Week 2: SIR Models & Epidemic Parameters

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Week 2 Overview

- Monday, August 2:
  - Relating SIR models to epidemic parameters
  - Estimating parameters in R
- Tuesday, August 3:
  - Guest lecture by Caroline Trotter
  - Modeling meningitis
  - Guided practice in R
- Thursday, August 5:
  - Using serological data for modeling
  - Guided practice in R

Objectives

- Understand how SIR models can be used to estimate epidemic determinants
- Learn new methods to estimate R0

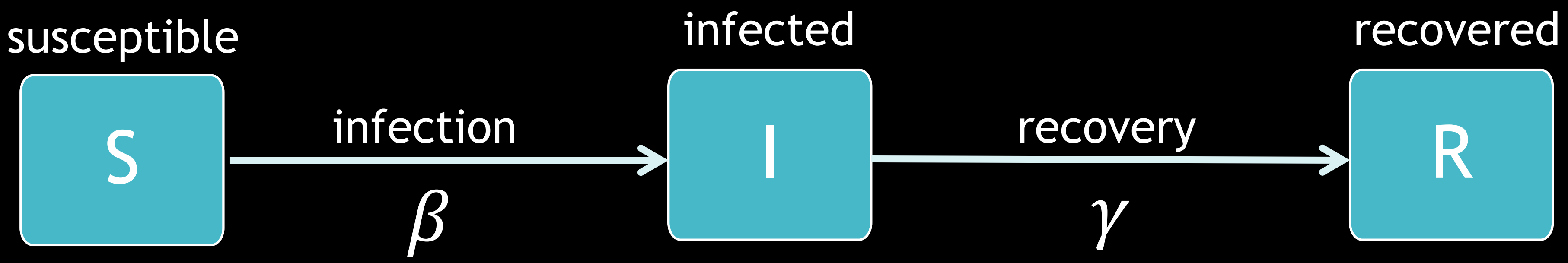
Post Questions in the Chat!

(or ask over microphone)

Workshop Schedule

Time	Topics
2:00—2:10 pm	~~Greetings~~
2:10—2:40 pm	SIR & R0 Relationship
2:40—2:50 pm	Break
2:50—3:15 pm	R0 & Final Epidemic Size
3:15—3:30 pm	R0 & Initial Growth
3:30—3:40 pm	Break
3:40—5:00 pm	R Session

SIR Model: Kermack & McKendrick



- β is a transmission coefficient
  - it is the probability of a susceptible becoming infected if they contact an infected person

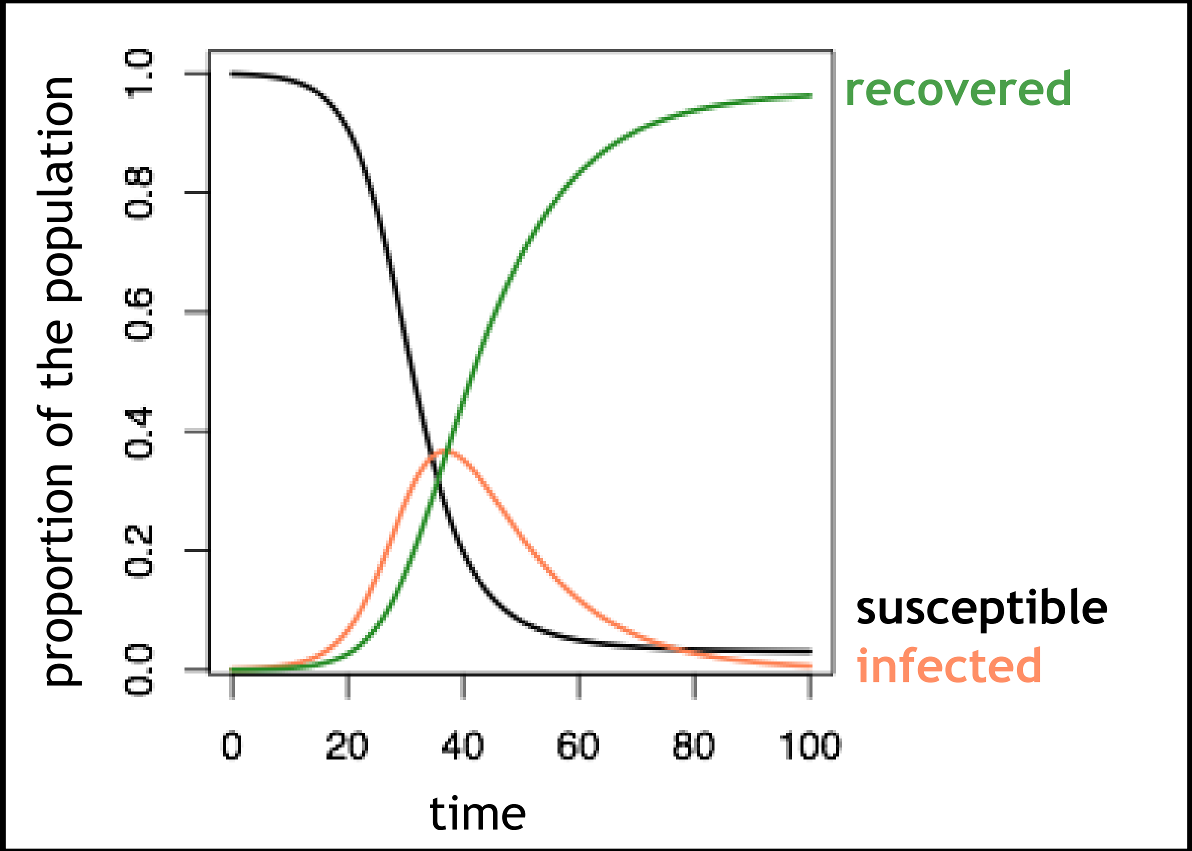
$$\frac{dS(t)}{dt} = -\beta S(t) I(t)$$

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

$$\frac{dR(t)}{dt} = \gamma I(t)$$

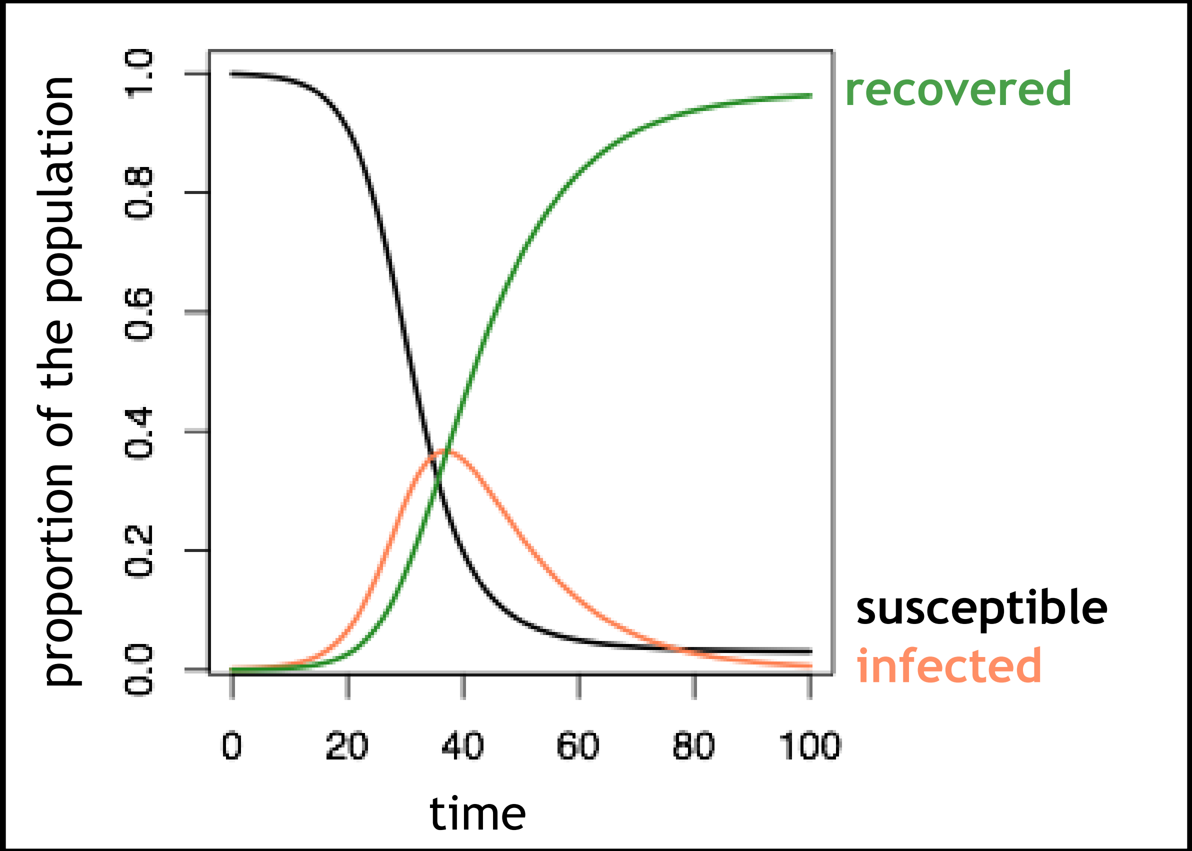
- γ is the recovery rate
  - 1/ γ is the duration of infectiousness

SIR Model Output



- We can examine the epidemic dynamics
- We will have values for S(t), I(t), and R(t) for each time step t
  - these can be expressed as population proportions and plotted
  - we can also find totals for each compartment at the end of the epidemic

SIR Model Output



- In our first examples last week, we input parameter values and starting values

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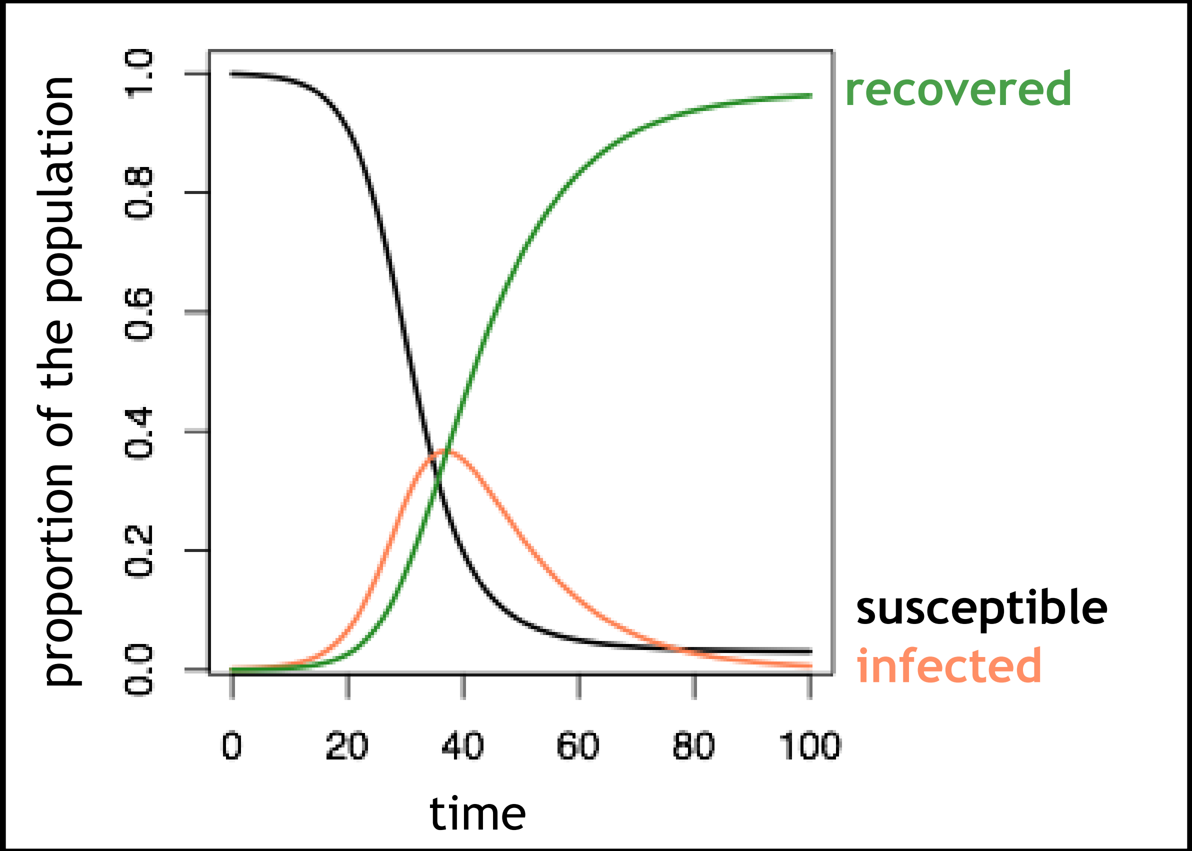

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  - parameter values for beta and gamma
  - starting values for number of people in each compartment S, I, R

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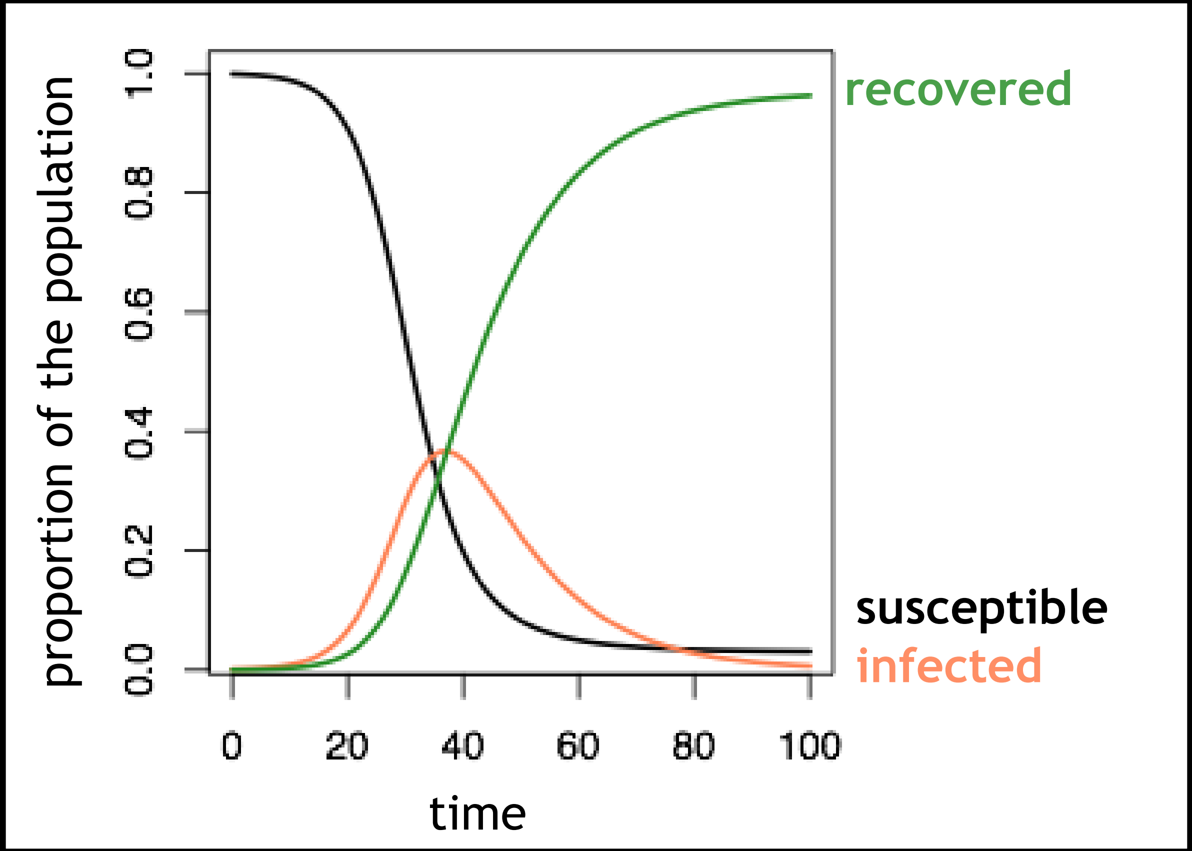
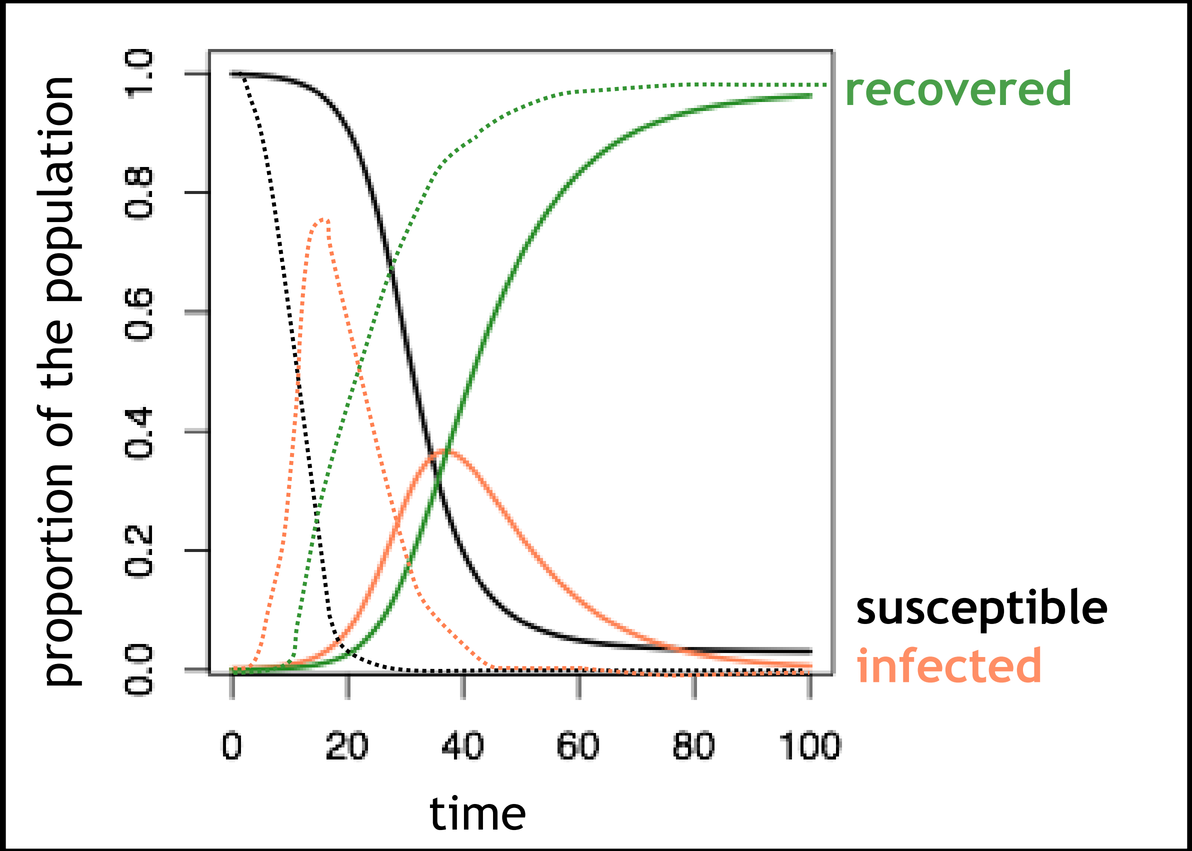


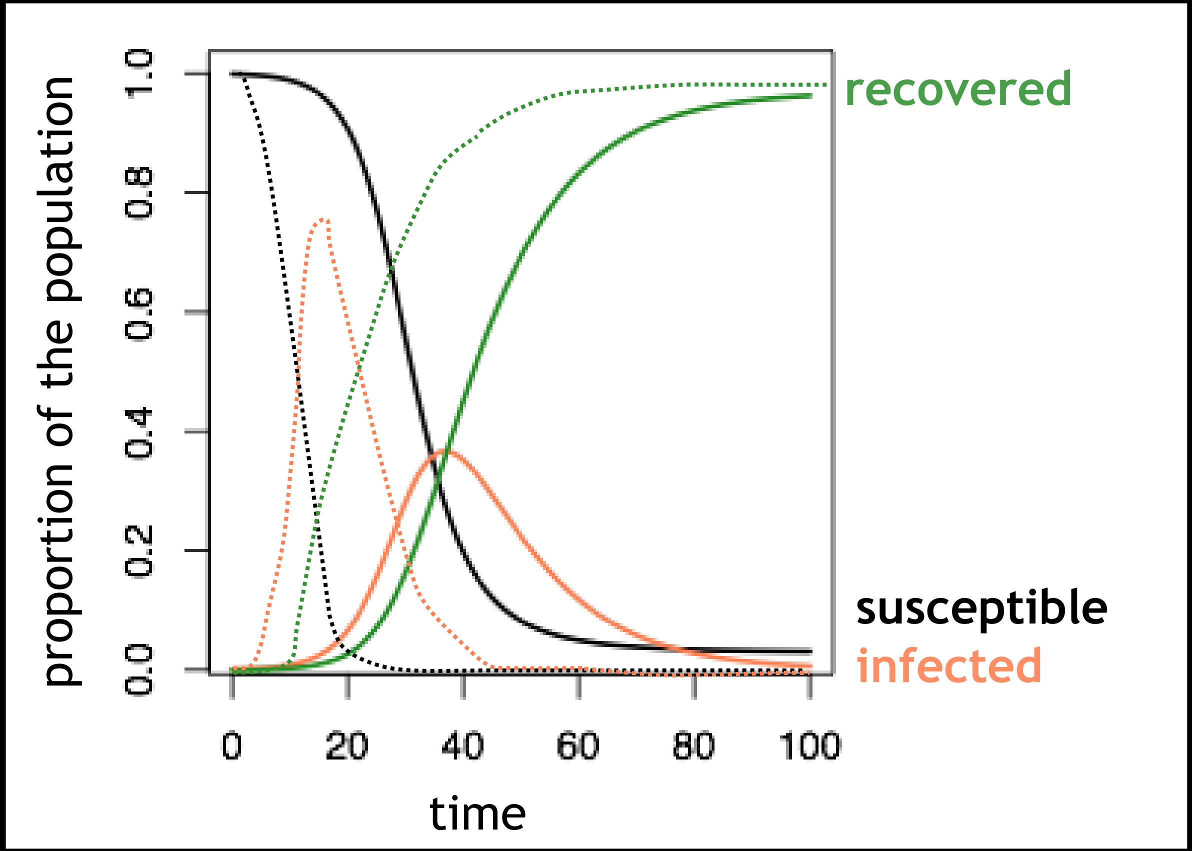
- In our first examples last week, we input parameter values and starting values
  - parameter values for beta and gamma
  - starting values for number of people in each compartment S, I, R
- What about our other epidemic determinants?

SIR Model Output



- Shape of curves will depend on epidemic determinants
  - solid lines → $R_0 = 3.6$
  - dotted lines → $R_0 = 13.2$

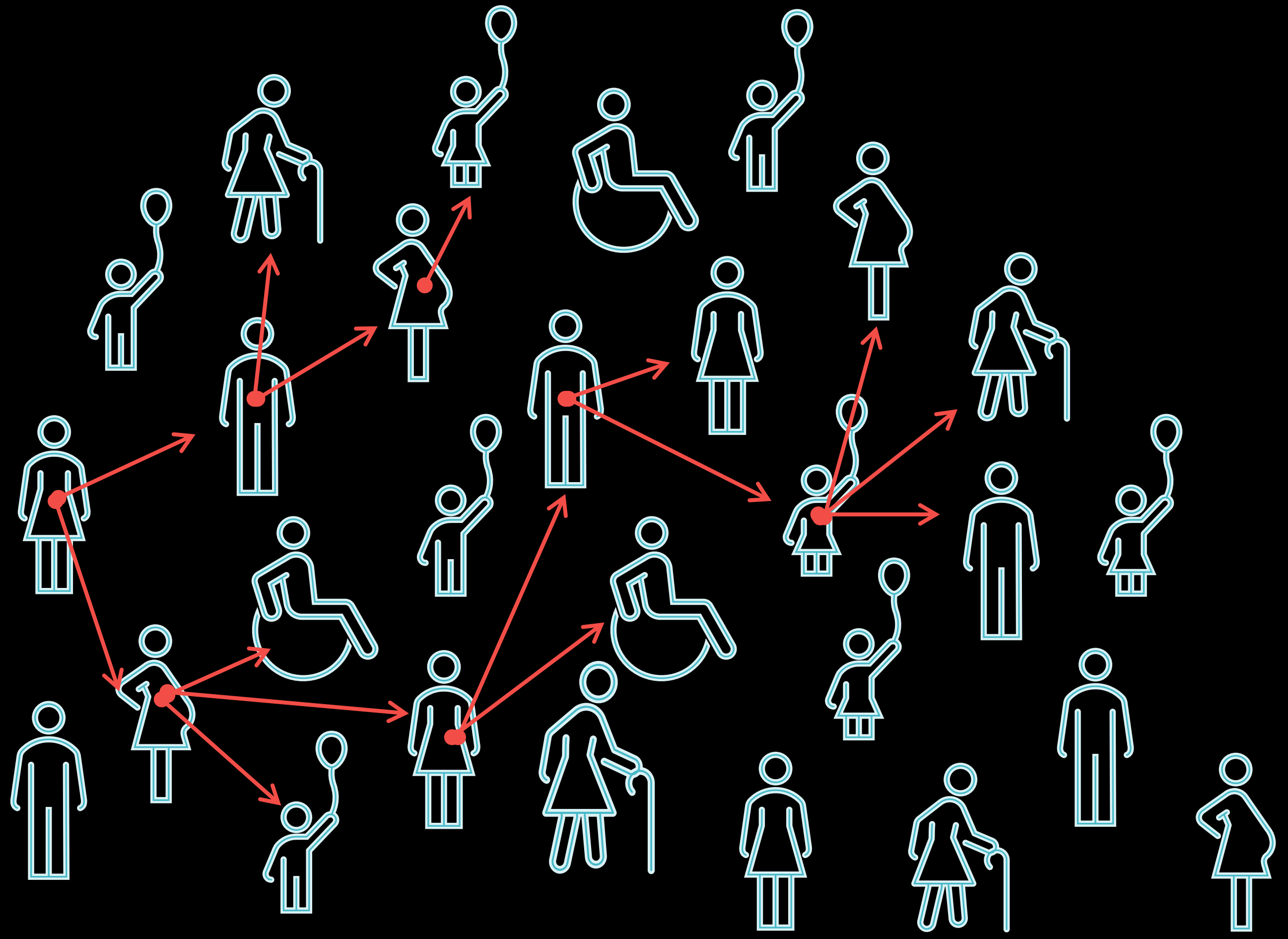
SIR Model Output



- Shape of curves will depend on epidemic determinants
  - solid lines → $R_0 = 3.6$
  - dotted lines → $R_0 = 13.2$
- What differences can we note about these two epidemics with two different basic reproductive numbers?

R_0 & SIR Models

- The calculation of R0 depends on the structure of the model being used
  - for our SIR model:
  - $R_0 = \frac{\beta N}{\gamma}$
  - ß = the transmission coefficient
  - γ = the recovery rate
  - N = the total population



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- Recall that our model assumes:
  - closed SIR structure
  - steady values for beta and gamma
  - random mixing

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- Recall that our model assumes:
  - closed SIR structure
  - steady values for beta and gamma
  - random mixing
- We may want to consider non-random mixing and add a contact rate *c* to the model
  - c=probability of contact
  - In this case:
  - $R_0 = \frac{\beta_c N c}{\gamma}$

R_0 & SIR Models

- What is R0 doing in our SIR model?
- Think about the beginning of the epidemic
  - R0 is appropriate because it is the start of the epidemic
  - R0 drives the number of people going into the infected compartment
  - everyone is susceptible
  - no one is infected

$$R_0 = \frac{\beta N}{\gamma}$$

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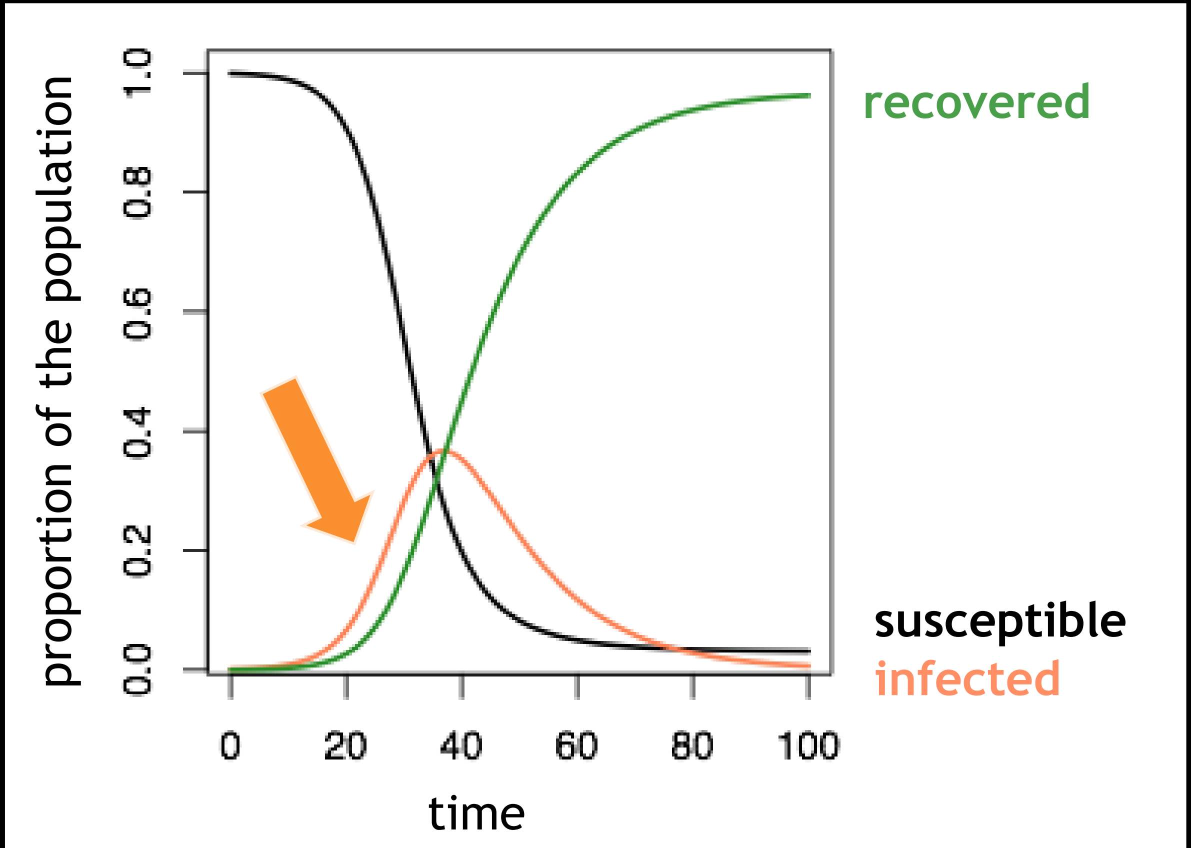
$\boxed{\beta S \approx \beta N}$

at the start of an epidemic, contact with anyone could result in an infection

$$R_0 = \frac{\beta N}{\gamma}$$

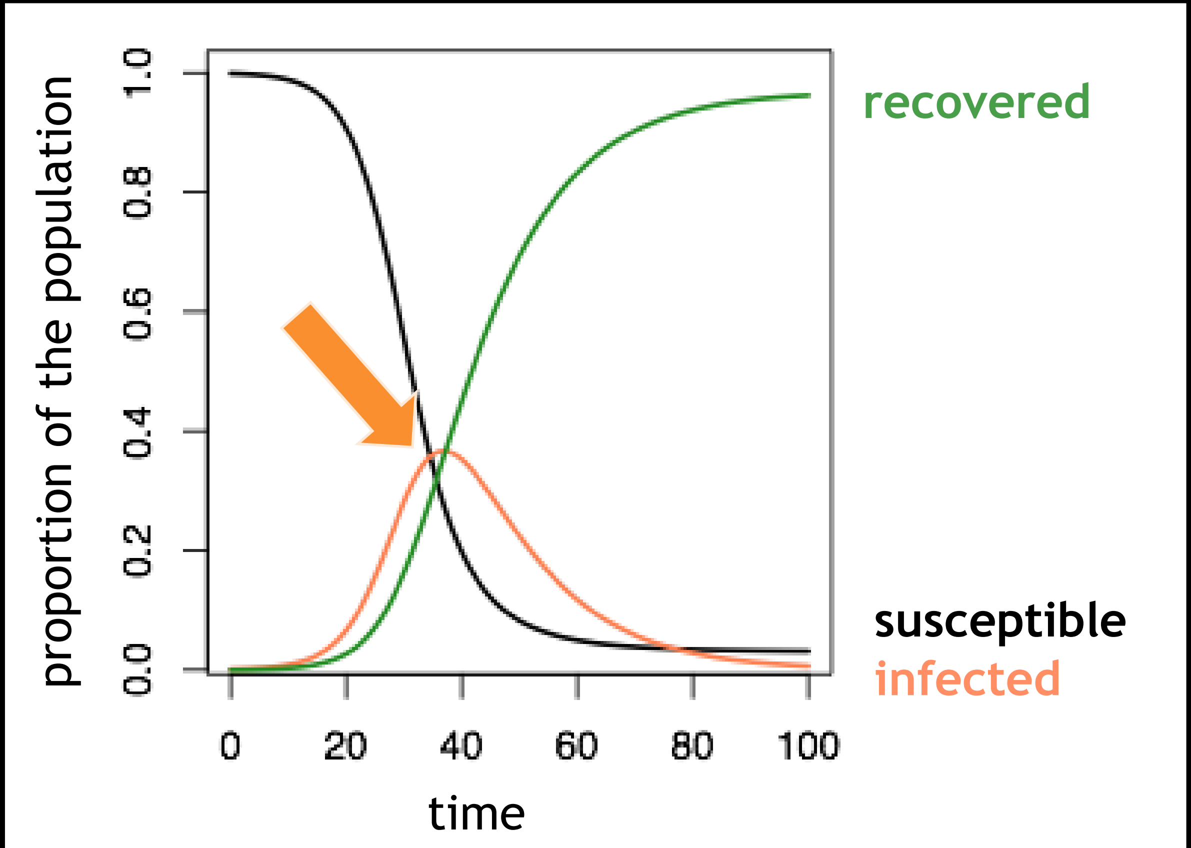
R_0 & Transmission Dynamics



- Early in the epidemic, the number infected is increasing
  - the rate of change is greater than 0

$$0 < \frac{dI(t)}{dt} = \beta S(t)I(t) - \gamma I(t)$$

R_0 & Transmission Dynamics



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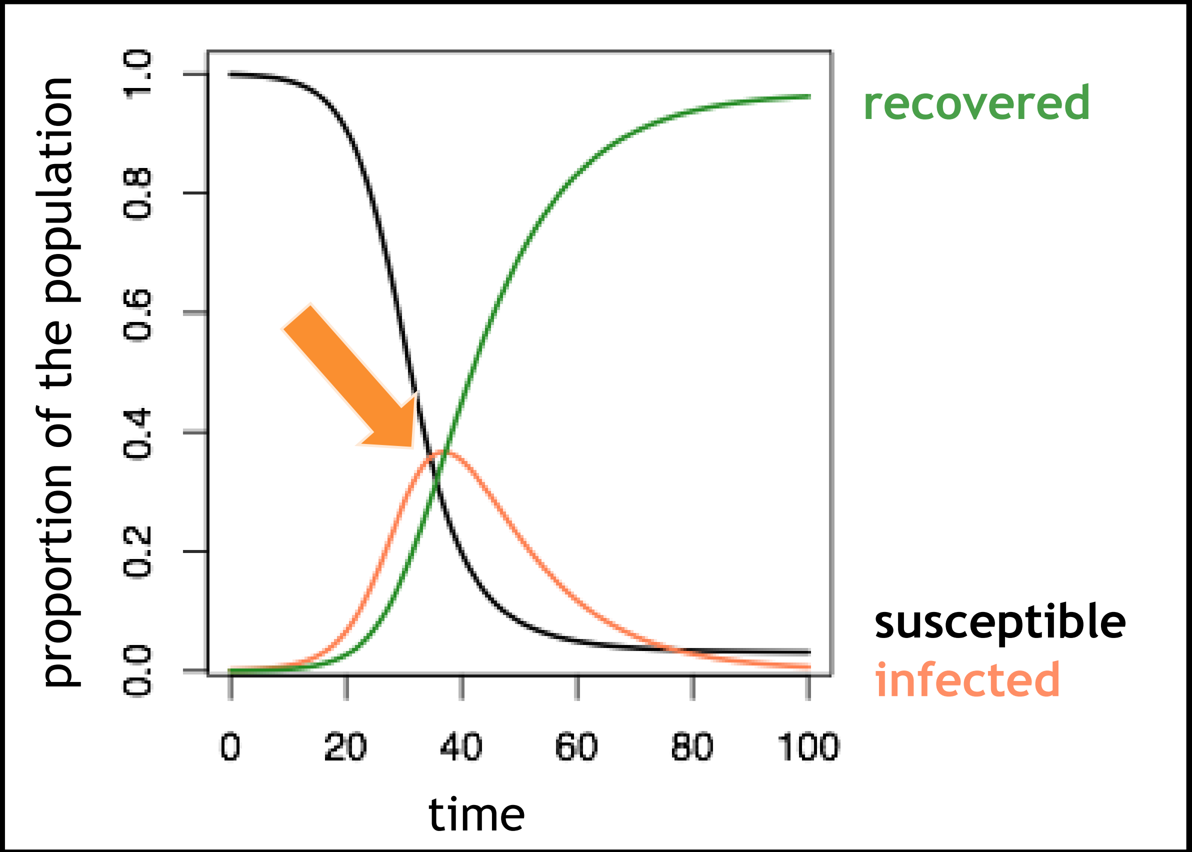

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$$0 = \frac{dI(t)}{dt} = \beta S(t)I(t) - \gamma I(t)$$

$$\beta S(t)I(t) = \gamma I(t)$$

$$\frac{\beta S(t)}{\gamma} = 1$$

Reproductive Number during Epidemic

R_0

- If population is fully susceptible:

$$R_0 = \frac{\beta N}{\gamma}$$

R

- If only a fraction of the population is susceptible (later in the epidemic)
  - only contacts that are susceptible (S/N) could lead to infection

$$R = \frac{\beta N}{\gamma}\frac{S}{N} = \frac{\beta S}{\gamma}$$

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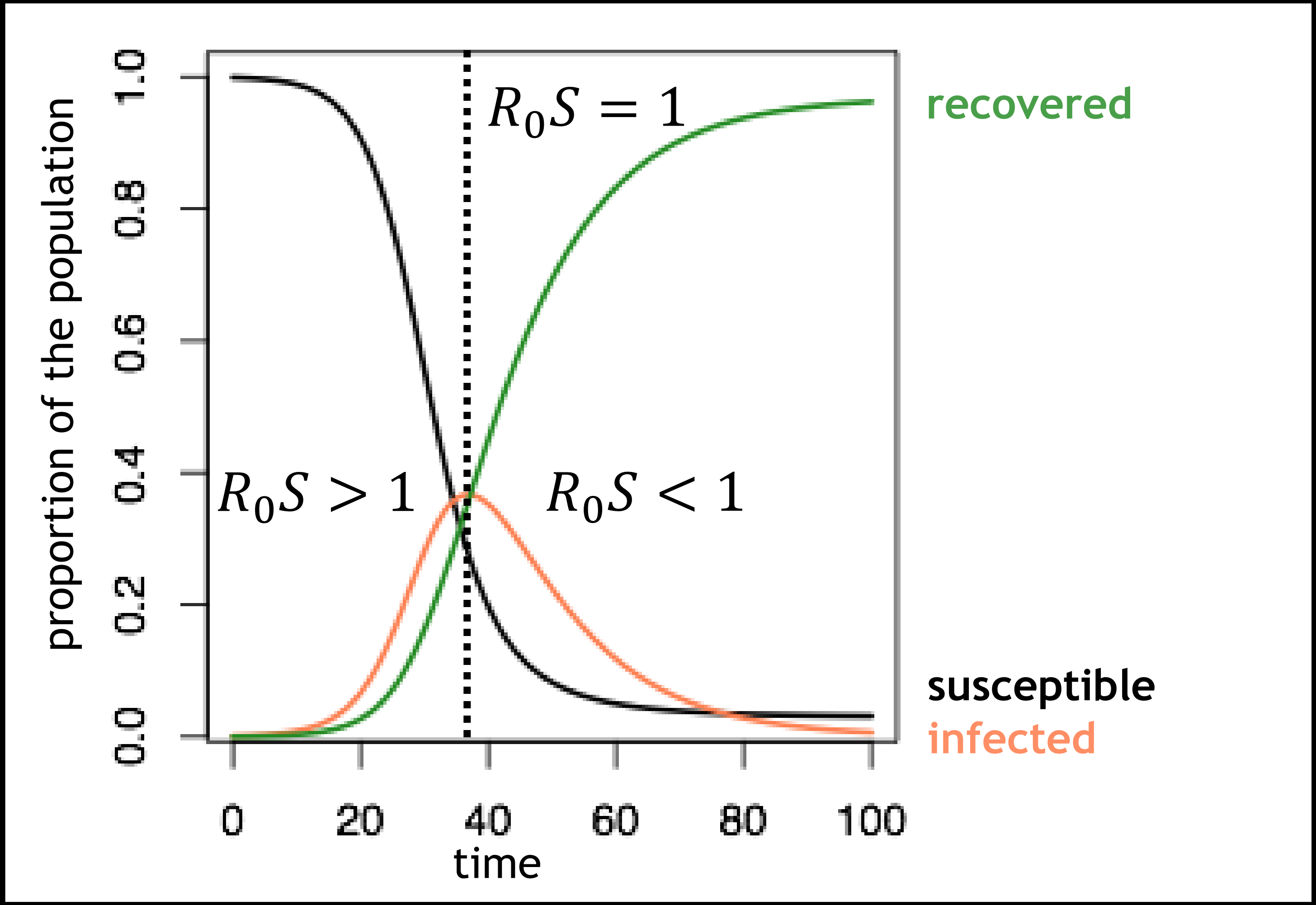
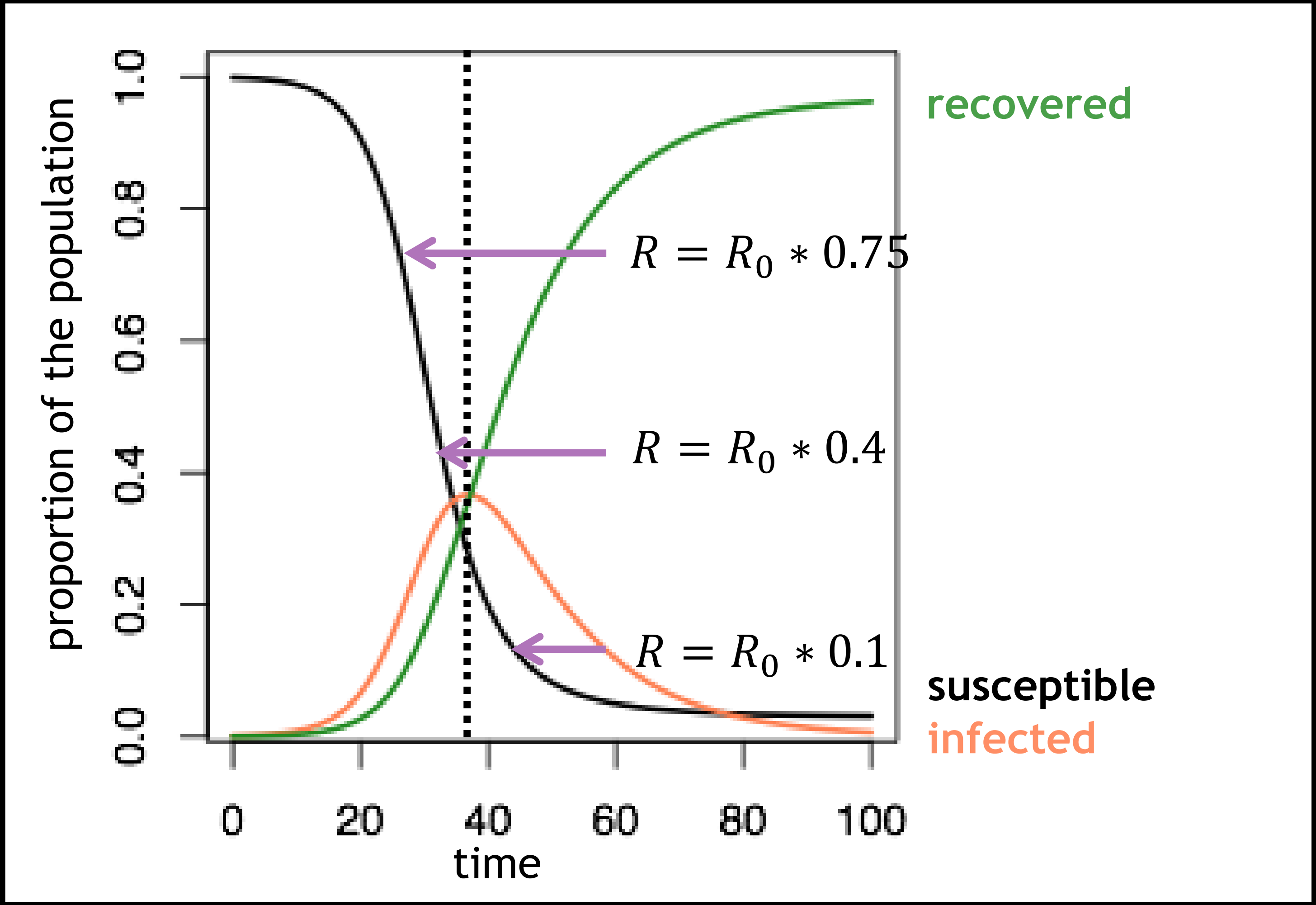
- Remember, on the previous slide we showed when this expression equals 1, the infection rate of change is 0

Reproductive Number during Epidemic

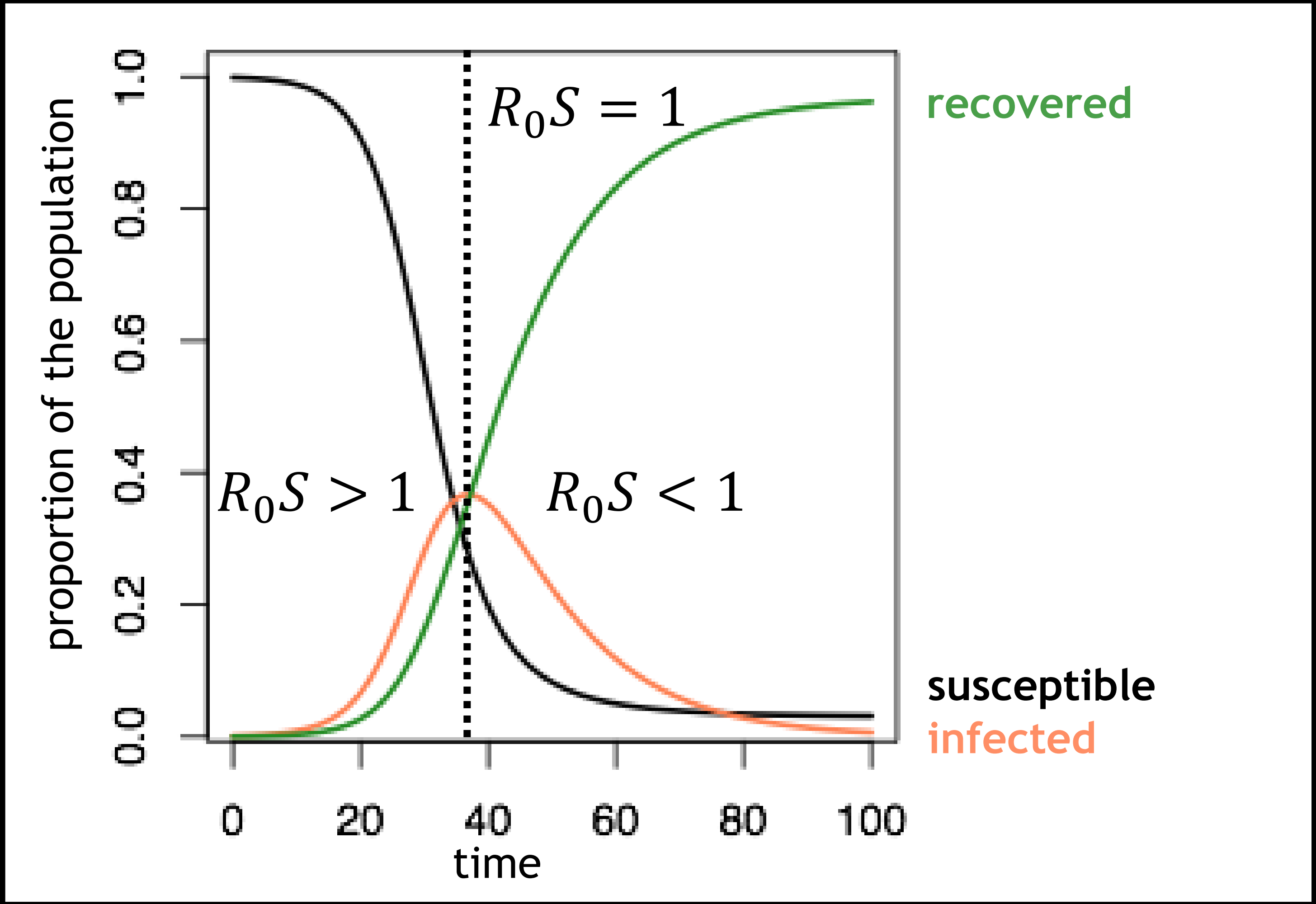


Reproductive Number during Epidemic



- Can translate R0 to R based on proportion of susceptibles at specific time points

Reproductive Number during Epidemic



- The basic reproductive number is driving the behavior of the epidemic
  - how we calculate R0 depends on the type of model
- During the epidemic, we can use the relationship between R0*S and 1 to see when the epidemic will increase, stabilize, or decrease

Questions?

10 minute break

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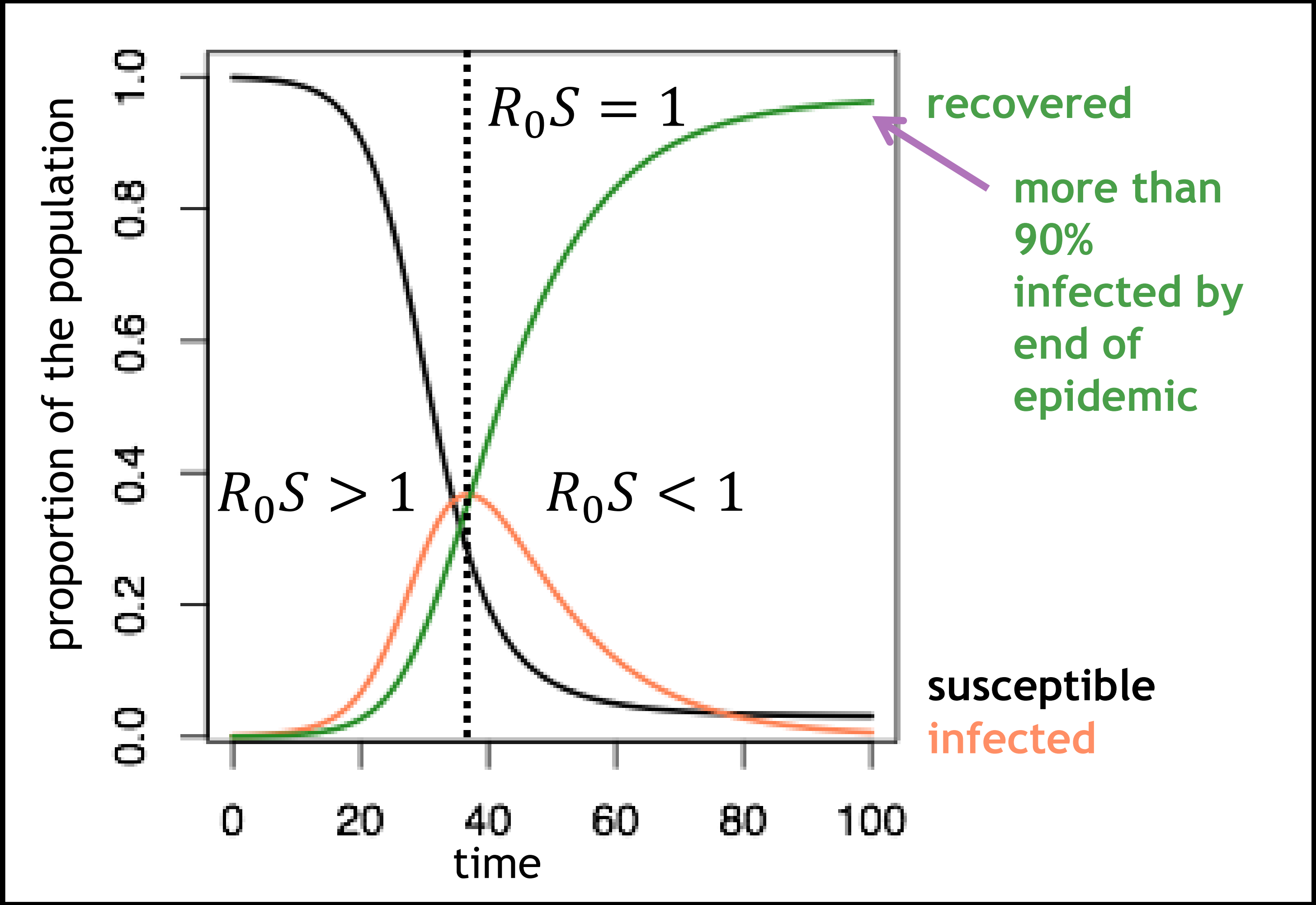
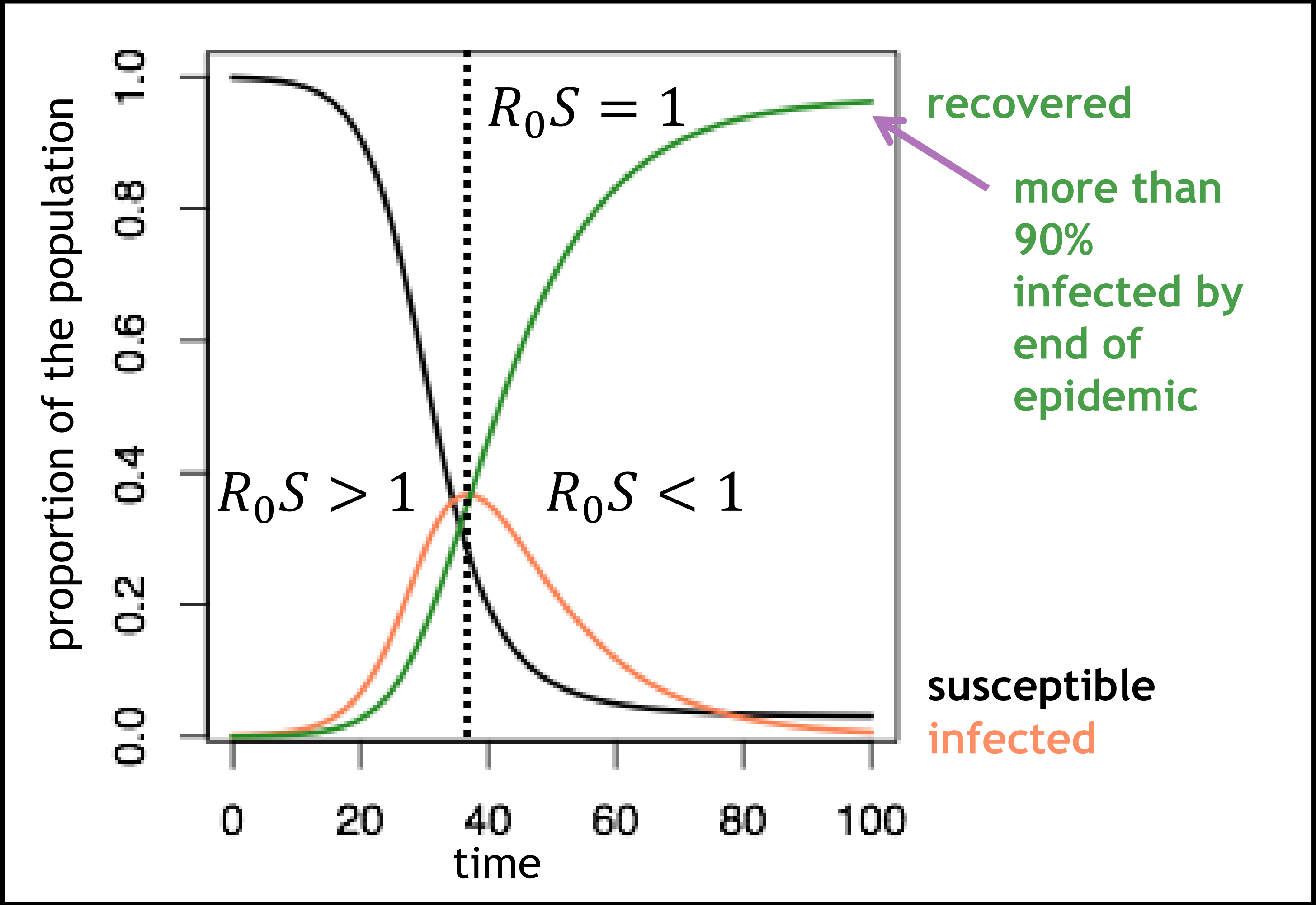
Reproductive Number & Final Size



- We also know the total proportion who got infected
  - whoever is in the "recovered" compartment at the end of the epidemic is someone who was infected
  - this can also be translated into an R0 value

Reproductive Number & Final Size



- But can we estimate the total number infected just using our modeling parameters?
  - yes we can!

Reproductive Number & Final Size

- Importantly:
  - $N = S(t) + I(t) + R(t)$
  - $1 = s(t) + i(t) + r(t)$

- N is our total population
- capitol S, I, R refers to the absolute number of people in the compartment
- lower-case s, i, r refers to the proportion in each compartment

Reproductive Number & Final Size

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- At the end of the epidemic, when $t = \infty$:
  - $1 = s(\infty) + r(\infty)$

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- N is our total population
- capitol S, I, R refers to the absolute number of people in the compartment
- lower-case s, i, r refers to the proportion in each compartment
- we are interested in calculating $r(\infty)$, which is the final epidemic size
- we need to rearrange some equations first

Reproductive Number & Final Size

- $\frac{ds/dt}{di/dt} = \frac{-\beta si}{\beta si - \gamma i}$

- Don't worry about memorizing these derivations…

Reproductive Number & Final Size

- $\frac{ds/\cancel{dt}}{di/\cancel{dt}} = \frac{-\beta si}{\beta si - \gamma i}$
- $\frac{ds}{di} = \frac{-1}{1-\frac{\gamma}{\beta s}}$

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- Don't worry about memorizing these derivations…
- this is possible because:
  - $R_0 = \frac{\beta N}{\gamma}$ and
  - $R = R_0 * s$

Reproductive Number & Final Size

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- $\left(1 - \frac{1}{R_0 s}\right) ds = -1 di$
- this gets integrated to:
- $s - \frac{1}{R_0} \ln s + i = c$

- Don't worry about memorizing these derivations…
- this is possible because:
  - $R_0 = \frac{\beta N}{\gamma}$ and
  - $R = R_0 * s$
- c is a constant

Reproductive Number & Final Size

- let’s use this equation

- since c is a constant, it is conserved; it is the same throughout the epidemic

Reproductive Number & Final Size

- let's use this equation
  - $s - \frac{1}{R_0} \ln s + i = c$
- since c is a constant, it is conserved; it is the same throughout the epidemic
  - remember everyone is susceptible at the start of the epidemic, and $t = \infty$ is the end of the epidemic
  - $\underbrace{1 - \frac{1}{R_0} \ln 1 + i(0)}_{\text{early epidemic}} = \underbrace{s(\infty) - \frac{1}{R_0} \ln s(\infty) + i(\infty)}_{\text{late epidemic}}$

Reproductive Number & Final Size

- let's use this equation
  - $s - \frac{1}{R_0}\ln s + i = c$
- since c is a constant, it is conserved; it is the same throughout the epidemic
  - remember everyone is susceptible at the start of the epidemic, and $t = \infty$ is the end of the epidemic
  - $1 - \cancel{\frac{1}{R_0}\ln 1} + \cancel{i(0)} = s(\infty) - \frac{1}{R_0}\ln s(\infty) + \cancel{i(\infty)}$
  - $1 = (1 - r(\infty)) - \frac{1}{R_0}\ln(1 - r(\infty))$

- remember at the end of the epidemic, when $t = \infty$:

$$1 = s(\infty) + r(\infty)$$
$$0 = i(\infty)$$

Reproductive Number & Final Size

- $1 = (1 - r(\infty)) - \frac{1}{R_0} \ln(1 - r(\infty))$
- $-R_0 r(\infty) = \ln(1 - r(\infty))$
- $r(\infty) = e^{-R_0 r(\infty)}$

Reproductive Number & Final Size

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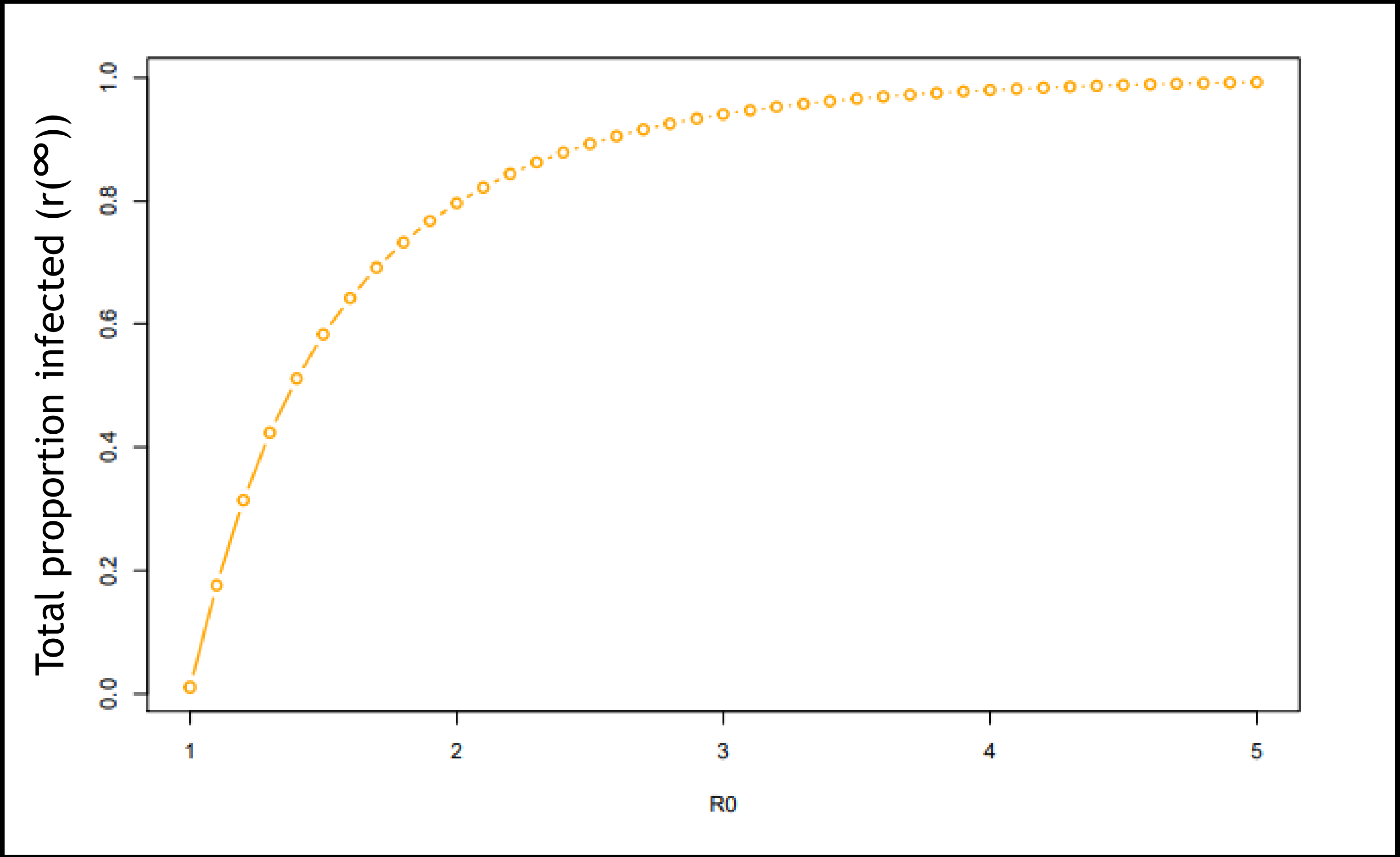
- the same term is on both sides
  - special type of equation that needs to be solved with a numeric solver
  - keeps trying values until one that works is discovered

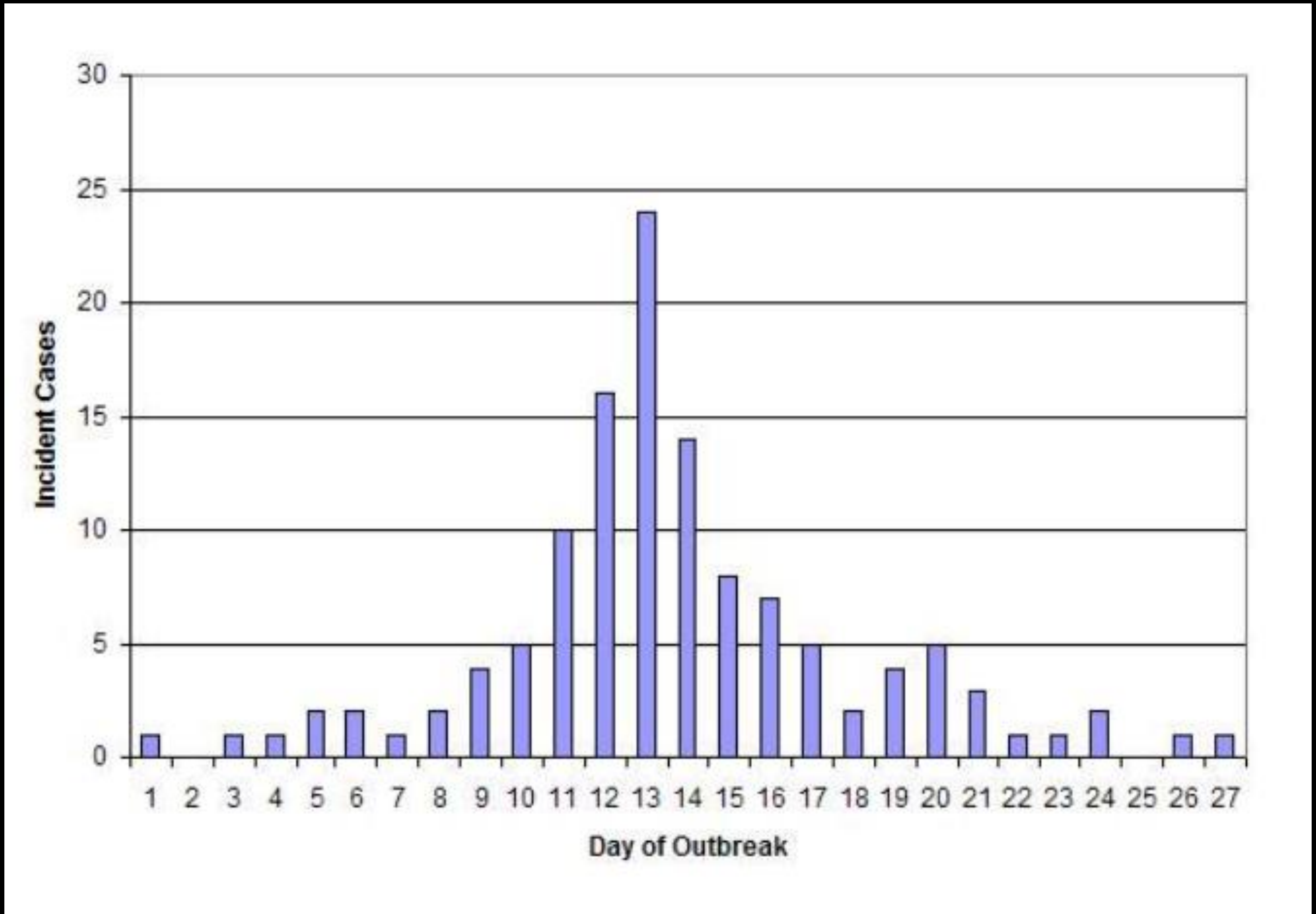


Reproductive Number & Final Size

- For R0>3, nearly everyone will get infected

Reproductive Number & Final Size

- When does this equation work?
  - $r(\infty) = e^{-R_0 r(\infty)}$
- We need to know:
  - s(0): we’ve assumed it is everyone
  - i(0): we assume this is so small we can ignore it
  - transmission conditions are stable
    - no controls introduced
    - no major changes in behavior
- there are more complex versions of this equation that don’t require the first two assumptions



- $r(\infty) = e^{-R_0 r(\infty)}$

Reproductive Number & Final Size

- Influenza B outbreak in a long-term care facility
- R0=1.5—2
- theoretical estimates:
  - $r(\infty) = 0.58 - 0.8$
  - $s(\infty) = 0.2 - 0.42$

Reproductive Number & Final Size

- We have this equation:
  - $r(\infty) = e^{-R_0 r(\infty)}$
- Which can be arranged as:
  - $R_0 = -\frac{\ln(1 - r(\infty))}{r(\infty)}$
- final epidemic size and basic reproductive number can be used to calculate each other if we already know one

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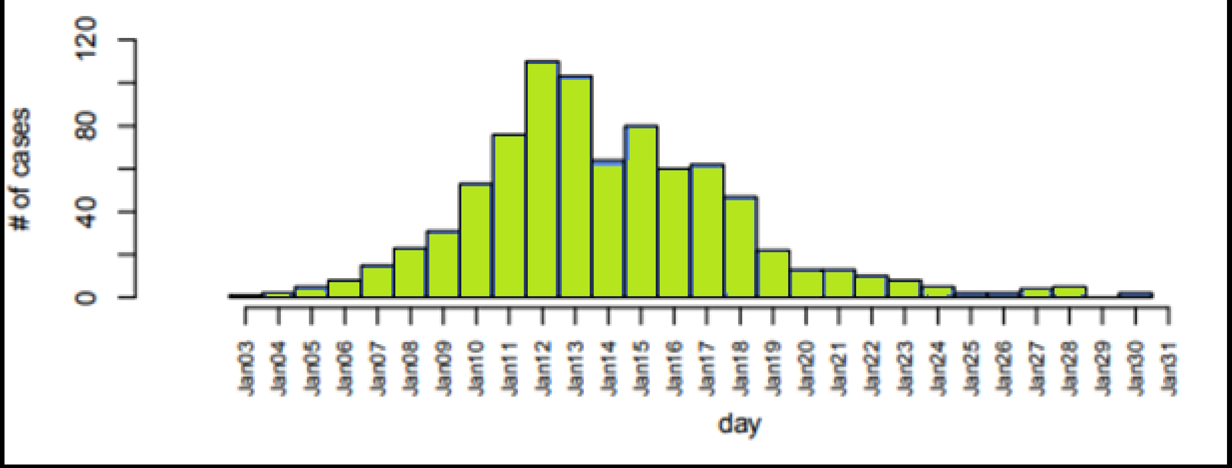
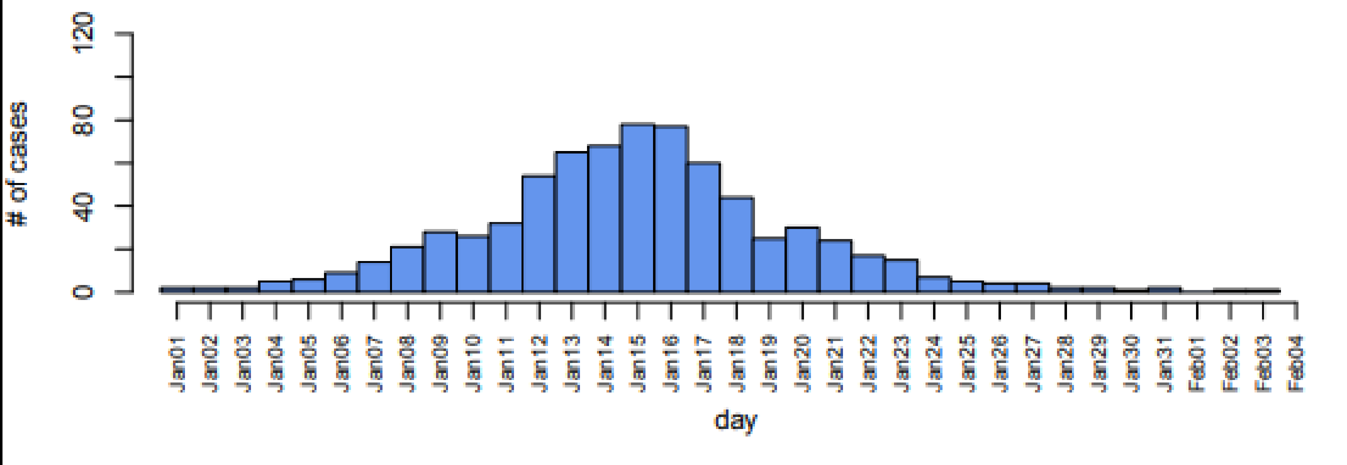
- Which can be arranged as:
  - $R_0 = -\frac{\ln(1-r(\infty))}{r(\infty)}$
- final epidemic size and basic reproductive number can be used to calculate each other if we already know one
- Without going through the derivation, there is another equation for calculating R0 from final size
  - $R_0 = \frac{N}{N-S(0)-R(\infty)} ln \frac{\mathrm{N}-R(\infty)}{S(0)}$

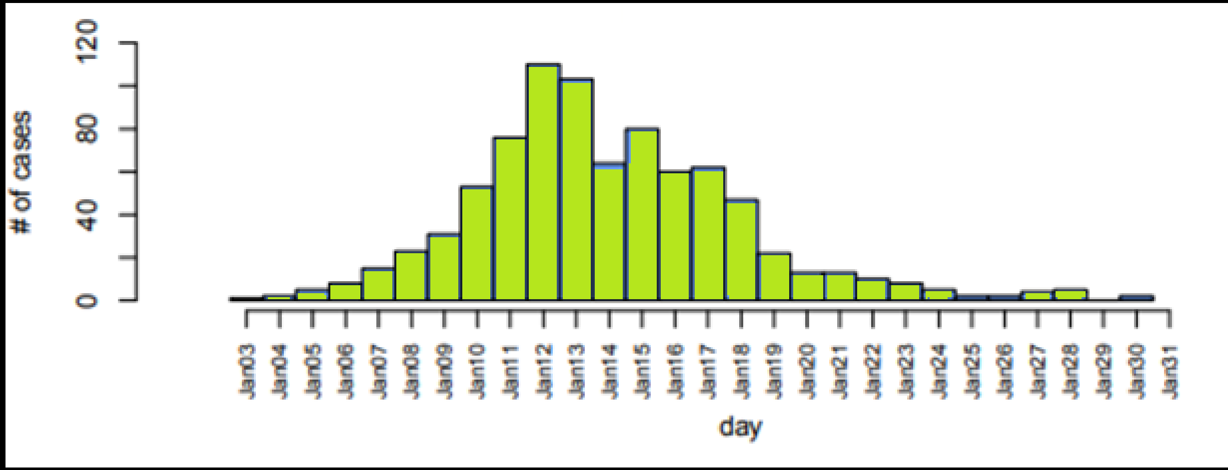


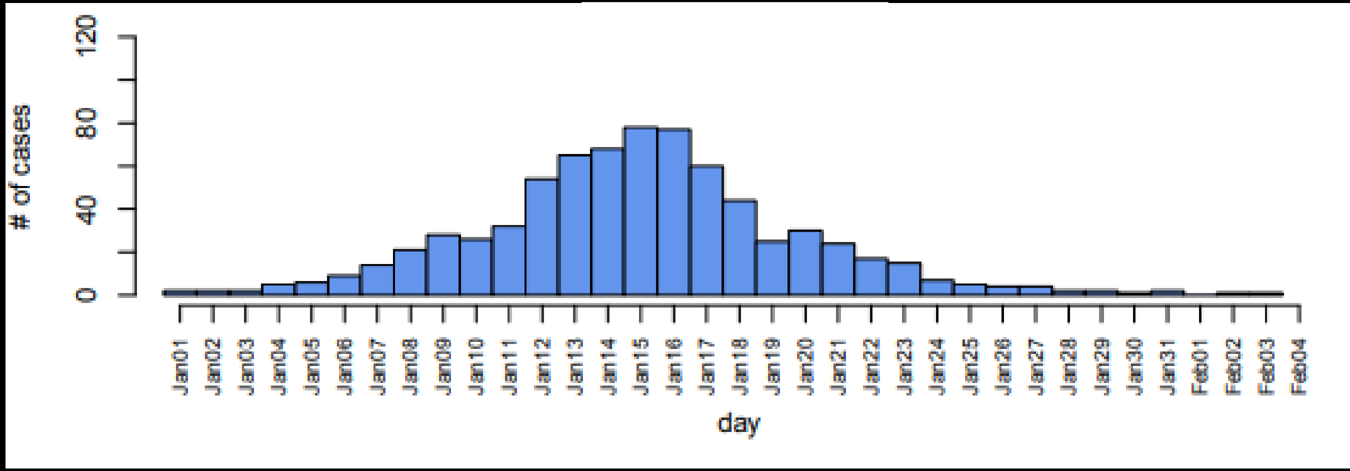


- $R_0 = \frac{N}{N-S(0)-R(\infty)} \ln \frac{\mathrm{N}-R(\infty)}{S(0)}$

Reproductive Number & Final Size

- Epidemic A
  - population=1.024
  - cases=826
- Epidemic B
  - population=952
  - cases=733





- $R_0 = \frac{N}{N - S(0) - R(\infty)} ln \frac{\mathrm{N} - R(\infty)}{S(0)}$
- $R_0 = \frac{1024}{1024 - 1023 - 826} ln \frac{1024 - 826}{1023} = 2.04$

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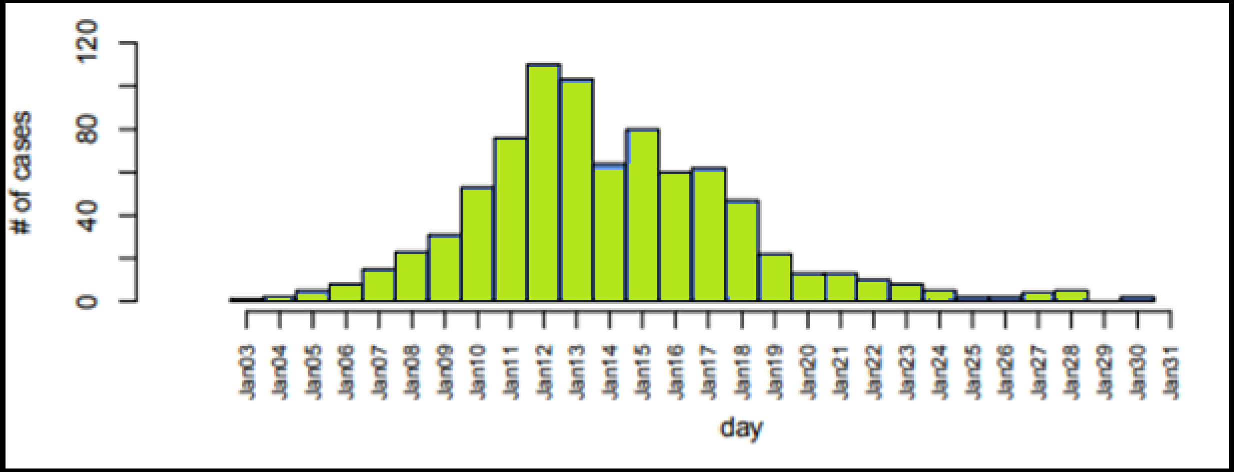

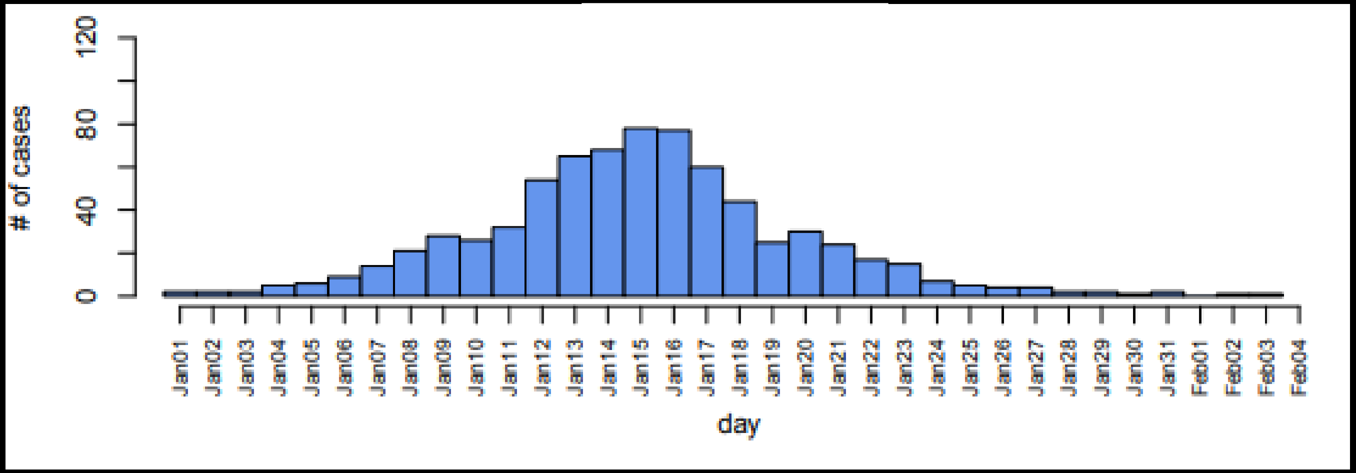

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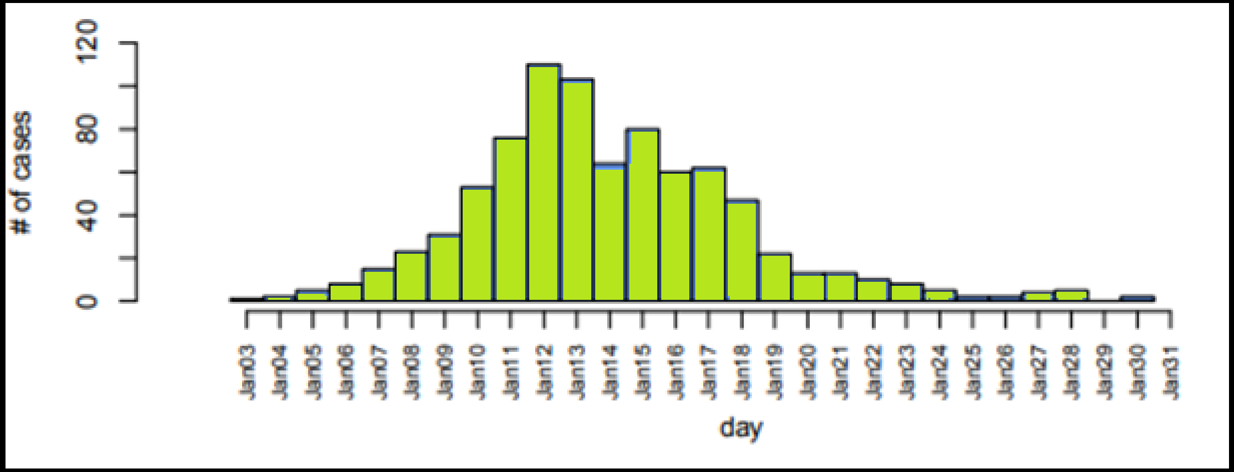
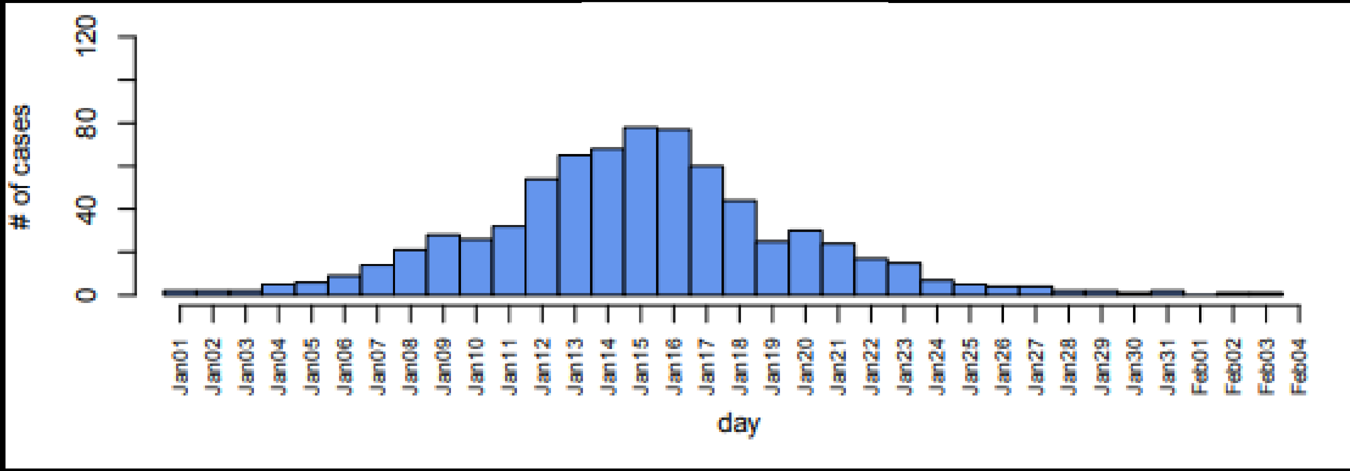
- $R_0 = \frac{1024}{1024-1023-826} ln \frac{1024-826}{1023} = 2.04$

Reproductive Number & Final Size

- Epidemic A
  - population=1.024
  - cases=826
  - R0=2.04
- Epidemic B
  - population=952
  - cases=733
  - R0=1.91





Reproductive Number & Early Size

- We can also use the cumulative number of cases early in an epidemic by fitting an exponential curve to the outbreak
- $R_0 = 1 + \frac{\ln(Y(t))/t}{\gamma}$
- Y(t)=cumulative number of cases at time t

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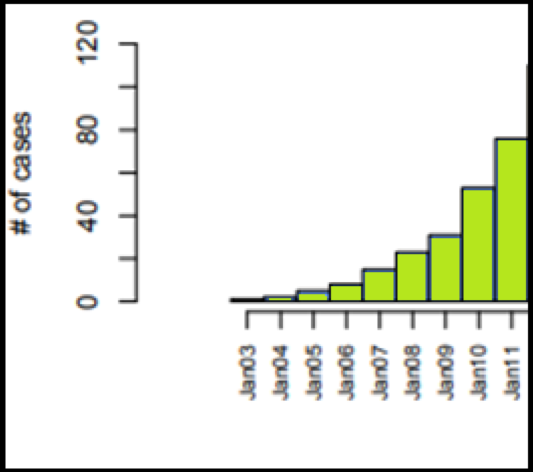
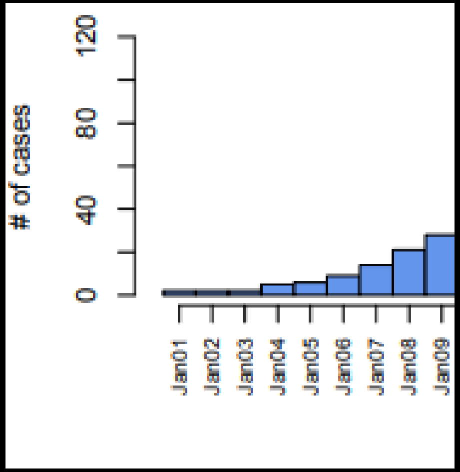


- Epidemic A
  - Y(t)=218
  - t=8
  - γ=1.5



- Epidemic B
  - Y(t)=89
  - t=8
  - γ=1.5

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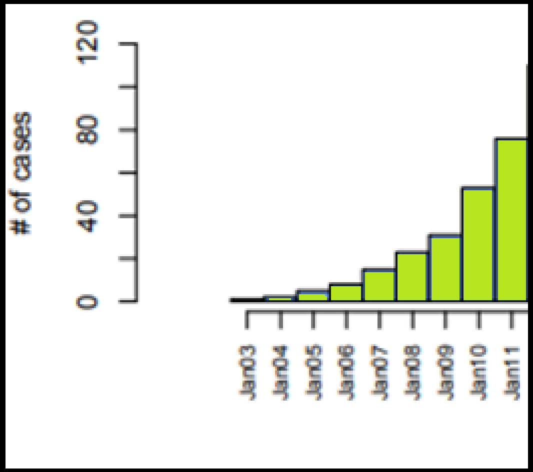

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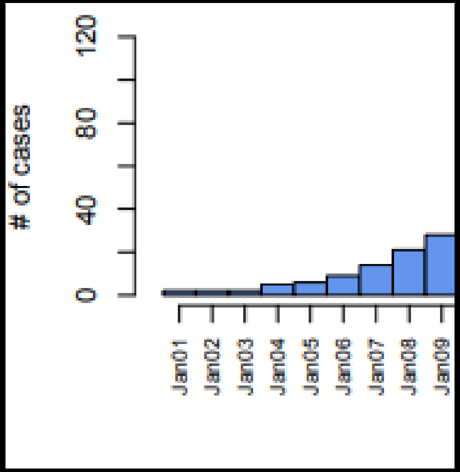
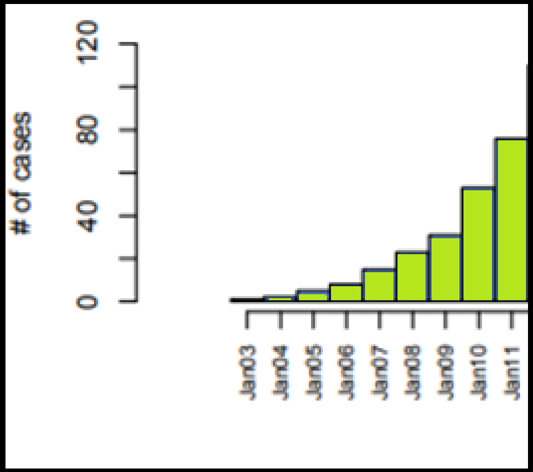
  - t=8
  - γ=1.5
  - R0=2.01

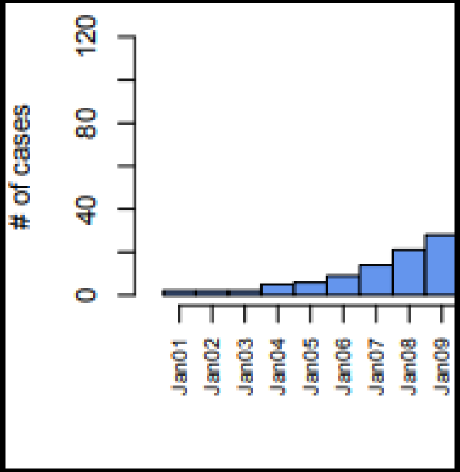


- Epidemic B
  - Y(t)=89
  - t=8
  - γ=1.5
  - R0=1.84

Reproductive Number & Early Size

- We can also use the cumulative number of cases early in an epidemic by fitting an exponential curve to the outbreak
- $$R_0 = 1 + \frac{\ln(Y(t))/_{t}}{\gamma}$$
- Y(t)=cumulative number of cases at time t



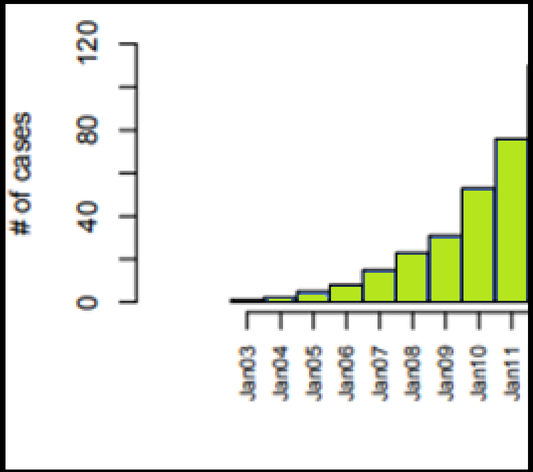


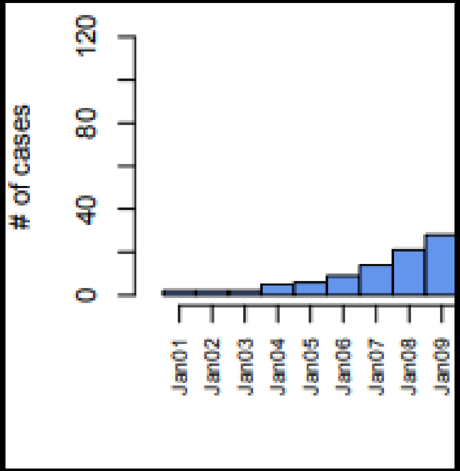
- Epidemic A
  - Y(t)=218
  - t=8
  - γ=1.5
  - R0=2.01

  - Y(t)=31
  - t=4
  - γ=1.5
  - R0=2.29

- Epidemic B
  - Y(t)=89
  - t=8
  - γ=1.5
  - R0=1.84

  - Y(t)=17
  - t=4
  - γ=1.5
  - R0=2.06





- Epidemic A
  - $Y(t)=218$
  - $t=8$
  - $\gamma=1.5$
  - $R0=2.01$

  - $Y(t)=31$
  - $t=4$
  - $\gamma=1.5$
  - $R0=2.29$

- Epidemic B
  - $Y(t)=89$
  - $t=8$
  - $\gamma=1.5$
  - $R0=1.84$

  - $Y(t)=17$
  - $t=4$
  - $\gamma=1.5$
  - $R0=2.06$

Method	Epidemic A R0	Epidemic B R0
Final epidemic size	2.04	1.91
Exponential at t=8	2.01	1.84
Exponential at t=4	2.29	2.06

Reproductive Number & Early Size

- We can also use the cumulative number of cases early in an epidemic by fitting an exponential curve to the outbreak
- $$R_0 = 1 + \frac{\ln(Y(t))/t}{\gamma}$$
- $Y(t)$=cumulative number of cases at time t

Workshop Schedule

Time	Topics
2:00–2:10 pm	~~Greetings~~
2:10–2:40 pm	~~SIR & R0 Relationship~~
2:40–2:50 pm	~~Break~~
2:50–3:15 pm	~~R0 & Final Epidemic Size~~
3:15–3:30 pm	~~R0 & Initial Growth~~
3:30–3:40 pm	Break
3:40–5:00 pm	R Session