

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:

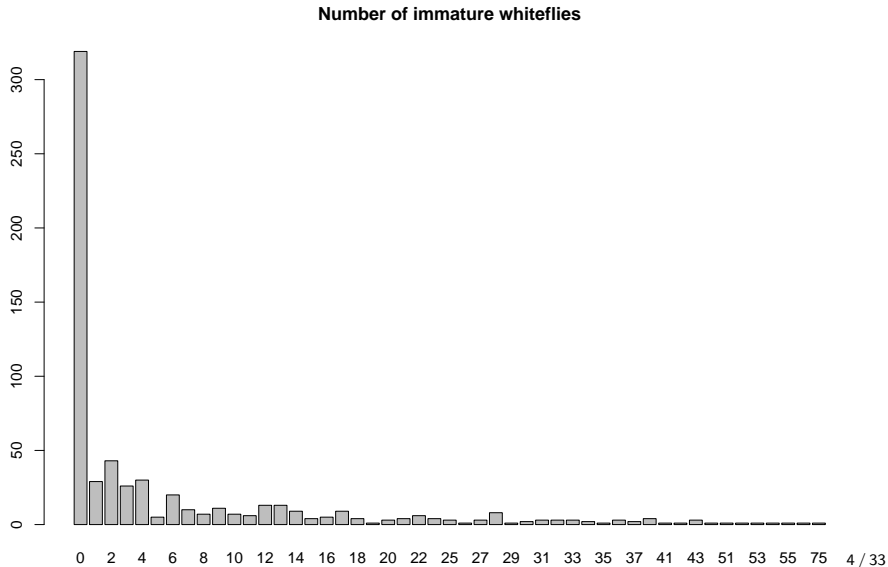
```
wf = read.csv('../data/whitefly.csv')  
head(wf)
```

	##	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 , $i = 1, \dots, N$ observations:

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

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

- ▶ 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

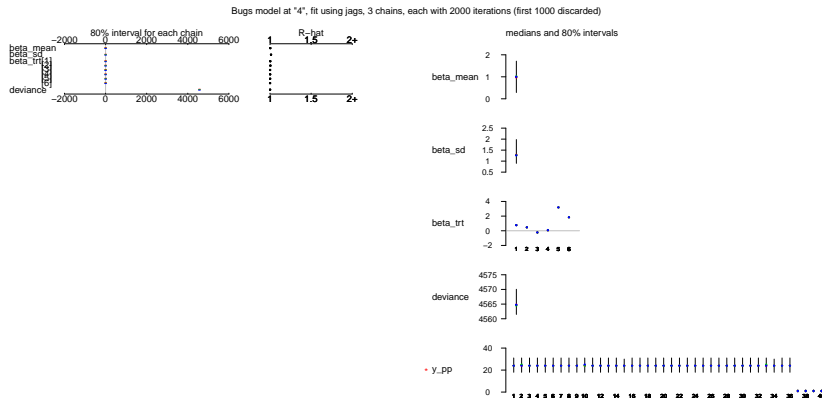
```
model_code = '  
model  
{  
  # Likelihood  
  for (i in 1:N) {  
    y[i] ~ dpois(lambda[i])  
    y_pp[i] ~ dpois(lambda[i])  
    log(lambda[i]) <- beta_trt[trt[i]]  
  }  
  # Priors  
  for (j in 1:N_trt) {  
    beta_trt[j] ~ dnorm(beta_mean, beta_sd^-2)  
  }  
  beta_mean ~ dnorm(0, 10^-2)  
  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)
```

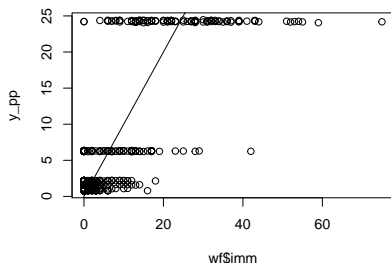
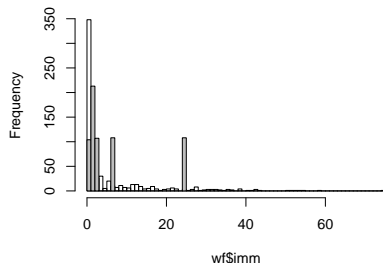


Some clear treatment effects - treatment 5 in particular

Did the model actually fit well?

```
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 =
plot(wf$imm, y_pp); abline(a = 0, b = 1)
```

Data vs posterior predictive fit



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:

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

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 $\text{Poisson}(0)$ distribution for the zeros, and a $\text{Poisson}(\lambda)$ distribution for the rest

Fitting the ZIP in JAGS

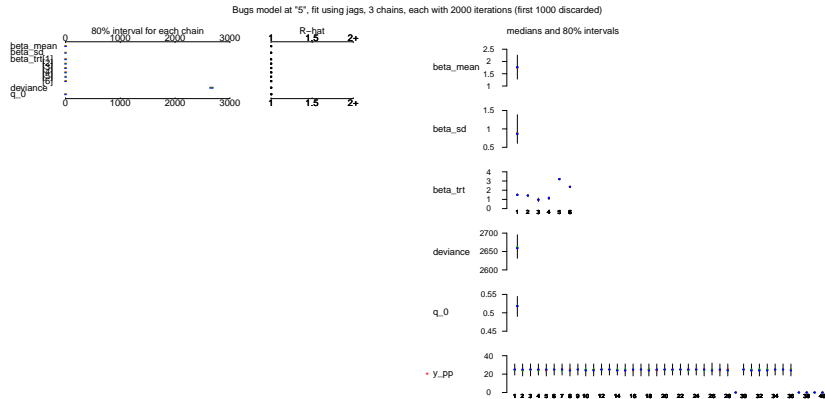
```
model_code = '  
model  
{  
  # Likelihood  
  for (i in 1:N) {  
    y[i] ~ dpois(lambda[i] * z[i] + 0.0001)  
    y_pp[i] ~ dpois(lambda[i] * z[i] + 0.0001)  
    log(lambda[i]) <- beta_trt[trt[i]]  
    z[i] ~ dbinom(q_0, 1)  
  }  
  # Priors  
  for (j in 1:N_trt) {  
    beta_trt[j] ~ dnorm(beta_mean, 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

```
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

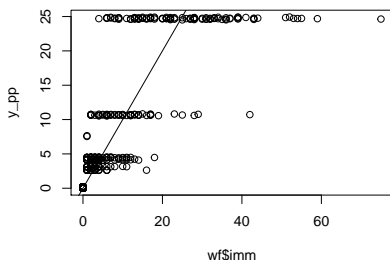
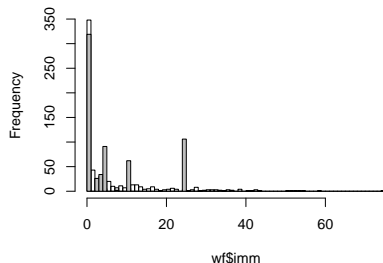
```
plot(jags_run)
```



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)
```

Data vs posterior predictive fit



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)  
}
```

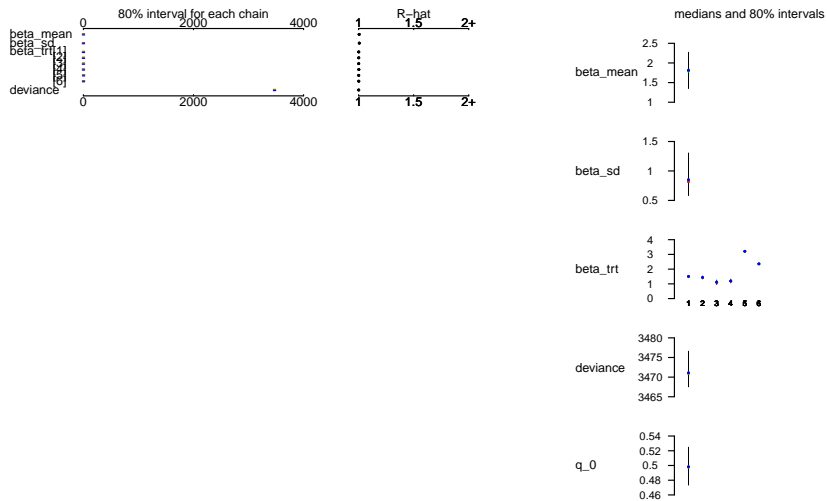
Running the model

```
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

```
plot(jags_run)
```

Bugs model at "6", fit using jags, 3 chains, each with 2000 iterations (first 1000 discarded)



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 $y_i = [y_{i1}, \dots, y_{iK}]$ 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

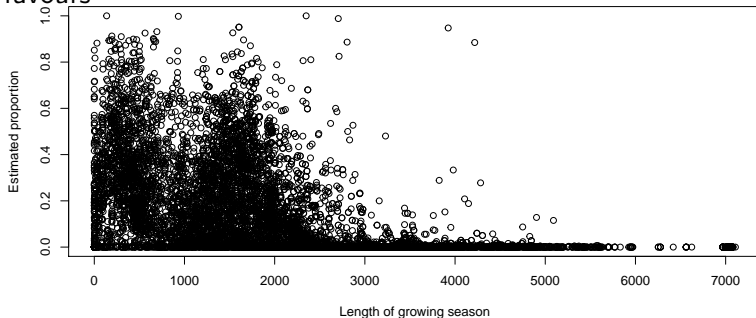
```
pollen = read.csv('../data/pollen.csv')  
head(pollen)
```

##	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:

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

or, for short:

$$y_i \sim \text{Mult}(S_i, p_i)$$

- ▶ 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.:

$$z_{ik} = \beta_0 + \beta_1 \text{GDD5}_i + \gamma_2 \text{MTCO}_i + \dots$$

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)

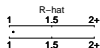
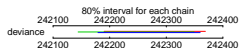
```
model_data = list(N = nrow(pollen[1:500,]),
                  y = pollen[1:500,3:9],
                  x = cbind(1, scale(cbind(pollen[1:500,1:2],
                                           pollen[1:500,1:2])),
                  S = pollen[1:500,10],
                  K = 5, # Number of covars
                  M = 7) # Number of categories

# Run the model
model_run = jags(data = model_data,
                 parameters.to.save = c("p"),
                 model.file = textConnection(model_code))
```

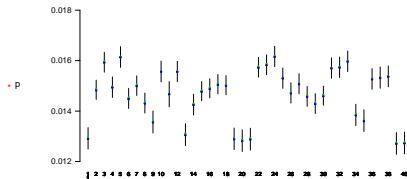
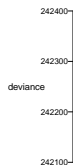
Results 1

```
plot(model_run)
```

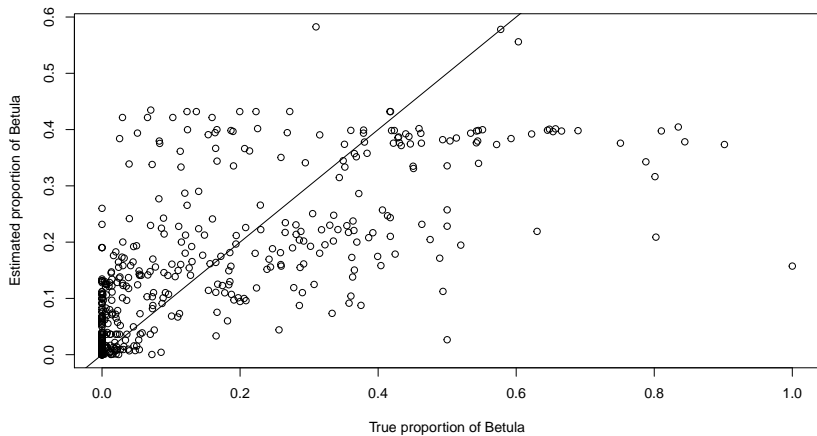
Bugs model at "4", fit using jags, 3 chains, each with 2000 iterations (first 1000 discarded)



medians and 80% intervals



Results 2



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