

The Coalescent Model

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The Coalescent Model

coalescent = „zusammenwachsend“

Outline

- ▶ Population Genetics and the Wright-Fisher-model
- ▶ The Coalescent
- ▶ Non-constant population-sizes
- ▶ Further extensions
- ▶ Summary

Population Genetics

(Shamelessly stealing Alexis' slides)

- ▶ Study of polymorphisms in a population
 - ▶ What are the processes that introduce polymorphisms in the population?
 - ▶ If a polymorphism exists in a population, will it be there for ever?
 - ▶ Is there some process that removes polymorphisms from the population?
 - ▶ Do the polymorphisms exhibit patterns?
 - ▶ ...

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- ▶ It can easily do calculations about the past
- ▶ It is very fast to compute
- ▶ It can easily be extended to represent a more complex reality

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Hardy-Weinberg

- ▶ Assuming an **infinite population size**, random mating, diploid population, no selection...
the allele-frequencies are constant
- ▶ Infinity is weird... $0.3 \times \infty = \infty$
- ▶ ...and unrealistic

Wright-Fisher

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- ▶ The likelihood for an allele to prevail is equal to its initial frequency

Wright-Fisher

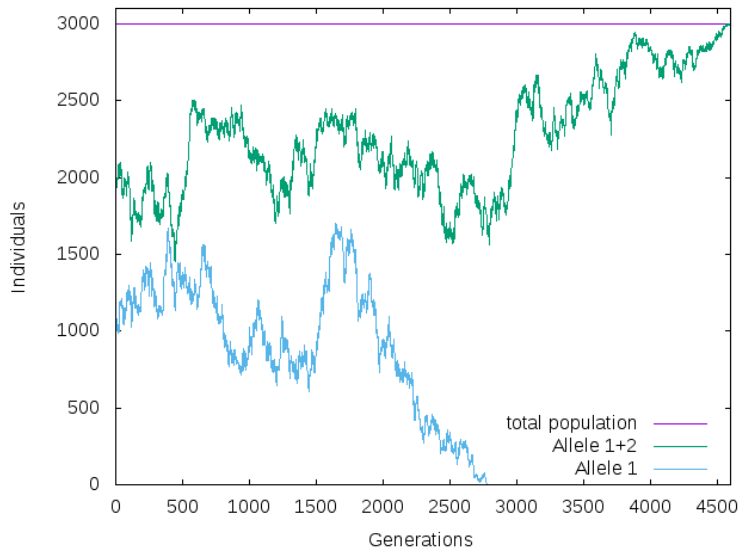


Figure 1: A simulation of three alleles under the model

Wright-Fisher (Individuals)

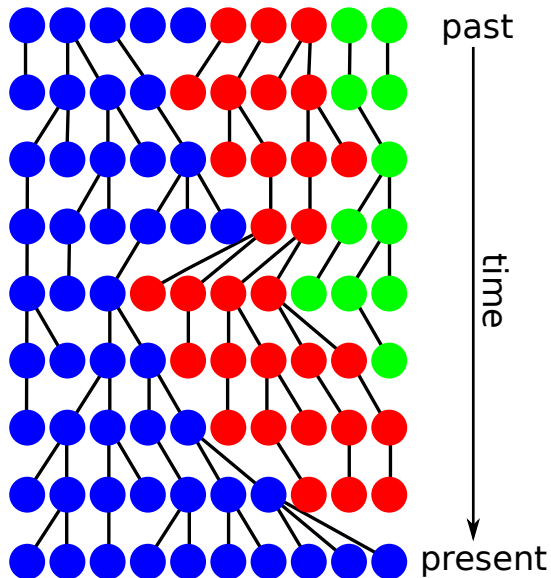


Figure 2: An evolutionary history in the model

Wright-Fisher (Individuals)

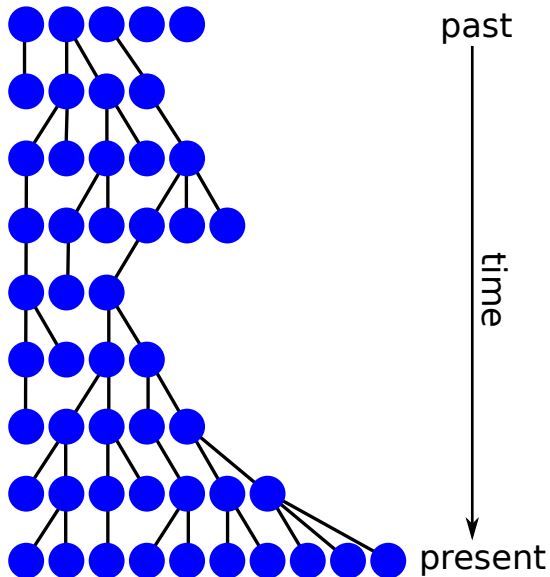


Figure 3: Extinct alleles removed

Wright-Fisher (Individuals)

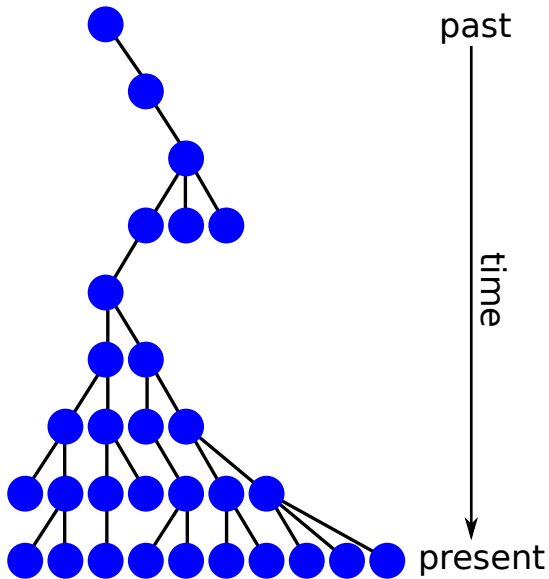


Figure 4: Surviving Tree

Wright-Fisher (MRCA)

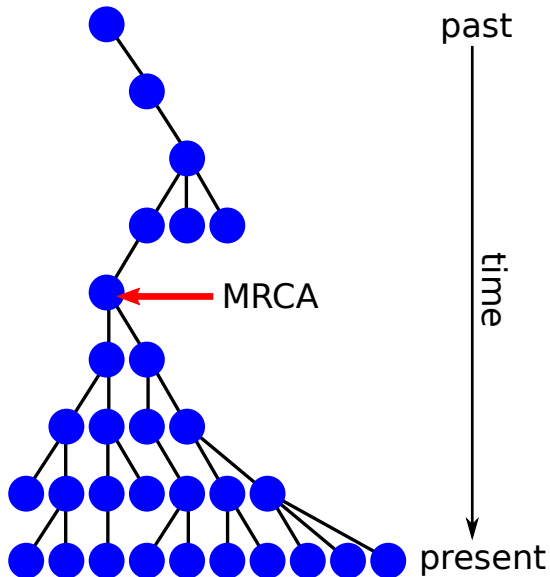


Figure 5: Most Recent Common Ancestor marked

Wright-Fisher (Coalescence-Events)

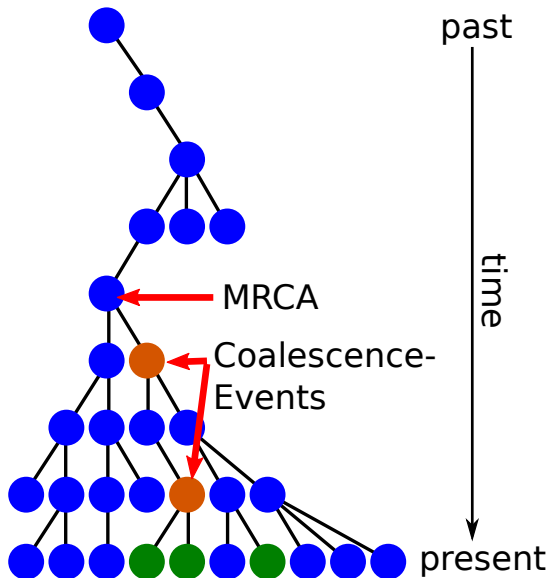


Figure 6: Coalescence-Events of the green individuals

The Coalescent Model

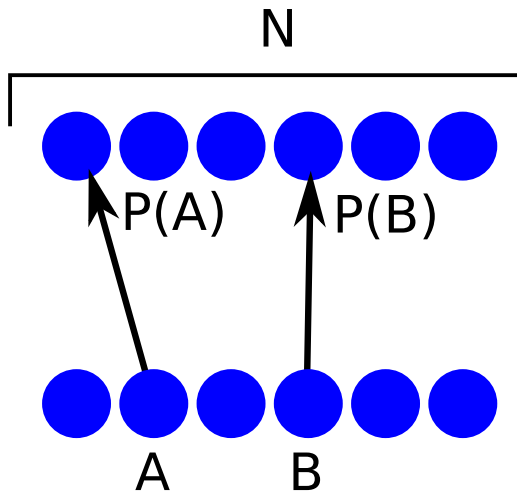


Figure 7: Two individuals and their parents

The Coalescent Model

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- ▶ In the previous t generations

$$1 - \left(\frac{N-1}{N}\right)^t$$

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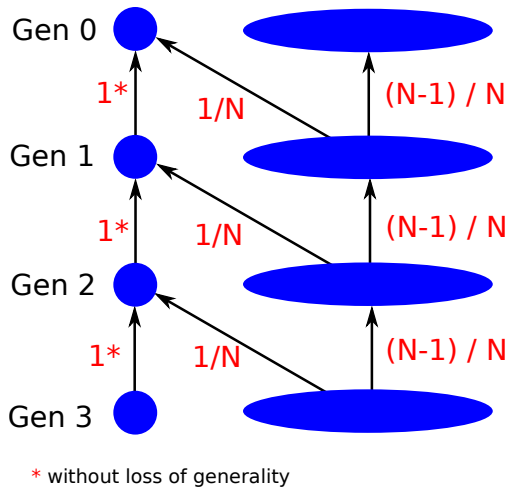


Figure 8: Likelihood of coalescence

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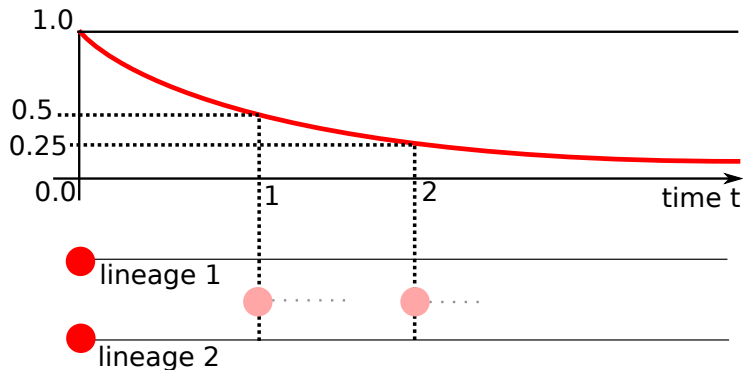
- ▶ Expected time for coalescence: $E(t) = N$

- ▶ Rescale: $\tau = \frac{t}{N}$:

$$\left(\frac{N-1}{N}\right)^{\lceil N\tau \rceil} \xrightarrow{N \rightarrow \infty} e^{-\tau}$$

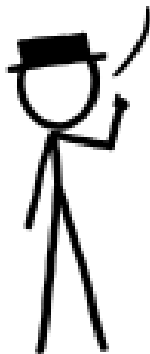
The Coalescent Model

⇒ The likelihood for two lineages to stay distinct over time is exponentially small!



Moar Lineages!!

WHAT IF WE TRIED
MORE ~~POWER?~~
lineages



More Lineages

- ▶ Likelihood of no coalescence in one generation and three lineages:

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- ▶ One generation, k lineages:

$$\frac{N-1}{N} \times \frac{N-2}{N} \times \cdots \times \frac{N-k+1}{N} = \prod_{i=1}^{k-1} \frac{N-i}{N}$$

More Lineages

- ▶ For some reason this is equal to:

$$\prod_{i=1}^{k-1} \frac{N-i}{N} = 1 - \frac{\binom{k}{2}}{N} + O\left(\frac{1}{N^2}\right) \approx 1 - \frac{\binom{k}{2}}{N}$$

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- ▶ There are $\binom{k}{2}$ ways to pick two lineages from a set of k lineages.
- ▶ Therefore a coalescence-event is $\binom{k}{2}$ -times as likely with k lineages than with 2
- ▶ **The number of coalescence-events grows quadratically with the number of lineages!**

More Lineages

Events getting exponentially rare

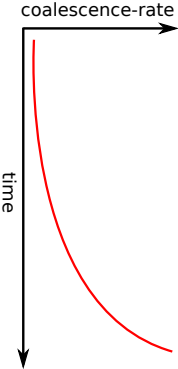
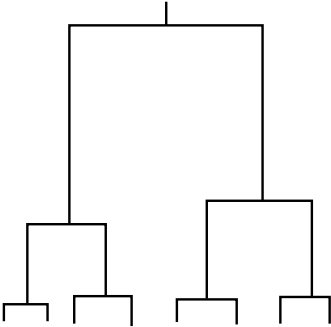
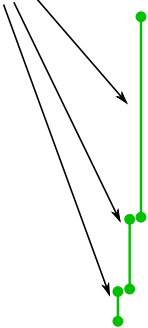


Figure 10: More lineages = faster coalescence

Properties

- ▶ Few deep furcations

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- ▶ Few deep furcations
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- ▶ Calculation is backward in times (Wright-Fisher: forward)
- ▶ Efficient: no calculation per individual or for extinct lineages

Non-constant population-sizes

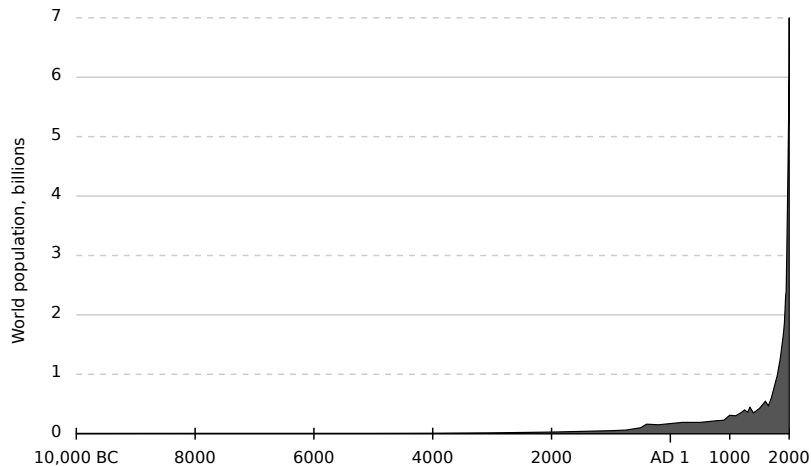


Figure 11: World population - not very constant [Wikimedia]

Non-constant population-sizes

- ▶ Non-constant, but known population-size
- ▶ Coalescence is more likely in small populations
- ▶ \Rightarrow Coalescence-rate changes over time

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- ▶ Coalescence is more likely in small populations
- ▶ \Rightarrow Coalescence-rate changes over time
- ▶ Simply rescale time.

Rescaling Time

- ▶ Before: t Generations corresponded to t/N units of coalescence-time
- ▶ Now: t Generations correspond to

$$\sum_{i=1}^t \frac{1}{N_i}$$

units of coalescence-time

- ▶ Note: for a constant population both formulas are equal

Rescaling Time - Example

- ▶ 5 Generations, with on average 5 individuals:

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- ▶ For non-constant $\{4, 4, 5, 6, 6\}$ individuals:

$$\tau = \sum_{i=1}^t \frac{1}{N_i} = \frac{1}{4} + \frac{1}{4} + \frac{1}{5} + \frac{1}{6} + \frac{1}{6} = \frac{31}{30}$$

note the lesser influence of the larger generations

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- ▶ **A generation with twice the size, will get halve the coalescence-time**

Rescaling Time - Exponential Growth

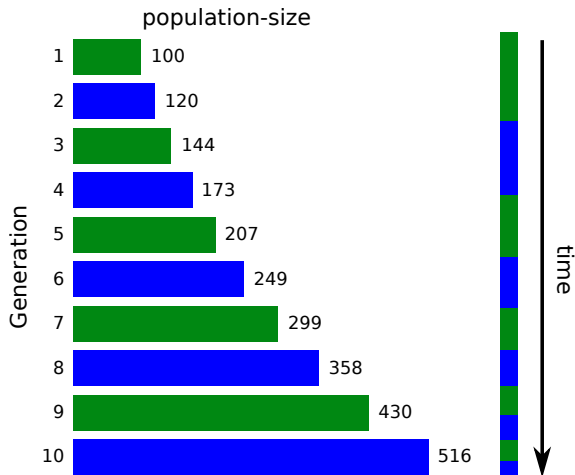


Figure 12: Exponentially growing population versus coalescence-time

Rescaling Time - Exponential Growth

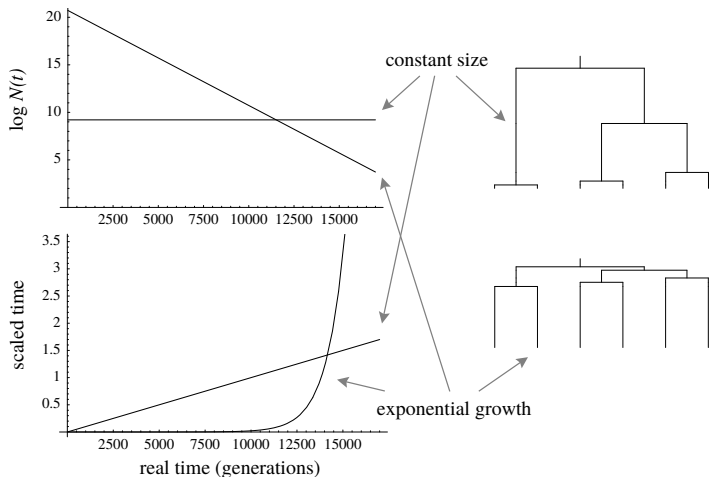


Figure 13: Exponentially growing and constant populations. Note the reverse time-scale! [Nordborg]

Rescaling Time - Applicability

- ▶ Approximation converges against theory for growing N
- ▶ Close enough for most purposes

Further Extensions

- ▶ Separated Populations
- ▶ Diploid Populations
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- ▶ Selection
- ▶ Multiple Species
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Coalescent:

Assuming non-overlapping generations. . .

An actual example

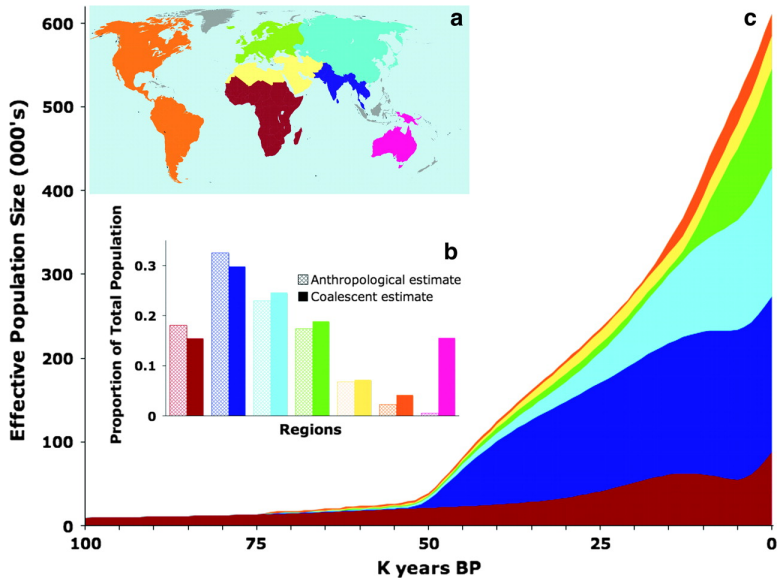


Figure 14: Coalescent vs. Anthropological Estimates [Atkinson et al.]

Software

Software that uses the coalescent model¹:

BEAST, COAL, CoaSim, DIYABC, DendroPy, GeneRecon, genetree, GENOME, IBDSim, IMA, Lamarc, Migraine, Migrate, MaCS, ms & msHOT, msms, Recodon and NetRecodon, SARG, simcoal2, TreesimJ

¹Source: https://en.wikipedia.org/wiki/Coalescent_theory

Summary

- ▶ The coalescent is the Wright-Fisher-model plus math
- ▶ Coalescent-events are, with exponential likelihood, relatively recent
- ▶ The more lineages there are, the more coalescence-events occur
- ▶ Non-Constant populations can be simulated by rescaling time
- ▶ The simulated time for a generation is anti-proportional to it's size

References

Content

- ▶ Magnus Nordborg, “Coalescent Theory”, March 2000

Software-list

- ▶ en.wikipedia.org/wiki/Coalescent_theory

Images

- ▶ Fig. 09: Randal Munroe: what-if.xkcd.com/13/
- ▶ Fig. 11: El T:
commons.wikimedia.org/wiki/File:Population_curve.svg
- ▶ Fig. 13: Magnus Nordborg: “Coalescent Theory”, 2000
- ▶ Fig. 14: Atkinson et al.: “mtDNA variation predicts population size in humans and reveals a major Southern Asian chapter in human prehistory”, 2008