The SIR Model

A Markov Chain model for disease spread

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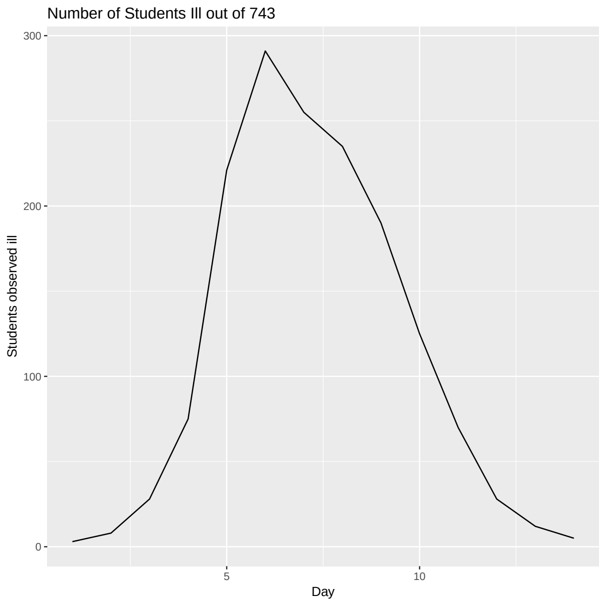
The Model

The Susceptible-Infected-Recovered model describes how populations respond to disease.

$$\mathbf{E}\begin{bmatrix} p_{S,t} \\ p_{I,t} \\ p_{R,t} \end{bmatrix} = \begin{bmatrix} a_{11} & 0 & 0 \\ a_{21} & a_{22} & 0 \\ 0 & a_{32} & 1 \end{bmatrix} \begin{bmatrix} p_{S,t-1} \\ p_{I,t-1} \\ p_{R,t-1} \end{bmatrix}$$

The matrix in the middle is the transition matrix. The number in column i, row j is the probability of moving from state i to state j at each transition.

Boarding School Data



Deriving the Likelihood

Our fourteen observations are not independent, so we can write the likelihood as:

$$f(x_1, x_2, ..., x_n | a_{12}, a_{32}) = f(x_1 | a_{12}, a_{32}) f(x_2 | x_1, a_{12}, a_{32}) ... f(x_n | x_{n-1}, a_{12}, a_{32})$$

Deriving the Likelihood

To address the fact that we didn't observe all states, we will sum over all possibilities. The R.V. R_i will represent the number of people recovered on day i.

$$f(x_i|x_{i-1}, a_{12}, a_{32}) = \sum_{j=0}^{n} f(x_i|x_{i-1}, a_{12}, a_{32}, R_i = j) \cdot Pr(R_i = j)$$

Deriving the Likelihood

We will iteratively calculate R_i as we move through the algorithm:

$$Pr(R_i = r + h) = \sum_{j=0}^{x_{i-1}} Pr(H_i = j | R_{i-1} = r - j) \cdot Pr(R_{i-1} = r - j)$$

Deriving the Likelihood

Now that we have R, we can calculate the probability of x_i given R_i

$$f(x_i|x_{i-1}, a_{12}, a_{32}, r) =$$

$$\sum_{h=0}^{x_{i-1}} \binom{x_{i-1}}{h} a_{32}^{h}(1-a_{32})^{x_{i-1}-h} \binom{n - x_{i-1} - r}{x_i - (x_{i-1} - h)} a_{12}^{x_i-(x_{i-1}-h)}(1-a_{12})^{n-r-x_i-h} I(x)$$

$$\text{where } I(x) = \begin{cases} 1 & \text{for } x_{i-1} - h \leq x_i \leq n - r \\ 0 & \text{otherwise} \end{cases}$$

Maximizing the Likelihood

The resulting likelihood involves a triple summation over time periods, possible values of R, and possible values of H (people healed), and two binomial densities. Needless to say, I didn't calculate the Hessian.

- Nelder-Mead constrained optimization (constraining both parameters between 0 and 1)
- Coded likelihood in C++ for faster evaluation

So...Did it work?

500 Simulations of each scenario

Pop.	No obs.	a_{12}	a_{32}	95% CI on $\hat{a}_{12}$	95% CI on $\hat{a}_{32}$
743	14	0.0848	0.3420	(0.0845, 0.0857)	(0.341, 0.345)
500	14	0.02	0.3	(0.020, 0.021)	(0.305, 0.319)
473	14	0.0848	0.3420	(0.084, 0.086)	(0.340, 0.345)
200	6	0.1	.3	(0.101, 0.104)	(0.301, 0.314)
100	14	0.2	0.7	(0.202, 0.206)	(0.700, 0.708)
100	14	0.7	0.2	(0.700, 0.707)	(0.222, 0.225)
100	14	0.5	0.5	(0.505, 0.513)	(0.534, 0.537)
50	20	0.1	0.3	(0.099, 0.104)	(0.282, 0.291)
20	8	0.4	0.3	(0.405, 0.422)	(0.304, 0.315)

Lack of Fit

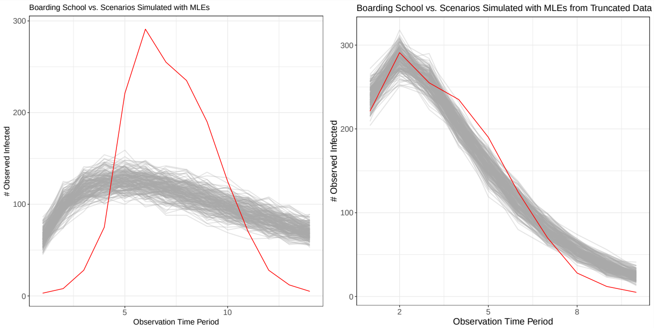
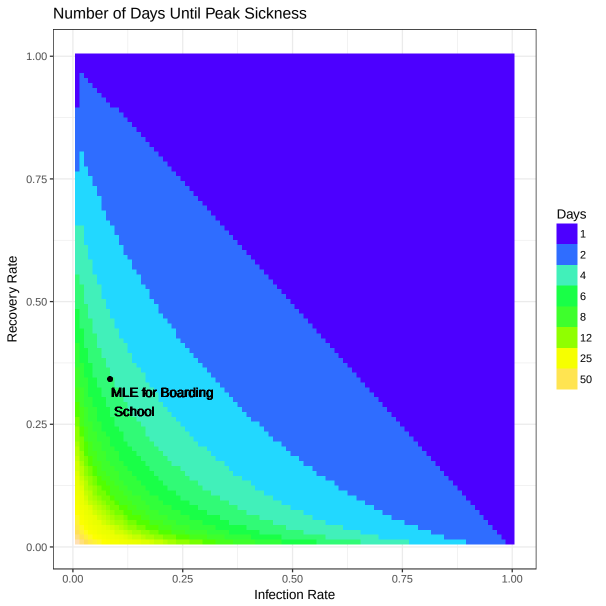
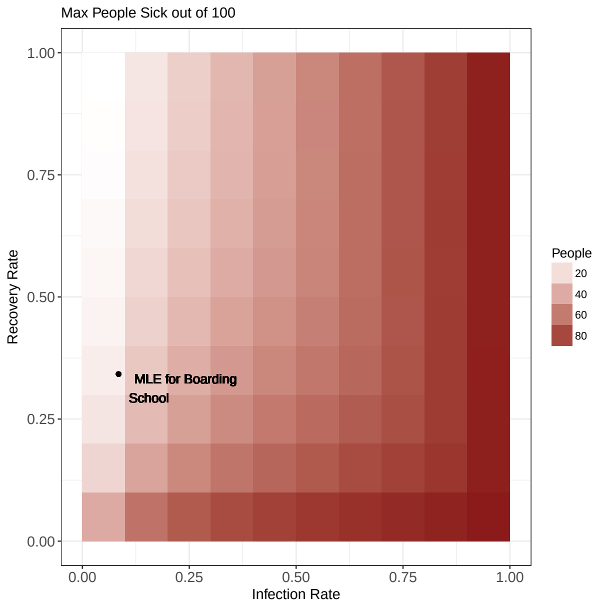


Figure 1: Actual data vs. 200 simulations using MLE as parameters for full dataset and dataset without first four days

Inference


Number of Days Until Peak Sickness
Recovery Rate
1.00
0.75
0.50
0.25
0.00
Infection Rate
0.00
0.25
0.50
0.75
1.00
MLE for Boarding School
Days
1
2
4
6
8
12
25
50

Inference


Max People Sick out of 100
Recovery Rate
1.00
0.75
0.50
0.25
0.00
Infection Rate
0.00
0.25
0.50
0.75
1.00
MLE for Boarding School
People
20
40
60
80

The end