Class 8: Partial pooling and zero-inflation

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Learning outcomes:

- Be able to fit some basic zero inflation and hurdle models
- Be able to understand and fit some multinomial modelling examples

Zero-inflation and hurdle models

- Let's introduce some new data. This is data from an experiment on whiteflies:

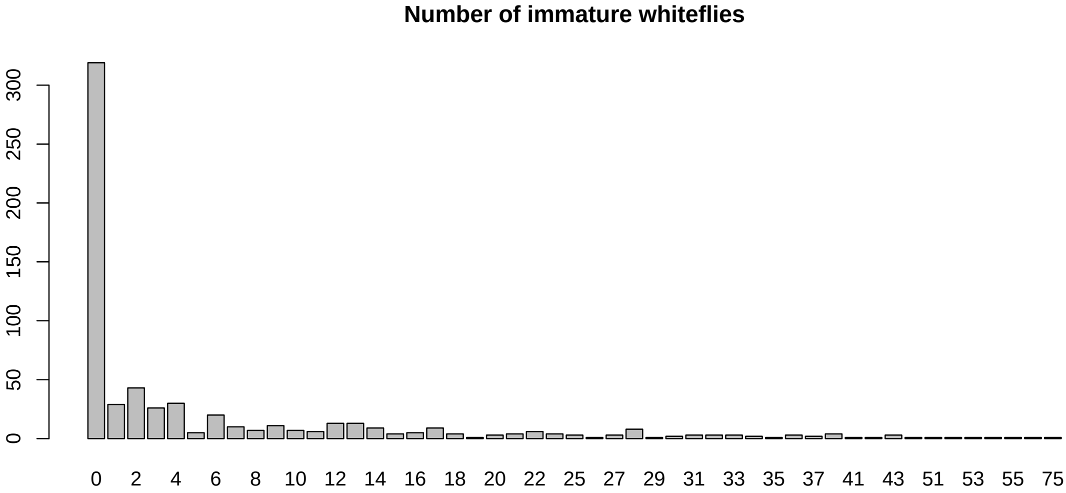
```
wf = read.csv('../data/whitefly.csv')
head(wf)
```

```
##   imm week block trt  n live plantid
## 1  15    1     3   5 12   11       1
## 2  16    2     3   5  8    6       1
## 3  28    3     3   5 10   10       1
## 4  17    4     3   5 10    8       1
## 5   9    5     3   5 10   10       1
## 6  28    6     3   5 10   10       1
```

The response variable here is the count `imm` of immature whiteflies, and the explanatory variables are `block` (plant number), `week`, and treatment `treat`.

Look at those zeros!

```
barplot(table(wf$imm),
        main = 'Number of immature whiteflies')
```



A first model

- These are count data so a Poisson distribution is a good start
- Let's consider a basic Poisson distribution model for Y_i, $i = 1, \ldots, N$ observations:

$$Y_i \sim Po(\lambda_i)$$

$$\log(\lambda_i) = \beta_{\mathrm{trt}_i}$$

- We'll only consider the treatment effect but we could run much more complicated models with e.g. other covariates and interactions

Fitting the model in JAGS

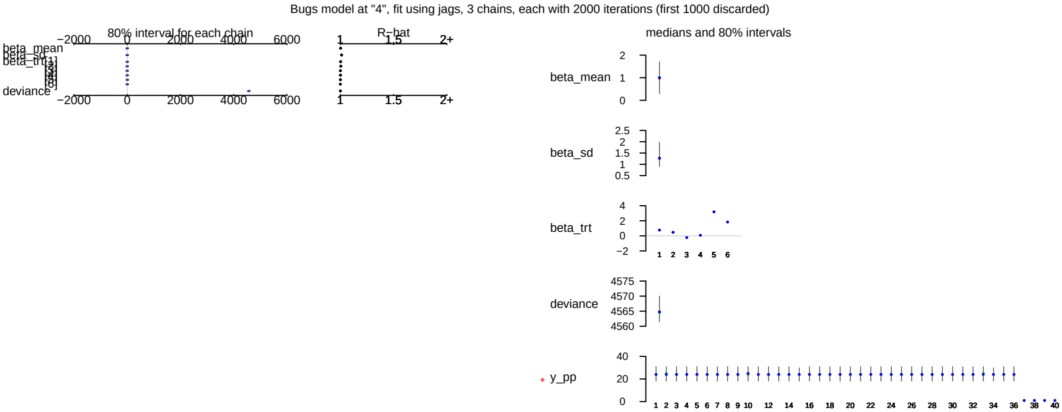
```
model_code = '
model
{
  # Likelihood
  for (i in 1:N) {
    y[i] ~ dpois(lambda[i])
    y_pp[i] ~ dpois(lambda[i])
    log(lambda[i]) <- beta_trt[trt[i]]
  }
  # Priors
  for (j in 1:N_trt) {
    beta_trt[j] ~ dnorm(beta_mean, beta_sd^-2)
  }
  beta_mean ~ dnorm(0, 10^-2)
  beta_sd ~ dt(0, 5, 1)T(0,)
}
'
```

Running the model

```
jags_run =
  jags(data = list(N = nrow(wf),
                   N_trt = length(unique(wf$trt)),
                   y = wf$imm,
                   trt = wf$trt),
       parameters.to.save = c('beta_trt', 'y_pp',
                              'beta_mean', 'beta_sd'),
       model.file = textConnection(model_code))
```

Results

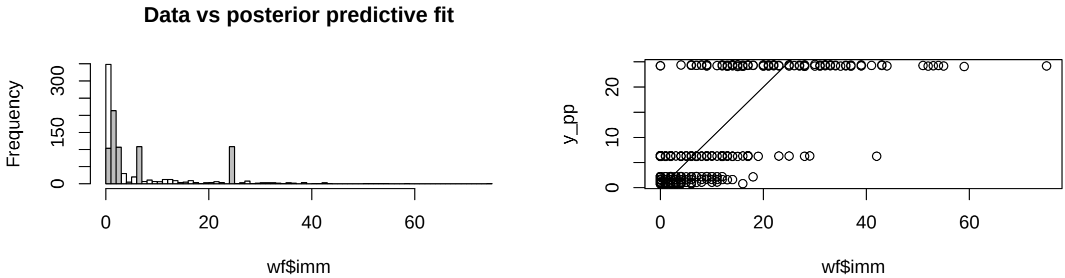
```
plot(jags_run)
```



Some clear treatment effects - treatment 5 in particular

Did the model actually fit well?

```r
y_pp = jags_run$BUGSoutput$mean$y_pp
par(mfrow=c(1,2))
hist(wf$imm, breaks = seq(0, max(wf$imm)),
     main = 'Data vs posterior predictive fit')
hist(y_pp, breaks = seq(0, max(wf$imm)), add = TRUE, col = 'gray')
plot(wf$imm, y_pp); abline(a = 0, b = 1)
```



What about the zeros?

- One way of broadening the distribution is through over-dispersion which we have already met:

$$\log(\lambda_i) \sim N(\beta_{\text{trt}_i}, \sigma^2)$$

- However this doesn't really solve the problem of excess zeros
- Instead there are a specific class of models called *zero-inflation* models which use a specific probability distribution. The zero-inflated Poisson (ZIP) with ZI parameter q_0 is written as:

$$p(y|\lambda) = \begin{cases} q_0 + (1 - q_0) \times Poisson(0, \lambda) & \text{if } y = 0 \\ (1 - q_0) \times Poisson(y, \lambda) & \text{if } y \neq 0 \end{cases}$$

Fitting models with custom probability distributions

- The Zero-inflated Poisson distribution is not included in Stan or JAGS by default. We have to create it
- It's possible to create new probability distributions in Stan
- It's a little bit fiddly to do so in JAGS, we have to use some tricks
- We will use JAGS to create a mixture of Poisson distributions; A Poisson(0) distribution for the zeros, and a Poisson(λ) distribution for the rest

Fitting the ZIP in JAGS

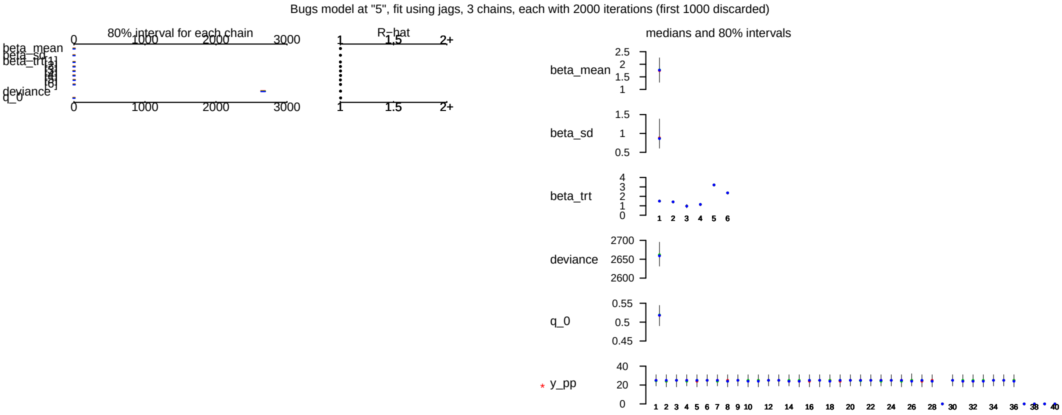
```
model_code = '
model
{
  # Likelihood
  for (i in 1:N) {
    y[i] ~ dpois(lambda[i] * z[i] + 0.0001)
    y_pp[i] ~ dpois(lambda[i] * z[i] + 0.0001)
    log(lambda[i]) <- beta_trt[trt[i]]
    z[i] ~ dbinom(q_0, 1)
  }
  # Priors
  for (j in 1:N_trt) {
    beta_trt[j] ~ dnorm(beta_mean, beta_sd^-2)
  }
  beta_mean ~ dnorm(0, 10^-2)
  beta_sd ~ dt(0, 5, 1)T(0,)
  q_0 ~ dunif(0, 1)
}
'
```

Running the model

```r
jags_run =
  jags(data = list(N = nrow(wf),
                   N_trt = length(unique(wf$trt)),
                   y = wf$imm,
                   trt = wf$trt),
       parameters.to.save = c('beta_trt','q_0', 'y_pp',
                              'beta_mean', 'beta_sd'),
       model.file = textConnection(model_code))
```

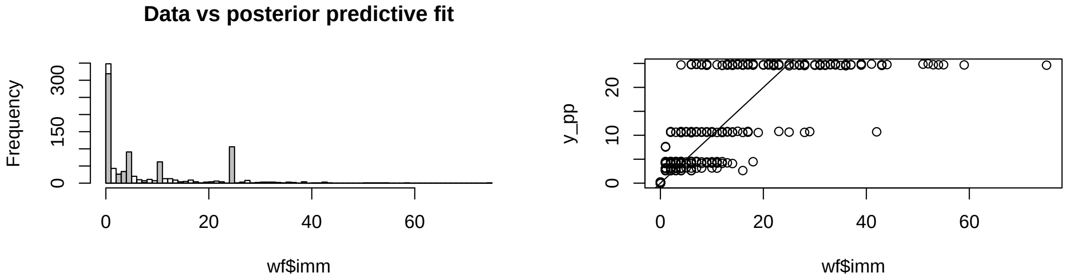
Results

```
plot(jags_run)
```



Did it work any better? - code

```
y_pp = jags_run$BUGSoutput$mean$y_pp
par(mfrow=c(1,2))
hist(wf$imm, breaks = seq(0, max(wf$imm)),
     main = 'Data vs posterior predictive fit')
hist(y_pp, breaks = seq(0, max(wf$imm)), add = TRUE, col = 'gray')
plot(wf$imm, y_pp); abline(a = 0, b = 1)
```



Some more notes on Zero-inflated Poisson

- This model seems to predict the number of zeros pretty well. It would also be interesting to perhaps try having a different probability of zeros (q_0) for different treatments
- It might be that the other covariates explain some of the zero behaviour
- We could further add in both zero-inflation and over-dispersion

An alternative: hurdle models

- ZI models work by having a parameter (here q_0) which is the probability of getting a zero, and so the probability of getting a Poisson value (which could also be a zero) is 1 minus this value
- An alternative (which is slightly more complicated) is a hurdle model where q_0 represents the probability of the *only way* of getting a zero. With probability (1-q_0) we end up with a special Poisson random variable which has to take values 1 or more
- In some ways this is richer than a ZI model since zeros can be deflated or inflated
- This is a bit fiddlier to fit in JAGS

A hurdle-Poisson model in JAGS

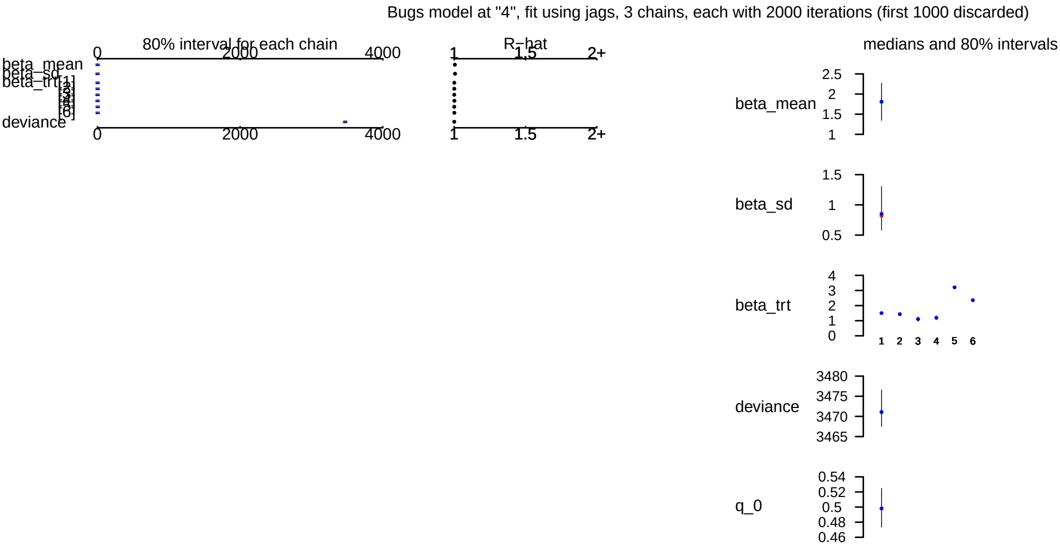
```
model_code = '
model
{
  # Likelihood
  for (i in 1:N) {
    y[i] ~ dpois(lambda[i])T(1,)
    log(lambda[i]) <- beta_trt[trt[i]]
  }
  for(i in 1:N_0) {
    y_0[i] ~ dbin(q_0, 1)
  }
  # Priors
  for (j in 1:N_trt) {
    beta_trt[j] ~ dnorm(beta_mean, beta_sd^-2)
  }
  beta_mean ~ dnorm(0, 10^-2)
  beta_sd ~ dt(0, 5, 1)T(0,)
  q_0 ~ dunif(0, 1)
}
'
```

Running the model

```
jags_run =
  jags(data = list(N = nrow(wf[wf$imm > 0,]),
                   N_trt = length(unique(wf$trt)),
                   y = wf$imm[wf$imm > 0],
                   y_0 = as.integer(wf$imm == 0),
                   N_0 = nrow(wf),
                   trt = wf$trt[wf$imm > 0]),
       parameters.to.save = c('beta_trt', 'q_0',
                              'beta_mean', 'beta_sd'),
       model.file = textConnection(model_code))
```

Results

```r
plot(jags_run)
```



Some final notes on ZI models

- To complete the Poisson-Hurdle fit we would need to simulate from a truncated Poisson model. This starts to get very fiddly though - see the `jags_examples` repository for worked examples
- We can extend these models further by using a better count distribution such as the negative binomial which has an extra over-dispersion parameter
- We can also add covariates into the zero-inflation component, though it is not always clear whether this is desirable

The multinomial distribution

- Multinomial data can be thought of as multivariate discrete data
- It's usually used in two different scenarios:
  1. For classification, when you have an observation falling into a single one of K possible categories
  2. For multinomial regression, where you have a set of counts which sum to a known value N
- We will just consider the multinomial regression case, whereby we have observations $y_i = [y_{i1}, \ldots, y_{iK}]$ where the sum $\sum_{k=1}^{K} y_{ik} = N_i$ is fixed
- The classification version is a simplification of the regression version

Some new data! - pollen

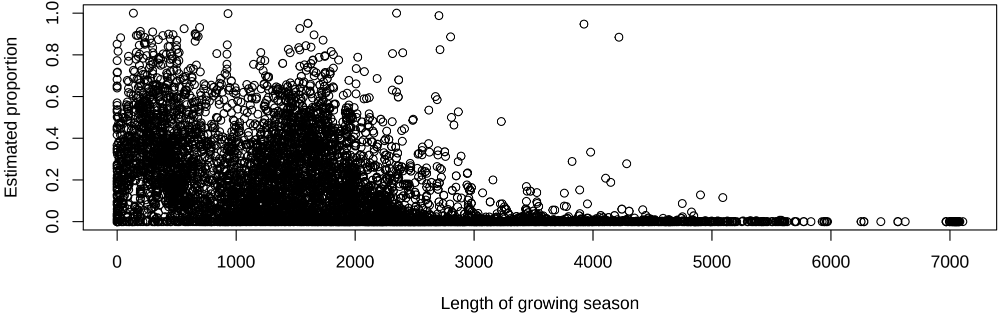
```
pollen = read.csv('../data/pollen.csv')
head(pollen)
```

```
##   GDD5 MTCO Abies Alnus Betula Picea Pinus.D Quercus.D Gramineae
## 1 1874 -7.9     0    50    158     7     721        22         0
## 2 1623 -5.5     0    38     28   302     537        19         0
## 3 1475 -4.7     0   276    183   110     136         0         0
## 4 1360 -8.8     0   111    354   141     364         0         0
## 5 1295 -6.9     0    91     50   151     708         0         0
## 6 1539 -7.8     0    51    194    82     673         0         0
```

These data are pollen counts of 7 varieties of pollen from modern samples with two covariates

Some plots

- The two covariates represent the length of the growing season (GDD5) and harshness of the winter (MTCO)
- The task is to find which climate regimes each pollen variety favours



A multinomial model

- The multinomial distribution is often written as:

  $$[y_{i1}, \dots, y_{iK}] \sim Mult(S_i, \{p_{i1}, \dots, p_{iK}\})$$

  or, for short:

  $$y_i \sim Mult(S_i, p_i)$$

- The key parameters here are the probability vectors p_i. It's these we want to use a link function on to include the covariates
- We need to be careful as each must sum to one: $\sum_{k=1}^{K} p_{ik} = 1$. Any link function must satisfy this constraint

Prior distributions on probability vectors

- When $K = 2$ we're back the binomial-logit we met in the first day, and we can use the logit link function
- When $K > 2$ a common function to use is the *soft-max* function:

$$p_{ik} = \frac{\exp(z_{ik})}{\sum_{j=1}^{K} \exp(z_{ij})}$$

- This is a generalisation of the logit function
- The next layer of our model sets, e.g.:

$$z_{ik} = \beta_0 + \beta_1 \mathrm{GDD5}_i + \gamma_2 \mathrm{MTCO}_i + \ldots$$

JAGS code

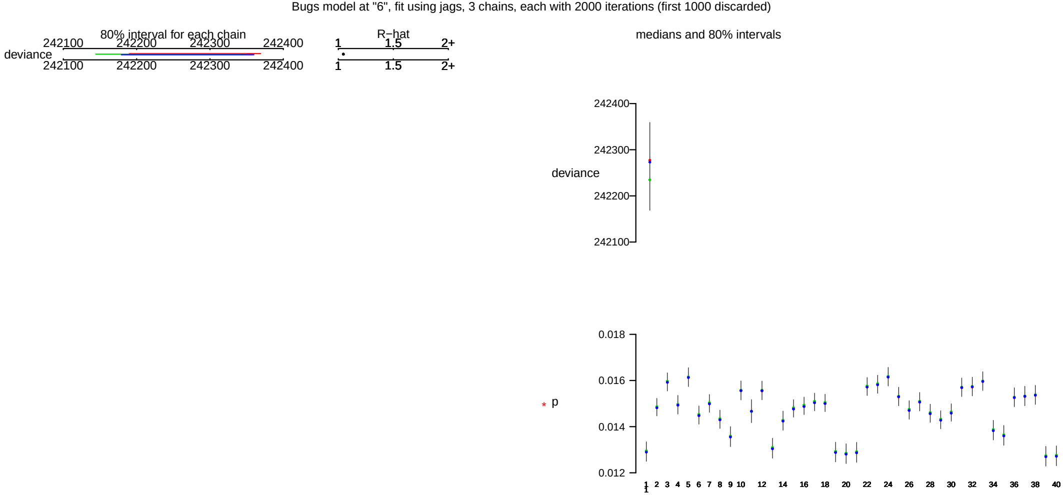
```
model_code = '
model
{
  # Likelihood
  for (i in 1:N) { # Observaton loops
    y[i,] ~ dmulti(p[i,], S[i])
    for(j in 1:M) { # Category loop
      exp_z[i,j] <- exp(z[i,j])
      p[i,j] <- exp_z[i,j]/sum(exp_z[i,])
      z[i,j] <- beta[j,]%*%x[i,]
    }
  }
  # Prior
  for(j in 1:M) {
    for(k in 1:K) {
      beta[j,k] ~ dnorm(0, 0.1^-2)
    }
  }
}
'
```

Let’s fit it (first 500 obs only)

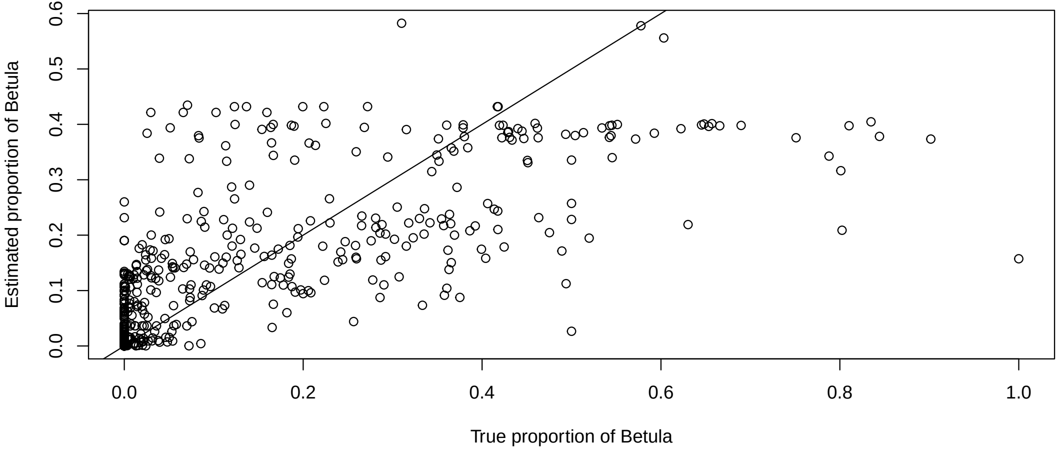
```r
model_data = list(N = nrow(pollen[1:500,]),
                  y = pollen[1:500,3:9],
                  x = cbind(1, scale(cbind(pollen[1:500,1:2],
                                           pollen[1:500,1:2]^2))),
                  S = pollen[1:500,10],
                  K = 5, # Number of covars
                  M = 7) # Number of categories
# Run the model
model_run = jags(data = model_data,
                 parameters.to.save = c("p"),
                 model.file = textConnection(model_code))
```

Results 1

```r
plot(model_run)
```



Results 2


Estimated proportion of Betula
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.0
0.2
0.4
0.6
0.8
1.0
True proportion of Betula

Notes about this model

- This model is not going to fit very well, since it is unlikely that a linear relationship between the covariates and the pollen counts will match the data
- It might be better to use e.g. a spline model (covered in the next class)
- Similarly we might need some complex interactions between the covariates as they are strongly linked
- We have constrained the parameters here so that the slopes and intercepts borrow strength across species. Does this make sense? What else could we do?

Some final notes about multinomial models

- These models can be a pain to deal with as there are tricky constraints on the β parameters to make them all sum to 1. Instead it's often easier to just put a tight prior distribution on them, e.g. $\beta \sim N(0, 0.1)$
- The `softmax` function is one choice but there are lots of others (logistic ratios, the Dirichlet distribution, . . .)
- Whilst the classification version of this model just has binary y_i (with just a single 1 in it, i.e. $S_i = 1$) most packages (including JAGS and Stan) have a special distribution (e.g. `dcat` in JAGS) for this situation

Summary

- We have fitted some zero inflated and hurdle Poisson models in JAGS
- We have seen a simple multinomial logistic regression