The Art of Mathematical Modeling

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"Remember that all models are wrong; the practical question is how wrong do they have to be to not be useful."

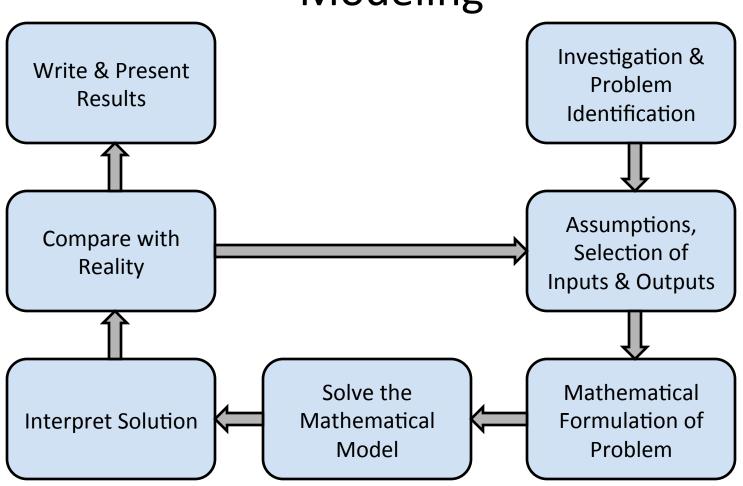
-OR-

"All models are wrong, but some are useful."

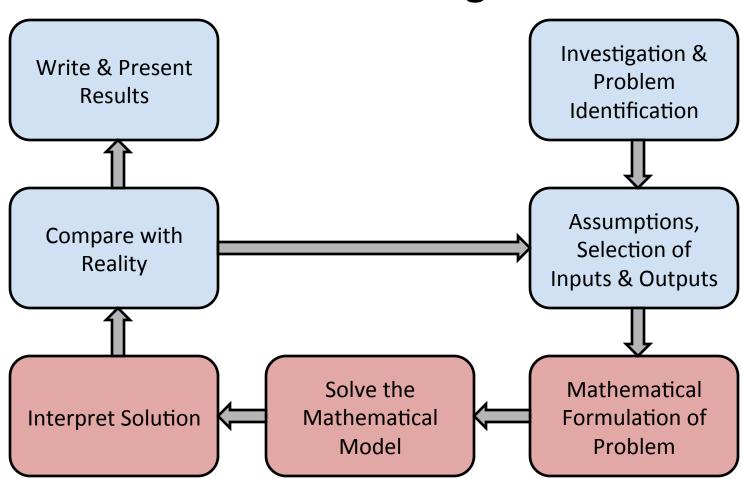
-George E. P. Box



General Process of Mathematical Modeling

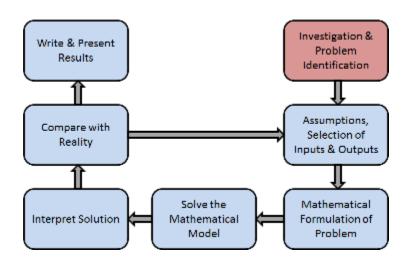


General Process of Mathematical Modeling



Example: Chickenpox

- How do we model a chickenpox epidemic?
 - An uninfected person is susceptible to chickenpox.
 - An infected person comes in contact with a susceptible person and infects this person.
 - After a period of time, the person recovers.

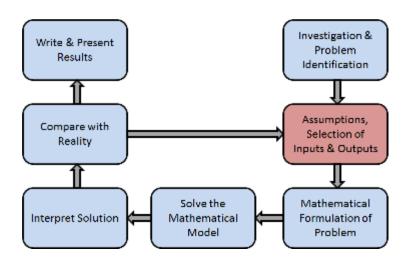


Assumptions

You could simplify the process for a single individual as:

$$S \to I \to R$$

where a person flows from susceptible, to infected, to removed. This is called an SIR model (Bailey, 1975).



Selection of Inputs

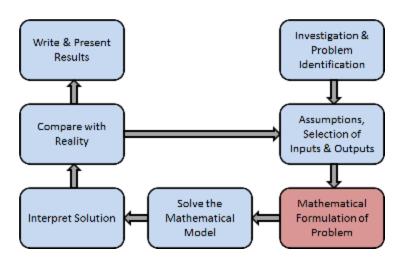
- Independent variables: Typically considered variables you have control over or are fixed.
 - Time* (t)
 - Space (x)
- Parameters: Arbitrary constants whose values characterize members of a system.
 - Infection rate (λ)
 - Recovery rate (r)

Selection of Outputs

- Dependent variables: The quantity you measure in the experiment and what is affected during the experiment.
 - Susceptible people (S)
 - Infected people (I)
 - Recovered people (R)

What kind of model?

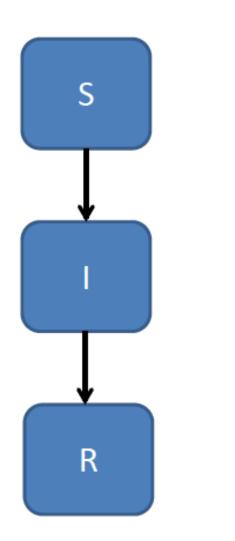
- Discrete or continuous in time?
 - Difference equations vs. differential equations.
- Discrete or continuous in space?
 - Compartment models vs. partial differential equations
- Deterministic or Stochastic?
 - Stochastic: Gillespie, stochastic differential equations, etc.
- Time delays?
 - Delay differential equations.



Example – SIR differential equations

- Continuous in time: neglect discrete events (such as going to work or school each day).
- <u>Neglect space</u>: system is well mixed. There are no local outbreaks.
- Neglect delays: individuals contagious as soon as infected.
- Neglect chance: If system is large enough, on average results are always the same.

SIR Model

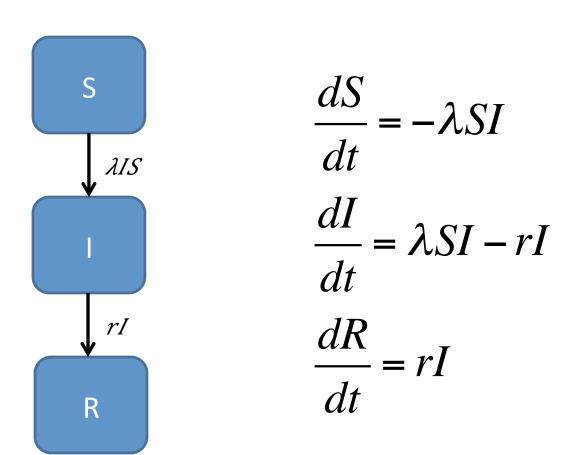


$$\frac{dS}{dt} = f(S, I)$$

$$\frac{dI}{dt} = g(S, I)$$

$$\frac{dR}{dt} = h(I)$$

SIR Model



Variables and Parameters

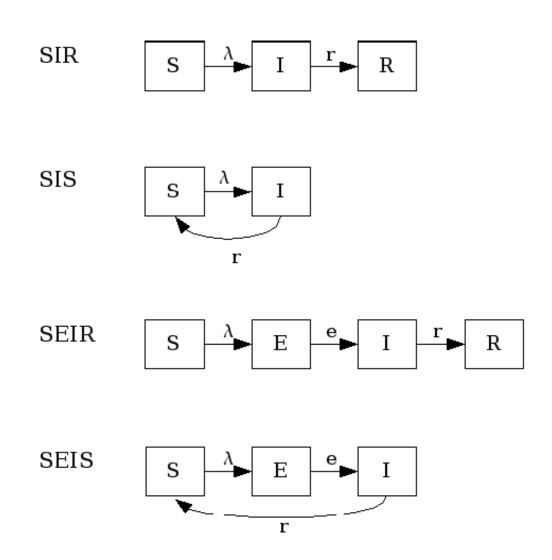
- Time (*t*) days
- Number Susceptible (S) number of people.
- Infected (I) number of people.
- Recovered (R) number of people.
- Infection rate (λ) (people *day)⁻¹
- Recovery rate (r) days⁻¹

$$\frac{dS}{dt} = -\lambda SI$$

$$\frac{dI}{dt} = \lambda SI - rI$$

$$\frac{dR}{dt} = rI$$

Other choices for epidemic models

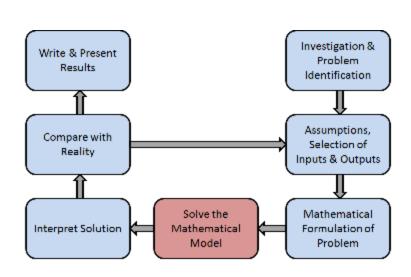


Rates

- Law of Mass Action for Infection (λSI)
 - Assumes infections are similar to reactions in molecular dynamics (random bumping).
- Recovery rate modeled as rl, where r is 1/ (number of days infectious).
 - All people recover at the same rate.

Solve the model

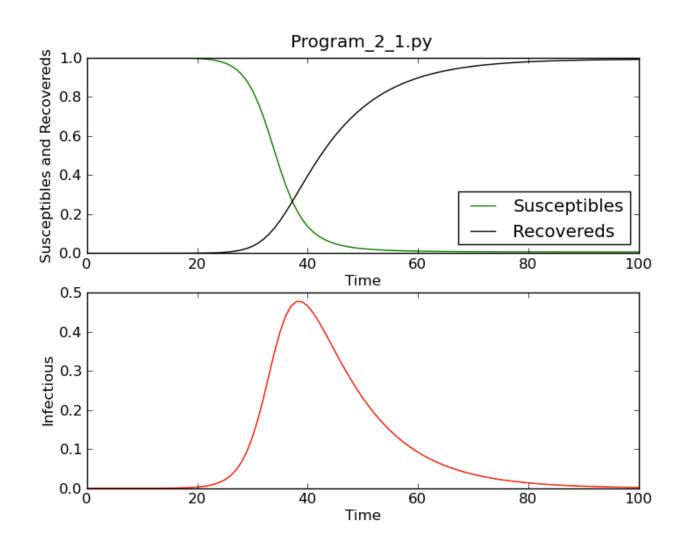
- Many commercial solvers are available for systems of differential equations.
- Matlab/Python codes available.
- Need to find reasonable parameter values.
 - Literature searches
 - Experiments
 - Best guess



Best guess at rates

- λ can be considered the average number of people one person would infect per day if everyone was susceptible.
 - Guess: 0.1 days⁻¹
- R is 1 divided by the average number of days you are infectious.
 - Guess: 0.5 (people*day)⁻¹
- Note that it usually takes 10-21 days to show symptoms (not including this yet).

SIR Results

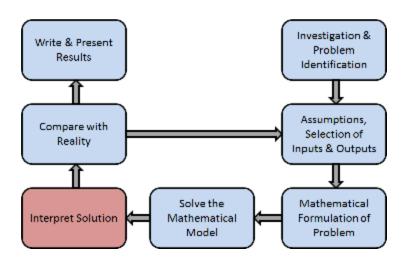


Interpret results

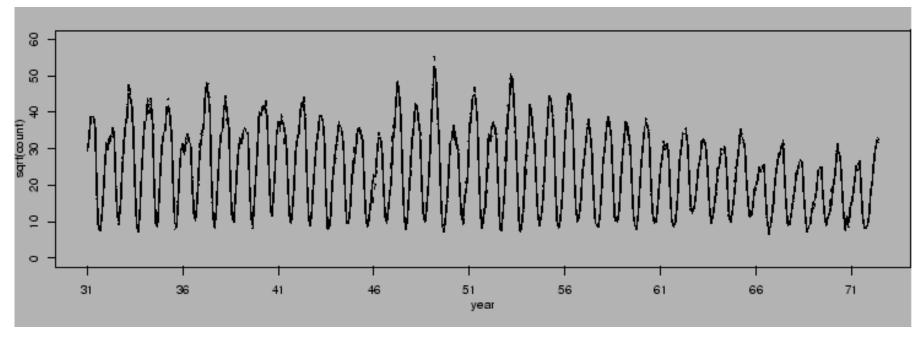
- Are the results reasonable?
- What is the behavior of the dependent variables as $t\rightarrow\infty$?

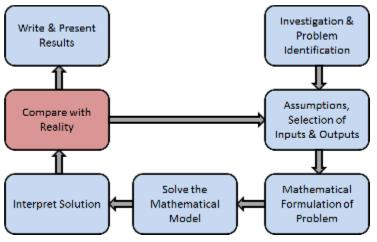
Do the dynamics make sense in terms of the

application?



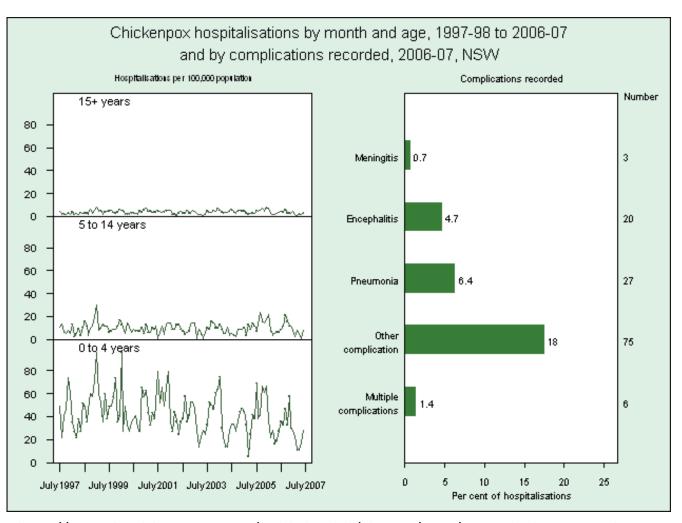
Chicken Pox Data





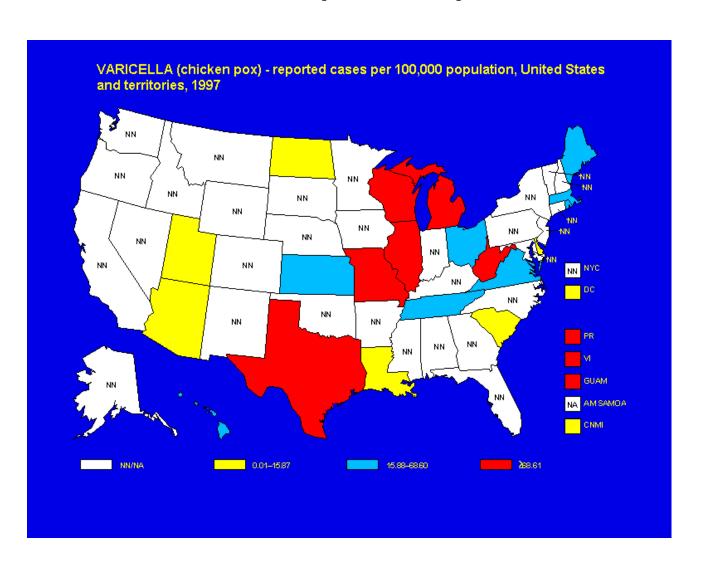
- Monthly reported number of chickenpox, New York City, 1931-1972.
- Source: Hipel and Mcleod (1994).

Age Structured Chickenpox Data

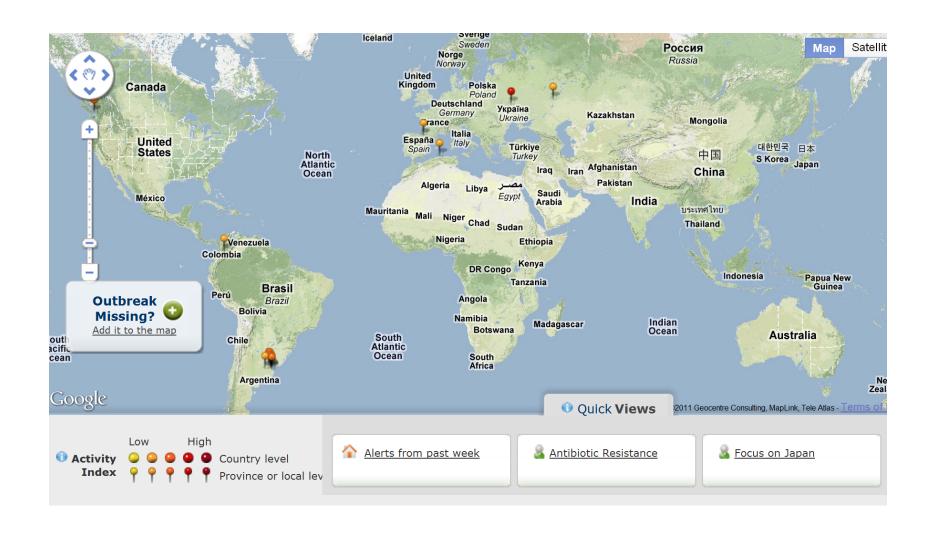


http://www.health.nsw.gov.au/publichealth/chorep/com/com_chickenpox_cxhos.asp

Chickenpox by State



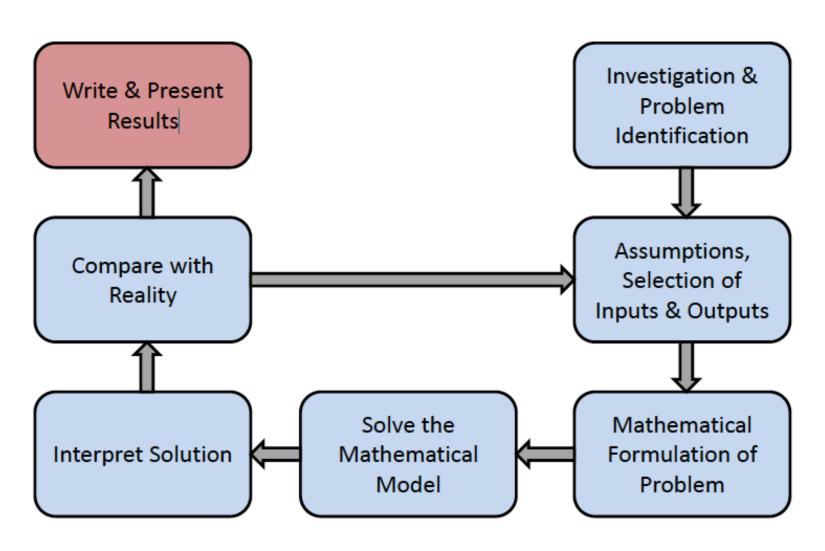
Current Global Outbreaks



Gleamviz global epidemic simulator

http://www.gleamviz.org/simulator/client/

Final step!



The most complex models aren't necessarily the most significant

"One the greatest scientific achievements of the 1990's was the development of a clear understanding of HIV pathogenesis aided by simple mathematical models. These simple formulations were enough to interpret clinical data, determining quantitative characteristics of the interaction between the HIV virus and the cells targeted by it. "

- From http://www.etsu.edu/cas/math/ cbmsDes.aspx