

distancer

Rich  l J.C. Bilderbeek & Rampal S. Etienne

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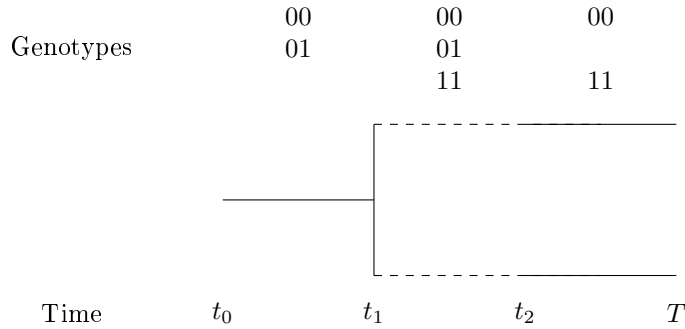


Figure 1: An incipient species phylogeny can be linked to population genetic processes: at time t_0 there were two genotypes present in the population (00 and 01). Branching starts at t_1 at the moment a genotype is introduced that allows a population with one extra species (11). At t_2 speciation is completed the linking genotype (01) has gone extinct

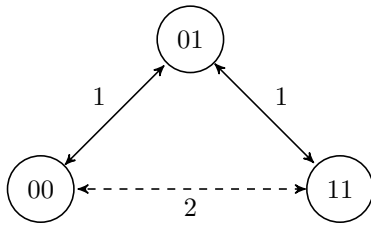


Figure 2: One species. The three nodes show the genotypes of the three individuals. The values above the edges show the genetic distance. If the edge is solid, these different genotypes can produce viable offspring. If the genetic distance exceeds a certain threshold, set to 1 in this example, these individual cannot produce viable offspring. These three individuals are considered one species. Would genotype '01' become absent, these would be two species (figure 3)

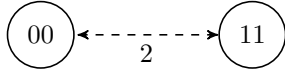


Figure 3: Two species. The two nodes show the genotypes of the two individuals. The values above the edges show the genetic distance. If the edge is solid, these different genotypes can produce viable offspring. If the genetic distance exceeds a certain threshold, set to 1 in this example, these individual cannot produce viable offspring. Would genotype '01' be introduced, these would become one species (figure 2)

1 Research questions [To be removed later]

- How well does the mechanistic IBM here mimic the PBD model?
 - (n)LTT, symmetry of phylogenies
- Without adding space, what are the statistics of phylogenies produced?
- Without adding one-dimensional space, what are the statistics of phylogenies produced?
- Without adding two-dimensional space, what are the statistics of phylogenies produced?
- Can the parameters be converted between IBM and PBD, using ML estimates?
- Which population dynamics resembles the PBD closest?
- Exists there a peripatric-like population dynamics that does have equal speciation-initiation rates for good and incipient species?

2 Abstract

The protracted birth-death (PBD) speciation model of Etienne & Rosindell 2012 add the key element of speciation taking time to birth-death speciation models.

The PBD model makes no claims about the biological mechanisms of speciation. It does mathematically follow peripatric speciation closest, yet sets speciation-initiation and extinction rate of incipient and good species to an equal value, to simplify the exploration of parameter space.

The model introduced in this paper is a mechanistic population genetics individual based model that shares many features of the PBD model and adds a biological meaning to all phylogenetic processes of the PBD model.

It additionally shows that peripatric speciation and equal speciation-initiation and extinction rate disagree by using maximum likelihood estimation. Phylogenies similar to the PBD model were obtained only when new founded populations were of identical population size of the ancestral population, which is a biological rarity.

We suggest to use different values of speciation-initiation and extinction rate of incipient and good species when assuming peripatric speciation and using the PBD model. We claim that this model opens up new research avenues from a mechanistical point-of-view in protracted speciation.

3 Introduction

Protracted speciation is introduced in Rosindell & Etienne 2010 and refined in Etienne & Rosindell 2012.

All PBD papers state that speciation is complex and do not single out a single mechanism.

This model mimics Etienne & Rosindell 2012 at the level of the individual.

4 Methods

All individuals and species are neutral.

Individuals are sexual and haploid.

Species Identity Genes (SIGs) are modeled like Melian et al., 2012 and allow for reproductive isolation and thus speciation (figures 2 and 3).

Ancestry Alleles (AAs) have no effect and are used to construct a phylogeny.

Create phylogeny

5 Results

Similar qualitative behavior

No pull-of-the-present

Parameter estimation from phylogenies using ML

6 Conclusion

7 Discussion

Density effects: the size of the population is related to extinction rate. One could argue that these are density (not: diversity) dependent effects. Use an infinite population size model, however, would be even less optimal: both the PBD and this model are stochastic; an infinite size population would eliminate all stochasticity.