

Should an individual based mechanism be implemented in the protracted birth death model?

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1. Abstract

Speciation models are used to construct phylogenetic trees. Most of the currently used models, including the protracted birth-death model, lack a mechanism on individual level. The models assume several constant factors to determine if a new lineage should arise or an old lineage should go extinct. An individual based model might give us more realistic phylogenies and answer evolutionary questions better than the currently used (protracted) birth-death model.

2. Introduction

2.1 Speciation models

2.1.1 The need for speciation models

Speciation models help us construct phylogenies to answer evolutionary biological questions. [REF 4] They are used to give a better understanding of speciation in nature.

2.1.2 Birth-death model (BD)

The standard birth-death model [5] shows an accelerating increase in the number of species. This is not shown in phylogenetic trees, which have a slowdown in the increase of number of lineages. [2] The birth-death model is one of the simplest of models [4] that has a constant speciation rate (λ) and a constant extinction rate (μ).

2.1.3 Protracted birth-death model (PBD)

By assuming that speciation is not instant and happens over a longer period of time we can change the birth-death model to a protracted birth-death model. “Good” species have a chance of making incipient species with rate b_g that will become good species with rate λ . Incipient can initiate speciation with rate b_i . Both good and incipient species can go extinct with rate μ_g and μ_i respectively. [2] [REF 4] The (P)BD model assumes the speciation is allopatric and therefor has no gene flow between two (incipient) species. Incipient species have two outcomes; they either go extinct or become a good species, whereas a good species can only go extinct eventually.

2.1.4 Relationship between birth-death and protracted birth-death

[2]

2.1.5 Other speciation models

[2] [REF]

2.1.6 Problems of speciation models

Speciation models, or models in general, tend to simplify the real world as much as possible. This is done to

2.2 The use of mechanisms to model speciation

2.2.1 Ecological and sexual selection (ESS)

The Ecological and sexual selection model of van Doorn en Weissing was made to be a more complete model to look at sympatric speciation [1]. To do this they combined older models with an ecological trait or some sort of sexual selection. The model leads to ecological differentiation, and mating strategies, which resulted in assortative mating.

2.2.2 Bateson-Dobzhansky-Müller (BDM)

[REF Jorik]

2.3 Differences protracted birth-death model and ecological and sexual selection model

[1] [2]

The original PBD model uses allopatric speciation [2] while the ESS model is focused on unravelling sympatric speciation. [1] With ESS gene flow between an old and a new species is still possible and will often result in a new species flowing back to the old species before they can branch off completely.

2.4 This study

This study compares the phylogenetic trees of the protracted birth-death model and ecological and sexual selection mechanism, by changing parameters to get the resulting trees as similar as possible. To do this the PBD model needs to be made sympatric. Therefor requires a parameter that simulates gene flow between incipient and good species right after branching off.

2.5 Novelty

2.6 Analysis

[3]

2.7 Expectations

3. Methods

3.1 Parameters

3.1.1 PBD

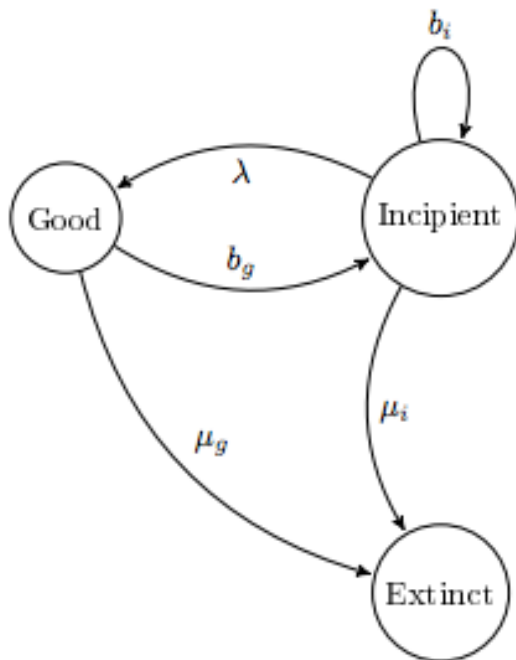


Figure 2: The states and transitions of a species. b_i : speciation-initiation rate of incipient species. b_g : speciation-initiation rate of good species. λ : speciation completion rate. μ_i : extinction rate of incipient species. μ_g : extinction rate of good species. Figure after Etienne et al, 2014, Evolution

[2]

3.1.2 Ecological and sexual selection model

[1]

3.2 Creating species trees

3.3 Analysis

3.3.1 nLTT

[3]

3.3.2 γ

The Gamma statistic (Pybus & Harvey 2000) is given by:

Pybus, O. & Harvey, P. (2000) Testing macro-evolutionary models using incom-

plete molecular phylogenies. Proceedings of the Royal Society B: Biological Sciences, 267, 2267–72.

3.4 Peripherals

3.4.1 Software

https://github.com/Lumphie/Research_phylogenies

3.4.2 Hardware

4. Results

5. Discussion

References

- [1] Van Doorn, G. S., & Weissing, F. J. (2001). *"Ecological versus sexual selection models of sympatric speciation."* Selection, 2, 17 - 40.
- [2] Etienne, Rampal S., and James Rosindell. (2011) *"Prolonging the past counteracts the pull of the present: protracted speciation can explain observed slowdowns in diversification."* Systematic Biology: syr091.
- [3] Janzen, Thijs, Höhna, Sebastian, Etienne, Rampal S. (2015) *"Approximate Bayesian Computation of diversification rates from molecular phylogenies: introducing a new efficient summary statistic, the nLTT."* Methods in Ecology and Evolution 6, 566 - 575.
- [4] ([My current work](#))
- [5] Kendall, D. G. (1948) *"On some modes of population growth giving rise to R.A. Fisher's logarithmic series distribution."* Biometrika, 35, 6 – 15.