Vaccination

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Introduction

- Our model simulates disease spread based on the amount of people vaccinated in the population.
- The goal is to show that disease spread is slower when more people are vaccinated.

Entities

- Humans
 - Vaccinated
 - Not vaccinated, not infected
 - Not vaccinated, infected
- Humans move around randomly
- There is a chance for infected humans to infect uninfected humans.

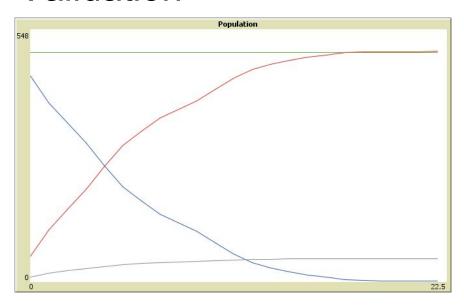
What are we looking for?

- Rate of infection as determined by the proportion of vaccinated people
- Graph; Amount of each entity vs. time

- Kermack and McKendrick derived differential equations [Proc. R. Soc. A, 115, 772 (1927)]
- This is called the "SIR Model"

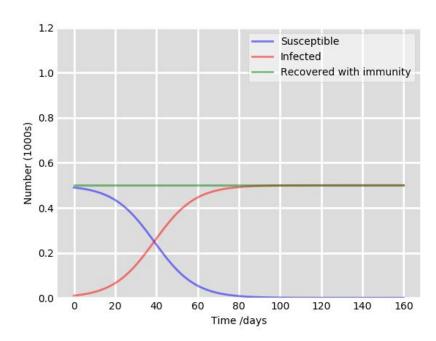
- S(t) are those susceptible but not yet infected with the disease;
- I(t) is the number of infectious individuals;
- R(t) are those individuals who have recovered from the disease and now have immunity to it.
- β = infection rate (arbitrary number; set to 0.2)
- Y = recovery rate (set to 0)

$$rac{\mathrm{d}S}{\mathrm{d}t} = -rac{eta SI}{N}, \ rac{\mathrm{d}I}{\mathrm{d}t} = rac{eta SI}{N} - \gamma I, \ rac{\mathrm{d}R}{\mathrm{d}t} = \gamma I.$$

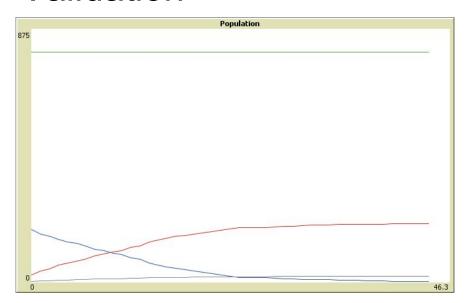


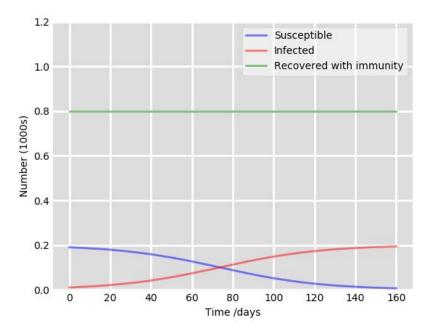
Our agent-based model implemented in NetLogo.

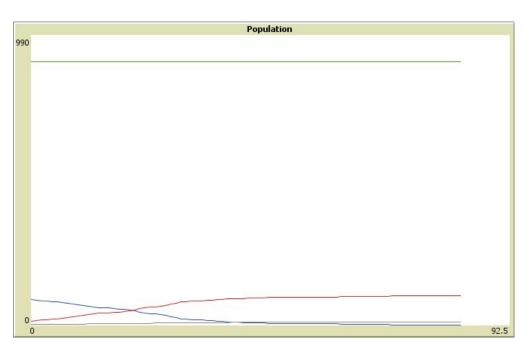
Green represents vaccinated, Blue for not vaccinated, and Red for infected.

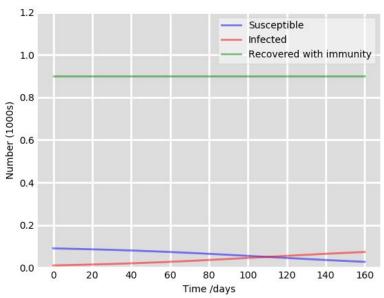


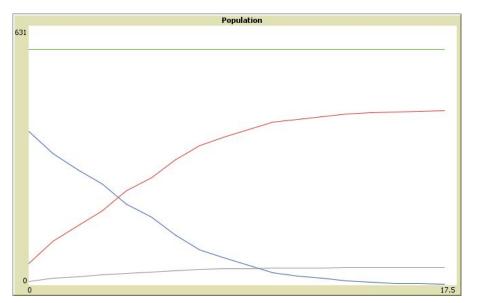
Kermack and McKendrick's mathematical model implemented in SciPy

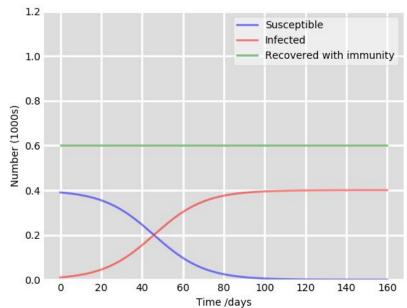












Recommendations

- More entities aside from infected, non-infected, and vaccinated humans
- Opportunity for infected individuals to be cured and become immune
- Try validating with other models