Statistical Methods

We developed several hierarchical Poisson-gamma models and ran these in R-statistics (3.1.2, 3.3.1) package "R2jags"[1] and JAGS (3.4.0, 4.20).[2] [3] The basic idea was to model the relative risk assuming a Poisson distribution between different areas correcting for age. The model itself is described in Lawson (p 75 and 111).[3] We aimed at accommodating extra variation by inclusion of a prior distribution for the relative risk – in this case a gamma distribution. Inference was primarily done with respect to the relative risk and its 95% credibility intervals. All parameters without the relative risk were with this respect nuisance parameters. The models assumed vague priors on the hyper-parameters, neglecting spatial correlation.

$$y_i|K_i \sim Poisson(K_i * e_i)$$
$$e_i = p_i * g$$
$$K_i \sim Gamma(\alpha , \beta)$$
$$M \sim Binomial(g,p)$$
$$g \sim Beta(1, 1)$$
$$\alpha = v^2/\delta^2$$
$$\beta = v/\delta^2$$
$$v \sim logNormal(1, 0.01)$$
$$\delta \sim halfNormal(0, 0.001)$$

The models were run with a burn-in of 5,000 iterations and a total length of Markov chain Monte Carlo (MCMC) of 10,000 iterations. We estimated these models without stratification by age and compared them to models that forced K_i to be equal within age groups. Models without forcing K_i to be equal between strata were estimated as well. We tested convergence of the MCMC-algorithm by trace plots, density plots, Geweke diagnostics, Gelman diagnostics, Heidelberg diagnostics and Raftery diagnostics. We selected the model with respect to the deviance information criterion (DIC). The deviance information criterion (DIC) has been proposed by Spiegelhalter et al. (2002; cited in Lawson)[3] and is widely used in Bayesian modelling. It is based on a comparison of the average deviance and the deviance of the posterior expected parameter estimates.

All diagnostics were done by the R package "coda"[4].

References

1. Su Y-S, Yajima M. *R2jags: Using R to Run 'JAGS'. R package version 0.5-7*, 2015. https://CRAN.R-project.org/package=R2jags.
2. Plummer M. *JAGS: A program for analysis of Bayesian graphical models using Gibbs sampling*, 2003. http://citeseer.ist.psu.edu/plummer03jags.html.
3. Lawson AB. *Bayesian Disease Mapping: Hierarchical Modeling in Spatial Epidemiology (2nd edition)*. Boca Raton: Chapman and Hall / CRC Press, 2013.
4. Plummer M, Best N, Cowles K, et al. CODA: Convergence Diagnosis and Output Analysis for MCMC. *R News* 2006;6:7-11

JAGS basic model code:

```
model
{
        for(i in 1:n)
                {
                observed[i]~dpois(mu[i])
                expected[i]<-p[i]*g
                mu[i]<-K[i]*expected[i]
                K[i]~dgamma(a,b)
                }
                M~dbin(g,N)
                g~dbeta(1,1)
                a<-pow(nu,2)/pow(sigma,2)
                b<-nu/pow(sigma,2)
                nu~dlnorm(1,.01)
                sigma~dnorm(0,0.001)I(0,)  # half-normal
}
```

JAGS model code with forcing to a common concentration factor between age groups:

```
model
{
        for(i in 1:n)
                {
                observed1[i]~dpois(mu1[i])
                mu1[i]<-K[i]*p1[i]*g1

                observed2[i]~dpois(mu2[i])
                mu2[i]<-K[i]*p2[i]*g2

                observed3[i]~dpois(mu3[i])
                mu3[i]<-K[i]*p3[i]*g3
                K[i]~dgamma(a,b)
                }
                M1~dbin(g1,p1)
                g1~dbeta(1,1)

                M2~dbin(g2,p2)
                g2~dbeta(1,1)

                M3~dbin(g3,p3)
                g3~dbeta(1,1)

                a<-pow(nu,2)/pow(sigma,2)
                b<-nu/pow(sigma,2)
                nu~dlnorm(1,.01)
                sigma~dnorm(0,0.001)I(0,)  # half-normal
}
```

JAGS model code with changing concentration factor between age-groups:

```
model
{
        for(i in 1:n)
                {
                observed1[i]~dpois(mu1[i])
                mu1[i]<-K1[i]*p1[i]*g1

                observed2[i]~dpois(mu2[i])
                mu2[i]<-K2[i]*p2[i]*g2

                observed3[i]~dpois(mu3[i])
                mu3[i]<-K3[i]*p3[i]*g3

                K1[i]~dgamma(a,b)
                K2[i]~dgamma(a,b)
                K3[i]~dgamma(a,b)
                }
                M1~dbin(g1,p1)
                g1~dbeta(1,1)
                M2~dbin(g2,p2)
                g2~dbeta(1,1)
                M3~dbin(g3,p3)
                g3~dbeta(1,1)

                a<-pow(nu,2)/pow(sigma,2)
                b<-nu/pow(sigma,2)
                nu~dlnorm(1,.01)
                sigma~dnorm(0,0.001)I(0,)  # half-normal
}
```