

Outline

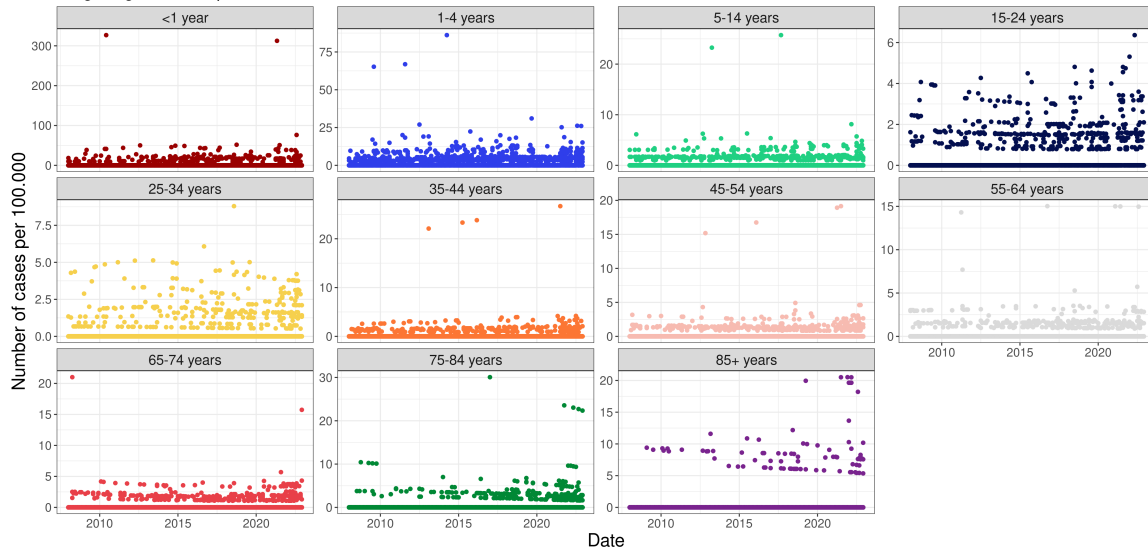
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 - Formulation

Date	ageGroup	y	n
2008-01-01	<1 year	2	10120
2009-01-01	<1 year	1	10288
2010-01-01	<1 year	1	10654
2011-01-01	<1 year	0	11199
...
2019-12-01	85+ years	1	14153
2020-12-01	85+ years	0	14613
2021-12-01	85+ years	2	14976
2022-12-01	85+ years	3	15203

Data exploration

VTEC / STEC

Shiga- og verotoxin producerende E. coli.



$$Y_t^a | u_t^a \sim \text{Pois}(w_t^a \lambda_a \exp(u_t^a)) \quad (1a)$$

$$u_t^a \sim \text{N}(0, \sigma^2) \quad (1b)$$

Implementation - Objective function in C++

```

#include <TMB.hpp>           // Links in the TMB libraries
template<class Type>
Type objective_function<Type>::operator() ()
{
    DATA_VECTOR(y);          // 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 = y.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;
}

```

Hierarchical Poisson Normal model

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
y <- dat %>%
  filter(caseDef == "Shiga- og veratotoxin producerende E. coli.") %>%
  group_by(Date, ageGroup) %>%
  mutate(y = sum(cases)) %>%
  select(Date, ageGroup, y, n)

compile(file = "PoissonLognormal.cpp") # Compile the C++ file
dyn.load(dynlib("PoissonLognormal")) # Dynamically link the C++ code

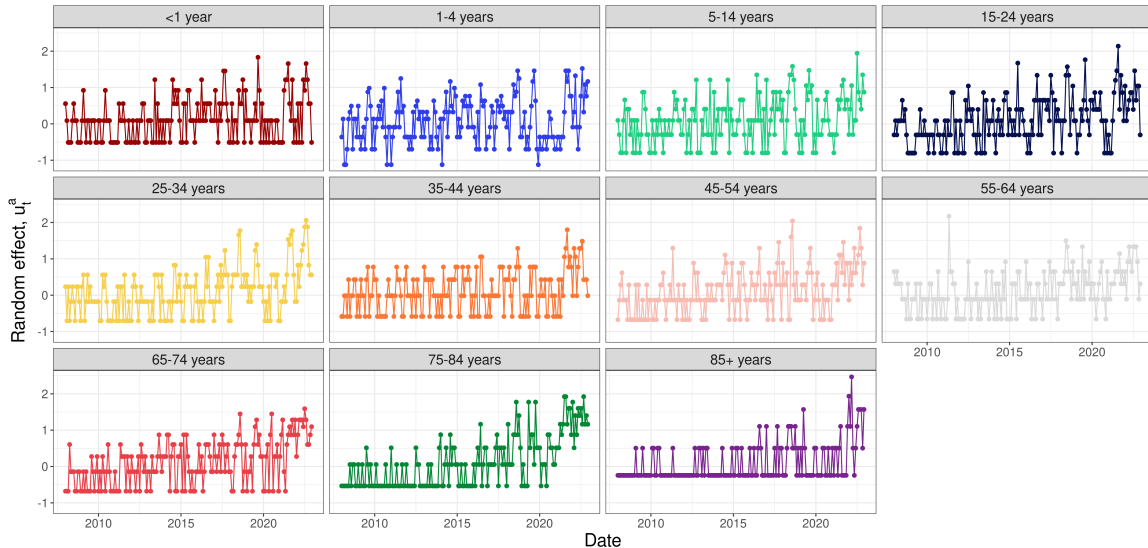
# Function and derivative
PoisLN <- MakeADFun(
  data = list(y = y$, ageGroup = y$ageGroup, w = y$n),
  parameters = list(u = rep(1, length(y$y)),
                    lambda = rep(1, nlevels(y$ageGroup)),
                    log_sigma_u = log(1)),
  random = "u",
  DLL = "PoissonLognormal"
)

opt <- nlminb(start = PoisLN$par, PoisLN$fn, PoisLN$gr, lower = c(0.01, 0.01))
```

Parameter	Estimate	Std. Error
$\log(\lambda_{<1year})$	8438.14	276.06
$\log(\lambda_{1-4years})$	34772.54	905.76
$\log(\lambda_{5-14years})$	18464.41	528.24
$\log(\lambda_{15-24years})$	19674.21	584.60
$\log(\lambda_{25-34years})$	15130.53	473.09
$\log(\lambda_{35-44years})$	11256.22	353.22
$\log(\lambda_{45-54years})$	13601.67	408.42
$\log(\lambda_{55-64years})$	13508.84	405.98
$\log(\lambda_{65-74years})$	14753.44	442.70
$\log(\lambda_{75-84years})$	10622.91	345.14
$\log(\lambda_{85+years})$	3586.71	158.77
$\log(\sigma_u)$	0.01	0.01

Hierarchical Poisson Normal model

Results

Shiga- og verotoxin producerende *E. coli*.

Hierarchical Poisson Gamma model

Formulation



$$Y_i | u_i \sim \text{Pois}(\lambda_i u_i) \quad (2a)$$

$$u_i \sim G(1, \phi) \quad (2b)$$

Hierarchical Poisson Gamma model

Probability function for Y



$$\begin{aligned} P[Y = y] &= g_Y(y; \lambda, \phi) \\ &= 1234 \end{aligned} \tag{3}$$

The probability function for the conditional distribution of Y for given u

$$f_{Y|u}(y; \lambda, u) = \frac{(\lambda u)^y}{y!} \exp(-\lambda u) \quad (4)$$

and the probability density function for the distribution of u is

$$f_u(u; \phi) = \frac{1}{\phi} \exp(-u/\phi) \quad (5)$$

Given (4) and (5), the probability function for the marginal distribution of Y is determined from

$$\begin{aligned} g_Y(y; \lambda, \phi) &= \int_{u=0}^{\infty} f_{Y|u}(y; \lambda, u) f_u(u; \phi) du \\ &= \int_{u=0}^{\infty} \frac{(\lambda u)^y}{y!} \exp(-\lambda u) \frac{1}{\phi} \exp(-u/\phi) du \\ &= \frac{1}{y! \phi} \int_{u=0}^{\infty} (\lambda u)^y \exp(-u(\lambda + 1/\phi)) du \end{aligned} \tag{6}$$