

# The Coalescent:

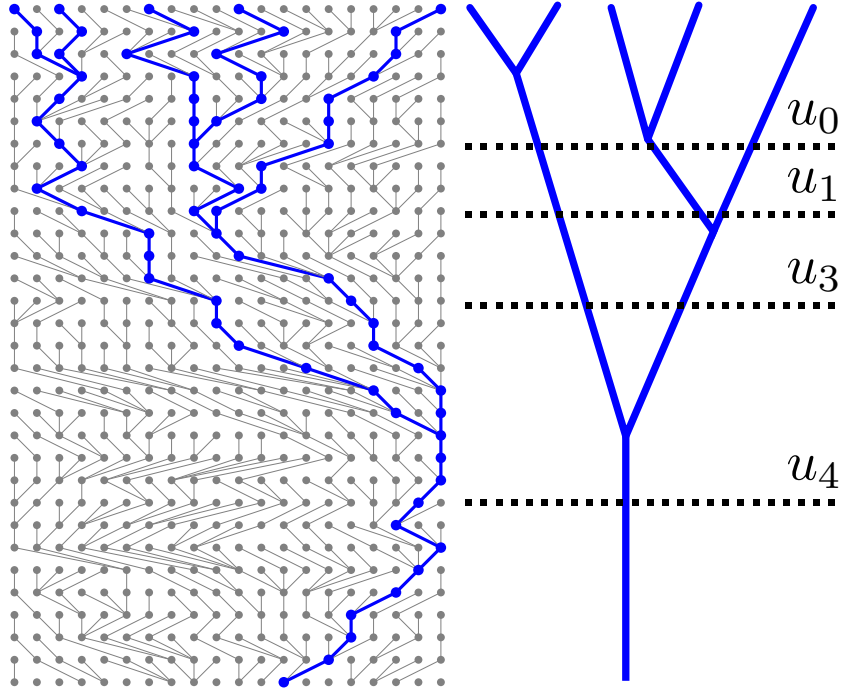
Inference using trees of individuals



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 #MolEvol2023  
@peterbeerli

# Kingman's coalescent



$$P(G|\Theta) = \prod_{j=0}^T e^{-u_j} \frac{k_j(k_j-1)}{\Theta} \frac{2}{\Theta}$$

$$\Theta = 4N_e\mu$$

- ◆ calculate the probability that we wait the time interval  $u$  until a coalescent
- ◆ calculate the probability of the particular coalescent event
- ◆ multiply these probabilities for all time intervals

# Extensions of the basic coalescence

Analogy #3



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# Extensions of the basic coalescence

- ◆ Population growth (two parameters), fluctuations, bottlenecks
- ◆ Migration among populations (potentially thousands, parameters)
- ◆ Population splitting (many parameters)
- ◆ Effect of assumption violation

# Extensions of the basic coalescent

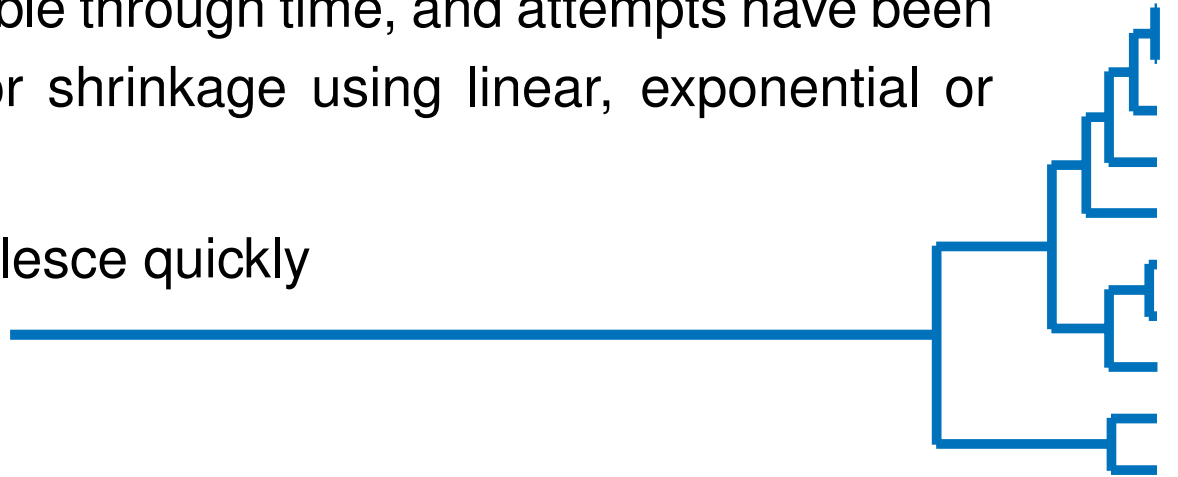
Populations are rarely completely stable through time, and attempts have been made to model population growth or shrinkage using linear, exponential or more general approaches.



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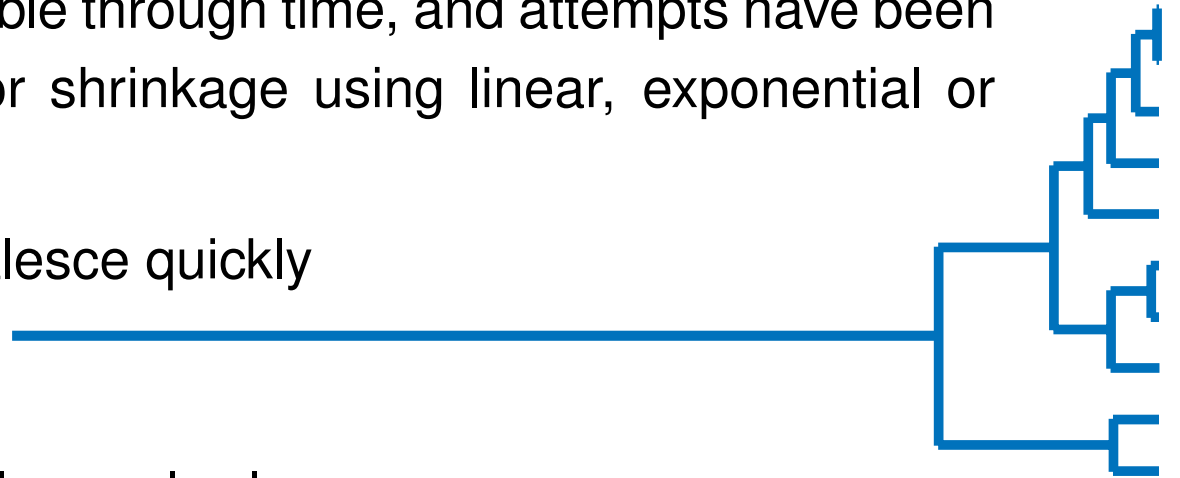
- ◆ In a small population lineages coalesce quickly



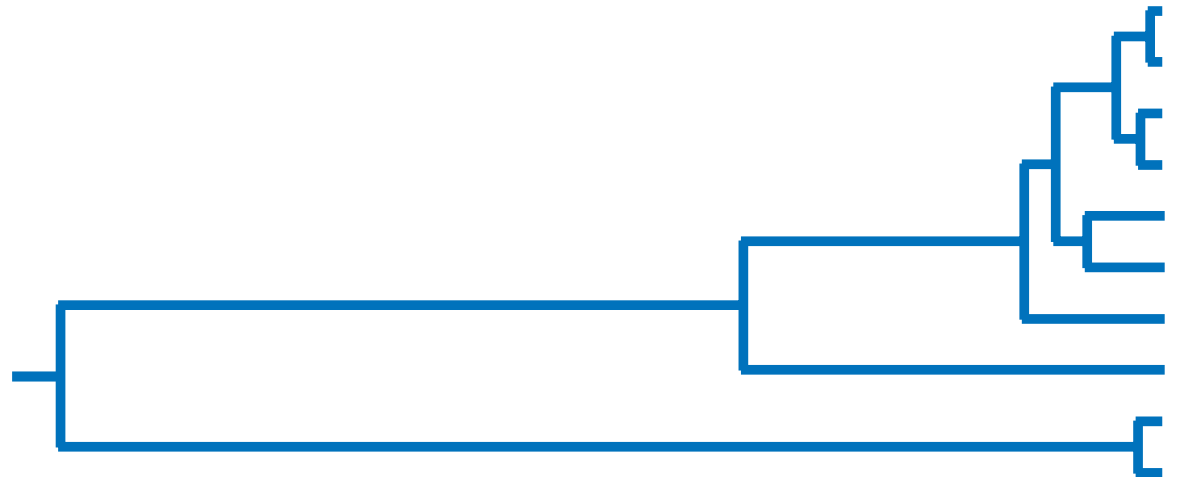
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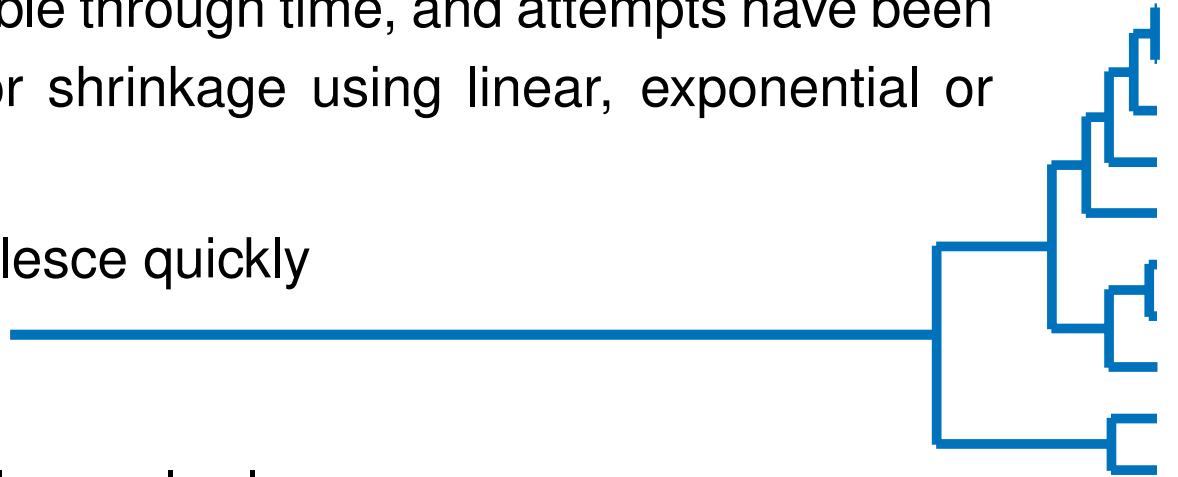
◆ In a large population lineages coalesce slowly



# Extensions of the basic coalescent

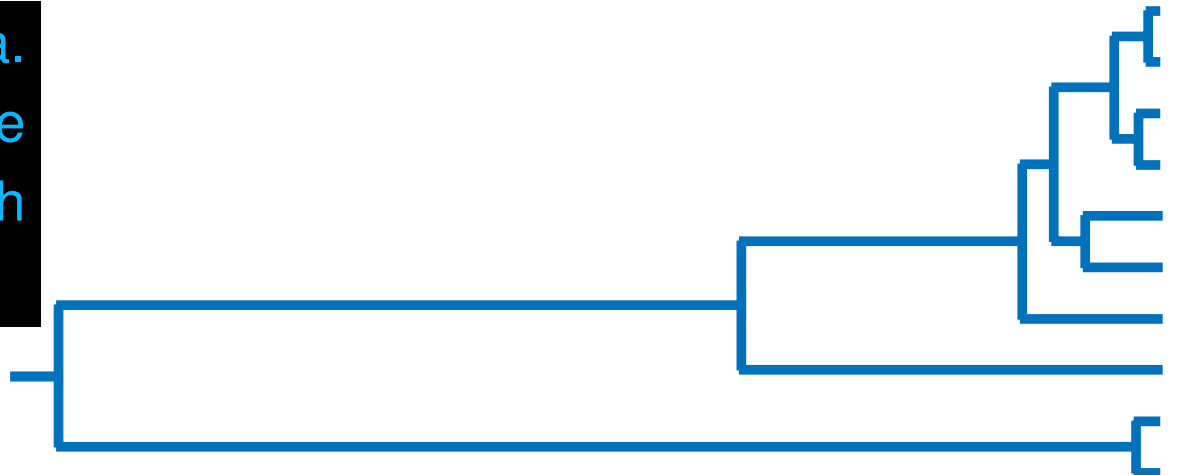
Populations are rarely completely stable through time, and attempts have been made to model population growth or shrinkage using linear, exponential or more general approaches.

◆ In a small population lineages coalesce quickly



◆ In a large population lineages coalesce slowly

This leaves a signature in the data.  
We can exploit this and estimate the population growth rate  $g$  jointly with the current population size  $\Theta$ .



# Extensions of the basic coalescent

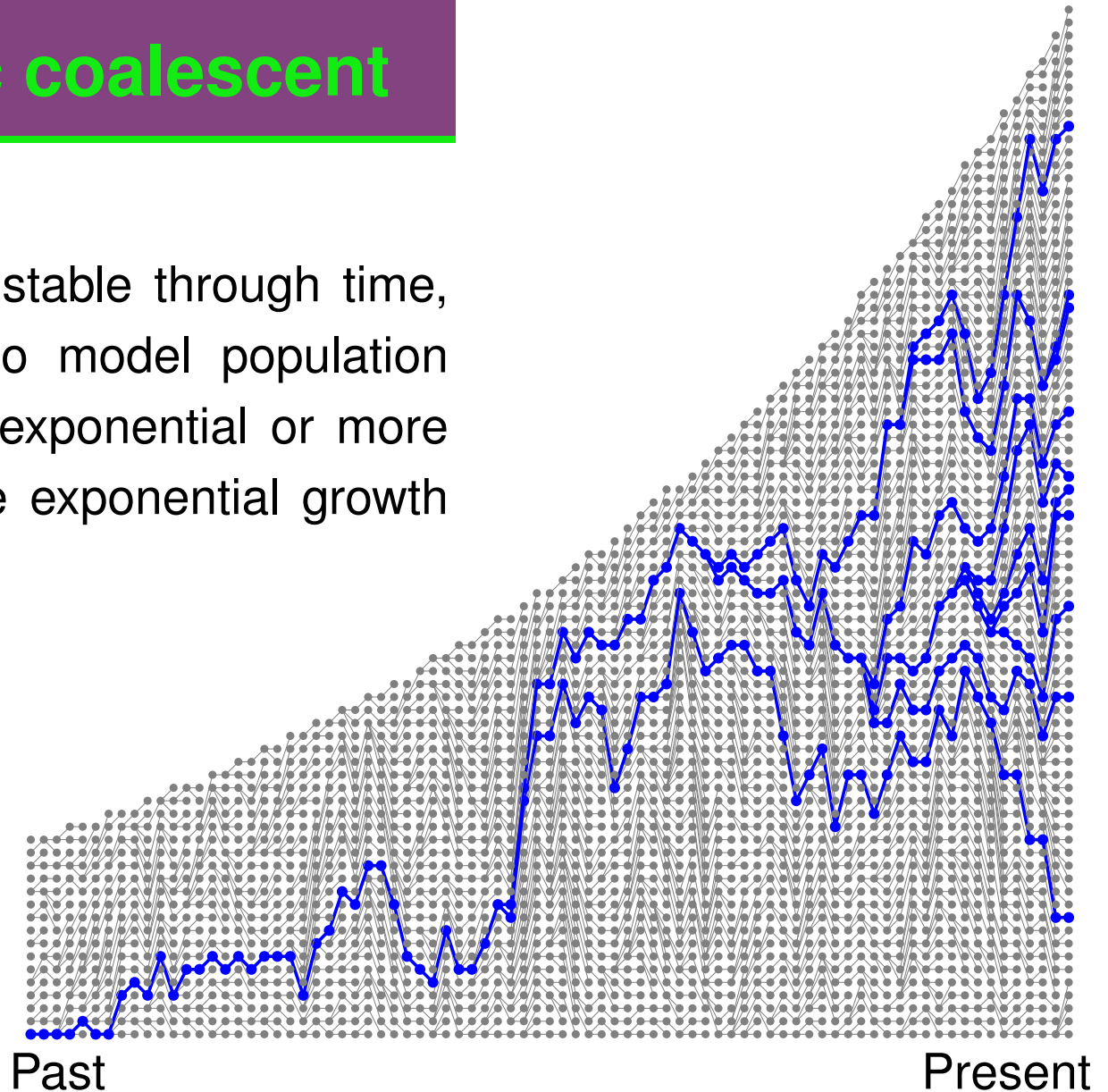
Populations are rarely completely stable through time, and attempts have been made to model population growth or shrinkage using linear, exponential or more general approaches. For example exponential growth could be modeled as

$$\frac{dN}{dt} = rN$$

$$N_t = N_0 e^{-rt}$$

$$N_0 = 80$$

$$r = 0.02$$



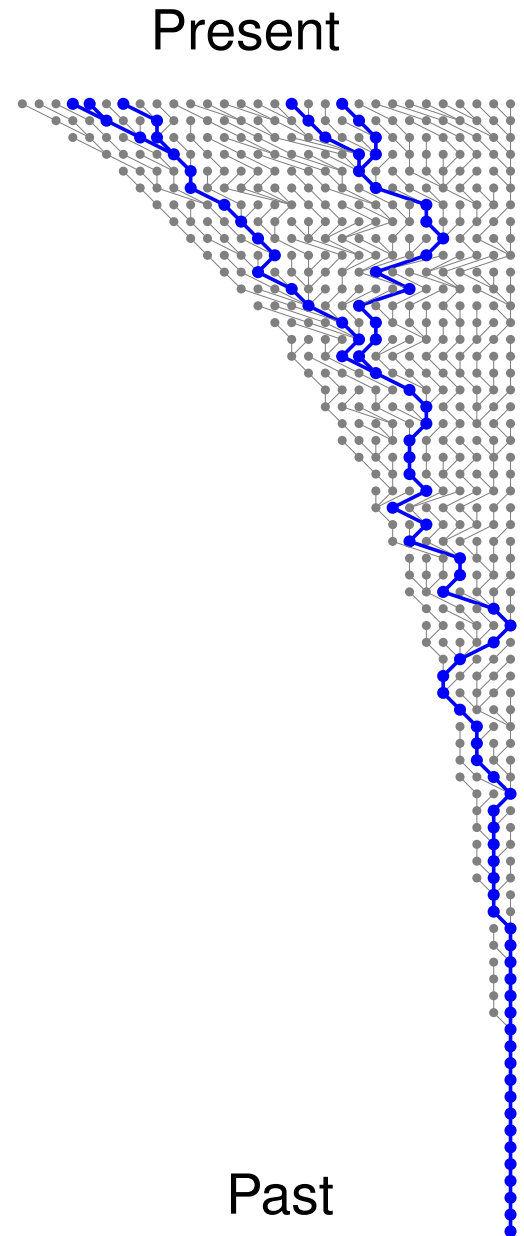
# Extensions of the basic coalescent

For constant population size we found

$$p(G|\Theta) = \prod_j e^{-u_j} \frac{k(k-1)}{\Theta} \frac{2}{\Theta}$$

Relaxing the constant size to exponential growth and using  $g = r/\mu$  leads to

$$p(G|\Theta_0, g) = \prod_j e^{-(t_j - t_{j-1}) \frac{k(k-1)}{\Theta_0 e^{-gt}}} \frac{2}{\Theta_0 e^{-gt}}$$

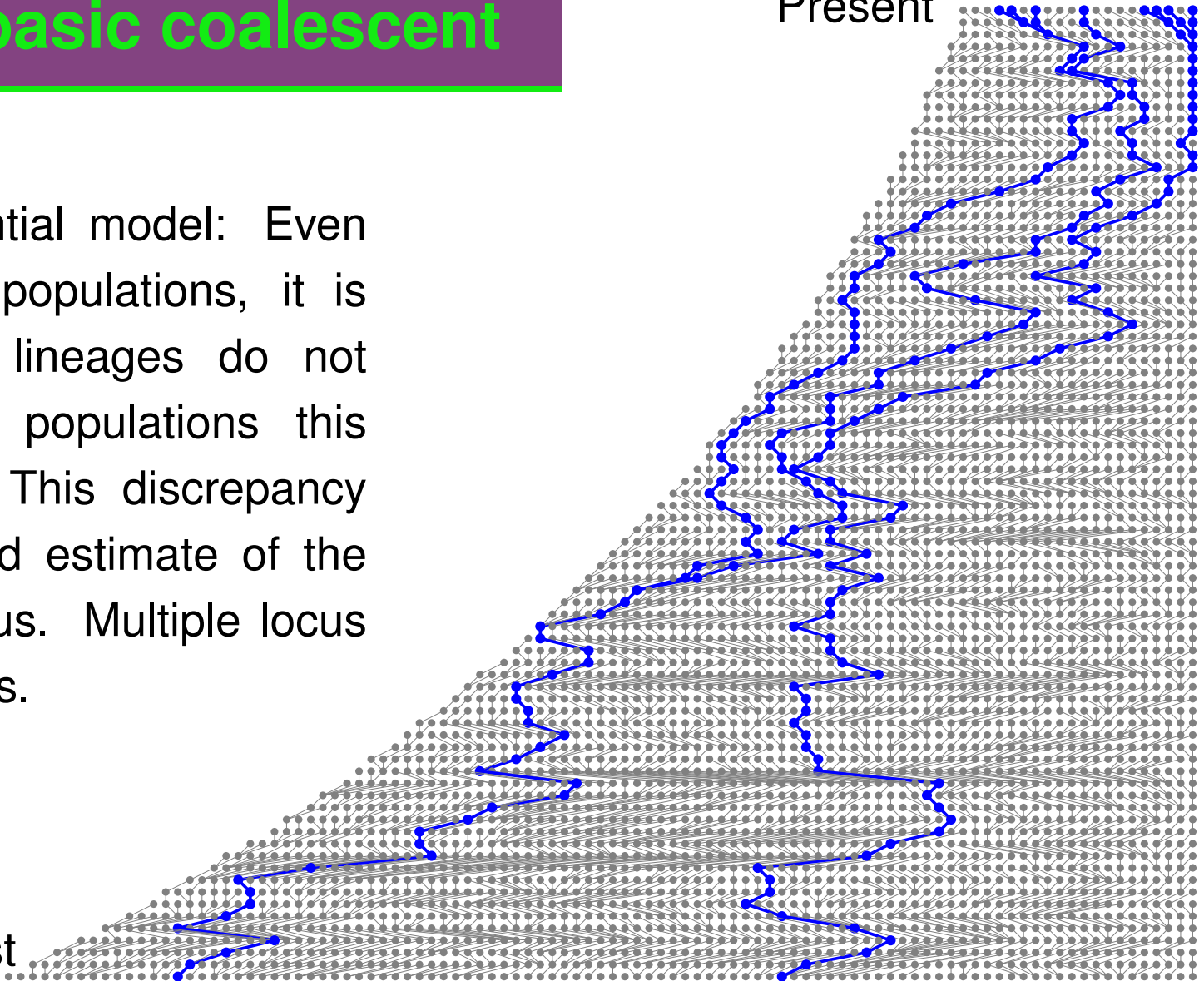


# Extensions of the basic coalescent

Problems with the exponential model: Even with moderately shrinking populations, it is possible that the sample lineages do not coalesce. With growing populations this problem does not occur. This discrepancy leads to an upwards biased estimate of the growth rate for a single locus. Multiple locus estimates improve the results.

Past

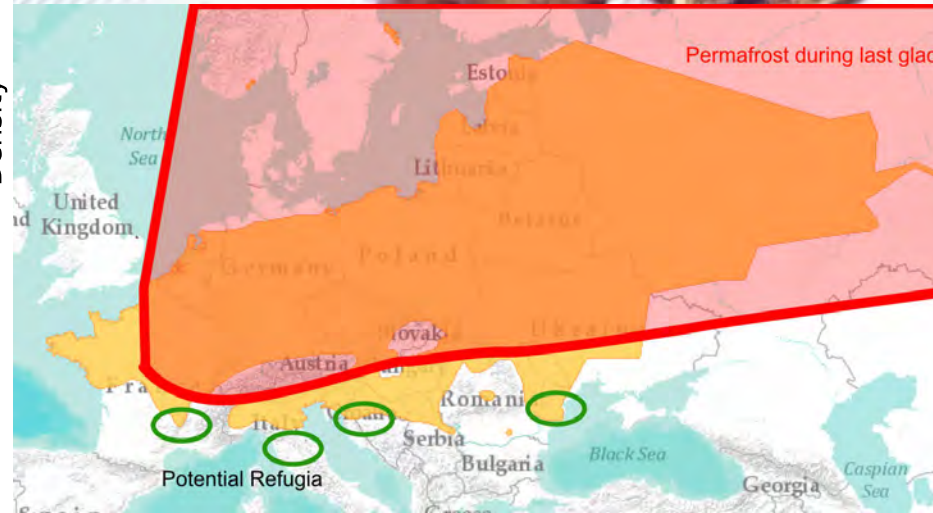
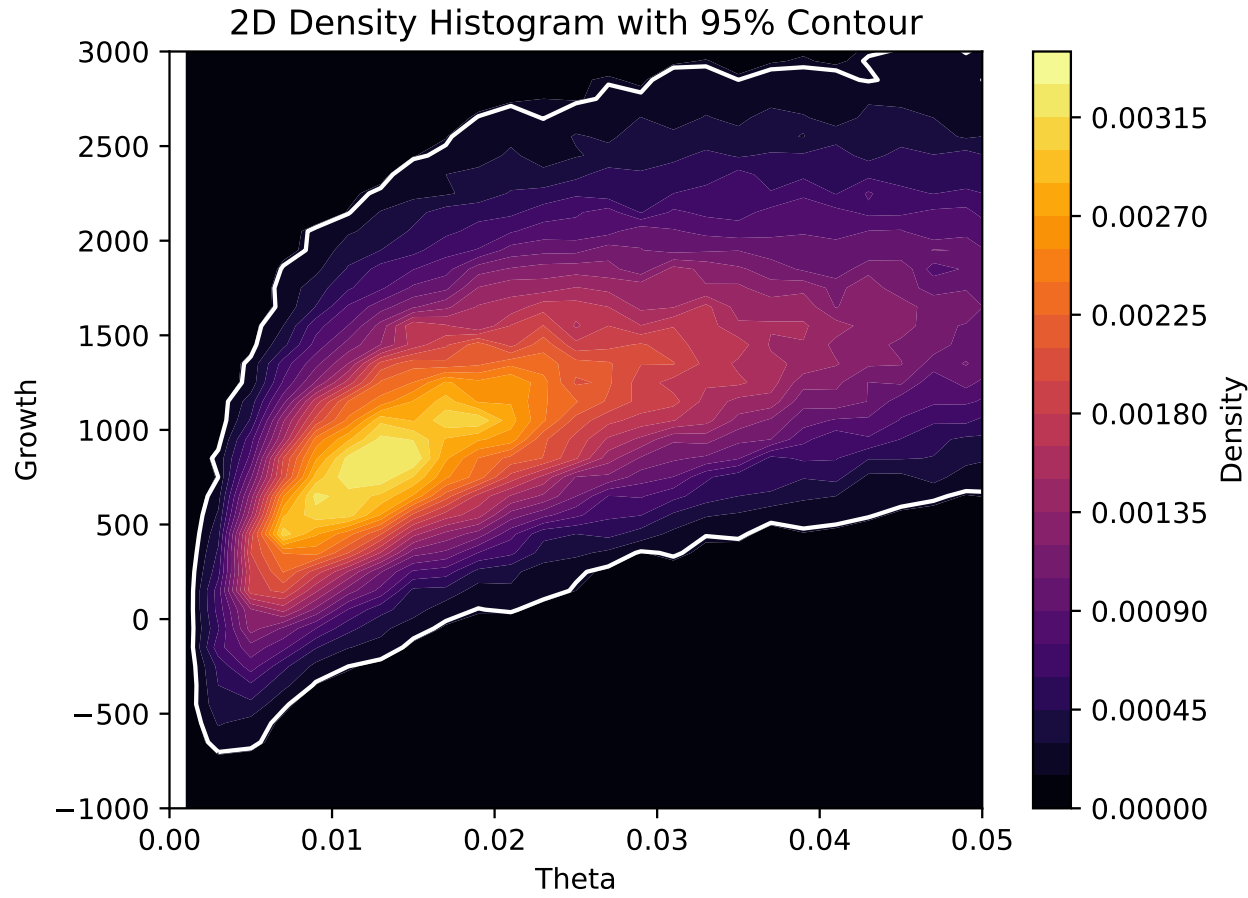
Present



# Grow-A-Frog



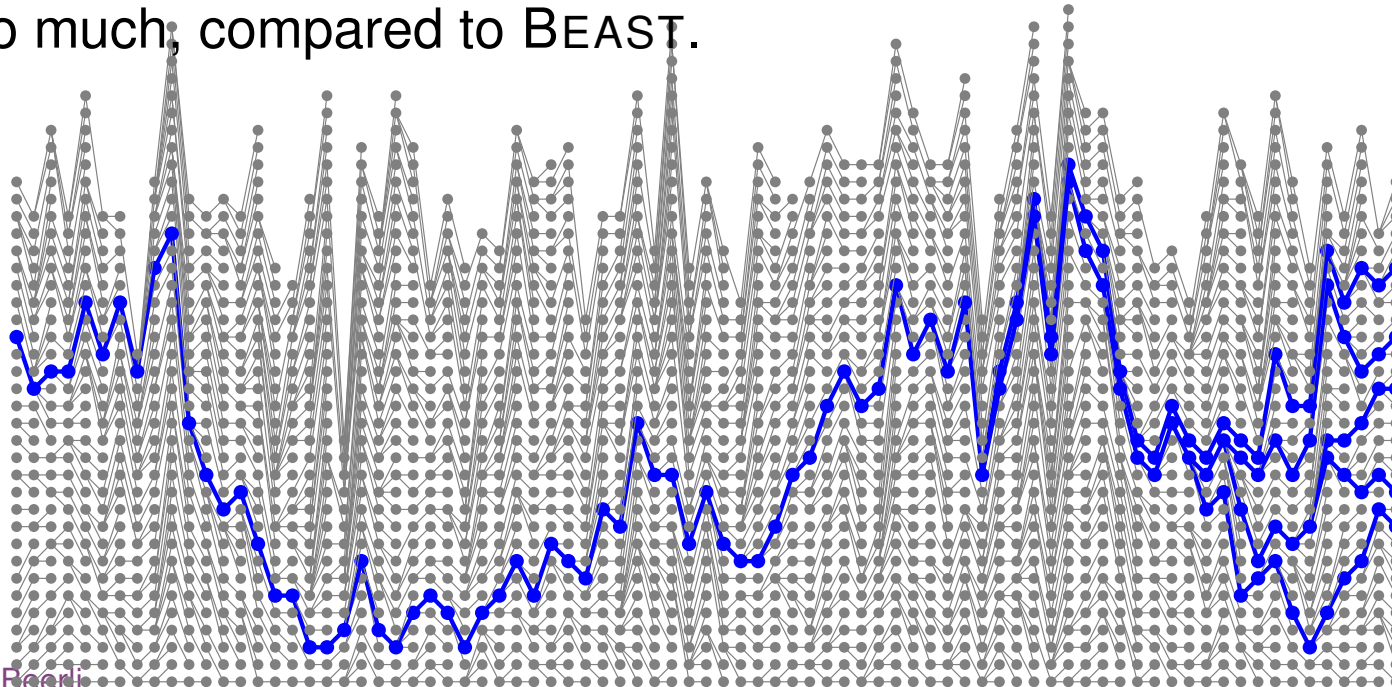
# Grow-A-Frog



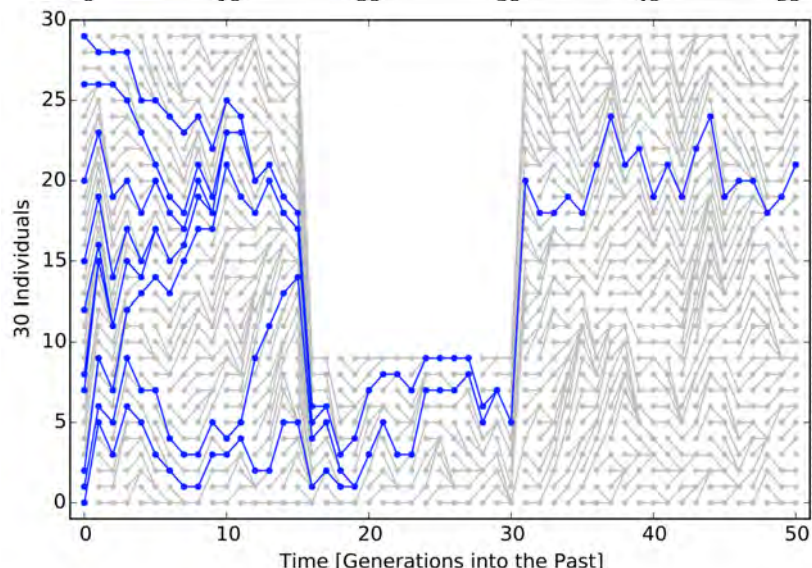
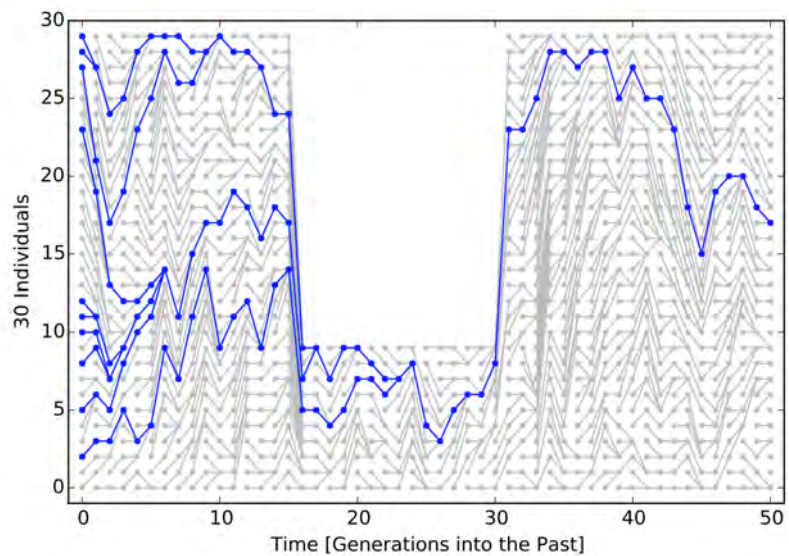
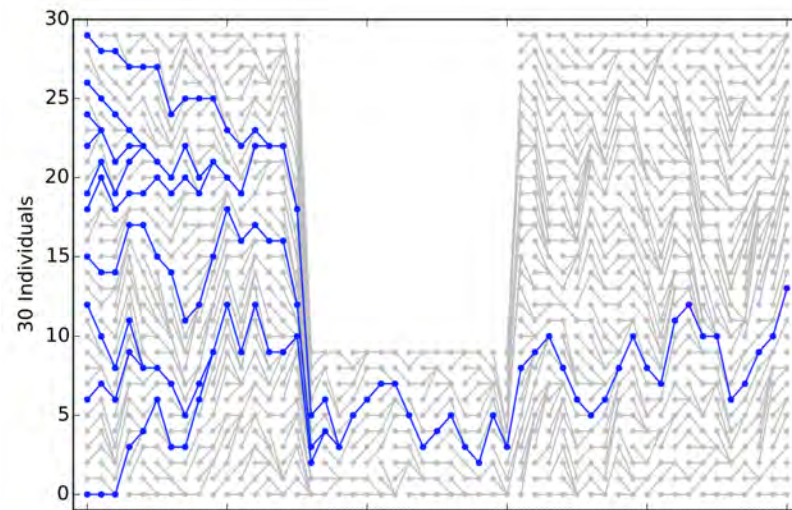
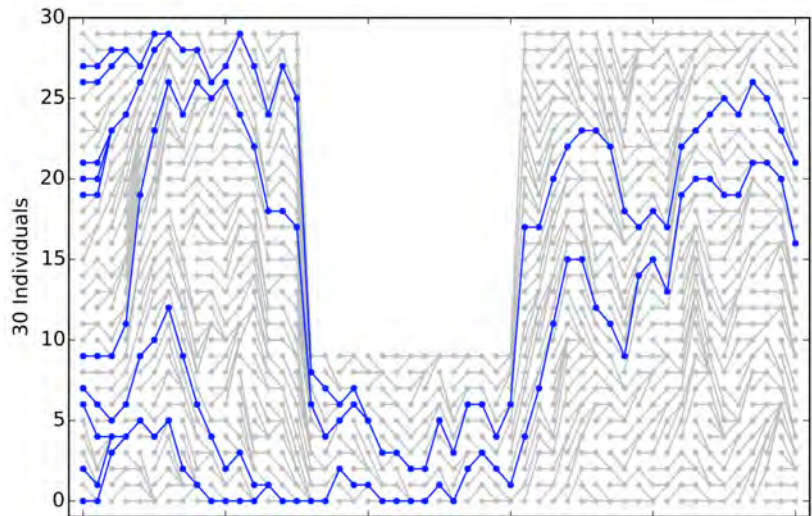


# Extensions of the basic coalescent

Random fluctuations of the population size are most often ignored. BEAST (and to some extent MIGRATE) can handle such scenarios. BEAST is using a full parametric approach (skyride, skyline) whereas MIGRATE uses a non-parametric approach for its skyline plots that has the tendency to smooth the fluctuations too much, compared to BEAST.

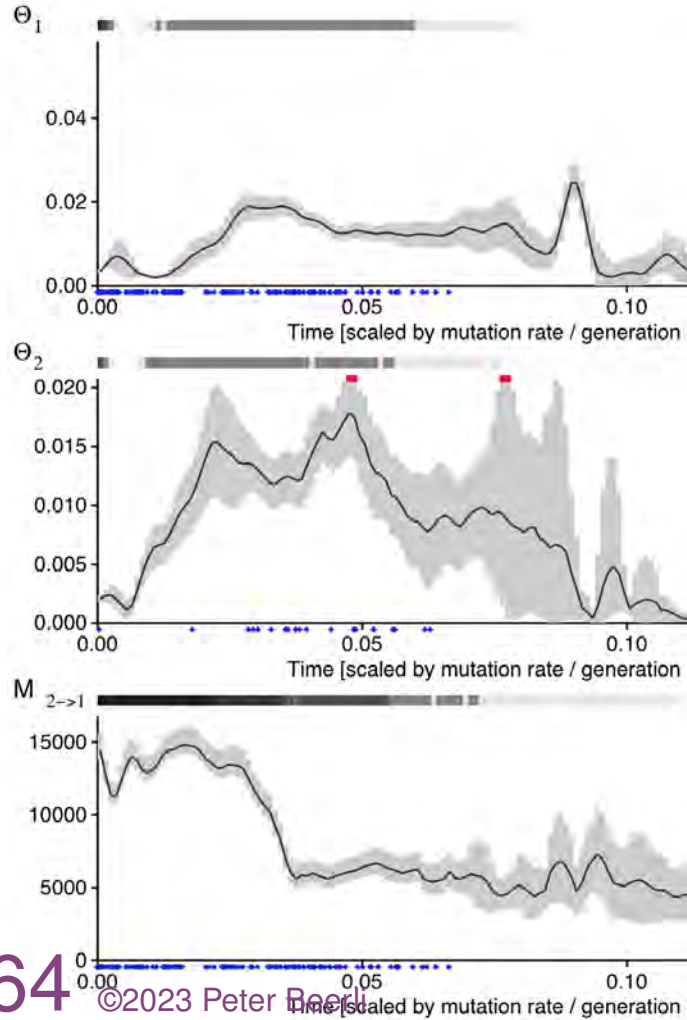


# Extensions of the basic coalescent

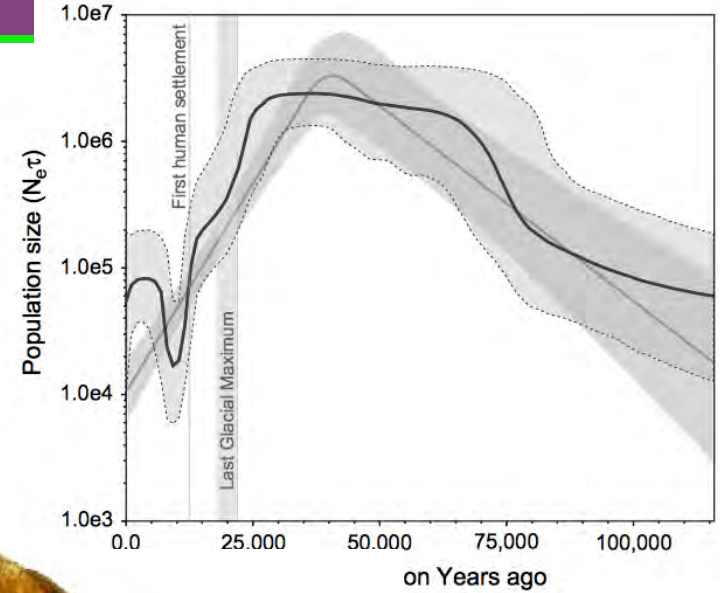


# Extensions of the basic coalescent

## MIGRATE



## BEAST



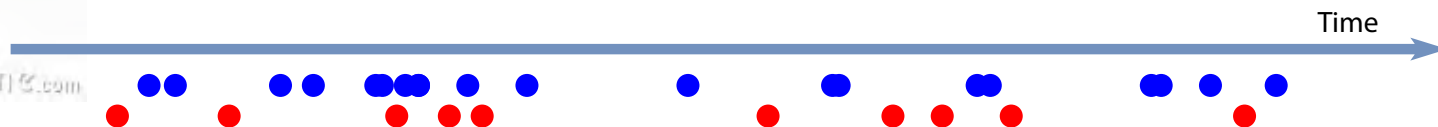
# Accommodating more events



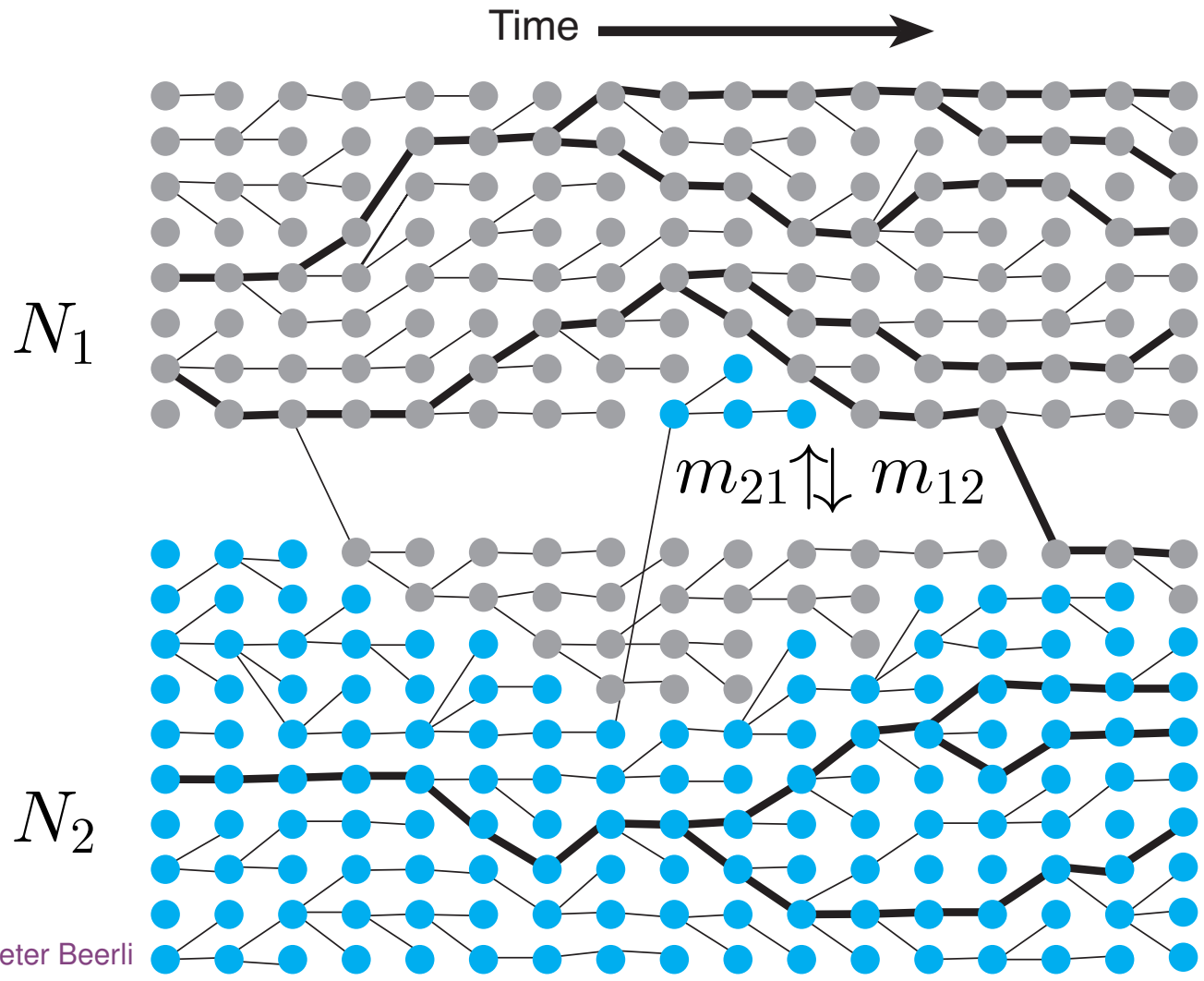
# An analogy



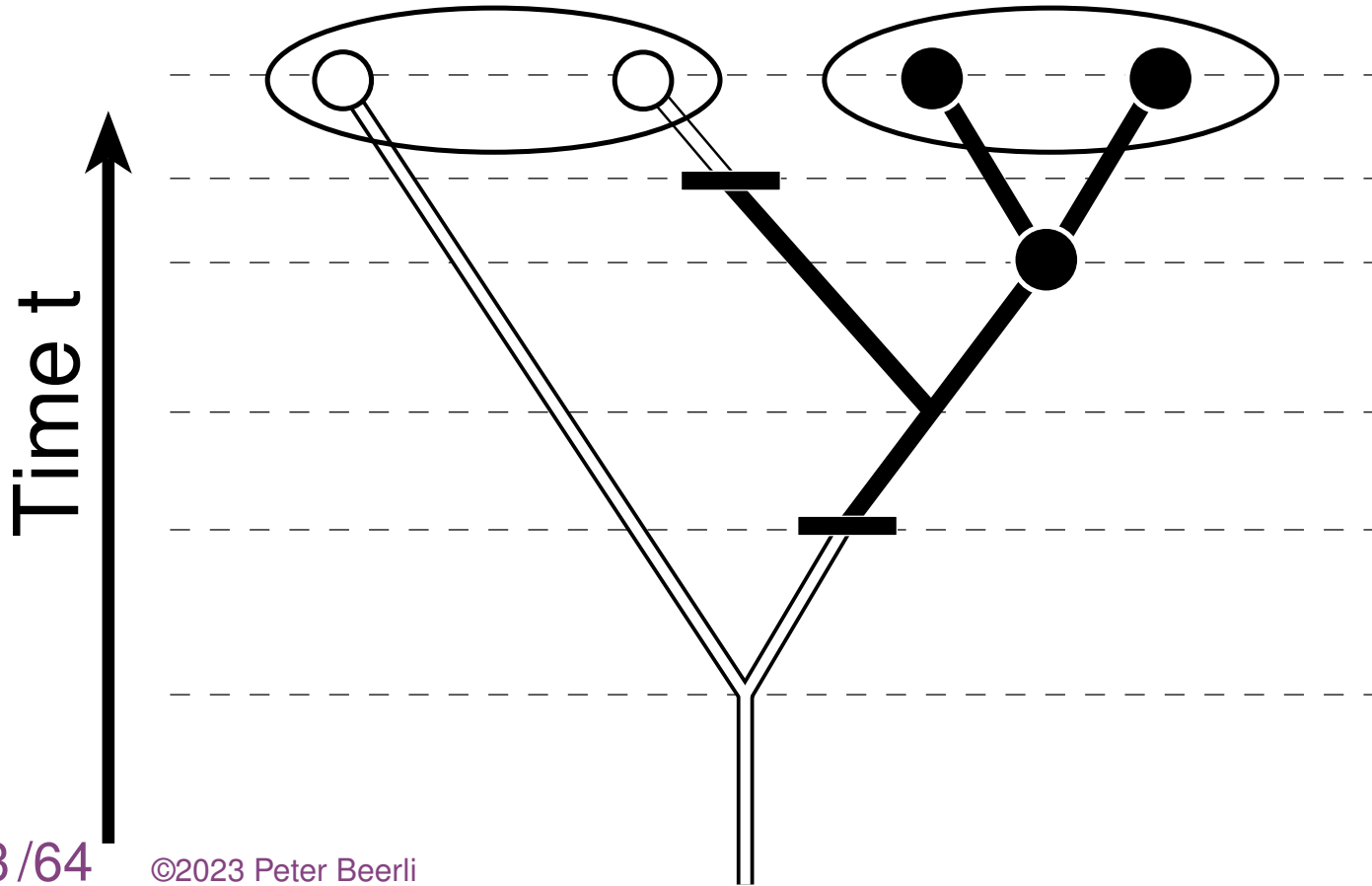
[dreamstime.com](https://www.dreamstime.com/stock-illustration-rotary-telephone-image-imagebank-gettyimages.com)



# Extensions of the basic coalescent



# Extensions of the basic coalescent

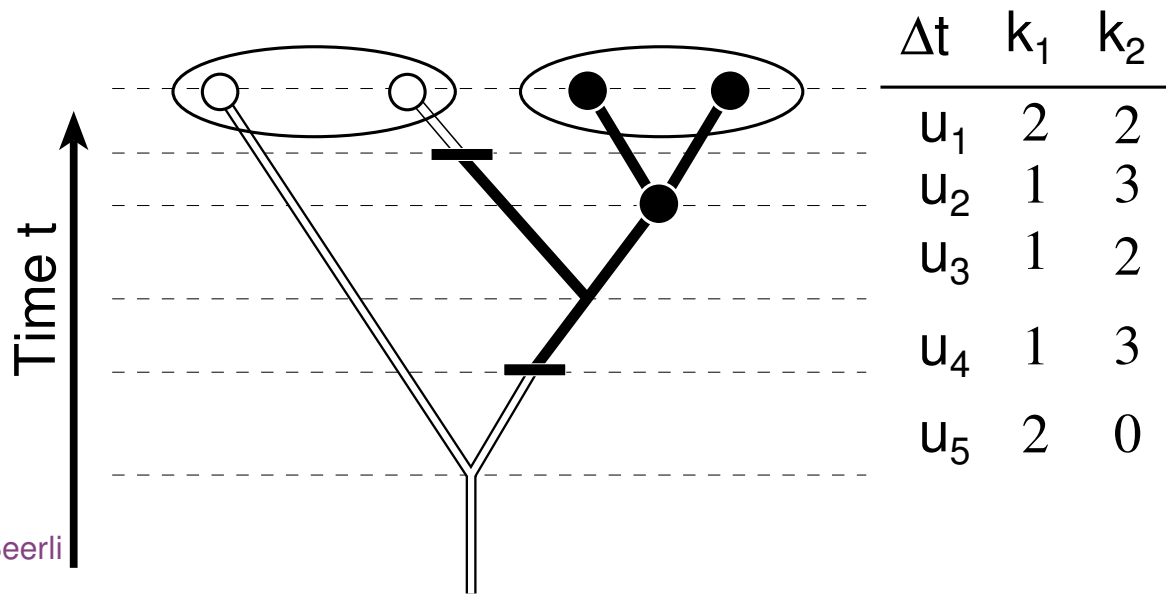


$\Delta t$	$k_1$	$k_2$
$u_1$	2	2
$u_2$	1	3
$u_3$	1	2
$u_4$	1	3
$u_5$	2	0

# Extensions of the basic coalescent

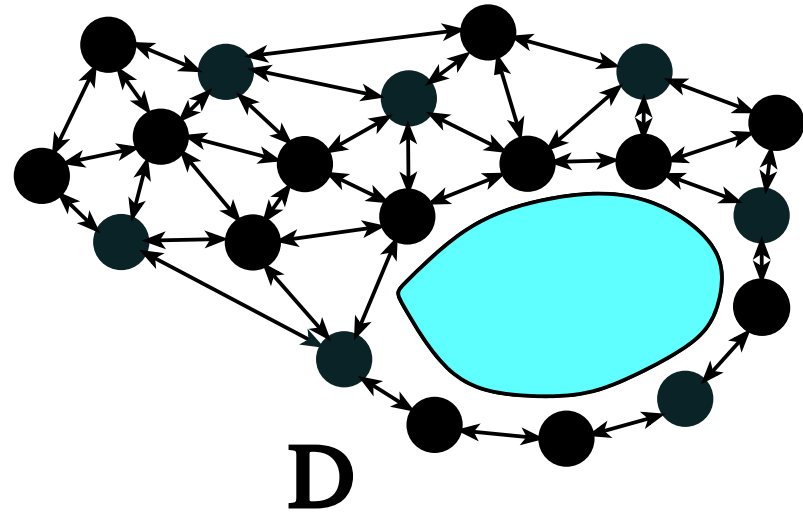
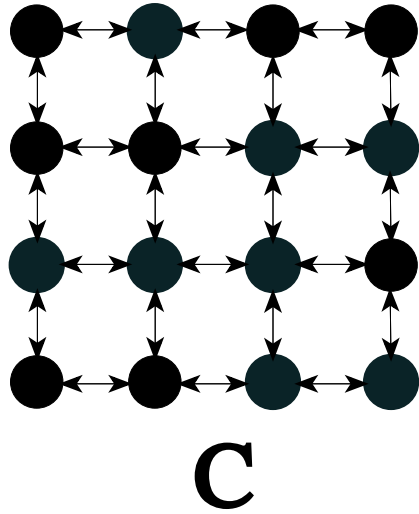
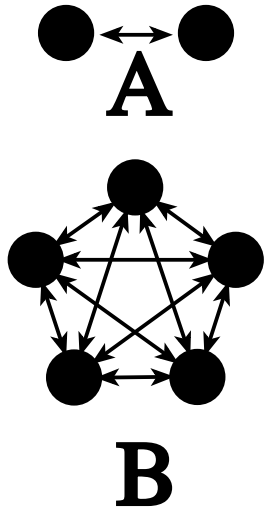
The single population coalescence rate is  $\frac{k(k-1)}{4N}$ .

Changes for two populations to  $\frac{k_1(k_1-1)}{\Theta_1} + \frac{k_2(k_2-1)}{\Theta_2} + k_1M_{2,1} + k_2M_{1,2}$





# Structured populations



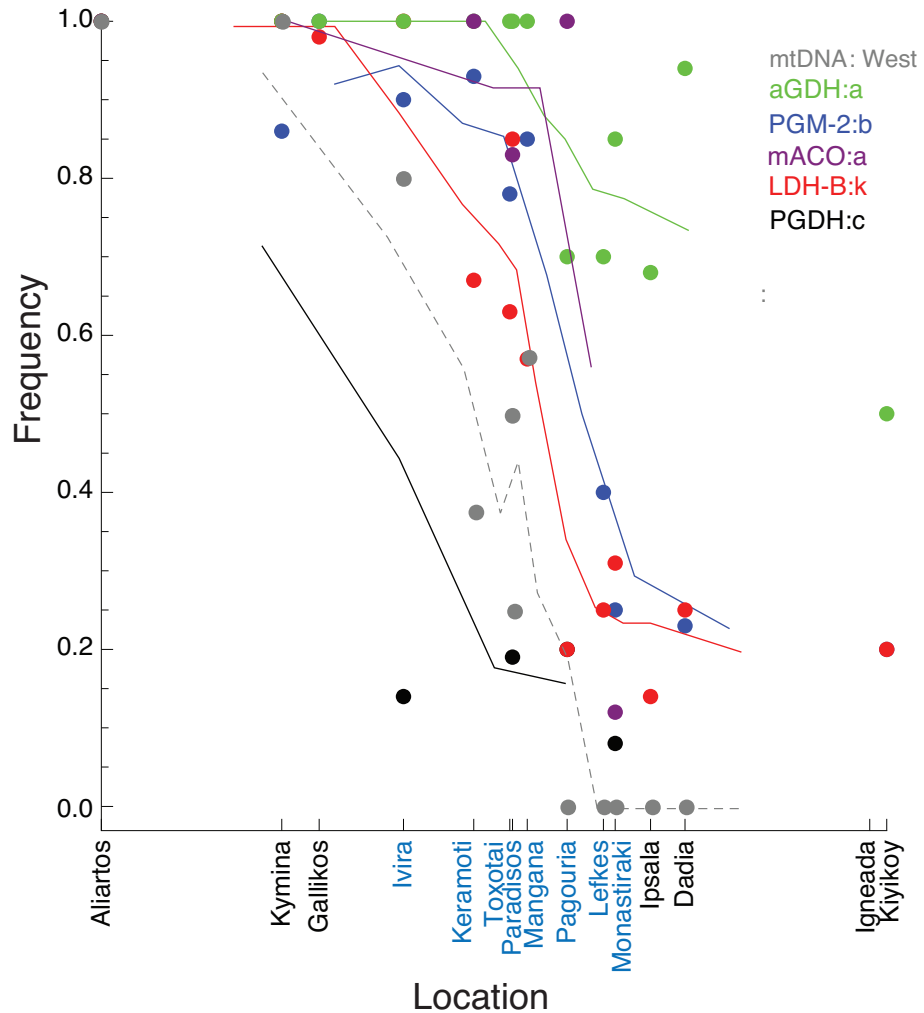
# Immigration into hybrid zone?



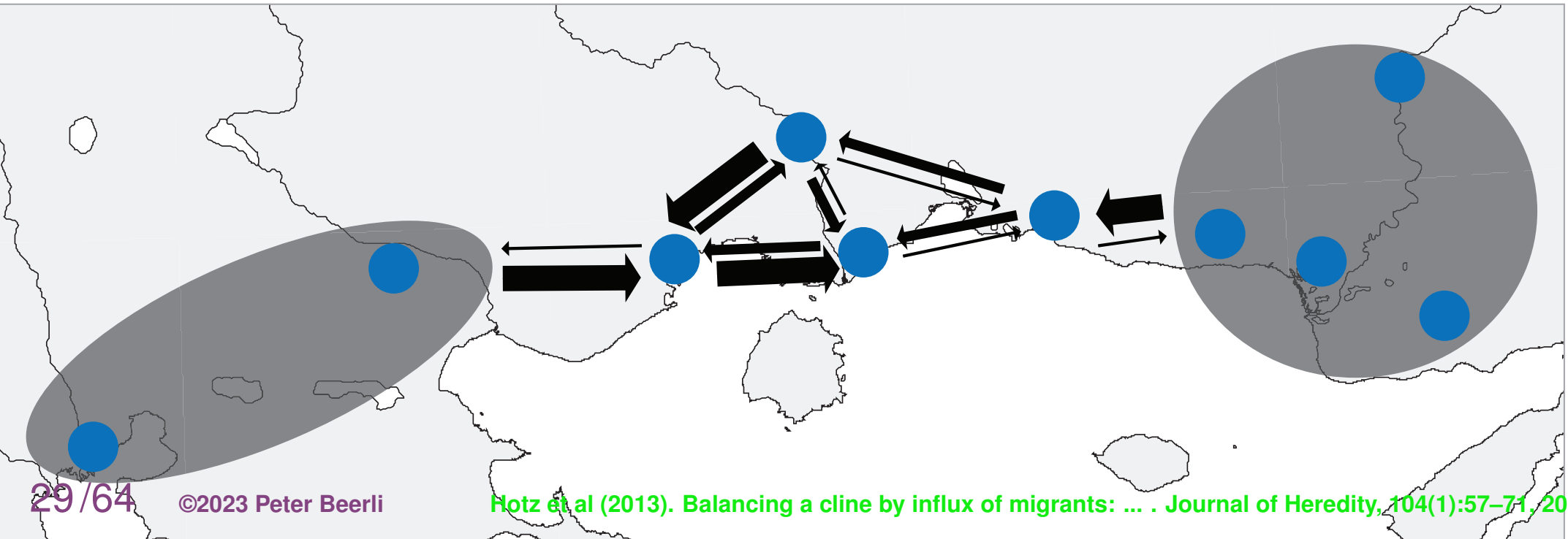
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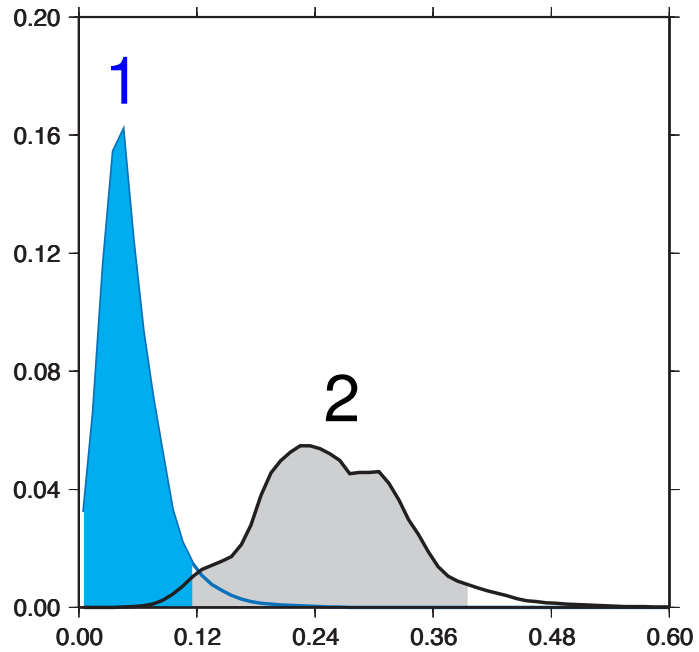


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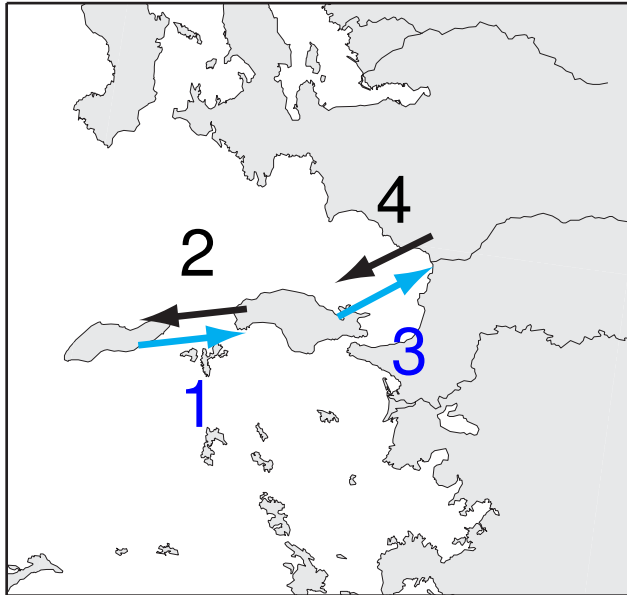


# Obvious migration pattern

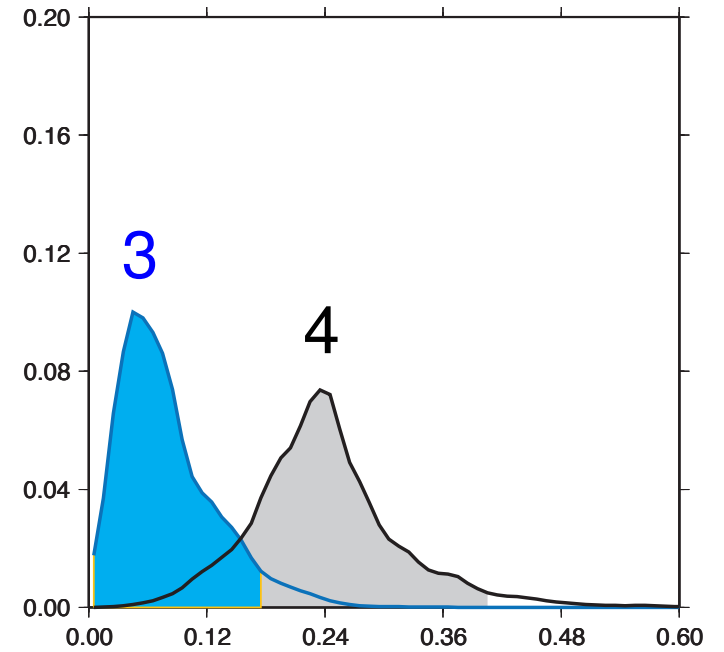
$$p(\mathcal{M}|D)$$



scaled migration rate



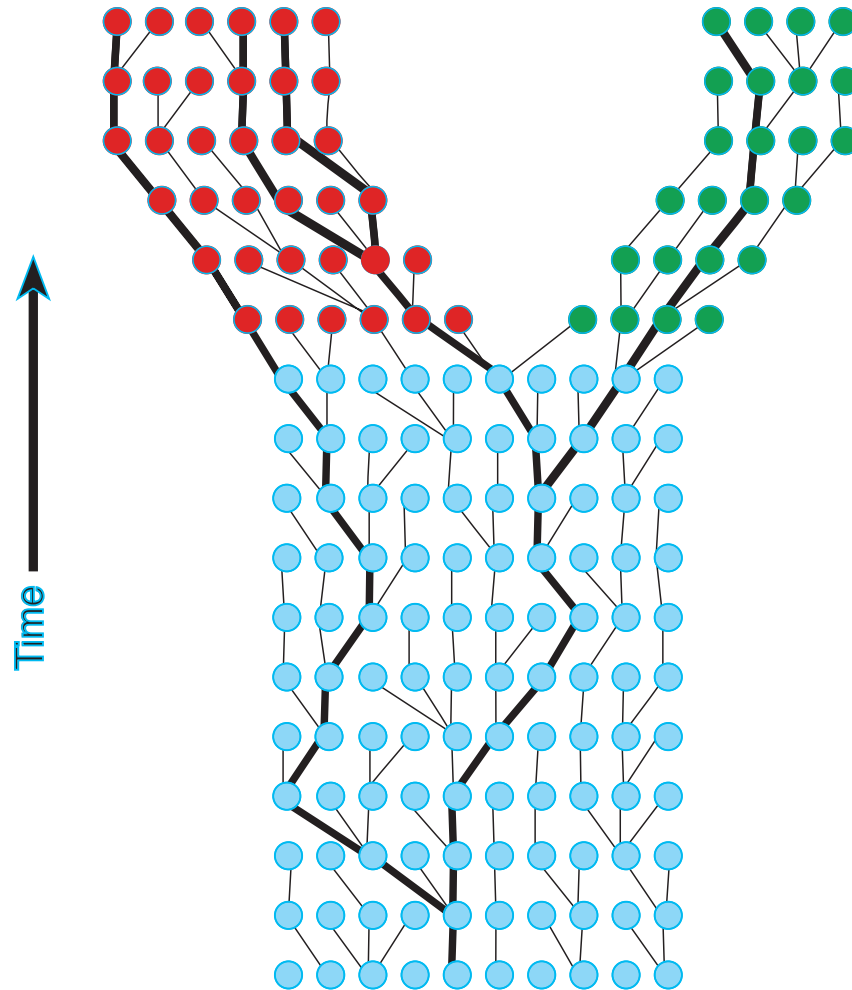
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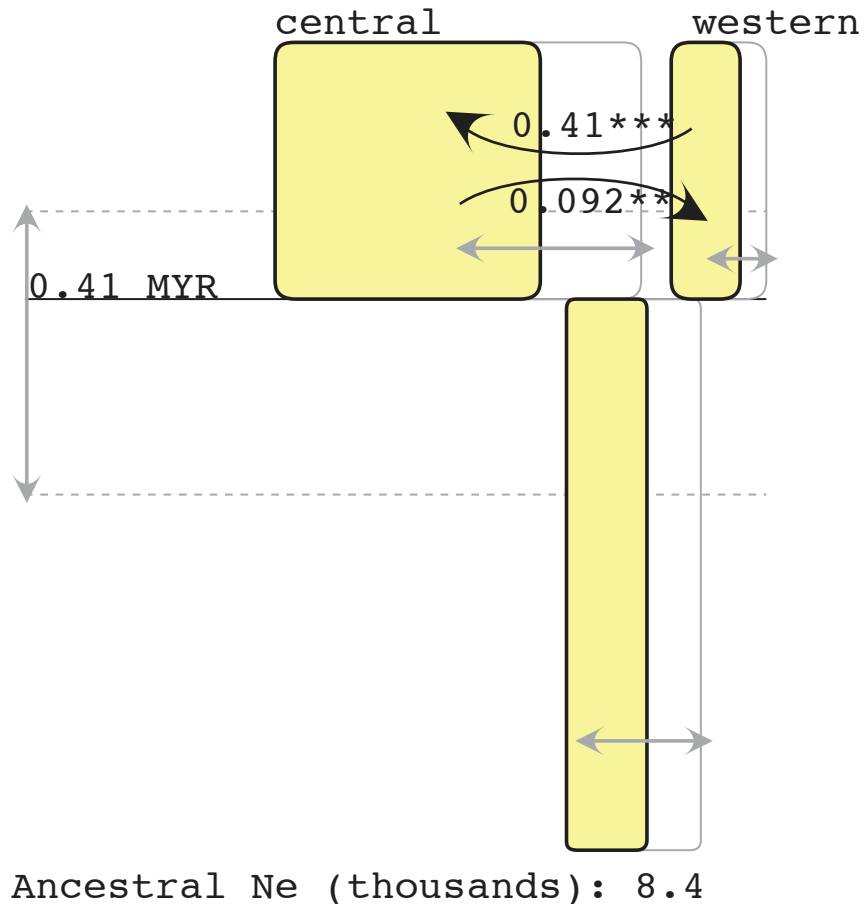
scaled migration rate



# Extensions of the basic coalescent



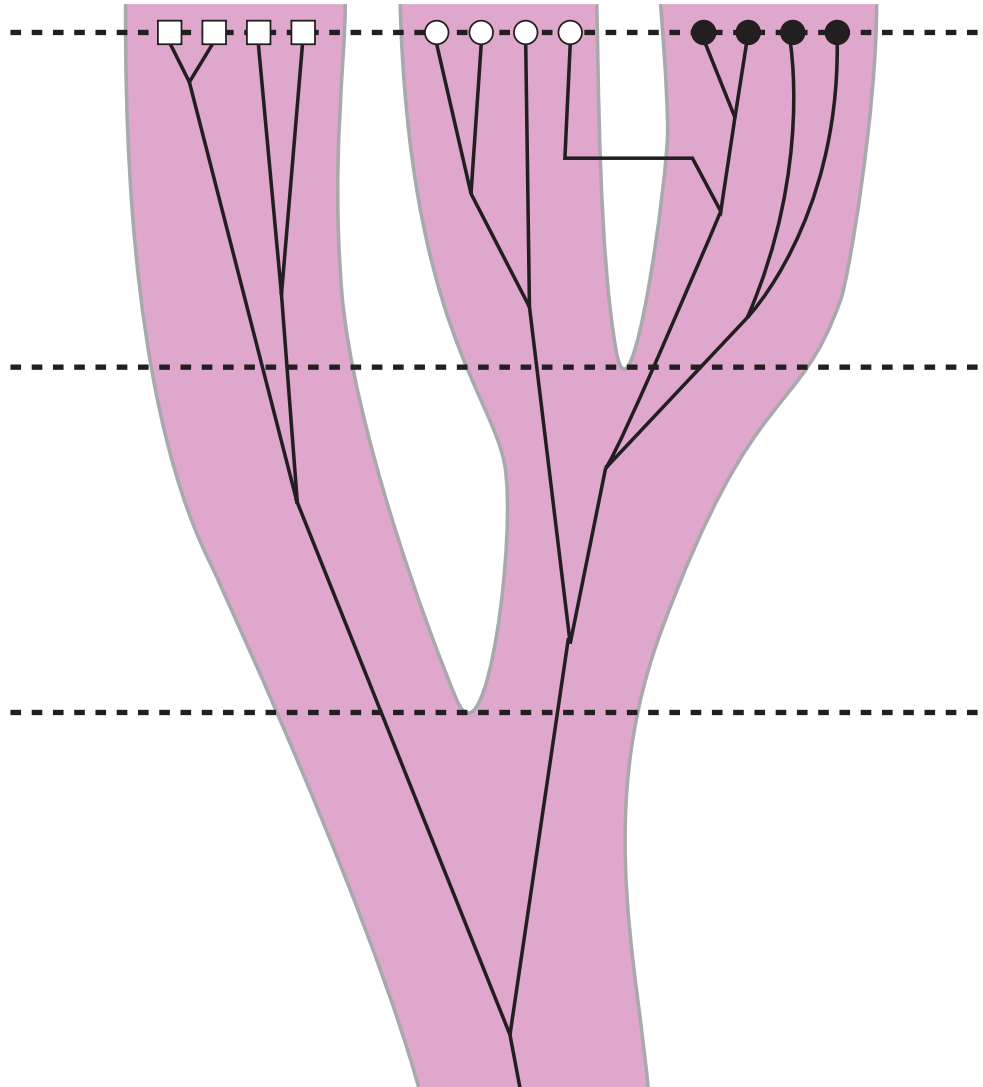
# Population splitting



IM: isolation with migration; co-estimation of divergence parameters, population sizes and migration rates. Not all datasets can separate migration from divergence, and multiple loci are helpful.



# Population splitting



# Population splitting

if we consider only a single individual that is today in population **A**. We also know that its ancestor was a member of population **B** then it will be only a matter of time to change the population label, but when?

Today

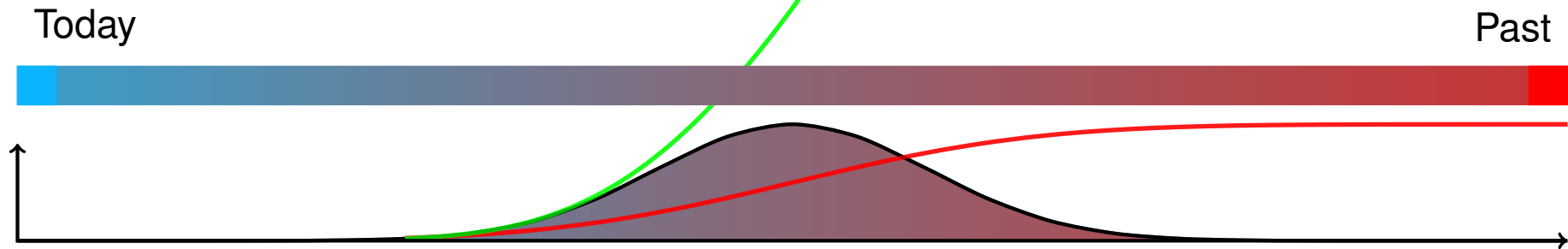


Past

(Beerli P., Ashki H., Mashayekhi S., and Palczewski M. 2022. Population divergence time estimation using individual lineage label switching. *G3 Genes – Genomes – Genetics*, 12(4), URL <https://doi.org/10.1093/g3journal/jkac040>.)

# Population splitting

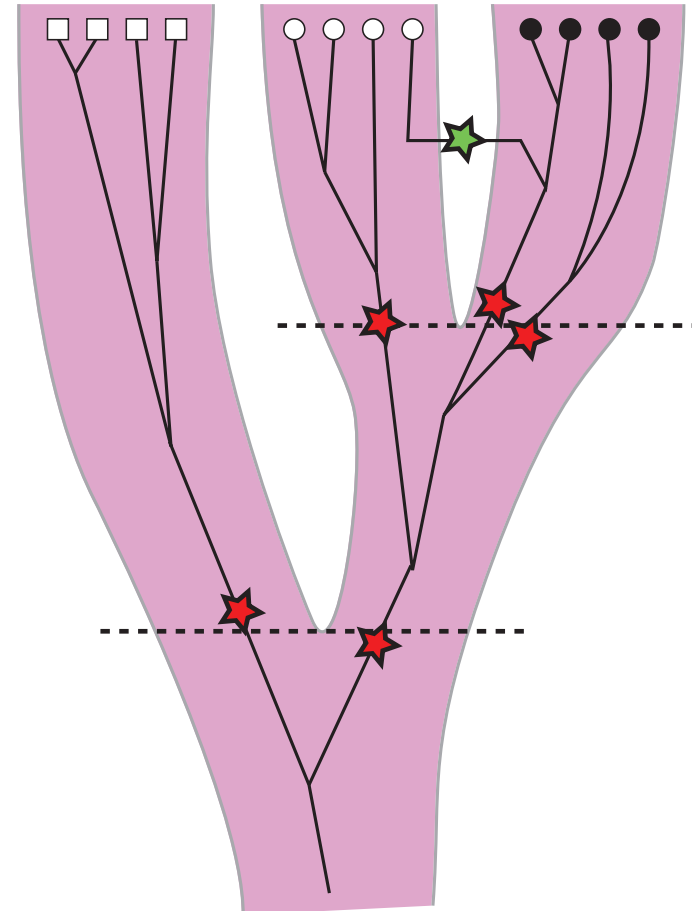
Looking backwards in time we could think about the risk of **A** turning into **B** which becomes larger and larger the further back in time the lineage goes. In the coalescence framework we are well accustomed to that thinking: we use the risk of a coalescent or the risk of a migration event. This risk can be expressed using the **hazard function** (or failure rate). Here we use the hazard function of the Normal distribution.



(Beerli P., Ashki H., Mashayekhi S., and Palczewski M. 2022. Population divergence time estimation using individual lineage label switching. *G3 Genes – Genomes – Genetics*, 12(4), URL <https://doi.org/10.1093/g3journal/jkac040>.)

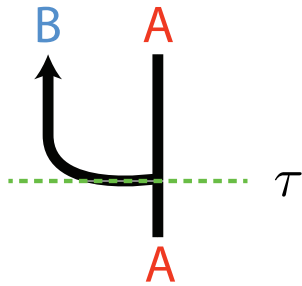
# Population splitting

One lineage is easy, but what about the genealogy? Each lineage is at risk of being in the ancestral population, thus we need to consider coalescences, migration events, and population label changing events. This results in genealogies that are realizations of migration and population splitting events.



# Population splitting

Comparison of estimated versus simulated divergence times for different number of loci



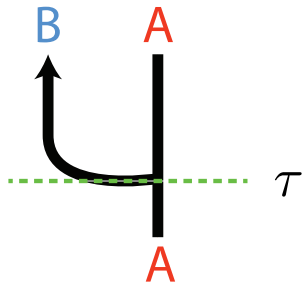
Model,  $\tau$   Genealogy

Genealogy  Sequence data

Sequence Data  Model   $\hat{\tau}$

# Population splitting

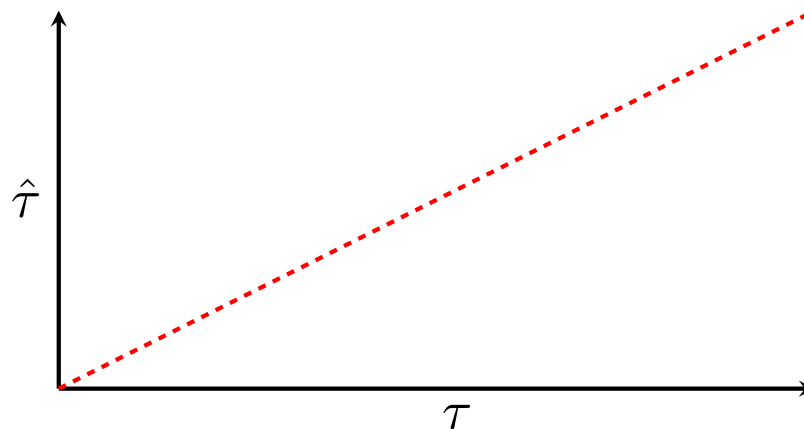
Comparison of estimated versus simulated divergence times for different number of loci



Model,  $\tau$   Genealogy

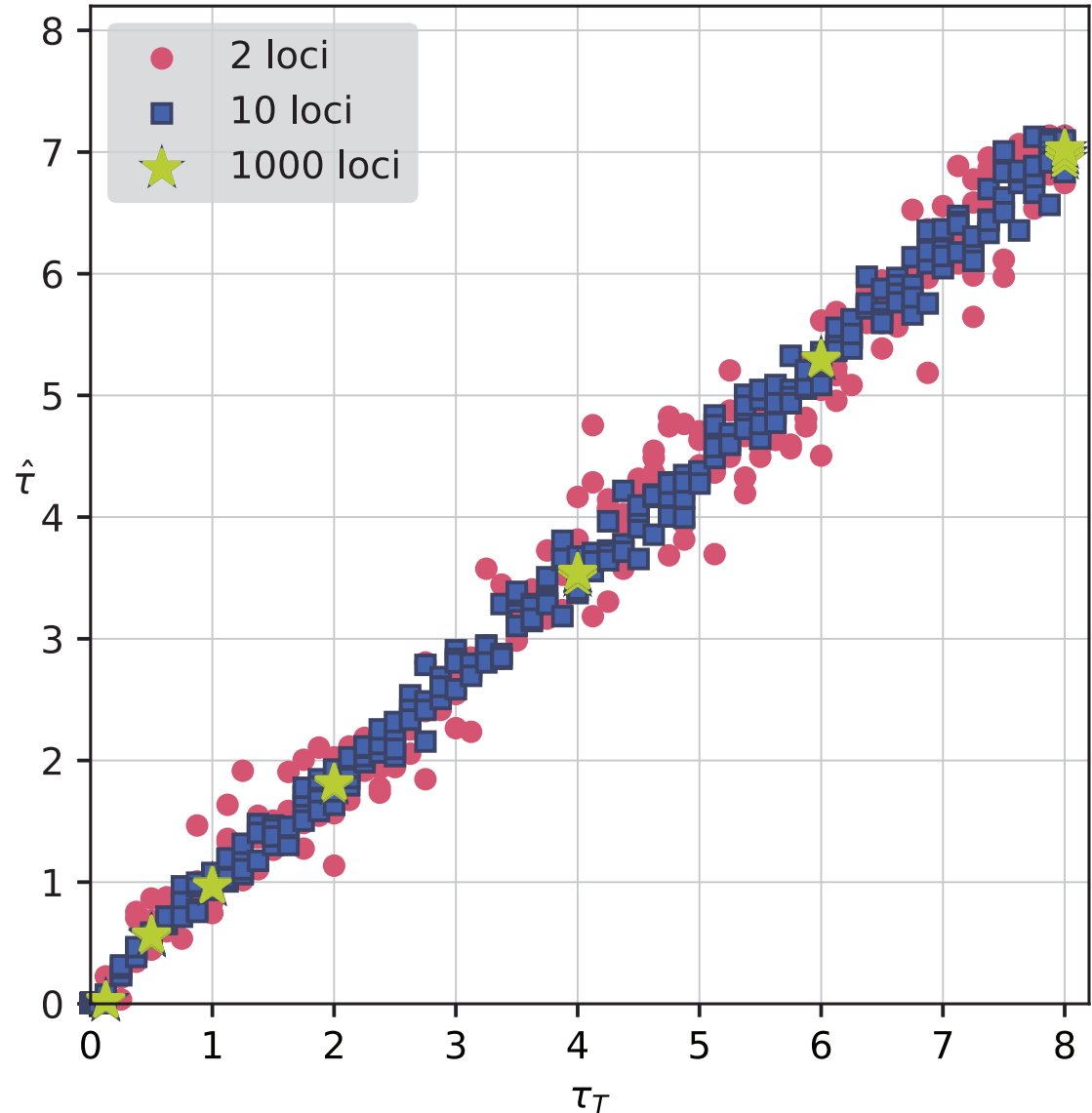
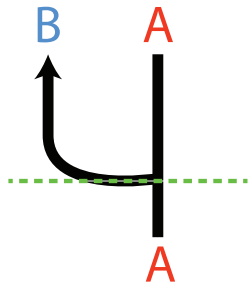
Genealogy  Sequence data

Sequence Data  Model   $\hat{\tau}$

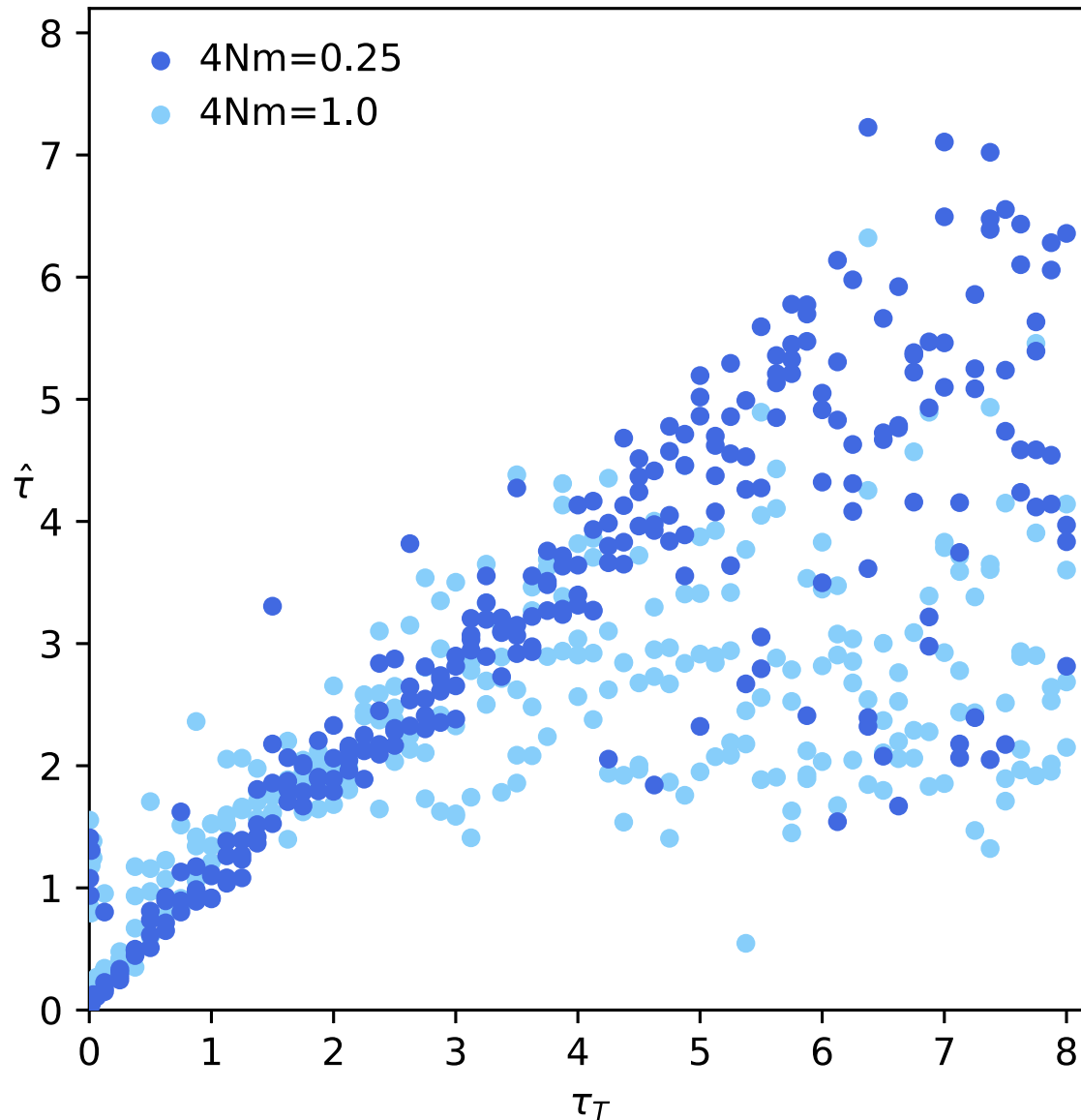
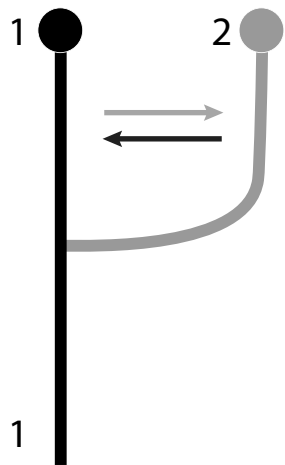


# Population splitting

Comparison of estimated versus simulated divergence times for different number of loci



# Population splitting





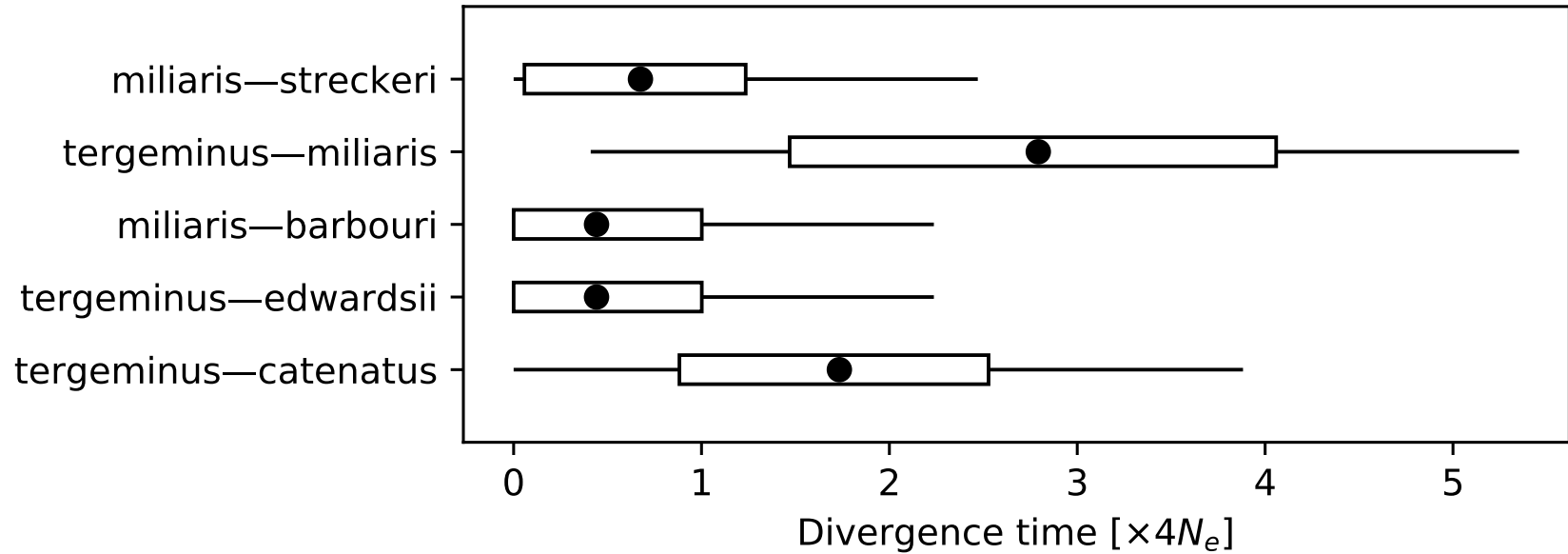
# Population splitting



# Phylogenetics of pygmy rattle snakes



# Population splitting



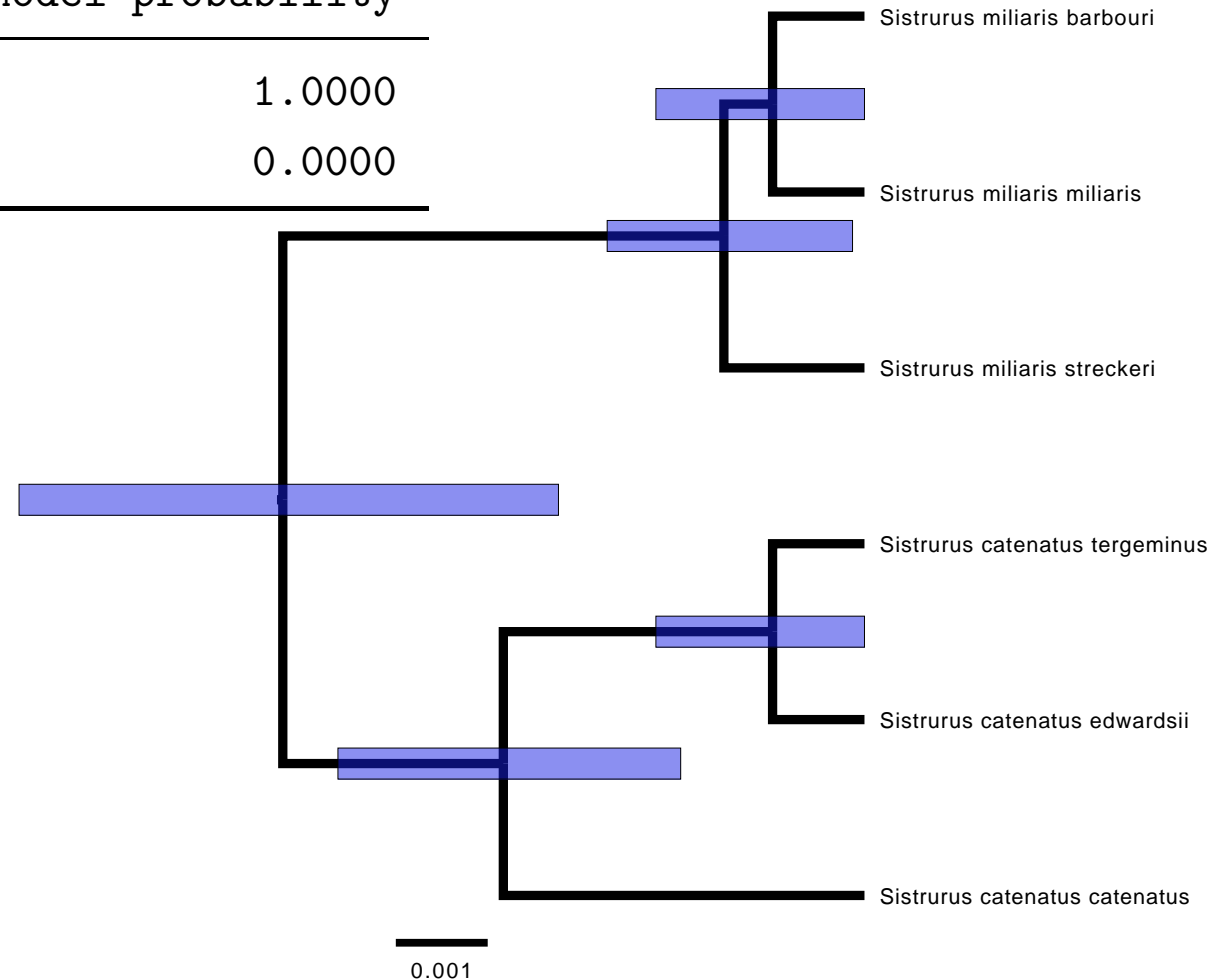
Estimation of splitting dates of 6 subspecies of pygmy rattlesnakes using MIGRATE (data from Kubatko et al. 2011)



# Population splitting: Pygmy rattle snakes

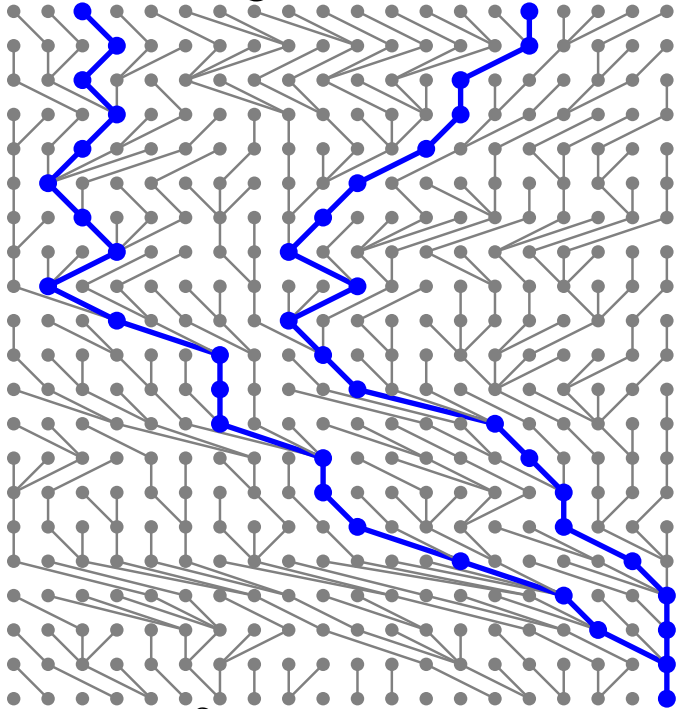
Estimation of splitting dates of 6 subspecies of pygmy rattle snakes using MIGRATE (data from Kubatko et al. 2011)

Model	Log(mL)	LBF	Model-probability
1: 3 species:	-15887.49	0.00	1.0000
2: 6 species:	-15961.95	-74.46	0.0000



# Offspring number is a random variable

Wright-Fisher

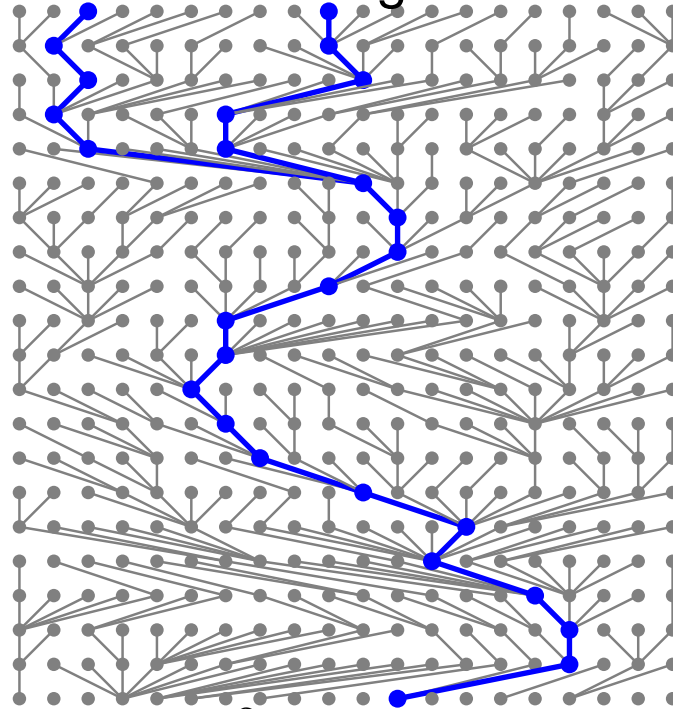


$$\sigma_{\text{offspring}}^2 \simeq 1$$

$$\mathbb{E}(t) = 2N$$

generation time  $g = 1$

Canning

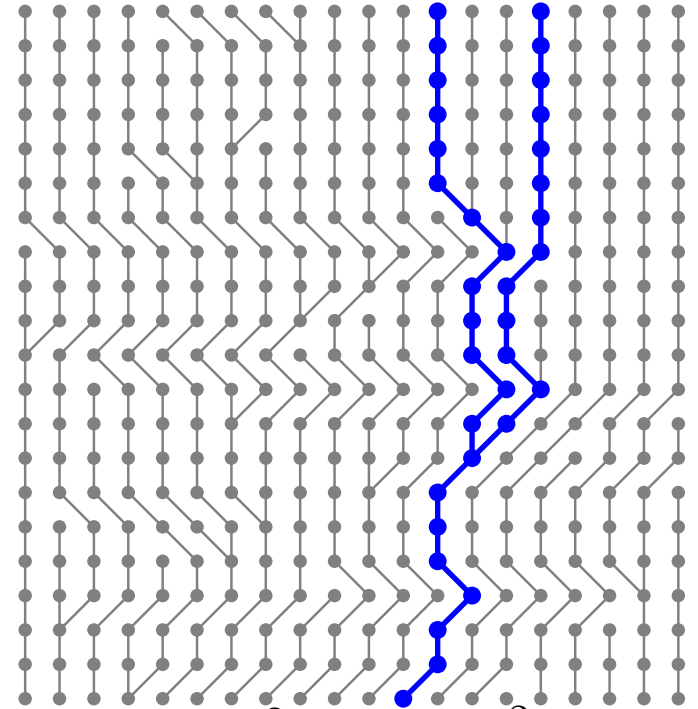


$$\sigma_{\text{offspring}}^2 = x$$

$$\mathbb{E}(t) = 2N/x$$

$g = 1$

Moran

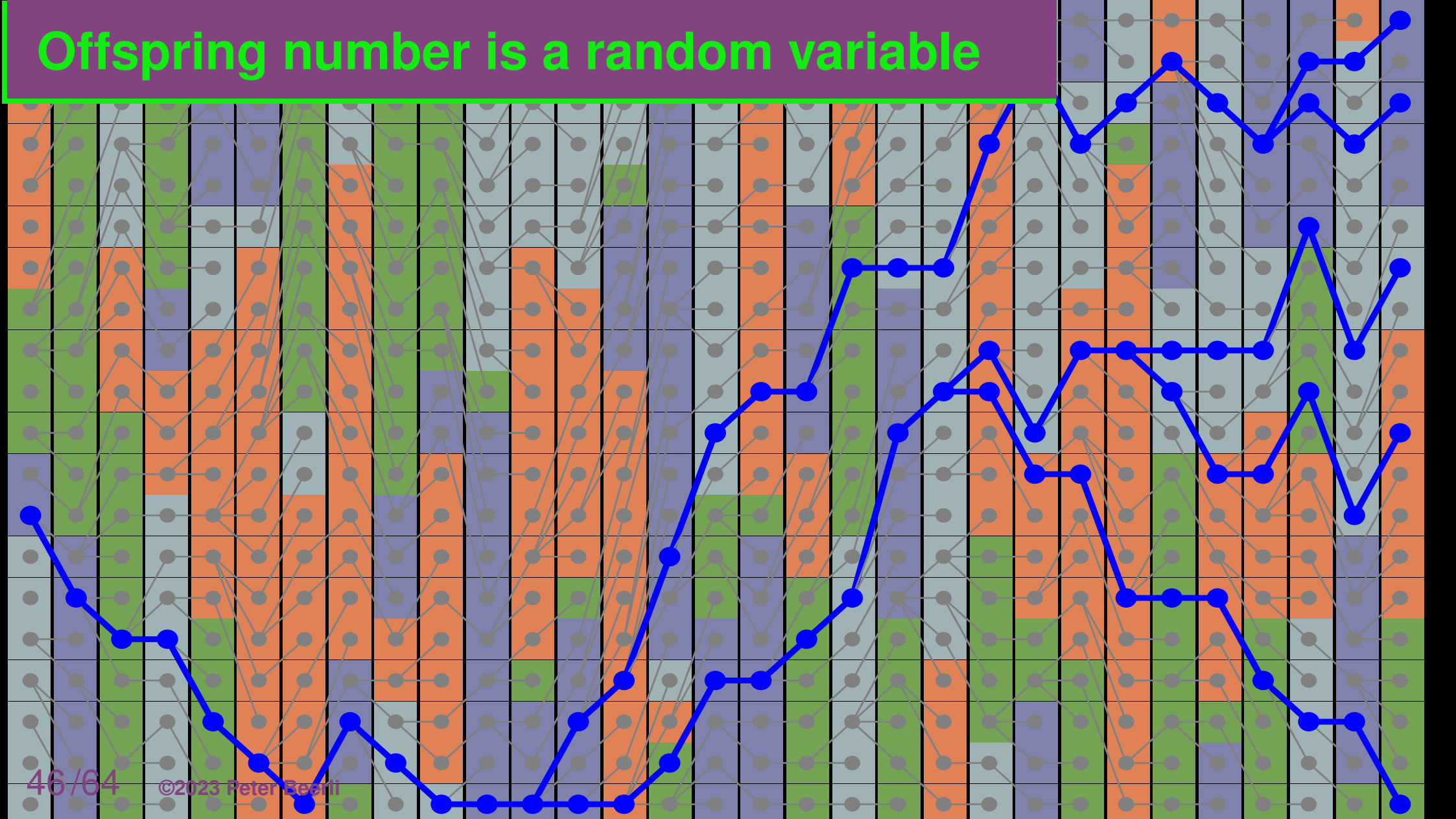


$$\sigma_{\text{offspring}}^2 = \frac{2}{2N}$$

$$\mathbb{E}(t) = \frac{1}{2}(2N)^2$$

$g = 2N$

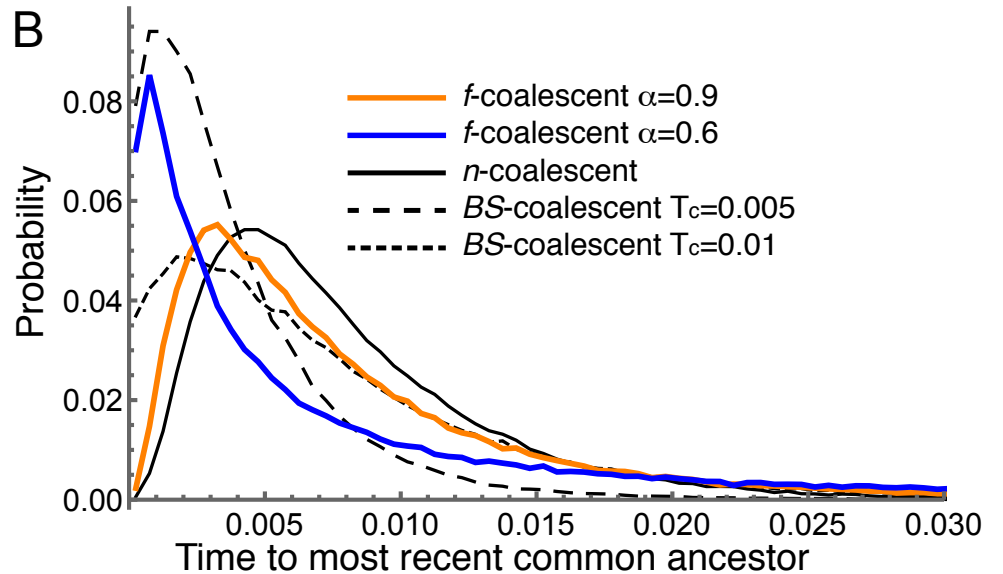
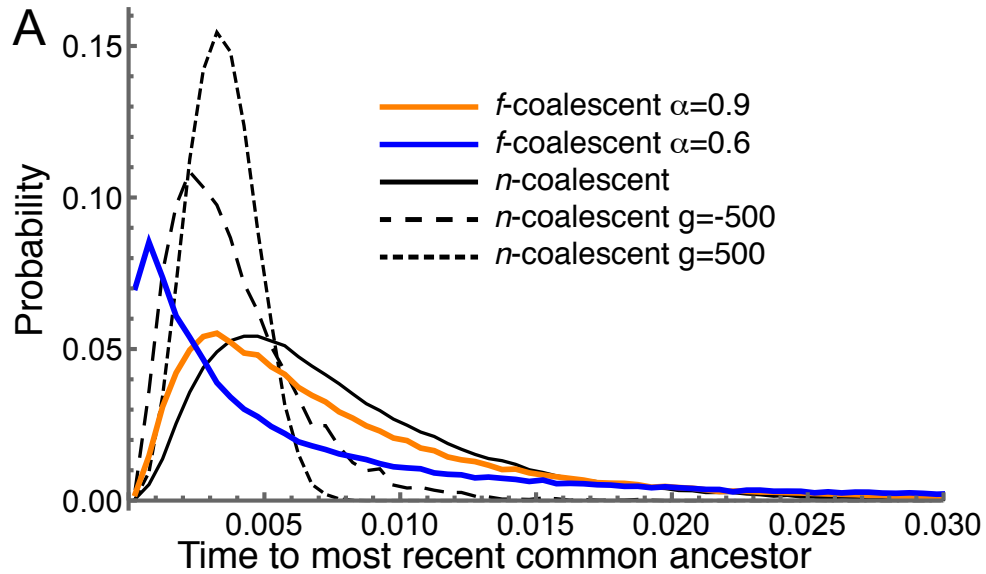
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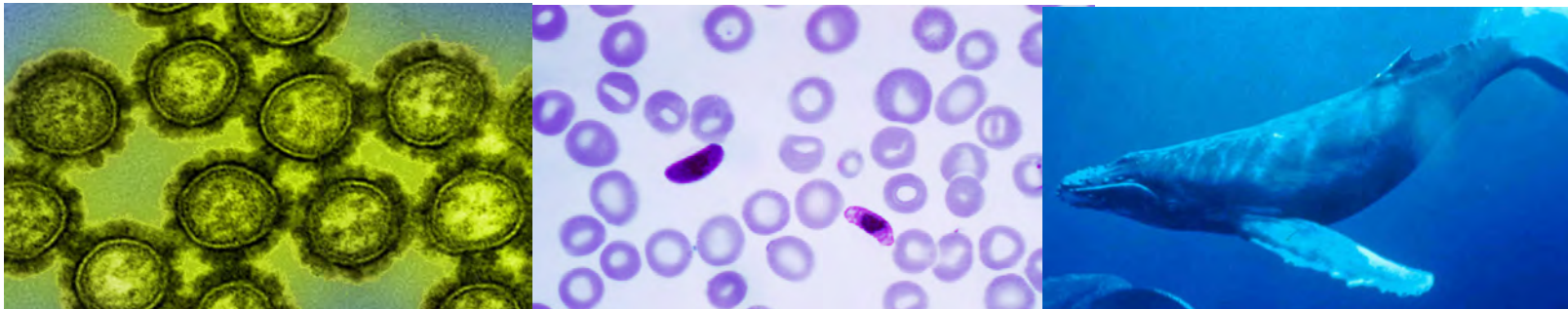
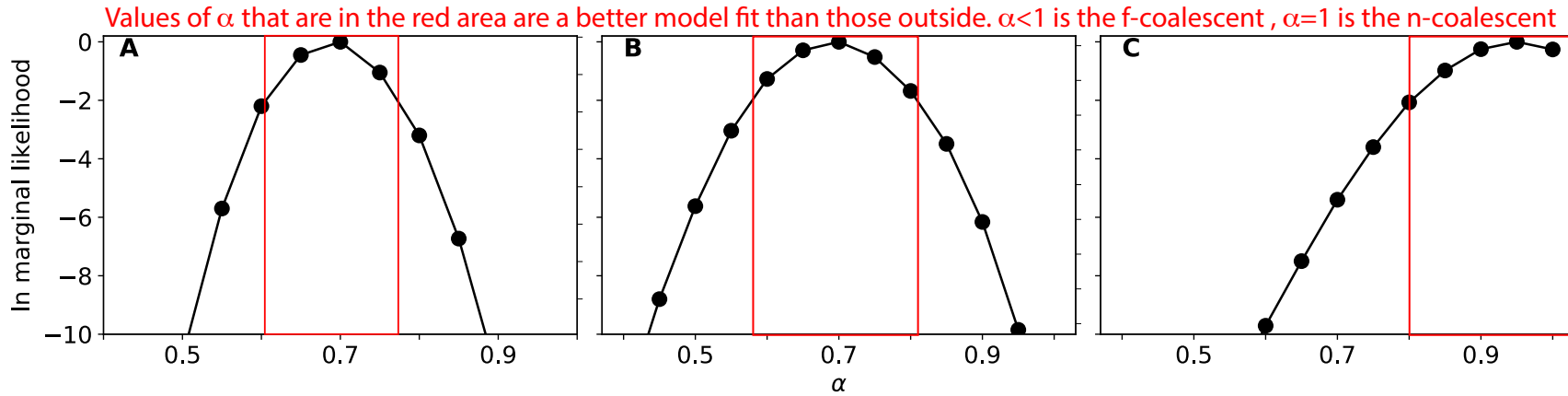
The habitat affects the potential of producing offspring and the quality differences are unpredictable. This will lead to a higher variance of the number of offspring: the Canning model allows arbitrary fixed variance of offspring number. We can treat this variance as a random variable.

# Extensions of Coalescence theory





# Different $\alpha$ : model comparison with real data



Model selection using relative marginal likelihoods of DNA sequence from the flu (H1N1), Malaria parasites, Humpback whales.

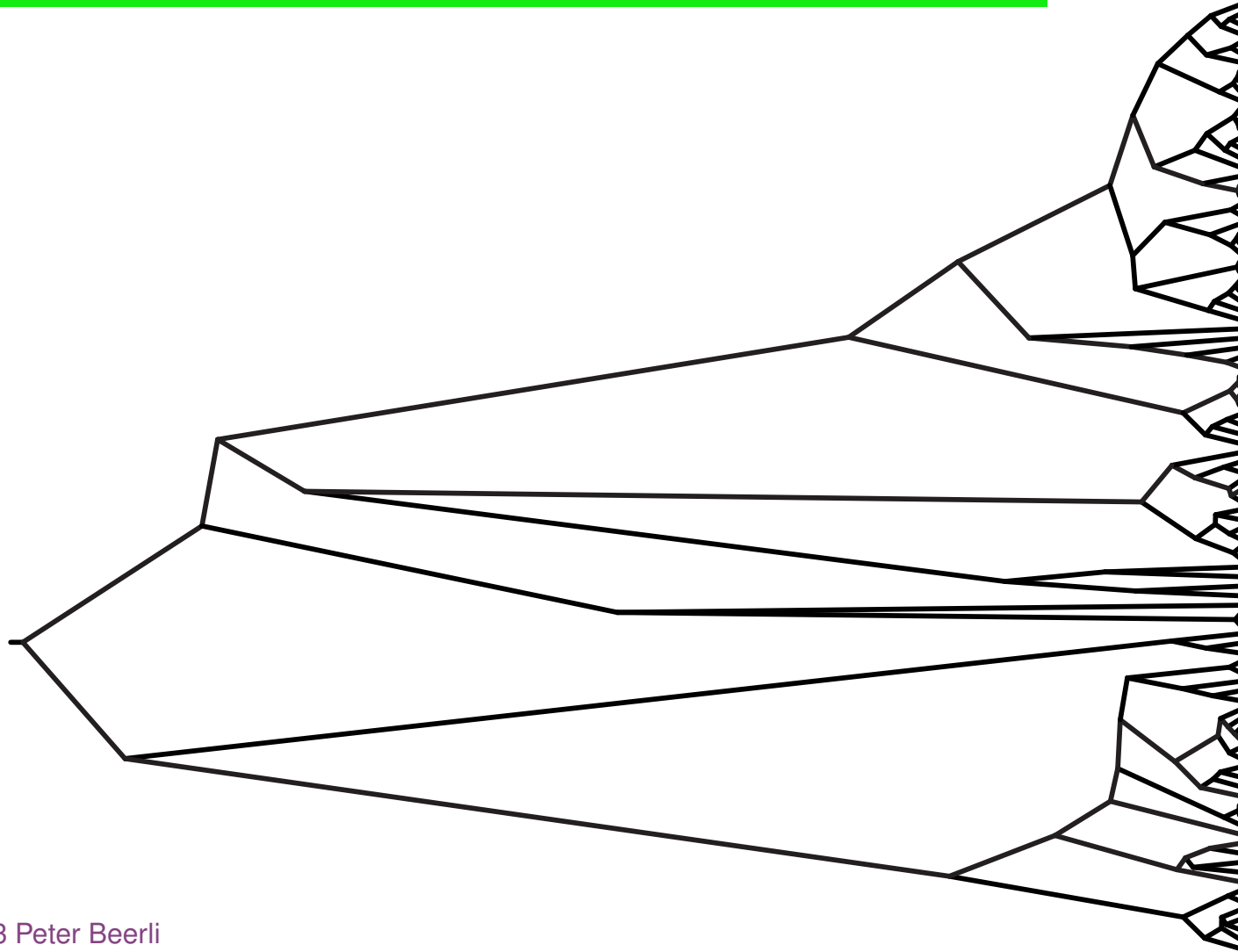
# Robustness of the coalescence



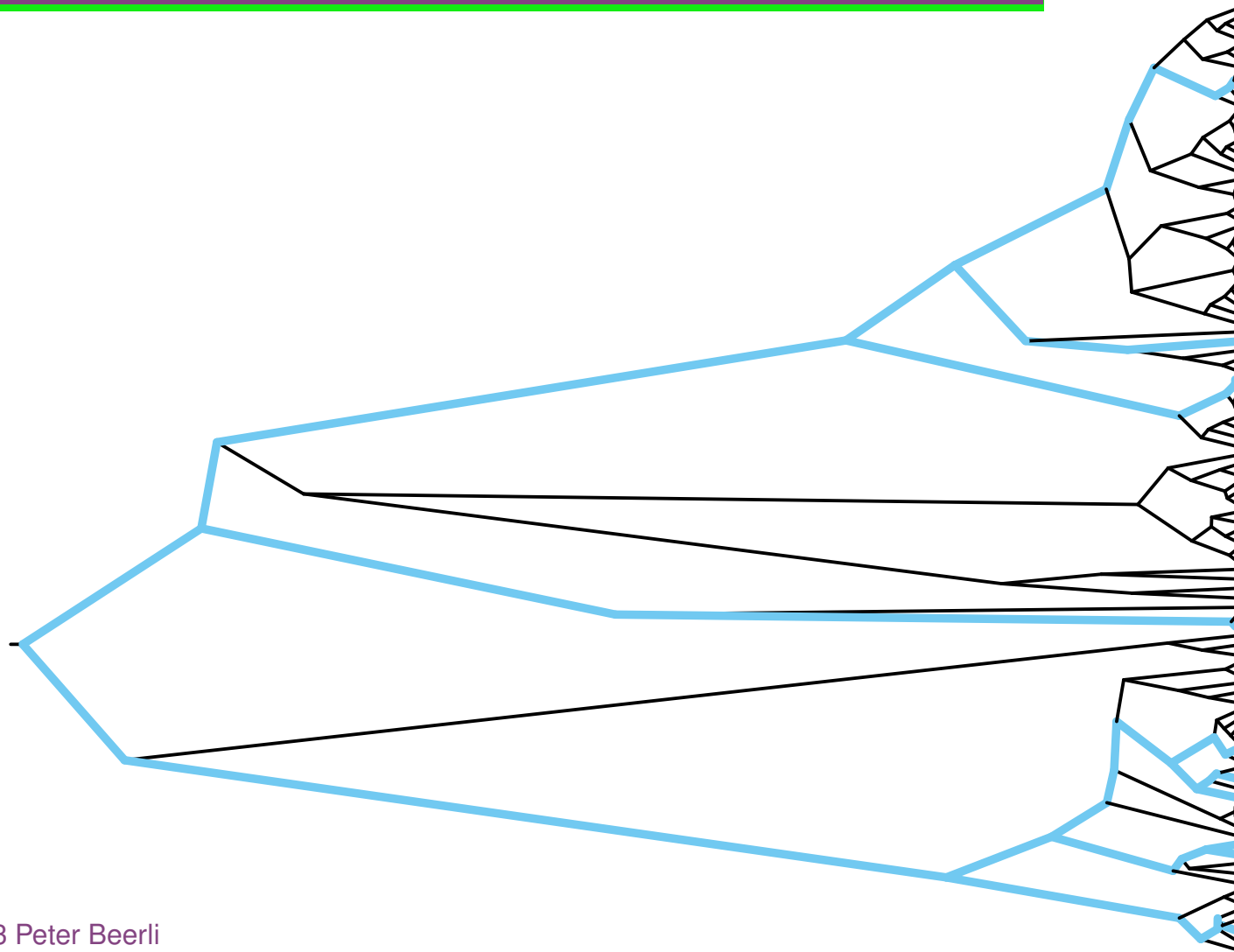
# Violating assumptions

- ◆ Required samples (small samples/ deep coalescence)
- ◆ Average over long time
- ◆ Recombination

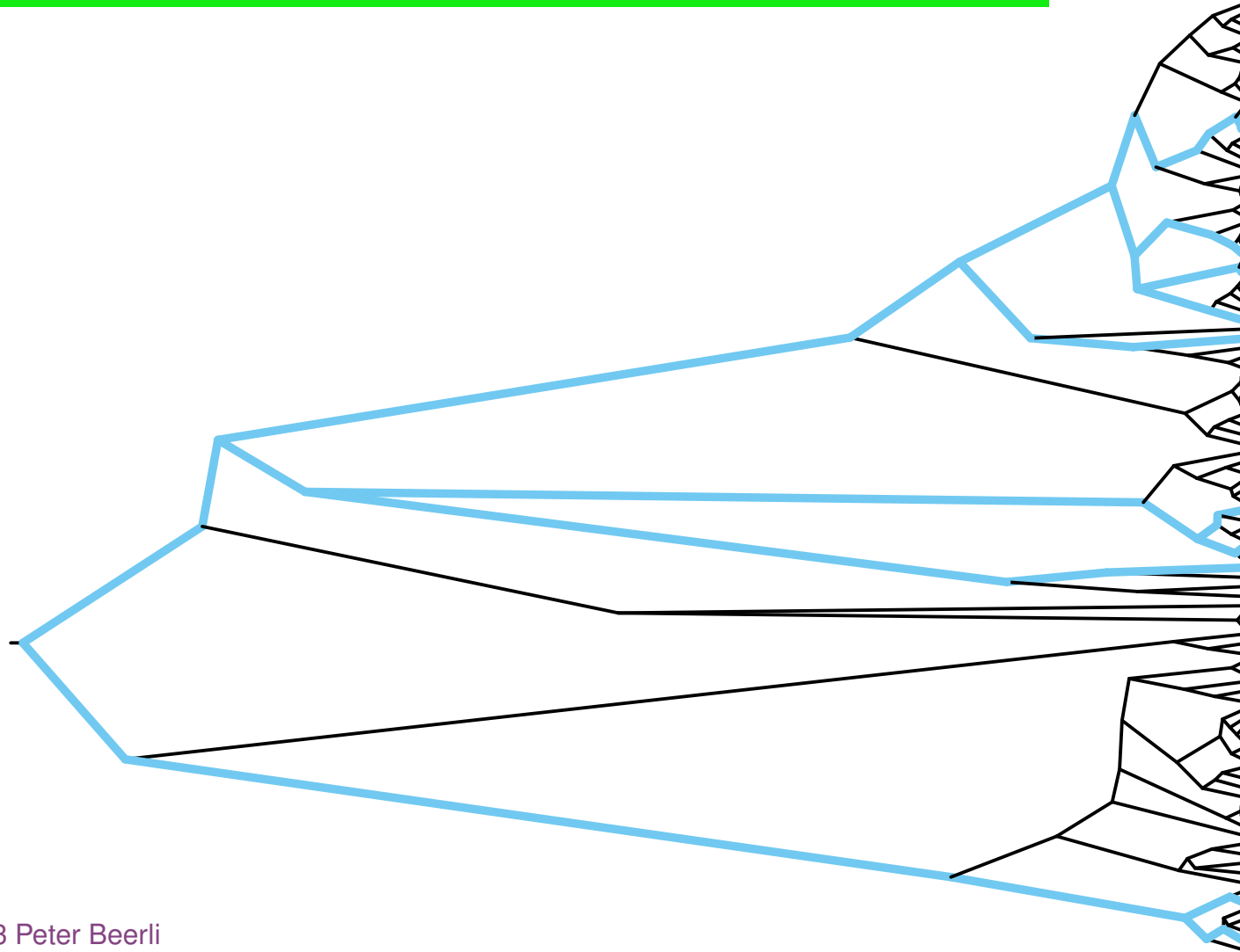
Required samples is small



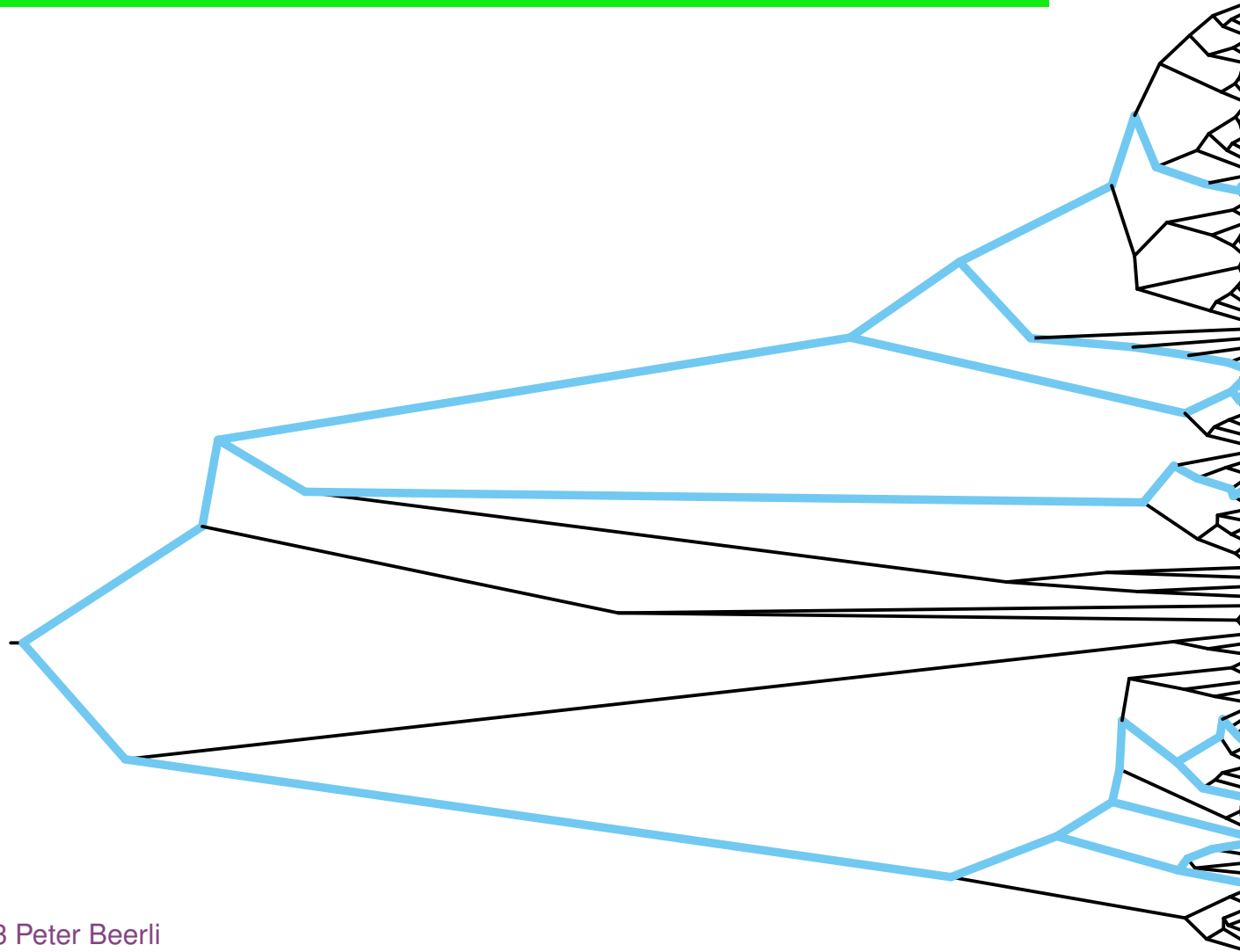
# Required samples is small



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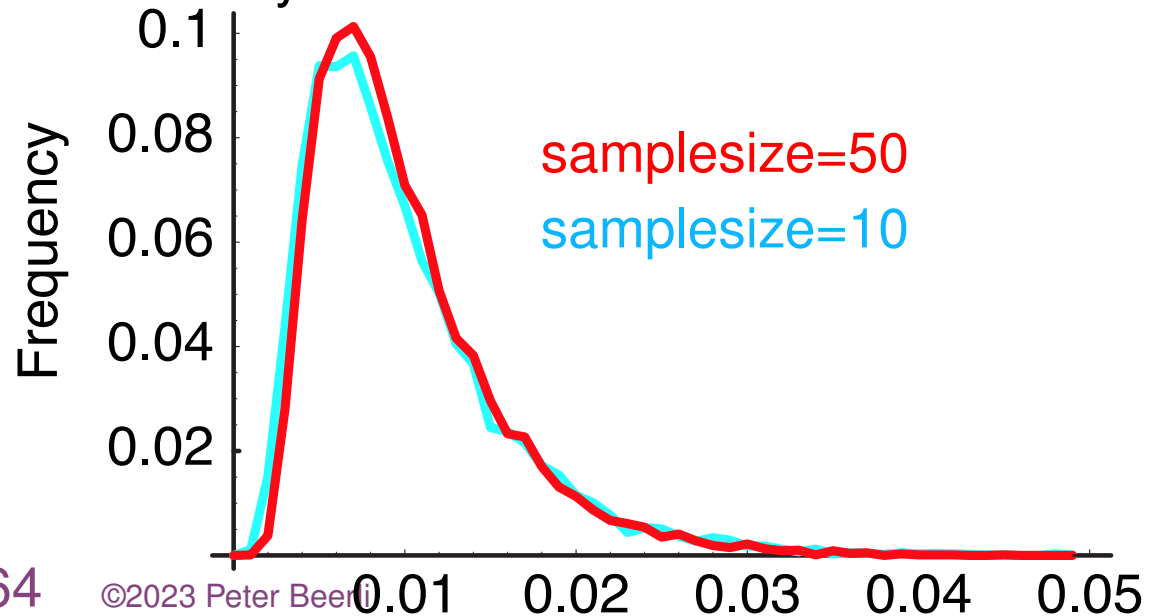


# Required samples is small



# Required samples is small

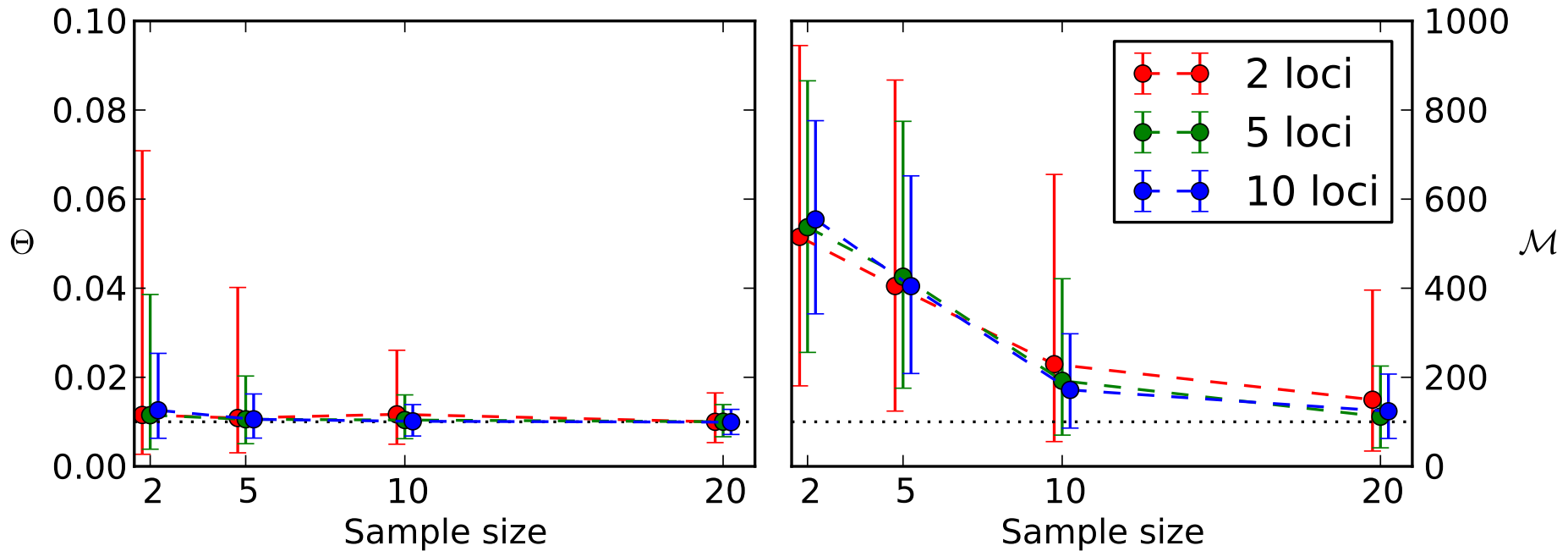
- ◆ The time to the most recent common ancestor is robust to different sample sizes.
- ◆ Simulated sequence data from a single population have shown that after 8 individuals you should better add another locus than more individuals.



Felsenstein (2005)  
Pluzhnikov and Donnelly  
(1996)



# Required number of samples is small

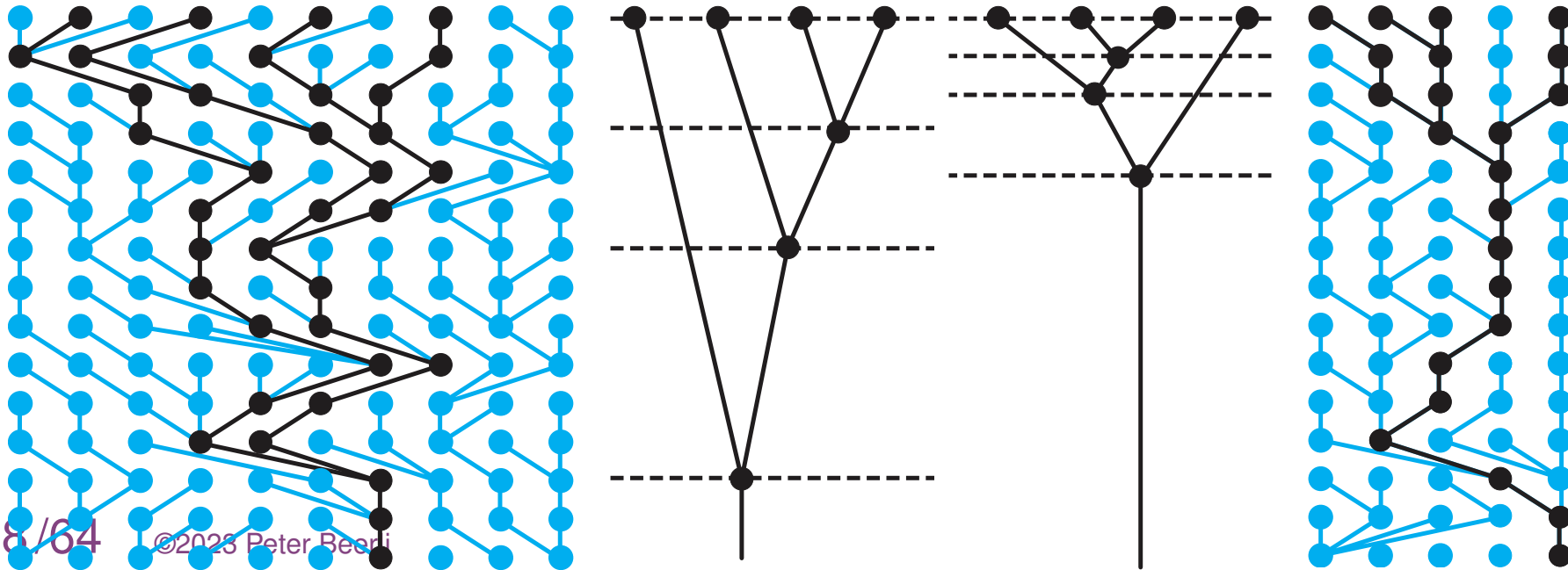


Medium variability DNA dataset: Mutation-scaled population size  $\Theta$  and mutation-scaled migration rate  $M$  versus sample size for 2, 5, and 10 loci. The true  $\Theta_T = 0.01$  is marked with the dotted gray line;  $M = 100$

# Average of parameters over long time

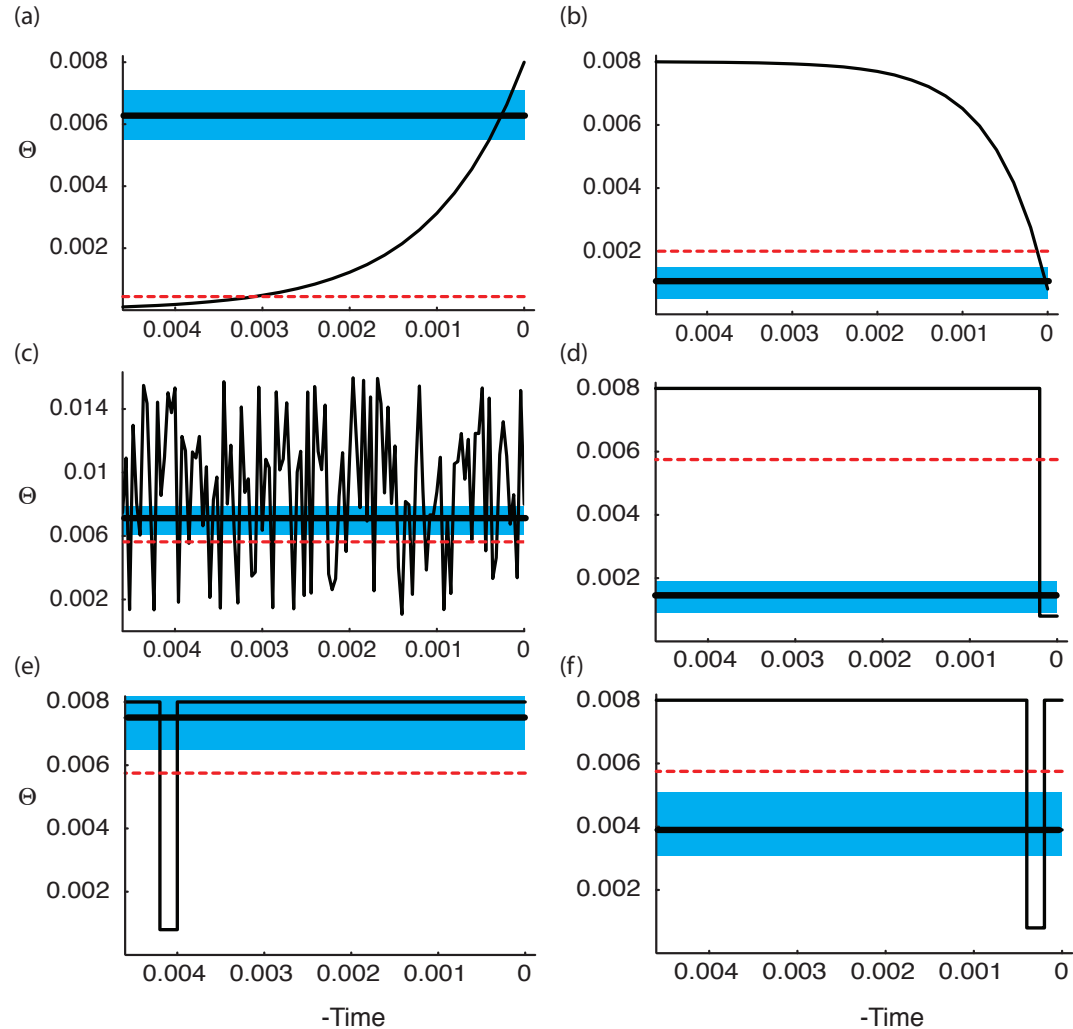
Researchers from the frequency-based camp claim that the coalescence-based methods are working on an evolutionary time-scale and therefore are not really usable in a conservation genetics or management context.

There is some truth to this claim because the time scale for the genealogies is in generations and with large populations such genealogies are deep, but ...



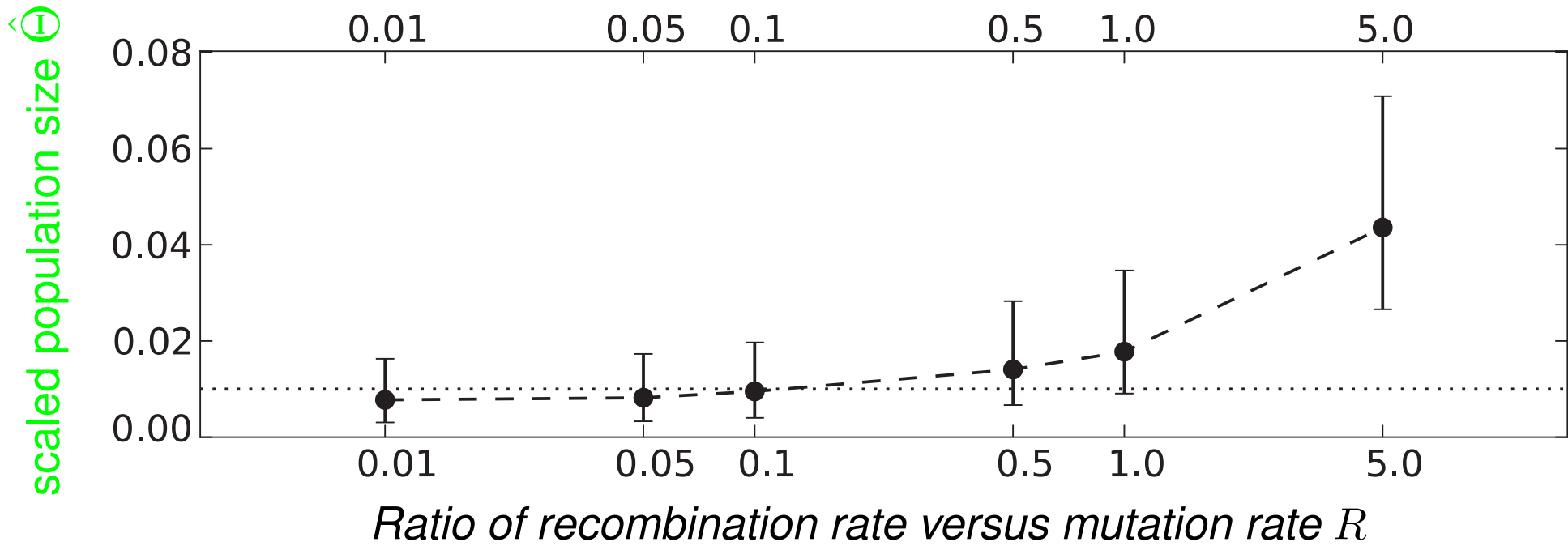
# Average of parameters over long time

- True value
- MIGRATE estimate
- Support interval
- - - Harmonic mean



# Ignoring recombination

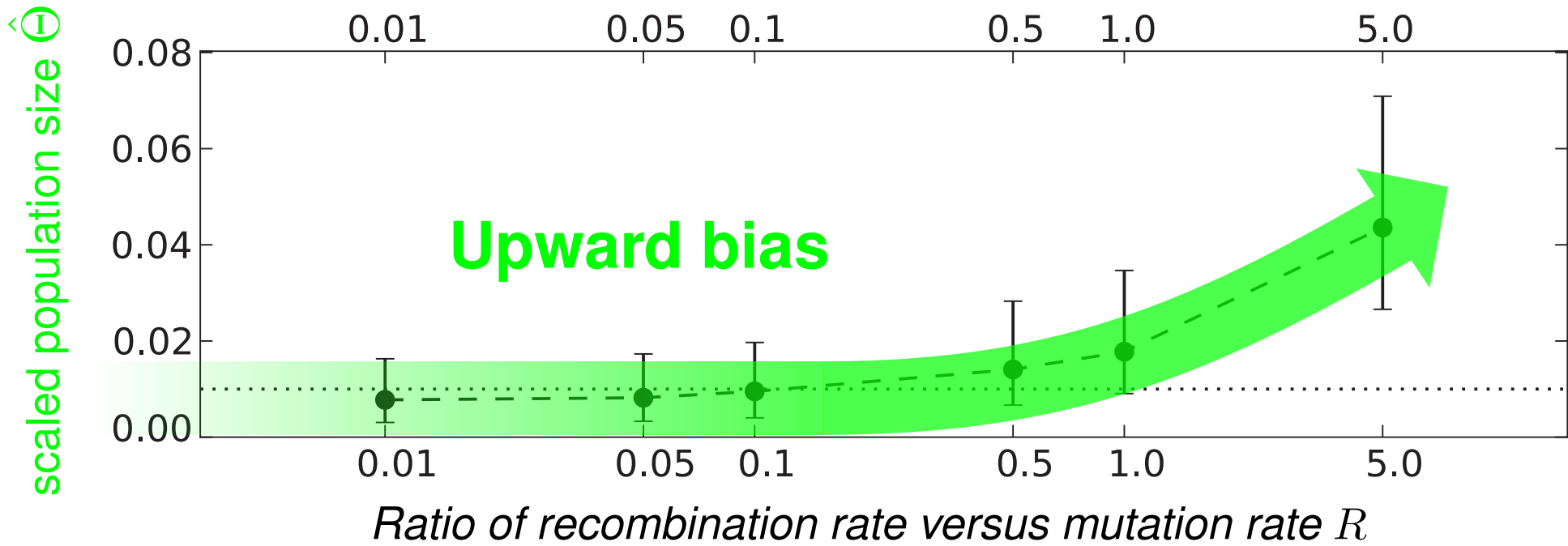
~500 simulated datasets



Averages with 95% credibility intervals of runs with different mutation-scaled recombination rates  $R = C/\mu$ . The dotted lines mark the 'true' values.

# Ignoring recombination

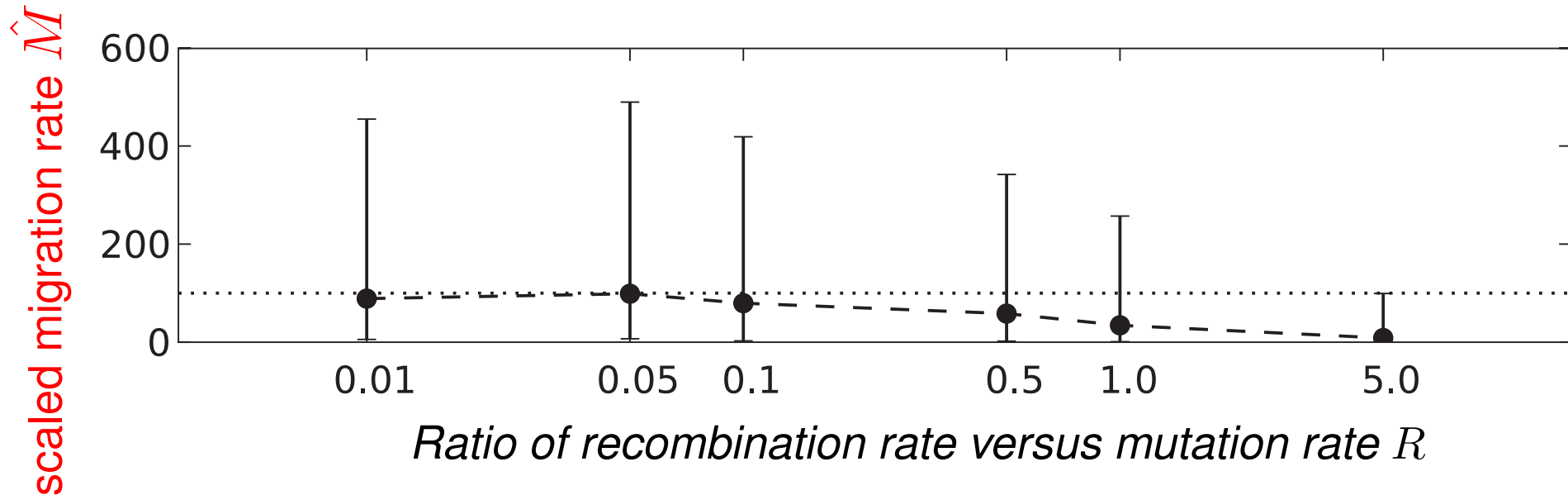
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Averages with 95% credibility intervals of runs with different mutation-scaled recombination rates  $R = C/\mu$ . The dotted lines mark the 'true' values.

# Ignoring recombination

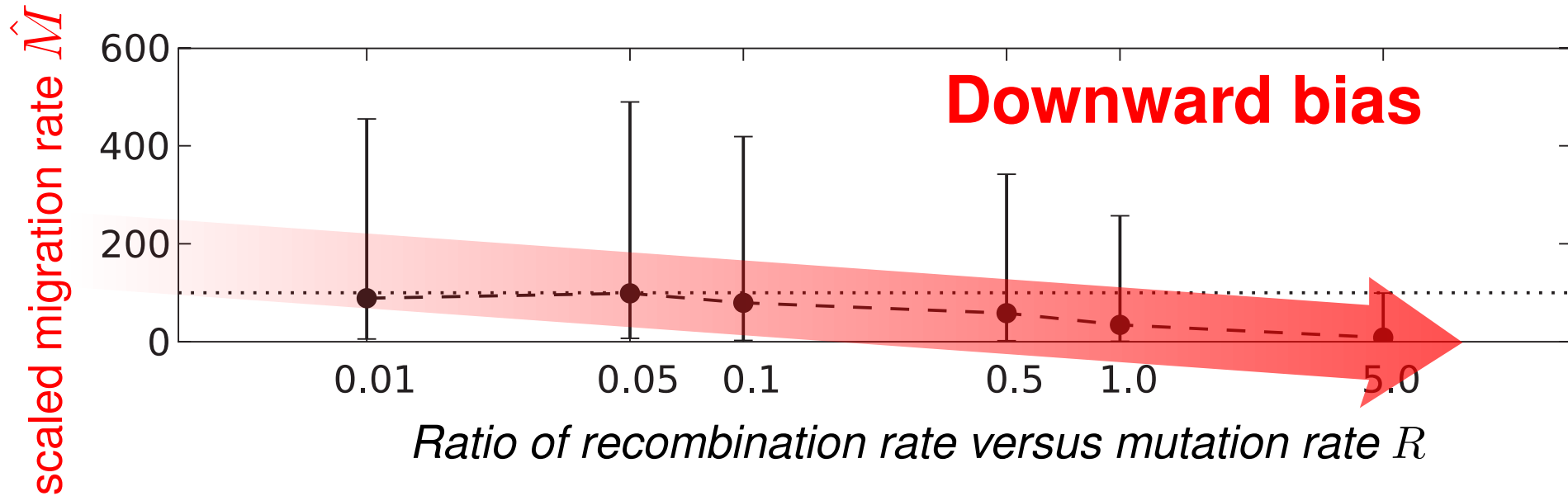
~500 simulated datasets



Averages with 95% credibility intervals of runs with different mutation-scaled recombination rates  $R = C/\mu$ . The dotted lines mark the 'true' values.

# Ignoring recombination

~500 simulated datasets



Averages with 95% credibility intervals of runs with different mutation-scaled recombination rates  $R = C/\mu$ . The dotted lines mark the 'true' values.

# Outlook

- ◆ We will have a lab later this week where you will learn about Bayesian model selection with MIGRATE using a lab where we differentiate between 8 simple population models that include "speciation" (or population splitting) with and without migration using a data set of complete genomes of Zika viruses.

