Introduction to Bayesian statistics with R
5. Case studies and GLMMs

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last updated: 2025-03-11

What is a Generalized Linear Model (or GLM)?

Survival of passengers on the Titanic ~ Class

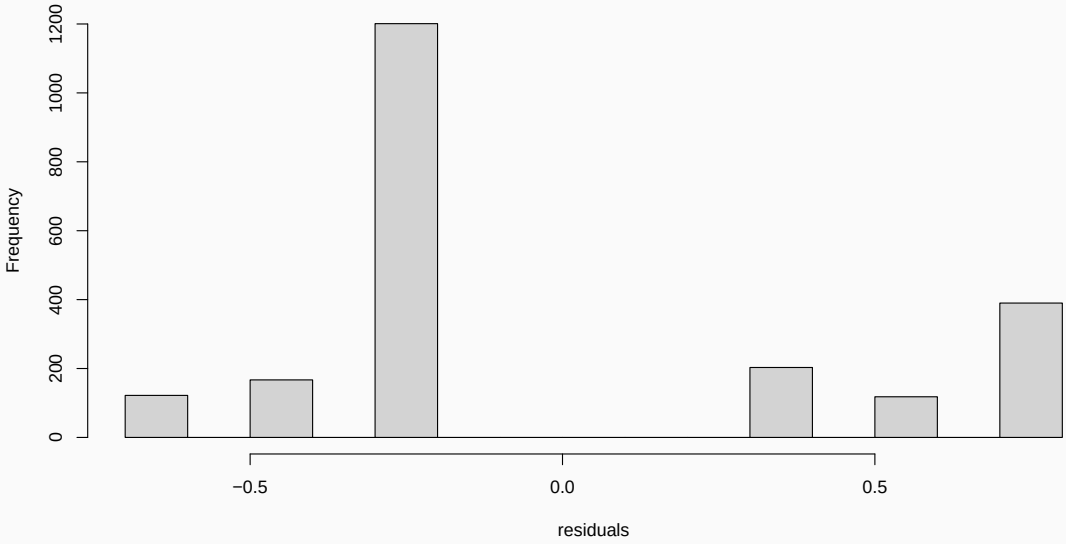
Read `titanic_long.csv` dataset.

```
titanic <- read.csv("dat/titanic_long.csv")
head(titanic)
#>   class   age  sex survived
#> 1 first adult male        1
#> 2 first adult male        1
#> 3 first adult male        1
#> 4 first adult male        1
#> 5 first adult male        1
#> 6 first adult male        1
```

Let's fit a linear model

```
titanic.lm <- lm(survived ~ class, data = titanic)
```

Clearly, the residuals are not normal!



Generalized linear models (GLMs)

- GLMs extend the linear model to scenarios that involve **non-normal error distributions**, hence the term generalized
- The **mean response** is expressed as a **linear function of the predictors** using a **link function**, hence the term linear

Generalized Linear Models

1. **Response variable**
   - Bernoulli/Binomial: Binary variables 0/1
   - Poisson: Counts 0, 1, 2, ...
   - Normal: Real values
   - etc
2. **Predictors** (continuous or categorical)
3. **Link function**
   - Gaussian: identity
   - Binomial: logit
   - Poisson: log
   - Type in `?family`

Bernoulli/Binomial distribution (logistic regression)

- Response variable: Yes/No (e.g. dead/alive, male/female, presence/absence)
- Link function: `logit`

$$\text{logit}(p) = \ln\left(\frac{p}{1-p}\right)$$

- Then, if predictor is x

$$\begin{aligned}
\text{Response} &\sim \text{Distribution}(\text{Mean Response}) \\
Y_i &\sim \text{Bernoulli}(p_i) \\
\text{logit}(p_i) &= a + b\, x_i \\
p_i = \text{logit}^{-1}(a + b\, x_i) &= \frac{e^{a+b\, x_i}}{1 + e^{a+b\, x_i}}
\end{aligned}$$

Poisson distributoin (Poisson regression)

- Response variable: Counts (0, 1, 2, 3...)
- Link function: `log`

$$\text{Response} \sim \text{Distribution}(\text{Mean Response})$$
$$Y_i \sim \text{Poisson}(\lambda_i)$$
$$\log(\lambda_i) = a + b\, x_i$$
$$\lambda_i = e^{a+b\, x_i}$$

Back to survival of Titanic passengers

How many passengers traveled in each class?

```
tapply(titanic$survived, titanic$class, length)
#>   crew  first second  third
#>    885    325    285    706
```

Back to survival of Titanic passengers

How many survived?

```
tapply(titanic$survived, titanic$class, sum)
#>   crew  first second  third
#>    212    203    118    178
```

Back to survival of Titanic passengers

What proportion survived in each class?

```
as.numeric(tapply(titanic$survived, titanic$class, mean))
#> [1] 0.2395480 0.6246154 0.4140351 0.2521246
```

Back to survival of Titanic passengers (package `dplyr`)

Arrange passenger survival according to class

```
library(dplyr)
summarise(group_by(titanic, class, survived), count = n())
```

Back to survival of Titanic passengers (package `dplyr`)

Same manipulation using the pipe operator %>%

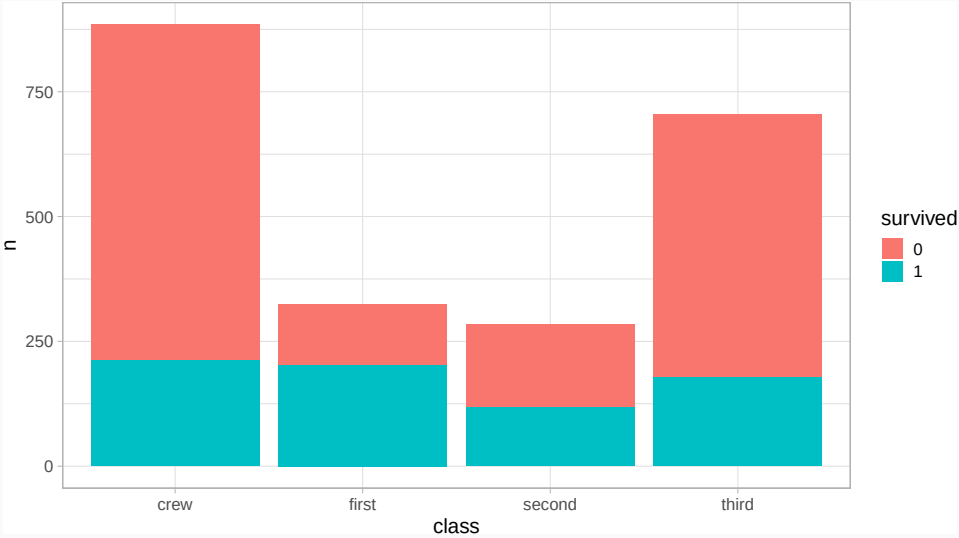
```
titanic %>%
  group_by(class, survived) %>%
  summarise(count = n())
```

Back to survival of Titanic passengers (package `dplyr`)

Arrange passenger survival according to class

```
#>    class survived   n
#> 1   crew        0 673
#> 2  third        0 528
#> 3   crew        1 212
#> 4  first        1 203
#> 5  third        1 178
#> 6 second        0 167
#> 7  first        0 122
#> 8 second        1 118
```

Or graphically. . .



Fitting GLMs in R: `glm` function

```
titanic.glm <- glm(survived ~ class, data = titanic, family = binomial)
#> # A tibble: 4 x 5
#>   term        estimate std.error statistic  p.value
#>   <chr>          <dbl>     <dbl>     <dbl>    <dbl>
#> 1 (Intercept)  -1.16      0.0788   -14.7   1.05e-48
#> 2 classfirst    1.66      0.139     12.0   4.97e-33
#> 3 classsecond   0.808     0.144      5.62  1.91e- 8
#> 4 classthird    0.0678    0.117      0.579 5.62e- 1
```

These estimates are on the logit scale!

Interpreting logistic regression outputs

Parameter estimates on the logit scale:

```
#> (Intercept)  classfirst classsecond  classthird
#> -1.15515905  1.66434399  0.80784987  0.06784632
```

We need to back-transform using the inverse logit function:

```
plogis(coef(titanic.glm)[1]) # crew survival probability
#> (Intercept)
#>    0.239548
```

Looking at the data, the proportion of crew who survived is:

```
sum(titanic$survived[titanic$class == "crew"]) /
  nrow(titanic[titanic$class == "crew", ])
#> [1] 0.239548
```

Probability of survival for 1st class passengers?

Needs to add intercept (baseline) to the parameter estimate:

```
plogis(coef(titanic.glm)[1] + coef(titanic.glm)[2])
#> (Intercept)
#>   0.6246154
```

Again this value matches the data:

```
sum(titanic$survived[titanic$class == "first"]) /
  nrow(titanic[titanic$class == "first", ])
#> [1] 0.6246154
```

Generalized linear *mixed* models (or GLMMs)

What are random effects?

- Mixed models include both fixed and random effects.
- Random effects are statistical parameters that attempt to explain noise caused by sub-populations of the population you are trying to model.
- A random-effect model assumes that the dataset being analysed consists of a hierarchy of different populations whose differences relate to that hierarchy.
- Measurement that come in groups. E.g. classrooms within schools, chapters within books, populations within species, frogs within ponds.
- Sex or age are not clusters; if we were to sample again, we would take the same levels, e.g. male/female and young/old.

Why do we need random effects?

- Model the clustering itself.
- Interested in variance components (environmental vs. genetic variance)
- Control for bias due to pseudoreplication (time, space, individual)

GLMM formulation

$$Y_{ij} \sim \text{Distribution}(\text{Mean Response}_{ij})$$

$$\text{Mean Response}_{ij} = \beta_{0j} + \beta_1 \, x_{i1} + \ldots + \beta_P \, x_{iP}$$

$$\beta_{0j} \sim \text{Normal}(\mu_{group}, \sigma^2_{group})$$

Model fitting in R

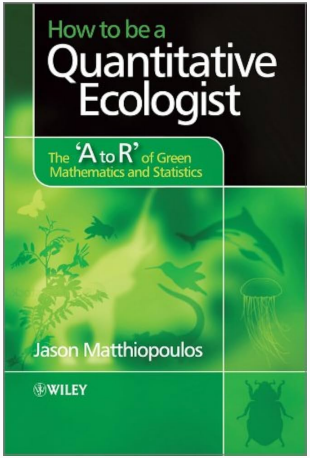
- Linear Mixed Models (LMMs) and Generalized Linear Mixed Models (GLMMs)

```
library(lme4)
my_LMM <- lmer(y ~ x + (1 | group)) # LMM
my_GLMM <- glmer(y ~ x + (1 | group), family = Distribution) # GLMM
```

- `x` is the fixed factor(s)
- `1` is the random factor(s), here the intercept
- `group` is for the grouping variable

GLMM with Poisson response

From Jason Matthiopoulos' book



Longitudinal study on coral reef

A survey of a coral reef uses 10 predefined linear transects covered by divers once every week. The response variable of interest is the abundance of a particular species of anemone as a function of water temperature. Counts of anemones are recorded at 20 regular line segments along the transect. The following piece of code will generate a data set with realistic properties according to the above design. Make sure you understand what it is doing. You might want to explain the script to the colleague next to you. Also, to try and make sense of the code of others, it is always good to plot and/or run small sections of the code.

Data generation

```
transects <- 10
data <- NULL
for (tr in 1:transects){
  # random effect (intercept)
  ref <- rnorm(1,0,.5)
  # water temperature gradient
  t <- runif(1, 18,22) + runif(1,-.2,0.2)*1:20
  # Anemone gradient (expected response)
  ans <- exp(ref -14 + 1.8 * t - 0.045 * t^2)
  # actual counts on 20 segments of the current transect
  an <- rpois(20, ans)
  data <- rbind(data, cbind(rep(tr, 20), t, an))
}
```

Our job

- Generate a data set using the anemone code.
- Using `NIMBLE` and `brms`, fit a GLMM with quadratic effect of temperature and a random intercept.
- Fit the same model to the same data in a Frequentist framework using function `lme4::glmer()`.
- Compare the estimates.

Make sense of the code

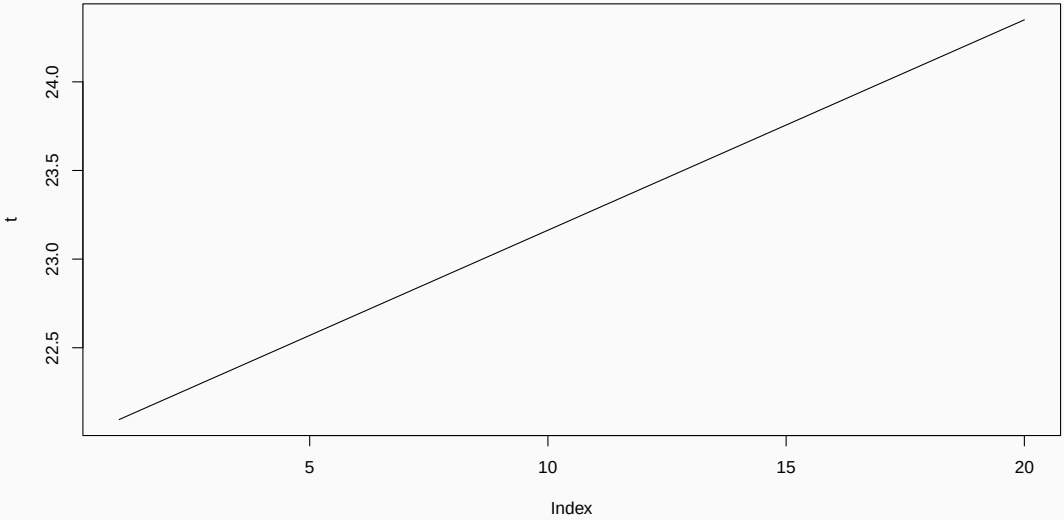
- Always difficult to make sense of the code of others.
- Good to plot and/or run small sections of the code.

Make sense of the code

```r
# random effect (intercept)
ref <- rnorm(1,0,.5)
# water temperature gradient
t <- runif(1, 18,22) + runif(1,-.2,0.2)*1:20

plot(t,type='l')
```

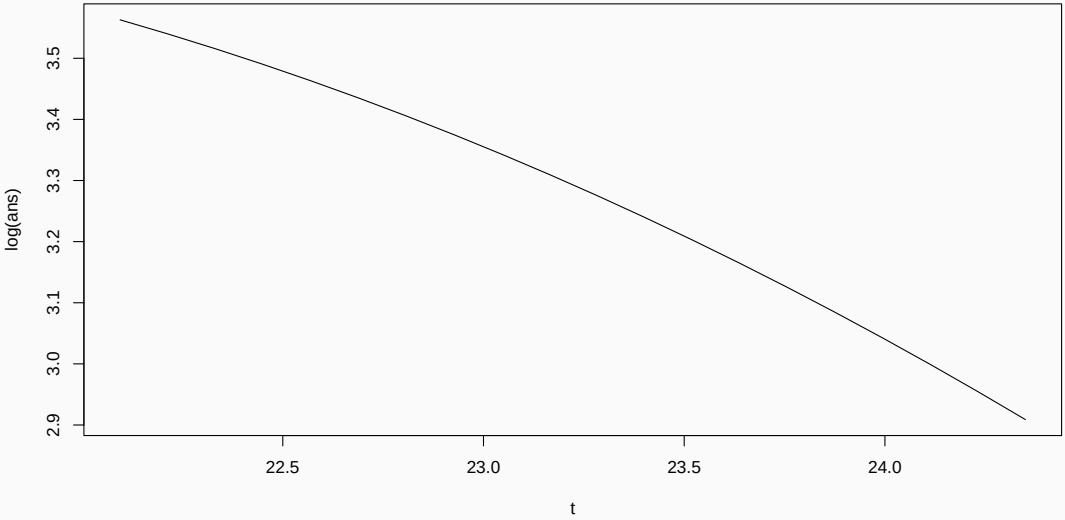
Make sense of the code



Make sense of the code

```
# Anemone gradient (expected response)
ans <- exp(ref -14 + 1.8 * t - 0.045 * t^2)
plot(t,log(ans),type='l')
```

Make sense of the code

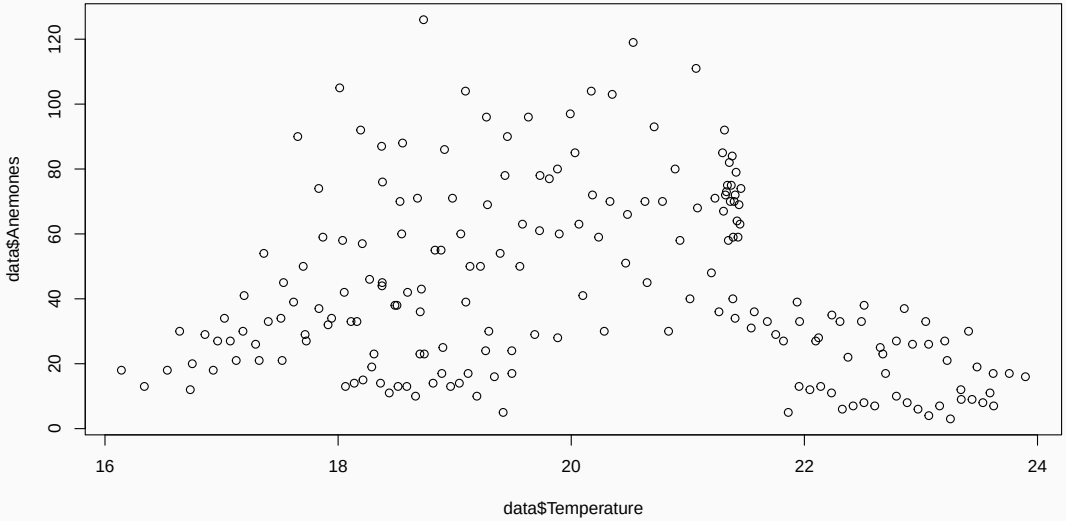


Make sense of the code

```
data <- data.frame(Transect = data[,1],
                   Temperature = data[,2],
                   Anemones = data[,3])

plot(data$Temperature, data$Anemones)
```

Make sense of the code



Write down model

$$\text{Count}_i \sim \text{Poisson}(\lambda_i) \quad \text{[likelihood]}$$

$$\log(\lambda_i) = a_{\text{TRANSECT[i]}} + b_1\,\text{temp}_i + b_2\,\text{temp}_i^2 \quad \text{[linear model]}$$

$$a_j \sim \text{Normal}(\bar{a}, \sigma) \quad \text{[prior for varying intercepts]}$$

$$\bar{a} \sim \text{Normal}(0, 1.5) \quad \text{[prior for population mean]}$$

$$\sigma \sim \text{Uniform}(0, 10) \quad \text{[prior for standard deviation]}$$

$$b_1, b_2 \sim \text{Normal}(0, 1.5) \quad \text{[prior for slopes]}$$

NIMBLE

Load package

```
library(nimble)
```

Standardize temperature covariate

```
boo <- data$Temperature
data$Temp <- (boo - mean(boo)) / sd(boo)
head(data)
#>   Transect Temperature Anemones        Temp
#> 1        1    19.88386       28 -0.09912526
#> 2        1    19.68686       29 -0.19824493
#> 3        1    19.48986       24 -0.29736459
#> 4        1    19.29286       30 -0.39648425
#> 5        1    19.09586       39 -0.49560392
#> 6        1    18.89886       25 -0.59472358
```

Model

```
model <- nimbleCode({
  for (i in 1:n){
    count[i] ~ dpois(lambda[i])
    log(lambda[i]) <- intercept[transect[i]] + slope[1] * x[i] + slope[2] * pow(x[i],2)
  }
  for (j in 1:nbtransects){
    intercept[j] ~ dnorm(mu.a, sd = sigma.a)
  }
  mu.a ~ dnorm(0, sd = 1.5)
  sigma.a ~ dunif(0, 10)
  slope[1] ~ dnorm(0, sd = 1.5)
  slope[2] ~ dnorm(0, sd = 1.5)
})
```

Data

```
my.constants <- list(n = nrow(data),
                     nbtransects = transects)
my.data <- list(x = data$Temp,
                count = data$Anemones,
                transect = data$Transect)
```

Initial values

```
init1 <- list(intercept = rnorm(transects), slope = rnorm(2),
              mu.a = rnorm(1), sigma.a = runif(1))
init2 <- list(intercept = rnorm(transects), slope = rnorm(2),
              mu.a = rnorm(1), sigma.a = runif(1))
initial.values <- list(init1, init2)
```

Parameters to monitor (and save)

```
parameters.to.save <- c("slope", "mu.a", "sigma.a")
```

Set up MCMC details

```
n.iter <- 5000
n.burnin <- 1000
n.chains <- 2
```

Run model

```
mcmc.output <- nimbleMCMC(code = model,
                          data = my.data,
                          constants = my.constants,
                          inits = initial.values,
                          monitors = parameters.to.save,
                          niter = n.iter,
                          nburnin = n.burnin,
                          nchains = n.chains)
```

Post-process results

```
library(MCMCvis)
MCMCsummary(object = mcmc.output, round = 2)
#>            mean   sd  2.5%   50% 97.5% Rhat n.eff
#> mu.a       3.61 0.27  3.04  3.63  4.10 1.00  4485
#> sigma.a    0.79 0.23  0.48  0.74  1.36 1.00   998
#> slope[1] -0.06 0.03 -0.11 -0.06  0.00 1.02   233
#> slope[2] -0.19 0.02 -0.23 -0.19 -0.15 1.01   302
```

Get regression coefficients

Convert regression coefficients from scaled to non-scaled and compare to values used to generate data (from https://stats.stackexchange.com/questions/361995/how-to-convert-coefficients-from-quadratic-function-from-scaled-to-not-scaled-co)

Pull two chains together:

```
samples <- rbind(mcmc.output$chain1,mcmc.output$chain2)
```

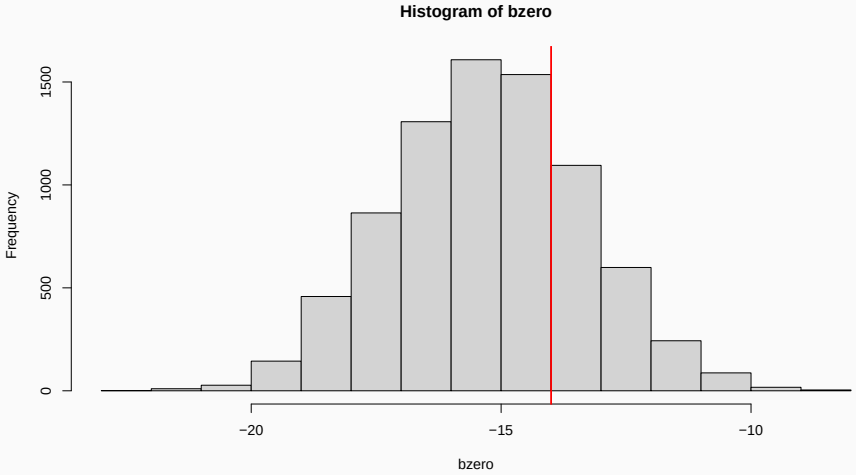
Get regression coefficients

```
sbzero <- samples[,'mu.a']
sbun <- samples[,'slope[1]']
sbdeux <- samples[,'slope[2]']

mu <- mean(boo)
sg <- sd(boo)
```

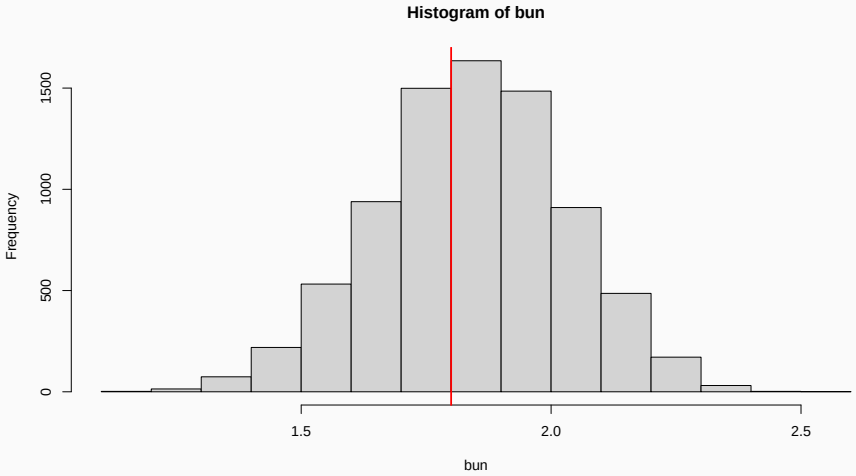
Get regression coefficients

```
bzero <- sbzero - sbun*mu/sg + sbdeux*mu^2/(sg^2)
hist(bzero)
abline(v = -14, col = "red", lwd = 2)
```



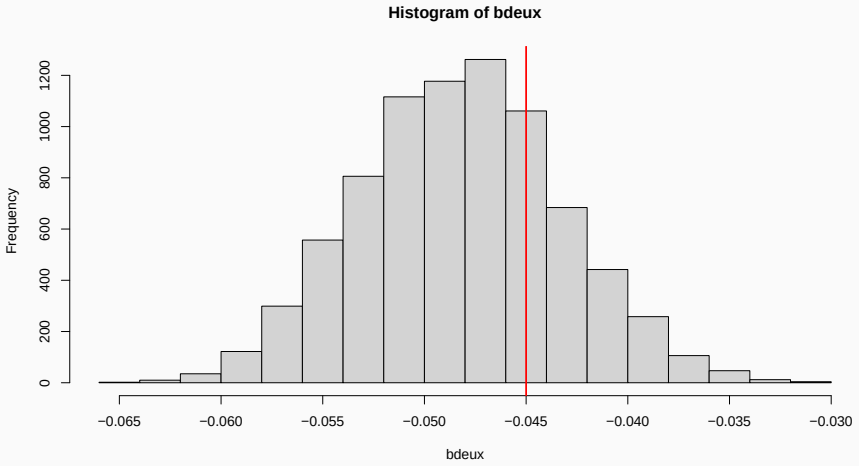
Get regression coefficients

```
bun <- sbdeux/sg - 2 * sbdeux * mu / (sg^2)
hist(bun)
abline(v = 1.8, col = "red", lwd = 2)
```



Get regression coefficients

```
bdeux <- sbdeux/(sg^2)
hist(bdeux)
abline(v = - 0.045, col = "red", lwd = 2)
```



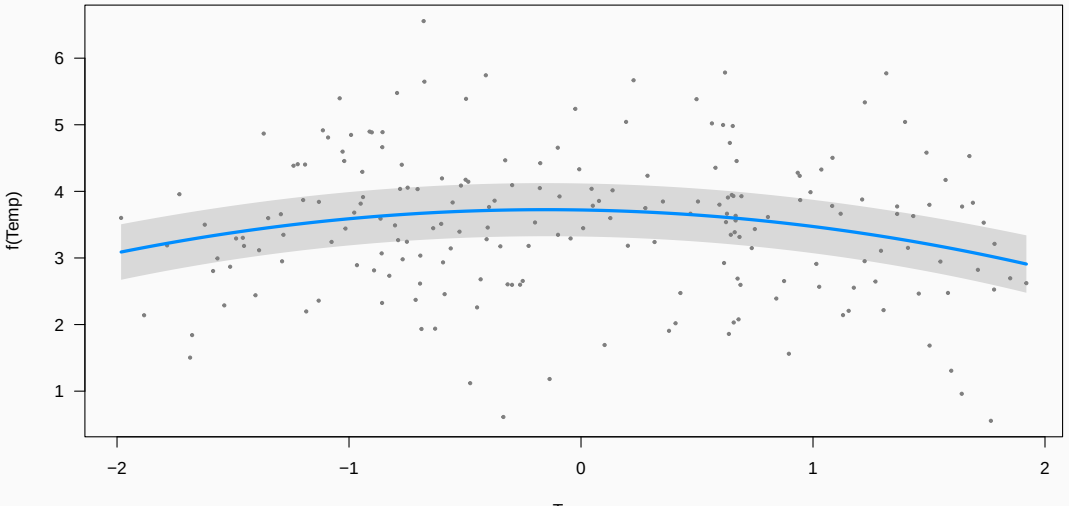
Frequentist approach

lme4 fit

```
library(lme4)
fit_lme4 <- glmer(Anemones ~ Temp + I(Temp^2) + (1 | Transect), data = data, family = poisson)
fit_lme4
#> Generalized linear mixed model fit by maximum likelihood (Laplace
#>   Approximation) [glmerMod]
#>  Family: poisson  ( log )
#> Formula: Anemones ~ Temp + I(Temp^2) + (1 | Transect)
#>    Data: data
#>       AIC       BIC    logLik  deviance  df.resid
#> 1357.6583 1370.8516 -674.8292 1349.6583       196
#> Random effects:
#>  Groups   Name        Std.Dev.
#>  Transect (Intercept) 0.639
#> Number of obs: 200, groups:  Transect, 10
#> Fixed Effects:
#> (Intercept)         Temp    I(Temp^2)
#>     3.72064     -0.05814     -0.19002
```

Visualize

```
visreg::visreg(fit_lme4, xvar = 'Temp')
```



brms

Implementation

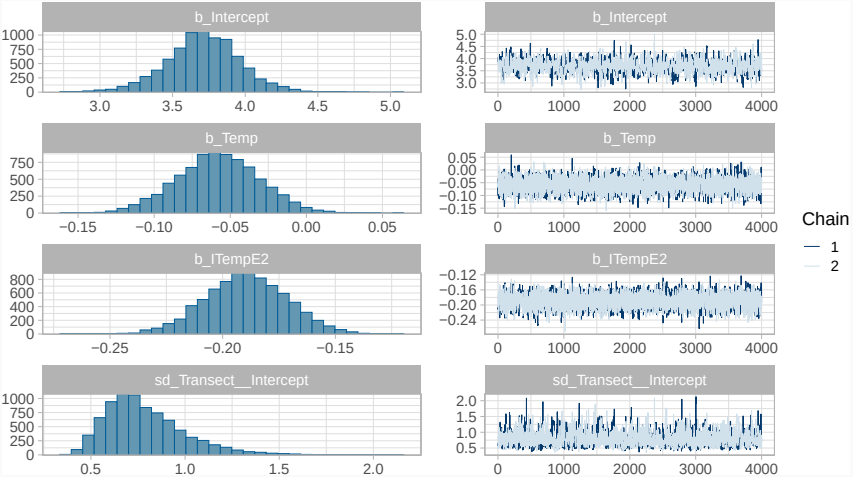
```
library(brms)
bayes.brms <- brm(Anemones ~ Temp + I(Temp^2) + (1 | Transect),
                  data = data,
                  family = poisson("log"),
                  chains = 2, # nb of chains
                  iter = 5000, # nb of iterations, including burnin
                  warmup = 1000, # burnin
                  thin = 1)
```

Numerical summaries

```
summary(bayes.brms)
#>  Family: poisson
#>   Links: mu = log
#> Formula: Anemones ~ Temp + I(Temp^2) + (1 | Transect)
#>    Data: data (Number of observations: 200)
#>   Draws: 2 chains, each with iter = 5000; warmup = 1000; thin = 1;
#>          total post-warmup draws = 8000
#>
#> Multilevel Hyperparameters:
#> ~Transect (Number of levels: 10)
#>                 Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
#> sd(Intercept)     0.79      0.22     0.48     1.31 1.00     1511     2441
#>
#> Regression Coefficients:
#>           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
#> Intercept     3.71      0.25     3.18     4.21 1.00     1160     1693
#> Temp         -0.06      0.03    -0.11    -0.01 1.00     4284     4289
#> ITempE2      -0.19      0.02    -0.23    -0.15 1.00     4876     4363
#>
#> Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
#> and Tail_ESS are effective sample size measures, and Rhat is the potential
#> scale reduction factor on split chains (at convergence, Rhat = 1).
```

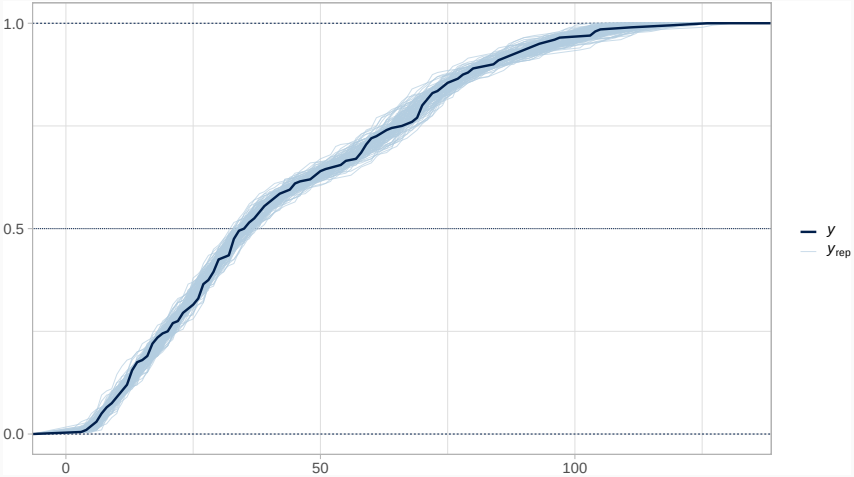
Convergence

```
plot(bayes.brms)
```



Quality of fit assessment

```
pp_check(bayes.brms, ndraws = 100, type = 'ecdf_overlay')
```



Model comparison

- What if we'd like to test the effect of temperature using WAIC?
- We fit a model with no effect of temperature:

```
bayes.brms2 <- brm(Anemones ~ 1 + (1 | Transect),
                   data = data,
                   family = poisson("log"),
                   chains = 2, # nb of chains
                   iter = 5000, # nb of iterations, including burnin
                   warmup = 1000, # burnin
                   thin = 1)
```

Model comparison

Then we compare both models, by ranking them with their WAIC:

```
waic1 <- waic(bayes.brms) # waic model w/ temperature
waic2 <- waic(bayes.brms2) # waic model wo/ temperature
data.frame(with_temp = waic1$waic,
           without_temp = waic2$waic)
#>   with_temp without_temp
#> 1  1308.948     1414.755
```

GLMM with binomial response

From a paper by Brice, Larsen and MacNulty (2021)

Received: 5 July 2021 | Revised: 10 August 2021 | Accepted: 30 September 2021

DOI: 10.1111/ele.13915

LETTER

ECOLOGY LETTERS WILEY

Sampling bias exaggerates a textbook example of a trophic cascade

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Funding information
National Science Foundation, Grant/Award Number: DGE-1633756; Yellowstone National Park; University of Wyoming-National Park Service Small Grant Program, Grant/Award Number: 1003867-USU; Utah State University

Editor: Tim Coulson

Abstract

Understanding trophic cascades in terrestrial wildlife communities is a major challenge because these systems are difficult to sample properly. We show how a tradition of non-random sampling has confounded this understanding in a textbook system (Yellowstone National Park) where carnivore [*Canis lupus* (wolf)] recovery is associated with a trophic cascade involving changes in herbivore [*Cervus canadensis* (elk)] behaviour and density that promote plant regeneration. Long-term data indicate a practice of sampling only the tallest young plants overestimated regeneration of overstory aspen (*Populus tremuloides*) by a factor of 4–7 compared to random sampling because it favoured plants taller than the preferred browsing height of elk and overlooked non-regenerating aspen stands. Random sampling described a trophic cascade, but it was weaker than the one that non-random sampling described. Our findings highlight the critical importance of basic sampling principles (e.g. randomisation) for achieving an accurate understanding of trophic cascades in terrestrial wildlife systems.

KEYWORDS

aspen, carnivore, elk, non-random sampling, predator indirect effects, preferred browsing height, sampling bias, trophic cascade, ungulate, wolf

Read in data

```
rawdat <- read_csv("dat/Aspen_Data.csv")
head(rawdat)
#> # A tibble: 6 x 6
#>    Plot  Year  Tree Browse Height Type
#>   <dbl> <dbl> <dbl>  <dbl>  <dbl> <chr>
#> 1     1  2008     1      1    115 5T
#> 2     1  2008     2      1    130 5T
#> 3     1  2008     3      1    113 5T
#> 4     1  2008     4      1    110 5T
#> 5     1  2008     5      0    132 5T
#> 6     1  2009     1      1    200 5T
```

Data collection (1)

We measured browsing and height of young aspen in 113 plots distributed randomly across the study area. Each plot was a 1 x 20 m belt transect located randomly within an aspen stand that was itself randomly selected from an inventory of stands with respect to high and low wolf-use areas. The inventory was a list of 992 grid cells (240 $\times$ 360 m) that contained at least one stand. A 'stand' was a group of tree-size aspen (more than 10 cm diameter at breast height) in which each tree was less than 30 m from every other tree. One hundred and thirteen grid cells were randomly selected from the inventory, one stand was randomly selected from each cell, and one plot was randomly established in each stand.

Data collection (2)

We measured aspen at the end of the growing season (late July–September), focusing on plants less than 600 cm tall and more than 1 year old, which we termed 'young aspen'. For each stand, we measured every young aspen within a plot ('random stems') and each of the five tallest young aspen within the stand ('5T stems'). For all young aspen, we measured browsing status (browsed or unbrowsed) and height of the leader (tallest) stem. A leader was 'browsed' if its growth from the previous growing season had been eaten, which we identified by a sharp, pruned edge at the base of the current year's growth. Most plots were measured nearly every year since 1999 and our analysis focused on data from 10 years (2007–2014, 2016–2017) in which sampled stands included measurements of random and 5T stems.

Data collection (3)

We combined measurements of 5T and random stems into one data set of all stems ($N = 18{,}623$) across all years ($N = 10$ years).

Our job

- Read in the data and get familiar with it.
- Using `NIMBLE` and `brms`, fit a GLMM with 'Browsed' as the response variable. Consider year and type of stems (random or 5T stems) as explanatory variables. Use stand identity as a random effect on the intercept.
- Fit the same model to the same data in a Frequentist framework using function `lme4::glmer()`.
- Compare the estimates.

Read in data

```
str(rawdat)
#> spc_tbl_ [18,792 x 6] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
#>  $ Plot  : num [1:18792] 1 1 1 1 1 1 1 1 1 1 ...
#>  $ Year  : num [1:18792] 2008 2008 2008 2008 2008 ...
#>  $ Tree  : num [1:18792] 1 2 3 4 5 1 2 3 4 5 ...
#>  $ Browse: num [1:18792] 1 1 1 1 0 1 0 0 0 0 ...
#>  $ Height: num [1:18792] 115 130 113 110 132 200 208 218 240 260 ...
#>  $ Type  : chr [1:18792] "5T" "5T" "5T" "5T" ...
#>  - attr(*, "spec")=
#>   .. cols(
#>   ..   Plot = col_double(),
#>   ..   Year = col_double(),
#>   ..   Tree = col_double(),
#>   ..   Browse = col_double(),
#>   ..   Height = col_double(),
#>   ..   Type = col_character()
#>   .. )
#>  - attr(*, "problems")=<externalptr>
```

Metadata

- Plot: individual identifier for each of 113 plots distributed randomly across the study area. Each plot was a 1×20 m belt transect located randomly within an aspen stand
- Year: year in which aspen was sampled
- Tree: individual identifier for each stem within a plot
- Browse: denotes the browsing status (browsed $= 1$,unbrowsed $= 0$) of the leader (tallest) stem. A leader was 'browsed' if its growth from the previous growing season had been eaten
- Height: height (cm) of the leader stem of each individual aspen
- Type: sampling method. Every young aspen within a plot is a "random" stem, and each of the five tallest young aspen within the stand is a "5T" stem.

Format data

```r
dat <- rawdat %>%
  transmute(y = Browse,
            type = if_else(Type == "5T", 1, 0), # numeric
            year = as.integer(Year) - 2006,     # year starts at 1
            id = as_factor(Plot))               # id is a factor
```

Write down model

$$\begin{aligned}
\text{Brwsed}_i &\sim \text{Bernoulli}(p_i) && \text{[likelihood]} \\
\text{logit}(p_i) &= a_{\text{ID[i]}} + b_1\ \text{year}_i + b_2\ \text{type}_i && \text{[linear model]} \\
a_j &\sim \text{Normal}(\bar{a}, \sigma) && \text{[prior for varying intercepts]} \\
\bar{a} &\sim \text{Normal}(0, 1.5) && \text{[prior for population mean]} \\
\sigma &\sim \text{Uniform}(0, 10) && \text{[prior for standard deviation]} \\
b_1, b_2 &\sim \text{Normal}(0, 1.5) && \text{[prior for slopes]}
\end{aligned}$$

NIMBLE

Load package

```
library(nimble)
```

Model

```
model <- nimbleCode({
  for (i in 1:n){
    y[i] ~ dbern(p[i])
    logit(p[i]) <- a[id[i]] + beta[1] * type[i] + beta[2] * year[i] + beta[3] * year[i] * type[i]
  }
  for (j in 1:nblevels){
    a[j] ~ dnorm(mu.a, sd = sigma.a)
  }
  for (k in 1:3){
    beta[k] ~ dnorm(0, sd = 1.5)
  }
  mu.a ~ dnorm(0, sd = 1.5)
  sigma.a ~ dunif(0,10)
})
```

Data

```
my.constants <- list(id = as.numeric(as_factor(dat$id)),
                     n = length(dat$y),
                     nblevels = length(levels(as_factor(dat$id))))
my.data <- list(y = dat$y,
                type = dat$type,
                year = dat$year)
```

Initial values

```
init1 <- list(mu.a = -0.5, sigma.a = 0.1, beta = rnorm(3))
init2 <- list(mu.a = 0.5, sigma.a = 0.5, beta = rnorm(3))
initial.values <- list(init1, init2)
```

Parameters to monitor (and save)

```
parameters.to.save <- c("mu.a", "sigma.a", "beta")
```

Set up MCMC details

```
n.iter <- 5000
n.burnin <- 1000
n.chains <- 2
```

Run model

```
mcmc.output <- nimbleMCMC(code = model,
                          data = my.data,
                          constants = my.constants,
                          inits = initial.values,
                          monitors = parameters.to.save,
                          niter = n.iter,
                          nburnin = n.burnin,
                          nchains = n.chains)
```

Post-process results

```
library(MCMCvis)
MCMCsummary(object = mcmc.output, round = 2)
#>           mean   sd  2.5%   50% 97.5% Rhat n.eff
#> beta[1] -0.43 0.09 -0.61 -0.43 -0.25 1.00   186
#> beta[2] -0.14 0.01 -0.15 -0.14 -0.12 1.02   130
#> beta[3] -0.08 0.01 -0.11 -0.08 -0.06 1.00   179
#> mu.a     1.57 0.13  1.31  1.57  1.82 1.00  1494
#> sigma.a  1.26 0.10  1.08  1.25  1.48 1.00   980
```

Visualize (1)

```
# pool two chains together
samples <- rbind(mcmc.output$chain1, mcmc.output$chain2)
nsim <- nrow(samples)

# get values sampled in posterior distribution of regression parameters
beta1 <- samples[,'beta[1]']
beta2 <- samples[,'beta[2]']
beta3 <- samples[,'beta[3]']
intercept <- samples[,'mu.a']

# predict
logitp_5T <- matrix(NA, nrow = nsim, ncol = 11)
logitp_random <- matrix(NA, nrow = nsim, ncol = 11)
for (i in 1:nsim){ # loop over simulations
  for (j in 1:11){ # loop over years
    logitp_5T[i,j] <- intercept[i] + beta1[i] * 1 + beta2[i] * j + beta3[i] * 1 * j
    logitp_random[i,j] <- intercept[i] + beta1[i] * 0 + beta2[i] * j + beta3[i] * 0 * j
  }
}

# back-transorm
p_5T <- plogis(logitp_5T)
p_random <- plogis(logitp_random)
```

Visualize (2)

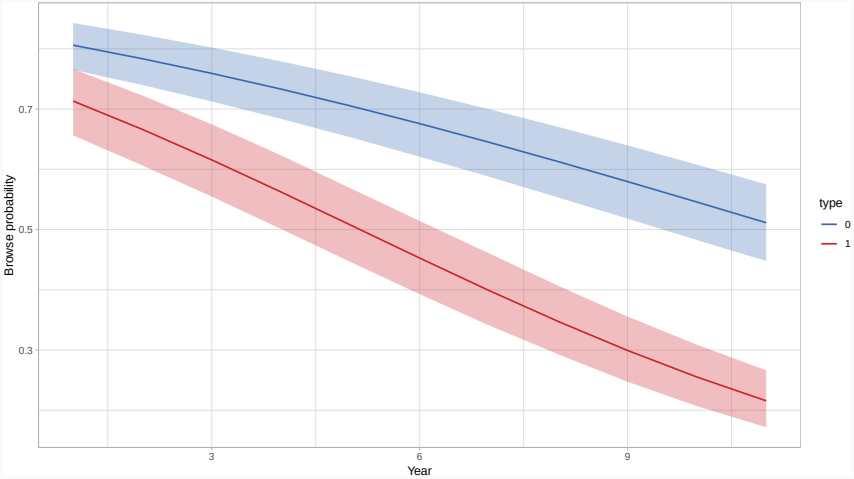
```r
# means and credible intervals
p_5T_mean <- apply(p_5T, 2, mean)
p_5T_inf <- apply(p_5T, 2, quantile, probs = 2.5/100)
p_5T_sup <- apply(p_5T, 2, quantile, probs = 97.5/100)

p_random_mean <- apply(p_random, 2, mean)
p_random_inf <- apply(p_random, 2, quantile, probs = 2.5/100)
p_random_sup <- apply(p_random, 2, quantile, probs = 97.5/100)
```

Visualize (3)

```
data.frame(year = c(1:11, 1:11),
           type = factor(c(rep(1, 11), rep(0, 11))),  # Convert type to a factor
           p_mean = c(p_5T_mean,p_random_mean),
           p_inf = c(p_5T_inf, p_random_inf),
           p_sup = c(p_5T_sup, p_random_sup)) %>%
  ggplot() +
  geom_ribbon(aes(x = year,
                  ymin = p_inf,
                  ymax = p_sup,
                  group = type,
                  fill = type),
              alpha = 0.3,
              show.legend = F) +
    geom_line(aes(x = year,
                  y = p_mean,
                  group = type,
                  color = type),
              size=0.7) +
  scale_color_manual(values = c("1" = "#CC2529", "0" = "#396AB1")) +
  scale_fill_manual(values = c("1" = "#CC2529", "0" = "#396AB1")) +
  xlab("Year")+
  ylab("Browse probability")+
  theme_light()
```

Visualize (3)



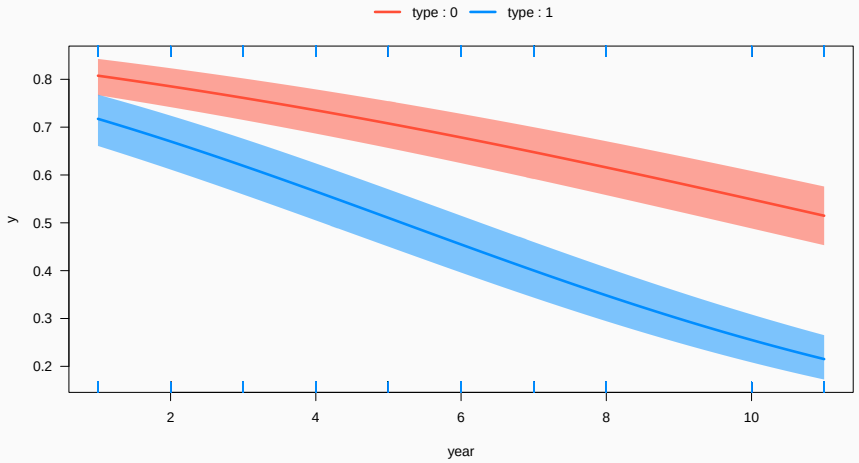
Frequentist approach

lme4 fit

```
library(lme4)
fit_lme4 <- glmer(y ~ type * year + (1|id), data = dat, family = "binomial")
fit_lme4
#> Generalized linear mixed model fit by maximum likelihood (Laplace
#>   Approximation) [glmerMod]
#>  Family: binomial  ( logit )
#> Formula: y ~ type * year + (1 | id)
#>    Data: dat
#>       AIC       BIC    logLik  deviance  df.resid
#>  21428.86  21468.02 -10709.43  21418.86     18618
#> Random effects:
#>  Groups Name        Std.Dev.
#>  id     (Intercept) 1.233
#> Number of obs: 18623, groups:  id, 113
#> Fixed Effects:
#> (Intercept)         type         year    type:year
#>     1.57173     -0.41777     -0.13750     -0.08506
```

Visualize

```
visreg::visreg(fit = fit_lme4, xvar = "year",
               by = "type", overlay = TRUE, scale = "response")
```



brms

Implementation

```
library(brms)
bayes.brms <- brm(y ~ type * year + (1|id),
                  data = dat,
                  family = bernoulli("logit"),
                  chains = 2, # nb of chains
                  iter = 5000, # nb of iterations, including burnin
                  warmup = 1000, # burnin
                  thin = 1)
```

Numerical summaries

```
summary(bayes.brms)
#>  Family: bernoulli
#>   Links: mu = logit
#> Formula: y ~ type * year + (1 | id)
#>    Data: dat (Number of observations: 18623)
#>   Draws: 2 chains, each with iter = 5000; warmup = 1000; thin = 1;
#>          total post-warmup draws = 8000
#>
#> Multilevel Hyperparameters:
#> ~id (Number of levels: 113)
#>               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
#> sd(Intercept)     1.25      0.10     1.08     1.46 1.00      947     1197
#>
#> Regression Coefficients:
#>           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
#> Intercept     1.57      0.13     1.31     1.83 1.00      404      810
#> type         -0.42      0.09    -0.59    -0.24 1.00     5716     5214
#> year         -0.14      0.01    -0.15    -0.12 1.00     8197     5558
#> type:year    -0.09      0.01    -0.11    -0.06 1.00     5668     5123
#>
#> Draws were sampled using sampling(NUTS). For each parameter, Bulk_ESS
#> and Tail_ESS are effective sample size measures, and Rhat is the potential
#> scale reduction factor on split chains (at convergence, Rhat = 1).
```

Convergence

```
plot(bayes.brms)
```