

## RE: First draft of Missouri Medicine article

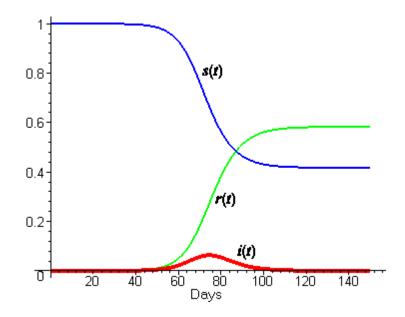


Inbox

Hi Steve,

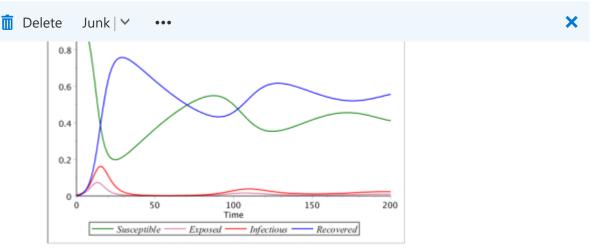
Congratulations! This is a well written article. There are a couple of areas of improvements:

- 1. The paragraph under herd immunity could be more accurate. Instead of using Rt, you could use R0 (the basic reproduction number). Then the herd immunity is calculated by 1-1/R0.
- 2. The section vaccination and reinfection models is fine. However, figure 3 is referring to an SIR model with "loss of immunity". Reinfection occurs due to loss of immunity.
- 3. Heterogeneity is only one of the concerns. It would be good to add a section about the limitations of compartmental models. For instance, in the section "Adding compartments to enhance the SIR model", a word of caution is needed: Due to lack of related data, the more compartments are added the harder it becomes to estimate the parameter values and to validate the model. For instance, we can never find the actual number of exposed individuals (E). Also, there are different levels of susceptibility. But it is a highly nontrivial task to determine the level of susceptibility according to the age gender or ethnicity. The other shortcoming of SIR models is that their outcomes are very limited. In the classic SIR model, regardless of the parameter values, we always get a bump for the infectious population, an inverted S shape for susceptible population and an shape for recovered population.

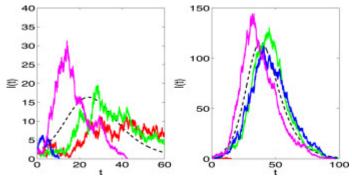


when we add exposed (E) with birth and death, we get some oscillations but the model will reach to a constant equilibrium which is known as an endemic equilibrium, see below. Here the outcomes are limited to convergence to a disease-free equilibrium (for R0<1) or convergence to an endemic equilibrium (for R0<1).

Reply all |



adding uncertainty can provide some interesting results, however the outcomes of stochastic SIR models are more or less the same as those of the deterministic ones. Note that in the following figures there are some simulations that shows the infection does not spread out and dies out. So, adding uncertainty tells us that RO>1 does not always imply an outbreak



- 4. It should be stressed out that one of the main contributions of compartmental models is to unpack the contribution of all factors and basic production number.
- 5. Even though, calculation of the basic reproduction number can be troublesome. Namely, different interpretations of disease characteristics can lead to different R0 expressions, which can lead to substantial inaccuracies in estimation of the herd immunity. See for example: Bani-Yaghoub, M., Gautam, R., Ivanek, R., van den Driessche, P., Shuai, Z. (2012) Reproduction numbers for infections with free-living pathogens growing in the environment, Journal of Biological Dynamics. 6 (2): 923-940

All the best, Majid

From: Simon, Stephen D. <simons@umkc.edu>

Sent: Friday, December 4, 2020 11:44 AM

To: Allsworth, Jenifer <allsworthj@umkc.edu>; Gaddis, Monica <gaddism@umkc.edu>; Bani Yaghoub, Majid

<baniyaghoubm@umkc.edu>

Subject: Fw: First draft of Missouri Medicine article

My boss asked me to write an article for Missouri Medicine, and I thought that an overview and explanation of the SIR models and variations might be fun to write about. This is an early draft. You all know a lot more about this than I do, so I would appreciate any suggestions you have. I am especially interested in beefing up the bibliography and I'm sure that you know the recently published literature better than I do.



If you have time to look this over, even just briefly, and offer suggestions, I would greatly appreciate it.

From: Simon, Stephen D.

Sent: Friday, December 4, 2020 11:39 AM

To: Nichols, Mark D.

Subject: First draft of Missouri Medicine article

The bibliography needs a lot of work, and I am getting feedback from some of our local experts, but here is a first draft of an article about COVID prediction models for Missouri Medicine.

It may or may not be Missouri Medicine is looking for. Let me know what you think.