

$R_0$  is used to represent the “basic reproduction number” of a pathogen. Epidemic expected to spread if this number  $> 1$  and expected not to spread if  $< 1$ .

(Crude) Rule of Thumb:

Vaccinate at least  $1 - 1/R_0$  to stop epidemic.

The number of **people** that **one sick person** will infect (on average) is called  $R_0$ . Here are the maximum  $R_0$  values for a few viruses.

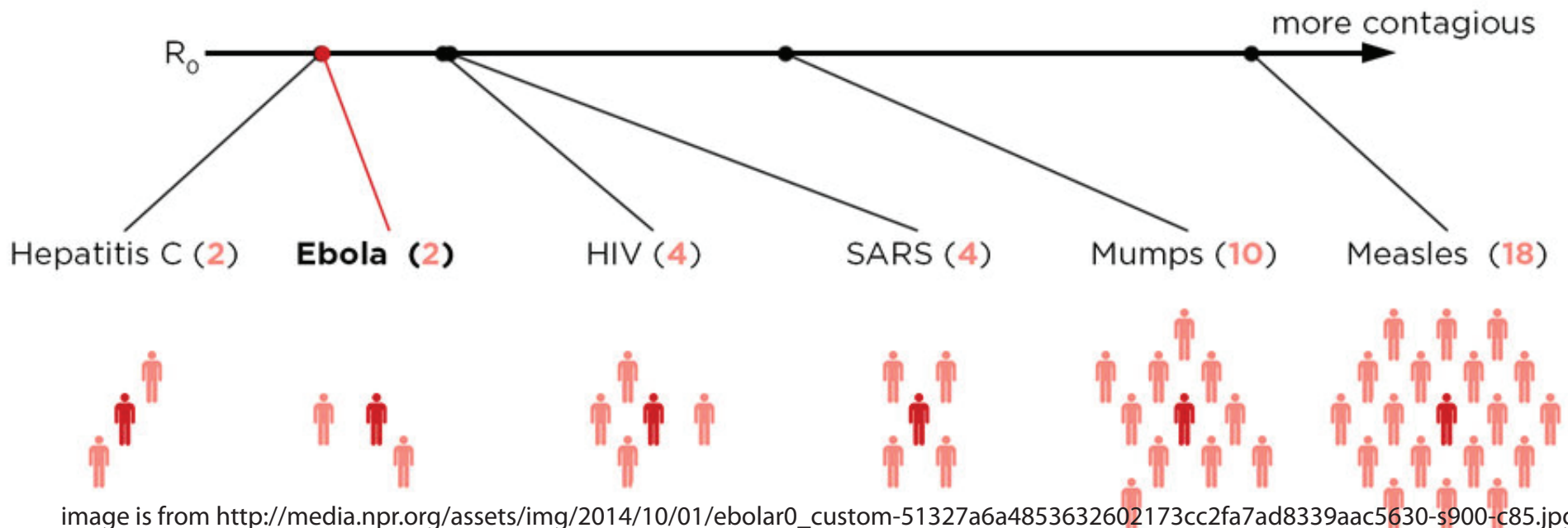


image is from [http://media.npr.org/assets/img/2014/10/01/ebolar0\\_custom-51327a6a4853632602173cc2fa7ad8339aac5630-s900-c85.jpg](http://media.npr.org/assets/img/2014/10/01/ebolar0_custom-51327a6a4853632602173cc2fa7ad8339aac5630-s900-c85.jpg)

$R_e$  is “effective reproduction number” (how many people on average does each newly infected person infect after the epidemic has been going for a while?)

$R_t$  is how many people on average does each person infect when the person is newly infected at time  $t$

$R_0$  for SARS-CoV-2?

Mean and Median of early pandemic estimates were respectively 3.28 and 2.79

(see <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7751056/>.)

But SARS-CoV-2 evolved! Unclear what would be a good estimate for recent strains...

# SIR models : **S**usceptible / **I**nfected / **R**ecovered

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

$$\frac{dI}{dt} = \beta SI - \delta I$$

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

Interactions between Susceptible and Infected depend on product of S and I.  
 $\beta$  describes rate at which these interactions become infections

$\delta$  is rate at which infected recover

t is time

( $\beta/\delta = R_0$  !)

SIR models are one sort of “Compartmental Model”



image is from

[http://sherrytowers.com/wp-content/uploads/2012/12/sir\\_compartment.jpg](http://sherrytowers.com/wp-content/uploads/2012/12/sir_compartment.jpg)

# Epidemiological model affects viral genealogy

Simulated genealogies for the four classes of epidemiological models considered, each starting with 250 homochronous tips.

**A. SIS / SIR / SIRS (Susceptible, Infected, Recovered)**

**B. Supershedding**

**C. Exposed but not yet infectious**

**D. Variable Infectious Period**

**E. Lines are expected lineages through time**

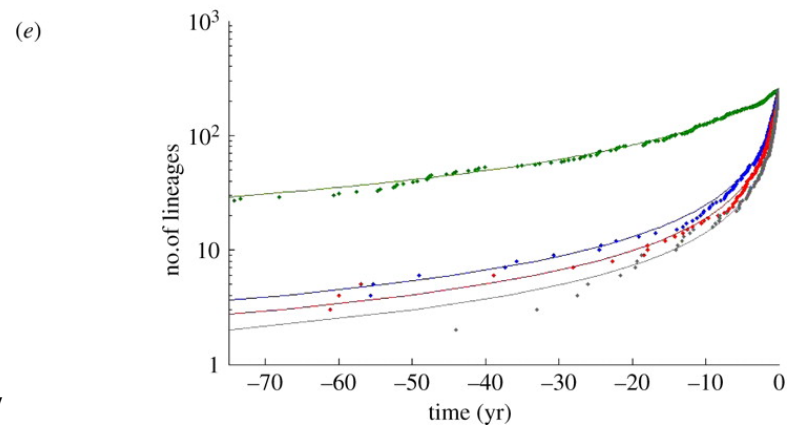
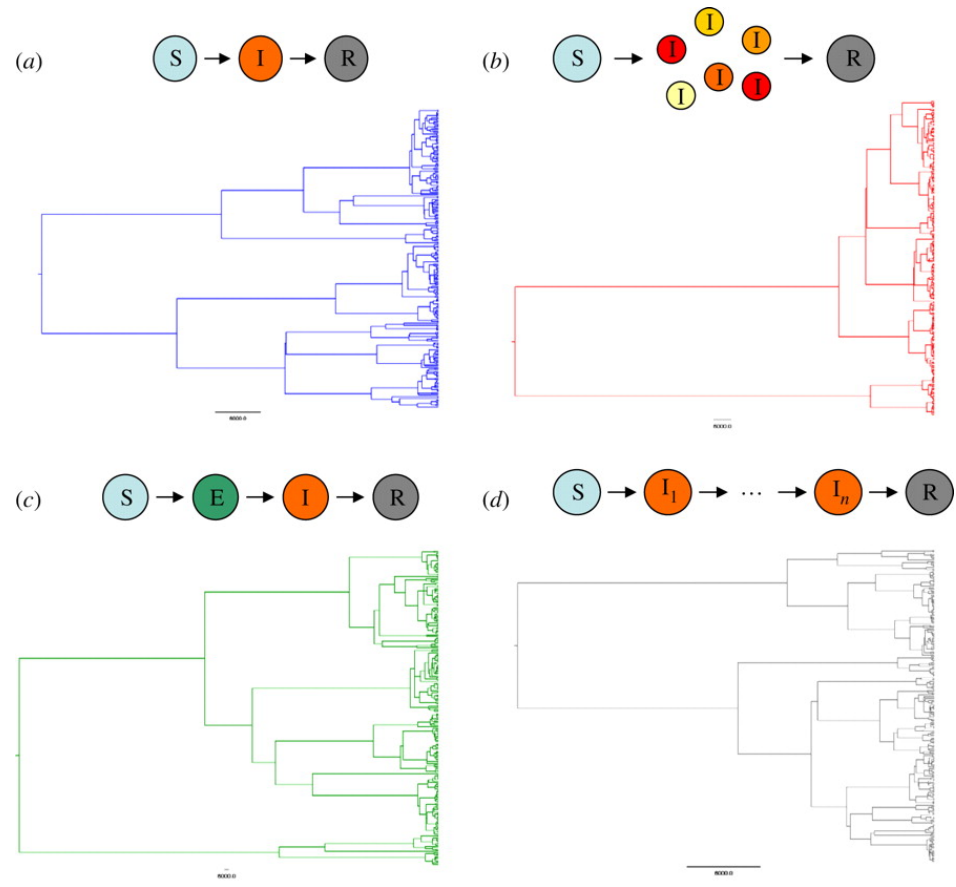
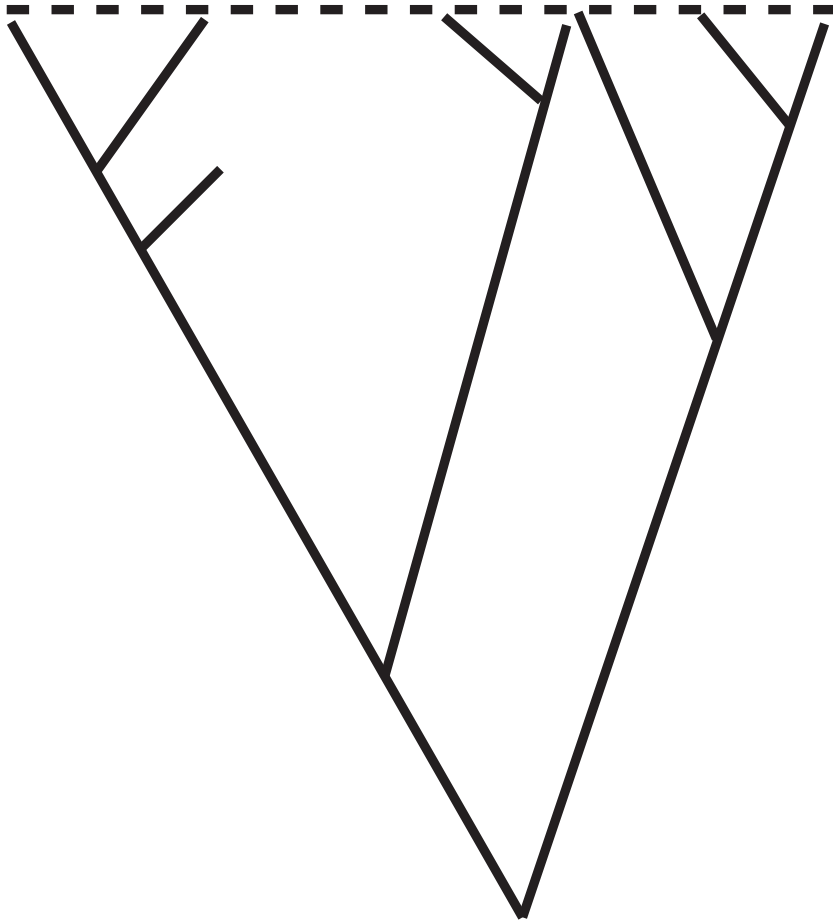


Figure 1 from Koelle K , and Rasmussen D A J. R. Soc. Interface 2012;9:997-1007 (slightly modified)

## Serially-Sampled Data



(1) Genetic data allow tree inference.

(2) Tree shows coalescence events.

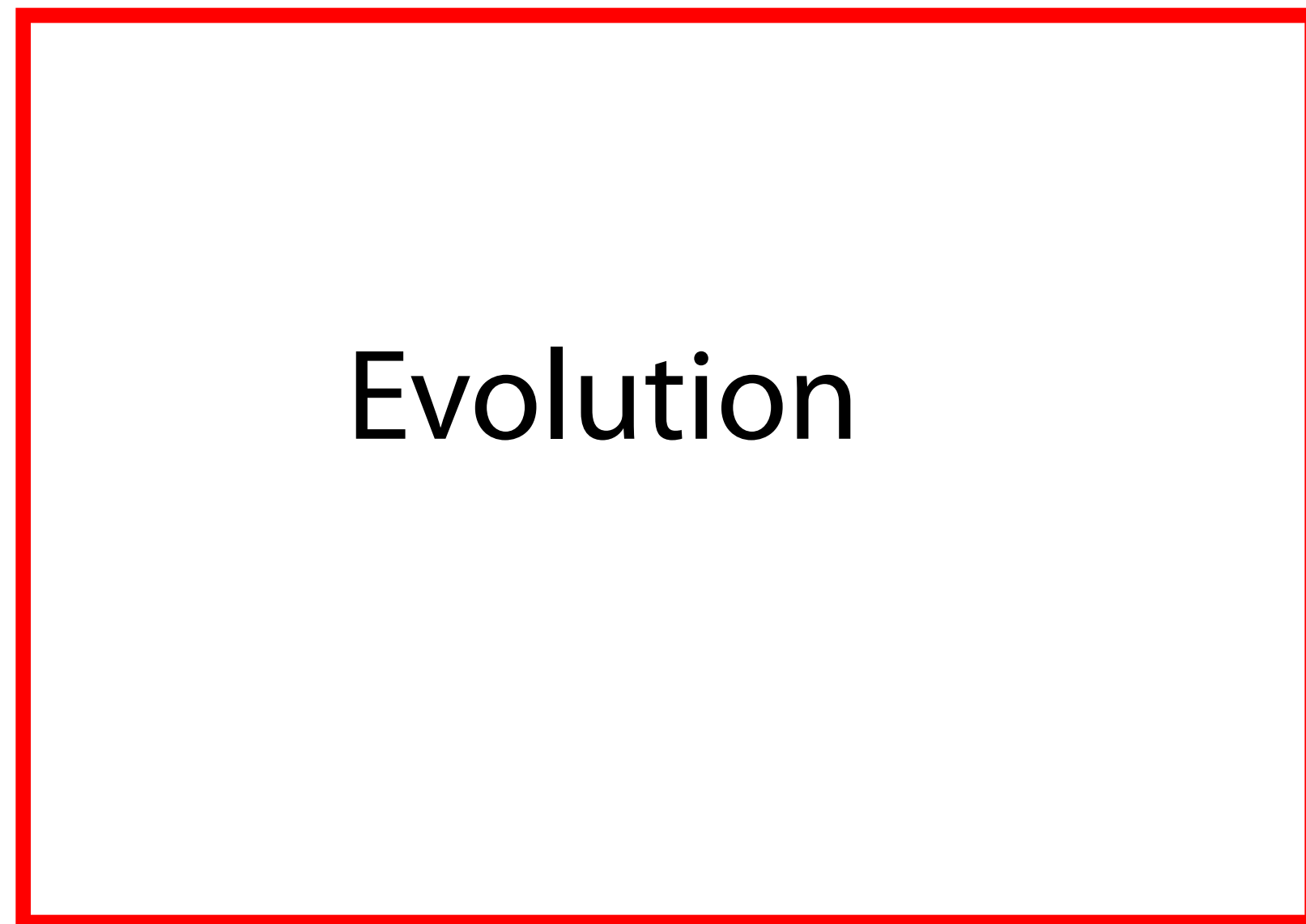
(3) Coalescences inform how population size (#infected people) has changed over time.

(4) This tells us about epidemiology parameters.

**Lots of uncertainty!**

**Initial SARS-CoV-2 Evo+Epi  
Studies limited by lack of viral  
genetic diversity**

*(pers. comm. David Rasmussen)*



Evolution affects  
treatment options  
and thereby host  
behavior & evolution



Behavior



Advances in  
treatment affect  
host behavior &  
thereby evolution

Oct. 13, 2017 NBC News Headline: "New California Law Reduces Penalty for Knowingly Exposing Someone to HIV"

"... Under current California law, it is felony offense punishable by 3 to 8 years in prison. The new law, which was signed by Brown on Oct. 6 and takes effect January 1, changes this to a misdemeanor, carrying a 6-month prison term — the same punishment as knowingly exposing someone to other communicable diseases. ..."

from <https://www.nbcnews.com/feature/nbc-out/new-california-law-reduces-penalty-knowingly-exposing-someone-hiv-n809416>