

**Appendix to:**

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Dynamics of measles epidemics: estimating scaling of transmission rates using a time series SIR model.

*Ecological Monographs.*

**Appendix A: Assumptions**

In order to estimate the parameters of the disease transmission in Eq. 1, we make a set of assumptions. Please note that some of these assumptions are likely to be fairly crude so that future improvements and qualifications should be anticipated.

A1. The true number of cases,  $I_t$ , can be approximated by the reported number of cases corrected for the underreporting rate.

A2. The sequence of reconstructed susceptibles  $z_t$  is assumed to be a fixed (i.e., nonrandom) covariate, and the mean number of susceptibles,  $\bar{S}$  is approximately constant through time.

A3. The spatial coupling process,  $\theta_t$ , represents a discrete non-negative stochastic process. For simplicity we assume this process to have a constant mean,  $E[\theta_t] = m$ . We further assume  $\theta_t$  to be independent of  $I_t$ .

A4. The transmission rate  $\beta_s$  is a time varying parameter with period one year, so that

$\beta_s \equiv \beta_{t \bmod s}$ , where  $s$  is the number of observations per year (i.e.,  $s = 26$  for biweekly data). In the estimation we secure this through using 26-dummy variables flagging each of the biweeks within the year.

A5. The data subsequent to extinction and prior to re-introduction of the disease, i.e. zero observations, are not informative about the model parameters.