Should a mechanism be implemented in the protracted birth death (PBD) model?

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September 01, 2016

1.   Abstract

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]

2.1.2   Birth Death (BD) model
[2]

2.1.3   Protracted Birth Death (PBD) model
[2]

2.1.4   Relationship between BD and PBD
[2]

2.1.5   Other speciation models
[2] [REF]

2.1.6   Problems of speciation models

2.2   The use of mechanisms to model speciation

2.2.1   Ecological and sexual selection model
[1]

2.2.2   Bateson-Dobzhansky-Müller (BDM) model
[REF Jorik]

2.3   Differences PBD and ecological and sexual selection model
[1] [2]

3.   Methods

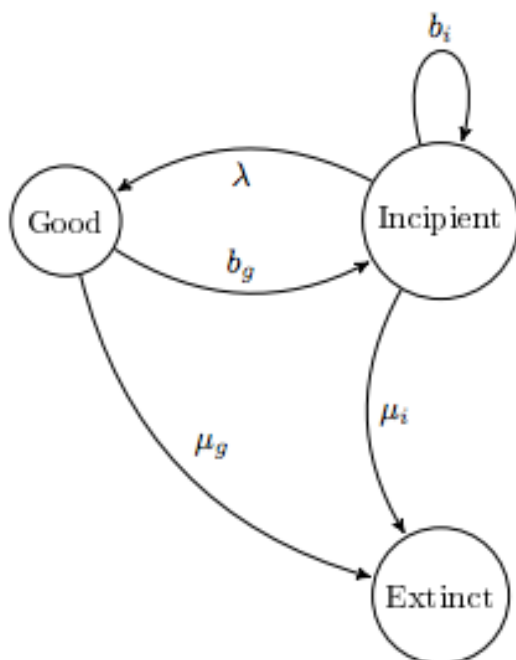## 3.1   Parameters

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 incomplete molecular phylogenies. Proceedings of the Royal Society B: Biological Sci- ences, 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

- 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. "Prolonging the past counteracts the pull of the present: protracted speciation can explain observed slowdowns in diversification." Systematic Biology (2011): syr091.
- [3] Janzen, Thijs, Höhna, Sebastian, Etienne, Rampal S. "Approximate Bayesia n Computation of diversificatio nrates from molecular phylogenies: introducing a newefficient summary statistic, the nLTT." Methods in ECology and Evolution (2015), 6, 566 - 575.
- [4] (My current work)