

PhD project overview

TECE meeting 2016-09-26



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www.github.com/richelbilderbeek/Science

PhD project question

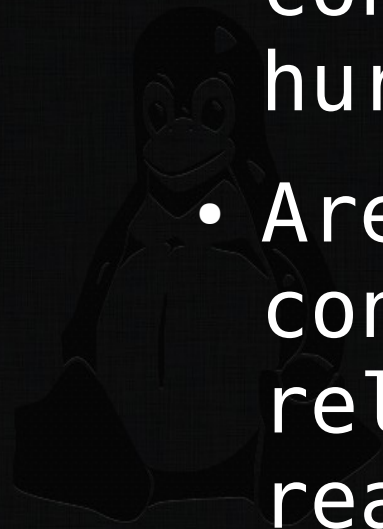
What if
reproductive
isolation
takes
time to
establish?

- In the context of phylogenetics
- What errors do our current tools make?
- How good are existing lineage-based models?
- Can we make mechanistic models?

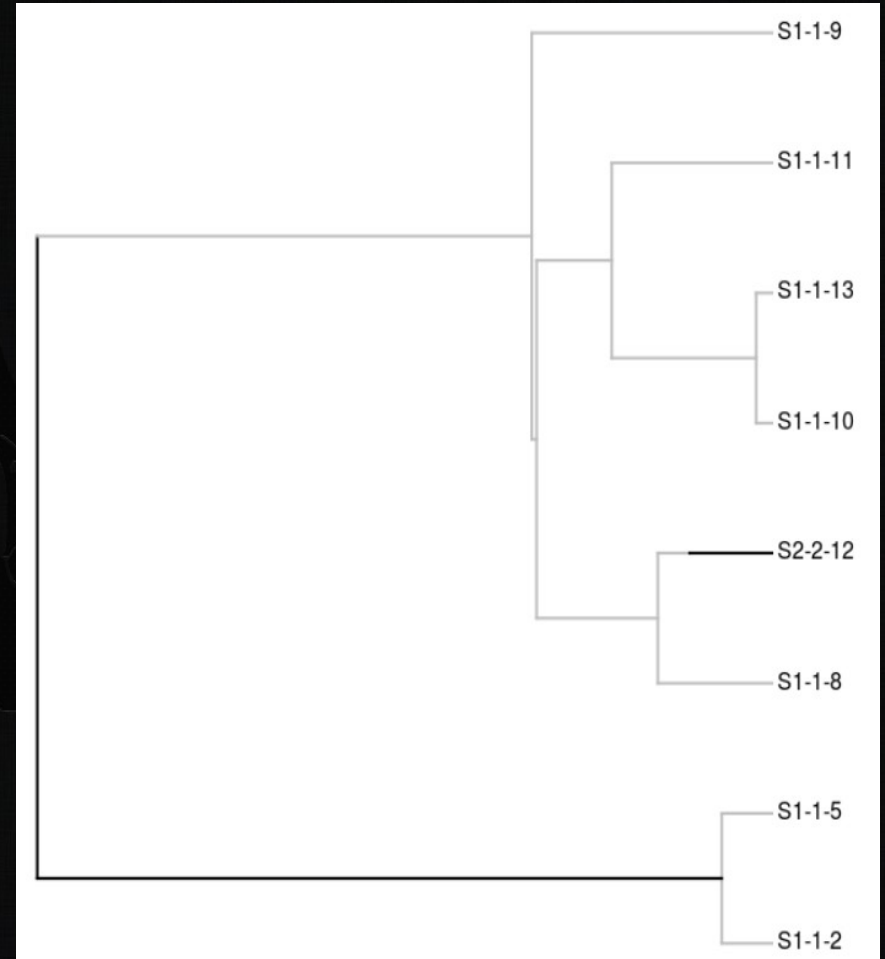
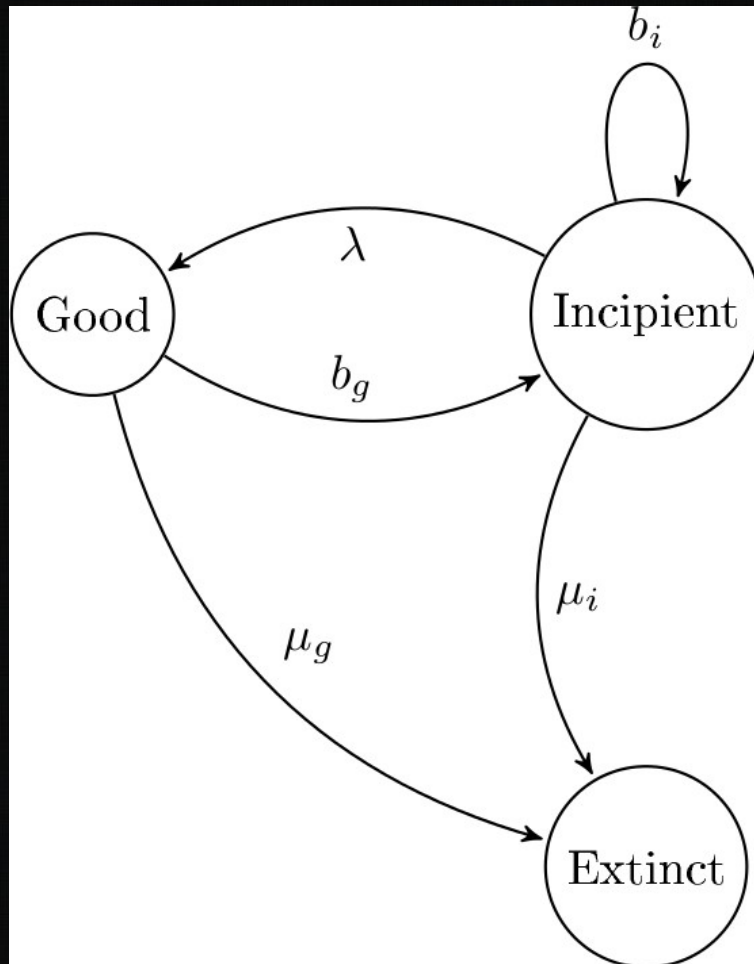
Project 1: BD on PBD

If reproductive isolation takes time to establish, what is the error made today in inferring a phylogeny?

- Under which conditions does it hurt?
- Are these conditions relevant and/or realistic?
- Tool used: BEAST2, assumes speciation is instantaneous

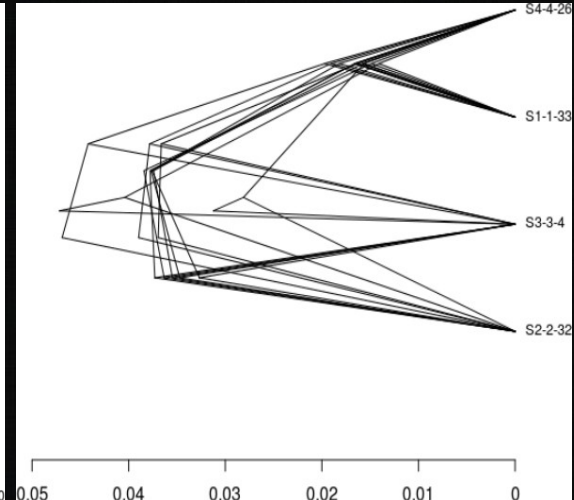
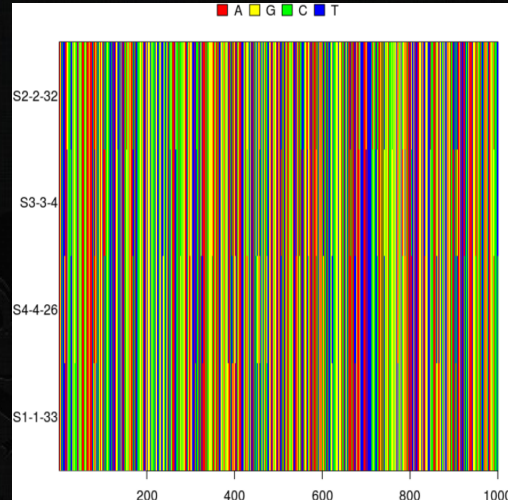
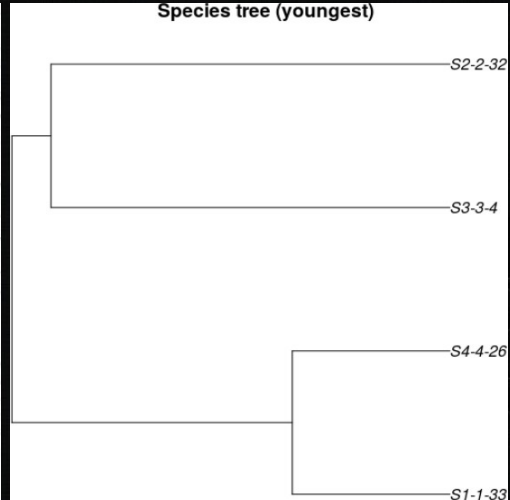
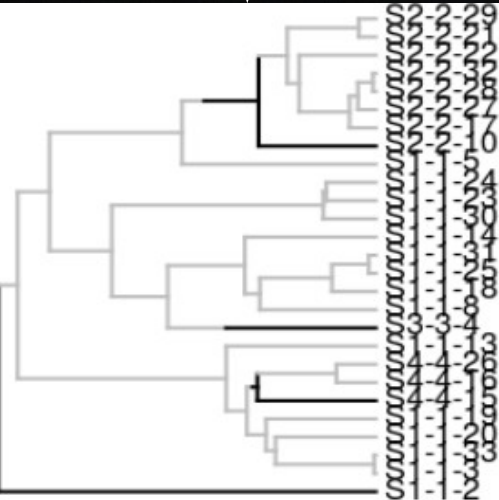


PBD model



Etienne, Rampal S., and James Rosindell. "Prolonging the past counteracts the pull of the present: protracted speciation can explain observed slowdowns in diversification." *Systematic Biology* (2011): syr091.

Approach

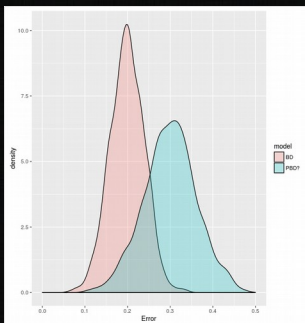


Simulate an
incipient
species tree

Sample species
trees

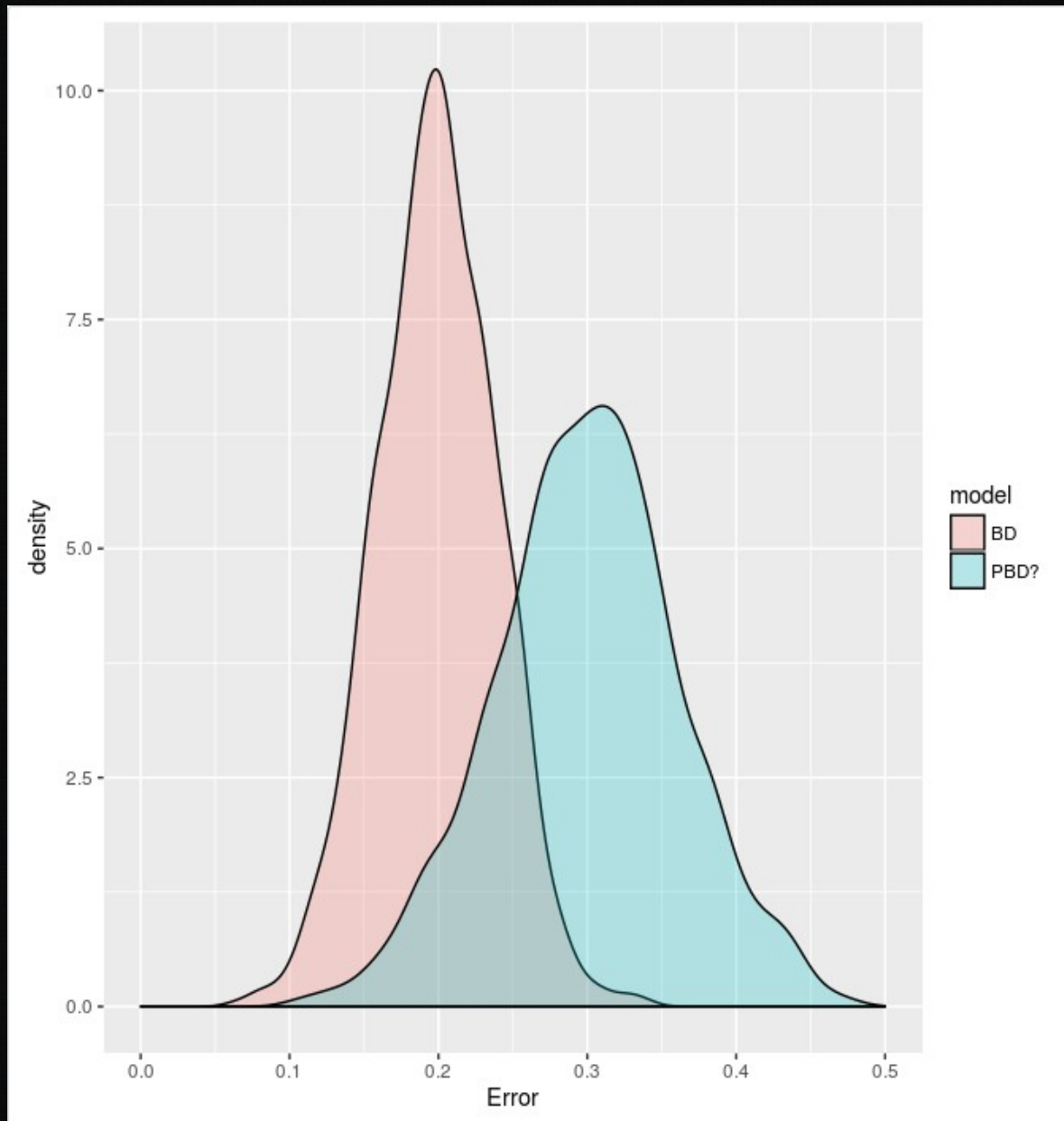
Simulate DNA
alignments

Infer species
tree posterior

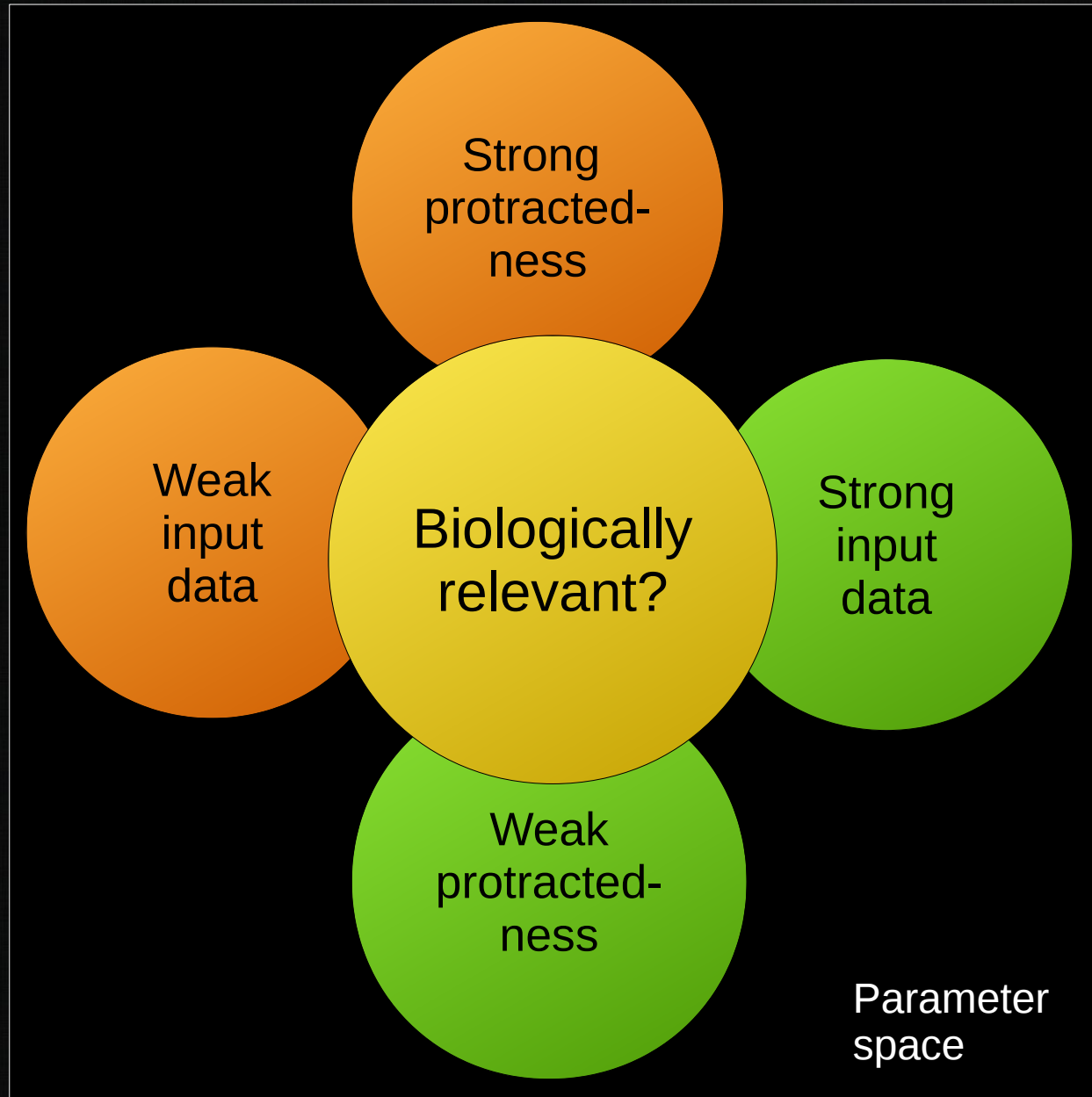


Measure difference/error

Goal



Predictions



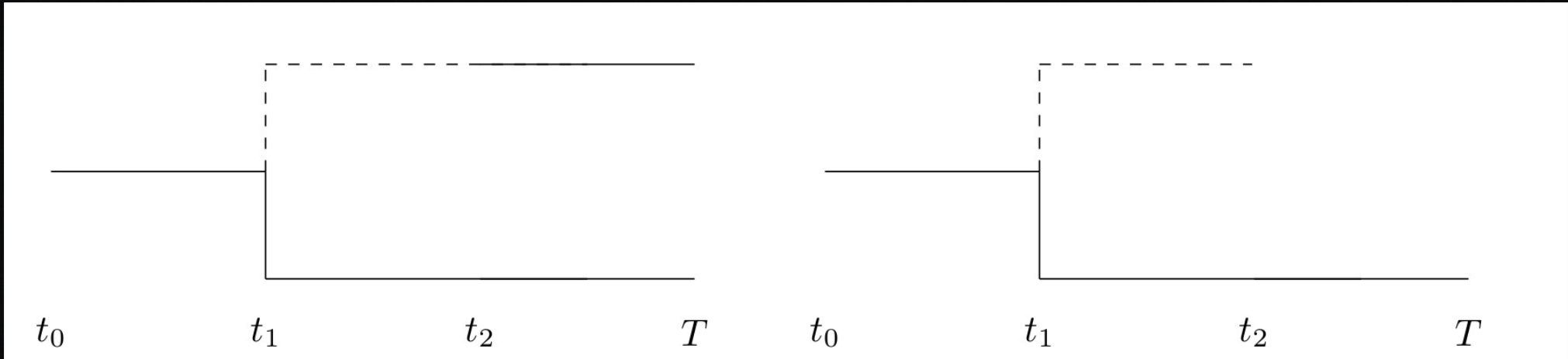
Project 2: phylogenesis

If reproductive isolation in nature takes time to establish, what kind of phylogenies do we expect?

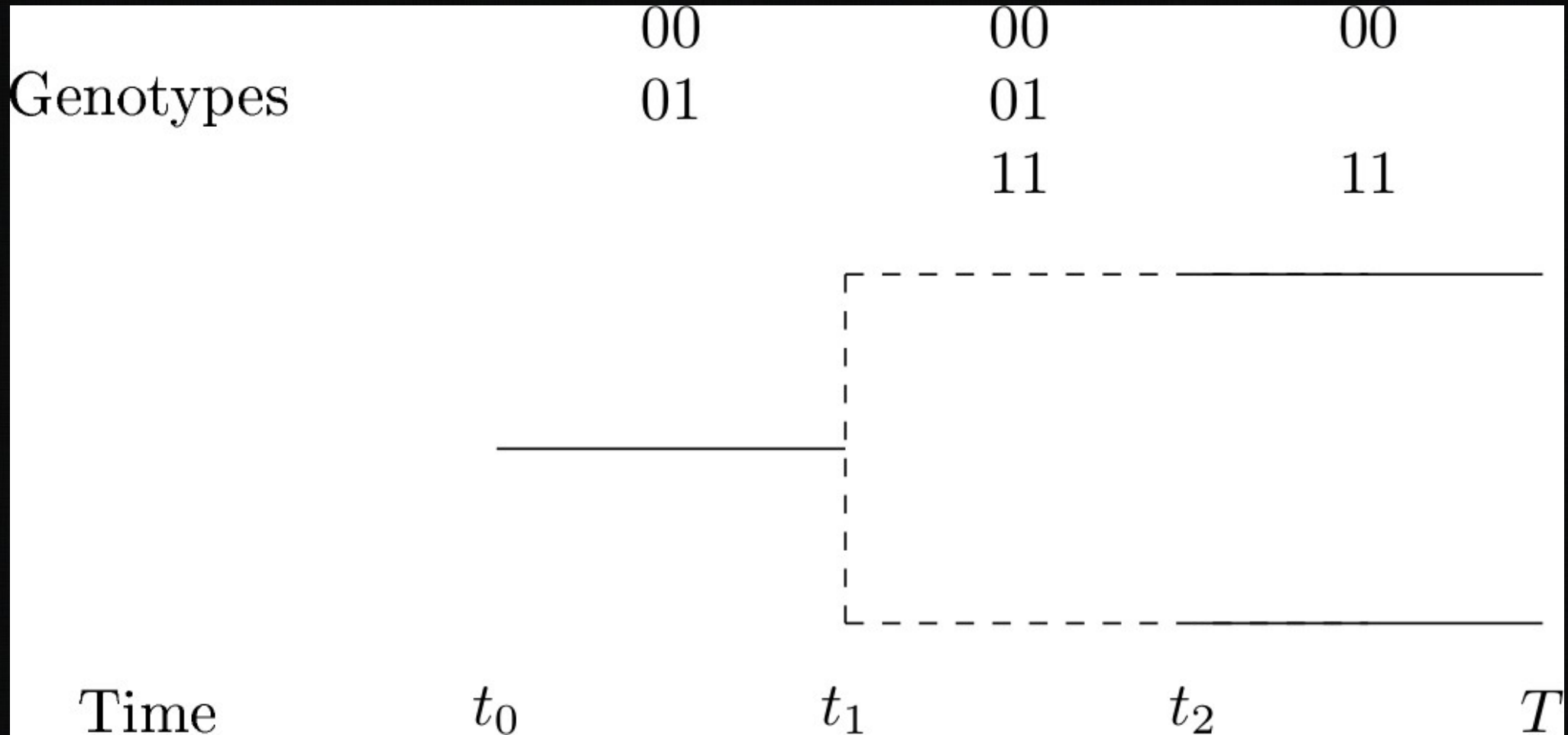
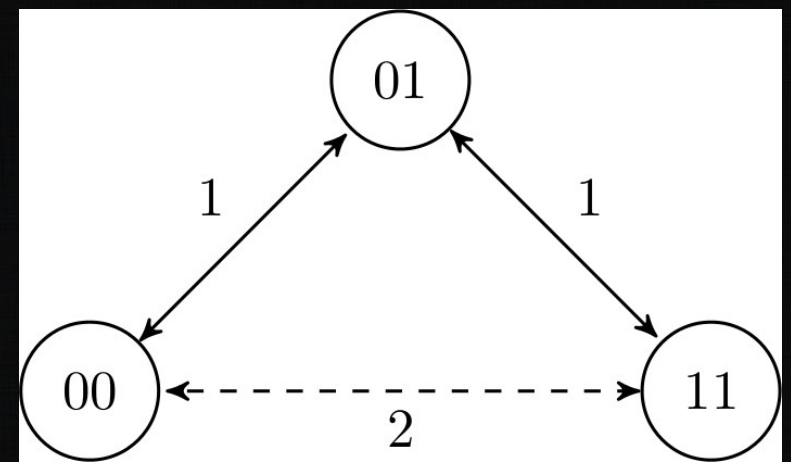
- Lineage-based
- Mechanistic



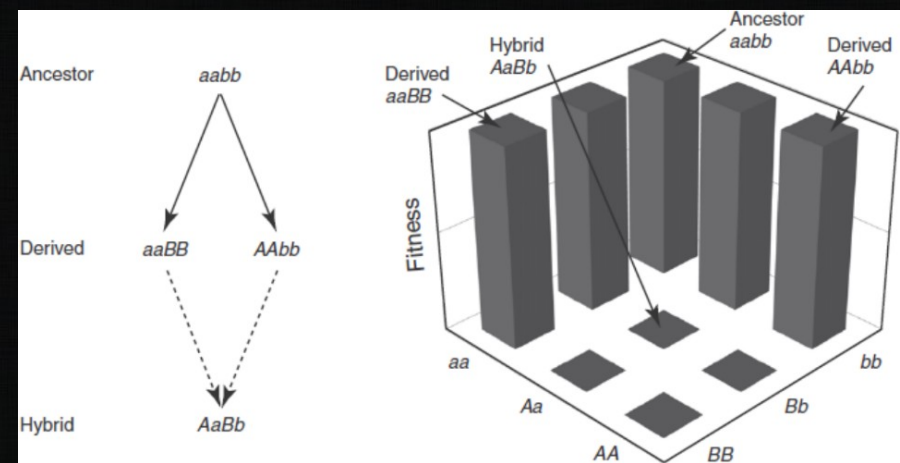
Interesting phylogenies



- Allopatric, peripatric, sympatric?
- What happens at t_1 and t_2 ?



Mallet J (2008) A species definition for the Modern Synthesis. Trends Ecol Evol 10: 294–299.



Genotypes

$aabb$
 $aaBB$

$aabb$
 $aaBB$
 $AAbb$

$aaBB$
 $AAbb$

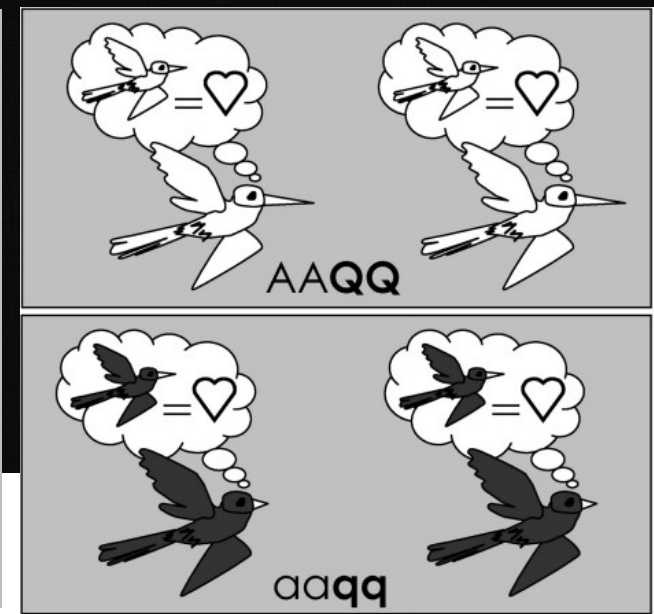
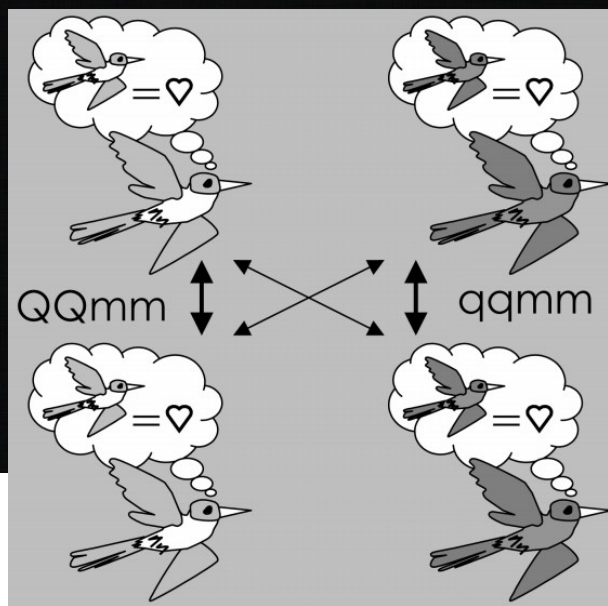
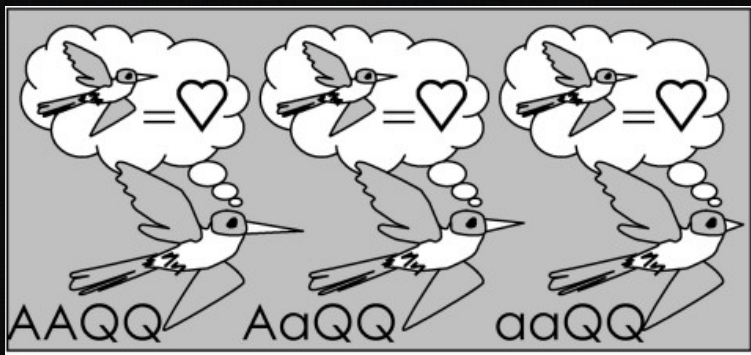
Time

t_0

t_1

t_2

T



Genotypes

Time

t_0

t_1

t_2

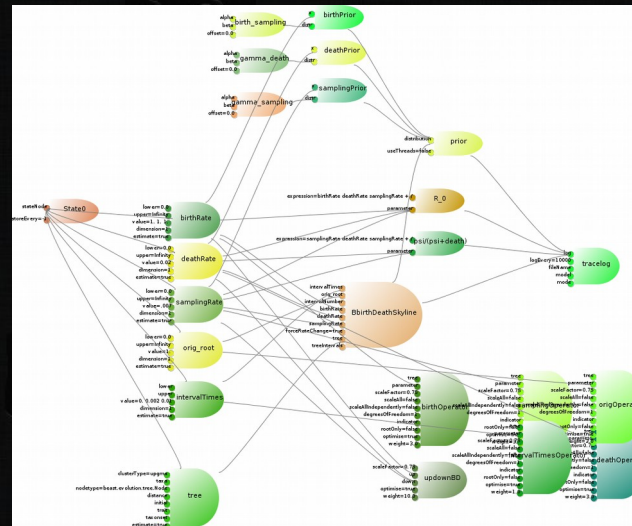
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Van Doorn, G. S., & Weissing, F. J. (2001). "Ecological versus sexual selection models of sympatric speciation." *Selection*, 2, 17 - 40.

Project 3: time

If
reproductive
isolation in
nature takes
time to
establish,
how well can
we infer it?

- Put PBD model in phylogenetic tool



BEAST 2: A Software Platform for Bayesian Evolutionary Analysis
Bouckaert, R., Heled, J., Kühnert, D., Vaughan, T., Wu, C-H., Xie, D., Suchard, MA., Rambaut, A., & Drummond, A. J. (2014). BEAST 2: A Software Platform for Bayesian Evolutionary Analysis. PLoS Computational Biology, 10(4), e1003537.
doi:10.1371/journal.pcbi.1003537

Project 4: question

If reproductive isolation in nature takes time to establish, what could be a fourth research question?

- Depends on other projects

