#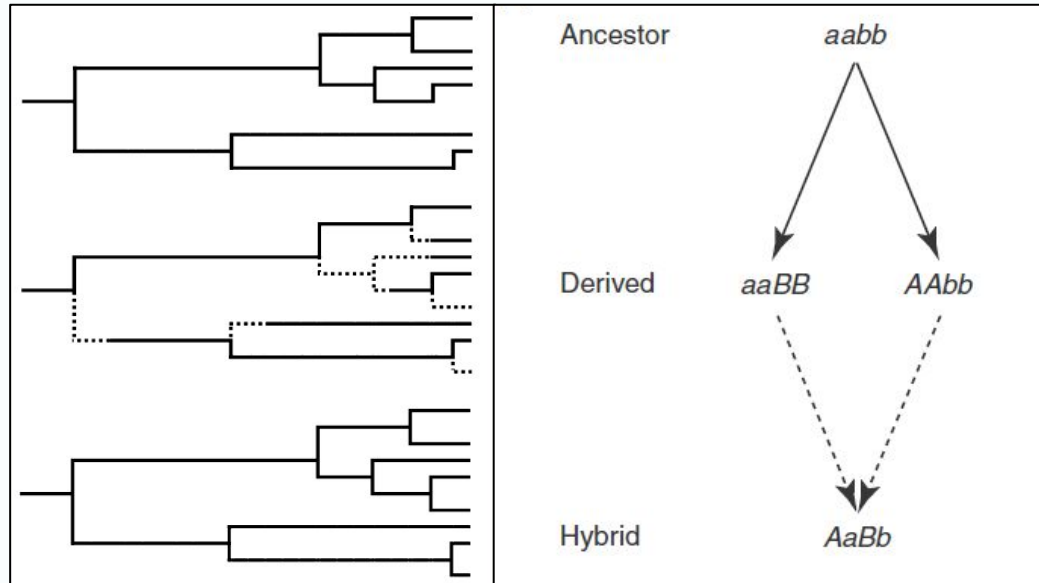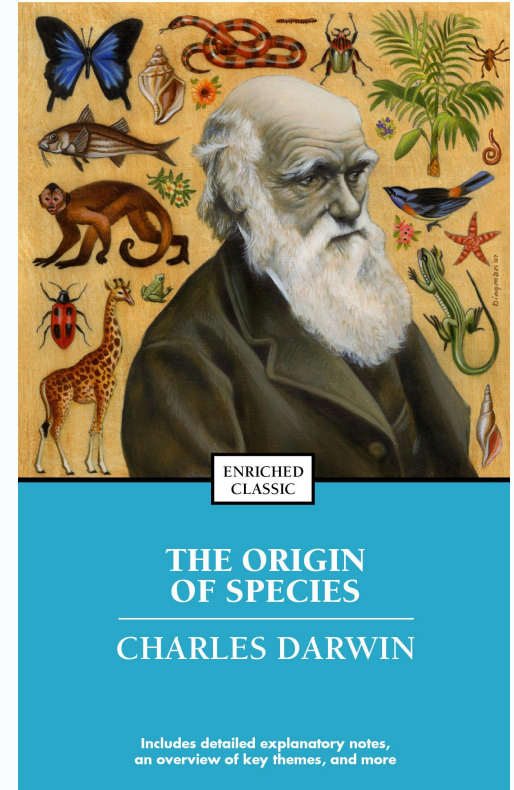 What are the differences in phylogenies based on the protracted birth-death model and the Bateson-Dobzhansky-Müller model?

By Jorik de Boer
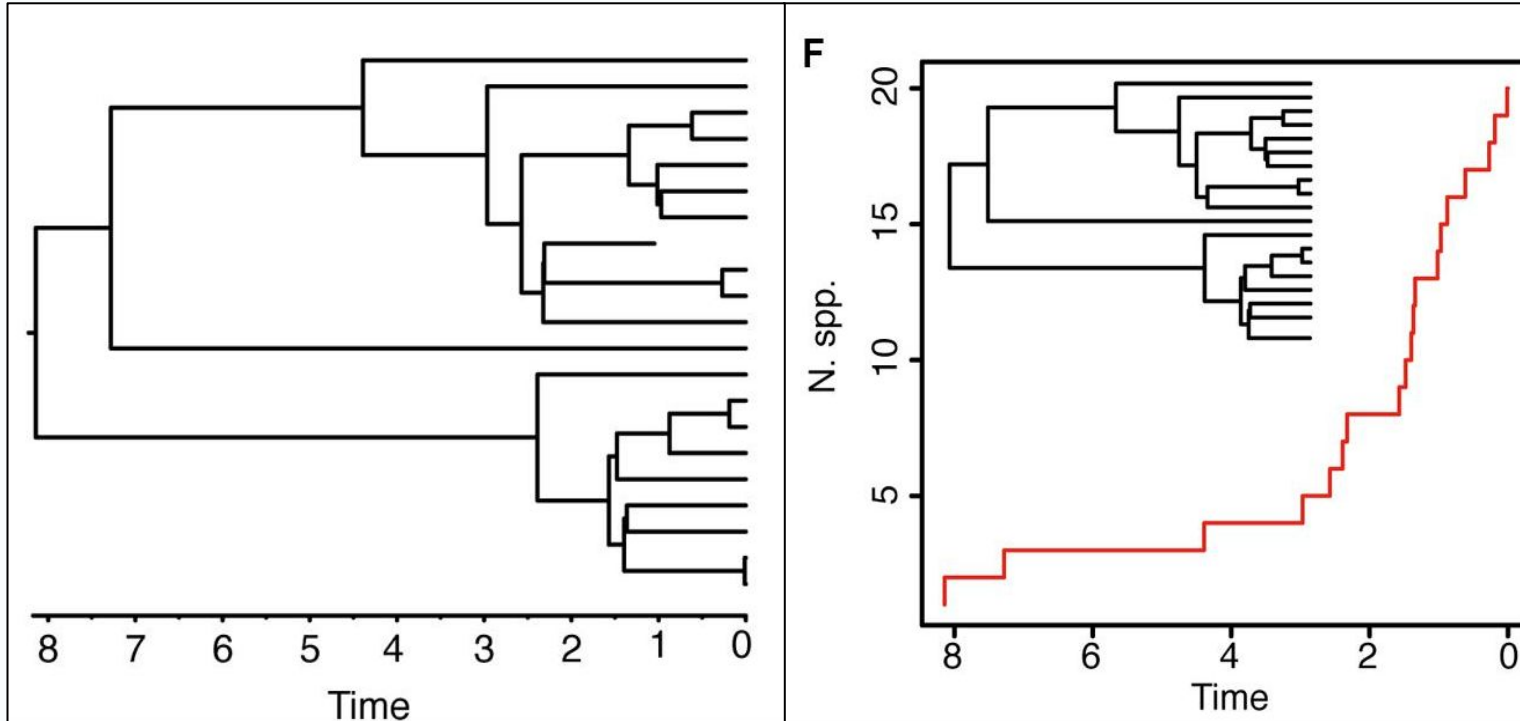

Master Ecology and Evolution
October 2016
Supervisor: Richèl Bilderbeek

Introduction

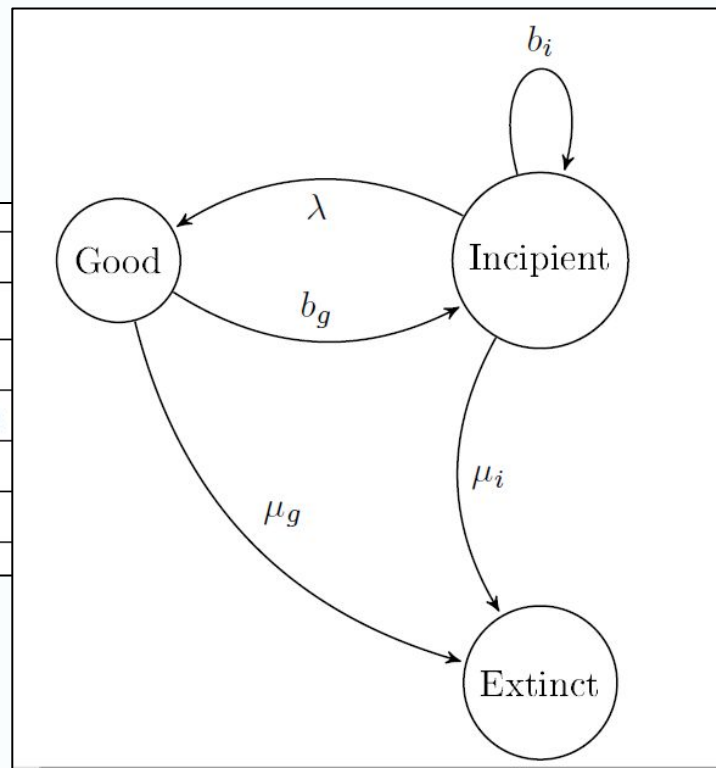# Background speciation models: BD-model

"Pull of the present"

Background speciation models: PBD-model
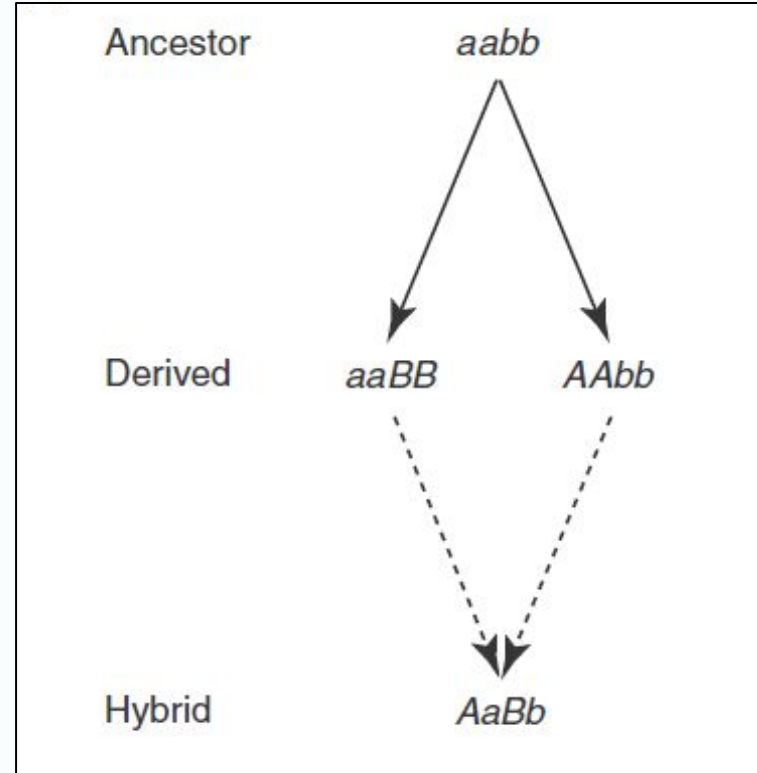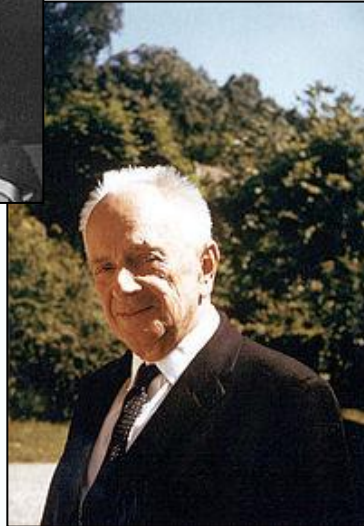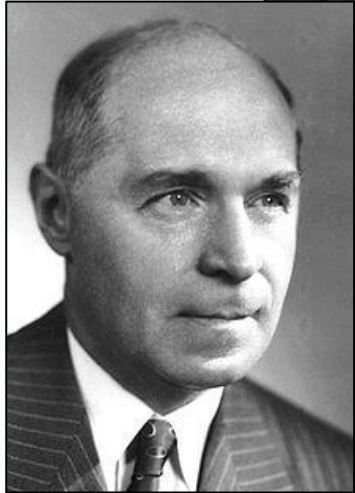
The protracted birth-death model

| Symbol	Description
μ_i	Extinction rate incipient species
μ_g	Extinction rate good species
b_i	Speciation initiation rate / birth rate incipient species
b_g	Speciation initiation rate / birth rate good species
λ	Speciation completion rate (SCR)

Background speciation models: BD & PBD-model
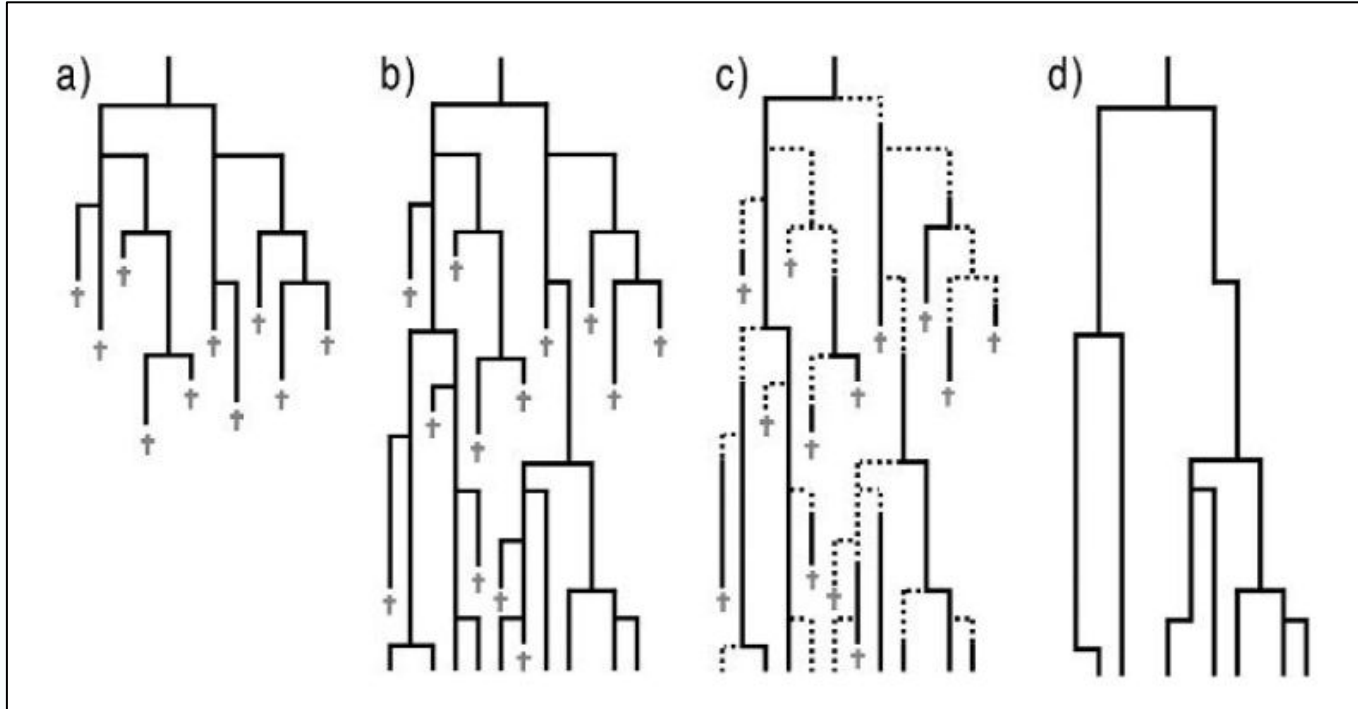
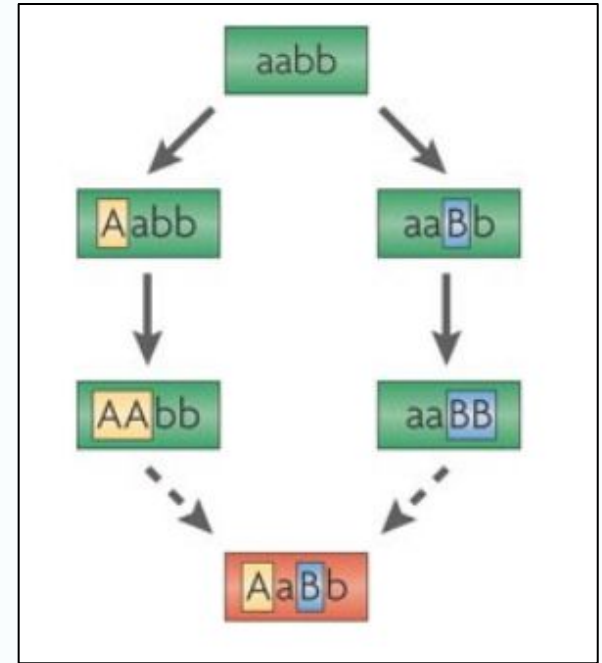# The Bateson-Dobzhansky-Müller model (1)

The Bateson-Dobzhansky-Müller model (2)
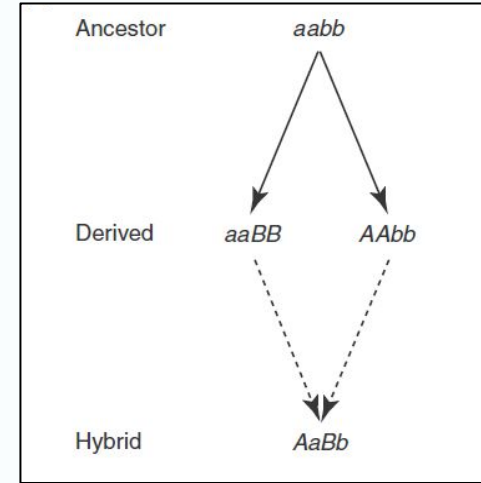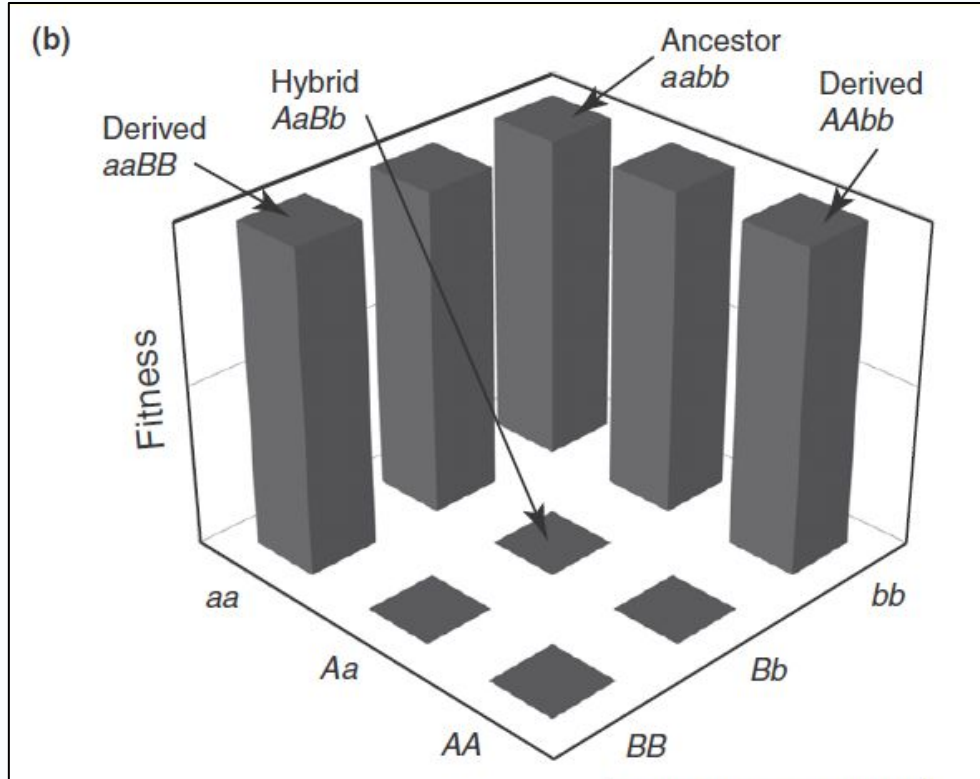
Bateson-Dobzhansky-Müller model characteristics

Two-populations and one-population scenario


```
0     1     2          0     1     2
ab => aB => aB         ab => Ab => AB
ab => ab => Ab
```

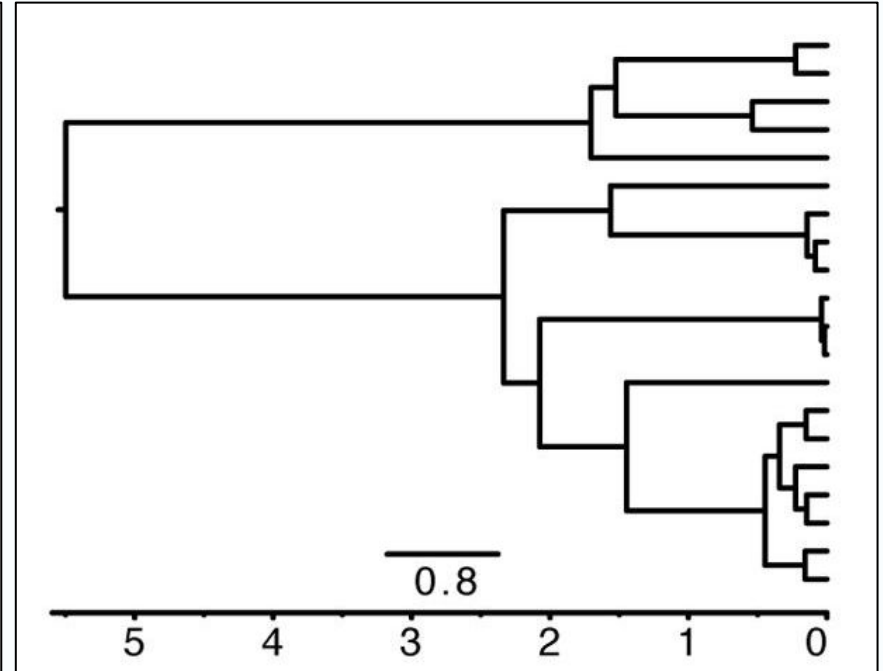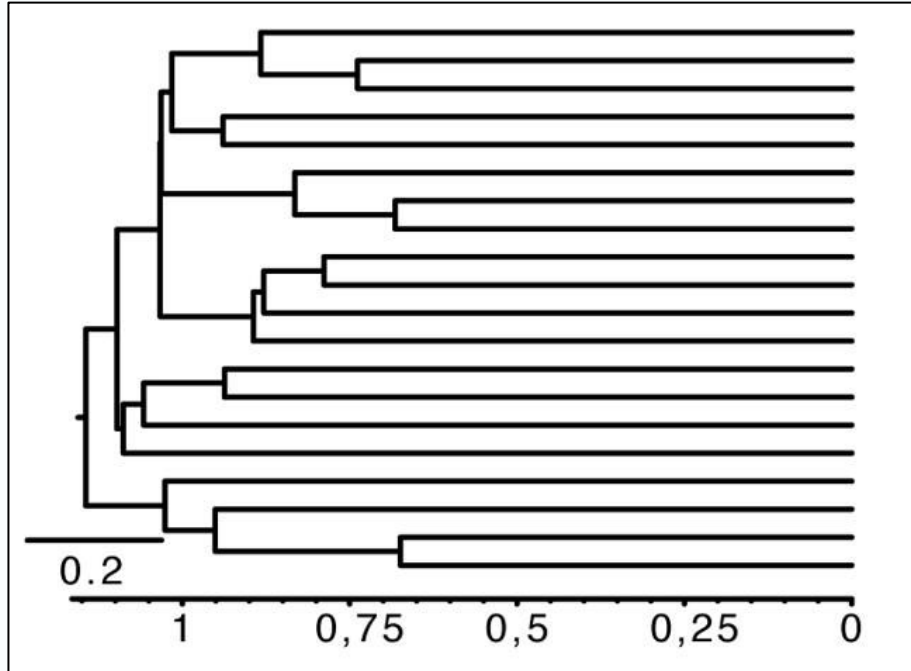a & B assumed incompatible

Biological context

Research Question

What are the differences in phylogenies based on the protracted birth-death model (PBD) and the Bateson-Dobzhansky-Müller model (BDM)?
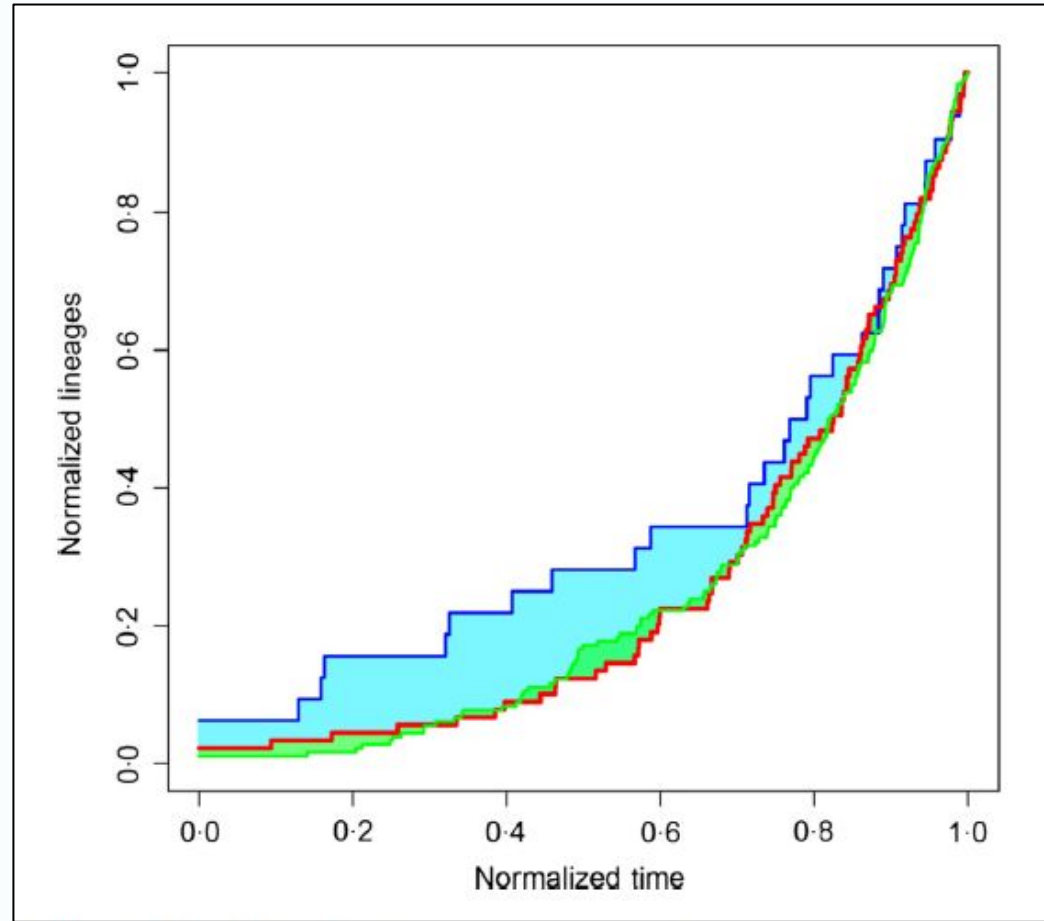
Summary statistics (1)

Gamma (γ) summary statistic, tree size and the Phylogenetic Diversity metric (PD)

Summary statistics (2)

Lineages through time (LTT) plot

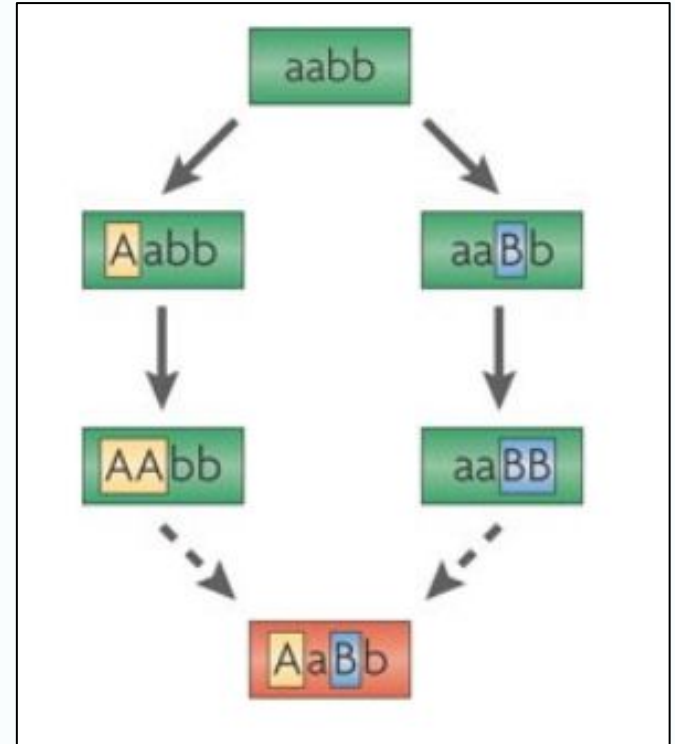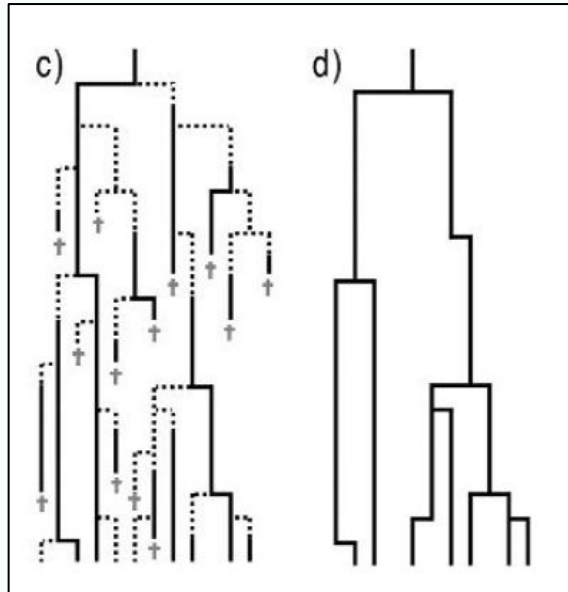Normalized lineages through time (nLTT) summary statistic

Assumptions

- Allopatric scenario, No migration

- No advantages or disadvantages for certain alleles

- Same mutation rates for different alleles

- Can be expanded in later stages

simple is beautiful.

Discussion

- Mechanistic model
- Differences and similarities PBD & BDM

Thank you for your attention!

Questions?