**German Measles Epidemic Model**

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**Journal of Statistical Software (2017, Section 5)**

The **basic model** implements a count of persons infected per region per week , using a negative binomial distribution for the mean :

**mean = endemic offset + AR(1) + influx from other regions**

**The first term on the rhs of the = is standard for count models – it reflects the fact that bigger regions will naturally have bigger counts. It looks slightly odd here as it is not just the log of regional population size, but is “modelled”.**

**The endemic (or region-specific) component can be further modelled as:**

**The seasonal term on the rhs of the above equation can be omitted as we have a very short ts so far (but it could be used to model weekly cycles in day-by-day models?)**

**The and coefficients can also modelled and the paper calls these “epidemic parameters”.**

**The paper goes on to implement more detailed models that use covariates and spatio-temporal .**

