

Phylogenetics

Introduction to
phylodynamics

RL-V3 MPP

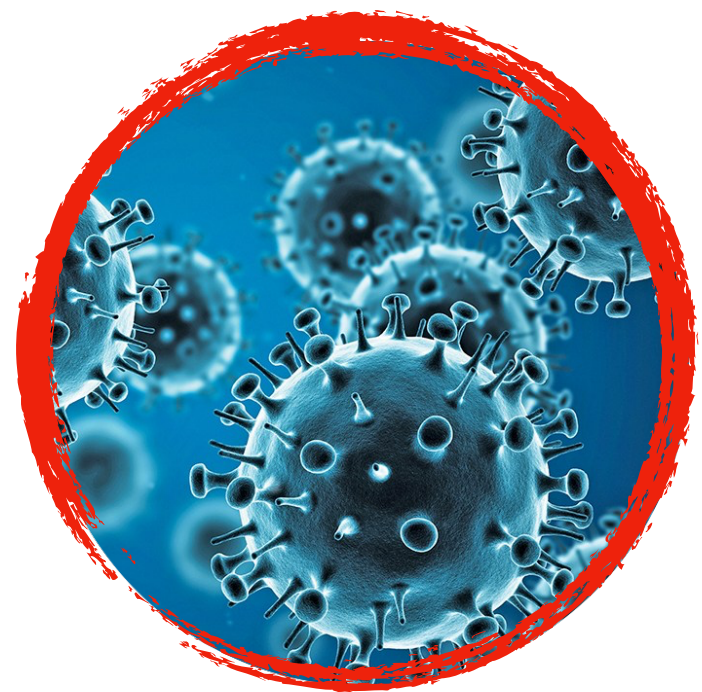
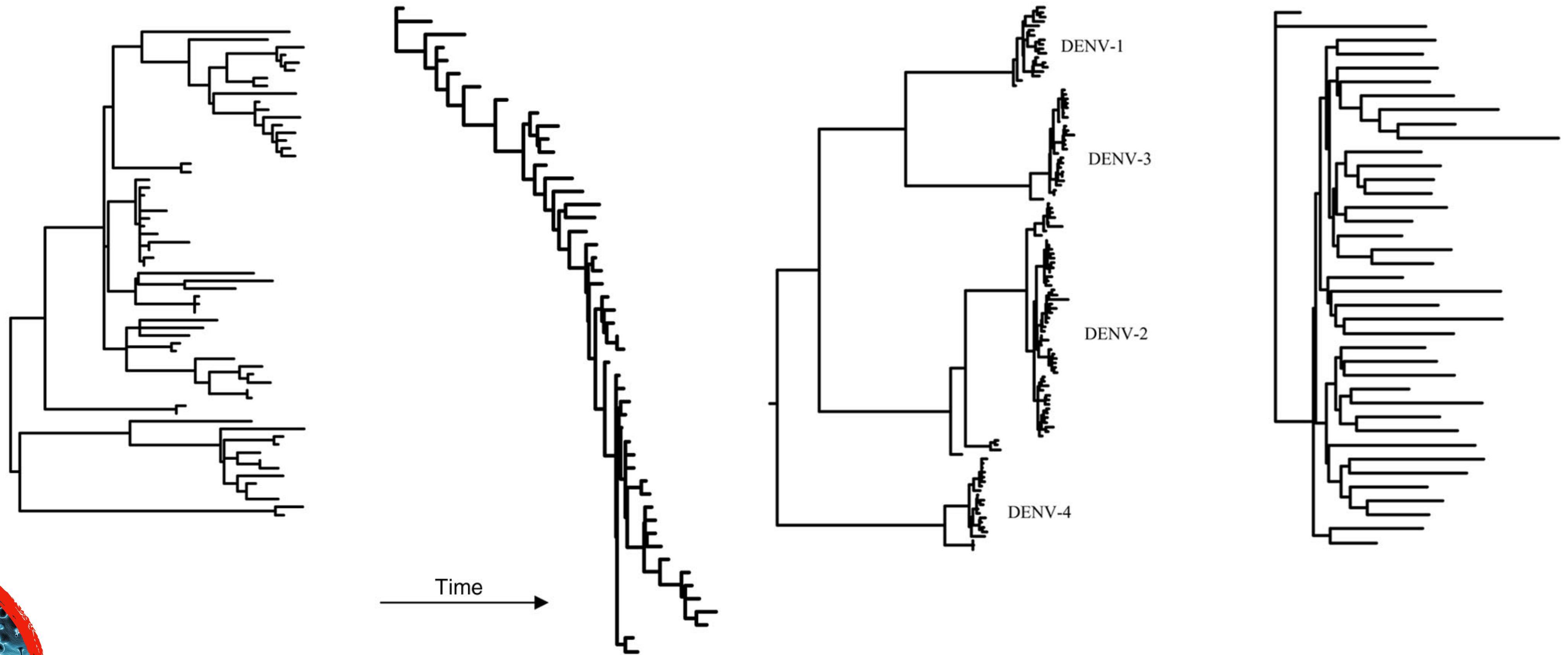
Rachel Warnock

28.04.2026



Recap: Bayesian phylodynamics

Tree shape is informative about underlying dynamics



This paper coined the term phylodynamics
Grenfell et al. 2004. Science

Bayesian divergence time estimation

The data

and / or

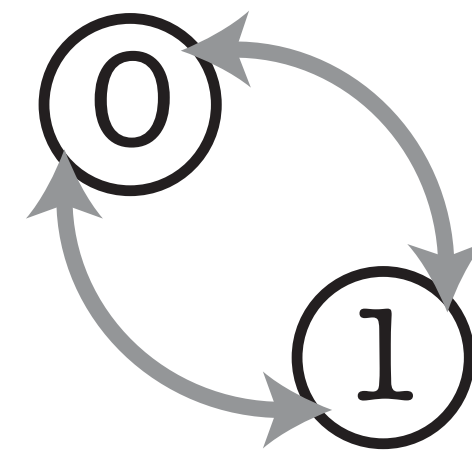
0101... ATTG...
1101... TTGC...
0100... ATTC...



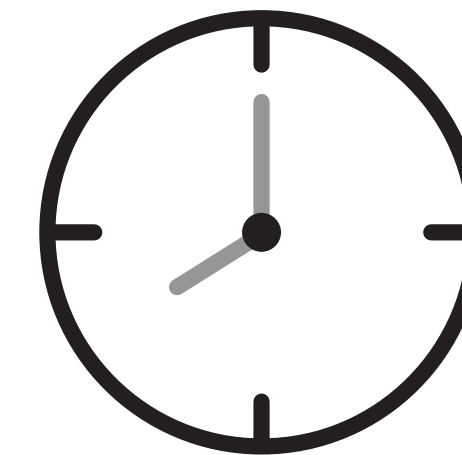
phylogenetics
characters

sample
ages

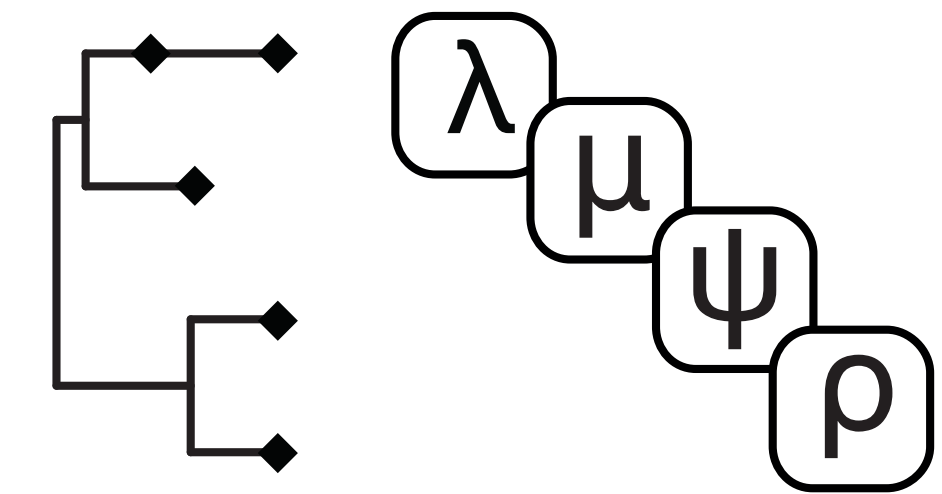
3 model components



substitution
model



clock
model



tree and tree
model

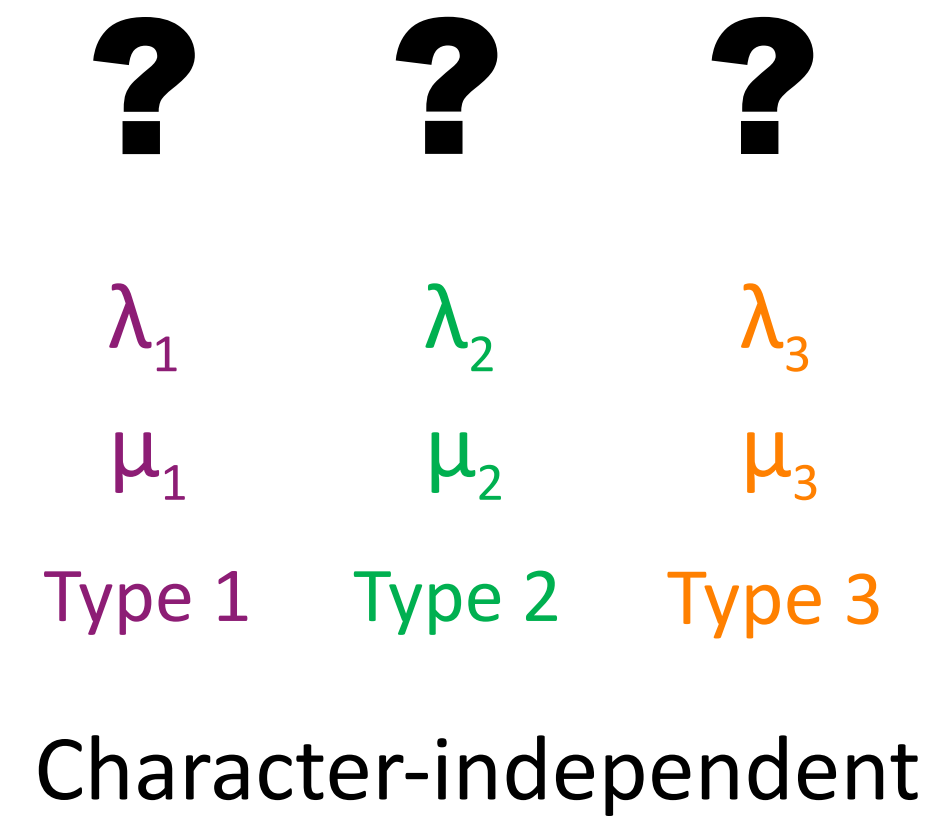
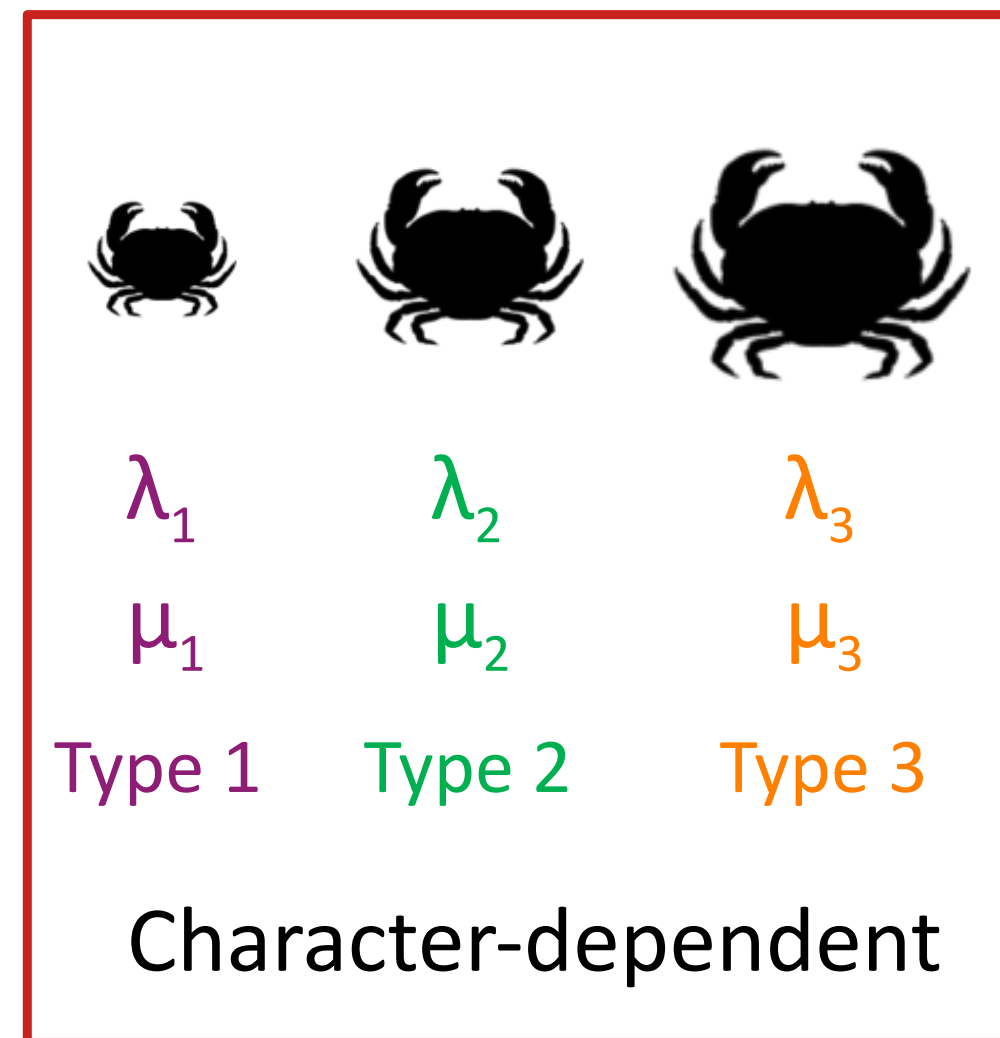
Bayesian divergence time estimation

$$P \left(\begin{array}{c} \text{Tree} \\ \lambda, \mu, \psi, \rho \\ \text{Clock} \end{array} \mid \begin{array}{c} 0101\dots \\ 1101\dots \\ 0100\dots \end{array} \text{Ear} \right) =$$

probability of the
time tree

$$\frac{P \left(\begin{array}{c} 0101\dots \\ 1101\dots \\ 0100\dots \end{array} \mid \begin{array}{c} \text{Tree} \\ \lambda, \mu, \psi, \rho \\ \text{Clock} \end{array} \right) P \left(\begin{array}{c} \text{Tree} \\ \text{Ear} \end{array} \mid \begin{array}{c} \lambda, \mu, \psi, \rho \end{array} \right) P \left(\begin{array}{c} \lambda, \mu, \psi, \rho \end{array} \right) P \left(\begin{array}{c} \text{Clock} \end{array} \right)}{P \left(\begin{array}{c} 0101\dots \\ 1101\dots \\ 0100\dots \end{array} \mid \text{Ear} \right)}$$

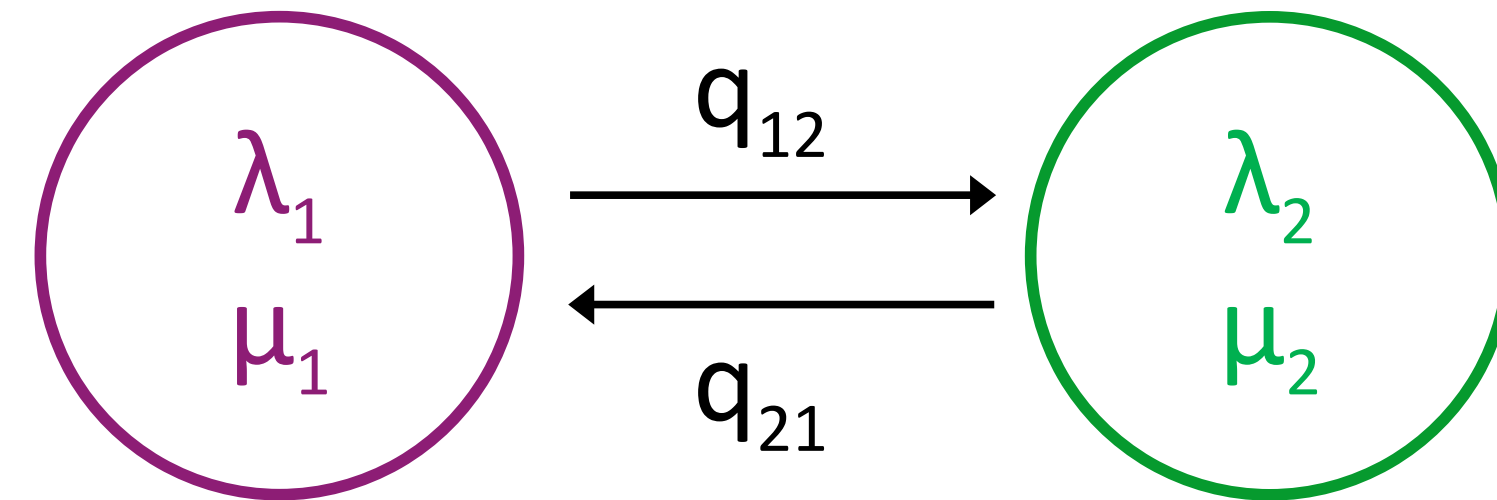
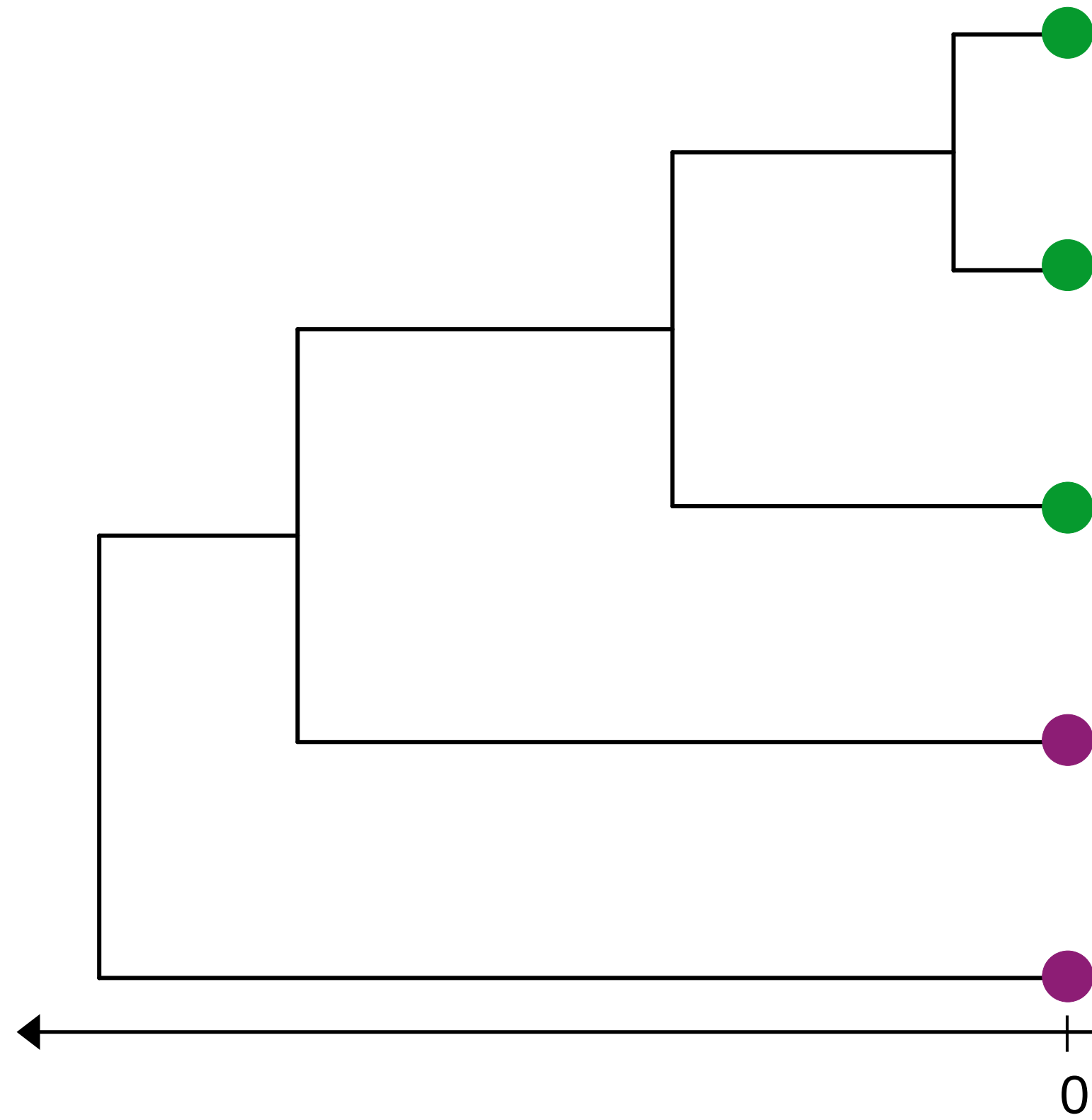
Character-dependent or independent?



In a character-dependent model:

The **number of types** is known and the **type at the tips** is known

The BiSSE/MuSSE/BDMM model



Parameters of the model:

λ_i – birth rates

μ_i – death rates

q_{ij} – transition rates

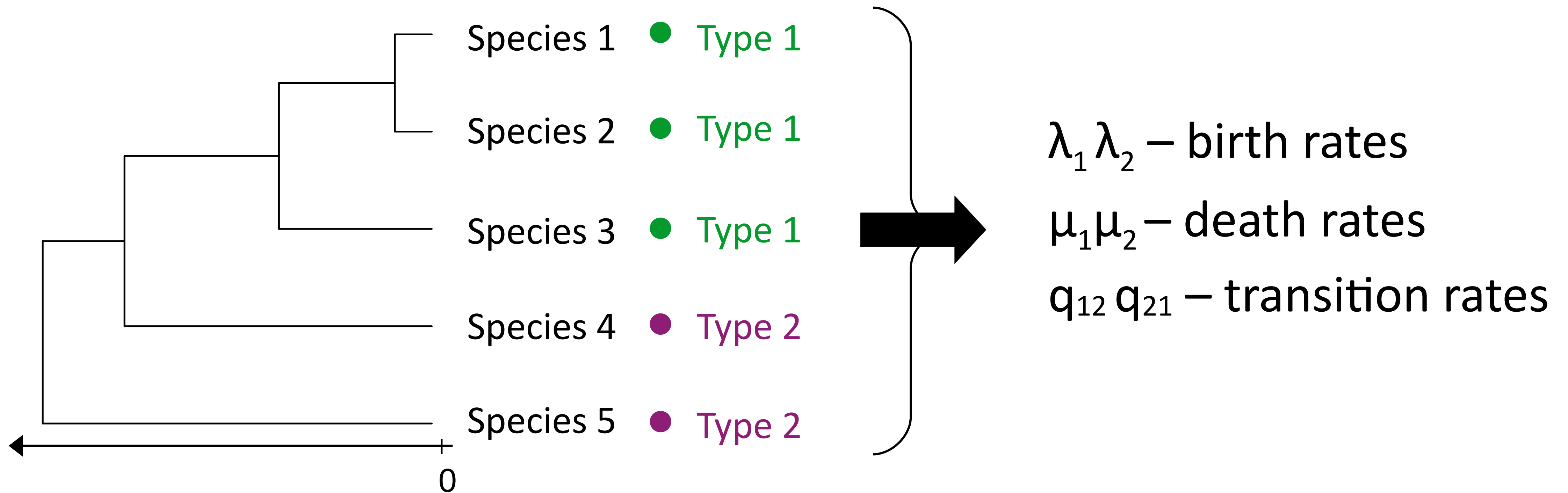
ρ/p – sampling probability

Maddison *et al.* **Sys. Bio.** 2007

Fitzjohn *et al.* **Sys. Bio.** 2009

Kühnert *et al.* **MBE** 2016

SSE/BDMM inference



BDMM-Prime



Tim Vaughan

The screenshot shows a web browser window with the URL `tgvaughan.github.io`. The page is titled "Table of Contents" and lists the following sections:

1. Introduction
2. Getting Started
3. Model specification using BEAUti
4. Sampling Latent Variables
5. Appendices
6. License

The main content area features a large black banner with the text "BDMM-Prime" in white, with the subtitle "Linear birth-death-sampling phylodynamics" below it. To the left of the text is a diagram of three squares connected by arrows, representing a birth-death process. Below the banner, the source code is listed as <https://github.com/tgvaughan/BDMM-Prime>.

1. Introduction

BDMM-Prime is a BEAST 2 package for performing phylodynamic inference under a variety of linear birth-death-sampling models with/without types.

1.1. Comparison with BDMM

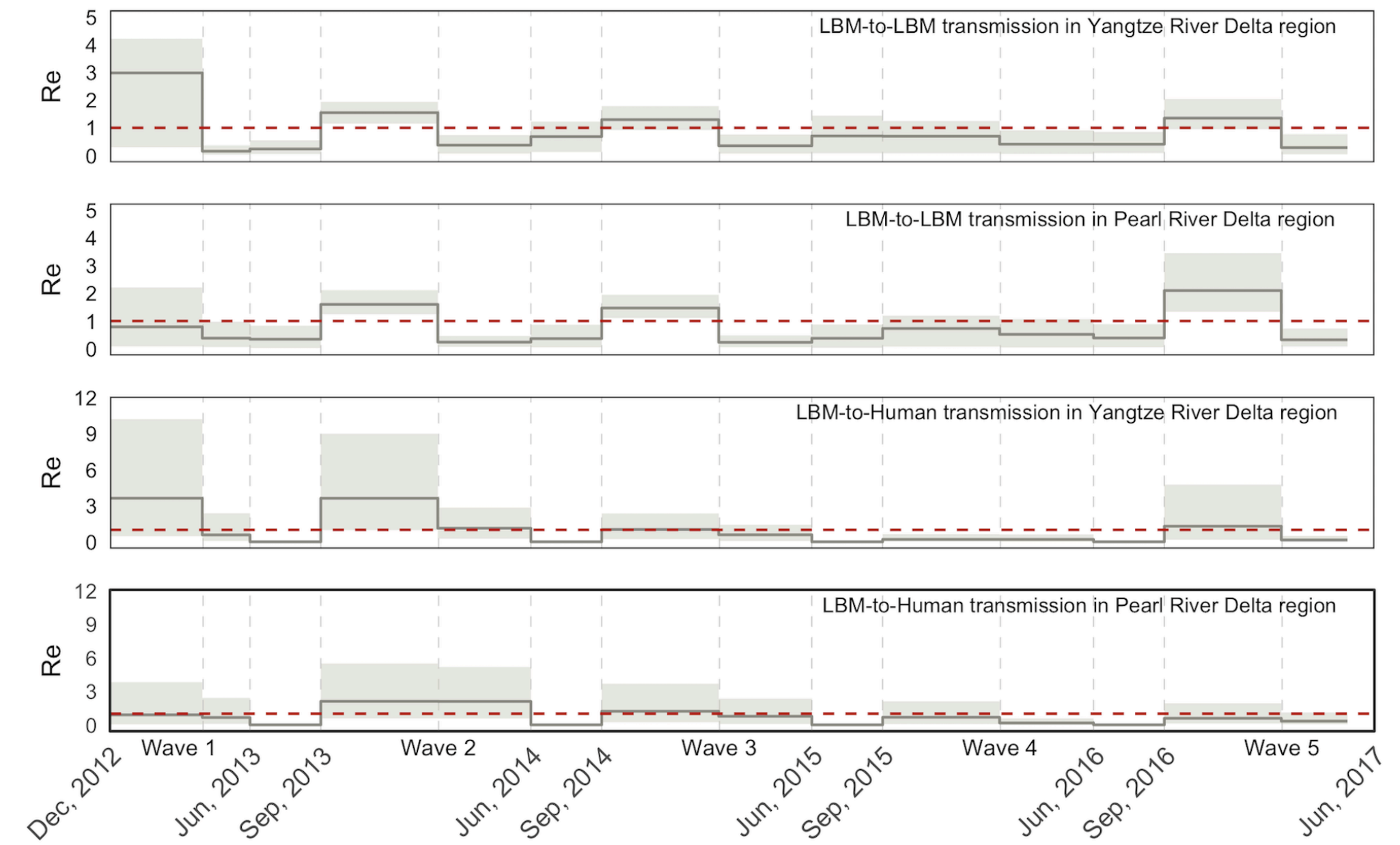
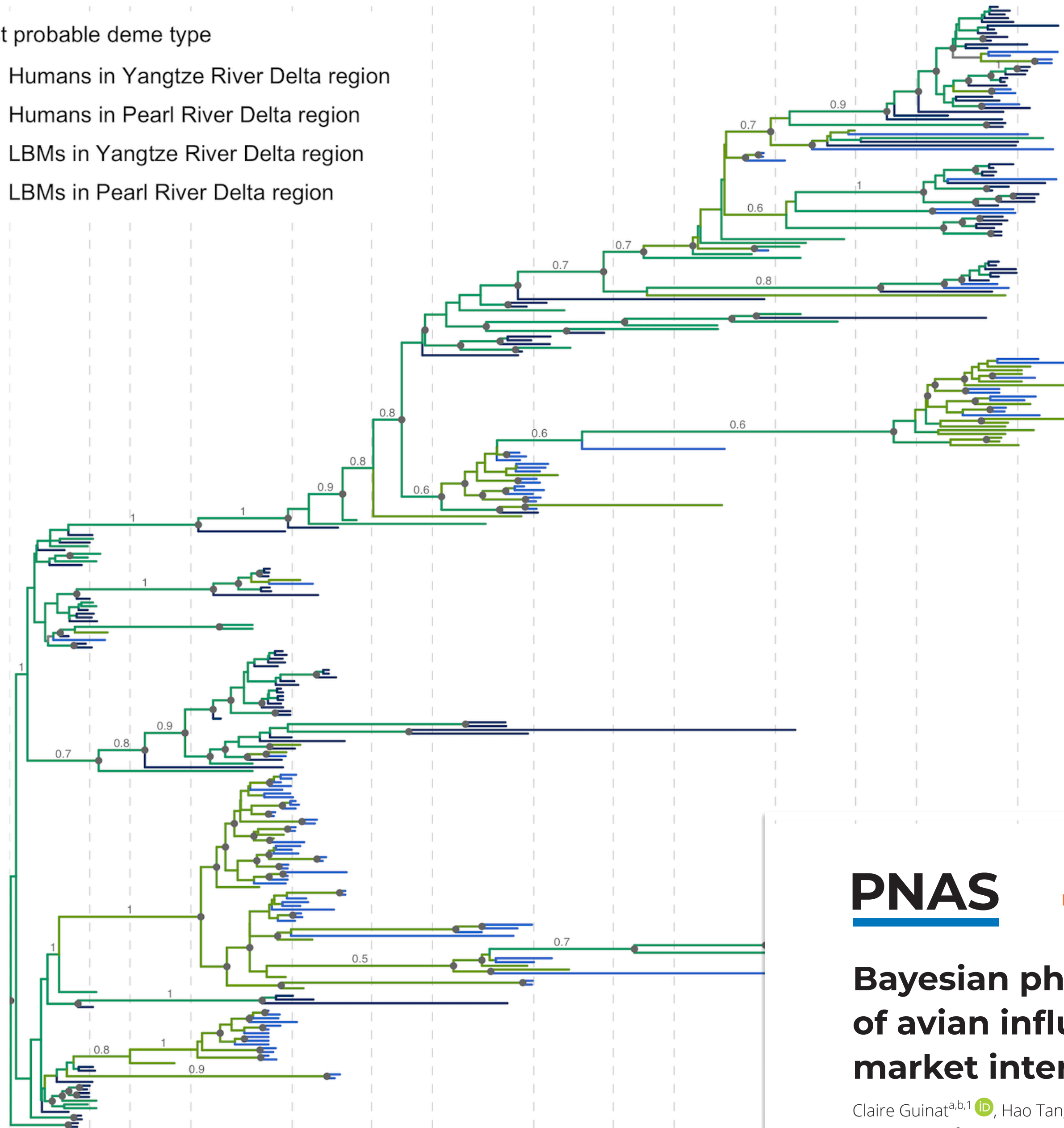
The BDMM-Prime project is a hard fork of the original [BDMM project](#). The intention is to extend the functionality of the original package, while improving its flexibility and ease of use. It incorporates the following enhancements:

- an improved BEAUti interface that allows a much more diverse range of analyses to be configured,
- automatic fall-back to analytical solutions for unstructured (single type) analyses, meaning BDMM-Prime can in principle be used in place of [BDSKY](#),
- use of stochastic mapping for efficient sampling of ancestral types

<https://tgvaughan.github.io>

Most probable deme type

- Humans in Yangtze River Delta region
- Humans in Pearl River Delta region
- LBMs in Yangtze River Delta region
- LBMs in Pearl River Delta region



PNAS

RESEARCH ARTICLE

EVOLUTION

OPEN ACCESS

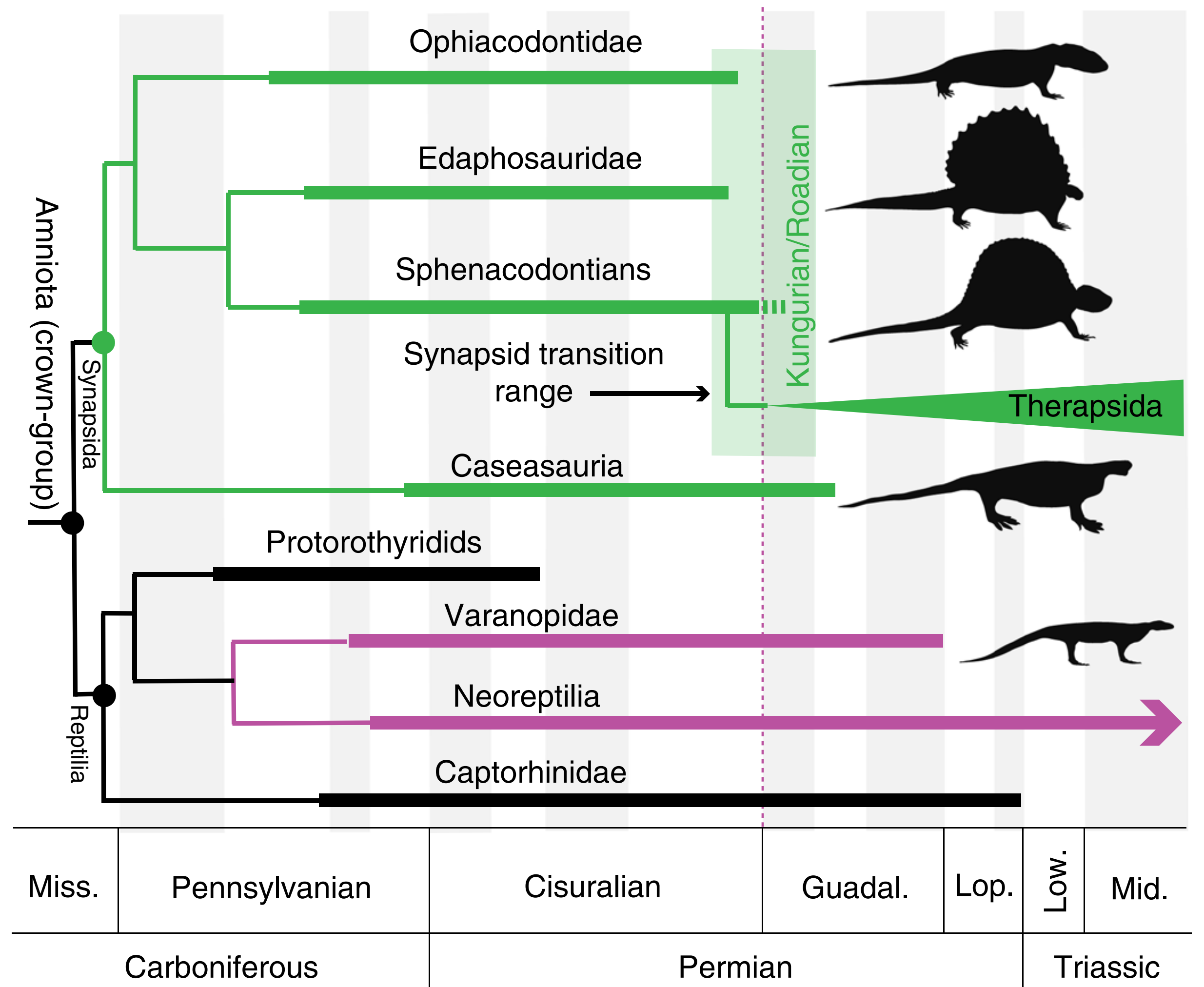


Bayesian phylodynamics reveals the transmission dynamics of avian influenza A(H7N9) virus at the human–live bird market interface in China

Claire Guinat^{a,b,1} , Hao Tang^c , Qiqi Yang^d , Cecilia Valenzuela Agü^{a,b} , Timothy G. Vaughan^{a,b} , Jérémie Scire^{a,b} , Hongjie Yu^e, Wei Wang^e, Zhiyuan Chen^e, Mariette F. Ducatez^f , and Tanja Stadler^{a,b}

Exercise

Both skyline and multi-type extensions of the FBD model are available via BDMM-Prime



- 70 fossils, spanning the Carboniferous to the Triassic
- Not all lineages are extinct
- 294 morphological characters
- Fossil ages plus locality information

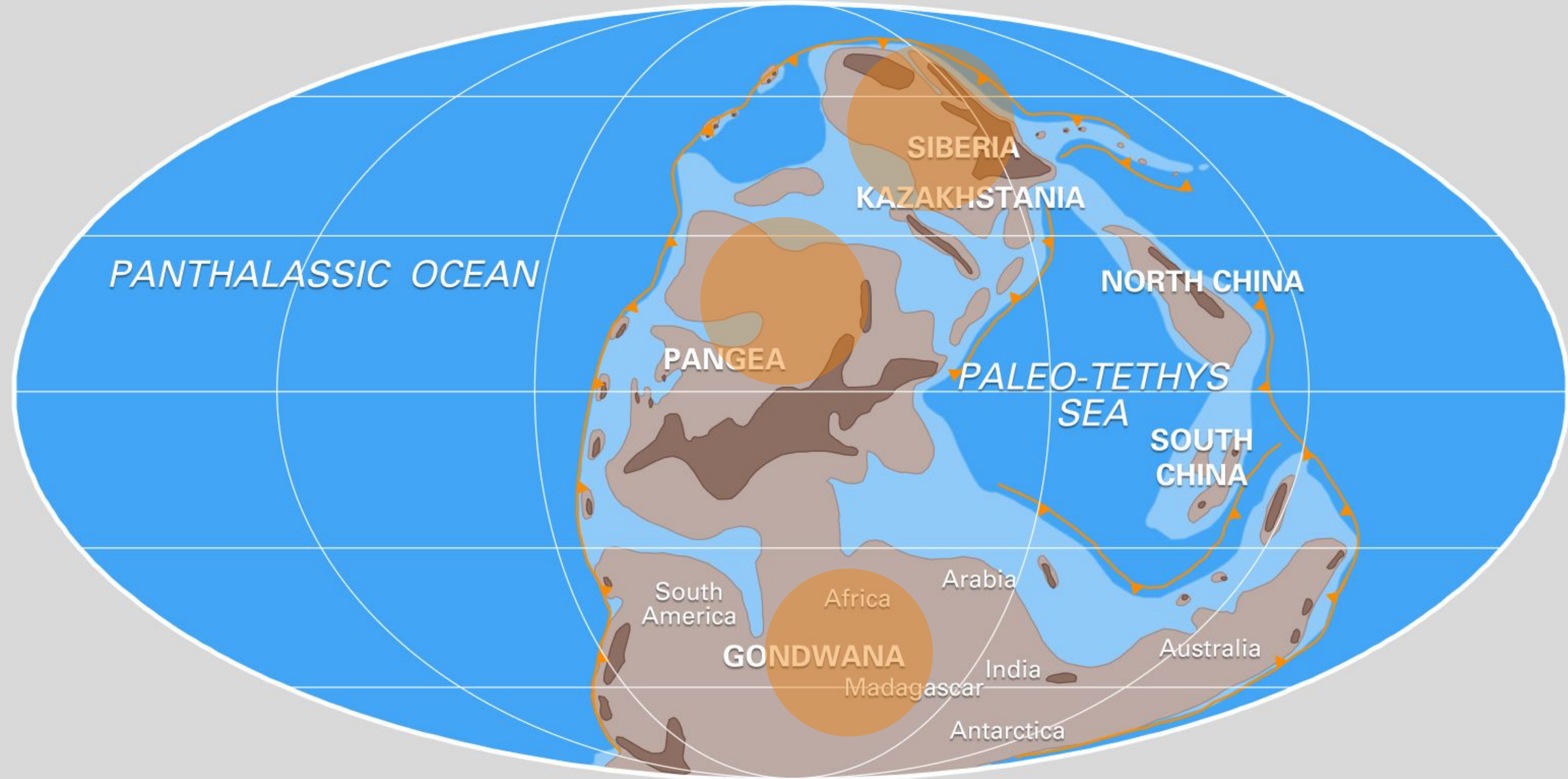
```

1 #NEXUS
2 [Data written by write.nexus.data.R, Tue Jun 17 20:12:20 2025]
3 BEGIN DATA;
4   DIMENSIONS NTAX=70 NCHAR=294;
5   FORMAT DATATYPE=STANDARD MISSING=? GAP=- INTERLEAVE=NO symbols="0123456789";
6   MATRIX
7     Gephyrostegus_bohemicus_Eu_309      00030000000000-000000?00000-030----0??
8     Seymouria_spp_NAm_288.51           00000000?00000-000000001200-01110000??
9     Tseajaia_campi_NAm_296.9           001-10000001?10001?10?00000-01111000??
10    Limnoscelis_paludis_NAm_298.61      001-1001?00110-001011200000-01100000??
11    Oedaleops_campi_NAm_296.21         100?21-0000111000??11?00100-011111000-
12    Eothyris_parkeyi_NAm_285.05        10??21-00001110001011?00100-01111101??
13    Vaughnictis_smithae_NAm_294.5      ?01-?0000001????????11????????0?????????
14    Eocasea_martini_NAm_300.45         ??012???0????????????????????0?????????
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16    Casea_broilii_NAm_283              100121-0001110-000000?00100-010----00-
17    Ennatosaurus_tecton_Eu_269.025     100221-0001110-0000112002010000----00-
18    Echinerpeton_intermedium_NAm_309   ??????1-?000????????????011????0111100?10
19    Archaeothyris_florensis_NAm_309    0?0?200?100??0-????????011????0211100?10

```

Ford and Benson. ([2019](#))

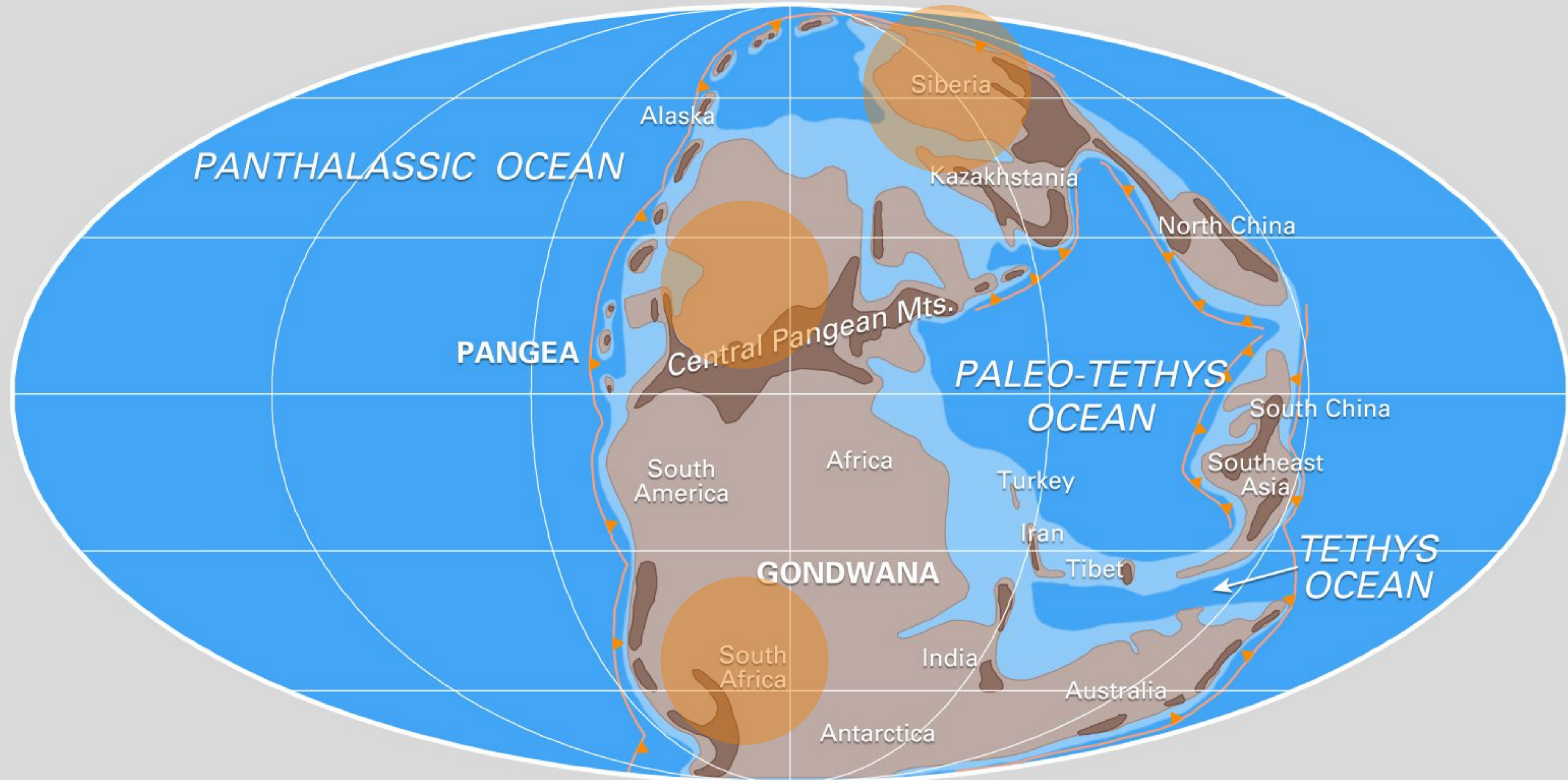
Late Carboniferous 306 million years ago



SOURCE: © 2001 C.R. Scotese, PALEOMAP Project

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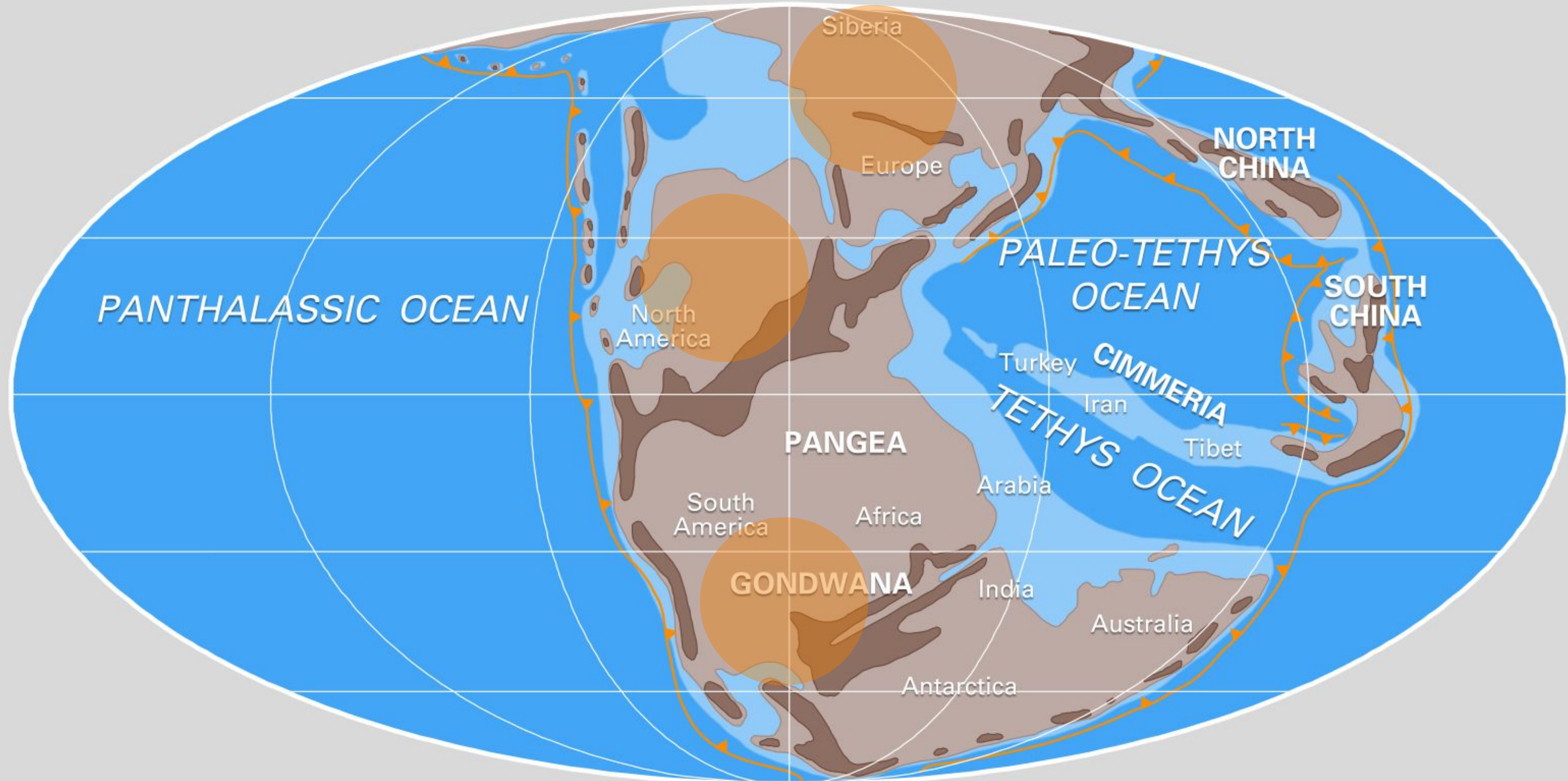
Late Permian 255 million years ago



SOURCE: © 2001 C.R. Scotese, PALEOMAP Project

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Early Triassic 237 million years ago

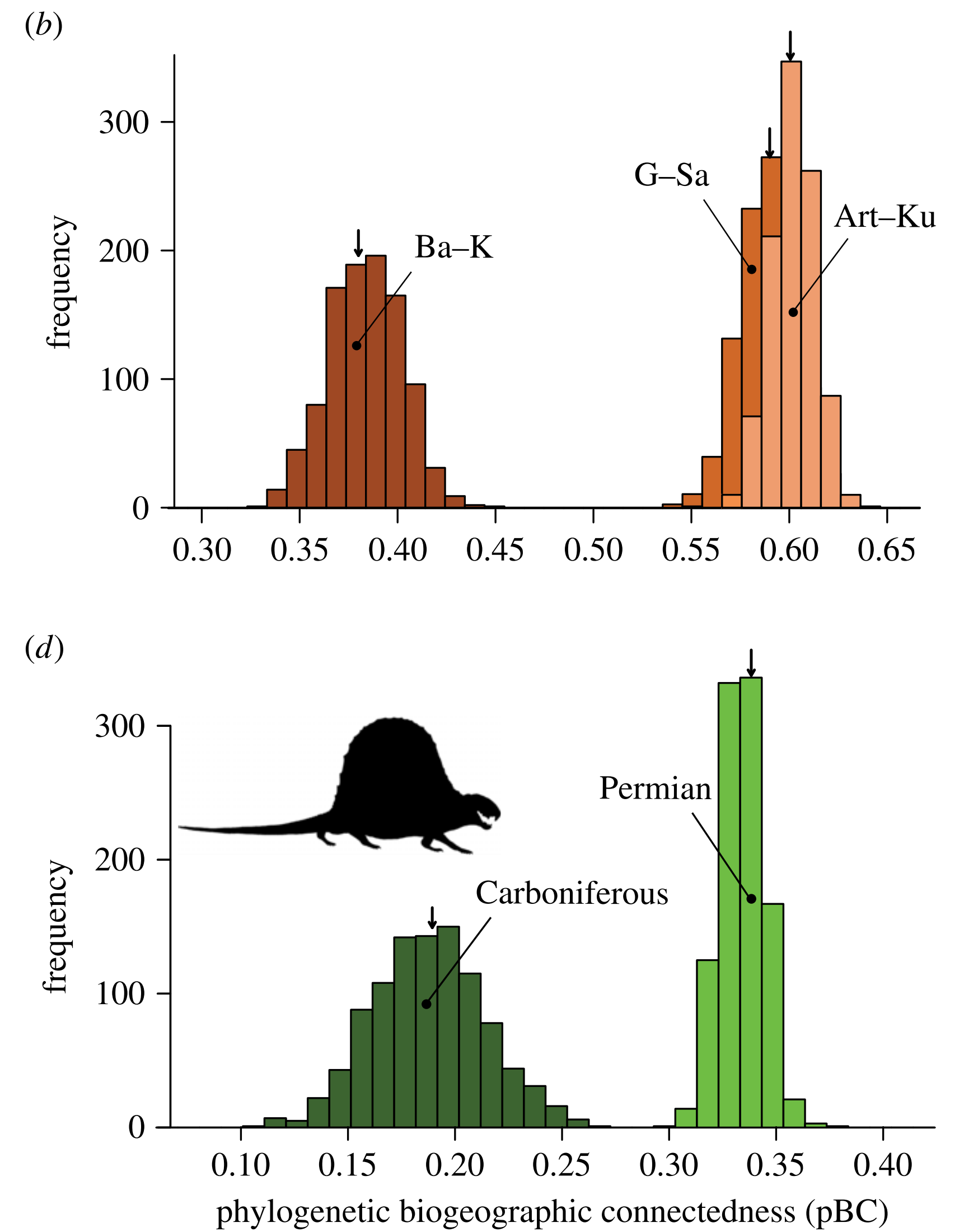
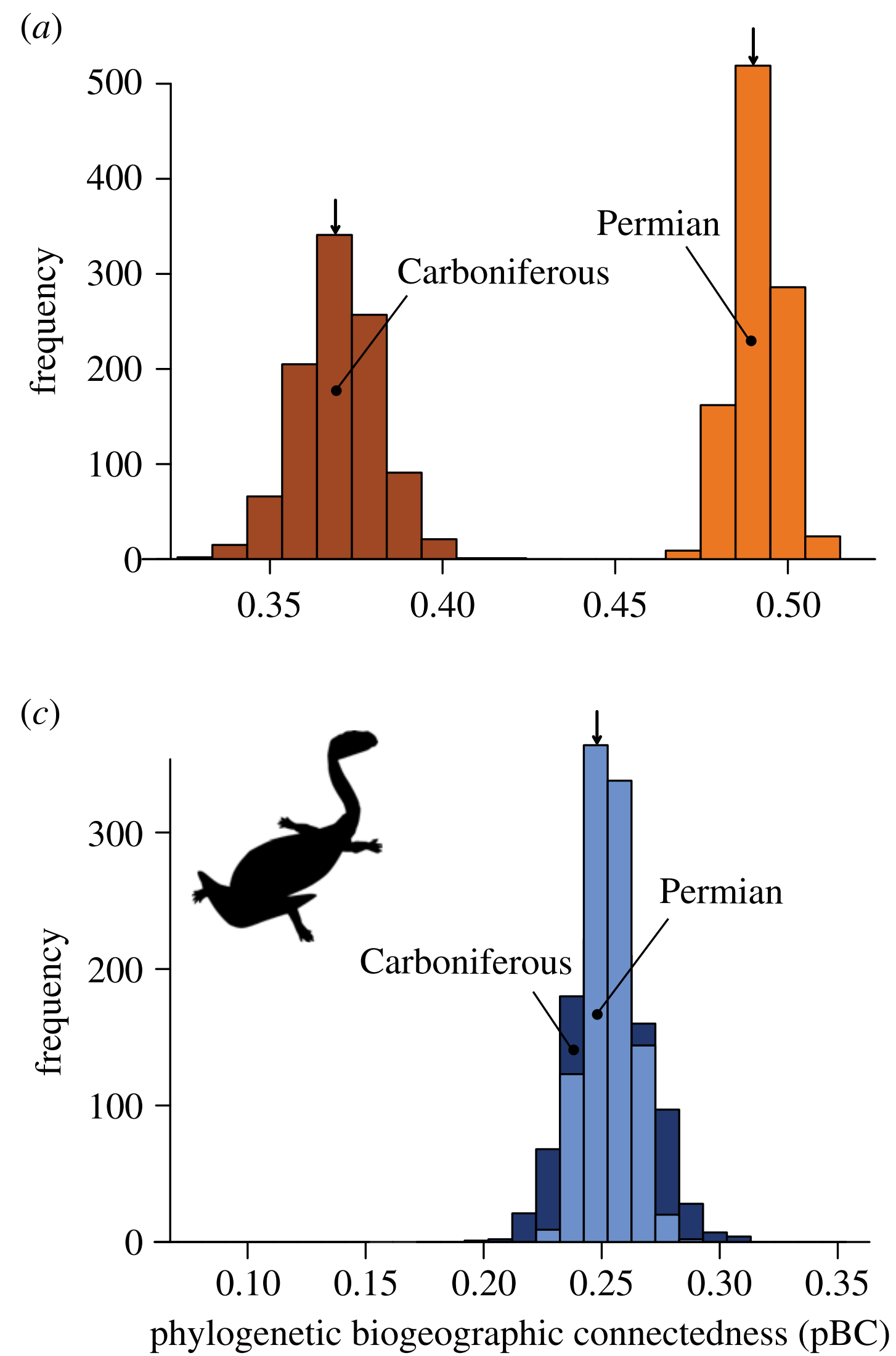


■ Mountains ■ Land ■ Shallow seas ■ Deep ocean basins —▲— Subduction zone (triangles point in the direction of subduction)

SOURCE: © 2001 C.R. Scotese, PALEOMAP Project

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Increased connectivity / migration is supported by different data and methods



Dunne et al. (2018)

BDMM-Prime checklist for macroevolution

We recommend always double checking your model parameters

Parameter	Notes
Birth (speciation) Rate – λ	usually estimated (time or lineage variable)
Death (speciation) Rate – μ	usually estimated (time or lineage variable)
Sampling (fossilisation) Rate – ψ	usually estimated (time or lineage variable)
Rho (extant sampling) Probability – ρ	usually fixed
Removal Probability – r	not applicable in macroevolution, fix to zero
Migration Rate – m	usually estimated (time or lineage variable)
Birth Rate Among Demes	not applicable in macroevolution, fix to zero