,
                          y = gamma),
                      size = 0.5,
                      col = grey(0.5))
p4 <- p4 + geom_smooth(data = V1a,
                       span = 0.9,
                       se = FALSE,
                       aes(x = dist,
```

```
                              y = gamma))
p4 <- p4 + xlab("Distance (km") + ylab("Sample variogram")
p4 <- p4 + theme(text = element_text(size=10))
p4
```

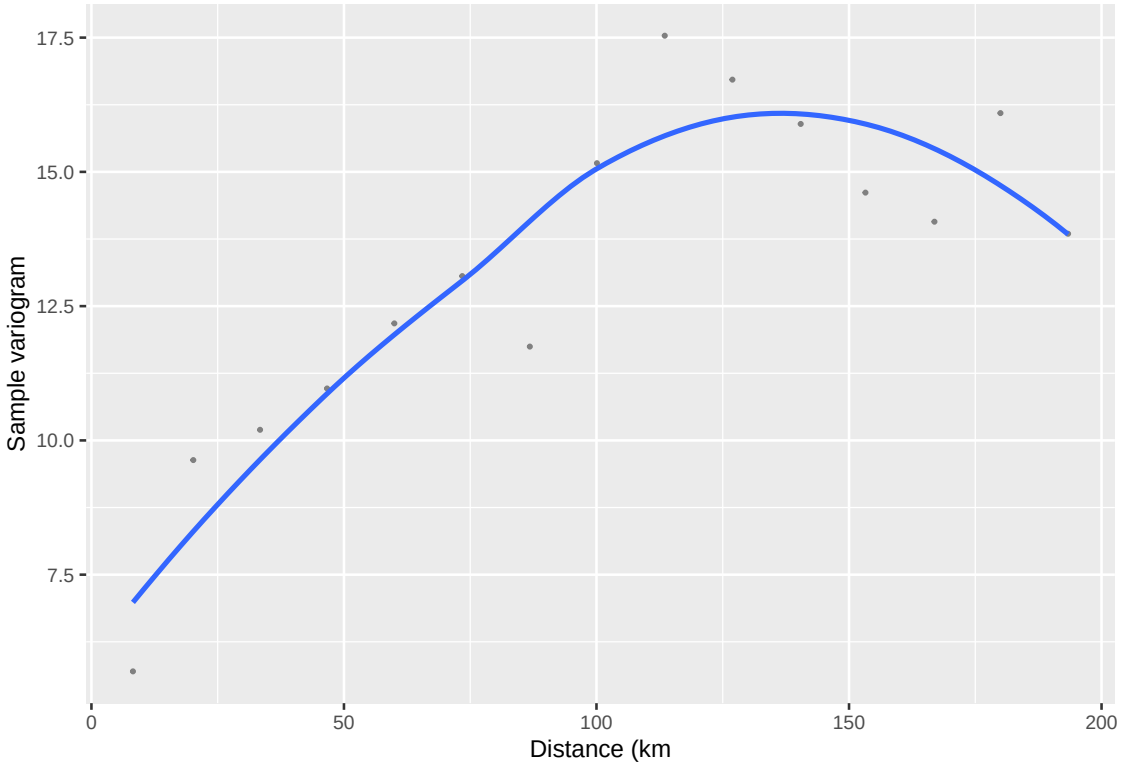


Figure 4.7: Sample variogram of the random effects.

In summary, the variogram also gives a clear indication of spatial dependency. The ultimate approach to determine whether there is really spatial dependency is to implement a model with spatial (or spatial-temporal) dependency and assess, for example, with the help of an AIC-related tool, whether the model improves.

The same exercise needs to be applied on the Pearson residuals, but because we have multiple Pearson residuals per site, this model validation step is less useful. The Pearson residuals also exhibit spatial dependency, but results are not presented here.

4.4.6 Zero inflation

There is more misery. The data set consists of 10673 observations. We can easily simulate 10673 values for the number of Red knots from the model. In a perfect world, these simulated 'number of Red knot' values are comparable to the observed 'number of Red knots'. If that would be the case then the model performs well. We can define 'similar' in many ways. One way is to look for whether the number of zeros in both data sets match. Let us explain this idea with some R code.

We first set the random seed so that we get the same results if we run the code again. We obtain the fitted values from the model (where fitted values are defined as intercept + year effect + random effects) and then simulate 10673 from a Poisson distribution using the fitted values from the model `M1`.

```
set.seed(1234)
N   <- nrow(CC2)
RK.Simulated <- rpois(n = N, lambda = CC2$mu1)
```

The `RK.Simulated` object contains simulated numbers of Red knots from the Poisson GLMM. In the simulated data we have 3641 values equal to 0, whereas we have 6665 for the observed data. It seems that the simulated data (which are truly Poisson) contain a fewer number of zeros. But this is only one set of simulated 'number of Red knot' values. We can easily do this 10,000 times, and for each simulated data set we determine the number of zeros. That is what the next block of R code does.

```
NSim <- 1000
Ysim <- simulate(M1, seed = 12345, nsim = NSim)
```

The `simulate` function simulates random effects from a normal distribution with mean 0, and the sigma is taken from the estimated model. Using the estimated regression parameters, it will then calculate the expected values, and the `rpois` function is used to simulate count data. Note that the simulation process itself can be improved by also simulating the regression parameters.

Now that we have 1,000 simulated sets of 'number of Red knots' we can calculate the numbers of zeros in each simulated data set and see how often we predict 0 times a zero, 1 times a zero, 2 times a zero, etc. We made a frequency plot of these values; see Figure 4.8. If the model can cope with the excessive number of zeros in the sampled data, then the red dot (representing the number of zeros in the observed Red knot values) would be within the range of the simulated values. That is not the case here, which means that the Poisson GLMM cannot cope with the 62.45% of zeros in the Red knot data. Therefore this model fails the model validation with respect to zero inflation, and it cannot be used for inferences. Further model improvement is required.

```
zeros <- vector(length = NSim)
for(i in 1:NSim){ zeros[i] <- sum(Ysim[,i] == 0)}
N <- nrow(CC2)
par(mfrow = c(1,1), cex.lab = 1.5, mar = c(5,5,2,2))
hist(100 * zeros / N,
     xlab = "Percentage of zeros",
     ylab = "Frequency",
     xlim = c(20, 80),
     main = "")
points(x = 100 * sum(CC2$RK == 0) / N,
       y = 0,
```

```
        pch = 16,
        cex = 5,
        col = 2)
```

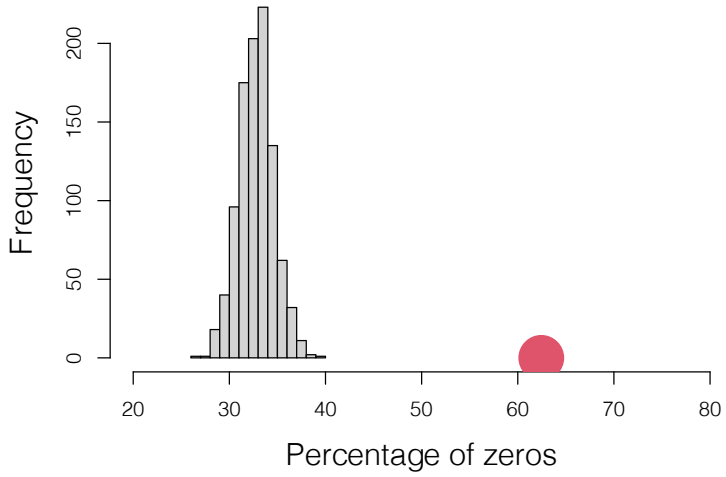


Figure 4.8: Results of a simulation study showing how often the Poisson GLMM predicts a zero. The red dot is the number of zeros in the observed Red knot data.

To assess whether the Poisson GLMM can cope with the excessive number of zeros in the Red knot data, we simulate a large number of truly Poisson data sets from the model. If the numbers of zeros in these simulated data sets are comparable to the numbers of zeros in the observed Red knot data, then the model performs well with respect to the zeros. Results indicate that the Poisson GLMM cannot cope with the excessive number of zeros in the Red knot data.

4.4.7 Explained variation

Using the `performance` package (Lüdecke et al., 2020) we can calculate an R^2 for the Poisson GLMM. The marginal R^2 below is the explained variation by the $\beta_2 \times \text{Year}_s$ term, also called the fixed part of the model. It hardly explains anything. The conditional R^2 is the variation in the Red knot data explained by the fixed effects and the random effects, which is nearly 98%. This means that the random effect `Site` explains a lot of variation. We suspect that this is due to many sites having lots of years with 0 red knots. Large negative random effects will model zero-inflated data rather well (the exponential of a large negative value is close to 0).

```
library(performance)
r2_nakagawa(M1)
```

```
## # R2 for Mixed Models
##
##   Conditional R2: 0.982
##      Marginal R2: 0.000
```

Note that this does not mean that there is no temporal trend. It only indicates that modelling the trend as $\beta_2 \times \text{Year}_s$ is not a good idea.

4.4.8 Summary of the Poisson GLMM

The Poisson GLMM is overdispersed, and the dispersion statistic is too large to ignore. Model validation of the Poission GLMM indicated two main problems: there is spatial correlation in the random effects, and the model cannot cope with the excessive number of Red knot values equal to 0. Model validation did not indicate any major non-linear year effects in the Pearson residuals. We are slightly surprised by this because in our experience trends over time tend to be non-linear for this type of data. To verify whether there really is no non-linear year effect, we will briefly run a generalised additive mixed model in the next section.

4.5 Poisson GAMM applied on the Red knot data

In the previous section we applied a Poisson GLMM, and model validation indicated that there was no non-linear year effect in the Pearson residuals. We are surprised by this, partly because of our experience with this type of data but also because Figure 3.8 did indicate a non-linear year effect for the absence/presence data. To put our minds at ease, we will verify that there really is no non-linear year effect. To do this we apply a Poisson generalised additive mixed-effects model (GAMM) on the Red knot data. Such a model is defined as follows.

$$\begin{array}{rcl} \text{RK}_{is} & \sim & \text{Poisson}\left(\mu_{is}\right) \\ \text{E}\left[\text{RK}_{is}\right] & = & \mu_{is} \\ \text{var}\left[\text{RK}_{is}\right] & = & \mu_{is} \\ \log\left(\mu_{is}\right) & = & \beta_1 + f(\text{Year}_s) + a_i \end{array} \tag{4.2}$$

The only difference between Equations (4.1) and (4.2) is the $\beta_2 \times \text{Year}_s$ and $f(\text{Year}_s)$. The $f(\text{Year}_s)$ is a smoother. The aim of the smoothing function of year is to obtain a curve that captures the general pattern of the Red knot counts-year relationship. Smoothers are explained in more detail in Wood (2017), Zuur et al. (2009), Zuur et al. (2015) and Zuur and Ieno (2018). For the moment it suffices to know that the smoother that we will apply in a moment has a mechanism that is called 'cross validation'. This tool determines the amount of smoothing of a smoother. Formulated differently, cross validation estimates the effective degrees of feeedom (edf). If the edf is 1, then the smoothing function $f(\text{Year}_s)$ is a straight line, and we might as well use the Poisson GLMM instead of the Poisson GAMM. The larger the edf, the less smooth is the smoothing function (which represents the year effect). Right now we are only interested in whether a GAMM gives an edf of 1 for the smoother $f(\text{Year}_s)$. If it does, then using a GAMM may give better results than a GLMM. We execute the Poisson GAMM with the following code.

```
G1 <- gamm4(RK ~ s(Year),
            random =~  (1| Site),
            data = CC2,
            family = poisson)
```

The `s(Year)` term implements the default smoother, which is a thin-plate regression spline. It is not important to know the exact mathematical details of this smoother. In Appendix A we explain that a smoother consists of a collection of so-called basis functions (we also call them Lego pieces). These basis functions are used as covariates, and each of them has an associated regression parameter. The `gamm4` function will use the `lme4` package (Bates et al., 2020) to estimate these regression parameters, together with all the other model components. The basis functions of the thin-plate regression spline are defined differently from the smoothers that we explain in Appendix A.

The estimated smoother is plotted in Figure 4.9. The edf of the smoother is 9, which is considerably larger than 1. This indicates that the year effect may be non-linear. At this stage we will refrain from trying to understand the shape of the smoother because we have not dealt yet with the overdispersion. The presence of unaccounted spatial and spatial-temporal dependency may have caused the non-linear pattern in the smoother. The bottom line is that we need to allow for a non-linear trend in the Red knot data.

```
plot(G1$gam)
```

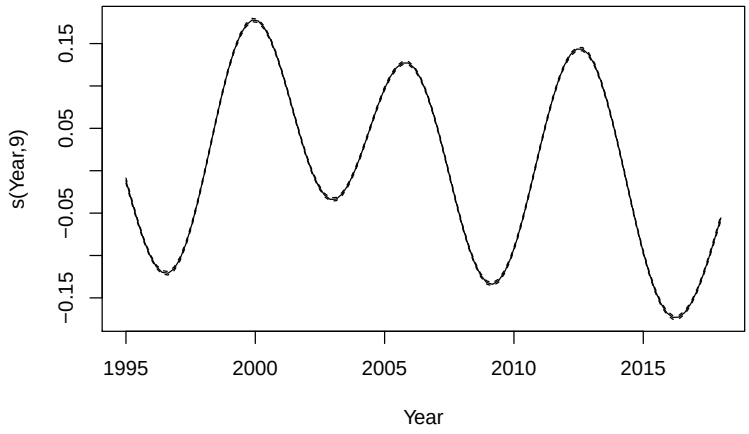


Figure 4.9: Estimated smoother for year obtained by a GAMM.

The Poisson GAMM is still overdispersed.

```
GE1 <- resid(G1$mer, type = "pearson")
Npar <- sum(G1$gam$edf) + 1 #'+1' is for sigma nest
N    <- nrow(CC2)
```

```
GE1  <- resid(G1$mer, type = "pearson")
OverdispGAMM <- sum(GE1^2) / (N - Npar)
OverdispGAMM
```

```
## [1] 497.8361
```

Following the same model validation steps as for the Poisson GLMM shows that we still have spatial dependency; see Figure 4.10.

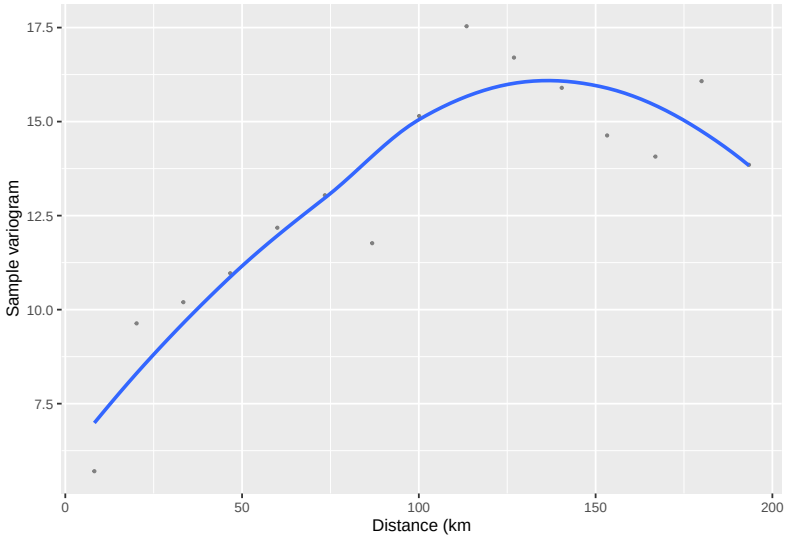


Figure 4.10: Sample variogram of the random effects of the Poisson GAMM.

4.6 What is next?

The Poisson GLMM is overdispersed, violates the spatial independence assumption and cannot cope with the excessive number of zeros in the Red knot data. At this stage we should not read too much into the shape of the smoother in Figure 4.9, as the GAMM needs to be extended so that it can cope better with the zero inflation and spatial-temporal dependency. During that process, the shape of the smoother may change. What it tells us now is that we should consider using a smoother in the model for the covariate `Year`.

When trying to fix the spatial dependency and zero-inflation problems we should not implement a model that attempts to solve all problems at once. Some of the problems may be due to the same cause; for example, lots of zeros next to one another is zero inflation but also spatial correlation. And if these zeros occur in sequential years, then the temporal smoother may also try to capture them. These are all scenarios for numerical estimation problems. We should really extend the model step by step. The question is then how to proceed, which problem do we tackle first. This is a matter of knowing the data, doing simple things first and addressing the underlying questions. Violation of independence is a more important problem than zero inflation. We will therefore apply models with spatial dependency in the next chapter.

Chapter 5

GAMM applied on the UK Red knot data in R-INLA

5.1 Model formulation

In this chapter we will apply a Poisson GAMM on the Red knot data from the UK in R-INLA. The reason for focusing on the UK data is to avoid excessively long computing time at this stage. The UK data were measured from 1975 onwards, and there is no need to remove the pre-1995 data for this country.

```
CC2 <- subset(CC, Country == "GB")
CC2 <- droplevels(CC2)
```

In Appendix A of this report we explain that a smoother is a collection of abstract mathematical functions. We show that the smoother of the covariate `Year` can be written as $f(\text{Year}) = X \times \beta$, where the matrix X contains columns with abstract mathematical functions, and the βs are the corresponding regression parameters. We also show in Appendix A how to execute a GAM as a linear regression model. We used the `lm` function to do this. The covariates in the `lm` function were the abstract mathematical functions in the matrix X. To understand the R code in this chapter, we assume that you are familiar with the code in Appendix A.

The Poisson GAMM that we will apply is defined in (5.1). We will use a smoother for the covariate year. It is the long-term trend present at all sites.

$$\begin{array}{rcl} \text{Counts}_{is} & \sim & \text{Poisson}\left(\mu_{is}\right) \\ \text{E}\left[\text{RK}_{is}\right] & = & \mu_{is} \\ \text{var}\left[\text{RK}_{is}\right] & = & \mu_{is} \\ \log\left(\mu_{is}\right) & = & \beta_1 + f(\text{Year}_s) + u_i \end{array} \tag{5.1}$$

Instead of $\beta \times \text{Year}_s$, which was used in the GLMM, the GAMM uses a smoothing function $f(\text{Year}_s)$.

Just as in the previous chapter, initial analysis showed that the Poisson GAMM is still overdispersed. The same holds for the Poisson models with spatial correlation that will be

applied in the next chapter. We therefore decided to also implement a negative binomial (NB) GAMM; see Equation (5.2).

$$\begin{array}{rcl} \text{Counts}_{is} & \sim & \text{NB}\left(\mu_{is}, \theta\right) \\ \text{E}\left[\text{RK}_{is}\right] & = & \mu_{is} \\ \text{var}\left[\text{RK}_{is}\right] & = & \mu_{is} + \frac{\mu_{is}^2}{\theta} \\ \log\left(\mu_{is}\right) & = & \beta_1 + f(\text{Year}_s) + u_i \end{array} \tag{5.2}$$

Note that this distribution has an extra parameter θ. For small values of θ, the NB distribution allows for a large variation of the counts. In our experience, the NB distribution is capable of dealing rather well with zero-inflated data.

5.2 Executing the Poisson GAMM in mgcv

We only need three lines of R code to execute the Poisson GAMM in the `gamm4` package (Wood and Scheipl, 2020) in R.

```
G1 <- gamm4(RK ~  s(Year),
            data = CC2,
            family = "poisson")
```

Instead of using the output of this model, we will execute the same model in R-INLA. The reason for this is that in R-INLA we can easily add spatial and spatial-temporal correlation. Doing this in the `gamm4` or `mgcv` packages is bound to result in numerical estimation problems. The only problem with executing the Poisson GAMM in R-INLA is that the required code is rather lengthy.

5.3 Executing the Poisson GAMM in R-INLA

In this section we will show how to execute a GAMM in R-INLA. The R code to do this is not well described in the literature, so we will therefore present and explain the code in detail. It is fully explained in Zuur and Ieno (2018).

In Appendix A we explain that a smoothing function of a covariate can be written as $X \times \beta$, and we also show how to obtain the basis functions (i.e. the columns of the X matrix). As explained in Appendix A we will keep the smoother relatively simple and use unpenalised cubic regression splines with 7 degrees of freedom.

We will apply a Poisson GAMM in which Year is modelled as a smoother. The native smoothers in R-INLA can be quite unstable, and we will therefore use unpenalised cubic regression splines with 7 degrees of freedom. This will result in a curve that is fairly smooth and will only pick up the main patterns of a covariate effect.

We use the `smoothCon` function from the `mgcv` package to obtain the basis functions of a smoother. This is the X matrix for a smoother.

```
NumKnots <- 8 #df = Number of knots - 1
Lego.Year <- smoothCon(s(Year, bs = "cr", k = NumKnots, fx = TRUE),
                       data = CC2, absorb.cons = TRUE)[[1]]
```

The `Lego.Year` component contains the knot positions and the basis functions, among other information. The X matrix is extracted below.

```
X.Year <- Lego.Year$X  #f(Year) = X.Year * beta
```

The object `X.Year` contains the 7 abstract mathematical functions that we will use as covariates in the model. This means that in order to estimate the smoother, we need to estimate 8 regression parameters (1 intercept + 7 parameters for the smoother).

The `inla` function will be used to execute the Poisson GAMM in R-INLA. Just like the `lm` and `glm` functions we can use the `data=` argument to provide the data. However, if there is spatial correlation, then we need to make adjustments in how we pass data to R-INLA. This is done with the so-called `stack` function.

When we apply models with spatial correlation then we need to use the `stack` function to combine the response variable, covariates and spatial correlation components. We might as well start using the `stack` function now as it means that in later chapters we only have to make small changes to the R code.

We don't have spatial correlation yet, but we might as well use the `stack` function at this stage of the analysis so that in later chapters we only have to make small modifications to the code. We use the `stack` function to combine all the data. The code for the `stack` function is explained in more detail in the next chapter.

```
N <- nrow(CC2)
StackPoissonGAMM <- inla.stack(
    tag = "Fit",
    data = list(RK = CC2$RK),
    A = list(1, 1, 1),
    effects = list(
       Intercept = rep(1, N),  #Intercept
       X.Year    = X.Year,     #f(Year) = X.Year * beta
       Site      = CC2$Site))  #random intercept
```

The last thing that we need to do is to specify a prior for the σ of the random intercept. As explained in Wang et al. (2018), the default gamma priors for variance parameters in R-INLA do not perform well for GLMMs, and it is recommended to use penalised complexity (PC) priors for such hyperparameters. A PC prior is defined as $P(\sigma > U) = \alpha$.

The task of the user is to select values for U and α, for example $P(\sigma > 4) = 0.05$. This states that the probability that the σ from the random intercept site is most likely smaller than 4. Such a prior is defined below.

```
priorpc <- list(prec = list(prior = "pc.prec",
                            param = c(4, 0.05)))
```

The choice for this prior may appear subjective, but we can easily get some idea of likely values for σ by applying a model without any covariates and inspecting the estimated σ for the random intercepts. In such a worst-case scenario, the value of σ is probably the largest that we may find. Wang et al. (2018) used a σ that is slightly larger than the σ obtained by a model without any covariates. One should also keep in mind that a σ of 4 implies that the majority of the random intercepts are between -1.96×4 and 1.96×4. And a random intercept of 7 or 8 means that the fitted values are around exp(7) or exp(8), which are rather large values.

For the regression parameters we use diffuse normal priors, and there is no urgent need to adjust these.

When we apply a GLMM or GAMM in R-INLA, an educated guess is required for the likely values of the σ of the random intercepts u_i, where $u_i \sim N(0, \sigma^2)$. The general recommendation is to use a penalised complexity prior for σ and specify some sort of upper limit for the likely values of σ via $P(\sigma > U) = 0.05$. Based on prior knowledge, initial data analysis and common sense, a sensible value for U needs to be selected.

We are now ready to execute the Poisson GAMM in R-INLA; see the code below.

```
Pois1 <- inla(RK ~ -1 + Intercept + X.Year +
                     f(Site, model = "iid", hyper = priorpc),
              data = inla.stack.data(StackPoissonGAMM),
              control.predictor = list(A = inla.stack.A(StackPoissonGAMM),
                                       link = 1),
              control.compute = list(dic = TRUE, waic = TRUE),
              control.inla = list(strategy='gaussian',
                                  int.strategy = 'eb'),
              family = "poisson")
```

We also execute the negative binomial GAMM; see the code below. We compared the results with those obtained by the frequentist package `glmmTMB`. Results were similar.

```
NB1 <- inla(RK ~ -1 + Intercept + X.Year +
                  f(Site, model = "iid", hyper = priorpc),
              data = inla.stack.data(StackPoissonGAMM),
              control.predictor = list(A = inla.stack.A(StackPoissonGAMM),
```

```
                                    link = 1),
            control.compute = list(dic = TRUE, waic = TRUE),
            control.inla = list(strategy='gaussian',
                                int.strategy = 'eb'),
            family = "nbinomial")
HyperMar <- NB1$marginals.hyperpar
theta.pd <- HyperMar$`size for the nbinomial observations (1/overdispersion)`
theta.pm <- inla.emarginal(function(x) x, theta.pd)
```

The reason that we execute the negative binomial GLMM is that we would like to use the posterior mean value of the parameter θ as a starting value for the spatial models that will be applied in later chapters. The NB GAMM produces a posterior mean of $\theta = 0.18$.

Once the model is finished, we have posterior mean values of all the regression parameters. We can also obtain fitted values and Pearson residuals. This allows us to assess the model for overdispersion and apply model validation. We still have spatial correlation in the random effects, and the Poisson GAMM cannot cope with the excessive number of zeros. The only problem that has been solved by the Poisson GAMM is the non-linear covariate effects.

We will not show any of these model validation graphs here. Instead, we will show how to plot the smoothers in the next section, before we apply models with spatial correlation.

5.4 Plotting the smoother in R-INLA

When we use the `plot` function after applying the `gamm4` or `gam` functions in a frequentist analysis, we get a graph of the smoother. There is no `plot` function that does this for the INLA smoothers. Instead, we have to implement a series of coding steps ourselves before we can visualise the smoothers. In essence, these are the same steps that the `plot` function does for a `gamm4` object.

In order to visualise or plot the smoother we need to perform a couple of steps. In short, we need to create a certain number (say 50) of made-up values for the covariate `Year`, and for these values we calculate the predicted counts. But because this is a smoother, we need to convert these made-up values into basis functions with the same knot locations as the original smoother. These new basis functions are then put into a stack (one stack per smoother) and then combined with the original stack. The code to do this is not presented here, but it is in the RMarkdown document that was used to generate this report.

Before we show the smoother, we need to mention one more point. Recall that the Poisson GLMM is of the form

$$\mu_{is} = e^{\text{Intercept}+f(\text{Year}_s)+u_i}$$

.

Using some high school mathematics, namely $e^{a+b} = e^a \times e^b$, we can write the link function as

$$\mu_{is} = e^{\text{Intercept}} \times e^{f(\text{Year}_s)} \times e^{u_i}$$

.

Figure 5.1A shows the $e^{f(\text{Year}_i)}$ component obtained by the Poisson GAMM, and panel B shows the component obtained by the negative binomial GAMM. Note that we applied the exponential function. This means that the curve shows the multiplication factor to obtain the expected values of the Red knot counts. Let us focus on the smoother obtained by the negative binomial GAMM in panel B. When year is around 2000 then we need to multiply the rest of the model by approximately 1.35 to obtain the fitted values. When the year values are between 1975 and 1988, we need to multiply the rest of the components by a value close to 0.8 to obtain the expected values.

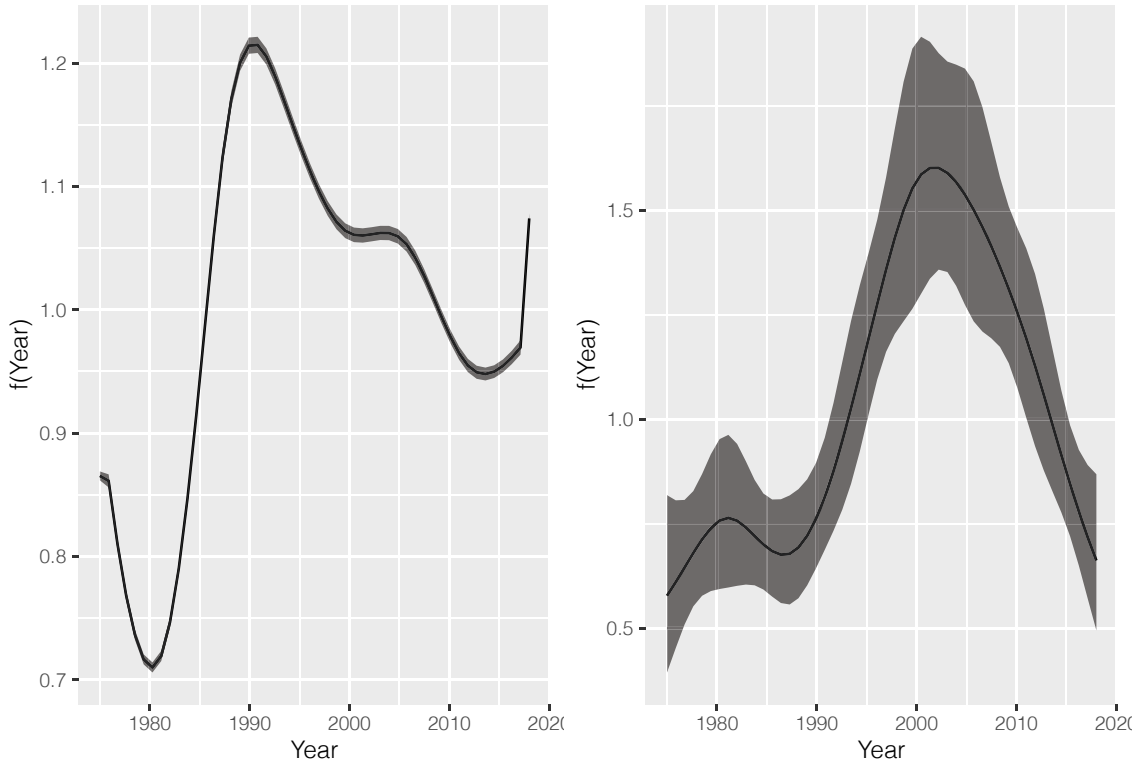


Figure 5.1: A: Posterior mean values and 95% credible intervals for the smoother obtained by the Poisson GAMM applied on the Red knot data from the UK. B: Posterior mean values and 95% credible intervals for the smoother obtained by the negative binomial GAMM applied on the Red knot data from the UK. The smoothers are unpenalised cubic regression splines with 7 df.

Finally, we have random effects. We extract them and combine them with the spatial coordinates of the site.

```
a_i <- NB1$summary.random$Site[,"mean"]
MyData.gamm <- data.frame(a_i = a_i,
                          Xkm    = tapply(CC2$Xkm,
                                          FUN = mean,
                                          INDEX = CC2$Site),
                          Ykm    = tapply(CC2$Ykm,
```

```
                                        FUN = mean,
                                        INDEX =CC2$Site),
                          Sign     = ifelse(a_i > 0, "Positive", "Negative"))
```

As discussed earlier in this section, we assume that the random intercepts are independently distributed. Figure 5.2 shows that this is not the case. Panel A shows a scatterplot of the spatial coordinates, and we have superimposed the sign of the random intercepts (obtained by the negative binomial GAMM). There is a clear grouping structure indicating spatial dependency in the random effects. Panel B shows a sample variogram of the random intercepts (of the negative binomial GAMM) and also indicates that there is spatial dependency to about 60 km. In summary, there is clear evidence that the random intercepts are spatially correlated. We therefore conclude that the Poisson GAMM and the NB GAMM are not good models, and further model extensions are required.

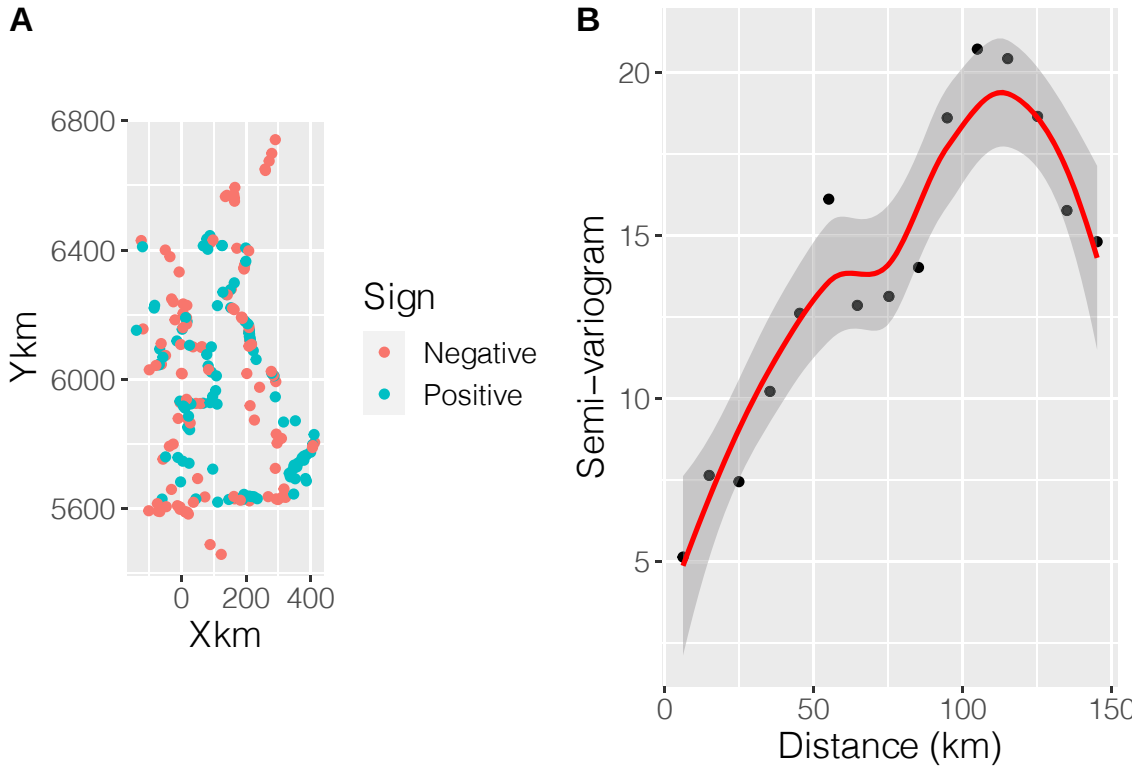


Figure 5.2: A: Plot of Xkm versus Ykm. Colours of the points are related to the sign of the posterior mean value of the random intercepts obtained by the negative binomial GAMM. B: Sample variogram of the posterior mean values of the random intercepts obtained by the negative binomial GAMM.

Chapter 6

Spatial GAM applied on the UK Red knot data

6.1 Introduction

In Chapter 5 we applied generalised additive mixed-effects models and estimated a temporal trend for the UK Red knot data. We used random effects to model dependency between all observations from the same site. We called these the u_is. We ended up with one u_i for each site i. One of the underlying assumptions of the GAMM is that these random intercepts u_i are independently distributed. However, model validation indicated that there is spatial dependency in these random effects, and that violates the model assumptions. In this chapter we will implement statistical models that allow for spatial dependency between the u_is. The models are estimated using the INLA method, which is implemented in the R-INLA package (Rue et al., 2020) in R.

In this report we avoid discussing technicalities of INLA. Instead, we focus on the conceptual points underlying INLA and show how to run a model with spatial correlation. We will also set the scene for the spatial-temporal GAMs that will be applied in Chapter 7. For a detailed discussion of R-INLA, see Blangiardo and Cameletti (2015), For a non-technical explanation plus a large number of case studies, see Zuur et al. (2017) and Zuur and Ieno (2018).

In this section we will apply Poisson, negative binomial, zero-inflated negative binomial and zero-altered negative binomial GAMs with spatial correlation.

6.2 Model formulation Poisson GAM with spatial correlation

The underlying questions are identical to those in Chapter 5. We will start with the following model.

$$\begin{array}{rcl} \text{RK}_{is} & \sim & \text{Poisson}\left(\mu_{is}\right) \\ \text{E}\left[\text{RK}_{is}\right] & = & \mu_{is} \\ \text{var}\left[\text{RK}_{is}\right] & = & \mu_{is} \\ \log\left(\mu_{is}\right) & = & \beta_1 + f(\text{Year}_s) + u_i \end{array} \tag{6.1}$$

RK_{is} is the number of Red knots at site i in year s. A smoother is used to model the effect of year. One may wonder what the difference is between the models in Equation (6.1) and Equation (5.1), which was presented in Section 5.1. The answer lies with the random effects u_i. In Section 5.1 the random intercepts u_i were independently distributed with mean 0 and variance σ^2. Note the word 'independently'. It implies that two random intercepts u_i and u_j are independent of each other, even if the corresponding sites are only 1 kilometer apart. In this section we will relax this assumption and allow the random effects u_i to be spatially correlated.

It should be noted that the spatially correlated random effects may represent real dependency, but also unmeasured covariate effects. It is not possible to discriminate between them, unless such covariates become available and are included in the model. The role of the spatially correlated random effects is to ensure that no residual spatial patterns are left. It also imposes dependency on the Red knot counts.

The only difference between the statistical models used in this chapter and those used in Chapter 4 is the independence assumption for the random effects. In this chapter we will allow them to be spatially correlated. This may affect the measures of uncertainty around the temporal trend.

6.3 Distances between sites

The purpose of the spatial correlation in the model is to capture small-scale dependency, where 'small' is relative to the distances between the sites. The first thing that we need to do is to define what is 'small' for these data. The left panel in Figure 6.1 shows a histogram of the distances between sites (in km). The right panel shows the cumulative distances. We would like to avoid the situation where the spatial correlation affects too many sites, so we limit it to about 10%-20% of the distance combinations. Spatial patterns on a larger scale may be captured with the covariates 'Xkm' and/or 'Ykm'. Based on Panels A and B in Figure 6.1 we label distances up to about 150 to 200 km as 'small'.

The spatial correlation is meant to capture only small-scale spatial dependency.

6.4 Defining the mesh

The spatial correlation in the GAM is modelled via the random effects u_i. When we applied the Poisson GAMM in Chapter 5 we assumed that the random effects u_i were independent and normal distributed, which we wrote as $u_i \sim N(0, \sigma_u^2)$. To allow for spatial dependency, we change the covariance structure and assume that the random intercepts are normal distributed with mean 0 and covariance matrix Ω.

$$u \sim N(0, \Omega)$$

The off-diagonal elements of Ω allow for correlation between the random effects at different locations. Estimating such a covariance matrix Ω has long been a major problem in

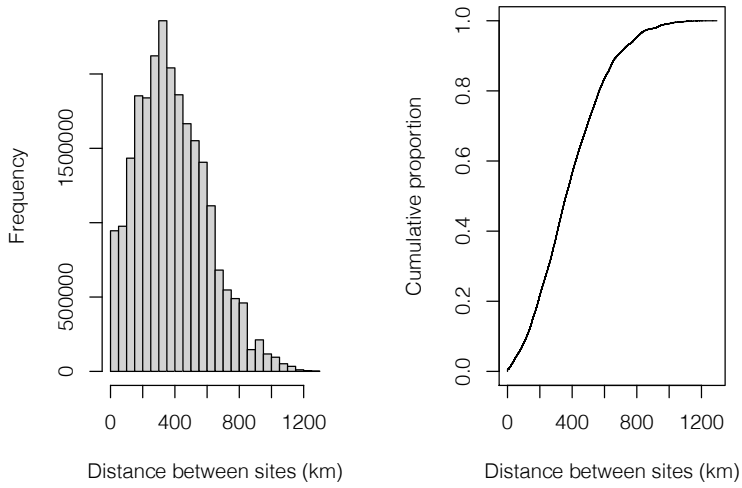


Figure 6.1: Left panel: Histogram of distances (km) between sites. Right panel: Cumulative distances between sites (km).

statistics. Rue et al. (2009) provided an efficient computing approach using integrated nested Laplace approximation (INLA), which is implemented in the R-INLA package in R. A brief outline is provided below. A more detailed, and non-technical explanation can be found in Blangiardo et al. (2013), Zuur et al. (2017), Zuur and Ieno (2018) or Wang et al. (2018).

Instead of estimating the random intercepts u_i directly, a grid is defined. This grid is called the 'mesh'; see Figure 6.2 for an example. The mesh consists of a large number of triangles that share vertices and corner points (also called nodes). The configuration of the triangles is such that a sampling site is either inside a triangle or on one of the three nodes. At each node there is a w_k. If a mesh has 2,000 nodes, there will be 2,000 of those w_ks. If a sampling location is inside a triangle, then the random intercept u_i is calculated as a weighted average of the three w_ks of the relevant triangle (nodes). The weights are given by the distances between the sampling location and the nodes of the relevant triangle. The covariance matrix Ω is also a function of the covariance matrix of the w_ks. So the problem of estimating the random intercepts u_i and its covariance matrix Ω shifts to estimating the w_ks and its covariance matrix.

In a model with spatial correlation, R-INLA does not estimate the random effects u_i directly. Instead it defines a dense grid of triangles. At each node of the triangle a w_k is estimated. Once we know the w_ks we can calculate the random effects u_i.

The R code below was used to generate and plot the mesh. In essence only the `RangeGuess` is a value that the user needs to select. All other settings can be kept as it is. We will discuss the code in more detail.

```
RangeGuess  <- 175  #in km
MaxEdge     <- RangeGuess / 5
```

```
Loc         <- cbind(CC2$Xkm, CC2$Ykm)
NonConvHull <- inla.nonconvex.hull(Loc, convex = -0.06)
mesh <- inla.mesh.2d(boundary = NonConvHull,
                     loc = Loc,
                     max.edge = c(1,5) * MaxEdge,
                     cutoff = MaxEdge / 5)
par(mfrow = c(1,1), mar = c(0, 0, 0, 0))
plot(mesh, asp=1, main = "")
points(Loc, col = 2, pch = 1, cex = 0.5)
```

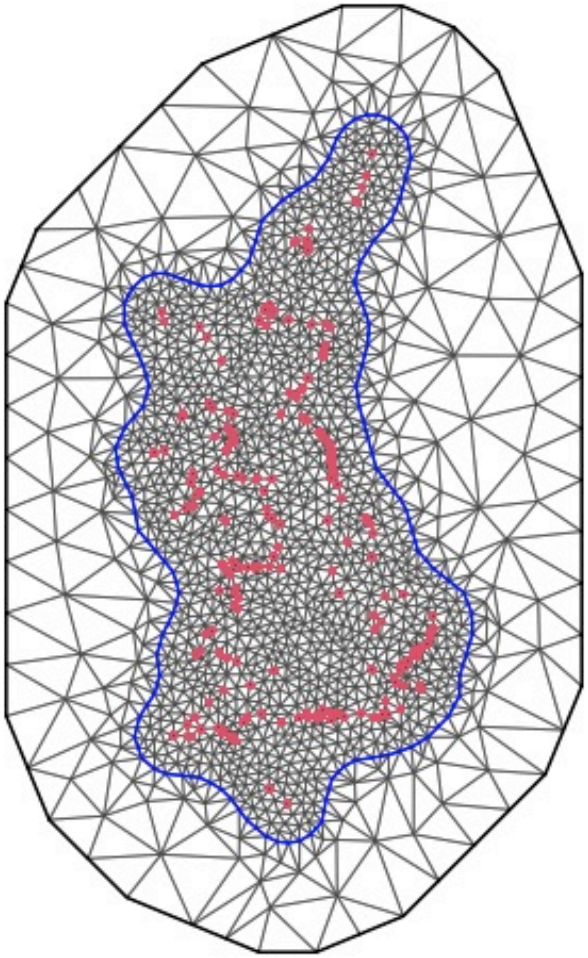


Figure 6.2: Mesh for the UK Red knot data.

We need not only the w_k but also its covariance matrix. Instead of trying to estimate the covariance matrix of the w_ks directly, a mathematical function is used to define the value of the correlation. This is done with the so-called Matérn correlation function. This function depends on the distance between sites. It has two parameters: a σ_u and a parameter κ (pronounced kappa). The parameter κ is linked to the range, which represents the distance at which spatial dependency diminishes. So in principle we can forget about the κ and only think about the range. If the range is large, then the spatial correlation covers large

areas; if the range is small, then it only affects sites close to one another. Hence, if R-INLA gives a very small range we might as well apply a model without spatial correlation.

For a given mesh, R-INLA will estimate the w_k values and its covariance matrix. Once we have these, we can calculate the u_is if we wish. The finer the mesh, the more accurate the solution but at a cost of more intensive computing. Behind the magical curtain of integrals and derivatives, R-INLA uses a complex mathematical function to define covariance between the w_ks as a function of distance between sites and two unknown parameters (the range and σ_u).

Let us return to the mesh in Figure 6.2 and the R code that we used to generate the mesh. There is an inner area and an outer area, separated by a blue line. It is recommended to use an outer area to avoid numerical estimation problems due to so-called boundary problems. This is a purely technical requirement. Because every extra node means we have to estimate an extra w_k value, it is preferable to use a less dense resolution in the outer area. The `max.edge = c(1, 5) * MaxEdge` causes a ratio of 1 to 5 between the resolutions in the inner and outer parts. This is a recommended ratio. The blue line that divides the inner and outer areas is obtained by putting a non-convex hull around the sampling location. There are different ways to control the density of the triangles, for example, with the maximum edge length of the triangles. When selecting the maximum edge value we should keep in mind the anticipated value of the range. Based on our desire to let the correlation affect sites that are separated by up to about 150-ish km, we selected a range of 175 km (this is `RangeGuess`). During initial analysis we also tried values of 125, 150 and 200 km. It is recommended to define the maximum edge length as a fifth of this value. The `cutoff` argument ensures that sampling locations that are within a distance that is smaller than the cut-off value are replaced by a single vertex. This is useful if there are sampling locations with the same spatial locations or if some are very close to one another. It avoids a mesh with lots of very small triangles in certain areas.

Before continuing we show the number of nodes.

```
mesh$n
```

```
## [1] 1589
```

Our mesh has 1589 observations. As we mentioned earlier, the more nodes we have, the more w_ks we use, and the more accurate the INLA approximation, but the longer the computing time. In general, a mesh with 1000 nodes (i.e. w_k values) takes only a few minutes on a fast computer. We can easily cope with meshes of higher density, although ultimately the choice of the mesh size depends on available computing power. In practice we choose the value of `RangeGuess` as large as computing time allows. Having said that, there will be a point at which increasing the value of `RangeGuess` no longer has any benefit. It is recommended to run the models with different mesh configurations and investigate whether there are any differences in the outcome.

From a practical point of view, we only need to choose the value of `RangeGuess` to generate a mesh. We defined it as 100 km.

6.5 Controlling the spatial dependency term

Next, we execute three commands. The first and third commands should be executed without making changes for different models and mesh configurations. They require no explanation at this stage. The second command does require some explanation.

```
A    <- inla.spde.make.A(mesh, loc = Loc)
spde <- inla.spde2.pcmatern(mesh,
                            prior.range = c(100, 0.05),
                            prior.sigma = c(5, 0.05))
w.index <- inla.spde.make.index('w', n.spde = spde$n.spde)
```

In Appendix A we explain smoothers. At this point in the reading of this report you may want to glance at that appendix. We start with the moving average and LOESS smoothers. We explain that the wiggliness of these smoothers is controlled by the size of the window that selects local points. Use a large window and the smoother is a straight line; use a small window and the smoother goes from point to point. We then introduce linear spline regression, quadratic spline regression and cubic spline regression models. The wiggliness of such smoothers can be controlled (partly) by the number of knots.

The spatial correlation term in the GAM is essentially a two-dimensional smoother of spatial coordinates. Again, there is a mechanism to control the wiggliness of such a smoother. We will discuss this mechanism now. The spatial correlation can be envisioned as a collection of mountains. If the value of the range is large, then there is only one, or perhaps a few, gently sloping mountains. If the range is small, then we may end up with lots of small-radius mountains. In addition to the width of a mountain there is also the height of a mountain. We can control this with the σ_u parameter. If σ_u is small, then the mountains are not very high, whereas a large σ_u will result in high mountains. So a large range and a large σ_u imply that we have a few, but high and wide, mountains. A small range with a large σ_u means lots of high mountains with a small diameter.

As we have already mentioned, one can also view the 'spatial dependency' term as a two-dimensional smoother of the spatial coordinates. If such a model is fitted with the `mgcv` package in R, then we use the notation `s(Xkm,Ykm)`, and we can control the shape of such a smoother with a term called the effective degrees of freedom (edf). A high value for edf means that we have a smoother that is rather non-smooth, whereas a smoother with a low edf results in a rather smooth two-dimensional shape.

The spatial correlation in the GAM is essentially a two-dimensional smoother of the spatial coordinates. We can control the amount of smoothing via the range and the σ_u. A large range and a small σ_u means that we have a rather smooth pattern, whereas a small range and a large σ_u means that we have a two-dimensional smoother that shows lots of small and high values, and may even result in a perfect fit.

When estimating the smoother in a GAM using the `mgcv` or `gamm4` packages in R, certain tools exist to estimate the optimal value for the amount of smoothing (i.e. the edf). This process is called cross-validation. But such a process is not available when determining the amount of smoothing that the 'spatial dependency' term is allowed to do. Instead we can specify likely values for the range and σ_u. Or formulated better, we specify non-likely values via so-called penalised complexity priors. This means that, *a priori*, we need to specify the values $range_0$ and $sigma_0$ (and also α_1 and α_2) in the following two expressions.

$$\begin{aligned} P(\text{range} < range_0) &= \alpha_1 \\ P(\sigma_u > \sigma_0) &= \alpha_2 \end{aligned}$$

In the R code above we use

$$\begin{aligned} P(\text{range} < 100 \text{ km}) &= 0.05 \\ P(\sigma_u > 5) &= 0.05 \end{aligned}$$

What we are saying here is that the probability that the range is smaller than 100 km is rather small, and the probability that σ_u is larger than 5 is also rather small. By increasing `range0` and decreasing `sigma0` we can force the spatial correlation to be smoother. Choosing these values is a matter of trial and error, prior knowledge and visual observation that the resulting smoother does not overfit the data. This sounds subjective, but in practice it is not too difficult to choose these values.

When we apply a spatial GLM or GAM in R-INLA, an educated guess is required for the likely values of the range (distance at which the spatial dependency diminishes) and the variation of the spatial random field (σ_u). This is done with penalised complexity priors. Using common sense, biological knowledge, results from initial analysis, expertise and some educated guess work, we need to specify values for range_0 in $P(\text{range} < \text{range}_0) > 0.05$ and σ_0 in $P(\sigma_u > \sigma_0) = 0.05$.

6.6 Stack for the GAM with spatial correlation

When using functions like `lm`, `glm`, `gam`, `glmer` or `glmmTMB` in R, the data can be specified with the `data = ...` argument. R-INLA uses the function `inla` to execute the models, but it has no `data = ...` argument, at least not when models with spatial correlation are executed. Instead we combine the response variable, covariates and the information about the w_ks in a so-called stack.

The stack is defined with the `inla.stack` function; see the R code below. In the `data` argument of this function we specify the counts of Red knots. In the `effects` part we define covariates.

The `A = list(1,1,...,A)` is perhaps the most confusing part of the stack. It requires modifications if covariates are added or removed. The problem is that the response variable and the covariates are measured at the sites, whereas the spatial dependency, defined on the nodes of the triangles, has a much higher resolution. In order to match the sampling locations with the nodes of the mesh we use the `1` as a sort of identify matrix and the

second `A` to map the `w_k`s to the response and covariates. Note that this stack is nearly the same as we used for the Poisson GAMM.

```
N <- nrow(CC2)
StackGAMSpatial <- inla.stack(
    tag = "Fit",
    data = list(RK = CC2$RK),
    A = list(1, 1, 1, A),
    effects = list(
       Intercept = rep(1, N),   #Intercept
       X.Year    = X.Year,      #f(Year) = X.Year * beta
       fsite     = CC2$Site,    #Random intercept
       w         = w.index))    #Spatial random field
```

The stack is a tool to combine data that is defined on different spatial scales (i.e. response and covariates at the sites and the w_ks at the nodes of the mesh).

6.7 Defining the formula

Now that we have done the hard work we are nearly ready to execute the GAM with spatial correlation in R-INLA. We only have to define the model formula.

```
Form1 <- RK ~ -1 + Intercept + X.Year + f(w, model = spde)
```

This formula states that the counts of the Red knots are modelled as a function of an intercept, a year effect and the spatial dependency. Note that the '−1' removes the standard intercept, and we use the newly defined `Intercept` from the stack. The reason for this odd way of coding an intercept is numerical stability of the software.

6.8 Executing the spatial GAMs in R-INLA

We are now ready to execute the spatial Poisson GAM.

```
Spat.Pois <- inla(Form1,
                  data = inla.stack.data(Stack50GAMSpatial),
                  control.predictor = list(A = inla.stack.A(Stack50GAMSpatial),
                                           link = 1),
                  control.compute = list(dic = TRUE, waic = TRUE),
                  #Faster calculation:
                  control.inla = list(strategy='gaussian',
                                      int.strategy = 'eb'),
                  family = "poisson")
```

The only piece of code that we did not show is adding the stacks that contain the 50 covariate values for the two smoothers so that we can plot them. This explains why we use `Stack50GAMSpatial` and not `StackGAMSpatial`.

Just as for the Poisson GLMM and Poisson GAMM, we need to extract the fitted values and calculate the Pearson residuals. We need to plot residuals versus fitted values, and versus all available covariates. The random effects are now allowed to be spatially correlated, so we do not need to check them for spatial dependency. We also need to simulate 1000 data sets from the model and see whether the model can cope with the excessive number of zeros. The Poisson GAM with spatial correlation was still overdispersed, which explains why we also execute the negative binomial GAM with spatial correlation.

```
Hyper.NB <- list(size = list(initial = theta.pm, fixed = TRUE))
Spat.NB <- inla(Form1,
                family = "nbinomial",
                data = inla.stack.data(Stack50GAMSpatial),
                control.predictor = list(A = inla.stack.A(Stack50GAMSpatial),
                                         link = 1),
                control.family = list(hyper = Hyper.NB),
                control.inla = list(strategy='gaussian',
                                    int.strategy = 'eb'),
                control.compute = list(dic = TRUE, waic = TRUE))
```

As an alternative to the negative binomial distribution, we can use the zero-inflated Poisson (ZIP) or the zero-inflated negative binomial (ZINB) distributions. The ZIP and ZINB distributions are explained in Zuur et al. (2012). These are just modifications of the Poisson and negative binomial distributions in the sense that they allow for an excessive number of zeros (zeros that cannot be explained with the covariates). We will apply ZIP and ZINB GAMs with spatial dependency. The same covariates are used.

We execute the ZIP and ZINB models as follows.

```
Spat.ZIP <- inla(Form1,
                 data = inla.stack.data(Stack50GAMSpatial),
                 control.predictor = list(A = inla.stack.A(Stack50GAMSpatial),
                                          link = 1),
                 control.compute = list(dic = TRUE, waic = TRUE),
                 #Faster calculation:
                 control.inla = list(strategy='gaussian',
                                     int.strategy = 'eb'),
                 family = "zeroinflatedpoisson1",)
```

```
Spat.ZINB <- inla(RK ~ -1 + Intercept + X.Year + f(w, model = spde),
                  data = inla.stack.data(Stack50GAMSpatial),
                  control.predictor = list(A = inla.stack.A(Stack50GAMSpatial),
```

```
                                    link = 1),
                control.compute = list(dic = TRUE, waic = TRUE),
                control.inla = list(strategy='gaussian',
                                    int.strategy = 'eb'),
                control.family = list(hyper = Hyper.NB),
                family = "zeroinflatednbinomial1")
```

6.9 Comparing models

To compare models with different sets of covariates or different dependency structures, we use the DIC and WAIC, which are Bayesian alternatives for the AIC. These are as follows.

```
##                           DIC         WAIC
## Poisson GAMM      5240502.16 2.285740e+06
## Poisson GAM + SRF 4807554.01 1.202780e+64
## NB GAMM             45669.55 4.584367e+04
## NB GAM + SRF        66759.86 6.889427e+04
## ZINB GAM + SRF      57696.48 5.901783e+04
```

The abbreviation 'SRF' stands for 'spatial random field' and represents the spatial dependency. The lower the DIC, the better the model, as judged by the DIC. Note that the Poisson GAM with spatial correlation has rather odd values for the DIC and WAIC. The posterior mean value of σ_u is 34 in the Poisson GAM with spatial correlation. This means that some of the w_k are excessively large. Its four largest values are 41.28, 46.12, 56.04 and 244.07. After applying the exponential function we end up with fitted values that are extremely large. This is the first indication that there are some serious problems with the analysis of these data. We tried to reduce the value of σ_u, but that caused other problems (i.e. a rather small range).

Note that the negative binomial GAMM has a lower DIC than the negative binomial GAM with spatial correlation. This is to be expected. The random effects in the NB GAMM have full flexibility, whereas in the NB GAM with spatial correlation, random effects of sites close to one another are forced to be similar. In this case, the model with restrictions is more limited in what it can do, and therefore its DIC is larger. However, the NB GAMM violates the independent assumption, so it is not a candidate model. The only four models that we should consider here are the models with spatial correlation. Of these, the zero-inflated negative binomial GAM with spatial correlation is considerably better than the other models, and we therefore focus on the ZINB GAM with spatial correlation in the next sections.

A model validation applied on the zero-inflated negative binomial GAM with spatial correlation did not indicate any major problems.

6.10 Results of the ZINB GAM with spatial dependency

Before presenting the results of the ZINB GAM with spatial correlation, we present the model formulation.

$$\begin{array}{rcl} \mathrm{RK}_{is} & \sim & \mathrm{ZINB}\left(\mu_{is}, \theta, \pi\right) \\ \mathrm{E}\left[\mathrm{RK}_{is}\right] & = & (1-\pi) \times \mu_{is} \\ \mathrm{var}\left[\mathrm{RK}_{is}\right] & = & (1-\pi) \times \mu_{is} \times (1 + \pi \times \mu_{is} + \frac{\mu_{is}}{\theta}) \\ \log\left(\mu_{is}\right) & = & \beta_1 + f(\mathrm{Year}_s) + u_i \end{array} \tag{6.2}$$

The term π is used to model the excessive number of zeros that cannot be modelled with the covariates in the count part of the model. When $\pi = 0$ we obtain the negative binomial distribution. In R-INLA, π cannot be modeled as a function of covariates. Instead, it is constant. The posterior mean value of π is 0.52.

The count part of the ZINB GAM with spatial correlation contains an intercept, the smoother for year and spatial correlation. The smoother is plotted in Figure 6.3. Just as before we have applied the exponential function, so along the y-axis we are visualising the multiplication factors to get the expected counts for Red knots.

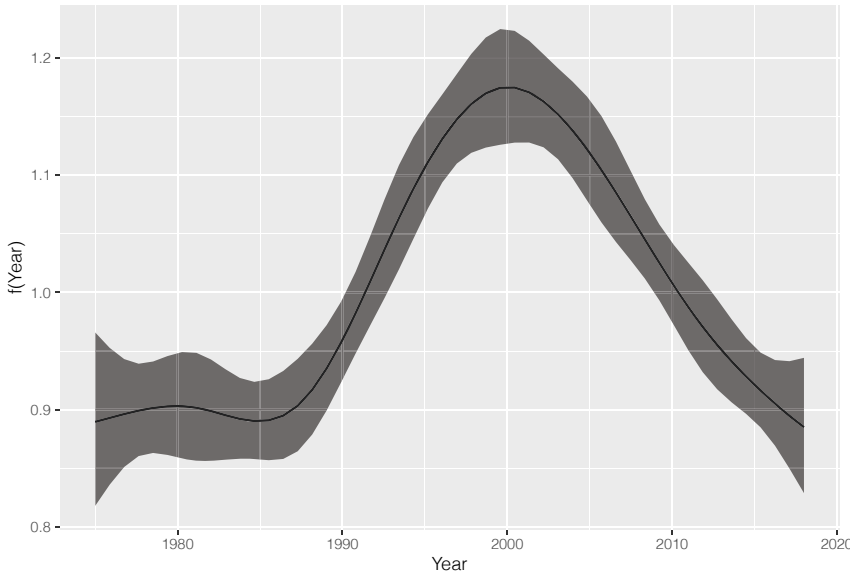


Figure 6.3: Posterior mean values and 95% credible intervals for the year smoother obtained by the ZINB GAM with spatial correlation applied on the UK Red knot data. The smoother is an unpenalised cubic regression spline with 7 df.

In Equation (6.2) we explained that the expected values of the ZINB GAM are given by

$$(1-\pi) \times e^{\mathrm{Intercept}} \times e^{f(\mathrm{Year}_s)} \times e^{u_i}$$

and we plotted the effects of year in Figure 6.3. When we plotted the smoother, we applied the exponential function. The ZINB GAM with spatial correlation has correlated random effects u_i. We explained that we estimate w_k values on a fine mesh. We can extract these w_ks and plot them; see Figure 6.4. Just as in Section 5.4 we can choose whether we want to plot the w_ks or e^{w_k}. We decided to plot the w_ks.

The interpretation of the spatial random field in Figure 6.4 is as follows. In those areas where we have dark red colours, the w_ks and therefore the u_is, are around 9. This means that the multiplication factor (to get the expected RK) due to the spatial correlation is

around exp(9) ≈ 8100. That is considerably more than the effect of the trend! In the dark purple areas, the w_k are around −5. This means that the multiplication factor to get the fitted values is around exp(−5) ≈ 0. In simple terms this means that we either have missing covariates or real spatial dependency that is causing higher expected values in the red areas and lower expected values in the purple areas. In the dark red areas the multiplication factor is more than 8000, and in the dark purple areas we probably have plenty of zero Red knots.

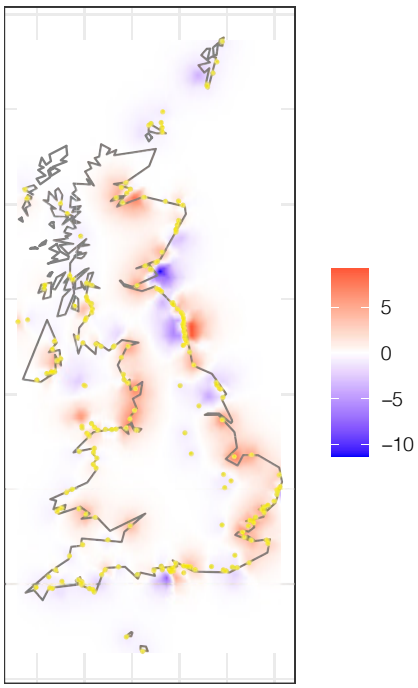


Figure 6.4: Spatial random field obtained by the ZINB GAM with spatial correlation. Yellow dots represent the sampling locations.

The underlying mathematical model for the spatial correlation in the GAM is the Matérn correlation function. The parameters of this correlation function are estimated by R-INLA, and its shape is presented in Figure 6.5.

The posterior mean value of the range is 30.15 km. If we quantify 'highly correlation' as correlation values between 0.8 and 1, then the Matérn correlation function in Figure 6.5 indicates that sites separated by up to around 50 km are highly correlated. And if we deem correlation between 0.5 and 0.8 and 'moderately correlated', then all sites that are separated by 50 to 100 km are deemed moderately correlated. Any sites separated by more than 30.15 km (which is the value of the range) have a very low correlation. The value of the range indicates that about 2% of the site combinations are affected by the spatial correlation.

6.11 Two major problems

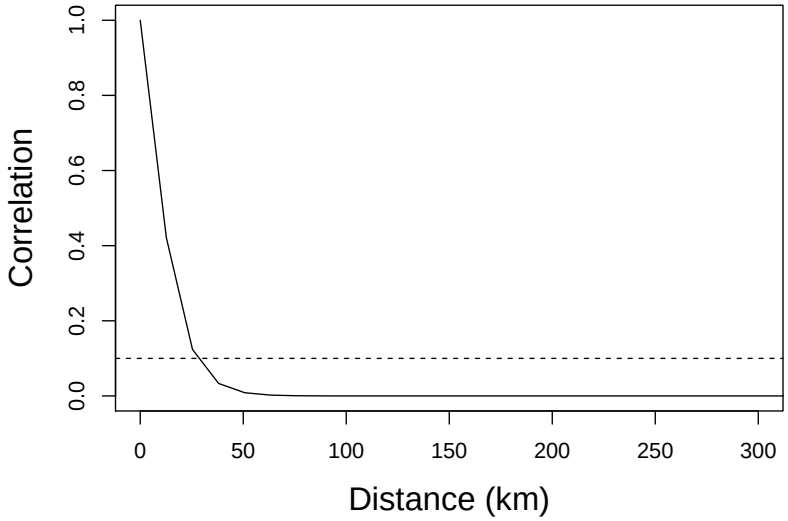


Figure 6.5: Matérn correlation function obtained by the ZINB GAM with spatial correlation applied on the UK Red knot data.

6.11.1 Correlation changing over time

There are two major problems with the spatial ZINB GAM (and all other spatial models that we have executed thus far), that may potentially limit its use. The Matérn correlation function allows that random effects of neighboring sites are correlated. But it does not allow for any temporal changes in the correlation. Formulated differently, the model assumes that two observations separated by (for example) 10 km are highly correlated, even if one observation was made in 1995 and the other in 2018. From a biological point of view it is unlikely that there is correlation between these two observations. The solution to this problem is to allow the spatial correlation to change over time. For this we need a GAM with spatial-temporal dependency. We will do this in the next chapter.

6.11.2 Small fitted values

The second problem becomes appearent when we plot the fitted values versus the observed data. The fitted values of the ZINB GAM with spatial correlation are obtained as follows.

```
N <- nrow(CC2)
mu <- Spat.ZINB$summary.fitted.values[1:N, "mean"]
Pi <- Spat.ZINB$summary.hyperpar[
           "zero-probability parameter for zero-inflated nbinomial_1",
           "mean"]
ExpCounts <- (1 - Pi) * mu
```

Once we have the fitted values `ExpCounts` of the ZINB GAM with spatial correlation, we plot them against the observed number of Red knots; see Figure 6.6. Note that the model is not able to fit the larger fitted values. The largest fitted value of the ZINB GAM with

spatial correlation is 5563.02. There are 364 observations on Red knots that are larger than 5563.02. If we want to predict population trends, then this is a major problem. Allowing for spatial random fields that change over time may improve this problem.

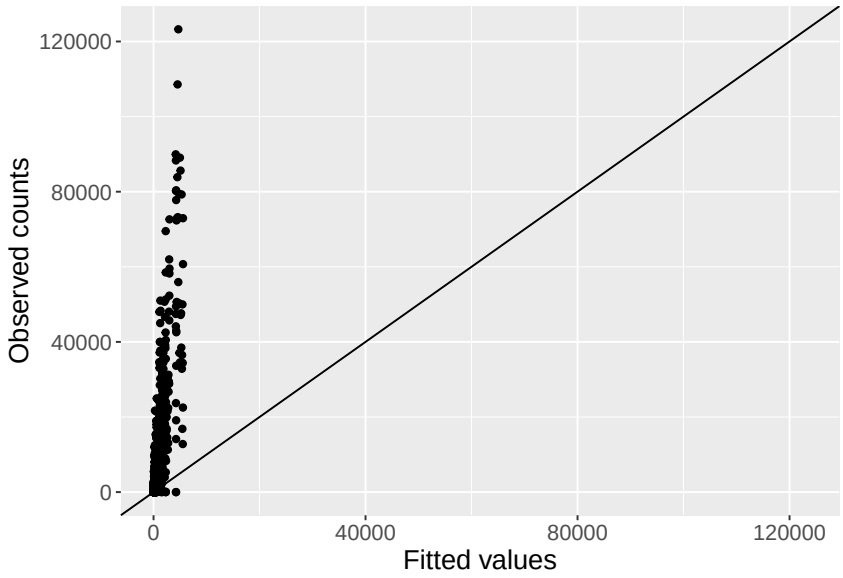


Figure 6.6: Observed data plotted versus the fitted values of the ZINB GAM with spatial correlation.

6.11.3 A small simulation study

In this subsection we will explain why the fitted values obtained by the ZINB GAM with spatial correlation produces fitted values that do not represent the larger Red knot observations very well. We will use a small simulation study for this.

We will simulate data from a zero-inflated Poisson GLM, but the same principles apply for the negative binomial and ZINB distributions. Suppose that we use the following ZIP GLM.

$$\begin{array}{rcl} Y_i & \sim & \text{ZIP}\left(\mu_i, \pi\right) \\ \text{E}\left[Y_i\right] & = & (1-\pi) \times \mu_i \\ \log\left(\mu_i\right) & = & 1 + 3 \times X_i \end{array} \tag{6.3}$$

This is a simple ZIP GLM in which we selected the intercept as 1, the slope for a covariate X_i as 3, and we will use $\pi = 0.75$. We will simulate 1,000 values for a covariate X_i by drawing values from a uniform distribution. Once we have the intercept (1), slope (7), covariate (`X`) and π (0.75),we can calculate the `mu` and simulate zero-inflated Poisson data (`Y`) with the `rzipois` function from the `VGAM` package (Yee, 2021).

```
set.seed(123)
library(VGAM)
X  <- sort(runif(1000))
mu <- exp(1 + 7 * X)
```

```
Pi <- 0.75
Y  <- rzipois(1000, lambda = mu, pstr0 = 0.75)
ZipData <- data.frame(X = X,
                      Y = Y)
```

The data frame `ZipData` contains the data that we would normally sample in the field. Figure 6.7 shows a frequency plot of the `Y` data and also a scatterplot of `Y` versus `X`. The percentage of observations in `Y` equal to 0 is 75.6%.

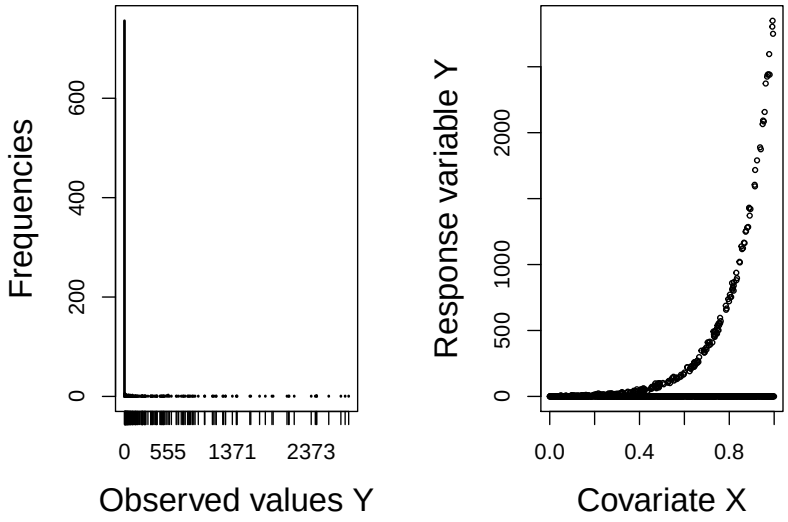


Figure 6.7: Left: Frequency plot of the simulated Y variable showing an excessive number of zeros. Right: Scatterplot of Y versus X. The horizontal line at 0 is in fact a series of observations that are all equal to 0.

When we apply a ZIP GLM on these data we obtain estimated values close to the original ones, as can be seen from the code below.

```
library(pscl)
M2 <- zeroinfl(Y ~ X | 1,
               data = ZipData)
summary(M2)
```

```
##
## Call:
## zeroinfl(formula = Y ~ X | 1, data = ZipData)
##
## Pearson residuals:
##     Min      1Q  Median      3Q     Max
## -0.5689 -0.5677 -0.5559 -0.4726  3.6030
##
## Count model coefficients (poisson with log link):
```

```
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.02435    0.01912   53.58   <2e-16 ***
## X            6.97005    0.02233  312.09   <2e-16 ***
##
## Zero-inflation model coefficients (binomial with logit link):
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.12749    0.07369    15.3   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of iterations in BFGS optimization: 5
## Log-likelihood: -1462 on 3 Df
```

Note that the `zeroinfl` function does not give π directly. Instead, we can calculate π via $\pi = \exp(1.12)/(1 + \exp(1.12)) = 0.76$.

The dispersion statistic of the ZIP GLM is 0.96, indicating that there is no overdispersion. Figure 6.8 shows the model fit of the ZIP. The red line is equal to $(1 - \pi) \times \mu_i$, and these are the expected values of the ZIP GLM. The green line is the π and the black line is the μ_i component. Note that the expected values of the ZIP (red line) are between the lines for the count data and the zeros. Many users of ZIP, NB and ZINB models are surprised to see that the expected values of the model are not going through the centre of the non-zero count data. The expected values of a ZIP are a weighted average of the count part of the model (μ_i) and the binary part (π). This explains why the fitted values obtained by the ZINB GAM with spatial correlation applied on the Red knot data produces fitted values that are considerably lower than the 90 largest observed values.

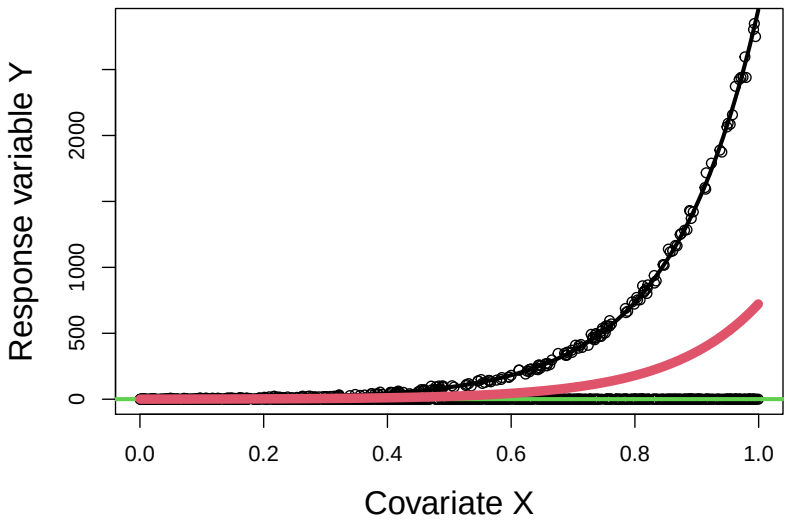


Figure 6.8: Fitted values of the ZIP (red line). The count part (red line) and binary part (green line) of the ZIP model are also presented.

Finally, we discuss why a quasi-Poisson model is not a good alternative. If we apply a Poisson GLM on these data, we get the following results.

```
M3 <- glm(Y ~ X,
          family = poisson,
          data = ZipData)
summary(M3)
```

```
##
## Call:
## glm(formula = Y ~ X, family = poisson, data = ZipData)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -36.297  -12.188   -4.189   -1.491   64.375
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.05506    0.01788    3.08  0.00207 **
## X            6.43910    0.02085  308.89  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 462296  on 999  degrees of freedom
## Residual deviance: 285285  on 998  degrees of freedom
## AIC: 286852
##
## Number of Fisher Scoring iterations: 6
```

The estimated slope of this model is diverting from what we selected (7), and the model has a dispersion statistic equal to 316.98, which indicates severe overdispersion. Actually, we choose the slope as 7 in this simulation study to mimic the amount of overdispersion that we obtained for the Red knot data. Some scientist apply a quasi-Poisson model when the Poisson is overdispersed. Such a model produces the same slope, but corrects the standard errors (of the Poisson GLM) by multiplying them with the square root of the dispersion statistic. This procedure is fine if the overdispersion in the Poisson GLM is small (<5), but it may produce biased parameter estimates for larger amounts of overdispersion. Below we apply the quasi-Poisson GLM on the simulated data.

```
M4 <- glm(Y ~ X,
          family = quasipoisson,
          data = ZipData)
summary(M4)
```

```
##
## Call:
## glm(formula = Y ~ X, family = quasipoisson, data = ZipData)
```

```
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -36.297  -12.188   -4.189   -1.491   64.375
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.05506    0.31833   0.173    0.863
## X            6.43910    0.37117  17.348   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasipoisson family taken to be 317.0195)
##
##     Null deviance: 462296  on 999  degrees of freedom
## Residual deviance: 285285  on 998  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 6
```

The standard error of the slope has now been corrected, but the 95% confidence interval just contains only the original value. We could have simulated data in which the quasi-Poisson produces biased parameter estimates. Hilbe (2014) argues that if there is overdispersion, then the cause of the problem has to be found, and this needs to be modelled accordingly. In other words, if there is severe overdispersion in a Poisson GLM or GAM, then quasi-Poisson should not be applied.

Chapter 7

GAM with spatial-temporal replicate correlation

In the previous chapter we applied negative binomial and zero-inflated negative binomial GAMs with spatial correlation. The spatial correlation was assumed to be constant over time. In this chapter we will apply the same two GAMs, except that we now allow the spatial correlation to change over time. The link function for both models is defined as follows.

$$\log(\mu_{is}) = \beta_1 + f(\text{Year}_{is}) + v_{is}$$

Note that we now use the notation v_{is} for the random intercepts. We discuss two options to model the spatial temporal random effects v_{is}. Both options will produce a set of w_ks for each year. This means that we will end up with 44 spatial random fields for the UK Red knots data, and we can plot these in 44 colour images. These spatial random fields may represent missing covariates, missing interactions or real dependency. The fundamental question is now how these spatial random fields change from year to year.

Option 1 is to use an auto-regressive correlation of order 1 (AR1). This means that we use

$$v_{i,s} = \rho \times v_{i,s-1} + u_{i,s}$$

We used a comma between the two subscripts to clearify the notation. The AR1 correlation states that the random effects in year s are a function of the random effects in year $s-1$. The random effects u_{is} are only spatially correlated and are modelled by the Matérn correlation function. The parameter ρ is unknown and needs to be estimated. If ρ is close to 1, then the spatial correlation in year s is similar to that of year $s-1$. Hence, we will end up with 44 colour images that change rather slowly over time.

Option 2 is the so-called replicate correlation. We get this if we force ρ to be 0. It means that in each year there is spatial correlation, as determined by the random effects u_{is}, but from year to year the location of the spatial correlation is allowed to change randomly. It means that in year $s-1$ we may have high values for the spatial random field in one part of the study area and in year s we can have high values in another part part. The strength of the spatial correlation, as quantified via the parameters for the Matérn correlation function, is assumed to be the same in all years.

The replicate correlation may be required for species that are dynamic in their spatial positions over time (e.g. birds), whereas the AR1 correlation may be more useful for species that are relatively stationary over time with respect to their spatial positions. In this report we will use the replicate correlation, for the simple reason that computing time is considerably shorter than for the AR1 model.

7.1 Projector matrix

We will use the same mesh as in Chapter 6. To implement a model in which the spatial correlation changes randomly from year to year, we need to inform R-INLA which observations belong to the same year. This needs to be coded via a vector with the values 1 1 1 2 2 2, etc. This is the variable `Repl` in the code below. It has the value 1 for all observations from 1975, 2 for all observations from 1976, etc.

```
Repl  <- CC2$Year - min(CC2$Year) + 1
NRepl <- length(unique(Repl))
```

The number of years is `NRepl` = 44. The number of observations per year varies between 114 and 185. The model will estimate a spatial random field for each year. The minimum number of sites per year that is required for this technique is about 50.

We need to define a projector matrix that contains 44 blocks of weighting factors. The argument `repl = Repl` in the `inla.spde.make.A` function below does that.

```
Arepl <- inla.spde.make.A(mesh = mesh,
                          loc  = Loc,
                          repl = Repl)
```

We also need to inform INLA that the spatial random field consists of 44 blocks.

```
wrepl.index <- inla.spde.make.index(
     name    = 'w',
     n.spde  = spde$n.spde,
     n.repl  = NRepl)
```

7.2 Defining the stack

The stack for the models with the replicate correlation is similar to that of the spatial models. We only changed is the projector matrix (`Arepl`), the name of the spatial random field (`wrepl.index`) and the name of the stack.

```
N <- nrow(CC2)
StackRepl <- inla.stack(
    tag = "Fit",
    data = list(RK = CC2$RK),
    A = list(1, 1, Arepl),
    effects = list(
       Intercept    = rep(1, N),      # Intercept
       X.Year       = X.Year,         # f(Year)
       w            = wrepl.index))  # Spatial-temporal correlation
All.StackRepl <- inla.stack(StackRepl,      #Observed data.
                            StackPr.Year)   #f(Year) for 50 values.
```

7.3 NB and ZINB GAMs with the replicate correlation

We execute the NB and ZINB GAMs with the replicate correlation with the following code.

```
Repl.NB <- inla(RK ~ -1 + Intercept + X.Year +
                      f(w, model = spde, replicate = w.repl),
            family = "nbinomial",
            #control.family = list(hyper = Hyper.NB),
            control.inla = list(strategy='gaussian',
                                int.strategy = 'eb'),
            data = inla.stack.data(All.StackRepl),
            control.predictor = list( A = inla.stack.A(All.StackRepl),
                                      link = 1),
            control.compute = list(dic = TRUE, waic = TRUE))
```

```
Repl.ZINB <- inla(RK ~ -1 + Intercept + X.Year +
                        f(w, model = spde, replicate = w.repl),
            family = "zeroinflatednbinomial1",
            #control.family = list(hyper = Hyper.NB),
            control.inla = list(strategy='gaussian',
                                int.strategy = 'eb'),
            data = inla.stack.data(All.StackRepl),
            control.predictor = list( A = inla.stack.A(All.StackRepl),
                                      link = 1),
            control.compute = list(dic = TRUE, waic = TRUE))
```

We compare both models with their DIC and WAIC values.

```
##                                DIC     WAIC
## NB GAM + replicate SRF    51120.37 51157.96
## ZINB GAM + replicate SRF 50802.27 51975.50
```

The ZINB GAM with the spatial replicate correlation has the lower DIC and WAIC values, and we will present the results of this model.

7.4 Results of the ZINB GAM with replicate correlation

The temporal trend is presented in Figure 7.1. It shows a nearly flat line with large 95% credible intervals, and it indicates that there are no major changes over time. Note that we have visualised $\exp(f(\text{Year}_{is}))$.

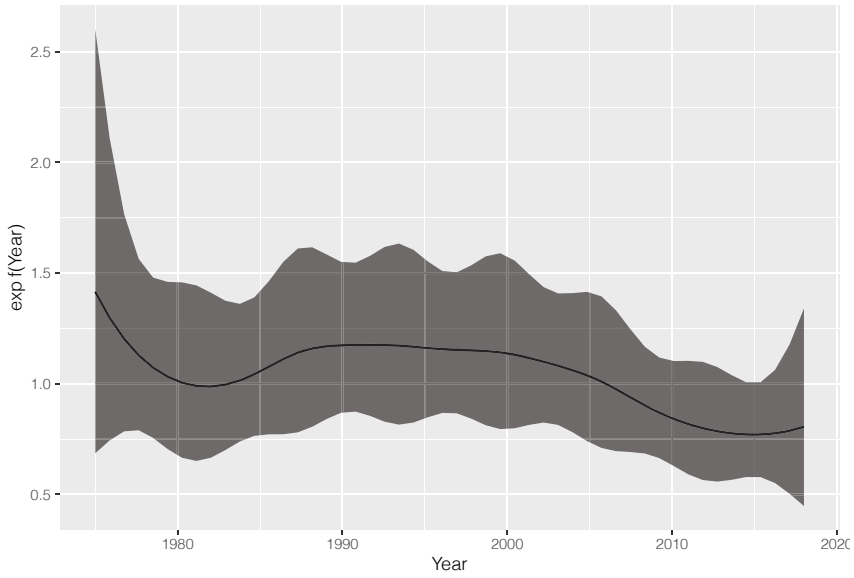


Figure 7.1: Posterior mean values and 95% credible intervals for the temporal trend obtained by the ZINB GAM with the spatial-temporal replicate correlation.

The model also produces a spatial random field for each year. We have plotted these in Figure 7.2. The dark red areas correspond to hotspots (higher abundances) of Red knots and the dark purple areas to coldspots (lower abundances). There are only minor changes over time, and if we compare the DICs of the models with spatial correlation and spatial-temporal correlation, then the spatial models are prefered. This indicates that there are only minor changes over time. An AR1 model gives a ϕ close to 1, which also indicates that there are minor changes over time.

These results can be interpreted in two ways. The first interpretation is that there are spatial patterns in the distribution of Red knot counts, but these do not change much over time. This would mean that a spatial ZINB GAM will be sufficient to describe the data, and that there is no need for spatial temporal models for this specific species. The second possible interpretation is that there are temporal changes, but numerical estimation problems prevent the model from estimating it. We noticed that the spatial-temporal models are rather sensitive to changes in the mesh configurations, priors and starting values. Closely related models sometimes gave rather different values for the range, θ and σ_u. To avoid excessively long computing time, we had to use `control.inla = list(strategy = 'gaussian', int.strategy = 'eb')`, which means that the software uses rather crude (though fast) approximation techniques to obtain the posterior distributions. This may be due to the rather large values for the

Figure 7.2: Posterior mean values of the spatial random field for each year by the ZINB GAM with the spatial-temporal replicate correlation.

counts, or high count values that are not spatially correlated. To further investigate which of these two is a plausible explanation, we will implement one more type of model, namely a hurdle model.

7.5 ZANB GAM with spatial-temporal correlation

7.5.1 Outline of ZANB analyses

As a final analysis of the UK Red knot data, we will apply a GAM with a zero-altered negative binomial (ZANB) distribution. This is also called a hurdle model. In a ZANB model we apply two separate analysis. We first apply a Bernoulli model on the absence/presence data, and then we apply a truncated negative binomial model on the presence-only data. Once we have applied these two models, we can combine the two components and calculate the expected values. These are then used to predict Red knots counts. We summarise the workflow below.

1. Apply Bernoulli GAM with spatial correlation on the absence/presence data of Red knots.
2. Apply a Bernoulli GAM with the spatial-temporal replicate correlation on the absence/presence data of Red knots. Compare the DIC and WAIC of both Bernoulli models.
3. Apply a zero-truncated negative binomial GAM with spatial correlation on the presence-only Red knot data. This is data in which the zeros are removed.
4. Apply a zero-truncated negative binomial GAM with spatial-temporal replicate correlation on the presence-only Red knot data. Compare the DIC and WAIC of both zero-truncated models.
5. Combine the relevant components of the Bernoulli and zero-truncated models to calculate expected values of the ZANB model.

We will provide the statistical formulation of the ZANB model towards the end of this section.

7.5.2 Bernoulli models

As explained above, a Bernoulli GAM with spatial correlation, and also with spatial temporal correlation, will be applied on the absence/presence data. The first thing that we need to do is to define a variable `RK01`, which represents absence (0) and presence (1) of Red knots.

```
CC2$RK01 <- ifelse(CC2$RK > 1, 1, 0)
```

The `RK01` variable will be the new response variable. From here onwards the R code and statistical analyses are nearly identical to that of the Poisson and negative binomial GAMs. All that we need to do is to change `family = "poisson"` to `family = "binomial"`. The R code is not presented here, but it is available in the RMarkdown file.

We executed both the Bernoulli GAM with spatial correlation and the Bernoulli GAM with spatial-temporal replicate correlation. The models were quite stable in the sense that mesh configurations, priors and starting values had minimal effect on the results.

```
##                                      DIC     WAIC
## Bernoulli GAM + SRF           5108.700 5069.976
## Bernoulli GAM + replicate SRF 8725.813 8693.941
```

Results show that the Bernoulli GAM with spatial correlation (that does not change over time) is better that the spatial-temporal model. This indicates that there are no major temporal changes over time in the probability of presence of Red knots at the sites in the UK.

The trends obtained by both models are presented in Figure 7.3. Their temporal patterns are similar, although the 95% credible intervals are smaller for the replicate model.

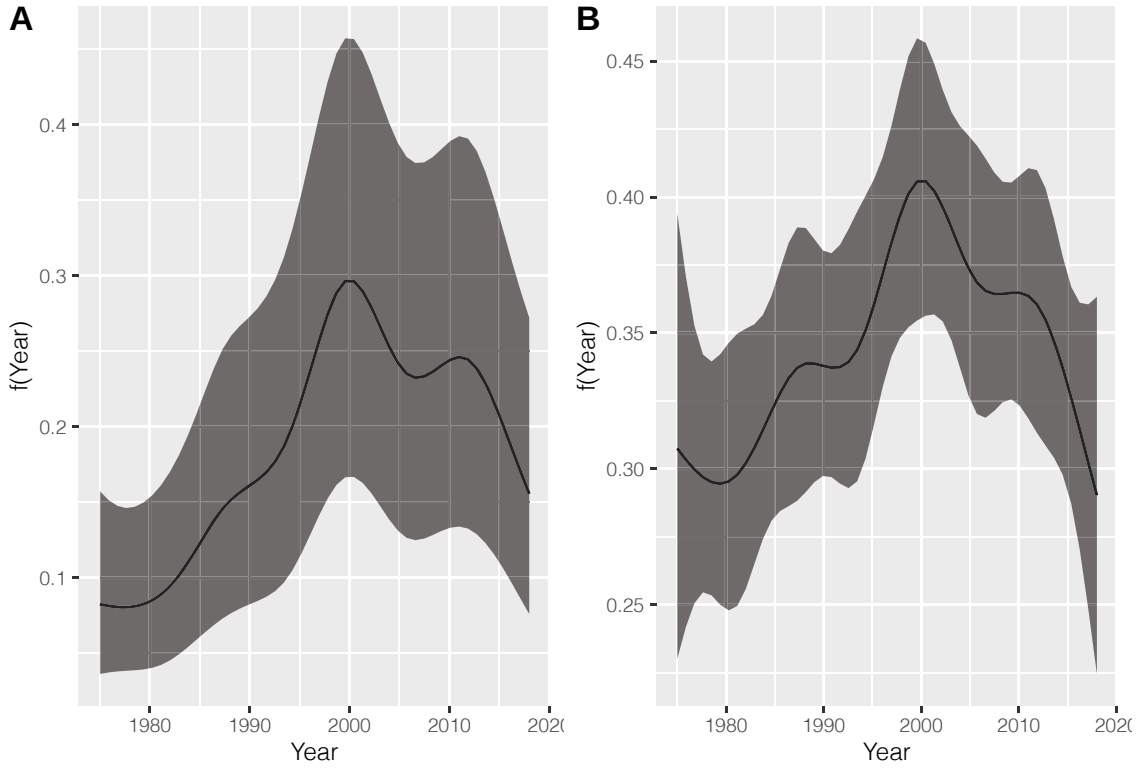


Figure 7.3: Posterior mean values and 95% credible intervals of the temporal trend obtained by the Bernoulli GAM with spatial correlation (panel A) and the Bernoulli GAM with spatial-temporal replicate correlation (panel B).

Figure 7.4 shows the spatial random field obtained by the Bernoulli GAM with spatial correlation. Sites in dark red areas have a higher probability of presence of Red knots, and sites in blue areas have a lower probability of presence.

Out of curiosity, we also plot the 44 spatial random fields obtained by the Bernoulli GAM with spatial-temporal replicate correlation; see Figure 7.5. There are indeed no major changes over time in the probability of presence for this specific species.

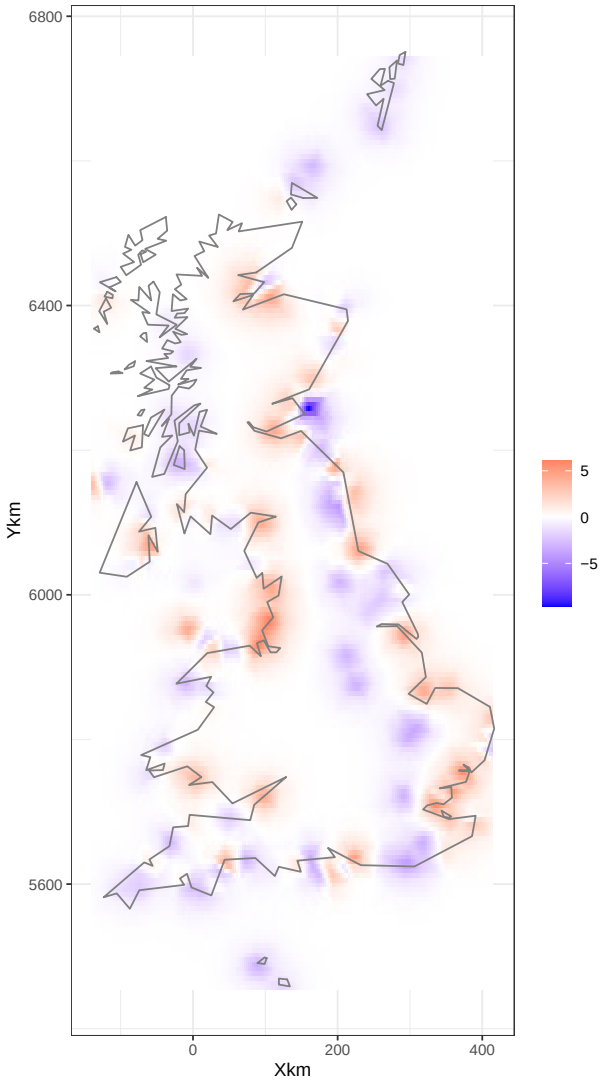


Figure 7.4: Posterior mean values of the spatial random field for each year by the Bernoulli GAM with the spatial correlation.

7.5.3 Truncated NB GAM with spatial-temporal correlation

In order to execute the zero-truncated negative binomial GAMs, we need to create a new response variable.

```
CC2$RKPos <- ifelse(CC2$RK > 0 , CC2$RK , NA)
```

The variable `RKpos` equals the observed Red knot data, but the value of 0 is replaced by an `NA`. Missing values (`NA`) will not influence the posterior distributions of the regression parameters in R-INLA. The alternative is to remove all the rows for which `RK` equals 0, but that generates some problems when we calculate the expected values of the ZANB model. Executing a zero-truncated NB requires fairly complicated R code and is discussed in detail in Zuur and Ieno (2018). We will not explain the code here.

Figure 7.5: Posterior mean values of the spatial random field for each year by the Bernoulli GAM with the spatial-temporal replicate correlation.

We first applied a zero-truncated NB GAM with spatial correlation, but the model did not converge. This indicates that the numerical estimations problems that we encountered throughout the analyses of this data set are linked to the count part of the data. The model with the spatial-temporal replicate correlation did converge. The temporal trend obtained by this model is presented in Figure 7.6, and the spatial random fields are presented in Figure 7.7. To show that we still have similar 'problems' as for the ZINB models, we have plotted the observed data (without the zeros) versus predicted values from the truncated NB GAM (with spatial-temporal correlation); see Figure 7.8. Just as for the ZINB GAMs, the fitted values are considerably lower than the observed values. Most likely this is due to the use of negative binomial distribution; its mean value is not necessarily at the centre of the data.

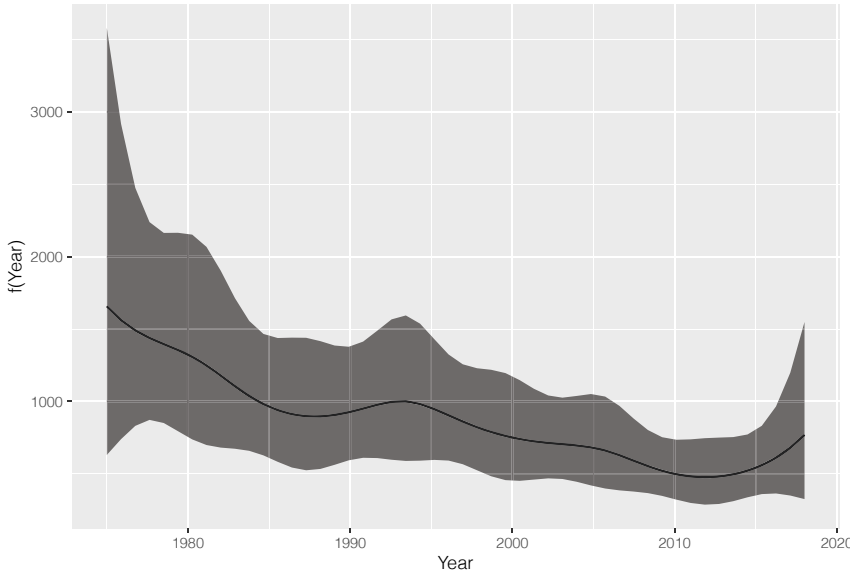


Figure 7.6: Posterior mean values of the spatial random field for each year obtained by the zero-truncated negative binomial GAM with the spatial-temporal replicate correlation.

7.5.4 ZANB model formulation

Once we have fitted the Bernoulli GAM and the zero-truncated NB GAM, we can extract the relevant components of the model and calculate the expected values of the ZANB model as follows. These are the ones that will be used for estimation of population trends. We have plotted these versus the observed data in Figure 7.9.

$$\begin{array}{rcl} \mathrm{RK}_{is} & \sim & \mathrm{ZANB}\left(\mu_{is}, \theta, \pi\right) \\ \mathrm{E}\left[\mathrm{RK}_{is}\right] & = & \frac{\pi_{is}}{1-P_0} \times \mu_{is} \\ P_0 & = & \left(\frac{\theta}{\mu_{is}+\theta}\right)^{\theta} \\ \mathrm{var}\left[\mathrm{RK}_{is}\right] & = & \frac{\pi_{is}}{1-P_0} \times (\mu_{is}^2 + \mu_{is} + \frac{\mu_{is}^2}{\theta}) - (\frac{\pi_{is}}{1-P_0} \times \mu_{is})^2 \\ \log\left(\mu_{is}\right) & = & \beta_1 + f(\mathrm{Year}_s) + v_{is} \\ \mathrm{logit}\left(\pi_{is}\right) & = & \gamma_1 + f(\mathrm{Year}_s) + z_{is} \end{array} \tag{7.1}$$

In the second model, a truncated negative binomial GAM is applied on the data without the zeros. This will given the μ_{is} and the θ.

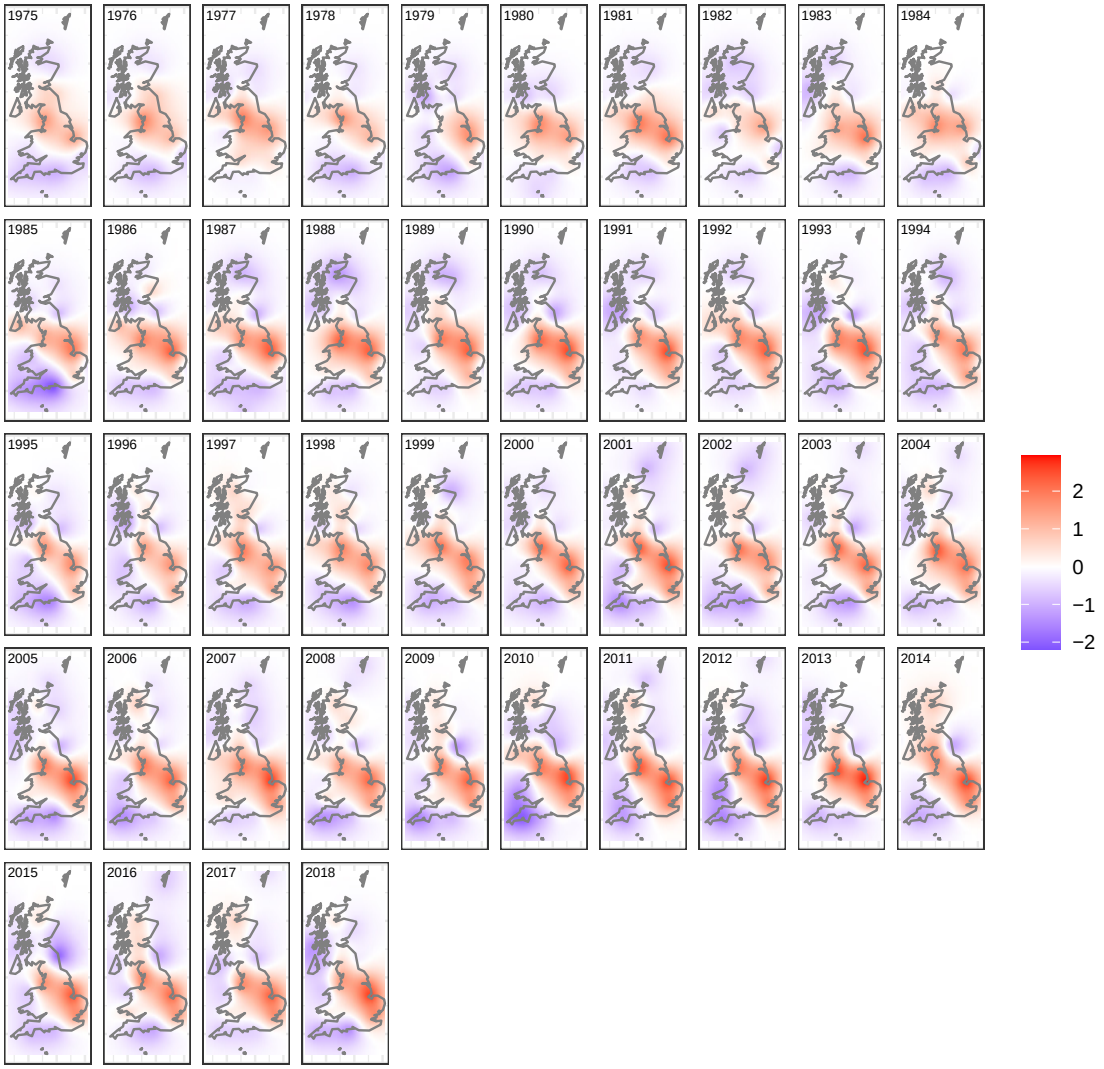


Figure 7.7: Posterior mean values of the spatial random field for each year obtained by the zero-truncated negative binomial GAM with the spatial-temporal replicate correlation.

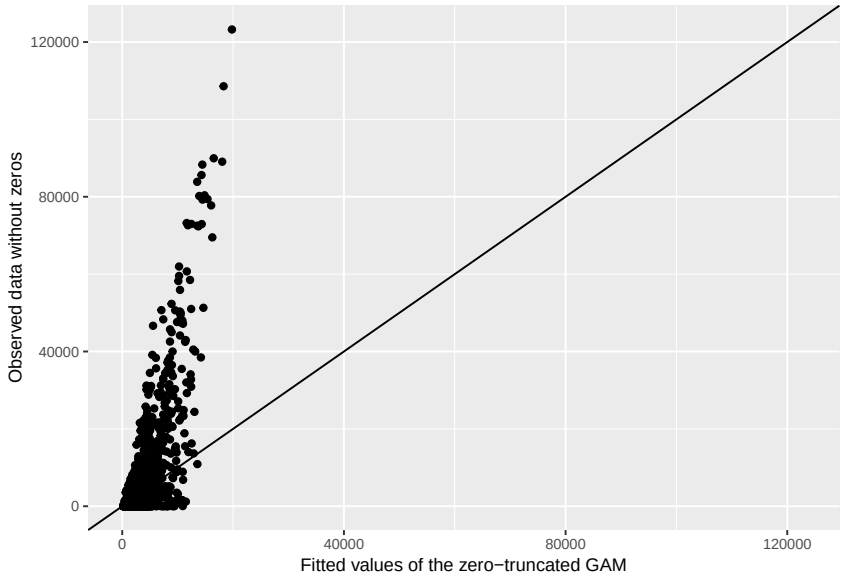


Figure 7.8: Observed number of Red knots (without zeros) and the fitted values of the zero-truncated NB GAM with spatial-temporal replicate correlation.

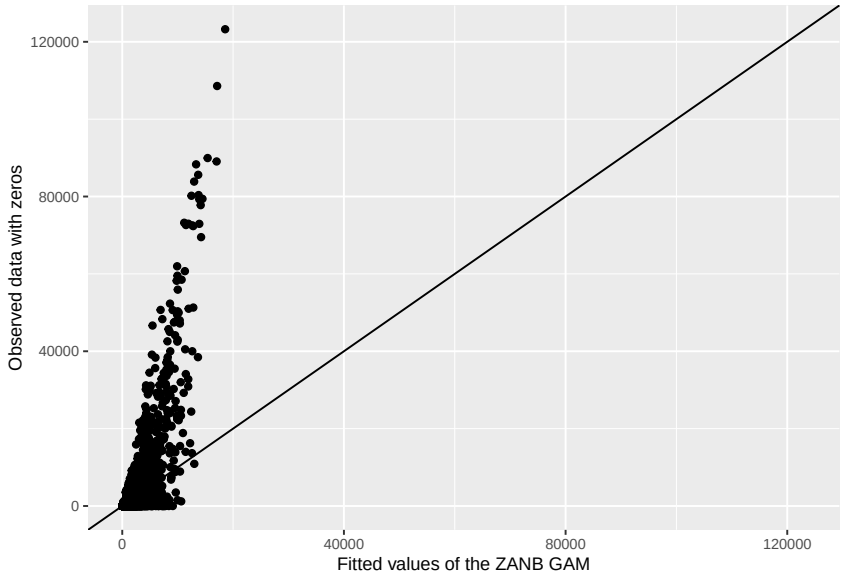


Figure 7.9: Observed number of Red knots and the fitted values of the ZANB GAM with spatial-temporal replicate correlation.

Chapter 8

Oystercatcher data

In this chapter we will apply the same methodology on the Oystercatcher data from South Africa.

8.1 Data preparation

In this section we will apply the same data preparation steps as in Section 3.1. We first import the data from the `HAEMOV2.csv` file, convert longitude and latitude into `Xkm` and `Ykm`, convert year into a categorical covariate and redefine `Count` as `OC`. Not all R code is presented here, but it is available in the RMarkdown file.

```
OC <- read.csv(file = "HAEMOV2.csv",
                      header = TRUE,
                      na.strings = "NA",
                      stringsAsFactors = TRUE)
source("HighstatLibV13.R")
```

8.2 Data exploration

8.2.1 Spatial locations

We first visualise the spatial locations on the sites; see Figure 8.1.

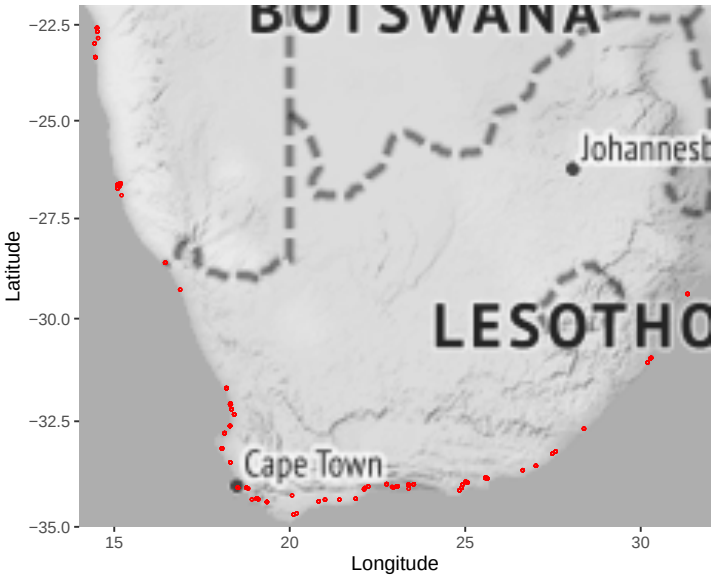


Figure 8.1: Sampling locations for all years.

When we split this up by year we can see that the spatial-temporal resolution of the data is not as good as for the Red knot data. For sure, we cannot make a distinction between the two countries. For spatial-temporal models, we need at least 50-ish observations per year. This is not always the case. We should at least omit the data from 1992 to 2001. Alternatively, we should consider a model without spatial-temporal correlation.

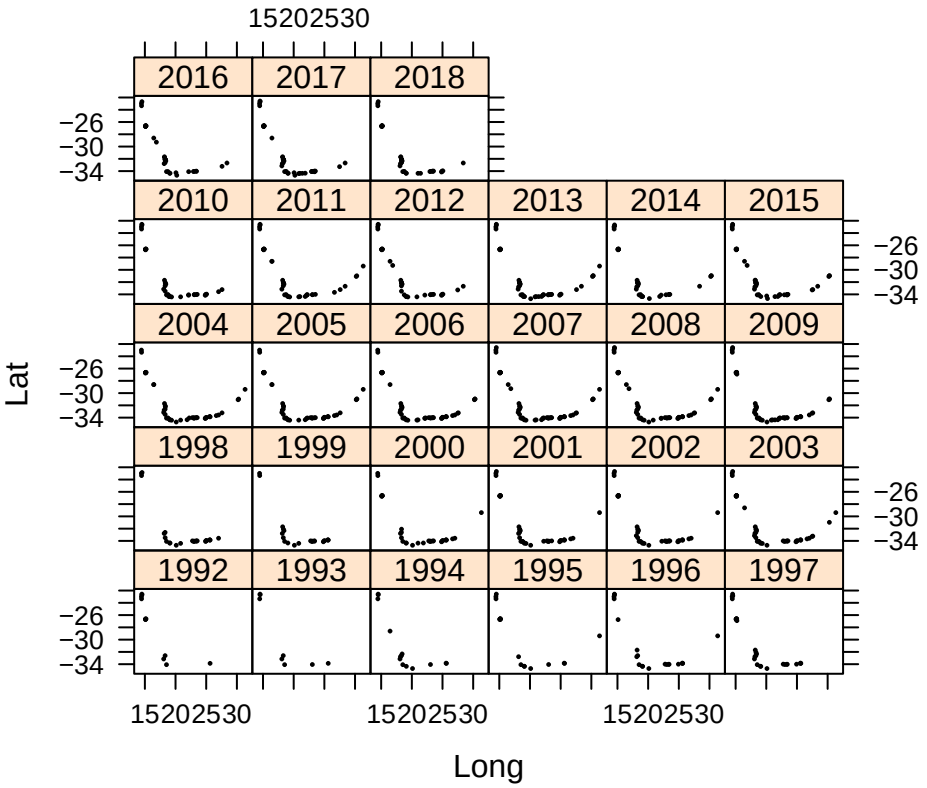


Figure 8.2: Sampling locations for each year.

We also visualised when the sites were sampled; see Figure 8.3. Note that a large number of sites were sampled rather inconsistently over time. This means that a trend over time may also reflect a change in sampling location.

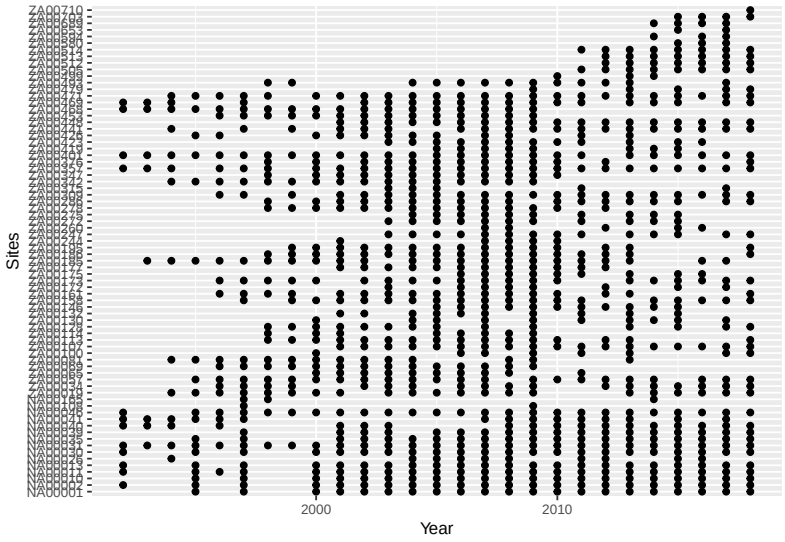


Figure 8.3: Visualisation of sampling. A dot is plotted if a site was sampled in a year.

8.2.2 Oystercatcher numbers versus year

We will now focus on the temporal trend in the Oystercatcher counts. Figure 8.4 shows the number of Oystercatchers for all sites versus year. A scatterplot smoother was added to aid the visual interpretation. There are no clear patterns, but this may be due to the large number of zeros and the large variation in the data.

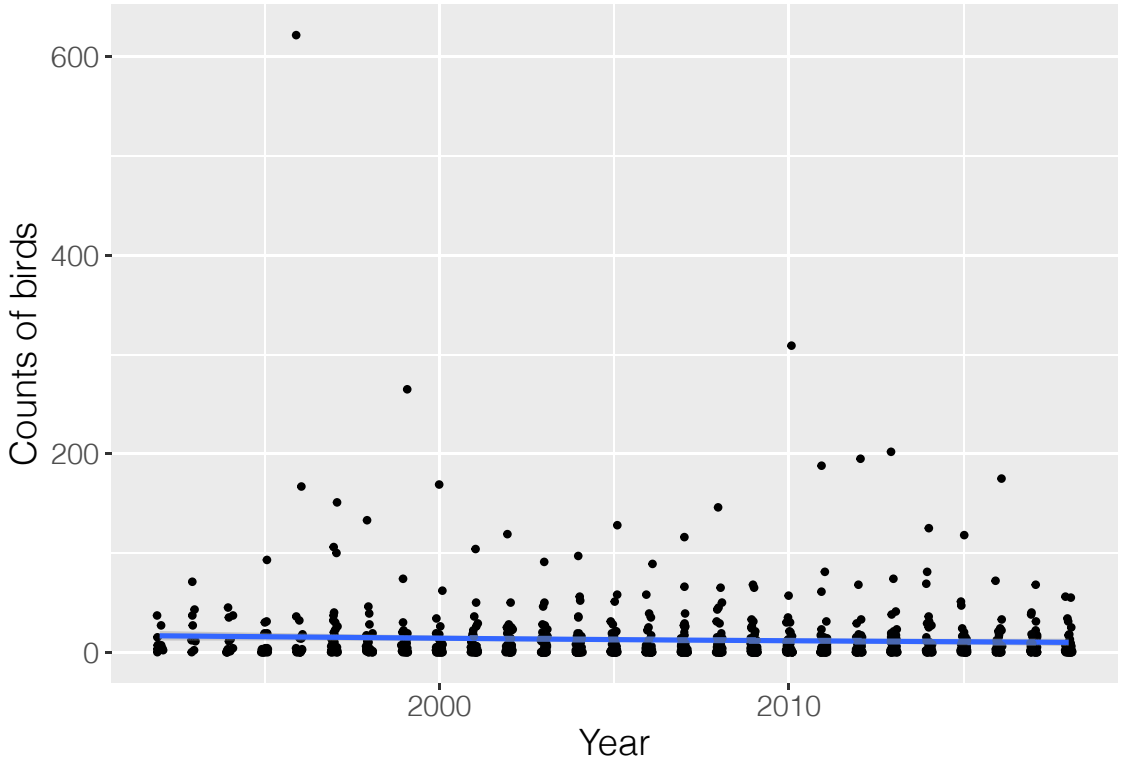


Figure 8.4: Scatterplot of number of birds versus year. A scatterplot smoother was added to aid visual interpretation.

8.2.3 Number of zeros

The number of zeros in the Oystercatcher data is 29.14%, which is relatively large. We also present the number of observations and the number of observations equal (and not equal) to zero by country; see the table below.

```
##    Number of observations Number of zeros Number of non-zeros % of zeros
## NA                    269              62                  207         23
## ZA                    740             232                  508         31
```

8.2.4 Conclusions

The number of observations per year is relatively low, perhaps too low to implement models with spatial-temporal correlation. The percentage of zeros is 29.14%, which is not as high as for the Red knot data, but we do expect zero-inflation issues.

8.3 Poisson GLMM

Our starting point is the same Poisson GLMM as in Equation (4.1).

```
#Without the outlier:
OC$Year.c <- MyStd(OC$Year)
M1 <- glmmTMB(Count ~ Year.c + (1| Site),
              data = OC,
              family = poisson)
```

We first check the model for overdispersion, which is indeed present.

```
E1   <- resid(M1, type = "pearson")
N    <- nrow(OC)
Npar <- length(fixef(M1)) + 1 #One sigma
Dispersion1 <- sum(E1^2) / (N - Npar)
Dispersion1
```

```
## [1] 16.49304
```

The amount of overdispersion is relatively large, and a detailed model validation was applied; see Figure 8.5. There is one observation that has a large Pearson residual.

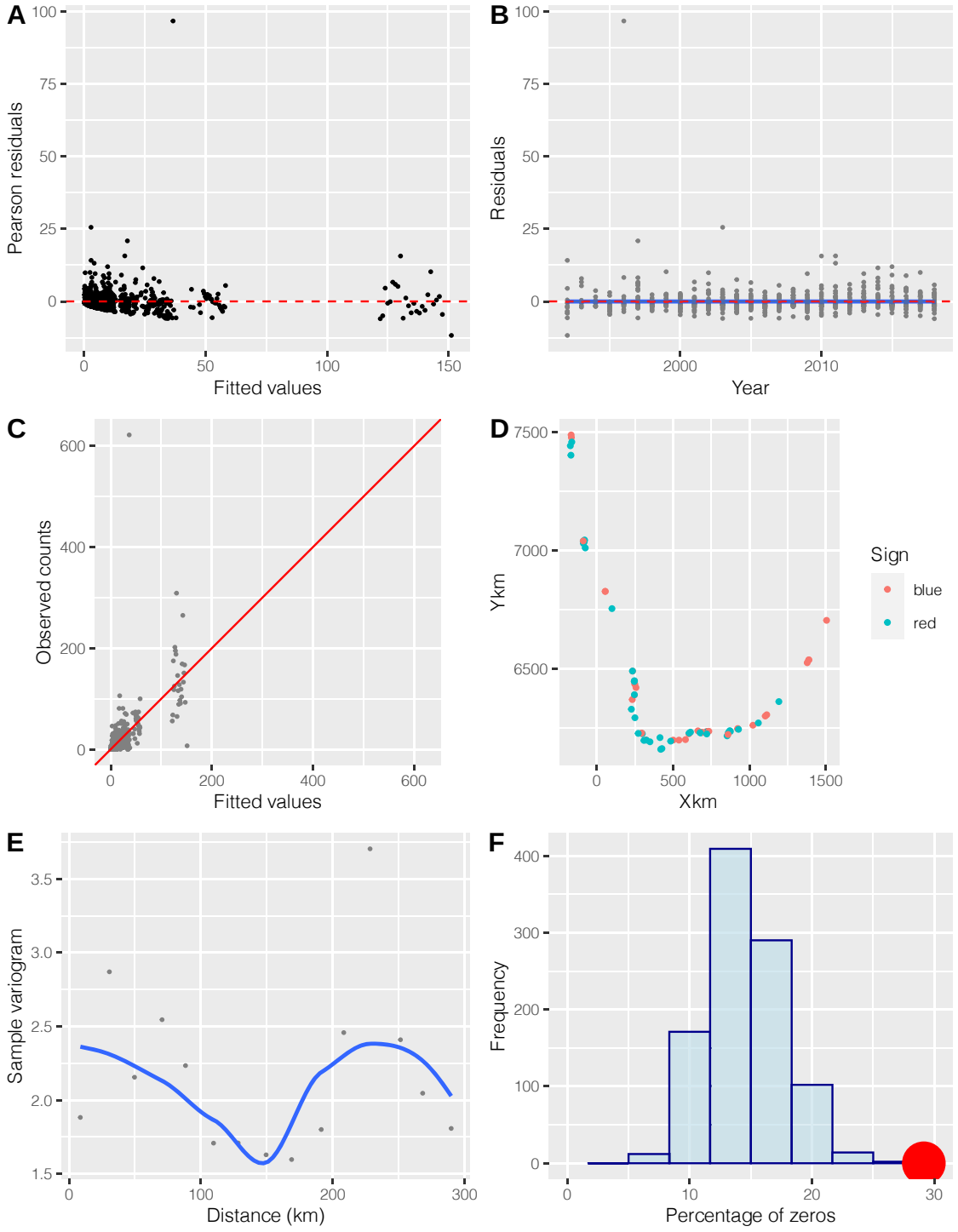


Figure 8.5: Model validation graphs for the Poisson GLMM applied on the Oystercatcher data. A: Pearson residuals versus fitted values. B: Pearson residuals versus the covariate year. Observed versus fitted values. C: Spatial locations of the sites. The colour of a dot is linked to the sign of a Pearson residual. D: Sample variogram of the random intercepts. E: Results of simulating 1,000 data sets from the model. The histogram is the percentage of zeros in the 1,000 simulated data sets. The red dot is the percentage of zeros for the observed data.

The variation explained by the covariate is minimal, but the random effects explain quite a lot.

```
library(performance)
r2_nakagawa(M1)
```

```
## # R2 for Mixed Models
##
##   Conditional R2: 0.921
##      Marginal R2: 0.001
```

Although it is not immediately obvious that we have to apply a GAM, we decide to give it a try.

```
G1 <- gamm4(Count ~ s(Year),
            random =~  (1| Site),
            data = OC,
            family = poisson)
```

The estimated smoother is presented in Figure 8.6 and shows that we do have a non-linear trend effect. Note that the shape of the smoother may well be linked to the unbalanced nature of the sampling of the sites.

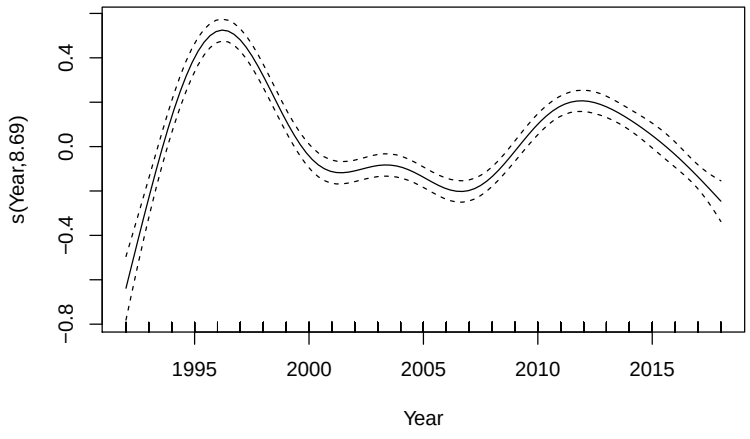


Figure 8.6: Estimated smoother for year obtained by a GAMM.

The Poisson GAMM is still overdispersed.

```
GE1 <- resid(G1$mer, type = "pearson")
Npar <- sum(G1$gam$edf) + 1 #'+1' is for sigma nest
N    <- nrow(OC)
GE1  <- resid(G1$mer, type = "pearson")
OverdispGAMM <- sum(GE1^2) / (N - Npar)
OverdispGAMM
```

```
## [1] 13.23961
```

The observation with the large Pearson residual is from site NA00011 in 1996. It is the observation with the largest observed value in Figure 8.4. Out of curiosity, we rerun all analysis without this observation. The overdispersion dropped to around 6. Panel A in 8.5 looked much better, but all other model validation tools produced similar graphs. The estimated smoother obtained by apply the GAMM on the data without this observation was similar as well. We decided not to remove this observation.

8.4 GAM with spatial correlation

We decided to apply a GAM with spatial correlation, although we were not 100% convinced whether this is needed. The left panel in Figure 8.7 shows a histogram of the distances between sites (in km). The right panel shows the the cumulative distances. Based on Figure 8.7 we label distances up to about 150-200 km as 'small'.

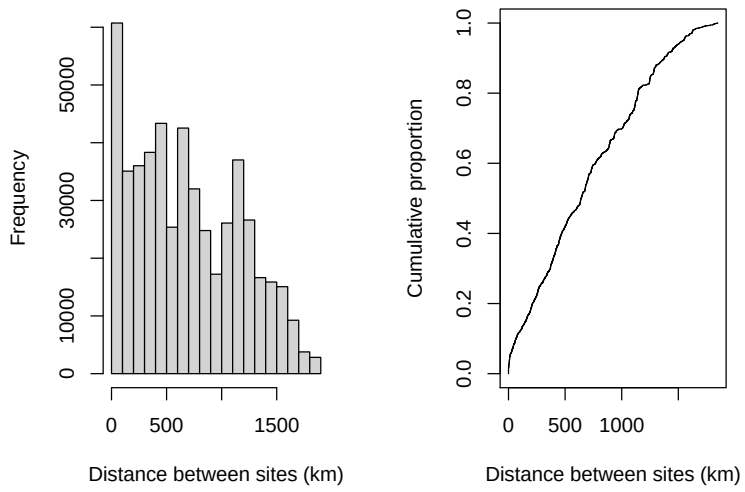


Figure 8.7: Left panel: Histogram of distances (km) between sites. Right panel: Cumulative distances between sites (km).

Using identical code as for the Red knot data we create a mesh; see Figure 8.8.

The mesh has 2090 nodes. We applied a Poisson GAMM with random effect site, a negative binomial GAMM with random effect site, a Poisson GAM with spatial correlation and a negative binomial GAM with spatial correlation. For the smoothing function of year, we

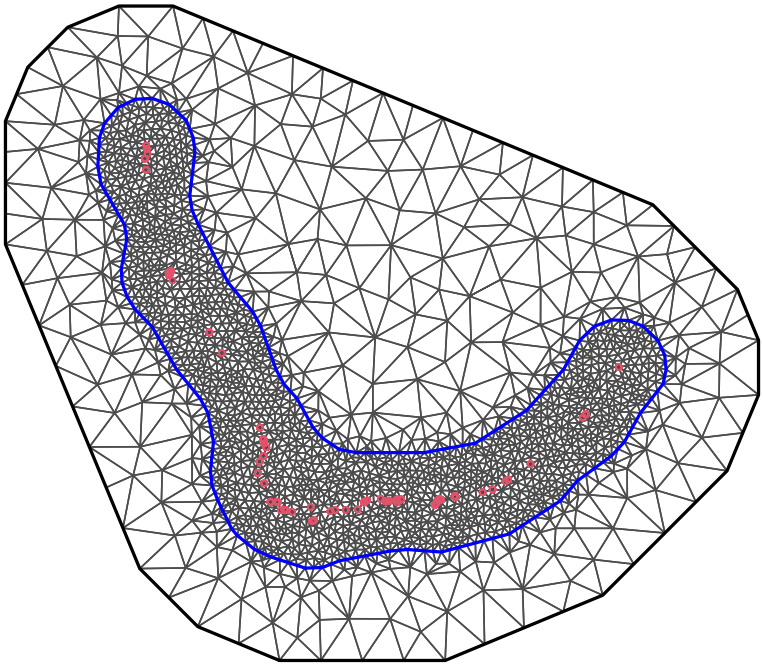


Figure 8.8: Mesh for the Oystercatcher data.

used a cubic regression spline with 7 knots. We used a PC prior of the form $P(\sigma > 2) = 0.05$ for the σ of the random intercepts. For the range we used $P(\text{Range} < 100) = 0.05$.

We compare all four models with the DIC and WAIC values. Clearly, the two negative binomial models are better than the Poisson models. The DIC and WAIC of the GAMM are lower than those of the GAM with spatial correlation. With the Red knot data we argued that the GAMM was violating the independence assumptions, and therefore it was not a good model. That argument does not hold here as there was no clear pattern in the sample variogram of the Pearson residuals. Hence, in principle the negative binomial GAMM may be sufficient for these data. But out of curiosity we will present the trends and spatial random field obtained by the spatial GAM.

```
##                          DIC      WAIC
## Poisson GAMM      9600.493 12260.983
## NB GAMM           5511.053  5558.011
## Poisson GAM + SRF 9973.889 12630.720
## NB GAM + SRF      5616.179  5658.759
```

8.4.1 Results of the spatial NB GAM

Figure 8.9 shows the posterior mean value and 95% credible intervals for exp(Intercept + $f(\text{Year}_{is})$). The trend shows a downward pattern from 1995 to 2000, a small increase around 2003, and a larger increase from 2007 to 2012, after which there are no major changes.

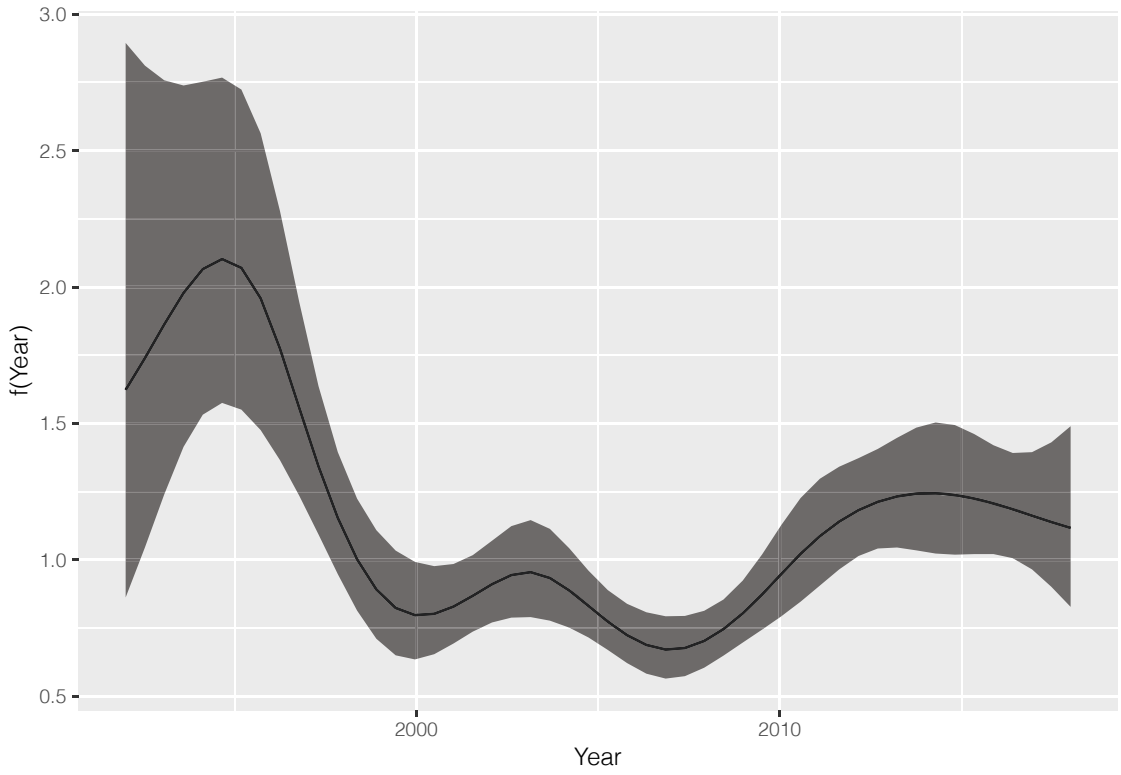


Figure 8.9: Posterior mean values and 95% credible intervals for the year effect obtained by the NB GAM with spatial correlation applied on the Oystercatcher data. The smoother is an unpenalised cubic regression spline with 7 df. We visualised exp(f(Year)).

The spatial random field is presented in Figure 8.10. Note that we have some rather large negative values of the spatial random field. These are probably sites with zero counts.

The fitted values of the NB GAM with spatial correlation are plotted versus the observed counts in Figure 8.11. Although the fit looks reasonably good, we have the impression that we are overfitting the data.

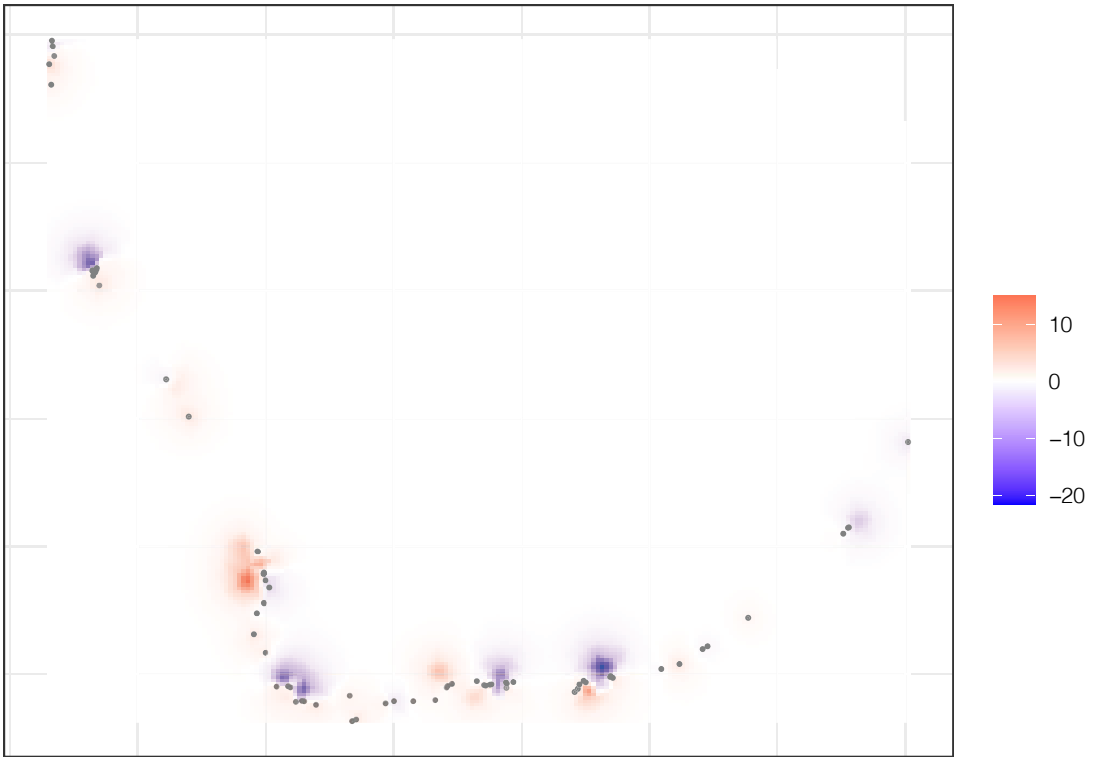


Figure 8.10: Spatial random field obtained by the NB GAM with spatial correlation. Yellow dots represent the sampling locations.

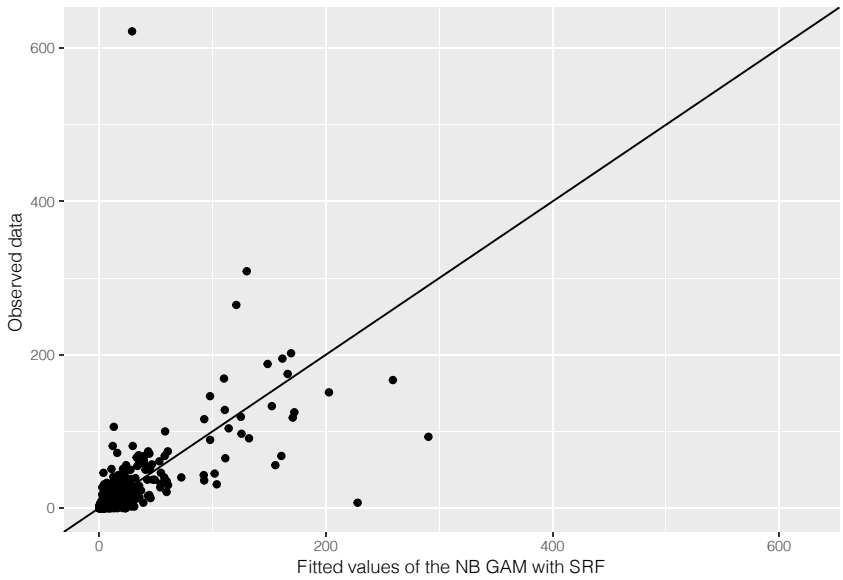


Figure 8.11: Observed number of oystercatchers and the fitted values of the NB GAM with spatial correlation.

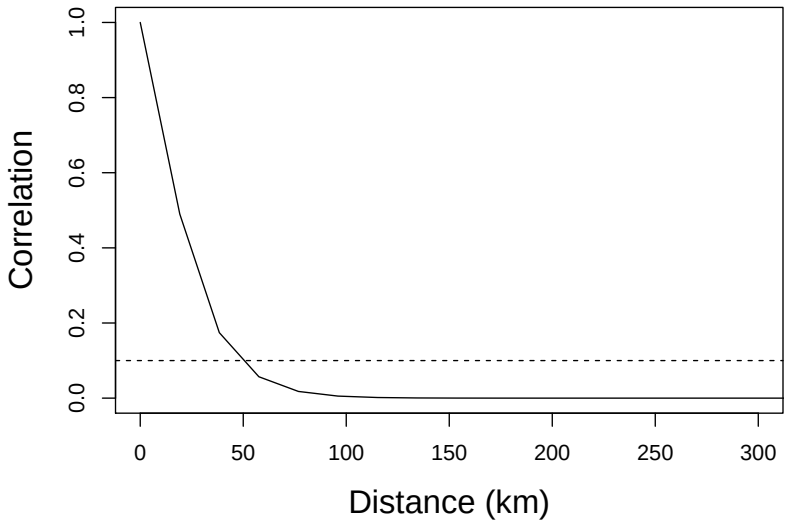


Figure 8.12: Matérn correlation function obtained by the NB GAM with spatial correlation applied on the Oystercatcher data.

Chapter 9

Comments

In this report we analysed count data from Red knots in the UK and Oystercatchers from South Africa. The aim was to provide a better approach than what is currently being used for these data, namely via TRIM. The TRIM approach predicts missing values, adds up the counts from all sites and then analyses the univariate time series using a quasi-Poisson GLM or GAM.

One of our criticism against this approach is that adding up data from all sites ignores any spatial dependency issues. The analysis presented in this report shows that there is strong spatial correlation. Aggregating spatially correlated data results in information loss and obscures important processes in the ecological system under study. Clark and Avery (1976) already warned against aggregation and explained concepts as aggregation bias of regression parameters. Furthermore, aggregation of Red knot counts for 500-ish sites means that the few rather abundant sites dominate the signal. One might as well only use the data from only those few sites.

Another criticism of the TRIM approach is that it used a quasi-Poisson approach if there is overdispersion. Such an approach should only be used if the overdispersion is up to about 5, not if the overdispersion is in the range of 500. Hilbe (2014) and Zuur et al. (2014), among many other publications, argue that overdispersion has a variety of causes.

1. Outliers in the response variable.
2. Missing covariates.
3. Missing interactions.
4. Covariate effects that are modelled as linear, whereas their effects are in fact non-linear.
5. Temporal and spatial dependency that are not taken into account.
6. Repeated measurements that are not taken into account.
7. Use of the wrong link function.
8. Zero inflation that is not taken into account by the model.

It is the task of the scientist to determine what is driving the overdispersion, and to extend the model in such a way that the source of the problem is modelled. Selecting the wrong approach may result in biased parameter estimates and the wrong ecological conclusions.

In this report we made an attempt to analyse the data using R-INLA. We only partly succeeded with this. The fact that the trends obtained by R-INLA do not look like the

trends obtained by TRIM is not the reason that we used the phrase 'partly succeeded'. The TRIM trend for the Red knot data is mainly determined by a few abundant sites. Zero-inflation issues are removed by aggregating data. However, when we analyse the data from all 500-ish sites, we do have to deal with zero-inflation issues. We used negative binomial GAMs and zero-inflated negative binomial GAMs with spatial (and spatial-temporal) correlation for this. We noticed that the trends obtained by the models did not fit the observed data well. It is important to realise what the negative binomial distribution and its zero-inflation cousin do. We will simulate 10,000 values from a negative binomial GLM. We will use an intercept of -2, a slope of 0.1 and $\theta = 0.1$ (which is a realistic value for the bird data sets that were analysed in this report).

```
set.seed(123)
X  <- sort(runif(10000, 1, 2))
mu <- exp(-2 + 0.1 * X )
Y  <-  rnbinom(10000, mu = mu, size = 0.1)
```

The simulated data are presented in Figure 9.1. The red line is the `mu`, and the fitted values of the model would be a line similar to the red line. Note that it is rather close to 0, which means that the non-zero data are fitted rather poorly. We noticed a similar pattern in Figure 6.8, where we showed the fitted value of a ZIP model. The actual fitted line of the model was in an area with no observed data at all. This is confusing for many scientists as they are used to the model fit of a linear regression model with a Gaussian distribution. In such models, the fitted line will go though the centre of the data. This is not necessarily the case for NB, ZINB and ZANB models.

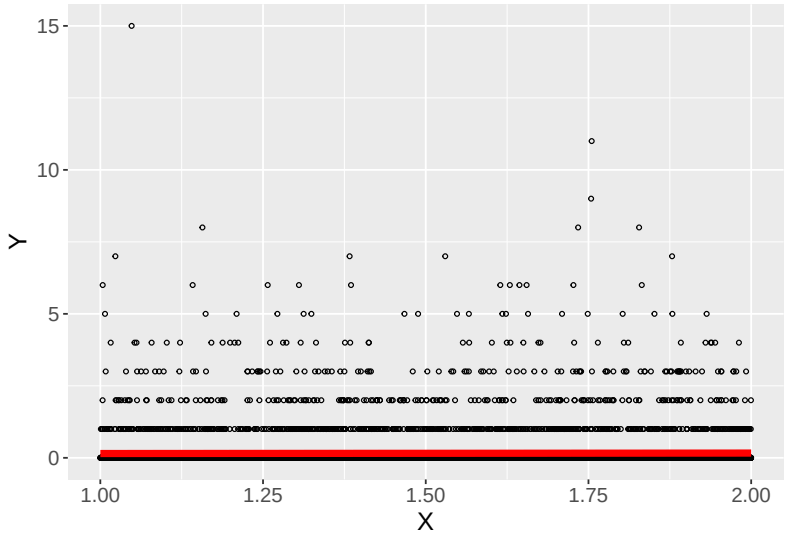


Figure 9.1: Simulated negative binomial data. The red line represents the mean of the distribution.

However, the use of the NB and ZINB distributions is not the main reason that the fit of the models is poor. The data are extremely noisy in the sense that one site can have 1 bird and the next site can have 100,000 birds in a specific year. A model with only a temporal trend and spatial correlation is not capable of describing these data well. It

would be better to add covariates to the model that are able to describe the patterns in the data.

Appendix A

Technical information on smoothers

Readers who are not interested in the technical background of basic smoothers may skip this appendix or just read the summary statements. The text below is partly based on Chapter 20 in Zuur and Ieno (2018).

Smoothing techniques constitute a scientific field in itself, and a large number of books and papers are available that discuss it in various degrees of complexity; see for example Hastie and Tibshirani (1990), Ruppert et al. (2003), Keele (2008), Yee (2015), Zuur et al. (2015), Wood (2017) and Zuur and Ieno (2018), to name just a few. The smoothers that will be used in later chapters are relatively complex. They are fully discussed in Zuur and Ieno (2018). In this appendix we discuss five basic smoothers. The reason for doing this is that by the time we reach the maths of the fifth smoother, you will understand the general principle of smoothers, and that is all that is needed for this report. The more advanced smoothers are all based on similar principles. Throughout this appendix we will ignore the fact that we have pseudo-replication. We also use the normal distribution for RK. This is just a didactic choice as it simplifies the explanation of smoothers.

A.1 Moving average and LOESS smoothers

Figure A.1A shows a scatterplot of RK versus year for the Red knot data. We would like to add a line that captures the main patterns in this scatterplot. One option is to connect sequential points in time, but such a graph is not very informative in this case. Another option is to add a straight line, but then we may be missing important patterns in the data.

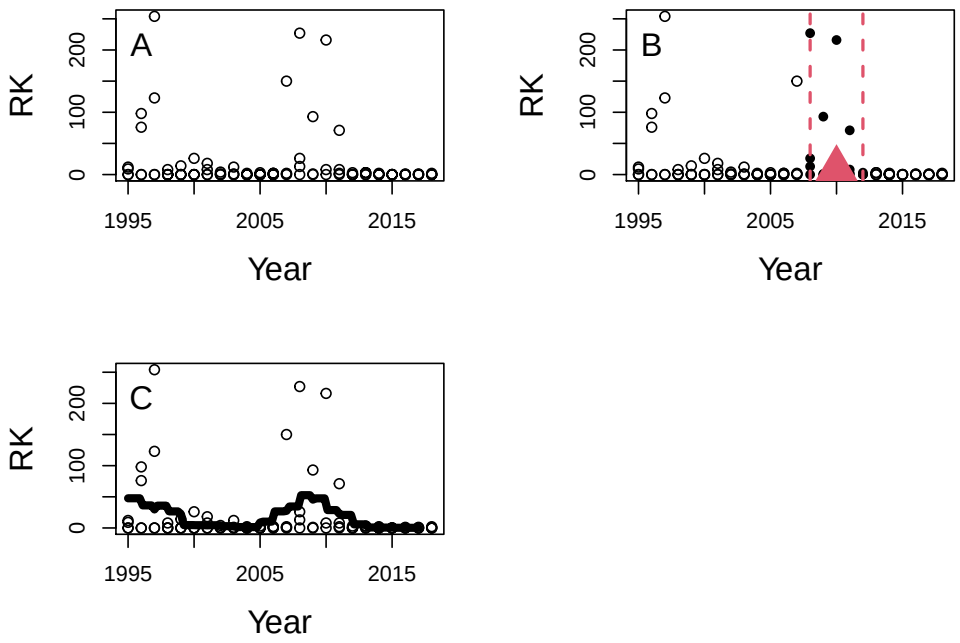


Figure A.1: A: Scatterplot of RK versus year for the Red knot data. B: Target value at 2010. The vertical dotted lines define a window from 2008 to 2012. C: Moving average smoother based on a window of 4 years.

A smoother is a line that attempts to visualise the important patterns in the data. Conceptually, the easiest smoother to explain is probably the moving average smoother. This smoother works as follows. Figure A.1B shows the same scatterplot as in Figure A.1A, except that we have added a window of 4 years around a target value, which in this case is the year 2010. The window is identified by the two vertical dotted lines. All points inside this window (which ranges from 2008 to 2012) are plotted as filled circles. The moving average technique takes the average of all the RK values *inside* this window. Instead of doing this at only one target value, the moving average smoother slides the window from left to right and each time takes the average. The resulting smoother is presented in Figure A.1C. The moving average smoother shows an increase from 2006 and reaches a plateau in 2012. This may be a real pattern, but it can also be due to a missing covariate, pseudo-replication or poor performance or usage of the smoothing technique. As to usage of the smoothing technique, we made a rather subjective decision to use a window of 4 years. We also could have used a window of 5 years, or a window of 1 year. In the former case we would have obtained a nearly straight line, whereas in the latter case we would have obtained a line that fluctuates considerably. So the size of the window determines how smooth the smoother is.

All smoothing techniques have a tuning mechanism that controls the amount of smoothing. This may be off-putting to some, but with no other options to model non-linear (temporal) patterns and with sensible use, smoothing techniques can be useful. However, the moving average smoother tends to produce rather wiggly curves, and we therefore continue with a slightly more advanced smoother.

Instead of taking the average of all points in a window, we can apply a linear regression using only the data inside a window. In such a linear regression model we can fit a

straight line or even a quadratic model. We could also down-weight observations that are further away from the target value, resulting in a smoothing technique that is called locally weighted smoothing (LOESS). Figure A.2 shows two examples of a LOESS smoother. Instead of specifying the boundaries of the window around the target it is possible to define the proportion of data points that should fall within a window and let the software figure out the boundaries. This proportion is called the span width. The larger the span width, the wider the window and the smoother the LOESS smoother, and vice versa. LOESS smoothers are available in various scatterplot functions in R, but for implementation in more advanced regression models (e.g. zero-inflated GLMs with spatial correlation) we prefer more advanced smoothing tools.

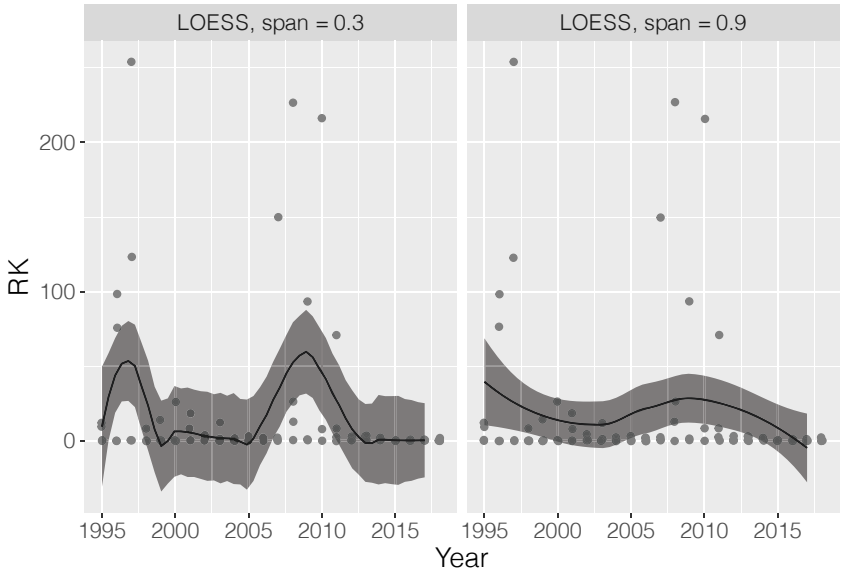


Figure A.2: LOESS smoother with a span of 0.3 and a span of 0.9.

The moving average smoother and the LOESS smoother are conceptually the easiest smoothers. They result in a curve that captures the general pattern in the data. We can control the shape of the curve via the size of a window that determines which points are used to calculate the smoother at a specific value.

A.2 Linear spline regression

The next smoother that we discuss is the linear spline regression. The underlying idea of spline regression is to separate the covariate `Year` into K segments and apply a bivariate linear regression model on the data of each segment. By connecting the regression lines for all segments we obtain a smoother. We will start our explanation of spline regression with $K = 2$ segments. The right panel in Figure A.2 gave the (vague) impression that there is a change in relationship at around 2012. We will fit a bivariate linear regression model on the data to the left of 2012 and also a bivariate linear regression model on the data to the right of 2012. We ensure that the lines are connected at 2012. The fit of such a model is presented in Figure A.3. Note that we have two lines with different slopes and

the lines intersect at the year 2012. If you are familiar with generalised additive models (GAMs), we just fitted a GAM with a Gaussian distribution, albeit with a super-simple smoother.

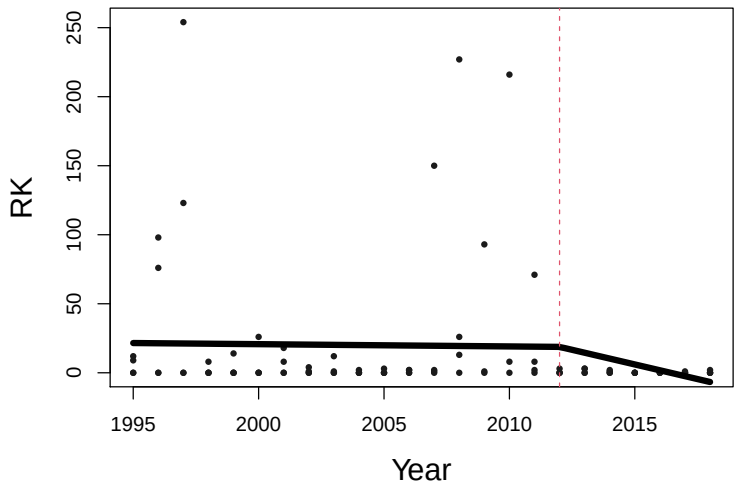


Figure A.3: Fit of a linear spline model with one internal knot at Year = 2012.

To show that GAMs are essentially just simple linear regression models (or GLMs), we dive a little bit more deeply into the R code for the linear spline regression. To fit the linear spline regression model in R we define (with the emphasis on define) a new mathematical function.

$$(Year_s - 2012)_+ = \begin{cases} 0 & \text{if } Year_s < 2012 \\ Year_s - 2012 & \text{if } Year_s \geq 2012 \end{cases}$$

Note the subscript '+' in this expression. It looks scary, but it defines the term $(Year_s - 2012)_+$ as being equal to 0 if $Year_s$ is smaller than 2012; otherwise it is equal to $Year_s - 2012$. It is just a definition; nothing else. Faraway (2006) gives an R function to calculate this new covariate.

```
rhs <- function(x, TH) ifelse(x >= TH, x-TH, 0)
```

This function is executed in R with `rhs(CC3$Year, 2012)` and gives the output $Year_s - 2012$ if $Year_s$ is larger than 2012, and 0 otherwise. Seeing is believing, and to see this in action we print the first 10 rows of $Year_s$ and $(Year_s - 2012)_+$ side by side.

```
SeeIt <- cbind(CC3$Year, rhs(CC3$Year, 2012))
colnames(SeeIt) <- c("Year", "(Year - 2012)+")
head(SeeIt, 10)
```

```
##       Year (Year - 2012)+
```

```
##  [1,] 1999              0
##  [2,] 2015              3
##  [3,] 2010              0
##  [4,] 1998              0
##  [5,] 2016              4
##  [6,] 2017              5
##  [7,] 2003              0
##  [8,] 2007              0
##  [9,] 2005              0
## [10,] 2009              0
```

The left column is `Year` and the right column is either equal to 0 (if the year is smaller than 2012) or `Year - 2012` if `Year` is larger than or equal to 2012. In the first 10 rows we have 9 values smaller than 2012, hence the zeros on the right. There is one row where year equals 2013. The newly defined variable is 1 (= 2013 – 2012).

We can now formulate the linear spline regression model with one knot at 2012 as follows.

$$RK_{is} = \beta_1 + \beta_2 \times Year_s + \beta_3 \times (Year_s - 2012)_+ + \epsilon_{is}$$

The ϵ_{is} is the usual residual term in a linear regression model; it is assumed to be normal distributed with mean 0 and (unknown) variance σ^2. The fancy expression above is shorthand notation for writing

$$RK_{is} = \begin{cases} \beta_1 + \beta_2 \times Year_s + \epsilon_{is} & \text{if } Year_s < 2012 \\ \beta_1 + \beta_2 \times Year_s + \beta_3 \times (Year_s - 2012) + \epsilon_{is} & \text{if } Year_s \geq 2012 \end{cases}$$

At $Year_s = 2012$, both expressions are the same, ensuring that the two lines touch each other at this year. The unknown regression parameters are β_1, β_2 and β_3 and the variance of the residuals. The R code to fit the model is as follows.

```
Mcsr <- lm(RK ~ Year  + rhs(Year, 2012), data = CC3)
```

Note that this is a linear regression model with two covariates. The function `rhs` creates the new covariate, and we end up with three estimated regression parameters. Once we have fitted the model it is quite easy to create Figure A.3. We can predict RK values for year values on a regular grid, say 100 values from 2002 to 2017. These values correspond to the smallest and largest year values, and the value of 100 is chosen arbitrarily.

```
ND <- data.frame(Year = seq(min(CC3$Year),
                            max(CC3$Year),
                            length = 100))
Pcsr <- predict(Mcsr, newdata = ND)
par(mfrow = c(1, 1), mar = c(5,5,2,2), cex.lab = 1.5)
plot(x = CC3$Year, y = CC3$RK,
     xlab = "Year", ylab = "RK",
     cex = 0.7, pch = 16, col = grey(0.1))
```

```
lines(x = ND$Year, y = Pcsr, lwd = 5)
abline(v = 2012, lty = 2)
```

The point where we separated the year gradient is called a knot. In Figure A.3 we use 1 internal knot and we also count the outer edges as knots; hence we used 3 knots in the model. The choice of Year = 2012 for the internal knot is rather subjective. It is more objective to use the quantiles of year for the knot positions. Another problem is how many knots we should use. Suppose we use 7 knots (i.e. 2 outer knots and 5 internal knots) and quantiles to choose the knot positions. In that case the values of these knots are as follows.

```
Knots <- quantile(CC3$Year, probs = seq(0, 1, length = 7))
Knots
```

```
##         0% 16.66667% 33.33333%        50% 66.66667% 83.33333%       100%
##     1995.0     1998.5     2002.0     2006.0     2011.0     2014.5     2018.0
```

The internal knots are at the 16.66%, 33.33%, 50%, 66.66% and 83.33% quantiles. These are the years 2005, 2008, 2010, 2013 and 2015. We fit a regression model with knots at these values.

```
Mcsr <- lm(RK ~ Year +
                  rhs(Year, Knots[2]) + rhs(Year, Knots[3]) +
                  rhs(Year, Knots[4]) + rhs(Year, Knots[5]) +
                  rhs(Year, Knots[6]), data = CC3)
```

Figure A.4 shows the model fit.

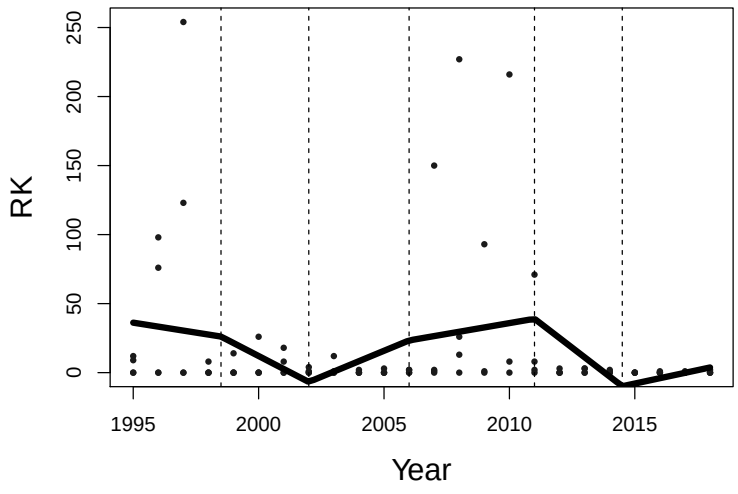


Figure A.4: Fit of the linear spline model with 5 internal knots.

The solid line in Figure A.4 is the smoother $f(Year)$. Its mathematical formulation is given below. We changed the regression parameters of the second part of the smoother from betas to bs for notational convenience.

$$\begin{aligned} f(Year_s) &= \beta_2 \times Year_s \\ &\quad b_1 \times (Year_s - 2005)_+ + \\ &\quad b_2 \times (Year_s - 2008)_+ + \\ &\quad b_3 \times (Year_s - 2010)_+ + \\ &\quad b_4 \times (Year_s - 2013)_+ + \\ &\quad b_5 \times (Year_s - 2015)_+ \end{aligned}$$

The problem with this notation is that when we use more knots, the equation gets rather lengthy. We can write the expression more compactly as follows.

$$f(Year_s) = \beta_2 \times Year_s + \sum_{j=1}^{K} b_j \times \left(Year_s - k_j\right)_+$$

where $K = 5$ internal knots and the k_j are the knot positions. The parameters β_2, b_1, b_2, ..., b_5 are unknown regression parameters that need to be estimated using linear regression, and $Year_s$ and the $\left(Year_s - k_j\right)_+$ terms are known covariates.

A smoother is nothing more than a collection of Lego pieces (i.e. abstract covariates defined at knots), and the corresponding regression parameters can be estimated with linear regression, GLM or GLMM procedures.

A.3 Quadratic and cubic spline regression

The smoother in Figure A.4 is not visually appealing due to the 'peaky' connection at the internal knots. To solve this problem we can increase the number of knots, but a linear spline regression tends to stay peaky, even for larger numbers of knots. The only solution to avoid peaky connections is to improve the smoother itself. The quadratic spline regression is defined by

$$f(Year_s) = \beta_2 \times Year_s + \beta_3 \times Year_s^2 + \sum_{j=1}^{K} b_j \times \left(Year_s - k_j\right)_+^2$$

This function produces a smoother that is less wiggly than the linear spline regression. We can even go one step further and define the cubic spline regression; such a smoother is less wiggly than the quadratic spline regression. The cubic spline regression is defined below.

$$f(Year_s) = \beta_2 \times Year_s + \beta_3 \times Year_s^2 + \beta_3 \times Year_s^3 + \sum_{j=1}^{K} b_j \times \left(Year_s - k_j\right)_+^3$$

The fit of the cubic spline regression is presented in Figure A.5.

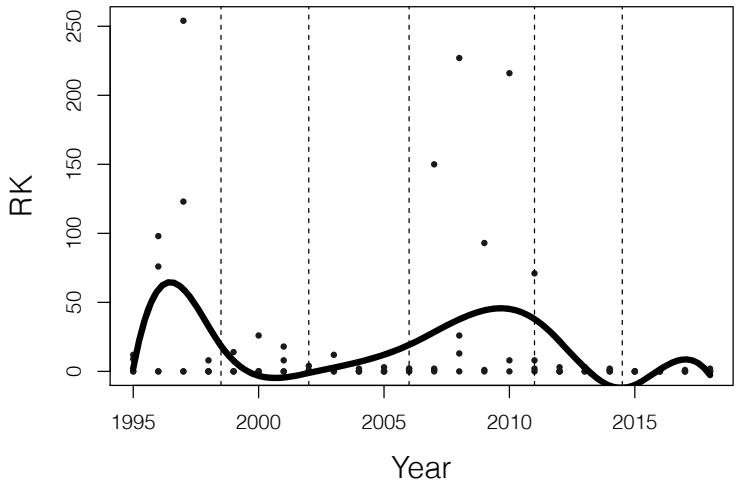


Figure A.5: Fit of the cubic spline model with 5 internal knots.

The difference between the linear, quadratic and cubic spline regression models is the Lego pieces that are used to define a smoother. The underlying principle is otherwise the same.

As can be seen from the equations of the linear, quadratic and cubic spline regression models, we do get a mathematical equation for a smoother, and this allows us to interpolate, predict, calculate confidence and prediction intervals, do hypothesis testing, etc. However, these equations are not particularly useful; they are merely the building blocks (or Lego pieces) of the smoother. Note that we did not include an intercept in any of the smoothers. The intercept is already specified in the linear regression model itself, and it is better not to include it into the smoother. This becomes an issue particularly if multiple smoothers are used. In such cases there will be only one intercept and none of the smoothers contains an intercept.

The basis of a smoother is defined as the set of covariates (also called basis functions) that are being used as known covariates by the smoother. The basis functions of the cubic spline regression smoother are as follows.

$$Year_s, Year_s^2, Year_s^3, (Year_s - 2005)_+^3, ..., (Year_s - 2015)_+^3$$

Different types of smoothers use different bases. Zuur and Ieno (2018) discuss more complex smoothers like thin-plate regression splines, O'Sullivan splines, B-splines, smoothing splines, random walk smoothers of orders 1 and 2, etc. In principle, there is no need to fully understand the technical details of these smoothers as all that they do is provide 'better' basis functions, where 'better' is with respect to the performance of the numerical estimation processes and aesthetics of a smoother (i.e. whether a smoother is not too wiggly and 'behaves well' at the edges).

The cubic spline regression contains small mathematical building blocks, which enable us to build up a smoother. The basis of a smoother is the set of basis functions (i.e. building blocks) that are used as covariates for the smoother.

Another point that we need to discuss is how to control the amount of smoothing. Specialised packages like `mgcv` (Wood, 2017) have tools that determine the optimal amount of smoothing (i.e. the optimal size of the window or the optimal span width). However, the underlying maths is rather complex. With multiple smoothers R-INLA is not very good at determining the optimal amount of smoothing (it sometimes results in a smoother that is too wiggly or at the other extreme, a flat horizontal line). In such cases it is better to control the amount of smoothing manually. Technically, we can use unpenalised cubic regression splines. These are explained in detail in Wood (2017) and used in combination with R-INLA in Zuur and Ieno (2018) In short, the data analyst specifies the amount of smoothing *a priori* and uses the `smooth.construct` function from the `mgcv` package (Wood, 2020) to obtain the basis functions (i.e. the Lego pieces). We suggest only allowing for a small amount of smoothing (in technical jargon this mean that we use smoothers with only three or four degrees of freedom). We will explain this in more detail when we do the analysis in R-INLA.

Bibliography

Bates, D., Maechler, M., Bolker, B., and Walker, S. (2020). *lme4: Linear Mixed-Effects Models using Eigen and S4*. R package version 1.1-26.

Blangiardo, M. and Cameletti, M. (2015). *Spatial and Spatio-Temporal Bayesian Models with R - INLA*. Chichester, UK: John Wiley & Sons.

Blangiardo, M., Cameletti, M., Baio, G., and Rue, H. (2013). Spatial and Spatio-Temporal Models with R-INLA. *Spatial and Spatio-Temporal Epidemiology*, 4:33–49.

Clark, W. a. V. and Avery, K. L. (1976). The Effects of Data Aggregation in Statistical Analysis. *Geographical Analysis*, 8(4):428–438. _eprint: https://onlinelibrary.wiley.com/doi/pdf/10.1111/j.1538-4632.1976.tb00549.x.

Hastie, T. J. and Tibshirani, R. J. (1990). *Generalized Additive Models*. Boca Raton, FL: CRC Press.

Hilbe, J. M. (2014). *Modeling Count Data*. Cambridge, UK: Cambridge University Press.

Keele, L. J. (2008). *Semiparametric Regression for the Social Sciences*. Chichester, UK: John Wiley & Sons.

Lüdecke, D., Makowski, D., Waggoner, P., Patil, I., and Ben-Shachar, M. S. (2020). *performance: Assessment of Regression Models Performance*. R package version 0.6.1.

Magnusson, A., Skaug, H., Nielsen, A., Berg, C., Kristensen, K., Maechler, M., van Bentham, K., Bolker, B., and Brooks, M. (2020). *glmmTMB: Generalized Linear Mixed Models using Template Model Builder*. R package version 1.0.2.1.

R Core Team (2020). *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria.

Rue, H., Lindgren, F., Simpson, D., Martino, S., Teixeira Krainski, E., Bakka, H., Riebler, A., and Fuglstad, G.-A. (2020). *INLA: Full Bayesian Analysis of Latent Gaussian Models using Integrated Nested Laplace Approximations*. R package version 20.03.17.

Rue, H., Martino, S., and Chopin, N. (2009). Approximate Bayesian Inference for Latent Gaussian Models by Using Integrated Nested Laplace Approximations. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, 71(2):319–392.

Ruppert, D., Wand, M. P., and Carroll, R. J. (2003). *Semiparametric Regression*. Cambridge, UK: Cambridge University Press.

Sarkar, D. (2020). *lattice: Trellis Graphics for R*. R package version 0.20-41.

Wang, X., Ryan, Y. Y., and Faraway, J. J. (2018). *Bayesian Regression Modeling with INLA*. Boca Raton, FL: Chapman & Hall.

Wickham, H., Chang, W., Henry, L., Pedersen, T. L., Takahashi, K., Wilke, C., Woo, K., Yutani, H., and Dunnington, D. (2020). *ggplot2: Create Elegant Data Visualisations Using the Grammar of Graphics*. R package version 3.3.3.

Wood, S. (2020). *mgcv: Mixed GAM Computation Vehicle with Automatic Smoothness Estimation*. R package version 1.8-33.

Wood, S. and Scheipl, F. (2020). *gamm4: Generalized Additive Mixed Models using mgcv and lme4*. R package version 0.2-6.

Wood, S. N. (2017). *Generalized Additive Models: An Introduction with R, Second Edition*. Boca Raton, FL: CRC Press.

Xie, Y. (2020). *bookdown: Authoring Books and Technical Documents with R Markdown*. R package version 0.21.

Yee, T. (2021). *VGAM: Vector Generalized Linear and Additive Models*. R package version 1.1-5.

Yee, T. W. (2015). *Vector Generalized Linear and Additive Models: With an Implementation in R*. New York: Springer-Verlag.

Zuur, A. F., Hilbe, J. M., and Ieno, E. N. (2014). *A Beginner's Guide to GLM and GLMM with R: A Frequentist and Bayesian Perspective for Ecologists*. Newburgh, UK: Highland Statistics.

Zuur, A. F. and Ieno, E. N. (2018). *Beginner's Guide to Spatial, Temporal and Spatial-Temporal Ecological Data Analysis with R-INLA, Volume 2: GAM and Zero-Inflated Models*. Newburgh, UK: Highland Statistics.

Zuur, A. F., Ieno, E. N., and Elphick, C. S. (2010). A Protocol for Data Exploration to Avoid Common Statistical Problems. *Methods in Ecology and Evolution*, pages (1):3–14.

Zuur, A. F., Ieno, E. N., and Saveliev, A. A. (2017). *Beginner's Guide to Spatial, Temporal and Spatial-Temporal Ecological Data Analysis with R-INLA: Using GLM and GLMM Volume I*. Newburgh, UK: Highland Statistics.

Zuur, A. F., Ieno, E. N., Walker, N., Saveliev, A. A., and Smith, G. M. (2009). *Mixed Effects Models and Extensions in Ecology with R*. Statistics for Biology and Health. New York: Springer-Verlag.

Zuur, A. F., Saveliev, A. A., and Ieno, E. N. (2012). *Zero Inflated Models and Generalized Linear Mixed Models with R*. Newburgh, UK: Highland Statistics.

Zuur, A. F., Saveliev, A. A., and Ieno, E. N. (2015). *A Beginner's Guide to Generalised Additive Mixed Models with R*. Newburgh, UK: Highland Statistics.