

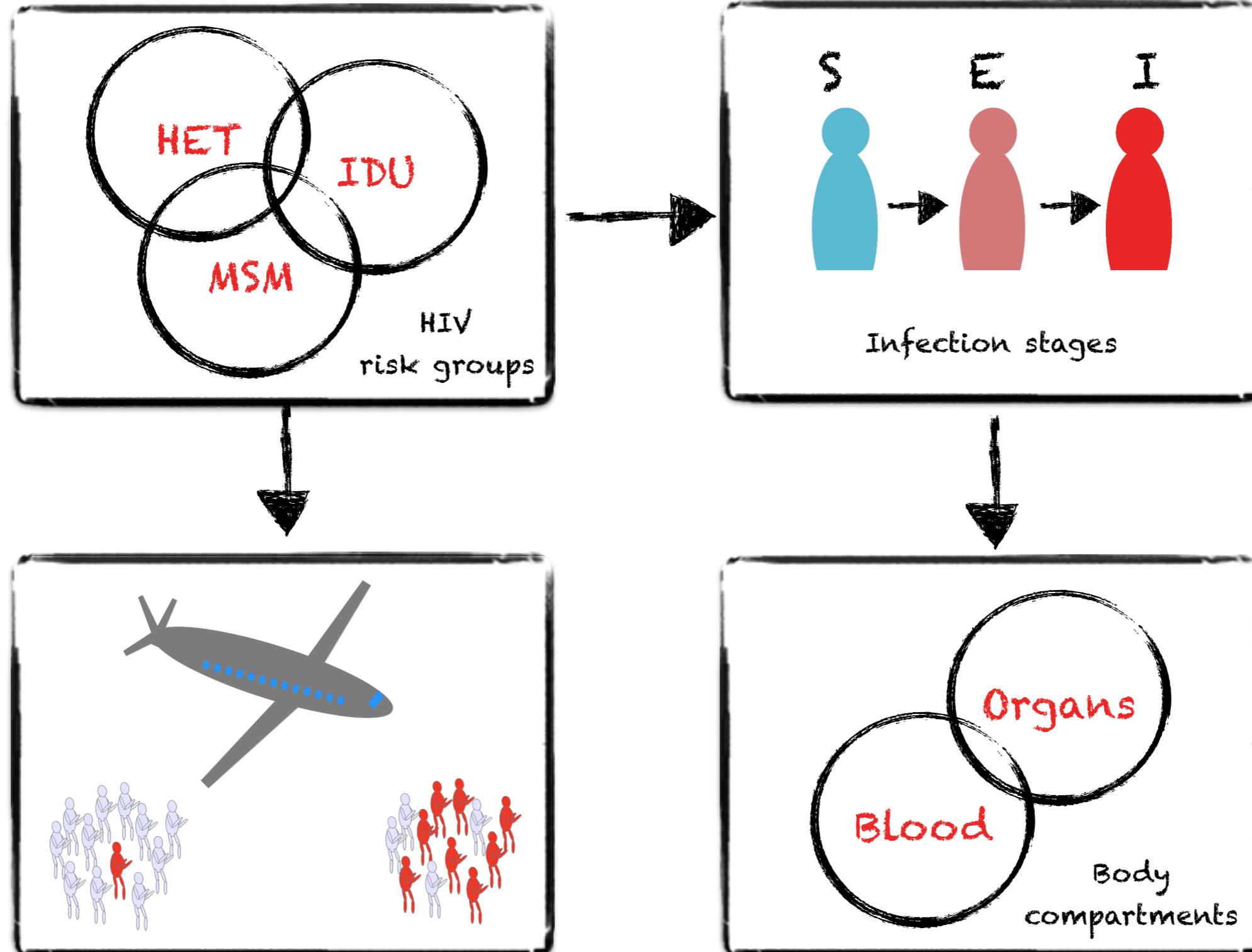
Phylodynamic inference

Denise Kühnert



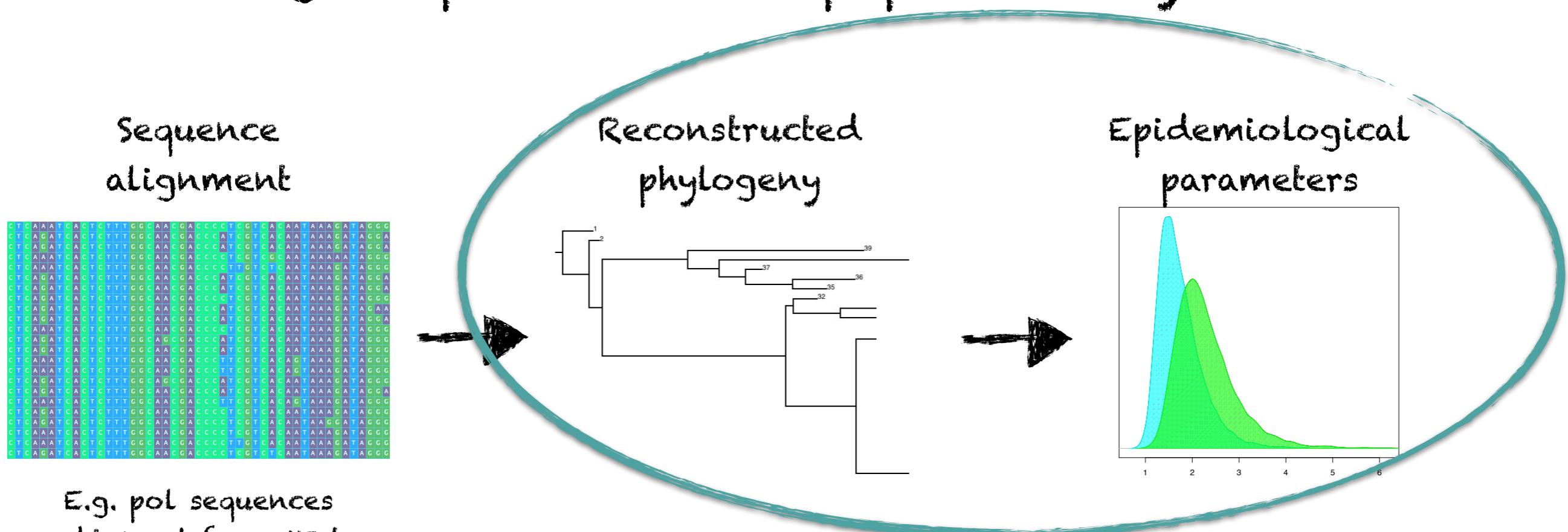
Transmission, Infection, Diversification & Evolution Group

Infectious Disease Dynamics are Manifold



Phylogenetic Inference

Pathogen genomes can track ecological processes and population dynamics

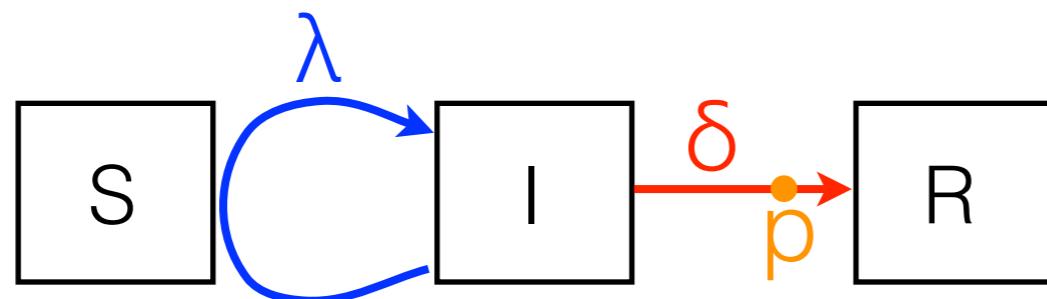


E.g. pol sequences obtained from HIV resistance testing

Joint reconstruction using Bayesian MCMC in BEAST

Birth-death models in phylogenetics

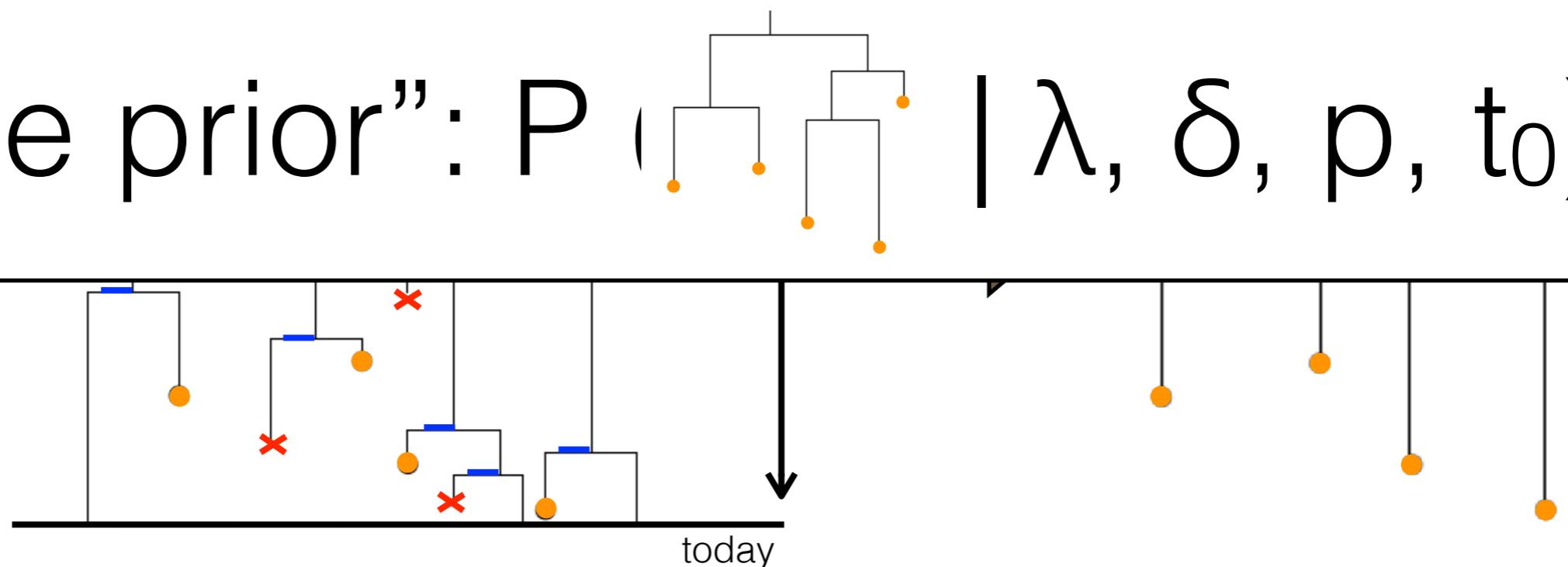
Birth-death
model for
epidemic
spread



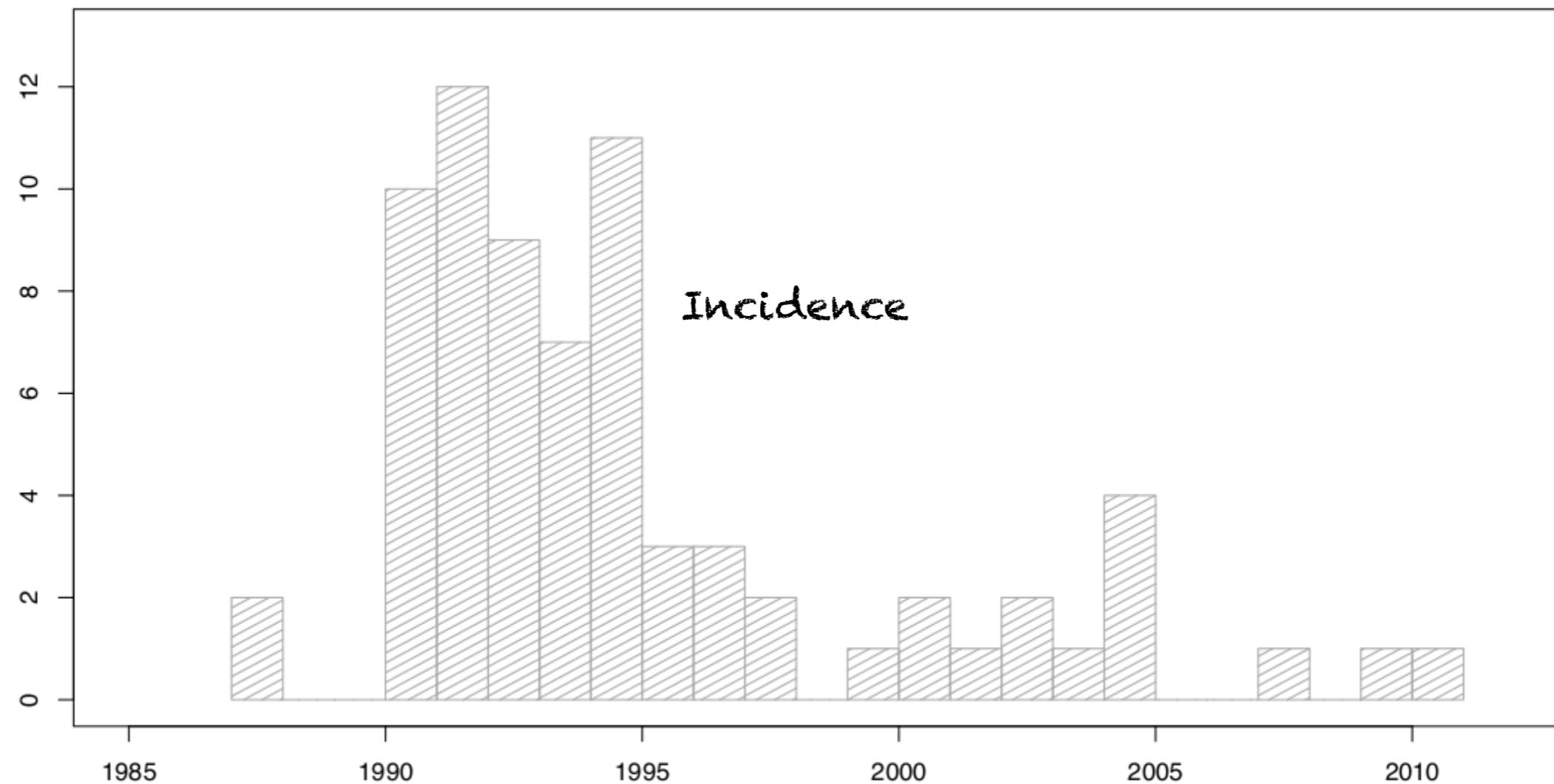
- transmission rate λ
- “becoming-non-infectious” rate δ
- sampling probability p

“Tree prior”: $P(\text{tree} | \lambda, \delta, p, t_0)$

genetic
trees

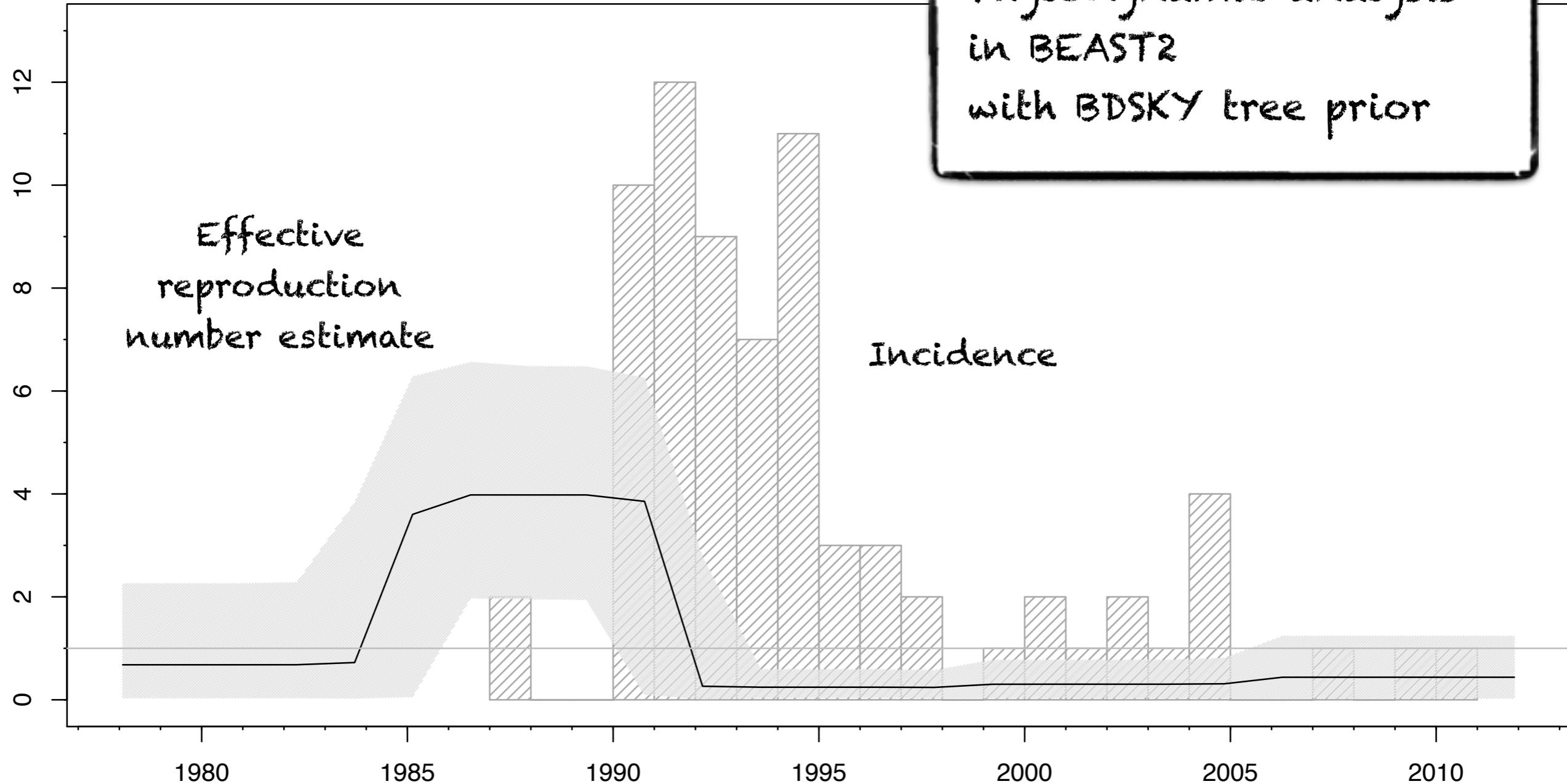


Mycobacterium Tuberculosis outbreak in Bern



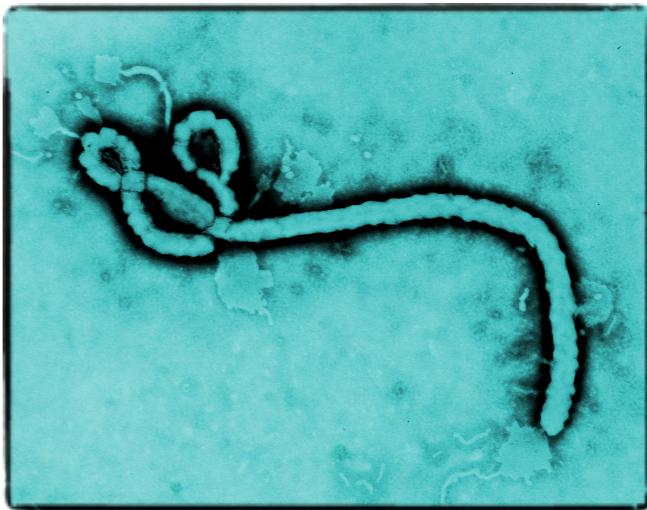
- 69 isolates from localized outbreak in Bern, Switzerland
- Initially samples from 1987-1993, then follow-up sample isolation
- Whole genome sequencing

Mycobacterium Tuberculosis: Case Data Does Not Tell the Whole Story

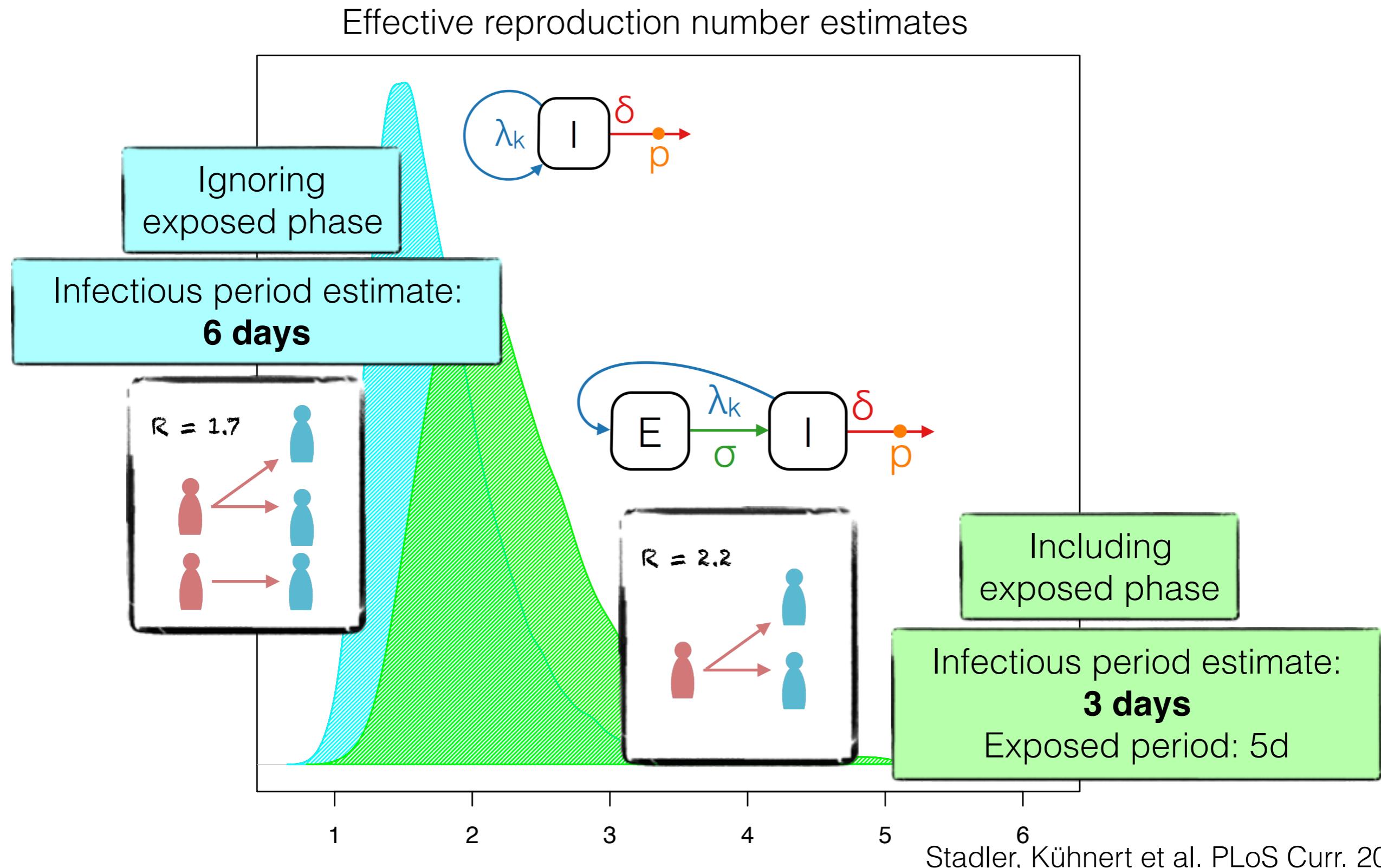


Ebola Virus Outbreak in Sierra Leone

- 72 sequences from Sierra Leone
- sampled between 26 May - 18 Juni
- Gire et al. 2014

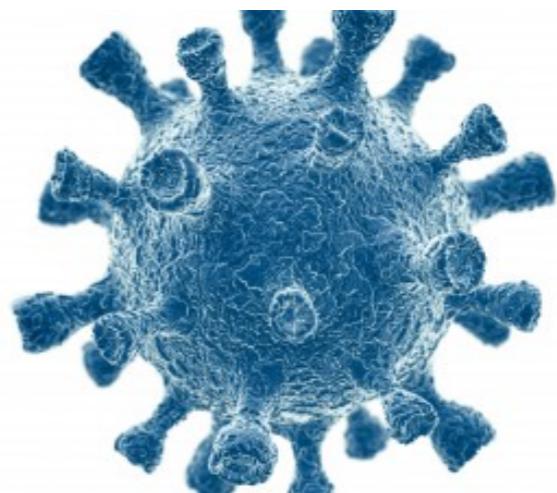


Ebola Virus Outbreak in Sierra Leone

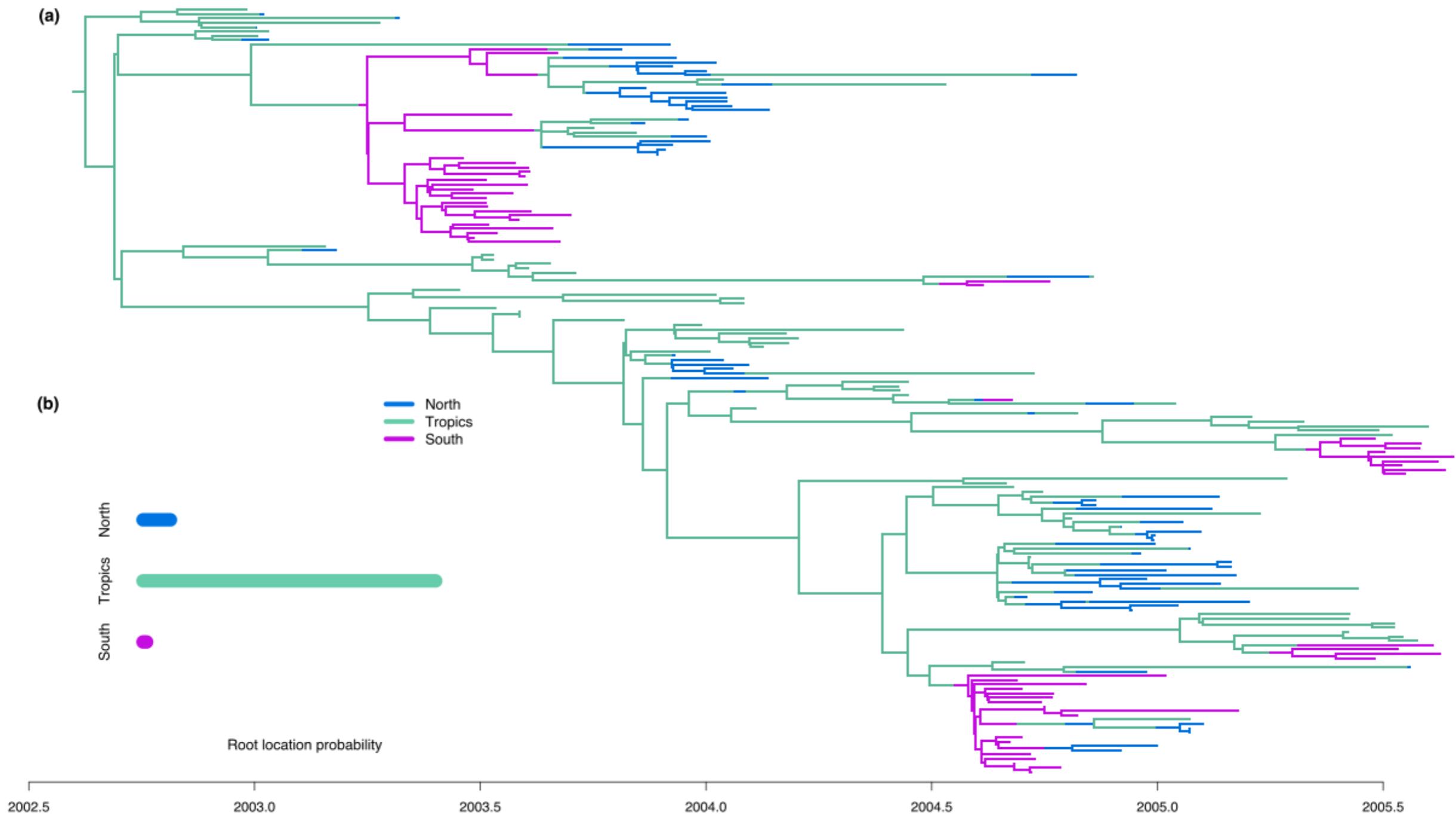


Global Influenza H3N2: Are the Tropics the Source?

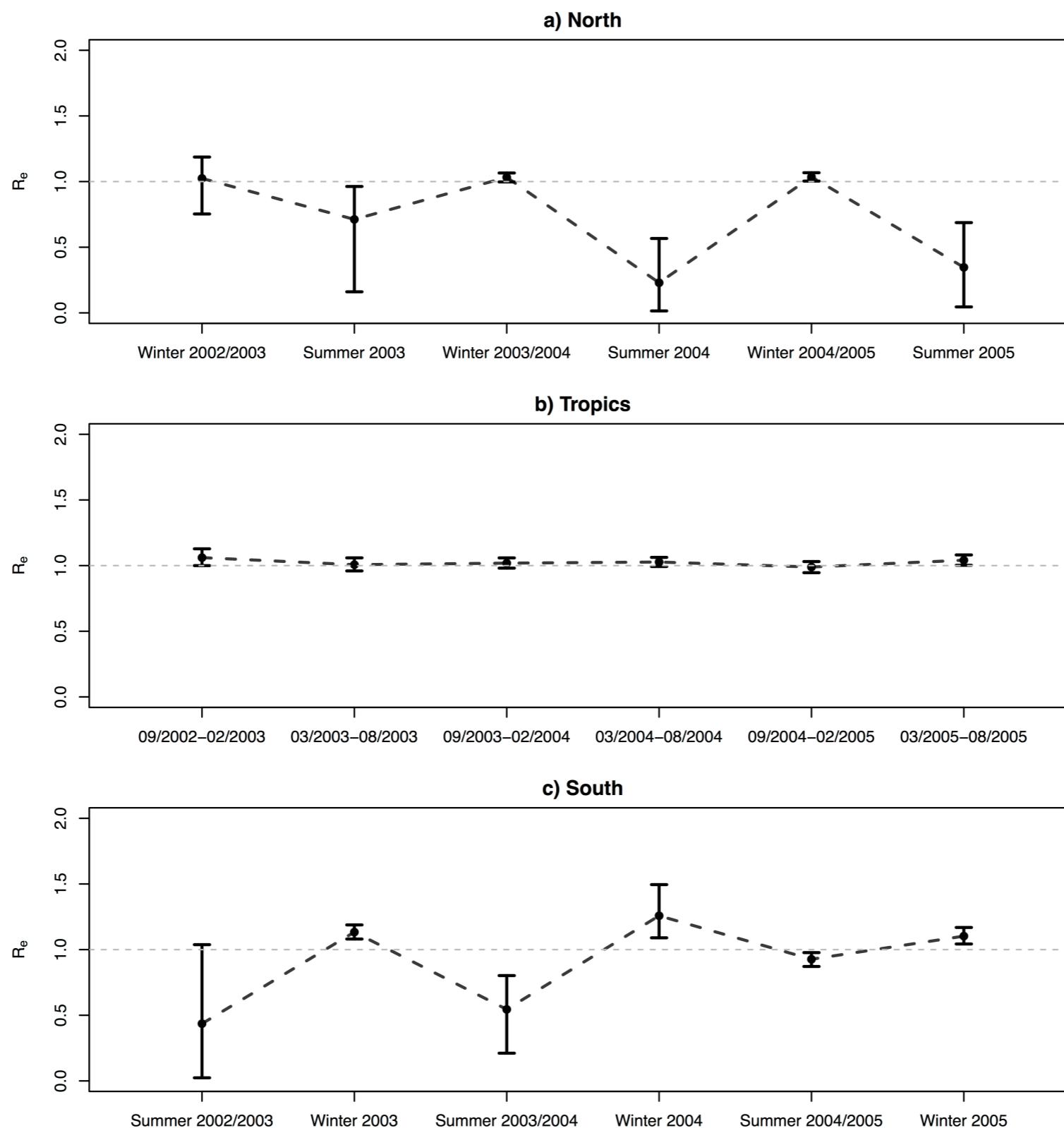
- 175 global HA gene sequences
- sampled between 2003-2005



Global Influenza H3N2: Are the Tropics the Source?



Global Influenza H3N2: Phylogenetics Can Reconstruct Seasonal Dynamics



Summary

TB

Phyldynamics gives further insight into Bernese outbreak: no or very few transmissions after 1992

Without phylogenetic analysis late cases may not have been associated with 1990s outbreak.

R_0 agrees with non-genetic estimates.

Sampling proportion lower than originally thought - probably missing patients from very rural areas.

Ebola

Phylogeographic analysis reconstructs temperate epidemiological dynamics

Flu

Posterior distribution of “coloured” phylogenies support a source in the tropics