



Webinar: The Role of Applied Math in Real-time Pandemic Response: How Basic Disease Models Work

Presented by:

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National Institute for Mathematical and Biological Synthesis, University of Tennessee, Knoxville With support from the National Science Foundation (DBI-1300426)

MEET YOUR MODERATOR



Louis J. Gross, PhD

Director, National Institute for Mathematical and Biological Synthesis (NIMBioS)

Director, The Institute for Environmental Modeling, University of Tennessee

Chancellor's Professor of Ecology and Evolutionary Biology and Mathematics, University of Tennessee



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Upcoming Webinars

Costs and benefits of defending against viral infection: Lessons from natural ecosystems

Date: 3:30 EDT Tuesday, April 7, 2020

Speaker: Dr. David Talmy, Asst. Professor, Microbiology, University of Tennessee, Knoxville

Moderator: NIMBioS Director Louis Gross, NIMBioS Director and Chancellor's Professor of Ecology and Evolutionary Biology and Mathematics at the University of Tennessee

Abstract: The COVID-19 virus is shaping Earth in unprecedented ways, for example by changing the rate at which humans release greenhouse gasses into the atmosphere. Yet, through their activity in natural ecosystems, viruses have been shaping Earth as a system for millions of years. In this presentation, I will consider diverse ways viruses may have shaped Earth as a system, and discuss the value of mathematical models for understanding factors which govern the dynamics of viral infections globally.

David Talmy grew up in London, England. He was trained in mathematics as an undergraduate at the University of Sussex. Dr. Talmy is an assistant professor in the Department of Microbiology at the University of Tennessee, Knoxville. He is also an affiliate faculty member at the National Institute for

Mathematical and Biological Synthesis. As a graduate, he transitioned into environmental research through a master's program at the University of York specifically tailored to train mathematicians in ecological research. His doctoral training was primarily at Plymouth Marine Laboratory in the UK, which houses one of the foremost European marine ecosystem





MEET YOUR PRESENTER



Nina Fefferman, PhD

Professor of Ecology and Evolutionary Biology and Mathematics, University of Tennessee

Director, The Mathematical Modeling Consulting Center, University of Tennessee

Associate Director, One Health Initiative, University of Tennessee



Webinar Objectives

- Understand how math models help us analyze and predict outbreaks
- Gain familiarity with concepts in the news about pandemics: R₀, "Flatten the Curve", etc.
- See how we can use models to design public health policy

The role of applied math in real-time pandemic response:

How basic disease models work

What Do Math Modelers Do?



Start with some problem in the world

- Complicated Interactions
- Zillions of possible factors
- Lots of different possible measurements / observations
- Lots of things we can't measure

We can use math to explain!



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Distill the world to abstract logic

Turn logic into equations



Lets us turn conceptual logic into quantitative calculations and predictions: Numbers



Lots of types of quantitative model methods

- Linear Algebra and Matrices
- Difference Equations
- Differential Equations
- ➢ Game Theory
- > Networks
- Cellular Automata
- Agent Based Models
- Statistical Models

The <u>details</u> of what you do in each of these are different, but the basic idea is the same:

Logic \rightarrow Equations \rightarrow Predictions

Let's Use Models to Understand Outbreaks



Measles (Gastañaduy et al. 2016)





West Nile virus (TX Dept of SHS, 2012)

Let's try to explain the pattern: Why do outbreaks end?

(even if we don't have a vaccine)





Measles (Gastañaduy *et al.* 2016)



West Nile virus (TX Dept of SHS, 2012)

Let's Abstract the Logic of Infections Together

What do we know about infectious diseases and how they work?



Healthy, Susceptible People Catch Infections From



Sick, Infectious People

What happens to Susceptible People?

A couple of steps:









3

2)

1)





Mathy things about what happens to Susceptible People





We need both Together this gives a **rate** of





Let's call it **Rate 1** and keep it for later









Let's call this one Rate 2



Susceptible People become Infectious at Rate1 and Recover at Rate 2

Abstract logic of our system is:

Now let's make our logic into equations





How many people will still be Susceptible tomorrow?

$$\begin{array}{c|c} S & \xrightarrow{Rate 1} & I & \xrightarrow{Rate 2} & R \end{array}$$

$$S_{tomorrow} = S_{today} - (Rate1) * S_{today} * I_{today}$$



How many people will be Infectious tomorrow?



$$S_{tomorrow} = S_{today} - (Rate1) * S_{today} * I_{today}$$





$$S_{tomorrow} = S_{today} - (Rate1) * S_{today} * I_{today}$$

*I*tomorrow



$$R_{tomorrow} = R_{today} + (Rate2) * I_{today}$$

The Complete Math!

$$S \xrightarrow{Rate 1} I \xrightarrow{Rate 2} R$$

$$S_{tomorrow} = S_{today} - (Rate1) * S_{today} * I_{today}$$

$I_{tomorrow} = I_{today} + (Rate1) * S_{today} * I_{today} - (Rate2) * I_{today}$



$$R_{tomorrow} = R_{today} + (Rate2) * I_{today}$$

This is really simple – Is it useful? YES

$$\begin{array}{c|c} S \end{array} \xrightarrow{Rate 1} & I \end{array} \xrightarrow{Rate 2} & R \end{array}$$

$$S_{tomorrow} = S_{today} - (Rate1) * S_{today} * I_{today}$$



$$R_{tomorrow} = R_{today} + (Rate2) * I_{today}$$

Let's go back to the question: Why do outbreaks end?



West Nile virus (TX Dept of SHS, 2012)

What is the pattern to explain?

- First the number of Infectious people goes up
- Then it goes down

Why?

Why do outbreaks end?

- First the number of Infectious people goes up
- Then it goes down

Notice:

This is a question just about the numbers of **Infectious People** over time

When will the number of Infectious people fit that pattern?

 $I_{tomorrow} = I_{today} + (Rate1) * S_{today} * I_{today} - (Rate2)I_{today}$ $I_{tomorrow}$ is increasing when

 $(Rate1) * S_{today} * I_{today} - (Rate2)I_{today} > 0$



the parts we add are bigger than the parts we subtract $I_{tomorrow} = I_{today} + (Rate1) * S_{today} * I_{today} - (Rate2)I_{today}$ This means:

Why you actually took algebra:

 $(Rate1)I_{today}S_{today} - (Rate2)I_{today} > 0$

 $(Rate1)I_{today}S_{today} > (Rate2)I_{today}$

 $(Rate1)S_{today} > (Rate2)$





I is increasing when $(Rate1)S_{today} > (Rate2)$

So what happens? Remember:

 $S_{tomorrow} = S_{today} - (Rate1)I_{today}S_{today}$

S can only decrease!

We **HAVE** to get **this** picture for I over time



This is also how we compare outbreaks

I is increasing when $(Rate1) * S_{today} > (Rate2)$

We can re-write as a ratio

 $\frac{(Rate1) * S_{today}}{(Rate2)} > 1$

This ratio at the start of an outbreak (when most people are Susceptible) is called R_0 for this model

The **bigger** the R_0 for a disease, the **worse** we expect the outbreak to be

Some R_0 values for our favorite diseases

Disease	\boldsymbol{R}_0
Measles	12-18
Smallpox	3.5-6
HIV/AIDS	2-5
COVID-19	1.4-3.9 ???
Influenza 1918	1.4 - 2.8
Ebola 2014	1.5 - 2.5
Influenza (seasonal)	0.9-2.1

We can estimate R_0 from equations or from observations of outbreak curves

Shamelessly copied from Wikipedia.org for this talk

But wait, we know diseases don't just go away permanently – What's going on?

Measles in China: Chao Ma et al. 2014

Fig. 1. Monthly numbers of measles cases, January 2005–October 2013, China



Rotavirus in Africa: Platts-Mills et al. 2017



Annual Flu Outbreaks: Potter 2008



Global Flu Pandemics: Potter 2008



Babies!

Measles in China: Chao Ma et al. 2014 Annual Flu Outbreaks: Potter 2008 Fig. 1. Monthly numbers of measles cases, January 2005–October 2013, China Thousands × 10³ No. of cases Year 2 З 4 5 6 III Berry III Frances and Berry Barry Bar Virus serotype A А В С D Е 2009 Onset by month 40-50 Death 0.5 1800 1900 2000 1700 Year

In reality, the number of Susceptibles ISN'T only decreasing

 $S_{tomorrow} =$

$S_{today} + S_{babies} - (Rate1)I_{today}S_{today}$



How much disease we can keep around the population is directly tied to the birth rate *(and if people lose immunity over time)* This is also why Vaccines can protect people who aren't even vaccinated

 $S_{tomorrow} =$

$$S_{today} - S_{vacc} - (Rate1)I_{today}S_{today}$$

Taking out enough Susceptibles so that $(Rate1)S_{today} \ge$ (Rate2) is the goal!



Called the "herd immunity threshold"

This really simple model is so powerful!



$$S_{tomorrow} = S_{today} - (Rate1) * S_{today} * I_{today}$$



$$R_{tomorrow} = R_{today} + (Rate2) * I_{today}$$

Let's use it to understand what we mean by "flatten the curve"



$$S_{tomorrow} = S_{today} - (Rate1) * S_{today} * I_{today}$$

It's all about Rate 1



 $S_{tomorrow} = S_{today} - (Rate1) * S_{today} * I_{today}$

If we can slow down Rate 1

 $S_{tomorrow} = S_{today} - (Rate1) * S_{today} * I_{today}$

$$I_{tomorrow} = I_{today} + (Rate1) * S_{today} * I_{today} - (Rate2) * I_{today}$$



- People move out of S more slowly
- I increases more slowly
- It takes **longer** to run out of **S**, but we **never** build up as many I at once

Keeps people alive - never run out of hospital beds

Remember how we got Rate 1?

It was a combination of:





This is how to slow down Rate 1

Social Distancing





Better Hygiene





This is how to slow down Rate 1

Social Distancing

Better Hygiene



Contact



Transmit Germs



Using just this, we can **predict**:

- How effective is shelter-in-place?
- How long do we need to continue sheltering?
- What percent of people have to shelter to shut down the outbreak?

Not all the answers can be obtained this easily...

- We usually use continuous averages instead
- Many diseases are more logically complicated
 - Different ways of being transmitted
 - Insect bites
 - Sexual contact
 - Contamination of an environment (fomite)
 - Mother to fetus
 - etc.
 - Delay between being infected and becoming infectious
 - Immunity can go away over time
 - Age-based differences
 - Seasonal/Climatological differences
 - Opportunistic infection
 - etc.

The logic and the math can look complicated

The logic of a Tuberculosis and HIV/AIDS model my students and I just published: ϕ^+_{\pm} S^+ γ_{q+1}^{+} DeNegre, Myers, Fefferman. Antibiotics 2020

The logic and the math can look complicated $\frac{dS_{--}}{dt} = -\beta_p^{--}S_{--}^{--}I_{all,p} - \beta_q^{--}S_{--}^{--}I_{all,q} + \rho^{--}R_{--}^{--} + \alpha(S_{--}^{--} + E_p^{--} + E_q^{--} + I_{p+}^{--} + R_{-+}^{--} + S_{++}^{++} + E_{q+}^{++} + E_{q+}^{++}$

The equations were worse:

The first 12 equations (out of 40) from a model to understand how different strains of TB would circulate in parts of Africa where there is already a high prevalence of AIDS in the population

But the basic ideas are EXACTLY THE SAME

$$\frac{dS_{-+}^{+-}}{dt} = -\beta_q^{+-}S_{-+}^{+-}I_{all,q} + \rho^{+-}R_{-+}^{+-} + \alpha(S_{-+}^{+-} + E_{q2}^{+-} + I_{q2}^{+-} + R_{-+}^{+-}) - (\omega + \omega_v)S_{-+}^{++} \\ \frac{dS_{--}^{++}}{dt} = -\beta_p^{++}S_{--}^{++}I_{all,p} - \beta_q^{++}S_{--}^{++}I_{all,q} + \rho^{++}R_{-+}^{++} - \omega S_{-+}^{++} \\ \frac{dS_{-+}^{++}}{dt} = -\beta_q^{++}S_{-+}^{++}I_{all,q} + \rho^{++}R_{-+}^{++} - \omega S_{-+}^{++} \\ I_{all,p} = I_{p+}^{--} + I_{p-}^{--} + I_{p-}^{--} + I_{p+}^{+-} + I_{p+}^{+-} + I_{p+}^{++} + I_{p+}^{++} + I_{p+}^{++} + I_{p+}^{++} \\ I_{all,q} = I_{q+}^{--} + I_{q-}^{--} + I_{q+}^{--} + I_{q+}^{+-} + I_{q+}^{+-} + I_{q+}^{++} \\ \frac{dE_{p-}^{--}}{dt} = \beta_p^{--}S_{--}^{--}I_{all,p} - \zeta_p^{--}E_p^{--} - \omega E_p^{--} \\ \frac{dE_{q}^{+-}}{dt} = \beta_q^{+-}S_{--}^{+-}I_{all,q} - \zeta_q^{--}E_q^{--} - \omega E_q^{--} \\ \frac{dE_{q}^{+-}}{dt} = \beta_q^{+-}S_{--}^{+-}I_{all,q} - \zeta_q^{+-}E_p^{+-} - (\omega - \omega_v)E_p^{+-} \\ \frac{dE_{q}^{++}}{dt} = \beta_q^{++}S_{--}^{+-}I_{all,q} - \zeta_q^{+-}E_q^{+-} - (\omega - \omega_v)E_q^{+-} \\ \frac{dE_{q}^{++}}{dt} = \beta_q^{++}S_{--}^{+-}I_{all,p} - \zeta_p^{++}E_p^{++} - \omega E_p^{++} \\ \end{bmatrix}$$

 $\frac{dS_{--}^{+-}}{dt} = -\beta_p^{+-}S_{--}^{+-}I_{all,p} - \beta_q^{+-}S_{--}^{+-}I_{all,q} + \rho^{+-}R_{--}^{+-} \\ +\alpha(S_{--}^{+-} + E_p^{+-} + E_q^{+-} + I_{p+}^{+-} + R_{--}^{+-} + S_{-+}^{+-} + E_{q2}^{+-} + R_{--}^{+-})$

 $-(\omega + \omega_v)S^{+-}$

DeNegre, Myers, Fefferman. Antibiotics 2020

The predictions our models make allow us to compare interventions

Model outcomes comparing mosquito control strategies to combat Zika virus in different cities



Stone, Schwab, Fonseca, Fefferman. PLoS NTD 2020

Sometimes we use predicted curves, sometimes we use theoretical thresholds

Together, these are the critical tools of mathematical epidemiology



 $\frac{(Rate1) * S_{today}}{(Rate2)}$ $R_0 =$

Moral: Math Models Keep Us All Safer

Thank you for your participation!

Questions? Please use the Question button on Zoom to post these

