Estimation and Dynamics in Household Disease Models

Casper Woroszylo and Grzegorz Rempala

Mathematical Bioscience Institute, the Ohio State University

Overview

Using cross-sectional data, we fit a dynamical model of infection. More specifically:

- 1. Determine household structure for a disease from 64 households within a 1 month period.
- 2. Use this likelihood and MLE estimates for parameters to generate data for households.
- 3. Derive functional equations for imputing susceptible and infective compartments.
- 4. Use generated averages of households to fit a dynamical model in steady state using a MCMC procedure. This provides point estimates as well as 95% credible intervals for the parameters and imputed states.

Household Structure

At the household level we have the number of Infants, Juveniles and Adults:

1. Healthy I, J, A

- 2. Diseased D_I , D_J , D_A
- 3. Contamination status (V)

	Ι	J	Α	DI	DJ	DA	V
()	0	2	0	0	0	0
()	1	2	0	0	1	0
()	1	7	0	0	0	0
()	4	6	0	0	0	1
-	1	3	5	0	1	3	0
()	5	3	0	0	0	1

Consider the following likelihood for a given household $(x_I, x_J, x_A, x_{DI}, x_{DJ}, x_{DA}, x_V)$:

 $\prod P[D_k = x_k | N_k = x_k + x_{Dk}, V = x_V]$ $k \in \! \{I, J, A\}$ $\times P[N_k = x_k + x_{Dk}]P[V = x_V]$

where

 $D_k|(N_k, V) \sim \text{Binomial}(N_k, p_k(V))$

 $N_k \sim \text{Poisson}(\lambda_k).$

We use this to generate **average** households.

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Dynamical System

We observe no diseased infants in the data. Hence we look at Juveniles (1) and Adults (2).

$$\begin{aligned} \frac{d}{dt}S_1 &= -\beta_{12}S_1I_2 - \beta_{11}S_1I_1 - \phi_1S_1V - \alpha_1S_1 \\ &+ \delta_1D_1 + (\gamma_1 - \nu_1)I_1 \\ \frac{d}{dt}S_2 &= -\beta_{21}S_2I_1 - \beta_{22}S_2I_2 - \phi_2S_2V - \alpha_2S_2 \\ &+ \delta_2D_2 + (\gamma_2 - \nu_2)I_2 \\ \frac{d}{dt}I_1 &= \beta_{21}S_2I_1 + \beta_{11}S_1I_1 + \phi_1S_1V - \gamma_1I_1 \\ \frac{d}{dt}I_2 &= \beta_{12}S_1I_2 + \beta_{22}S_2I_2 + \phi_2S_2V - \gamma_2I_2 \\ \frac{d}{dt}D_1 &= \alpha_1S_1 + \nu_1I_1 - \delta_1D_1 \\ \frac{d}{dt}D_2 &= \alpha_2S_2 + \nu_2I_2 - \delta_2D_2 \end{aligned}$$

The system represents the average behavior of the system over time.

Since the epidemic is not taking off, we can assume that the data come from steady state period, meaning the average state of a household is not changing with respect to time.

end citation formats

Bibliography

Gelman, A., Carlin, J. B., Stern, H. S., Dunson, D. B., Vehtari, A., and Rubin, D. B. 2013. *Bayesian Data Analysis*, 3rd Edition. Chapman & Hall/CRC Press, London. Casella, George, and Roger L. Berger. Statistical Inference. Pacific Grove, Calif: Brooks/Cole Pub. Co, 1990.

MCMC and Synthetic Likelihood

The Susceptible and Infectives are not observed. We can impute them using functional forms of non-diseased individuals:

$$\begin{split} \tilde{D}_1 &= S_1 + I_1 = \left(\frac{\gamma_1}{\beta_{11}I_1 + \beta_{12}I_2 + \phi_1} + 1\right)I_1 \\ &= f_1^{\theta_1}(I_1, I_2) \end{split}$$
 2. Ini
III Initial I

$$\tilde{D}_2 = S_2 + I_2 = \left(\frac{\gamma_2}{\beta_{22}I_2 + \beta_{21}I_1 + \phi_2} + 1\right)I_2 \qquad 3. 1$$
$$= f_2^{\theta_2}(I_1, I_2) \qquad 4. 1$$

$$\tilde{D}_1 = \frac{(\alpha_1 - \nu_1)I_1 + \delta_1 D_1}{\alpha_1 - \nu_1}$$

$$D_{1} = \frac{1}{\alpha_{1}}$$

$$= f_{3}^{\theta_{3}}(I_{1})$$

$$\tilde{D}_{2} = \frac{(\alpha_{2} - \nu_{2})I_{2} + \delta_{2}D_{2}}{\alpha_{2}}$$

$$l_{1} \propto \exp\left(\sum_{i=1}^{B} (\tilde{d}_{i}^{1} - (f_{1}^{\theta_{1}} + f_{3}^{\theta_{3}})/2)^{2}/2\sigma_{1}^{2}\right),$$

$$l_{2} \propto \exp\left(\sum_{i=1}^{B} (\tilde{d}_{i}^{2} - (f_{2}^{\theta_{2}} + f_{4}^{\theta_{4}})/2)^{2}/2\sigma_{2}^{2}\right).$$

$$=f_4^{oldsymbol{ heta}_4}(I_2)$$

Results

The following are results are for the posterior means, standard deviations, and associated credible inter vals in the settings V = 1 and V = 0. We generated 100 average households of size 50.

	MC_mean	MC_sd	2.50%	97.50%		MC_mean	MC_sd	2.50%	97.50%
beta11	0.5350	0.4056	0.0366	1.5541	beta11	0.5316	0.4191	0.0454	1.6545
beta12	0.5128	0.4041	0.0417	1.5410	beta12	0.4824	0.4220	0.0313	1.5507
phi1	0.5254	0.3991	0.0540	1.5526	gamma1	0.7024	0.4806	0.0733	1.9213
gamma1	0.6371	0.4382	0.0798	1.6457	beta11	0.4742	0.4037	0.0429	1.6455
beta22	0.4801	0.3796	0.0364	1.5018	beta21	0.4882	0.3670	0.0323	1.3771
beta21	0.5266	0.4094	0.0388	1.5610	gamma2	0.7316	0.5022	0.0824	1.9509
phi2	0.5537	0.4279	0.0376	1.7793	alpha1	0.8006	0.4851	0.1282	1.9710
gamma2	0.7937	0.6352	0.0761	2.3740	nu1	0.2656	0.1995	0.0165	0.750
alpha1	0.7401	0.4461	0.1541	1.8767	delta1	0.6647	0.4867	0.0573	1.9252
nu1	0.2514	0.1844	0.0333	0.7074	alpha2	0.7496	0.4683	0.1345	1.9672
delta1	0.6994	0.4830	0.0621	1.9595	nu2	0.2228	0.1773	0.0199	0.6745
alpha2	0.8236	0.4810	0.1446	2.0287	delta2	0.6649	0.4925	0.0585	1.8735
nu2	0.2233	0.1777	0.0138	0.6557	11	1.7448	0.4658	0.6885	2.508
delta2	0.6217	0.4502	0.0561	1.8455	12	3.7009	0.8404	1.6611	4.950
11	1.6693	0.3838	0.8531	2.3165					
12	4.2566	0.6144	2.8644	5.1508	E!	e 2: MCM	C	E 0	VI O

Figure 1: MCMC results: n = 50, V = 1

Contact

Email: woroszylo.1@osu.edu Site: casperw.github.io

- Outline of MCMC procedure (V=0,1 separately):
 - 1. Simulate average households (e.g. 50 households) B times.
 - itialize Gamma priors on parameters and I_1,I_2
 - Draw from posterior of parameters via M-H
- 4. Draw from posterior of I_1, I_2 via M-H using

5. Repeat 3 and 4 until chain converges.

 $\mathbf{Iguic} \mathbf{Z}_{\bullet} \text{ interview results. If } = \mathbf{U}_{\bullet}, \mathbf{V} = \mathbf{U}$