

Coalescent theory and the population genetics of molecular evolution

Molecular Epidemiology of Infectious Diseases
Lecture 4

February 3rd, 2020

Coalescent models
track the ancestry
of sampled
lineages backwards
through time.

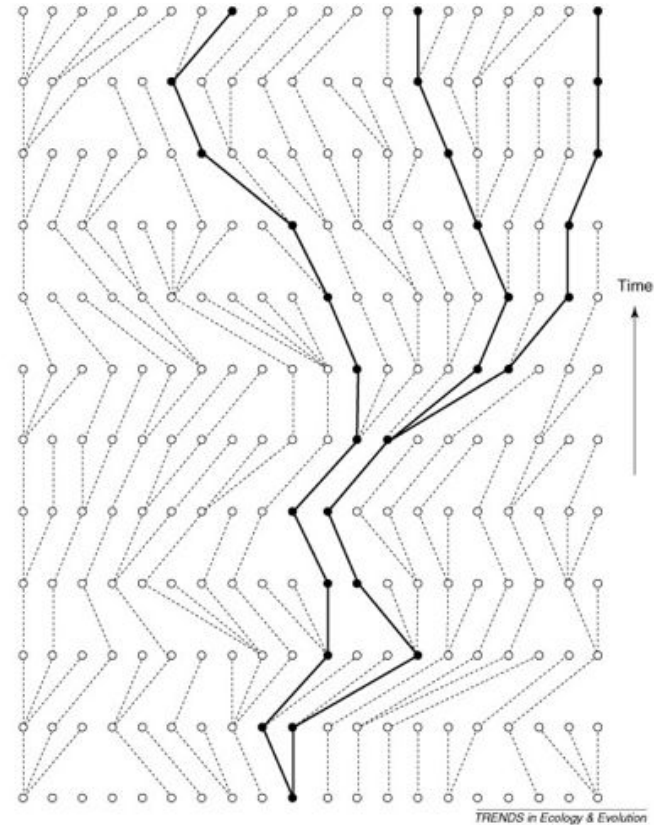


John Goddard, The Tree of Man's Life (1649)

Basic coalescent theory

Coalescent theory describes the ancestral relationships (i.e. genealogy) of individuals sampled from a larger population.

The sampled lineages are embedded within the full ancestral history of the population.



Kuhner *et al.* (2008)

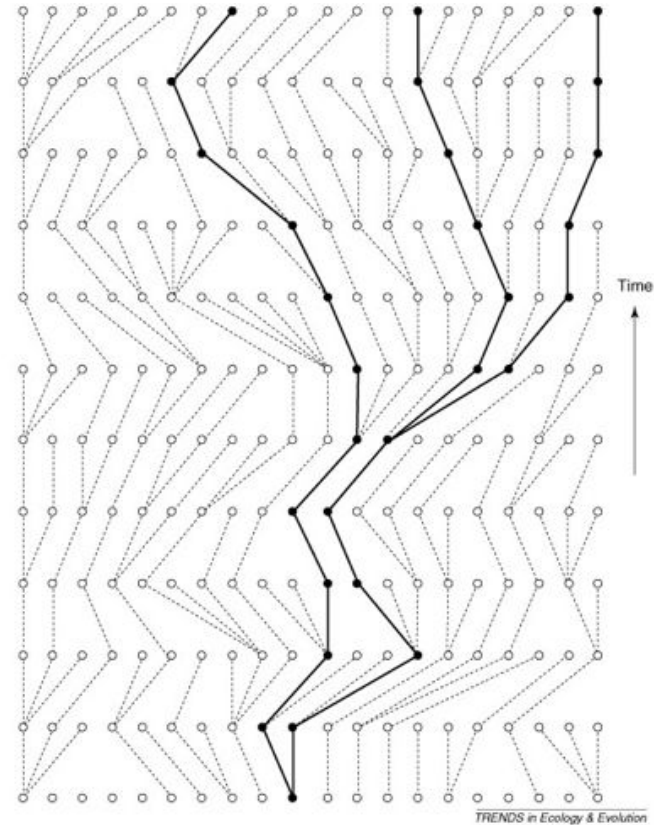
Wright-Fisher assumptions

Coalescent theory is largely based on simple demographic models like the Wright-Fisher model

Constant population size of N haploid individuals

Discrete, non-overlapping generations

Reproduction is a stochastic process such that individuals leave a random number of offspring.



TRENDS in Ecology & Evolution

Kuhner *et al.* (2008)

Basic coalescent theory

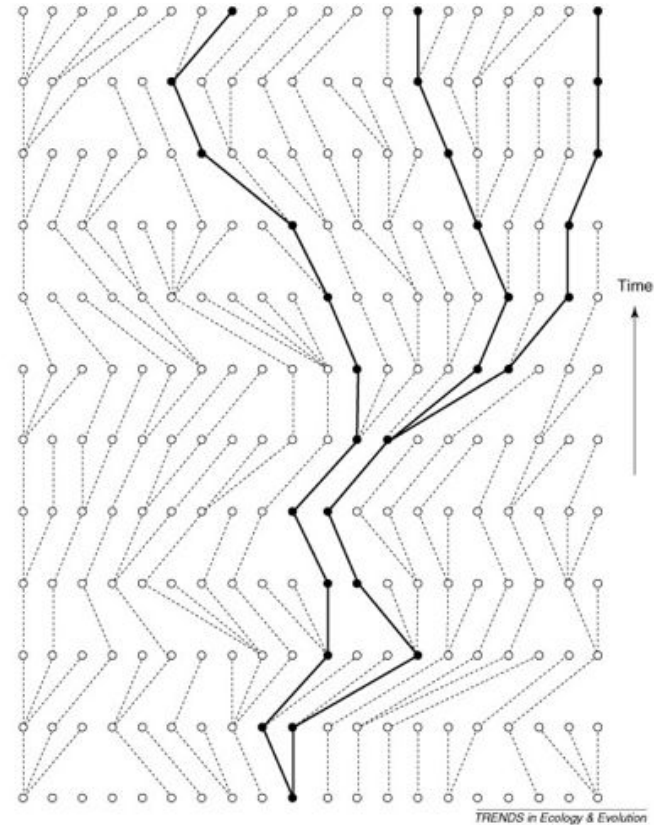
Because reproduction is random, the ancestral relationships among individuals is also viewed as a stochastic process that generates random coalescent trees.



Basic coalescent theory

The probability of two lineages coalescing per generation is:

$$p_{coal} = \frac{1}{N}$$



Kuhner *et al.* (2008)

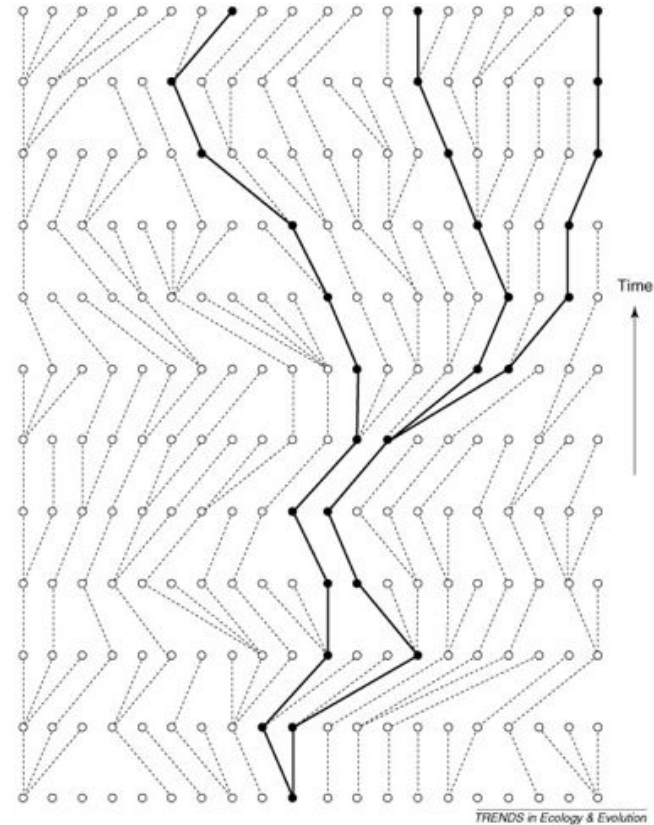
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$$Pr(X = n) = (1 - p_{coal})^{n-1} p_{coal}$$



Kuhner *et al.* (2008)

Basic coalescent theory

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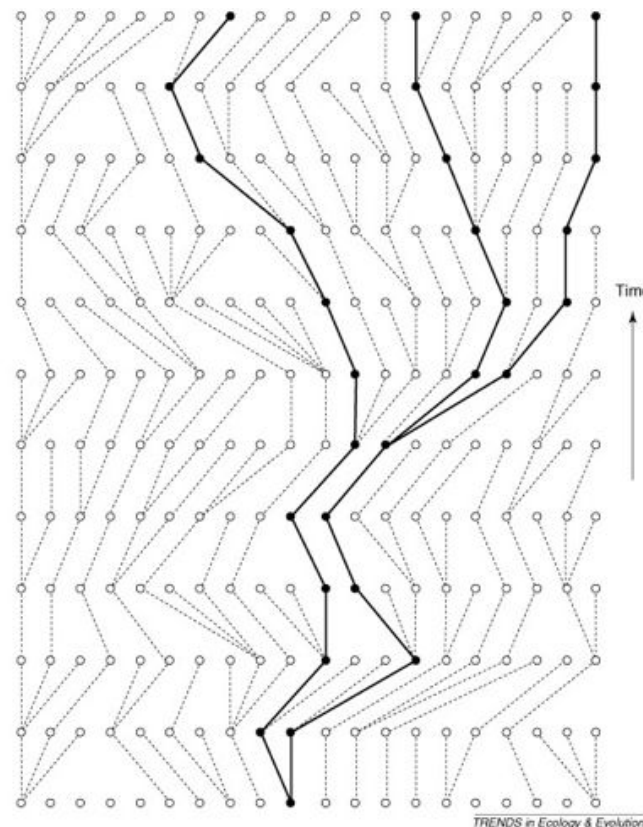
$$p_{coal} = \frac{1}{N}$$

The probability of coalescing after n generations is:

$$Pr(X = n) = (1 - p_{coal})^{n-1} p_{coal}$$

In continuous time:

$$Pr(X = t) = \lambda e^{-\lambda t} \quad \lambda = p_{coal} = \frac{1}{N}$$

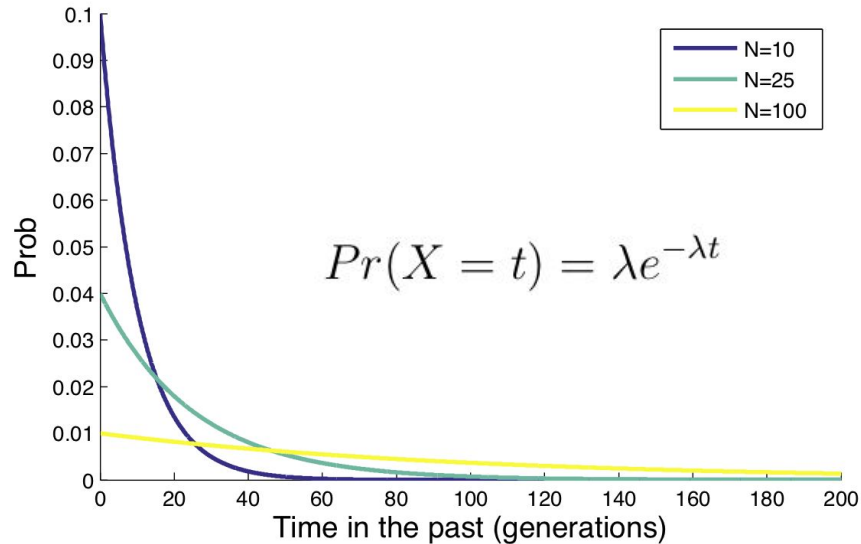


TRENDS in Ecology & Evolution

Kuhner et al. (2008)

Basic coalescent theory

The waiting time for a pair of lineages to coalesce is exponentially distributed.



A slightly more general coalescent model

The coalescent rate increases with the the amount of reproductive variance σ^2 in the population:

$$\lambda_{coal} = \frac{\sigma^2}{N}$$

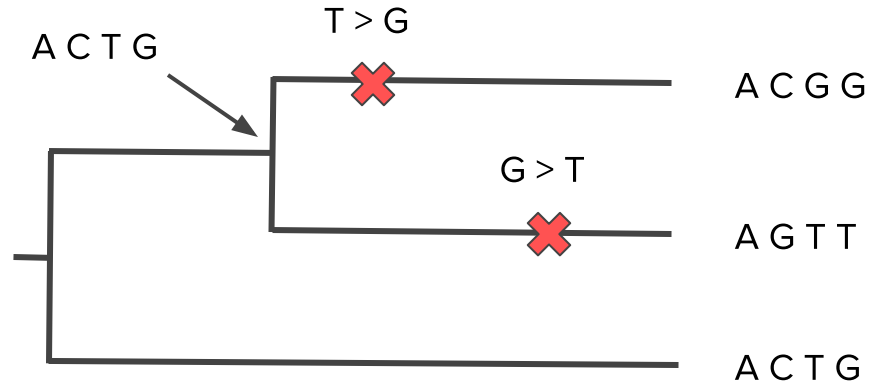
We can define an **effective population size N_e** :

$$N_e = \frac{N}{\sigma^2}$$

More generally then, the coalescent rate is:

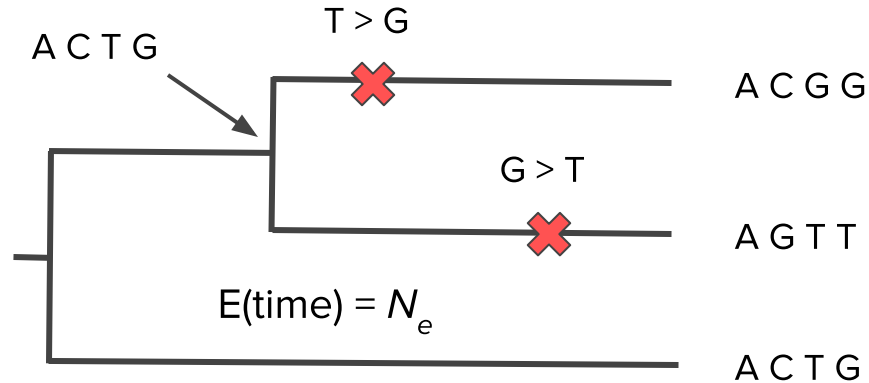
$$\lambda_{coal} = \frac{1}{N_e}$$

Coalescent trees with mutations



Most coalescent models assume mutations are neutral such that mutations occur independently of the coalescent process.

Coalescent trees and genetic diversity



Genetic diversity depends directly on both the mutation rate μ and the coalescent rate. The expected average pairwise diversity is: $\theta = 2N_e\mu$

Now with more than two lineages

With k lineages present, the coalescent rate becomes:

$$\lambda_{coal} = \frac{\binom{k}{2}}{N_e}$$

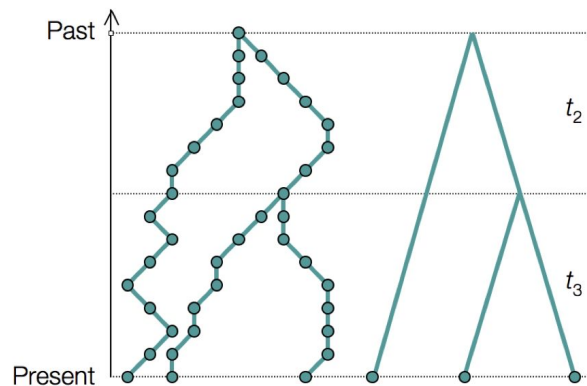
The binomial coefficient gives the total number of lineage pairs that could have coalesced:

$$\binom{k}{2} = \frac{k(k-1)}{2}$$

The coalescent likelihood

For a tree with n samples and $n-1$ coalescent events we can compute the likelihood of the tree as:

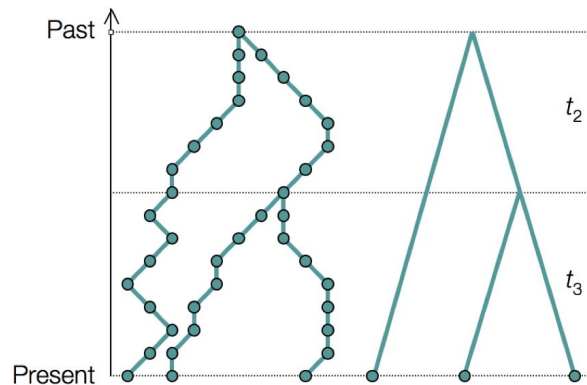
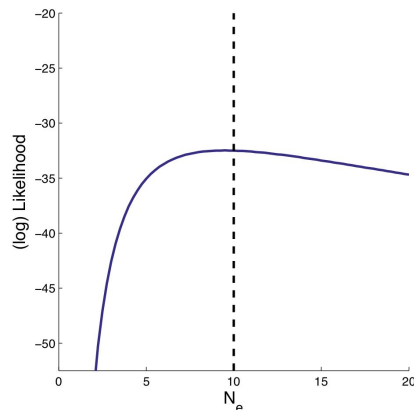
$$L(T|N_e) = \frac{1}{N_e^{(n-1)}} \prod_{k=2}^n \exp \left(- \frac{\binom{k}{2}}{N_e} t_k \right)$$



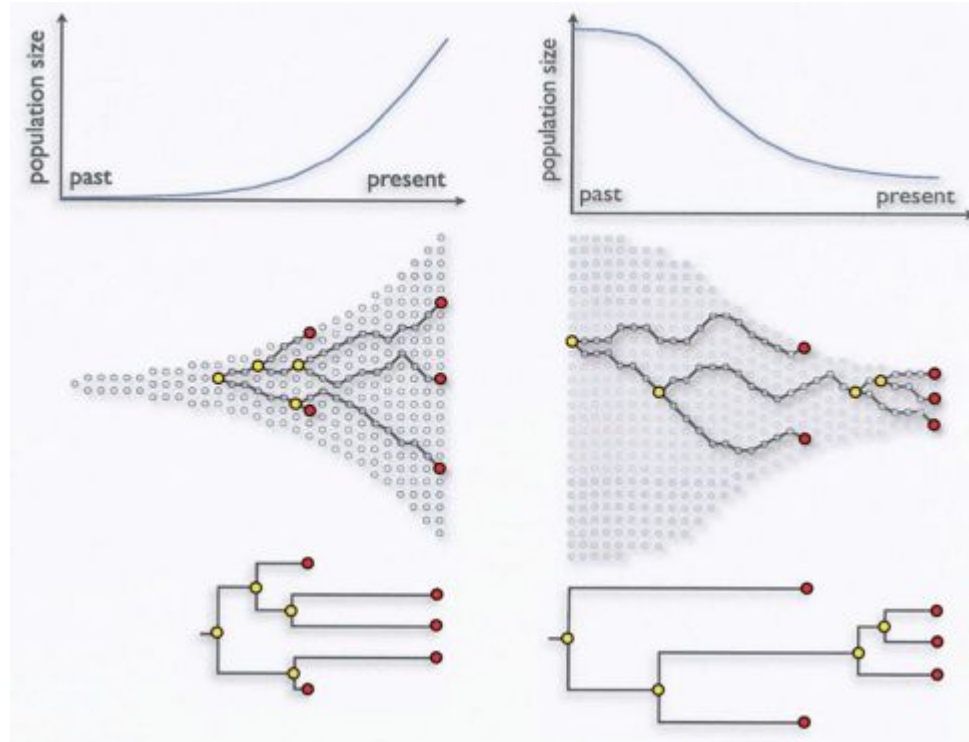
Coalescent-based inference

We can therefore infer demographic parameters like N_e from a known phylogeny.

$$L(T|N_e) = \frac{1}{N_e^{(n-1)}} \prod_{k=2}^n \exp \left(- \frac{\binom{k}{2}}{N_e} t_k \right)$$



The signal of population size change



Modeling population size changes

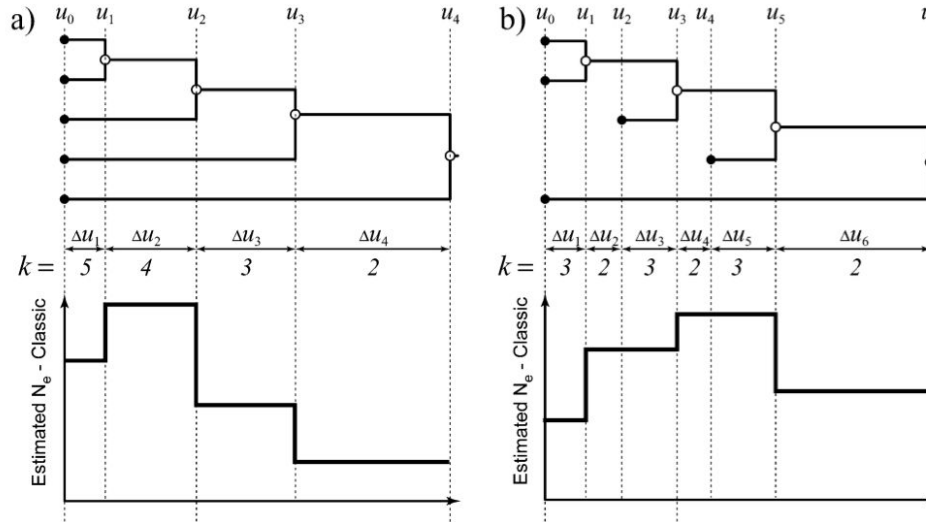
Parametric models assume population sizes change according to some population dynamic model (e.g. exponential growth)

Nonparametric methods allow population sizes to change over time in an unconstrained manner.

- Bayesian Skyline (Drummond *et al.*, 2005)
- Bayesian Skygrid (Minin *et al.*, 2008)

Nonparametric approaches

Generally assume population sizes change over time in a piecewise-constant manner.



Bayesian skyline

Assumes that the population size can only change at a fixed number of change points.

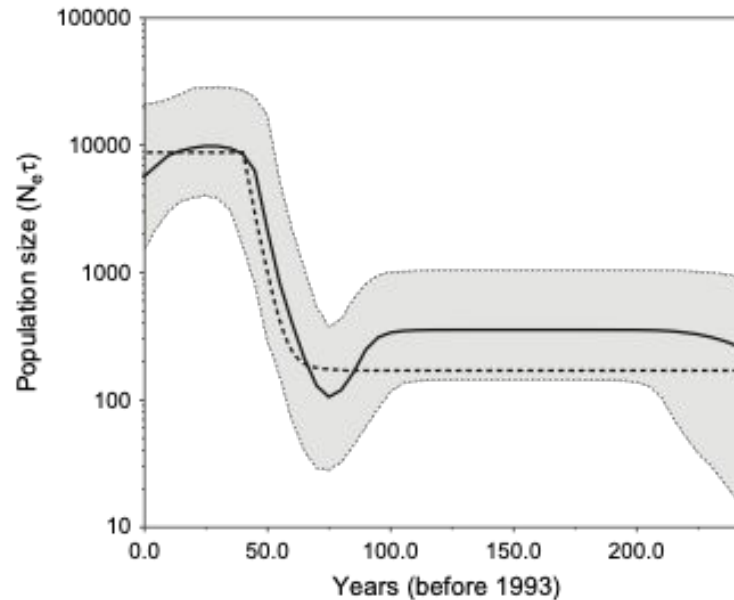
Uses Bayesian MCMC to integrate (average) over all possible change point positions in addition to N_e within each interval/epoch.

Intervals can contain multiple coalescent events allowing for better estimates of N_e

Produces a smoothed estimate of N_e through time with credible intervals.

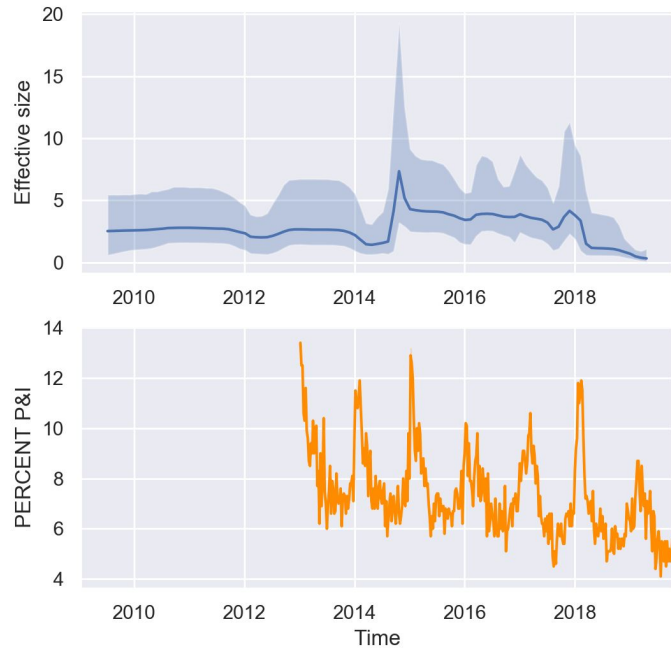
Bayesian skyline plots

Bayesian skyline estimates of for Hepatitis C virus in Egypt

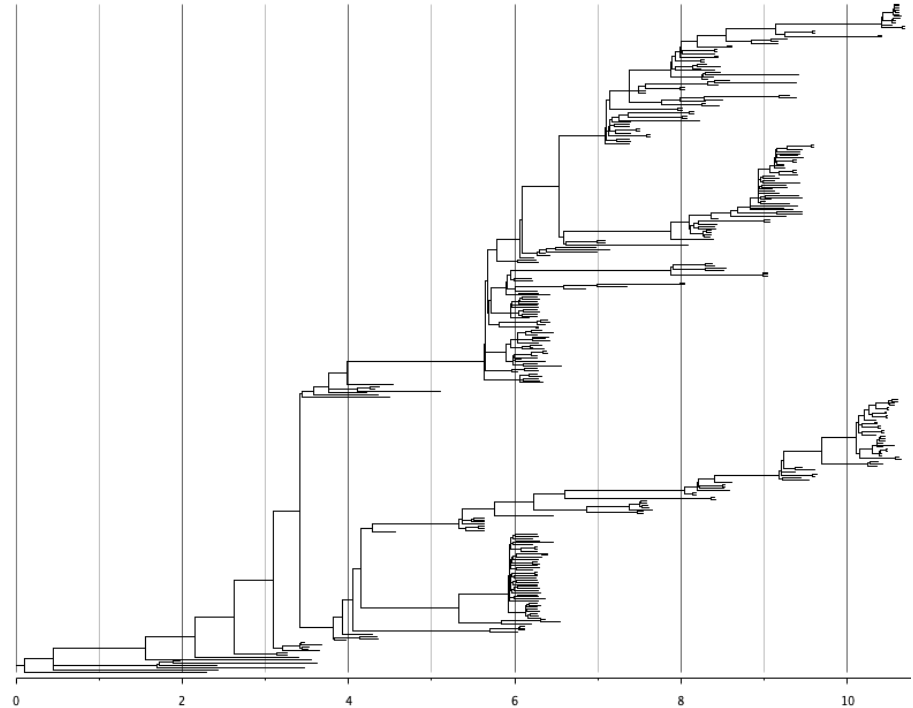
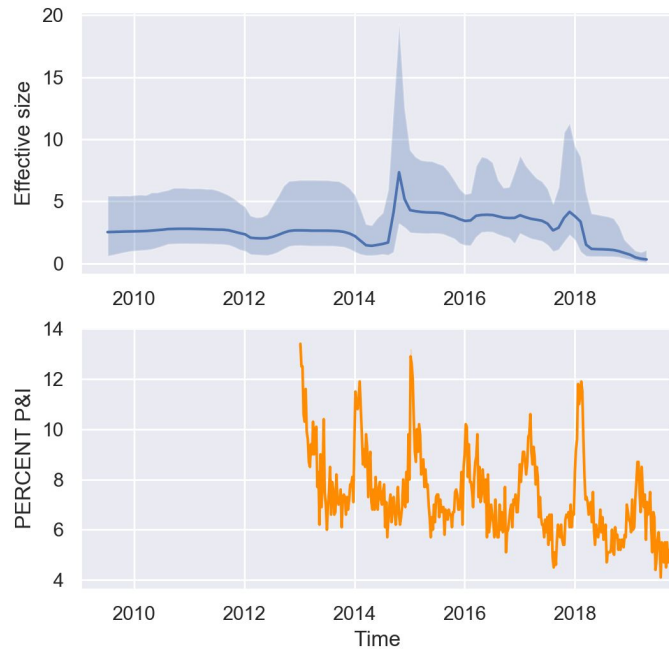


Drummond *et al.* (2005)

Bayesian skyline plots for H3N2 in NC



Bayesian skyline plots for H3N2 in NC

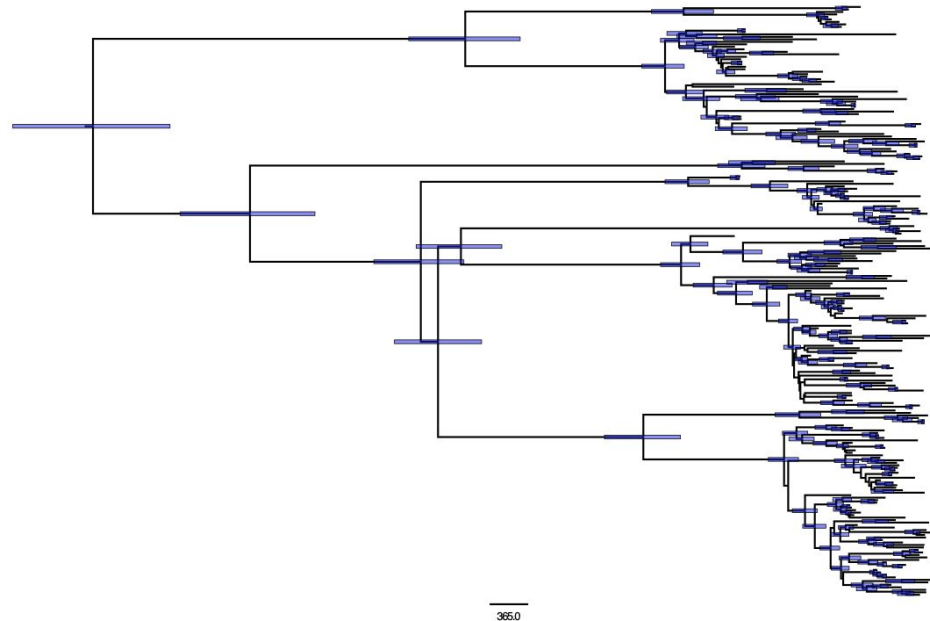
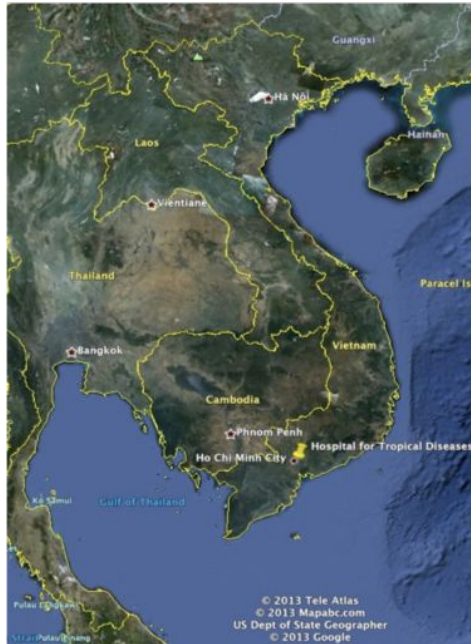


Limitations of simple coalescent models

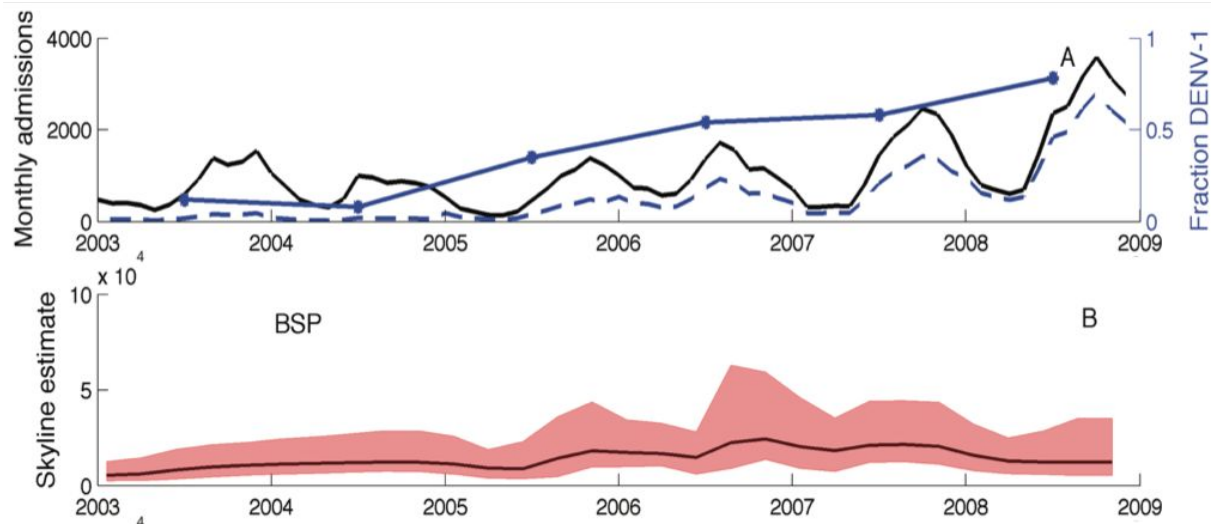
Other forces beyond population dynamics strongly shape phylogenies:

- Reproductive variance
- Population/spatial structure
- Selection
- Recombination (if ignored)

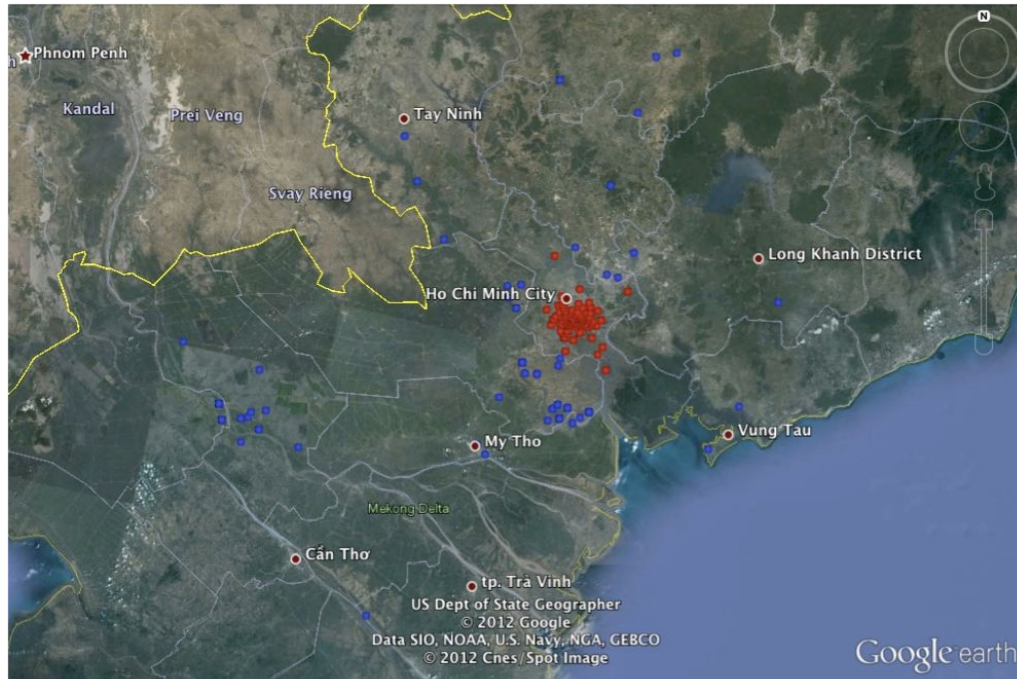
Dengue in southern Vietnam



Bayesian skyline estimates



Spatial structure



The problem with population structure

Standard coalescent models assume that all lineages in the tree are **exchangeable**.

Exchangeability here means that any lineage is equally likely to coalesce with any other lineage in the tree.

Many forms of population structure violate this key assumption.

The structured coalescent

Relaxes the exchangeability assumption by letting lineages move between different populations.

Each lineage pair is allowed to coalesce at a different rate λ_{ij} based on the locations of lineages i and j :

$$L(T|\theta) = \prod_{k=2}^n \lambda_{ij} \exp \left[- \sum_i^k \sum_{j>i}^k \lambda_{ij} t_k \right]$$

However, inference is much more difficult because we must now also infer the location of each lineage through time.

The Migrate-n model

A structured coalescent model with migration between n subpopulations or demes

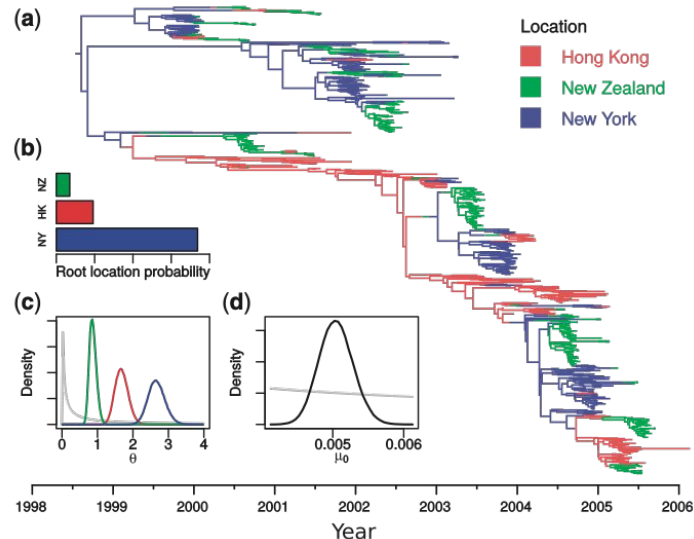
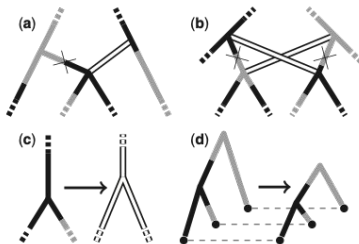
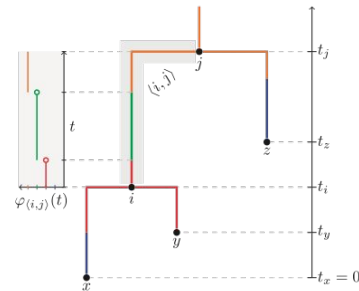
Model is parameterized in terms of a migration rate matrix M and a vector of effective population sizes θ :

$$M = \begin{bmatrix} 0 & m_{1,2} & \cdots & m_{1,n} \\ m_{2,1} & 0 & \cdots & m_{2,n} \\ \vdots & \vdots & \ddots & \vdots \\ m_{n,1} & m_{n,2} & \cdots & 0 \end{bmatrix} \quad \Theta = \begin{bmatrix} N_e^1 \\ N_e^2 \\ \vdots \\ N_e^n \end{bmatrix}$$

Model allows for likelihood-based inference of M and θ BUT we need to use MCMC to sample full **migration histories** along each lineage

Migrate-N and MultiTypeTree

MCMC implementations of the structured coalescent like MIGRATE and MultiTypeTree (Vaughan *et al.*, 2014) sample migration histories on trees



Phylogeography with the SC

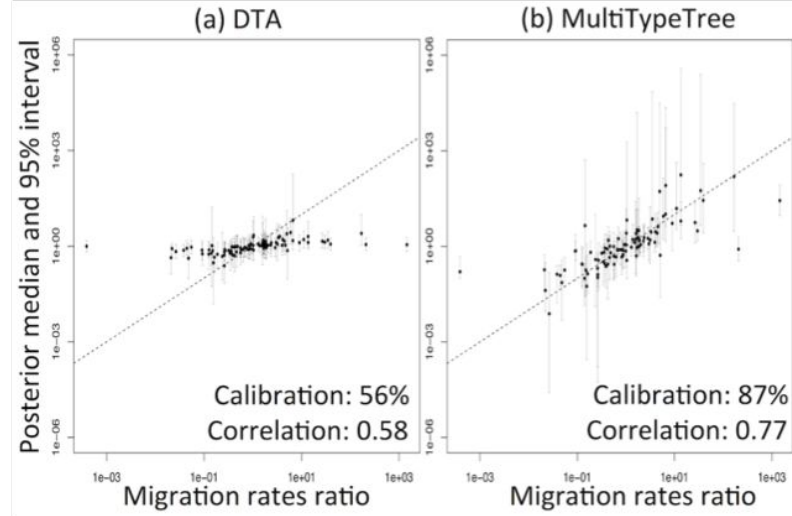
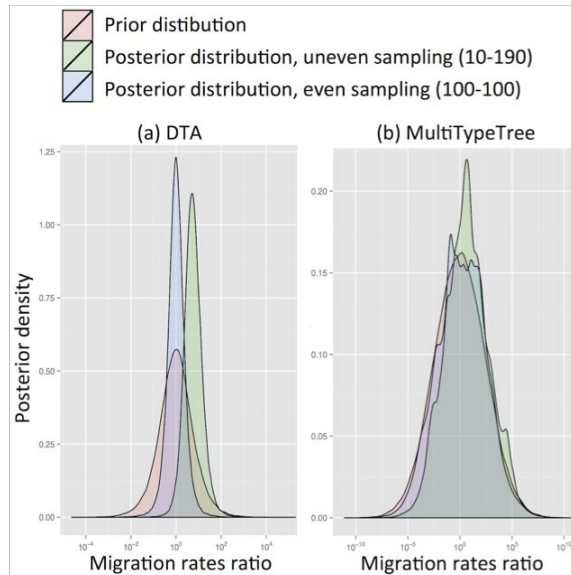
The structured coalescent has become an attractive alternative to discrete-trait analysis (DTA) for phylogeography

DTA treats sampling locations as informative about the migration process whereas the SC conditions on sampling locations.

DTA can therefore be highly biased by disproportionate sampling while the SC is more robust to uneven sampling.

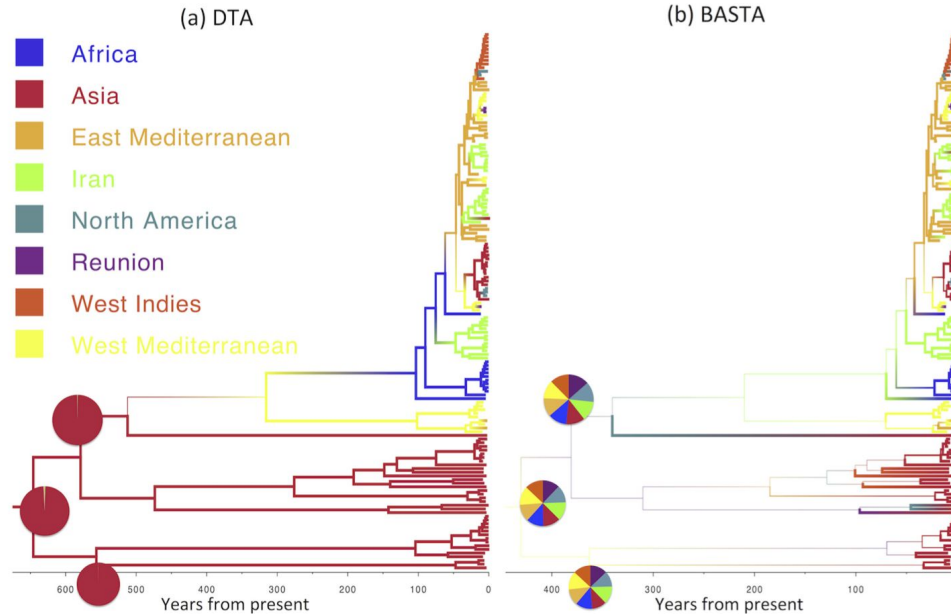
DTA vs. the SC

Uneven sampling strongly biases DTA but not the structured coalescent.



DTA vs. the SC

DTA is also over confident in assigning ancestral state probabilities.



DTA vs. the SC

Structured coalescent models improve statistical performance but are fundamentally limited by the need to sample migration histories on trees.

This does not allow for very efficient MCMC sampling due to strong correlations between the migration histories and model parameters. Generally limited to about 5 or 6 states and trees $1000 < \text{tips}$.

But what if there was a way to efficiently “integrate over” migration histories and therefore average over all possible paths a lineage could have taken?

The Volz (2012) Structured Coalescent

Rather than explicitly sampling migration histories, we can probabilistically track the movement of each lineage back through time.

We can then write pairwise coalescent rates in terms of lineage state probabilities

p_{ik}

$$\lambda_{ij} = \sum_k^m \sum_l^m \frac{f_{kl}}{y_k y_l} (p_{ik} p_{jl} + p_{il} p_{jk})$$

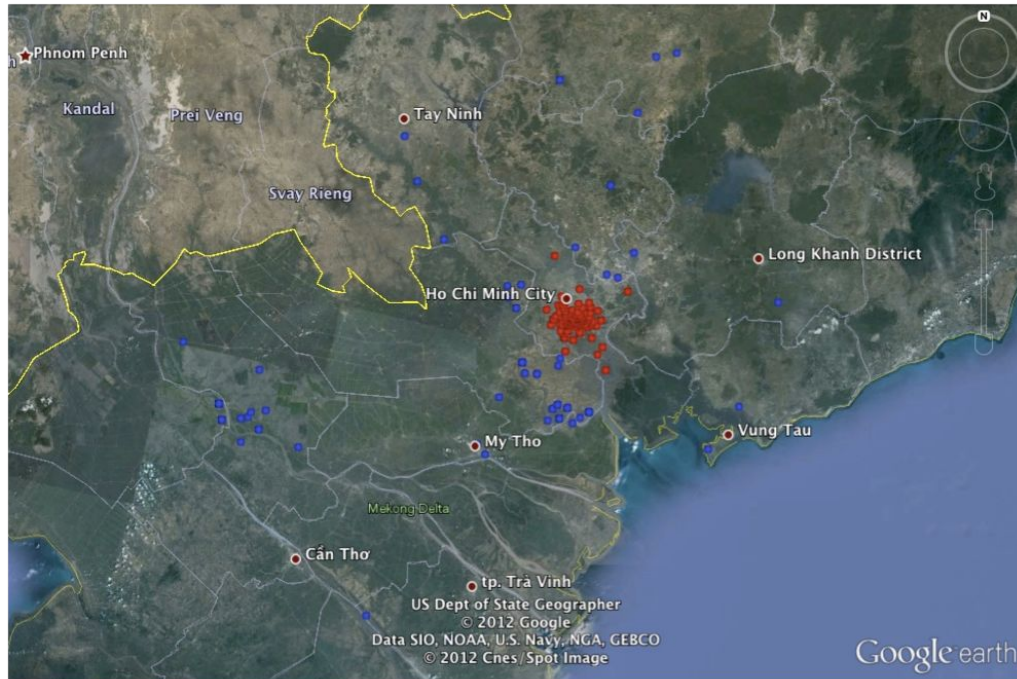
The Volz (2012) Structured Coalescent

Lineage state probabilities p_{ik} can then be tracked backwards in time using a system of master equations (ODEs) based on the transition rates g_{kl} :

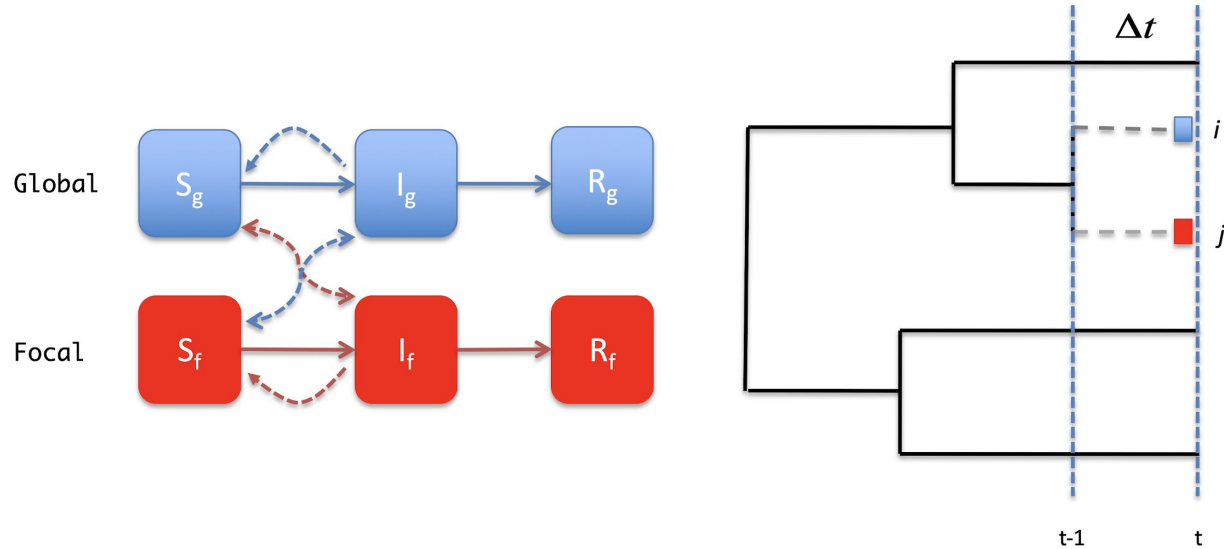
$$\frac{d}{dt}p_{ik} = \sum_k^m (p_{il}g_{kl} - p_{ik}g_{lk})$$

This assumes that the state of each lineage is completely independent of all other lineages. We'll revisit this assumption later!

Spatial structure



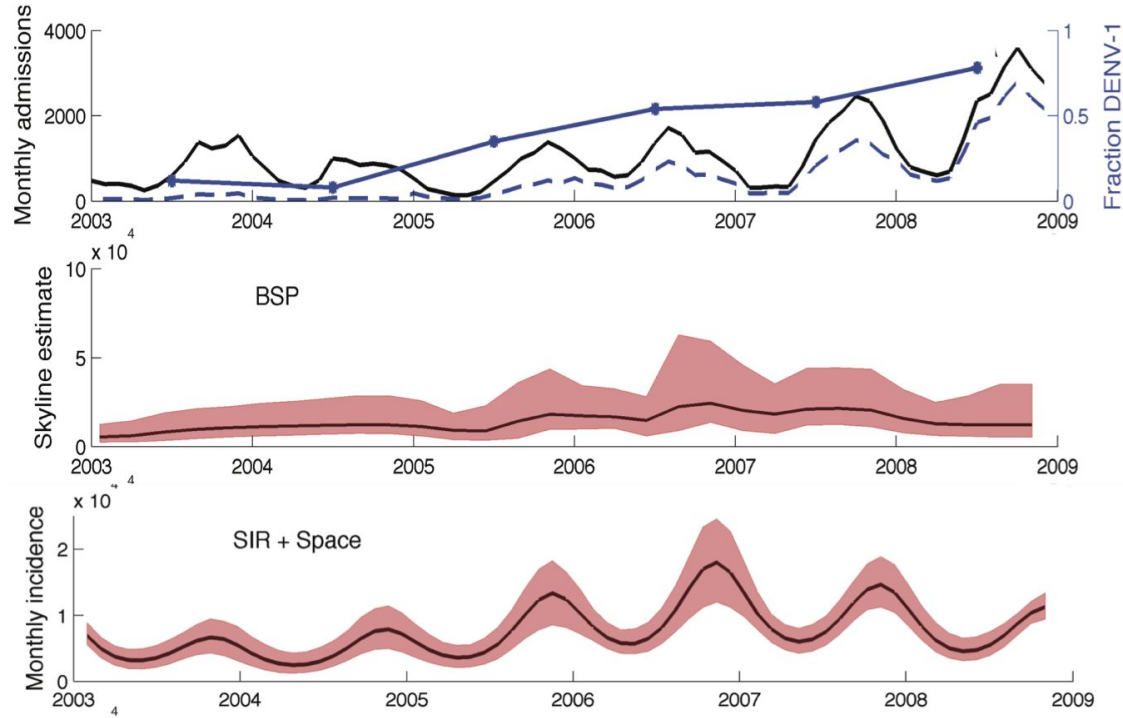
Spatial SIR model



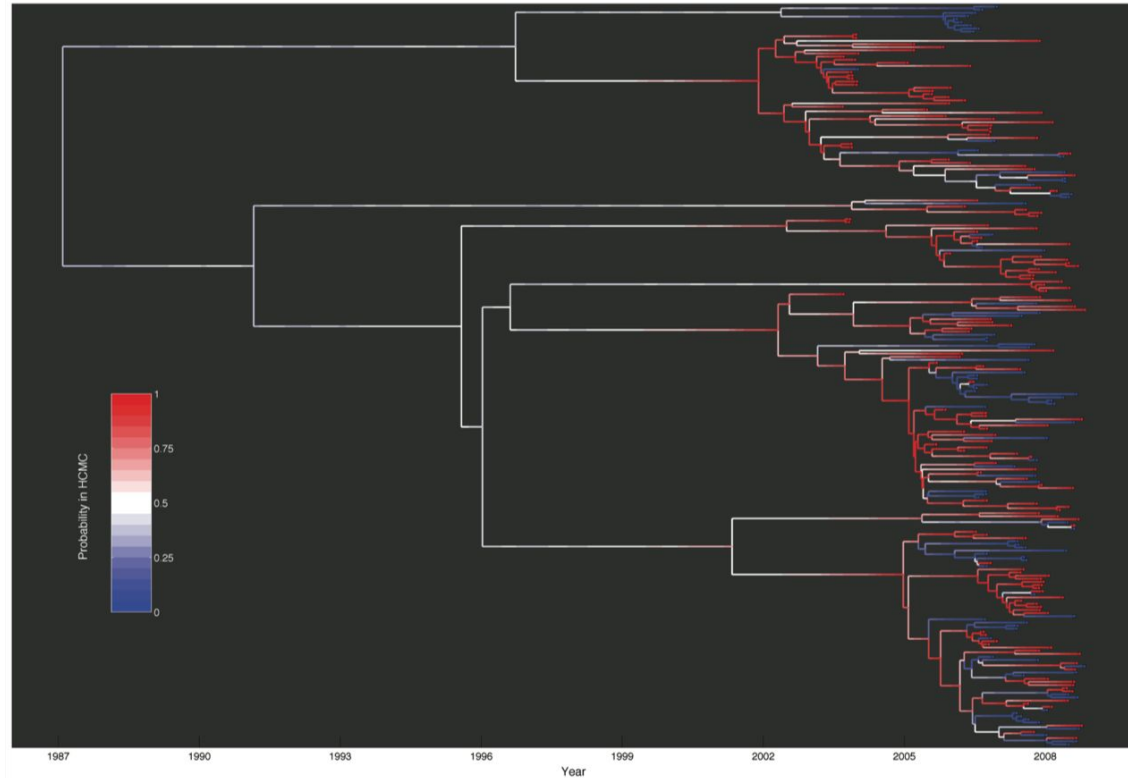
Structured coalescent
model:

$$\lambda_{ij} = \sum_k^m \sum_l^m \frac{\beta_{kl} \frac{S_l}{N_l} I_k}{I_k I_l} (p_{ik} p_{jl} + p_{il} p_{jk})$$

Estimates accounting for spatial structure



Movement of lineages



MASCOT

The MASCOT package for BEAST 2 implements a structured coalescent model that tracks lineage states probabilistically as in Volz (2012).

Uses an improved approximation to track lineage state probabilities

Allows for inference of pop sizes, migration rates and ancestral states

Can also use GLMs to predict migration rates based on explanatory variables

Conclusions

Coalescent models relate phylogenies of sampled lineages back to the larger demographic history of a population.

Coalescent methods can be used to reconstruct past population dynamics but other forces, especially population structure, also shape trees.

Structured coalescent models generalize coalescent models and are incredibly useful for modeling different forms of population structure.

SC models improve upon earlier discrete-trait phylogeographic methods but are less computationally efficient. Newer approaches like MASCOT that approximate lineage state probabilities offer a promising alternative.