

Intro to infectious disease modeling (in R)

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All materials at: github.com/SineadMorris/trainings

Objectives



Background & practical concepts



Construct a simple disease model: SIR example



Extend this model to fit a particular need



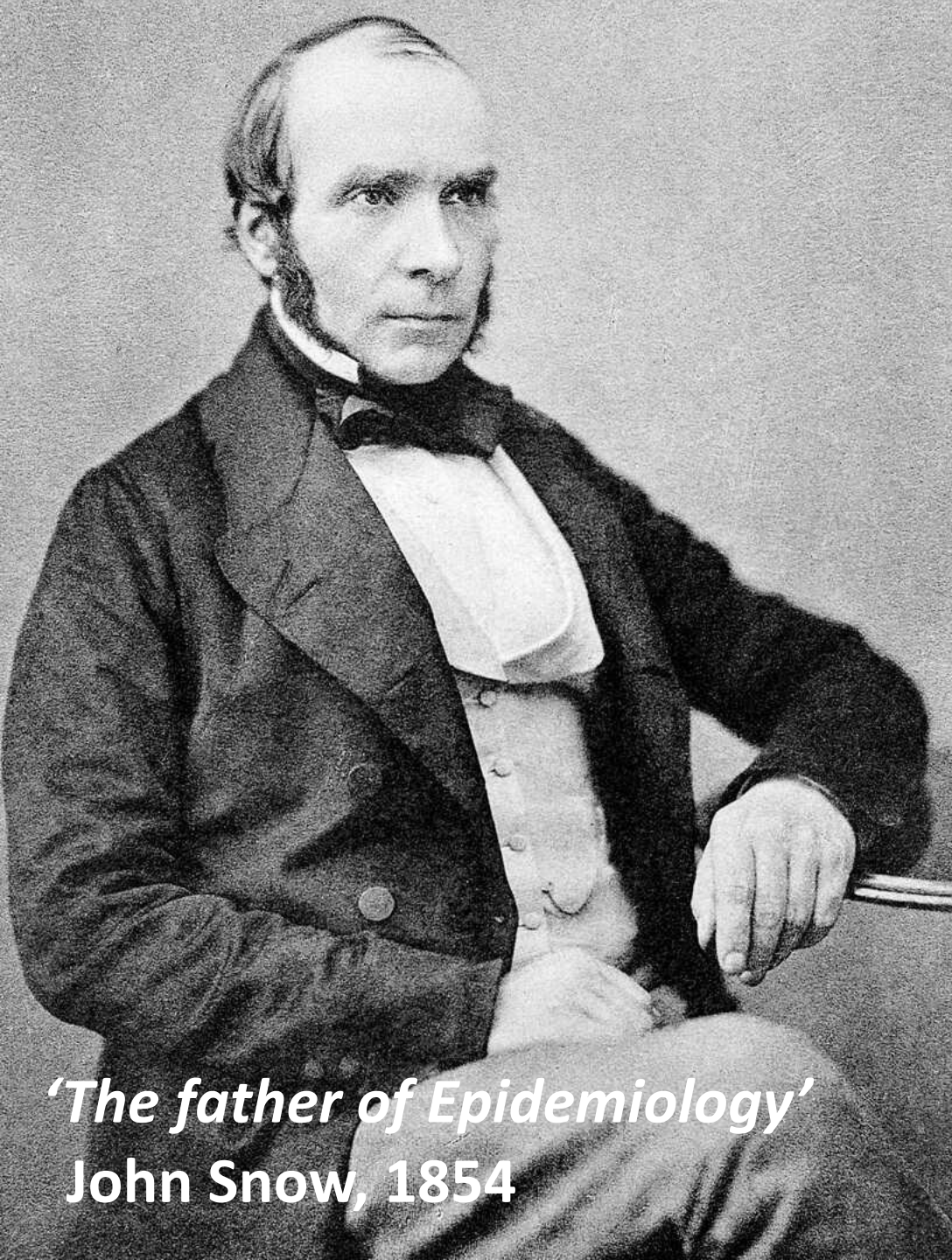
Code a model in R



Time for Qs & additional resources



Background & practical concepts



'The father of Epidemiology'
John Snow, 1854



NOTE
Boundary within which all the Deaths are indicated, is shown thus, ————
Divisions between Sub-Districts, thus, ————
Boundary of equal distance between Broad Street Pump and other Pumps, thus, ————

SCALE 30 INCHES TO A MILE.

The parents of Infectious Disease Modeling



Hilda
Hudson



Ronald
Ross



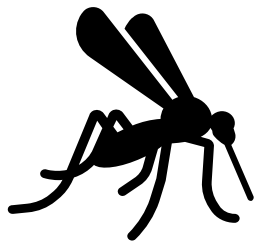
Anderson
McKendrick



William
Kermack

1915-17

1927-33

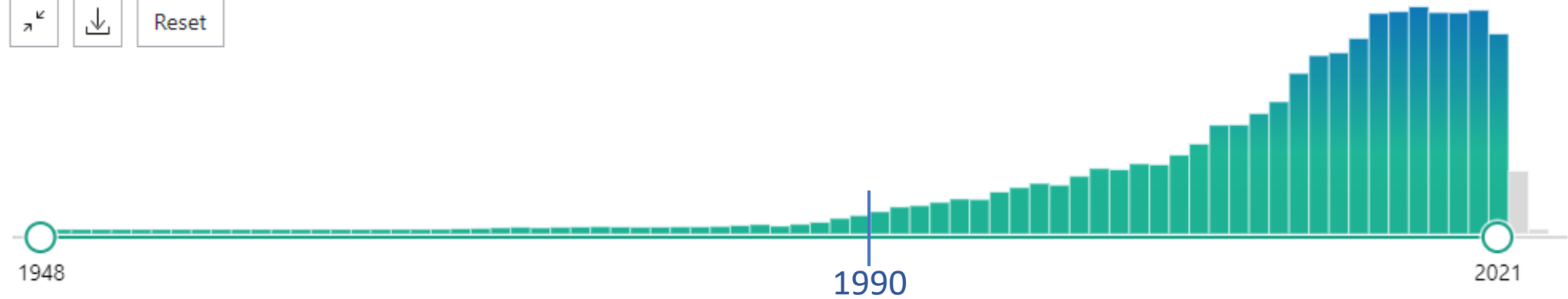


Since the 1980/90s the field has been steadily growing

RESULTS BY YEAR

54,884 results

Page 1 of 5,489



SCIENCE • CORONAVIRUS

What Are Mathematical Models Of Covid-19?

February 4, 2022
9:17 AM EST
Last Updated 6 months ago

United Kingdom

Britain's pandemic modellers say future large waves of COVID possible

CURRENT EVENTS

The Math of Ending the Pandemic: Exponential Growth and Decay

Mathematical model suggests a clue as to when COVID-19 pandemic will turn into an endemic

COVID-19

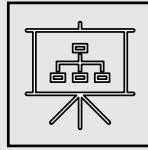
Exponential growth bias: The numerical error behind Covid-19



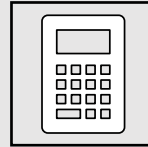
A model is just a
(mathematical)
description of how
we think a disease
spreads



Forecasting / prediction



Scenario analysis



Estimate unknown quantities

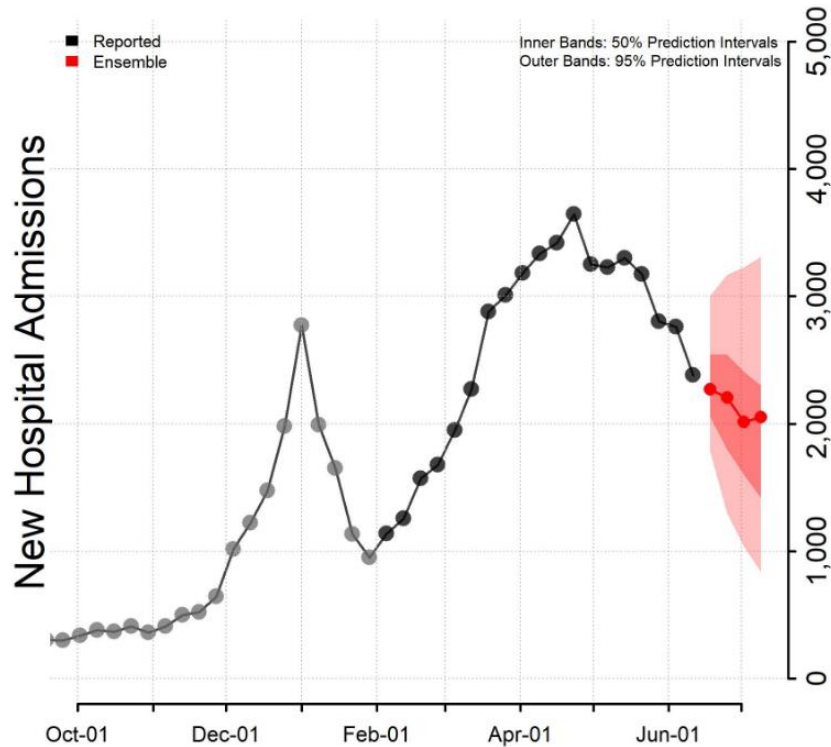


Inference / explaining patterns



Forecasting / prediction

(e.g. how many cases will there be next week?)

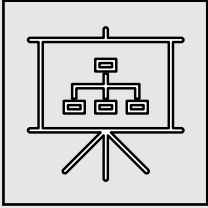


Ex: [FluSight Challenge](#)

Forecasting flu each season (2013+)

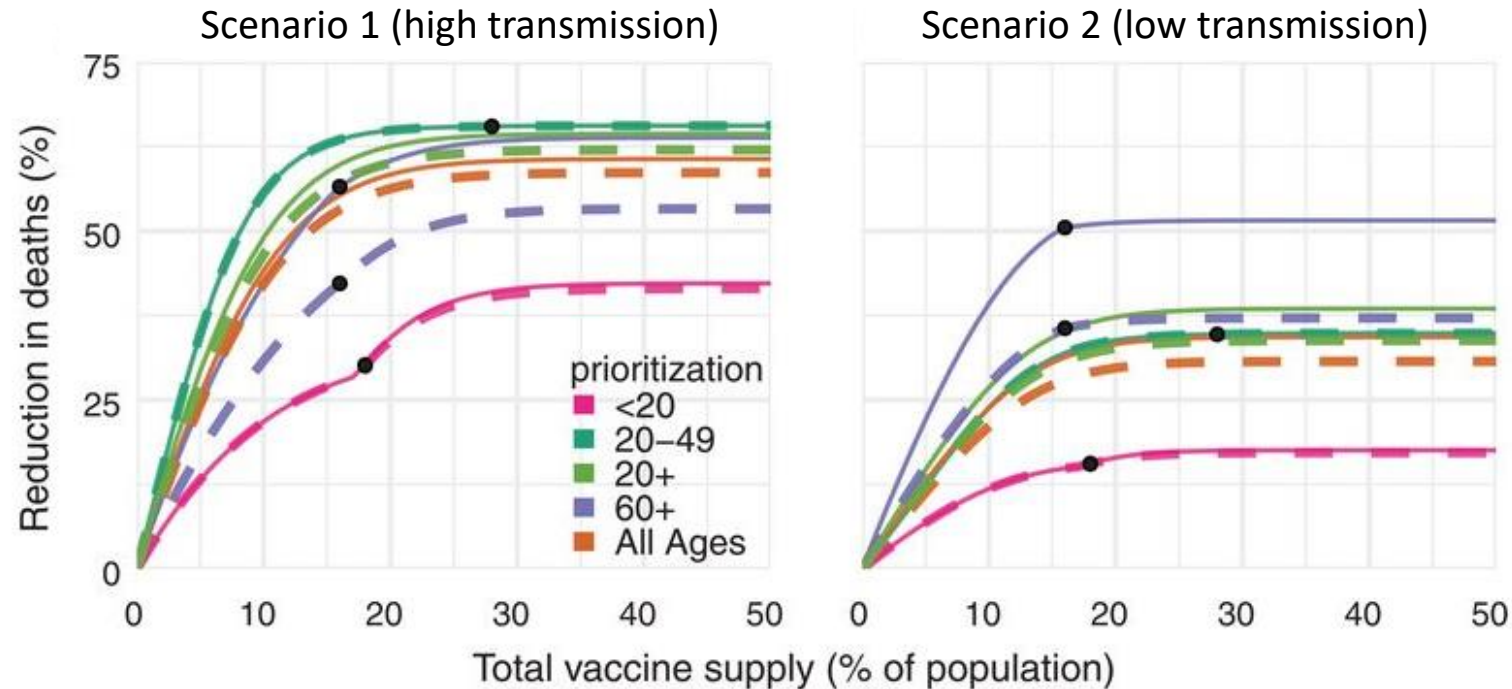
Each week teams predicted hospitalizations 1-4+ wks ahead

Uses include: short-term planning / decision-making



Scenario analysis

(e.g. what *could happen* in situation A vs B vs?)

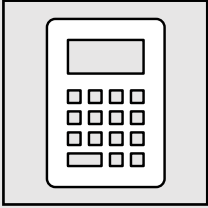


Ex: COVID vax ([Bubar et al 2021](#))

Compare age prioritization
High/low transmission

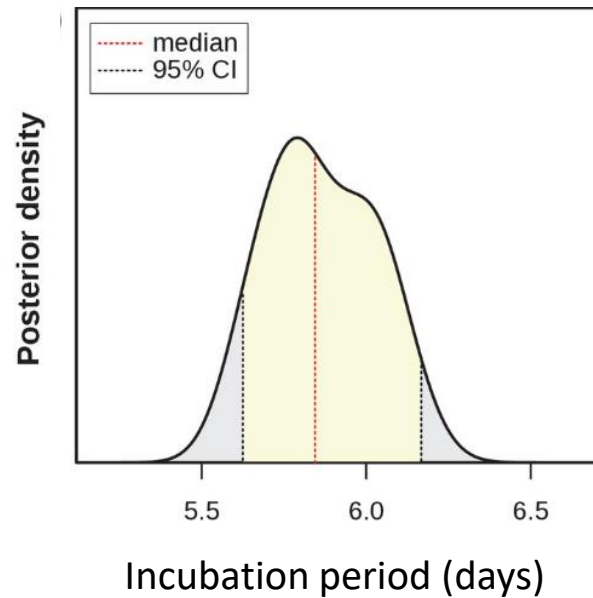
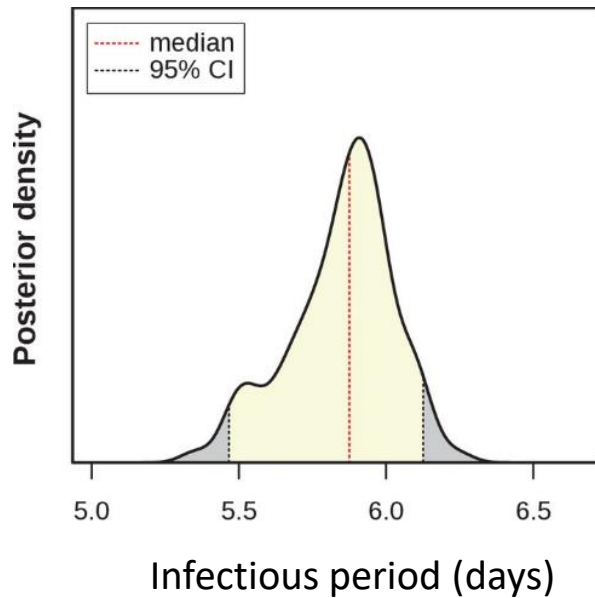
Uses include:

- explore different hypotheses
- long-term planning / assessment



Estimate unknown quantities

(e.g. what is the infectious period?)



Ex: Zika virus ([Lourenco et al 2017](#))

Fit model to case data to estimate parameters

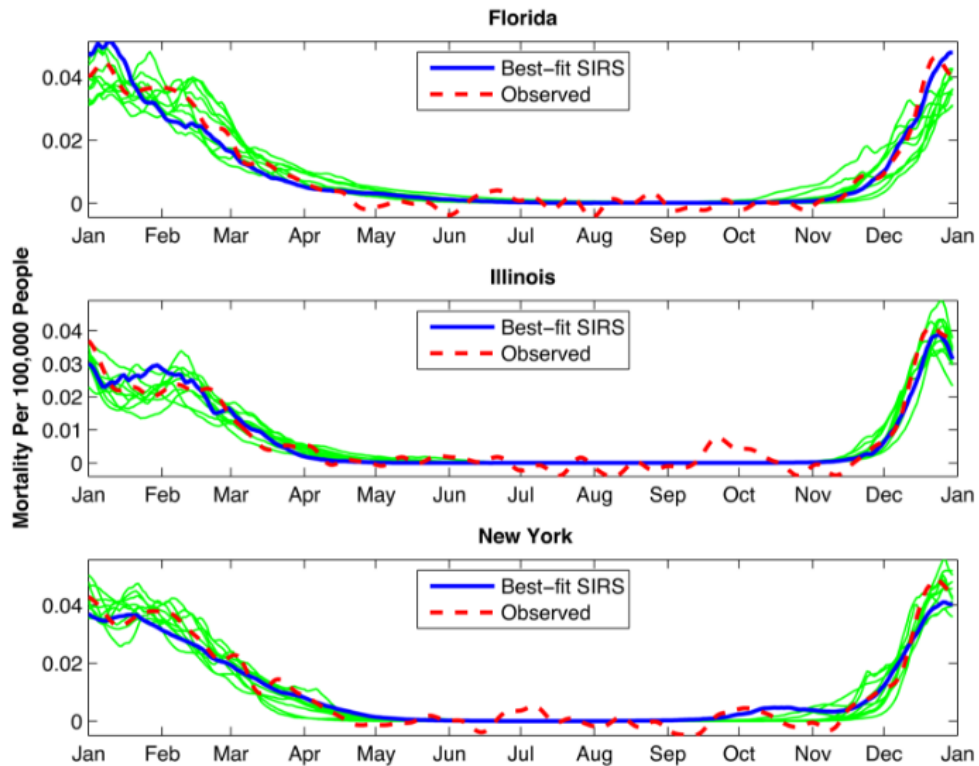
Uses include:

- Understanding disease (e.g. natural history)
- Policy design
- Better inputs for future models



Inference / explaining patterns

(e.g. why are outbreaks seasonal?)



Ex: [Shaman et al \(2010\)](#)

Showed that absolute humidity could be one driver of seasonality

Uses include:

- Understanding drivers/mechanisms of spread
- Policy design
- Building more accurate models



Compartmental models

For a particular pathogen / population:

- Define **general health states** that occur during infection progression
e.g. susceptible, then infected & infectious, then recovered
- Assume **people move through states** at certain rates
- **Transmission equally likely** to occur between anyone (“well-mixed” assumption)

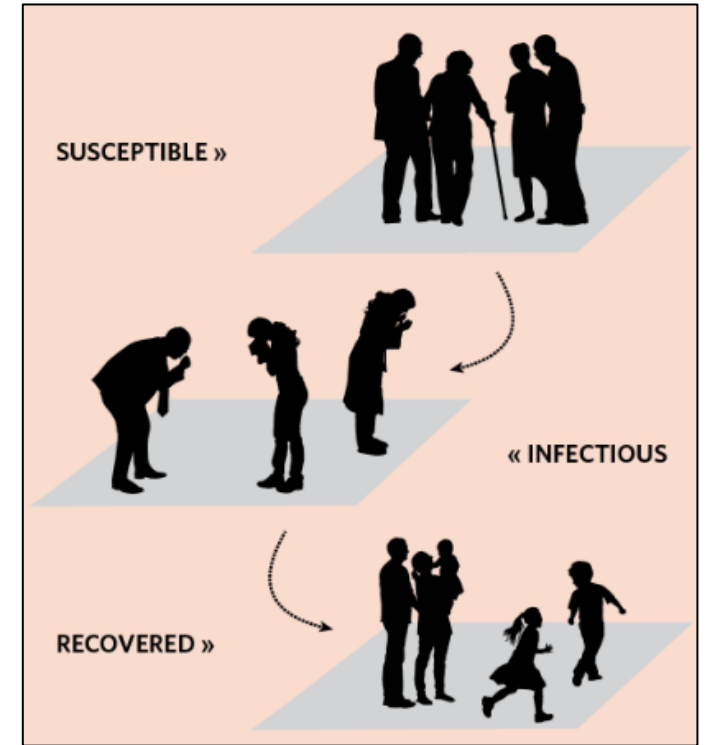


Image source: The Scientist



Basic reproduction number (R_0)

Average # new infections caused by one infected person in a **fully susceptible** population

$$\begin{array}{rclclcl}
 (\text{\# infections / day}) & \times & (\text{\# days infectious}) & & & \\
 \text{per infected person} & & & & & \\
 \\
 \text{e.g.} & 1 & \times & 4 & = & 4
 \end{array}$$

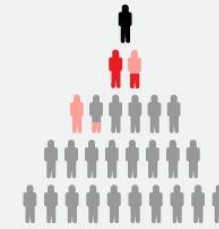
Effective reproduction number (R_t)

Average # new infections caused by one infected person in a **partially susceptible** population

$$\begin{array}{rclclcl}
 (\text{\# infections / day}) & \times & (\text{\# days infectious}) & \times & \text{fraction at risk} & \\
 \text{per infected person} & & & & & \\
 \\
 \text{e.g.} & 1 & \times & 4 & \times & 0.5 & = & 2
 \end{array}$$

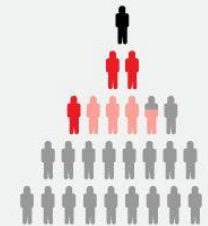
How contagious is a disease?

Scientists use "R naught," or R_0 , to estimate how many other people one sick person is likely to infect

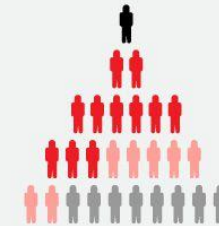


2019-nCoV
1.4-3.3

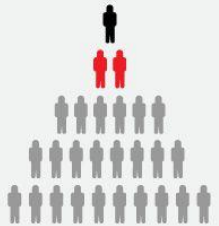
*This estimate is preliminary and likely to change



Zika
3-6.6

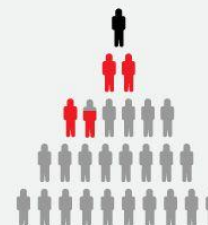


Measles
11-18

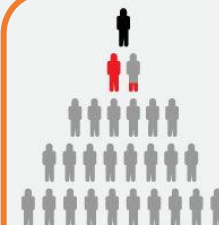


Ebola
2

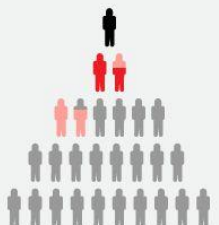
*An early estimate based on the Colombia outbreak in 2015



HIV
3.6-3.7



Seasonal flu
1.3



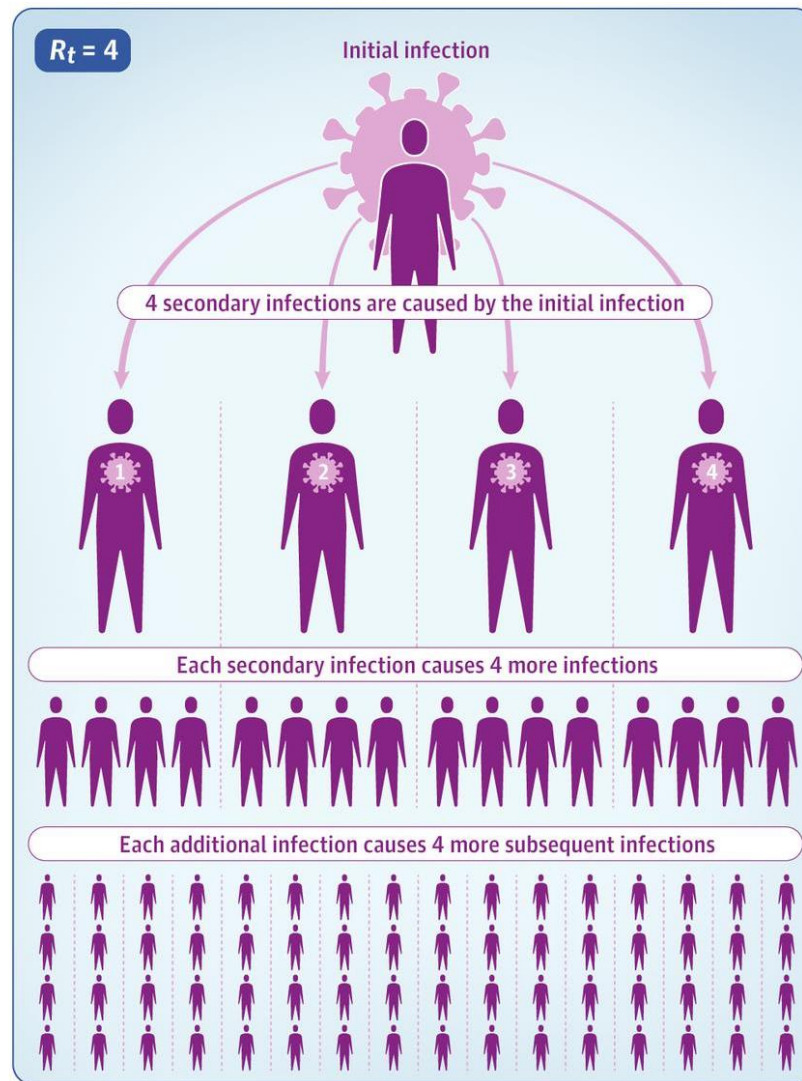
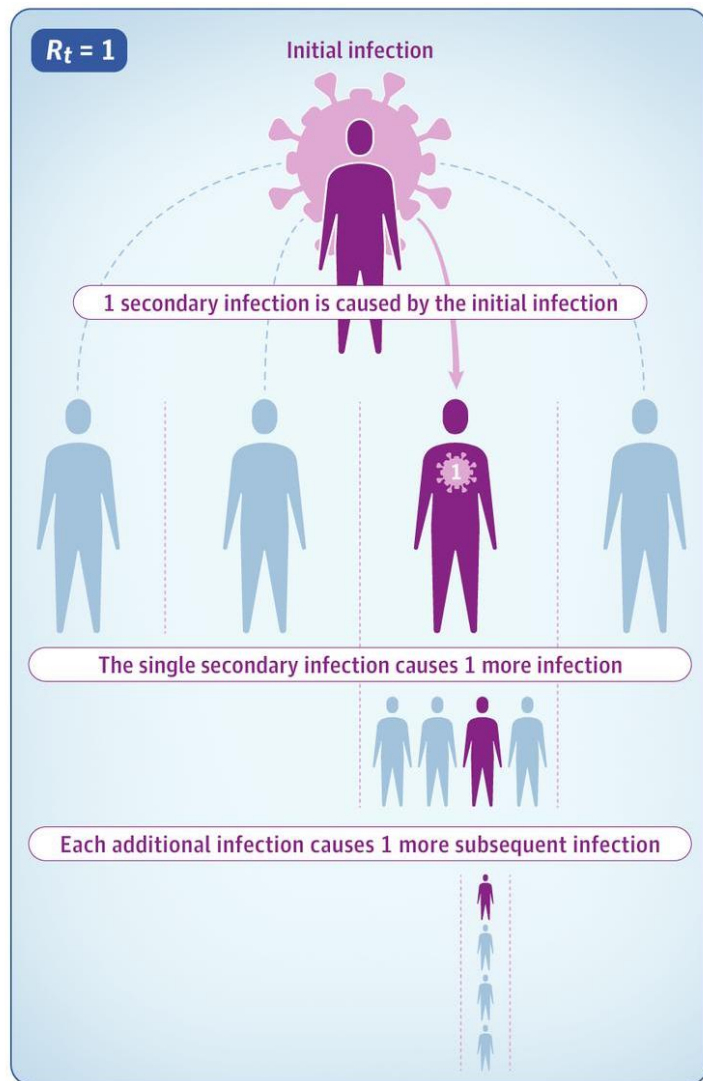
Norovirus
1.6-3.7

*An estimate based on Réunion Island in 2006

SOURCES: Travel Medicine, PLOS One, JAMA Pediatrics, MDPI, NCBI, New England Journal of Medicine, "The Spread and Control of Norovirus Outbreaks Among Hospitals in a Region"



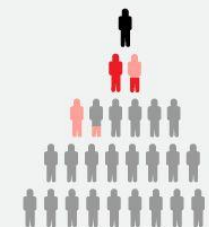
Basic reproduction number (R_0)



Iceland Monitor

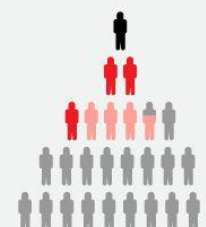
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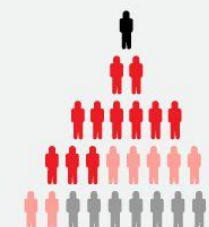


2019-nCoV
1.4-3.3

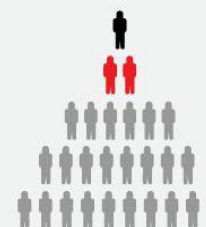
*This estimate is preliminary
and likely to change



Zika
3-6.6

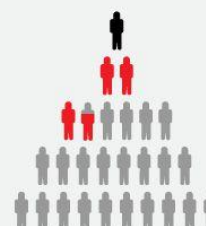


Measles
11-18



Ebola
2

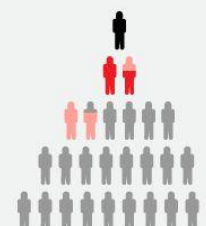
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3.6-3.7



Seasonal flu
1.3



Norovirus
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SOURCES: Travel Medicine, PLOS One, JAMA Pediatrics, MDPI, NCBI, New England Journal of Medicine, "The Spread and Control of Norovirus Outbreaks Among Hospitals in a Region"

Vox

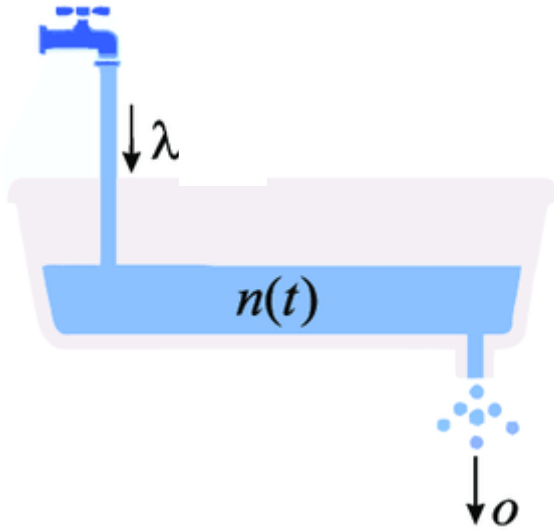


Construct a simple disease model: SIR example



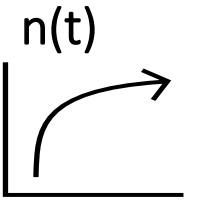
Ordinary differential equations (ODEs)

How much water is in the bath?



Need to know:

1. how much we started with, i.e. $n(0)$
2. how it **changes over time**,
i.e. how much is **flowing in (λ)** vs **flowing out (o)**



$$\frac{dn}{dt} = \lambda - o$$

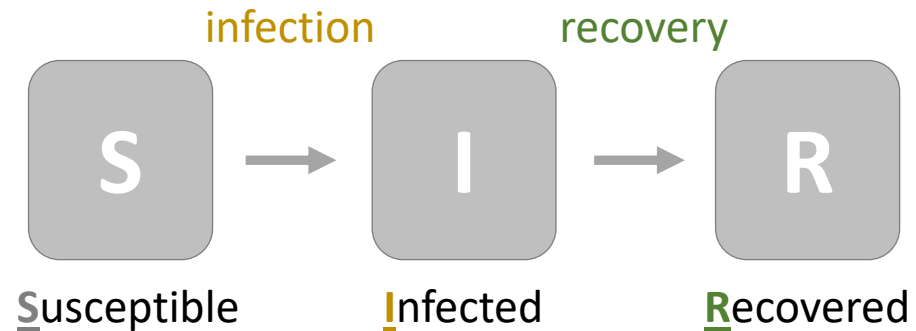
Change over time = flow in - flow out



Constructing the SIR model

Model outbreak of influenza during a single season:

- unvaccinated population (of size N)
- assume immediately infectious upon infection
- assume after infection, immune for rest of season



Describe **flows**
between
compartments

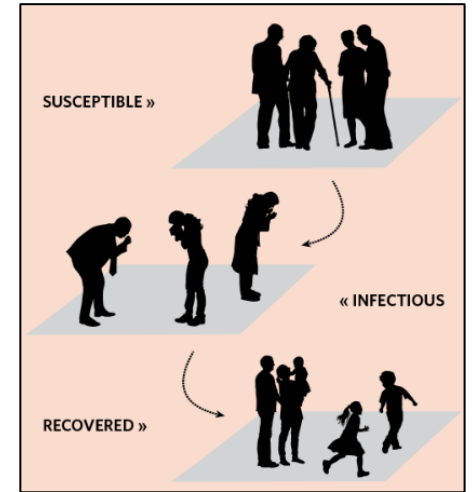


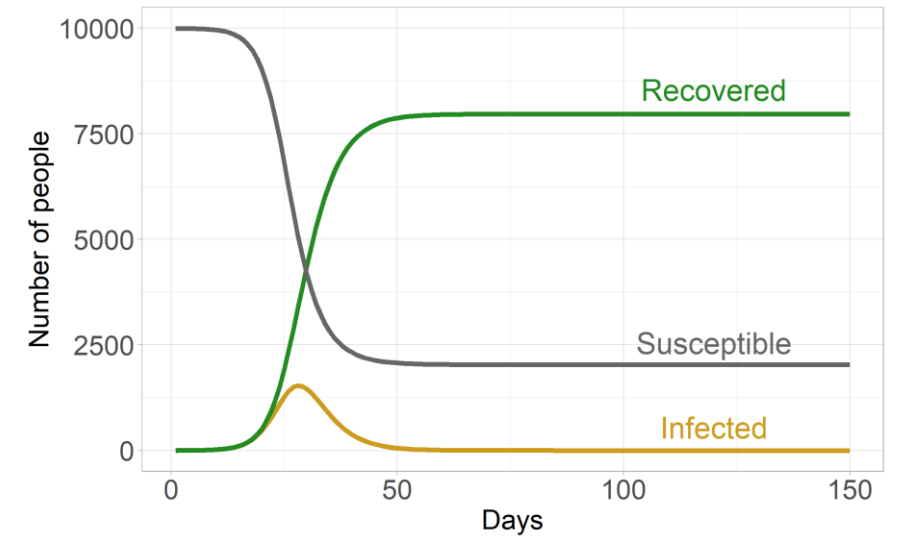
Image source: The Scientist



Constructing the SIR model

Model outbreak of influenza during a single season:

- unvaccinated population (of size N)
- assume immediately infectious upon infection
- assume after infection, immune for rest of season



$$\frac{dS}{dt} = -\beta S I$$

$$\frac{dI}{dt} = \beta S I - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$



Constructing the SIR model

Model outbreak of influenza during a single season:

- unvaccinated population (of size N)
- assume immediately infectious upon infection
- assume after infection, immune for rest of season

infections / day
per infected person

$$\beta S$$

x

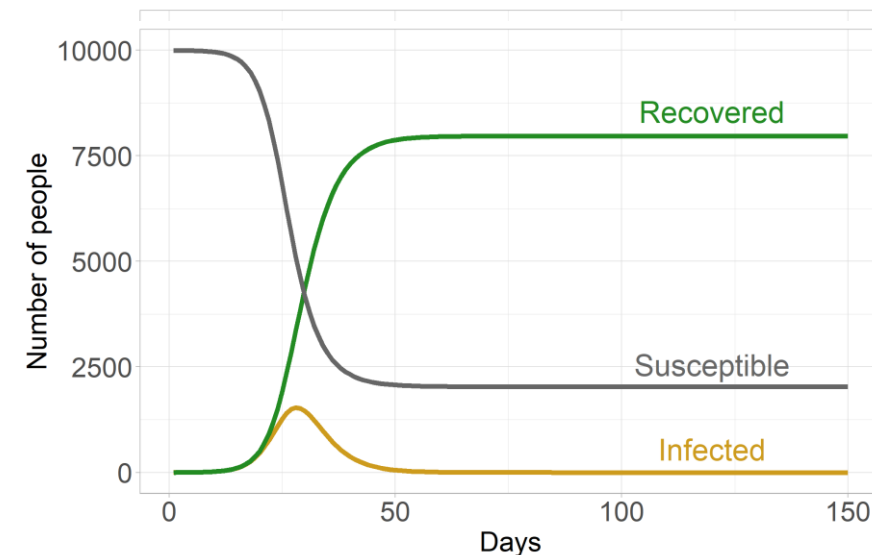
days infectious

x

$$1/\gamma$$

$$R_0 = \beta S \times \frac{1}{\gamma} = \beta N \times \frac{1}{\gamma} = \frac{\beta N}{\gamma}$$

Fully suscept.



$$\frac{dS}{dt} = -\beta S I$$

$$\frac{dI}{dt} = \beta S I - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

γ = rate of
recovery

$\frac{1}{\gamma}$ = time to
recovery



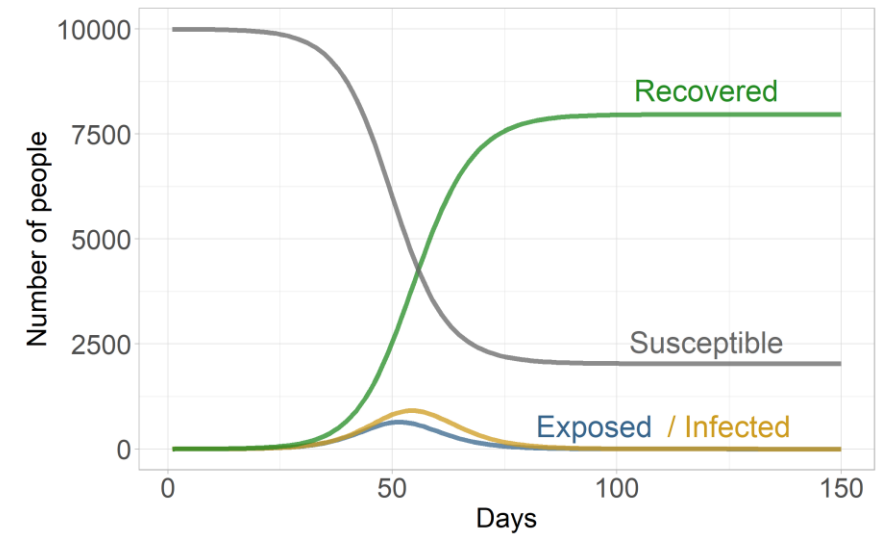
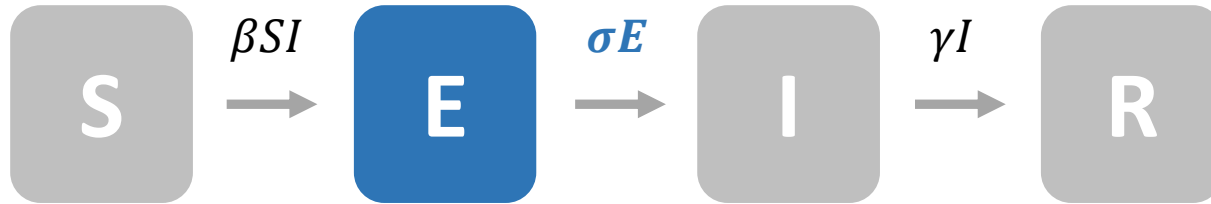
Case studies: Adapting the model to different needs



#1 “Have you included *latent infection*?”

Model outbreak of influenza during a single season:

- unvaccinated population
- assume after infection, immune for rest of season
- period of *latent infection* **before** people become infectious



$$\frac{dS}{dt} = -\beta S I$$

$$\frac{dE}{dt} = \beta S I - \sigma E$$

$$\frac{dI}{dt} = \sigma E - \gamma I$$

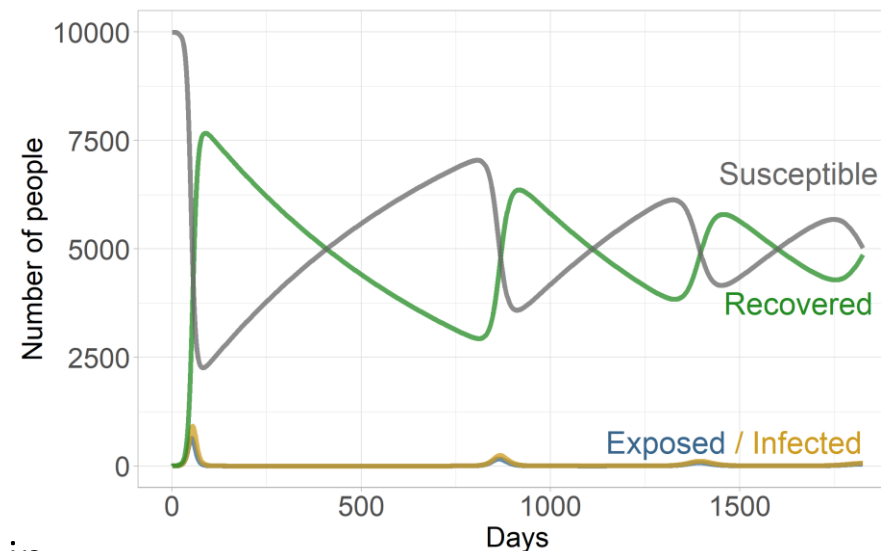
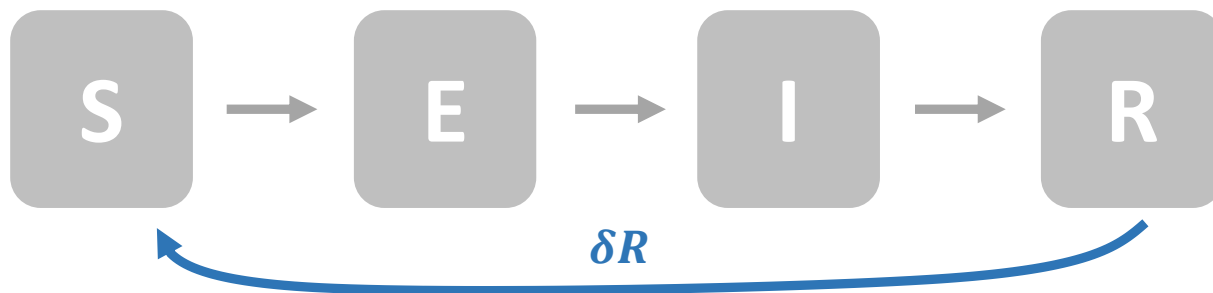
$$\frac{dR}{dt} = \gamma I$$



#2 “...and *waning immunity*?”

Model outbreak of influenza during **multiple** seasons:

- unvaccinated population
- period of latent infection before people become infectious
- assume people **lose immunity** and become fully susceptible again



$$\frac{dS}{dt} = -\beta S I + \delta R$$

$$\frac{dE}{dt} = \beta S I - \sigma E$$

$$\frac{dI}{dt} = \sigma E - \gamma I$$

$$\frac{dR}{dt} = \gamma I - \delta R$$

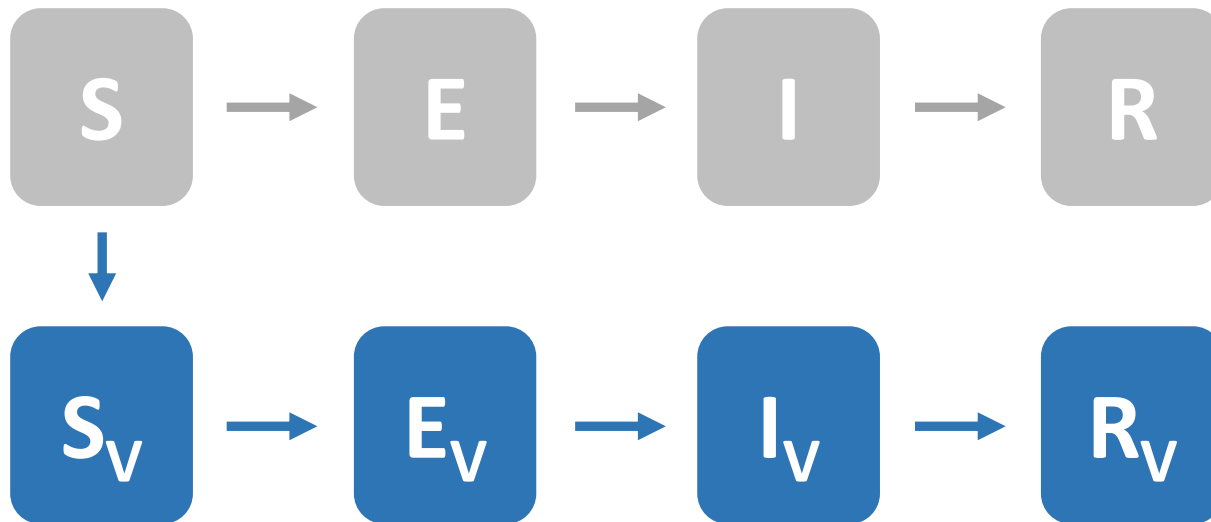


#3 “...or *vaccination*?”

→ SEIR*V* model

Model outbreak of influenza during a *single* season:

- assume after infection, immune for rest of season
- period of latent infection before people become infectious
- susceptible people can be *vaccinated*



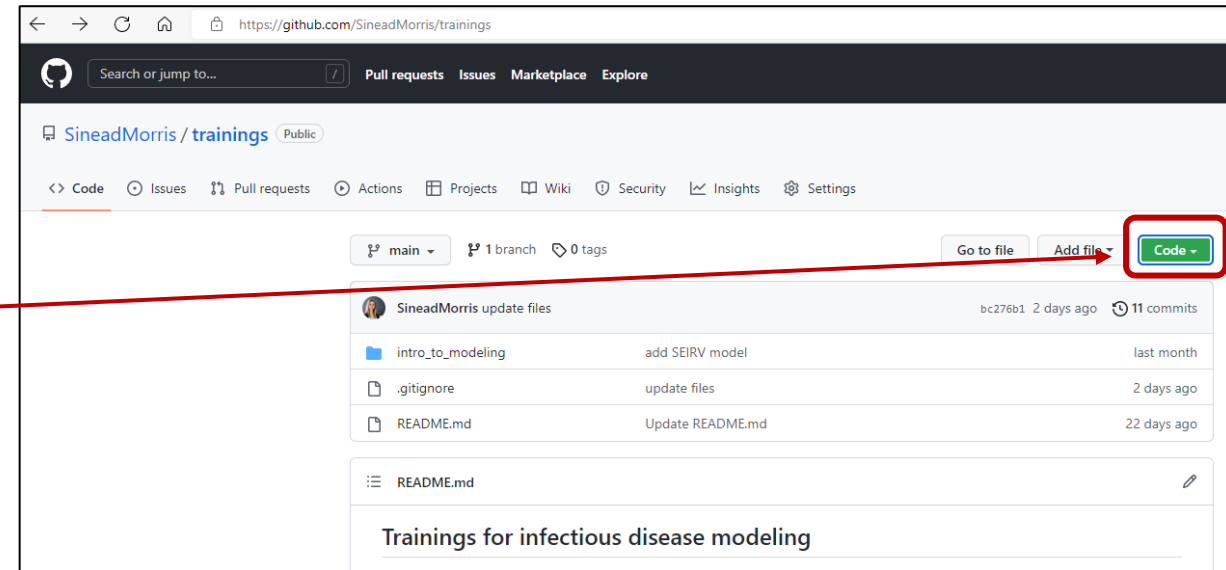


Code a model in R



Materials at:

github.com/SineadMorris/trainings



Files in 'intro_to_modeling':

- SIR_model.Rmd -- code to simulate the SIR model
- SIR_model_extra.Rmd -- same analysis, with a few extra bells & whistles
- SEIR_model.Rmd -- code to simulate the SEIR model
- SEIRS_model.Rmd -- code to simulate the SEIRS model
- SEIRV_model.Rmd -- code to simulate the SEIRV model



(Optional) Exercise



Try adding **latent infection** to `SIR_model.Rmd`

(without looking at `SEIR_model.Rmd`!)



Additional Qs & resources

Applied Research & Modeling Team (ARM)

[SCBS](#) at CDC

CDC R User Group ([RUG](#))

NCIRD Data Science [DOJO](#)

R packages: `flumodels`, `epiestim`, `tidyverse`, `patchwork`, `scico`

R tutorials / help: [Harvard online](#), [Applied Epi R Handbook](#), stackoverflow/google

Modeling tutorials: [ICI3D lectures & code](#), [Imperial coursera](#), [Penn State coursera](#)

