Speciation takes time:
a conceptual individual-based model
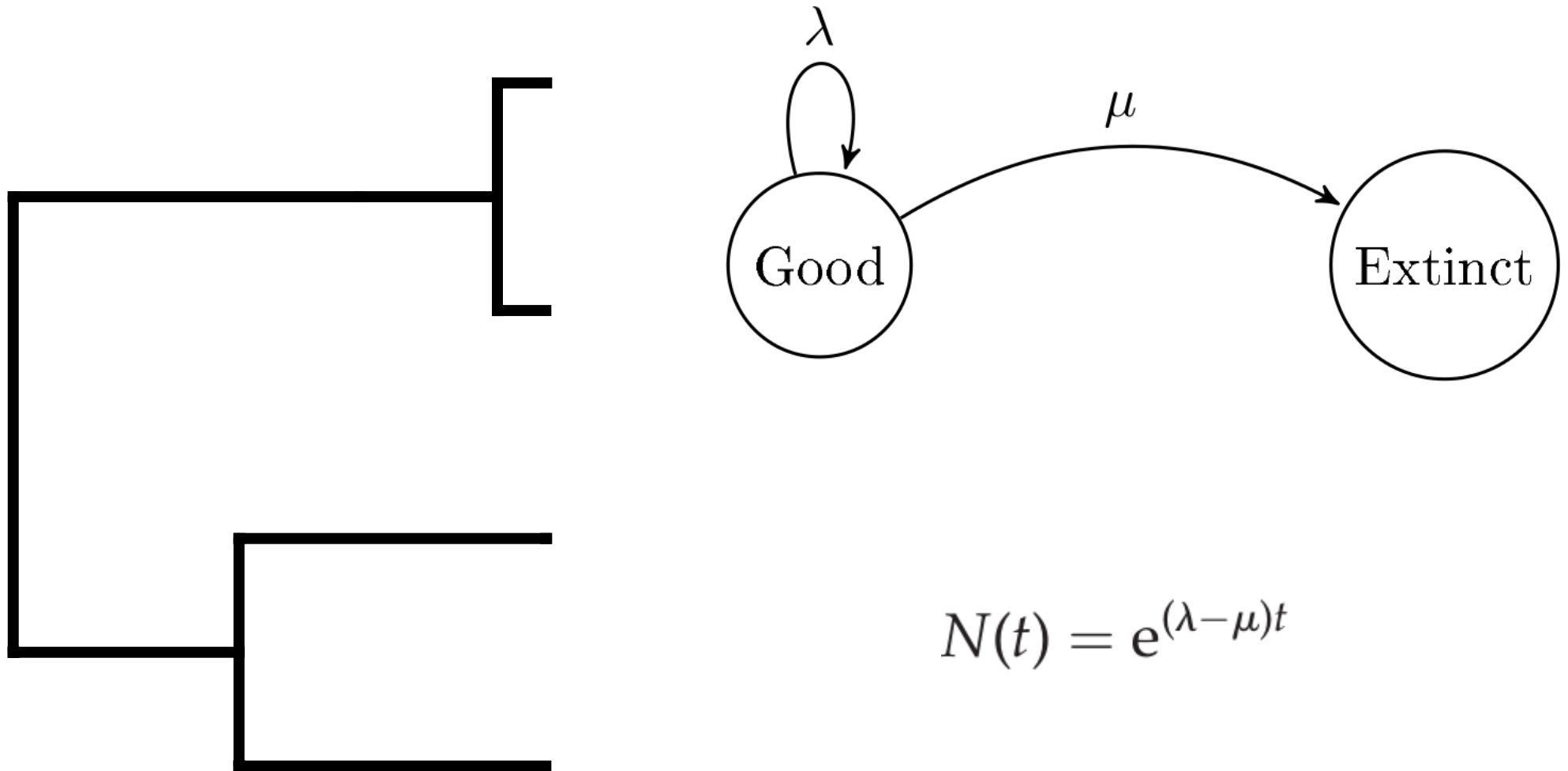
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GELIFES
Groningen Institute for Evolutionary Life Sciences

Thermoanaerobacter tengcongensis
Clostridium acetobutylicum
Clostridium tetani
Clostridium perfringens
Phytoplasma Onion yellows
Mycoplasma mycoides
Mycoplasma mobile
Mycoplasma pulmonis
Ureaplasma parvum
Mycoplasma penetrans
Mycoplasma gallisepticum
Mycoplasma pneumoniae
Mycoplasma genitalium
Staphylococcus epidermidis
Staphylococcus aureus MW2
Staphylococcus aureus N315
Staphylococcus aureus Mu50
Listeria innocua
Listeria monocytogenes F2365
Listeria monocytogenes EGD
Bacillus halodurans
Oceanobacillus iheyensis
Bacillus subtilis
Bacillus anthracis
Bacillus cereus ATCC 10987
Bacillus cereus ATCC 14579
Lactobacillus plantarum
Lactobacillus johnsonii
Enterococcus faecalis
Lactococcus lactis
Streptococcus pneumoniae R6
Streptococcus pneumoniae TIGR4
Streptococcus mutans
Streptococcus agalactiae III
Streptococcus agalactiae V
Streptococcus pyogenes M1
Streptococcus pyogenes MGAS8232
Streptococcus pyogenes MGAS3
Streptococcus pyogenes SSI-
Streptococcus pyogenes
Fibrobacter succinogenes
Chlorobium tepidum
Porphyromonas gingiv
Bacteroides thetaiota
Chlamydia muridar
Chlamydia trachom
Chalmydophila
Chlamydophila
Chlamydia pn
Chlamydia p
Chlamydia
Gemmata
Rhodopire
Leptospira
Leptospira
Borrelia b
Treponem
Treponem
Bifidobact
Tropherym
Tropheryma
Streptomyc
Streptomyce
Corynebacter
Corynebacter
Corynebacteri
Corynebacteri
Mycobacteri
Mycobacterium
Mycobacterium lep
Myco

Pan troglodytes
Homo sapiens
Rattus norvegicus
Mus musculus
Gallus gallus
Danio rerio
Takifugu rubripes
Anopheles gambiae
Drosophila melanogaster
Caenorhabditis elegans
Caenorhabditis briggsae
Saccharomyces cerevisiae
Eremothecium gossypii
Schizosaccharomyces pombe
Dictyostelium discoideum
Oryza sativa
Arabidopsis thaliana
Cyanidioschyzon merolae
Plasmodium falciparum
Cryptosporidium hominis
Thalassiosira pseudonana
Leishmania major
Giardia lamblia

Methanococcus maripaludis
Methanococcus jannaschii
Methanobacterium thermautotrophicum
Methanopyrus kandleri
Pyrococcus horikashii
Pyrococcus abyssi
Pyrococcus furiosus
Methanosarcina mazei
Methanosarcina acetivorans
Halobacterium sp. NRC-1
Archaeoglobus fulgidus
Thermoplasma volcanium
Thermoplasma acidophilum
Sulfolobus solfataricus
Sulfolobus tokodaii
Aeropyrum pernix
Pyrobaculum aerophilum
Nanoarchaeum equitans

Shigella flexneri 2a 301
Shigella flexneri 2a 245TT
Escherichia coli K12
Escherichia coli O6
Escherichia coli O157:H7
Escherichia coli EDL933
Salmonella typhi
Salmonella
Yersinia pestis KIM
Yersinia pestis

# Instantaneous birth-death model

$$N(t) = e^{(\lambda - \mu)t}$$

Stadler, Tanja, et al. "How well can the exponential-growth coalescent approximate constant-rate birth–death population dynamics?." Proc. R. Soc. B. Vol. 282. No. 1806. The Royal Society, 2015.
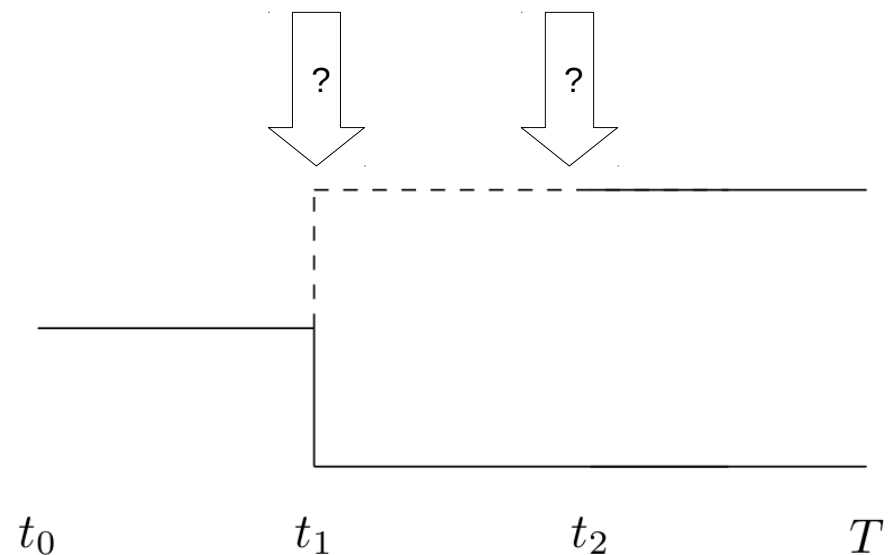
Protracted birth-death model
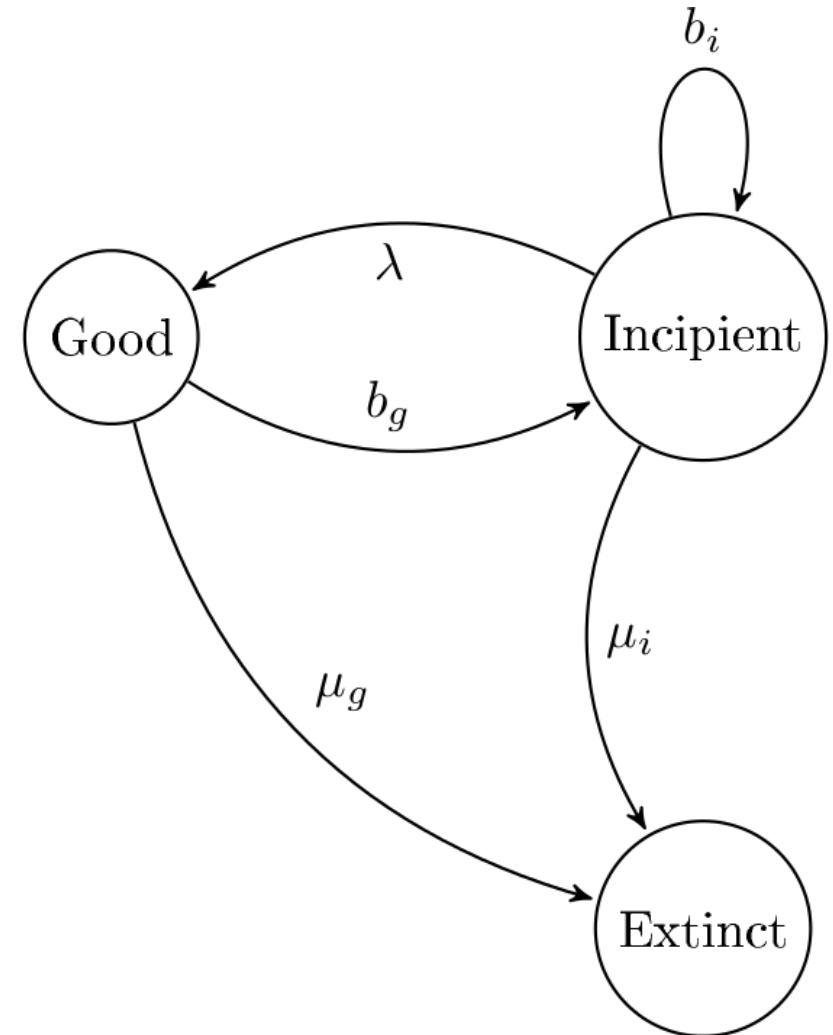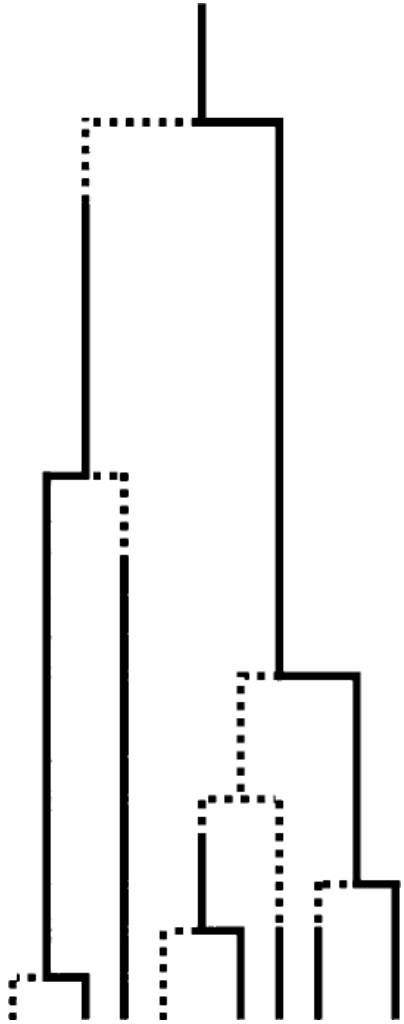
Etienne, Rampal S., and James Rosindell. "Prolonging the past counteracts the pull of the present: protracted speciation can explain observed slowdowns in diversification." Systematic Biology 61.2 (2012): 204-213.

Lineages through time
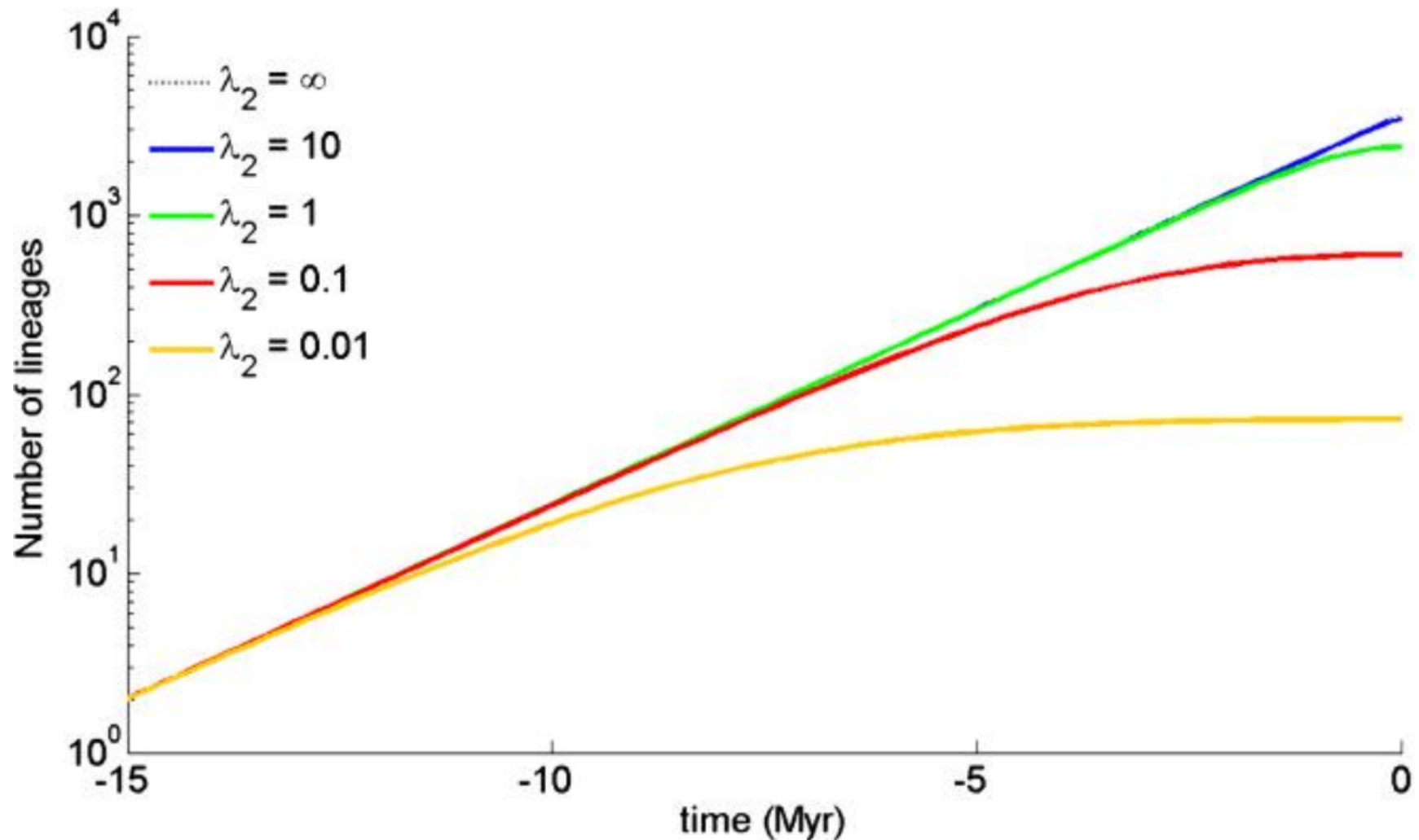
Etienne, Rampal S., and James Rosindell. "Prolonging the past counteracts the pull of the present: protracted speciation can explain observed slowdowns in diversification." Systematic Biology 61.2 (2012): 204-213.

Mechanism?

- No gene flow, thus allopatric speciation?

Here, […] we deliberately do not assume a specific mechanism for speciation but only recognize […] that it is gradual rather than instantaneous

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 61.2 (2012): 204-213.

Research question

- Can we verbally offer a biological explanation?
- Can we put this in an IBM at the species level?
- If yes, how much do these approaches match?

t_0 $\qquad$ t_1 $\qquad$ t_2 $\qquad$ T
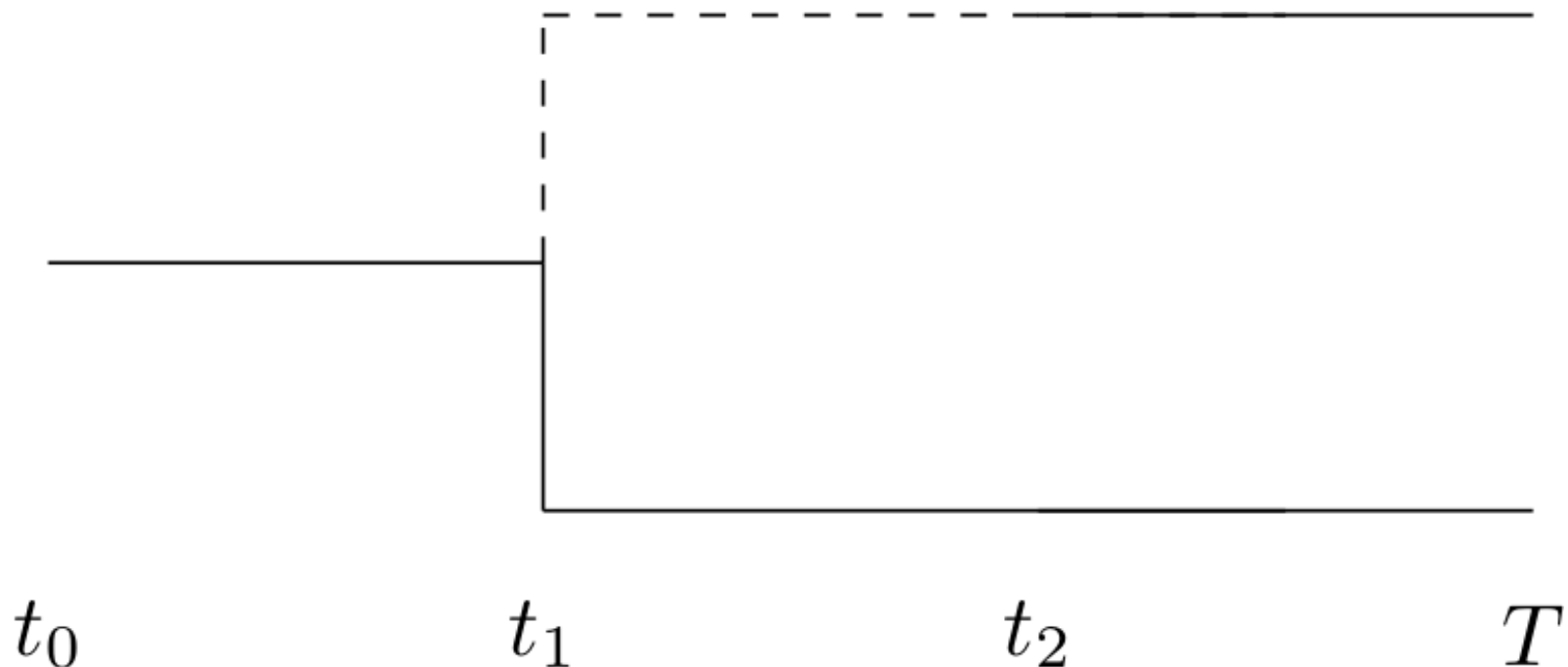
Speciation models

- Bateson-Dobzhansky-Muller
  - Two loci, two alleles per locus

- 'Van Doorn'
  - Species trait and species preference

- Mallet
  - Minimum genetic similarity threshold

Mallet J (2008) A species definition for the Modern Synthesis. Trends Ecol Evol 10: 294–299.
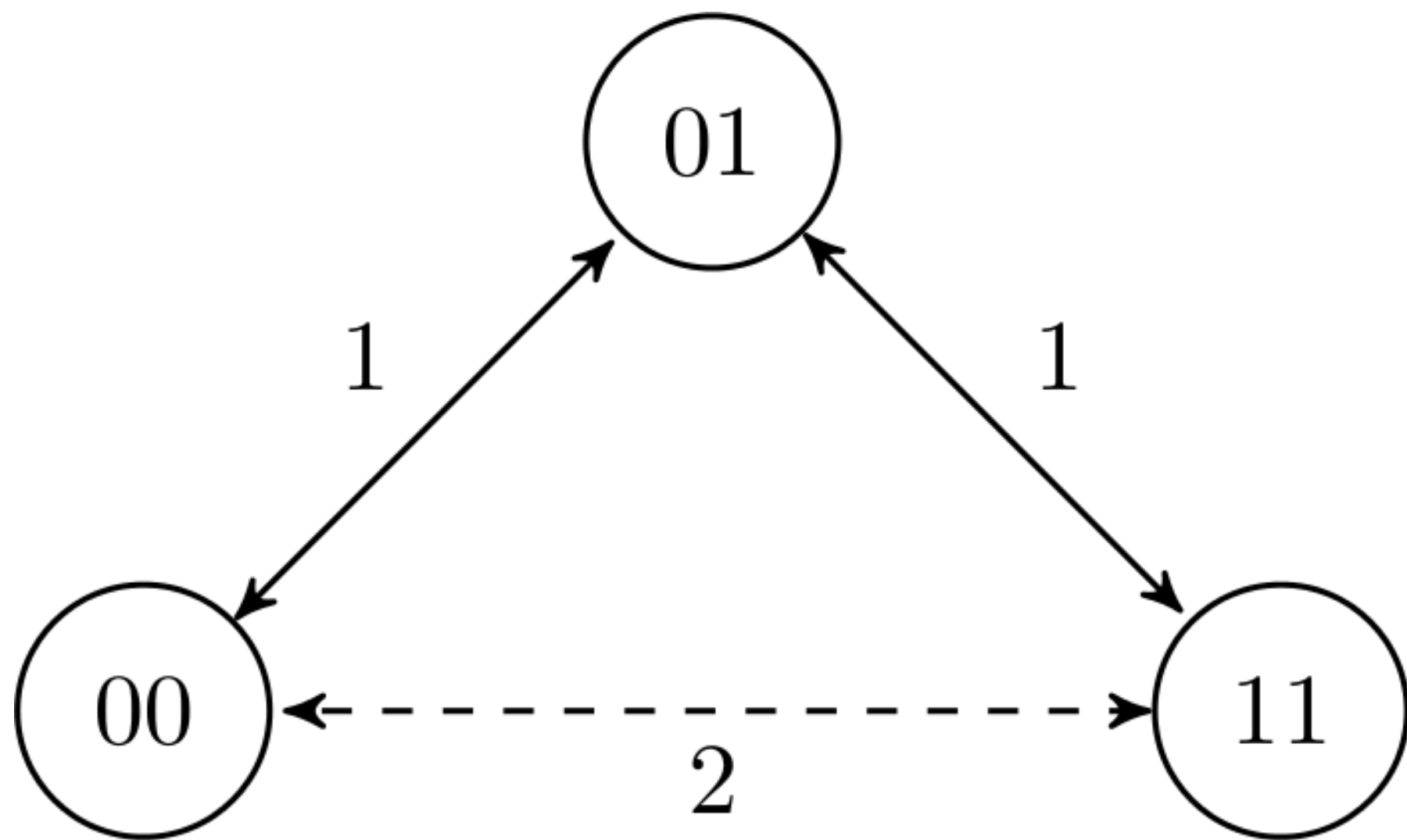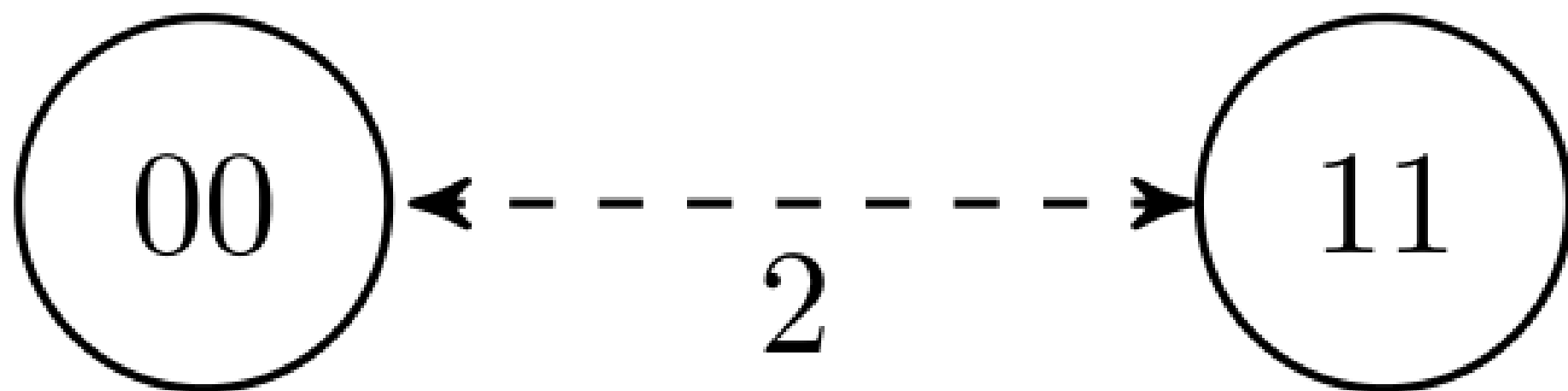
	00	00	00
Genotypes	01	01	01
		11	11

	t_0	t_1	t_2	T
Time				
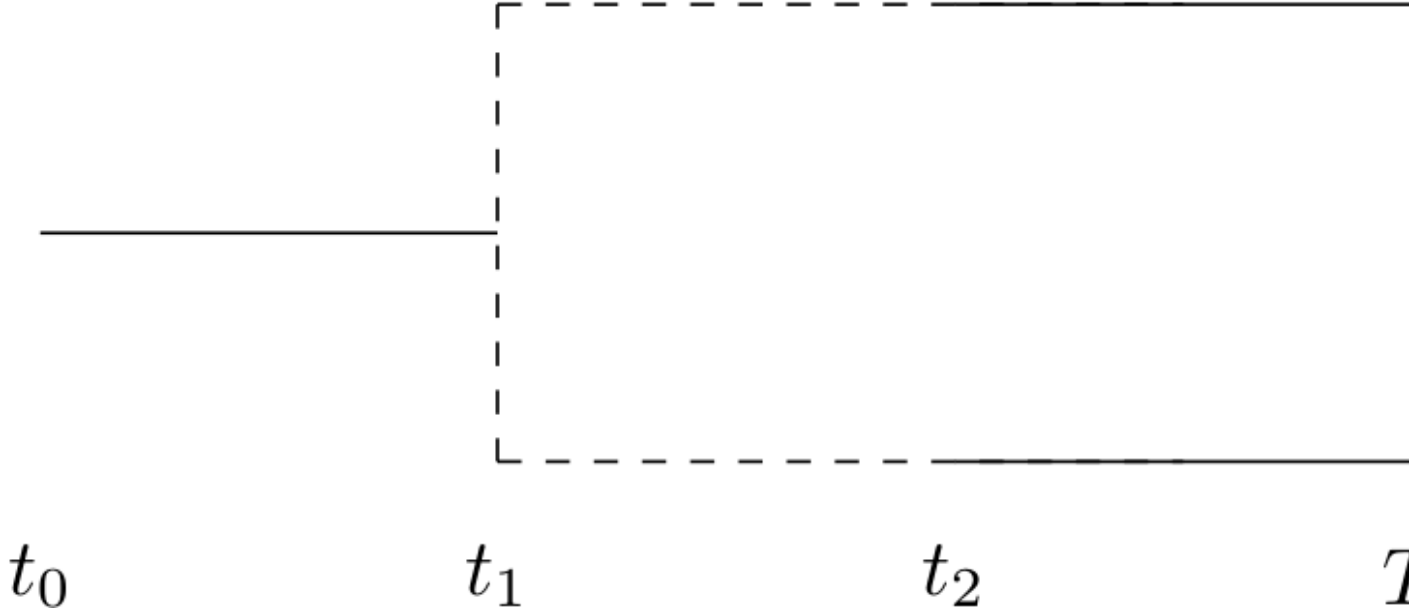
Verbal biological explanation

- A speciation-initiation event happens when there is the <u>possibility</u> of a new species

- A speciation-completion event happens when the linking genotype is lost

Individual

- *Number of SIL*

- Haploid

00
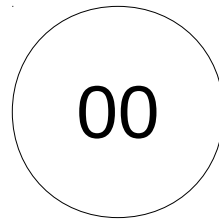
Population

- *Population size*
- Random mating
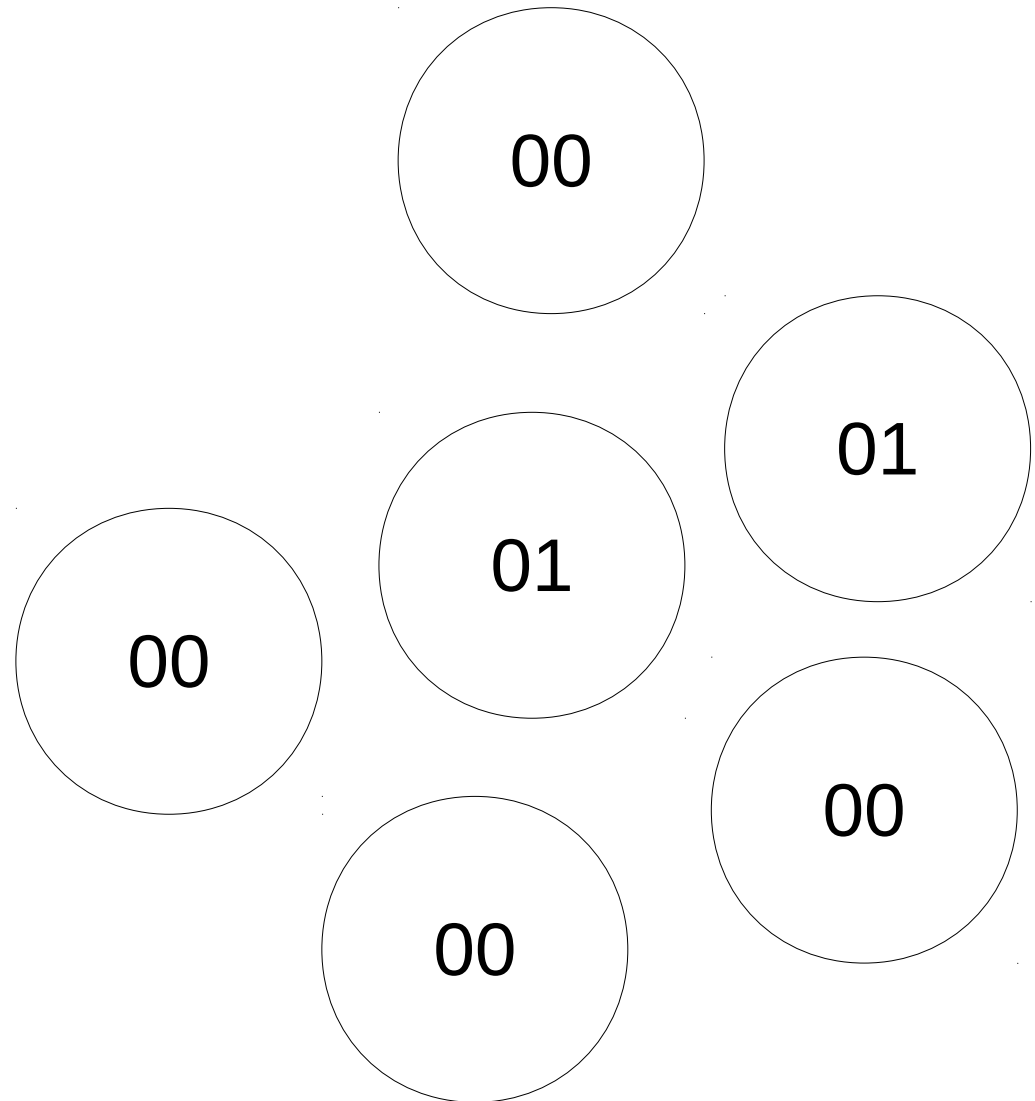
Generation

- Random father
- Random mother
- Random individual to be replaced
- Alleles inherit independently
- Father and mother must be of same species
- *Maximum genetic distance*
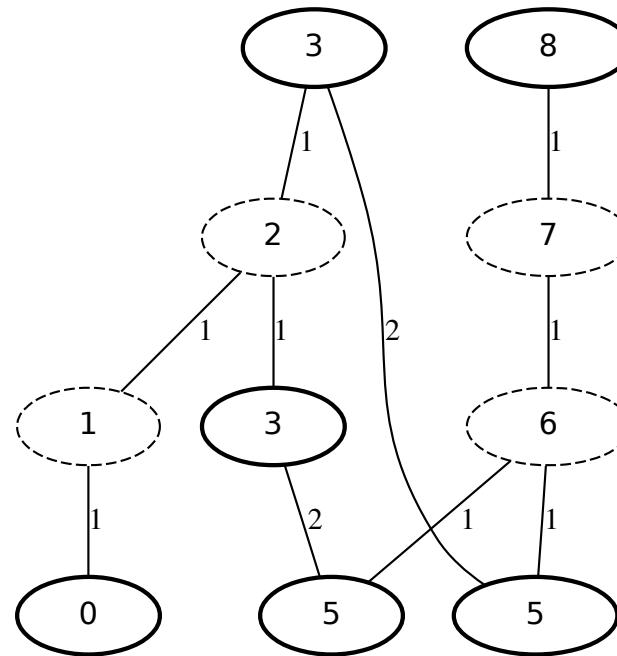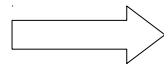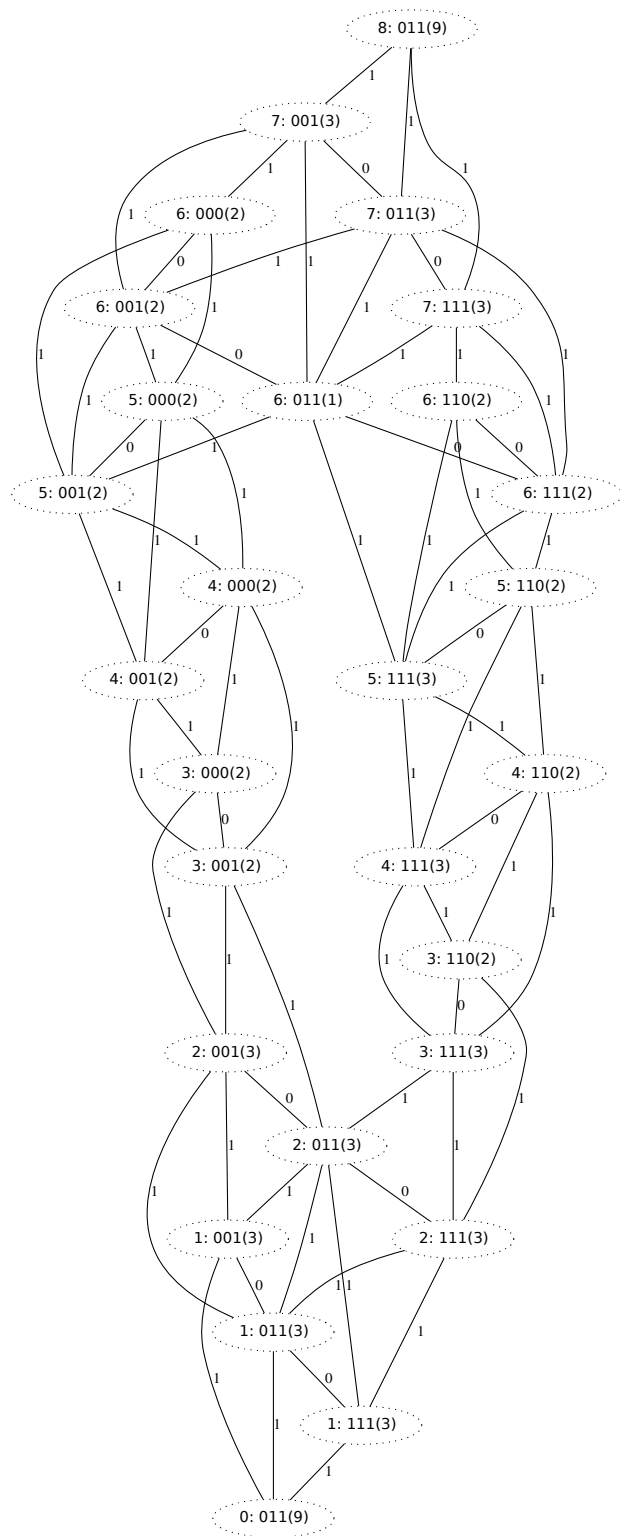- *Chance of one SIL mutation*
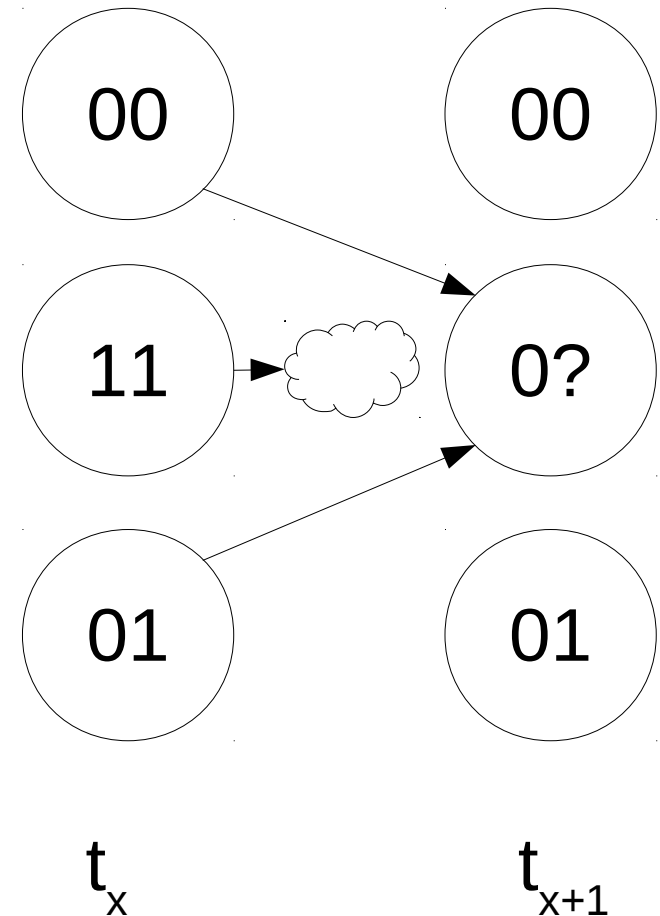
Research questions

- How similar are the incipient-species trees between LBM and IBM?

- Can we convert the model parameters?

- When adding a neutral DNA sequence, where do our current tools estimate the branching points?
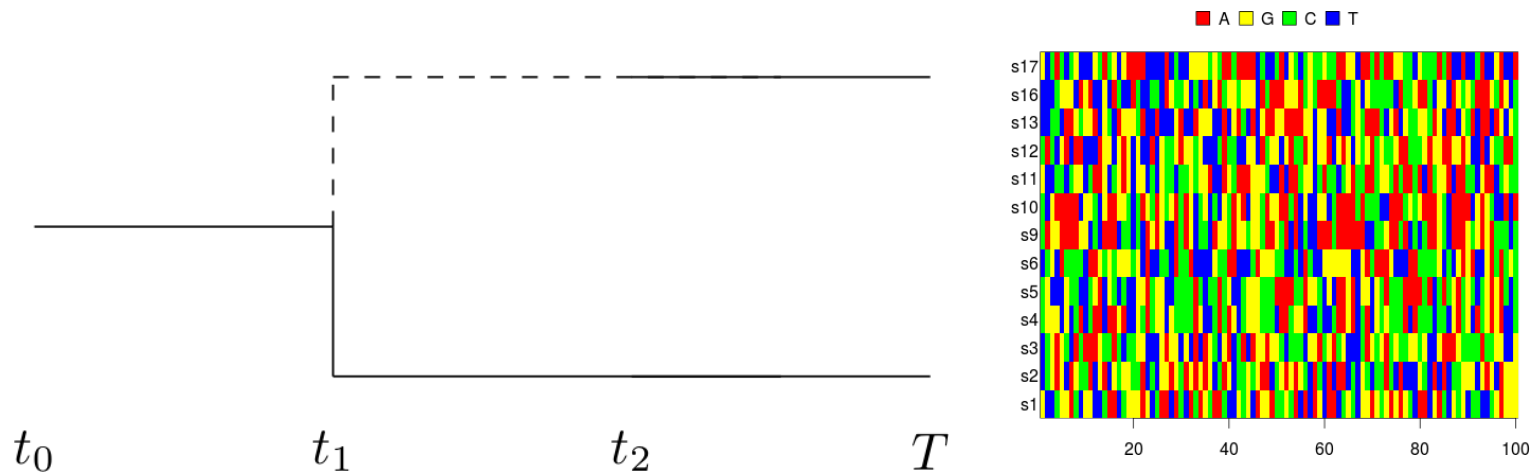
Results in progress
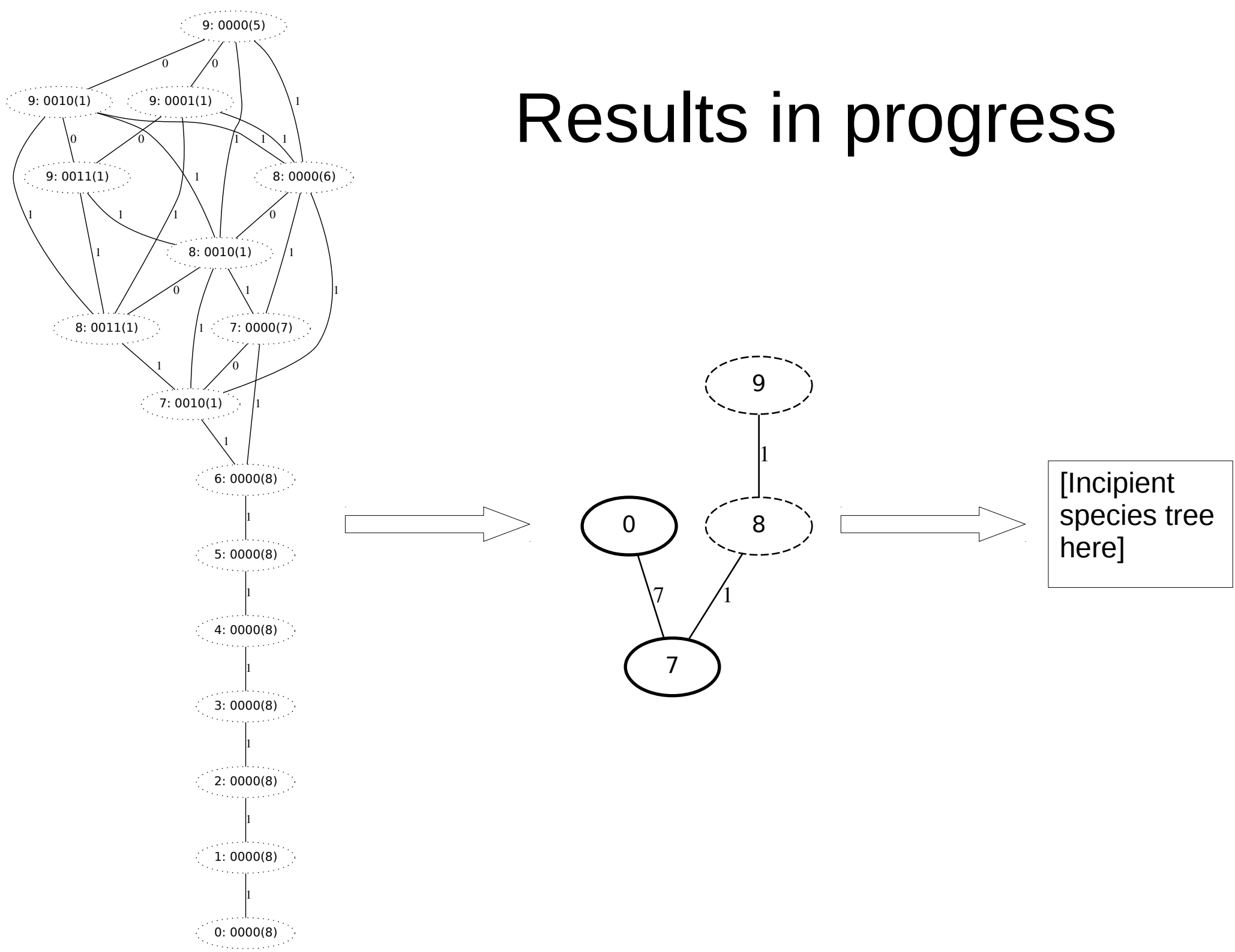
Results in progress
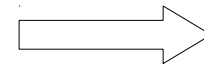
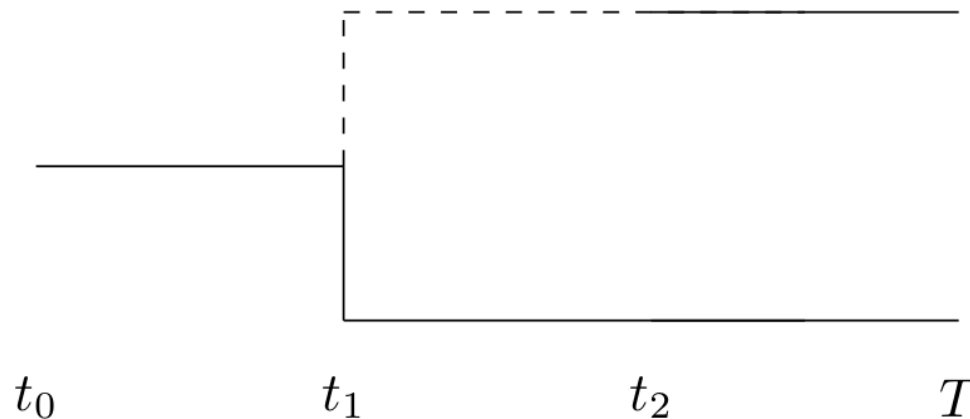[Incipient species tree here]

Results in progress

- More SIL → more species

- Population size smaller → more species

- Higher mutation rate → more species

Insights

For analytical tractability [...], we must assume that all rates of speciation-initiation are equal

Smaller population size
$\to$
more species

t_0 $\qquad$ t_1 $\qquad$ t_2 $\qquad$ T

Etienne, Rampal S., Hélène Morlon, and Amaury Lambert. "Estimating the duration of speciation from phylogenies." Evolution 68.8 (2014): 2430-2440.

This means assuming populations are seperated in equal halves!

Conclusion

- This IBM offers a conceptual biological explanation of the processes in an incipient species tree

- How well the incipient species trees match is in progress

Discussion

- Still only a conceptual mechanism

- One of many speciation models

- Density (not diversity) dependent effects due to limited population sizes?