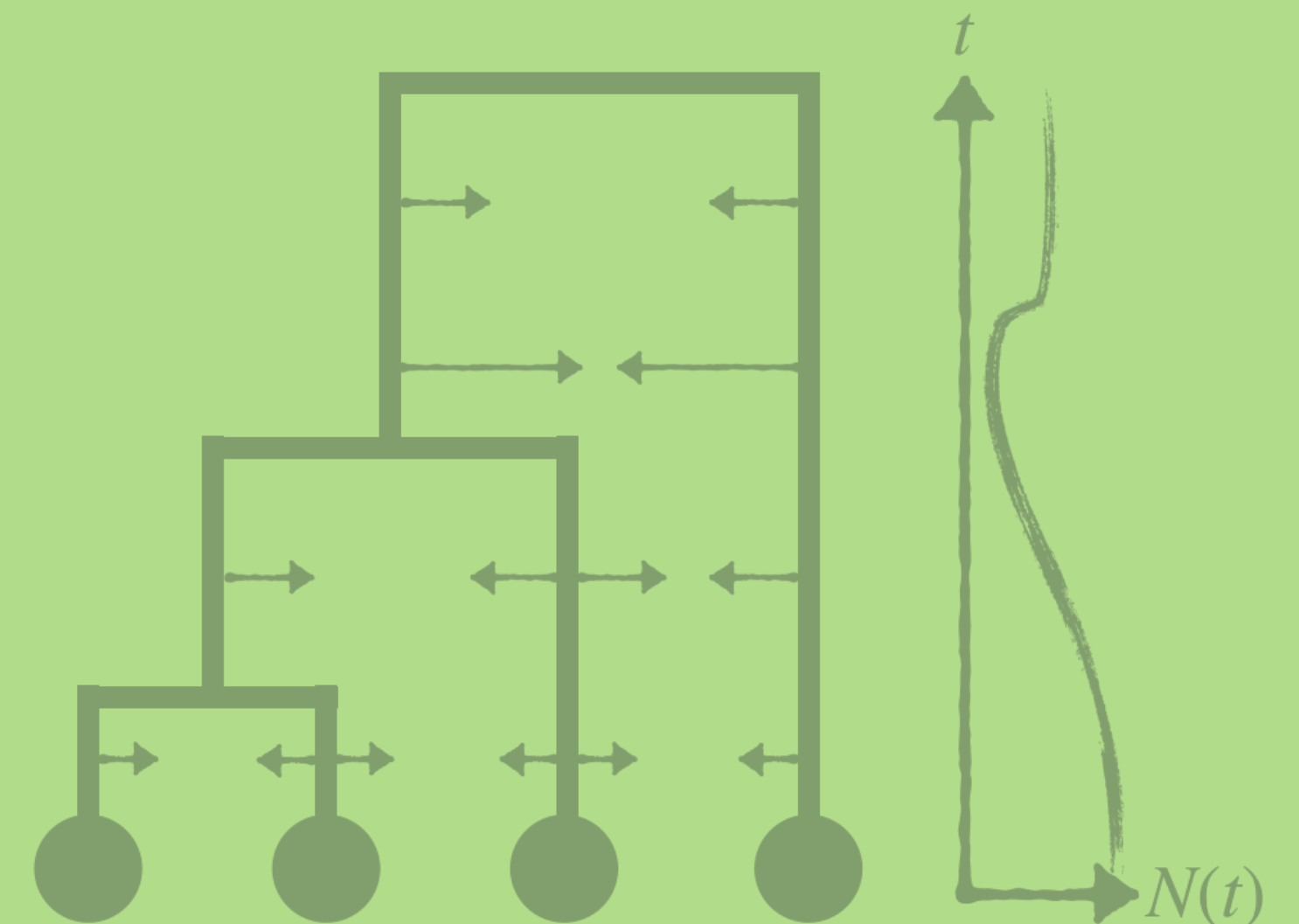


GENOME 541: population genetic inference

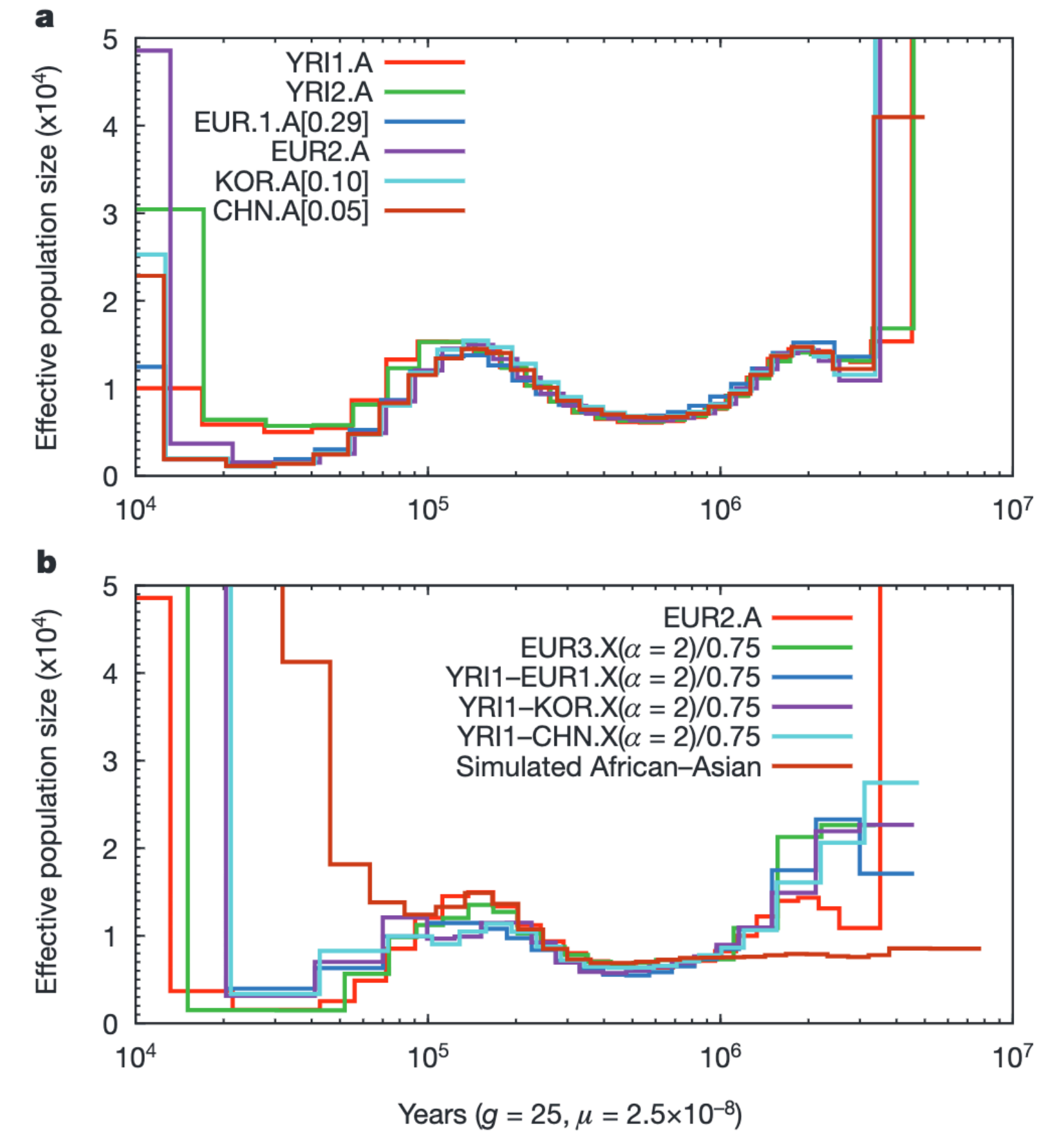
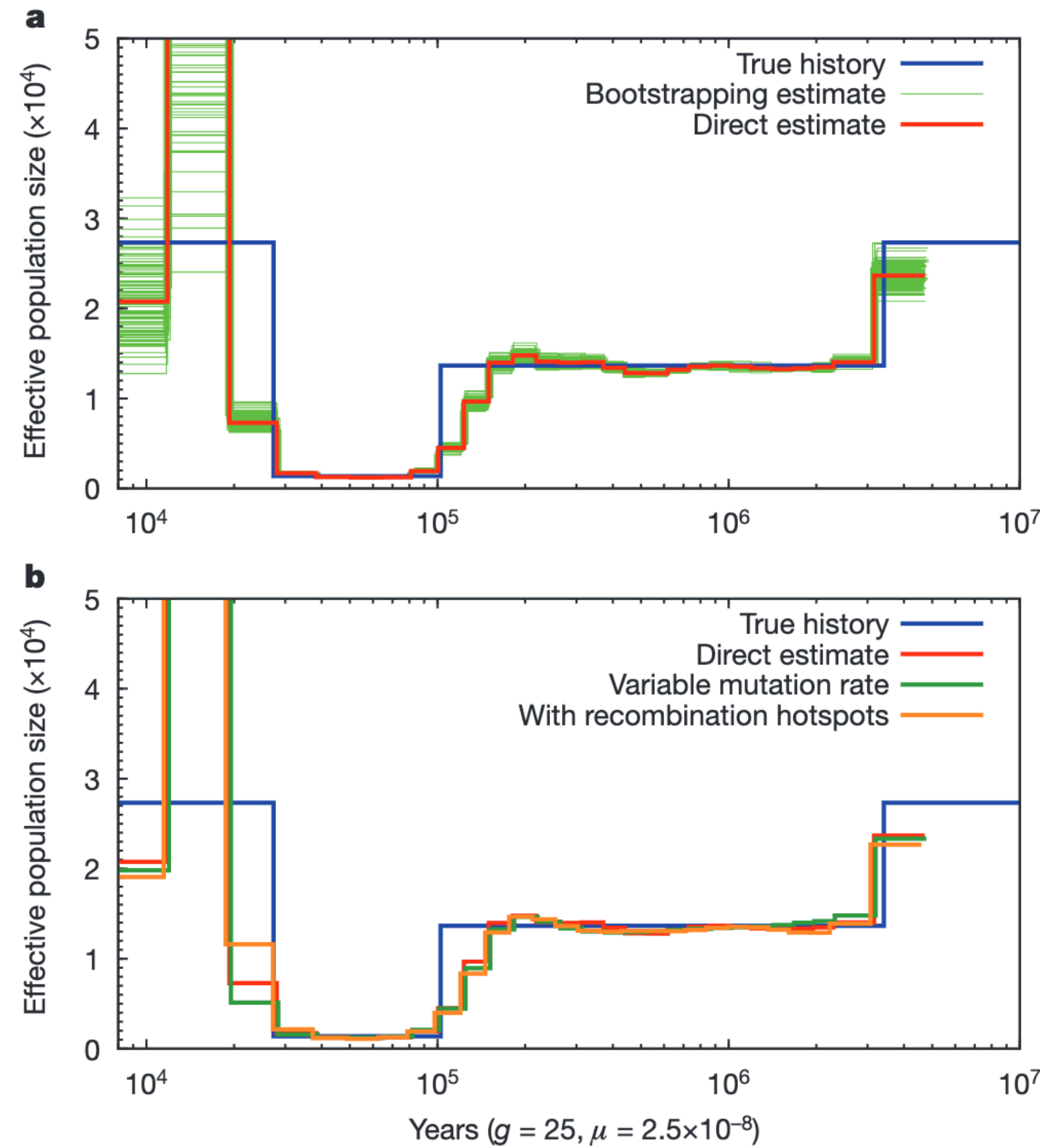
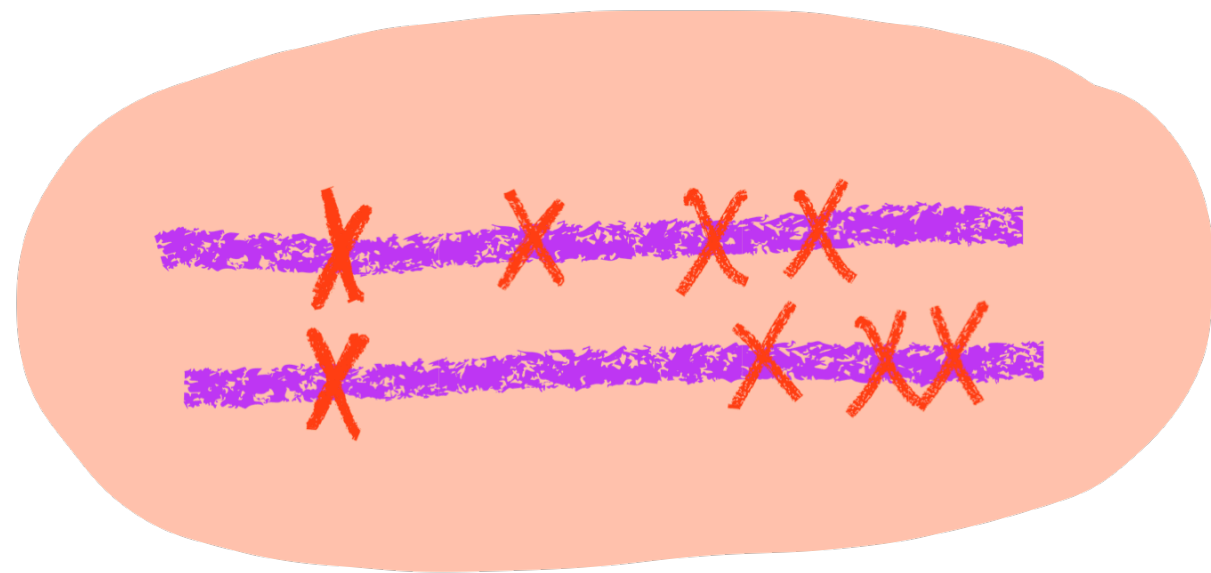
I. The coalescent (again)

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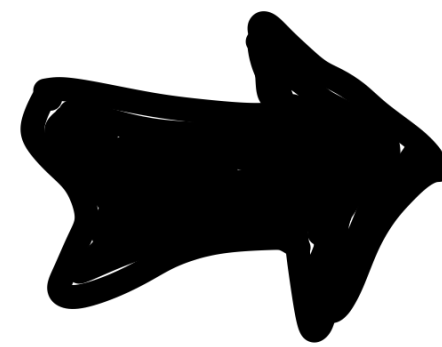
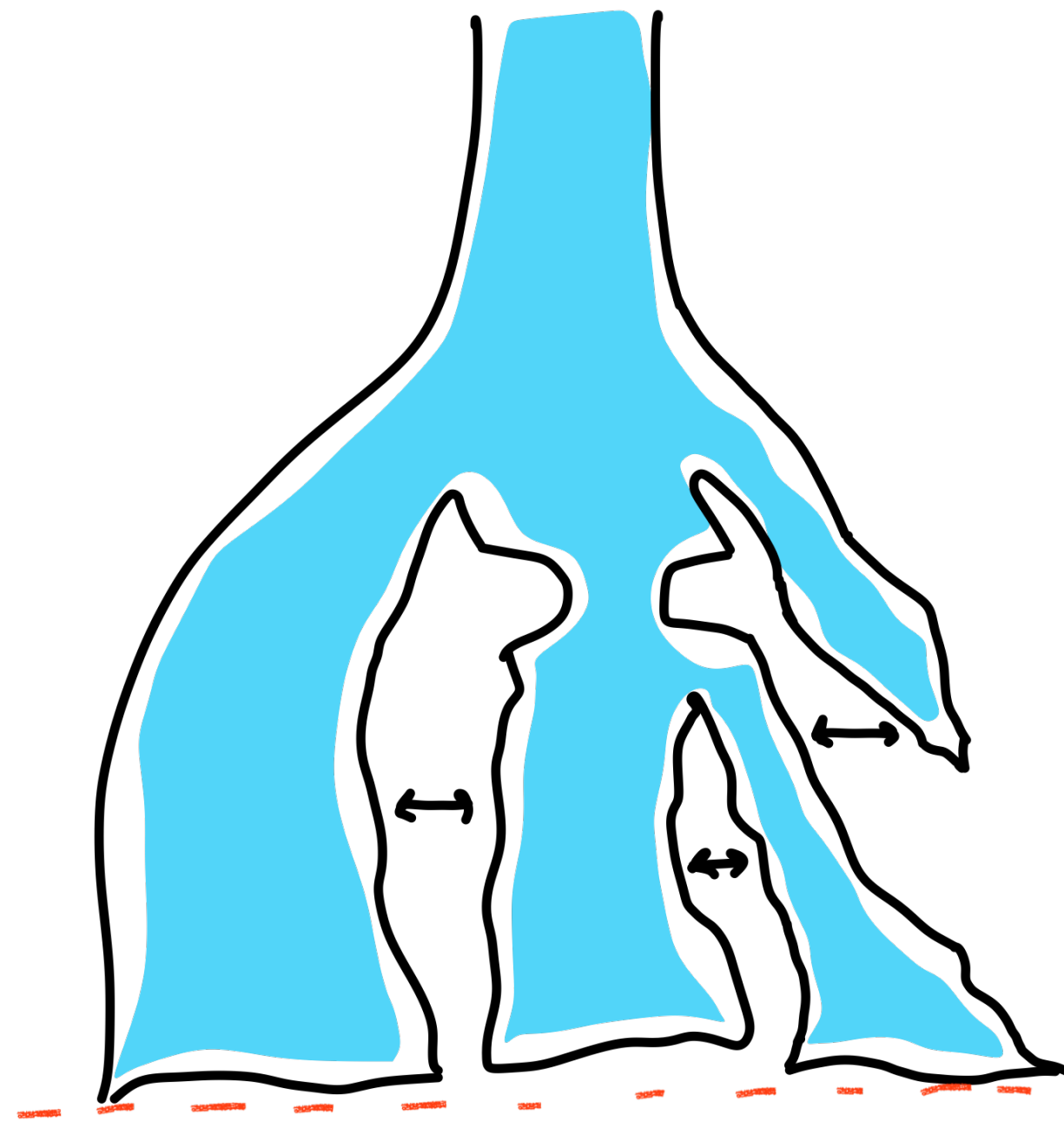
Inference of human population history from individual whole-genome sequences

Heng Li^{1,2} & Richard Durbin¹

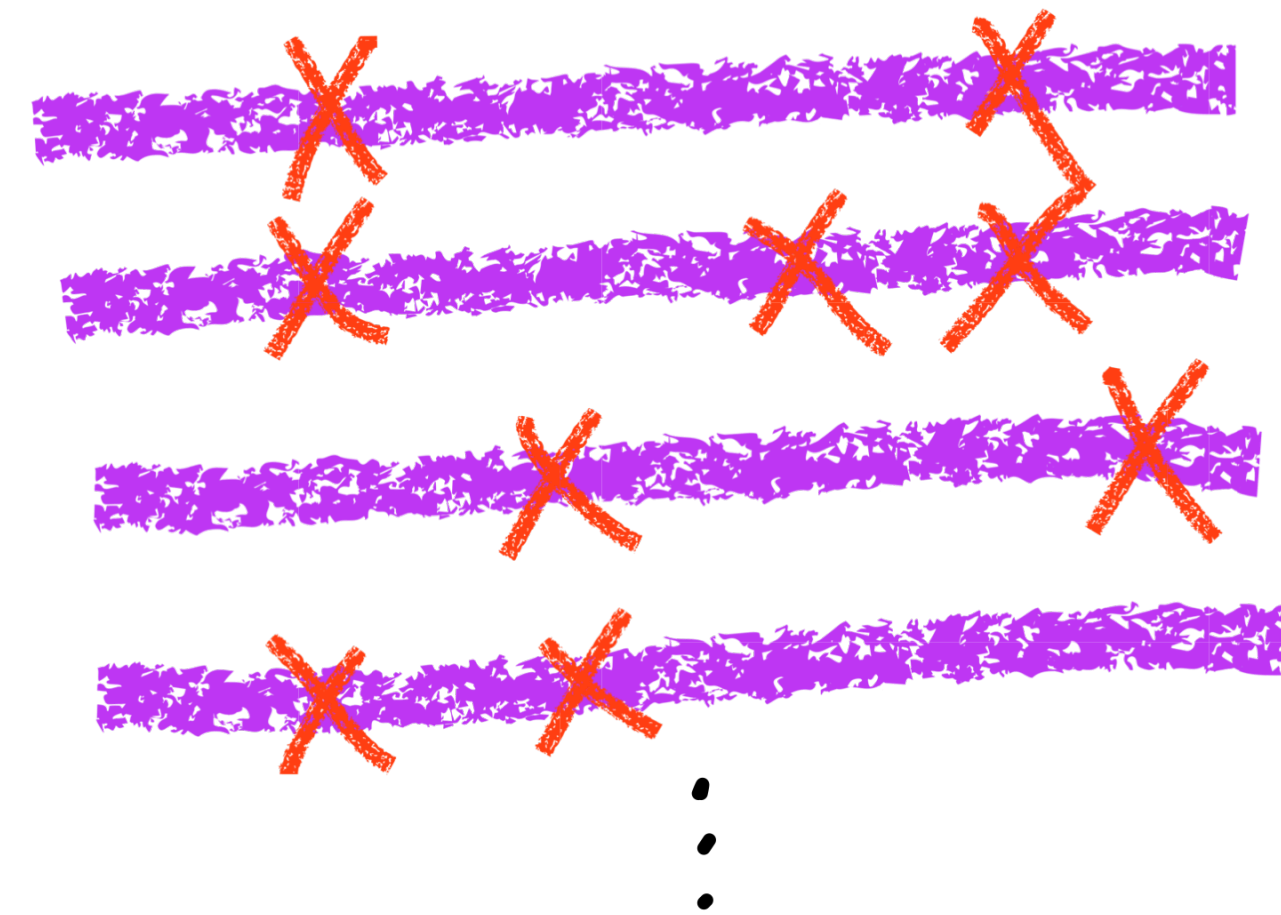


The big picture

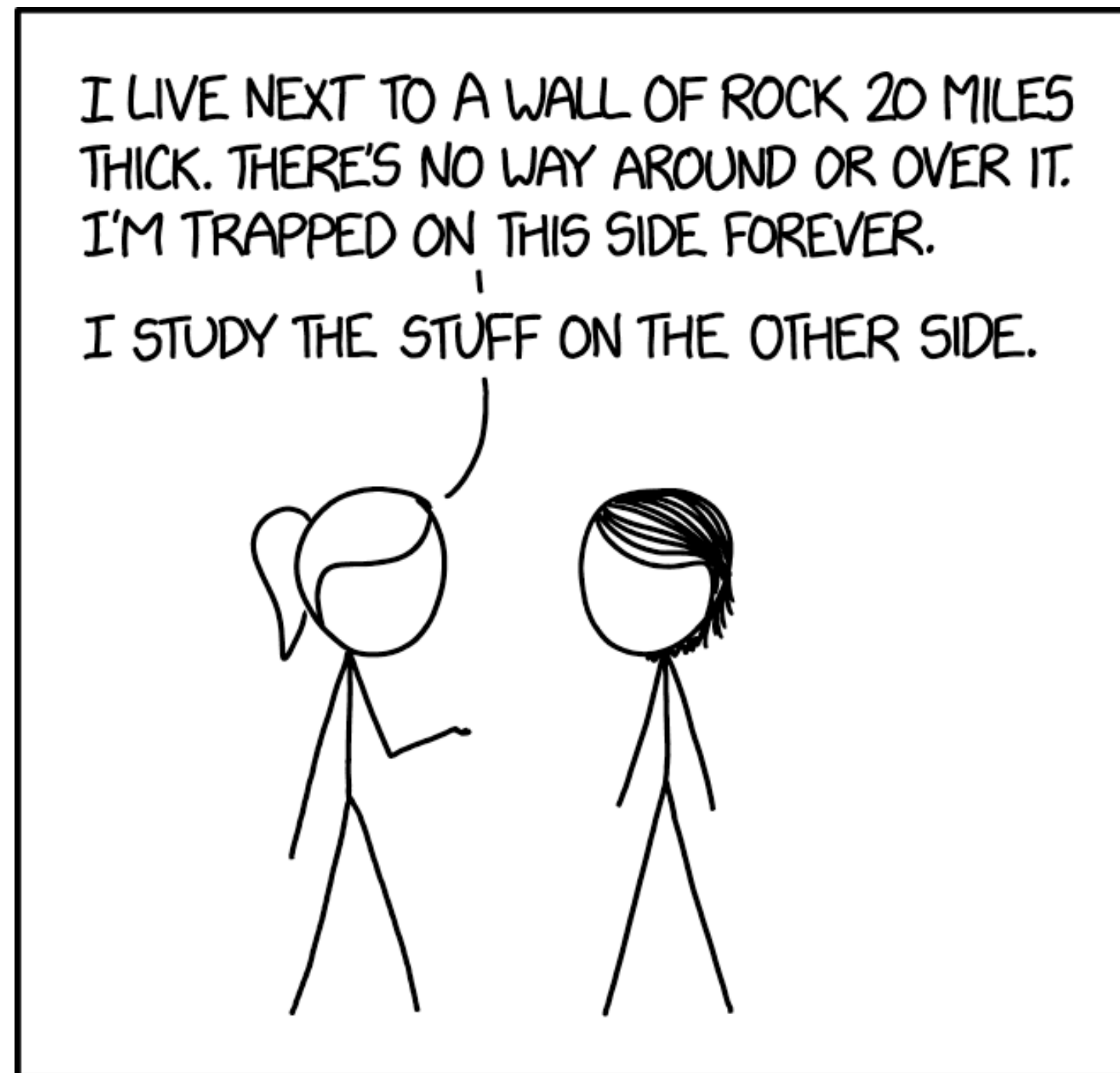
Evolutionary
Process



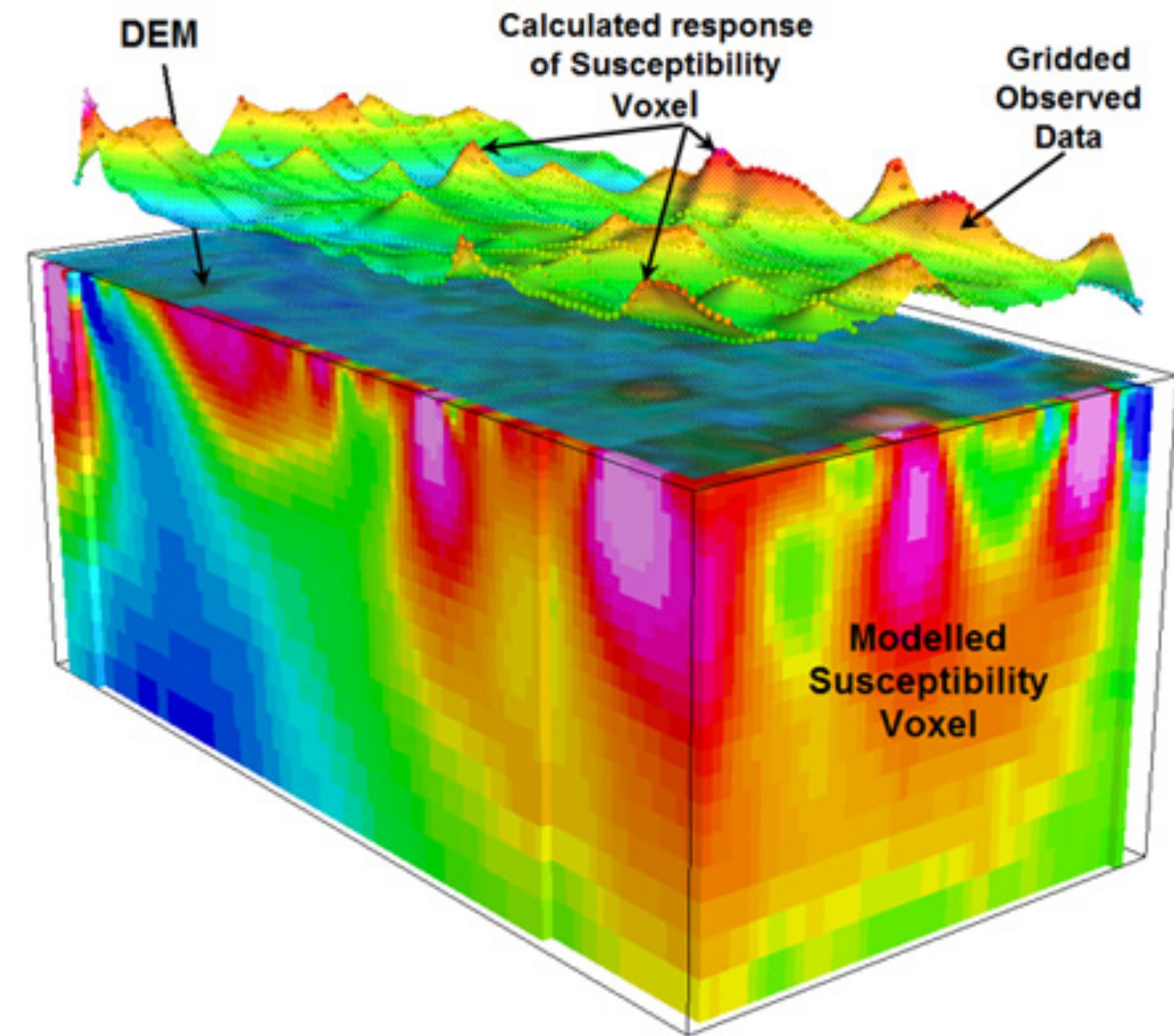
Genetic
Variation



Inverse problems



MANTLE GEOLOGY SEEMS LIKE THE MOST FRUSTRATING FIELD.

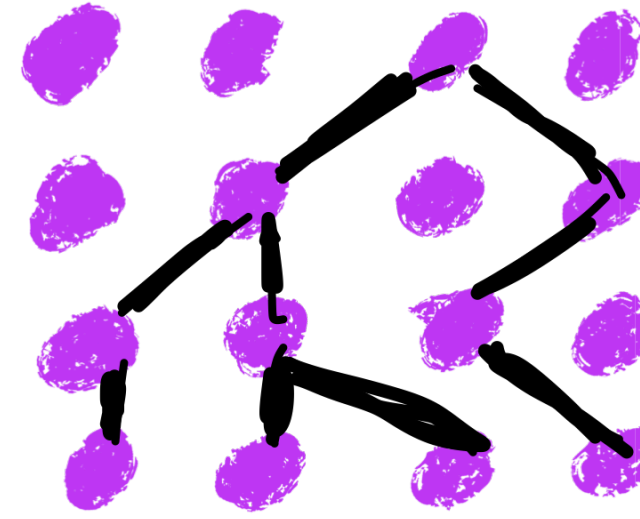


$$g(x) = \int K(x, y) f(y) dy$$

data ↑ *model* ↑ *stuff we want to know about* ↑

Inference frameworks

Wright-Fisher process at the core



Summary statistics and simple calculations
(small data, simple population)

Π : average pairwise divergence

S : # segregating sites

T_D : deviation from neutrality

Probabilistic models
(big data, more complex populations)

Forward time:

- PDEs / diffusion

- selective sweeps



Reverse time:

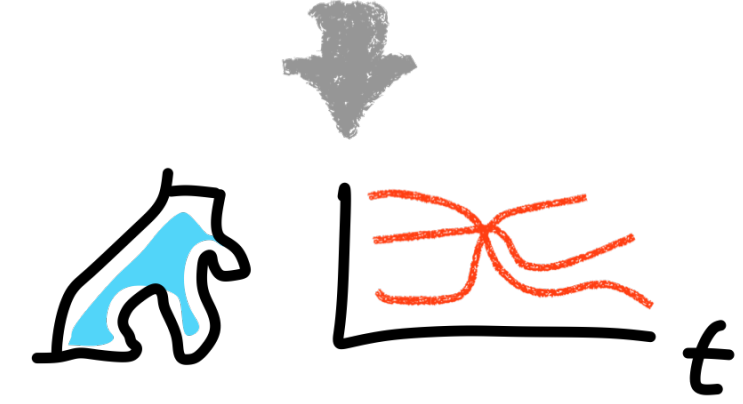
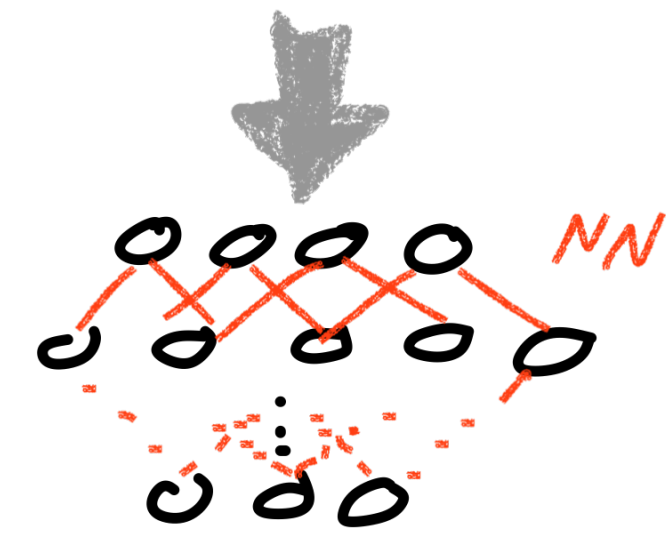
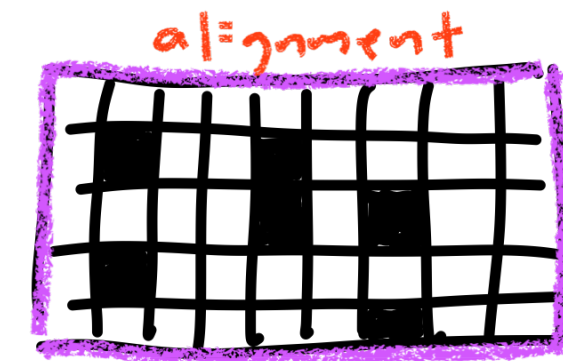
- coalescent genealogy

- coalescent HMM



Machine learning
(big data, arbitrarily complex population)

Supervised learning



Problem

The Wright-Fisher process is wrong!

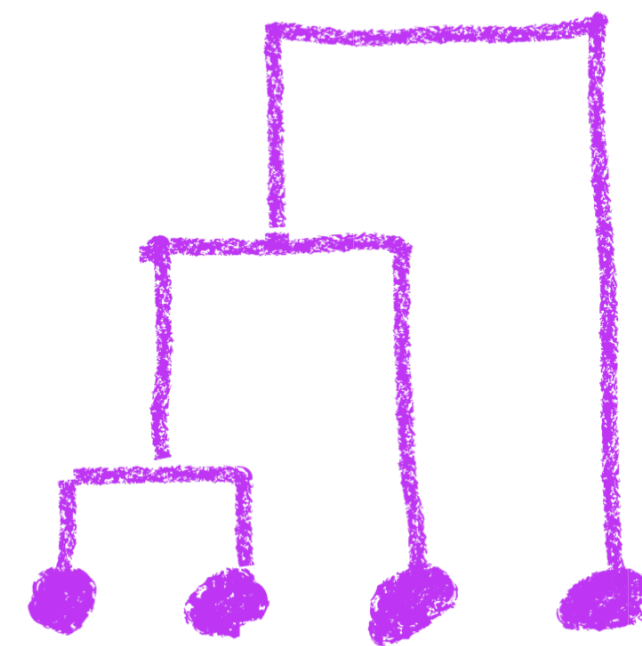
Question: what's missing w/ WF model?

It turns out...



Universe of models
(WF just one)

big N



The coalescent limit

Universality

$$PV = nRT$$

Oh nos, where are the molecules?

Cole-escient theory

Inspired by GENOME 551 with Cole Trapnell

- 20 students in a class, numbered 1, 2, ..., 20
- Each day of class, professor rolls 20-sided die to choose a student to call on

Question: How many classes do I expect it to take me to get called on?

Each class I get called w/ Prob. $\frac{1}{20}$

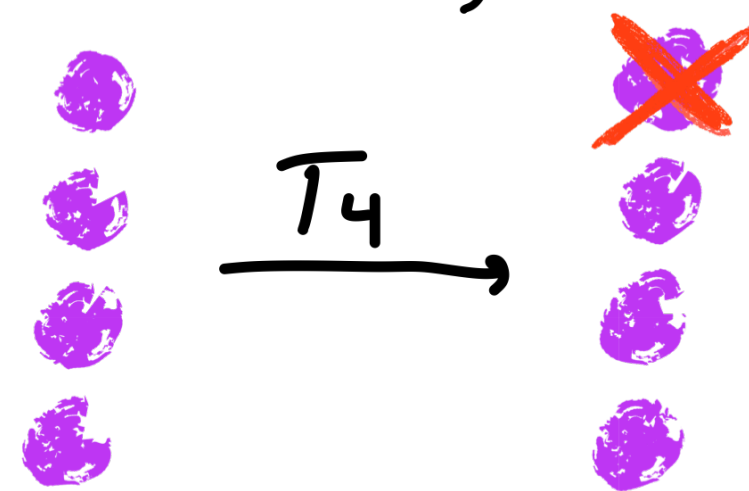
$$\implies E[T] = \frac{1}{\frac{1}{20}} = 20 \text{ classes}$$

Cole-escient theory

Question: How many classes do you expect until all 20 students have been called on?

When there are i students left to call on, the prob of rolling one of these remaining i is $\frac{i}{20}$

$$\mathbb{E}[T_i] = \frac{1}{i/20} = \frac{20}{i}$$



$i = 20, 19, \dots, 1$

So

$$\begin{aligned} \mathbb{E}[T_{20 \rightarrow 0}] &= \mathbb{E}[T_{20}] + \mathbb{E}[T_{19}] + \dots + \mathbb{E}[T_1] \\ &= 1 + \frac{20}{19} + \dots + \frac{20}{1} = 1 + 20 \sum_{i=1}^{19} \frac{1}{i} \approx 72 \end{aligned}$$

Cole-escient theory

Generalize: Class size N (and N -sided die)
sample of $n \leq N$ students

$$E[T_{n \rightarrow 0}] = \sum_{i=1}^n E[T_i] = \sum_{i=1}^n \frac{1}{i/N} = N \sum_{i=1}^n \frac{1}{i}$$

$$p = \frac{i}{N}$$

Each interval is geometrically distributed

$$P(T_i = t_i) = \frac{i}{N} \left(1 - \frac{i}{N}\right)^{t_i - 1}$$

$$p(t_i) \approx \frac{i}{N} e^{-\frac{i}{N} t_i}$$

↑
(continuous)

for large N :
→ approx. exponential dist.



Memoryless:

$$P(t_i | t_{i+1}) = P(t_i)$$

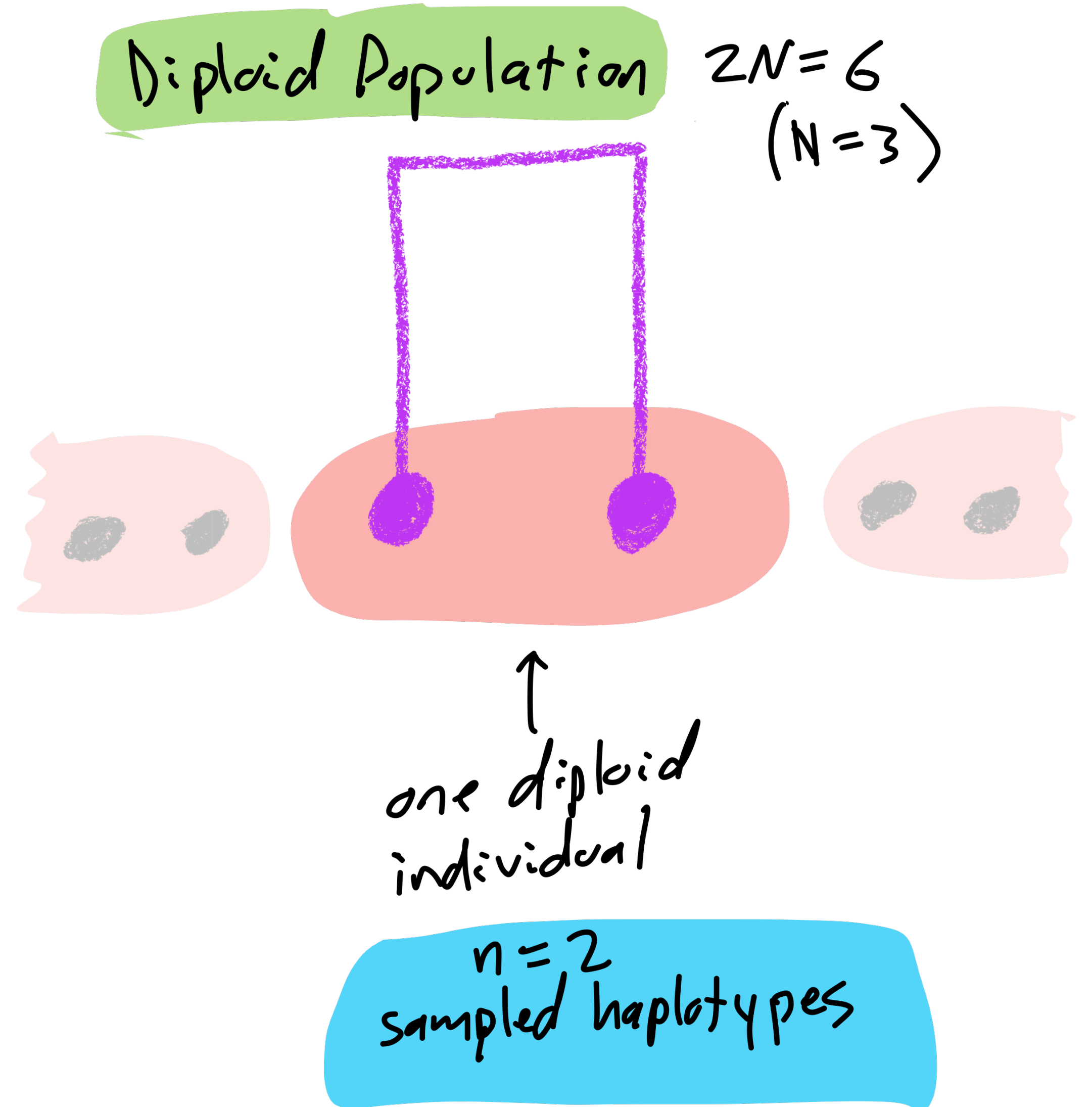
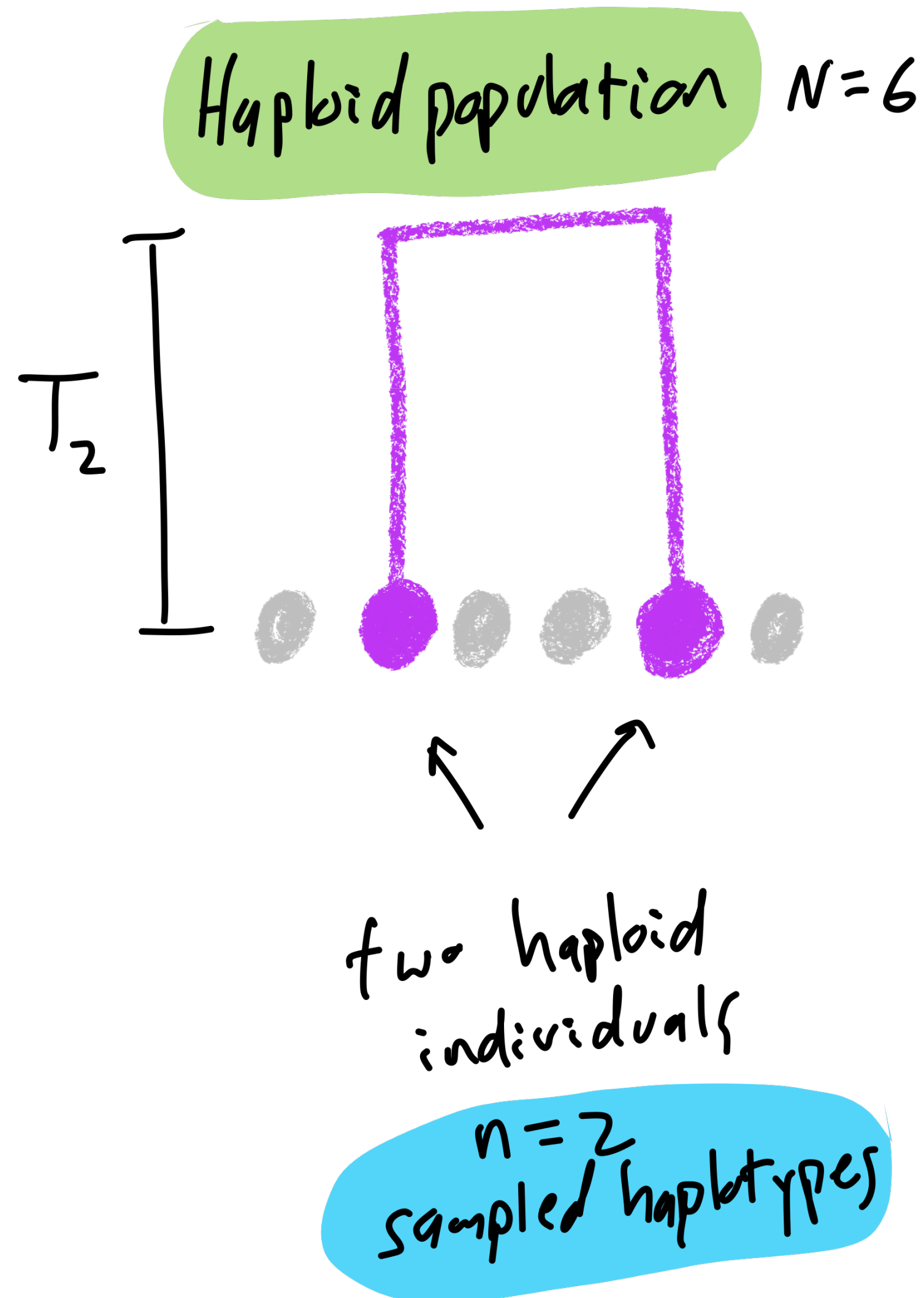
Coalescent theory

Only slightly fancier

	<u>Cole-esc</u> ent	<u>coalescent</u>
time	classes into the future	generations into the past
events	dice rolls, one student	coalescences, pairs of individuals
rate of events w/ i individuals	i ← students uncalled $\frac{i}{N}$ ← class size	$\binom{i}{2} \leftarrow = \frac{1}{2}i(i-1)$, # pairs $\frac{1}{2N}$ ← population size ↑ if diploid

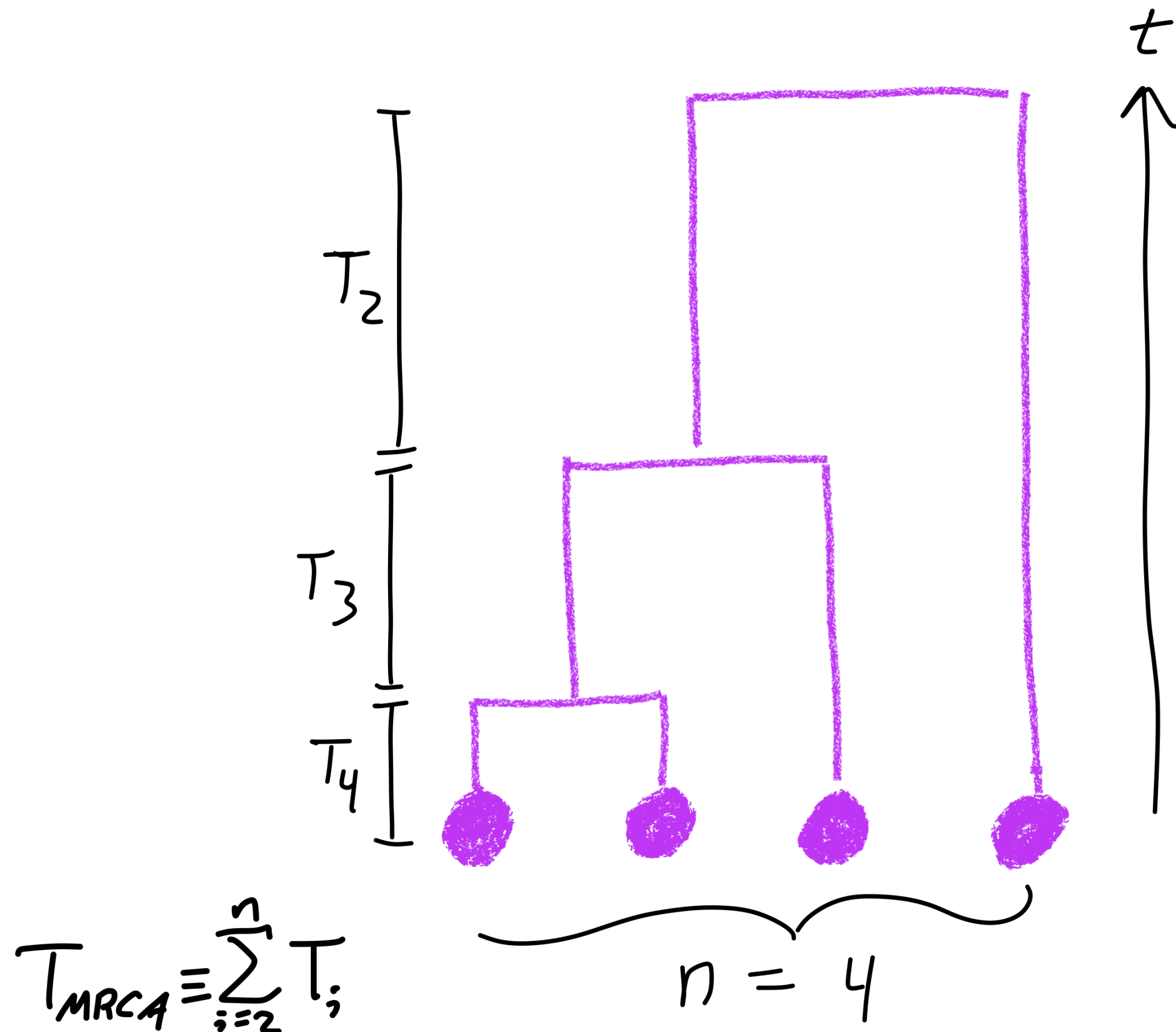
Coalescent theory

Watch those factors of 2!



Coalescent theory

Updating the previous results



"intercoalescence"
times

$$E[T_i] = \frac{2N}{\binom{i}{2}}$$

Exp. dist.

$$p(t_i) = \frac{\binom{i}{2}}{2N} e^{-\frac{\binom{i}{2}}{2N} t_i}$$

- Each pair is a process w/ rate $\frac{2}{2N}$
- The pairs race to coalesce

Coalescent theory

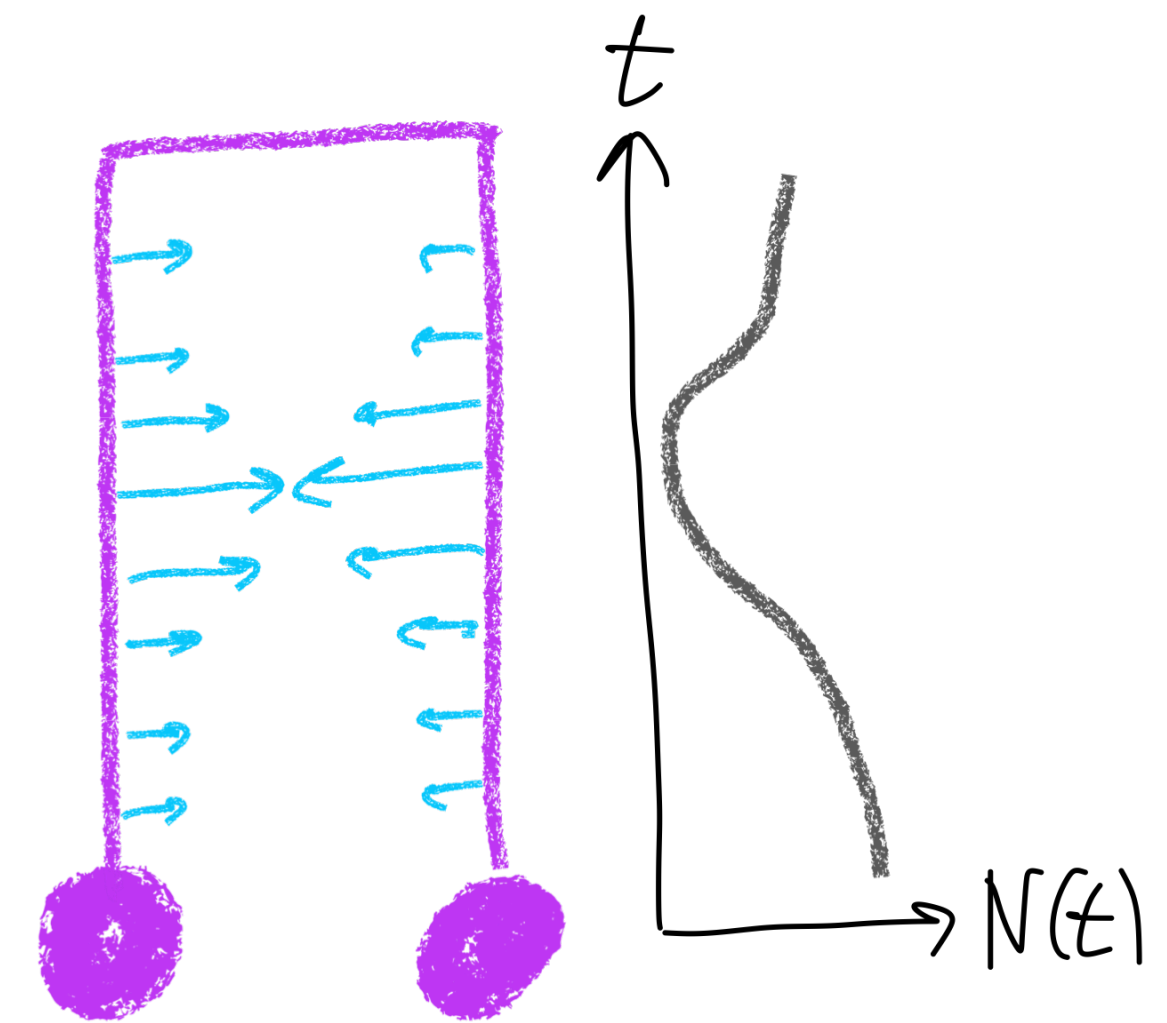
Population size determines coalescence rate

What if population size varies over time? $N(t)$

[Like students adding/dropping mid-quarter in coalescent theory]

$N(t)$ distorts time scale from the standard coalescent

- time compressed when $N(t)$ is small
- time stretched when $N(t)$ is large



The details:

$$P(T_i = t_i) = \frac{\binom{i}{2}}{2N_{t_i}} \prod_{j=2}^{t_i-1} \left(1 - \frac{\binom{i}{2}}{2N_j}\right)$$

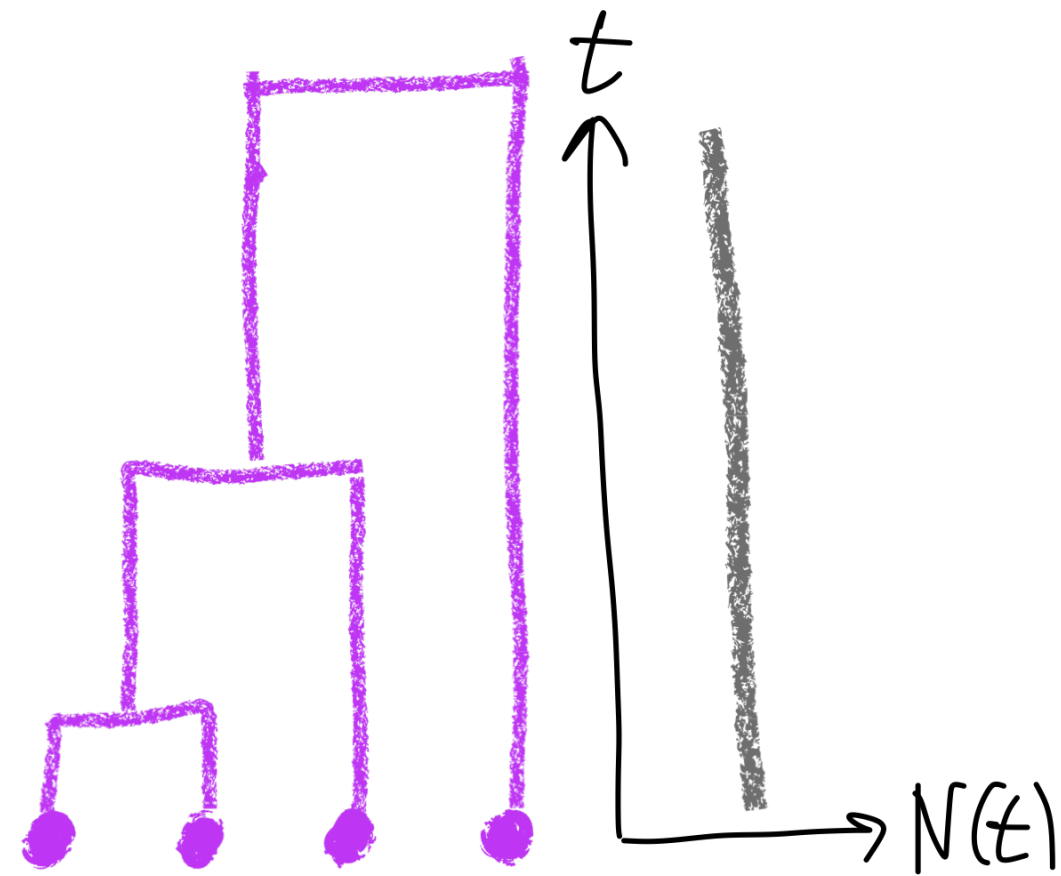
big $N \rightarrow P(t_i) = \frac{\binom{i}{2}}{2N(t_i)} \exp\left(-\binom{i}{2} \int_0^t \frac{ds}{2N(s)}\right)$

inhomogeneous Poisson process

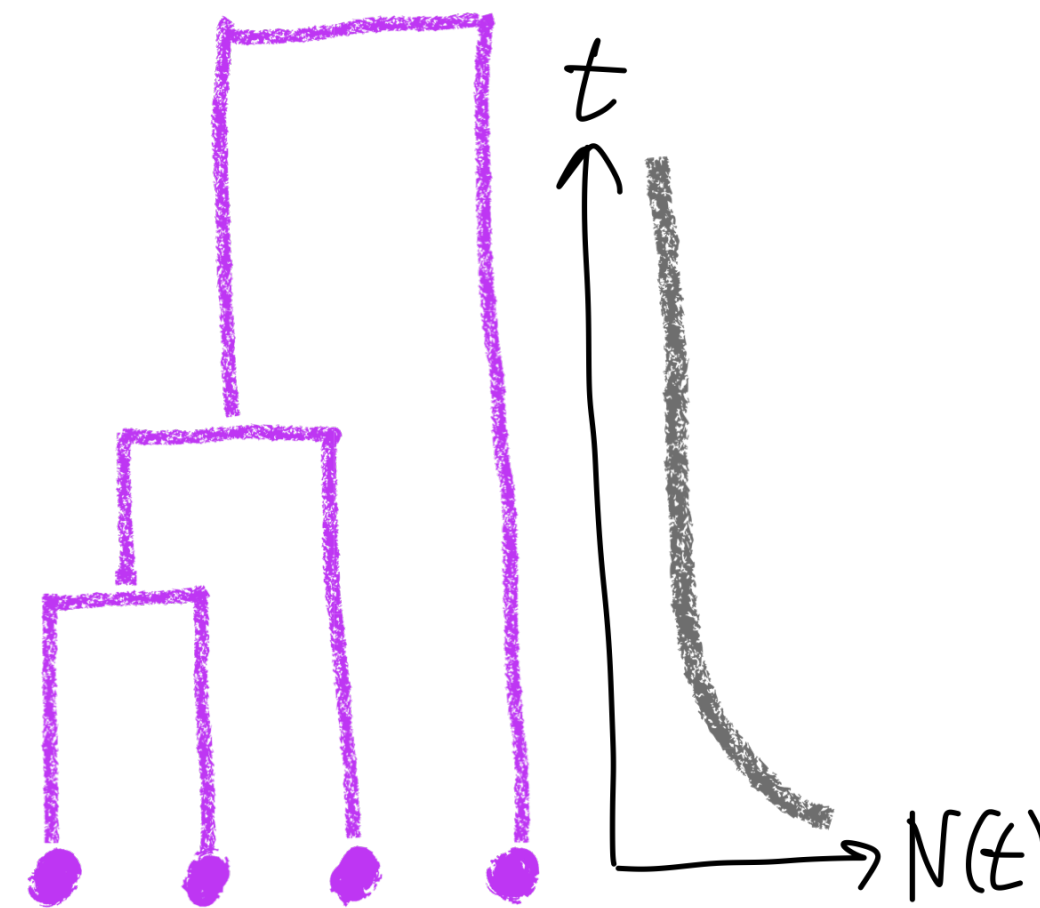
Coalescent theory

Population size determines coalescence rate

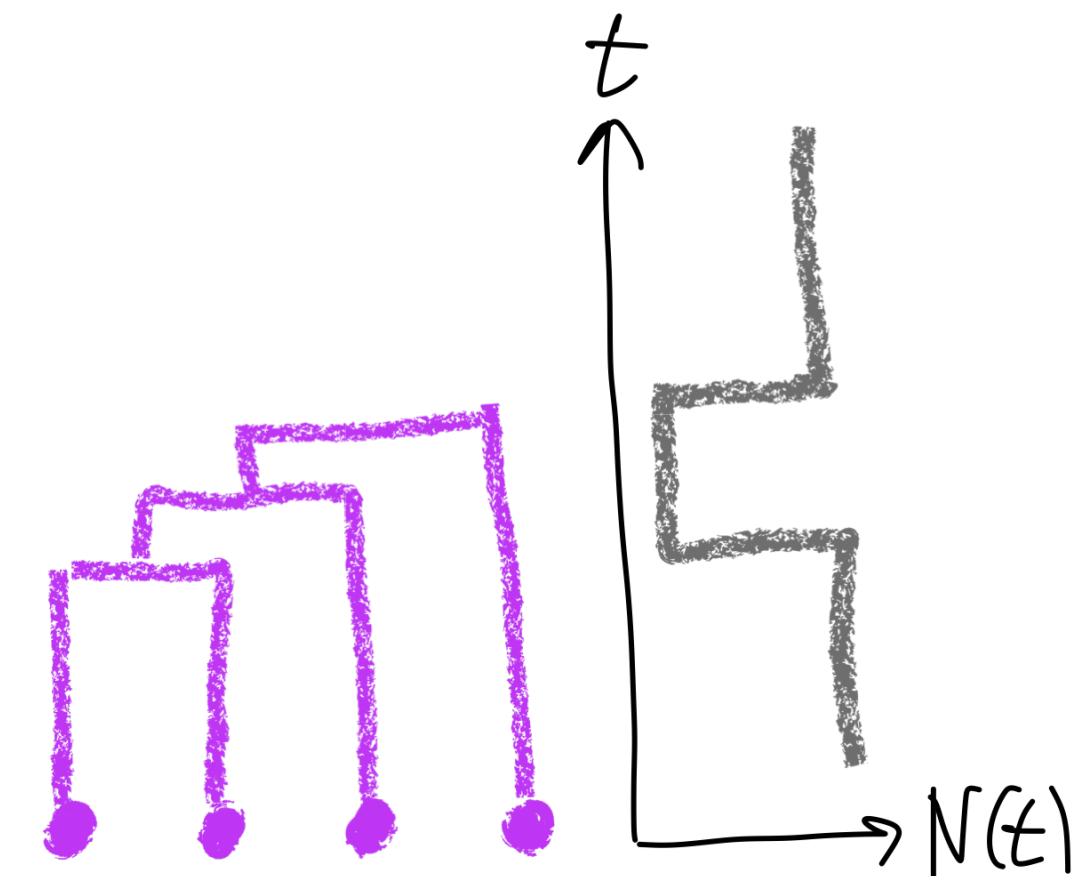
Constant



Exponential growth

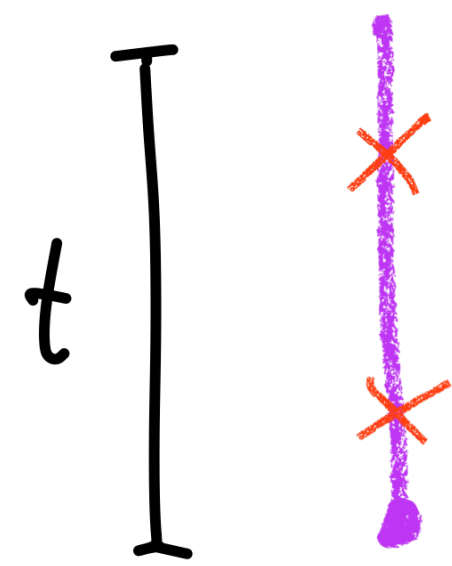


Bottleneck



Coalescent theory

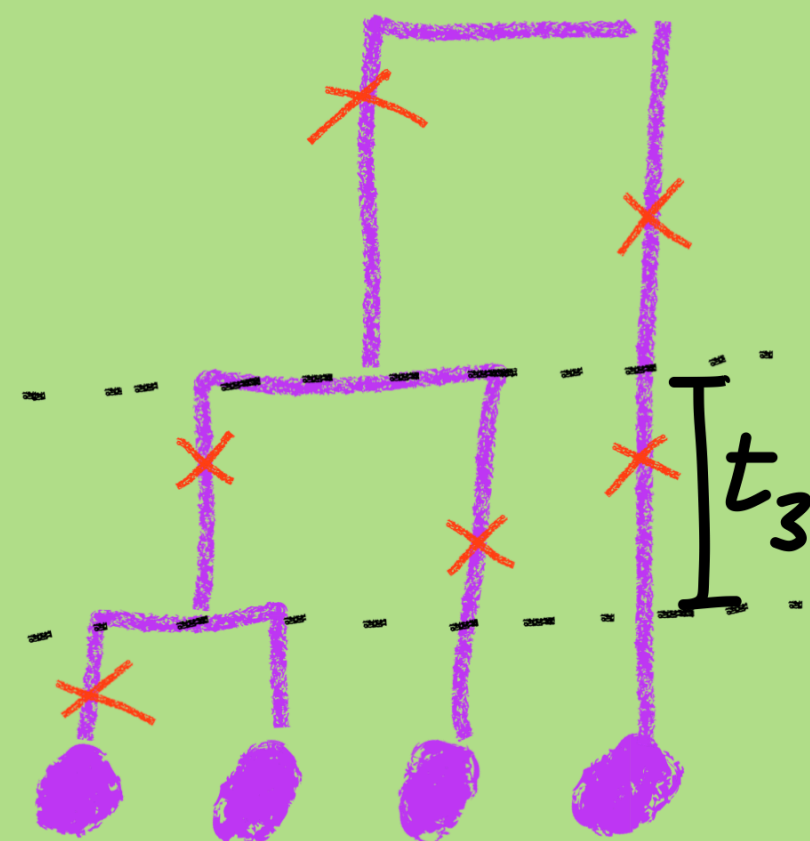
Mutations



mutations on branch of length t
is Poisson rv w/ mean μt

$$IP(k | t) = \frac{(\mu t)^k e^{-\mu t}}{k!}$$

↑ mutations per genome per generation



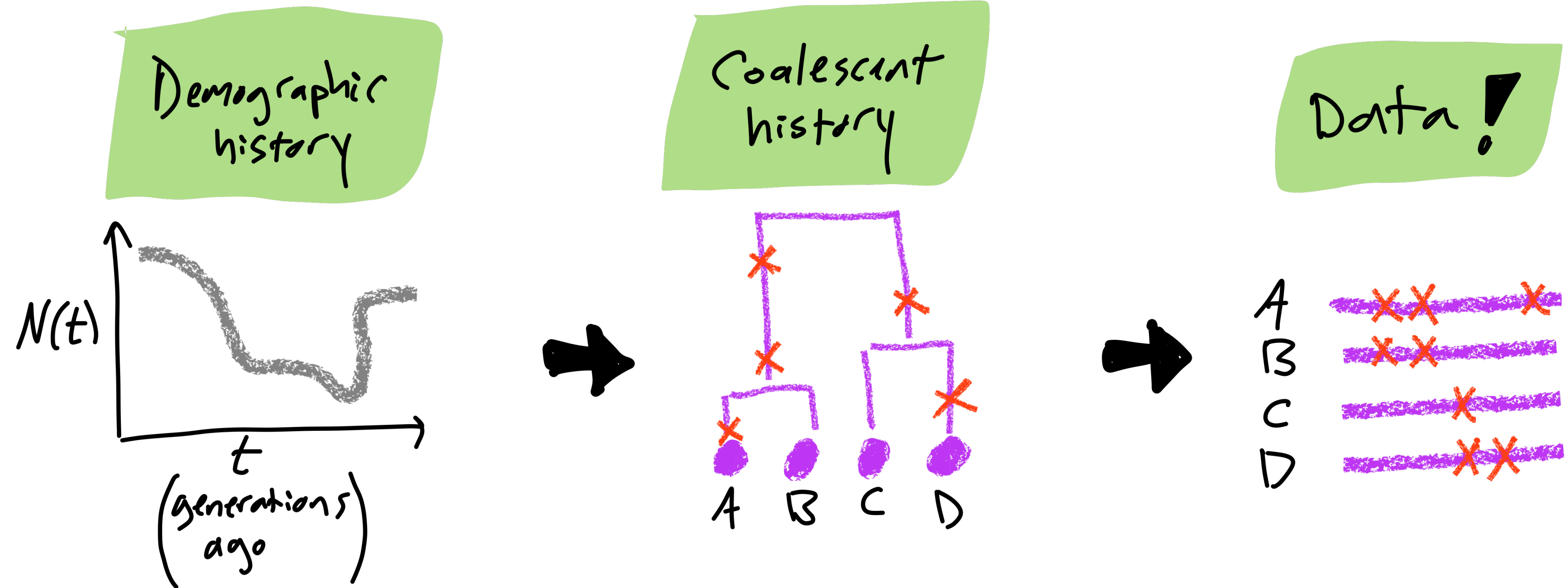
mutations in intercoalescent interval i , of length t_i , is Poisson rv w/mean

$$i \mu t_i$$

↑ # lines in interval i ← duration of interval i

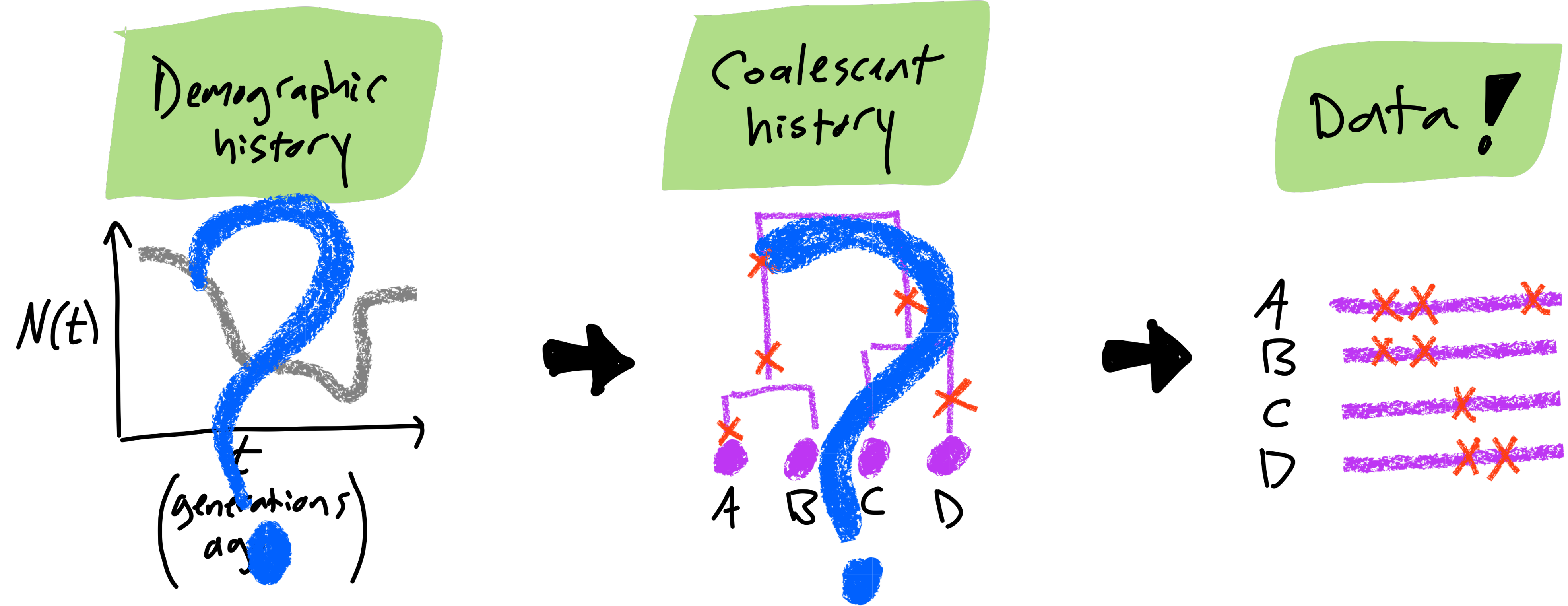
Coalescent theory

Genetic diversity



Coalescent theory

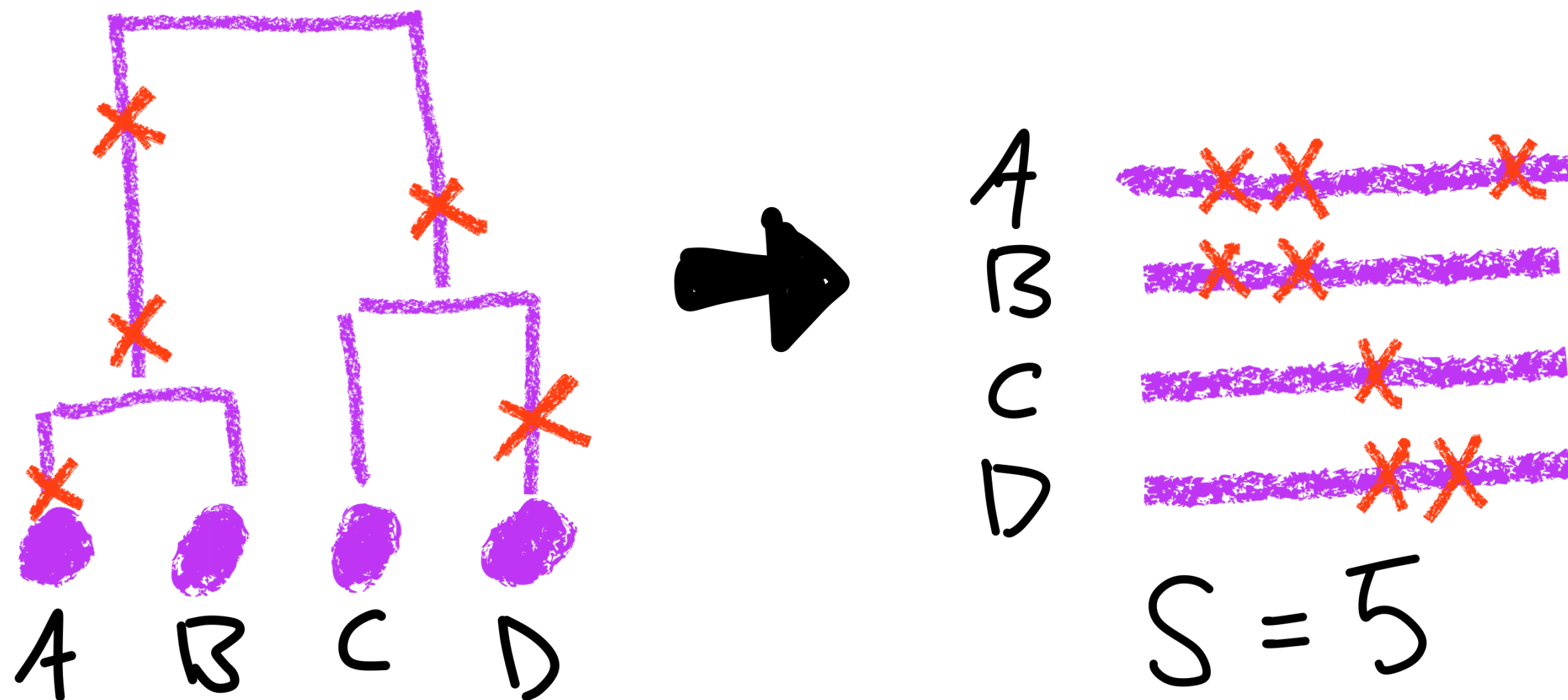
Genetic diversity



Coalescent theory

Genetic diversity

segregating sites, S , equals # mutations in the sample's history (infinite sites approximation)



Constant N case:

$$E[S] = \mu E[T_{\text{total}}]$$

$$= \mu \sum_{i=2}^n i E[T_i]$$

$$= \mu \sum_{i=2}^n i \frac{2N}{\binom{n}{i}}$$

$$= 4\mu N \sum_{i=1}^{n-1} \frac{1}{i}$$

total branch length

Recap

Good to know for homework

Intercoalescent times are indep. exponential rvs

intercoalescent interval i diploid pop size $2N$ # sampled haplotypes

$$T_i \sim \exp\left(\frac{2N}{\binom{i}{2}}\right), \text{ for } i = n, n-1, \dots, 2$$

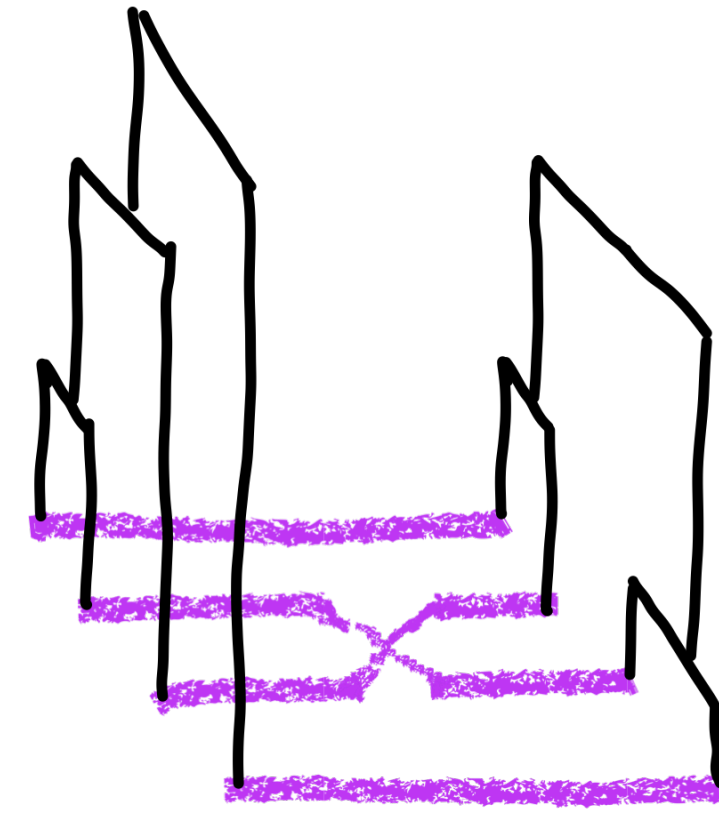
mutations on branches are indep. Poisson rvs

$$k \sim \text{Pois}(Mt)$$

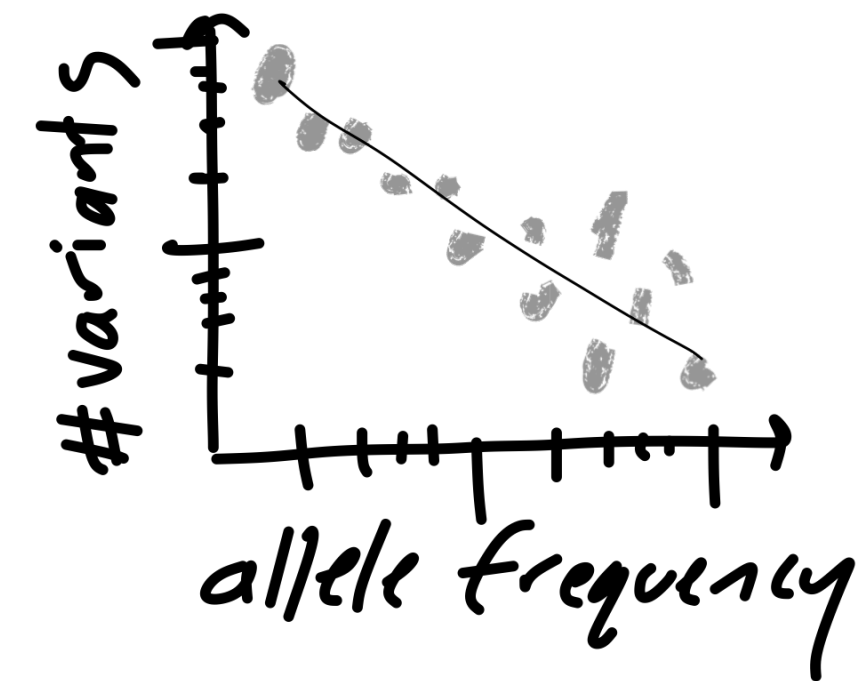
mutations mutation rate branch length

Next time

- The coalescent with recombination



- Sample Frequency Spectrum (SFS)



- Coalescent hidden Markov model

