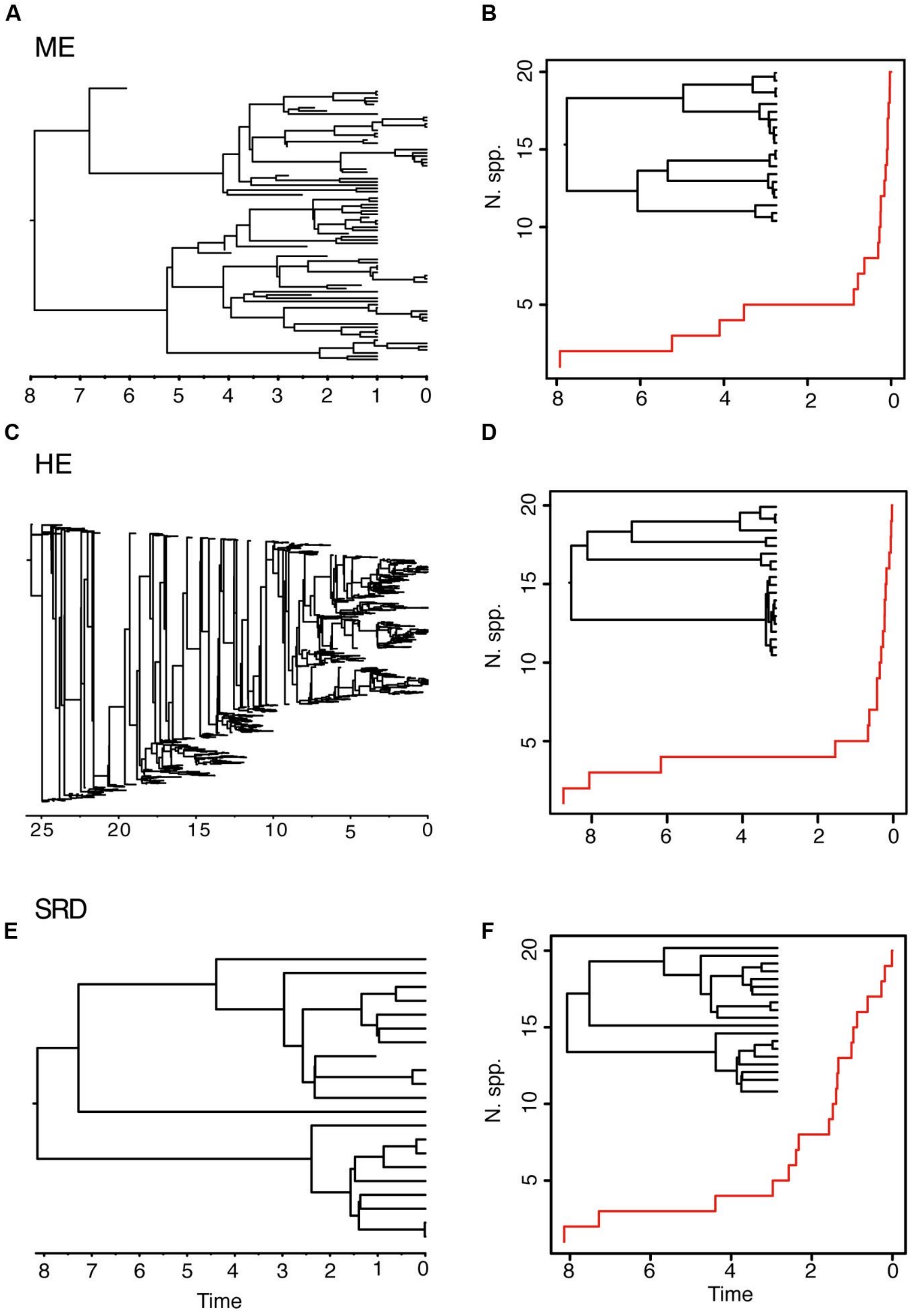
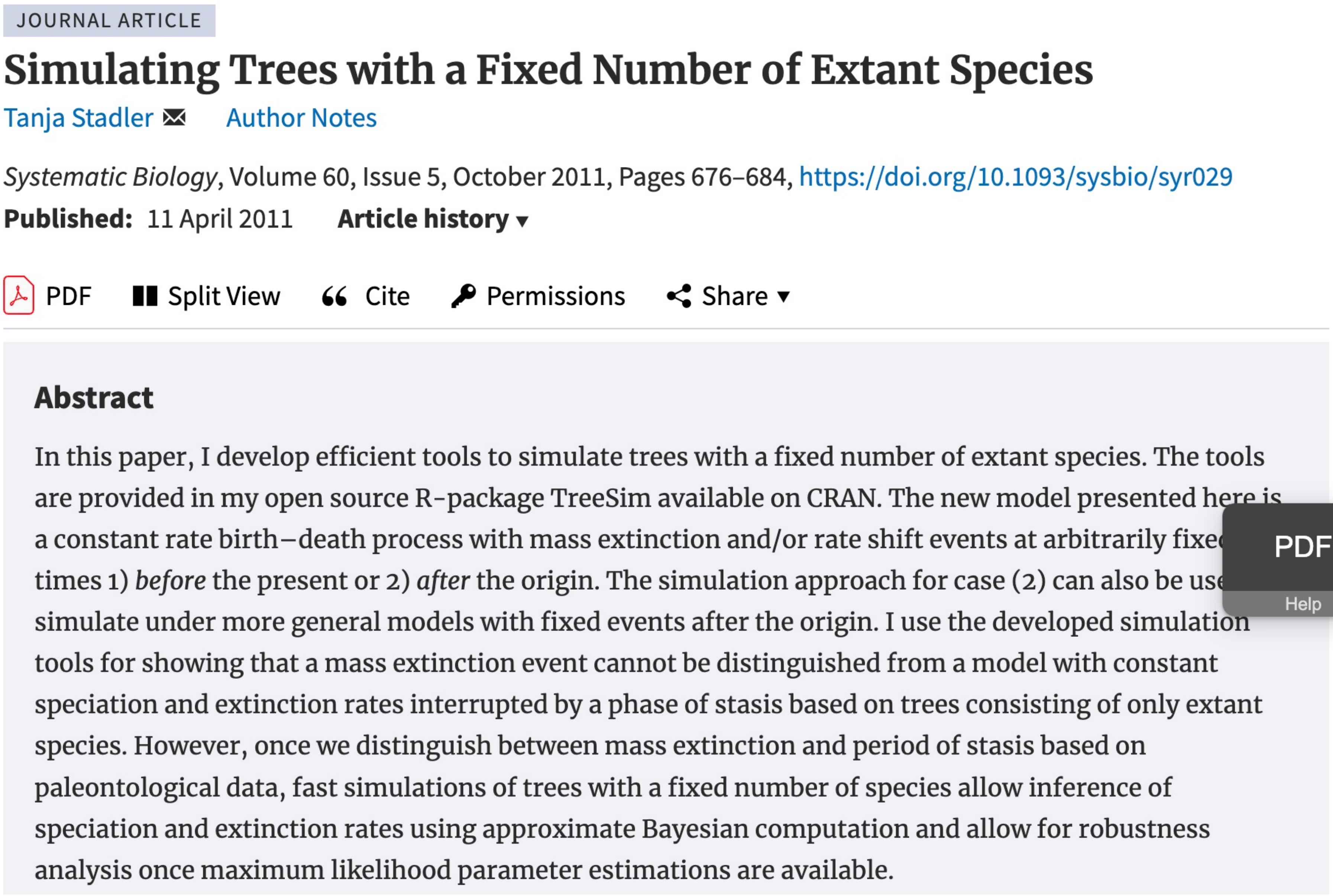
# Estimación de Eventos de Extinción Masiva



**Sanmartín & Meseguer, 2016**



# Simulating Trees with a Fixed Number of Extant Species

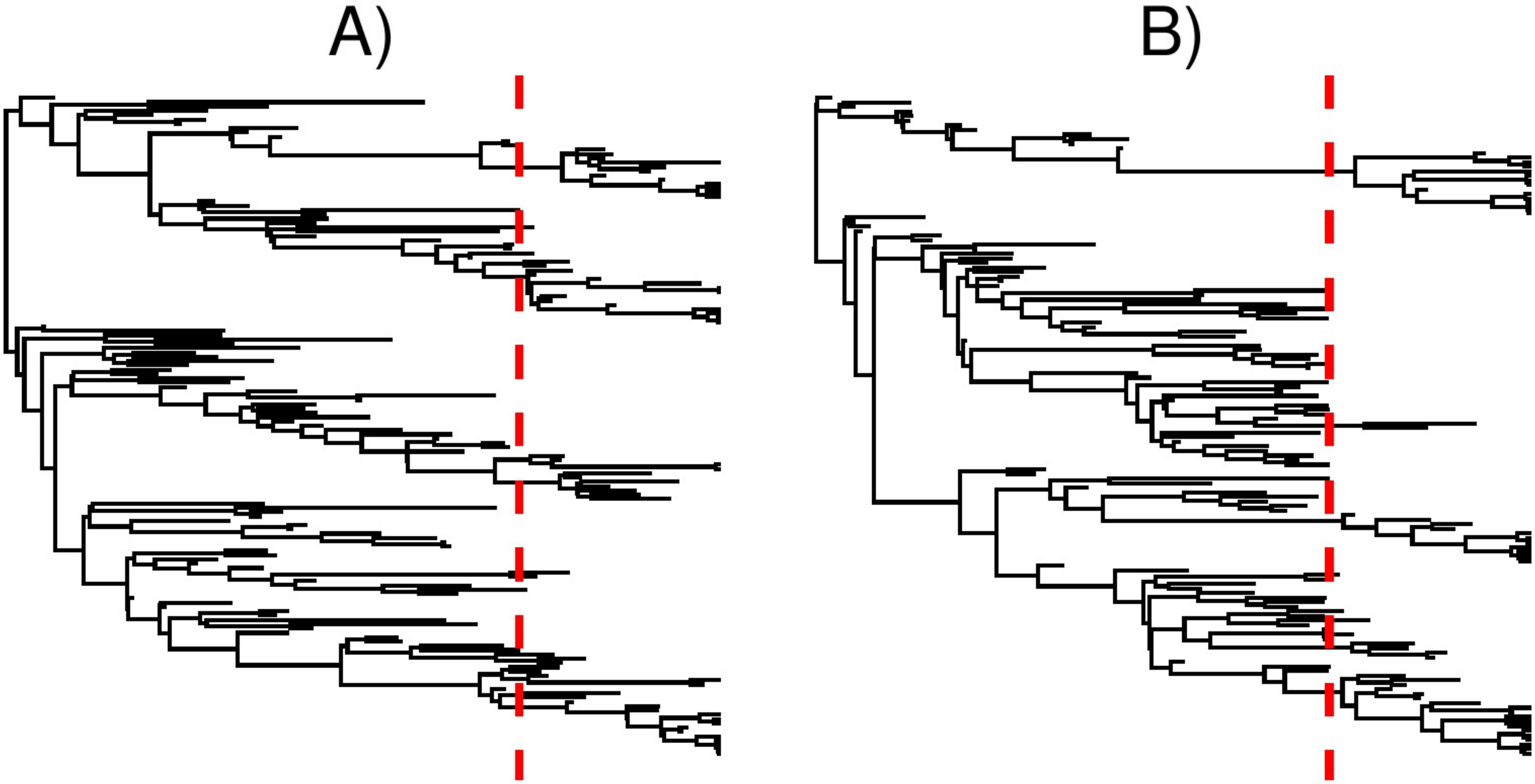
Tanja Stadler ✉ Author Notes

*Systematic Biology*, Volume 60, Issue 5, October 2011, Pages 676–684, https://doi.org/10.1093/sysbio/syr029

**Published:** 11 April 2011 **Article history** ▾

## Abstract

In this paper, I develop efficient tools to simulate trees with a fixed number of extant species. The tools are provided in my open source R-package TreeSim available on CRAN. The new model presented here is a constant rate birth–death process with mass extinction and/or rate shift events at arbitrarily fixe times 1) *before* the present or 2) *after* the origin. The simulation approach for case (2) can also be use simulate under more general models with fixed events after the origin. I use the developed simulation tools for showing that a mass extinction event cannot be distinguished from a model with constant speciation and extinction rates interrupted by a phase of stasis based on trees consisting of only extant species. However, once we distinguish between mass extinction and period of stasis based on paleontological data, fast simulations of trees with a fixed number of species allow inference of speciation and extinction rates using approximate Bayesian computation and allow for robustness analysis once maximum likelihood parameter estimations are available.



https://revbayes.github.io/tutorials/divrate/efbdp_me.html

***bd.shifts.optim***

**(TreePar R package)**

***bd.densdep.optim***

```
bd.shifts.optim(x, c(sampling, shifts), grid, start, end,

yule = FALSE, ME = FALSE, survival = 1)
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**Longitud de las ramas**

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**Porcentaje de efectividad del muestreo,**
**número de veces que ha cambiado la tasa de diversificación**
**o número de eventos de extinción masiva**

```
bd.shifts.optim(x, c(sampling, shifts), grid, start, end,

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```
bd.shifts.optim(x, c(0.84,1), grid, start, end,
yule = FALSE, ME = FALSE, survival = 1)
```

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**(TreePar R package)**

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**“ventana” de actualización**

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bd.shifts.optim(x, c(sampling, shifts), grid, start, end,

yule = FALSE, ME = FALSE, survival = 1)
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bd.shifts.optim(x, c(0.84, 1), 0.2, start, end,
yule = FALSE, ME = FALSE, survival = 1)
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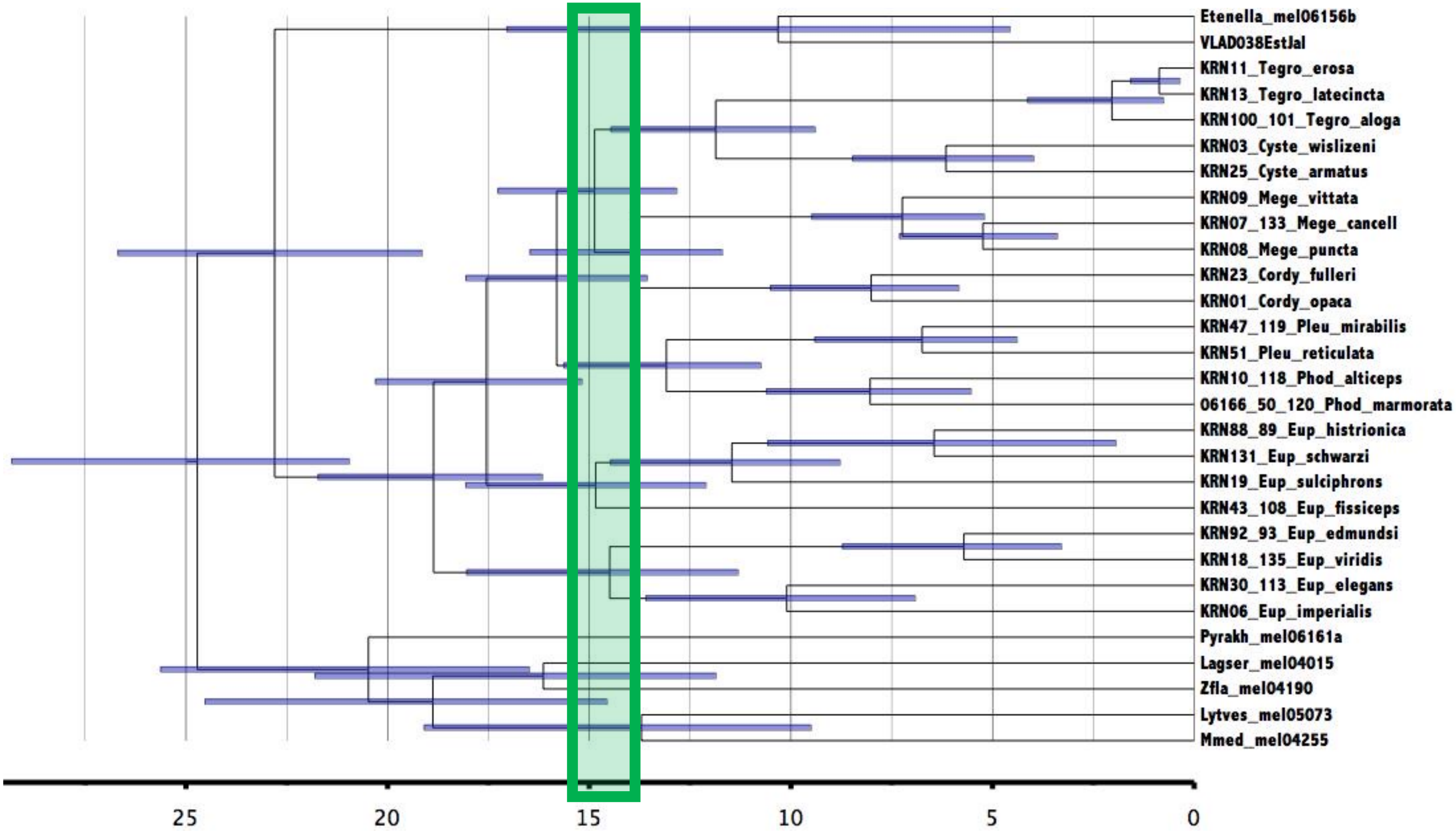
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KRN08_Mege_puncta
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KRN10_118_Phod_alticeps
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KRN30_113_Eup_elegans
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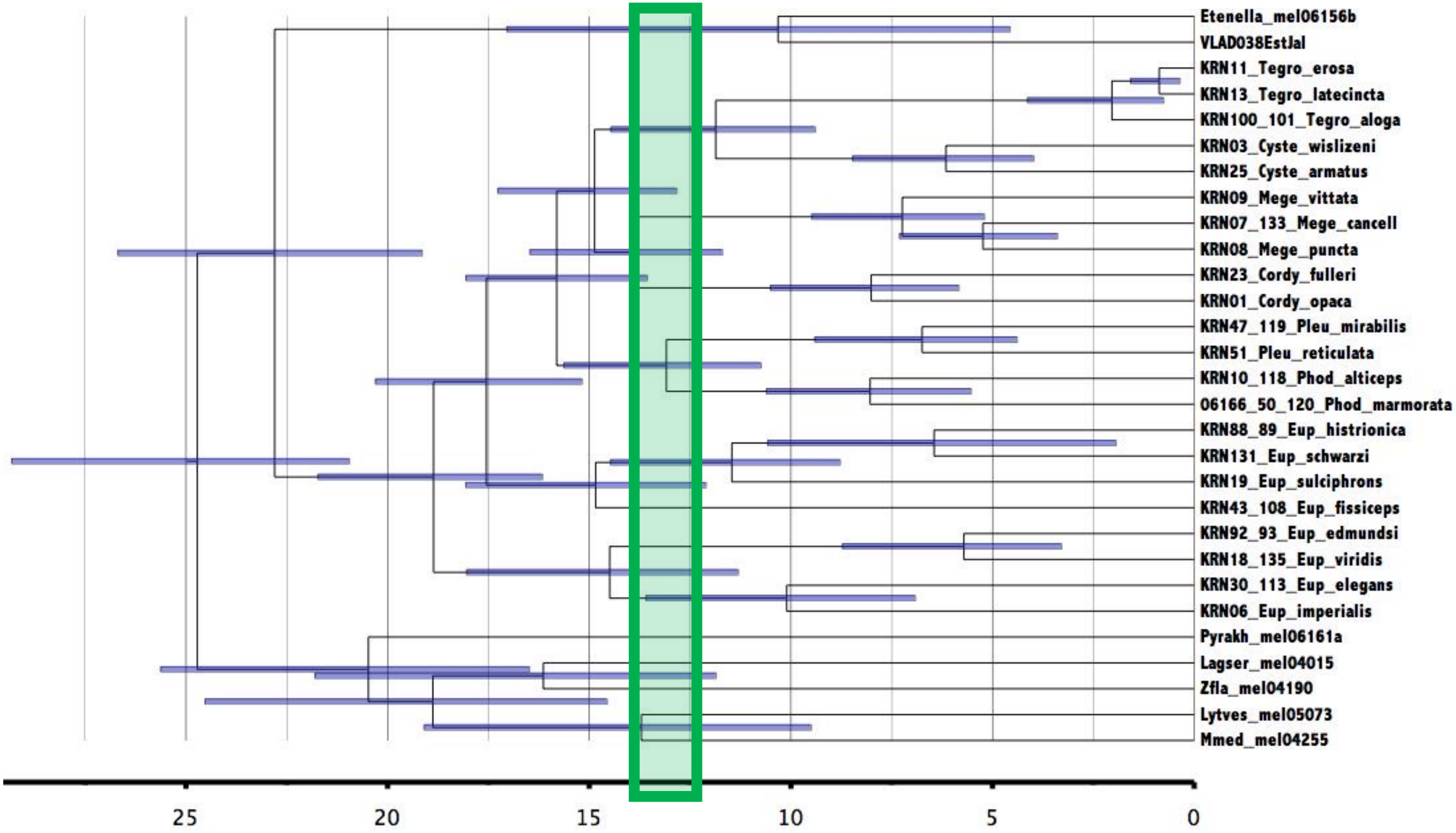
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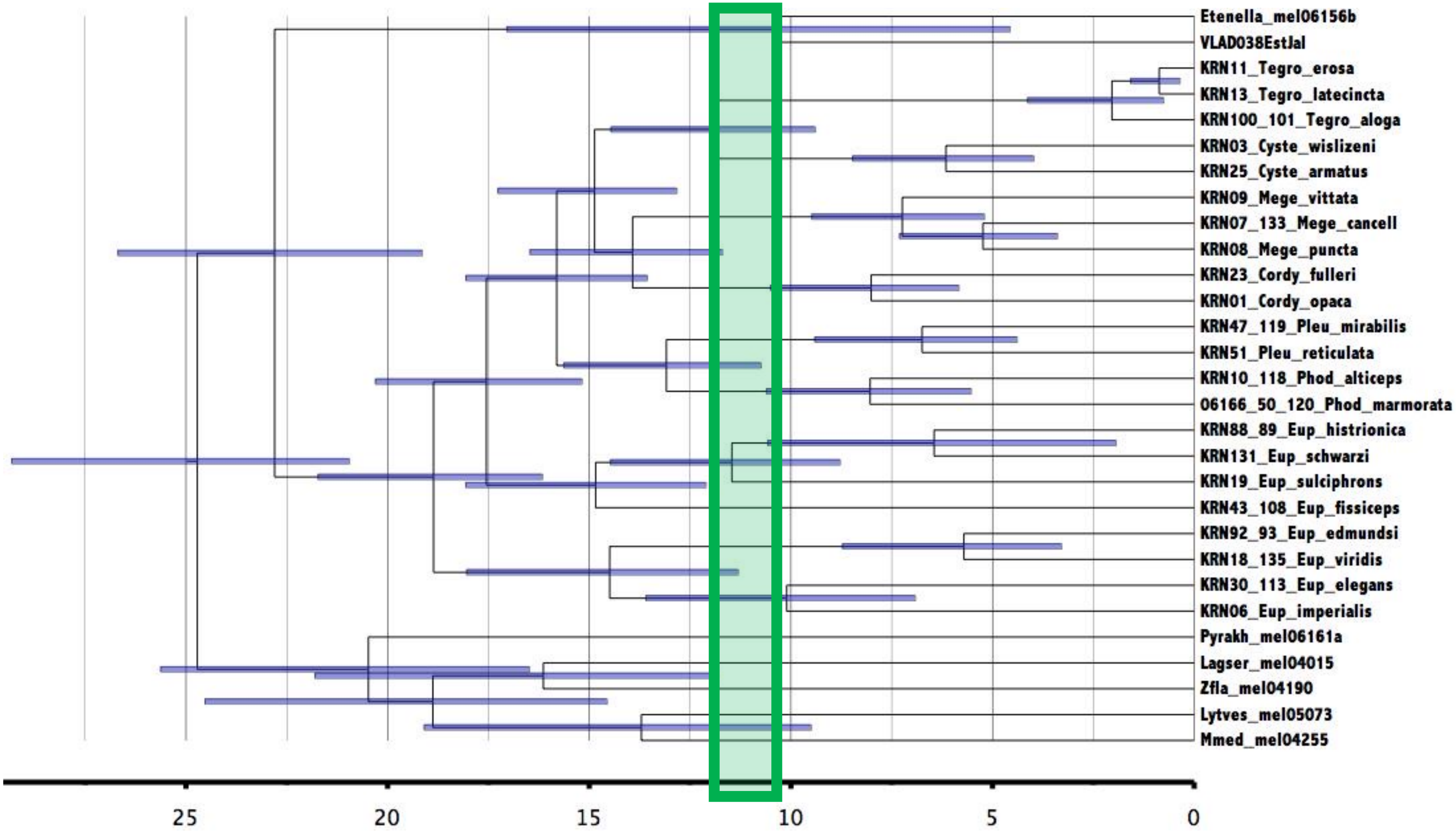
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```
bd.shifts.optim(x, c(sampling, shifts), grid, start, end,

yule = FALSE, ME = FALSE, survival = 1)
```

```
bd.shifts.optim(x, c(0.84, 1), 0.2, 0.5522438, end,
yule = FALSE, ME = FALSE, survival = 1)
```

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***bd.densdep.optim***

**Último evento de especiación**

⬇

```
bd.shifts.optim(x, c(sampling, shifts), grid, start, end,

yule = FALSE, ME = FALSE, survival = 1)
```

```
bd.shifts.optim(x, c(0.84, 1), 0.2, 0.5522438, 19.9102699,
yule = FALSE, ME = FALSE, survival = 1)
```

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```
bd.shifts.optim(x, c(sampling, shifts), grid, start, end,

yule = FALSE, ME = FALSE, survival = 1)
```

$\mu = 0$ Siempre false cuando estimamos

$\mu \neq 0$ MEE

```
bd.shifts.optim(x, c(0.84, 1), 0.2, 0.5522438, 19.9102699,
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⬆

**Considera Eventos de**
**Extinción Masiva (MEE)**
**en la filogenia**

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bd.shifts.optim(x, c(sampling, shifts), grid, start, end,

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```

**Usa N para condicionar el valor de likelihood**

```
bd.shifts.optim(x, c(0.84, 1), 0.2, 0.5522438, 19.9102699,
yule = FALSE, ME = FALSE, survival = 1)
```

- Birth-Death-Shift model.

Stadler, 2011; PNAS

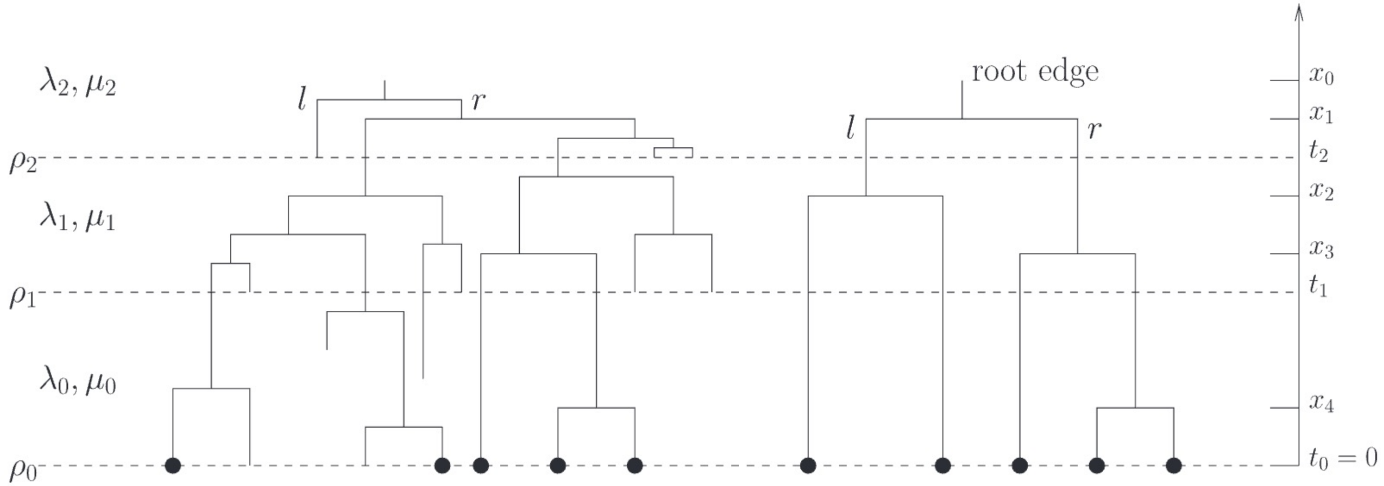
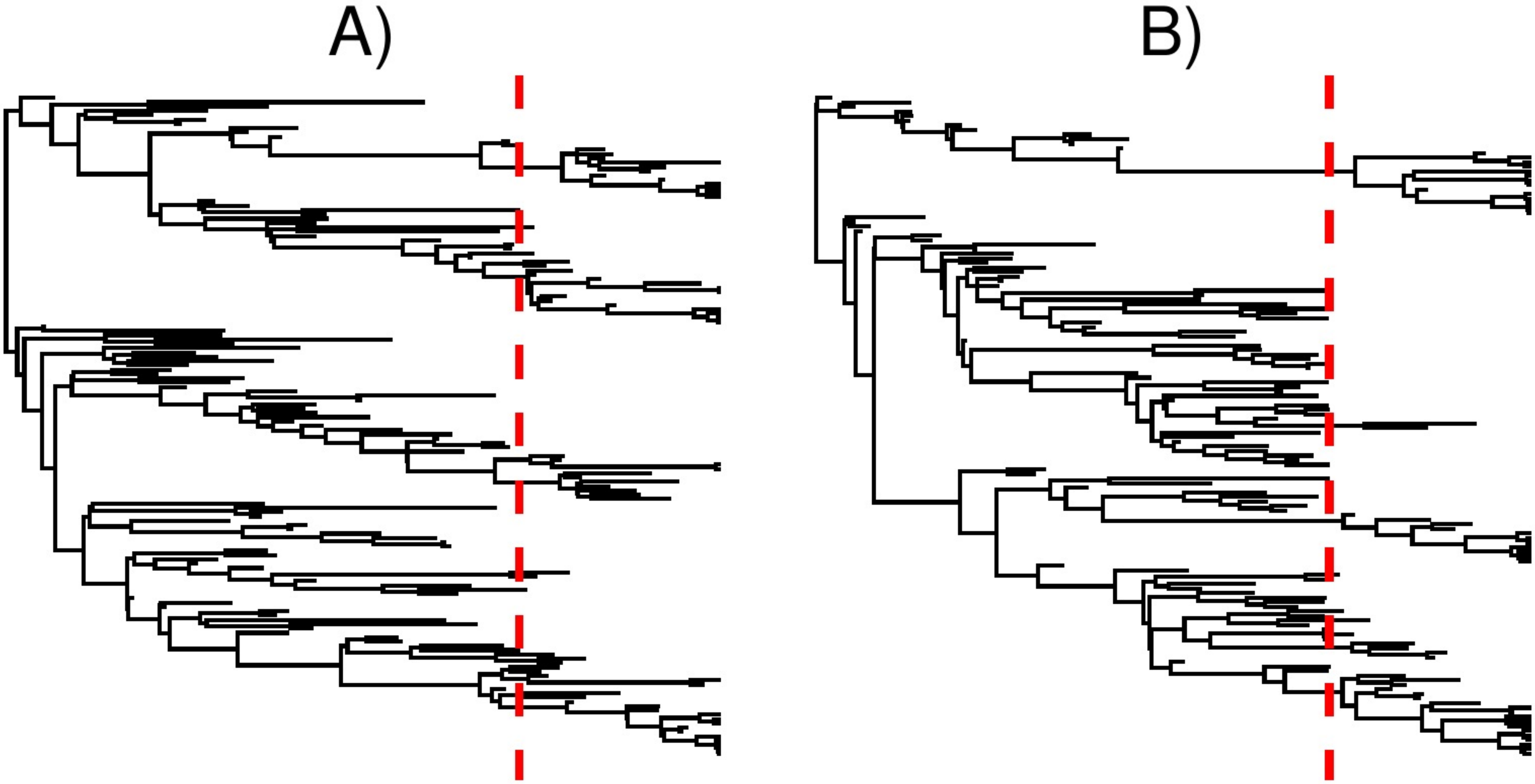


**Fig. 5.** Tree notation. (*Left*) An example of a tree that evolved under the birth–death shift process. The sampled species are denoted with a solid circle. (*Right*) The corresponding sampled tree with root edge. The labels *l* and *r* are suppressed on most branches for clarity.



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Research Article | Open Access

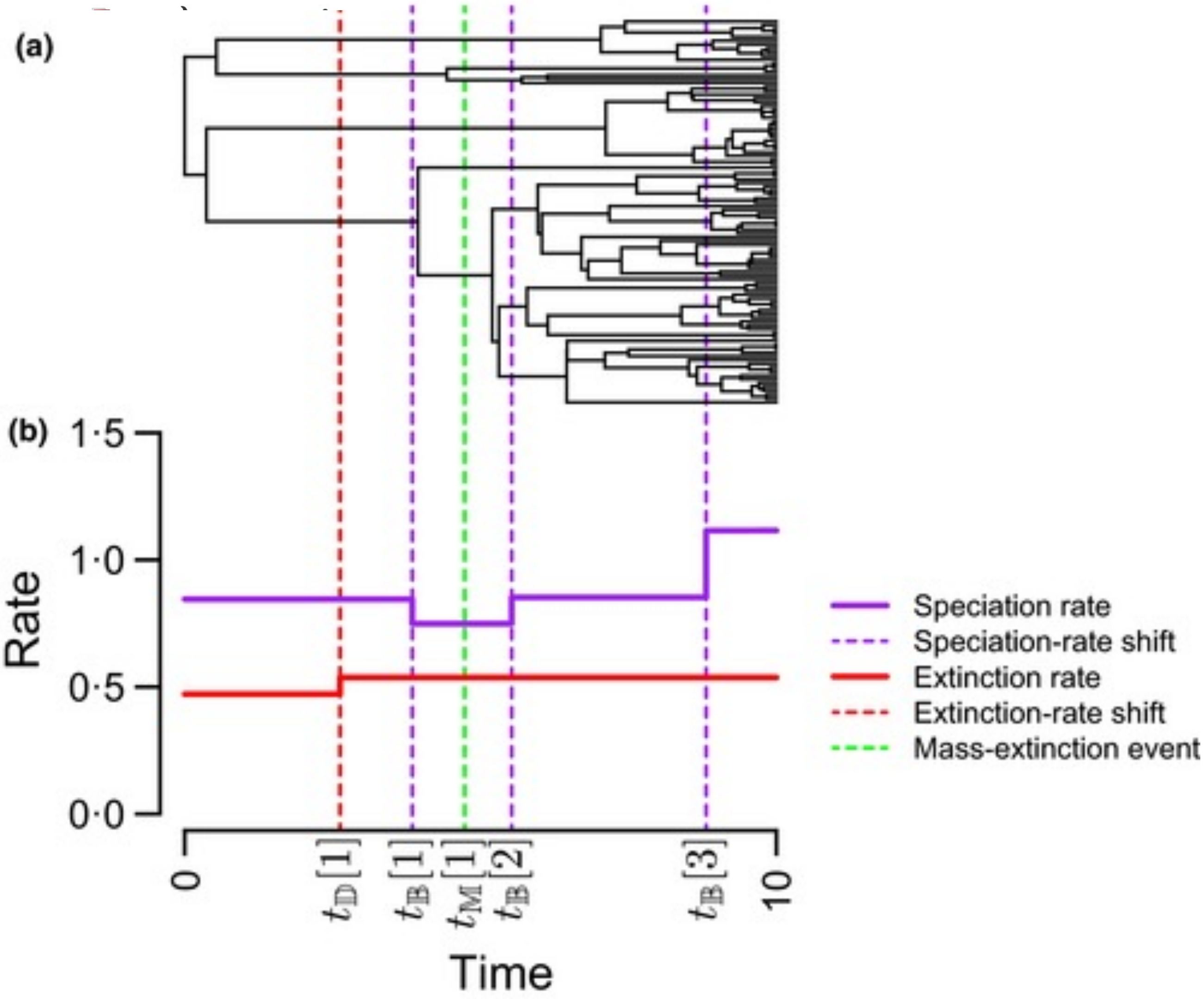
# A Bayesian approach for detecting the impact of mass-extinction events on molecular phylogenies when rates of lineage diversification may vary

Michael R. May, Sebastian Höhna, Brian R. Moore

First published: 26 March 2016 | https://doi.org/10.1111/2041-210X.12563 | Citations: 78

**Table 1.** CoMET-model parameters and their interpretation.

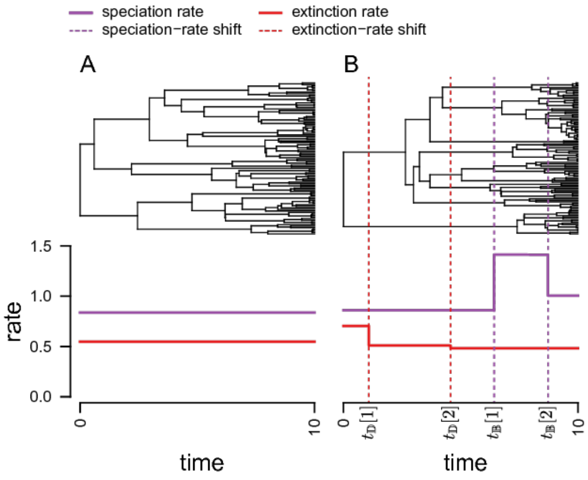
| Parameter | Interpretation |
|---|---|
| $\Psi$ | Labelled history with divergence times |
| $\tau$ | Tree topology |
| $\mathbb{T}$ | Vector of divergence times |
| $\mathbb{B}$ | Vector of speciation rates per interval |
| $b_i$ | Speciation rate in the interval $t_{\mathbb{B}}[i-1]$ to $t_{\mathbb{B}}[i]$ |
| $\mathbb{T}_{\mathbb{B}}$ | Vector of times of the speciation-rate changes |
| $t_{\mathbb{B}}[i]$ | Time of the $i$ th speciation-rate change |
| $k_{\mathbb{B}}$ | Number of speciation-rate changes |
| $\mathbb{D}$ | Vector of extinction rates per interval |
| $d_i$ | Extinction rate in the interval $t_{\mathbb{D}}[i-1]$ to $t_{\mathbb{D}}[i]$ |
| $\mathbb{T}_{\mathbb{D}}$ | Vector of times of the extinction-rate changes |
| $t_{\mathbb{D}}[i]$ | Time of the $i$ th extinction-rate change |
| $k_{\mathbb{D}}$ | Number of extinction-rate changes |
| $\mathbb{P}$ | Vector of the survival probabilities per mass-extinction event |
| $\rho_i$ | Survival probability of the $i^{\text{th}}$ mass-extinction event |
| $\mathbb{T}_{\mathbb{M}}$ | Vector of times of the mass-extinction events |
| $t_{\mathbb{M}}[i]$ | Time of the $i^{\text{th}}$ mass-extinction event |
| $k_{\mathbb{M}}$ | Number of mass-extinction events. |

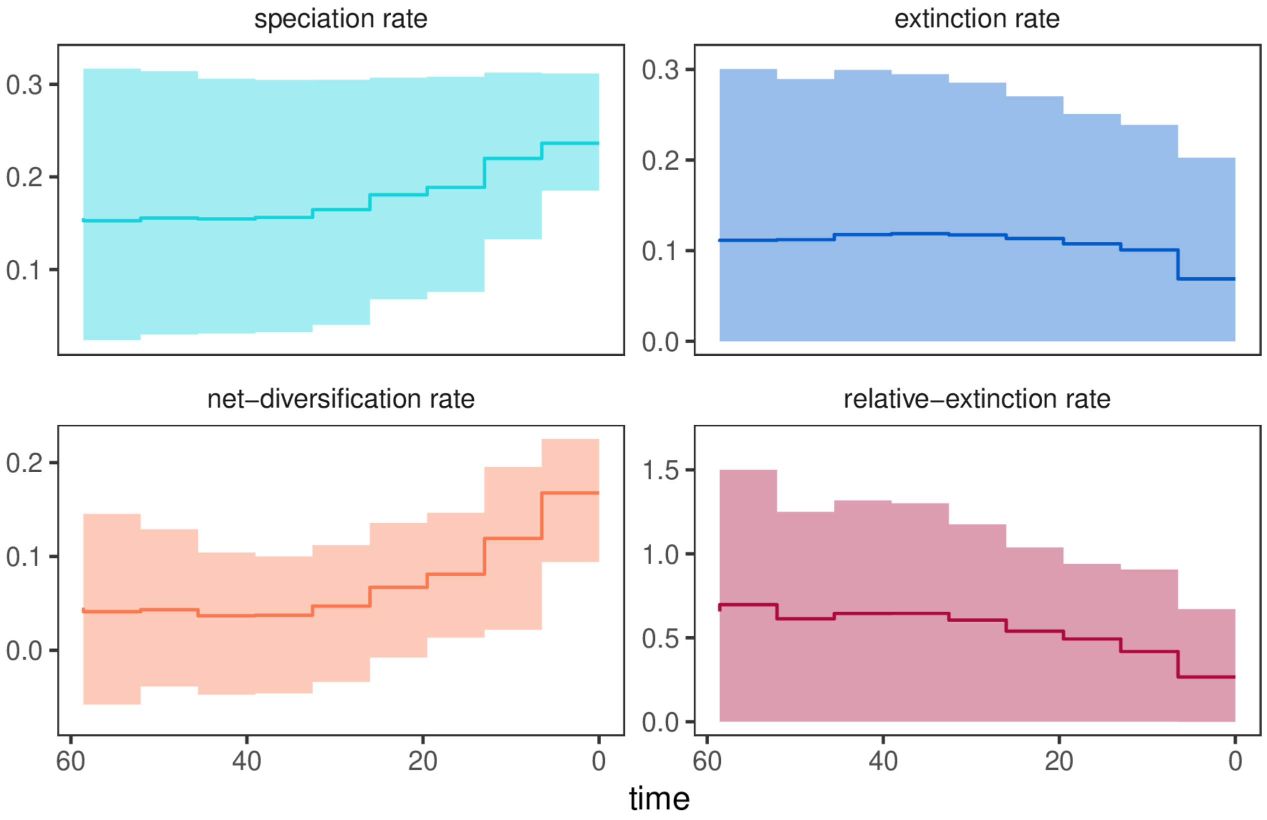


# Modelos episódicos de nacimiento-muerte y fosilización

## Episodic fossilized Birth-Death models

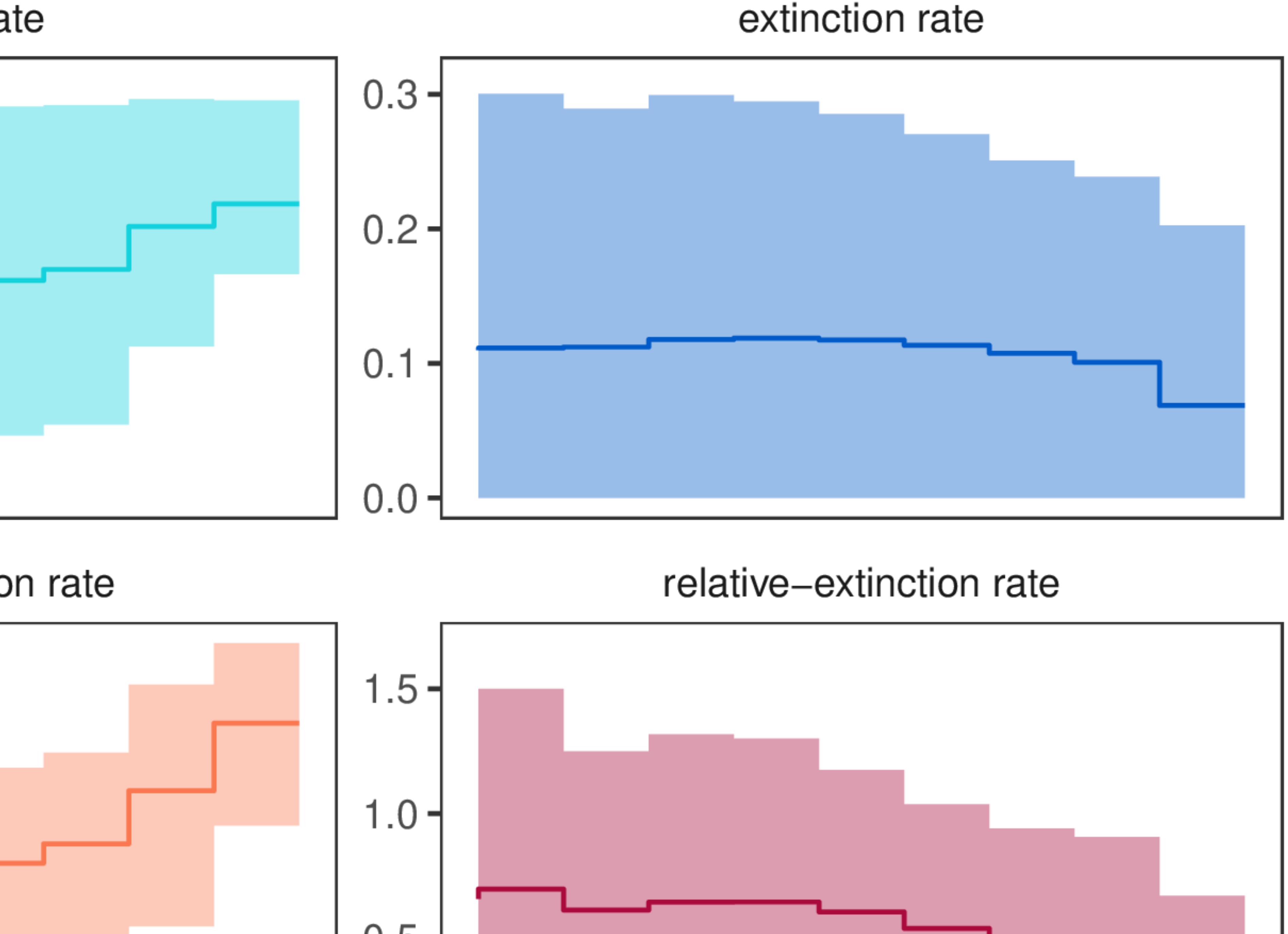
Höhna 2015; J. Theor Biol. Magee and Höhna 2021; bioRxiv.:426715





Distribución Horseshoe Markov

- Auto correlación de las tasas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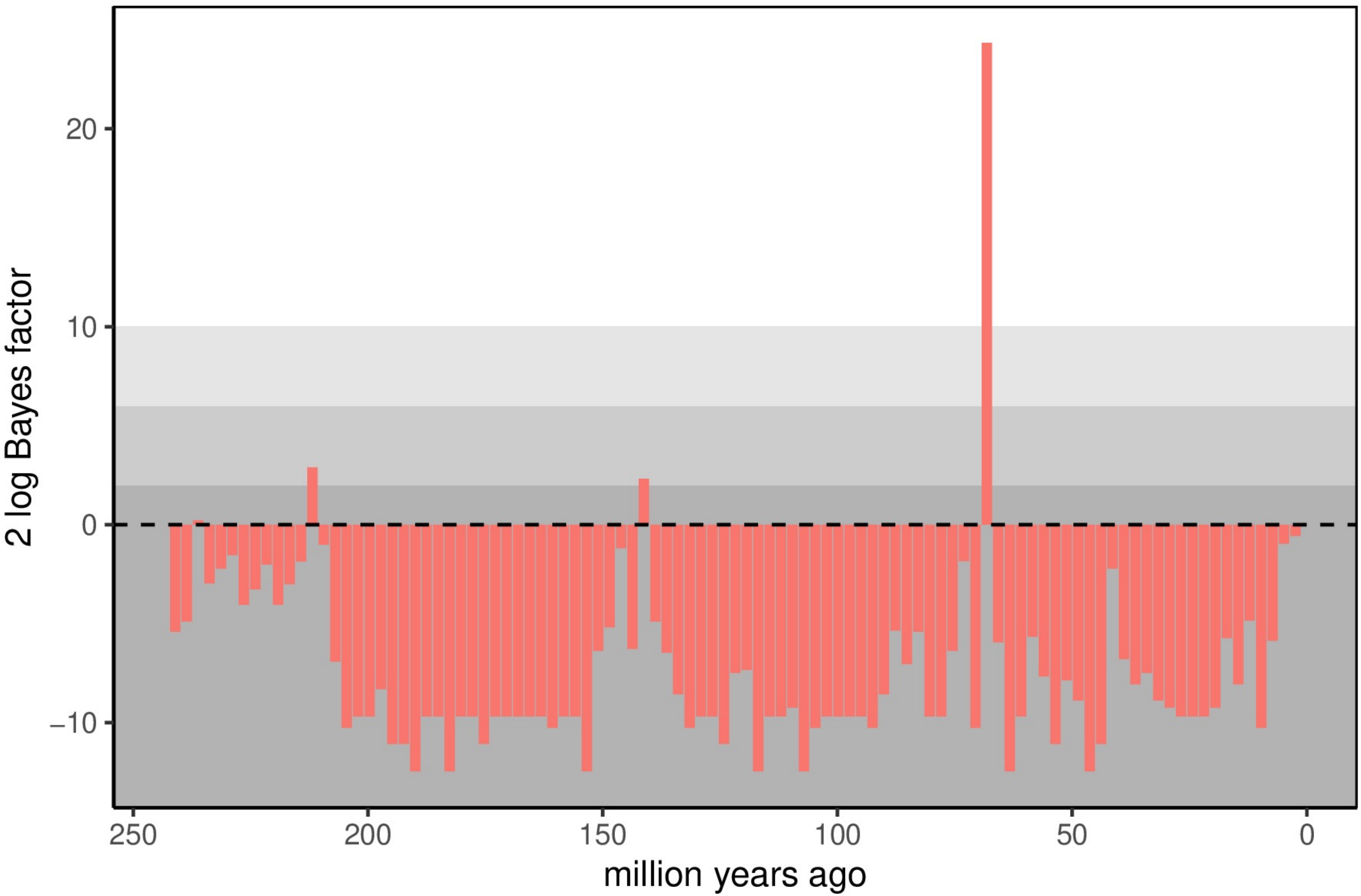
1.0



https://revbayes.github.io/tutorials/divrate/efbdp_me.html

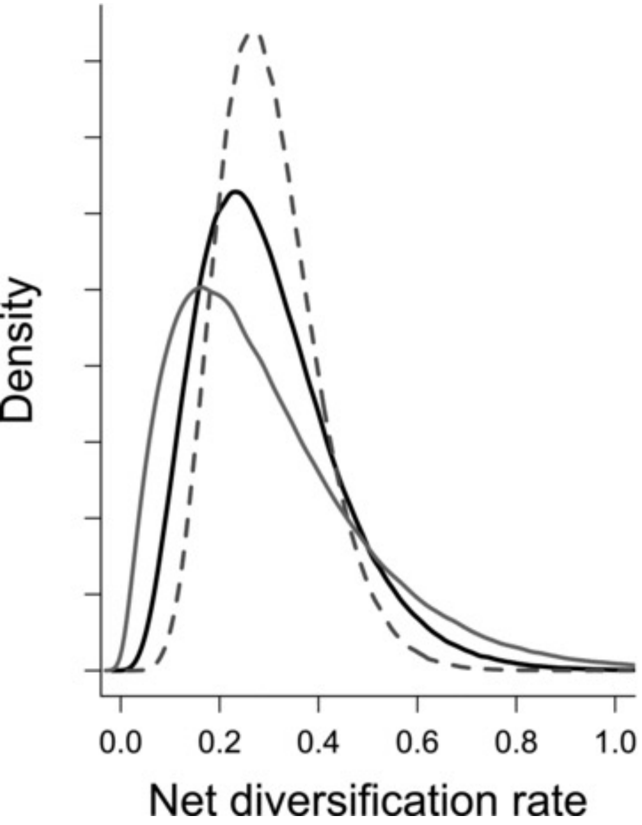
JOURNAL ARTICLE

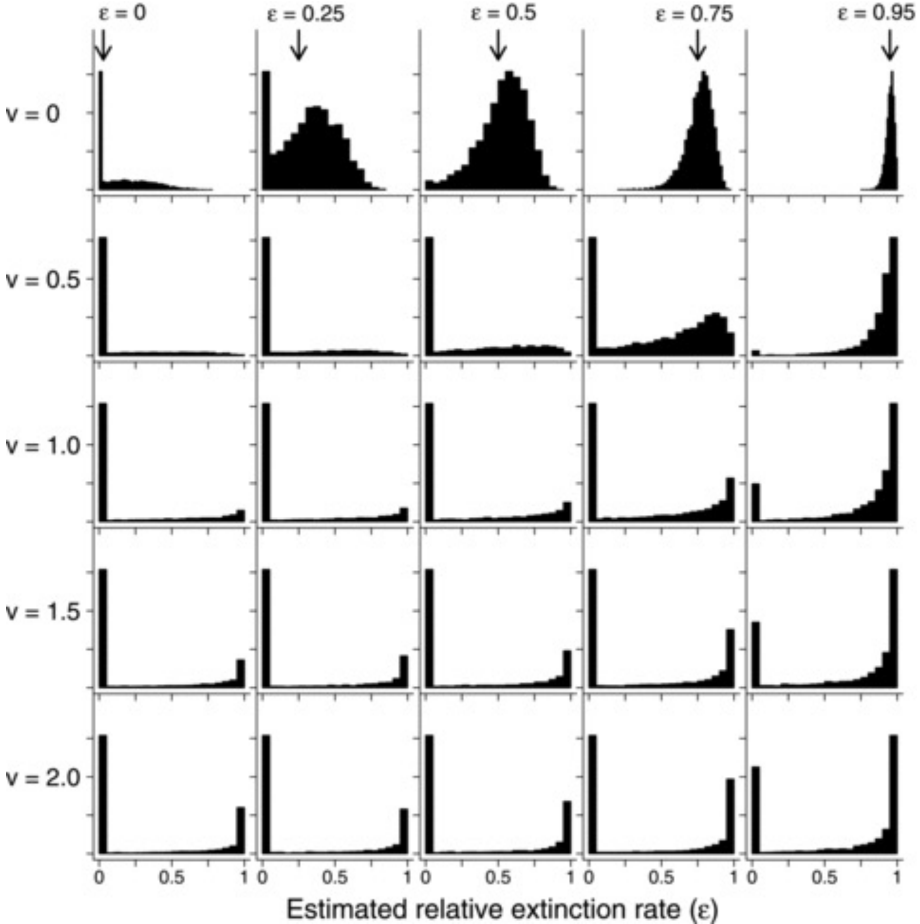
# EXTINCTION RATES SHOULD NOT BE ESTIMATED FROM MOLECULAR PHYLOGENIES

Daniel L. Rabosky

*Evolution*, Volume 64, Issue 6, 1 June 2010, Pages 1816–1824, https://doi.org/10.1111/j.1558-5646.2009.00926.x

**Published:** 01 June 2010 **Article history** ▾





nature ecology & evolution

PERSPECTIVE

PUBLISHED: 23 MAY 2017 | VOLUME: 1 | ARTICLE NUMBER: 0165

# Five palaeobiological laws needed to understand the evolution of the living biota

Charles R. Marshall

**Box 1 | Five palaeobiological laws needed to understand the evolution of the living biota and the reasons for their significance.**

**First law: lineages become extinct.** The extinction of lineages, like the death of individuals, is an integral part of the evolutionary process, even though extinct lineages are hidden from view when only analysing living species.

**Second law: species longevity = 1/extinction rate.** (1) Species are geologically short-lived. (2) Thus, the living biota represents only a tiny subsample of all species that have existed (for example, the living mammal species represent ~4% of all post-Cretaceous mammal species).

**Third law: the average origination rate ≈ the average extinction rate.** (1) Except perhaps for the youngest evolutionary radiations, molecular phylogenetic analyses that yield zero or low extinction rates compared with origination rates are almost certainly wrong. (2) Origination rates derived from molecular phylogenies are typically much too low, as they fail to take into account the origin of extinct species. (3) Rates of origination and extinction measured in the fossil record are typically high.

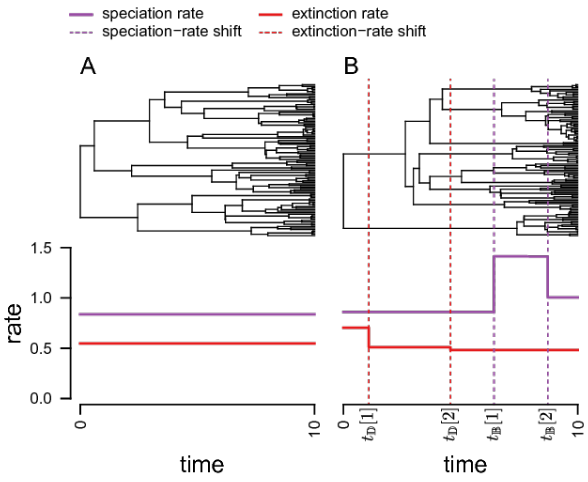
**Fourth law: species richness results from time varying origination and extinction rates.** Evolutionary models, whether used directly or as priors, that treat evolution as a pure birth (Yule) process, or as one with fixed origination and extinction rates should be avoided if possible, unless it is demonstrated that their use does not lead to biased results.

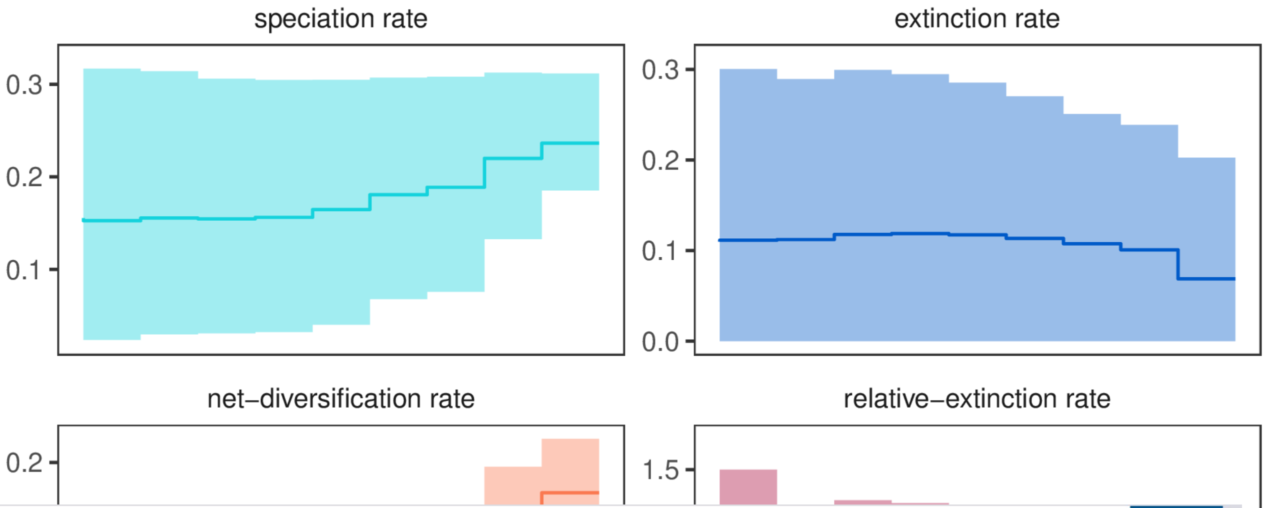
**Fifth law: extinction erases a clade's history.** (1) Ancestral character states observed in the fossil record are sometimes completely unanticipated given the living biota. (2) Diversity trajectories (for example, LTT plots) derived from molecular phylogenies often bear little resemblance to diversity trajectories seen in the fossil record—they are of little use when trying to infer the history of a group.

# Modelos episódicos de nacimiento-muerte y fosilización

Episodic fossilized Birth-Death models

Höhna 2015; J. Theor Biol. Magee and Höhna 2021; bioRxiv.:426715





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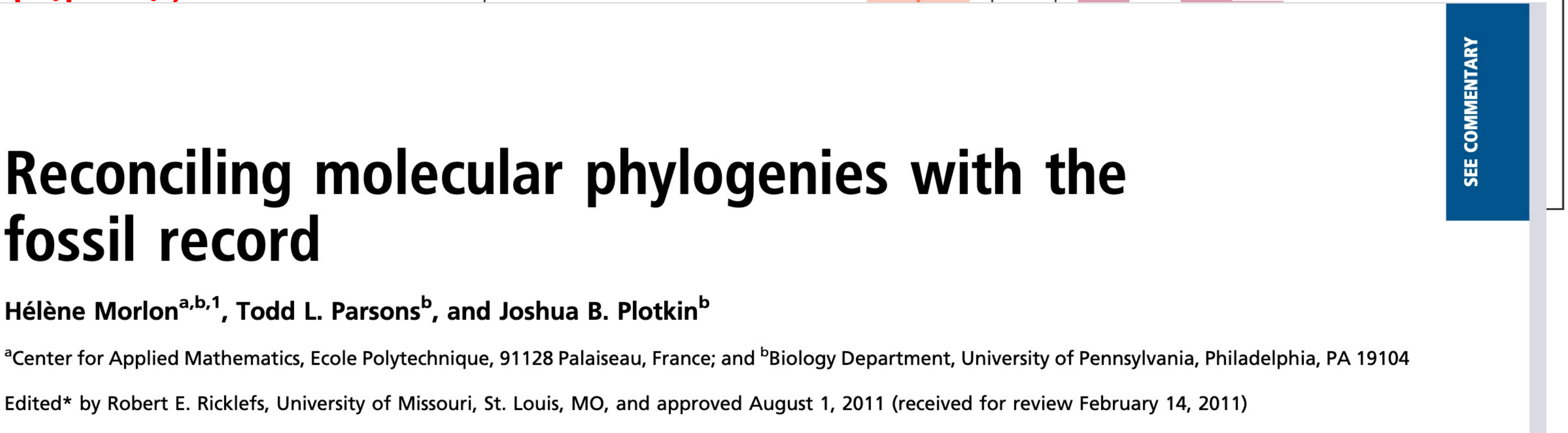

- **Reconciling molecular phylogenies with the fossil record**

**Hélène Morlon[a,b,1], Todd L. Parsons[b], and Joshua B. Plotkin[b]**

[a]Center for Applied Mathematics, Ecole Polytechnique, 91128 Palaiseau, France; and [b]Biology Department, University of Pennsylvania, Philadelphia, PA 19104

Edited* by Robert E. Ricklefs, University of Missouri, St. Louis, MO, and approved August 1, 2011 (received for review February 14, 2011)

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