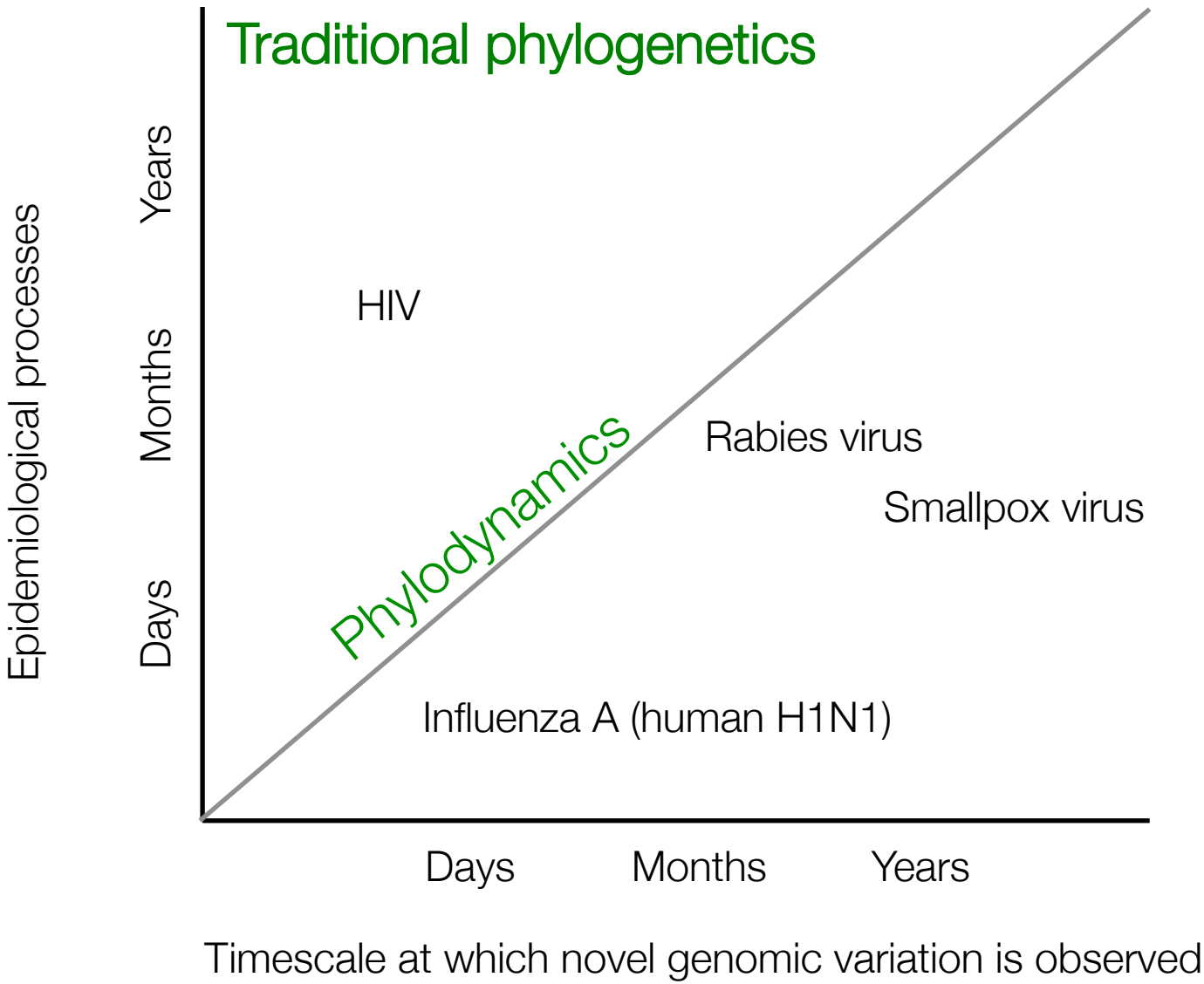
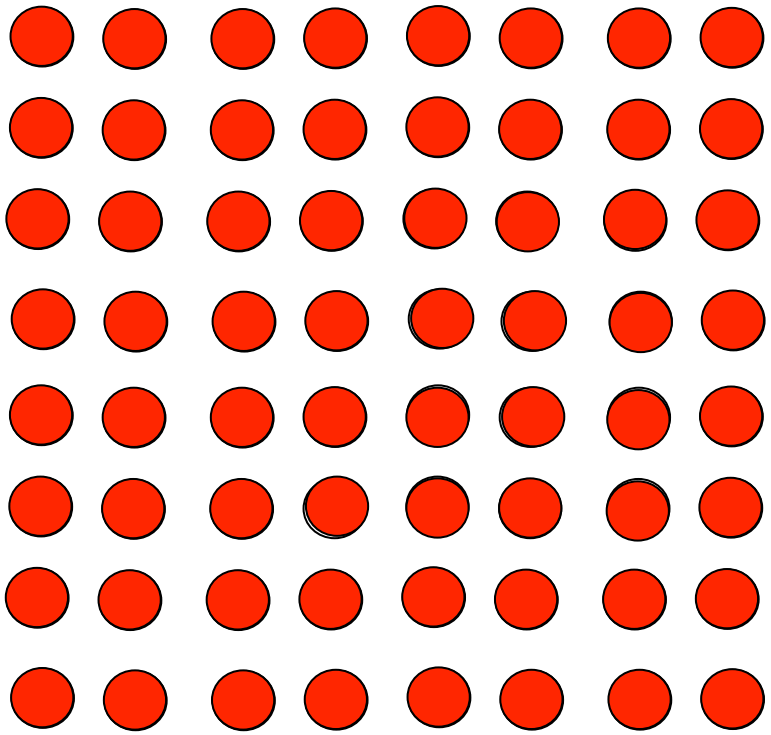
Lecture 2.4:
Infectious disease phylodynamics



From Biek et al. 2013 *Trends Ecol Evol*

The basic reproductive number

The basic reproductive number: R_0



R_0 is the average number of secondary infections in a **fully susceptible** population

R_0>1 Infection can spread

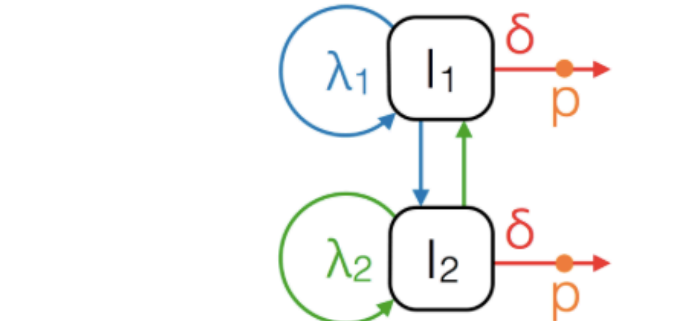
R_0<1 Infection will die out

R_0 for some diseases

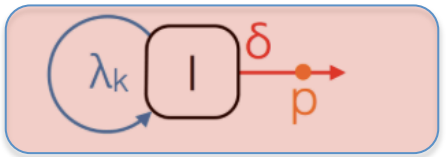
Measles	>12
HIV	2 – 5
Ebola	2.2 (Stadler et al. 2014)
TB	3.4 (Tanaka et al. 2006)

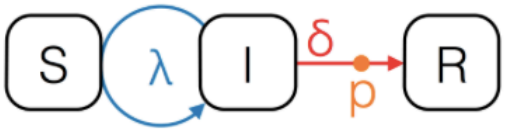
The basic reproductive number: R_0

- Can depend on many factors:
  - Duration of infection
  - Incubation period
  - Host immunity
  - Behavioral changes
- Some of these can be modeled using compartmental models:



- λ — infection rate
- σ — incubation rate
- δ — becoming-noninfectious rate
- p — sampling probability





From Stadler et al. 2014 *PLOS Current Outbreaks*

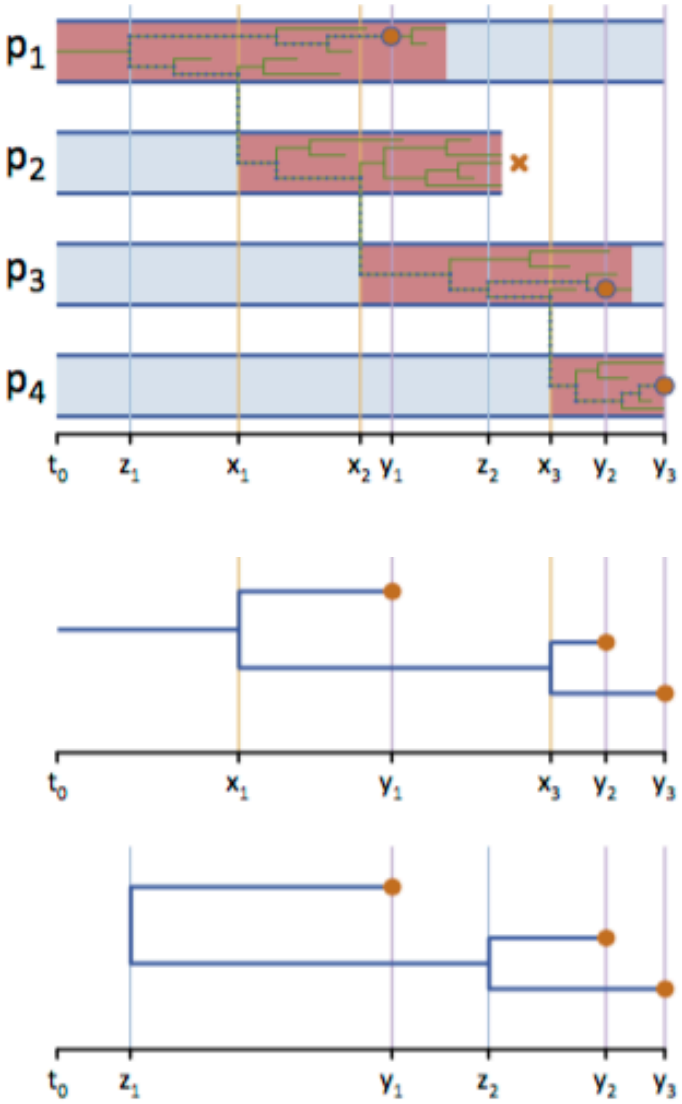
Phylogenetic epidemiology

Phylogenetics trees and infection

Complete transmission tree

Sampled transmission tree

Reconstructed genealogy



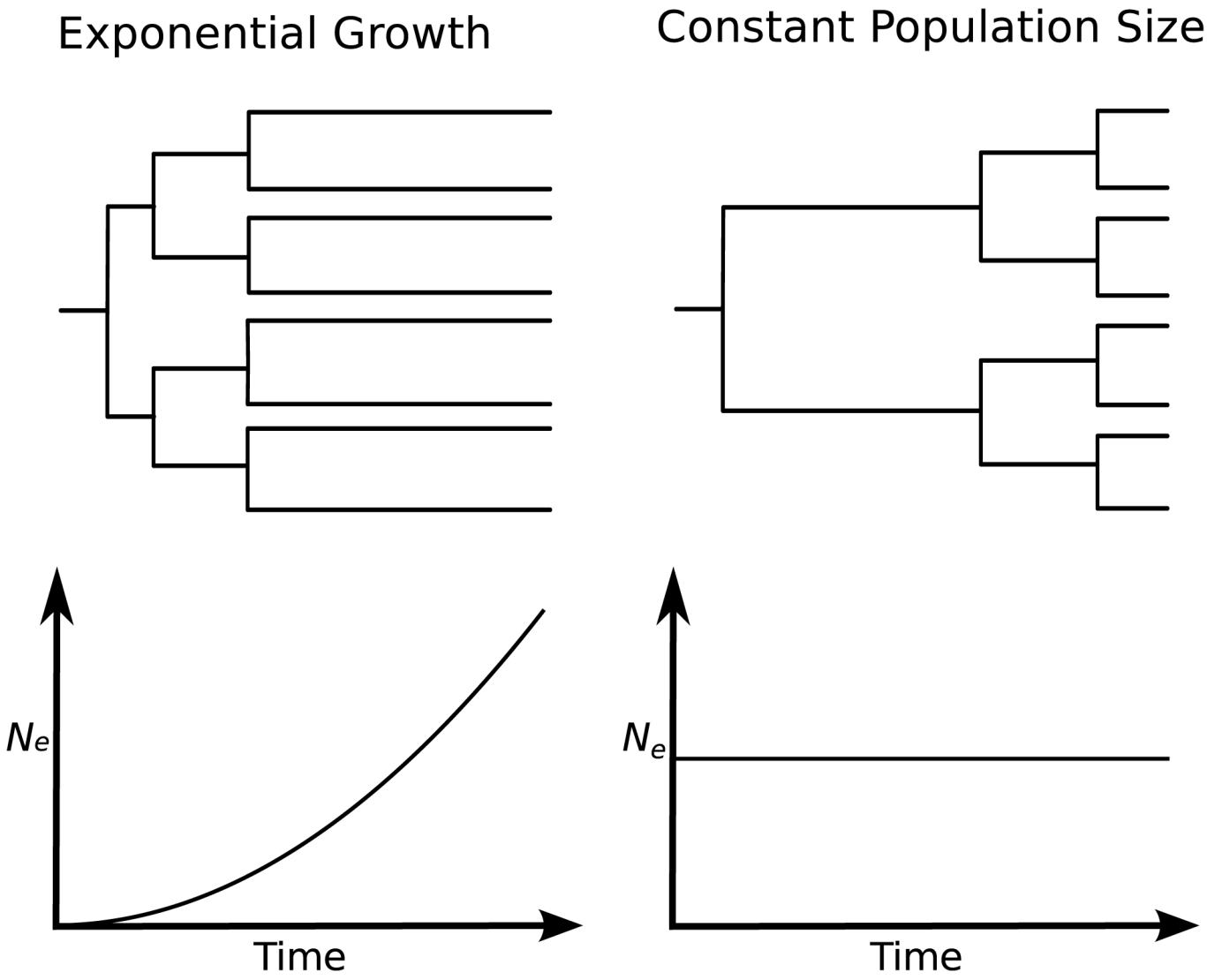
Account for sampling fraction

Assume that the sampled tree and reconstructed genealogy are equal

The genealogies have no information about who infected whom

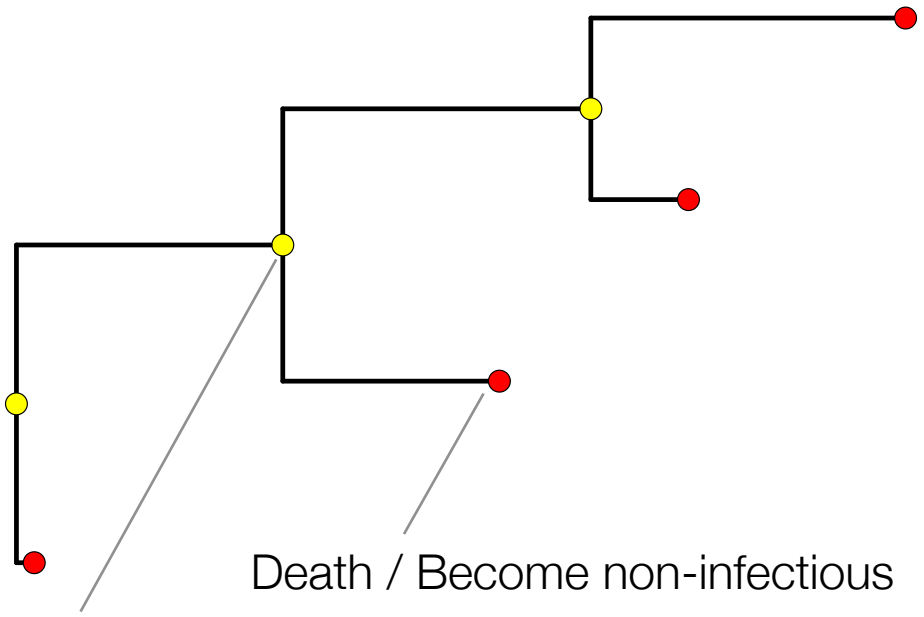
From du Pleiss and Stadler 2015 *Trends in Microb*

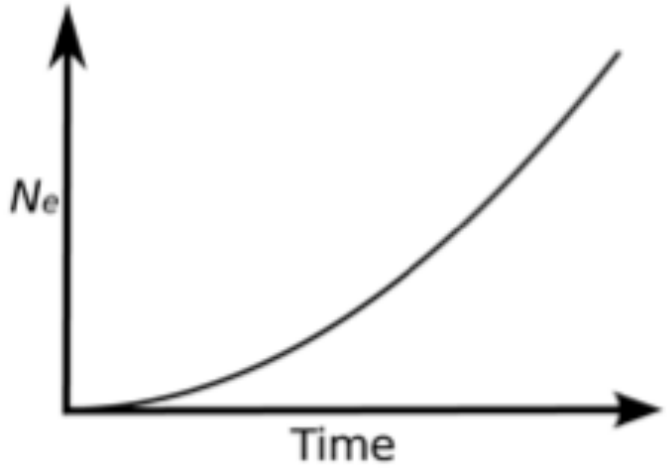
Estimating population size: the coalescent



From Volz et al. 2013 *PLOS Comp Biol*

Estimating R_0: coalescent phylodynamics





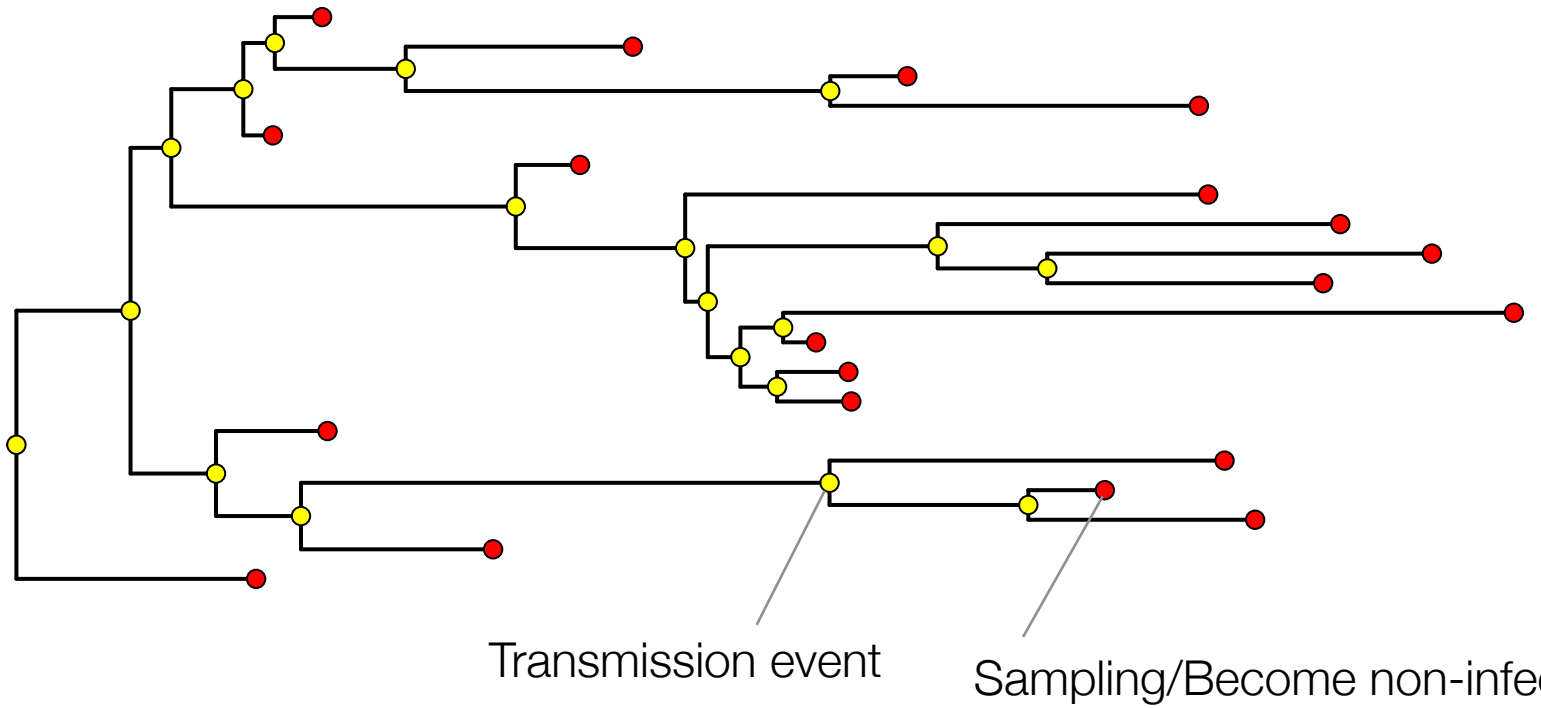
$N(t) = N_0 e^{-rt}$

$r = (R_0 - 1) / D$

r: exponential growth rate
N_0: initial population size
N(t): population size at time t

R_0: basic reproductive ratio
D: duration of infection

Estimating R_0: Birth-Death models



λ: transmission rate (birth)

δ = sampling + death/recovered

$$R_0 = \lambda / \delta$$

Skyline methods

- Coalescent and Birth-Death methods assume constant parameters
- This assumption can be relaxed
  - Birth Death Skyline
  - Coalescent Skyline

$R_e(t)$ is R_0 at time t, $R_e(0) = R_0$

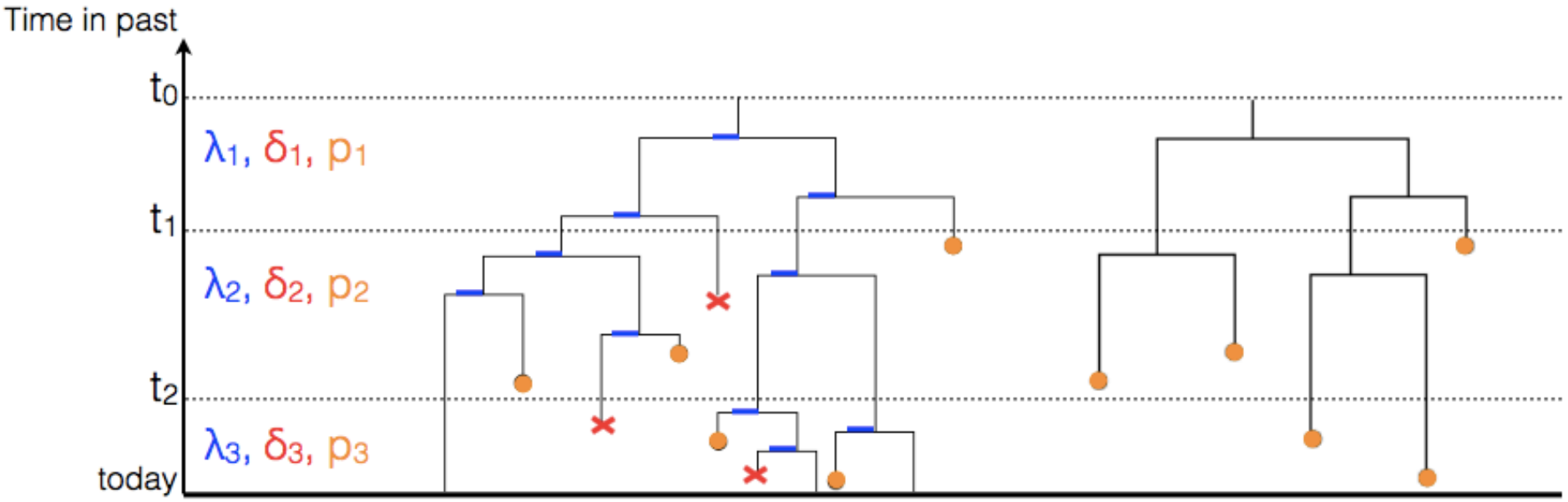
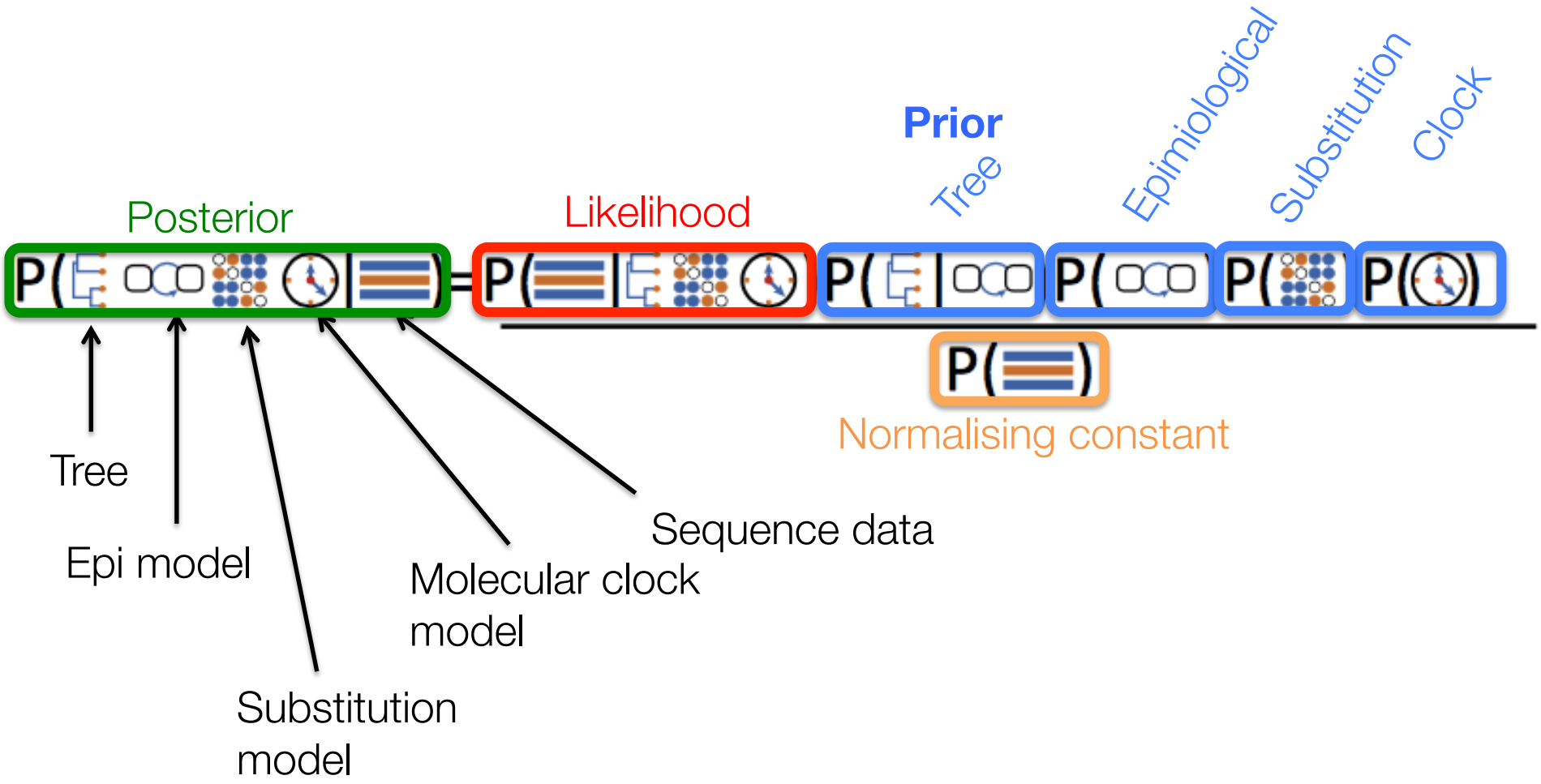


Image modified from Tanja Stadler's slides

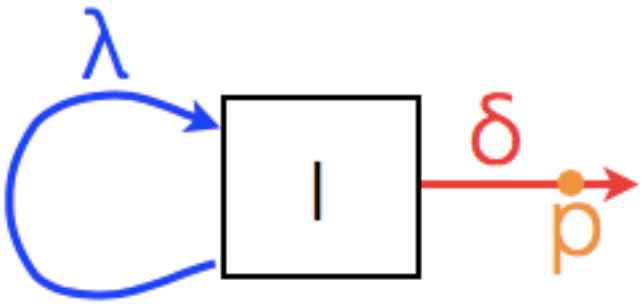
Modelling framework

Bayesian approach



Compartmental models

Birth-Death



$$R_0 = \lambda / (\delta)$$

λ = transmission rate

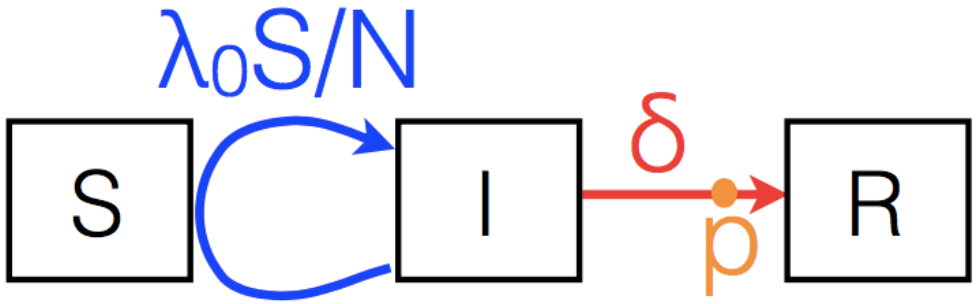
δ = becoming non-infectious rate

ρ = sampling probability

From Stadler et al. 2014 *PLOS Current Outbreaks*

Compartmental models

Birth-Death Susceptible-infected-recovered



$R_0 = \lambda_0 / \delta$

N=S+I+R

$\lambda(S) = \lambda_0 S/N$

λ = transmission rate

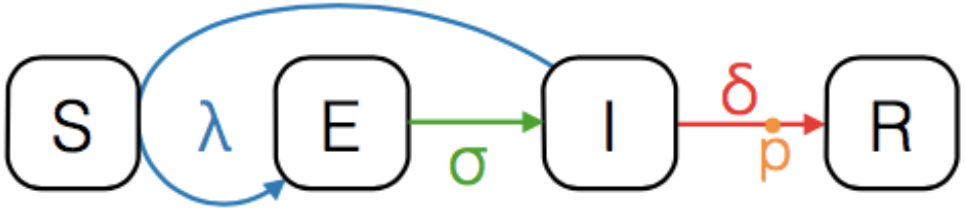
δ = becoming non-infectious rate

ρ = sampling probability

From Stadler et al. 2014 *PLOS Current Outbreaks*

Compartmental models

Birth-Death Exposed-infected-recovered



λ = transmission rate

δ = becoming non-infectious rate

ρ = sampling probability

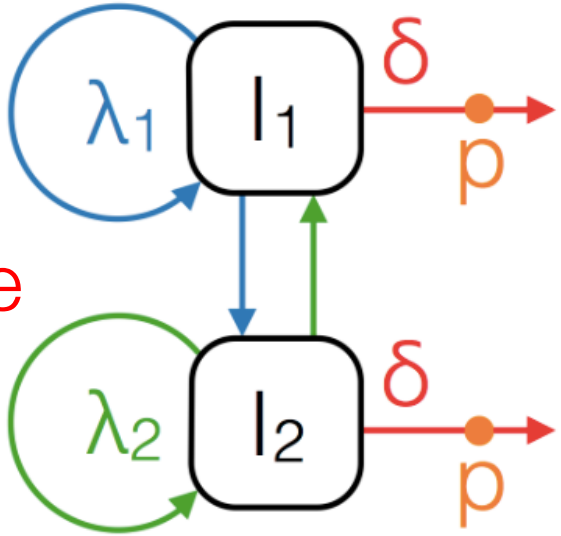
σ = incubation rate

From Stadler et al. 2014 *PLOS Current Outbreaks*

Compartmental models

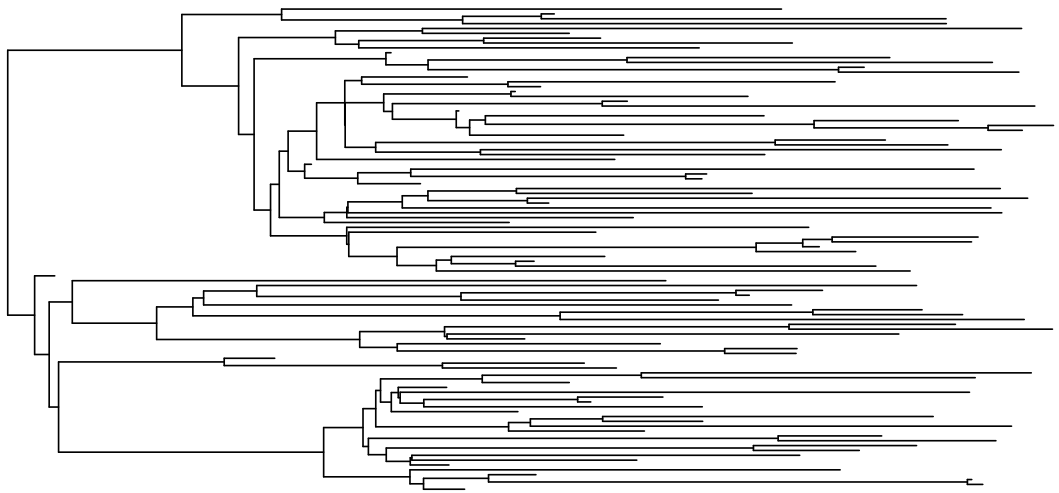
Birth-Death super-spreading

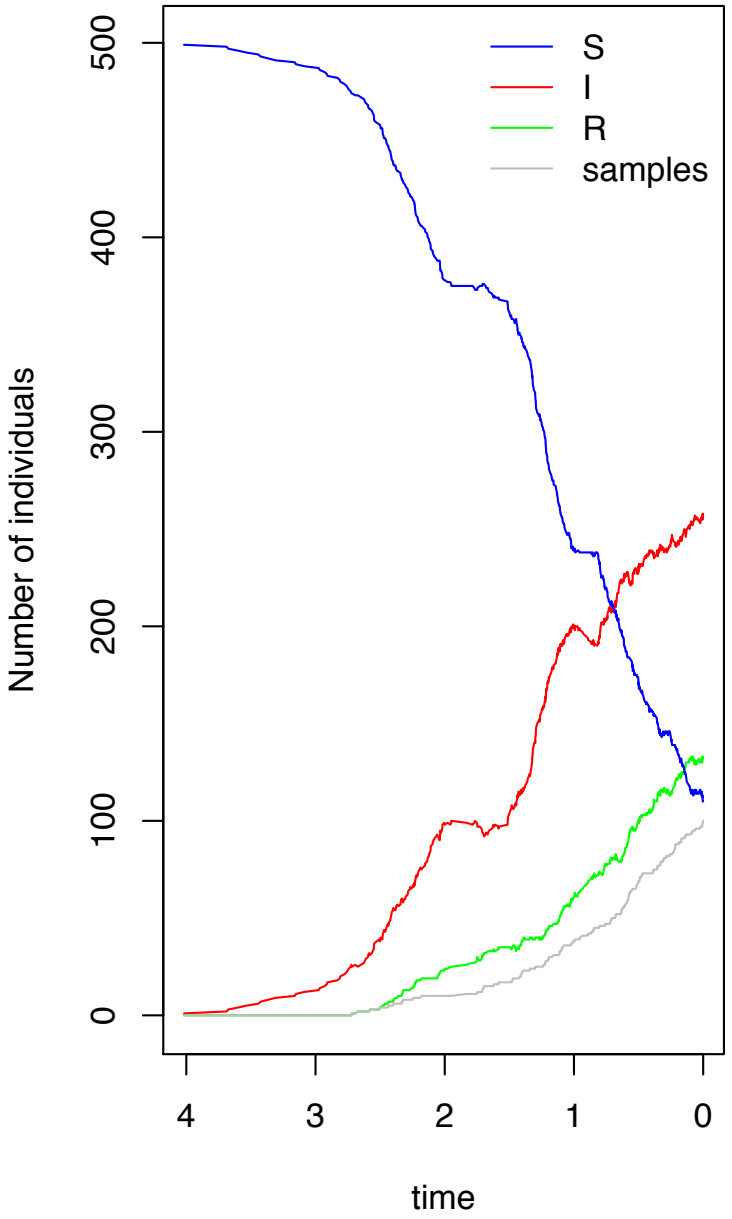
λ_1 = transmission rate 1
λ_2 = transmission rate 2
δ = becoming non-infectious rate
ρ = sampling probability



From Stadler et al. 2014 *PLOS Current Outbreaks*

Simulating trajectories





MASTER (BEAST2)
(Vaughan and Drummond 2013)
TreeSim (Stadler 2011)

Useful references

Kühnert, Denise, et al. "Simultaneous reconstruction of evolutionary history and epidemiological dynamics from viral sequences with the birth–death SIR model." *Journal of the Royal Society Interface* 11.94 (2014): 20131106.

du Plessis, Louis, and Tanja Stadler. "Getting to the root of epidemic spread with phylodynamic analysis of genomic data." *Trends in microbiology* 23.7 (2015): 383-386.

Go to Practical 4: Phylogenetic epidemiology in BEAST