

Point count data analysis: How to violate assumptions and get away with it

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2019-06-13

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Preface

This book provides material for the workshop *Analysis of point-count data in the presence of variable survey methodologies and detection error* at the [AOS 2019 conference](#) by Peter Solymos.

The book and related materials in this repository is the basis of a full day workshop (8 hours long with 3 breaks).

Prior exposure to [R](#) language is necessary (i.e. basic R object types and their manipulation, such as arrays, data frames, indexing) because this is not covered as part of the course. Check [this intro](#).

About the book and the course

You'll learn

- how to analyze your point count data when it combines different methodologies/protocols/technologies,
- how to violate assumptions and get away with it.

This book/course is aimed towards ornithologists analyzing field observations, who are often faced by data heterogeneities due to field sampling protocols changing from one project to another, or through time over the lifespan of projects, or trying to combine ‘legacy’ data sets with new data collected by recording units. Such heterogeneities can bias analyses when data sets are integrated inadequately, or can lead to information loss when filtered and standardized to common standards. Accounting for these issues is important for better inference regarding status and trend of bird species and communities.

Analysts of such ‘messy’ data sets need to feel comfortable with manipulating the data, need a full understanding the mechanics of the models being used (i.e. critically interpreting the results and acknowledging assumptions and limitations), and should be able to make informed choices when faced with methodological challenges.

The course emphasizes critical thinking and active learning. Participants will be asked to take part in the analysis: first hand analytics experience from start to finish. We will use publicly available data sets to demonstrate the data manipulation and analysis. We will use freely available and open-source R packages.

The expected outcome of the course is a solid foundation for further professional development via increased confidence in applying these methods for field observations.

About the author

Peter Solymos is an ecologist (molluscs, birds), he is pretty good at stats (modeling, detectability, data cloning, multivariate), an R programmer (vegan, detect, ResourceSelection, pbapply), sometimes he teaches (like the contents of this book).

Installing R and RStudio

Follow the instructions at the [R website](#) to download and install the most up-to-date base R version suitable for your operating system (the latest R version at the time of writing these instructions is 3.6.0).

Having RStudio is not absolutely necessary, but some of our course material will follow a syntax that is close to RStudio's [R markdown](#) notation, so having RStudio will make our life easier. RStudio is also available for different operating systems. Pick the open source desktop edition from [here](#) (the latest RStudio Desktop version at the time of writing these instructions is 1.2.1335).

Installing required packages

```
pkgs <- c("bookdown", "detect", "devtools", "dismo", "forecast",
  "glmnet", "gbm", "intrval", "knitr", "lme4", "maptools", "mefa4",
  "mgcv", "MuMIn", "opticut", "partykit", "pscl", "raster",
  "ResourceSelection", "shiny", "sp", "unmarked", "visreg")
to_inst <- setdiff(pkgs, rownames(installed.packages()))
if (length(to_inst))
  install.packages(to_inst, repos="https://cloud.r-project.org/")
devtools::install_github("psolymos/bSims")
devtools::install_github("psolymos/QPAD")
devtools::install_github("borealbirds/paired")
devtools::install_github("borealbirds/lhreg")
still_missing <- setdiff(c(pkgs, "bSims", "paired", "lhreg", "QPAD"),
  rownames(installed.packages()))
if (length(still_missing)) {
  cat("The following packages could not be installed:\n",
    paste("\t-", pkgs, collapse="\n"), "\n")
} else {
```

```
cat("You are all set! See you at the workshop.\n")
}
```

Here is a preprint version of Norman Matloff's *The Art of R Programming* book: <http://heather.cs.ucdavis.edu/~matloff/132/NSPpart.pdf>. Check out Chapters 1–6 if you want to brush up your R skills.

Installing the book

The **bookdown** package can be installed from CRAN or Github:

```
install.packages("bookdown")
# or the development version
# devtools::install_github("rstudio/bookdown")

## clean up
bookdown::clean_book(TRUE)
## rendering the book
bookdown::render_book('index.Rmd', 'bookdown::gitbook')
bookdown::render_book('index.Rmd', 'bookdown::pdf_book')
bookdown::render_book('index.Rmd', 'bookdown::epub_book')
```

To compile this example to PDF, you need XeLaTeX. You are recommended to install TinyTeX (which includes XeLaTeX): <https://yihui.name/tinytex/>.

How this works



This is an exercise.



This is a note.



This is a warning.

Acknowledgments

List here all the wonderful folks who helped with this book.

Chapter 1

Introduction

All assumptions are violated, but some are more than others

A comparison of apples and oranges occurs when two items or groups of items are compared that cannot be practically compared ([Wikipedia](#)). The way we measure things can have a big impact on the outcome of that measurement. For example, you might say that “I saw 5 robins walking down the road”, while I might say that “I only saw one robin while sitting on my porch”. Who say more robins? If looking at only the numeric results, you saw more robins than me. But this seems like an apples to oranges comparison.

To compare apples to apples, we need to agree on a comparable measurement scheme, or at least figure out how does *effort* affect the observations.

Effort in our example can depend on, e.g. the *area* of the physical space searched, the amount of *time* spent, etc. The outcome might further affected by weather, time of year, time of day, location, experience and skill level of the observer.

All these factors can affect the observed count. Which brings us to the definition of a *point count*: a trained observer records all the birds seen and heard from a point count station for a set period of time within a defined distance radius.

Point count duration and distance have profound effect on the counts, as shown in Figure 1.1 showing that a 10-min unlimited distance count is roughly 300% increased compared to 3-min 50-m counts (averaged across 54 species of boreal songbirds, ([Matsuoka et al., 2014](#))).

Point counts are commonly used to answer questions like:

- How many? (Abundance, density, population size)
- Is this location part of the range? (0/1)
- How is abundance changing in space? (Distribution)
- How is abundance changing in time? (Trend)
- What is the effect of a treatment on abundance?

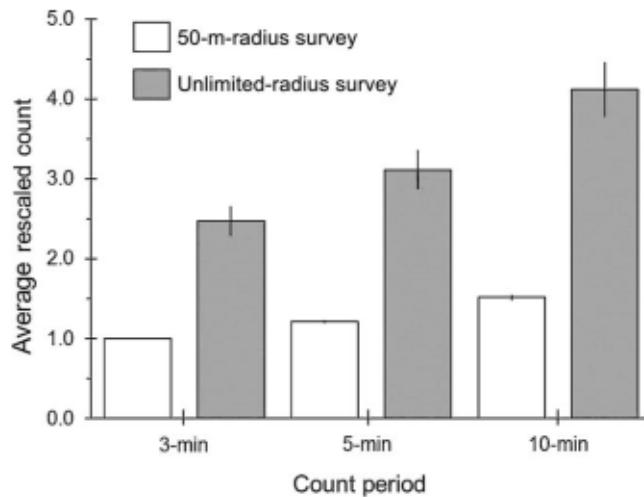


Figure 1.1: Effects of duration and distance on mean counts, from [@matsuoka2014].

1.1 Design-based approaches

Standards and recommendations can maximize efficiency in the numbers of birds and species counted, minimize extraneous variability in the counts.

But programs started to deviate from standards: “*For example, only 3% of 196,000 point counts conducted during the period 1992–2011 across Alaska and Canada followed the standards recommended for the count period and count radius*” ((Matsuoka et al., 2014)). Figure 1.2 show how point count protocol varies across the boreal region of North America.

Exercise



- In what regard can protocols differ?
- What might drive protocol variation among projects?
- Why have we abandoned following protocols?

1.2 Model-based approaches

Detection probabilities might vary even with fixed effort (we’ll cover this more later), and programs might have their own goals and constraints (access, training, etc). These constraints would make it almost impossible, and potentially costly to set up very specific standards.

Labour intensive methods for unmarked populations have come to the forefront, and computing power of personal computers opened the door for model-based approaches, that can accomodate more variation given enough information in the observed data. These methods often rely on ancillary information and often some sort of replication.

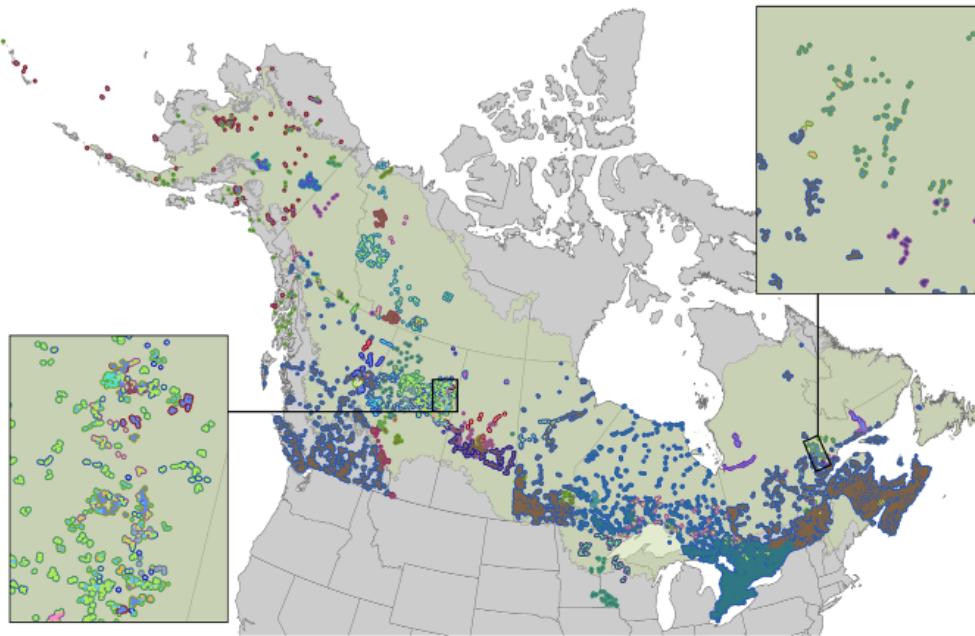


Figure 1.2: Survey methodology variation (colors) among contributed projects in the Boreal Avian Modelling (BAM) data base, from [@barker2015].

Some of the commonly used model-based approaches are:

- double observer ([Nichols et al. 2000](#)),
- distance sampling ([Buckland et al. 2001](#)),
- removal sampling ([Farnsworth et al. 2002](#)),
- multiple visit occupancy ([MacKenzie et al. 2002](#)),
- multiple visit abundance ([Royle 2004](#)).

Models come with assumptions, such as:

- population is closed during multiple visits,
- observers are independent,
- all individuals emit cues with identical rates,
- spatial distribution of individuals is uniform,
- etc.

Although assumptions are everywhere, we are really good at ignoring and violating them.



Exercise

Can you mention some assumptions from everyday life?

Can you explain why we neglect/violate assumptions in these situations?

Assumptions are violated, because we seek simplicity. The main question we have to ask: *does it matter in practice* if we violate the assumptions?

1.3 Our approach

In this book and course, we will critically evaluate common assumptions made when analyzing point count data using the following approach:

1. we will introduce a concept,
2. understand how we can infer it from data,
3. then we recreate the situation *in silico*,
4. and see how the outcome changes as we make different assumptions.

It is guaranteed that we will violate every assumption we make. To get away with it, we need to understand how much is too much, and whether it has an impact in practice. If there is a practical consequence, we will look at ways to minimize that effects – so that we can safely ignore the assumption.

Chapter 2

Organizing and Processing Point Count Data

All data are messy, but some are missing

2.1 Introduction

It is often called *data processing*, *data munging*, *data wrangling*, *data cleaning*. None of these expressions capture the dread associated with the actual activity. Luckily, this book and course is not about data manipulation, and we can gladly skip these steps. But keep in mind, in real life, you'll often have to worry about at least four things that can go wrong:

1. space (e.g. wrong UTM zones, errors),
2. time (ISO format please),
3. taxonomy (unknowns, mis-identifications),
4. something else (if there were no errors, check again).

This chapter sets you up for the required data skills for the rest of the book/course.

2.2 Prerequisites

```
library(mefa4)          # data manipulation
library(raster)         # reading raster files
library(sp)              # spatial data manipulation
load("_data/josm/josm.rda") # load bird data
rr <- stack("_data/josm/landcover-hfi2016.grd") # rasters
```

2.3 R basics

This short document is intended to help you brush up your R skills. If you feel that these R basics are not very familiar, I suggest to take a look at some introductory R books, such as this preprint version of Norman Matloff's *The Art of R Programming* book: <http://heather.cs.ucdavis.edu/~matloff/132/NSPpart.pdf>, check out Chapters 1–6.

R is a great calculator:

```
1 + 2
```

Assign a value and print an object using = or <- (preferred in this book):

```
(x = 2) # shorthand for print
print(x)
x == 2 # logical operator, not assignment
y <- x + 0.5
y # another way to print
```

Logical operators come handy:

```
x == y # equal
x != y # not equal
x < y # smaller than
x >= y # greater than or equal
```

Vectors and sequences are created most often by the functions `c`, `:`, `seq`, and `rep`:

```
x <- c(1, 2, 3)
x
1:3
seq(1, 3, by = 1)

rep(1, 5)
rep(1:2, 5)
rep(1:2, each = 5)
```

When doing operations with vectors remember that values of the shorter object are recycled:

```
x + 0.5
x * c(10, 11, 12, 13)
```

Indexing and ordering vectors is a fundamental skill:

```
x[1]
x[c(1, 1, 1)] # a way of repeating values
x[1:2]
x[x != 2]
x[x == 2]
```

```
x[x > 1 & x < 3]
order(x, decreasing=TRUE)
x[order(x, decreasing=TRUE)]
rev(x) # reverse
```

See how NA values can influence sorting character vectors:

```
z <- c("b", "a", "c", NA)
z[z == "a"]
z[!is.na(z) & z == "a"]
z[is.na(z) | z == "a"]
is.na(z)
which(is.na(z))
sort(z)
sort(z, na.last=TRUE)
```

There are a few special values:

```
as.numeric(c("1", "a")) # NA: not available (missing or invalid)
0/0 # NaN: not a number
1/0 # Inf
-1/0 # -Inf
```

Matrices and arrays are vectors with dimensions, elements are in same mode:

```
(m <- matrix(1:12, 4, 3))
matrix(1:12, 4, 3, byrow=TRUE)

array(1:12, c(2, 2, 3))
```

Many objects have attributes:

```
dim(m)
dim(m) <- NULL
m
dim(m) <- c(4, 3)
m
dimnames(m) <- list(letters[1:4], LETTERS[1:3])
m
attributes(m)
```

Matrice and indices:

```
m[1:2,]
m[, 2]
m[, 2]
m[, 2, drop=FALSE]
m[2]
```

```
m[rownames(m) == "c",]
m[rownames(m) != "c",]
m[rownames(m) %in% c("a", "c", "e"),]
m[!(rownames(m) %in% c("a", "c", "e"))]
```

Lists and indexing:

```
l <- list(m = m, x = x, z = z)
l
l$ddd <- sqrt(l$x)
l[2:3]
l[["ddd"]]
```

Data frames are often required for statistical modeling. A data frame is a list where length of elements match and elements can be in different mode.

```
d <- data.frame(x = x, sqrt_x = sqrt(x))
d
```

Inspect structure of R objects:

```
str(x)
str(z)
str(m)
str(l)
str(d)
str(as.data.frame(m))
str(as.list(d))
```

Get summaries of these objects:

```
summary(x)
summary(z)
summary(m)
summary(l)
summary(d)
```

2.4 JOSM data set

The data is based on the project *Cause-Effect Monitoring Migratory Landbirds at Regional Scales: understand how boreal songbirds are affected by human activity in the oil sands area* (2.1 and 2.2, (Mahon et al., 2016)). JOSM stands for Joint Oil Sands Monitoring. Look at the source code in the `_data/josm` directory of the book if you are interested in data processing details. We skip that for now.

Surveys were spatially replicated because:

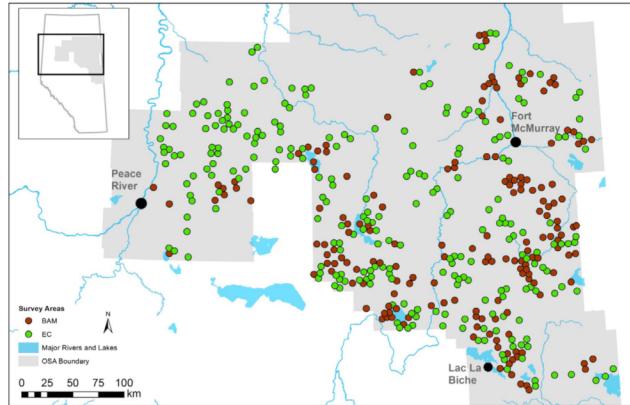
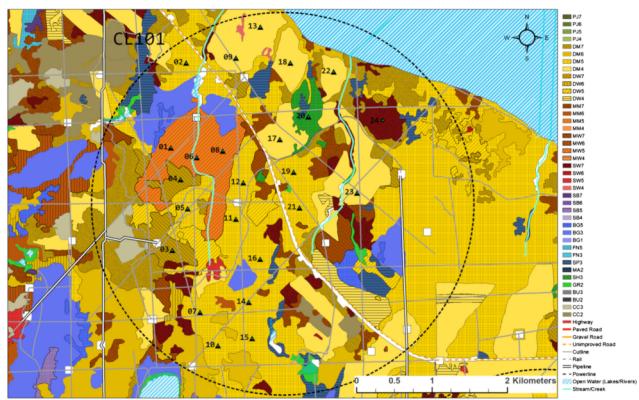


Figure 2.1: JOSM bird data survey locations from [@mahon2016].



- we want to make inferences about a population,
- full census is out of reach,
- thus we take a sample of the population
- that is representative and random.
- Ideally, sample size should be as large as possible,
- it reduces variability and
- increases statistical power.

Survey locations were picked based on various criteria:

- stratification (land cover),
- gradients (disturbance levels),
- random location (control for unmeasured effects),
- take into account historical surveys (avoid, or revisit),
- access, cost (clusters).

The `josm` object is a list with 3 elements:

- `surveys`: data frame with survey specific information,
- `species`: lookup table for species,
- `counts`: individual counts by survey and species.

```
names(josm)
```

```
## [1] "surveys" "species" "counts"
```

Species info: species codes, common and scientific names. The table could also contain taxonomic, trait, etc. information as well.

```
head(josm$species)
```

At the survey level, we have coordinates, date/time info, variables capturing survey conditions, and land cover info extracted from 1 km² resolution rasters.

```
colnames(josm$surveys)
```

```
##  [1] "SiteID"          "SurveyArea"       "Longitude"        "Latitude"
##  [5] "Date"             "StationID"        "ObserverID"       "TimeStart"
##  [9] "VisitID"          "WindStart"         "PrecipStart"      "TempStart"
## [13] "CloudStart"        "WindEnd"           "PrecipEnd"         "TempEnd"
## [17] "CloudEnd"          "TimeFin"           "Noise"            "OvernightRain"
## [21] "DateTime"          "SunRiseTime"       "SunRiseFrac"      "TSSR"
## [25] "OrdinalDay"        "DAY"               "Open"              "Water"
## [29] "Agr"               "UrbInd"            "SoftLin"          "Roads"
## [33] "Decid"             "OpenWet"            "Conif"            "ConifWet"
```

The count table contains one row for each unique individual of a species (`SpeciesID` links to the species lookup table) observed during a survey (`StationID` links to the survey attribute table). Check the data dictionary in `_data/josm` folder for a detailed explanation of each column.

```
str(josm$counts)

## 'data.frame': 52372 obs. of 18 variables:
## $ ObservationID: Factor w/ 57024 levels "CL10102-130622-001",...: 1 2 3 4 5 6 8 9 10 ...
## $ SiteID       : Factor w/ 4569 levels "CL10102","CL10106",...: 1 1 1 1 1 1 1 1 2 2 ...
## $ StationID    : Factor w/ 4569 levels "CL10102-1","CL10106-1",...: 1 1 1 1 1 1 1 1 2 2 ...
## $ TimeInterval : int 1 1 1 1 5 5 1 1 1 1 ...
## $ Direction    : int 1 2 2 2 1 4 4 4 1 1 ...
## $ Distance     : int 1 2 2 1 3 3 2 1 1 1 ...
## $ DetectType1  : Factor w/ 3 levels "C","S","V": 2 2 2 2 1 1 2 2 2 2 ...
## $ DetectType2  : Factor w/ 3 levels "C","S","V": NA ...
## $ DetectType3  : Factor w/ 3 levels "C","S","V": NA ...
## $ Sex          : Factor w/ 4 levels "F","M","P","U": 2 2 2 2 4 4 2 2 2 2 ...
## $ Age          : Factor w/ 6 levels "A","F","J","JUV",...: 1 1 1 1 1 1 1 1 1 ...
## $ Activity1    : Factor w/ 17 levels "BE","CF","CH",...: 5 5 5 5 NA NA NA 5 5 NA ...
## $ Activity2    : Factor w/ 17 levels "48","BE","CF",...: NA NA NA NA NA NA NA NA NA ...
## $ Activity3    : Factor w/ 7 levels "CF","DC","DR",...: NA NA NA NA NA NA NA ...
## $ ActivityNote : Factor w/ 959 levels "AGITATED","AGITATED CALLING",...: NA NA NA NA ...
## $ Dur          : Factor w/ 3 levels "0-3min","3-5min",...: 1 1 1 1 3 3 1 1 1 ...
## $ Dis          : Factor w/ 3 levels "0-50m","50-100m",...: 1 2 2 1 3 3 2 1 1 1 ...
## $ SpeciesID   : Factor w/ 150 levels "ALFL","AMBI",...: 107 95 95 107 46 43 140 95 1
```

2.5 Cross tabulating species counts

Take the following dummy data frame (long format):

```
(d <- data.frame(
  sample=factor(paste0("S", c(1,1,1,2,2)), paste0("S", 1:3)),
  species=c("BTNW", "OVEN", "CANG", "AMRO", "CANG"),
  abundance=c(1, 1, 2, 1, 1),
  behavior=rep(c("heard", "seen"), c(4, 1)))
str(d)

## 'data.frame': 5 obs. of 4 variables:
## $ sample  : Factor w/ 3 levels "S1","S2","S3": 1 1 1 2 2
## $ species : Factor w/ 4 levels "AMRO","BTNW",...: 2 4 3 1 3
## $ abundance: num 1 1 2 1 1
## $ behavior : Factor w/ 2 levels "heard","seen": 1 1 1 1 2
```

We want to add up the abundances for each sample (rows) and species (column):

```
(y <- Xtab(abundance ~ sample + species, d))
```

```
## 3 x 4 sparse Matrix of class "dgCMatrix"
##      AMRO BTNW CANG OVEN
```

```
## S1      .    1    2    1
## S2      1    .    1    .
## S3      .    .    .    .
```

y is a sparse matrix, that is a very compact representation:

```
object.size(d[,1:3])
```

```
## 2328 bytes
```

```
object.size(y)
```

```
## 2160 bytes
```

Notice that we have 3 rows, but d\$sample did not have an S3 value, but it was a level. We can drop such unused levels, but it is generally not recommended, and we need to be careful not to drop samples where no species was detected (this can happen quite often depending on timing of surveys)

```
Xtab(abundance ~ sample + species, d, drop.unused.levels = TRUE)
```

```
## 2 x 4 sparse Matrix of class "dgCMatrix"
##   AMRO BTNW CANG OVEN
## S1      .    1    2    1
## S2      1    .    1    .
```

A sparse matrix can be converted to ordinary matrix

```
as.matrix(y)
```

```
##   AMRO BTNW CANG OVEN
## S1      0    1    2    1
## S2      1    0    1    0
## S3      0    0    0    0
```

The nice thing about this cross tabulation is that we can filter the records without changing the structure (rows, columns) of the table:

```
Xtab(abundance ~ sample + species, d[d$behavior == "heard",])
```

```
## 3 x 4 sparse Matrix of class "dgCMatrix"
##   AMRO BTNW CANG OVEN
## S1      .    1    2    1
## S2      1    .    .    .
## S3      .    .    .    .
```

```
Xtab(abundance ~ sample + species, d[d$behavior == "seen",])
```

```
## 3 x 4 sparse Matrix of class "dgCMatrix"
##   AMRO BTNW CANG OVEN
## S1      .    .    .    .
```

```
## S2 . . 1 .
## S3 . . . .
```

Now let's do this for the real data. We have no abundance column, because each row stands for exactly one individual. We can add a column with 1's, or we can just count the number of rows by using only the right-hand-side of the formula in `Xtab`. `ytot` will be our total count matrix for now.

We also want to filter the records to contain only Songs and Calls, without Vvisual detections:

```
table(josm$counts$DetectType1, useNA="always")
```

```
##
##      C      S      V  <NA>
##  9180 41808 1384      0
```

We use `SiteID` for row names, because only 1 station and visit was done at each site:

```
ytot <- Xtab(~ SiteID + SpeciesID, josm$counts[josm$counts$DetectType1 != "V",])
```

See how not storing 0's affect size compared to the long formar and an ordinary wide matrix

```
## 2-column data frame as reference
tmp <- as.numeric(object.size(
  josm$counts[josm$counts$DetectType1 != "V", c("StationID", "SpeciesID")]))
## spare matrix
as.numeric(object.size(ytot)) / tmp
```

```
## [1] 0.1366
## dense matrix
as.numeric(object.size(as.matrix(ytot))) / tmp
```

```
## [1] 1.106
## matrix fill
sum(ytot > 0) / prod(dim(ytot))
```

```
## [1] 0.04911
```

Check if counts are as expected:

```
max(ytot) # this is interesting
```

```
## [1] 200
sort(apply(as.matrix(ytot), 2, max)) # it is CANG
```

```
## BUFF BWTE COGO COHA DCCO GWTE HOLA NHOW NSHO RTHU WWSA CANV NOPI AMBI AMCO
## 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1
## AMGO BAEA BAOR BEKI BOWA CONI CSWA EAPH GBHE GCTH GGOW GHOW HOWR LEOW MERL
## 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
```

```

## NESP NOGO NOHA NSWO PBGR RBGU RTHA SAVS SPSA WBNU BRBL CAGU MYWA SNBU VEER
##   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1
## AMKE AMWI BADO BARS BBWO BHCO BLBW BLPW BLTE BWHA COGR DOWO EAKI HAWO KILL
##   2   2   2   2   2   2   2   2   2   2   2   2   2   2   2   2   2
## LEYE NAWA NOPO OSFL OSPR PIWO PUFI RNDU SORA SSHA COSN AMCR AMRO ATTW BHVI
##   2   2   2   2   2   2   2   2   2   2   2   2   2   2   3   3   3
## BOCH BRCR BTNW CMWA FOSP FRGU GCKI MAWR MOWA NOFL PHVI SACR SOSA SOSP SPGR
##   3   3   3   3   3   3   3   3   3   3   3   3   3   3   3   3   3
## TRES WETA WIWA WIWR YBSA FOTE BAWW BBWA BCCH BLJA CAWA CONW COTE GRYE NOWA
##   3   3   3   3   3   3   4   4   4   4   4   4   4   4   4   4   4
## NRWS OCWA REVI RNGR RUBL RWBL WAVI WEWP WISN YBFL YWAR ALFL AMRE CHSP CORA
##   4   4   4   4   4   4   4   4   4   4   4   4   4   5   5   5   5
## EVGR HETH LCSP RBGR RBNU RCKI SWSP CCSP COYE DEJU LEFL LISp MAWA OVEN RUGR
##   5   5   5   5   5   5   6   6   6   6   6   6   6   6   6   6   6
## SWTH BOGU MALL GRAJ PAWA WTSP YRWA COLO TEWA AMPI WWCR CEDW PISI RECR CANG
##   6   7   7   8   8   8   8   9   12  12  20  23  50  51  200

## lyover (FO) flock (FL) beyond 100m distance
head(josm$counts[
  josm$counts$SiteID == rownames(ytot)[which(ytot[, "CANG"] == 200)] &
  josm$counts$SpeciesID == "CANG",])

```

We can check overall mean counts:

```
round(sort(colMeans(ytot)), 4)
```

```

## BUFF BWTE COGO COHA DCCO GWTE HOLA NHOW NSHO RTHU
## 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
## WWSC CANV NOPI GBHE GCTH GHOW LEOW NOHA RBGU BRBL
## 0.0000 0.0000 0.0000 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002 0.0002
## CAGU AMCO BAEA BARS NESP NOGO NOPO NSWO RNDU SNBU
## 0.0002 0.0004 0.0004 0.0004 0.0004 0.0004 0.0004 0.0004 0.0004 0.0004 0.0004
## VEER BEKI CSWA MERL SAVS SSHA MYWA AMKE BAOR OSPR
## 0.0004 0.0007 0.0007 0.0007 0.0007 0.0007 0.0007 0.0009 0.0009 0.0009 0.0009
## SPGR WBNU AMGO AMWI BOWA CONI EAPH HOWR NRWS BLTE
## 0.0009 0.0009 0.0011 0.0011 0.0011 0.0011 0.0011 0.0011 0.0011 0.0011 0.0013
## COGR EAKI GGOW NAWA COSN COTE FRGU MAWR FOTE KILL
## 0.0013 0.0013 0.0013 0.0013 0.0013 0.0015 0.0015 0.0015 0.0015 0.0015 0.0018
## RTHA BADO BLBW AMBI PBGR SPSA AMPI BHCO BWHA SOSP
## 0.0020 0.0024 0.0024 0.0028 0.0028 0.0028 0.0028 0.0031 0.0037 0.0042
## RUBL MALL PUFI DOWO SORA LEYE ATTW HAWO RNGR BBWO
## 0.0044 0.0046 0.0048 0.0059 0.0068 0.0094 0.0096 0.0101 0.0101 0.0107
## BLJA BOGU AMCR EVGR RWBL OSFL LCSP TRES FOSP WEWP
## 0.0134 0.0140 0.0166 0.0169 0.0169 0.0186 0.0193 0.0201 0.0217 0.0232
## WIWA PIWO RECR SOSA YWAR GCKI BLPW CAWA SACR BTNW
## 0.0236 0.0256 0.0269 0.0269 0.0291 0.0304 0.0306 0.0315 0.0322 0.0335

```

```

##  NOWA  OCWA  BRCR  CCSP  COLO  PHVI  CONW  CEDW  RUGR  MOWA
## 0.0341 0.0359 0.0381 0.0385 0.0387 0.0394 0.0429 0.0449 0.0475 0.0477
##  WAVI  BCCH  BOCH  NOFL  SWSP  GRYE  WWCR  AMRO  RBNU  BBWA
## 0.0582 0.0593 0.0593 0.0622 0.0659 0.0685 0.0751 0.0757 0.0766 0.0810
##  CMWA  BHVI  COYE  YBFL  YBSA  AMRE  BAWW  LEFL  WETA  WISN
## 0.0812 0.0814 0.0814 0.0873 0.0878 0.0889 0.0963 0.0974 0.1086 0.1280
##  CORA  WIWR  ALFL  MAWA  PISI  RBGR  LISP  DEJU  GRAJ  CANG
## 0.1401 0.1466 0.1582 0.1727 0.1775 0.1832 0.2169 0.2725 0.2898 0.3018
##  PAWA  REVI  RCKI  HETH  CHSP  SWTH  WTSP  OVEN  YRWA  TEWA
## 0.3053 0.3344 0.3898 0.4344 0.4460 0.7402 0.8091 0.8831 0.8934 1.2221

```

2.6 Joining species data with predictors

Let's join the species counts with the survey attributes. This is how we can prepare the input data for regression analysis.

```

spp <- "OVEN" # which species
josm$species[spp,]

compare_sets(rownames(josm$surveys), rownames(ytot))

##           xlength ylength intersect union xbutnoty ybutnotx
## labels      4569      4569      4569  4569        0        0
## unique      4569      4569      4569  4569        0        0

x <- josm$surveys
x$y <- as.numeric(ytot[rownames(x), spp])

```

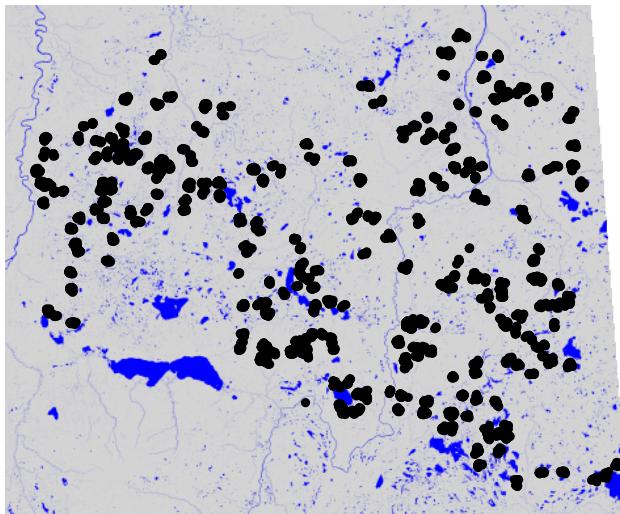
2.7 Explore predictor variables

Put the locations on the map:

```

xy <- x[,c("Longitude", "Latitude")]
coordinates(xy) <- ~ Longitude + Latitude
proj4string(xy) <- "+proj=longlat +ellps=GRS80 +datum=NAD83 +no_defs"
xy <- spTransform(xy, proj4string(rr))
col <- colorRampPalette(c("lightgrey", "blue"))(100)
plot(rr[["Water"]], col=col, axes=FALSE, box=FALSE, legend=FALSE)
plot(xy, add=TRUE, pch=19, cex=0.5)

```



Exercise



Explore the data to understand the distributions and associations. Use `summary`, `table`, `hist`, `plot` (bivariate, scatterplot matrix), etc.

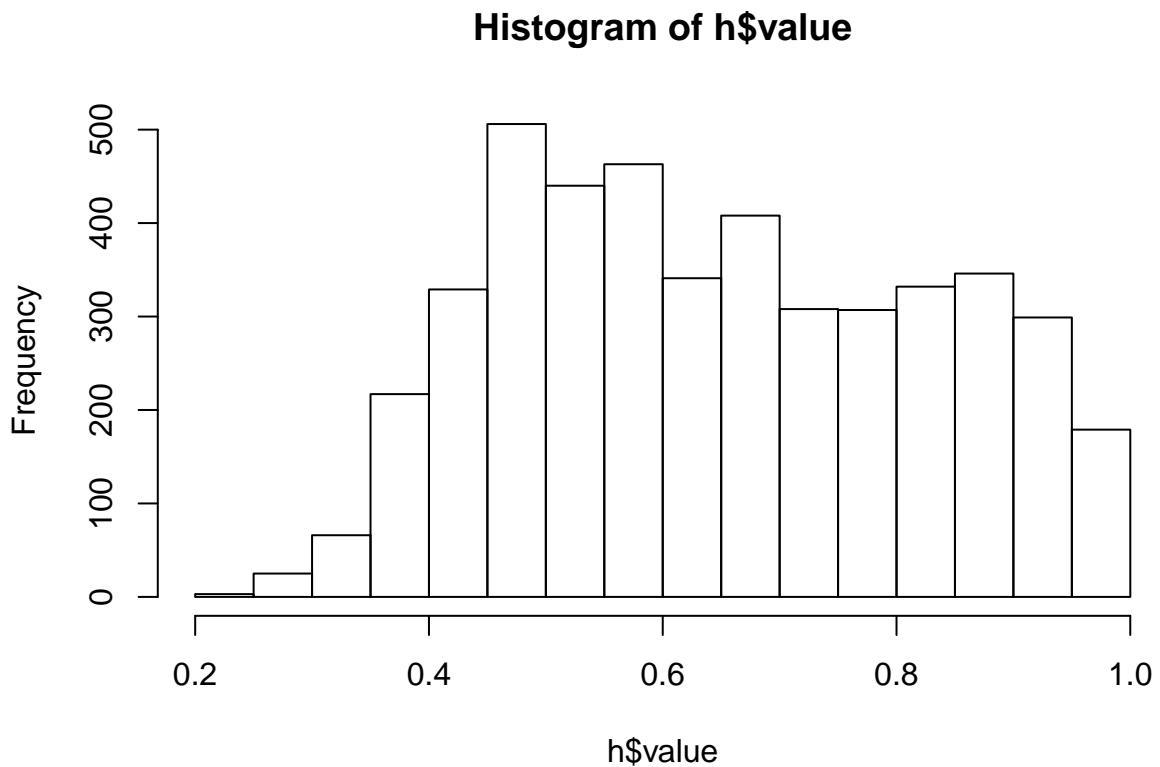
2.8 Derived variables

Add up some of the compositional variables into meaningful units:

```
x$FOR <- x$Decid + x$Conif + x$ConifWet # forest
x$AHF <- x$Agr + x$UrbInd + x$Roads # 'alienating' human footprint
x$WET <- x$OpenWet + x$ConifWet + x$Water # wet + water
```

Classify surveys locations based on dominant land cover type:

```
cn <- c("Open", "Water", "Agr", "UrbInd", "SoftLin", "Roads", "Decid",
       "OpenWet", "Conif", "ConifWet")
h <- find_max(x[,cn])
hist(h$value)
```



```
table(h$index)
```

```
##          Open      Water      Agr UrbInd SoftLin Roads Decid OpenWet
##            12        10       4     14      0      2   2084      160
##      Conif ConifWet
##      745    1538
```

```
x$HAB <- droplevels(h$index) # drop empty levels
```


Chapter 3

A Primer in Regression Techniques

All models are wrong, but some are useful – Box

3.1 Introduction

This chapter will provide all the foundations we need for the coming chapters. It is not intended as a general and all-exhaustive introduction to regression techniques, but rather the minimum requirement moving forwards. We will also hone our data processing and plotting skills.

3.2 Prerequisites

```
library(mefa4)                      # data manipulation
library(mgcv)                        # GAMs
library(pscl)                         # zero-inflated models
library(lme4)                          # GLMMs
library(MASS)                          # Negative Binomial GLM
library(partykit)                     # regression trees
library(intrval)                      # interval magic
library(opticut)                      # optimal partitioning
library(visreg)                       # regression visualization
library(ResourceSelection)            # marginal effects
library(MuMIn)                        # multi-model inference
source("functions.R")                 # some useful stuff
load("_data/josm/josm.rda")          # JOSM data
```

Let's pick a species, Ovenbird (OVEN), that is quite common and abundant in the data set. We put together a little data set to work with:

```
spp <- "OVEN"

ytot <- Xtab(~ SiteID + SpeciesID , josm$counts[josm$counts$DetectType1 != "V",])
ytot <- ytot[,colSums(ytot > 0) > 0]
x <- data.frame(
  josm$surveys,
  y=as.numeric(ytot[rownames(josm$surveys), spp]))
x$FOR <- x$Decid + x$Conif+ x$ConifWet # forest
x$AHF <- x$Agr + x$UrbInd + x$Roads # 'alienating' human footprint
x$WET <- x$OpenWet + x$ConifWet + x$Water # wet + water
cn <- c("Open", "Water", "Agr", "UrbInd", "SoftLin", "Roads", "Decid",
       "OpenWet", "Conif", "ConifWet")
x$HAB <- droplevels(find_max(x[,cn])$index) # drop empty levels
x$DEC <- ifelse(x$HAB == "Decid", 1, 0)

table(x$y)

## 
##    0     1     2     3     4     5     6 
## 2493   883   656   363   132    29    13
```

3.3 Poisson null model

The null model states that the expected values of the count at all locations are identical: $E[Y_i] = \lambda$ ($i = 1, \dots, n$), where Y_i is a random variable that follows a Poisson distribution with mean λ : $(Y_i | \lambda) \sim \text{Poisson}(\lambda)$. The observation (y_i) is a realization of the random variables Y at site i , these observations are independent and identically distributed (i.i.d.), and we have n observations in total.

Saying the the distribution is Poisson is an assumption in itself. For example we assume that the variance equals the mean ($V(\mu) = \mu$).

```
mP0 <- glm(y ~ 1, data=x, family=poisson)
mean(x$y)

## [1] 0.8831
mean(fitted(mP0))

## [1] 0.8831
exp(coef(mP0))

## (Intercept)
##      0.8831
```

```
summary(mP0)

##
## Call:
## glm(formula = y ~ 1, family = poisson, data = x)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.33   -1.33   -1.33    1.02    3.57
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.1243    0.0157  -7.89  2.9e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
## Null deviance: 7424.8 on 4568 degrees of freedom
## Residual deviance: 7424.8 on 4568 degrees of freedom
## AIC: 12573
##
## Number of Fisher Scoring iterations: 6
```

The `family=poisson` specification implicitly assumes that we use a logarithmic link function, that is to say that $\log(\lambda) = \beta_0$, or equivalently: $\lambda = e^{\beta_0}$. The mean of the observations equal the mean of the fitted values, as expected.

The logarithmic function is called the link function, its inverse, the exponential function is called the inverse link function. The model family has these conveniently stored for us:

```
mP0$family
```

```
##
## Family: poisson
## Link function: log
```

```
mP0$family$linkfun
```

```
## function (mu)
## log(mu)
## <environment: namespace:stats>
```

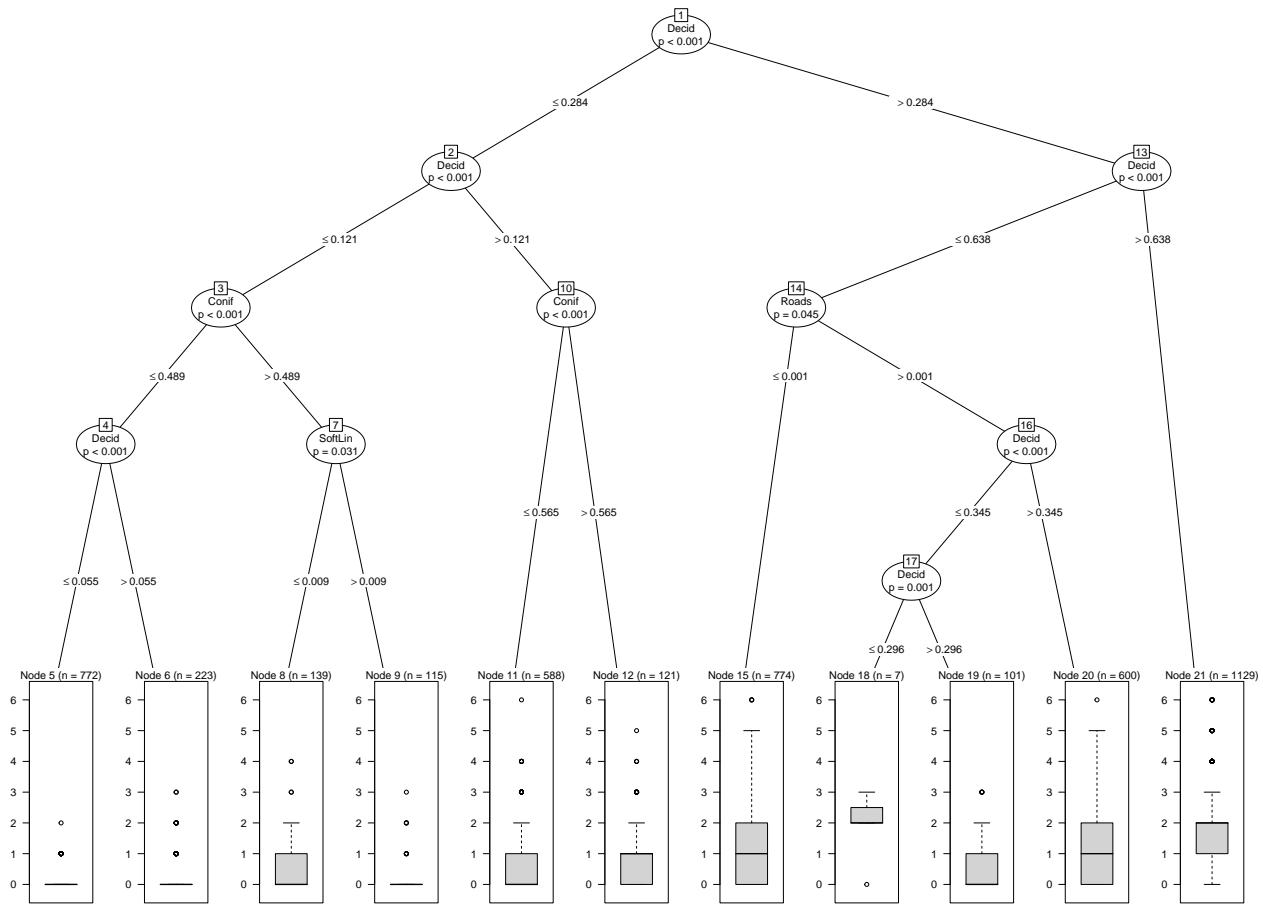
```
mP0$family$linkinv
```

```
## function (eta)
## pmax(exp(eta), .Machine$double.eps)
## <environment: namespace:stats>
```

3.4 Exploring covariates

Now, in the absence of info about species biology, we are looking at a blank page. How should we proceed? What kind of covariate (linear predictor) should we use? We can do a quick and dirty exploration to see what are the likely candidates. We use a regression tree (`ctree` refers to conditional trees). It is a nonparametric method based on binary recursive partitioning in a conditional inference framework. This means that binary splits are made along the predictor variables, and the explanatory power of the split is assessed based on how it maximized difference between the splits and minimized the difference inside the splits. It is called conditional, because every new split is conditional on the previous splits (difference can be measured in many different ways, think e.g. sum of squares). The stopping rule in this implementation is based on permutation tests (see `?ctree` or details and references).

```
mCT <- ctree(y ~ Open + Water + Agr + UrbInd + SoftLin + Roads +
  Decid + OpenWet + Conif + ConifWet, data=x)
plot(mCT)
```



The model can be seen as a piecewise constant regression, where each bucket (defined by the splits along the tree) yields a constant predictions based on the mean of the observations in the bucket. Any new data classified into the same bucket will get the same value. There is no notion of uncertainty (confidence or prediction intervals) in this nonparametric model.

But we see something very useful: the proportion of deciduous forest in the landscape seems to be vary influential for Ovenbird abundance.

3.5 Single covariate

With this new found knowledge, let's fit a parametric (Poisson) linear model using `Decid` as a predictor:

```
mP1 <- glm(y ~ Decid, data=x, family=poisson)
```

```
mean(x$y)
```

```
## [1] 0.8831
```

```
mean(fitted(mP0))
```

```
## [1] 0.8831
```

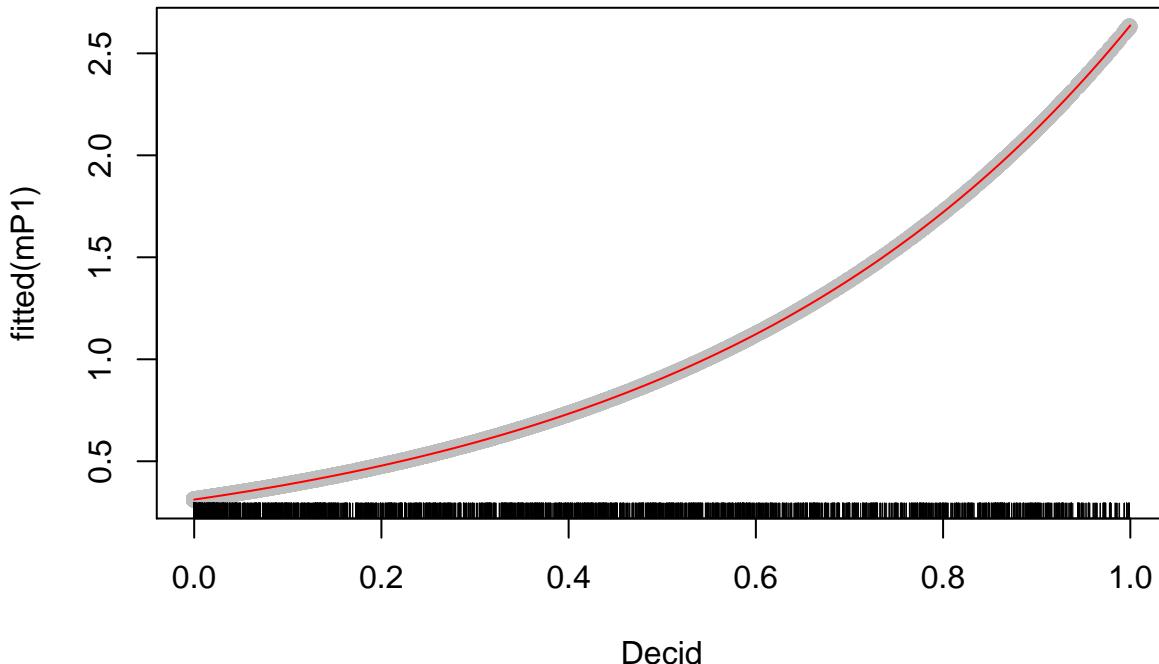
```
coef(mP1)
```

```
## (Intercept)      Decid
##       -1.164      2.134
```

Same as before, the mean of the observations equal the mean of the fitted values. But instead of only the intercept, now we have 2 coefficients estimated. Our linear predictor thus looks like: $\log(\lambda_i) = \beta_0 + \beta_1 x_{1i}$. This means that expected abundance is e^{β_0} where `Decid`=0, $e^{\beta_0}e^{\beta_1}$ where `Decid`=1, and $e^{\beta_0+\beta_1 x_1}$ in between.

The relationship can be visualized by plotting the fitted values against the predictor, or using the coefficients to make predictions using our formula:

```
dec <- seq(0, 1, 0.01)
lam <- exp(coef(mP1)[1] + coef(mP1)[2] * dec)
plot(fitted(mP1) ~ Decid, x, pch=19, col="grey")
lines(lam ~ dec, col=2)
rug(x$Decid)
```



The model summary tells us that residuals are not quite right (we would expect 0 median and symmetric tails), in line with residual deviance being much higher than residual degrees of freedom (these should be close if the Poisson assumption holds). But, the `Decid` effect is significant (meaning that the effect size is large compared to the standard error):

```
summary(mP1)
```

```
## 
## Call:
## glm(formula = y ~ Decid, family = poisson, data = x)
## 
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max 
## -2.291  -0.977  -0.790   0.469   4.197 
## 
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)    
## (Intercept) -1.1643    0.0352 -33.1   <2e-16 ***
## Decid       2.1338    0.0537  39.7   <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: 7424.8 on 4568 degrees of freedom
## Residual deviance: 5736.9 on 4567 degrees of freedom
## AIC: 10887
```

```
##  
## Number of Fisher Scoring iterations: 6
```

We can compare this model to the null (constant, intercept-only) model:

```
AIC(mP0, mP1)
```

```
BIC(mP0, mP1)
```

```
model.sel(mP0, mP1)
```

```
## Model selection table
```

```
## (Intercept) Decid df logLik AICc delta weight
```

```
## mP1 -1.1640 2.134 2 -5442 10887 0 1
```

```
## mP0 -0.1243 1 -6285 12573 1686 0
```

```
## Models ranked by AICc(x)
```

```
R2dev(mP0, mP1)
```

	R2	R2adj	Deviance	Dev0	DevR	df0	dfR	p_value			
## mP0	0.00	0.00	0.00	7424.78	7424.78	4568.00	4568.00	<2e-16 ***			
## mP1	0.23	0.23	1687.87	7424.78	5736.91	4568.00	4567.00	<2e-16 ***			
## ---											
## Signif. codes:	0	'***'	0.001	'**'	0.01	'*'	0.05	'. '	0.1	' '	1

AIC uses the negative log likelihood and the number of parameters as penalty. Smaller value indicate a model that is closer to the (unknowable) true model (caveat: this statement is true only asymptotically, i.e. it holds for very large sample sizes). For small samples, we often use BIC (more penalty for complex models when sample size is small), or AICc (as in MuMin::model.sel).

The other little table returned by R2dev shows deviance based (quasi) R^2 and adjusted R^2 for some GLM classes, just for the sake of completeness. The Chi-squared based test indicates good fit when the p -value is high (probability of being distributed according the Poisson).

None of these two models is a particularly good fit in terms of the parametric distribution. This, however does not mean these models are not useful for making inferential statements about ovenbirds. How useful these statements are, that is another question. Let's dive into confidence and prediction intervals a bit.

```
B <- 2000
```

```
alpha <- 0.05
```

```
xnew <- data.frame(Decid=seq(0, 1, 0.01))
```

```
CI0 <- predict_sim(mP0, xnew, interval="confidence", level=1-alpha, B=B)
```

```
PI0 <- predict_sim(mP0, xnew, interval="prediction", level=1-alpha, B=B)
```

```
CI1 <- predict_sim(mP1, xnew, interval="confidence", level=1-alpha, B=B)
```

```
PI1 <- predict_sim(mP1, xnew, interval="prediction", level=1-alpha, B=B)
```

```
## nominal coverage is 95%
```

```
sum(x$y %in% predict_sim(mP0, interval="prediction", level=1-alpha, B=B) [,c("lwr", "upr")])
```

```

## [1] 0.9619
sum(x$y %[]% predict_sim(mP1, interval="prediction", level=1-alpha, B=B) [,c("lwr", "upr")]

## [1] 0.9711

```

A model is said to have good *coverage* when the prediction intervals encompass the right amount of the observations. When the nominal level is 95% ($100 \times (1 - \alpha)$, where α is Type I. error rate), we expect 95% of the observations fall within the 95% *prediction interval*. The prediction interval includes the uncertainty around the coefficients (confidence intervals, uncertainty in $\hat{\lambda}$) and the stochasticity coming from the Poisson distribution ($Y_i \sim Poisson(\hat{\lambda})$).

The code above calculate the confidence and prediction intervals for the two models. We also compared the prediction intervals and the nomial levels, and those were quite close (ours being a bit more conservative), hinting that maybe the Poisson distributional assumption is not very bad after all, but we'll come back to this later.

Let's see our confidence and prediction intervals for the two models:

```

yj <- jitter(x$y, 0.5)

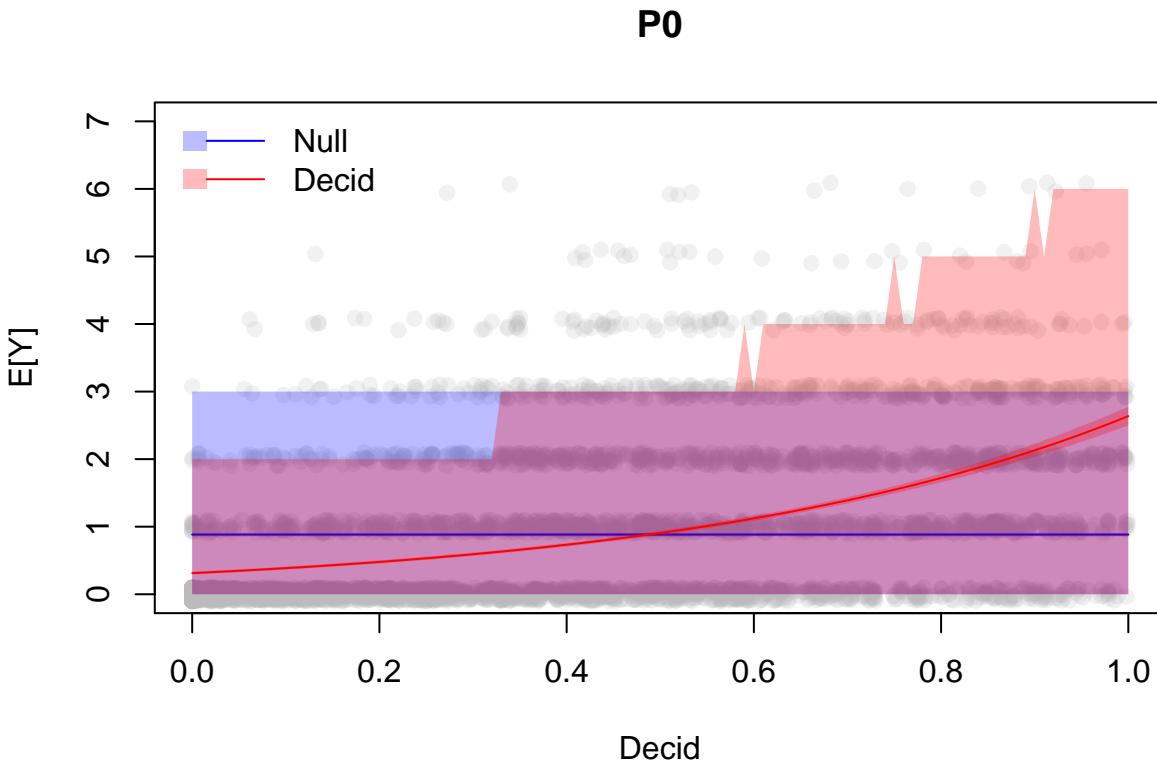
plot(yj ~ Decid, x, xlab="Decid", ylab="E[Y]",
      ylim=c(0, max(PI1$upr)+1), pch=19, col="#bbbbbb33", main="P0")

polygon(c(xnew$Decid, rev(xnew$Decid)),
        c(PI0$lwr, rev(PI0$upr)), border=NA, col="#0000ff44")
polygon(c(xnew$Decid, rev(xnew$Decid)),
        c(CI0$lwr, rev(CI0$upr)), border=NA, col="#0000ff44")
lines(CI0$fit ~ xnew$Decid, lty=1, col=4)

polygon(c(xnew$Decid, rev(xnew$Decid)),
        c(PI1$lwr, rev(PI1$upr)), border=NA, col="#ff000044")
polygon(c(xnew$Decid, rev(xnew$Decid)),
        c(CI1$lwr, rev(CI1$upr)), border=NA, col="#ff000044")
lines(CI1$fit ~ xnew$Decid, lty=1, col=2)

legend("topleft", bty="n", fill=c("#0000ff44", "#ff000044"), lty=1, col=c(4,2),
       border=NA, c("Null", "Decid"))

```

**Exercise**

What can we conclude from this plot?



Coverage is comparable, so what is the difference then?

Which model should I use for prediction and why? (Hint: look at the non overlapping regions.)

3.6 Additive model

Generalized additive models (GAMs) are semiparametric, meaning that parametric assumptions apply, but responses are modelled more flexibly.

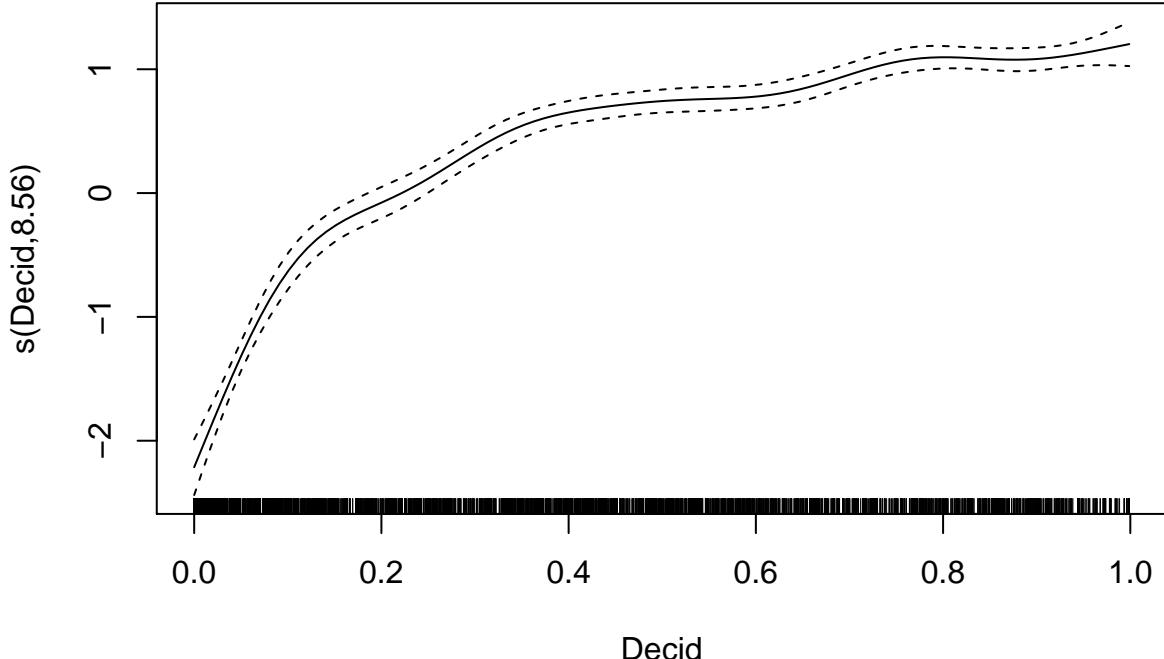
```
mGAM <- mgcv::gam(y ~ s(Decid), x, family=poisson)
summary(mGAM)
```

```
##
## Family: poisson
## Link function: log
##
## Formula:
## y ~ s(Decid)
##
```

```

## Parametric coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.5606     0.0283   -19.8   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Approximate significance of smooth terms:
##             edf Ref.df Chi.sq p-value
## s(Decid) 8.56    8.94  1193  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## R-sq.(adj) =  0.239    Deviance explained =  29%
## UBRE = 0.15808  Scale est. = 1          n = 4569
plot(mGAM)

```

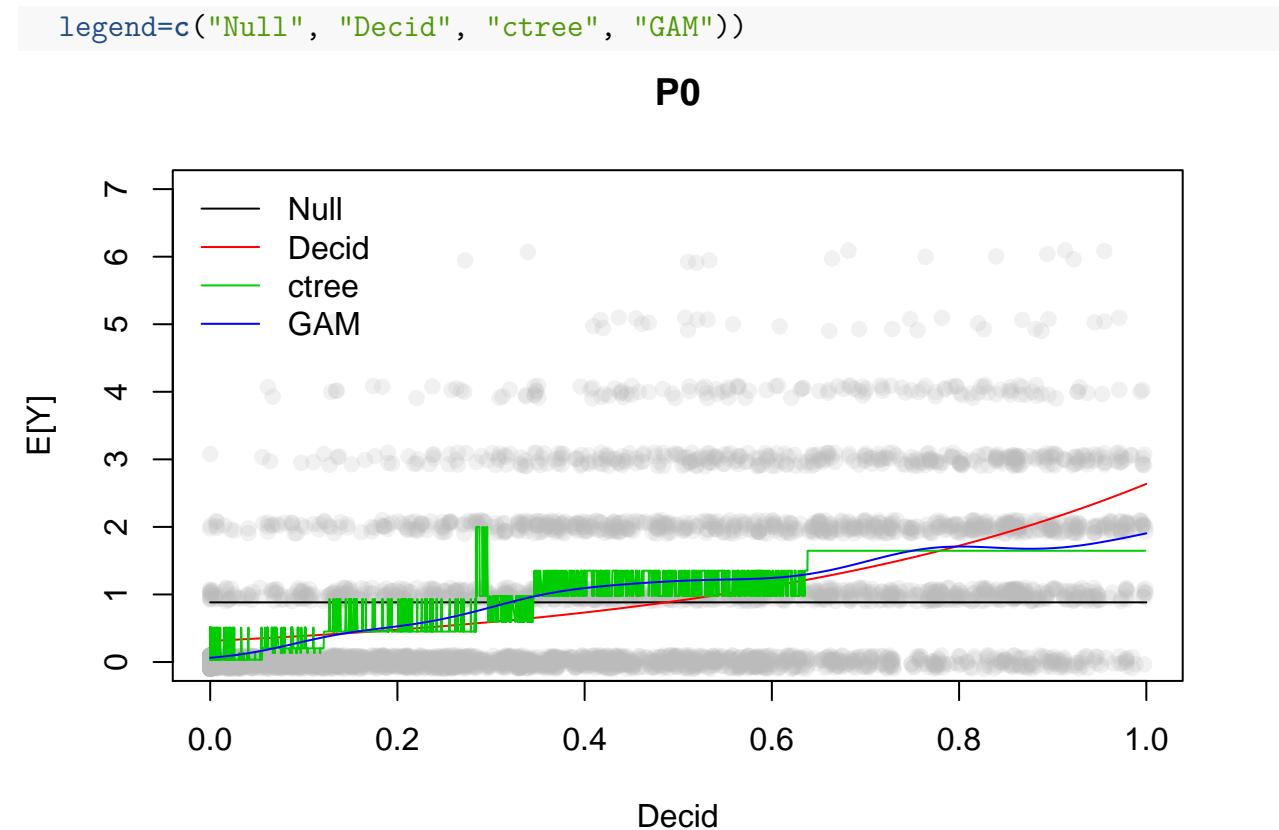


```

fitCT <- predict(mCT, x[order(x$Decid),])
fitGAM <- predict(mGAM, xnew, type="response")

plot(yj ~ Decid, x, xlab="Decid", ylab="E[Y]",
      ylim=c(0, max(PI1$upr)+1), pch=19, col="#bbbbbb33", main="P0")
lines(CI0$fit ~ xnew$Decid, lty=1, col=1)
lines(CI1$fit ~ xnew$Decid, lty=1, col=2)
lines(fitCT ~ x$Decid[order(x$Decid)], lty=1, col=3)
lines(fitGAM ~ xnew$Decid, lty=1, col=4)
legend("topleft", bty="n", lty=1, col=1:4,

```

**Exercise**

Play with GAM and other variables to understand response curves:

```
plot(mgcv::gam(y ~ s(variable_name)), data=x, family=poisson)
```

3.7 Nonlinear terms

We can use polynomial terms to approximate the GAM fit:

```
mP12 <- glm(y ~ Decid + I(Decid^2), data=x, family=poisson)
mP13 <- glm(y ~ Decid + I(Decid^2) + I(Decid^3), data=x, family=poisson)
mP14 <- glm(y ~ Decid + I(Decid^2) + I(Decid^3) + I(Decid^4), data=x, family=poisson)
model.sel(mP1, mP12, mP13, mP14, mGAM)

## Model selection table
##      (Int)    Dcd   Dcd^2   Dcd^3   Dcd^4 s(Dcd) class df logLik  AICc
## mGAM -0.5606                               +  gam  9  -5209 10438
## mP14 -2.6640 16.640 -38.60  41.470 -16.31      glm  5  -5215 10441
## mP13 -2.3910 11.400 -16.31   8.066      glm  4  -5226 10461
## mP12 -1.9240  6.259  -3.97      glm  3  -5269 10544
```

```

## mP1  -1.1640  2.134          glm   2  -5442 10887
##           delta weight
## mGAM    0.00   0.84
## mP14   3.31   0.16
## mP13  23.42   0.00
## mP12 106.04   0.00
## mP1  449.60   0.00
## Models ranked by AICc(x)

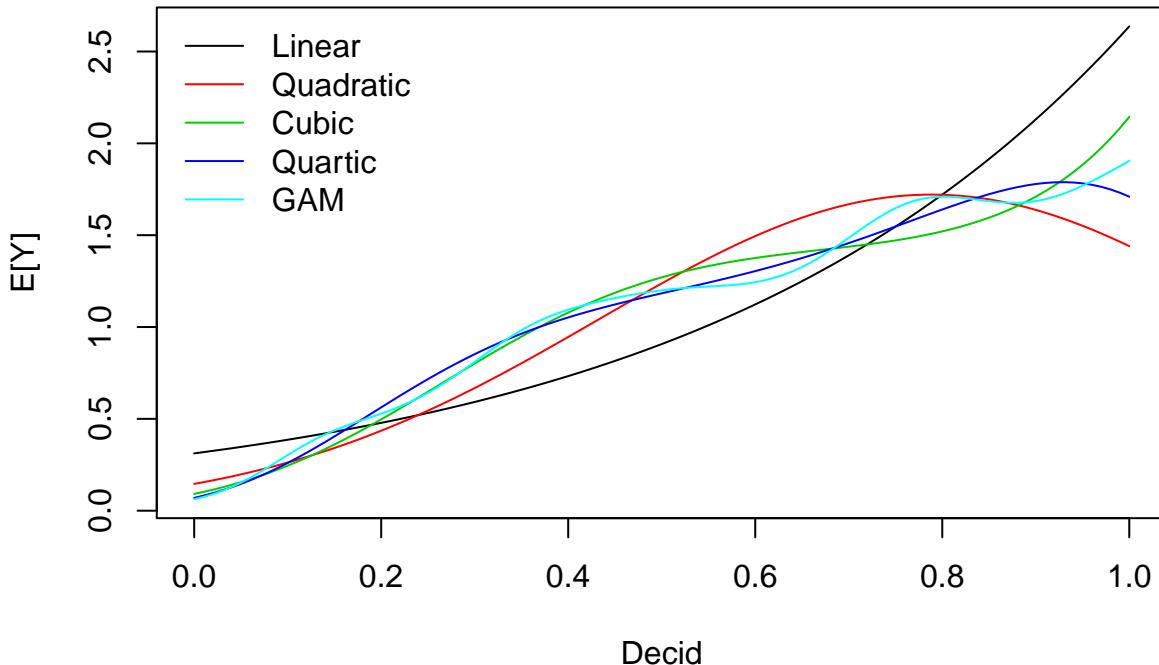
```

Not a surprise that the most complex model won. GAM was more complex than that.

```

pr <- cbind(
  predict(mP1, xnew, type="response"),
  predict(mP12, xnew, type="response"),
  predict(mP13, xnew, type="response"),
  predict(mP14, xnew, type="response"),
  fitGAM)
matplot(xnew$Decid, pr, lty=1, type="l",
  xlab="Decid", ylab="E[Y]")
legend("topleft", lty=1, col=1:5, bty="n",
  legend=c("Linear", "Quadratic", "Cubic", "Quartic", "GAM"))

```



Let's see how these affect our prediction intervals:

```

CI12 <- predict_sim(mP12, xnew, interval="confidence", level=1-alpha, B=B)
PI12 <- predict_sim(mP12, xnew, interval="prediction", level=1-alpha, B=B)
CI13 <- predict_sim(mP13, xnew, interval="confidence", level=1-alpha, B=B)
PI13 <- predict_sim(mP13, xnew, interval="prediction", level=1-alpha, B=B)

```

```

CI14 <- predict_sim(mP14, xnew, interval="confidence", level=1-alpha, B=B)
PI14 <- predict_sim(mP14, xnew, interval="prediction", level=1-alpha, B=B)

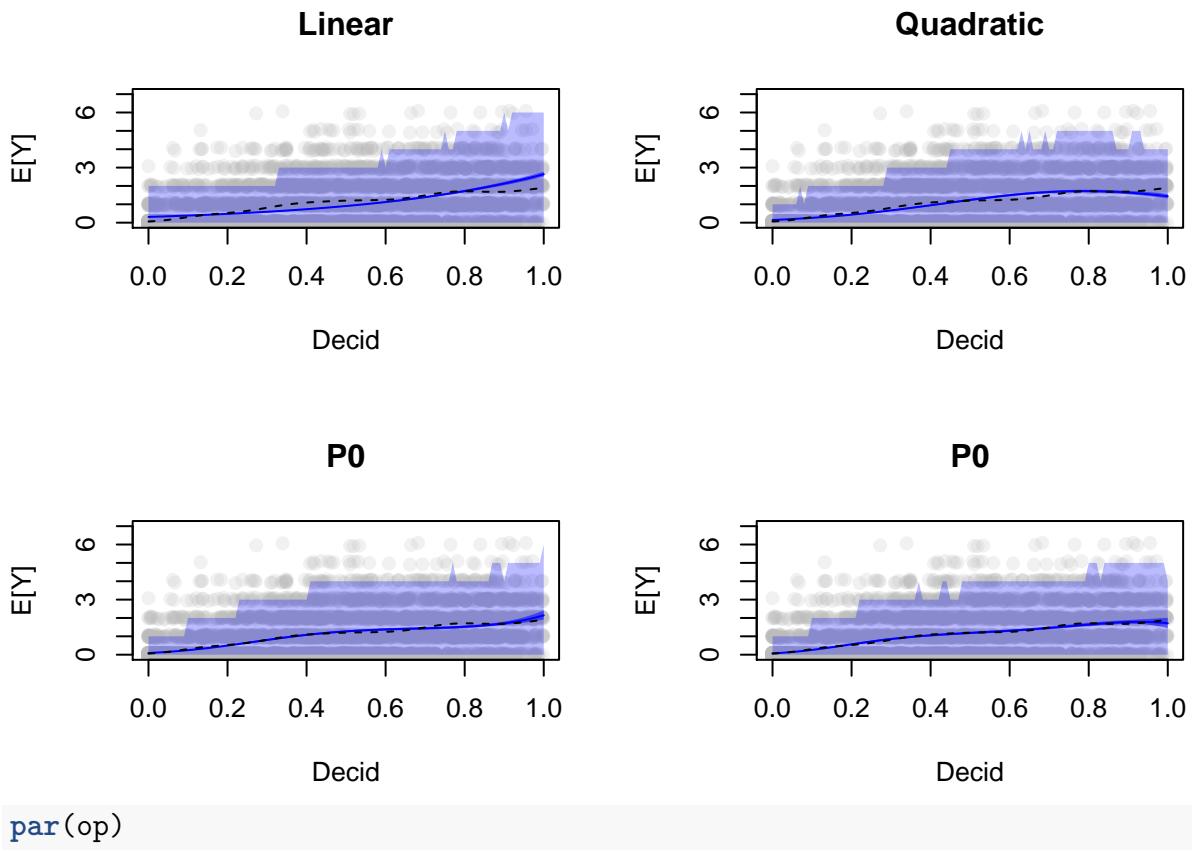
op <- par(mfrow=c(2,2))
plot(yj ~ Decid, x, xlab="Decid", ylab="E[Y]",
      ylim=c(0, max(PI1$upr)+1), pch=19, col="#bbbbbb33", main="Linear")
polygon(c(xnew$Decid, rev(xnew$Decid)),
        c(PI1$lwr, rev(PI1$upr)), border=NA, col="#0000ff44")
polygon(c(xnew$Decid, rev(xnew$Decid)),
        c(CI1$lwr, rev(CI1$upr)), border=NA, col="#0000ff88")
lines(CI1$fit ~ xnew$Decid, lty=1, col=4)
lines(fitGAM ~ xnew$Decid, lty=2, col=1)

plot(yj ~ Decid, x, xlab="Decid", ylab="E[Y]",
      ylim=c(0, max(PI1$upr)+1), pch=19, col="#bbbbbb33", main="Quadratic")
polygon(c(xnew$Decid, rev(xnew$Decid)),
        c(PI12$lwr, rev(PI12$upr)), border=NA, col="#0000ff44")
polygon(c(xnew$Decid, rev(xnew$Decid)),
        c(CI12$lwr, rev(CI12$upr)), border=NA, col="#0000ff88")
lines(CI12$fit ~ xnew$Decid, lty=1, col=4)
lines(fitGAM ~ xnew$Decid, lty=2, col=1)

plot(yj ~ Decid, x, xlab="Decid", ylab="E[Y]",
      ylim=c(0, max(PI1$upr)+1), pch=19, col="#bbbbbb33", main="PO")
polygon(c(xnew$Decid, rev(xnew$Decid)),
        c(PI13$lwr, rev(PI13$upr)), border=NA, col="#0000ff44")
polygon(c(xnew$Decid, rev(xnew$Decid)),
        c(CI13$lwr, rev(CI13$upr)), border=NA, col="#0000ff88")
lines(CI13$fit ~ xnew$Decid, lty=1, col=4)
lines(fitGAM ~ xnew$Decid, lty=2, col=1)

plot(yj ~ Decid, x, xlab="Decid", ylab="E[Y]",
      ylim=c(0, max(PI1$upr)+1), pch=19, col="#bbbbbb33", main="PO")
polygon(c(xnew$Decid, rev(xnew$Decid)),
        c(PI14$lwr, rev(PI14$upr)), border=NA, col="#0000ff44")
polygon(c(xnew$Decid, rev(xnew$Decid)),
        c(CI14$lwr, rev(CI14$upr)), border=NA, col="#0000ff88")
lines(CI14$fit ~ xnew$Decid, lty=1, col=4)
lines(fitGAM ~ xnew$Decid, lty=2, col=1)

```



3.8 Categorical variables

Categorical variables are expanded into a *model matrix* before estimation. The model matrix usually contains indicator variables for each level (value 1 when factor value equals a particular label, 0 otherwise) except for the *reference category* (check `relevel` if you want to change the reference category).

The estimate for the reference category comes from the intercept, the rest of the estimates are relative to the reference category. In the log-linear model example this means a ratio.

```
head(model.matrix(~DEC, x))
```

```
##           (Intercept) DEC
## CL10102          1   1
## CL10106          1   0
## CL10108          1   0
## CL10109          1   1
## CL10111          1   1
## CL10112          1   1
```

```
mP2 <- glm(y ~ DEC, data=x, family=poisson)
summary(mP2)
```

```

## 
## Call:
## glm(formula = y ~ DEC, family = poisson, data = x)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.691  -0.921  -0.921   0.449   4.543
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.8577    0.0308  -27.8 <2e-16 ***
## DEC          1.2156    0.0358   33.9 <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: 7424.8 on 4568 degrees of freedom
## Residual deviance: 6095.5 on 4567 degrees of freedom
## AIC: 11246
##
## Number of Fisher Scoring iterations: 6
coef(mP2)

```

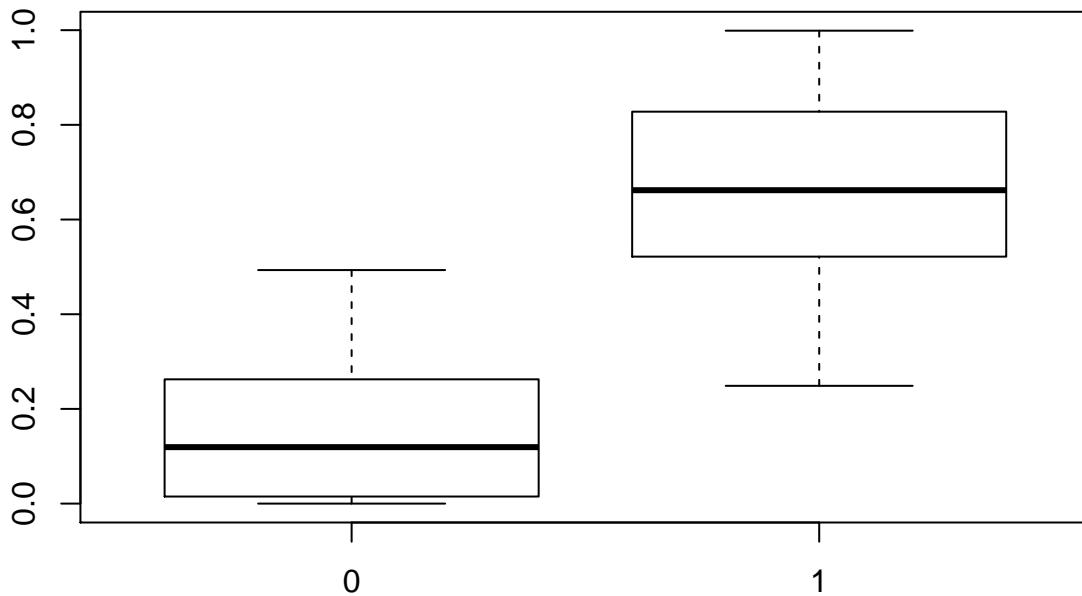
```

## (Intercept)      DEC
## -0.8577       1.2156

```

The estimate for a non-deciduous landscape is e^{β_0} , and it is $e^{\beta_0}e^{\beta_1}$ for deciduous landscapes. Of course such binary classification at the landscape (1 km^2) level doesn't really makes sense for various reasons:

```
boxplot(Decid ~ DEC, x)
```



```
model.sel(mP1, mP2)
```

```
## Model selection table
## (Intercept) Decid DEC df logLik AICc delta weight
## mP1 -1.1640 2.134      2 -5442 10887  0.0     1
## mP2 -0.8577 1.216      2 -5621 11246 358.6    0
## Models ranked by AICc(x)
```

```
R2dev(mP1, mP2)
```

```
##          R2      R2adj Deviance      Dev0      DevR      df0      dfR p_value
## mP1  0.23  0.23 1687.87 7424.78 5736.91 4568.00 4567.00 <2e-16 ***
## mP2  0.18  0.18 1329.23 7424.78 6095.55 4568.00 4567.00 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Having estimates for each land cover type improves the model, but the model using continuous variable is still better

```
mP3 <- glm(y ~ HAB, data=x, family=poisson)
summary(mP3)
```

```
##
## Call:
## glm(formula = y ~ HAB, family = poisson, data = x)
##
## Deviance Residuals:
##      Min      1Q  Median      3Q      Max
## -1.691  -0.873  -0.817   0.449   4.832
##
## Coefficients:
```

```

##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.386     0.577  -2.40  0.0163 *
## HABWater    1.030     0.690   1.49  0.1357
## HABAgr      0.693     0.913   0.76  0.4477
## HABUrbInd   0.134     0.764   0.17  0.8612
## HABRoads   -10.916    201.285  -0.05  0.9567
## HABDecid    1.744     0.578   3.02  0.0025 **
## HABOpenWet   0.422     0.591   0.71  0.4755
## HABConif     0.913     0.579   1.58  0.1150
## HABConifWet  0.288     0.579   0.50  0.6185
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
## Null deviance: 7424.8 on 4568 degrees of freedom
## Residual deviance: 5997.2 on 4560 degrees of freedom
## AIC: 11161
##
## Number of Fisher Scoring iterations: 10
model.sel(mP1, mP2, mP3)

## Model selection table
##          (Intrc) Decid DEC HAB df logLik  AICc delta weight
## mP1 -1.1640  2.134           2  -5442 10887  0.0      1
## mP3 -1.3860           + 9  -5572 11162 274.4      0
## mP2 -0.8577  1.216           2  -5621 11246 358.6      0
## Models ranked by AICc(x)

R2dev(mP1, mP2, mP3)

##          R2  R2adj Deviance    Dev0    DevR      df0      dfR p_value
## mP1  0.23  0.23 1687.87 7424.78 5736.91 4568.00 4567.00 <2e-16 ***
## mP2  0.18  0.18 1329.23 7424.78 6095.55 4568.00 4567.00 <2e-16 ***
## mP3  0.19  0.19 1427.55 7424.78 5997.23 4568.00 4560.00 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

The prediction in this case would look like: $\log(\lambda_i) = \beta_0 + \sum_{j=1}^{k-1} \beta_j x_{ji}$, where we have k factor levels (and $k - 1$ indicator variables besides the intercept).

Here is a general way of calculating fitted values or making predictions based on the design matrix (X) and the coefficients (b) (column ordering in X must match the elements in b) given a parametric log-linear model object and data frame df :

```

b <- coef(object)
X <- model.matrix(formula(object), df)

```

```
exp(X %*% b)
```

3.9 Multiple main effects

We can keep adding variables to the model in a forwards-selection fashion. `add1` adds variables one at a time, selecting from the scope defined by the formula:

```
scope <- as.formula(paste("~ FOR + WET + AHF +", paste(cn, collapse="+")))
tmp <- add1(mP1, scope)
tmp$AIC_drop <- tmp$AIC - tmp$AIC[1] # current model
tmp[order(tmp$AIC),]
```

```
## Single term additions
##
## Model:
## y ~ Decid
##          Df Deviance   AIC AIC_drop
## ConifWet  1    5638 10791    -96.5
## Conif     1    5685 10838    -49.4
## WET       1    5687 10839    -48.1
## Water     1    5721 10873    -13.7
## FOR       1    5724 10876    -11.0
## OpenWet   1    5728 10880    -6.9
## Open      1    5730 10882    -4.7
## Roads     1    5733 10885    -1.9
## AHF       1    5734 10886    -0.7
## <none>    5737 10887    0.0
## Agr       1    5736 10888    1.2
## UrbInd   1    5736 10889    1.5
## SoftLin   1    5737 10889    1.6
```

It looks like `ConifWet` is the best covariate to add next because it leads to the biggest drop in AIC, and both effects are significant.

```
mP4 <- glm(y ~ Decid + ConifWet, data=x, family=poisson)
summary(mP4)
```

```
##
## Call:
## glm(formula = y ~ Decid + ConifWet, family = poisson, data = x)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -2.237   -0.996   -0.679    0.447    4.439
```

```

## 
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.7014    0.0556 -12.61  <2e-16 ***
## Decid       1.6224    0.0719  22.57  <2e-16 ***
## ConifWet    -0.9785    0.0993  -9.86  <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: 7424.8 on 4568 degrees of freedom
## Residual deviance: 5638.4 on 4566 degrees of freedom
## AIC: 10791
## 
## Number of Fisher Scoring iterations: 6

```

`drop1` is the function opposite of `add1`, it assesses which term should be dropped from a more saturated model:

```

formula_all <- y ~ Open + Agr + UrbInd + SoftLin + Roads +
Decid + OpenWet + Conif + ConifWet +
OvernightRain + TSSR + DAY + Longitude + Latitude

tmp <- drop1(glm(formula_all, data=x, family=poisson))
tmp$AIC_drop <- tmp$AIC - tmp$AIC[1] # current model
tmp[order(tmp$AIC),]

```

```

## Single term deletions
## 
## Model:
## y ~ Open + Agr + UrbInd + SoftLin + Roads + Decid + OpenWet +
##     Conif + ConifWet + OvernightRain + TSSR + DAY + Longitude +
##     Latitude
##          Df Deviance   AIC AIC_drop
## OvernightRain  1    5500 10674    -2.0
## Roads          1    5500 10674    -1.9
## SoftLin        1    5500 10675    -1.6
## Agr            1    5501 10675    -1.4
## <none>          5500 10676    0.0
## Decid          1    5505 10679    3.0
## OpenWet        1    5505 10679    3.1
## Conif          1    5508 10682    6.0
## UrbInd         1    5511 10685    8.7
## Longitude      1    5519 10693   16.5
## TSSR           1    5524 10698   21.8

```

```

## ConifWet      1    5528 10703     26.4
## DAY          1    5529 10703     26.7
## Open         1    5531 10705     28.7
## Latitude     1    5580 10754     78.2

```

The `step` function can be used to automatically select the best model based on adding/dropping terms:

```

mPstep <- step(glm(formula_all, data=x, family=poisson),
  trace=0) # use trace=1 to see all the steps
summary(mPstep)

```

```

##
## Call:
## glm(formula = y ~ Open + UrbInd + Decid + OpenWet + Conif + ConifWet +
##       TSSR + DAY + Longitude + Latitude, family = poisson, data = x)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q      Max
## -2.763  -0.986  -0.674   0.451   4.624
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -5.88293   1.30223  -4.52  6.3e-06 ***
## Open        -3.47428   0.65867  -5.27  1.3e-07 ***
## UrbInd      -1.66883   0.54216  -3.08  0.00208 **
## Decid        0.83372   0.25957   3.21  0.00132 **
## OpenWet      -0.74076   0.30238  -2.45  0.01430 *
## Conif        -0.88558   0.26566  -3.33  0.00086 ***
## ConifWet     -1.89423   0.27170  -6.97  3.1e-12 ***
## TSSR        -1.23416   0.24984  -4.94  7.8e-07 ***
## DAY         -2.87970   0.52686  -5.47  4.6e-08 ***
## Longitude    0.03831   0.00877   4.37  1.2e-05 ***
## Latitude     0.20930   0.02309   9.06 < 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: 7424.8 on 4568 degrees of freedom
## Residual deviance: 5501.1 on 4558 degrees of freedom
## AIC: 10669
##
## Number of Fisher Scoring iterations: 6

```

3.10 Interaction

When we consider interactions between two variables (say x_1 and x_2), we really referring to adding another variable to the model matrix that is a product of the two variables ($x_{12} = x_1x_2$):

```
head(model.matrix(~x1 * x2, data.frame(x1=1:4, x2=10:7)))
```

```
##   (Intercept) x1 x2 x1:x2
## 1           1  1 10   10
## 2           1  2  9   18
## 3           1  3  8   24
## 4           1  4  7   28
```

Let's consider interaction between our two predictors from before:

```
mP5 <- glm(y ~ Decid * ConifWet, data=x, family=poisson)
summary(mP5)
```

```
##
## Call:
## glm(formula = y ~ Decid * ConifWet, family = poisson, data = x)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -2.081  -1.022  -0.484   0.374   4.321
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.5604    0.0566  -9.9   <2e-16 ***
## Decid       1.2125    0.0782   15.5   <2e-16 ***
## ConifWet    -2.3124    0.1490  -15.5   <2e-16 ***
## Decid:ConifWet 5.3461    0.3566   15.0   <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: 7424.8 on 4568 degrees of freedom
## Residual deviance: 5395.2 on 4565 degrees of freedom
## AIC: 10549
##
## Number of Fisher Scoring iterations: 6
model.sel(mP0, mP1, mP4, mP5)

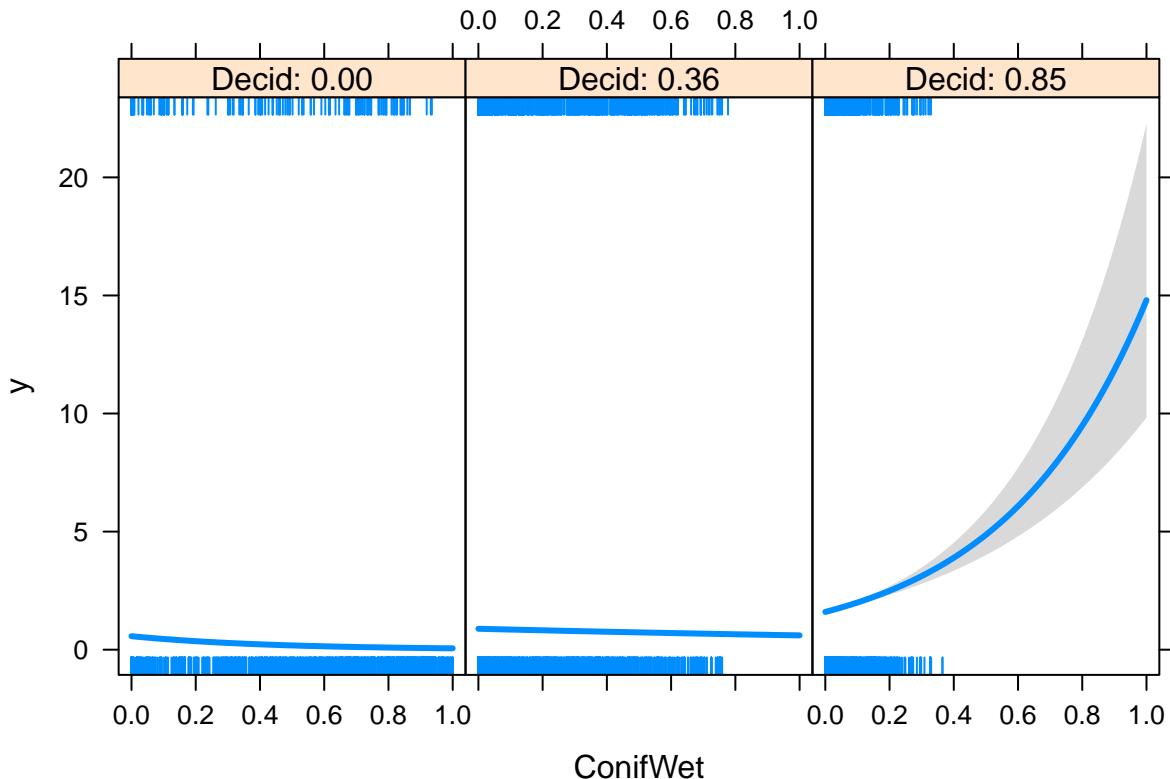
## Model selection table
```

```
##          (Int)     Dcd      CnW CnW:Dcd df logLik  AICc delta weight
## mP5 -0.5604 1.213 -2.3120    5.346  4 -5271 10549   0.0      1
## mP4 -0.7014 1.622 -0.9785           3 -5392 10791 241.2      0
## mP1 -1.1640 2.134           2 -5442 10887 337.7      0
## mP0 -0.1243           1 -6285 12573 2023.6      0
## Models ranked by AICc(x)
```

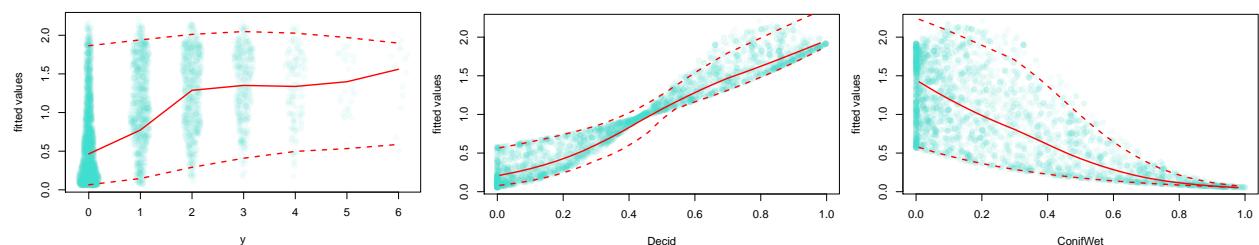
The model with the interaction is best supported, but how do we make sense of this relationship? We can't easily visualize it in a single plot. We can either

1. fix all variables (at their mean/meadian) and see how the response is changing along a single variable: this is called a *conditional* effect (conditional on fixing other variables), this is what `visreg::visreg` does;
2. or plot the fitted values against the predictor variables, this is called a *marginal* effects, and this is what `ResourceSelection::mep` does.

```
visreg(mP5, scale="response", xvar="ConifWet", by="Decid")
```

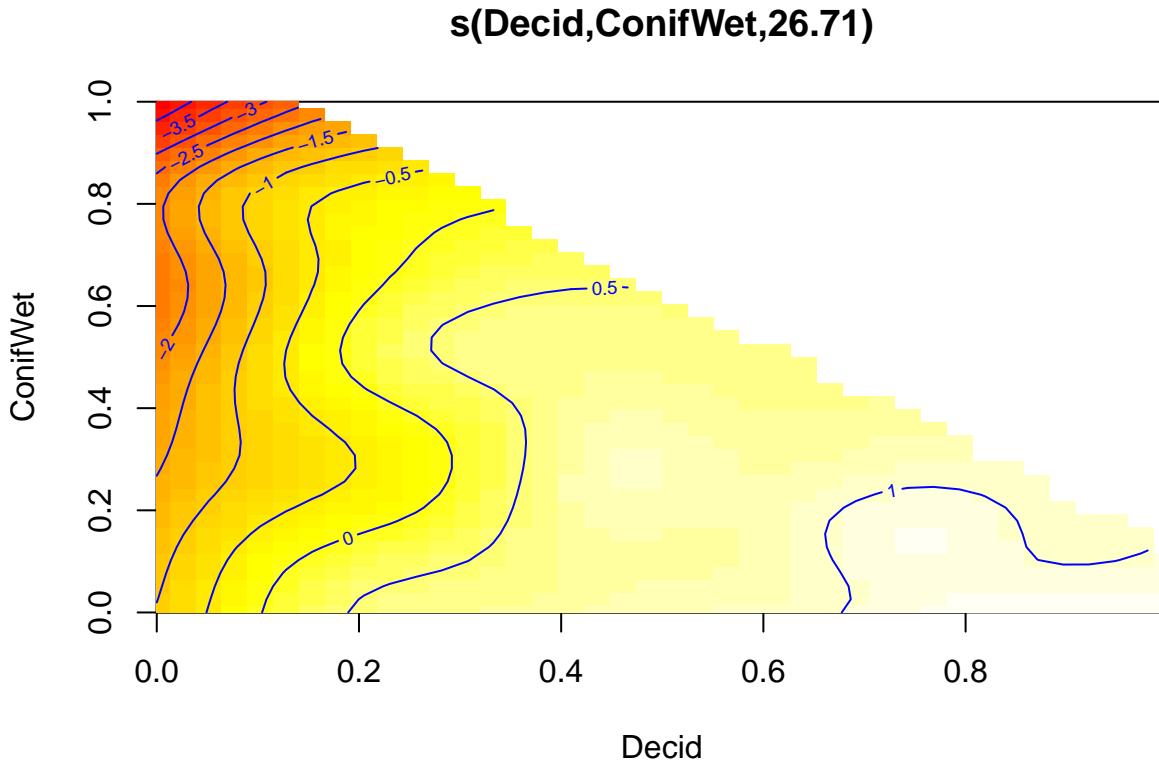


```
mep(mP5)
```



Let's use GAM to fit a bivariate spline:

```
mGAM2 <- mgcv:::gam(y ~ s(Decid, ConifWet), data=x, family=poisson)
plot(mGAM2, scheme=2, rug=FALSE)
```



Final battle of Poisson models:

```
model.sel(mP0, mP1, mP12, mP13, mP14, mP2, mP3, mP4, mP5, mGAM, mGAM2)
```

```
## Model selection table
##          (Int)    Dcd   Dcd^2   Dcd^3   Dcd^4    DEC HAB      CnW CnW:Dcd s(Dcd)
## mGAM2 -0.6251
## mGAM  -0.5606
## mP14  -2.6640 16.640 -38.60 41.470 -16.31
## mP13  -2.3910 11.400 -16.31  8.066
## mP12  -1.9240  6.259  -3.97
## mP5   -0.5604  1.213
## mP4   -0.7014  1.622
## mP1   -1.1640  2.134
## mP3   -1.3860
## mP2   -0.8577
## mP0   -0.1243
##          s(Dcd,CnW) class df logLik AICc   delta weight
## mGAM2      +  gam 27 -5160 10376     0.00     1
## mGAM        gam  9 -5209 10438    61.11     0
## mP14        glm  5 -5215 10441    64.42     0
```

```

## mP13          glm  4  -5226 10461   84.53    0
## mP12          glm  3  -5269 10544  167.14    0
## mP5           glm  4  -5271 10549  172.99    0
## mP4           glm  3  -5392 10791  414.18    0
## mP1           glm  2  -5442 10887  510.71    0
## mP3           glm  9  -5572 11162  785.06    0
## mP2           glm  2  -5621 11246  869.35    0
## mP0           glm  1  -6285 12573 2196.58    0
## Models ranked by AICc(x)

```

```
R2dev(mP0, mP1, mP12, mP13, mP14, mP2, mP3, mP4, mP5, mGAM, mGAM2)
```

##	R2	R2adj	Deviance	Dev0	DevR	df0	dfR	p_value			
## mP0	0.00	0.00	0.00	7424.78	7424.78	4568.00	4568.00	< 2e-16 ***			
## mP1	0.23	0.23	1687.87	7424.78	5736.91	4568.00	4567.00	< 2e-16 ***			
## mP12	0.27	0.27	2033.44	7424.78	5391.34	4568.00	4566.00	< 2e-16 ***			
## mP13	0.29	0.28	2118.06	7424.78	5306.72	4568.00	4565.00	7.6e-14 ***			
## mP14	0.29	0.29	2140.17	7424.78	5284.61	4568.00	4564.00	3.4e-13 ***			
## mP2	0.18	0.18	1329.23	7424.78	6095.55	4568.00	4567.00	< 2e-16 ***			
## mP3	0.19	0.19	1427.55	7424.78	5997.23	4568.00	4560.00	< 2e-16 ***			
## mP4	0.24	0.24	1786.40	7424.78	5638.38	4568.00	4566.00	< 2e-16 ***			
## mP5	0.27	0.27	2029.60	7424.78	5395.18	4568.00	4565.00	< 2e-16 ***			
## mGAM	0.29	0.29	2152.63	7424.78	5272.15	4568.00	4559.00	5.5e-13 ***			
## mGAM2	0.30	0.30	2250.35	7424.78	5174.43	4568.00	4539.00	8.4e-11 ***			
## ---											
## Signif. codes:	0	'***'	0.001	'**'	0.01	'*'	0.05	'. '	0.1	' '	1

Of course, the most complex model wins but the Chi-square test is still significant (indicating lack of fit). Let's try different error distribution.

3.11 Different error distributions

We will use the 2-variable model with interaction:

```
mP <- glm(y ~ Decid * ConifWet, data=x, family=poisson)
```

Let us try the Negative Binomial distribution first. This distribution is related to Binomial experiments (number of trials required to get a fixed number of successes given a binomial probability). It can also be derived as a mixture of Poisson and Gamma distributions (see [Wikipedia](#)), which is a kind of hierarchical model. In this case, the Gamma distribution acts as an i.i.d. random effect for the intercept: $Y_i \sim Poisson(\lambda_i)$, $\lambda_i \sim Gamma(e^{\beta_0 + \beta_1 x_{1i}}, \gamma)$, where γ is the Gamma variance.

The Negative Binomial variance (using the parametrization common in R functions) is a function of the mean and the scale: $V(\mu) = \mu + \mu^2/\theta$.

```

mNB <- glm.nb(y ~ Decid * ConifWet, data=x)
summary(mNB)

##
## Call:
## glm.nb(formula = y ~ Decid * ConifWet, data = x, init.theta = 3.5900635,
##         link = log)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.860  -0.985  -0.451   0.317   3.803
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.5905    0.0630  -9.38   <2e-16 ***
## Decid        1.2459    0.0892  13.97   <2e-16 ***
## ConifWet     -2.3545    0.1605 -14.67   <2e-16 ***
## Decid:ConifWet 5.6945    0.4009  14.20   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(3.59) family taken to be 1)
##
## Null deviance: 6089.3 on 4568 degrees of freedom
## Residual deviance: 4387.7 on 4565 degrees of freedom
## AIC: 10440
##
## Number of Fisher Scoring iterations: 1
##
##
##          Theta:  3.590
##          Std. Err.:  0.425
##
## 2 x log-likelihood:  -10430.448

```

Next, we look at zero-inflated models. In this case, the mixture distribution is a Bernoulli distribution and a count distribution (Poisson or Negative Binomial, for example). The 0's can come from both the zero and the count distributions, whereas the >0 values can only come from the count distribution: $A_i \sim Bernoulli(\varphi)$, $Y_i \sim Poisson(A_i\lambda_i)$.

The zero part of the zero-inflated models are often parametrized as probability of zero ($1 - \varphi$), as in the `pscl::zeroinfl` function:

```

## Zero-inflated Poisson
mZIP <- zeroinfl(y ~ Decid * ConifWet | 1, x, dist="poisson")
summary(mZIP)

```

```

## 
## Call:
## zeroinfl(formula = y ~ Decid * ConifWet | 1, data = x, dist = "poisson")
##
## Pearson residuals:
##    Min     1Q Median     3Q    Max
## -1.218 -0.700 -0.339  0.378  8.951
##
## Count model coefficients (poisson with log link):
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.3241    0.0651  -4.98  6.5e-07 ***
## Decid        1.0700    0.0860   12.44 < 2e-16 ***
## ConifWet     -2.4407    0.1564  -15.60 < 2e-16 ***
## Decid:ConifWet 5.9373    0.3840   15.46 < 2e-16 ***
##
## Zero-inflation model coefficients (binomial with logit link):
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.613     0.103   -15.6 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of iterations in BFGS optimization: 12
## Log-likelihood: -5.21e+03 on 5 Df
## Zero-inflated Negative Binomial
mZINB <- zeroinfl(y ~ Decid * ConifWet | 1, x, dist="negbin")
summary(mZINB)

```

```

## 
## Call:
## zeroinfl(formula = y ~ Decid * ConifWet | 1, data = x, dist = "negbin")
##
## Pearson residuals:
##    Min     1Q Median     3Q    Max
## -1.190 -0.689 -0.338  0.361  8.956
##
## Count model coefficients (negbin with log link):
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.3873    0.0732  -5.29  1.2e-07 ***
## Decid        1.1195    0.0911   12.29 < 2e-16 ***
## ConifWet     -2.4230    0.1589  -15.25 < 2e-16 ***
## Decid:ConifWet 5.9227    0.3963   14.94 < 2e-16 ***
## Log(theta)    2.6504    0.5305    5.00  5.9e-07 ***
##
## Zero-inflation model coefficients (binomial with logit link):

```

```

##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.861      0.193   -9.64 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Theta = 14.159
## Number of iterations in BFGS optimization: 22
## Log-likelihood: -5.2e+03 on 6 Df

```

Now we compare the four different parametric models:

```
AIC(mP, mNB, mZIP, mZINB)
```

Our best model is the Zero-inflated Negative Binomial. The probability of observing a zero as part of the zero distribution is back transformed from the zero coefficient using the inverse logit function:

```
unname(plogis(coef(mZINB), "zero")) # P of 0
```

```
## [1] 0.1346
```

Now we use the scale parameter to visualize the variance functions for the Negative Binomial models (the 1:1 line is the Poisson model):

```
mNB$theta
```

```
## [1] 3.59
```

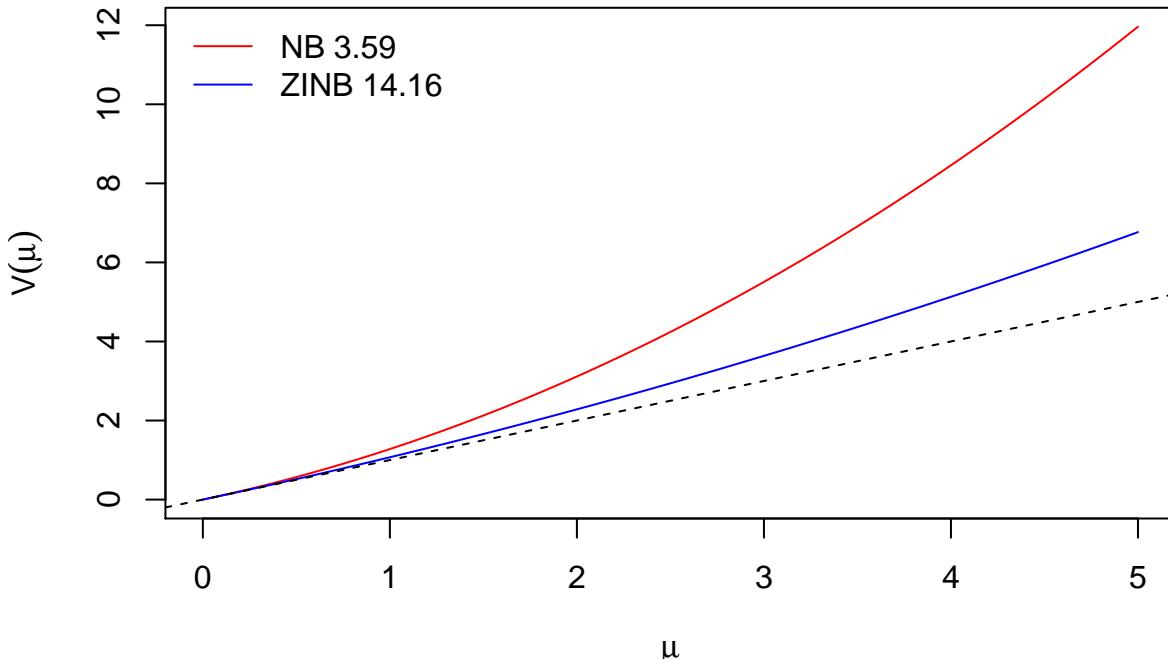
```
mZINB$theta
```

```
## [1] 14.16
```

```

mu <- seq(0, 5, 0.01)
plot(mu, mu + mu^2/mNB$theta, type="l", col=2,
     ylab=expression(V(mu)), xlab=expression(mu))
lines(mu, mu + mu^2/mZINB$theta, type="l", col=4)
abline(0,1, lty=2)
legend("topleft", bty="n", lty=1, col=c(2,4),
       legend=paste(c("NB", "ZINB"), round(c(mNB$theta, mZINB$theta), 2)))

```



Exercise



How can we interpret these different kinds of overdispersion (zero-inflation and higher than Poisson variance)?

What are some of the biological mechanisms that can contribute to the overdispersion?

It is also common practice to consider generalized linear mixed models (GLMMs) for count data. These mixed models are usually considered as Poisson-Lognormal mixtures. The simplest, so called i.i.d., case is similar to the Negative Binomial, but instead of Gamma, we have Lognormal distribution: $Y_i \sim Poisson(\lambda_i)$, $\log(\lambda_i) = \beta_0 + \beta_1 x_{1i} + \epsilon_i$, $\epsilon_i \sim Normal(0, \sigma^2)$, where σ^2 is the Lognormal variance on the log scale.

We can use the `lme4::glmer` function: use `SiteID` as random effect (we have exactly n random effects).

```
mPLN1 <- glmer(y ~ Decid * ConifWet + (1 | SiteID), data=x, family=poisson)
summary(mPLN1)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson  ( log )
## Formula: y ~ Decid * ConifWet + (1 | SiteID)
## Data: x
##
##      AIC      BIC  logLik deviance df.resid
##    10423    10455    -5206     10413      4564
```

```

## 
## Scaled residuals:
##   Min    1Q Median    3Q   Max
## -1.150 -0.629 -0.288  0.418  5.469
## 
## Random effects:
##   Groups Name        Variance Std.Dev.
##   SiteID (Intercept) 0.294     0.542
##   Number of obs: 4569, groups: SiteID, 4569
## 
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.7518    0.0675 -11.1   <2e-16 ***
## Decid       1.2847    0.0920   14.0   <2e-16 ***
## ConifWet    -2.3380    0.1625  -14.4   <2e-16 ***
## Decid:ConifWet 5.6326    0.4118   13.7   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Correlation of Fixed Effects:
##          (Intr) Decid  ConfWt
## Decid    -0.895
## ConifWet  -0.622  0.644
## Decid:CnfWt 0.176 -0.379 -0.700

```



Note

The number of unknowns we have to somehow estimate is now more than the number of observations we have. How is that possible?

Alternatively, we can use `SurveyArea` as a grouping variable. We have now $m < n$ random effects, and survey areas can be seen as larger landscapes within which the sites are clustered: $Y_{ij} \sim Poisson(\lambda_{ij})$, $\log(\lambda_{ij}) = \beta_0 + \beta_1 x_{1ij} + \epsilon_i$, $\epsilon_i \sim Normal(0, \sigma^2)$. The index i ($i = 1, \dots, m$) defines the cluster (survey area), the j ($j = 1, \dots, n_i$) defines the sites within survey area i ($n = \sum_{i=1}^m n_i$).

```

mPLN2 <- glmer(y ~ Decid * ConifWet + (1 | SurveyArea), data=x, family=poisson)
summary(mPLN2)

```

```

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: y ~ Decid * ConifWet + (1 | SurveyArea)
## Data: x
## 
```

```

##      AIC      BIC logLik deviance df.resid
## 10021    10053   -5006     10011      4564
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -1.739 -0.643 -0.320  0.355  6.535
##
## Random effects:
## Groups   Name        Variance Std.Dev.
## SurveyArea (Intercept) 0.295    0.543
## Number of obs: 4569, groups: SurveyArea, 271
##
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.7459    0.0783 -9.53   <2e-16 ***
## Decid       1.1967    0.0984 12.16   <2e-16 ***
## ConifWet    -2.3213    0.1686 -13.77   <2e-16 ***
## Decid:ConifWet 5.5346    0.3977 13.92   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) Decid  ConfWt
## Decid   -0.808
## ConifWet -0.610  0.628
## Decid:CnfWt 0.162 -0.325 -0.670

```

In the battle of distributions (keeping the linear predictor part the same) the clustered GLMM was best supported:

```

tmp <- AIC(mP, mNB, mZIP, mZINB, mPLN1, mPLN2)
tmp$delta_AIC <- tmp$AIC - min(tmp$AIC)
tmp[order(tmp$AIC),]

```



Exercise

What are some of the biological mechanisms that can lead to the clustered GLMM being the best model?

3.12 Count duration effects

Let's change gears a bit now, and steer closer to the main focus of this book. We want to account for methodological differences among samples. One aspect of methodologies involve

variation in total counting duration. We'll now inspect what that does to our observations.

First, we create a list of matrices where counts are tabulated by surveys and time intervals for each species:

```
ydur <- Xtab(~ SiteID + Dur + SpeciesID ,
  josm$counts[josm$counts$DetectType1 != "V",])
```

We use the same species (`spp`) as before and create a data frame indluring the cumulative counts during 3, 5, and 10 minutes:

```
y <- as.matrix(ydur[[spp]])
head(y)

##          0-3min 3-5min 5-10min
## CL10102      3      0      0
## CL10106      0      0      0
## CL10108      0      0      0
## CL10109      2      0      1
## CL10111      2      0      0
## CL10112      2      0      0

colMeans(y) # mean count of new individuals

##  0-3min 3-5min 5-10min
## 0.67367 0.09346 0.11600

cumsum(colMeans(y)) # cumulative counts

##  0-3min 3-5min 5-10min
## 0.6737 0.7671 0.8831

x <- data.frame(
  josm$surveys,
  y3=y[, "0-3min"],
  y5=y[, "0-3min"]+y[, "3-5min"],
  y10=rowSums(y))

table(x$y3)

## 
##   0    1    2    3    4    5    6
## 2768  922  576  226   61   14    2

table(x$y5)

## 
##   0    1    2    3    4    5    6
## 2643  894  632  285   87   24    4
```

```
table(x$y10)
```

```
##  
##    0     1     2     3     4     5     6  
## 2493  883  656  363  132   29   13
```

If we fit single-predictor GLMs to these 3 responses, we get different fitted values, consistent with our mean counts:

```
m3 <- glm(y3 ~ Decid, data=x, family=poisson)  
m5 <- glm(y5 ~ Decid, data=x, family=poisson)  
m10 <- glm(y10 ~ Decid, data=x, family=poisson)  
mean(fitted(m3))
```

```
## [1] 0.6737
```

```
mean(fitted(m5))
```

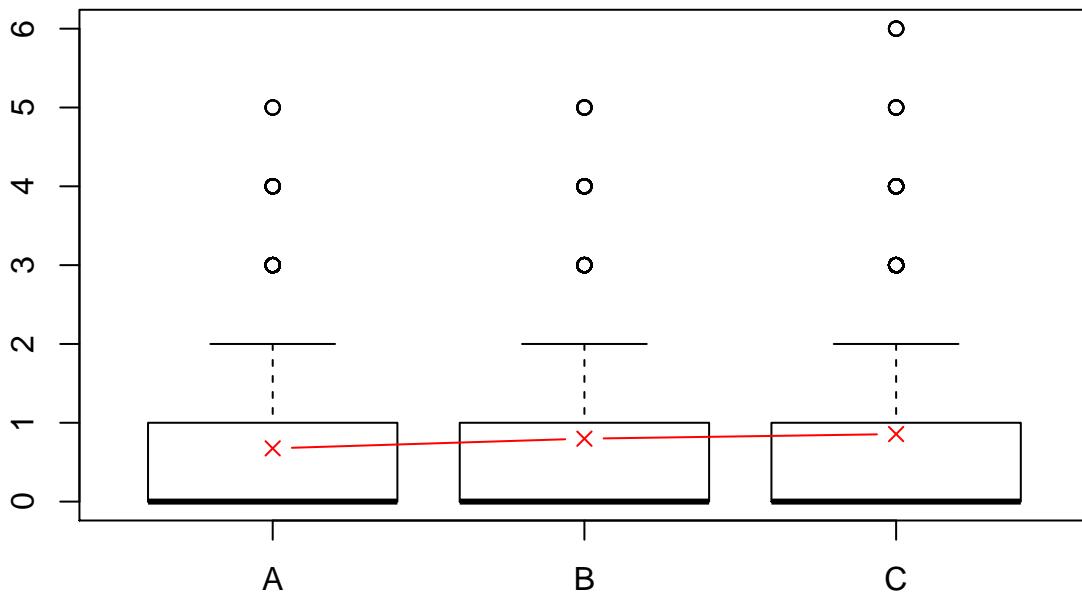
```
## [1] 0.7671
```

```
mean(fitted(m10))
```

```
## [1] 0.8831
```

Using the multiple time interval data, we can pretend that we have a mix of methodologies with respect to count duration:

```
set.seed(1)  
x$meth <- as.factor(sample(c("A", "B", "C"), nrow(x), replace=TRUE))  
x$y <- x$y3  
x$y[x$meth == "B"] <- x$y5[x$meth == "B"]  
x$y[x$meth == "C"] <- x$y10[x$meth == "C"]  
boxplot(y ~ meth, x)  
sb <- sum_by(x$y, x$meth)  
points(1:3, sb[,1]/sb[,2], col=2, type="b", pch=4)
```



We can estimate the effect of the methodology:

```
mm <- glm(y ~ meth - 1, data=x, family=poisson)
summary(mm)
```

```
##
## Call:
## glm(formula = y ~ meth - 1, family = poisson, data = x)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.309  -1.263  -1.162   0.369   3.616
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## methA     -0.3929     0.0309 -12.70 < 2e-16 ***
## methB     -0.2255     0.0289  -7.79 6.6e-15 ***
## methC     -0.1550     0.0277  -5.60 2.1e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
## Null deviance: 7225.2 on 4569 degrees of freedom
## Residual deviance: 6941.8 on 4566 degrees of freedom
## AIC: 11657
##
## Number of Fisher Scoring iterations: 6
```

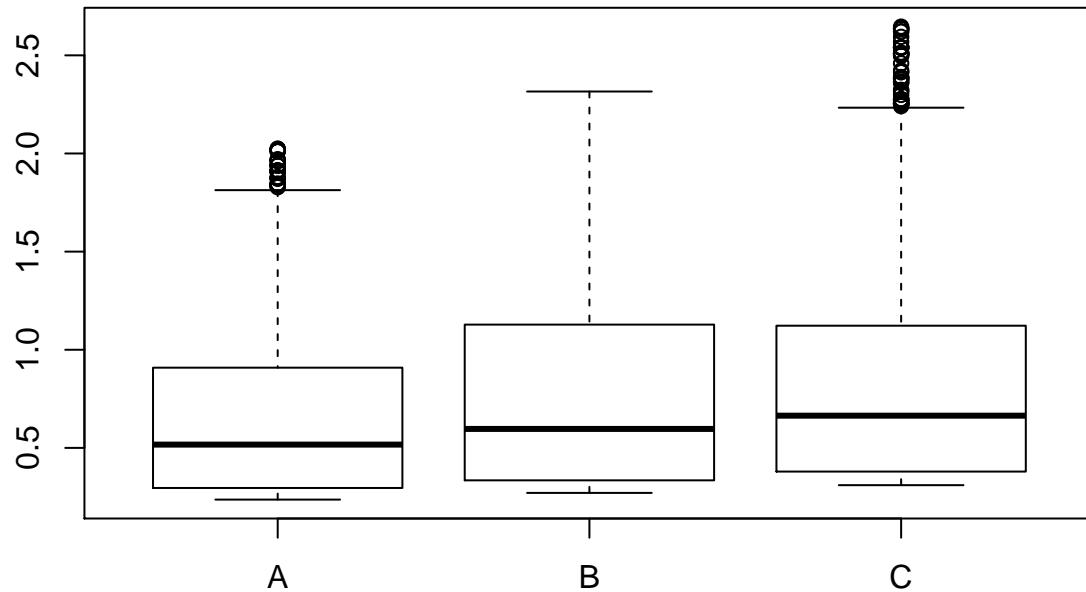
```
exp(coef(mm))

##  methA  methB  methC
## 0.6751 0.7981 0.8564
```

Or the effect of the continuous predictor and the method (discrete):

```
mm <- glm(y ~ Decid + meth, data=x, family=poisson)
summary(mm)
```

```
##
## Call:
## glm(formula = y ~ Decid + meth, family = poisson, data = x)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -2.278  -0.939  -0.736   0.457   4.201
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.4416    0.0457 -31.56  < 2e-16 ***
## Decid        2.1490    0.0574  37.43  < 2e-16 ***
## methB        0.1347    0.0424   3.18   0.0015 **
## methC        0.2705    0.0415   6.51   7.3e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
## Null deviance: 6976.3 on 4568 degrees of freedom
## Residual deviance: 5442.7 on 4565 degrees of freedom
## AIC: 10159
##
## Number of Fisher Scoring iterations: 6
boxplot(fitted(mm) ~ meth, x)
```



```
exp(coef(mm))
```

```
## (Intercept) Decid methB methC
## 0.2365 8.5766 1.1442 1.3106
```

The fixed effects adjusts the means well:

```
cumsum(colMeans(y))
```

```
## 0-3min 3-5min 5-10min
## 0.6737 0.7671 0.8831
mean(y[,1]) * c(1, exp(coef(mm))[3:4])

## methB methC
## 0.6737 0.7708 0.8829
```

But it is all relative, depends on reference methodology/protocol. The problem is, we can't easily extrapolate to a methodology with count duration of 12 minutes, or interpolate to a methodology with count duration of 2 or 8 minutes. We need somehow to express time expenditure in minutes to make that work. Let's try something else:

```
x$tmax <- c(3, 5, 10)[as.integer(x$method)]
mm <- glm(y ~ Decid + I(log(tmax)), data=x, family=poisson)
summary(mm)
```

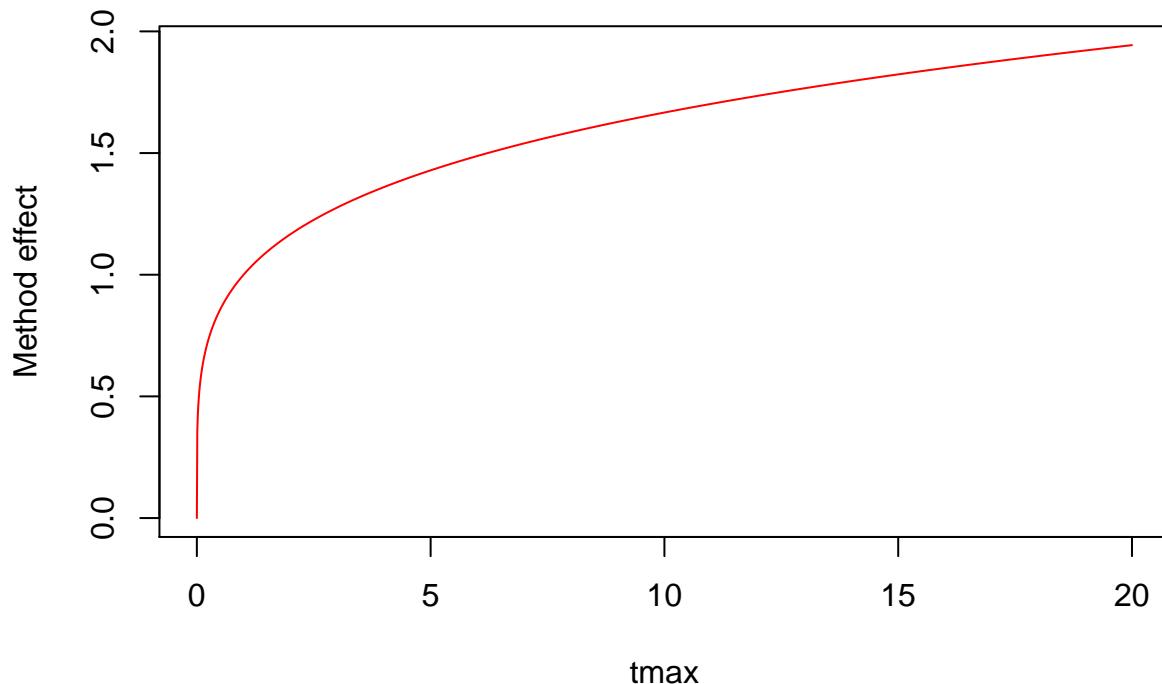
```
##
## Call:
## glm(formula = y ~ Decid + I(log(tmax)), family = poisson, data = x)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.3425  -0.9250  -0.5000  -0.0750   1.3425
```

```

## -2.284 -0.939 -0.731  0.453  4.195
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.6777     0.0702 -23.91 < 2e-16 ***
## Decid        2.1504     0.0574  37.48 < 2e-16 ***
## I(log(tmax)) 0.2218     0.0340   6.53 6.7e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
## Null deviance: 6976.3 on 4568 degrees of freedom
## Residual deviance: 5443.0 on 4566 degrees of freedom
## AIC: 10158
##
## Number of Fisher Scoring iterations: 6

tmax <- seq(0, 20, 0.01)
plot(tmax, exp(log(tmax) * coef(mm)[3]), type="l",
     ylab="Method effect", col=2)

```



Now we are getting somewhere. But still, this function keep increasing monotonically.

**Exercise**

What kind of function would we need and why?
What is the underlying biological mechanism?

3.13 Count radius effects

Before solving the count duration issue, let us look at the effect of survey area. We get a similar count breakdown, but now by distance band:

```
ydis <- Xtab(~ SiteID + Dis + SpeciesID ,
  josm$counts[josm$counts$DetectType1 != "V",])

y <- as.matrix(ydis[[spp]])
head(y)

##          0-50m 50-100m 100+m
## CL10102     1       2      0
## CL10106     0       0      0
## CL10108     0       0      0
## CL10109     1       2      0
## CL10111     1       0      1
## CL10112     0       2      0

colMeans(y) # mean count of new individuals

##    0-50m 50-100m   100+m
## 0.29241 0.49223 0.09849

cumsum(colMeans(y)) # cumulative counts

##    0-50m 50-100m   100+m
## 0.2924 0.7846 0.8831

x <- data.frame(
  josm$surveys,
  y50=y[, "0-50m"],
  y100=y[, "0-50m"]+y[, "50-100m"])

table(x$y50)

## 
##    0    1    2    3    4    5
## 3521 792 228 25   2   1
```

```
table(x$y100)

##
##    0     1     2     3     4     5     6
## 2654  833  647  316   92   20    7
```

We don't consider the unlimited distance case, because the survey area there is unknown (although we will ultimately address this problem later). We compare the counts within the 0-50 and 0-100 m circles:

```
m50 <- glm(y50 ~ Decid, data=x, family=poisson)
m100 <- glm(y100 ~ Decid, data=x, family=poisson)
mean(fitted(m50))

## [1] 0.2924

mean(fitted(m100))

## [1] 0.7846

coef(m50)

## (Intercept)      Decid
##      -2.265      2.126

coef(m100)

## (Intercept)      Decid
##      -1.327      2.209
```

3.14 Offsets

Offsets are constant terms in the linear predictor, e.g. $\log(\lambda_i) = \beta_0 + \beta_1 x_{1i} + o_i$, where o_i is an offset. In the survey area case, an offset might be the log of area surveyed. The logic for this is based on point processes: intensity is a linear function of area under a homogeneous Poisson point process. So we can assume that $o_i = \log(A_i)$, where A stands for area.

Let's see if using area as offset makes our models comparable:

```
m50 <- glm(y50 ~ Decid, data=x, family=poisson,
            offset=rep(log(0.5^2*pi), nrow(x)))
m100 <- glm(y100 ~ Decid, data=x, family=poisson,
              offset=rep(log(1^2*pi), nrow(x)))
coef(m50)

## (Intercept)      Decid
##      -2.024      2.126
```

```
coef(m100)

## (Intercept)      Decid
## -2.471        2.209

mean(exp(model.matrix(m50) %*% coef(m50)))

## [1] 0.3723

mean(exp(model.matrix(m100) %*% coef(m100)))

## [1] 0.2498
```

These coefficients and mean predictions are much closer to each other, but something else is going on.

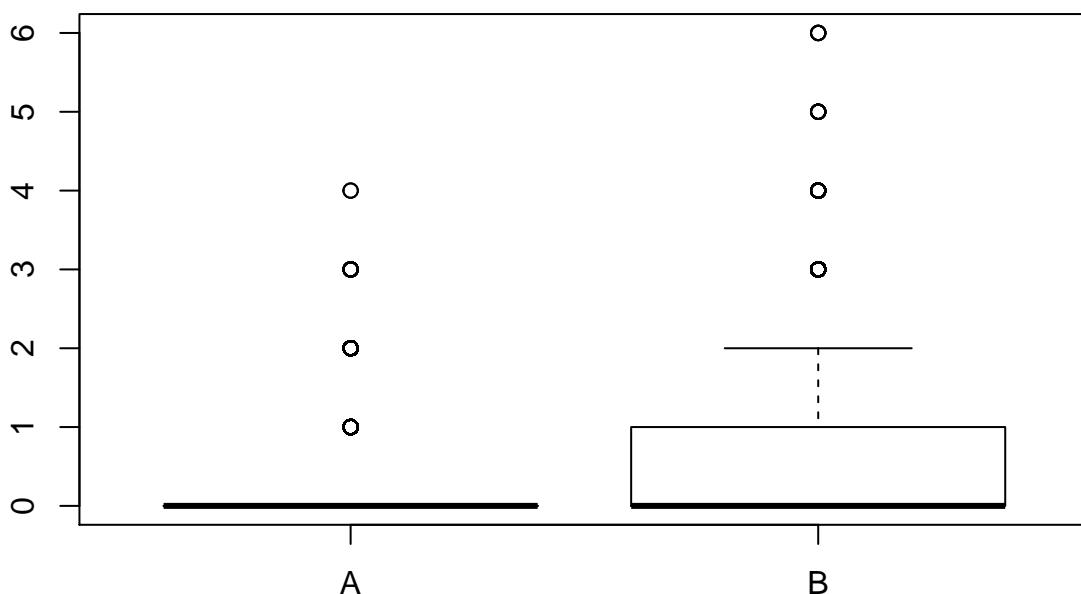


Exercise

Can you guess why we cannot make abundances comparable using log area as as offset?

We pretend again, that survey area varies in our data set:

```
set.seed(1)
x$meth <- as.factor(sample(c("A", "B"), nrow(x), replace=TRUE))
x$y <- x$y50
x$y[x$meth == "B"] <- x$y100[x$meth == "B"]
boxplot(y ~ meth, x)
```



Methodology effect:

```

mm <- glm(y ~ meth - 1, data=x, family=poisson)
summary(mm)

##
## Call:
## glm(formula = y ~ meth - 1, family = poisson, data = x)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.256  -1.256  -0.775   0.228   3.731
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## methA     -1.2040    0.0375 -32.10  <2e-16 ***
## methB     -0.2370    0.0240  -9.87  <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: 7299.4 on 4569 degrees of freedom
## Residual deviance: 5587.9 on 4567 degrees of freedom
## AIC: 9066
##
## Number of Fisher Scoring iterations: 6
exp(coef(mm))

```

```

## methA methB
## 0.300 0.789

```

Predictor and method effects:

```

mm <- glm(y ~ Decid + meth, data=x, family=poisson)
summary(mm)

```

```

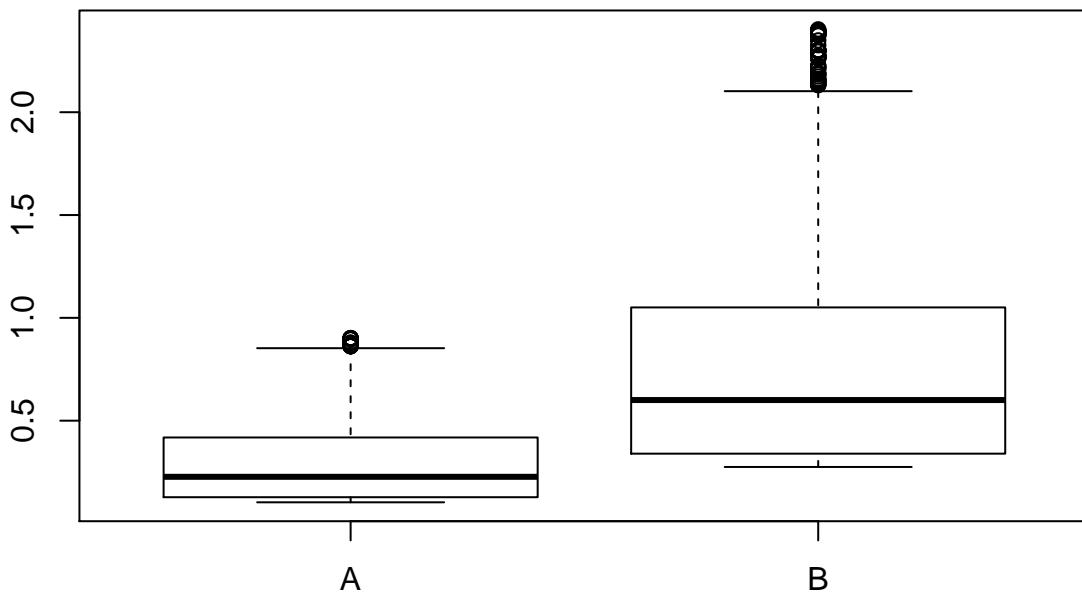
##
## Call:
## glm(formula = y ~ Decid + meth, family = poisson, data = x)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -2.185  -0.847  -0.584   0.274   4.347
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)

```

```

## (Intercept) -2.2719      0.0554     -41.0    <2e-16 ***
## Decid        2.1706      0.0690      31.4    <2e-16 ***
## methB        0.9804      0.0445      22.0    <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: 6110.2  on 4568  degrees of freedom
## Residual deviance: 4531.0  on 4566  degrees of freedom
## AIC: 8011
##
## Number of Fisher Scoring iterations: 6
boxplot(fitted(mm) ~ meth, x)

```



```

exp(coef(mm))

## (Intercept)      Decid      methB
## 0.1031       8.7632     2.6654

cumsum(colMeans(y))[1:2]

## 0-50m 50-100m
## 0.2924  0.7846

mean(y[,1]) * c(1, exp(coef(mm))[3])

##           methB
## 0.2924 0.7794

```

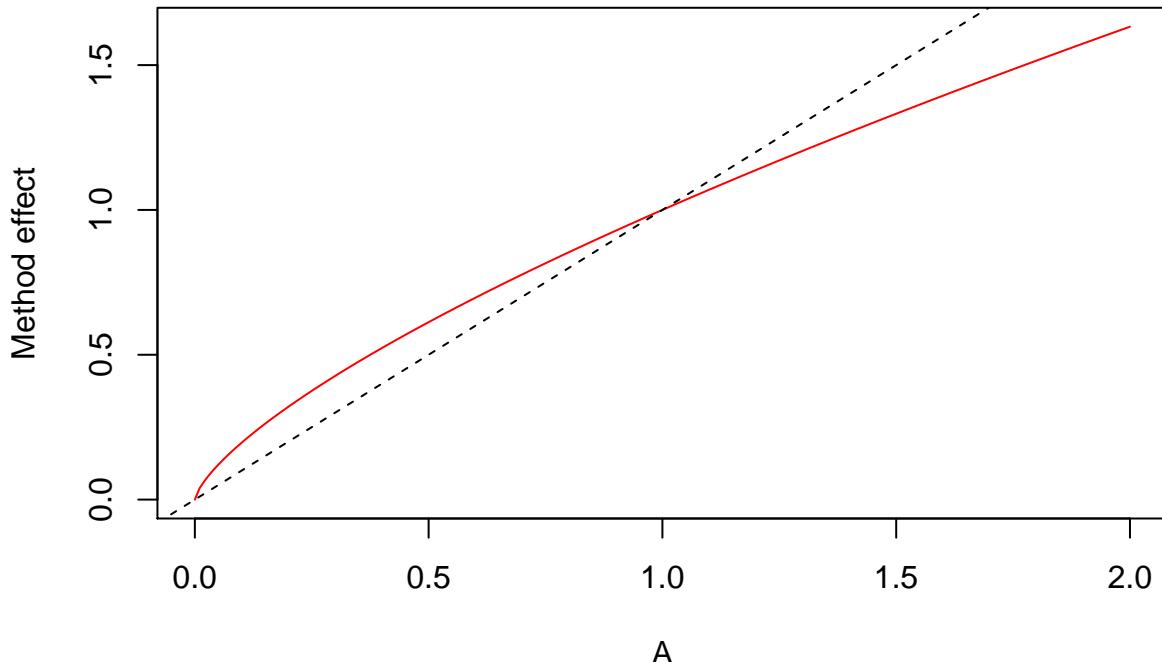
Use log area as continuous predictor: we would expect a close to 1:1 relationship on the

abundance scale.

```
x$logA <- log(ifelse(x$meth == "A", 0.5, 1)^2*pi)
mm <- glm(y ~ Decid + logA, data=x, family=poisson)
summary(mm)
```

```
##
## Call:
## glm(formula = y ~ Decid + logA, family = poisson, data = x)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -2.185  -0.847  -0.584   0.274   4.347
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.1011    0.0513  -40.9  <2e-16 ***
## Decid        2.1706    0.0690   31.4  <2e-16 ***
## logA         0.7072    0.0321   22.0  <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: 6110.2 on 4568 degrees of freedom
## Residual deviance: 4531.0 on 4566 degrees of freedom
## AIC: 8011
##
## Number of Fisher Scoring iterations: 6

A <- seq(0, 2, 0.01) # in ha
plot(A, exp(log(A) * coef(mm)[3]), type="l",
      ylab="Method effect", col=2)
abline(0, 1, lty=2)
```

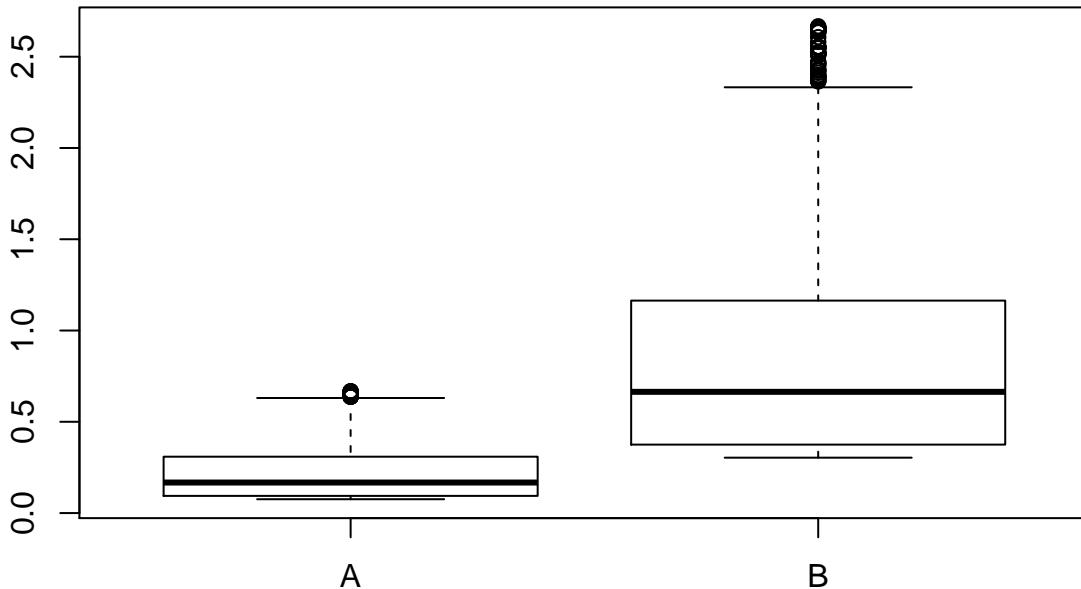


The offset forces the relationship to be 1:1 (it is like fixing the $\log A$ coefficient to be 1):

```
mm <- glm(y ~ Decid, data=x, family=poisson, offset=x$logA)
summary(mm)
```

```
##
## Call:
## glm(formula = y ~ Decid, family = poisson, data = x, offset = x$logA)
##
## Deviance Residuals:
##      Min      1Q      Median      3Q      Max
## -2.302  -0.836  -0.512   0.260   4.219
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.3374     0.0453  -51.6   <2e-16 ***
## Decid        2.1758     0.0690   31.5   <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: 5671.1 on 4568 degrees of freedom
## Residual deviance: 4609.2 on 4567 degrees of freedom
## AIC: 8087
##
## Number of Fisher Scoring iterations: 6
```

```
boxplot(fitted(mm) ~ meth, x)
```



```
cumsum(colMeans(y)) [1:2]
```

```
##    0-50m 50-100m
##  0.2924  0.7846
```

```
c(0.5, 1)^2*pi * mean(exp(model.matrix(mm) %*% coef(mm))) # /ha
```

```
## [1] 0.2200 0.8798
```



Exercise

Why did we get a `logA` coefficient that was less than 1 when theoretically we should have gotten 1?

Predictions using offsets in `glm` can be tricky. The safest way is to use the matrix product `(exp(model.matrix(mm) %*% coef(mm) + <offset>))`. We can often omit the offset, e.g. in the log area case we can express the prediction per unit area. If the unit is 1 ha, as in our case, $\log(1)=0$, which means the mean abundance per unit area can be calculated by omitting the offsets all together.

Chapter 4

Behavioral Complexities

4.1 Introduction

We have reviewed so far how to fit *naive* models to estimate the expected value of the observed counts, λ . So what is this λ ? Here are some definitions for further discussion:

- **relative abundance:** λ without any reference to nuisance variables, but possibly standardized by design, or nuisance variables used as fixed effects,
- **abundance:** $N = \lambda/C$, C is a correction factor and N refers to the number of individuals within the area surveyed – the problem is that we cannot measure this directly (this is a latent variable), moreover the survey area is also often unknown (i.e. for unlimited distance counts),
- **occupancy:** the probability that the survey area is occupied, this is really equivalent to the indicator function $N > 0$,
- **density** $D = N/A = \lambda/AC$, abundance per unit area – same problems as above: both N and A are unknowns.

Our objective in the following chapters is to work out the details of estimating abundance and density in some clever ways through learning about the nature of the mechanisms contributing to C .

4.2 Prerequisites

```
library(bSims)                      # simulations
library(detect)                      # multinomial models
source("functions.R")                # some useful stuff
load("_data/josm/josm.rda") # JOSM data
set.seed(1)
```

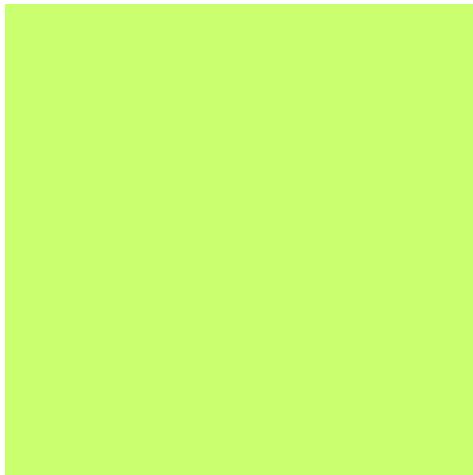
4.3 A world with birds in it

Build a landscape: extent is given in 100 m units

```
(l <- bsims_init(extent=10))
```

```
## bSims landscape
## 1 km x 1 km
## stratification: H

plot(l)
```

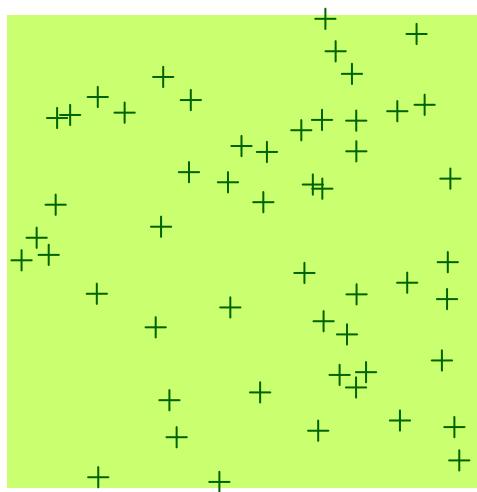


We have a 100 ha landscape that we populate with birds, 1 bird / ha using a Poisson spatial point process. As a result, we have N birds in the landscape, $N \sim Poisson(\lambda)$, $\lambda = DA$:

```
(a <- bsims_populate(l, density=0.5))
```

```
## bSims population
## 1 km x 1 km
## stratification: H
## total abundance: 52

plot(a)
```

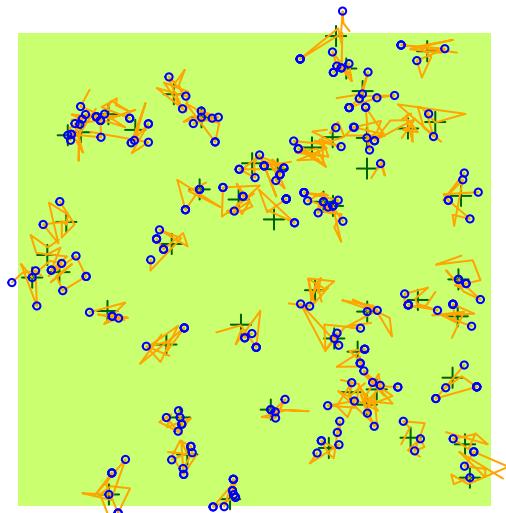


The locations can be seen as nest locations. But birds don't just stay at one place. They move and vocalize:

```
(b <- bsims_animate(a,
  vocal_rate=0.5, duration=10,
  move_rate=1, movement=0.25))
```

```
## bSims events
## 1 km x 1 km
## stratification: H
## total abundance: 52
## total duration: 10

plot(b)
```



```
e <- get_events(b)
summary(e)
```

	x	y	t	v
--	---	---	---	---

```

## Min.   :-5.121   Min.   :-5.158   Min.   :0.044   Min.   :1
## 1st Qu.:-1.510   1st Qu.:-2.446   1st Qu.:2.450   1st Qu.:1
## Median : 0.679   Median : 0.733   Median :4.913   Median :1
## Mean    : 0.433   Mean    : 0.195   Mean    :4.955   Mean    :1
## 3rd Qu.: 2.339   3rd Qu.: 2.714   3rd Qu.:7.097   3rd Qu.:1
## Max.    : 4.785   Max.    : 5.455   Max.    :9.970   Max.    :1
##           i
## Min.   : 1.0
## 1st Qu.:13.0
## Median :24.0
## Mean   :25.5
## 3rd Qu.:37.0
## Max.   :52.0

v <- get_events(b, vocal_only=TRUE)

## check vocal rates: no mixture
phi <- 0.5
br <- c(3, 5, 10)
#br <- 1:10
l <- bsims_init(10)
p <- bsims_populate(l, 1)
a <- bsims_animate(p, vocal_rate=phi)
o <- bsims_detect(a, tau=Inf) # detect all
d <- get_detections(o, first_only=TRUE)
i <- cut(d$t, c(0, br), include.lowest = TRUE)
table(i)
Y1 <- matrix(as.numeric(table(i)), nrow=1)
D1 <- matrix(br, nrow=1)
(phihat <- exp(cmulti.fit(Y1, D1, type="rem")$coef))
plot(stepfun(d$t, (0:nrow(d))/nrow(d)), do.points=FALSE, xlim=c(0,10))
curve(1-exp(-phihat*x), add=TRUE, col=2)
points(br, cumsum(table(i))/sum(table(i)), cex=2, col=4)
curve(1-exp(-phihat*x), add=TRUE, col=4)

## check vocal rates: finite mixture
phi <- c(10, 0.5)
mix <- c(0.2, 0.8)
#br <- c(3, 5, 10)
br <- 1:10
l <- bsims_init(10)
p <- bsims_populate(l, 10)
a <- bsims_animate(p, vocal_rate=phi, mixture=mix)
o <- bsims_detect(a, tau=Inf) # detect all
d <- get_detections(o, first_only=TRUE)

```

```

i <- cut(d$t, c(0, br), include.lowest = TRUE)
table(i)
Y1 <- matrix(as.numeric(table(i)), nrow=1)
D1 <- matrix(br, nrow=1)
cf <- cmulti.fit(Y1, D1, type="mix")$coef # log.phi, logit.c
(phihat <- exp(cf[1]))
(mixhat <- c(1-plogis(cf[2]), plogis(cf[2])))

plot(stepfun(d$t, (0:nrow(d))/nrow(d)), do.points=FALSE, xlim=c(0,10))
curve(1-mix[2]*exp(-phi[2]*x), add=TRUE, col=2)
points(br, cumsum(table(i))/sum(table(i)), cex=2, col=4)
curve(1-mixhat[2]*exp(-phihat*x), add=TRUE, col=4)

# play with intervals

```

Need to explain survival models and removal model related stats

Here comes the real data analysis

Behaviour related stuff

constant p (time as covariate)

time varying p

finite mix

time varying p/c

rate, count, time-to-event

Chapter 5

The Detection Process

EDR, tau constant

truncated, unlimited

variable tau: habitat effect (continuous case?)

discrete: land cover, observer effects

contrast fixed effects with offsets – motivation for ARU

Chapter 6

Dealing with Recordings

integration challenges

calibration (exponential/cloglog approximation)

fixed effects

paired

sensor sensitivity - EDR

Chapter 7

A Closer Look at Assumptions

break thos assumptions

Chapter 8

Understanding Roadside Surveys

directional diff in signal transmission

Chapter 9

Miscellaneous Topics

model selection and conditional likelihood

variance/bias trade off

error propagation

MCMC?

N-mixture ideas

phylogenetic and life history/trait stuff

PIF methods

These are just reminders, to be deleted later

You can label chapter and section titles using `{#label}` after them, e.g., we can reference Chapter 1. If you do not manually label them, there will be automatic labels anyway.

Figures and tables with captions will be placed in `figure` and `table` environments, respectively.

```
par(mar = c(4, 4, .1, .1))
plot(pressure, type = 'b', pch = 19)
```

Reference a figure by its code chunk label with the `fig:` prefix, e.g., see Figure 9.1. Similarly, you can reference tables generated from `knitr::kable()`, e.g., see Table 9.1.

```
knitr::kable(
  head(iris, 20), caption = 'Here is a nice table!',
  booktabs = TRUE
)
```

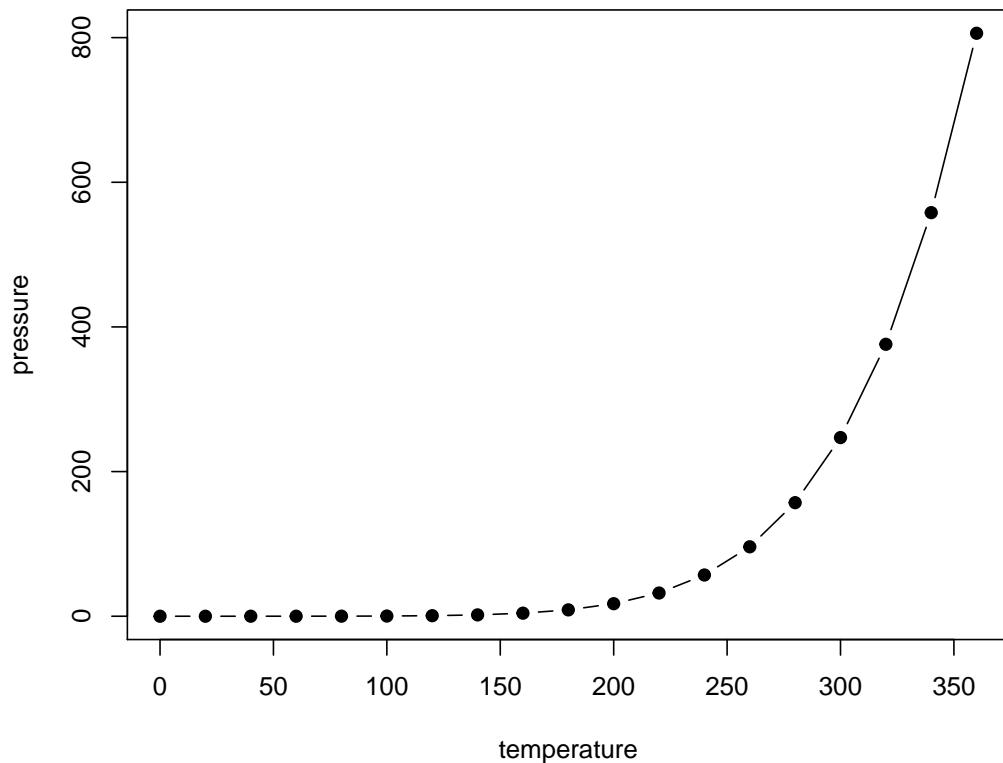


Figure 9.1: Here is a nice figure!

9.1 Binomial model and censoring

Try cloglog with a rare species, like BOCH

```
#spp <- "OVEN" # which species
spp <- "BOCH" # which species
#spp <- "CAWA" # which species

x <- data.frame(
  josm$surveys,
  y=as.numeric(ytot[rownames(x), spp]))
x$y01 <- ifelse(x$y > 0, 1, 0)

table(x$y)

mP <- glm(y ~ Decid * ConifWet, x, family=poisson)
mBc <- glm(y01 ~ Decid * ConifWet, x, family=binomial("cloglog"))
mBl <- glm(y01 ~ Decid * ConifWet, x, family=binomial("logit"))

coef(mP)
coef(mBc)
```

Table 9.1: Here is a nice table!

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
5.1	3.5	1.4	0.2	setosa
4.9	3.0	1.4	0.2	setosa
4.7	3.2	1.3	0.2	setosa
4.6	3.1	1.5	0.2	setosa
5.0	3.6	1.4	0.2	setosa
5.4	3.9	1.7	0.4	setosa
4.6	3.4	1.4	0.3	setosa
5.0	3.4	1.5	0.2	setosa
4.4	2.9	1.4	0.2	setosa
4.9	3.1	1.5	0.1	setosa
5.4	3.7	1.5	0.2	setosa
4.8	3.4	1.6	0.2	setosa
4.8	3.0	1.4	0.1	setosa
4.3	3.0	1.1	0.1	setosa
5.8	4.0	1.2	0.2	setosa
5.7	4.4	1.5	0.4	setosa
5.4	3.9	1.3	0.4	setosa
5.1	3.5	1.4	0.3	setosa
5.7	3.8	1.7	0.3	setosa
5.1	3.8	1.5	0.3	setosa

```

coef(mB1)

plot(fitted(mBc) ~ fitted(mP), col=4,
      ylim=c(0, max(fitted(mP))), xlim=c(0, max(fitted(mP))))
points(exp(model.matrix(mBc) %*% coef(mBc)) ~ fitted(mP), col=2)
abline(0,1)

```

9.1.1 Optimal partitioning

```

oc <- opticut(as.matrix(ytot) ~ 1, strata = x$HAB, dist="poisson")
plot(oc)

```

9.1.2 Optilevels

When we have categorical or compositional (when e.g. proportions add up to 1, also called the unit sum constraint) data, we often want to simplify and merge classes or add up columns.

We can do this based on the structural understanding of these land cover classes (call all treed classes Forest, like what we did for FOR, WET and AHF).

Alternatively, we can let the data (the birds) tell us how to merge the classes. The algorithm does the following:

1. fit model with all classes,
2. order estimates for each class from smallest to largest,
3. merge classes that are near each others, 2 at a time, moving from smallest to largest,
4. compare ΔAIC or ΔBIC values for the merged models and pick the smallest,
5. treat this best merged model as an input in step 1 and star over until Δ is negative (no improvement).

Here is the code for simplifying categories using the `opticut::optilevels` function:

```
M <- model.matrix(~HAB-1, x)
colnames(M) <- levels(x$HAB)
ol1 <- optilevels(x$y, M, dist="poisson")
sort(exp(coef(bestmodel(ol1))))
## estimates
exp(ol1$coef)
## optimal classification
ol1$rank
data.frame(combined_levels=ol1$levels[[length(ol1$levels)]])
```

Here is the code for simplifying compositional data:

```
ol2 <- optilevels(x$y, x[,cn], dist="poisson")
sort(exp(coef(bestmodel(ol2))))
## estimates
exp(ol2$coef)
## optimal classification
ol2$rank
head(groupSums(as.matrix(x[,cn]), 2, ol2$levels[[length(ol2$levels)]]))
```

Bibliography

- Mahon, C. L., Holloway, G., Sólymos, P., Cumming, S. G., Bayne, E. M., Schmiegelow, F. K. A., and Song, S. J. (2016). Community structure and niche characteristics of upland and lowland western boreal birds at multiple spatial scales. *Forest Ecology and Management*, 361:99–116.
- Matsuoka, S. M., Mahon, C. L., Handel, C. M., Sólymos, P., Bayne, E. M., Fontaine, P. C., and Ralph, C. J. (2014). Reviving common standards in point-count surveys for broad inference across studies. *Condor*, 116:599–608.