### Generalized Linear Models

Lecture 10. Count data models III. Models with excess zeros

#### Data with excess zeros

There are too many zeros (probability distribution suggests less), thus there are so-called 'false' zeros and 'true' zeros

#### Motivating examples

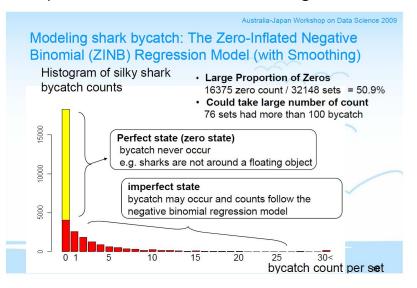
- Small claims not reported in non-life insurance
- Defective products in a manufacturing process (Lambert, 1992)
- Absent days because of sick-leave (Lam et al, 2006)
- Domestic violence cases (Famoye, Singh, 2006)
- Shark counting via bycatch

Tools and examples about how to deal with zero-modified data:

Zuur, A.F., Ieno, E.N., Walker, N., Saveliev, A.A., Smith, G.M. (2009). *Mixed Effects Models and Extensions in Ecology with R* 

http://www.springer.com/life+sciences/ecology/book/978-0-387-87457-9

## Example 1. Zero inflation in estimating the shark count



### Example 2: Zero inflation in teeth data

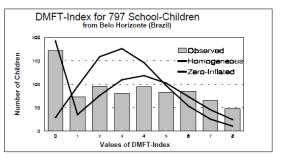


Figure 1: DMFT distribution at begin of study

#### DMFT index - Decay, Missing, Filled Teeth - counts problematic teeth

Source: Böhning, Dietz, Schlattmann (1997). Zero inflated Count Models and their Applications in Public Health and Social Science. In: Applications of Latent Trait and Latent Class Models in the Social Sciences, Ch 32, p 334.

### Approach 1. Zero inflated model

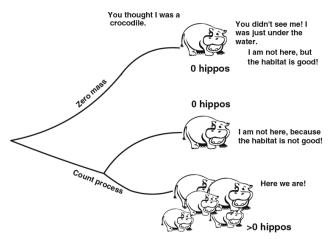


Fig. 11.5 Sketch of the underlying principle of mixture models (ZIP and ZINB). In counting hippos at sites, one can measure a zero because the habitat is not good (the hippos don't like the covariates), or due to poor experimental design and inexperienced observers (or experienced observers but difficult to observe species)

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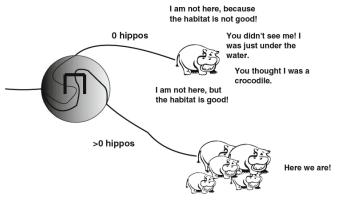


Fig. 11.4 Sketch of a two-part, or hurdle model. There are two processes; one is causing zeros versus non-zeros, the other process is explaining the non-zero counts. This is expressed with the hurdle in the *circle*; you have to cross it to get non-zero counts. The model does not make a distinction between the different types of zeros

Source: Zuur et al. 2009

## Zero Inflated (ZI) model. Setup (1)

#### Problem: too many zeros

**Idea:** we divide the data in two imaginary groups:

- First group only zeros (the **false** zeros). This group is also called the observations with zero mass
- Second group the count data, which may produce zeros (true zeros) and values larger than zero.

#### Note that

- We are not actively splitting the data in two groups; it is just an assumption that we have these two groups.
- We do not know which of the observations with zeros belong to a specific group.

## Zero Inflated (ZI) model. Setup (2)

#### Assume now that the data comes from

- the process of (false) zeros with probability  $\pi, \ \ 0 \le \pi < 1$
- ullet the counting process with probability  $1-\pi$

Then we have

$$\mathbf{P}{Y = 0} = \pi + (1 - \pi)p(0)$$

$$\mathbf{P}{Y = y} = (1 - \pi)p(y), \quad y = 1, 2, ...$$
(\*\*)

#### p(y) – Poisson or NB pmf

The resulting model is a certain mixture of models:

- for the binary part (Bernoulli process) we use logit or probit link
- for the counting process we apply Poisson or NB model

# ZIP model (Zero Inflated Poisson)

Let us start with Poisson model with pmf

$$p(y_i; \mu_i) = \frac{\exp(-\mu_i)\mu_i^{y_i}}{y_i!},$$

i.e. we estimate counts with the Poisson model  $\mu_i = \mu_i(\beta) = \exp(\mathbf{x}_i^T \beta)$ 

Let us also have a process generating zeros:  $\pi_i = \pi_i(\gamma)$ 

Now the relations (\*) and (\*\*) from previous slide allow us to write

#### ZIP model

$$\begin{aligned} \mathbf{P}\{Y_i = 0\} &= \pi_i(\gamma) + (1 - \pi_i(\gamma)) \exp(-\mu_i(\beta)) \\ \mathbf{P}\{Y_i = y_i\} &= (1 - \pi_i(\gamma)) \frac{\exp(-\mu_i(\beta))[\mu_i(\beta)]^{y_i}}{y_i!}, \ y_i = 1, 2, ... \end{aligned}$$

 $\beta$  – parameter vector of the counting process  $\gamma$  – parameter vector the process generating zeros

### ZIP model: mean and variance

Since  $\mathbf{P}(\mathbf{Y}_i = y_i) = (1 - \pi_i)p(y_i)$ , the mean of the response is:

$$\mathbf{E}(Y_i) = \mu_i (1 - \pi_i)$$

and to find the variance, we use

$$\mathbf{D}(Y_i) = \mathbf{E}(Y_i^2) - (\mathbf{E}Y_i)^2 = (1 - \pi_i)(\mu_i + \mu_i^2) - (1 - \pi_i)^2 \mu_i^2$$

Thus the variance of the response is

$$\mathbf{D}(Y_i) = \mu_i (1 - \pi_i)(1 + \mu_i \pi_i)$$

Variance is greater than the mean:  $\mathbf{D}(Y_i) > \mathbf{E}(Y_i)$ 

⇒ excessive number of (false) zeros causes overdispersion!

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## Estimation of ZIP model

To estimate parameter  $\gamma$ , often a *logit*-model is used (to estimate the probability of zeros!):

$$\ln \frac{\pi_i(\boldsymbol{\gamma})}{1 - \pi_i(\boldsymbol{\gamma})} = \boldsymbol{w}_i^T \boldsymbol{\gamma}, \quad \pi_i(\boldsymbol{\gamma}) = \frac{\exp(\boldsymbol{w}_i^T \boldsymbol{\gamma})}{1 + \exp(\boldsymbol{w}_i^T \boldsymbol{\gamma})}$$

If the zero-model is *logit*, the mean of ZIP model is

$$\mathbf{E}(Y_i) = \frac{\exp(\mathbf{x}_i^T \boldsymbol{\beta})}{1 + \exp(\mathbf{w}_i^T \boldsymbol{\gamma})}$$

Another common choice for estimating  $\gamma$  is probit-model  $\pi_i(\gamma) = \Phi(\mathbf{w}_i^T \gamma)$ 

Now, the arguments of the ZIP model are divided into two groups:

• arguments of the counting process, x:

$$\mu_i(\boldsymbol{\beta}) = \mu_i(\boldsymbol{x}_i^T \boldsymbol{\beta})$$

• arguments of the zero-generating process, w:

$$\pi_i(\boldsymbol{\gamma}) = \pi_i(\boldsymbol{w}_i^T \boldsymbol{\gamma})$$

Usually  $x_i$  and  $w_i$  differ

## Log-likelihood for ZIP model

Log-likelihood of ZIP model consists of log-likelihood of zero-model and log-likelihood of Poisson model

If zero-model is logit:

$$\begin{split} I(\boldsymbol{y}; \boldsymbol{\beta}, \boldsymbol{\gamma}) &= \sum_{i: y_i = 0} \ln[\exp(\boldsymbol{w}_i^T \boldsymbol{\gamma}) + \exp(-\exp(\boldsymbol{x}_i^T \boldsymbol{\beta}))] \\ &+ \sum_{i: y_i > 0} [y_i \boldsymbol{x}_i^T \boldsymbol{\beta} - \exp(\boldsymbol{x}_i^T \boldsymbol{\beta}) - \ln y_i!] - \sum_{i=1}^n \ln[1 + \exp(\boldsymbol{w}_i^T \boldsymbol{\gamma})] \end{split}$$

If zero-model is probit:

$$I(\mathbf{y}; \boldsymbol{\beta}, \boldsymbol{\gamma}) = \sum_{i: y_i = 0} \ln[\Phi(\mathbf{w}_i^T \boldsymbol{\gamma}) + (1 - \Phi(\mathbf{w}_i^T \boldsymbol{\gamma})) \exp(-\exp(\mathbf{x}_i^T \boldsymbol{\beta}))] + \sum_{i: y_i > 0} [\ln(1 - \Phi(\mathbf{w}_i^T \boldsymbol{\gamma})) - \exp(\mathbf{x}_i^T \boldsymbol{\beta}) + y_i \mathbf{x}_i^T \boldsymbol{\beta} - \ln y_i!]$$

### Example. Australian doctor visits

The dataset contains information for approximately 5,000 Australian individuals about the number and possible determinants of doctor visits that were made during a two-week interval.

#### Variables used for modelling:

- doctorco response variable, the number of visits
- sex 0/1 (male/female)
- age age/100 (people over 72 are coded to age 72)
- illness number of illnesses during 2 weeks (1, .., 5; over 5 coded to 5)
- income income (in 1000AUD)
- hscore health score (bigger score means worse health)

#### Arguments used:

- In zero-model: only age was used (as empirical studies show that younger people tend to not go to a doctor)
- In counting model: all mentioned arguments

# How do we know that we have excess zeros? (1)

Simplest way is to compare the amount of zeros in data with the amount estimated by model:

```
# Apply Poisson and NB models
modelP=glm(doctorco~sex+age+illness+hscore,family="poisson",data=docvisit)
library(MASS)
modelNB=glm.nb(doctorco~sex+age+illness+hscore,data=docvisit)
data_counts = table(docvisit$doctorco) # actual counts in data
# counts by Poisson model
lambda=fitted(modelP)
modelP_counts = NA
for (i in (0:9)) {
  modelP_counts[i+1] = nrow(docvisit)*mean(dpois(i,lambda=lambda))
}
```

# How do we know that we have excess zeros? (2)

```
# counts by NB model
mu = fitted(modelNB)
k = modelNB$theta
modelNB counts = NA
for (i in (0:9)) {
  modelNB_counts[i+1] = nrow(docvisit)*mean(dnbinom(i,mu=mu,size=k))
}
# Comparison of counts
> rbind(data_counts, modelP_counts, modelNB_counts)
data_counts 4141.000 782.000 174.0000 30.00000 24.000000
modelP_counts 3923.240 1027.489 192.3367 36.83231
modelNB counts 4162.377 711.002 193.1876 66.62437 27.385283
                                 6
data_counts 9.000000 12.0000000 12.00000000 5.00000000 1.000000000
modelP_counts 1.768392
                         0.401649 0.08806722 0.01824272 0.003535122
```

modelNB counts 12.849942 6.654180 3.70833122 2.18477570 1.343859220

# Example solution in R. ZIP model (1)

```
> library(pscl)
> modelZIP1 = zeroinfl(doctorco~sex+age+illness+income+hscore | age,
           dist="poisson", link="logit", data=docvisit)
> summary(modelZIP1)
Count model coefficients (poisson with log link):
          Estimate Std. Error z value Pr(>|z|)
sex 0.12474 0.06265 1.991 0.0465 *
age -0.20144 0.20192 -0.998 0.3185
illness 0.23971 0.02013 11.906 < 2e-16 ***
income -0.16805 0.09118 -1.843 0.0653.
hscore 0.08775 0.01006 8.723 < 2e-16 ***
Zero-inflation model coefficients (binomial with logit link):
          Estimate Std. Error z value Pr(>|z|)
(Intercept) 1.0945 0.1673 6.543 6.03e-11 ***
   -2.3300 0.3654 -6.376 1.82e-10 ***
age
. . .
Number of iterations in BFGS optimization: 17
Log-likelihood: -3500 on 8 Df
```

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# Example solution in R. ZIP model (1)

```
> modelZIP2 = zeroinfl(doctorco~sex+illness+hscore | age,
           dist="poisson",link="logit", data=docvisit)
> summary(modelZIP2)
Count model coefficients (poisson with log link):
          Estimate Std. Error z value Pr(>|z|)
sex 0.14999 0.06029 2.488 0.0129 *
illness 0.24005 0.01991 12.056 <2e-16 ***
hscore 0.08948 0.01002 8.933 <2e-16 ***
Zero-inflation model coefficients (binomial with logit link):
          Estimate Std. Error z value Pr(>|z|)
(Intercept) 1.0164 0.1297 7.836 4.64e-15 ***
age -2.1570 0.2690 -8.019 1.07e-15 ***
Number of iterations in BFGS optimization: 14
Log-likelihood: -3502 on 6 Df
```

# ZINB model (Zero Inflated Negative Binomial )

Idea is very similar to ZIP model, the difference is that the Poisson count model is substituted with the NB model

Let us recall the pmf of NB distribution:

$$p(y_i; \mu_i, k) = \frac{\Gamma(k + y_i)}{y_i! \ \Gamma(k)} \ \left(\frac{k}{k + \mu_i}\right)^k \left(1 - \frac{k}{k + \mu_i}\right)^{y_i}$$

We again have

- a counting process, with  $\mu_i = \mu_i(\beta) = \exp(\mathbf{x}_i^T \beta)$
- ullet a process generating zeros  $\pi_i(oldsymbol{\gamma})$

#### ZINB model

$$\mathbf{P}\{Y_i = 0\} = \pi_i(\gamma) + [1 - \pi_i(\gamma)] (\frac{k}{k + \mu_i(\beta)})^k 
\mathbf{P}\{Y_i = y_i\} = [1 - \pi_i(\gamma)] p(y_i; \mu_i, k), \ y_i = 1, 2, ...$$

$$eta$$
 – parameter vector of the counting process  $\gamma$  – parameter vector the process generating zeros

Main choices to estimate  $\pi_i$  are again logit or probit model

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### Mean and variance of ZINB model

Mean of the response variable is

$$\mathbf{E}(Y_i) = \mu_i (1 - \pi_i)$$

Now, assuming the zero model is logit, we can proceed and obtain

$$\mathbf{E}(Y_i) = \frac{\exp(\boldsymbol{x}_i^T \boldsymbol{\beta})}{1 + \exp(\boldsymbol{w}_i^T \boldsymbol{\gamma})}$$

Variance of the response variable is

$$\mathbf{D}(Y_i) = \mu_i (1 - \pi_i) (\mu_i + \frac{\mu_i^2}{k}) + \mu_i^2 (\pi_i^2 + \pi_i)$$

Clearly  $\mathbf{D}(Y_i) > \mathbf{E}(Y_i)$ 

# Example solution in R. ZINB model (1)

```
> modelZINB1=zeroinfl(doctorco~sex+age+illness+income+hscore|age,
           dist="negbin", link="logit", data=docvisit)
> summary(modelZINB1)
. . .
Count model coefficients (negbin with log link):
          Estimate Std. Error z value Pr(>|z|)
sex 0.20288 0.07085 2.863 0.004191 **
age 0.27688 0.25984 1.066 0.286614
illness 0.27450 0.02397 11.453 < 2e-16 ***
income -0.15122 0.10311 -1.467 0.142500
hscore 0.10969 0.01355 8.096 5.66e-16 ***
Log(theta) -0.38889 0.10685 -3.640 0.000273 ***
Zero-inflation model coefficients (binomial with logit link):
          Estimate Std. Error z value Pr(>|z|)
(Intercept) 0.7688 0.8535 0.901 0.3677
age -8.8293 4.0542 -2.178 0.0294 *
. . .
Log-likelihood: -3381 on 9 Df
```

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# Example solution in R. ZINB model (2)

```
> modelZINB2 = zeroinfl(doctorco~sex+illness+hscore | age,
            dist="negbin",link="logit",data=docvisit)
> summary(modelZINB2)
. . .
Count model coefficients (negbin with log link):
          Estimate Std. Error z value Pr(>|z|)
sex 0.23801 0.06887 3.456 0.000549 ***
illness 0.28089 0.02380 11.800 < 2e-16 ***
hscore 0.11050 0.01351 8.181 2.81e-16 ***
Log(theta) -0.32524 0.10261 -3.170 0.001526 **
Zero-inflation model coefficients (binomial with logit link):
          Estimate Std. Error z value Pr(>|z|)
(Intercept) 0.8226 0.4855 1.694 0.09023.
age -7.4834 2.2866 -3.273 0.00107 **
Theta = 0.7224
```

Number of iterations in BFGS optimization: 26 Log-likelihood: -3384 on 7 Df

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# Hurdle model (also called ZA (Zero Altered) model)

#### Setup:

- too many zeros in data
- zeros in count process are not of interest

#### Two-step process:

- binary process that models the probability of event that the counting process starts
- ② counting process (without zeros)

### Hurdle (ZA) model

$$\mathbf{P}\{Y_i = 0\} = f_1(0) 
\mathbf{P}\{Y_i = y_i | Y_i > 0\} = f_2(y_i) \frac{1 - f_1(0)}{1 - f_2(0)}, \ y_i = 1, 2, \dots$$
(\*\*\*)

where  $f_1$  and  $f_2$  are some pmf-s (corresponding to binary process and count process)

## Deriving the probabilities for Hurdle model

To explain the formula (\*\*\*), let us look at the setup in more details:

- First step: a binary process C:
  - C = 0 counting is not yet started,  $P\{C = 0\} = f_1(0)$ • C = 1 – 'hurdle is crossed' and counting is started,  $P\{C = 1\} = 1 - f_1(0)$
- ② Second step: the conditional distribution of the counting process (given C=1, i.e. 'hurdle is crossed') is found:

$$\mathbf{P}\{Y_i = y_i | C = 1\} = \frac{f_2(y_i)}{1 - f_2(0)}, \ y_i = 1, 2, \dots,$$

where  $f_2$  is the (non-conditional) pmf of the counting process

Now, since

 $P\{Y_i = y_i\} = P\{Y_i = y_i | C = 1\}P\{C = 1\} = P\{Y_i = y_i | C = 1\}(1 - f_1(0)),$  the equation (\*\*\*) follows:

$$\mathbf{P}\{Y = y_i | Y > 0\} = \frac{f_2(y_i)}{1 - f_2(0)} (1 - f_1(0))$$

# Poisson Hurdle (ZAP) model

Notation and assumptions:

- $f_2$  pmf of count model (Poisson)
- $\bullet$   $f_1$  pmf of zero model (logistic/normal: logit/probit-link for binary model)

### Poisson Hurdle (ZAP) logit model

$$p(y_i, \mu_i | y_i > 0) = \frac{[1 - \mathbf{P}\{Y_i = 0\}] \exp(-\mu_i) \mu_i^{y_i}}{[1 - \exp(-\mu_i)] y_i!} = \frac{\exp(-\mu_i) \mu_i^{y_i}}{[1 + \exp(\eta_{i0})] [1 - \exp(-\mu_i)] y_i!}$$

where

• 
$$\mathbf{P}{Y_i = 0} = \frac{\exp(\eta_0)}{1 + \exp(\eta_{i0})}$$

• 
$$\eta_{0i} = \ln \frac{\pi_i}{1-\pi_i} = \boldsymbol{w}_i^T \boldsymbol{\gamma}, \ \pi_i = \mathbf{P}\{Y_i = 0\}, \ \mu_i = \exp(\boldsymbol{x}_i^T \boldsymbol{\beta})$$

- $\mathbf{w}_i$  argument vector for zero model
- x<sub>i</sub> − argument vector for count model

The derivation of NB Hurdle model (ZANB) is analogous

### Mean and variance of ZA models

ZAP model:

$$\mathbf{E}(Y_i) = \frac{1 - \pi_i}{1 - \exp(-\mu_i)} \mu_i$$

$$\mathbf{D}(Y_i) = \frac{1 - \pi_i}{1 - \exp(-\mu_i)} (\mu_i + \mu_i^2) - \left(\frac{1 - \pi_i}{1 - \exp(-\mu_i)} \mu_i\right)^2$$

ZANB model:

$$\mathbf{E}(Y_i) = \frac{1 - \pi_i}{1 - P_0} \mu_i, \text{ where } P_0 = \left(\frac{k}{\mu_i + k}\right)^k$$

$$\mathbf{D}(Y_i) = \frac{1 - \pi_i}{1 - P_0} \left(\mu_i + \mu_i^2 + \frac{\mu_i^2}{k}\right) - \left(\frac{1 - \pi_i}{1 - P_0} \mu_i\right)^2$$

The mean and variance can be used to calculate Pearson residuals

### Difference of ZI and ZA models

NB! An important difference is that in R

- in ZIP and ZINB, the binomial GLM models the probability of a **false zero versus other types of data**,
- in ZAP and ZANB, the binomial GLM models the probability of presence versus absence

Hence, the estimated regression parameters obtained by ZAP and ZANB should have opposite signs compared to those obtained by ZIP and ZINB due to the definition of  $\pi_i$ .

In other words, assuming that  $\pi_i$  corresponds to the probability of zeros, we should interpret the R output for ZA models as either

• 
$$logit(1-\pi_i) = ln \frac{1-\pi_i}{\pi_i} = \boldsymbol{w}_i^T \boldsymbol{\gamma}$$
, or

$$\bullet$$
 logit $(\pi_i) = \ln \frac{\pi_i}{1-\pi_i} = -\boldsymbol{w}_i^T \boldsymbol{\gamma}$ 

## Example solution in R. ZAP model (1)

Log-likelihood: -3619 on 8 Df

```
> modelZAP1 = hurdle(doctorco~sex+age+illness+income+hscore | age,
           dist="poisson",link="logit",data=docvisit)
> summary(modelZAP1)
. . .
Count model coefficients (truncated poisson with log link):
         Estimate Std. Error z value Pr(>|z|)
sex -0.13048 0.08908 -1.465 0.142996
age -0.05724 0.21614 -0.265 0.791133
illness 0.10324 0.02931 3.523 0.000427 ***
income -0.33740 0.14077 -2.397 0.016539 *
hscore 0.06879 0.01265 5.436 5.44e-08 ***
Zero hurdle model coefficients (binomial with logit link):
         Estimate Std. Error z value Pr(>|z|)
1.85287 0.16727 11.08 <2e-16 ***
age
. . .
Number of iterations in BFGS optimization: 14
```

# Example solution in R. ZAP model (2)

```
> modelZAP2=hurdle(doctorco~illness+hscore+income | age,
         dist="poisson",link="logit",data=docvisit)
> summary(modelZAP2)
Count model coefficients (truncated poisson with log link):
         Estimate Std. Error z value Pr(>|z|)
illness 0.10060 0.02864 3.512 0.000445 ***
hscore 0.06991 0.01258 5.557 2.74e-08 ***
income -0.27016 0.12831 -2.105 0.035250 *
Zero hurdle model coefficients (binomial with logit link):
         Estimate Std. Error z value Pr(>|z|)
age 1.85287 0.16727 11.08 <2e-16 ***
Number of iterations in BFGS optimization: 16
Log-likelihood: -3621 on 6 Df
```

# Example solution in R. ZANB model (1)

```
> modelZANB1=hurdle(doctorco~sex+age+illness+income+hscore | age,
           dist="negbin",link="logit",data=docvisit)
> summary(modelZANB1)
. . .
Count model coefficients (truncated negbin with log link):
           Estimate Std. Error z value Pr(>|z|)
(Intercept) -10.83240 37.96271 -0.285 0.7754
sex -0.11067 0.14721 -0.752 0.4522
age -0.24472 0.36378 -0.673 0.5011
illness 0.12985 0.04986 2.605 0.0092 **
income -0.33252 0.20842 -1.595 0.1106
hscore 0.10451 0.02617 3.994 6.5e-05 ***
Log(theta) -10.75455 37.96275 -0.283 0.7770
Zero hurdle model coefficients (binomial with logit link):
          Estimate Std. Error z value Pr(>|z|)
age 1.85287 0.16727 11.08 <2e-16 ***
Theta: count = 0
Number of iterations in BFGS optimization: 32
Log-likelihood: -3490 on 9 Df
```

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## Example solution in R. ZANB model (2)

```
> modelZANB2=hurdle(doctorco~illness+hscore | age,
           dist="negbin",link="logit",data=docvisit)
> summary(modelZANB2)
. . .
Count model coefficients (truncated negbin with log link):
           Estimate Std. Error z value Pr(>|z|)
(Intercept) -11.65889 47.28034 -0.247 0.80522
illness 0.13020 0.04832 2.695 0.00705 **
hscore 0.10722 0.02609 4.110 3.96e-05 ***
Log(theta) -11.22227 47.28088 -0.237 0.81238
Zero hurdle model coefficients (binomial with logit link):
          Estimate Std. Error z value Pr(>|z|)
1.85287 0.16727 11.08 <2e-16 ***
age
Theta: count = 0
Number of iterations in BFGS optimization: 61
Log-likelihood: -3491 on 6 Df
```

### Which models to choose?

Different aspects that need to be considered while choosing models for count data:

- overdispersion in data (including non-zero part): Poisson vs NB
- too many zeros (overdispersion in zero part), depending on situation: ZI or ZA models

5 different types of zeros are discussed in (Zuur et al., 2009, p 270)

- structural zeros true zeros
- 2 design errors e.g., wrong area or wrong season for counting
- Observer errors
- 4 'errors' of the subject of counting the habitat is suitable, but site is not used
- naughty naughts; bad zeros obvious errors (need to be deleted)

Type 1 ( $true\ negative$ ), is taken into account by ZI models Types 2–4 are false negatives, which actually are not of interest

### Which model fits best?

Different tools are available to compare the models:

- AIC, BIC
- Likelihood ratio test for nested models)
   Poisson vs NB; ZIP vs ZINB
- Vuong's test (closeness test) for nonnested models
   ZIP vs Poisson; ZINB vs NB

### Vuong's test

Hypothesis that 2 models  $f: F_{\theta}$  and  $g: G_{\gamma}$  are close:  $H_0: E(\ln \frac{f(y)}{g(y)}) = 0$ 

The corresponding test statistic is a difference of weighted log-likelihoods:

$$V = rac{\ln LR_n(\hat{ heta}_n,\hat{\gamma}_n)}{n^{1/2}\omega_n} \stackrel{ extstyle{a}}{
ightarrow} N(0,1)$$

 $\ln LR_n = I_n^f(\hat{\theta}_n) - I_n^g(\hat{\gamma}_n)$  (log-likelihoods),  $\omega_n$  – weights

Think, e.g.:  $F_{\theta}$ :ZIP, ZINB  $G_{\gamma}$ : Poisson, NB

Decision rules (significance level  $\alpha = 0.05$ ):

If  $V>1.96\Rightarrow F_{ heta}$  is better than  $\mathcal{G}_{\gamma}$ 

If  $V < -1.96 \Rightarrow G_{\gamma}$  is better than  $F_{\theta}$ 

If  $|V| \leq 1.96 \Rightarrow$  models are equally good

#### Weights:

$$\omega_n^2 = \frac{1}{n} \sum_{t=1}^n \left[ \ln \frac{f(y_t|z_t, \hat{\theta}_n)}{g(y_t|z_t, \hat{\gamma}_n)} \right]^2 - \left[ \frac{1}{n} \sum_{t=1}^n \ln \frac{f(y_t|z_t, \hat{\theta}_n)}{g(y_t|z_t, \hat{\gamma}_n)} \right]^2$$

Quang H. Vuong (b. 1953 Paris), Professor in University of Pennsylvania (economics)

# Example continued. Comparison of models (1)

```
> library(lmtest)
> lrtest(modelNB,modelP)
Likelihood ratio test
Model 1: doctorco ~ sex + age + illness + hscore
Model 2: doctorco ~ sex + age + illness + hscore
 #Df LogLik Df Chisq Pr(>Chisq)
1 6 -3385.9
2 5 -3650.5 -1 529.11 < 2.2e-16 ***
> vuong(modelP,modelZIP2)
Vuong Non-Nested Hypothesis Test-Statistic:
(test-statistic is asymptotically distributed N(0,1) under the
null that the models are indistinguishible)
   ______
            Vuong z-statistic H_A p-value
                   -5.481430 model2 > model1 2.1095e-08
Raw
```

AIC-corrected -5.444507 model2 > model1 2.5974e-08 BIC-corrected -5.323503 model2 > model1 5.0894e-08

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## Example continued. Comparison of models (2)

#### > vuong(modelNB,modelZIP2)

```
        Vuong
        z-statistic
        H_A
        p-value

        Raw
        5.500703 model1 > model2 1.8914e-08

        AIC-corrected
        5.548084 model1 > model2 1.4441e-08

        BIC-corrected
        5.703362 model1 > model2 5.8733e-09
```

#### > vuong(modelNB,modelZINB2)

```
-----
```

```
      Vuong
      z-statistic
      H_A p-value

      Raw
      -0.5144592 model2 > model1 0.30347

      AIC-corrected
      -0.3001882 model2 > model1 0.38202

      BIC-corrected
      0.4020304 model1 > model2 0.34383
```

#### > vuong(modelNB,modelZANB2)

\_\_\_\_\_

```
        Vuong
        z-statistic
        H_A
        p-value

        Raw
        6.329138 model1 > model2 1.2327e-10

        AIC-corrected
        6.329138 model1 > model2 1.2327e-10

        BIC-corrected
        6.329138 model1 > model2 1.2327e-10
```

## Example continued. Comparison of models (3)

#### Final decision?