Lab 6: Modeling Epidemics Part II



Today's Lab

- 1. Talk through how to evaluate model assumptions and modify models to fit disease biology
- 2. Work through an example with Covid data
- 3. Let you start developing models for your given diseases



Modifying Compartmental Models

SIR is a useful, classic framework. However, it may not fit in all situations!

Example: Cholera, a diarrheal disease caused by the O1 strain of the bacteria *Vibrio cholerae*. Transmission is largely waterborne, and the pathogen can asexually replicate in water.



Does SIR make sense for Cholera? How could we modify it?

(Some) Assumptions of the SIR Model

- Homogeneous Mixing of Populations
- Constant Population Size
- Infection probability increases linearly with # of infecteds
- Permanent, perfect immunity after recovering
- Every individual has the same susceptibility
- Recovery rate is exponentially distributed

dSdt-dIdt dR= dI

Modifying Compartmental Models for Cholera (from Codeço 2001)

$$\frac{dS}{dt} = n(H - S) - a\lambda(B)S$$
$$\frac{dI}{dt} = a\lambda(B)S - rI$$
$$\frac{dB}{dt} = B(nb - mb) + eI$$

(Note: Codeço here doesn't keep track of the recovered class here)



How do we decide between contenting models?

Remember AIC?

If we're using maximum likelihood to fit our models, we already have likelihood values-easy to convert for the sake of comparison!

$$AIC = -2\ln(L) + 2k$$

Occam's Razor



"When faced with two equally good hypotheses, always choose the simpler."

Case Study: Can we improve a model for COVID-19?

COVID-19: Caused by SARS-CoV2

- Global pandemic, beginning at the end of 2019
- Directly transmitted through respiratory droplets.
- Many infected individuals experience an infectious asymptomatic period preceding noticing they're sick. A minority of individuals may never experience symptoms at all, while still being able to infect other



Two Potential Models for Covid-19



$$\begin{aligned} \frac{dS}{dt} &= -\beta SI \\ \frac{dI}{dt} &= \beta SI - dI \\ \frac{dR}{dt} &= dI \end{aligned}$$

Draw this model

$$\frac{dS}{dt} = -\beta_1 SI - \beta_2 SA$$
$$\frac{dA}{dt} = \beta_2 SA - \alpha_1 A - \alpha_2 A$$
$$\frac{dI}{dt} = \beta_1 SI - \gamma 1I + \alpha_1 AI$$
$$\frac{dR}{dt} = \gamma 1I + \alpha_2 A$$

Which model fits better?

Let's use maximum likelihood estimation to see!

Your case data: Weekly COVID-19 deaths in Richland county from the "first wave" of infection, From mid-march 2020 to the beginning of June.



Disease Modeling Project: Your Task

- 1. Take a real dataset and create an epidemic model to represent it
 - a. Describe what changes you need to make compared to the SIR model
 - b. Be able to describe the aspects of the system that inspired you to make that change
- 2. Fit the model to data and present your param estimates
 - a. Compare your results to primary lit and see if they're supported. Discuss why there might be differences between your result and others
- 3. Describe what aspects of the system change when you incorporate this additional wrinkle
 - a. What sorts of dynamics/patterns might you be missing if you treat it like an SIR system?
- 4. Present your findings in a clear and effective scientific presentation (12min, 3min for questions)
 - a. Presentation date: March 13th

Possible Diseases + Datasets

- 1. The 1918 Influenza Epidemic in the US (city-level case data)
- 2. The 2020 Covid-19 epidemic in the US (county-level case data)
- 3. 2018 Measles outbreak in Chad (data from: <u>https://reliefweb.int/disaster/ep-2018-000075-tcd</u>, summarized in <u>this master's thesis</u>)
- 4. HIV in humans (Cape Verde or Morocco) https://link.springer.com/chapter/10.1007/978-3-030-49896-2_6
- 5. Rabies: https://zenodo.org/records/5015975
- 6. Ebola:<u>https://data.humdata.org/dataset/guinea-ebola-evd-2021-subnational-cases-deaths-h</u> ospitalisations-and-contact-tracing
- 7. Malaria
- 8. Lyme Disease
- 9. Avian Conjunctivitis (Mycoplasma gallisepticum)
- 10. Daphnia disease
- 11. White Nose in Bats

Sources

Codeço, C. T. (2001). Endemic and epidemic dynamics of cholera: the role of the aquatic reservoir. BMC Infectious diseases, 1(1), 1-14.

Gao, Z., Xu, Y., Sun, C., Wang, X., Guo, Y., Qiu, S., & Ma, K. (2021). A systematic review of asymptomatic infections with COVID-19. Journal of Microbiology, Immunology and Infection, 54(1), 12-16.

Juul, J. L., Græsbøll, K., Christiansen, L. E., & Lehmann, S. (2021). Fixed-time descriptive statistics underestimate extremes of epidemic curve ensembles. Nature physics, 17(1), 5-8.

Ying, L., & Xiaoqing, T. (2021). COVID-19: Is it safe now? Study of asymptomatic infection spread and quantity risk based on SAIR model. Chaos, Solitons & Fractals: X, 6, 100060.

Data: <u>https://www.nytimes.com/interactive/2021/us/covid-cases.html</u> <u>https://github.com/nytimes/covid-19-data/tree/master</u>