

Models

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Outline



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Data exploration VTEC / STEC

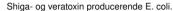


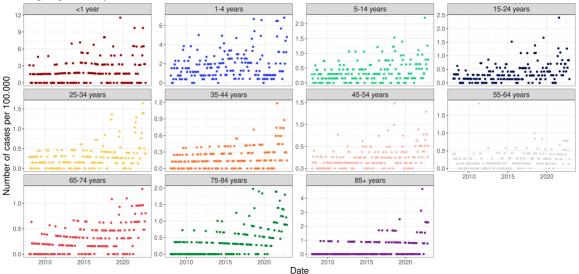
Date	ageGroup	у	n
2008-01-01	<1 year	2	64137
2008-01-01	1-4 years	2	259910
2008-01-01	5-14 years	2	680529
2008-01-01	15-24 years	1	631724
2022-12-01	55-64 years	2	773073
2022-12-01	65-74 years	5	621965
2022-12-01	75-84 years	4	449423
2022-12-01	85+ years	3	132181

Data exploration

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VTEC / STEC





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Fomulation

$$Y_{it}|u_{it} \sim \text{Pois}\left(w_{it}\lambda_i \exp(u_{it})\right)$$
 (1a)

$$u_{it} \sim N(0, \sigma_i^2)$$
 (1b)



Implementation - Objective function in C++

```
// Links in the TMB libraries
#include <TMB.hpp>
template<class Type>
Type objective_function<Type>::operator() ()
 DATA VECTOR(v):
                                       // Data vector transmitted from R
 DATA VECTOR(w)
                               // Data vector transmitted from R
 DATA_FACTOR(ageGroup);
                               // Data factor transmitted from R
 PARAMETER VECTOR(u):
                                   // Random effects
 // Parameters
 PARAMETER VECTOR(lambda):
                              // Parameter value transmitted from R
 PARAMETER(log_sigma_u):
                                       // Parameter value transmitted from R
 Type sigma_u = exp(log_sigma_u);
 int nobs = v.size();
 Type mean ran = Type(0):
 int j;
 Type f = 0;
                           // Declare the "objective function" (neg. log. likelihood)
 for(int i=0; i < nobs: i++){
   f -= dnorm(u[i],mean_ran,sigma_u,true);
   j = ageGroup[i];
   f -= dpois(y[i],exp(log(lambda[j])-log(w[j]))*exp(u[i]),true);
 return f;
```



Implementation - Call from R

```
# Import libraries
library(readr)
library(dplyr)
library(TMB)
# Import the data
dat <- read rds(file = "../../data/processed/dat.rds")
# Only consider some of the data
v <- dat %>%
 filter(caseDef == "Shiga- og veratoxin producerende E. coli.") %>%
  group_by(Date, ageGroup) %>%
  mutate(y = sum(cases)) \%>\%
  select(Date, ageGroup, y, n)
compile(file = "PoissonLognormal.cpp") # Compile the C++ file
dvn.load(dvnlib("PoissonLognormal")) # Dunamically link the C++ code
# Function and derivative
PoisLN <- MakeADFun(
  data = list(y = y$y, ageGroup = y$ageGroup, w = y$n),
 parameters = list(u = rep(1, length(y$y)),
                   lambda = rep(1, nlevels(y$ageGroup)),
                   log_sigma_u = log(1)),
 random = "u".
 DLL = "PoissonLognormal"
opt <- nlminb(start = PoisLN$par, PoisLN$fn, PoisLN$gr, lower = c(0.01, 0.01))
```

Hierachical Poisson-Normal model

Results



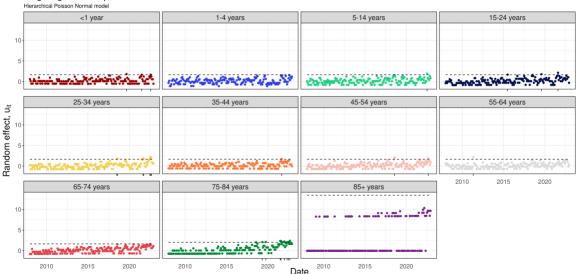
ageGroup	λ	σ
$<\!1$ year	2.38	1.01
1-4 years	2.61	1.01
5-14 years	2.63	1.01
15-24 years	2.64	1.01
25-34 years	2.62	1.01
35-44 years	2.60	1.02
45-54 years	2.63	1.01
55-64 years	2.62	1.01
65-74 years	2.61	1.01
75-84 years	2.52	1.25
85+ years	1.16	8.18

Hierachical Poisson-Normal model



Results

Shiga- og veratoxin producerende E. coli.



Formulation



$$Y_{it}|u_{it} \sim \operatorname{Pois}(\lambda_i u_{it})$$
 (2a)

$$u_{it} \sim G(1/\beta_i, \beta_i)$$
 (2b)

Probability function for *Y*

$$P[Y = y] = g_{Y}(y; \lambda, \beta)$$

$$= \frac{\lambda^{y}}{y!\Gamma(1/\beta)\beta^{1/\beta}} \frac{\beta^{y+1/\beta}\Gamma(y+1/\beta)}{(\lambda\beta+1)^{y+1/\beta}}$$

$$= \frac{\Gamma(y+1/\beta)}{\Gamma(1/\beta)y!} \frac{1}{(\lambda\beta+1)^{1/\beta}} \left(\frac{\lambda\beta}{\lambda\beta+1}\right)^{y}$$

$$= \left(\frac{y+1/\beta-1}{y}\right) \frac{1}{(\lambda\beta+1)^{1/\beta}} \left(\frac{\lambda\beta}{\lambda\beta+1}\right)^{y}, \text{ for } y = 0, 1, 2, \dots$$

$$(3)$$

where we have used the convention

The marginal distribution of Y is a negative binomial distribution, $Y \sim NB(1/\beta, 1/(\lambda\beta + 1))$

Proof

The probability function for the conditional distribution of Y for given \boldsymbol{u}

$$f_{Y|u}(y;\lambda,u) = \frac{(\lambda u)^y}{y!} \exp(-\lambda u)$$
 (5)

and the probability density function for the distribution of \boldsymbol{u} is

$$f_u(u;\beta) = \frac{1}{\beta \Gamma(1/\beta)} \left(\frac{u}{\beta}\right)^{1/\beta - 1} \exp(-u/\beta)$$
 (6)

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Proof

Given (5) and (6), the probability function for the marginal distribution of Y is determined from

$$g_{Y}(y;\lambda,\beta) = \int_{u=0}^{\infty} f_{Y|u}(y;\lambda,u) f_{u}(u;\beta) du$$

$$= \int_{u=0}^{\infty} \frac{(\lambda u)^{y}}{y!} \exp(-\lambda u) \frac{1}{\beta \Gamma(1/\beta)} \left(\frac{u}{\beta}\right)^{1/\beta - 1} \exp(-u/\beta) du$$

$$= \frac{\lambda^{y}}{y! \Gamma(1/\beta) \beta^{1/\beta}} \int_{u=0}^{\infty} u^{y+1/\beta} \exp\left(-u(\lambda \beta + 1)/\beta\right) du$$
(7)



In (7) it is noted that the integrand is the *kernel* in the probability density function for a Gamma distribution, $G\left(y+1/\beta,\beta/(\lambda\beta+1)\right)$. As the integral of the density shall equal one, we find by adjusting the norming constant that

$$\int_{u=0}^{\infty} u^{y+1/\beta} \exp\left(-u/\left(\beta/(\lambda\beta+1)\right)\right) du = \frac{\beta^{y+1/\beta}\Gamma(y+1/\beta)}{(\lambda\beta+1)^{y+1/\beta}}$$
(8)

and then (3) follows

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Inference on individual group means

Consider the hierarchical Poisson-Gamma model in (2), and assume that a value Y=y has been observed. Then the conditional distribution of u for given Y=y is a Gamma distribution,

$$u|Y = y \sim G(y + 1/\beta, \beta/(\lambda\beta + 1))$$
 (9)

with mean

$$E[u|Y=y] = \frac{y\beta + 1}{\lambda\beta + 1} \tag{10}$$

and variance

$$V[u|Y=y] = \frac{(y\beta^2 + \beta)}{(\lambda\beta + 1)^2}$$
(11)

Proof



The conditional distribution is found using Bayes Theorem

$$g_{u}(u|Y=y) = \frac{f_{y,u}(y,u)}{g_{Y}(y;\lambda,\phi)}$$

$$= \frac{f_{y|u}(y;u)g_{u}(u)}{g_{Y}(y;\lambda,\beta)}$$

$$= \frac{1}{g_{Y}(y;\lambda,\beta)} \left(\frac{(\lambda u)^{y}}{y!} \exp(-\lambda u) \frac{1}{\beta \Gamma(1/\beta)} \left(\frac{u}{\beta}\right)^{1/\beta-1} \exp(-u/\beta)\right)$$

$$\propto u^{y+1/\beta-1} \exp(-u(\lambda\beta+1)/\beta)$$
(12)

We identify the *kernel* of the probability density function

$$u^{y+1/\beta-1}\exp(-u(\lambda\beta+1)/\beta) \tag{13}$$

as the kernel of a Gamma distribution, $G(y+1/\beta,\beta/(\lambda\beta+1))$



Implementation - Define negative likelihood function in R

```
# Define the negative likelihood function for the marginal distribution of Y
nll.age <- function(theta, data){
 # Extract counts
 v <- data$v
 # Extract agegroups
 ageGroup <- data$ageGroup
 # Extract number of agegroups
 n.ageGroup <- n_distinct(data$ageGroup)
 # Define parameters
 lambda <- theta[1:n.ageGroup]</pre>
 beta <- theta[(n.ageGroup+1):(n.ageGroup*2)]
 # Construct the size and probability for the negative binomial distribution
 r <- 1/beta
 p <- 1/(lambda*beta+1)
 # Initilize the log-likelihood
 11 <- 0
 for(i in 1:nrow(data)){
   11 = 11 + dnbinom(x = y[i],
                      size = r[ageGroup[i]],
                      prob = p[ageGroup[i]],
                      log = TRUE)
 # Return the negative log-likelihood
 -11
```

Results



ageGroup	λ	β
<1 year	1.24	0.33
1-4 years	4.57	0.36
5-14 years	2.47	0.42
15-24 years	2.57	0.48
25-34 years	2.08	0.57
35-44 years	1.47	0.20
45-54 years	1.88	0.39
55-64 years	1.77	0.25
65-74 years	1.89	0.40
75-84 years	1.45	1.08
85+ years	0.50	0.97

Hierachical Poisson-Gamma model

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Results

Shiga- og veratoxin producerende E. coli.

