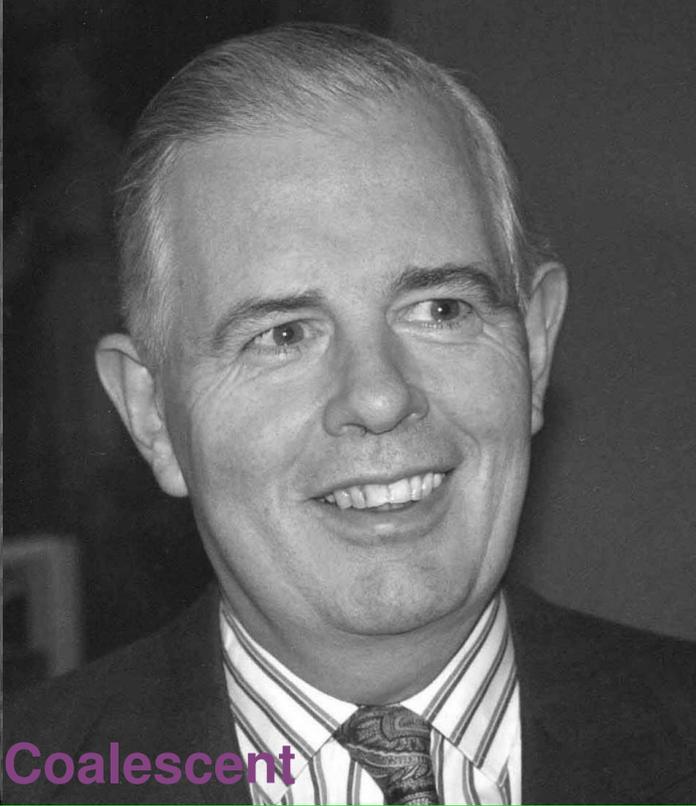


# Fractional Coalescent:

A new coalescent theory based on a non-Markovian Poisson process



Exponentials



Coalescent



Mittag-Leffler function

Somayeh Mashayekhi and Peter Beerli  
Scientific Computing, Florida State University



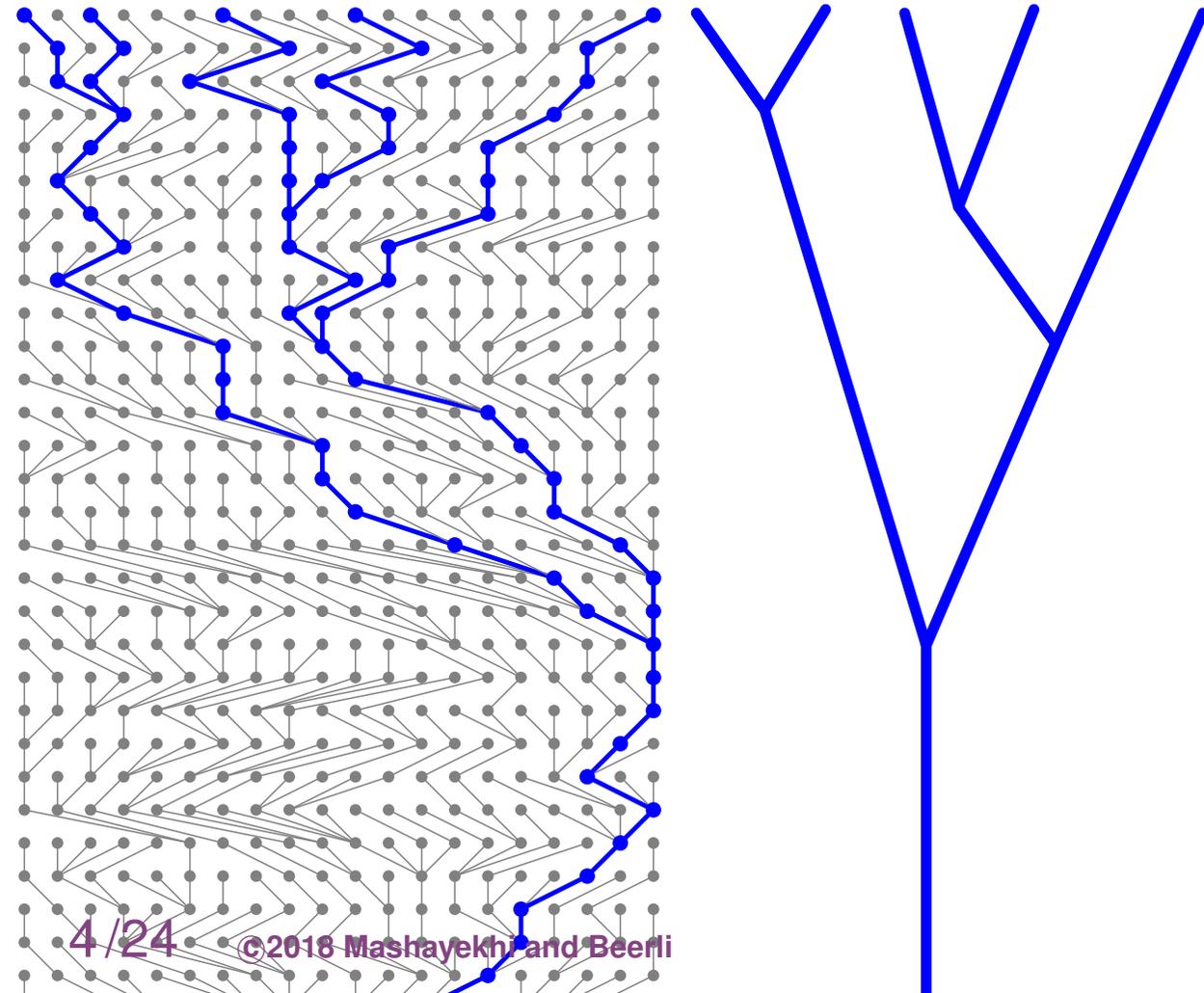
@somayehmashayek  
@peterbeerli



# Coalescence theory



# Coalescence theory



Using  $\tau$  scaled by  $1/N$  generations, two lineages remain distinct with probability

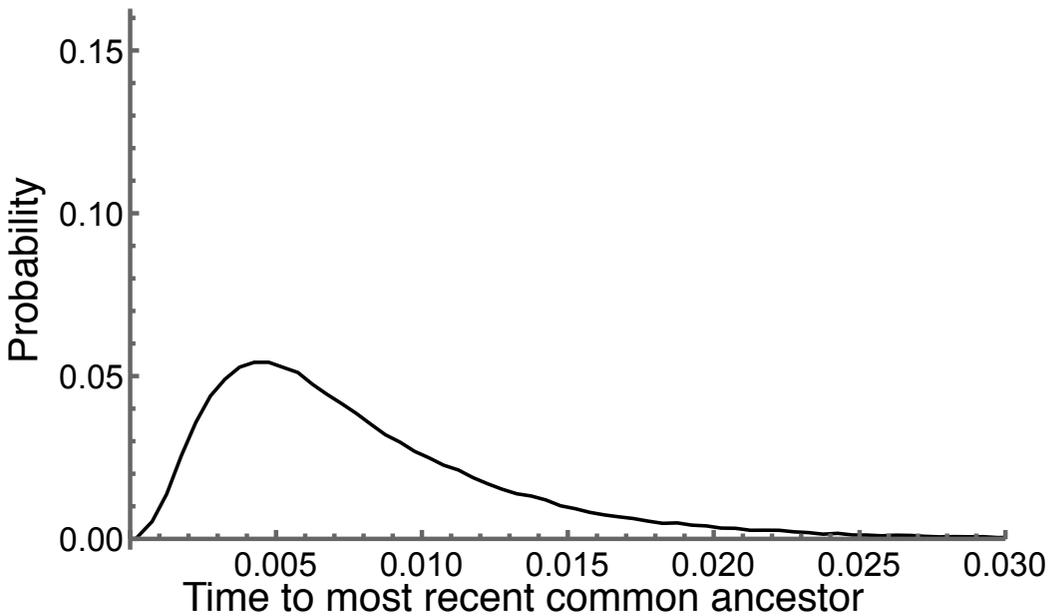
$$\left(1 - \frac{1}{N}\right)^{N\tau} \rightarrow e^{-\tau},$$

as  $N$  goes to  $\infty$ . Kingman's  $n$ -coalescent generalized the two-lineages framework to  $k$  lineages by changing  $\tau \rightarrow \tau \binom{k}{2}$ :

$$\left(1 - \frac{\binom{k}{2}}{N}\right)^{N\tau} \rightarrow e^{-\binom{k}{2}\tau},$$

as  $N$  goes to  $\infty$ . With  $\tau = t/N$  the familiar coalescence formula  $e^{-t \binom{k}{2}/N}$  emerges.

# Coalescent is a convolution of exponential distributions



Sample size  $n = 5$

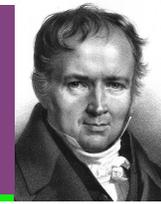
$$p(t|N, k) = e^{-t \binom{k}{2} / N} \frac{\binom{k}{2}}{N}$$

$$p(G|N, n) = \prod_{k=2}^{k=n} p(t|N, k) = \prod_{k=2}^{k=n} e^{-t \binom{k}{2} / N} \frac{1}{\binom{k}{2}}$$

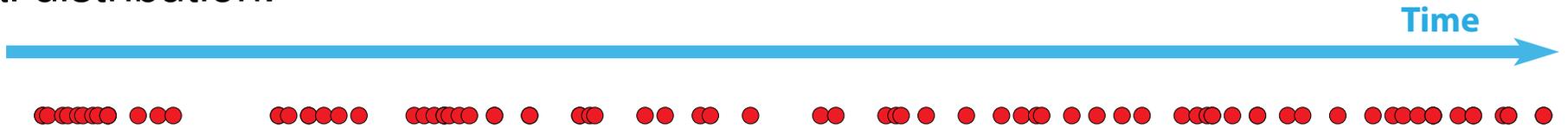
Scaling the time and the population size using mutation we get the familiar

$$p(G|\Theta, n) = \prod_{k=2}^{k=n} \left( e^{-t \frac{k(k-1)}{\Theta}} \frac{2}{\Theta} \right) \quad \text{with} \quad \Theta = 2N\mu$$

# Poisson process and waiting time

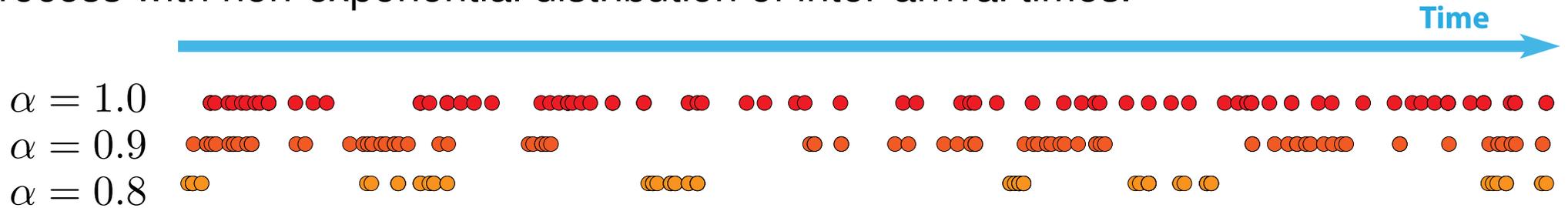


The coalescent rate changes with every coalescent, but with a fixed rate we recognize the randomness in the waiting time more easily! When coalescence events are rare then the Poisson process is a good model for the arrival of the events, the process has no memory and the waiting times between coalescent events are drawn from an exponential distribution.



# Fractional Poisson process and waiting time

The fractional Poisson distribution extends the standard Poisson distribution with an additional parameter  $\alpha$  adding variability of the waiting times. The time interval between each pair of consecutive counts follows the non-exponential power-law distribution with parameter  $0 < \alpha \leq 1$ . Thus, the fractional Poisson process is a non-Markovian counting process with non-exponential distribution of inter-arrival times.



# Poisson process and number of offsprings

When the population size is large (and constant), the number of offspring of each individual is approximated by a Poisson distribution.

The probability of having  $n$  offspring per  $x$  generation

$$P(n, x) = \frac{(\bar{n}x)^n}{n!} e^{-\bar{n}x},$$

the parameter  $\bar{n}$  is the average number of offspring per generation.

# Fractional Poisson process and number of offspring

The fractional Poisson distribution extends the standard Poisson distribution with an additional parameter  $\alpha$  adding variability to the number of offspring per individual, we can calculate the probability of  $n$  offsprings in  $x$  generations as

$$P(n, x) = \frac{(\bar{\zeta} x^\alpha)^n}{n!} \sum_{k=0}^{\infty} \frac{(k+n)!}{k!} \frac{(-\zeta x^\alpha)^k}{\Gamma(\alpha(k+n) + 1)}$$

# Fractional Poisson distribution and number of offspring

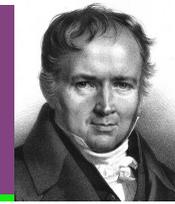
The fractional Poisson distribution extends the standard Poisson distribution with an additional parameter  $\alpha$  adding variability to the number of offspring per individual, we can calculate the probability of  $n$  offsprings in  $x$  generations as

$$P(n, x) = \frac{(\bar{\zeta} x^\alpha)^n}{n!} \sum_{k=0}^{\infty} \frac{(k+n)!}{k!} \frac{(-\zeta x^\alpha)^k}{\Gamma(\alpha(k+n) + 1)}$$

This includes the standard Poisson distribution, with  $\bar{\zeta} = \bar{n}$ , for example  $\bar{n} = 1$  for the Wright-Fisher model, and  $\alpha = 1$  the fractional Poisson becomes

$$P(n, x) = \frac{x^n}{n!} \sum_{k=0}^{\infty} \frac{(k+n)!}{k!} \frac{(-x)^k}{\Gamma(k+n+1)} = \frac{x^n}{n!} \sum_{k=0}^{\infty} \frac{(k+n)!}{k!} \frac{(-x)^k}{(k+n)!} = \frac{x^n}{n!} e^{-x}$$

# Using the Fractional Poisson distribution



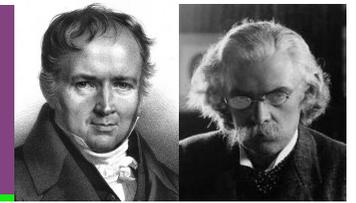
If we assume that the expected number of offspring depends on  $\alpha$ , then the probability that two randomly selected individuals have not the same parent in the previous generation is

$$1 - \frac{1}{\Gamma(\alpha + 1)N},$$

Using time  $\tau^\alpha$  scaled by  $1/N$  generations, two lineages remain distinct with probability

$$\left(1 - \frac{1}{\Gamma(1 + \alpha)N}\right)^{N\tau^\alpha} \longrightarrow e^{-\frac{\tau^\alpha}{\Gamma(\alpha+1)}} \xrightarrow{\alpha=1} e^{-\tau}$$

# Using the Fractional Poisson distribution



If we assume that the expected number of offspring depends on  $\alpha$ , then the probability that two randomly selected individuals have not the same parent in the previous generation is

$$1 - \frac{1}{\Gamma(\alpha + 1)N},$$

More interesting are results with  $\alpha < 1$ : Using time  $\tau^\alpha$  scaled by  $1/N$  generations, two lineages remain distinct with probability

$$\left(1 - \frac{1}{\Gamma(1 + \alpha)N}\right)^{N\tau^\alpha} \longrightarrow e^{-\frac{\tau^\alpha}{\Gamma(\alpha+1)}} \rightarrow \mathcal{E}_\alpha(-\tau^\alpha)$$

# Mittag-Leffler function and Exponential function

The Mittag-Leffler function

$$\mathcal{E}_\alpha(x) = \sum_{n=0}^{\infty} \frac{x^n}{\Gamma(\alpha n + 1)}, \quad \alpha > 0, x \in \mathcal{C}.$$

generalizes the exponential function, with  $\alpha=1$  the Mittag-Leffler becomes the Exponential function

$$= \sum_{n=0}^{\infty} \frac{x^n}{\Gamma(n + 1)} = \sum_{n=0}^{\infty} \frac{x^n}{n!} = e^x.$$

# Mittag-Leffler function and Exponential Distribution

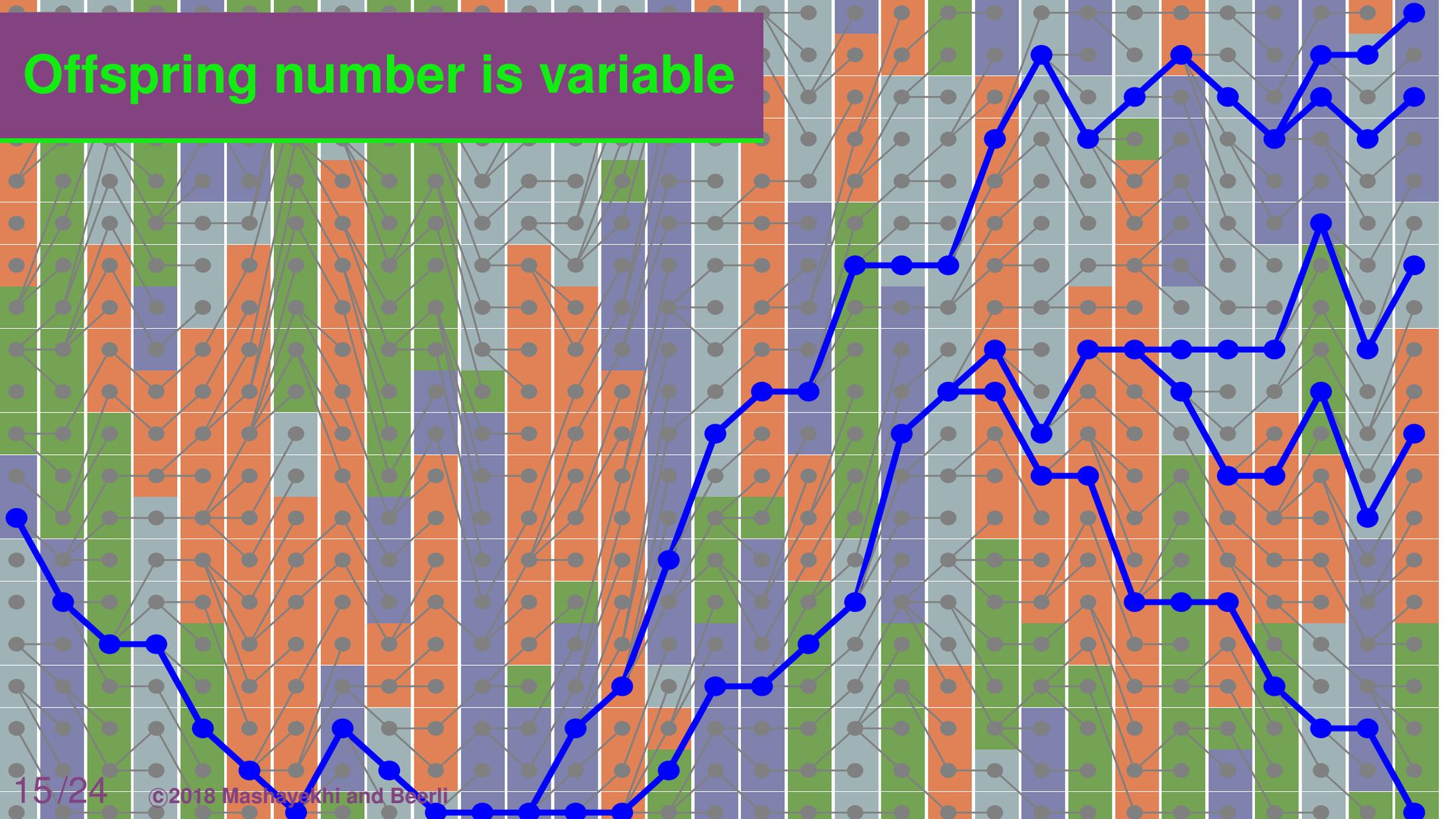
The Mittag-Leffler function can be expressed as a mixture of exponentials

$$\mathcal{E}_\alpha(-\lambda x^\alpha) = \int_0^\infty \omega(\kappa, \alpha) e^{-\kappa x} d\kappa,$$

where  $\omega(\kappa, \alpha)$  is a probability density. The discrete form can be written as

$$\mathcal{E}_\alpha(-\lambda x^\alpha) = \sum_k \omega(\kappa_k, \alpha) \left(1 - \kappa_k \frac{1}{n}\right)^{xn}.$$

Offspring number is variable



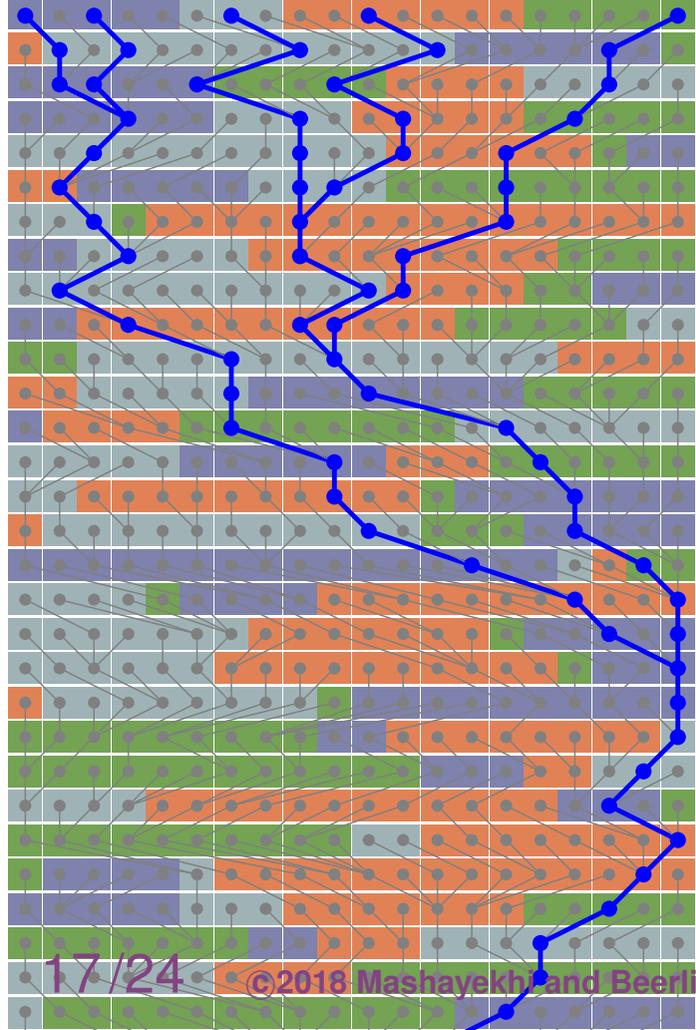
# Offspring number is variable

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.

# Offspring number is variable

The Canning model allows an arbitrary fixed variance of offspring number  $\sigma$ . We can extend the Canning model and treat this variance as a random variable.

$$P\{\text{not coal} \mid \sigma^2 = \sigma_j^2\} = \left(1 - \frac{\sigma_j^2}{N}\right)^{N\tau}.$$



# Offspring number is variable

The Canning model allows an arbitrary fixed variance of offspring number  $\sigma$ . We can extend the Canning model and treat this variance as a random variable.

$$P\{\text{not coal} \mid \sigma^2 = \sigma_j^2\} = \left(1 - \frac{\sigma_j^2}{N}\right)^{N\tau}.$$

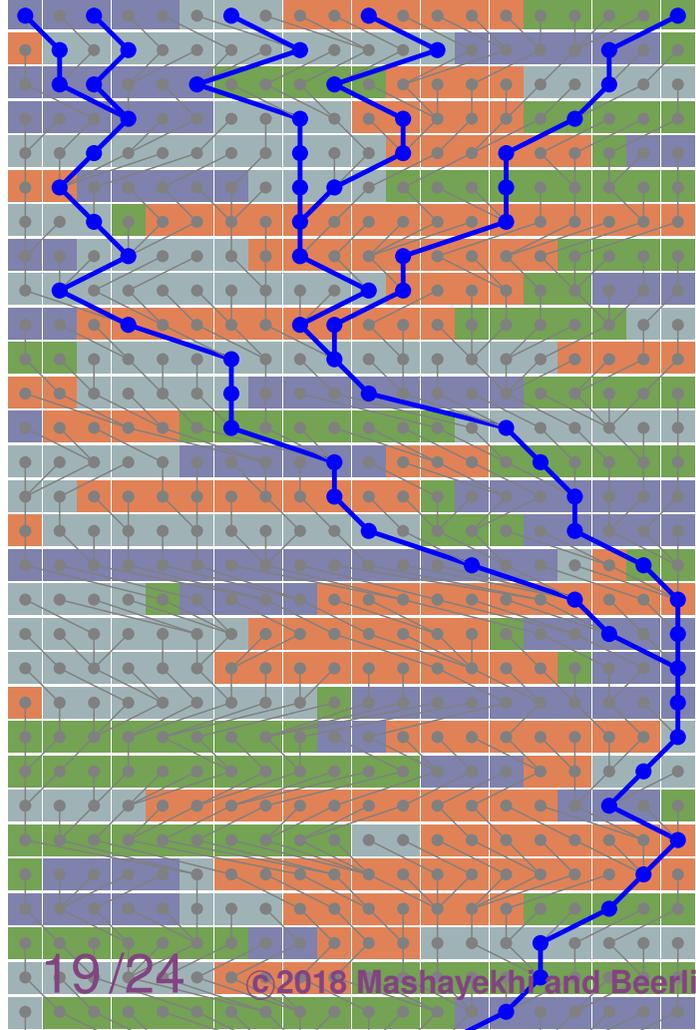
The Mittag-Leffler function with parameter  $\alpha$  can be used to approximate this system:

$$\mathcal{E}_\alpha(-\tau^\alpha) = \sum_j \omega(\sigma_j^2, \alpha) \left(1 - \sigma_j^2 \frac{1}{N}\right)^{N\tau}$$

For more than two lineages the waiting time to the next coalescent is

$$\mathcal{E}_\alpha\left(-\binom{k}{2}\tau^\alpha\right)$$

# Offspring number is variable



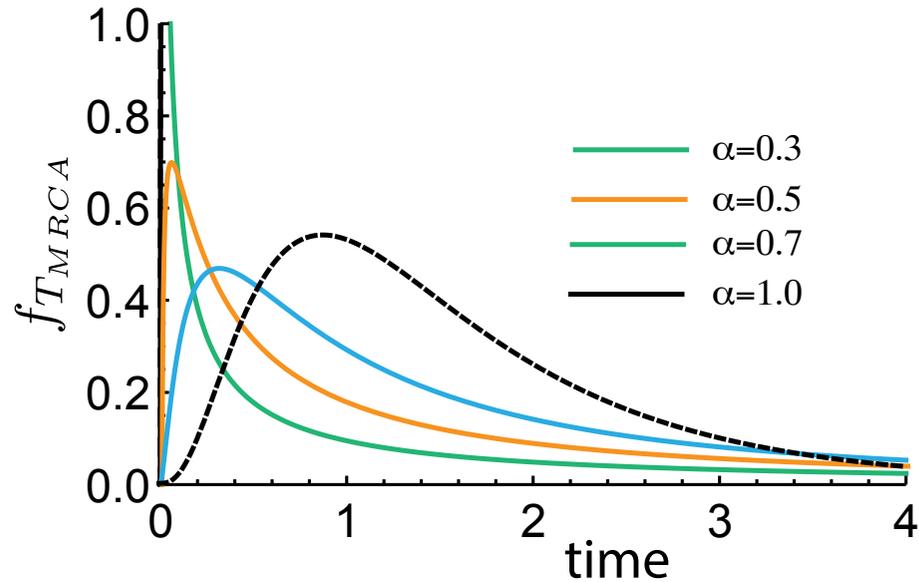
When we replace the scaled time  $\tau$  with  $\frac{u_k}{(N\mu)^{\frac{1}{\alpha}}}$ , where  $u_k$  has been scaled by mutation ( $\mu^{\frac{1}{\alpha}}$ ), we can rewrite

$$\mathcal{E}_\alpha\left(-\binom{k}{2}\frac{u_k^\alpha}{N\mu}\right) \rightarrow \mathcal{E}_\alpha\left(-\frac{k(k-1)}{\Theta}u_k^\alpha\right).$$

finally, using  $\lambda_k = \frac{k(k-1)}{\Theta}$  with  $\Theta = 2N\mu$ , we can get the fractional equivalent of Kingman's coalescent"

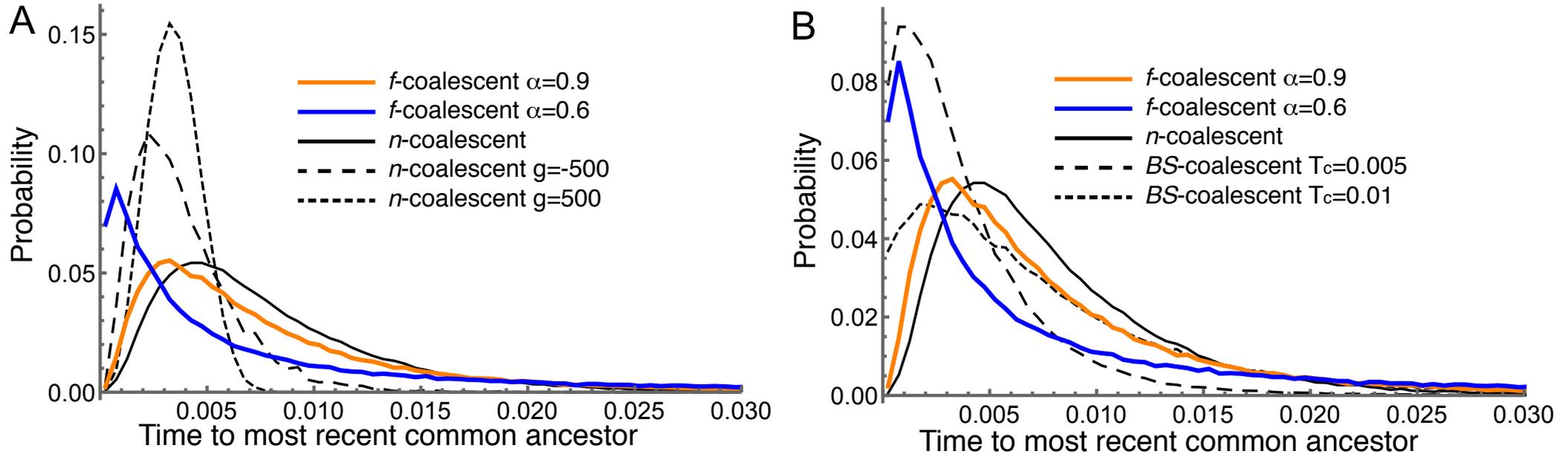
$$p(G|\Theta, n) = \prod_{k=2}^n u_k^{\alpha-1} \frac{2}{\Theta} \mathcal{E}_\alpha(-\lambda_k u_k^\alpha)$$

# Time to the most recent common ancestor



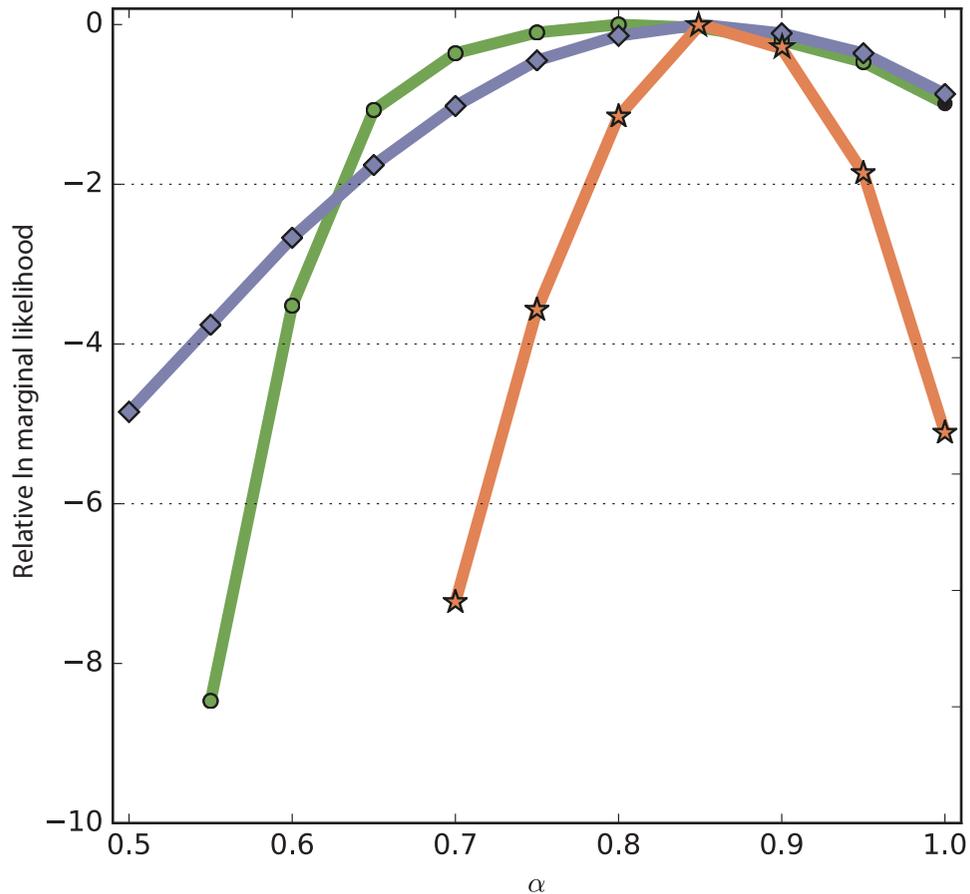
Analytical distribution of the probability of the time to the most recent common ancestor for various  $\alpha$  for a samples size of  $n = 5$ .

# Time to the most recent common ancestor: Comparison



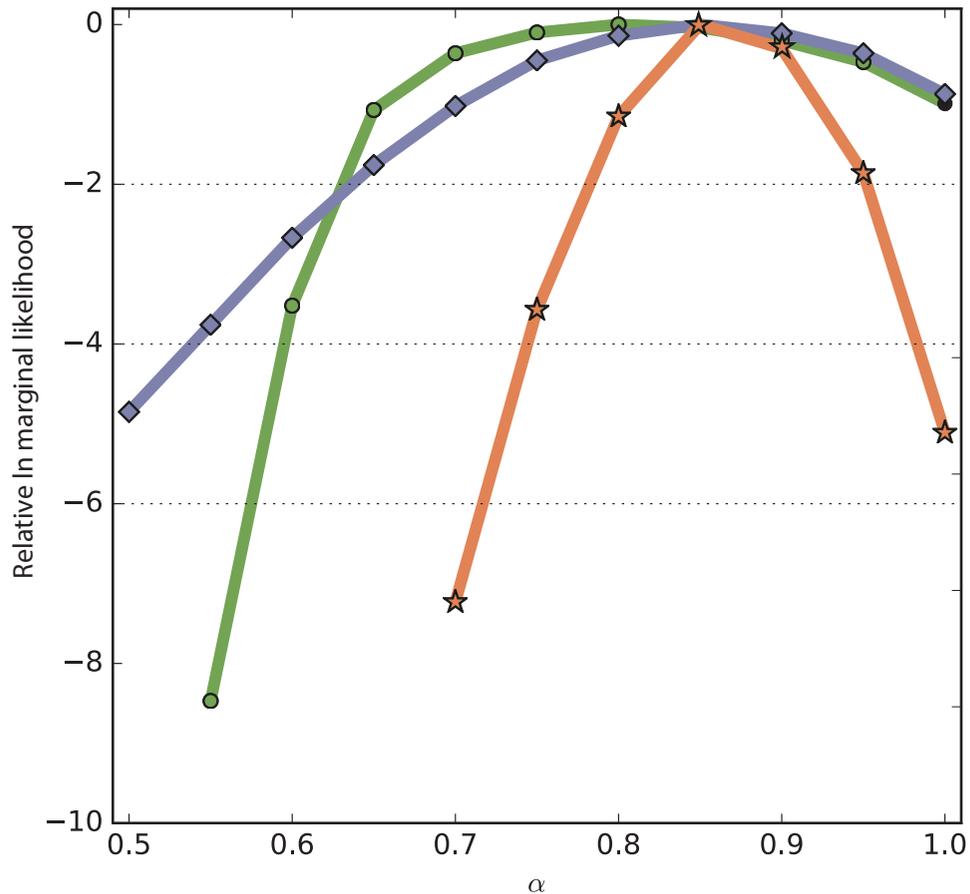
Empirical distribution of the time of the most recent common ancestor for various coalescents: (A) strictly bifurcating; (B) *fractional* coalescent versus  $n$ -coalescent and multifurcating Bolthausen-Sznitman coalescent. The x-axis is truncated at 0.03. Each curve represent a histogram of 100,000 draws of the TMRCA.

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



Model selection using relative marginal likelihoods of a *Plasmodium falciparum* (circle), a H1N1 influenza (star), and a Humpback whale mtDNA (diamond) dataset.

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



Model selection using relative marginal likelihoods of a *Plasmodium falciparum* (circle), a H1N1 influenza (star), and a Humpback whale mtDNA (diamond) dataset.

Influenza model with  $\Theta$  and growth is 118 ln mL units worse than best model!

Thank you



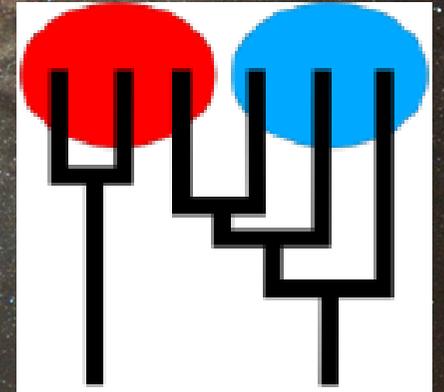
Lucrezia Bieler



National Science  
Foundation



Florida State University



<http://popgen.sc.fsu.edu>