# Phylogeography and structured populations

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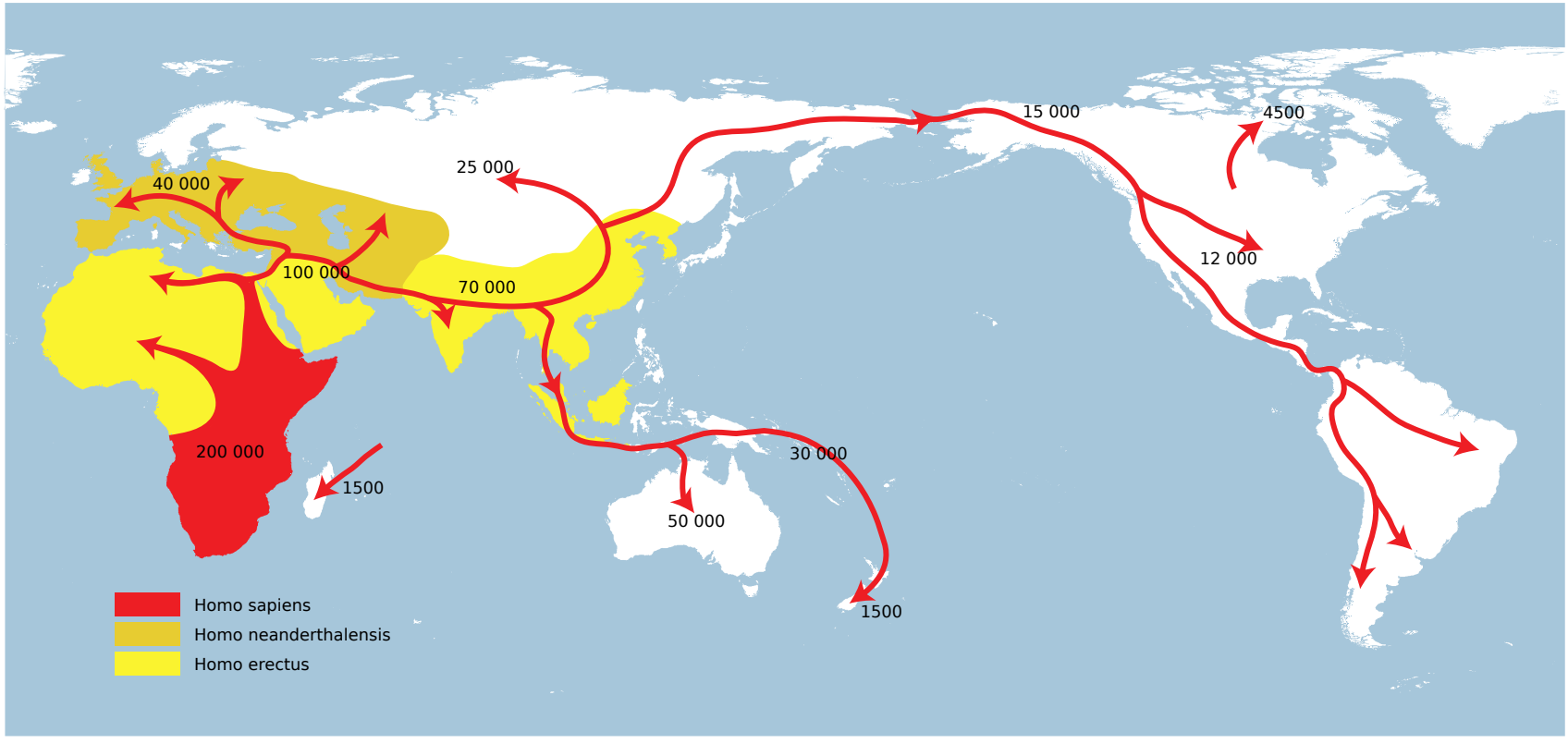
# What is Phylogeography?

Phylogeography is a field of study concerned with the principles and processes governing the geographic distributions of genealogical lineages, especially those within and among closely related species.

Avise (2000)

# What is Phylogeography?

Early human migrations:




Wikipedia

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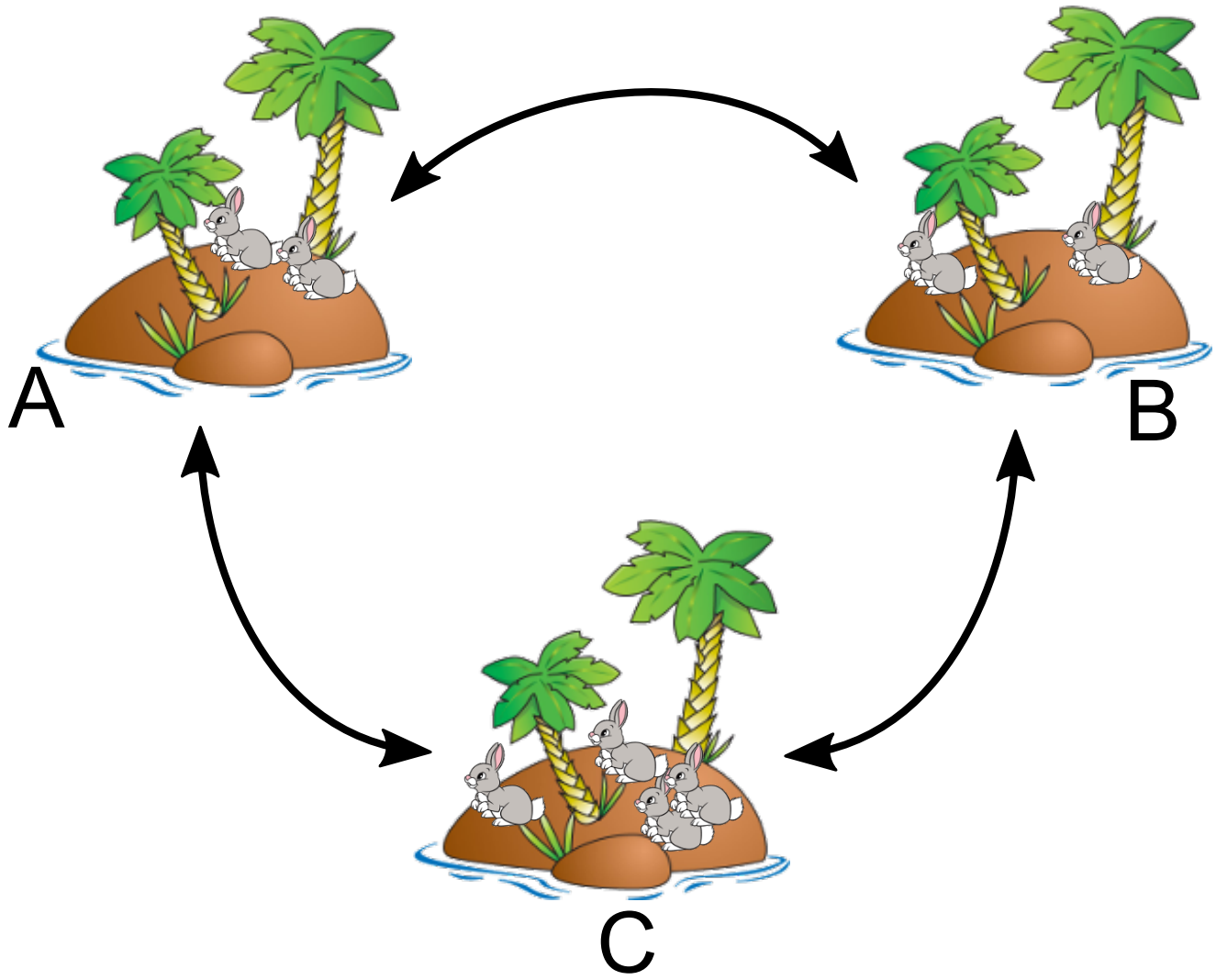
  - *et cetera!*

# Generalized island models and demes

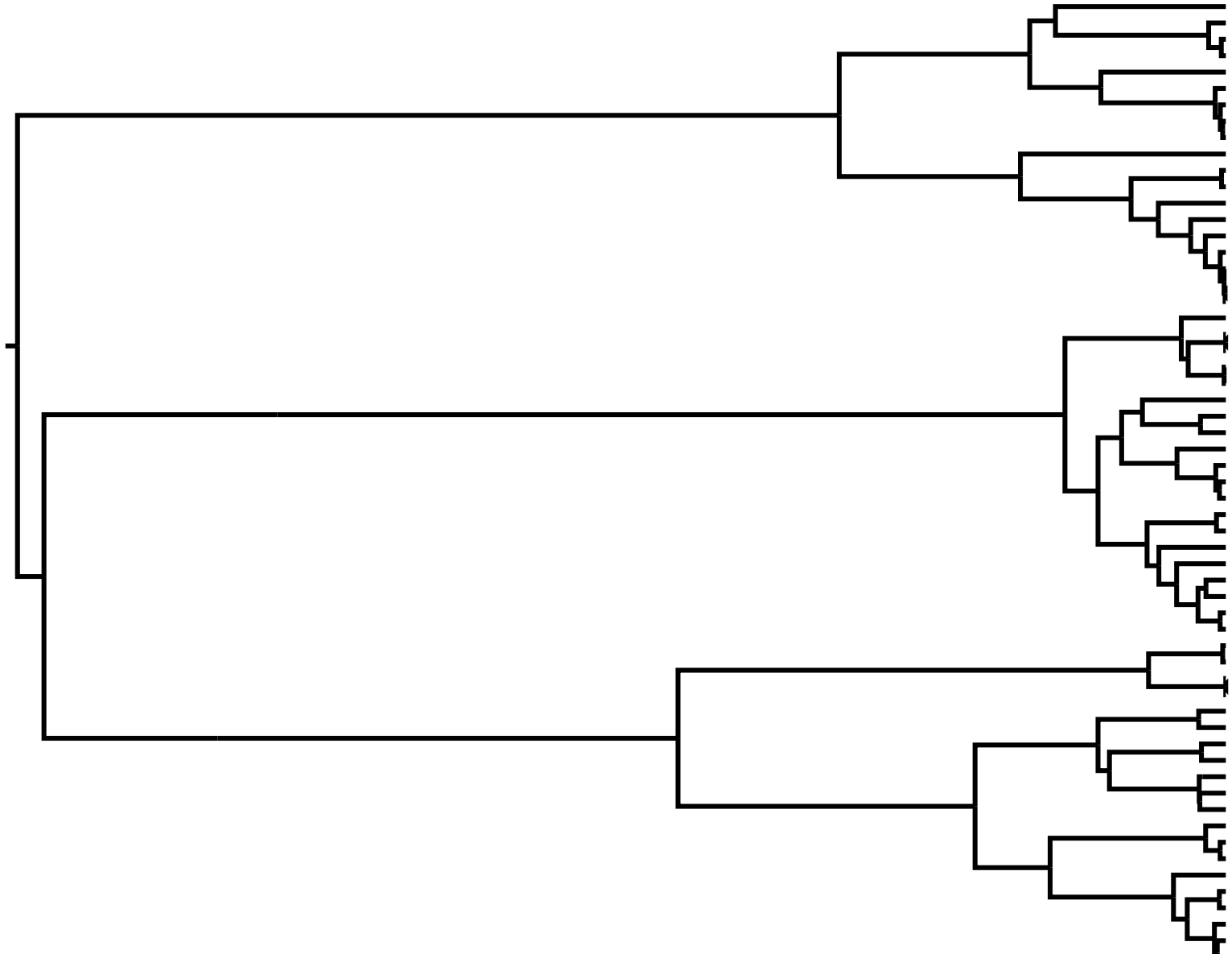
The island model is a common discrete model of spatial structure:




Locations are sometimes referred to as *demes*.

# Effect of population structure on trees

Population structure can have a very strong effect on the shape of the trees sampled from that population:

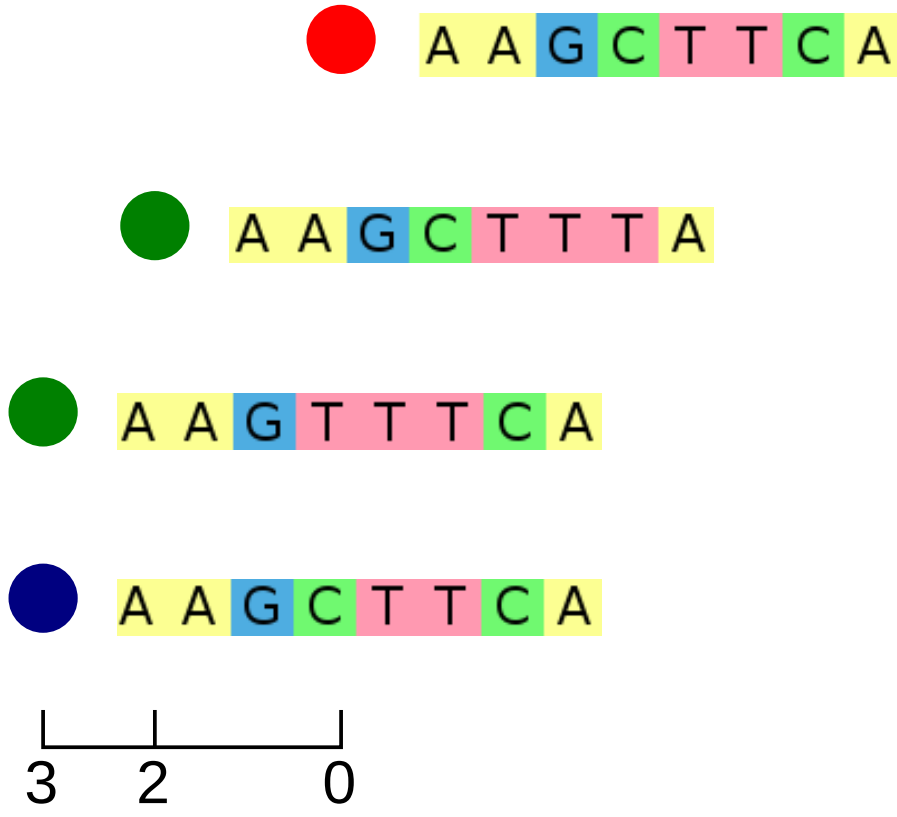


# Phylogeographic inference data

| Sample | Sequence | Location | Age/Time |
|---|---|---|---|
| 1 | A A G C T T C A | Place A | 0 |
| 2 | A A G C T T T A | Place B | 2 |
| 3 | A A G T T T C A | Place B | 3 |
| 4 | A A G C T T C A | Place C | 3 |

# Phylogeographic inference questions

Common questions include:



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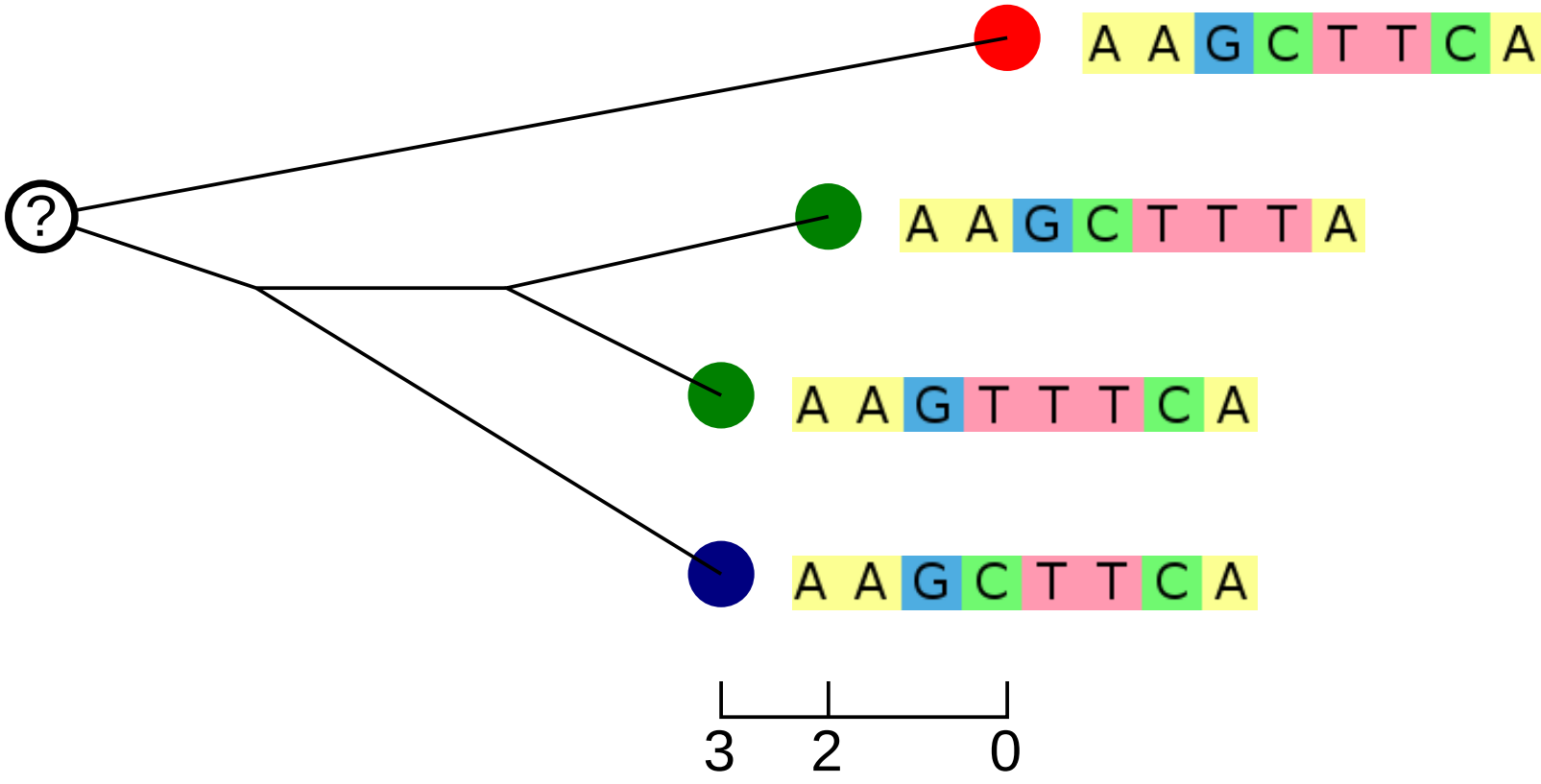

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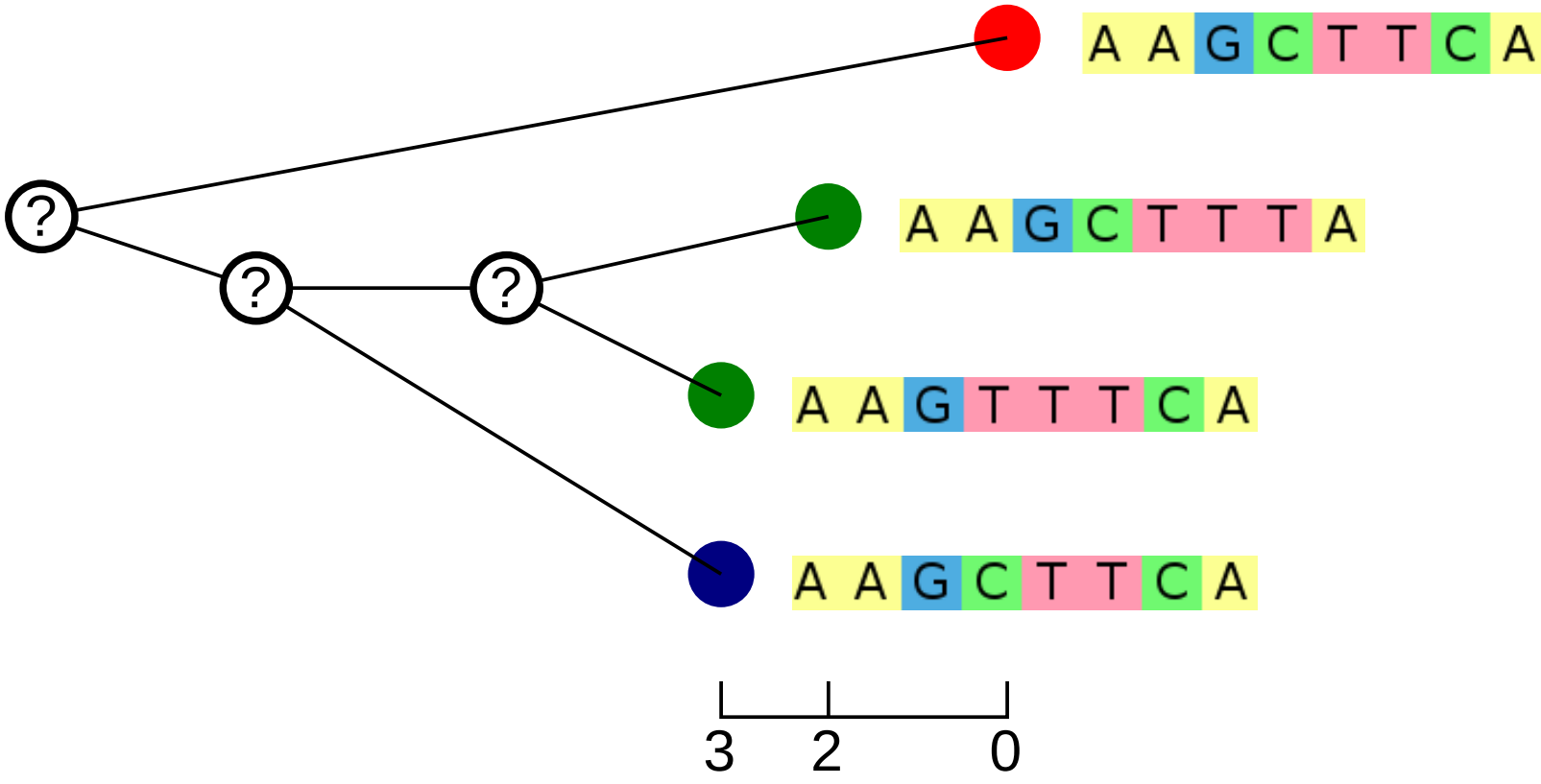

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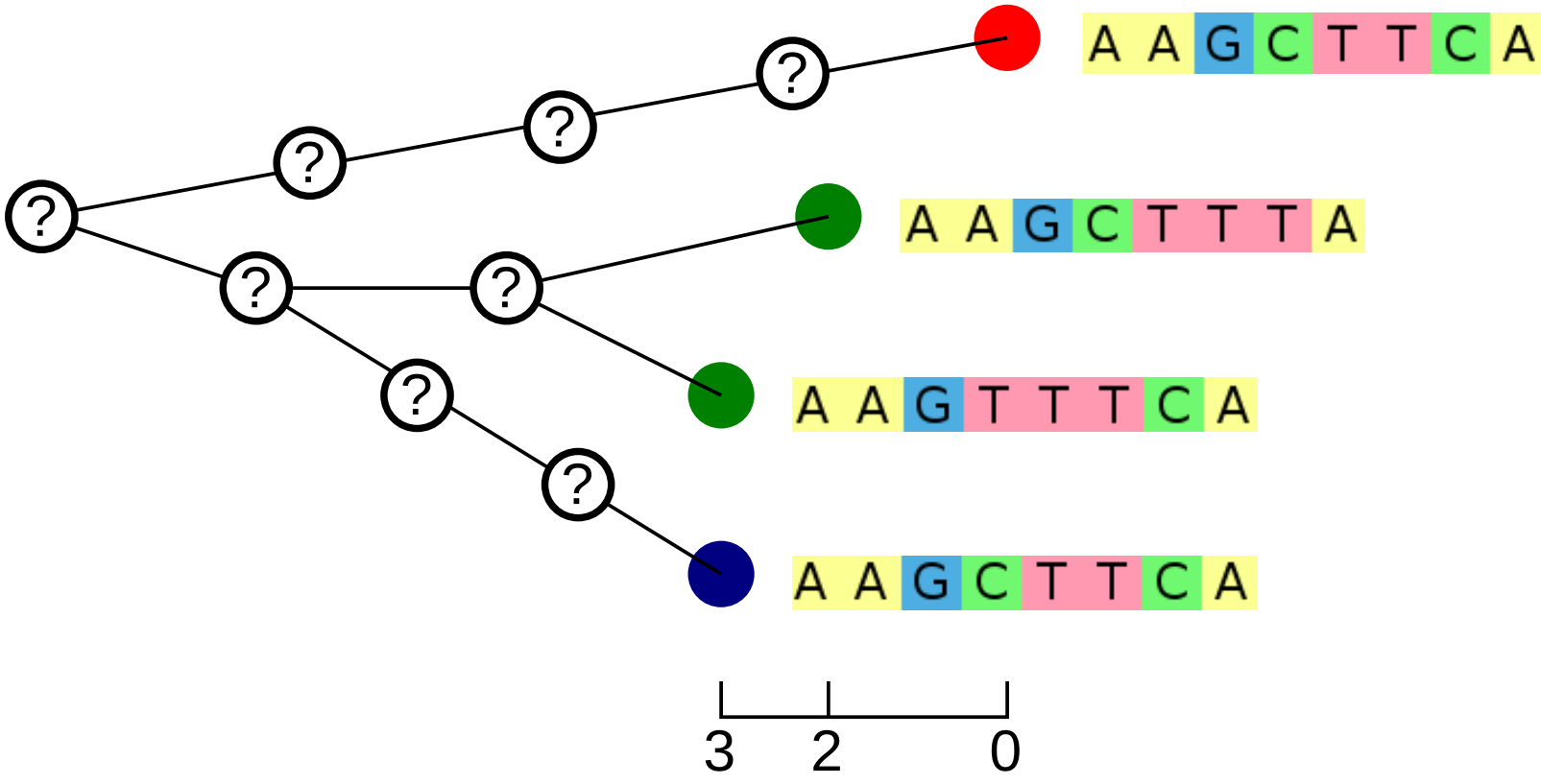

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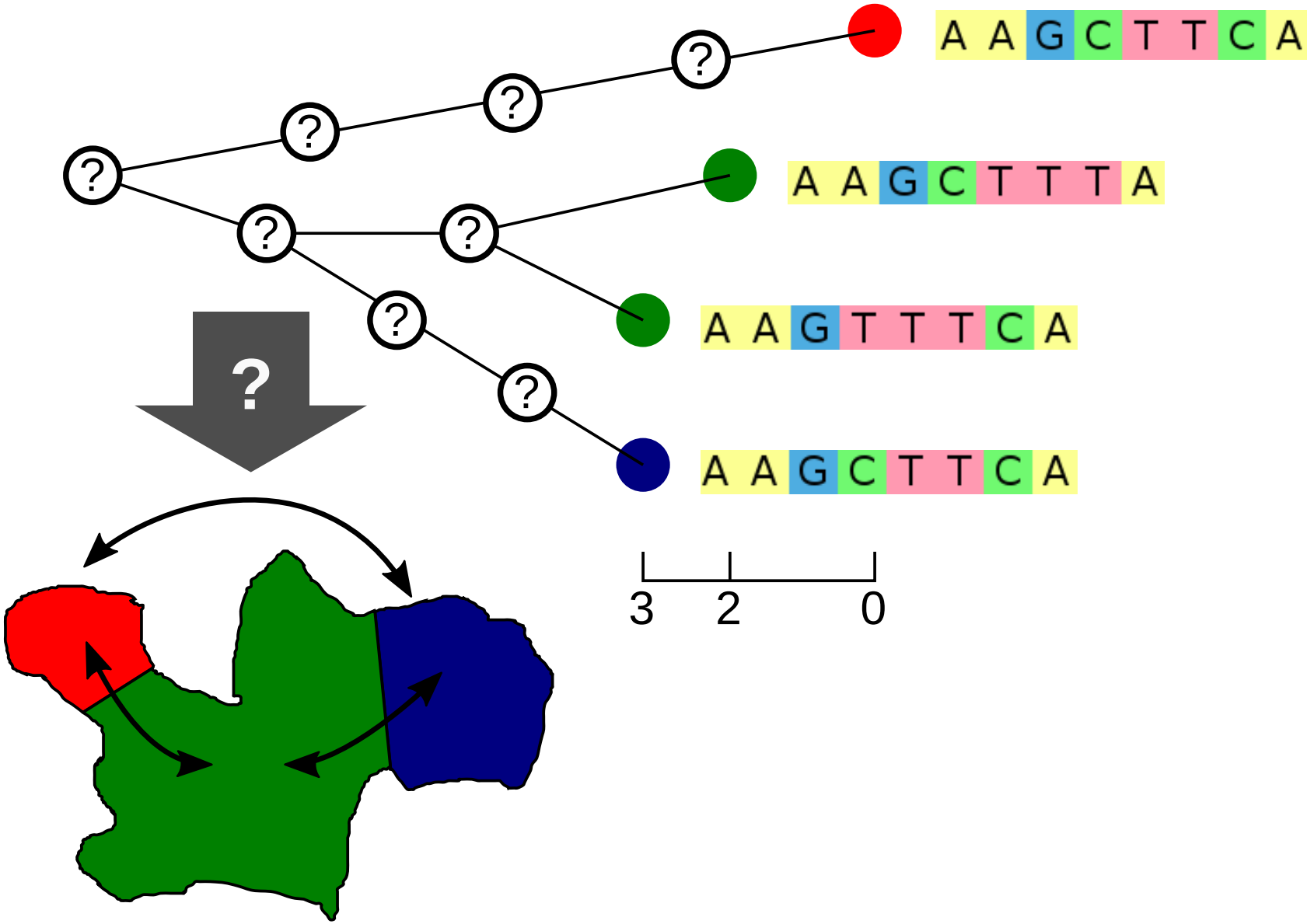

# Bayesian Phylogeographic Inference?

The usual phylogenetic posterior is:

$$P(T, \mu, \theta|A) = \frac{1}{P(A)} P(A|T, \mu) P(T|\theta) P(\mu) P(\theta)$$

where

$P(A|T, \mu)$ is a the *tree likelihood*,

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Where does geography fit in?

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- **Mugration models (also Discrete Trait Analysis):**
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- **Structured population models:**
  - Given sequences and locations, what is the probability of the tree?
  - Currently mostly discrete.
  - Many extend the structured coalescent framework of Hudson (1990) and Notohara (1990).
  - Others extend the birth-death-sampling framekwork of Stadler (2010).

# Part I

## Mugration models

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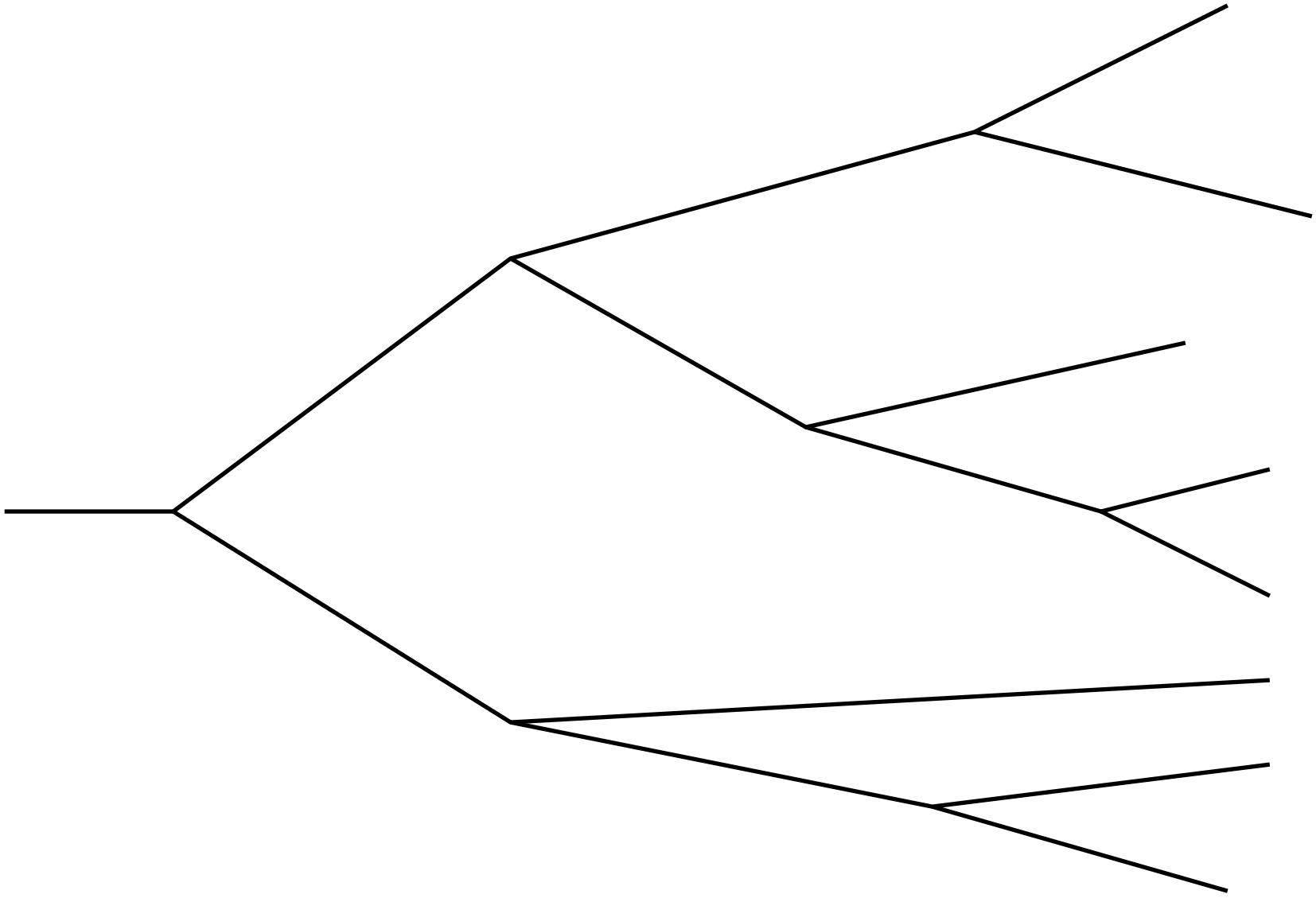

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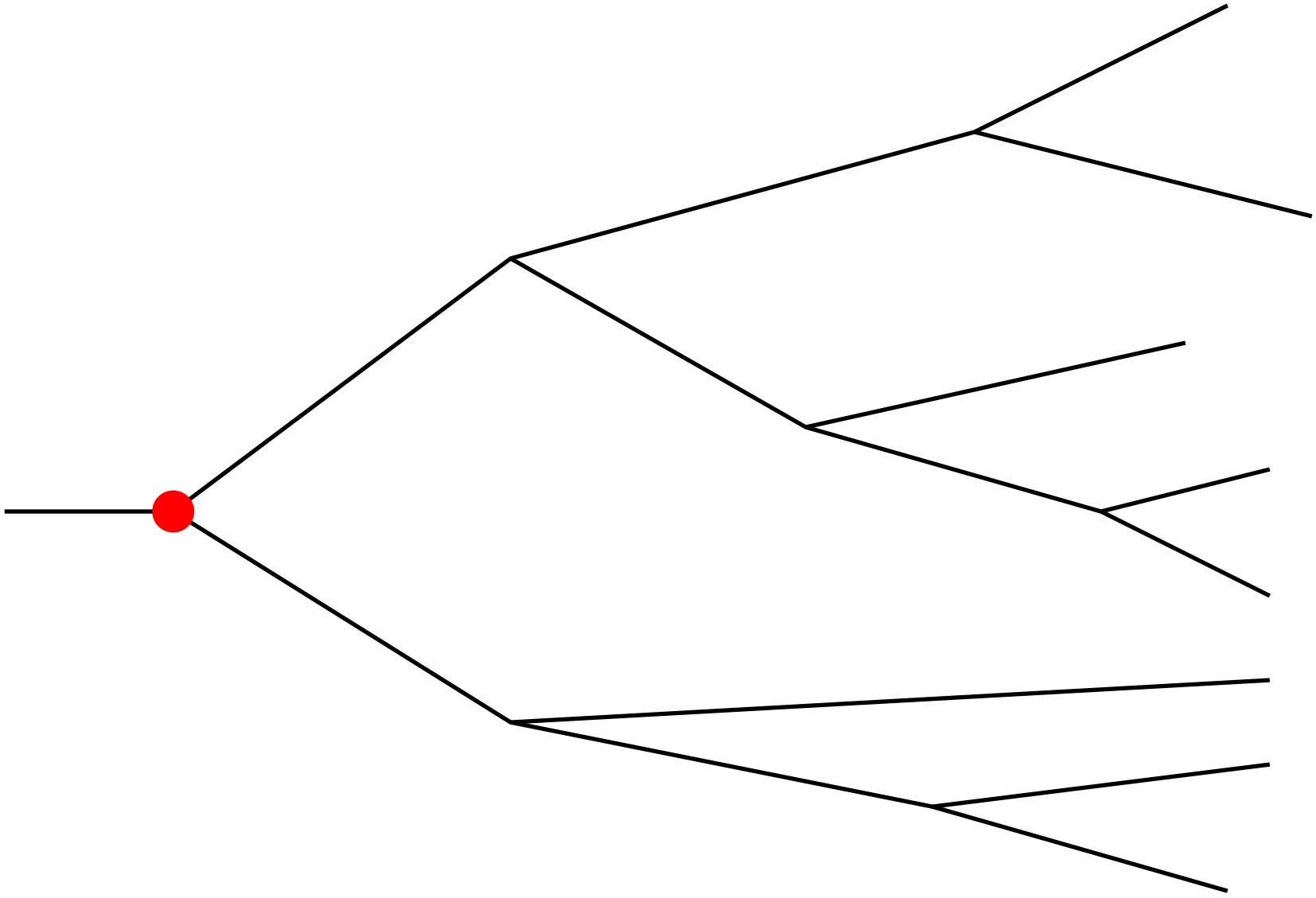

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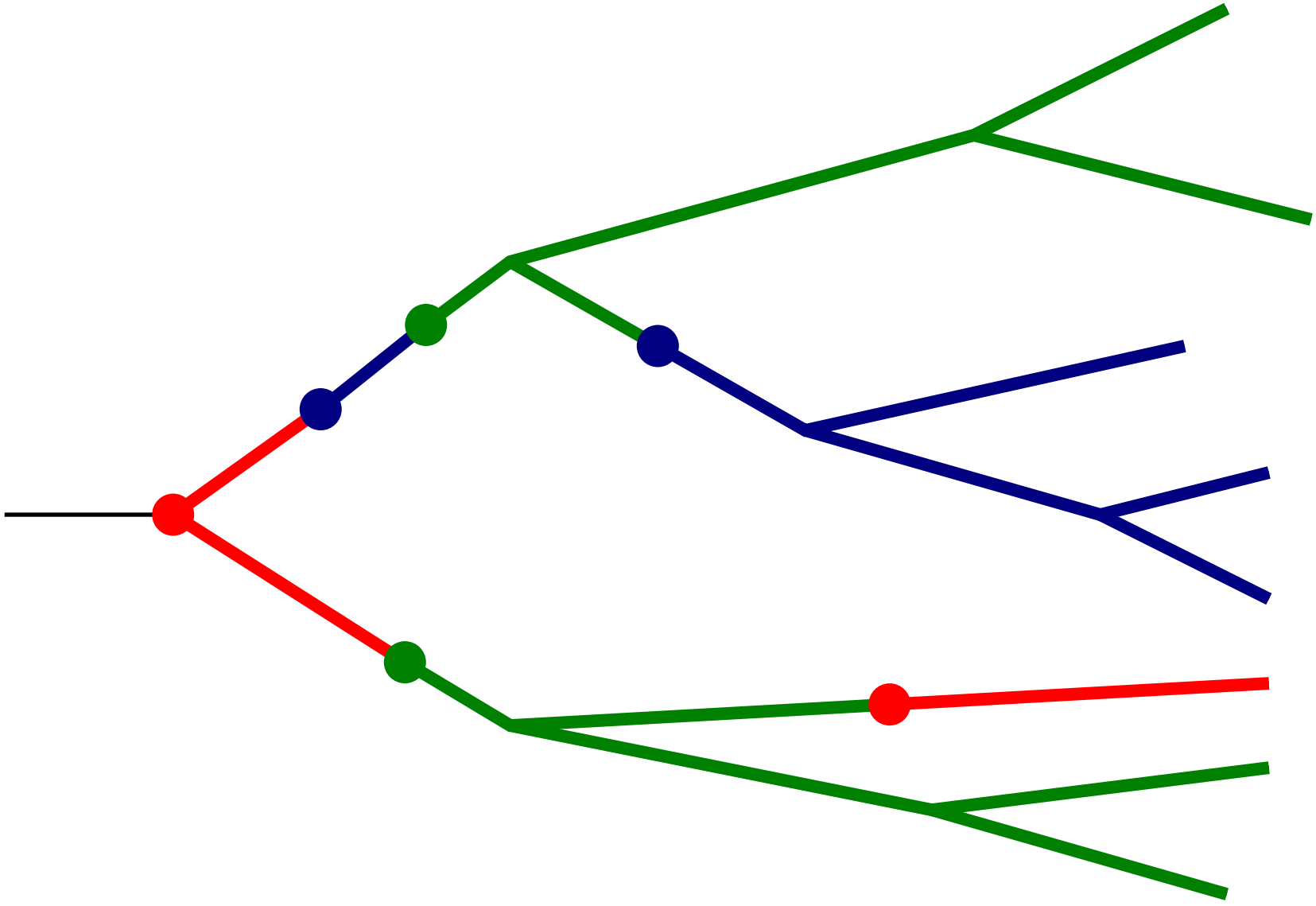

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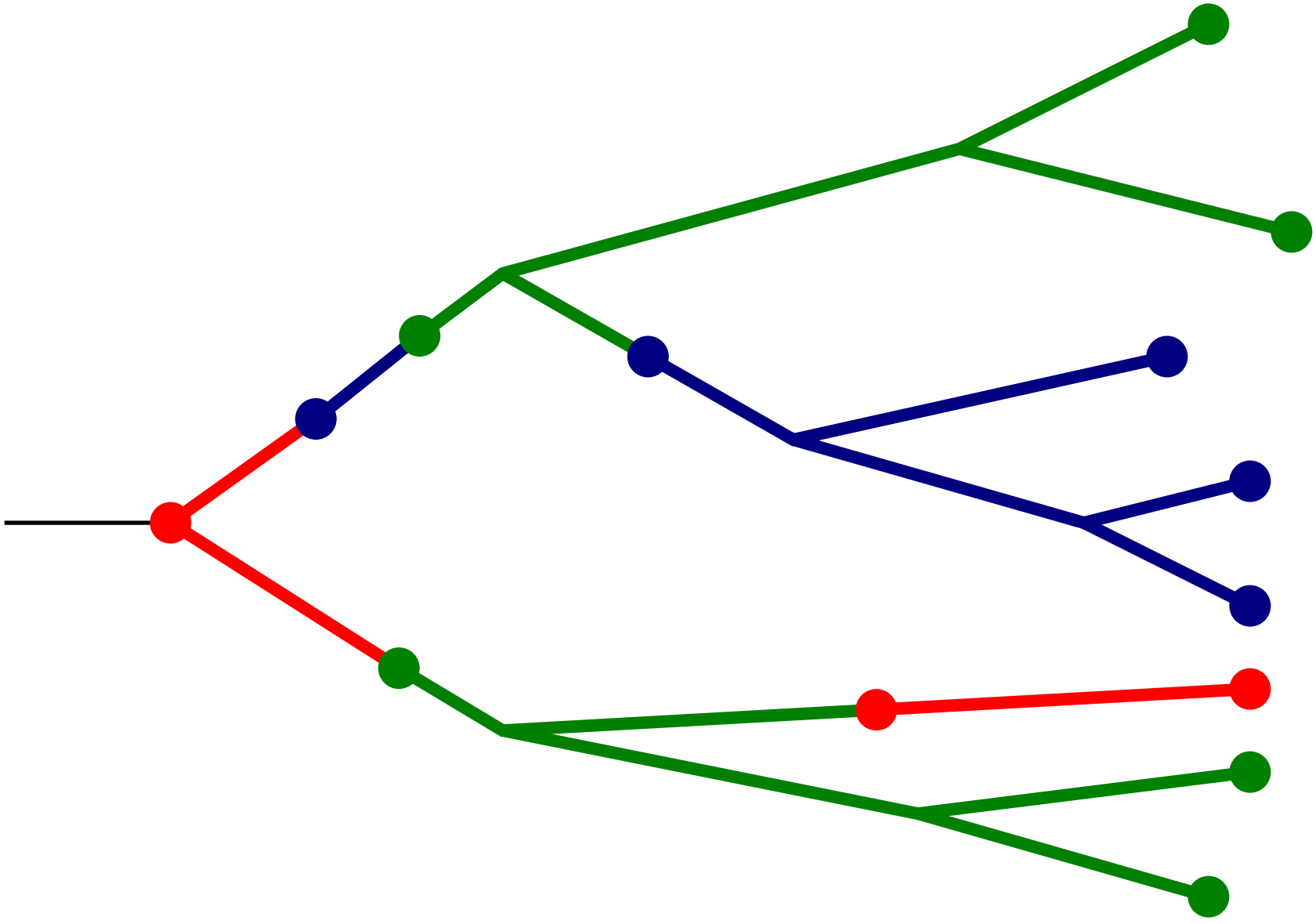

# Mugration Inference: Modified tree likelihood

The standard phylogenetic posterior is modified:

$$P(T, \mu, \theta|A, L) = \frac{1}{P(A, L)} P(A|T, \mu) P(L|T, M) \times P(T|\theta) P(\mu) P(M) P(\theta)$$

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Notice the similarity between the two likelihood terms.

**Mugration models treat location as just another trait/character.**

# Mugration transition matrix

The matrix $\mathrm{M}$ is often assumed to be symmetric and thus describe a reversible process. In exact analogy to the GTR model of nucleotide evolution, we can expand:

$$\mathrm{M} = \mathfrak{m}\mathrm{S}\Pi \tag{1}$$

where

- $\mathfrak{m}$ is the average overall transition rate,
- $\mathrm{S}$ is the normalized transition rate matrix, and
- $\Pi$ is a diagonal matrix containing the equilibrium probabilities for each location in the long term.

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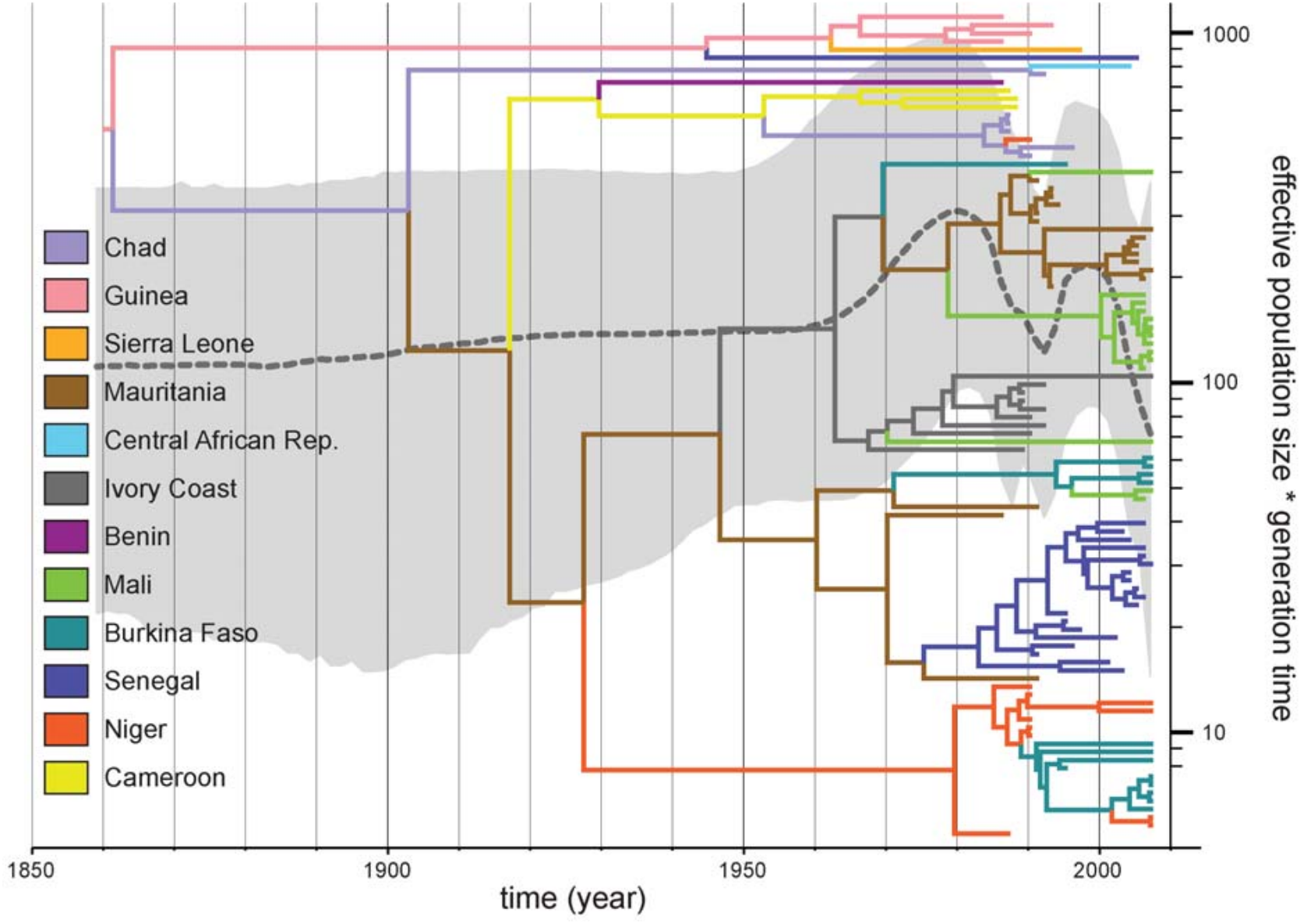
- Mugration models use sample location as data.
- Just as for genetic data, non-random sampling procedures will **bias results**.
- This isn't a property of the generative model, just the way it is conditioned. (Conditioning on sampling location would prevent the use of regular unstructured tree priors.)




Analysis of "Africa 2" rabies virus, Lemey et al. (2009)

# Part II

## Structured coalescent models

# Wright-Fisher model

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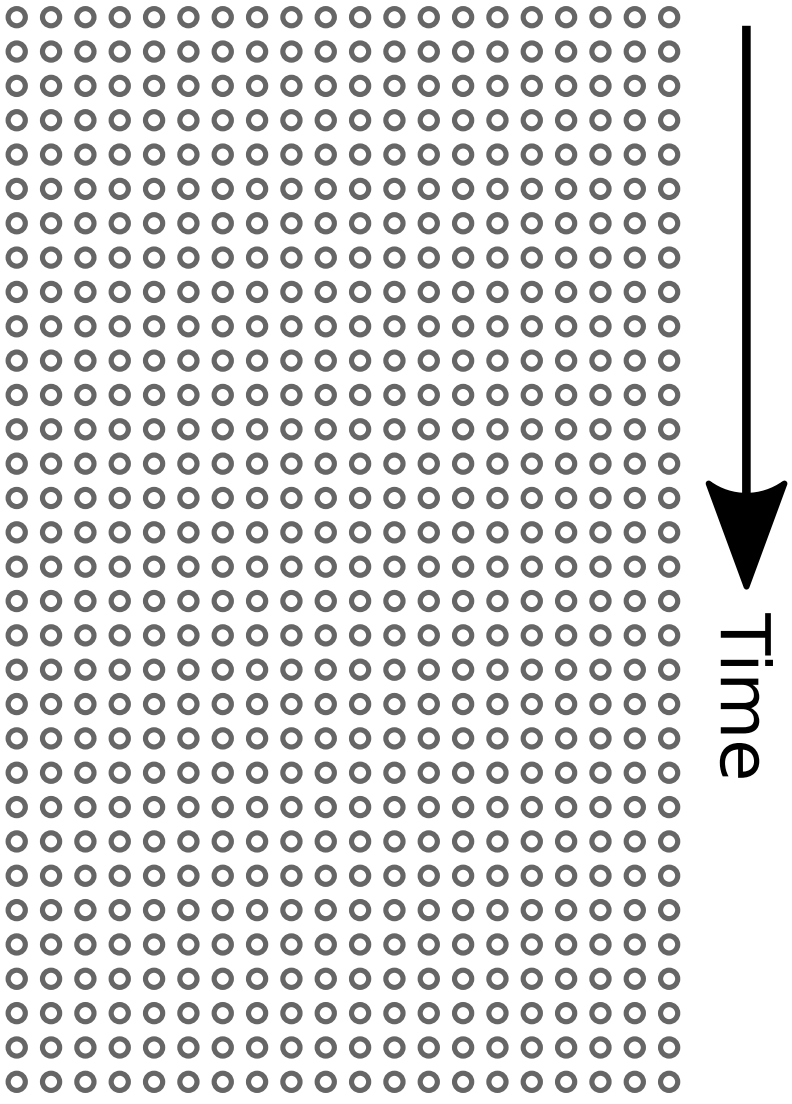

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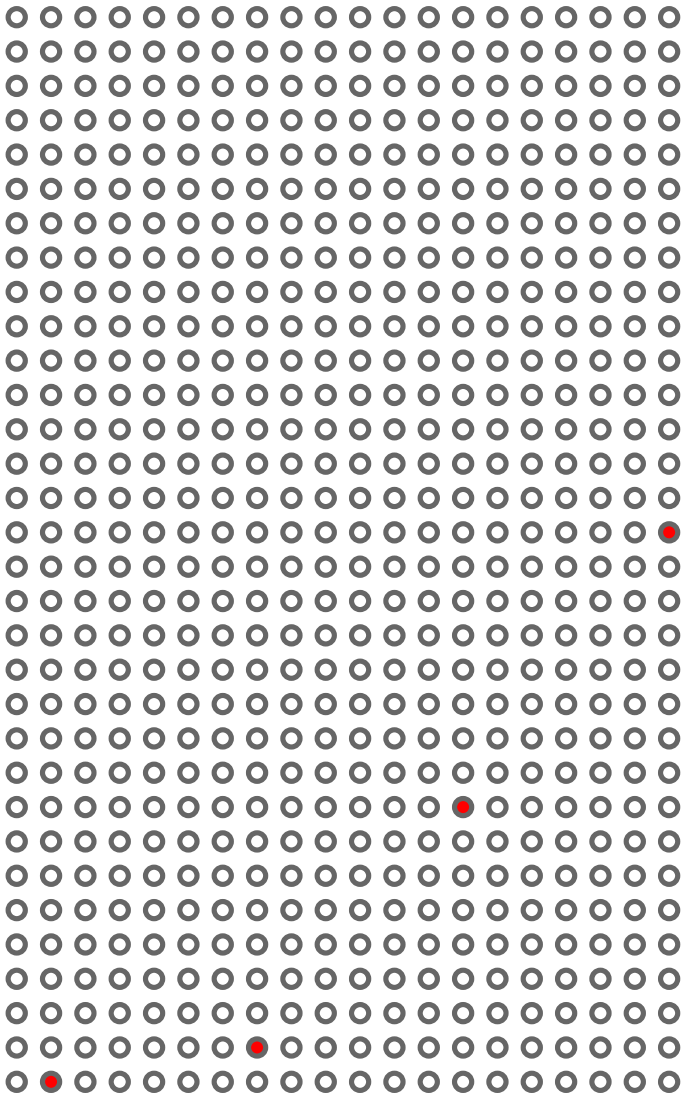

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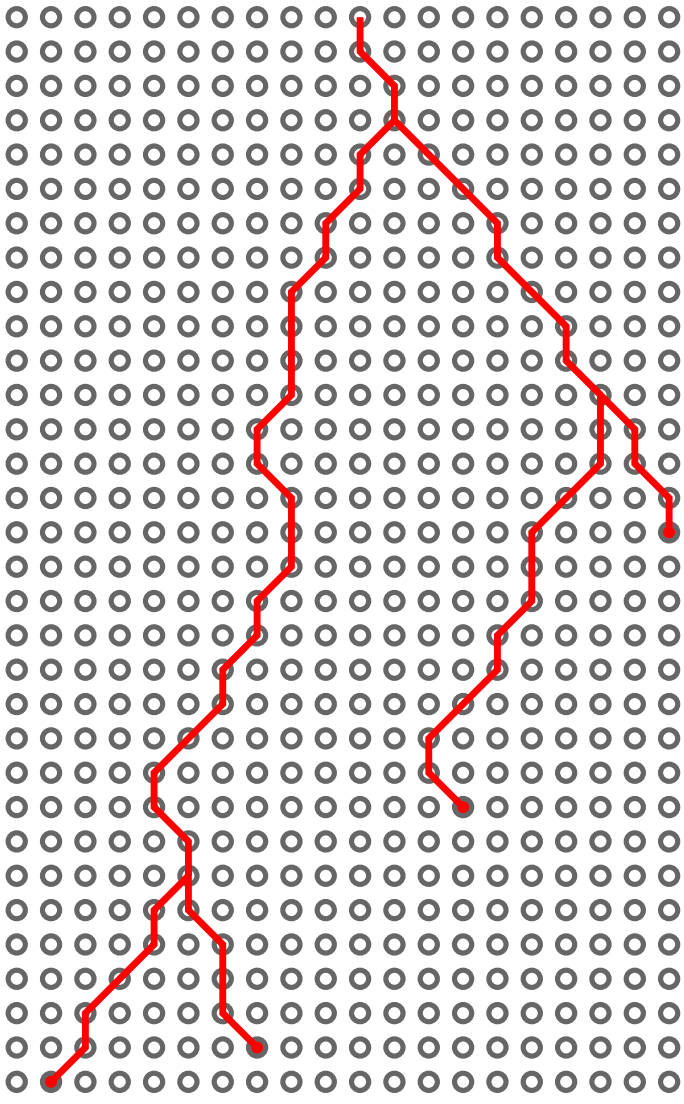

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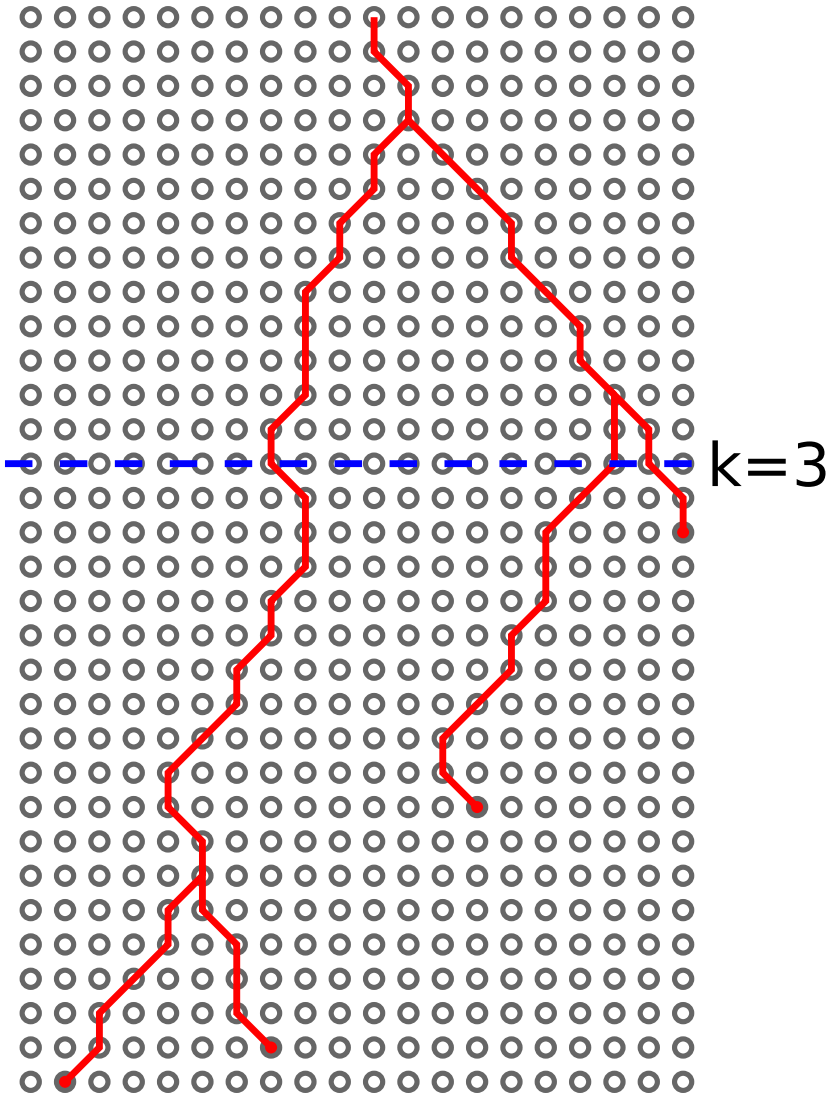
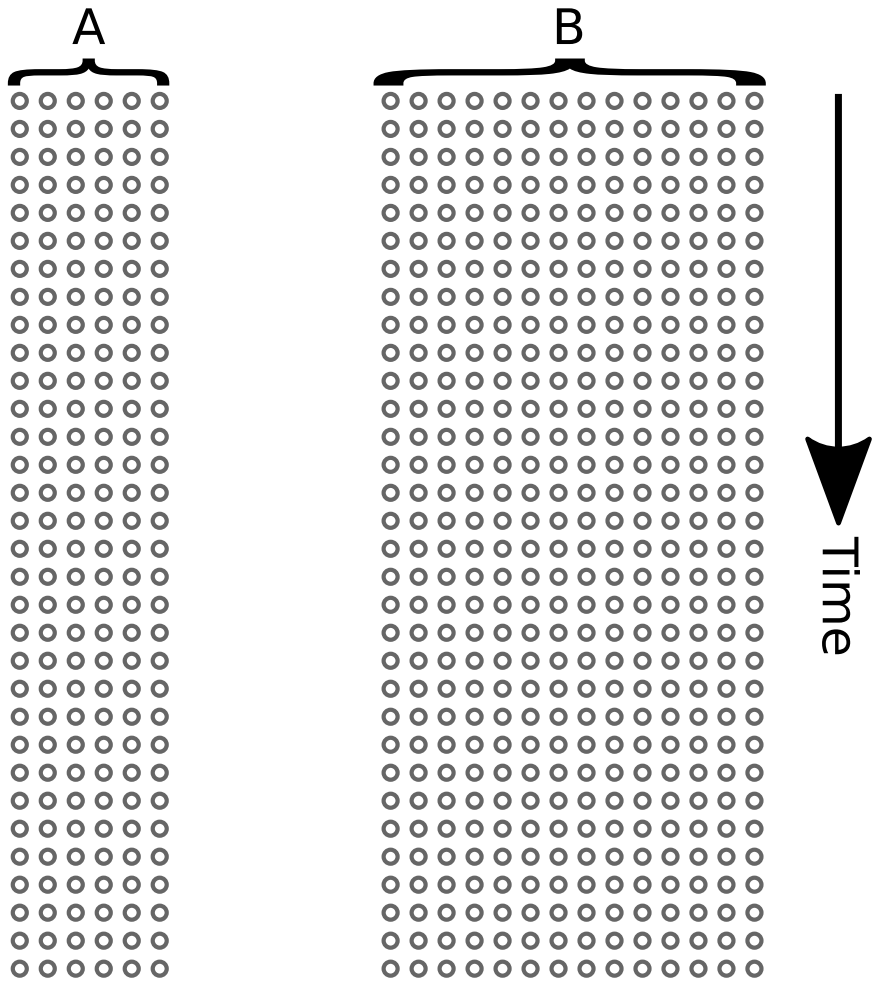



Probability of coalescence per generation:

$$\sim \binom{k}{2} \frac{1}{N}$$

# Partitioned Wright-Fisher model



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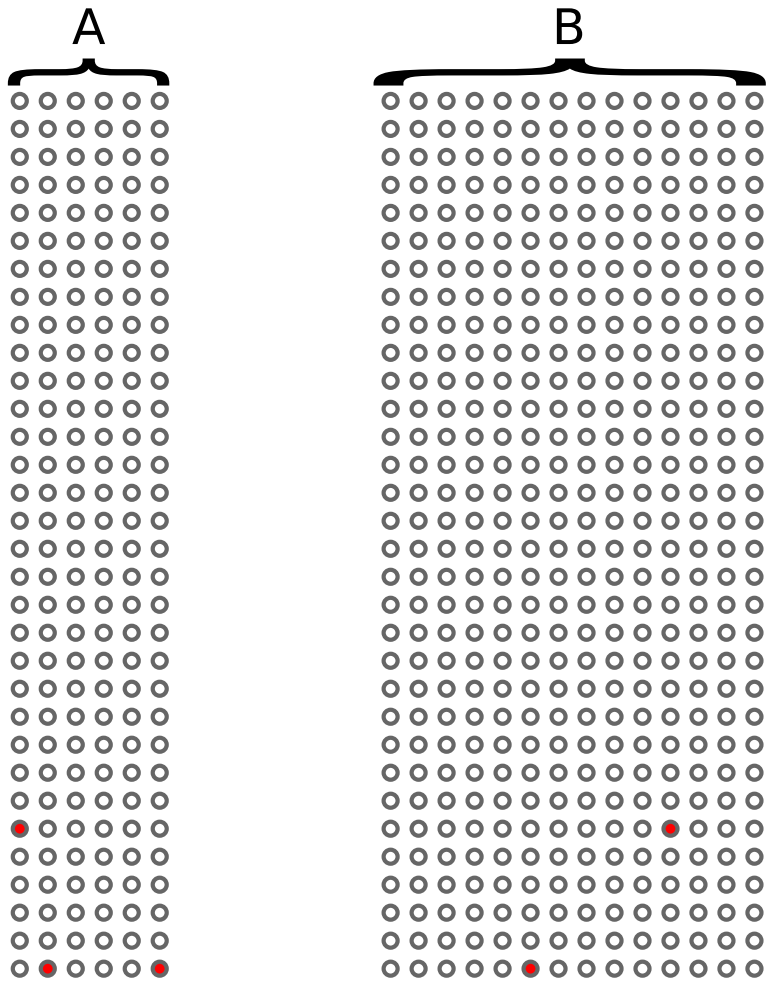

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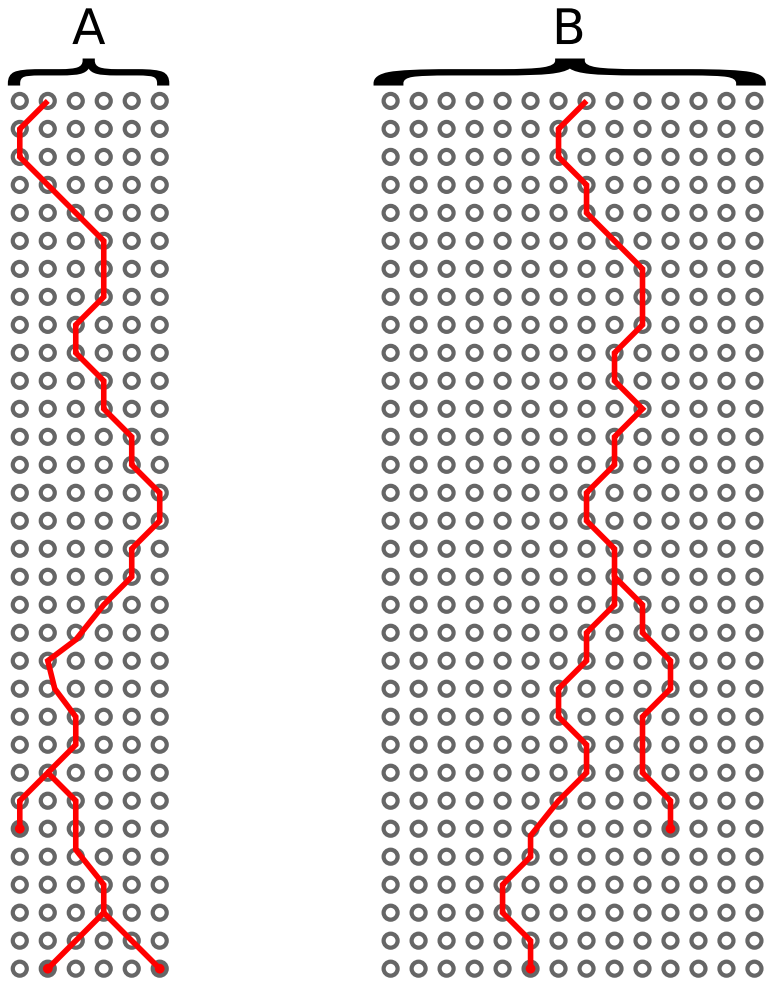

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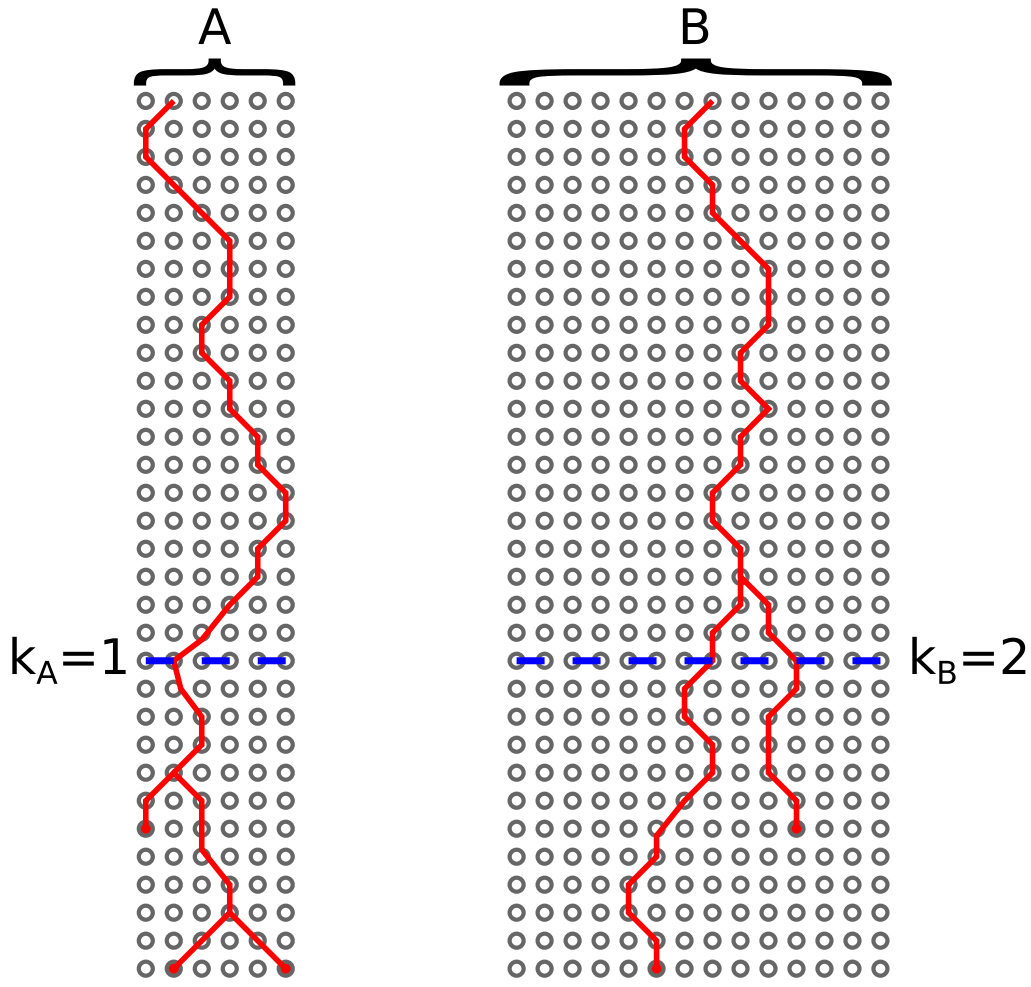


Probability of coalescence per generation in A:

$$\binom{k_A}{2}\frac{1}{N_A}$$

Probability of coalescence per generation in B:

$$\binom{k_B}{2}\frac{1}{N_B}$$

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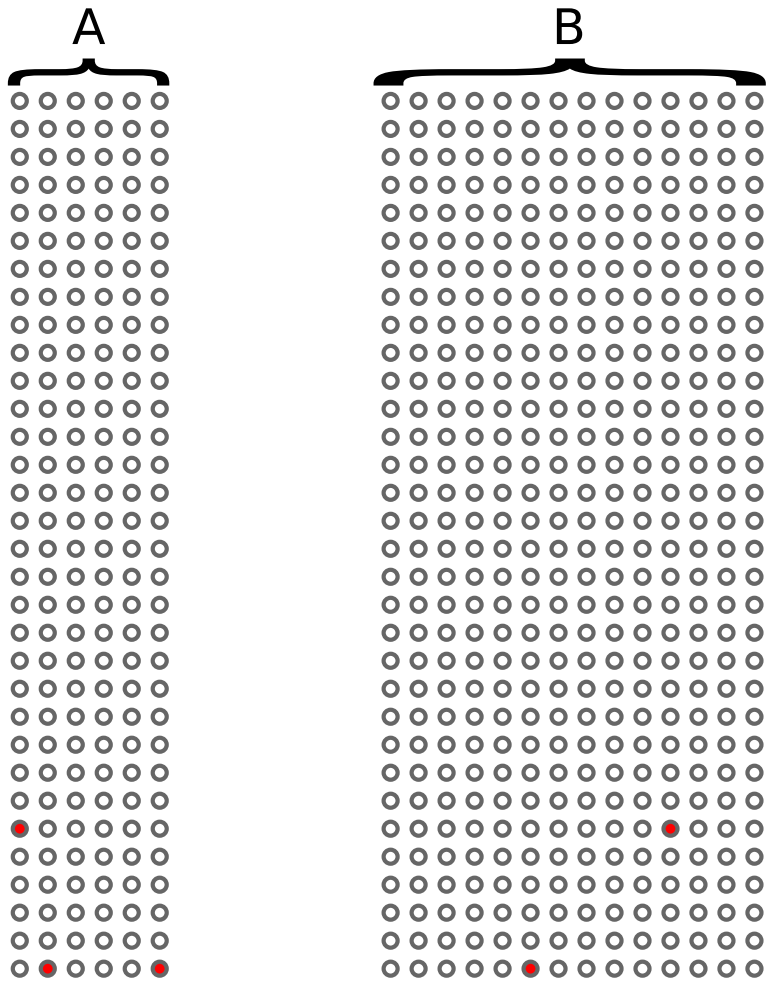

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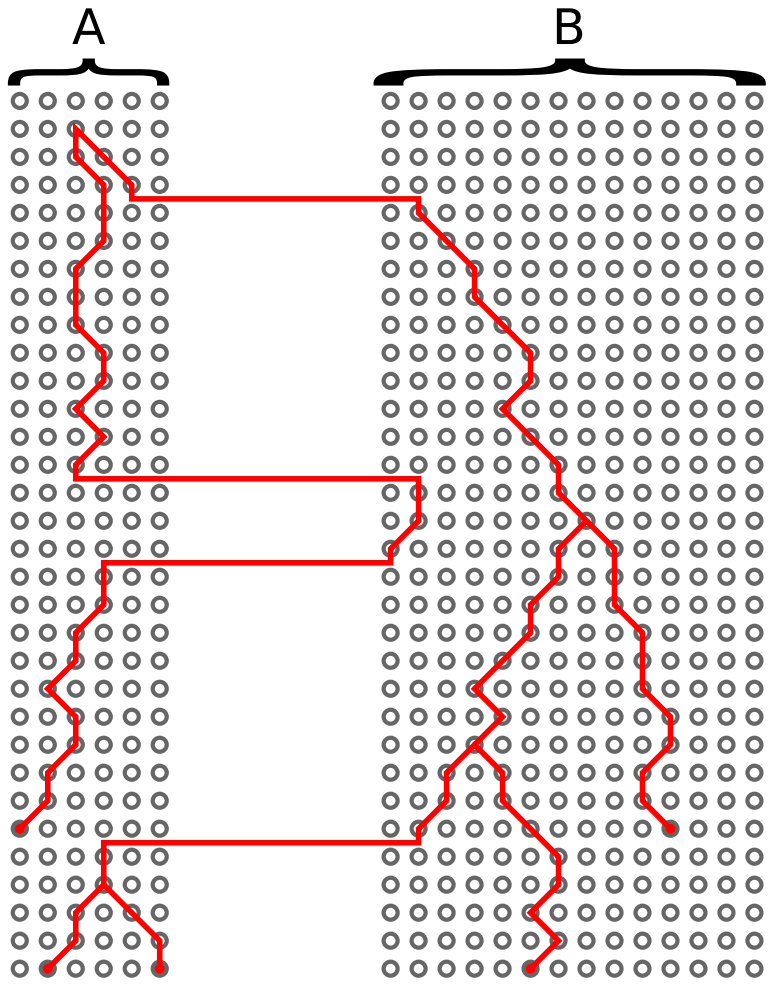

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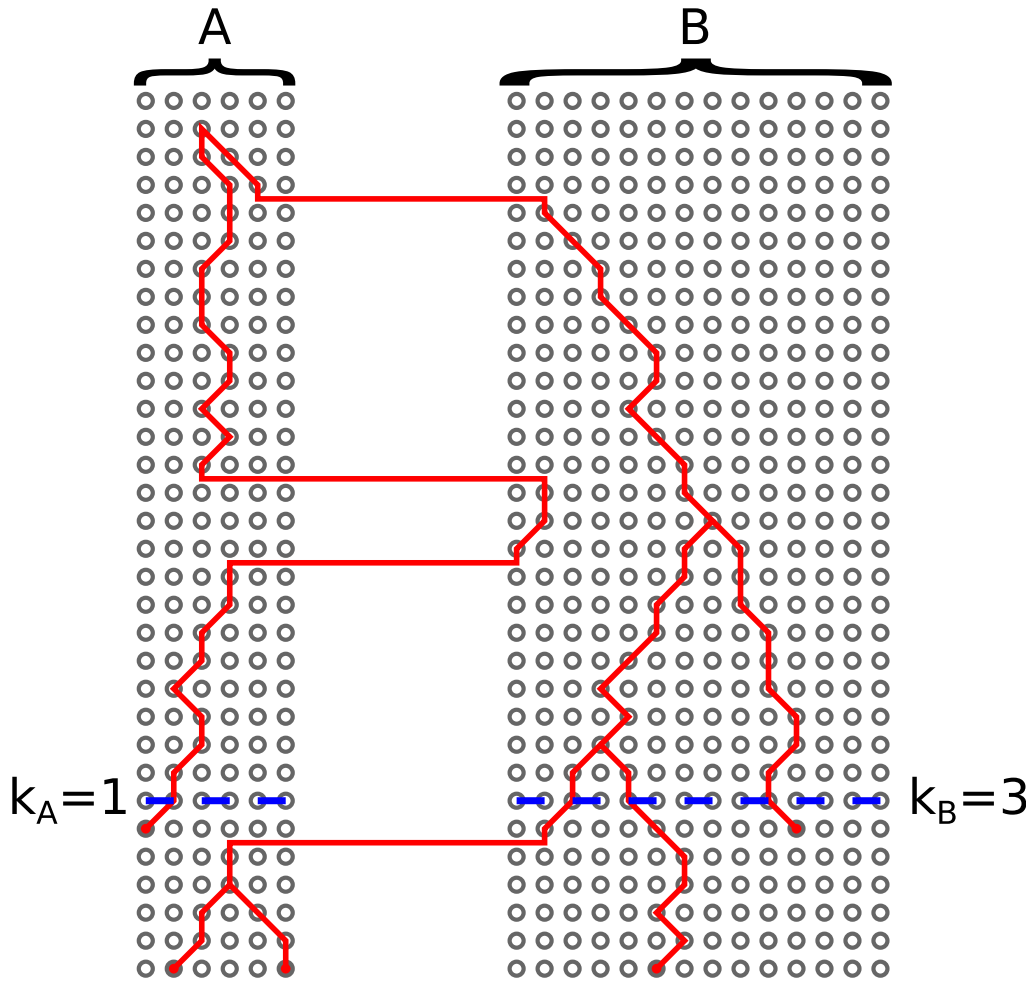


Probability of migration from $A \rightarrow B$ per individual in $A$:

$$q_{AB}$$

Probability of single lineage migration from $B \rightarrow A$ (**backward time**):

$$m_{BA} = q_{AB} \frac{N_A}{N_B}$$

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Backwards-in-time Markov process that generates both the sampled tree and ancestral locations.
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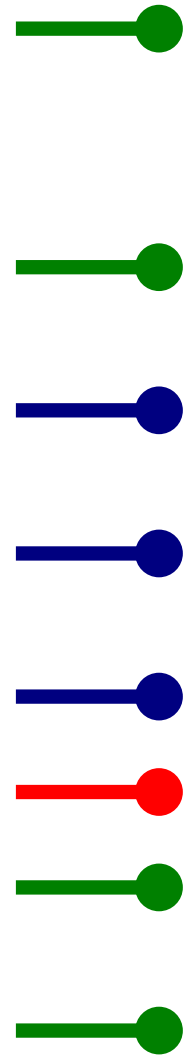

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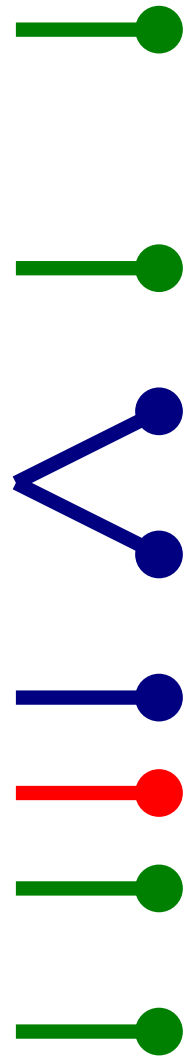

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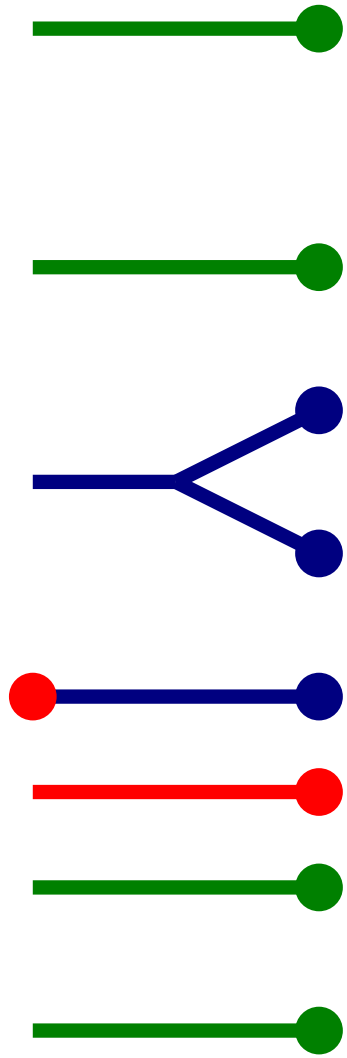

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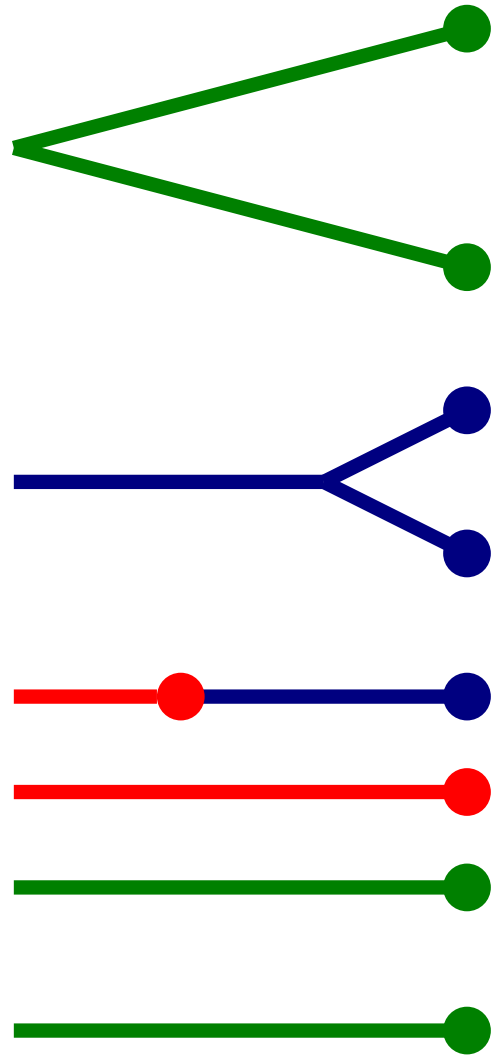

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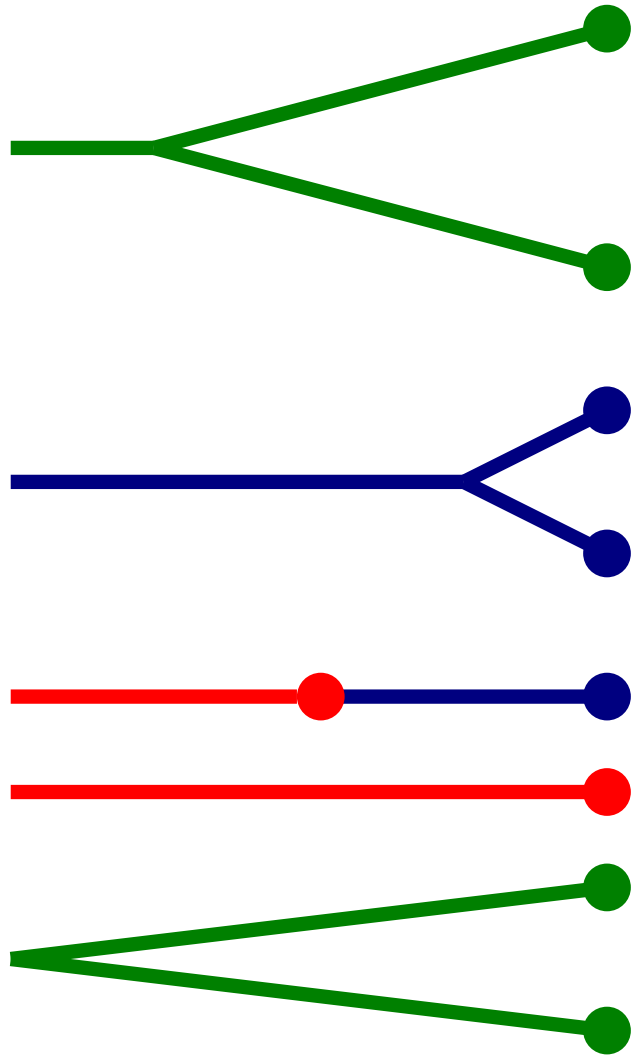

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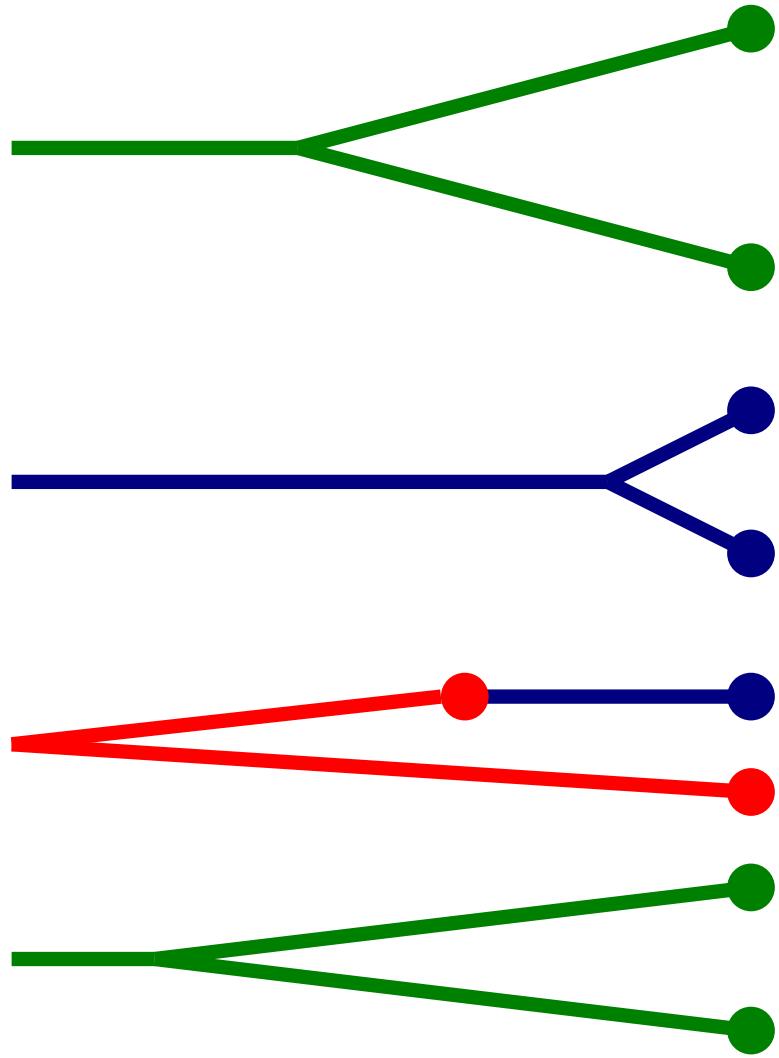

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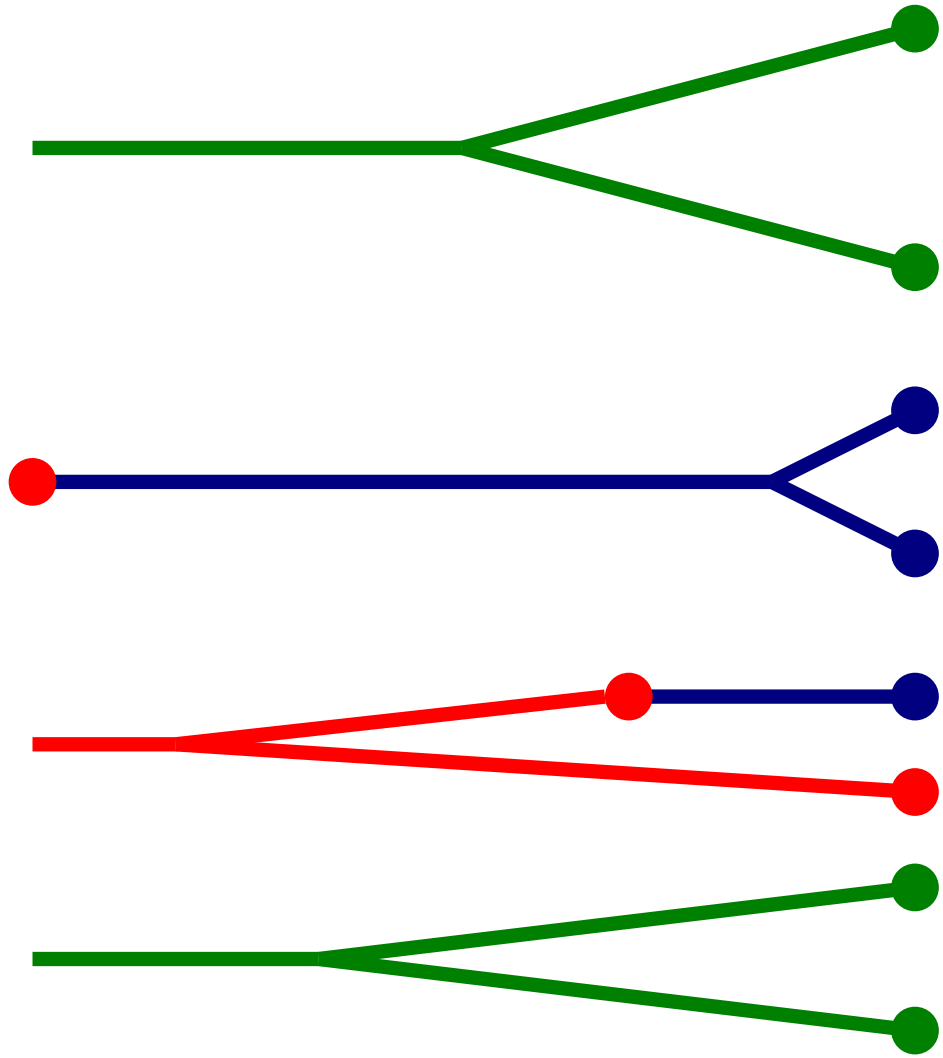

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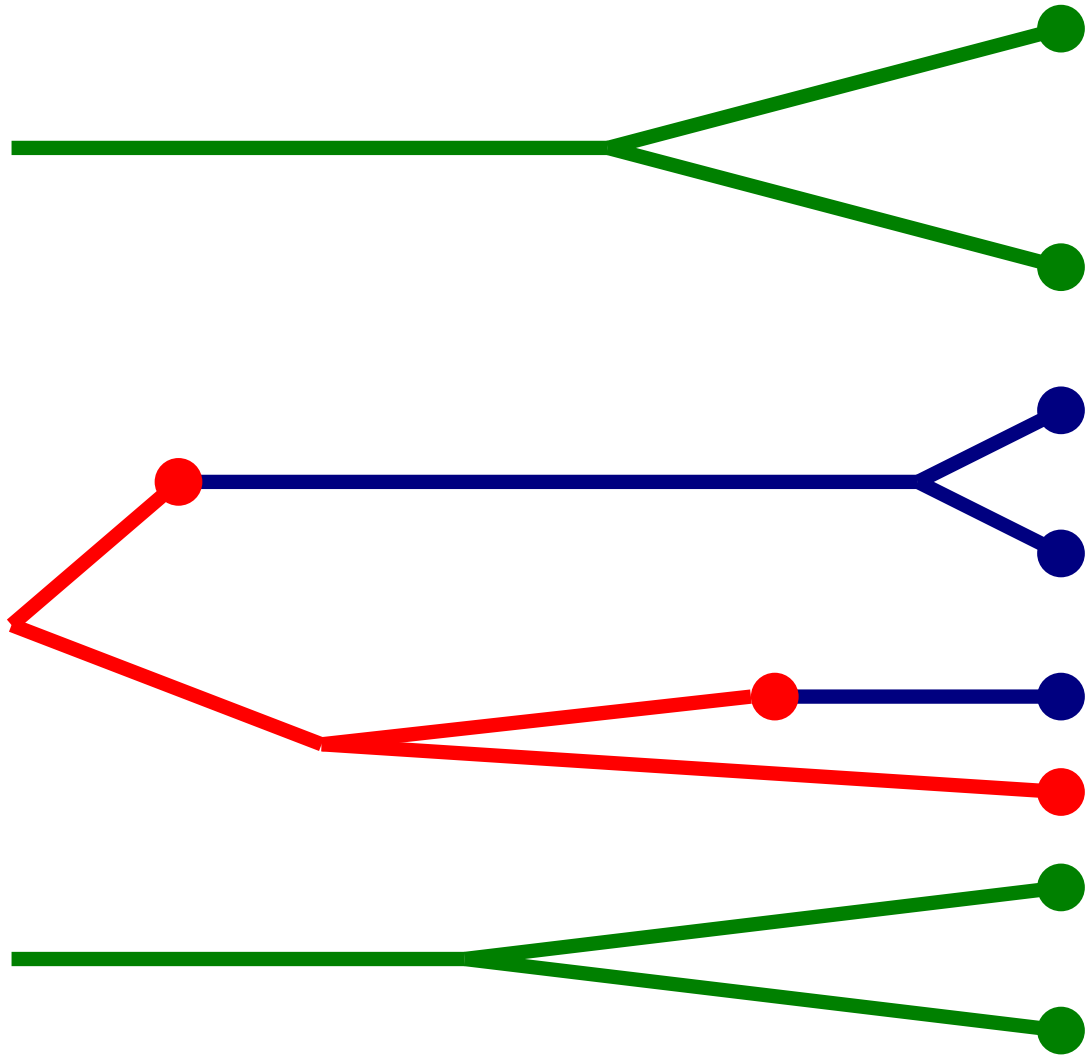

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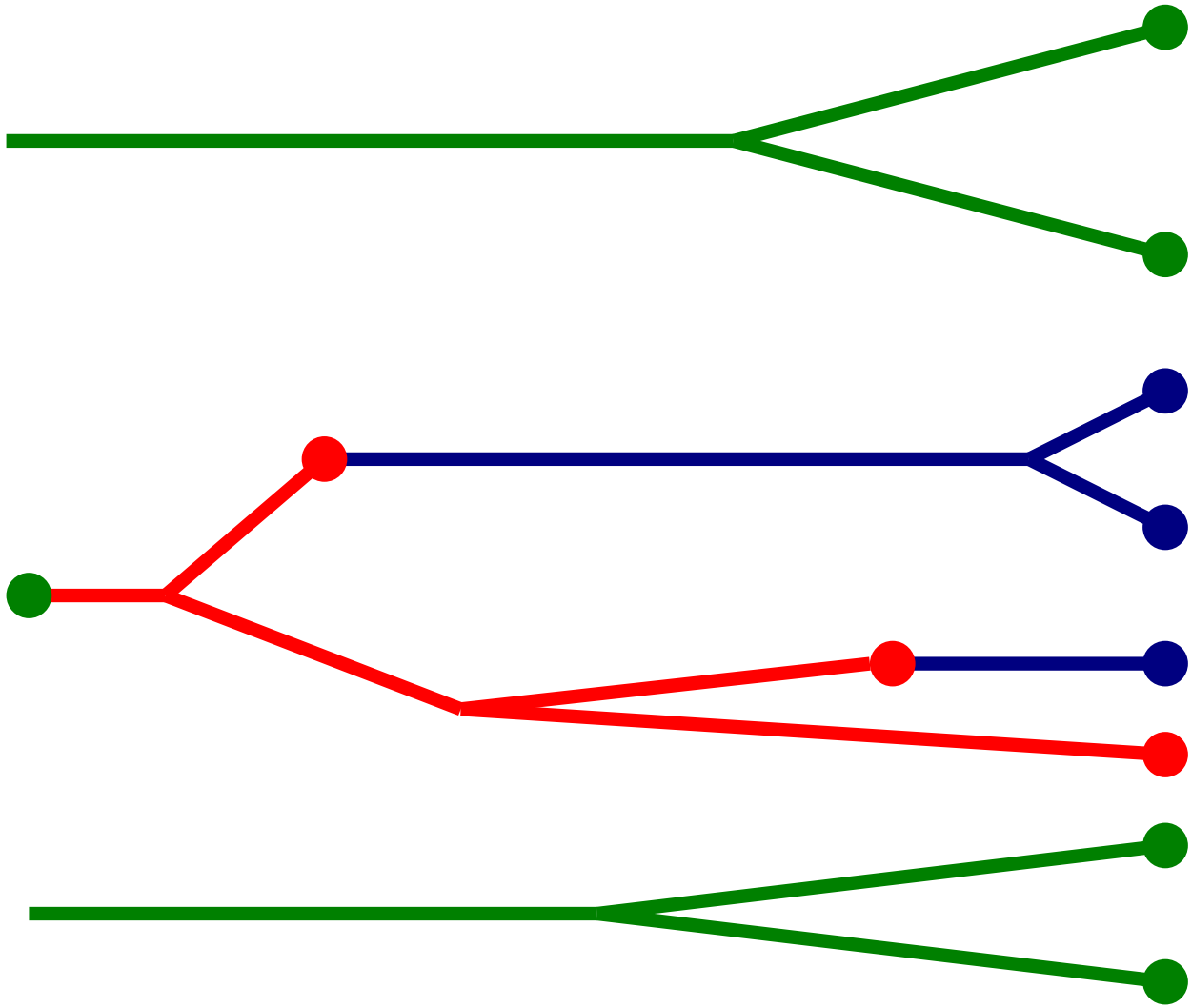

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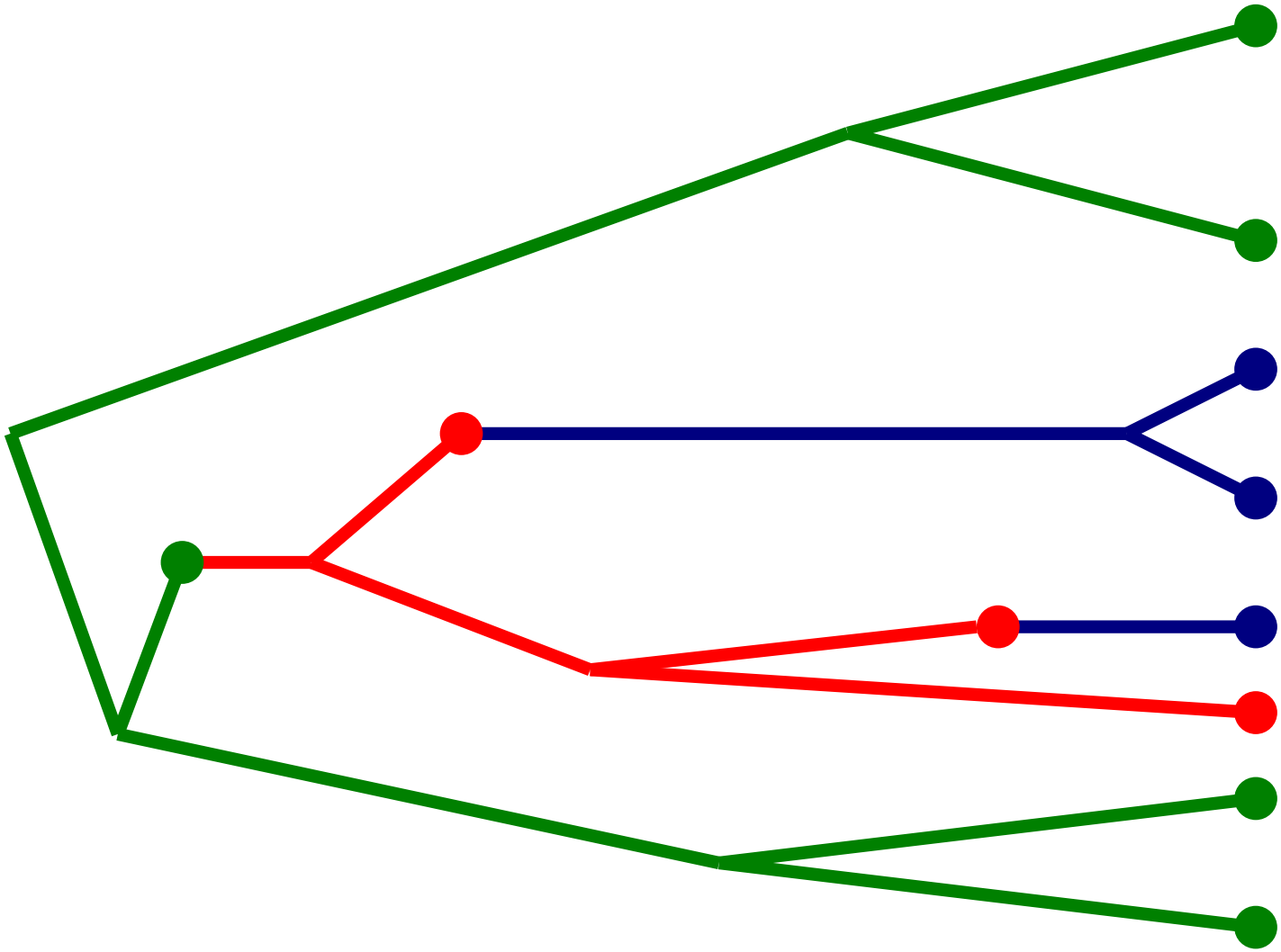

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Again, the standard phylogenetic posterior is modified:

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- Sample distribution not used as data.
- Uneven sampling can reduce inference power, but will *not* bias results!

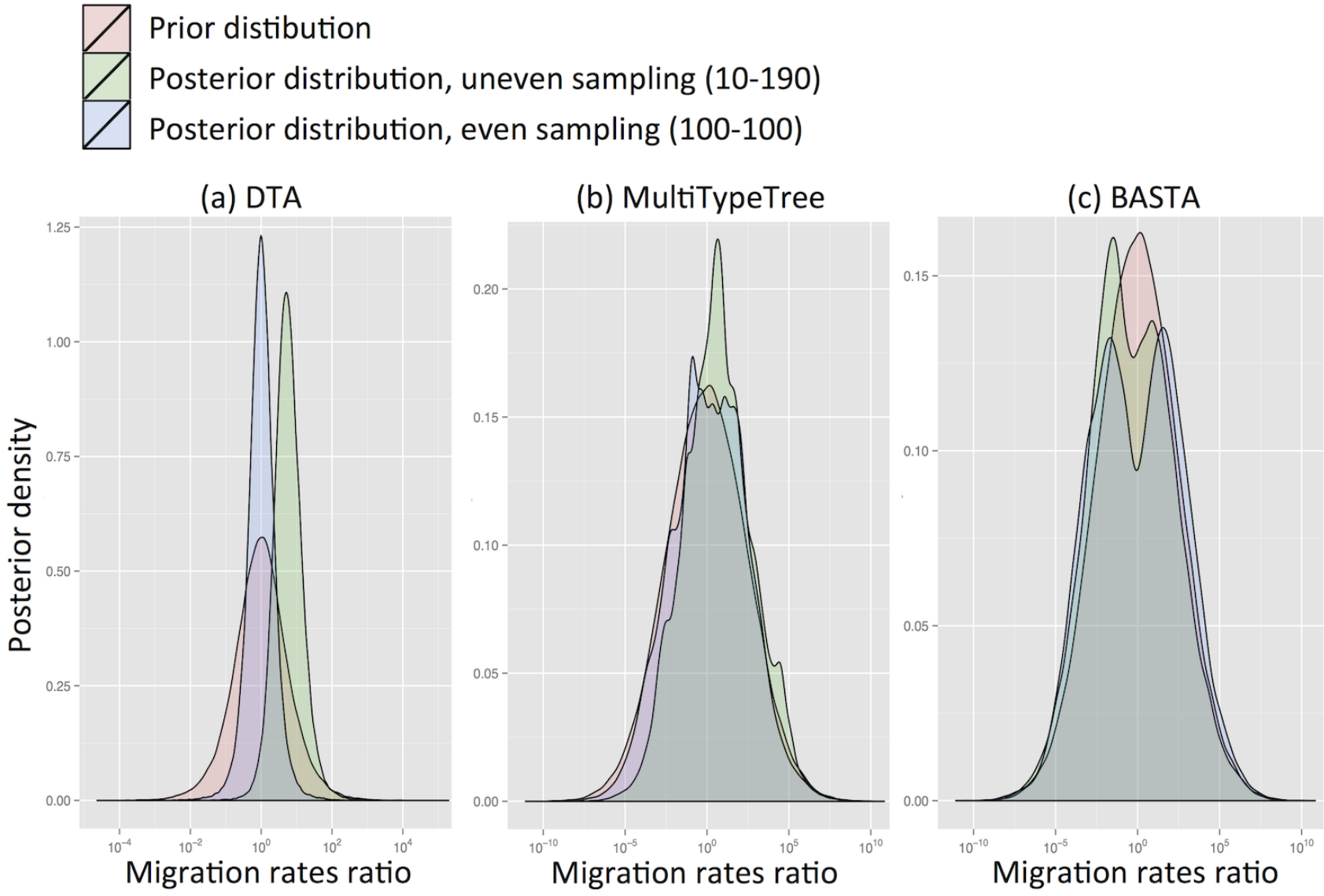
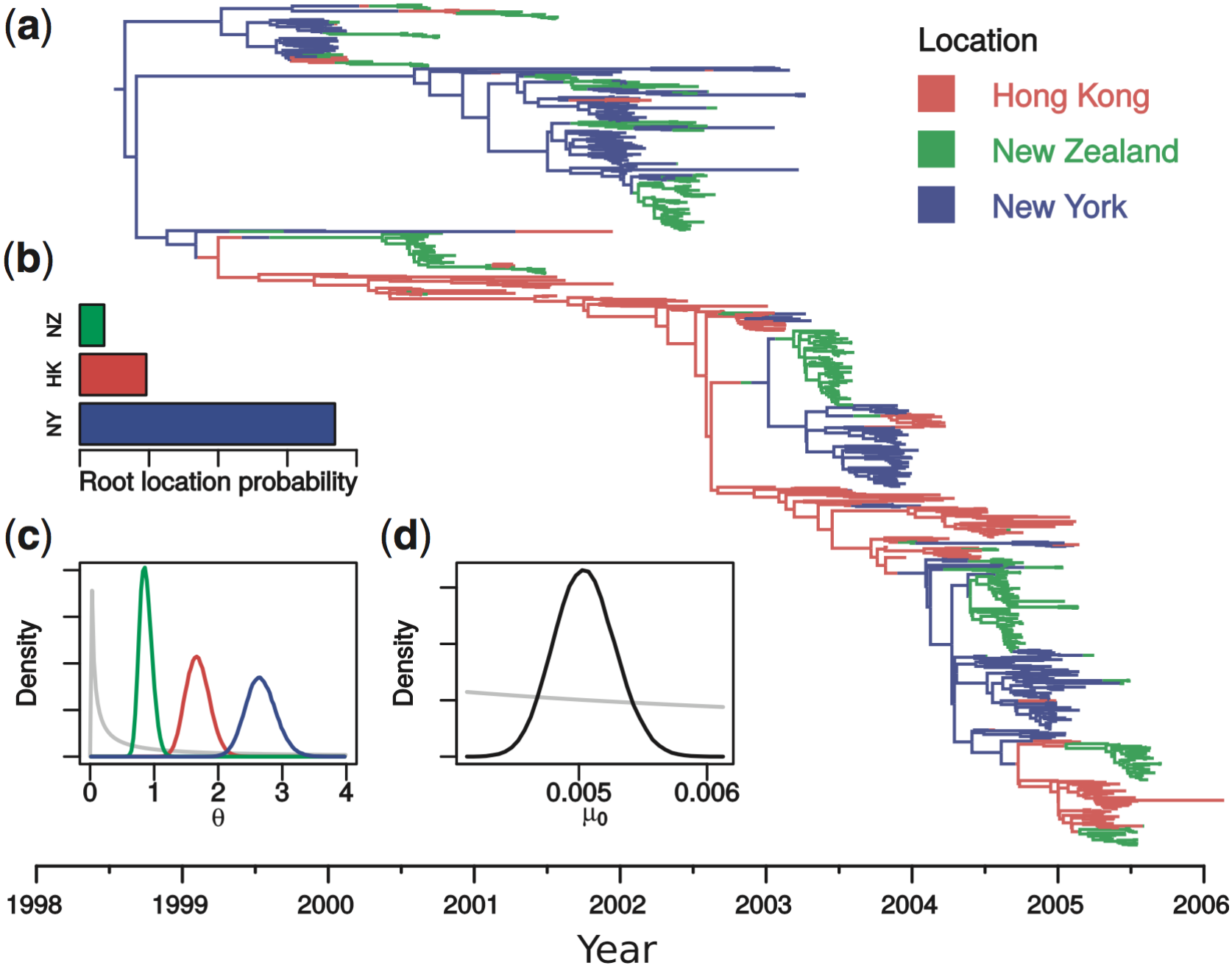



Figure 2, De Maio et al. (2015)




Inference of H3N2 movement usinc SC, Vaughan et al. (2014)

# Part III

## Structured birth-death-sampling models

# Structured birth-death-sampling models

- Introduced by Kühnert et al. (2016).
- A birth-death model of population dynamics in which individuals are permitted to change location due to discrete migration events.
- Sampling process is explicitly modelled.
- Birth and death rates may be location-dependent: not "neutral"! (Tree shape affected by structure.)
- Inference is performed using modified tree prior.

# Examples: two-type structured birth-death models

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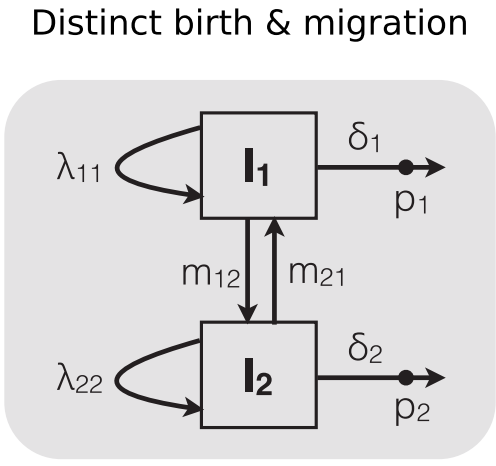


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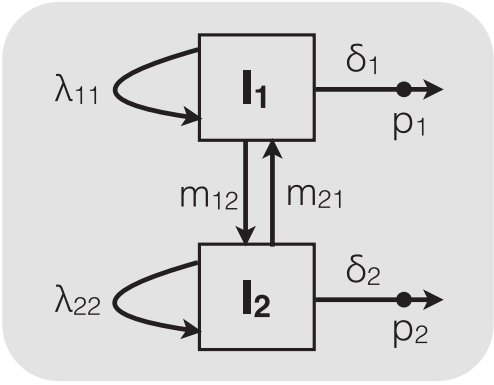
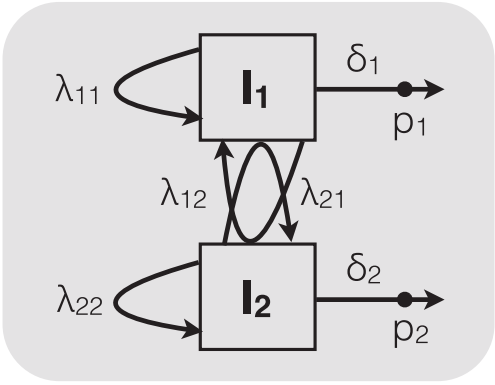
# Examples: two-type structured birth-death models

Distinct birth & migration




Simultaneous birth & migration

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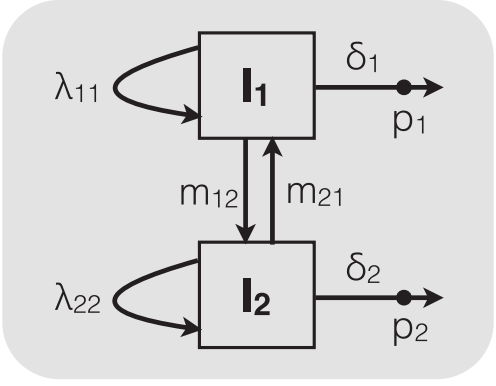


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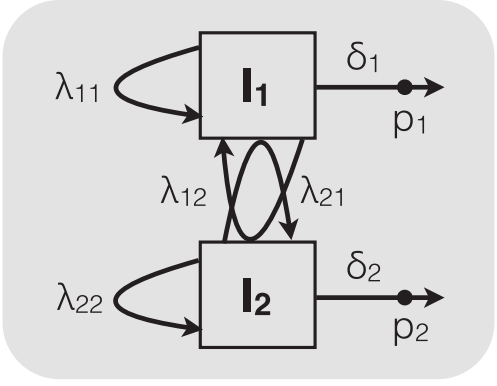
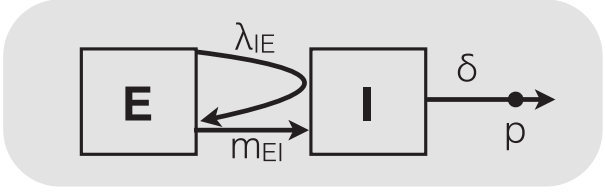



Hybrid model

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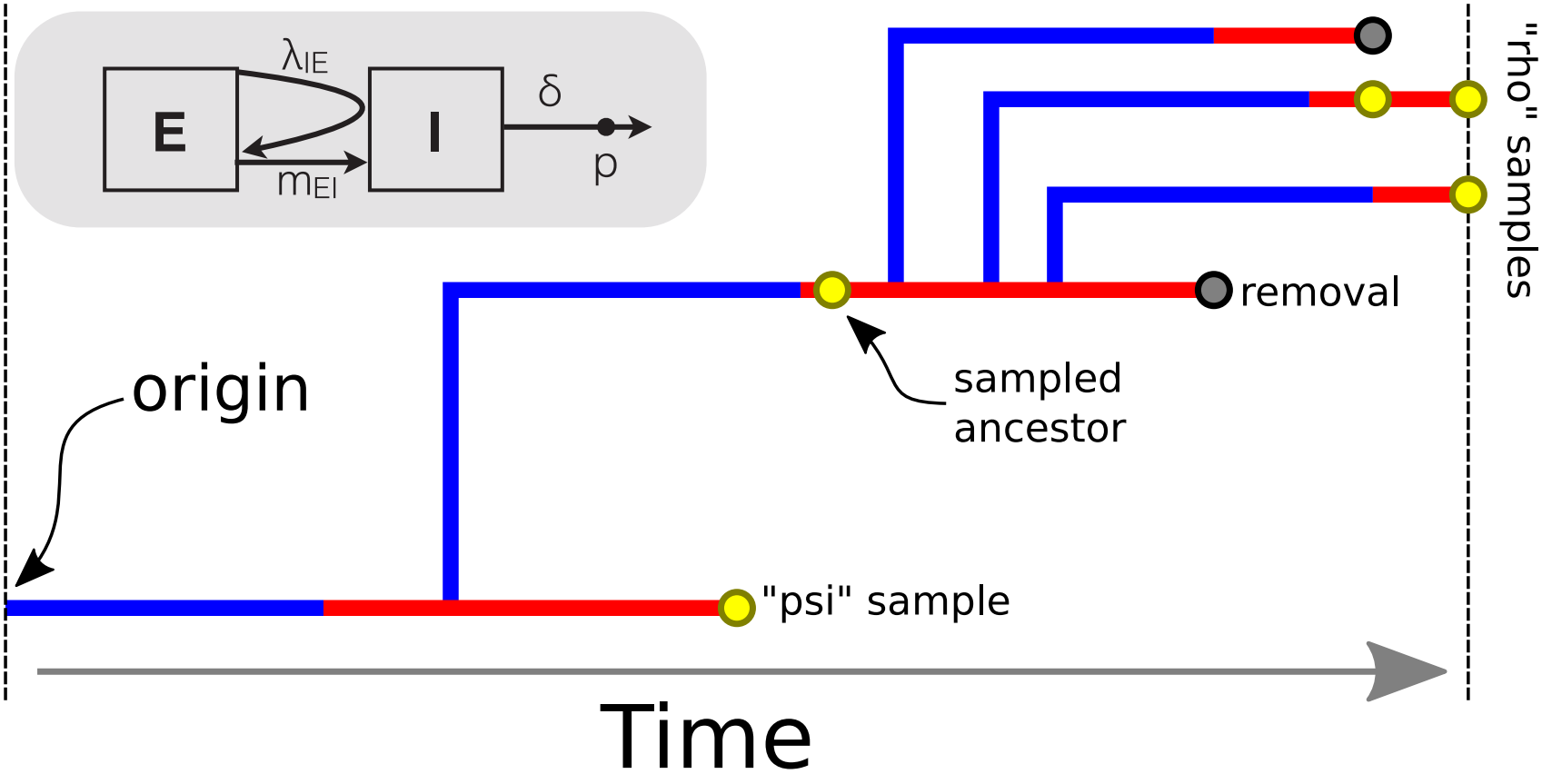

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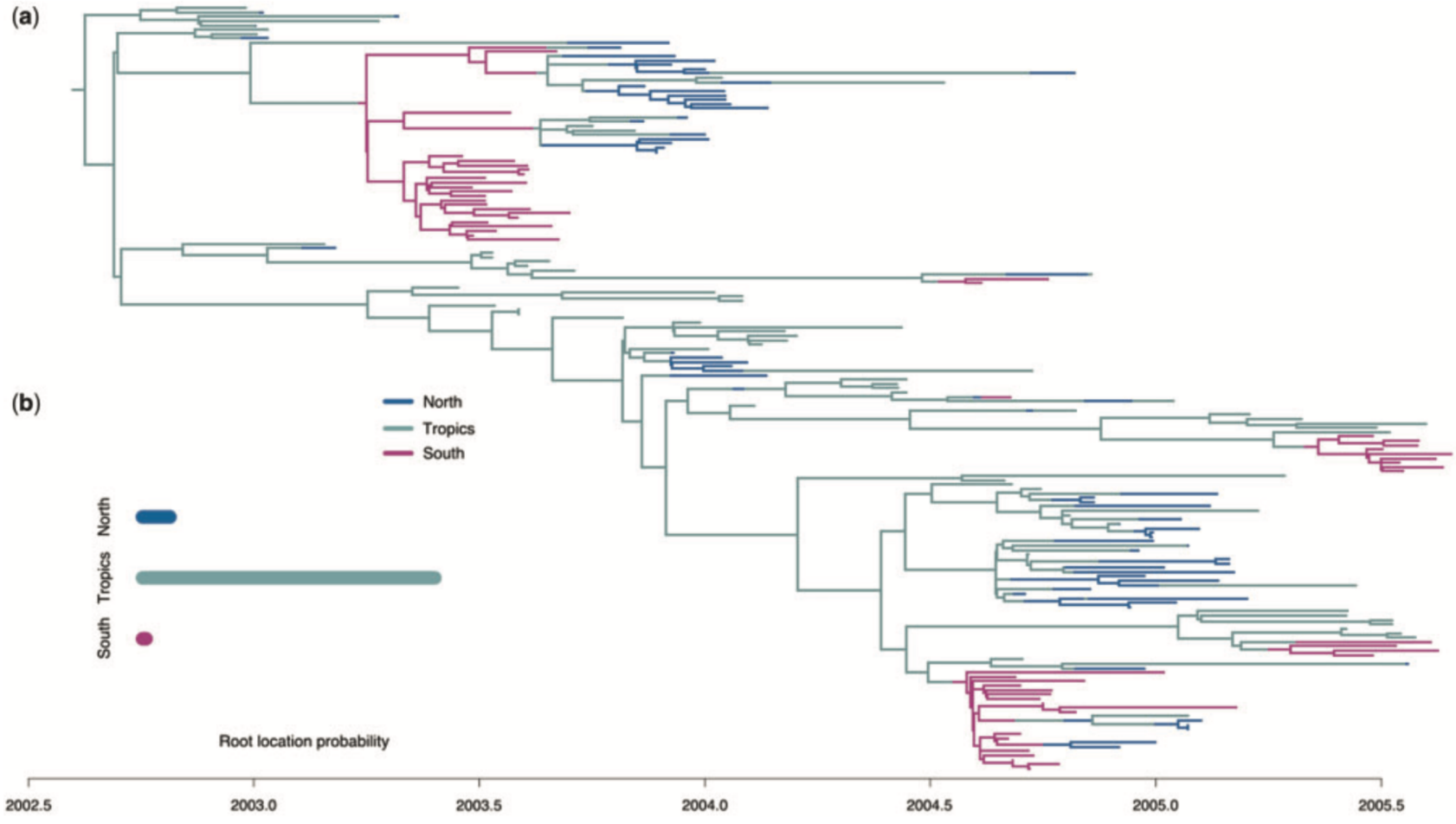
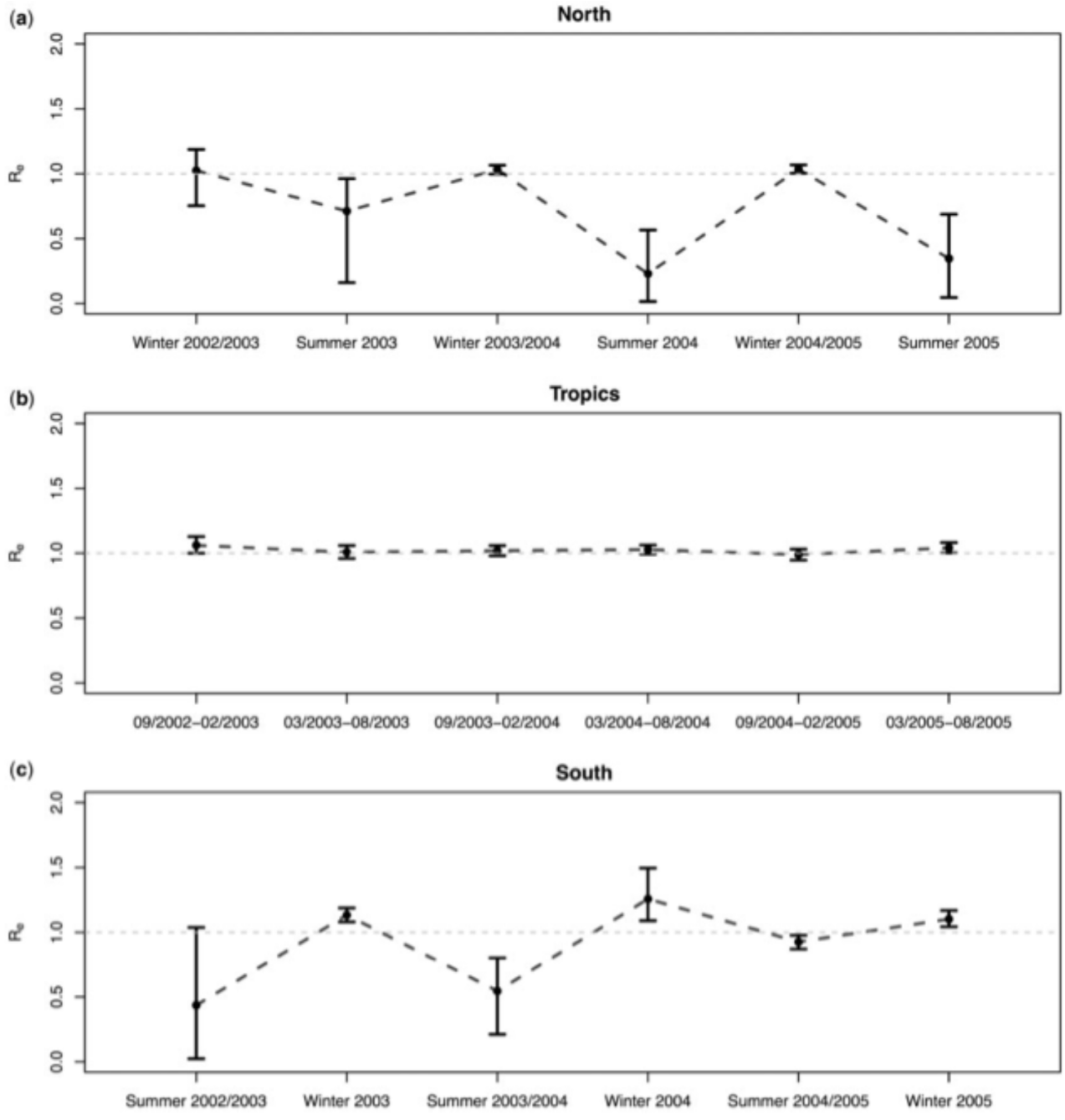
- Jointly estimating the spatial distribution of sampling rates allows non-uniform sampling to be appropriately handled.
- In contrast with the vanilla SC model, modelling the sampling process can provide additional inference power.




Analysis of H3N2 under BDMM, Kühnert et al. (2016).

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# Part IV

# Conclusions

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- Models such as the structured coalescent and the birth-death-sampling with migration (BDMM) models explicitly capture this effect.
- All models discussed make specific assumptions about the sampling process. Be careful that your data satisfy the assumptions of the model you use.

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