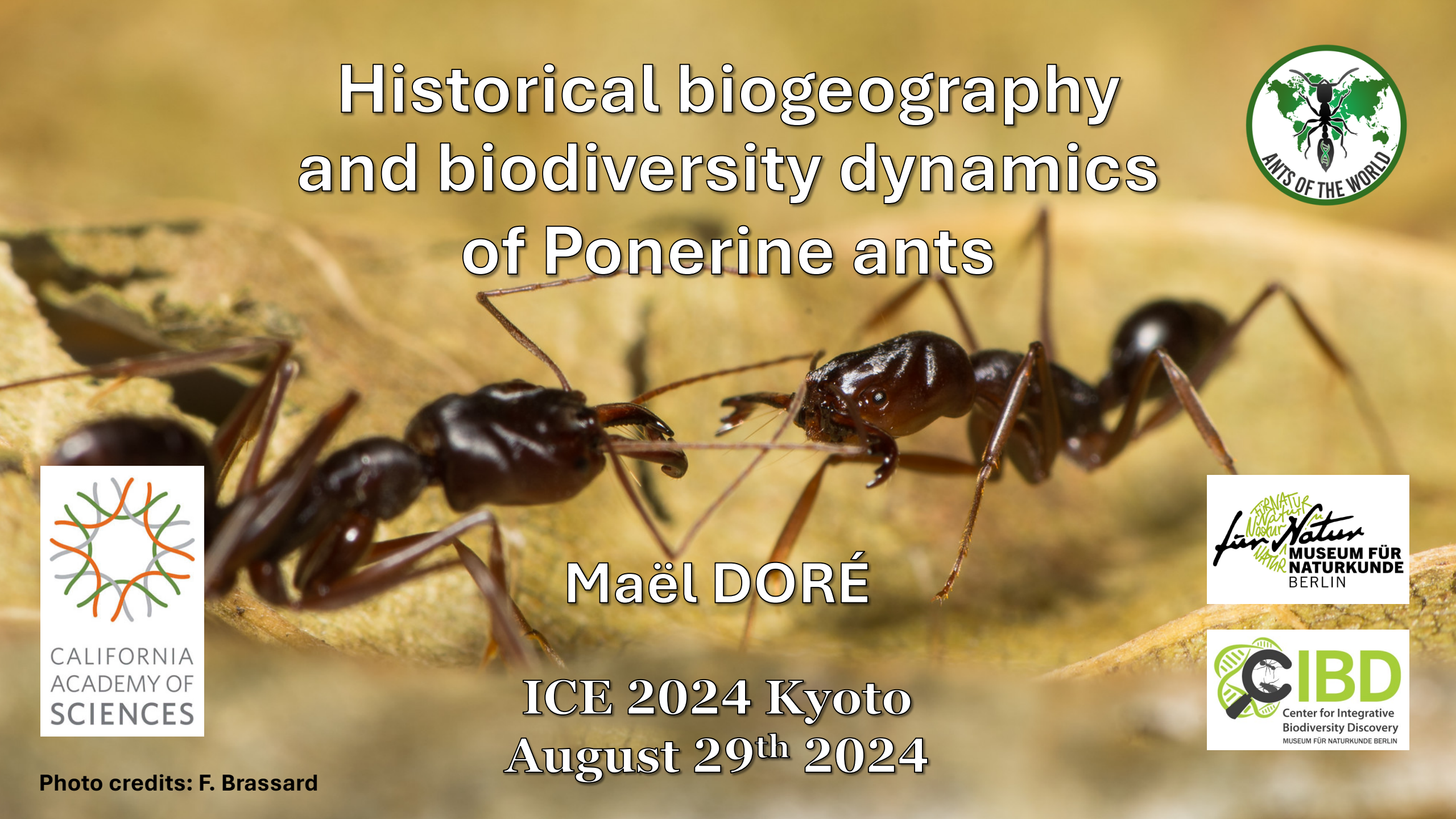
Historical biogeography and biodiversity dynamics of Ponerine ants



Maël DORÉ

ICE 2024 Kyoto
August 29th 2024

Photo credits: F. Brassard

Ponerinae Subfamily

Top 3 ant subfamily for **diversity**
with 50 genera and ca. **1,400 species**

Predatory ants: include the **trap-jaw** ants (Anochetus, Odontomachus)

High diversity of **mandible shapes** related to **diet specialization**

Plesiomorphic robust morphology

Include the **largest ant species**: *Dinoponera gigantea*

Formicinae	Myrmicinae	**Ponerinae**
3,300 sp.	7,200 sp.	**1,400 sp.**
22%	48%	**10%**

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Photo Credits: Magdalena Sorger

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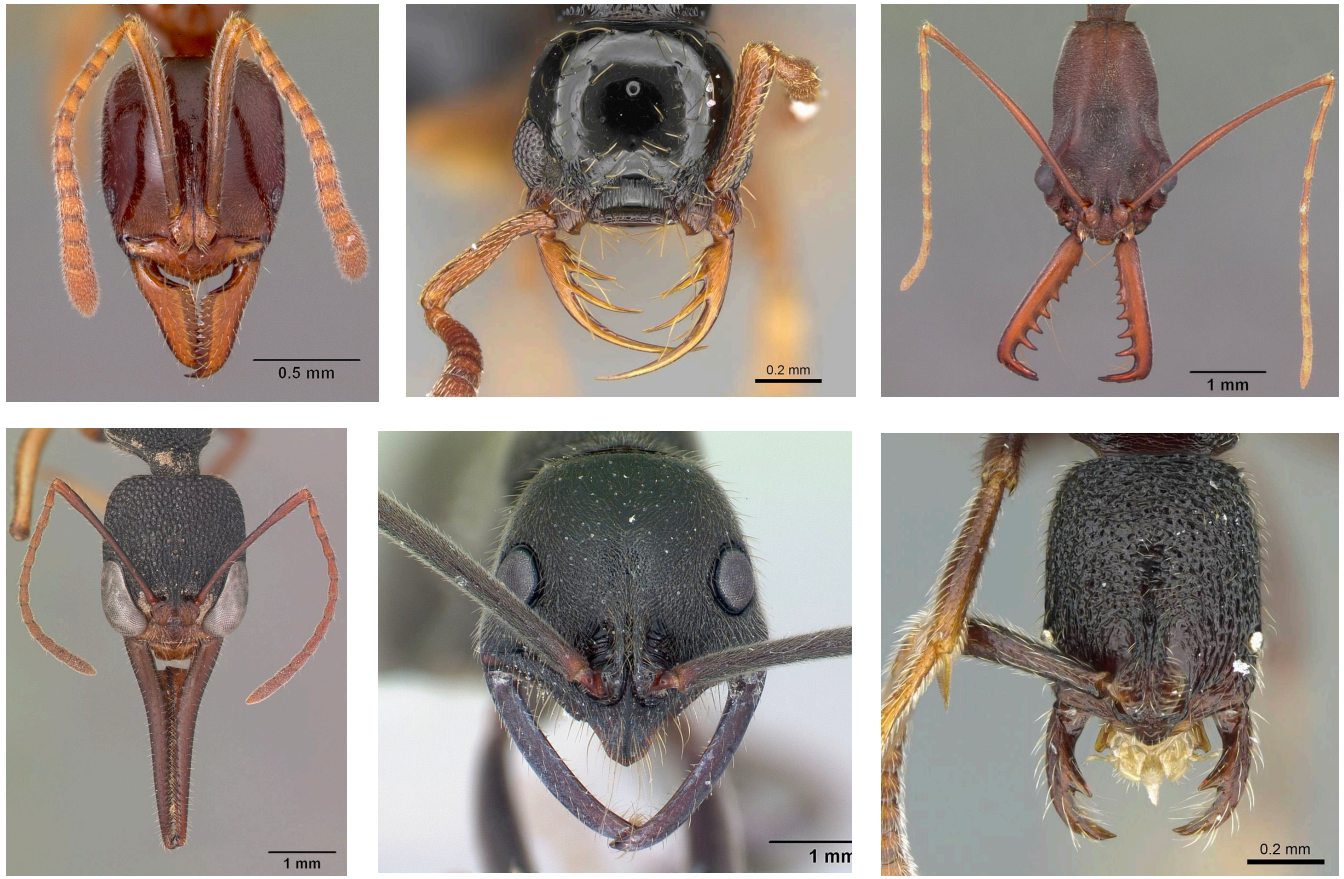

Source: AntWeb

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Photo Credits: Tatyana Kolesnikova

Dinoponera gigantea in Belem, Brazil
Up to 40 mm

Current diversity

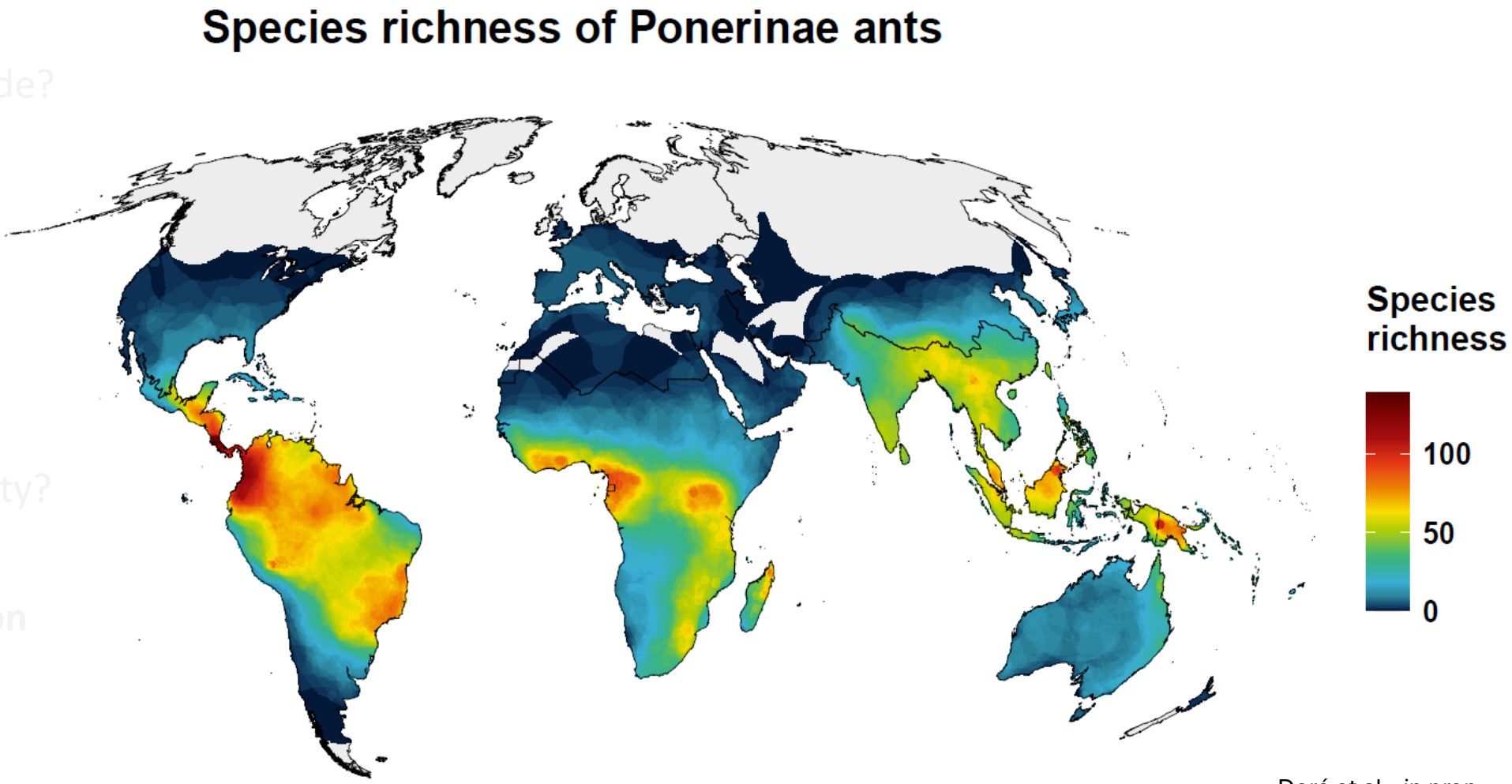
1/ **Origin** of the clade?

2/ Source of diversity?

In situ **diversification**

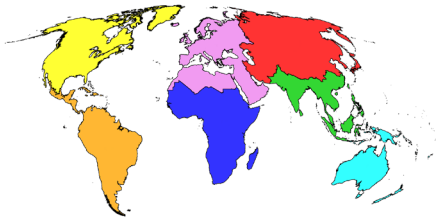
vs.

Dispersal



Doré et al., *in prep.*

Current diversity



Species richness of Ponerinae ants

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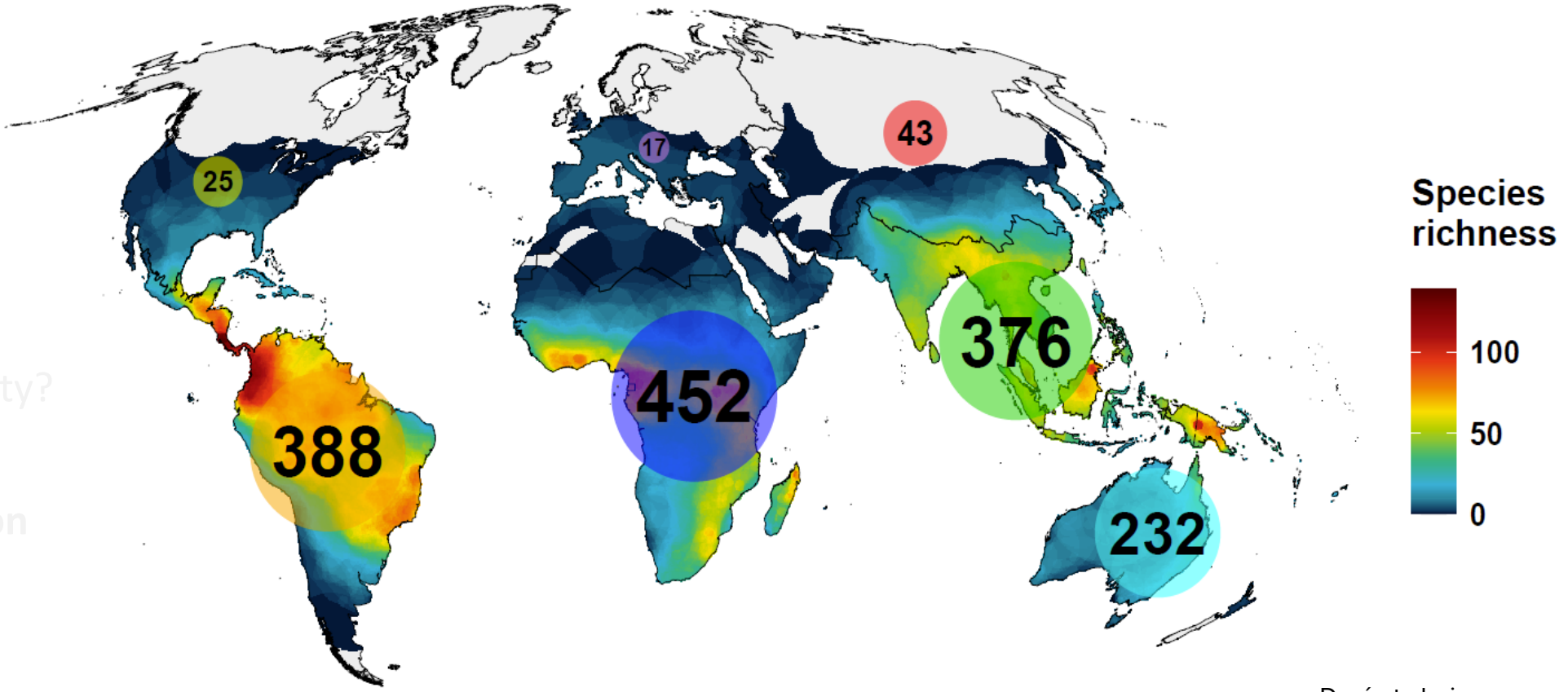

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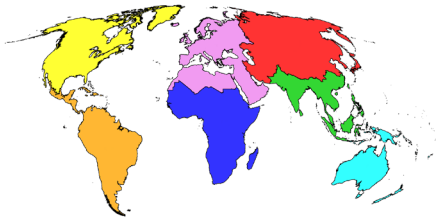

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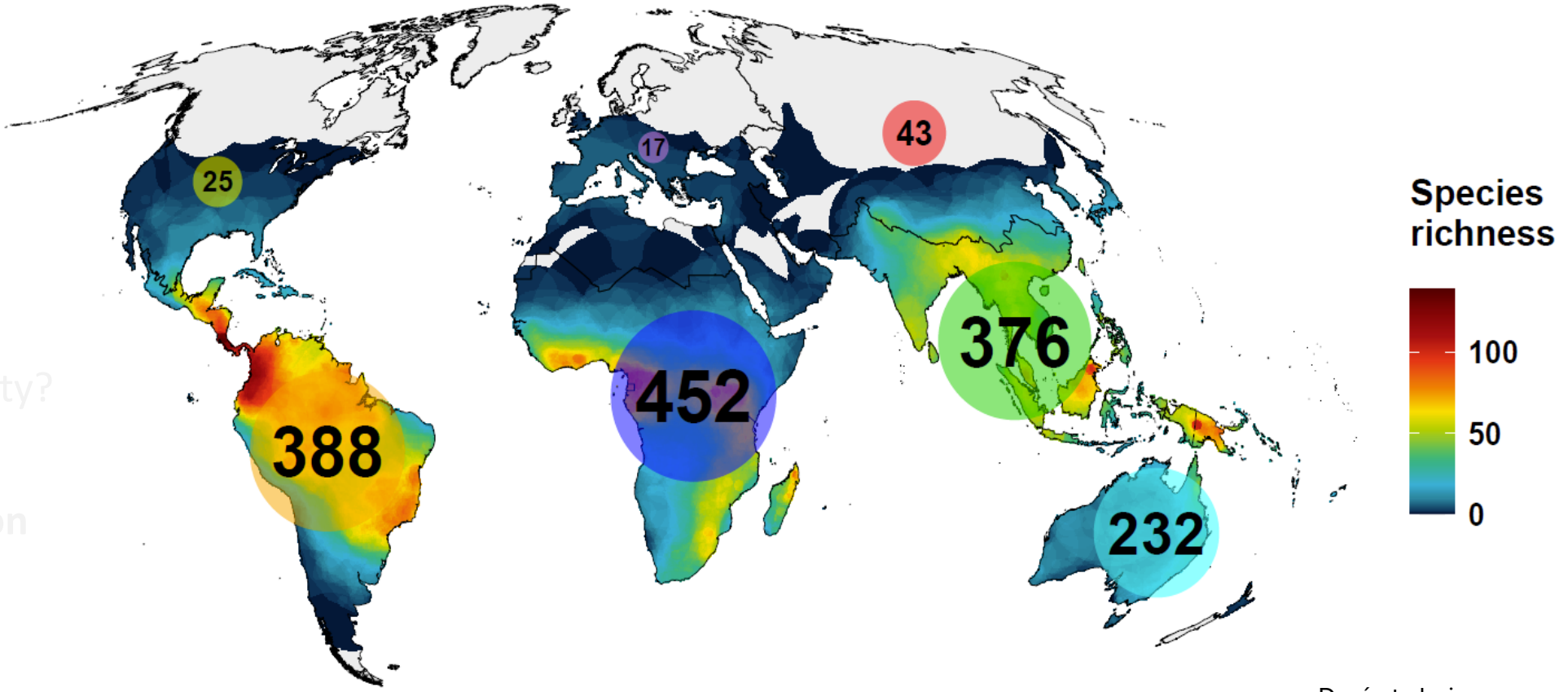

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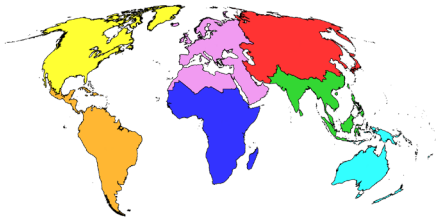

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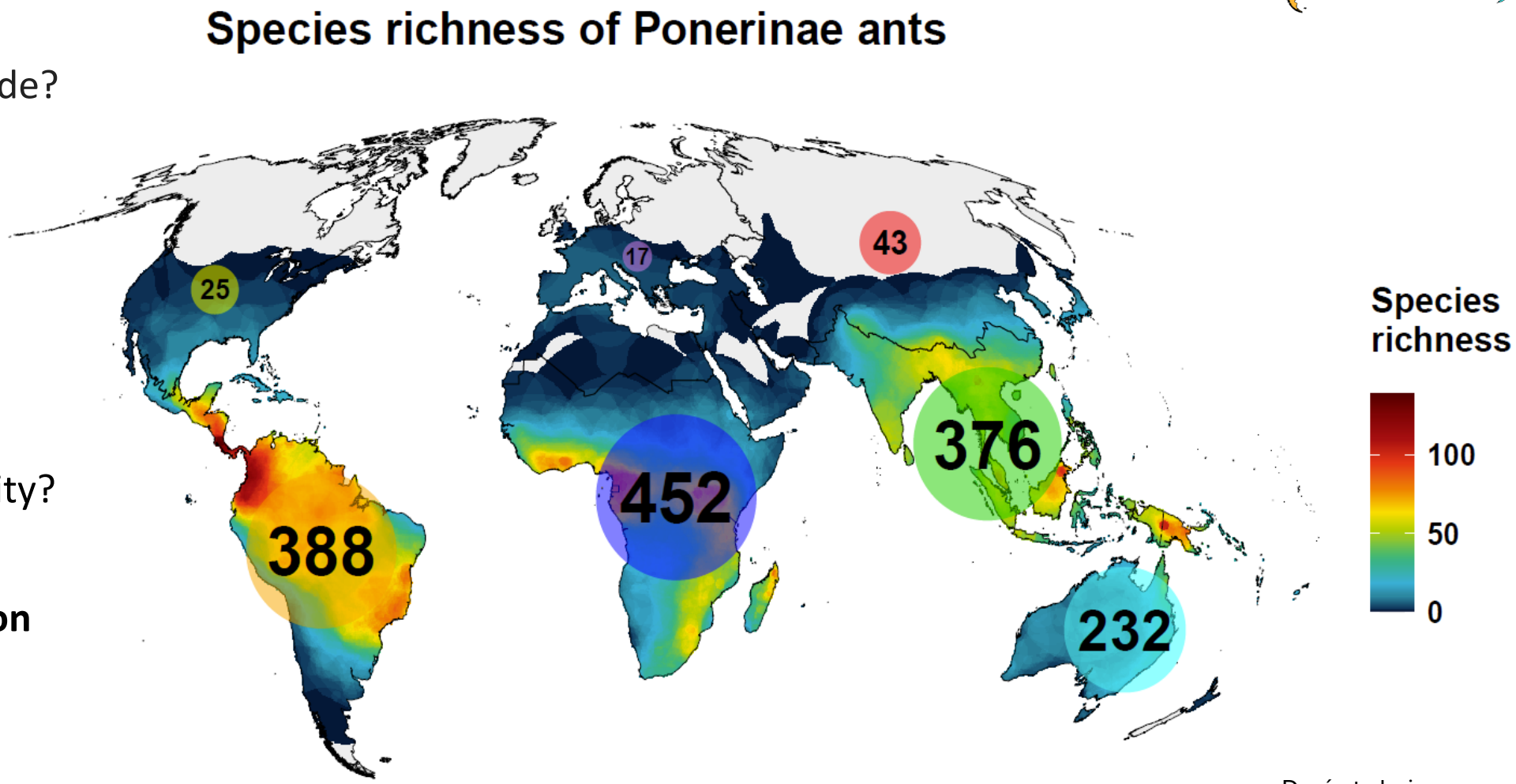

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Phylogenomic methods

Taxa sampling: 789 species (51.4%)
among all 50 Genera (100%)

Molecular data: 2,365 **UCE loci** = 1.05 M sites

Phylogenetic inferences: ML in **IQ-Tree**
with **SWSC partitioning**

Sensitivity analyses:
Inference method x Loci filtering x
Partitioning scheme x Divergence dating

Grafting of missing species:
Impute all 745 valid species with no UCE data using
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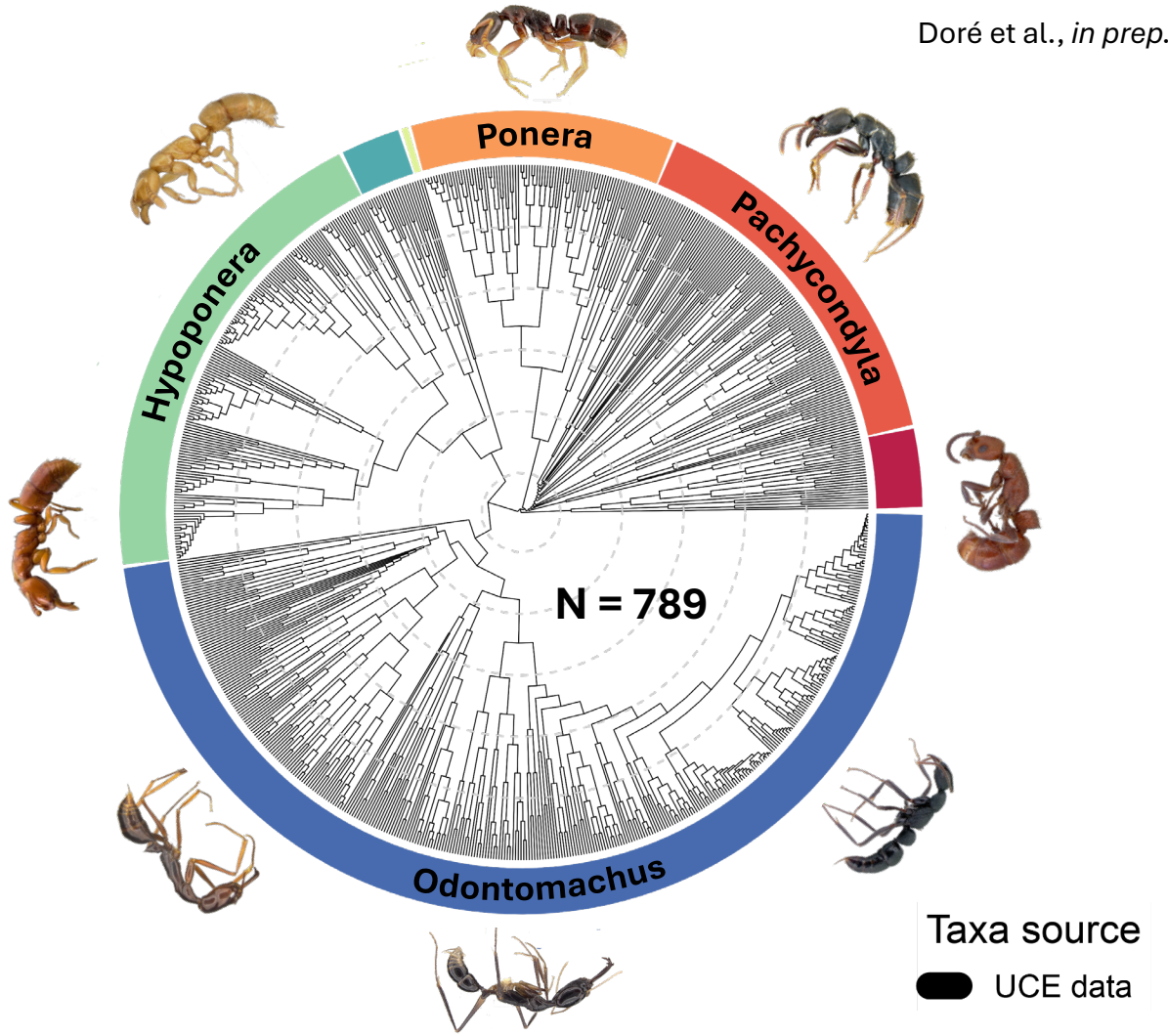

New species-level phylogeny for Ponerinae

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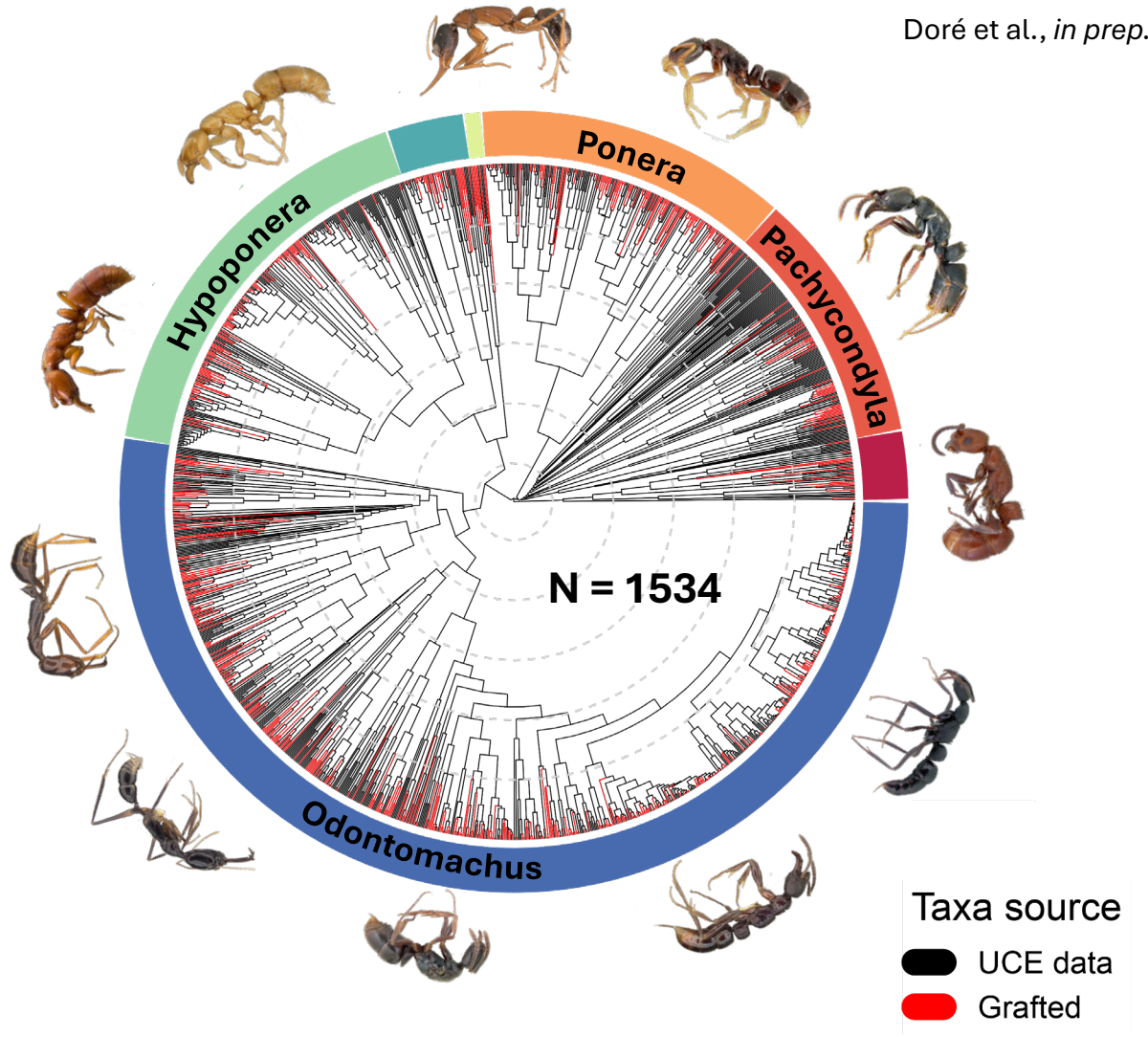

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Biogeographic data

Occurrence sources:

- AntWeb (62,301 records)
- GABI/AntMap (93,557 records)

Bioregions as defined in AntWeb

Data curation:

- Automatic and visual checks
  - *CoordinateCleaner* (Zizka et al., 2019)
- Geogazeeting
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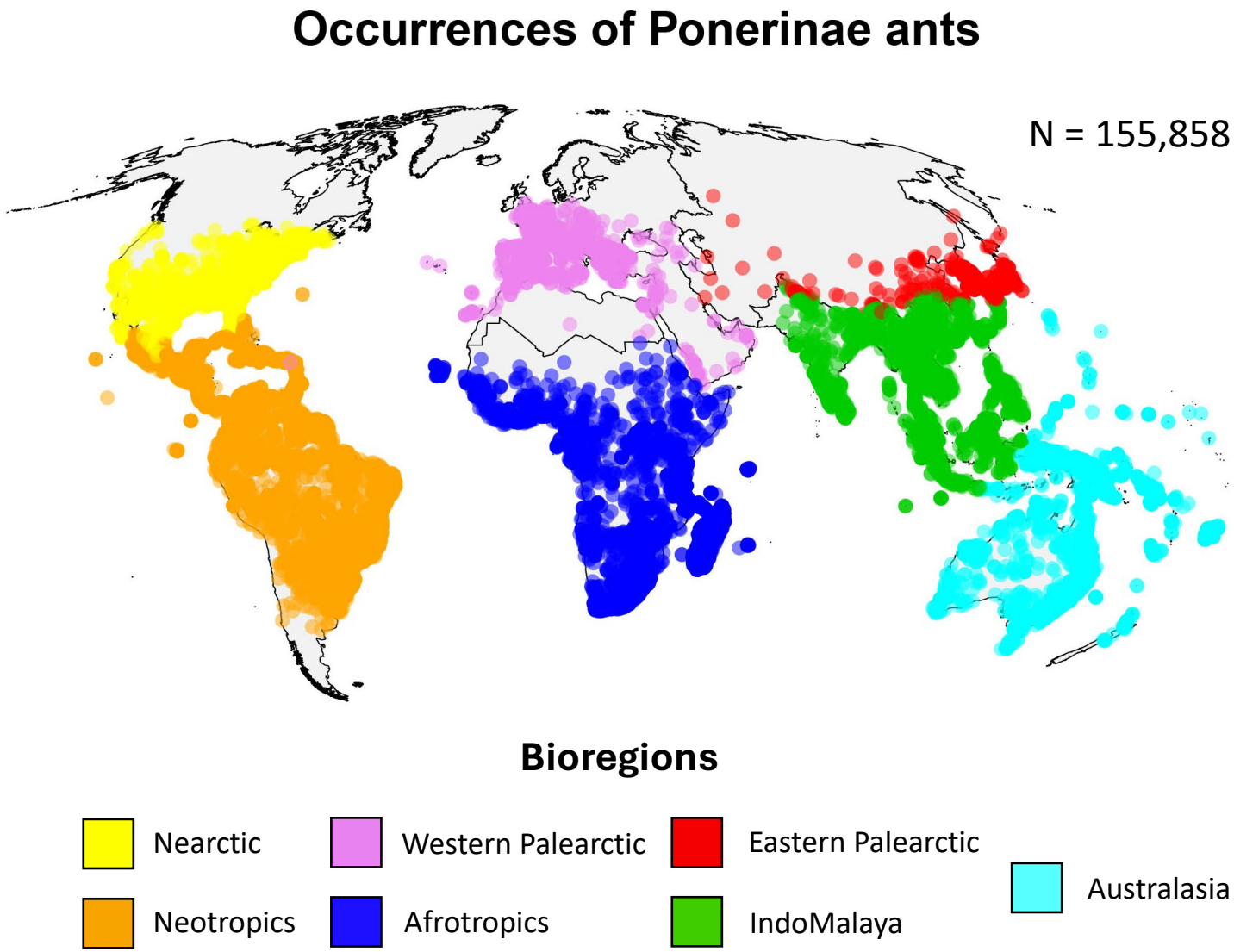
- Accuracy estimates

Final database: 155,858 records

- 105,574 records from **GPS**
- 50,284 records from **locality**



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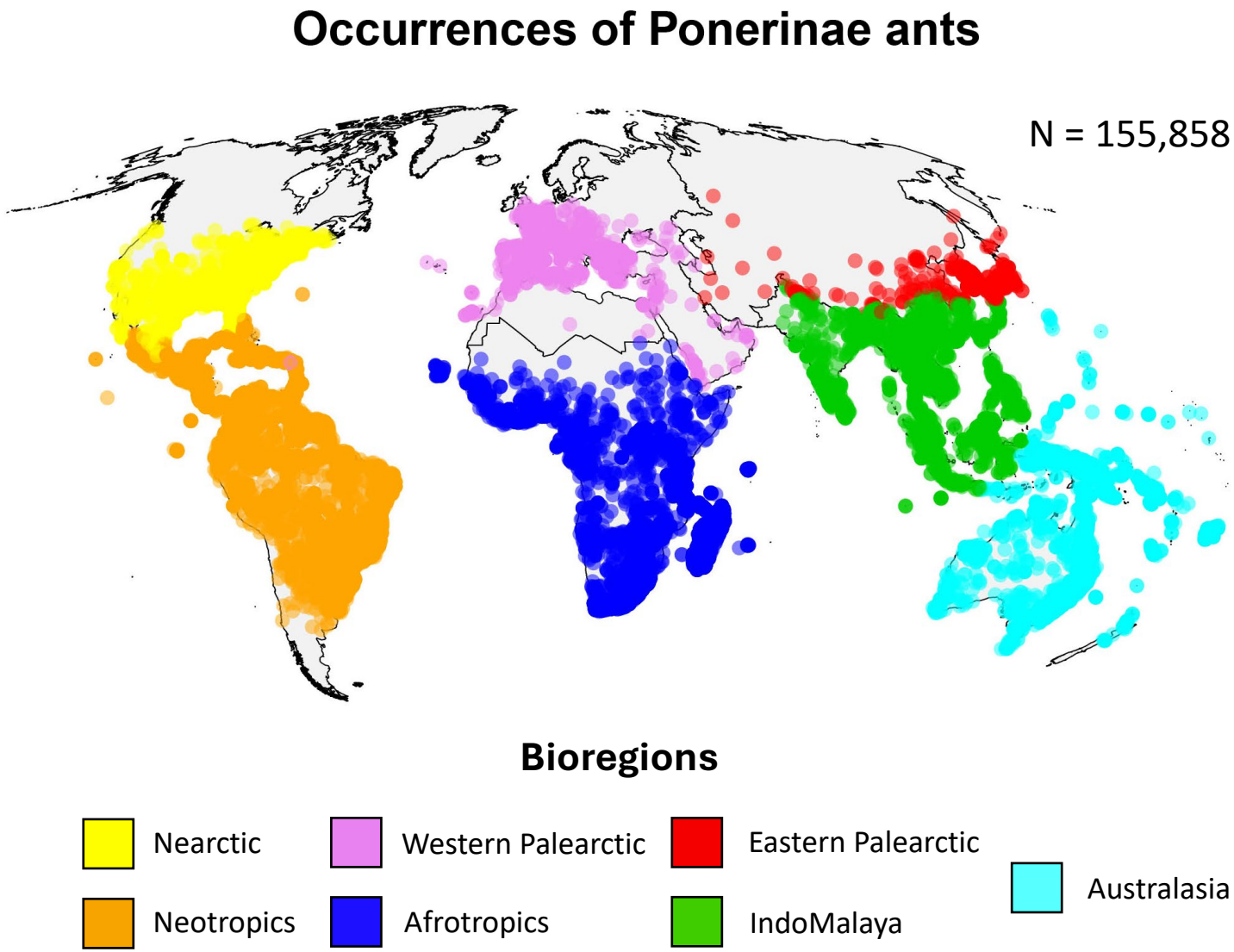
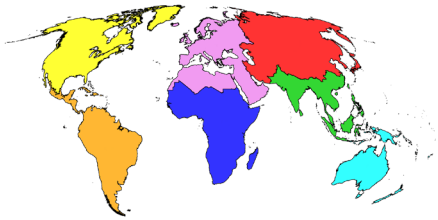


Biogeographic methods



BioGeoBEARS framework:

- DIVALIKE, DEC, DIVALIKE + J, DEC + J
- Model selection based on AICc
- Best model = **Time-stratified DEC + J**

Model of **continental connectivity**

Ancestral Range Estimates (ARE):

- Marginal likelihoods of node ranges

Biogeographic Stochastic Mapping (BSM):

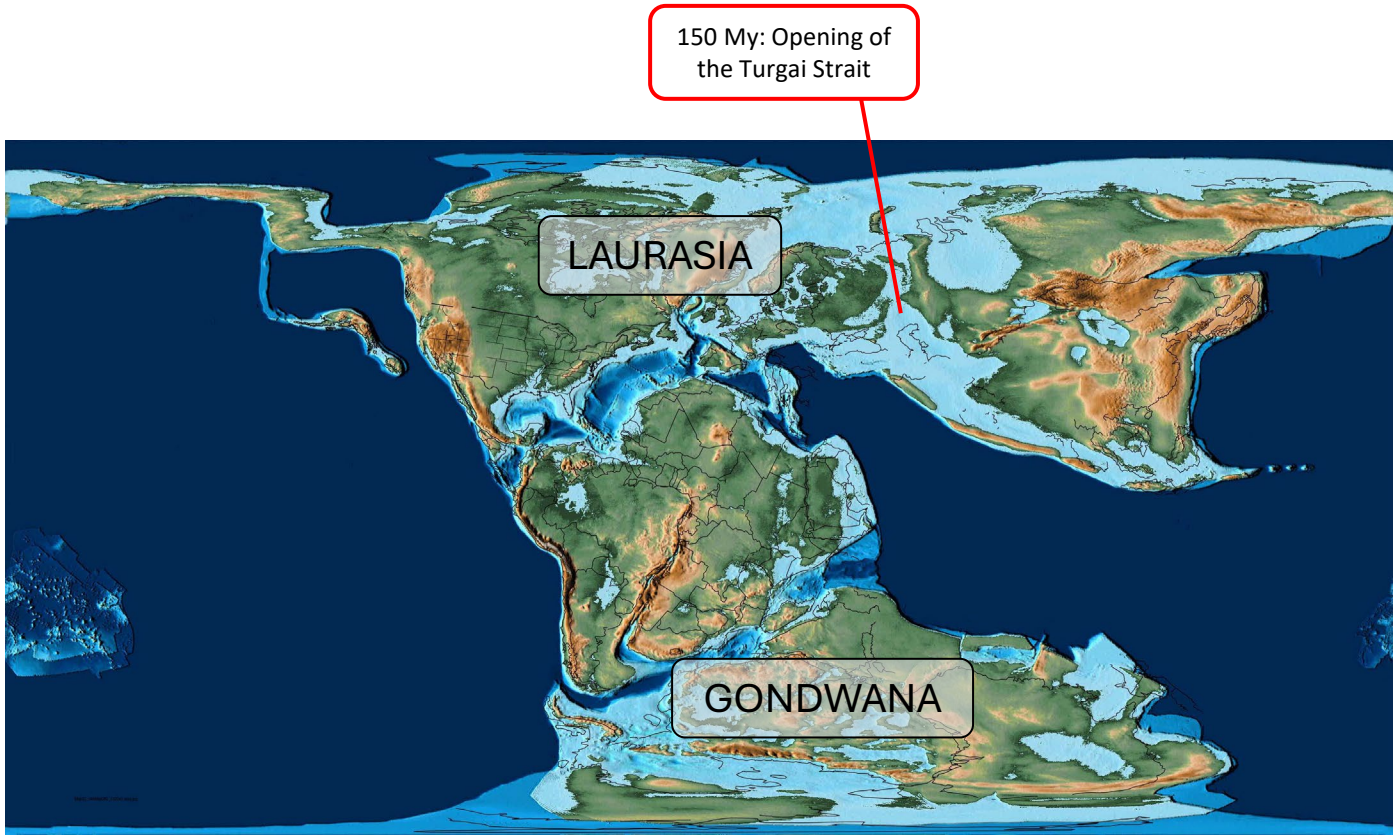
- Simulation of **biogeographic histories** compatible with ancestral ranges estimates
- Summary statistics across 1000 BSM

Model comparison

	DEC+J	DIVALIKE+J	DIVALIKE	DEC
logLk	-2154	-2205	-4391	-4467
# params	3	3	2	2
AICc	4313	4416	8787	8939
Δ AICc	**0**	103	4474	4626
Akaike weights	**100 %**	0 %	0 %	0 %
d	0.007	0.008	0.030	0.024
e	0.000	0.000	0.019	0.020
y	0.994	0.991	1.000	1.000
v	0.994	0.991	1.000	1.000
s	0.994	-	-	1.000
j	0.019	0.018	-	-

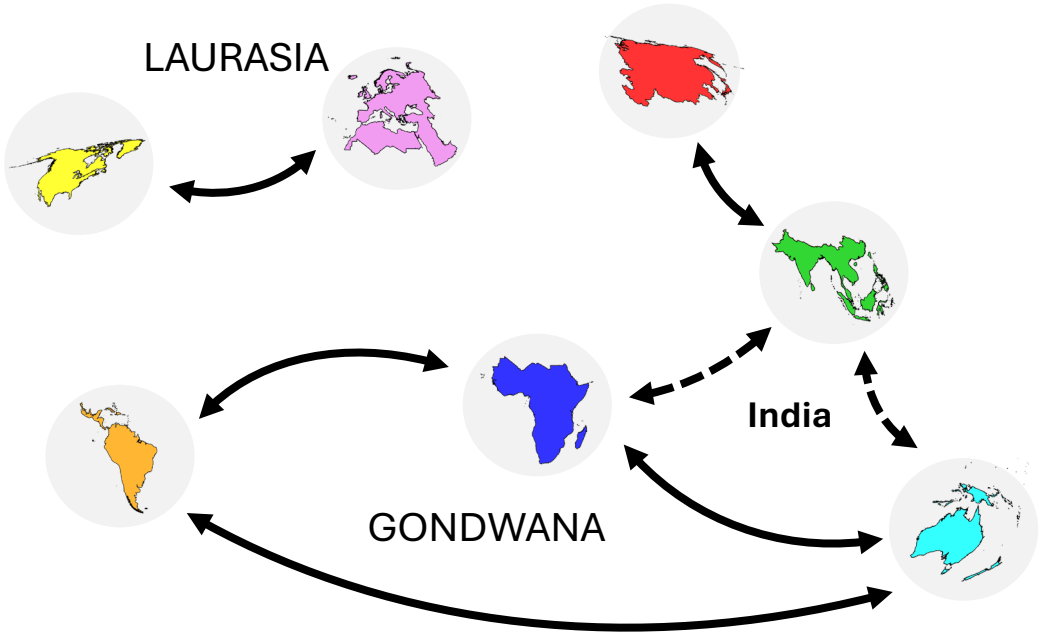
Doré et al., *in prep.*

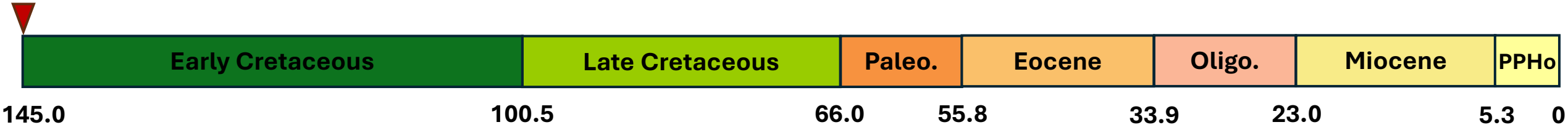
Biogeographic methods



Source: PALEOMAP Project by C. Scotese

Early Cretaceous
145.0 My





Biogeographic methods

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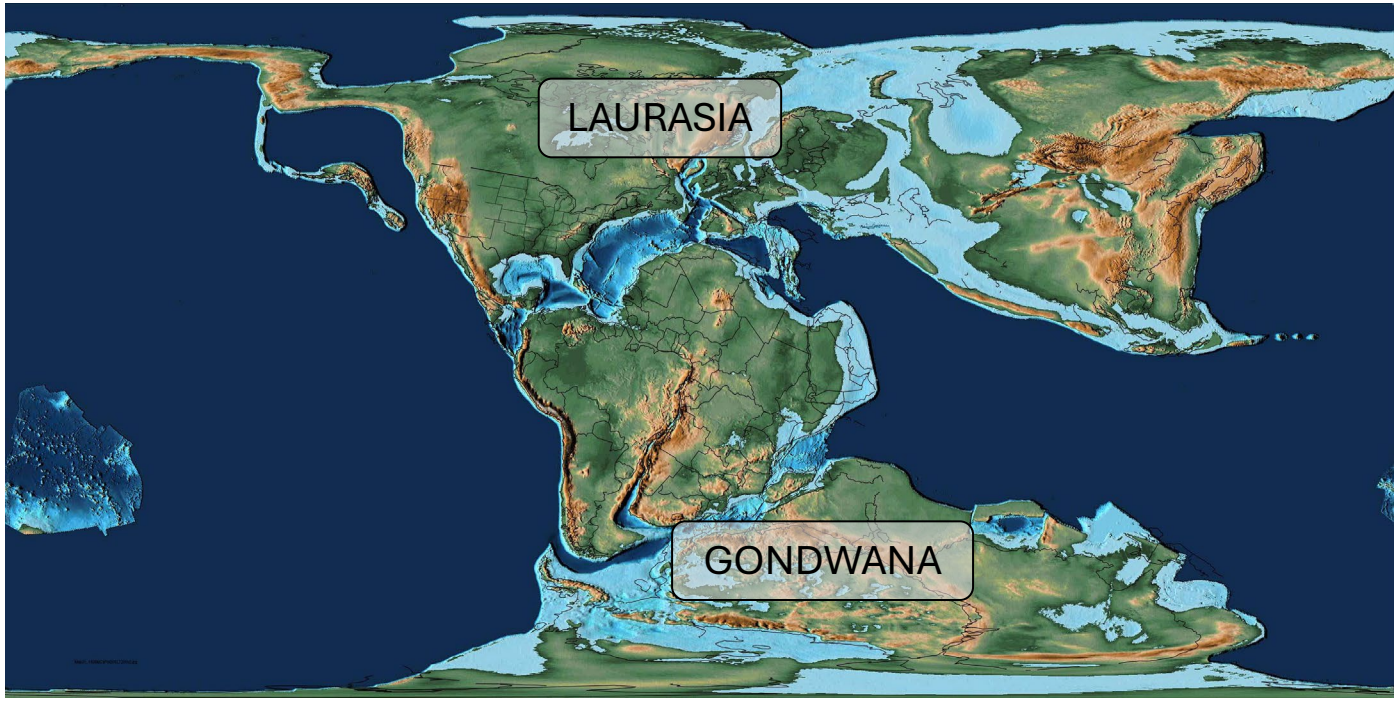
140.0 My



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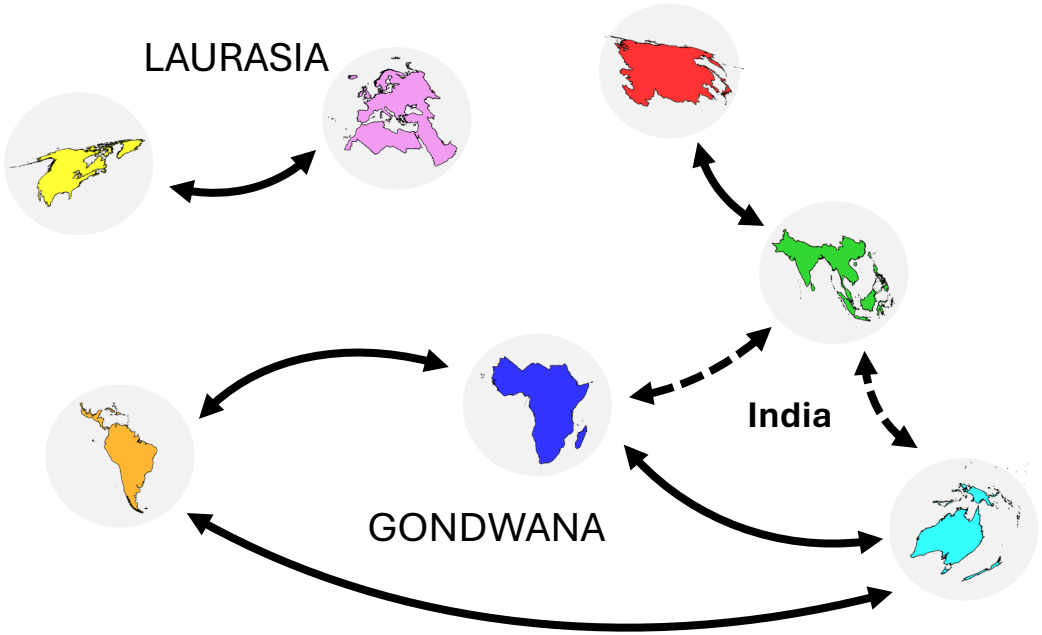

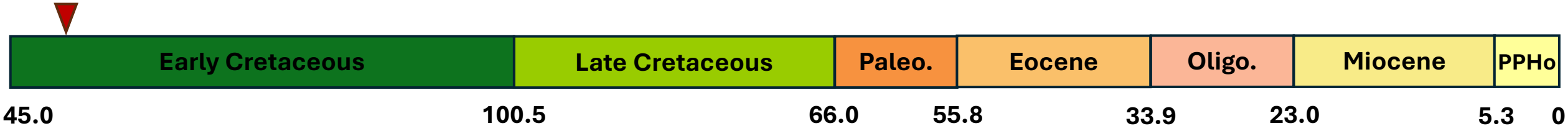

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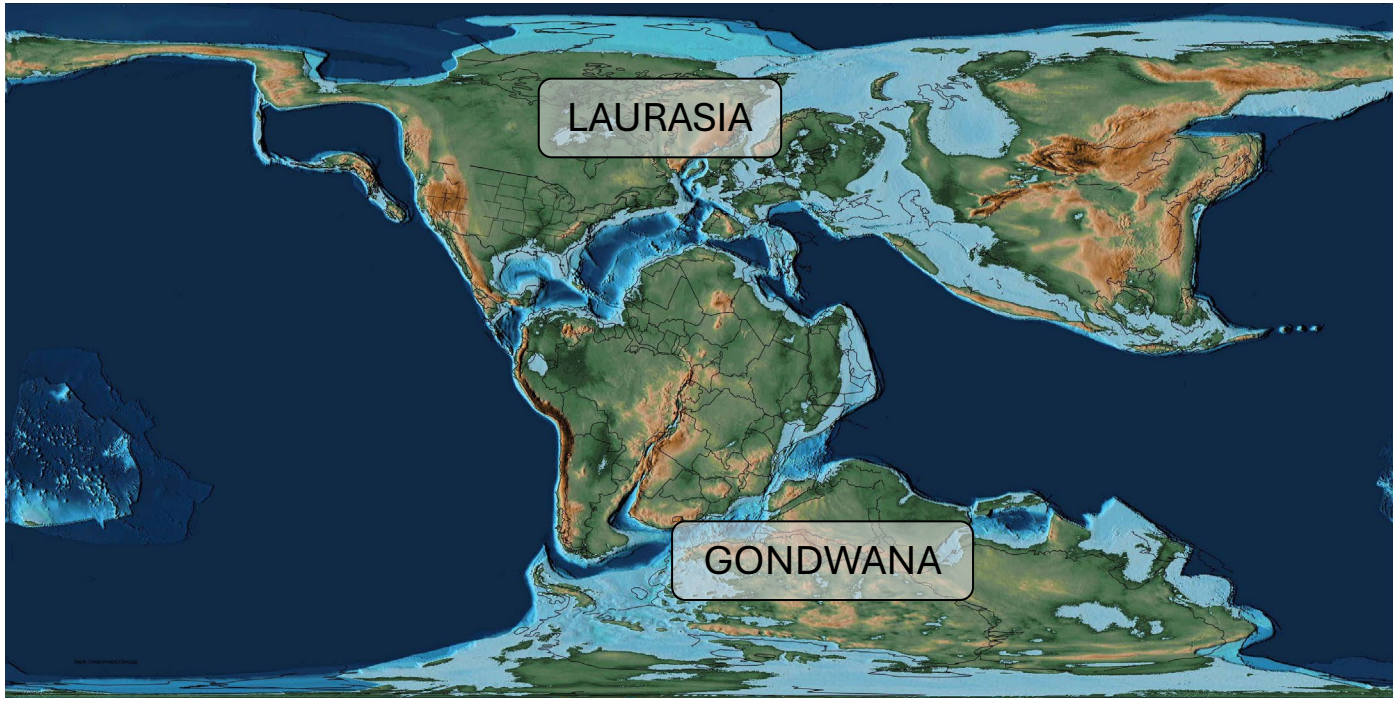
135.0 My



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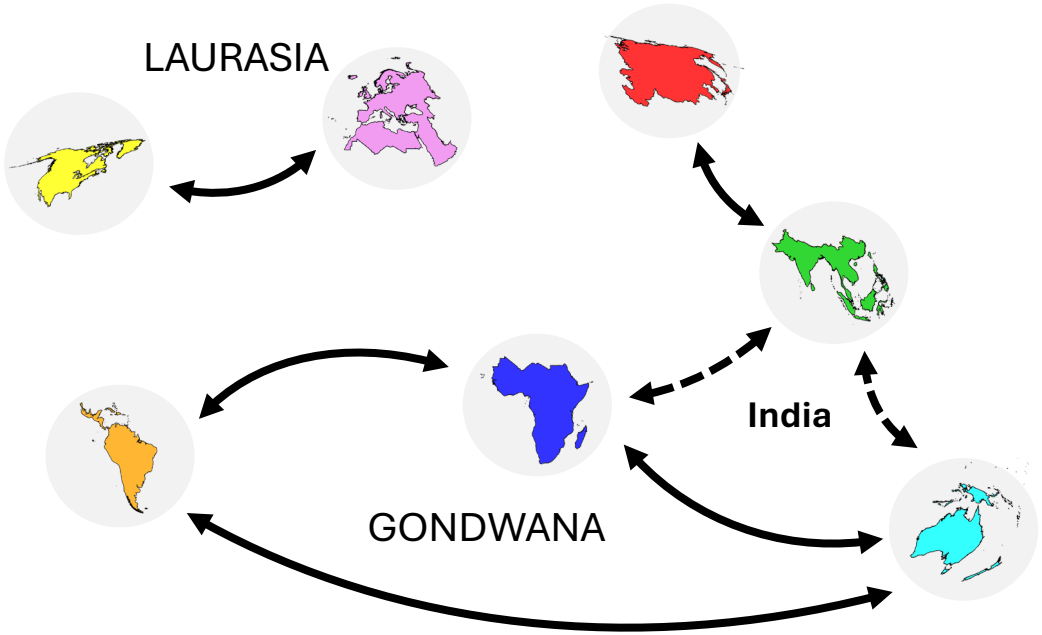

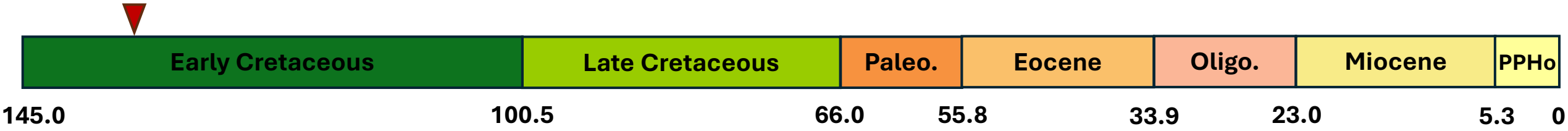

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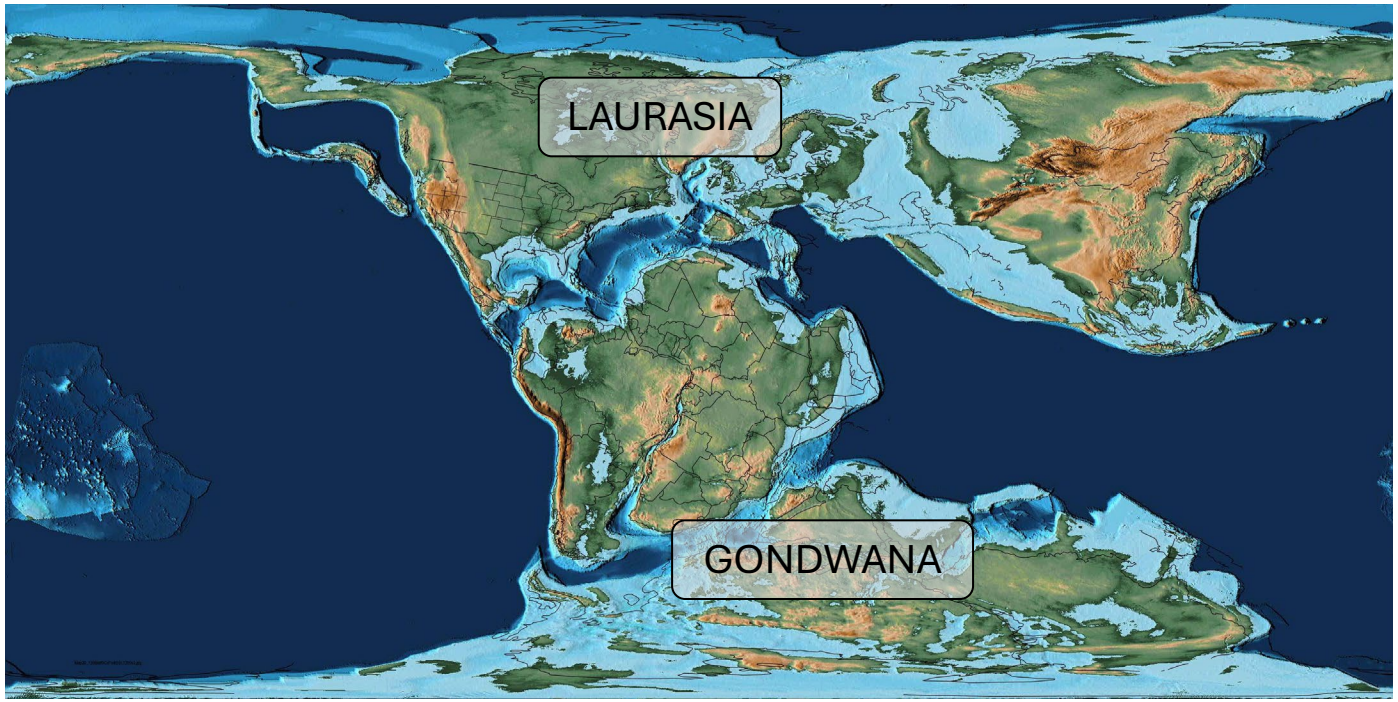

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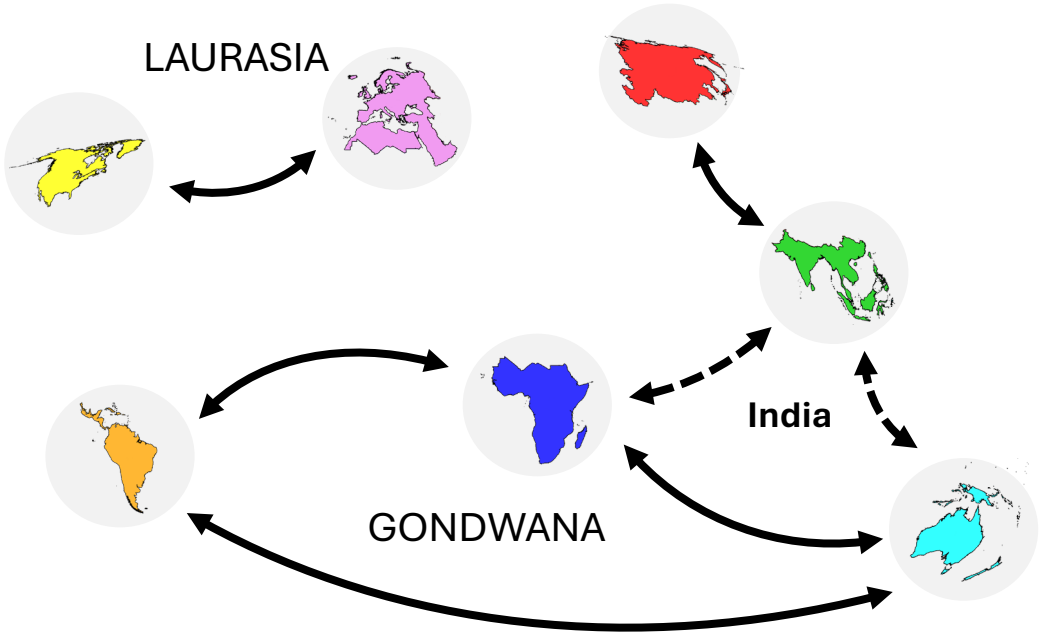

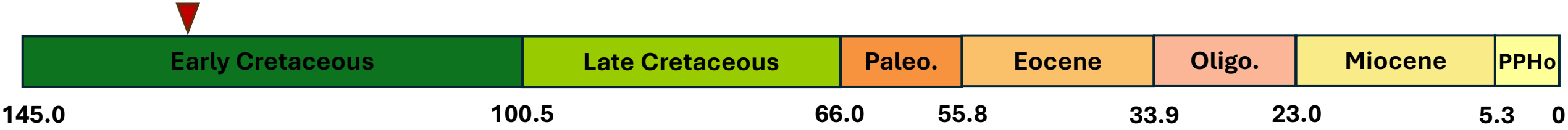

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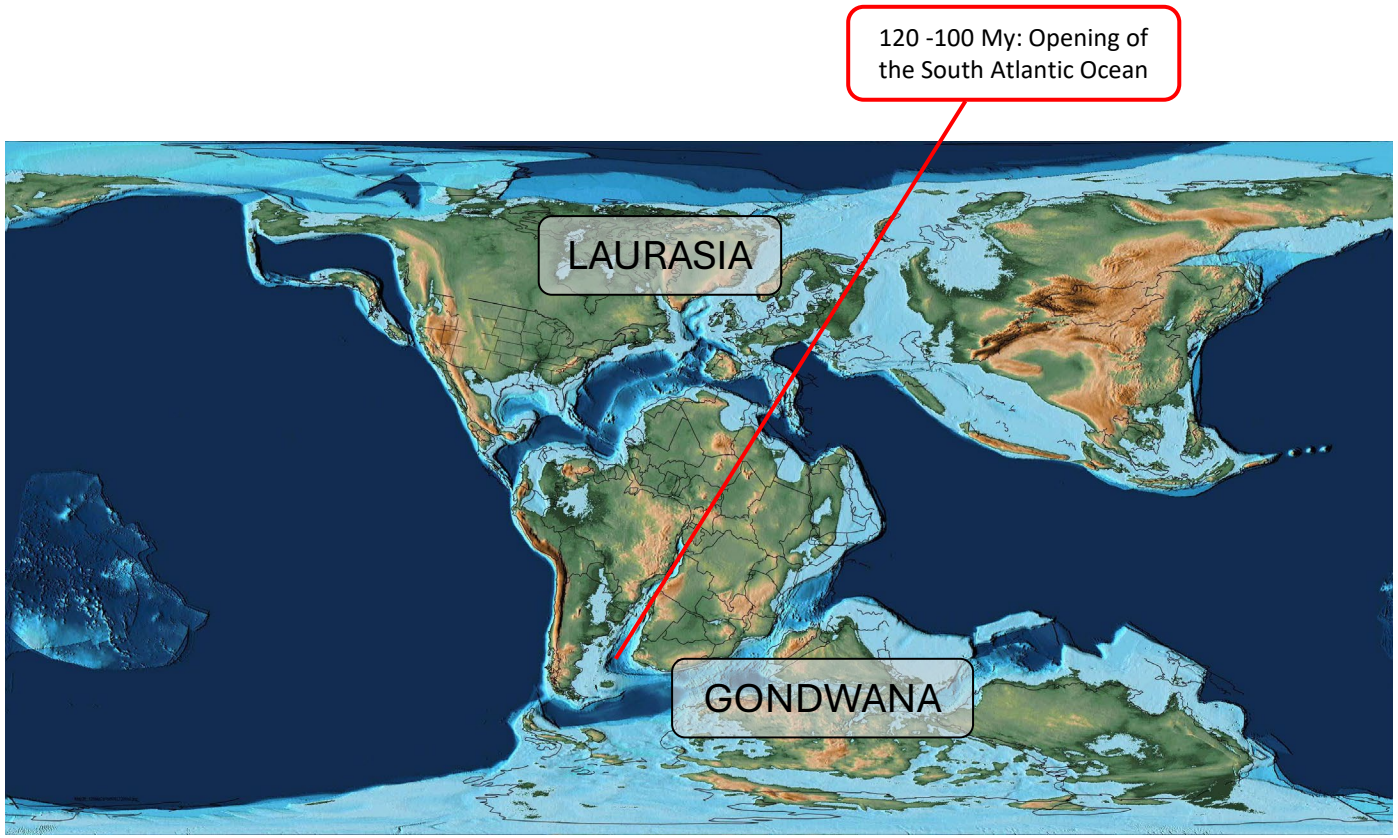

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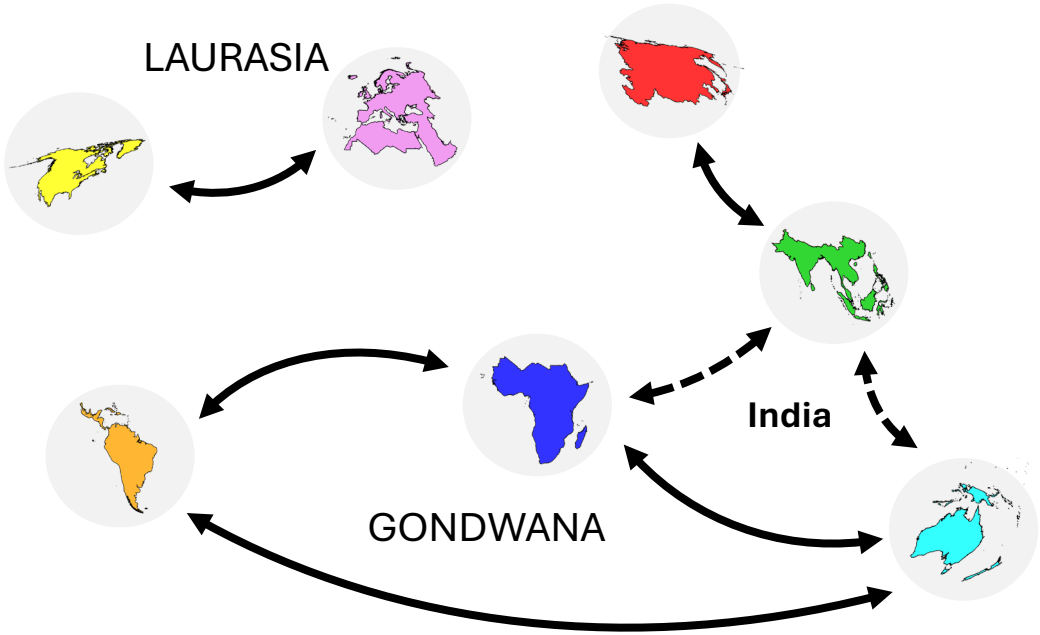
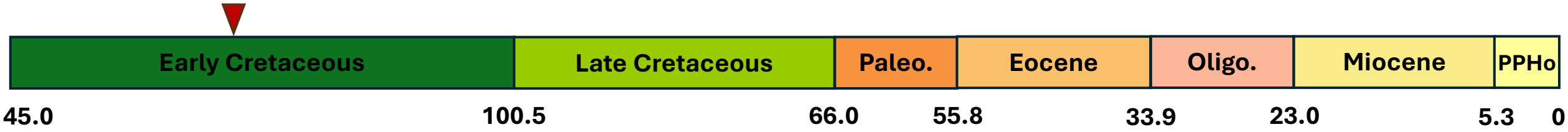
Early Cretaceous
125.0 My





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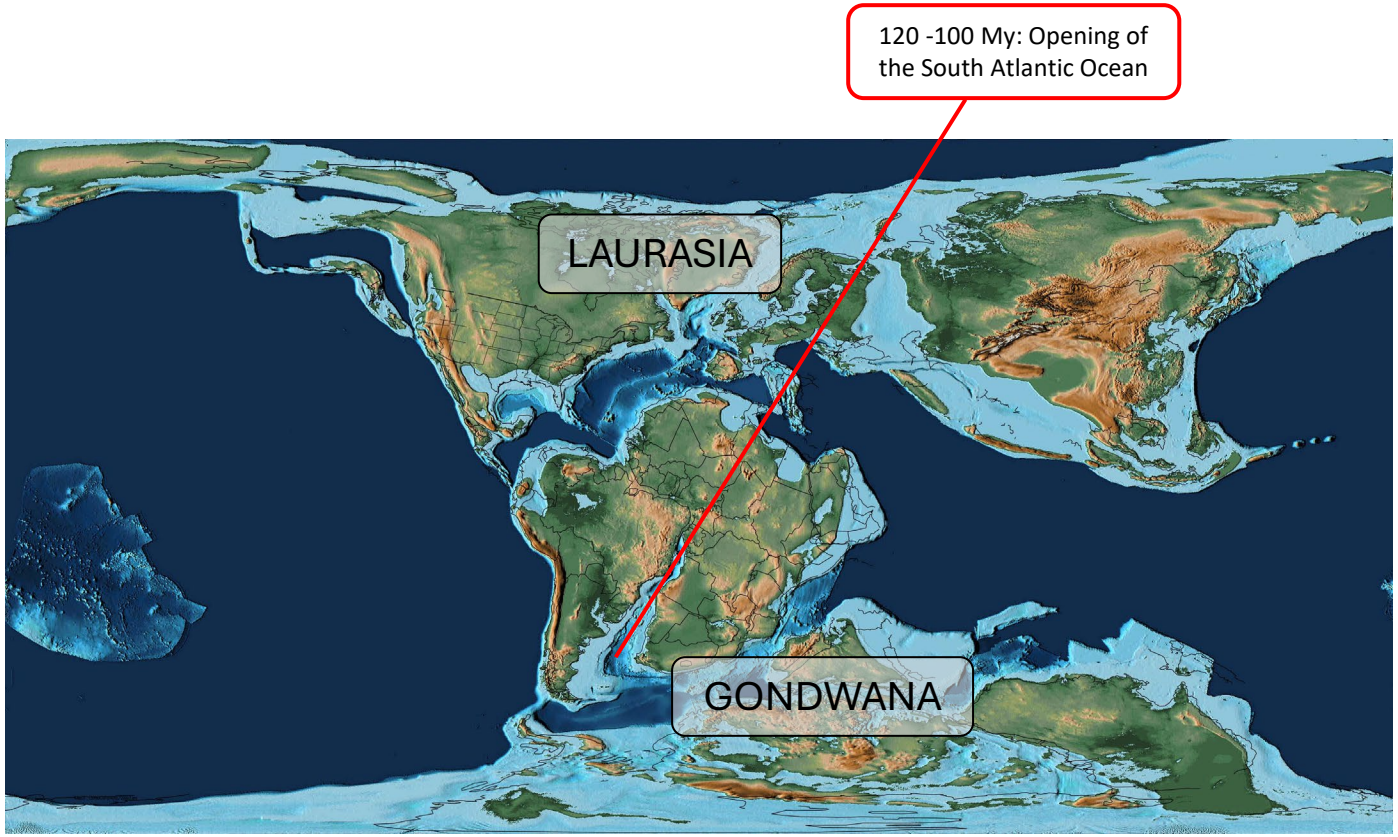

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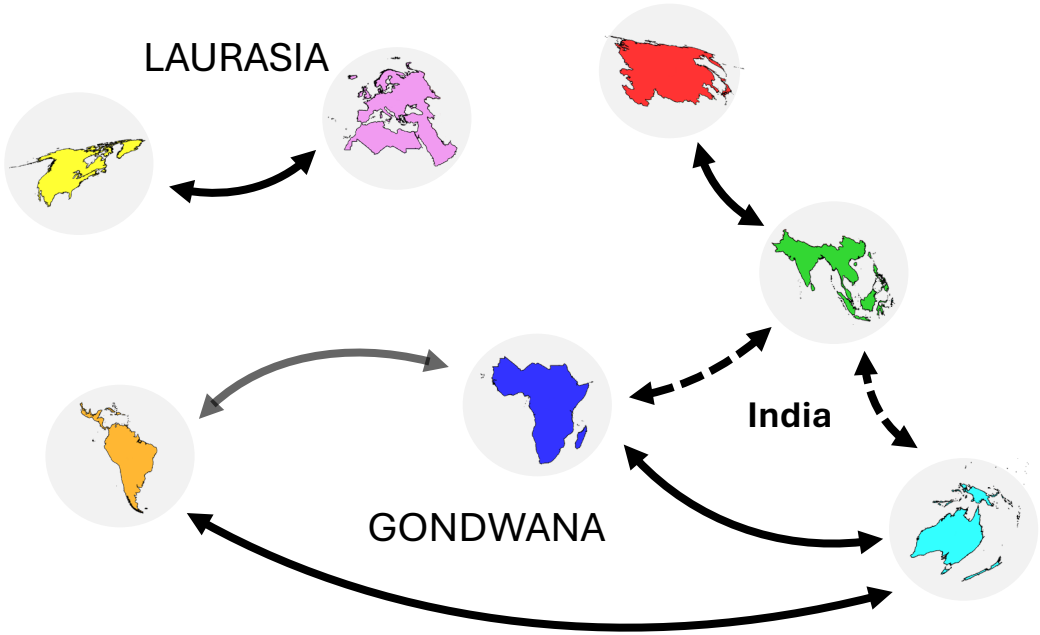

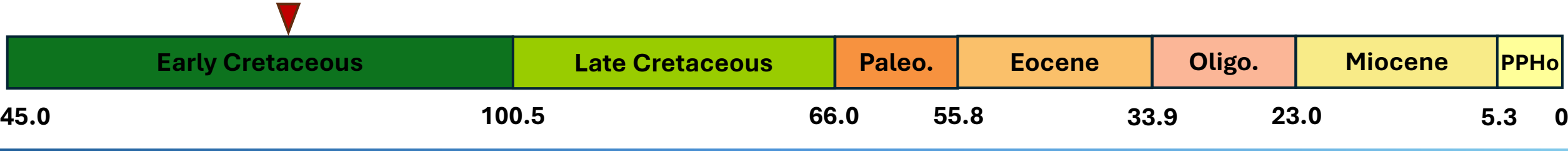

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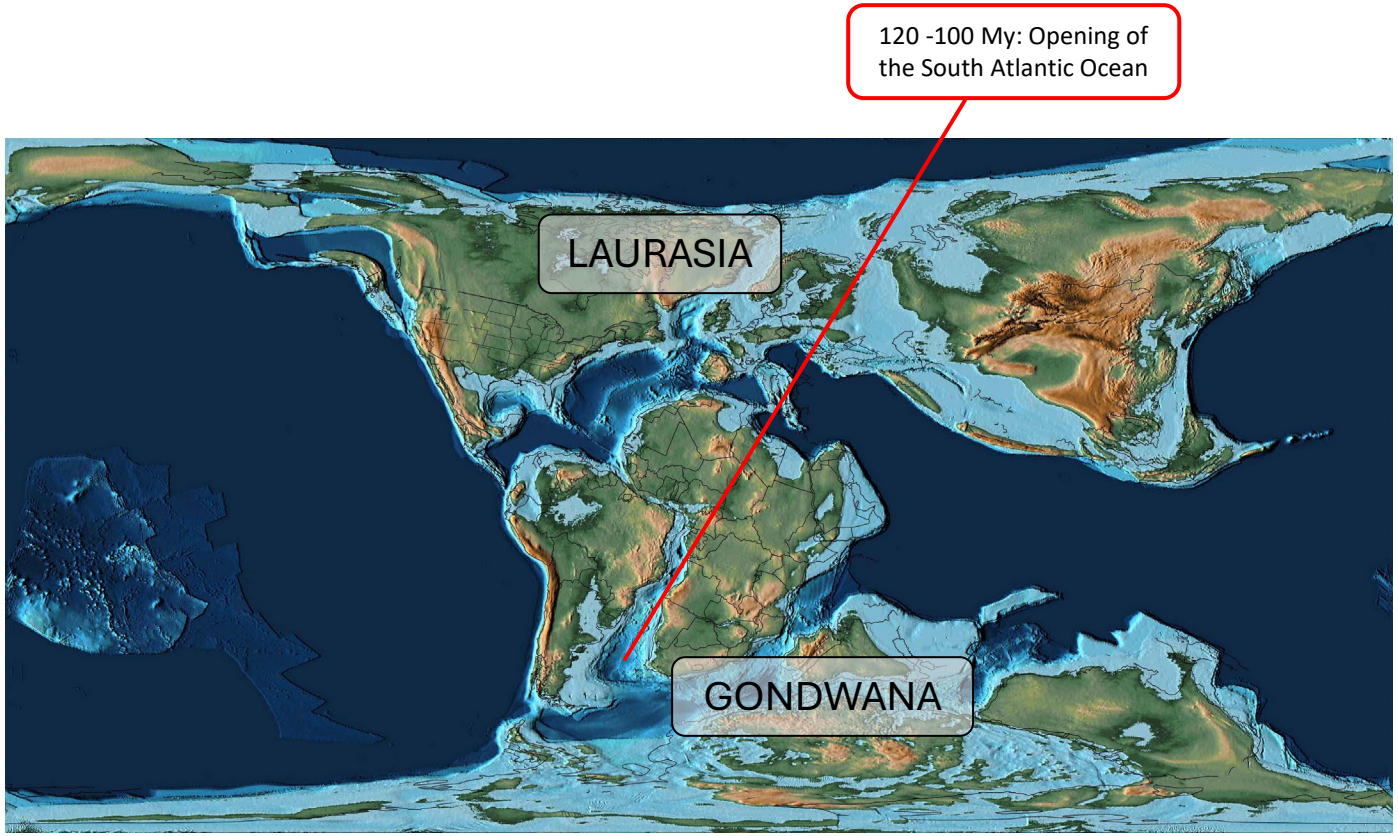

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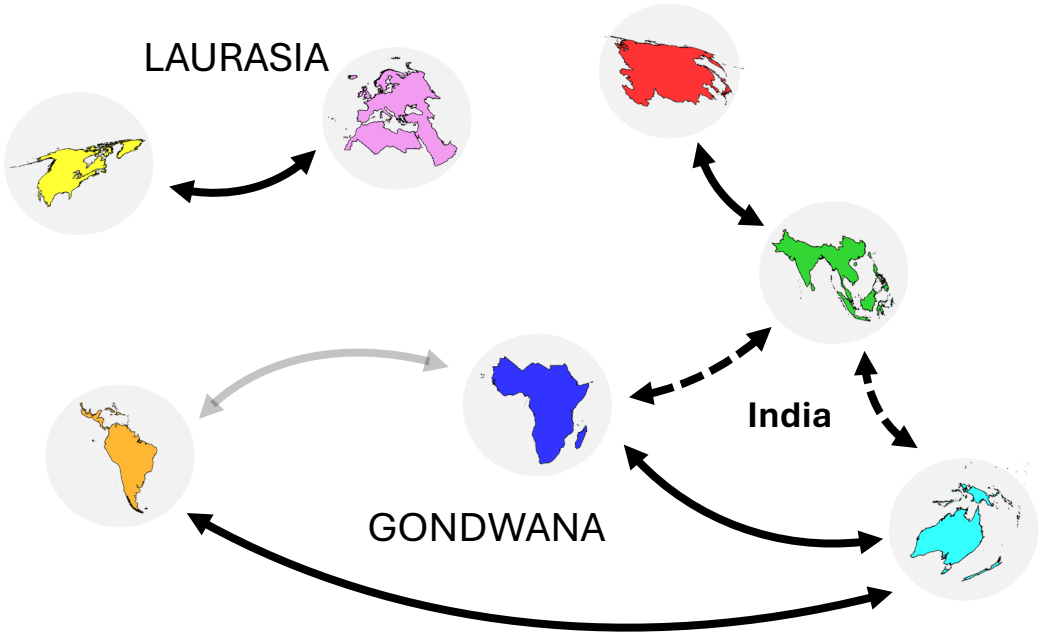

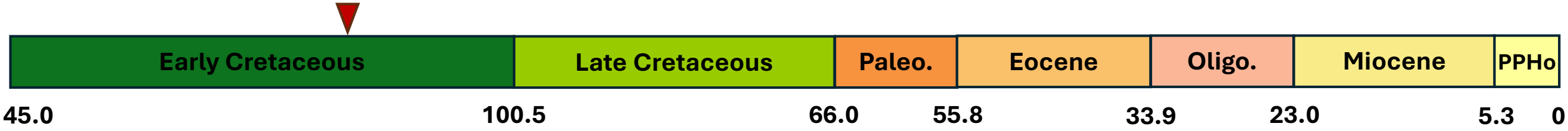

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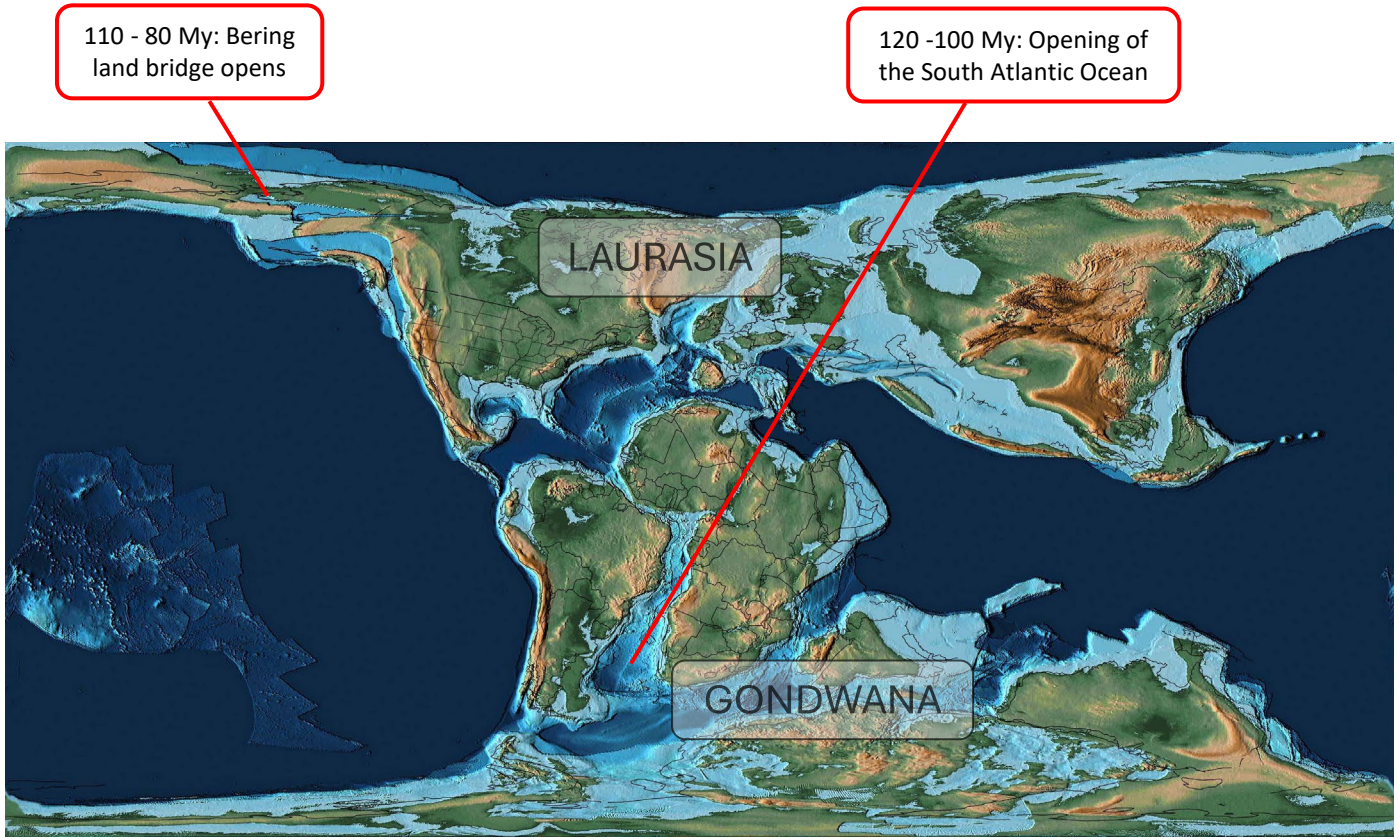

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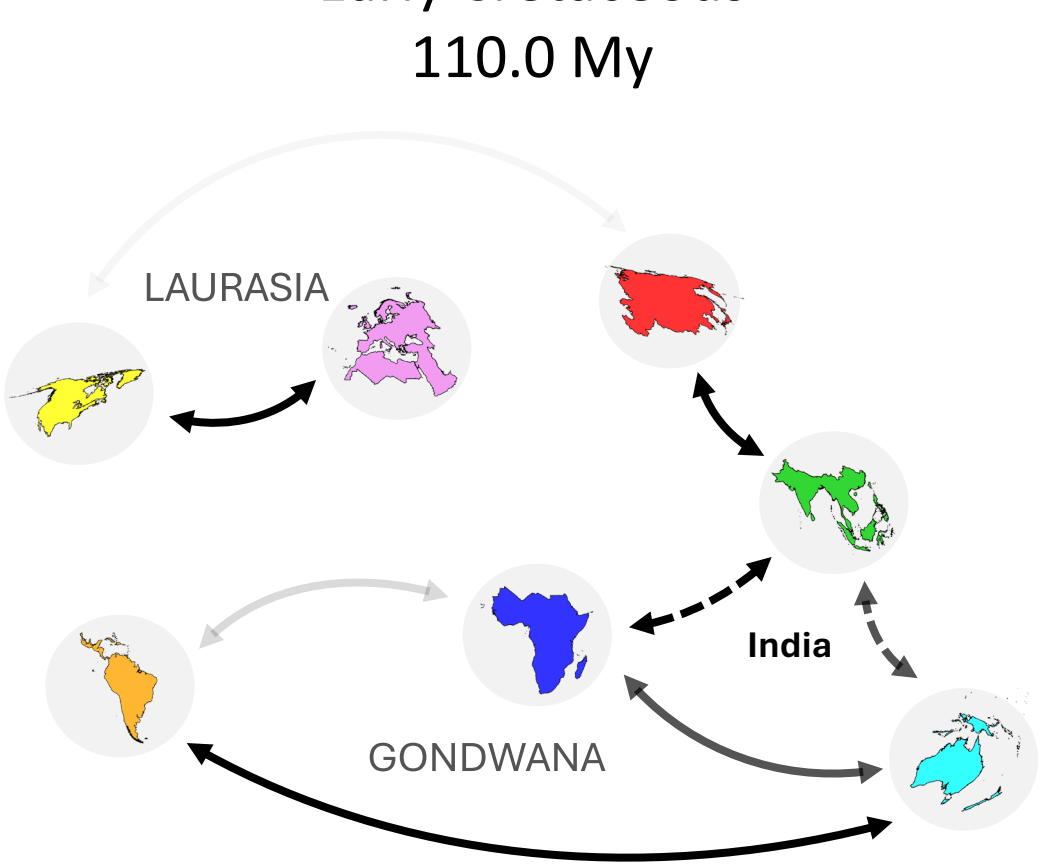

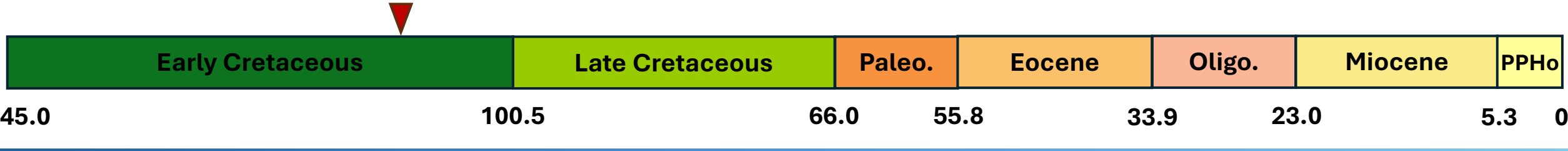

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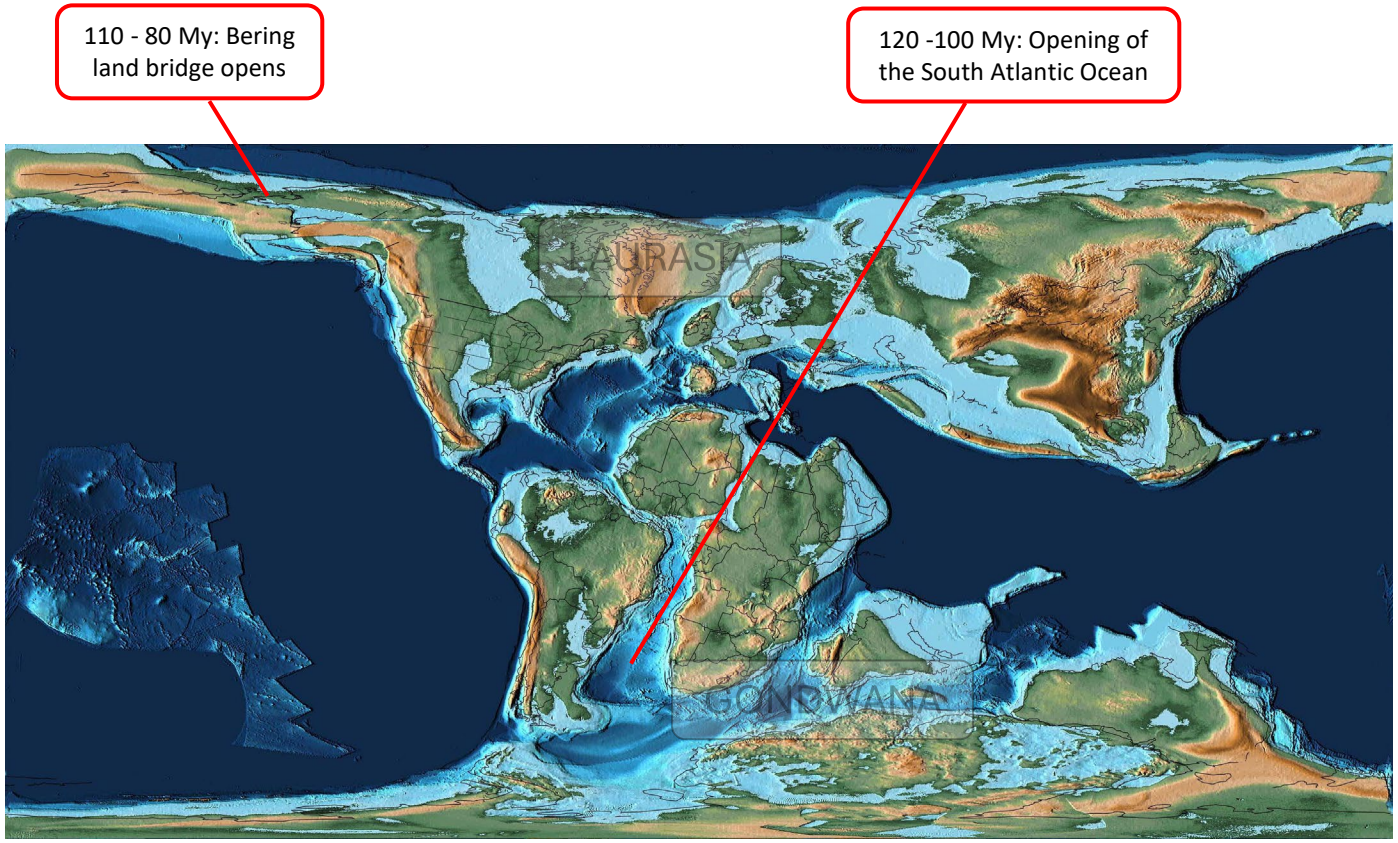

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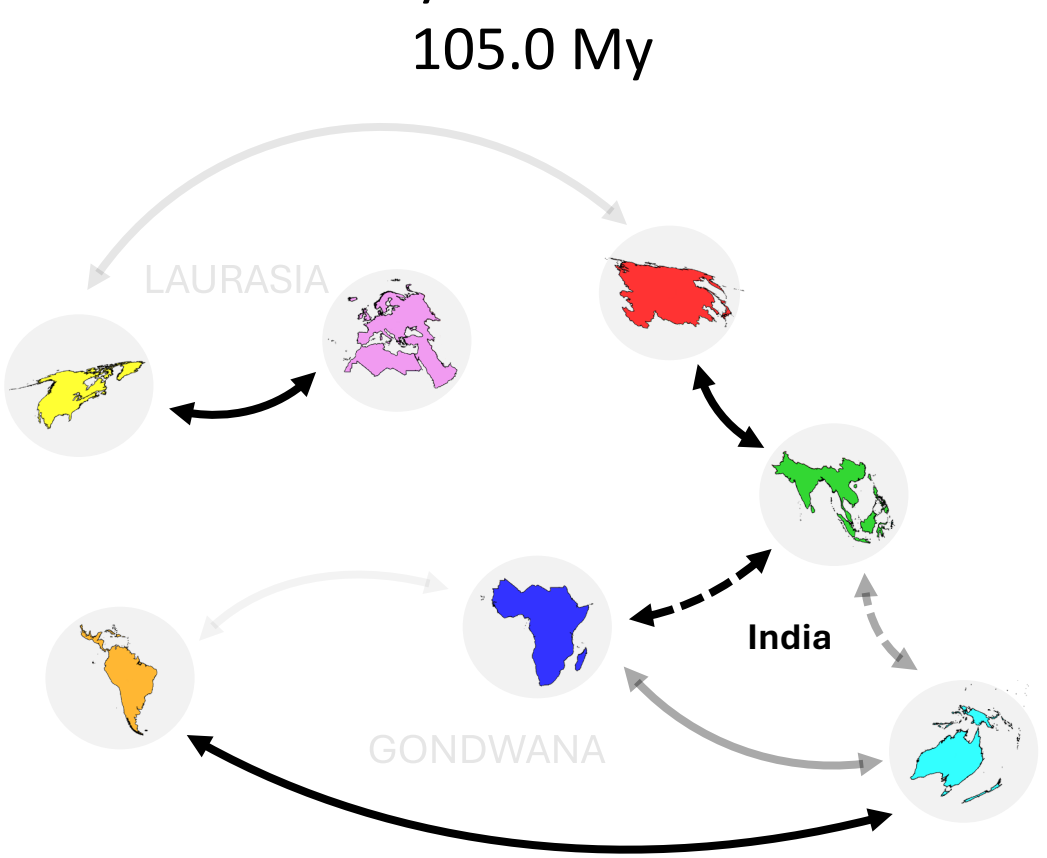

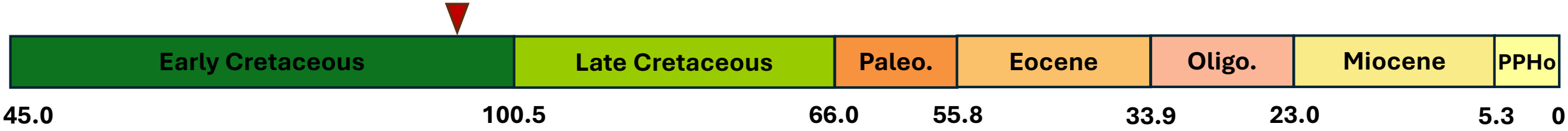

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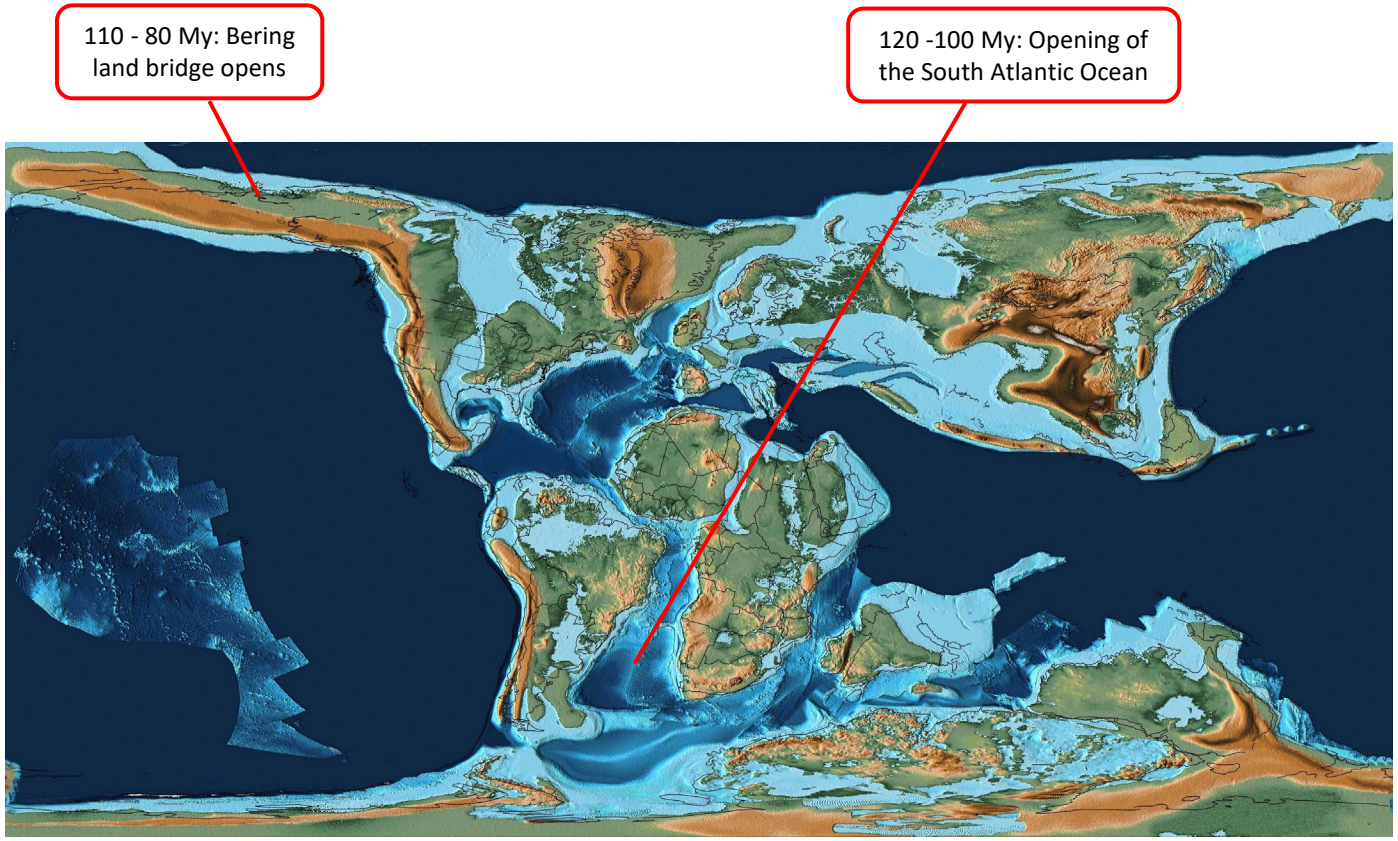
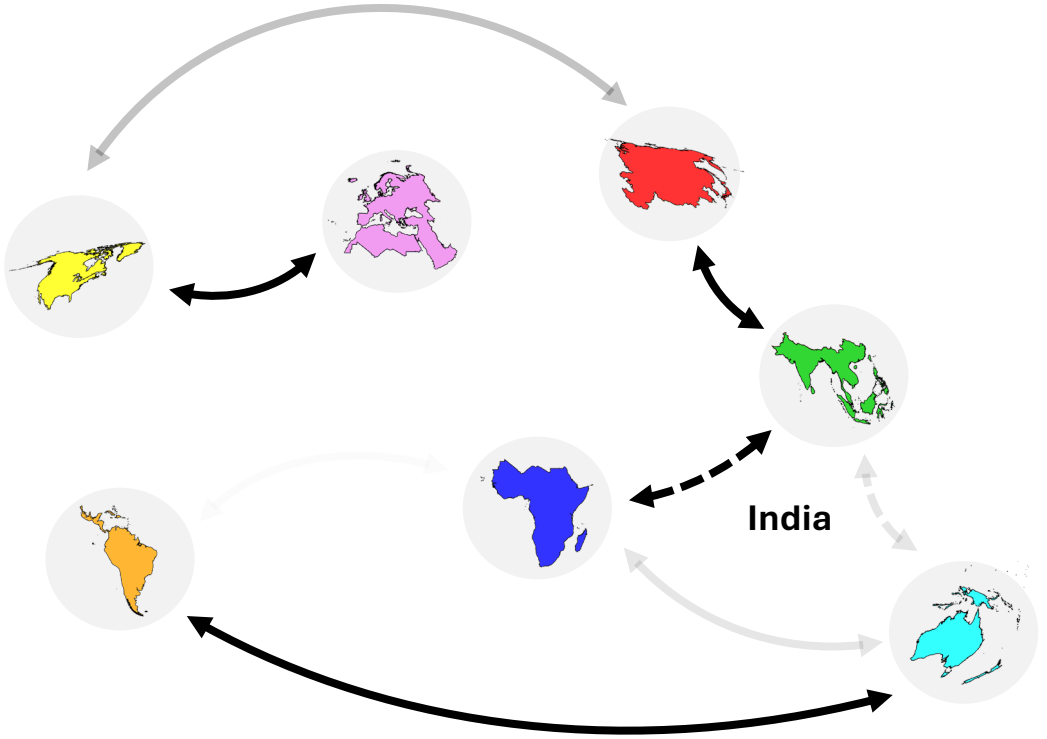
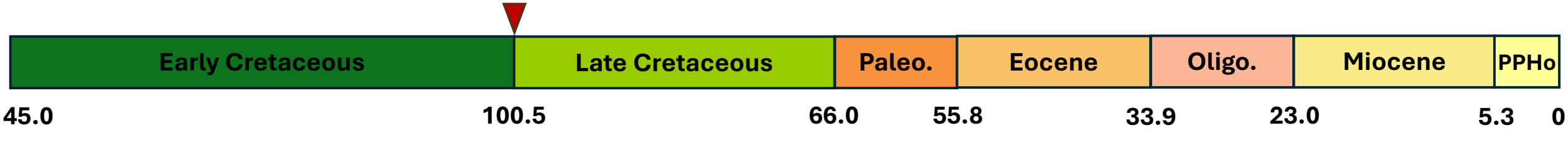


Source: PALEOMAP Project by C. Scotese

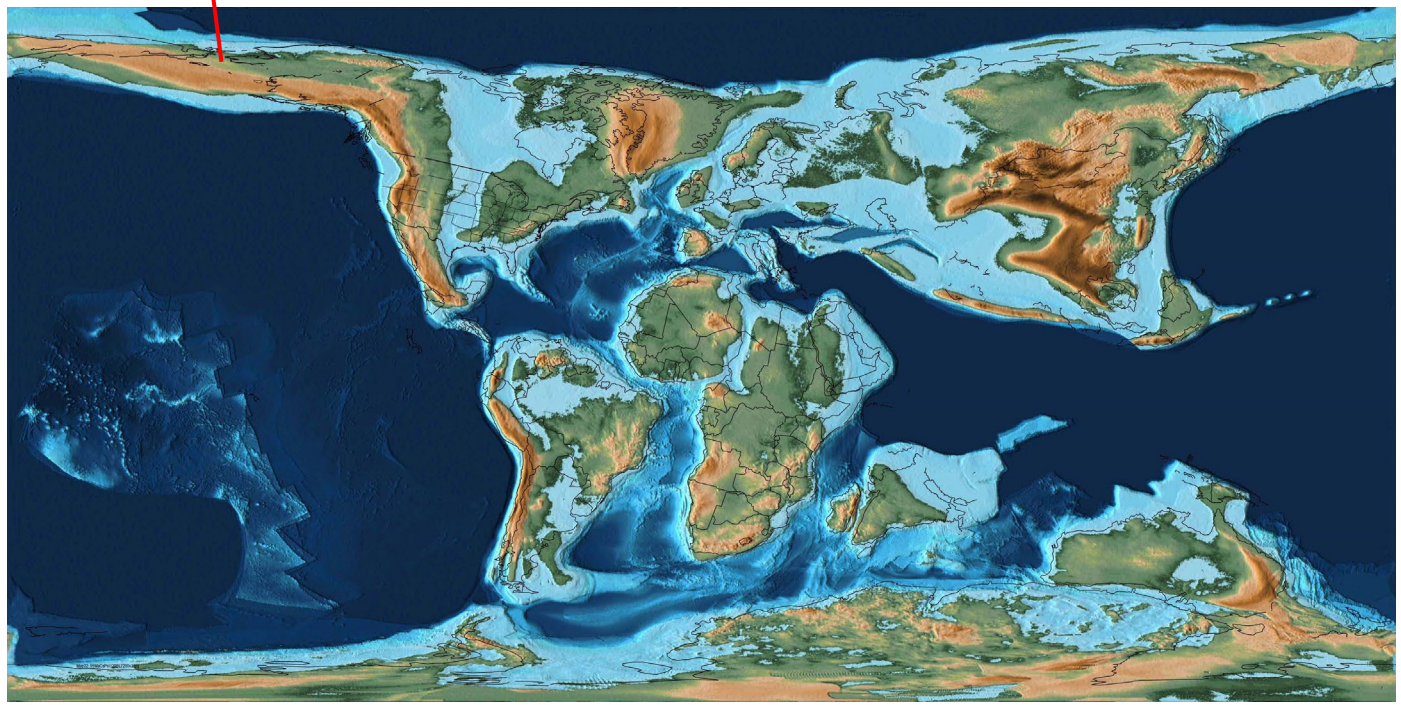
Early to Late Cretaceous
100.5 My





Biogeographic methods

110 - 80 My: Bering land bridge opens



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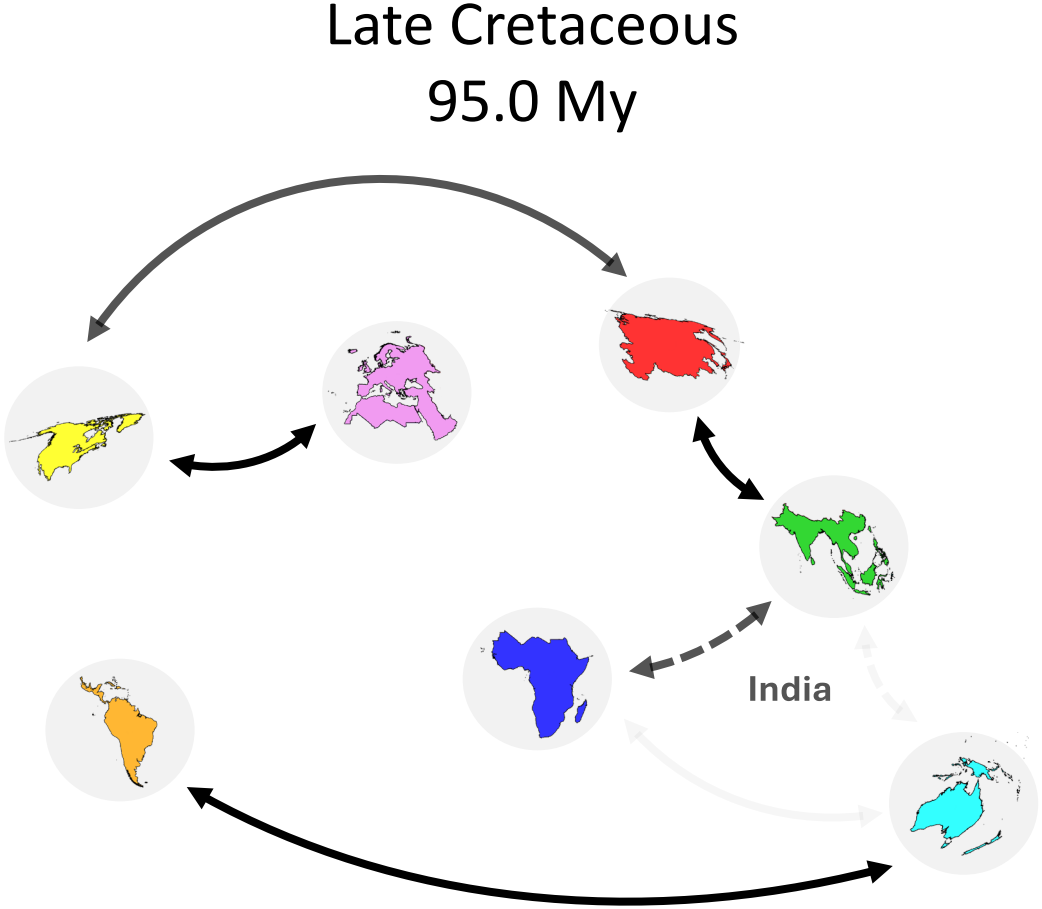
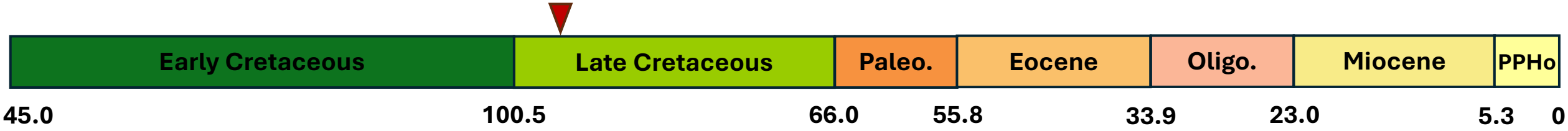
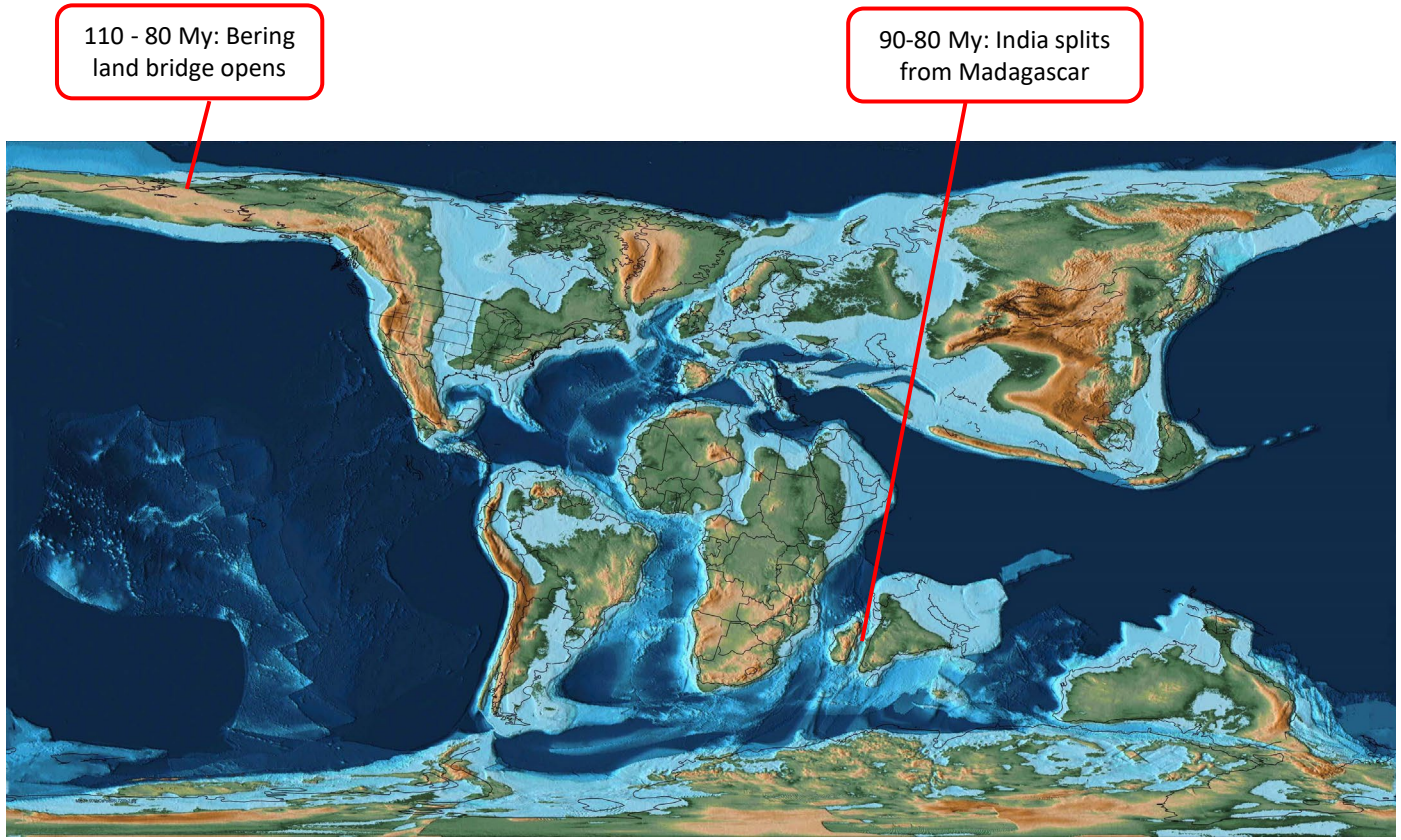
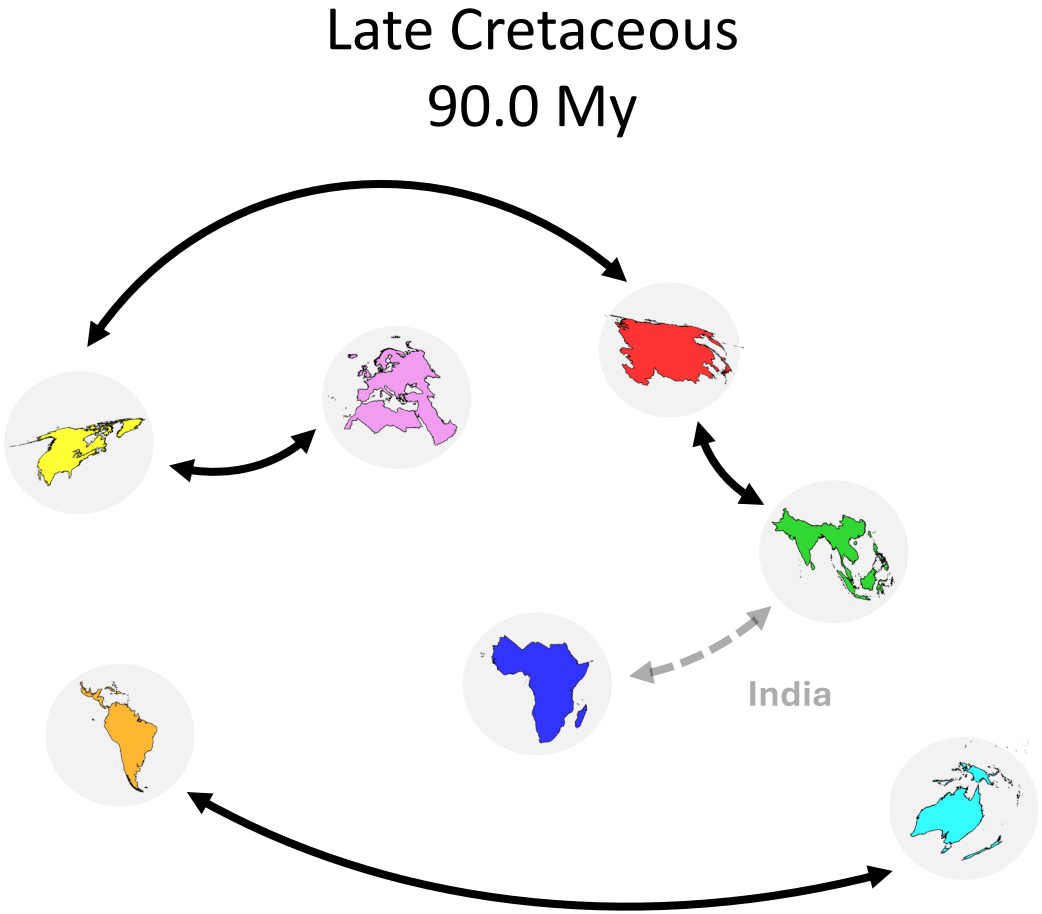


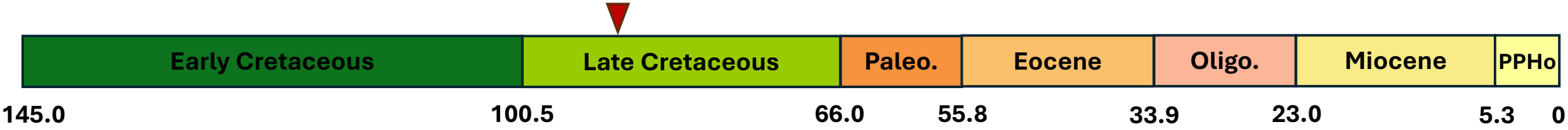


Biogeographic methods



Source: PALEOMAP Project by C. Scotese

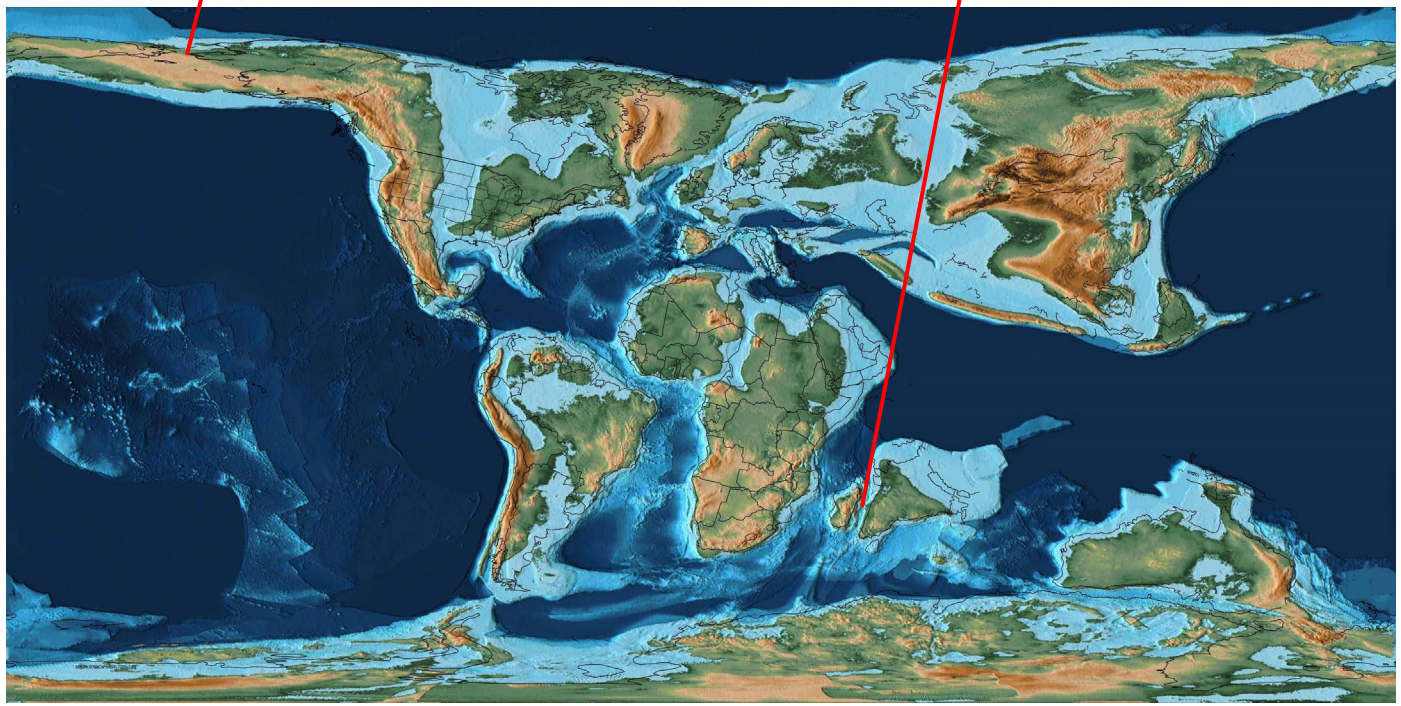




Biogeographic methods

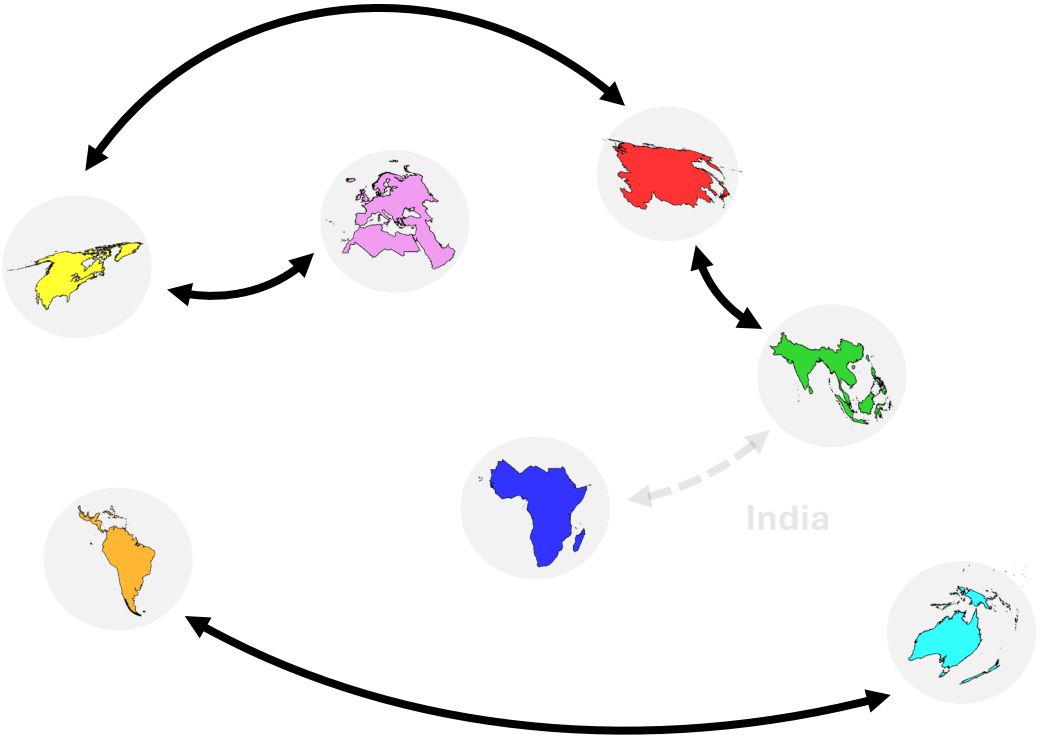
110 - 80 My: Bering land bridge opens

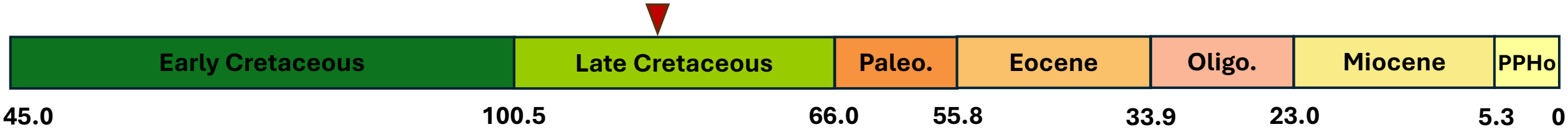
90-80 My: India splits from Madagascar



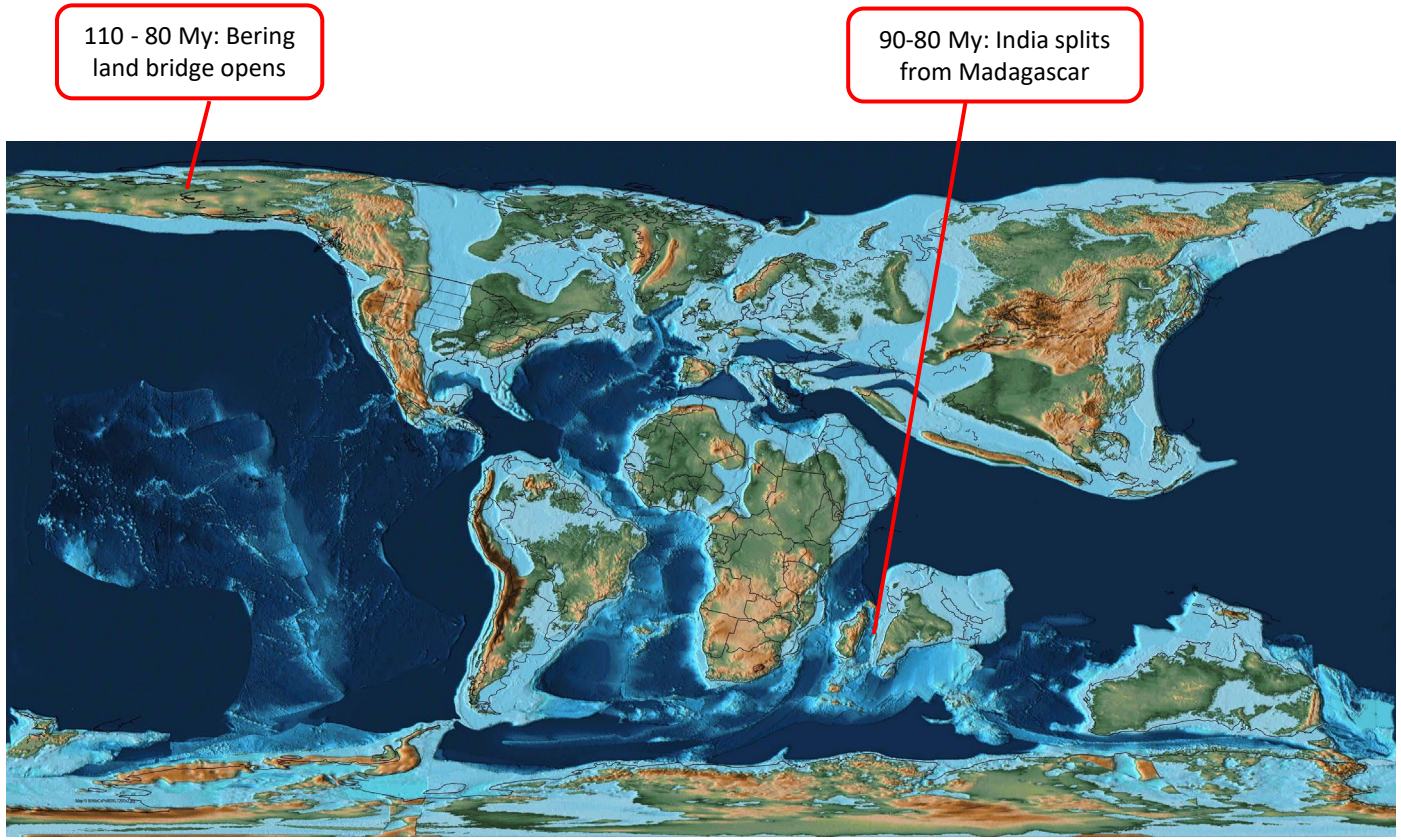
Source: PALEOMAP Project by C. Scotese

Late Cretaceous
85.0 My

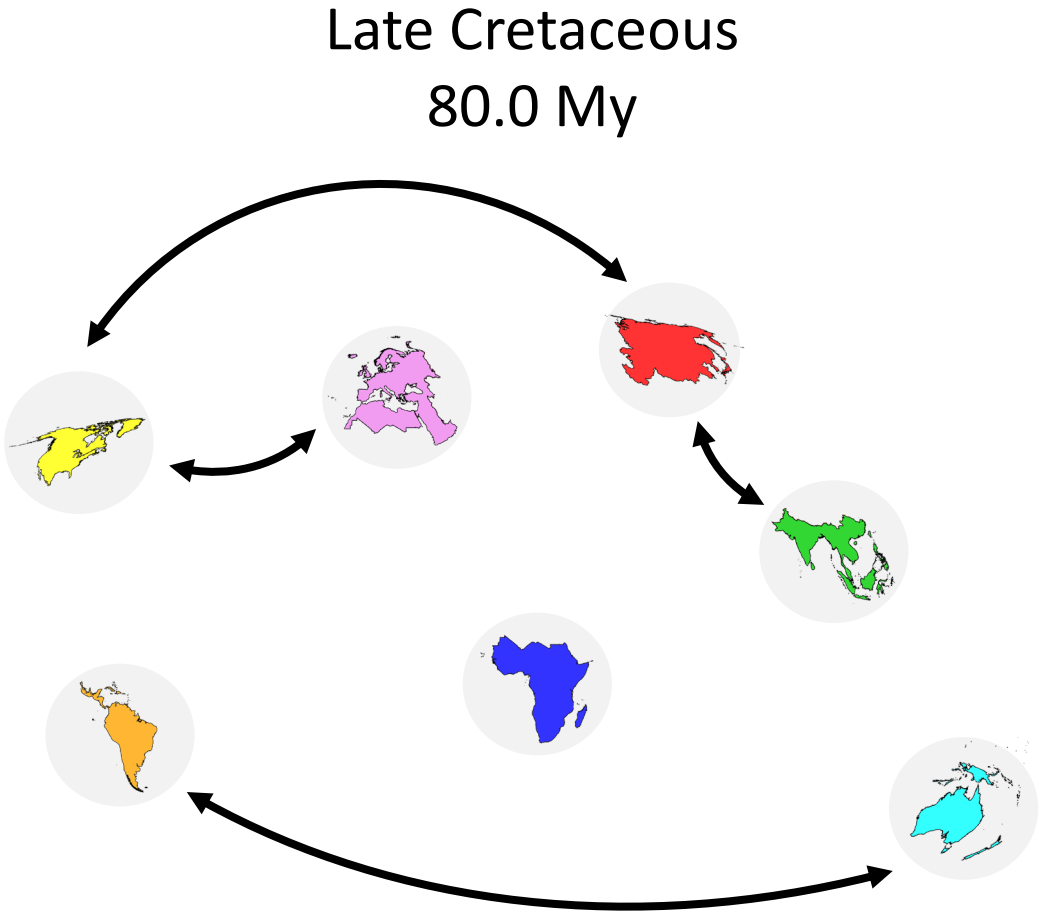


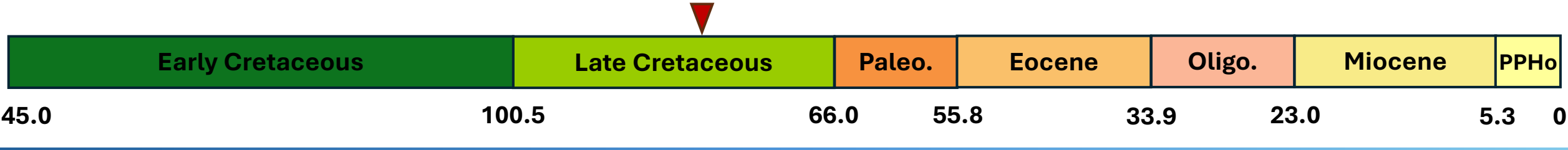


Biogeographic methods

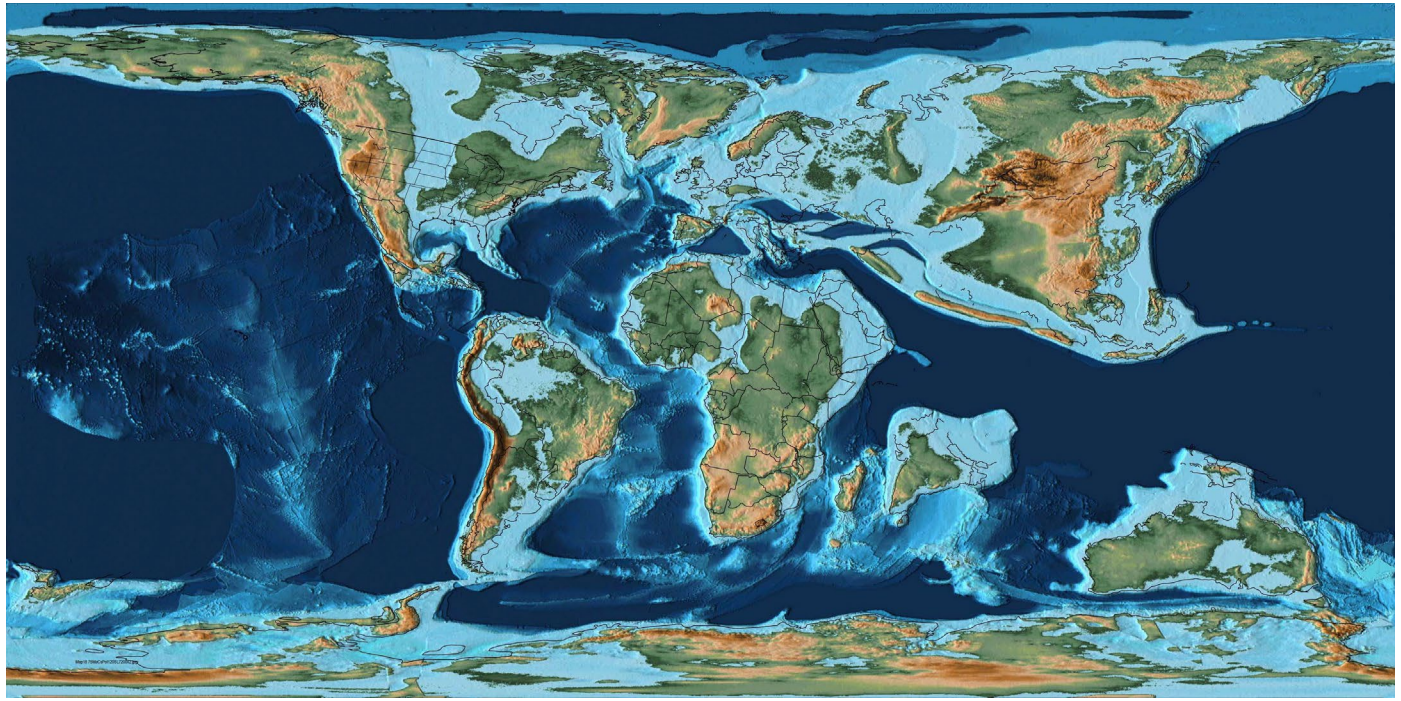


Source: PALEOMAP Project by C. Scotese

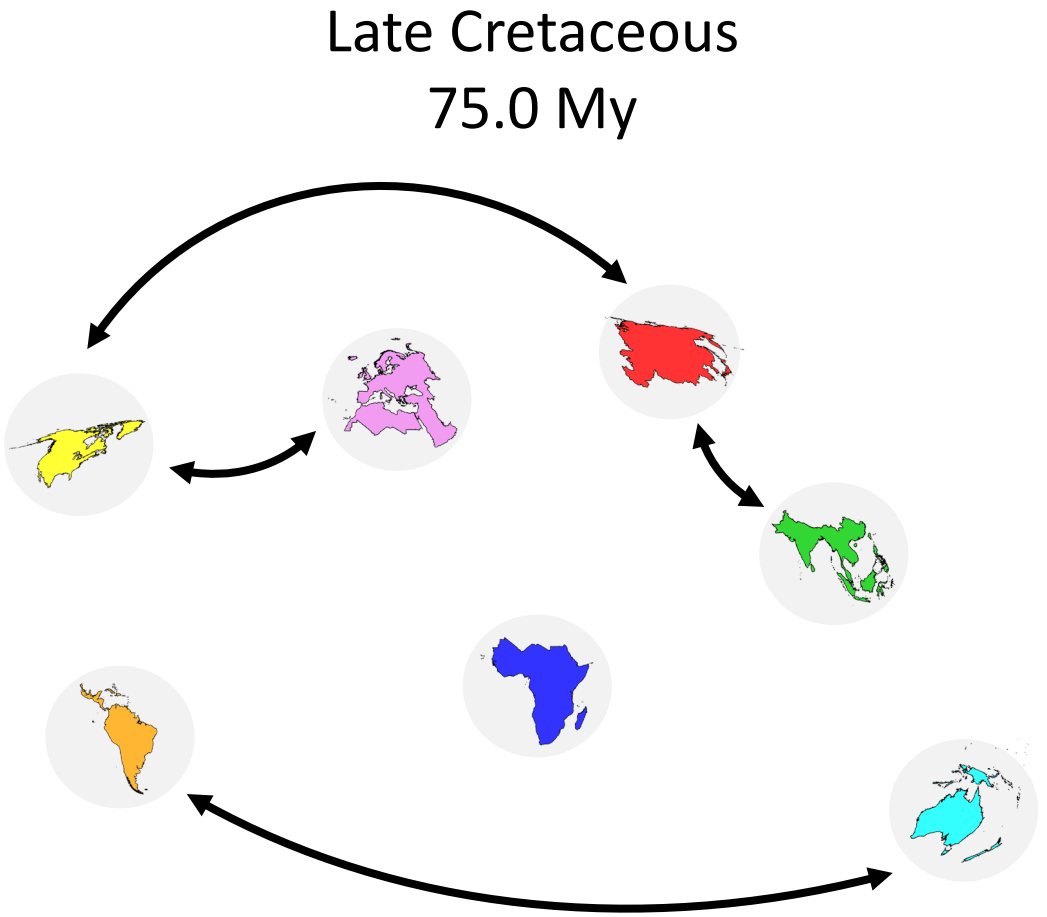


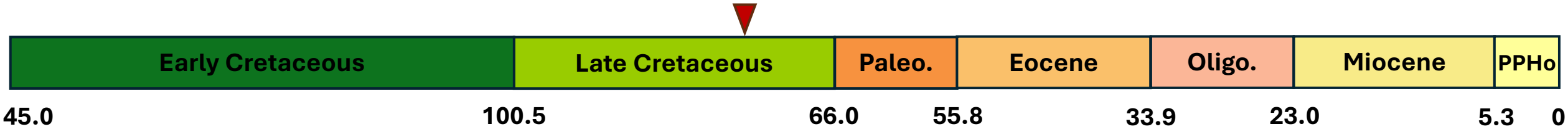


Biogeographic methods

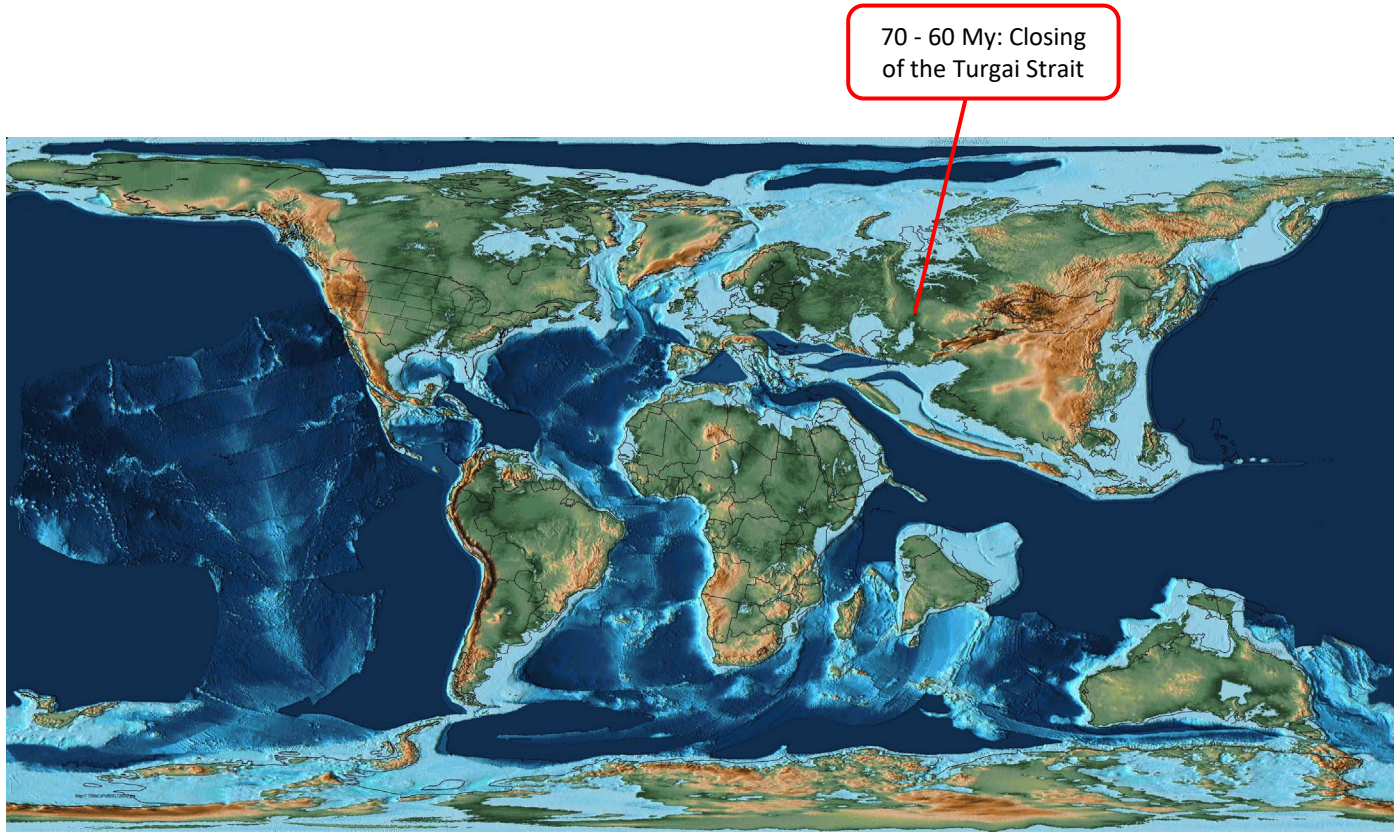


Source: PALEOMAP Project by C. Scotese

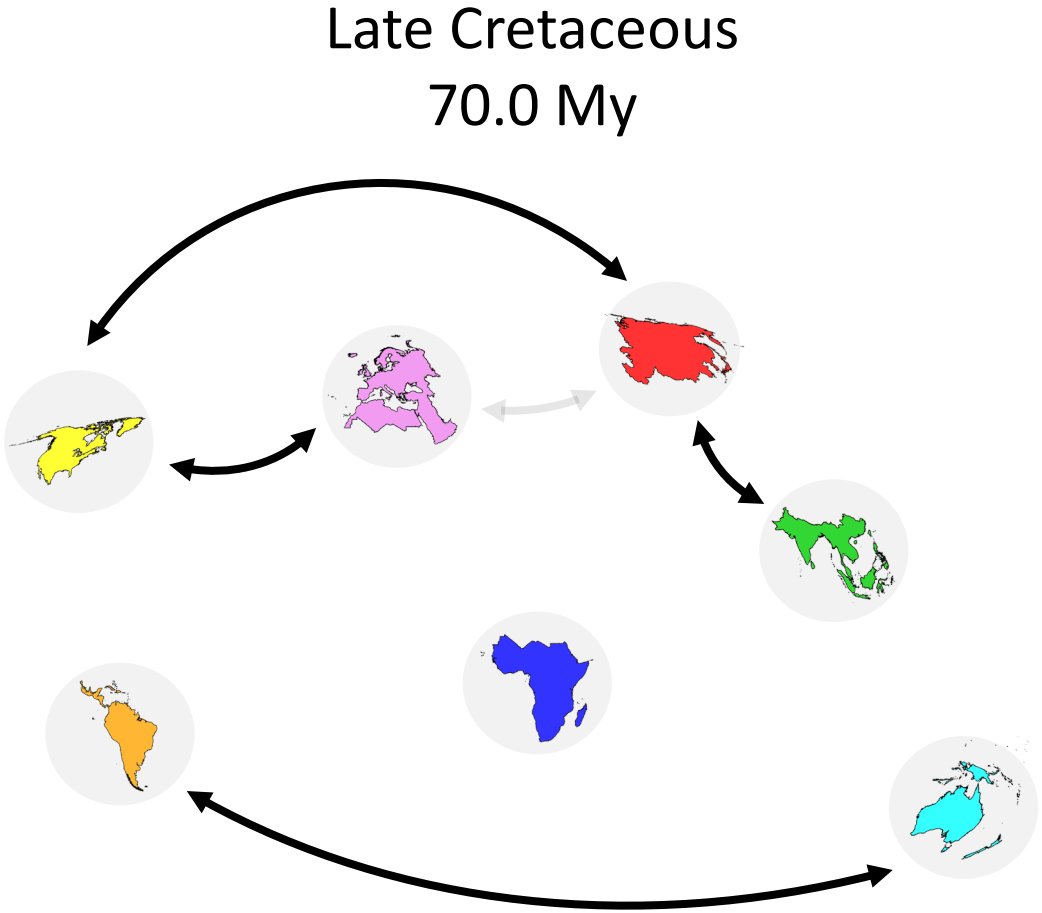


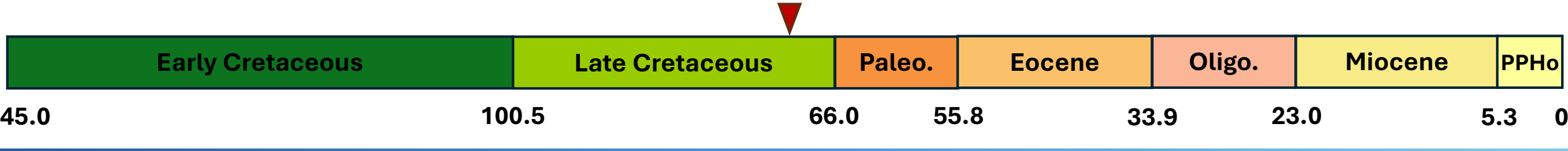


Biogeographic methods

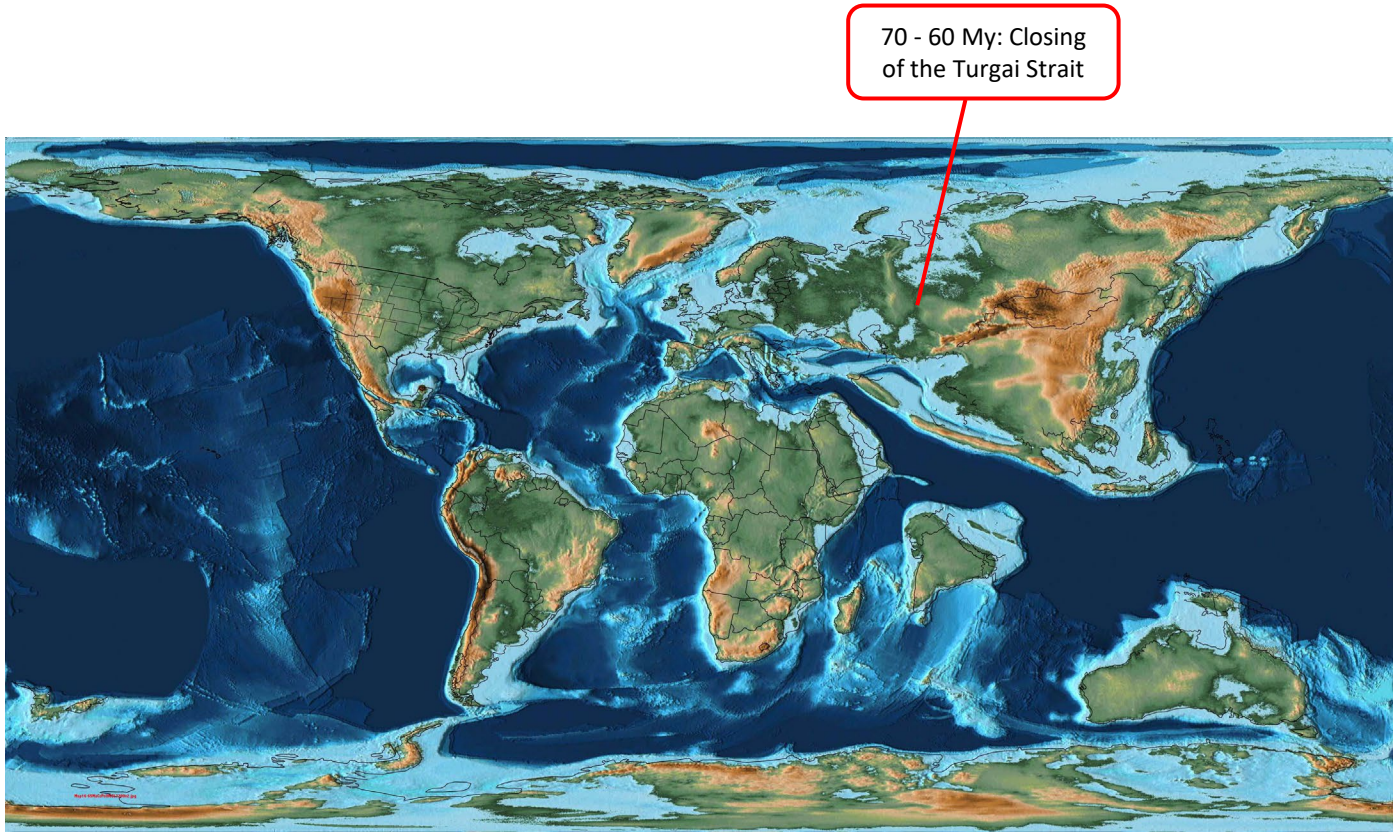


Source: PALEOMAP Project by C. Scotese



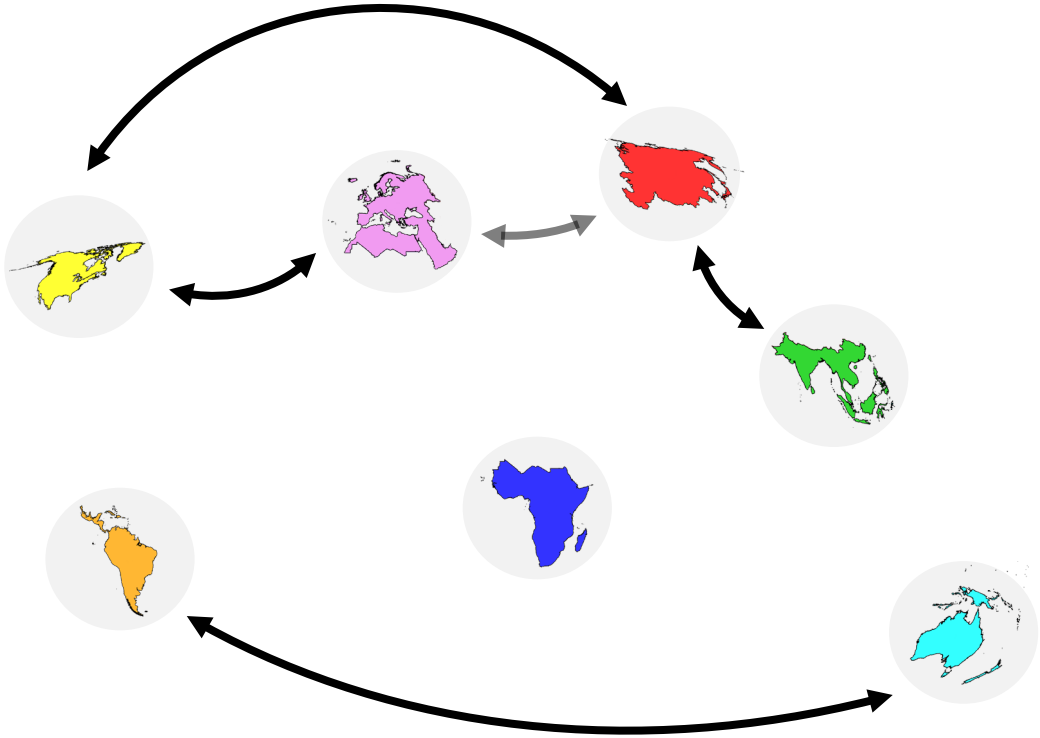


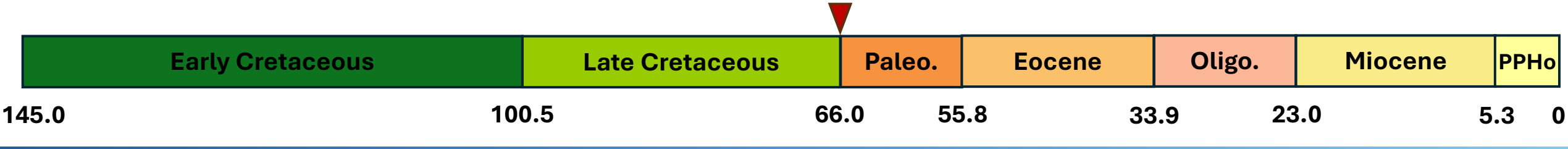
Biogeographic methods



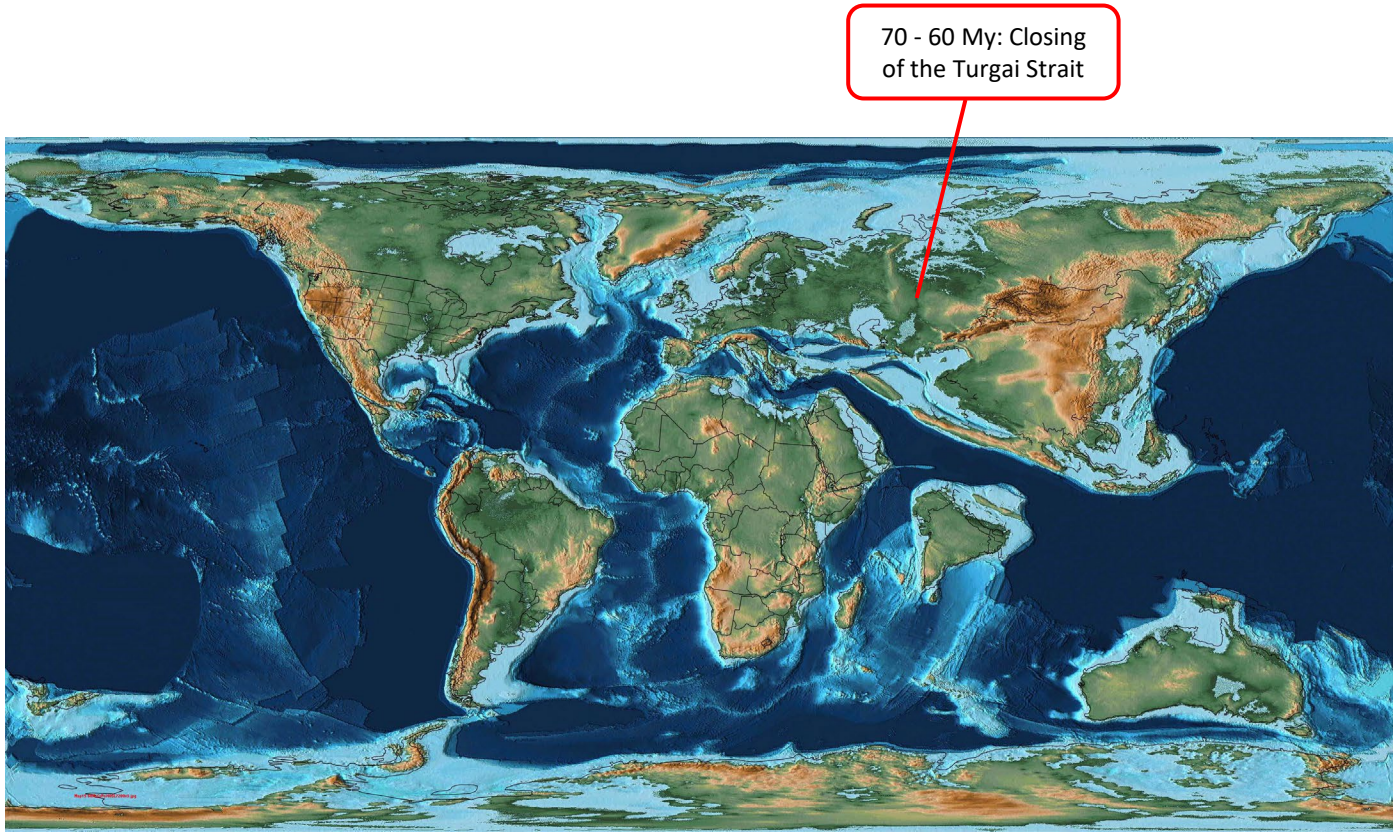
Source: PALEOMAP Project by C. Scotese

Late Cretaceous to Paleocene
66.0 My

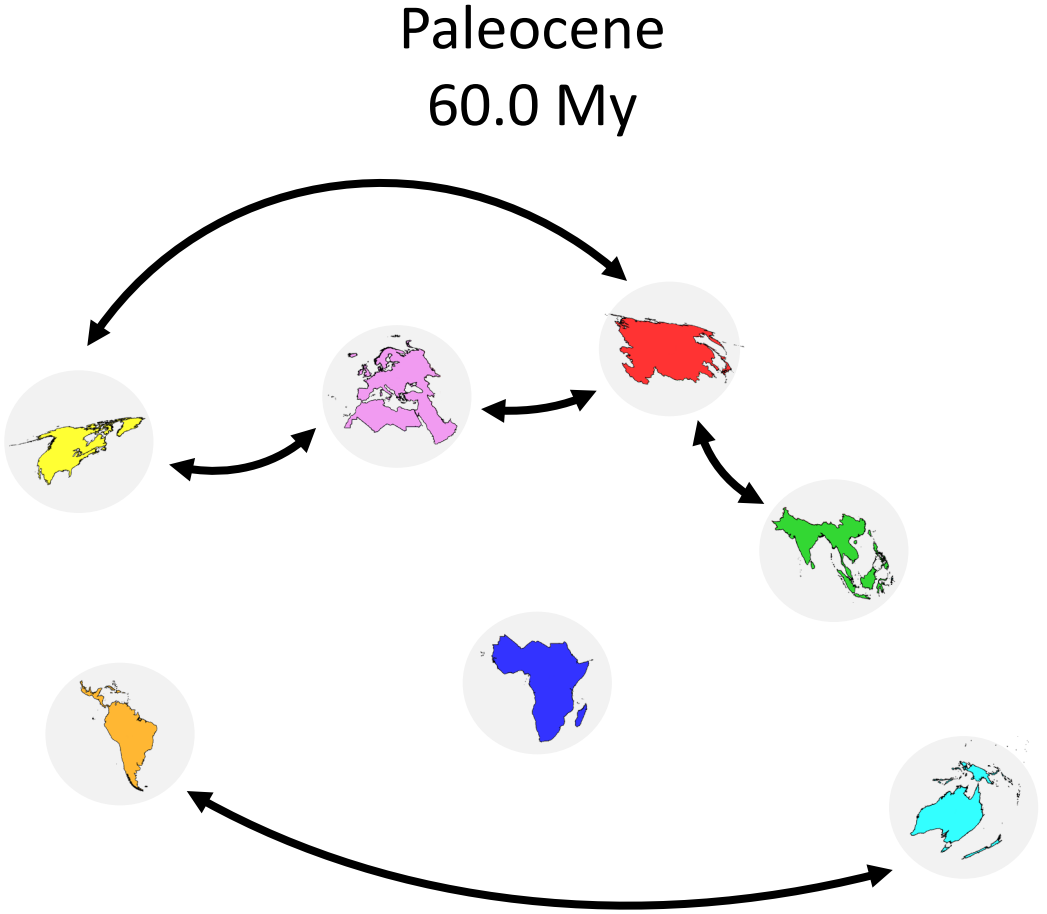


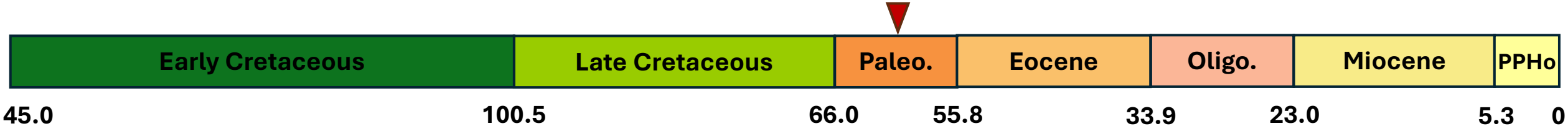


Biogeographic methods

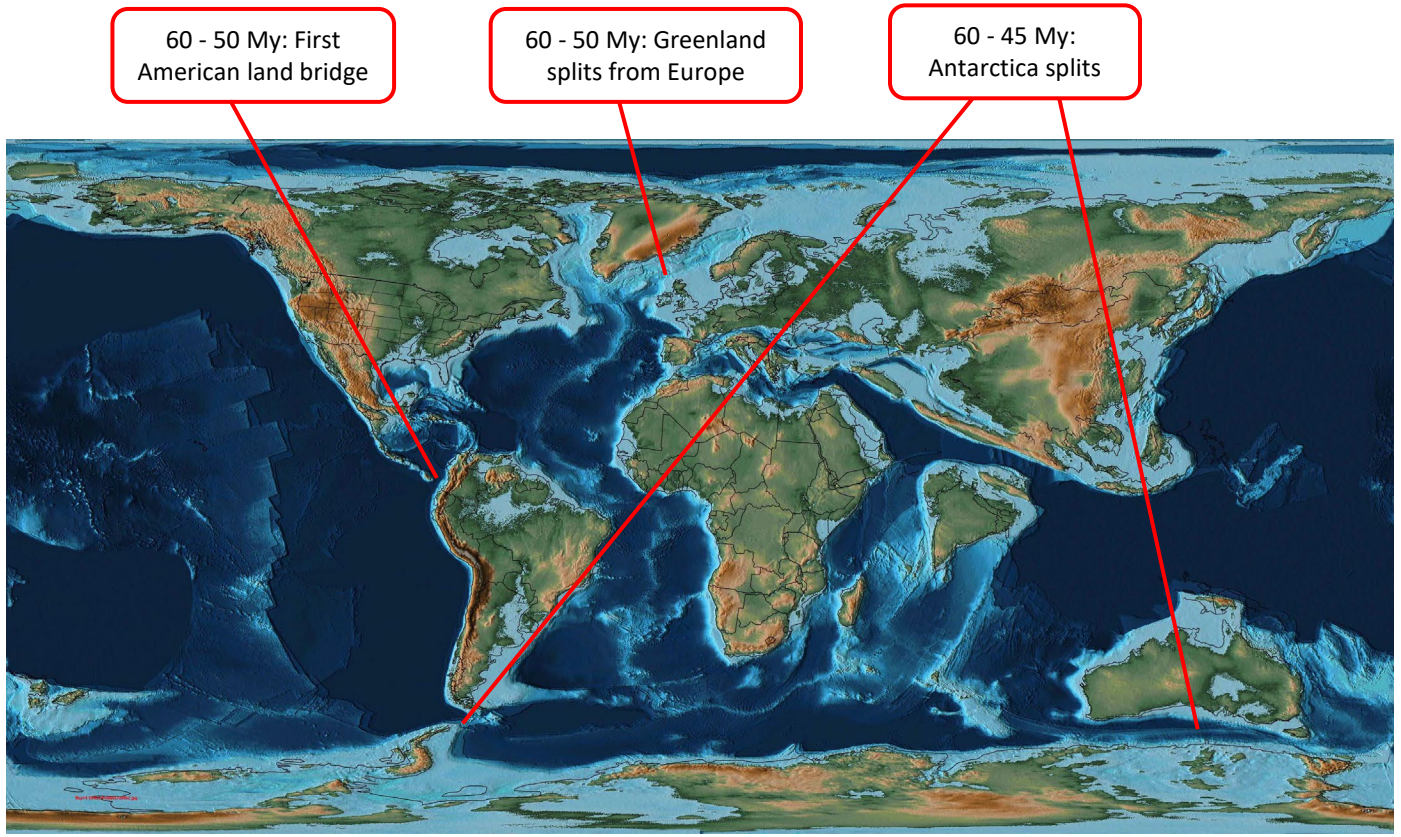


Source: PALEOMAP Project by C. Scotese



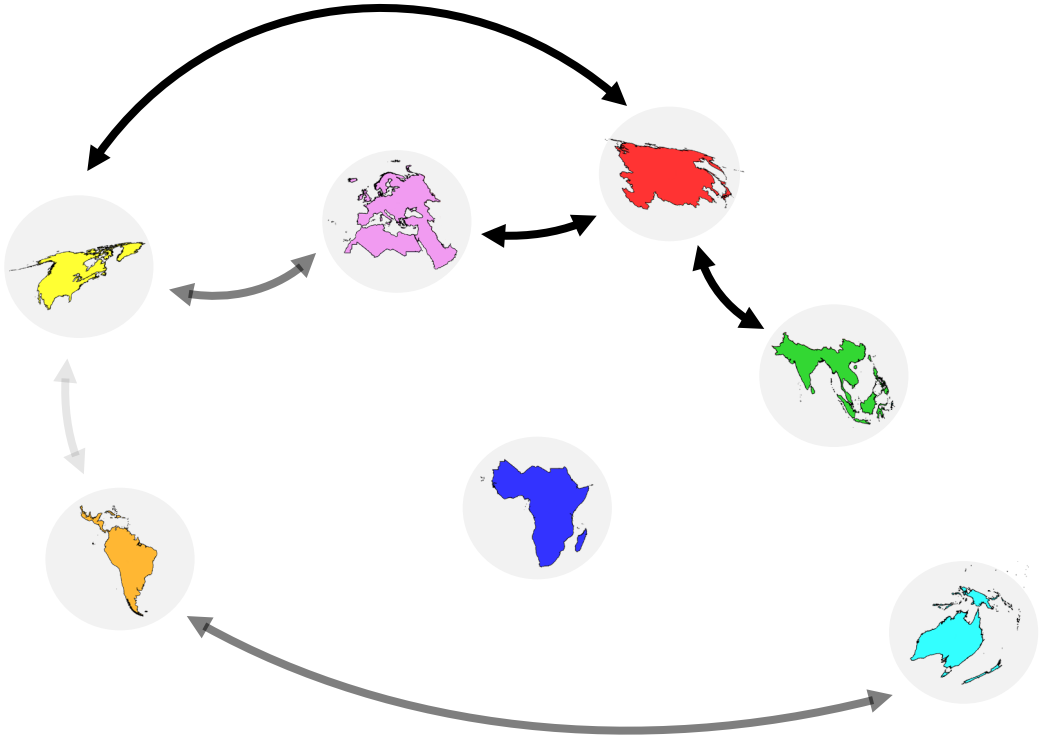


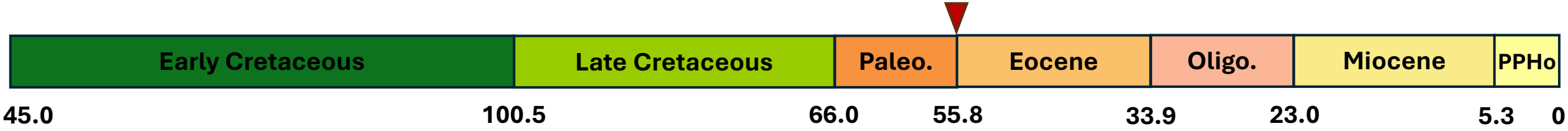
Biogeographic methods



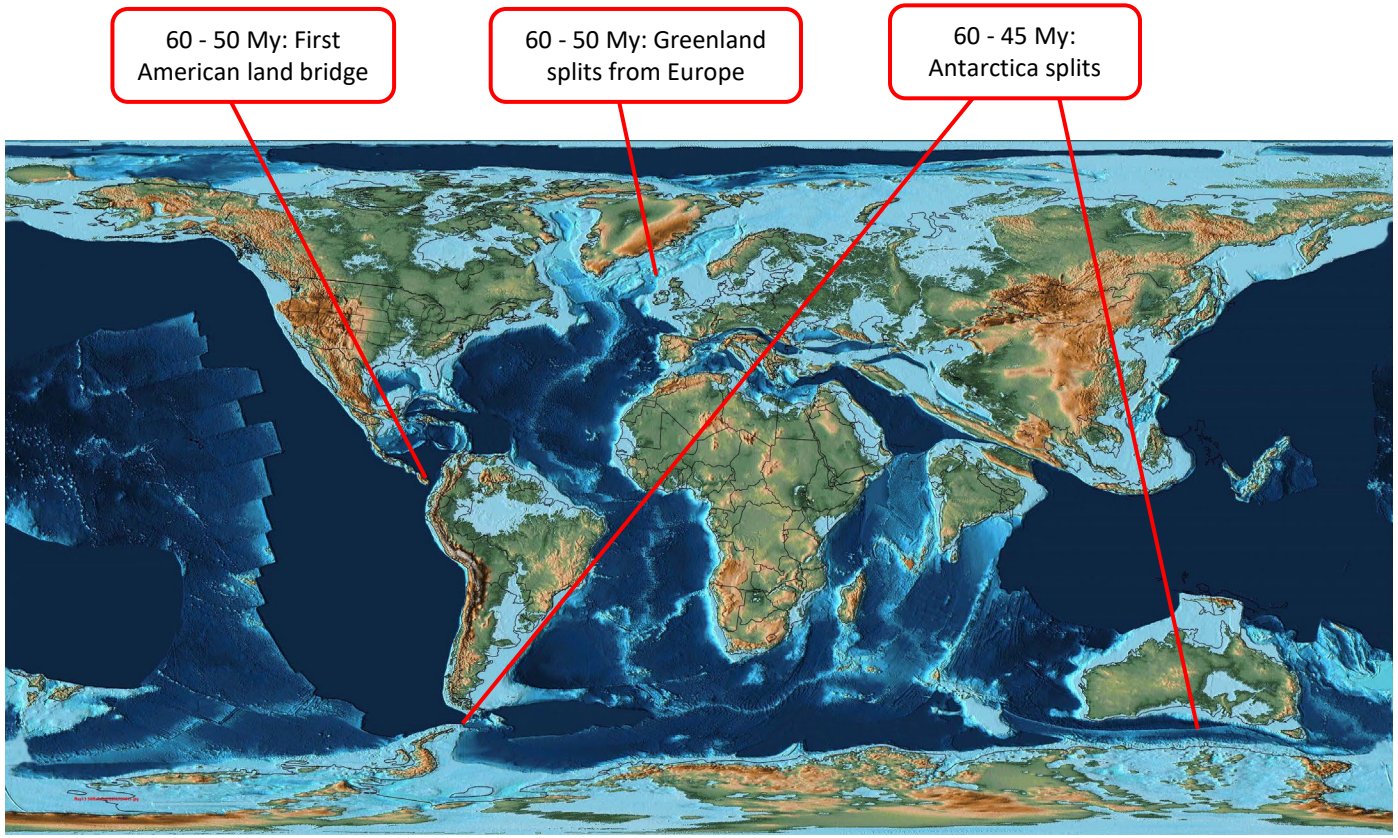
Source: PALEOMAP Project by C. Scotese

Paleocene to Eocene
55.8 My

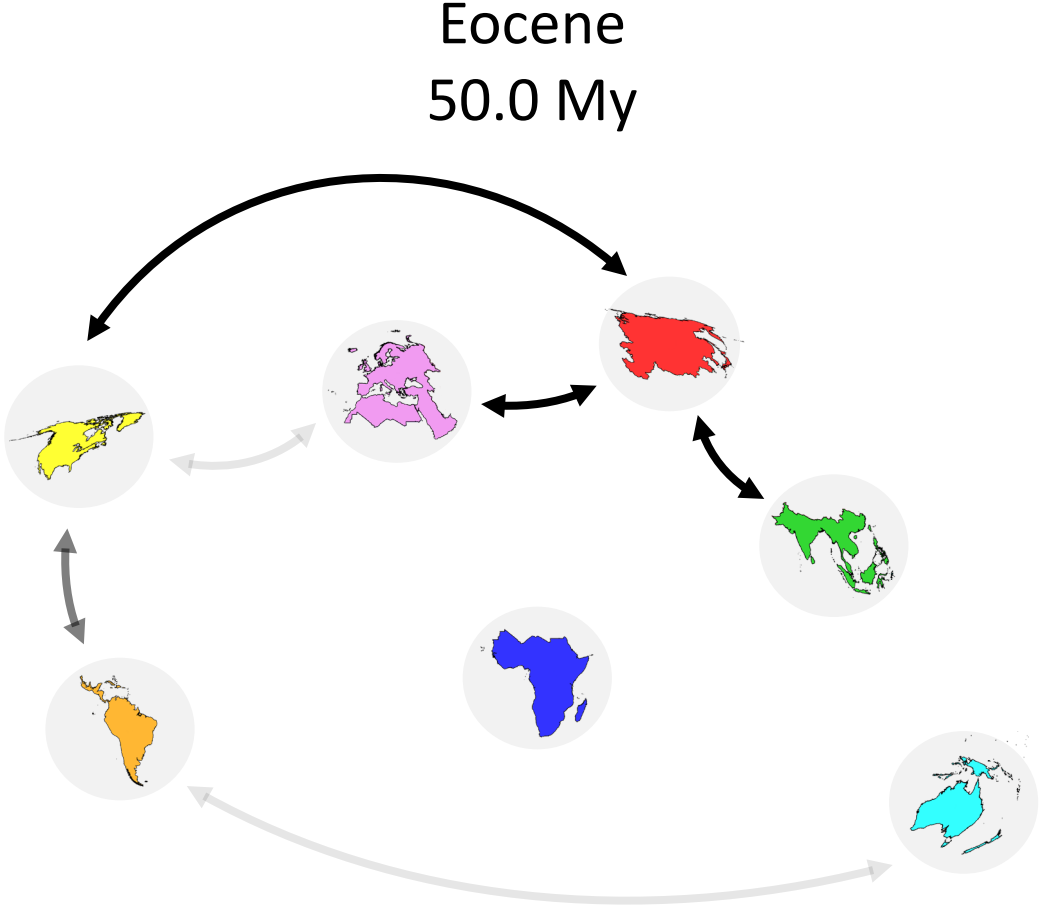


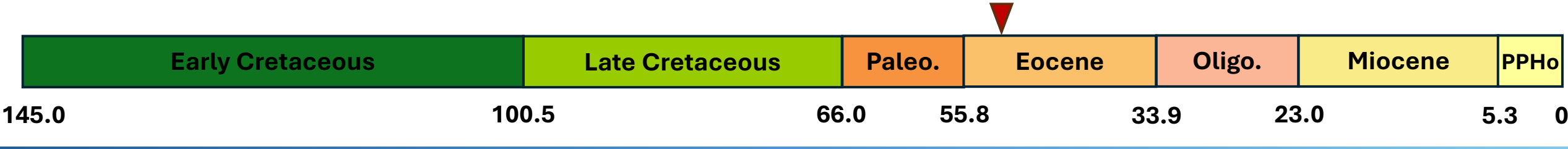


Biogeographic methods

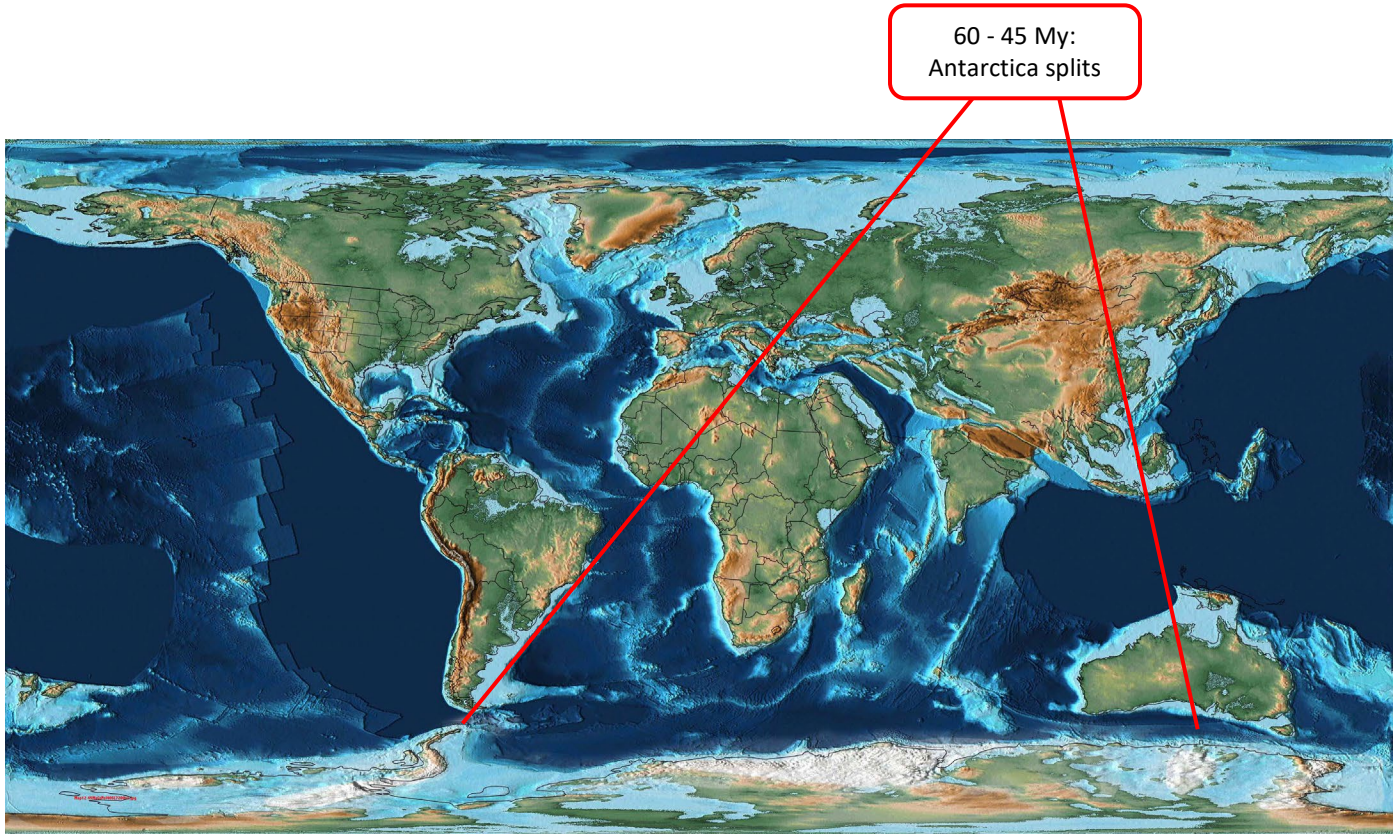


Source: PALEOMAP Project by C. Scotese

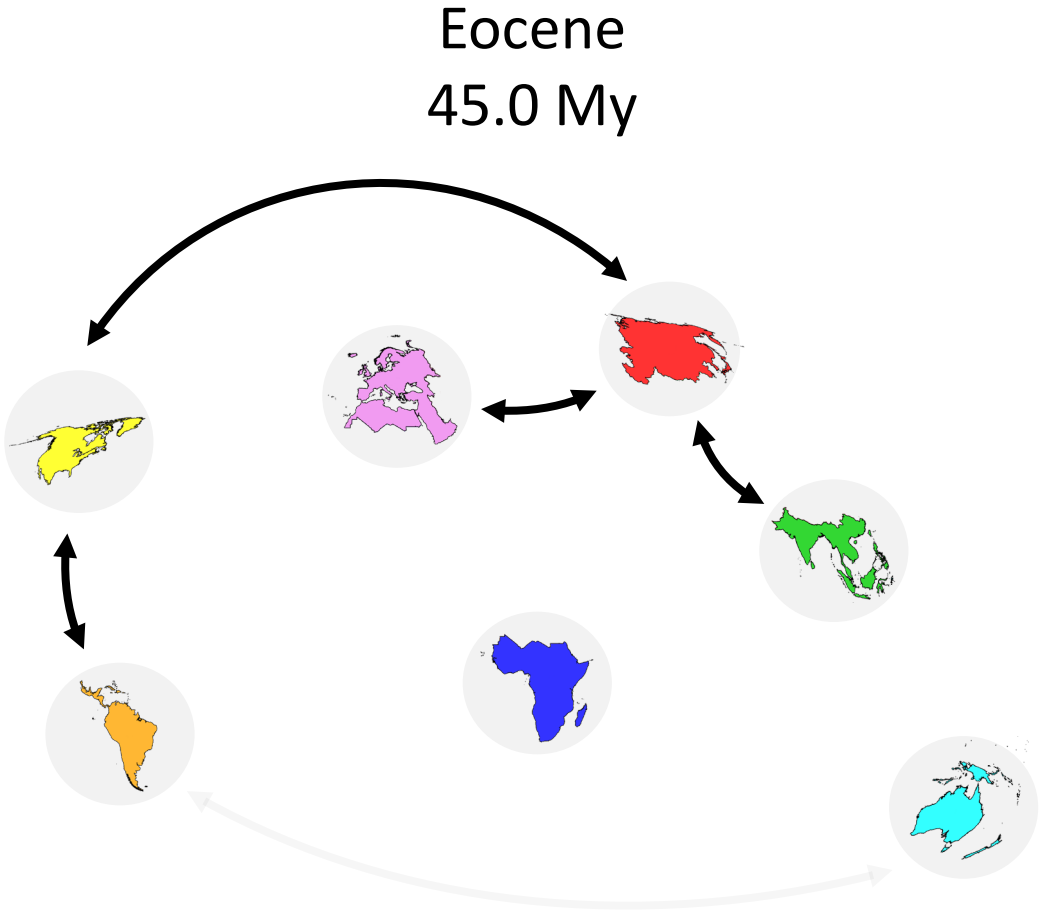


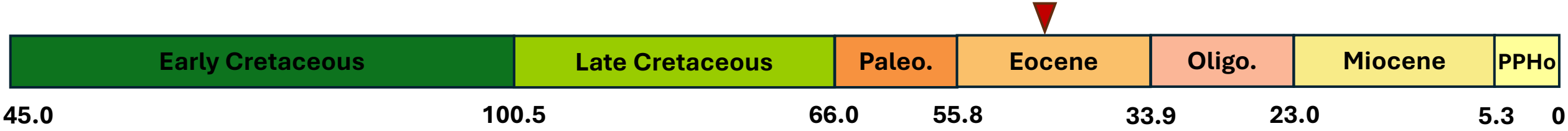


Biogeographic methods

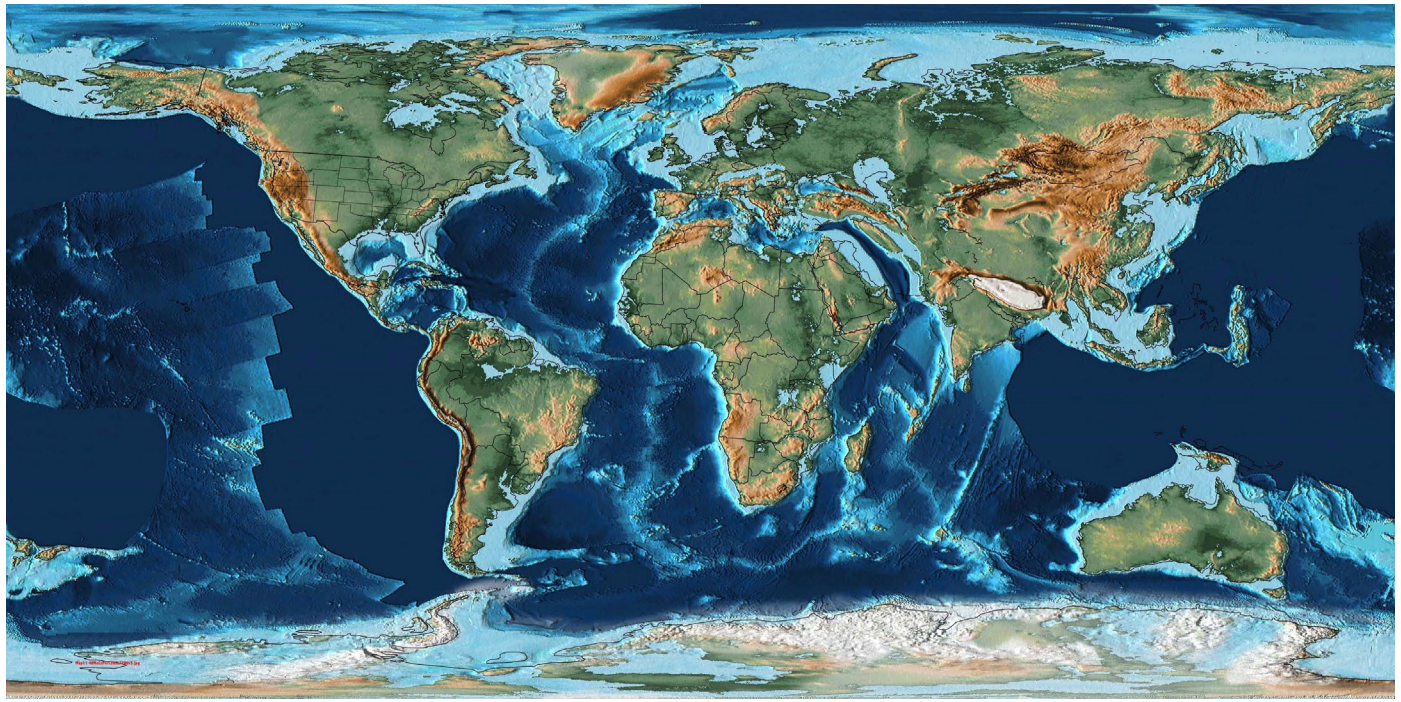


Source: PALEOMAP Project by C. Scotese

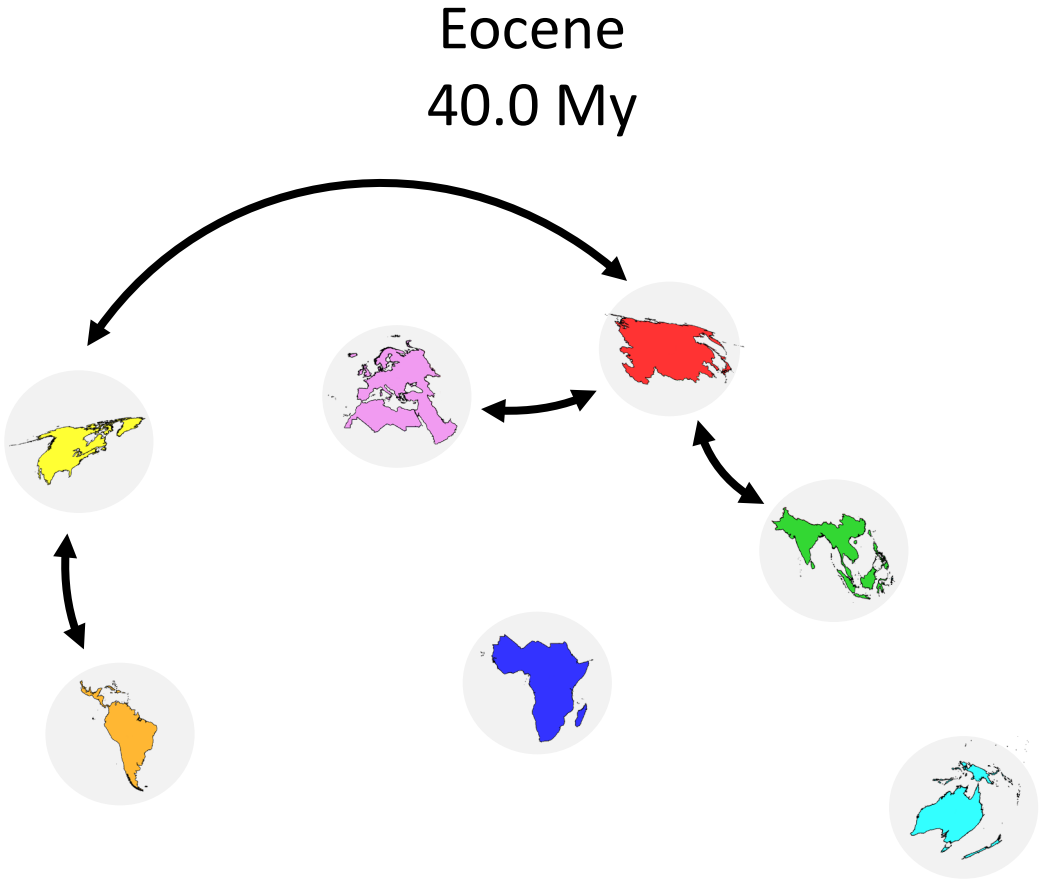


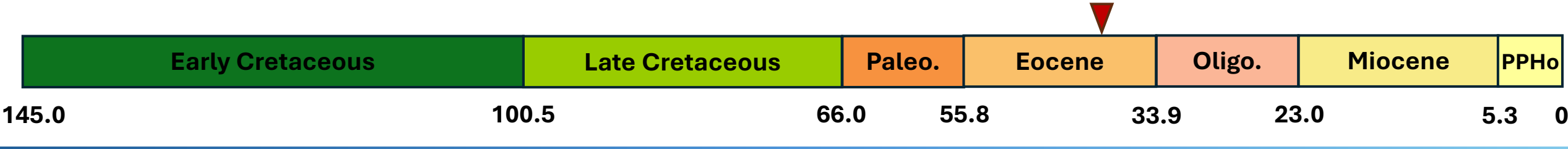


Biogeographic methods

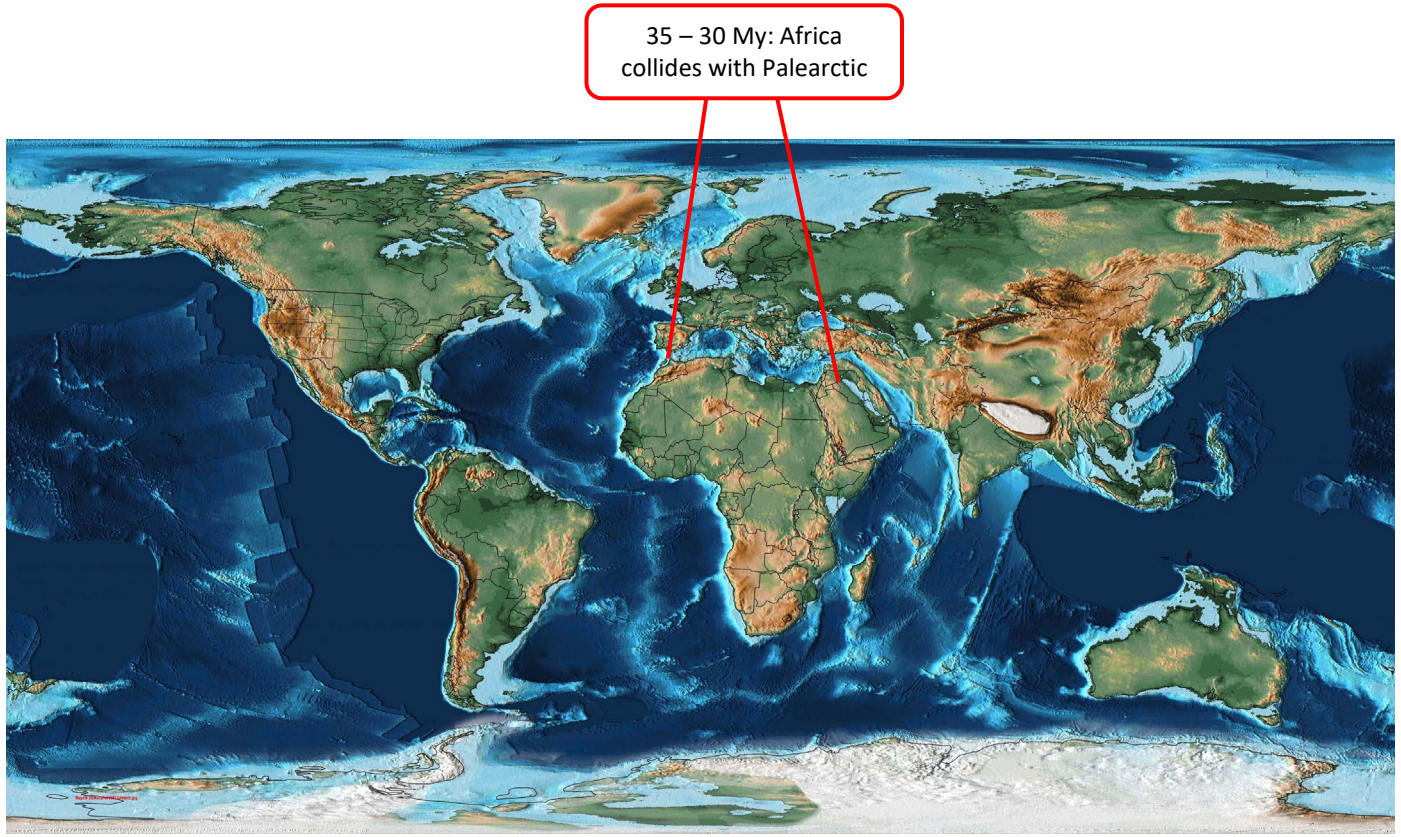


Source: PALEOMAP Project by C. Scotese



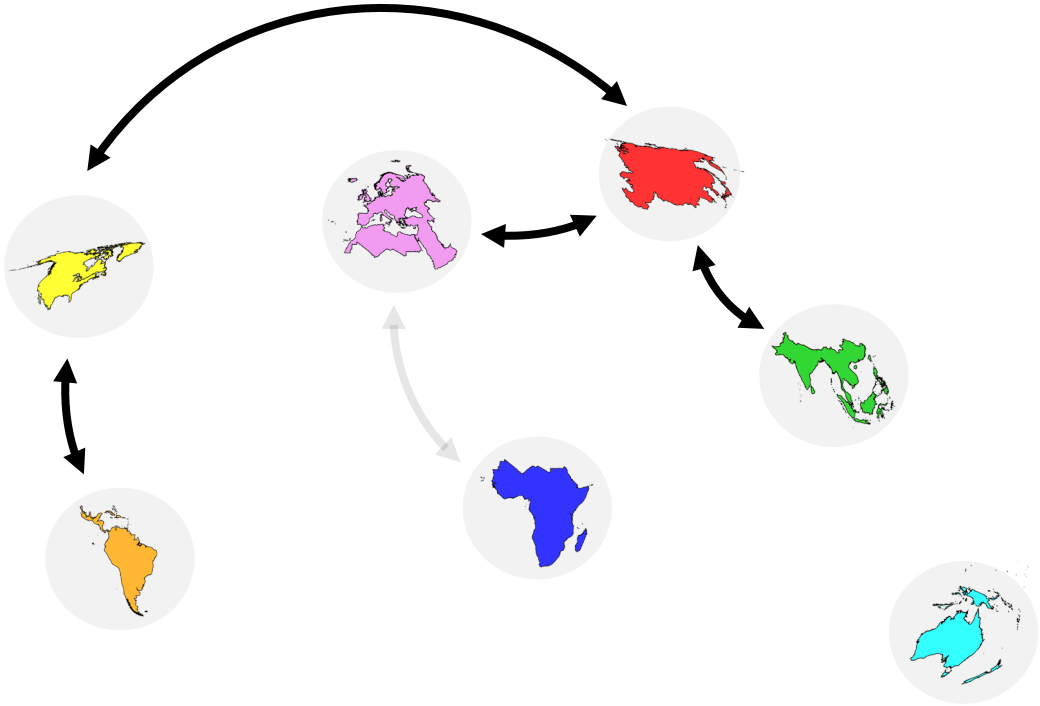


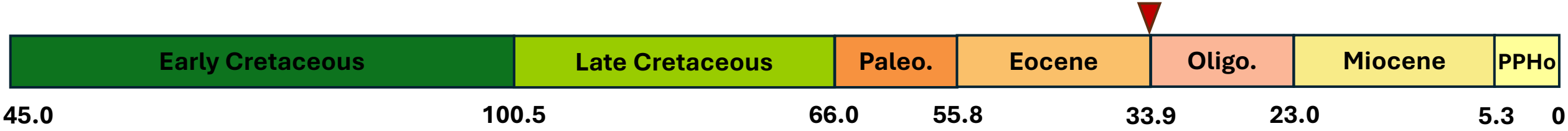
Biogeographic methods



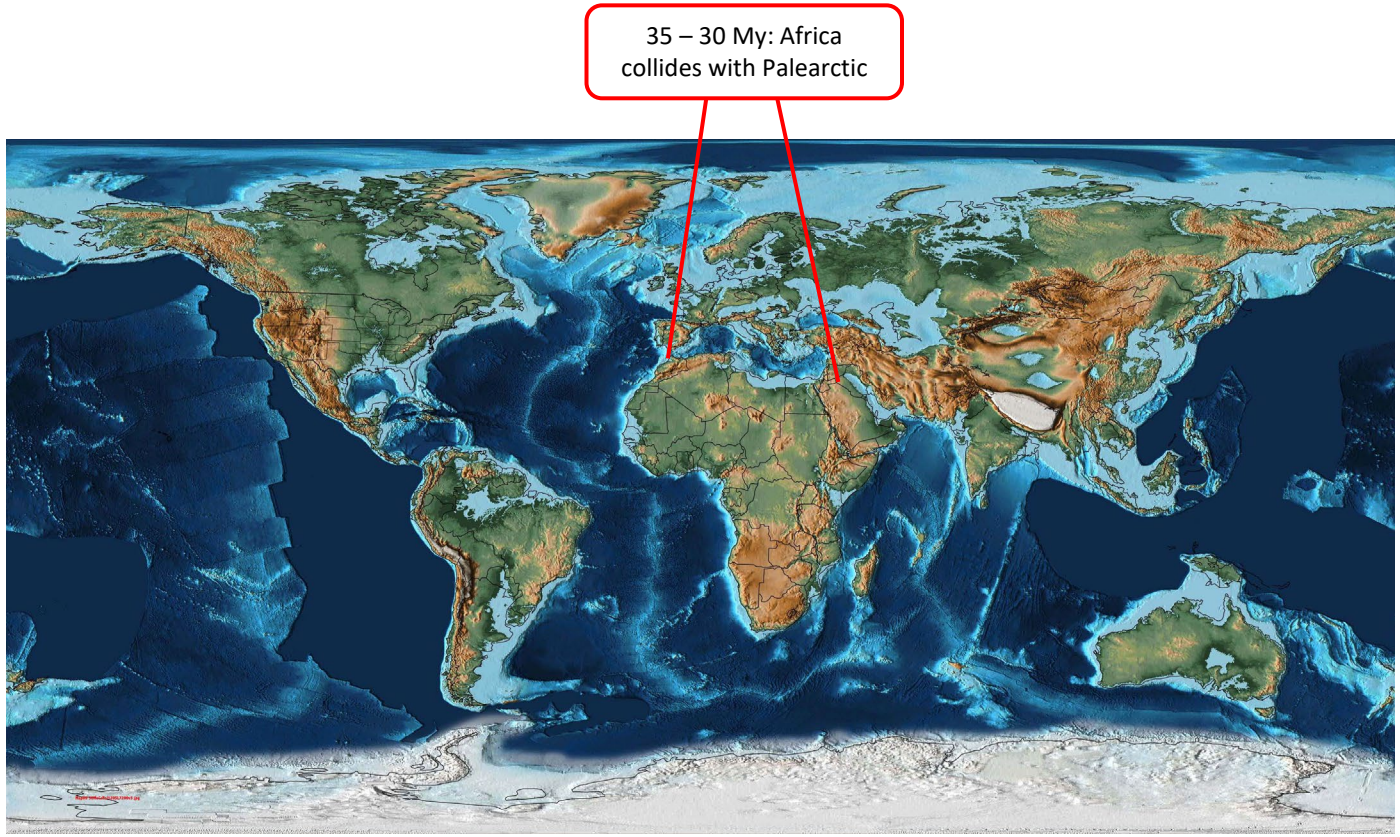
Source: PALEOMAP Project by C. Scotese

Eocene to Oligocene
33.9 My

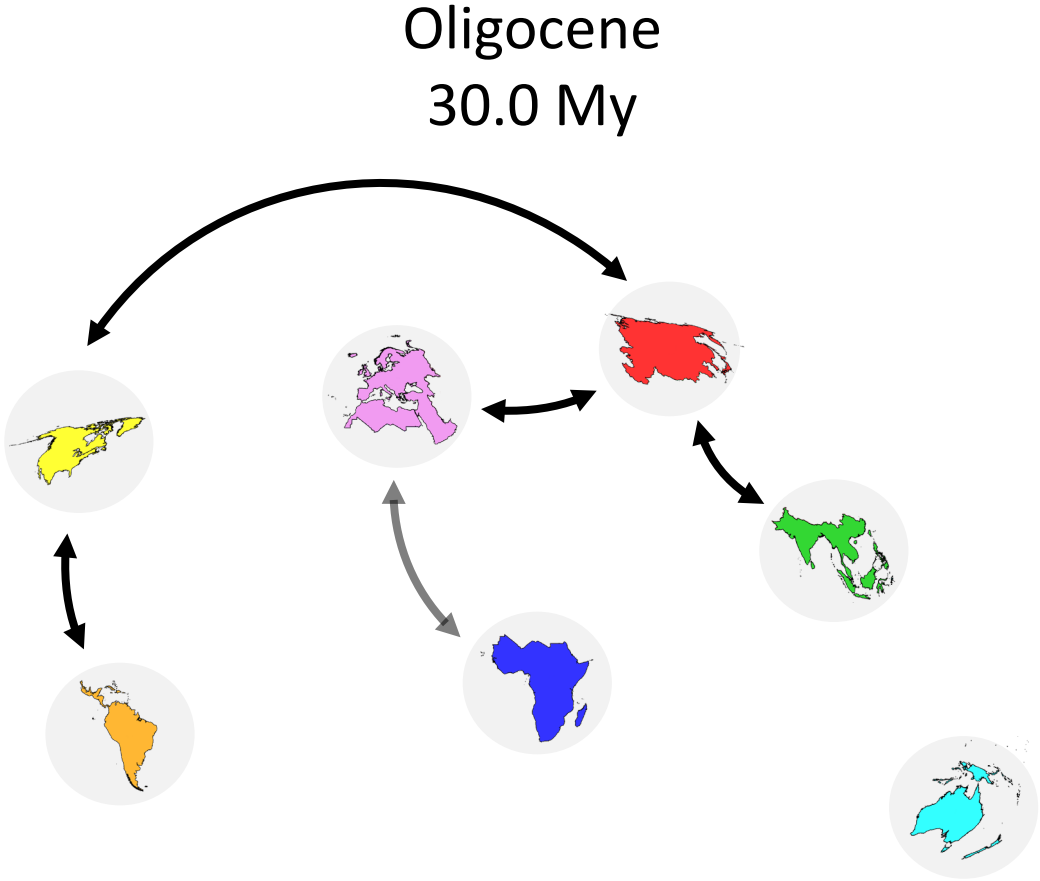


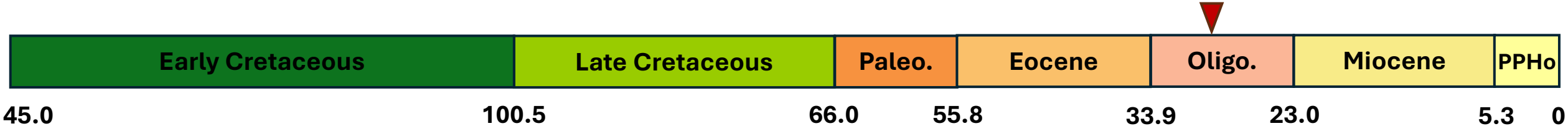


Biogeographic methods

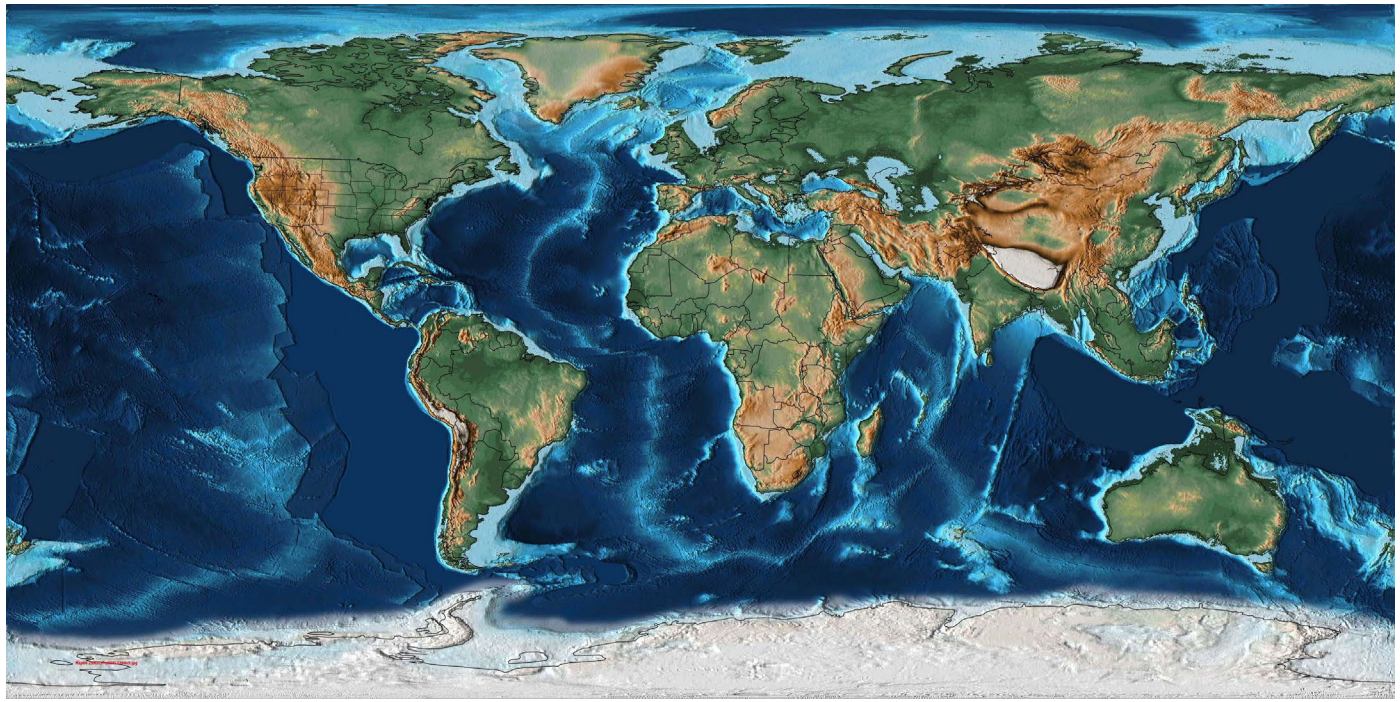


Source: PALEOMAP Project by C. Scotese



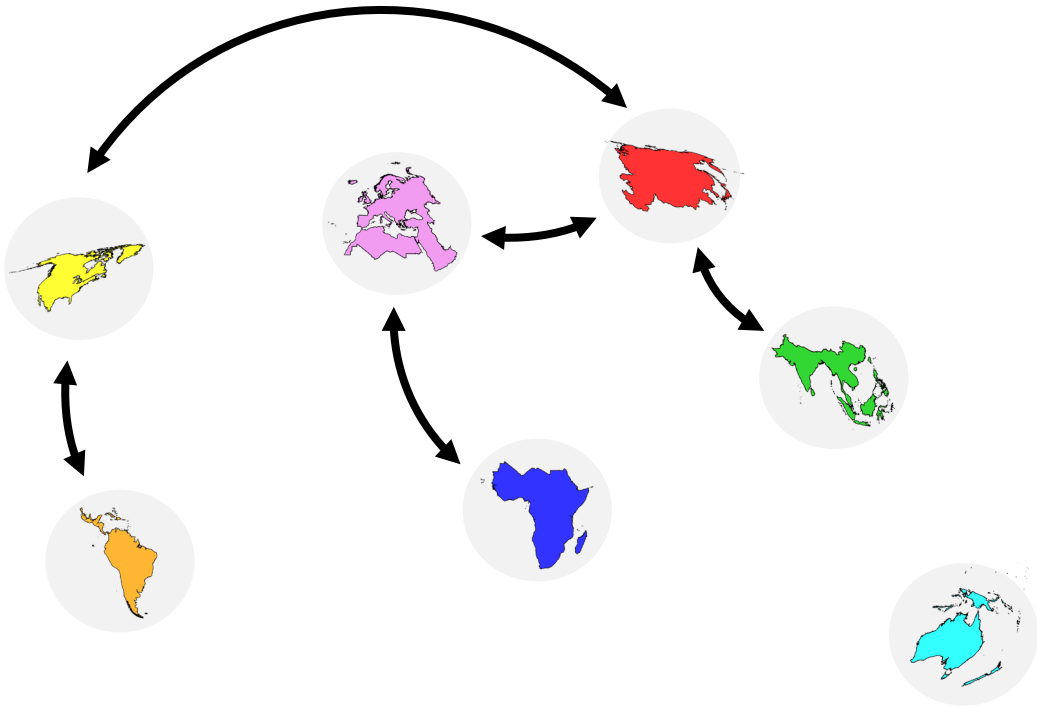


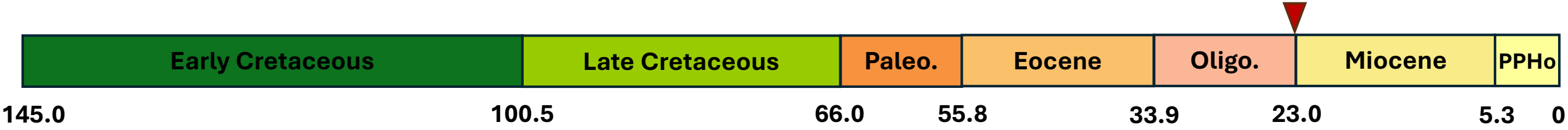
Biogeographic methods



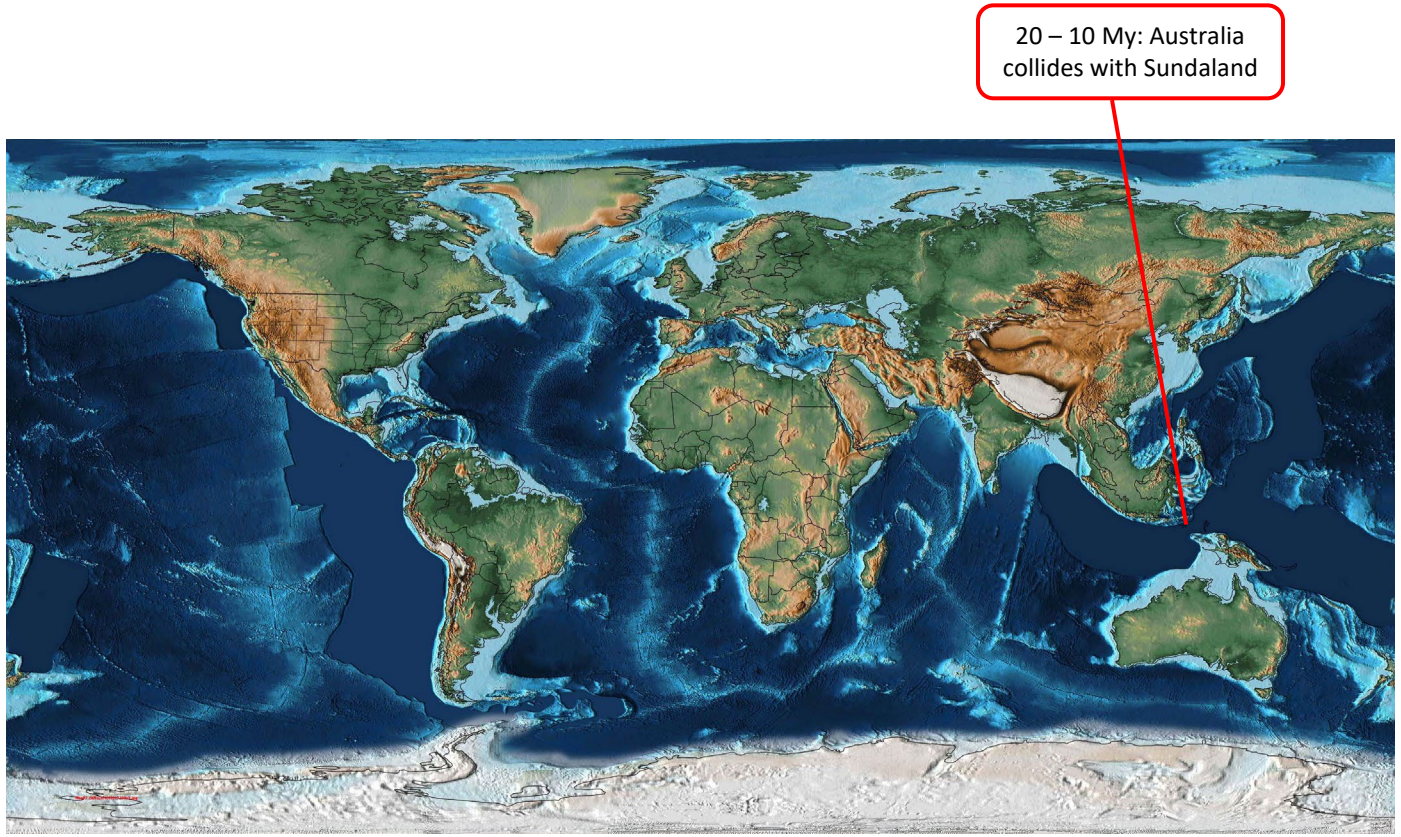
Source: PALEOMAP Project by C. Scotese

Oligocene to Miocene
23.0 My

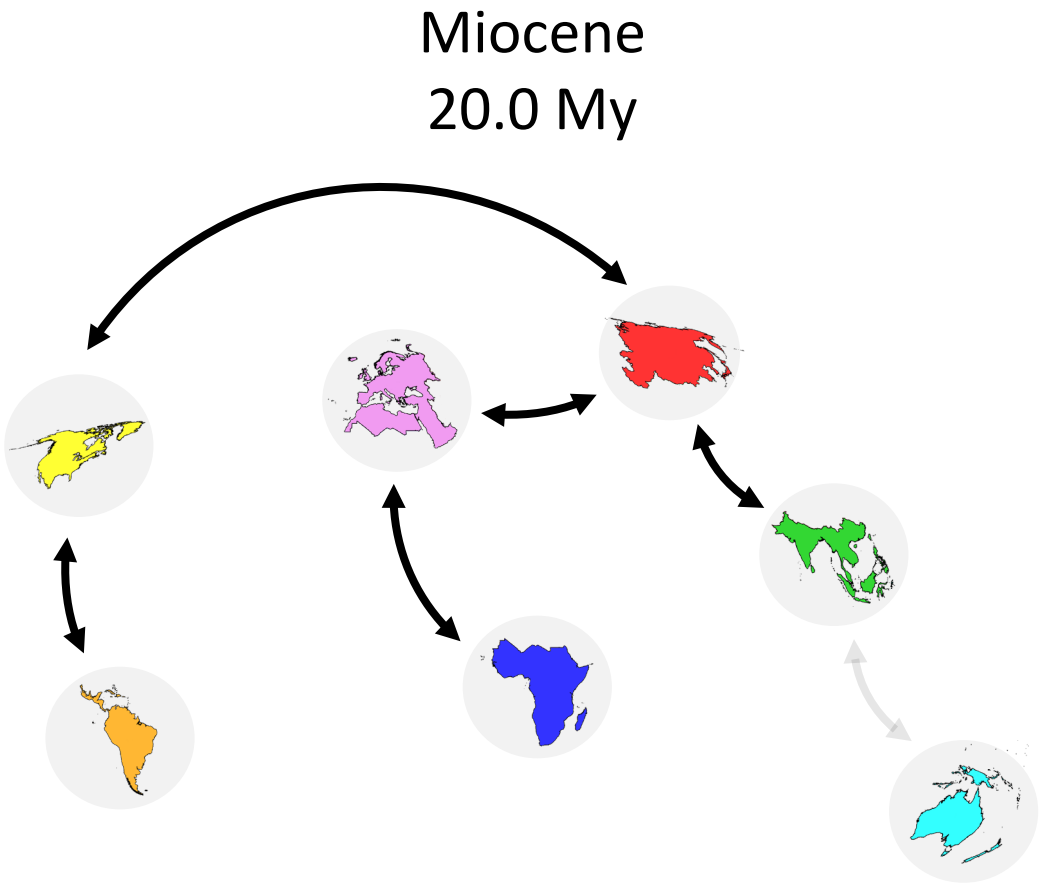


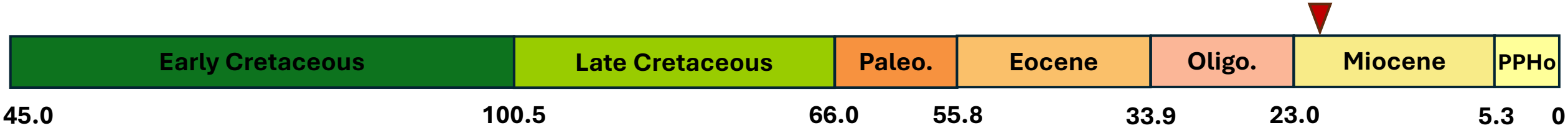


Biogeographic methods

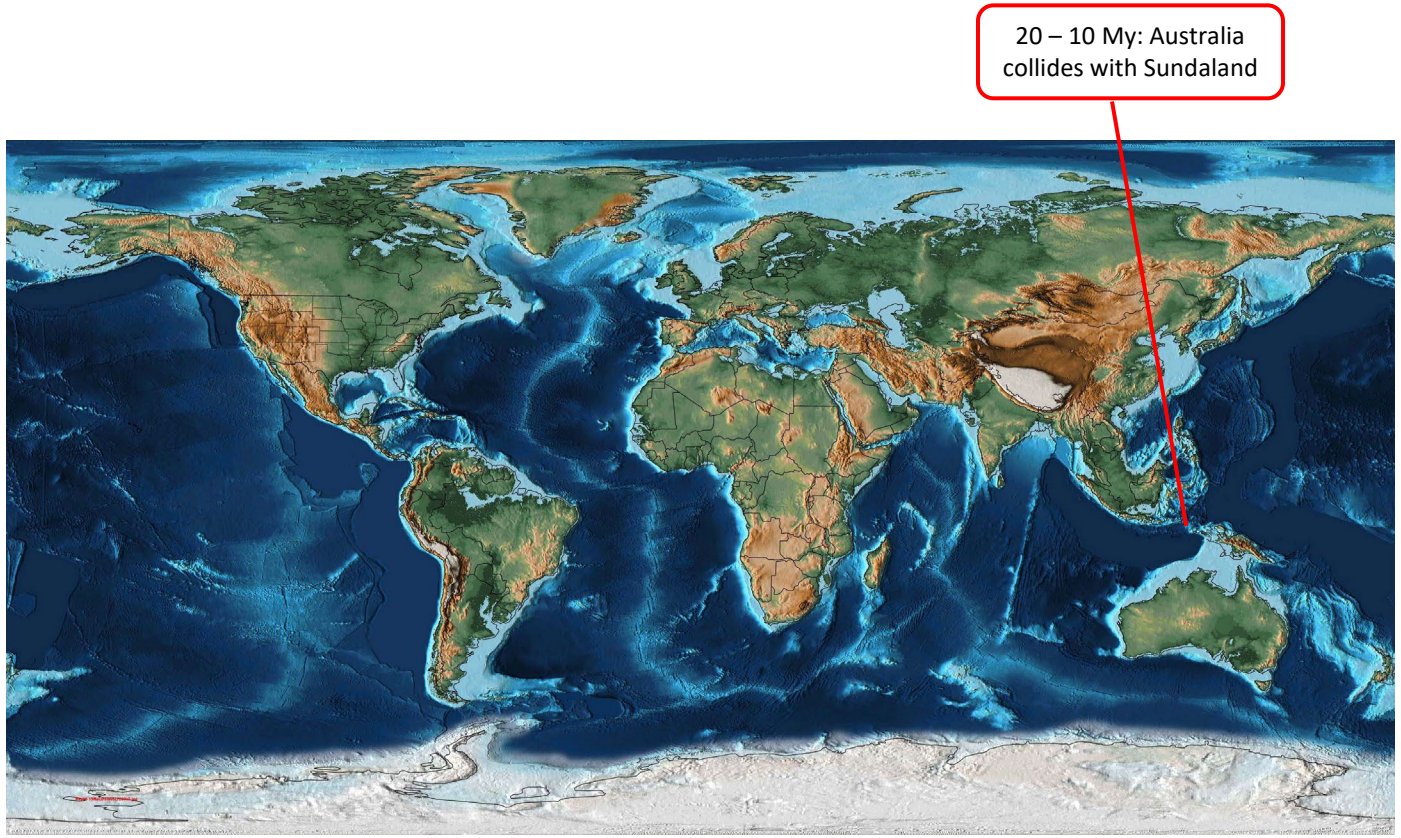


Source: PALEOMAP Project by C. Scotese

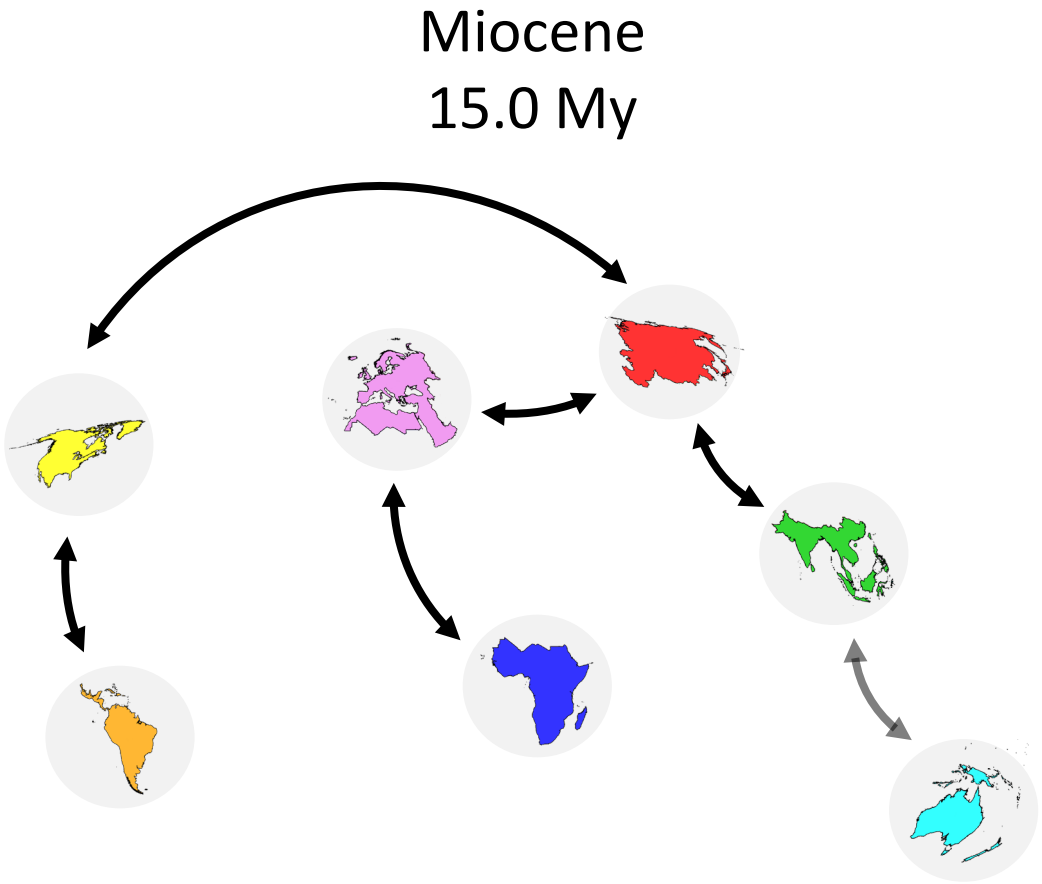


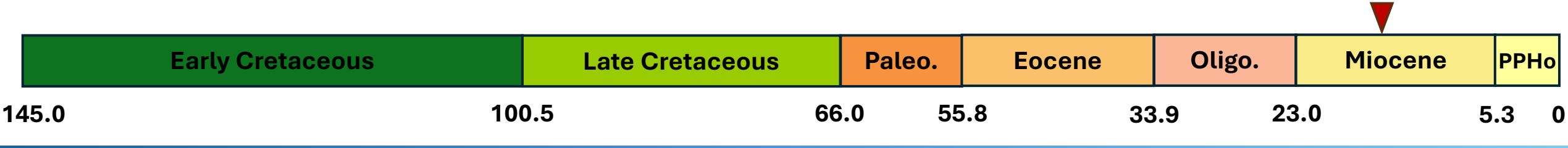


Biogeographic methods

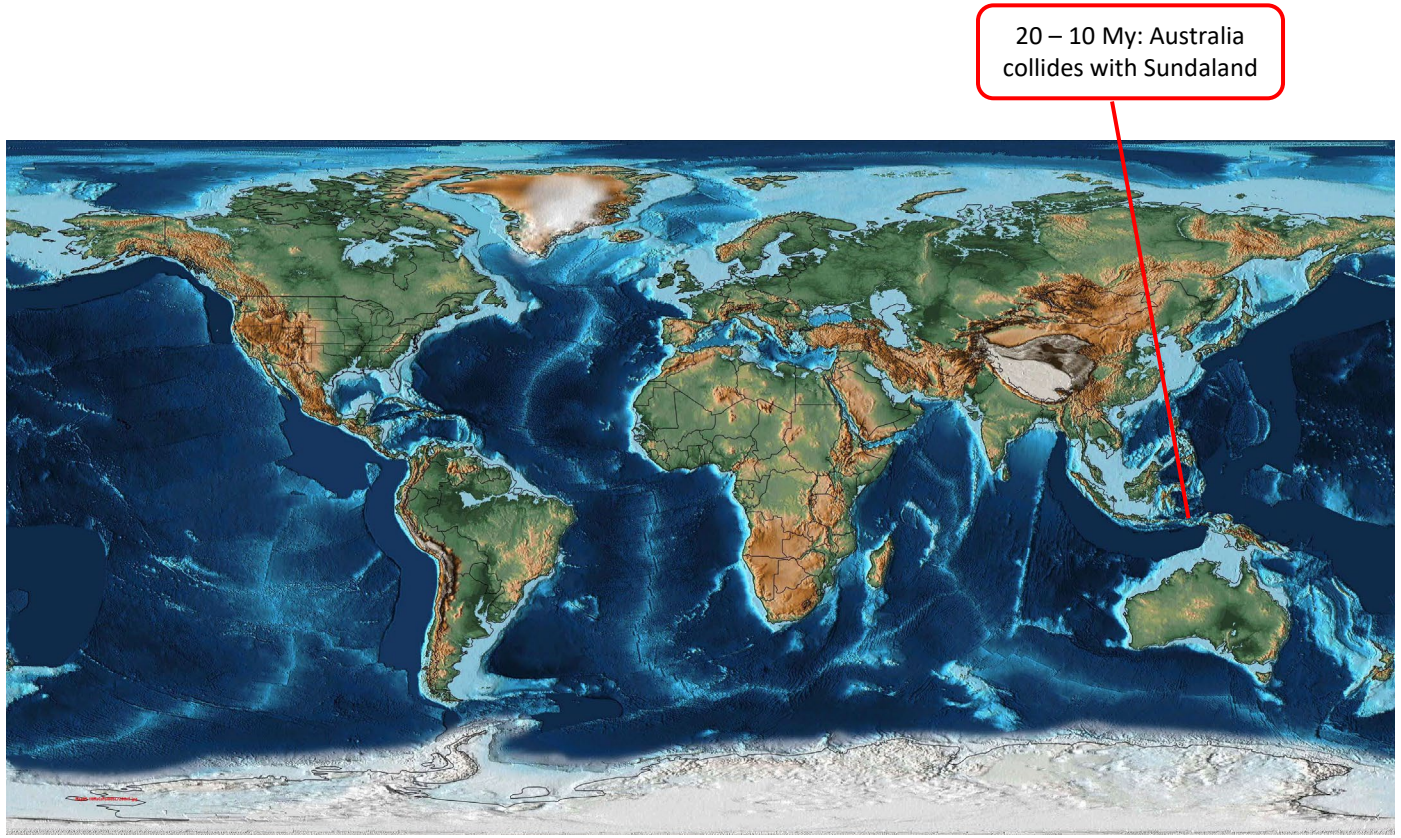


Source: PALEOMAP Project by C. Scotese

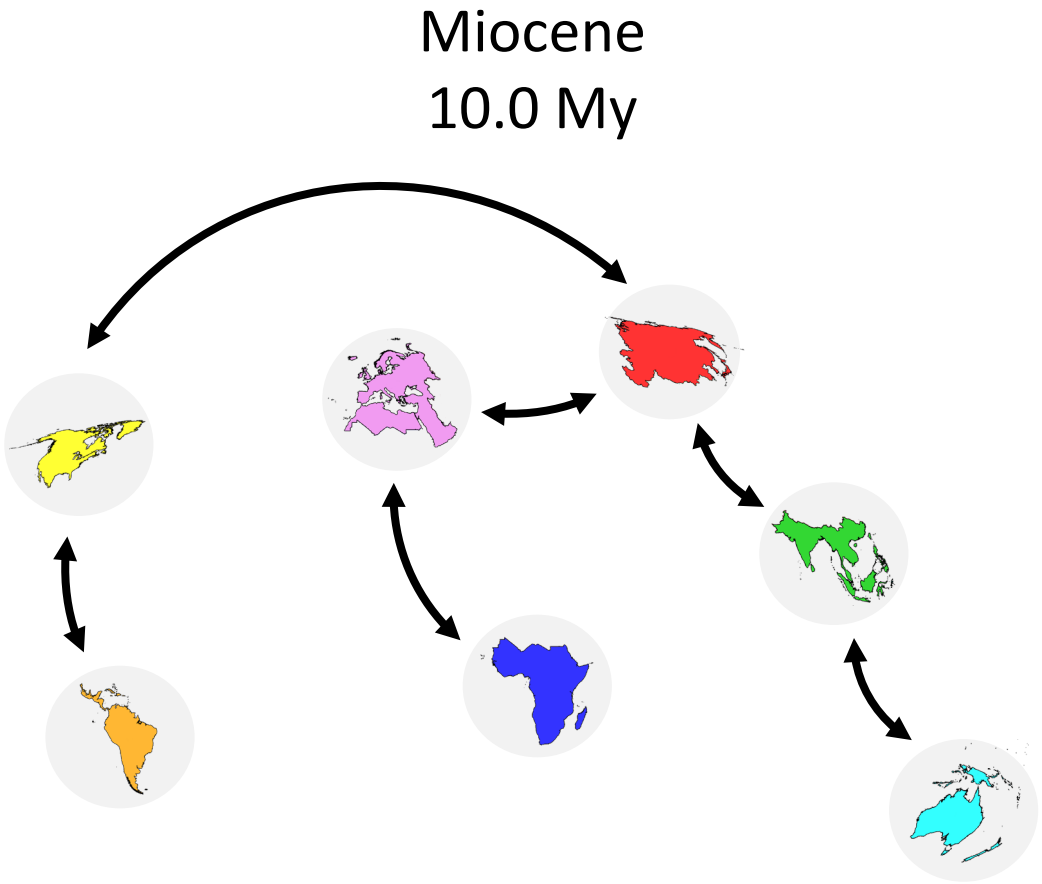


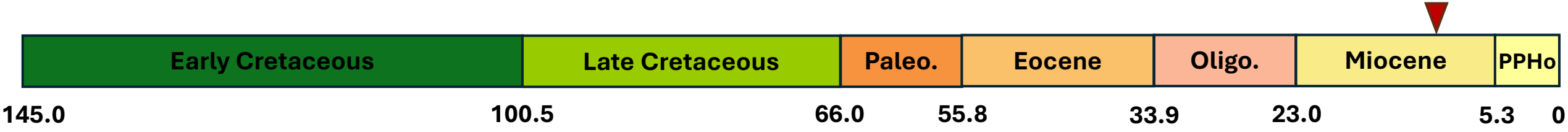


Biogeographic methods

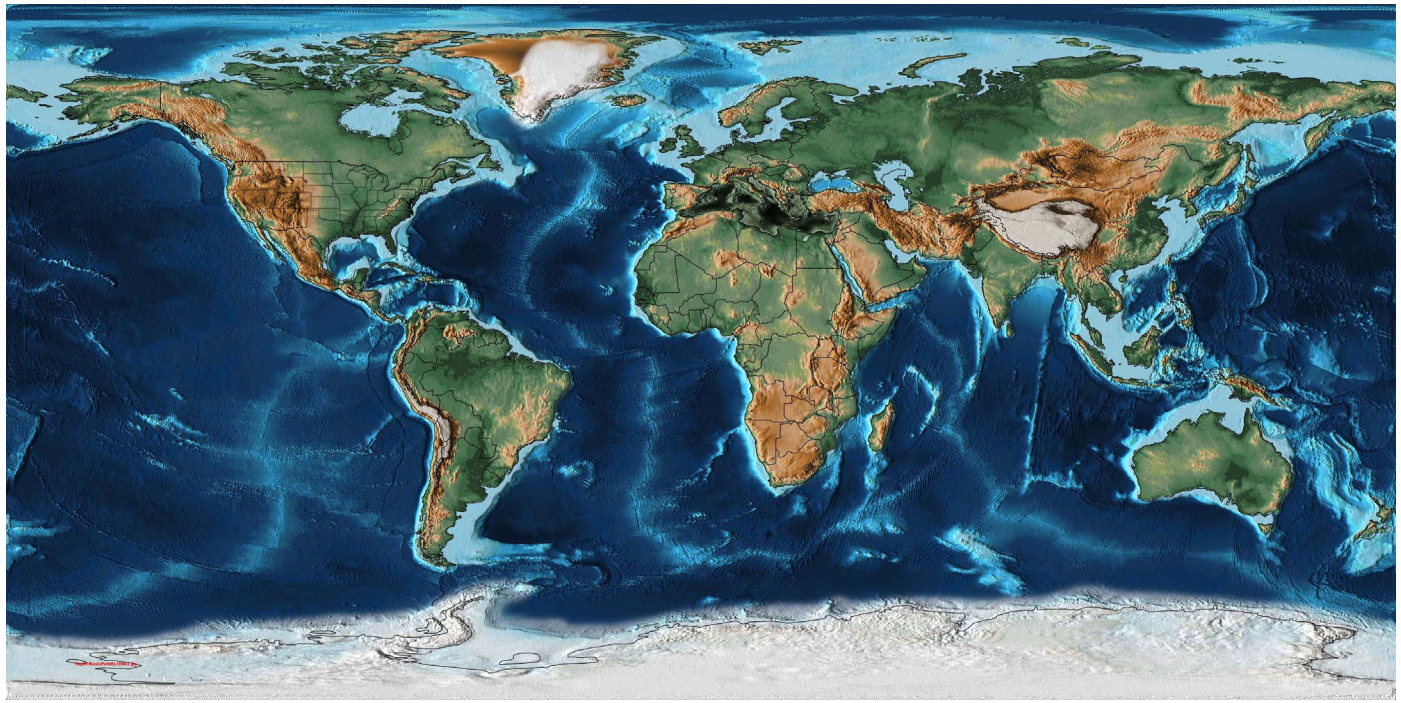


Source: PALEOMAP Project by C. Scotese



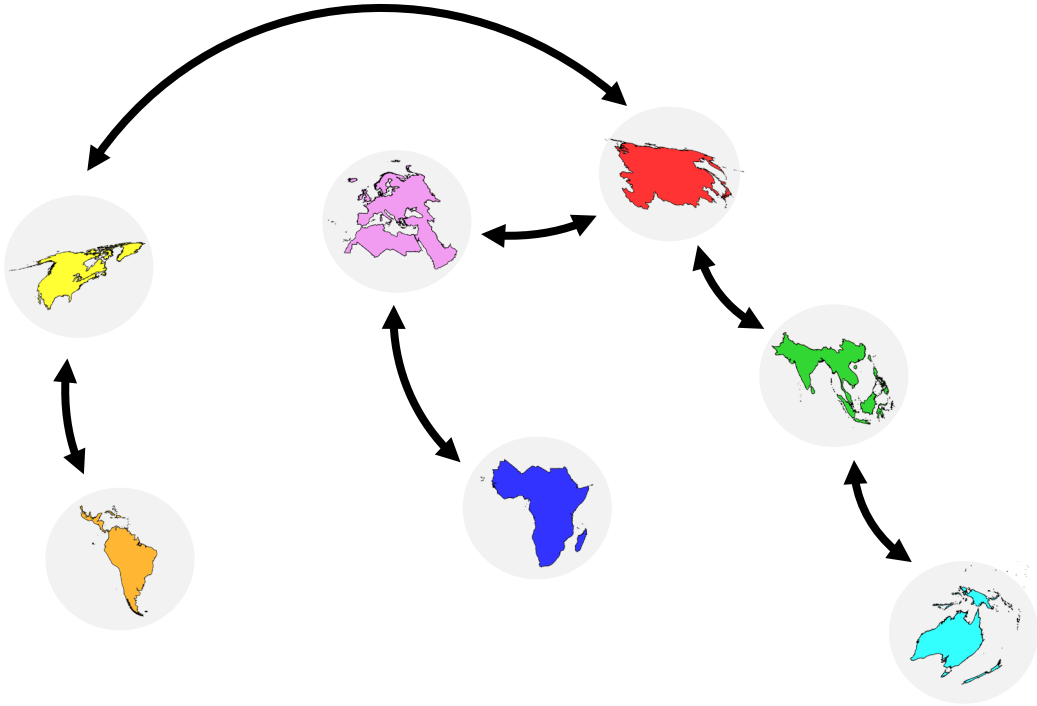


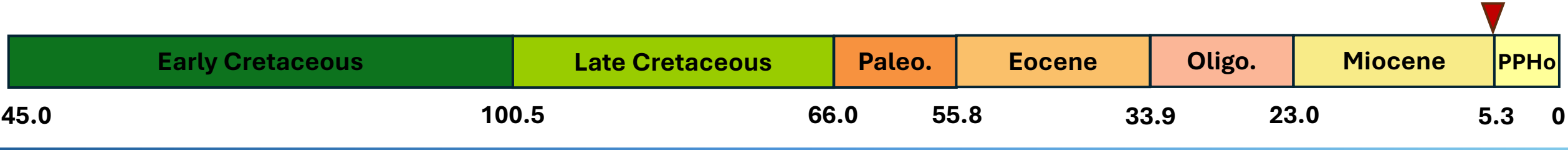
Biogeographic methods



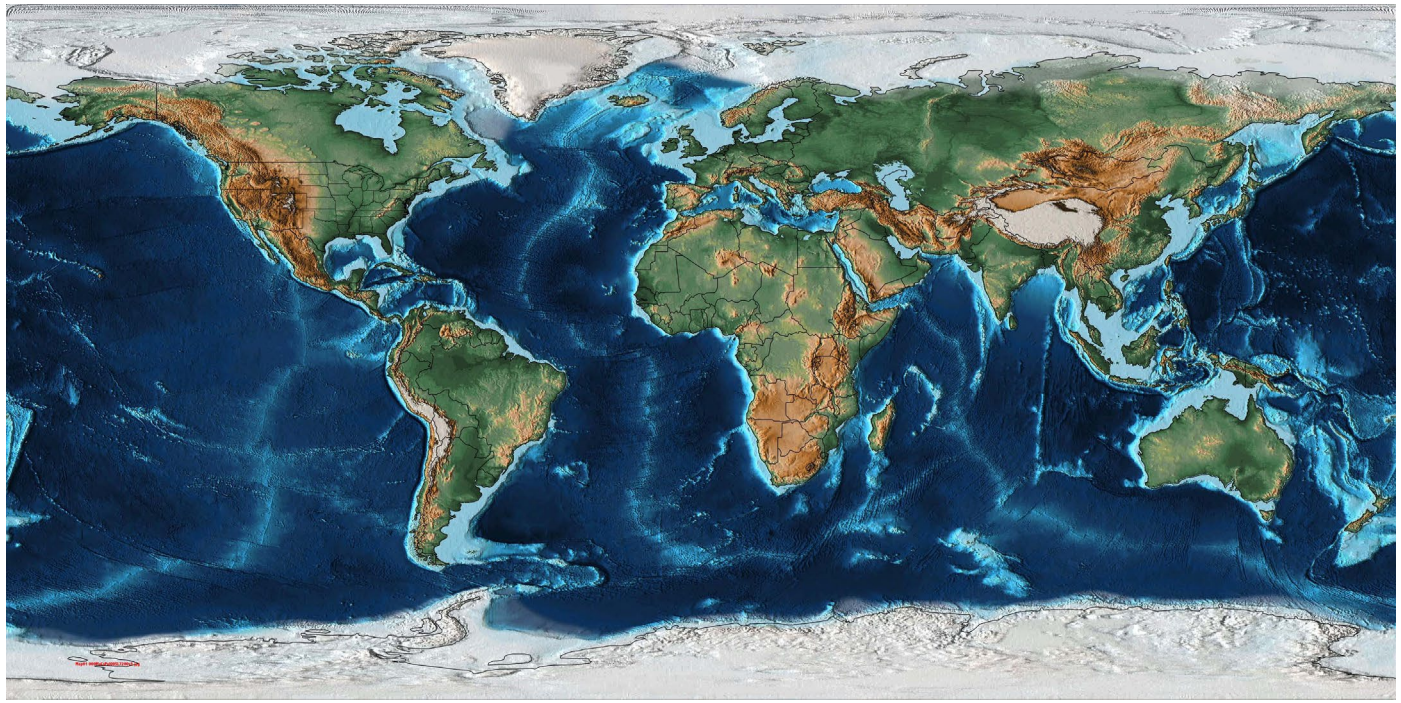
Source: PALEOMAP Project by C. Scotese

Miocene to Plio-Pleisto-Holocene
5.3 My

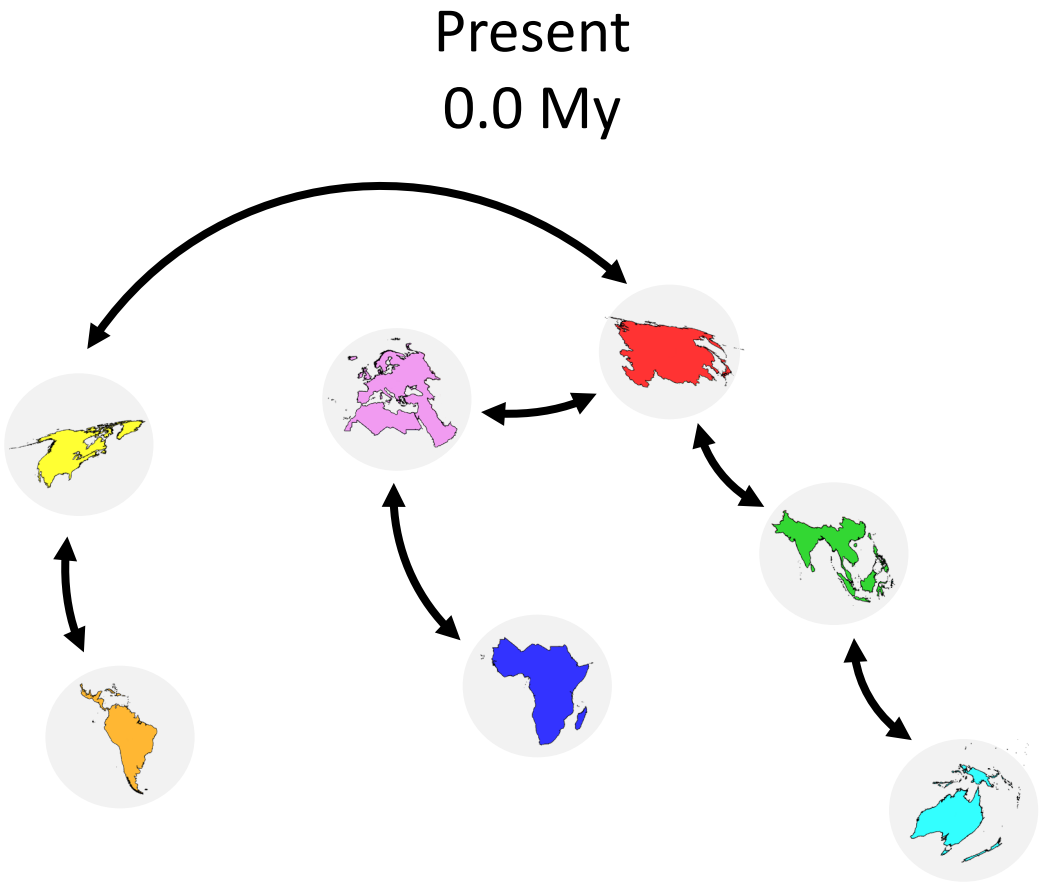


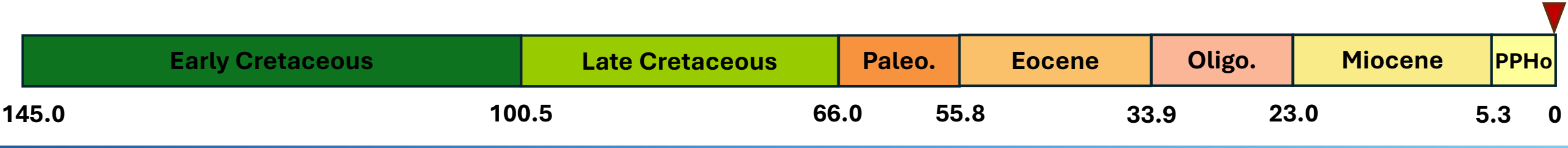


Biogeographic methods

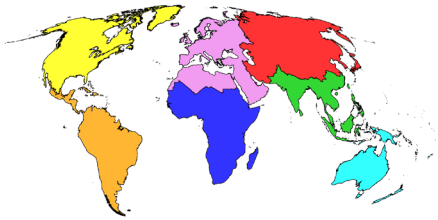


Source: PALEOMAP Project by C. Scotese





Biogeographic methods



BioGeoBEARS framework:

- DIVALIKE, DEC, DIVALIKE + J, DEC + J
- Model selection based on AICc
- Best model = **Time-stratified DEC + J**

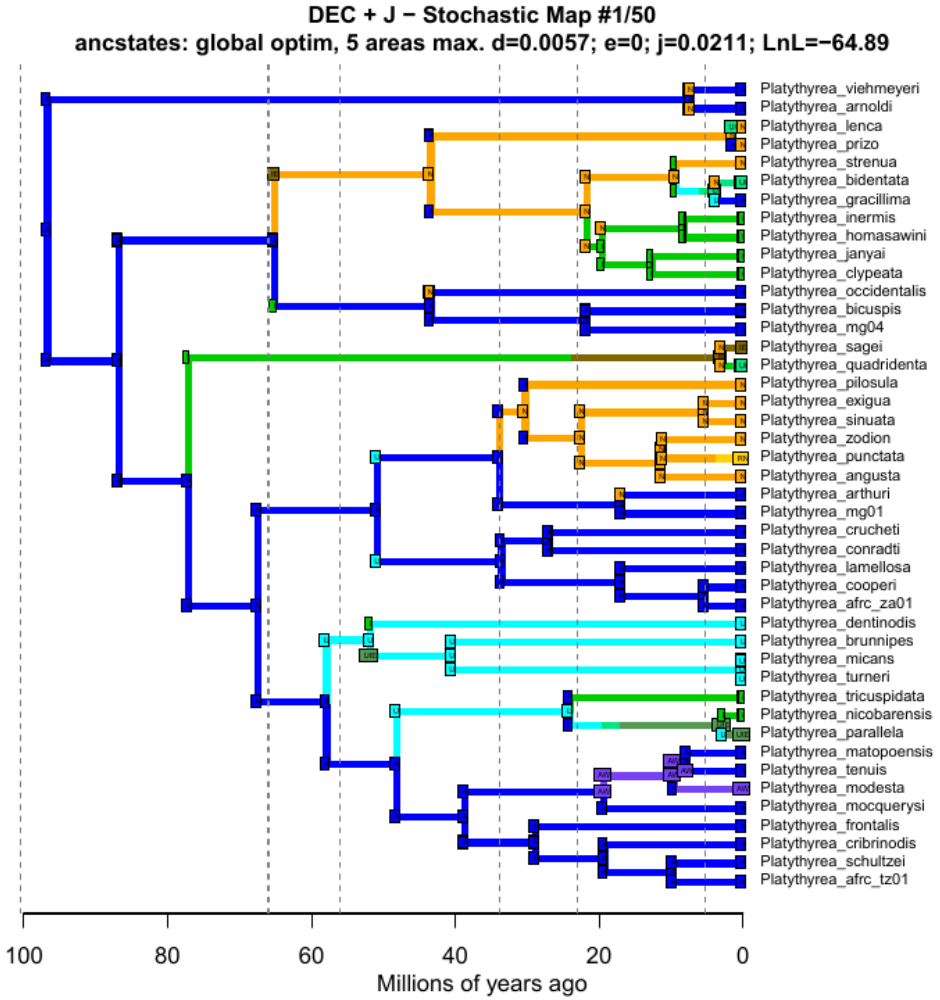
Model of **continental connectivity**

Ancestral Range Estimates (ARE):

- Marginal likelihoods of node ranges

Biogeographic Stochastic Mapping (BSM):

- Simulation of **biogeographic histories** compatible with ancestral ranges estimates
- Summary statistics across 1000 BSM



Origins of clades

Overall picture:

- Some important **regional radiations**
- Many **independent colonizations**

Origins of S&S clades:

- **Afrotropics**: Platytherea, Plectroctena, Hypoponera
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Origin of Ponerinae:

Afrotropics + **Neotropics** [+ **Indo(Malaya)**]

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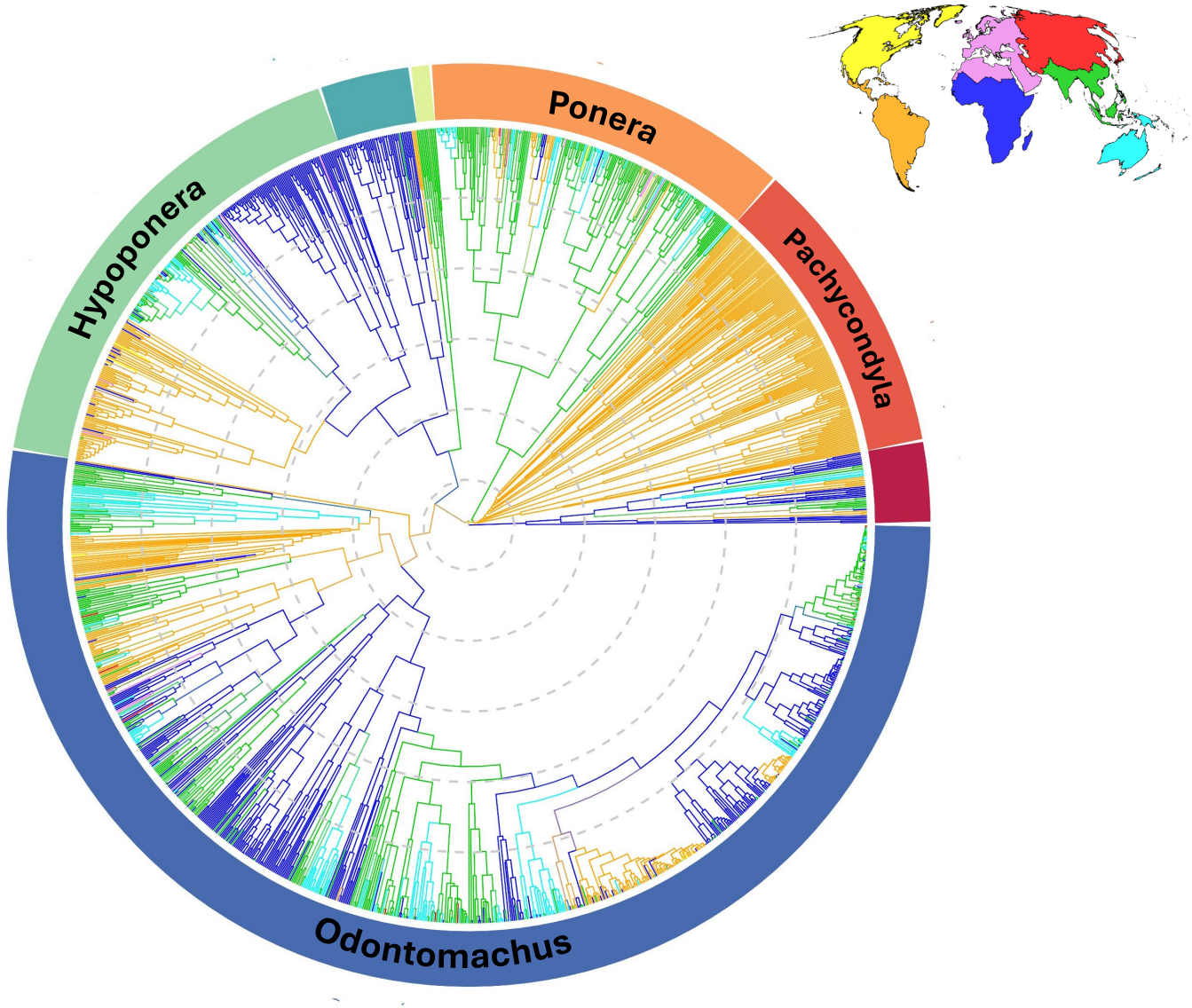
Gondwana



Ancestral Range Estimates
All Ponerinae species

Doré et al., *in prep.*

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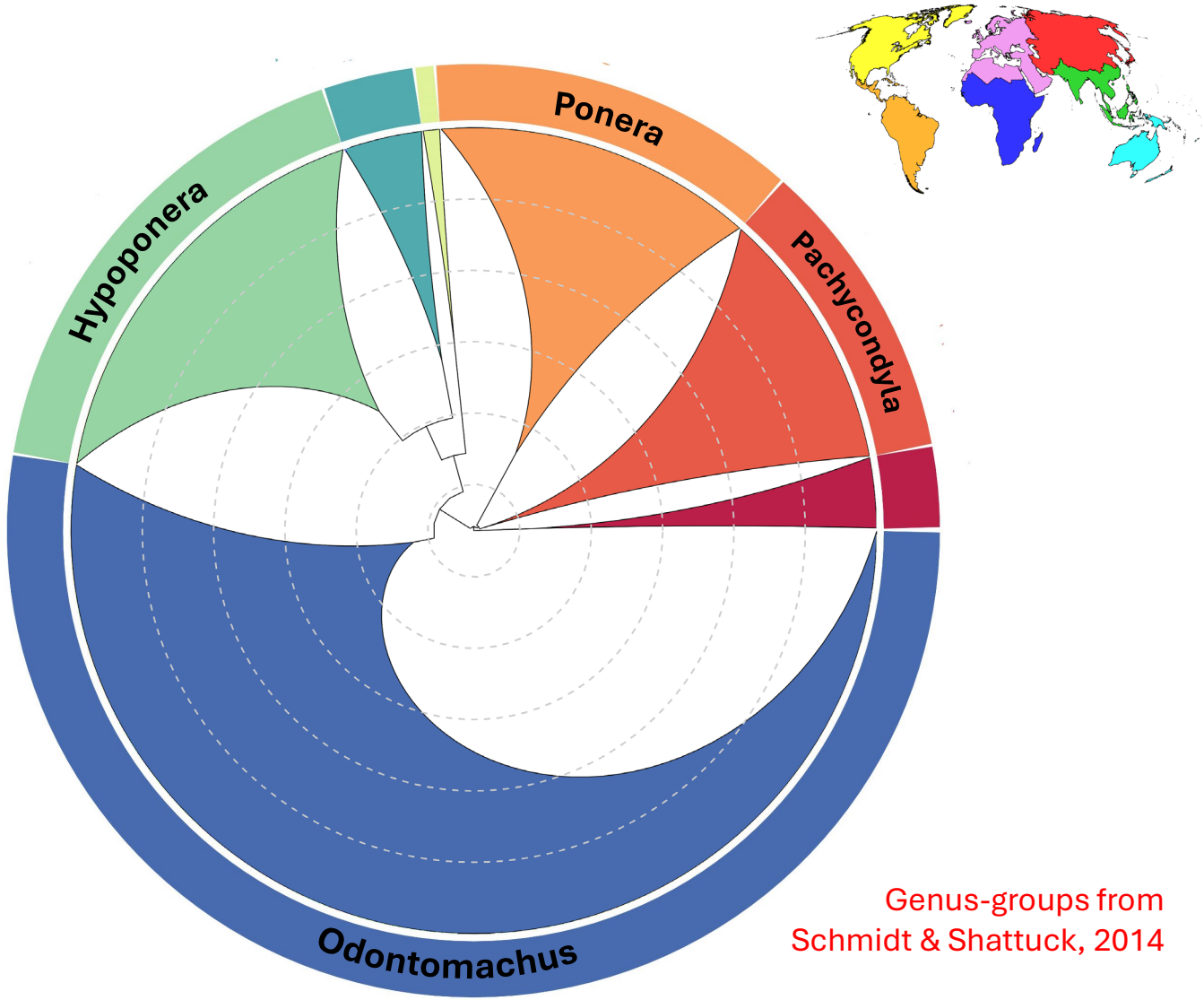
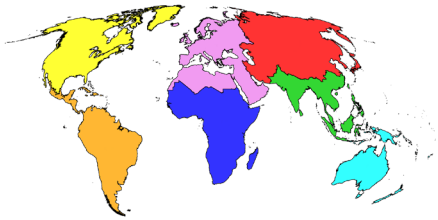


Genus-groups from Schmidt & Shattuck, 2014

Ancestral Range Estimates
S&S Genus-groups

Doré et al., *in prep.*

Origins of clades



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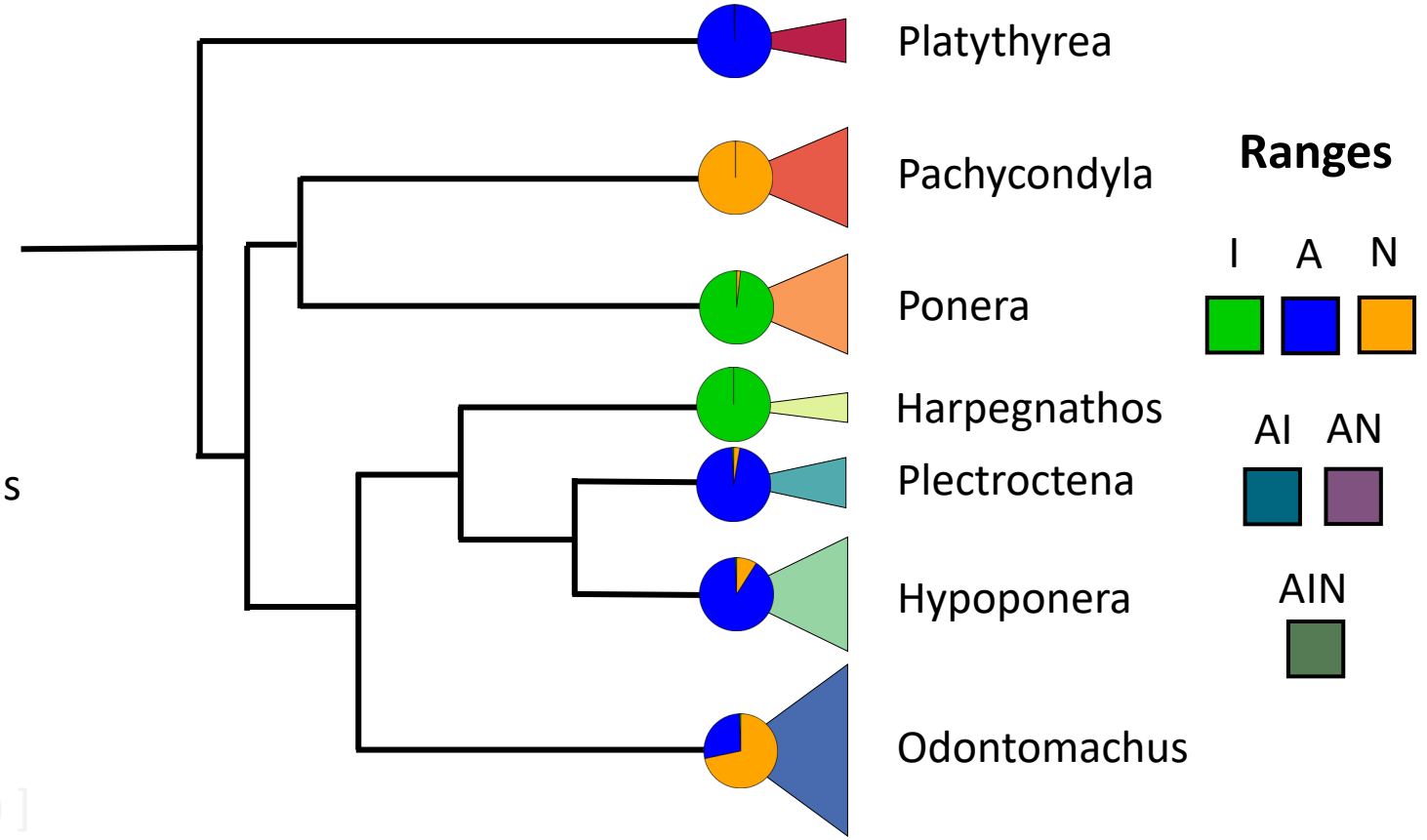

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Doré et al., *in prep.*

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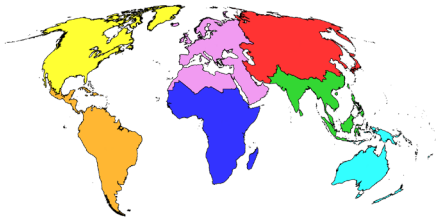

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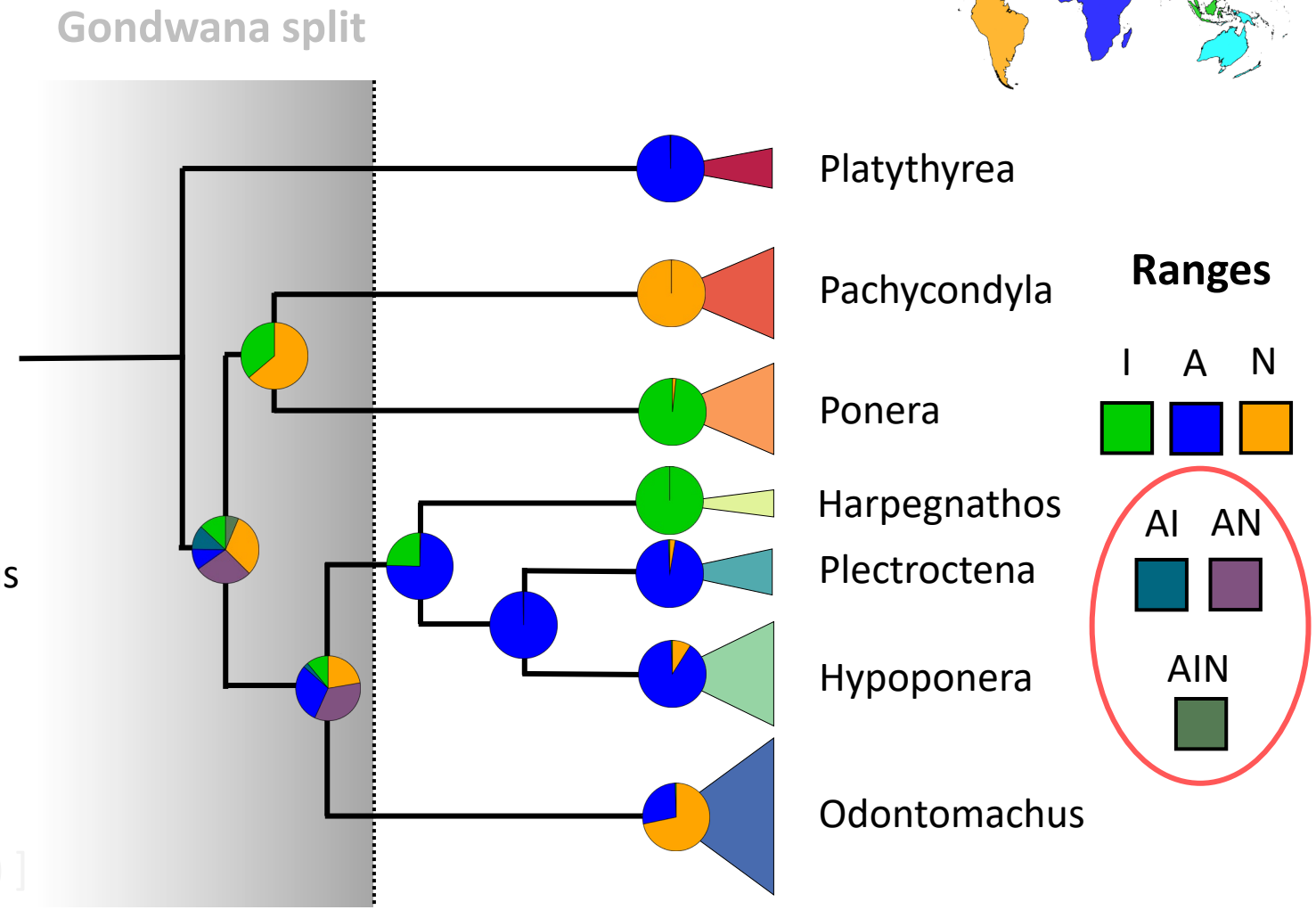

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Doré et al., *in prep.*

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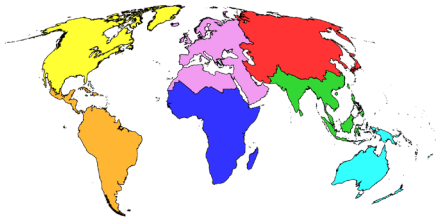

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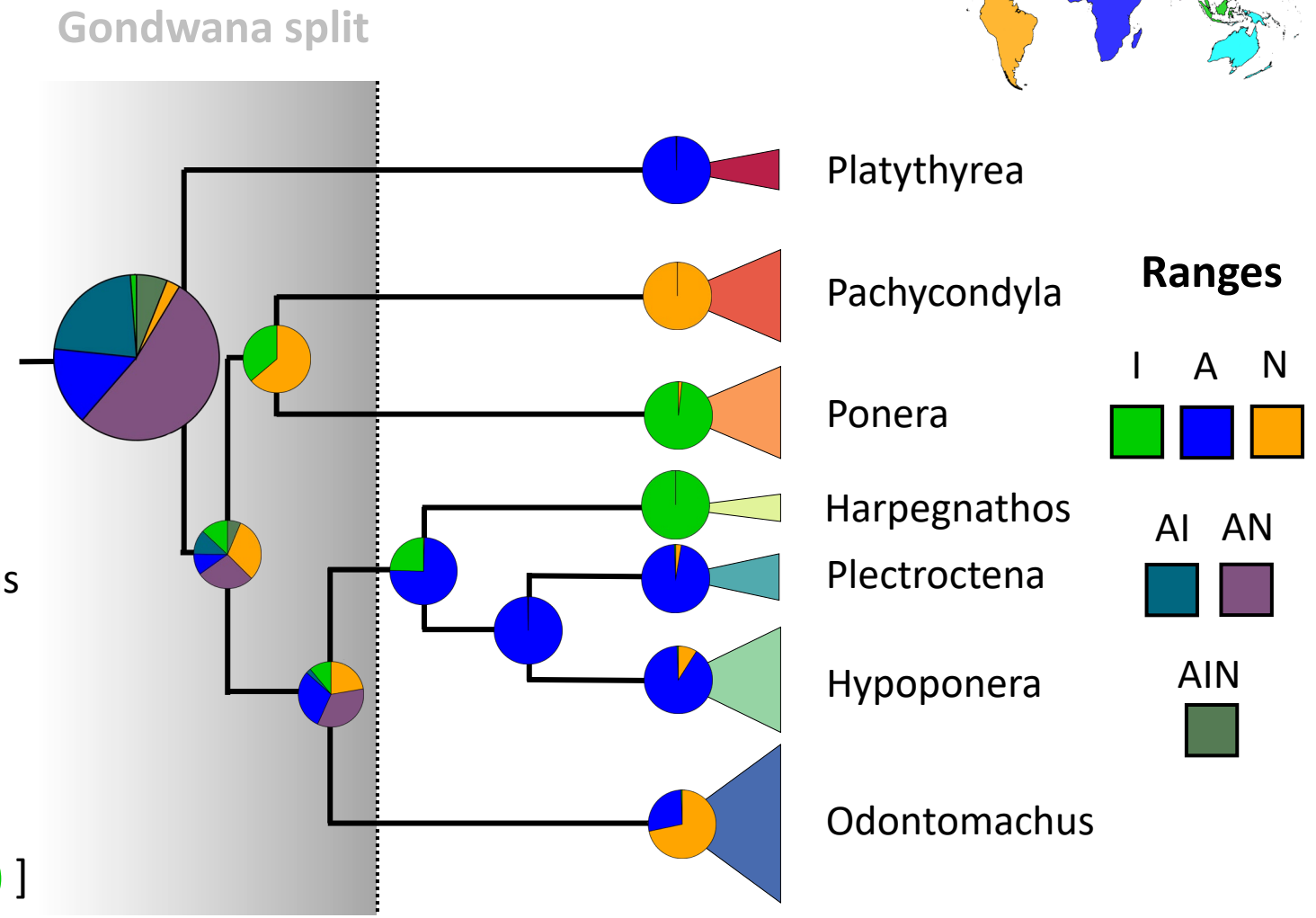
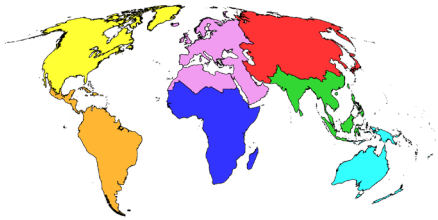
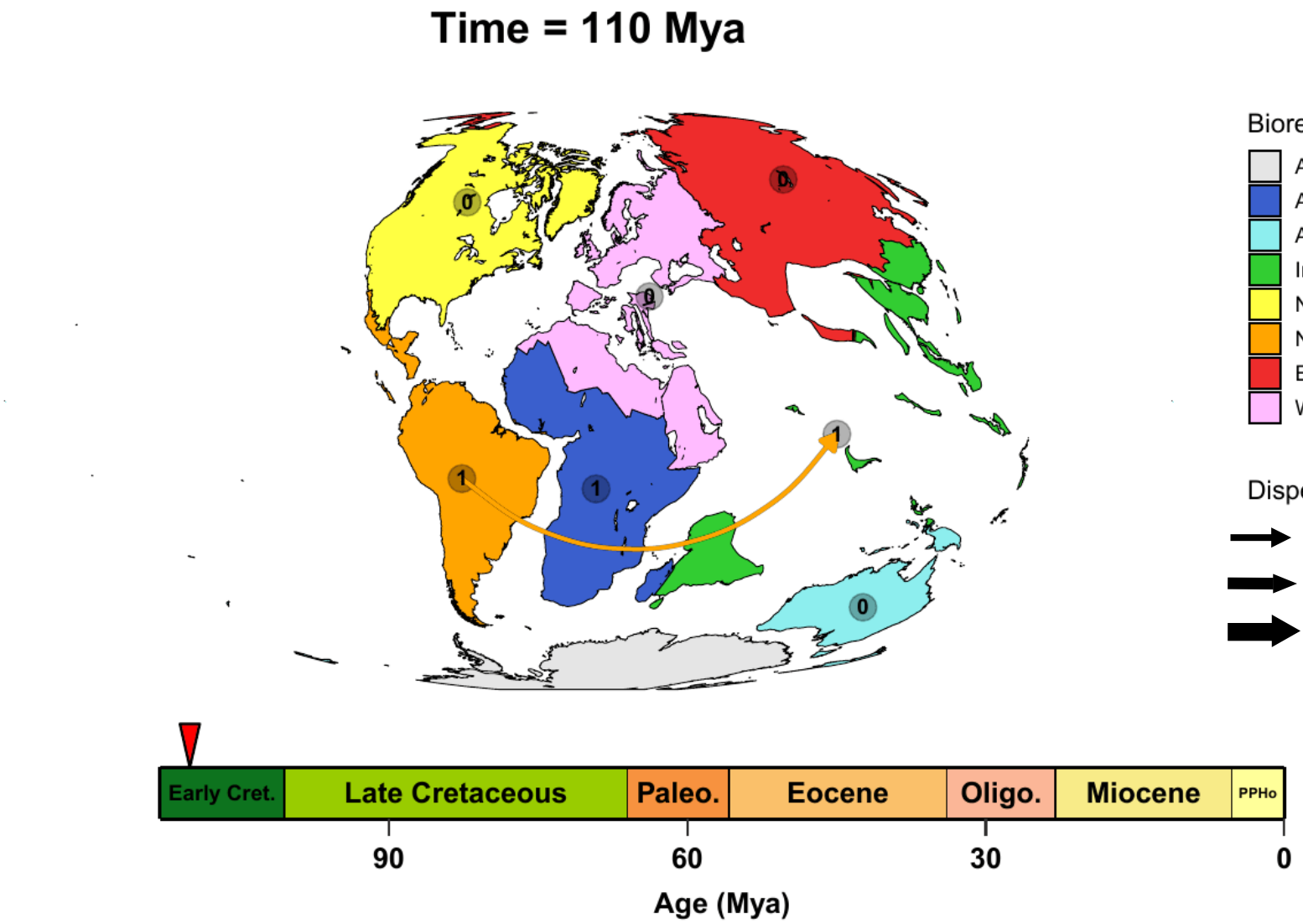


Ancestral Range Estimates
S&S Genus-groups

Doré et al., *in prep.*

Dispersal events in time





Doré et al., *in prep.*

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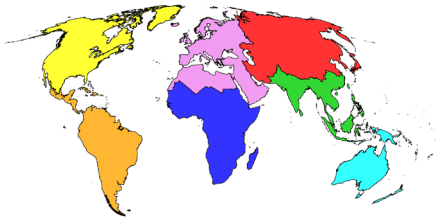
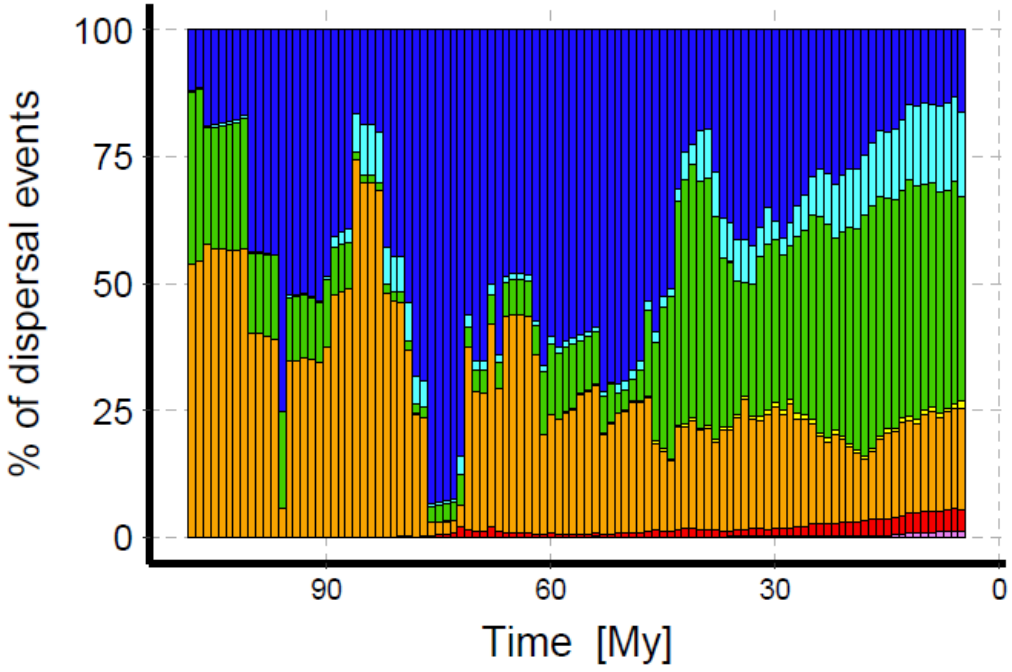


Dispersal events
per Source bioregions



Dispersal events
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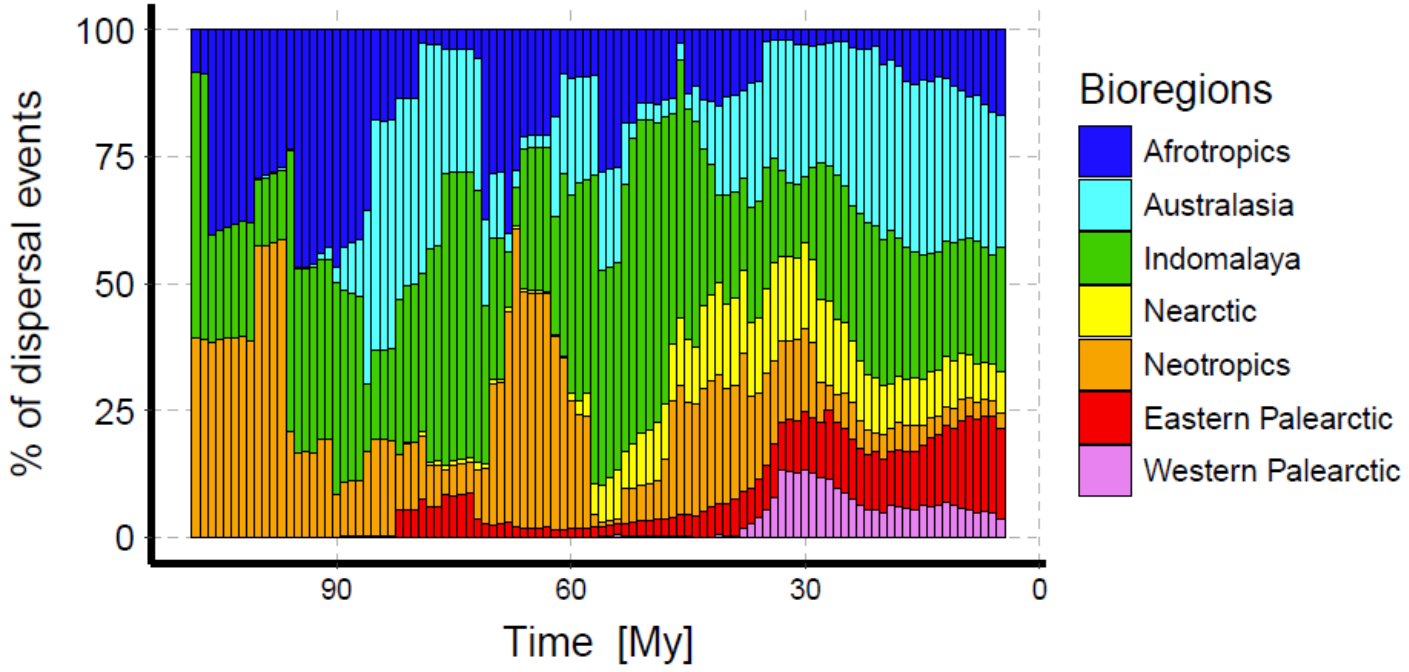

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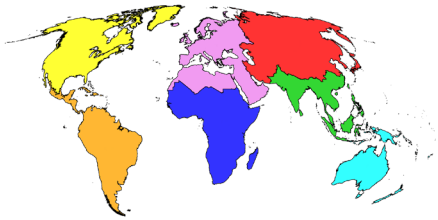

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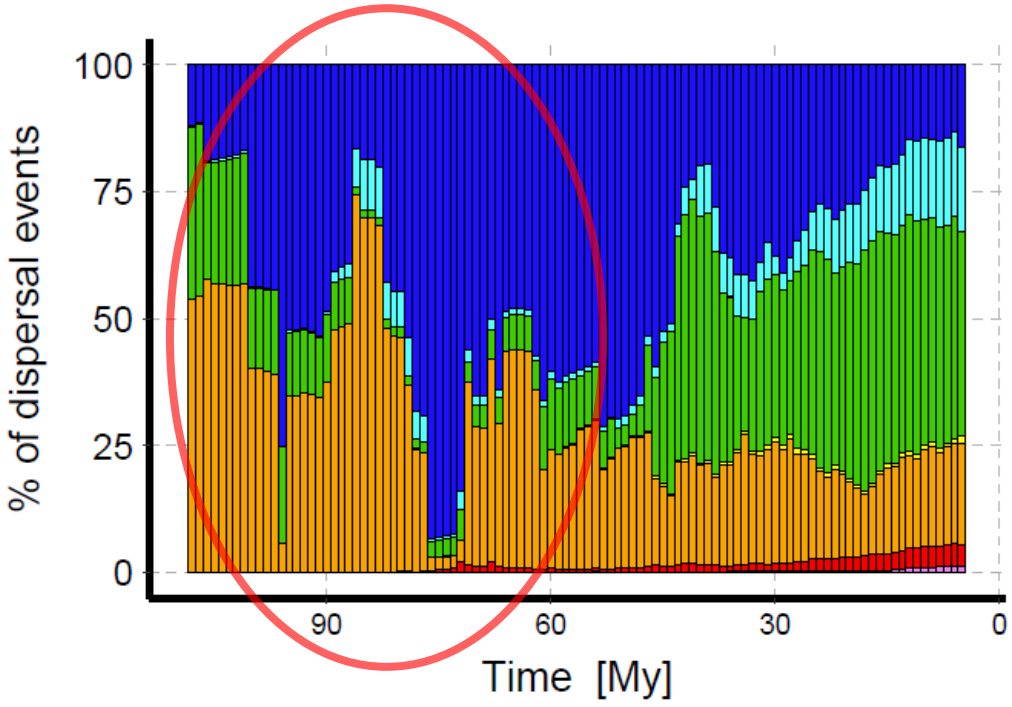

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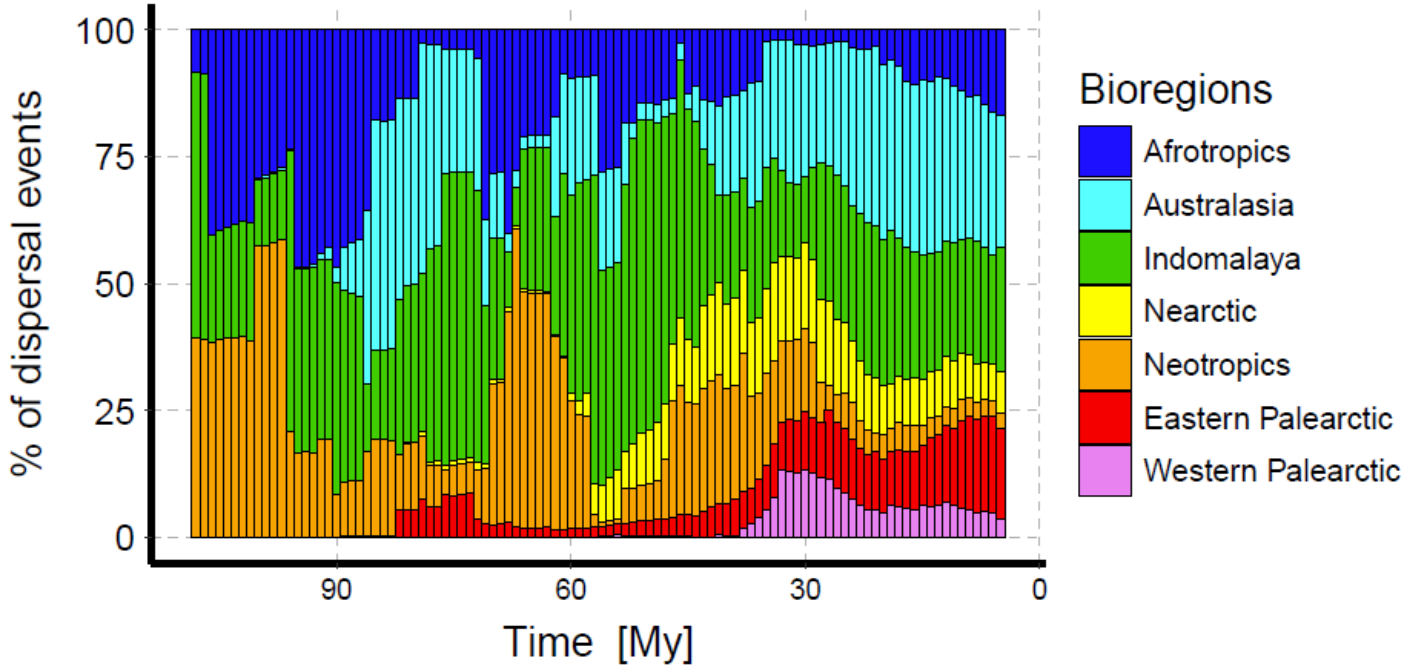

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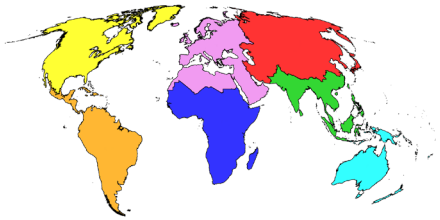

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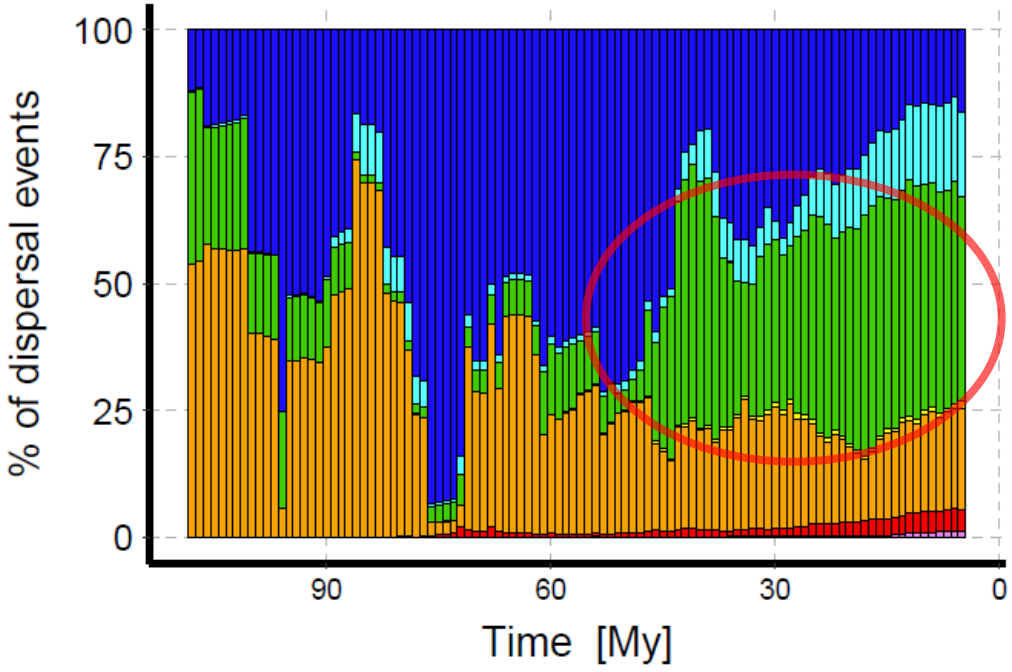

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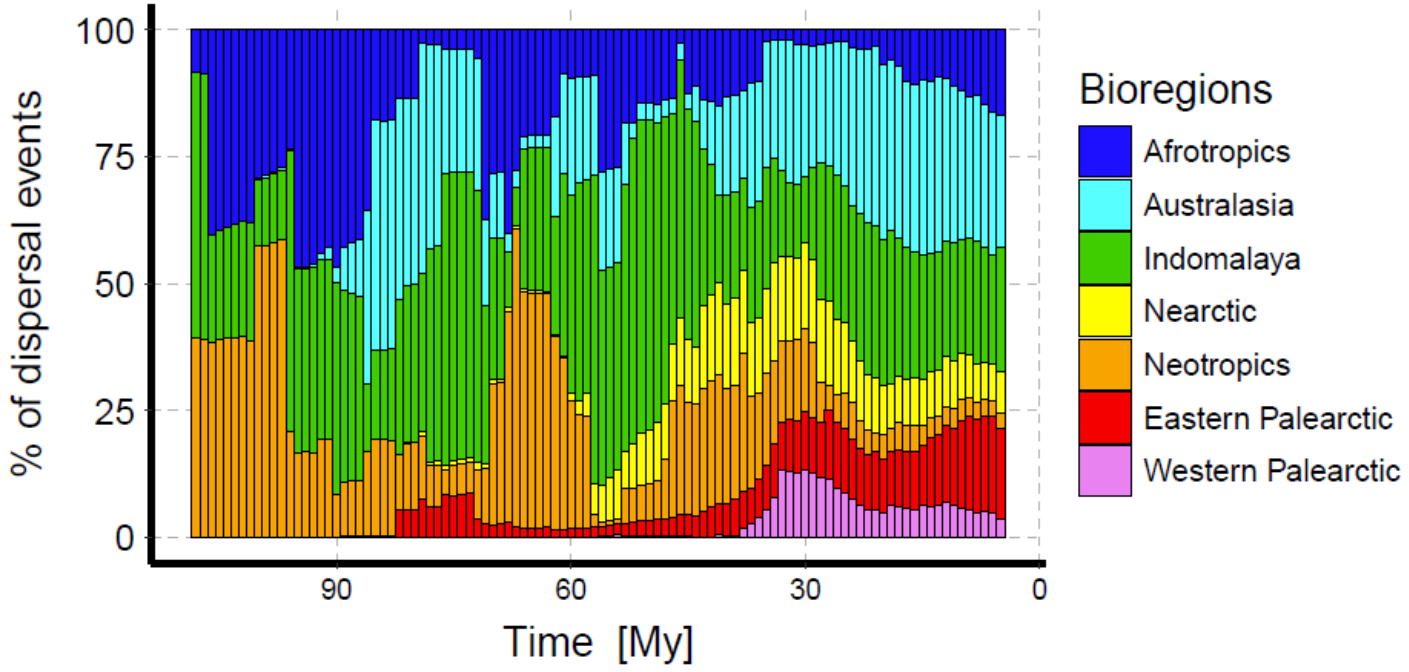

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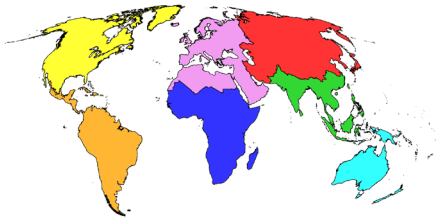

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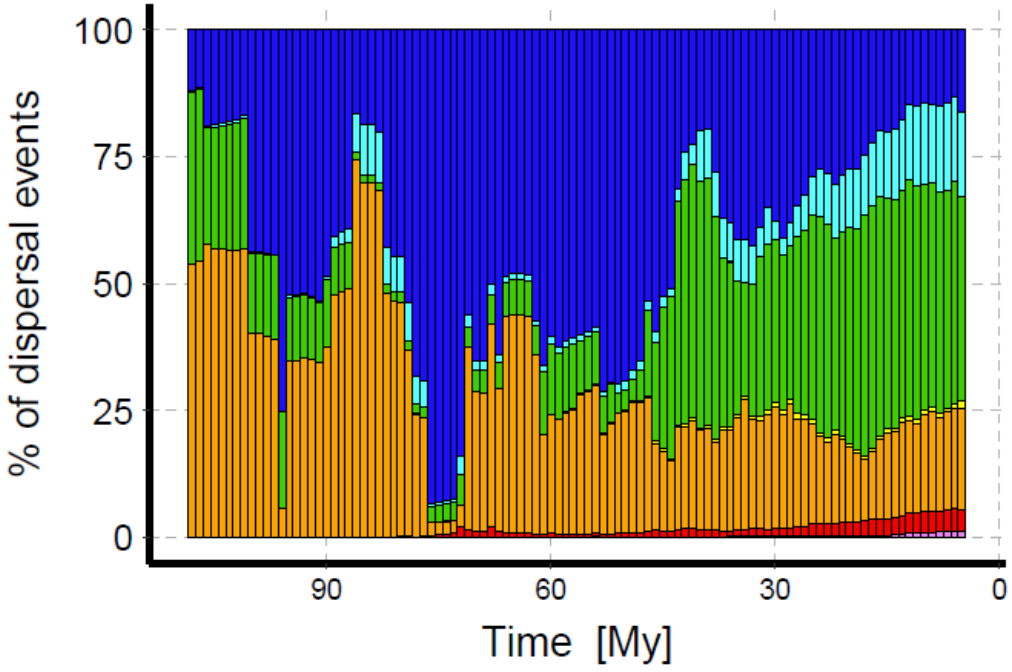

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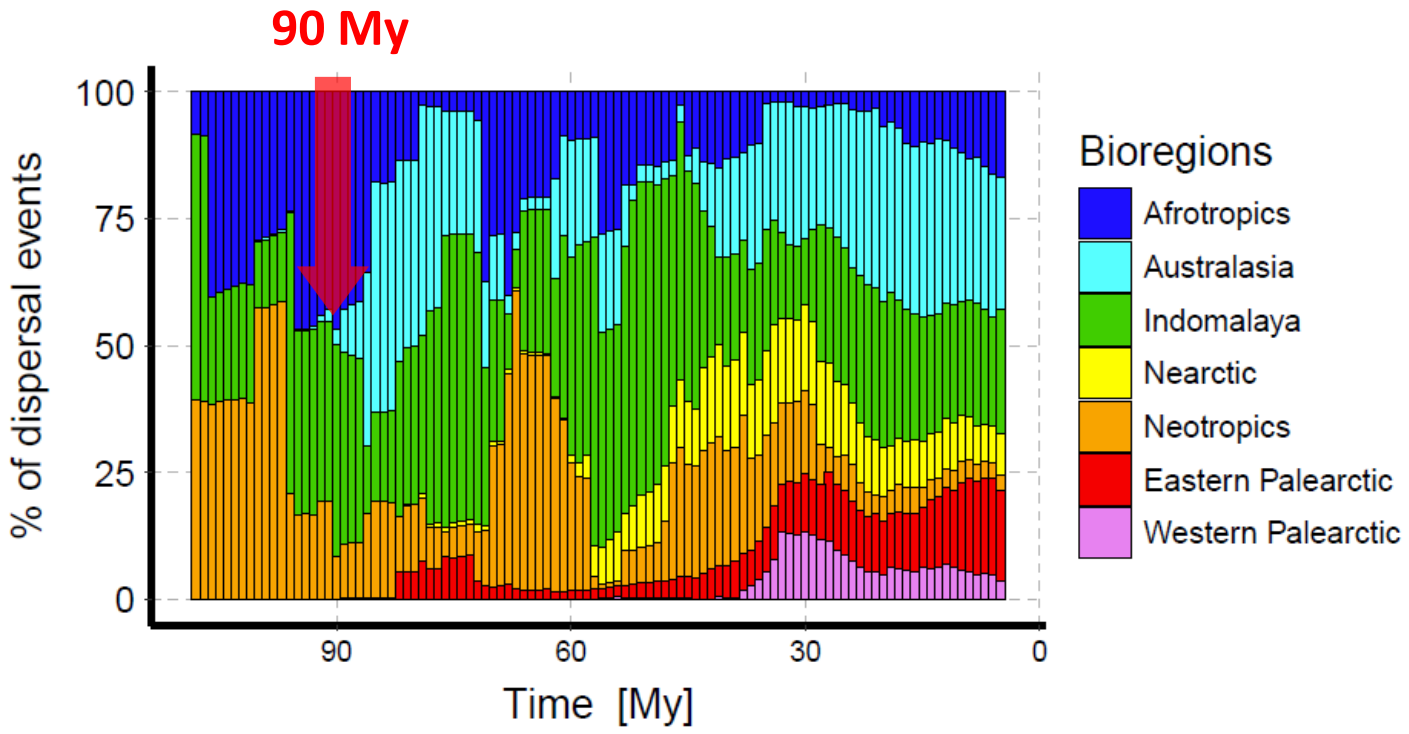

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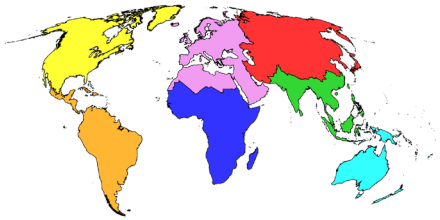

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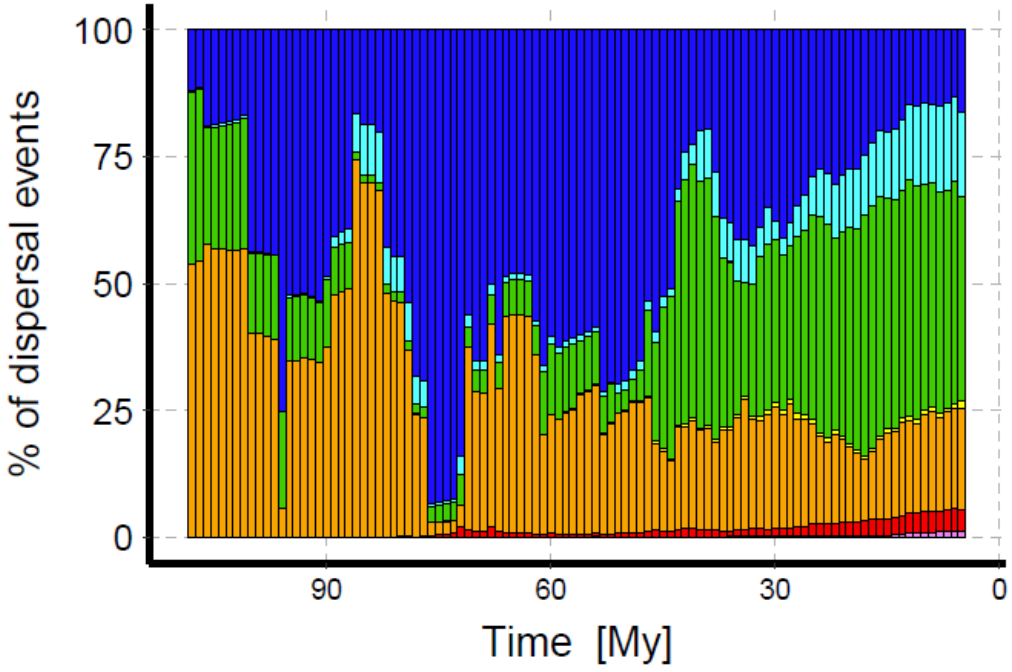

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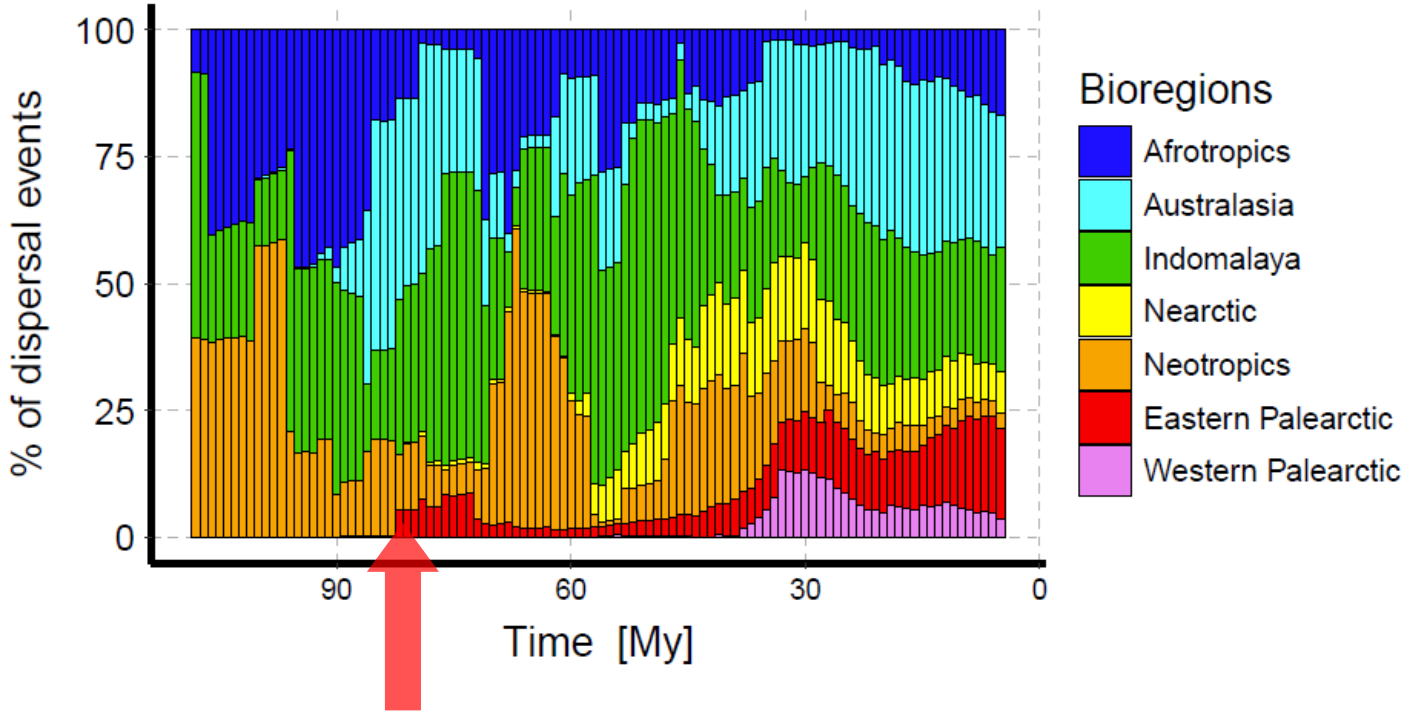

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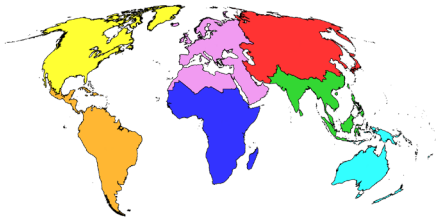

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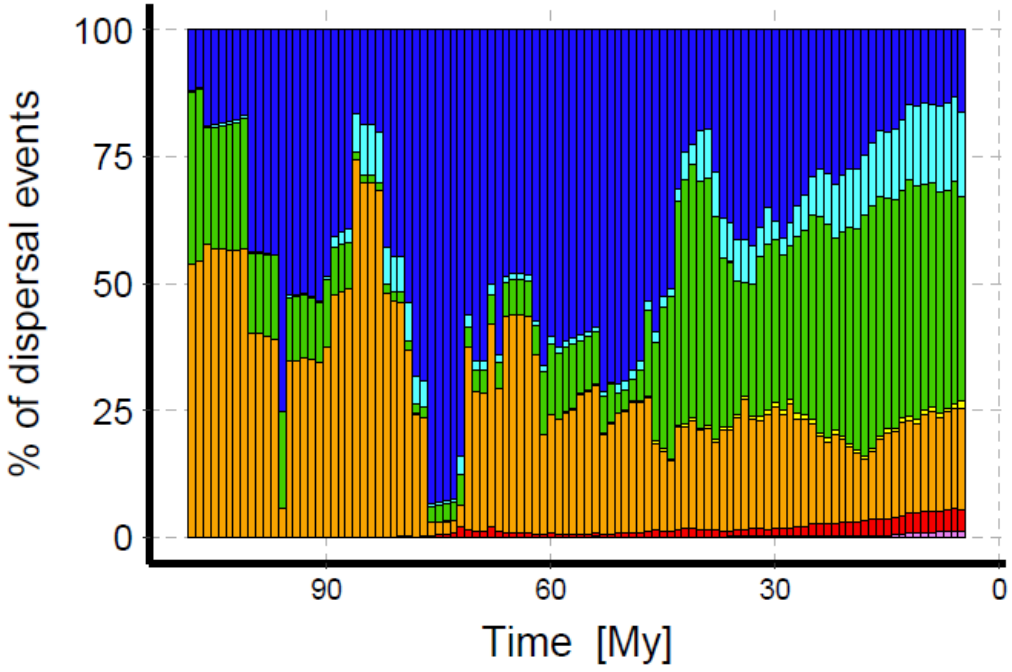

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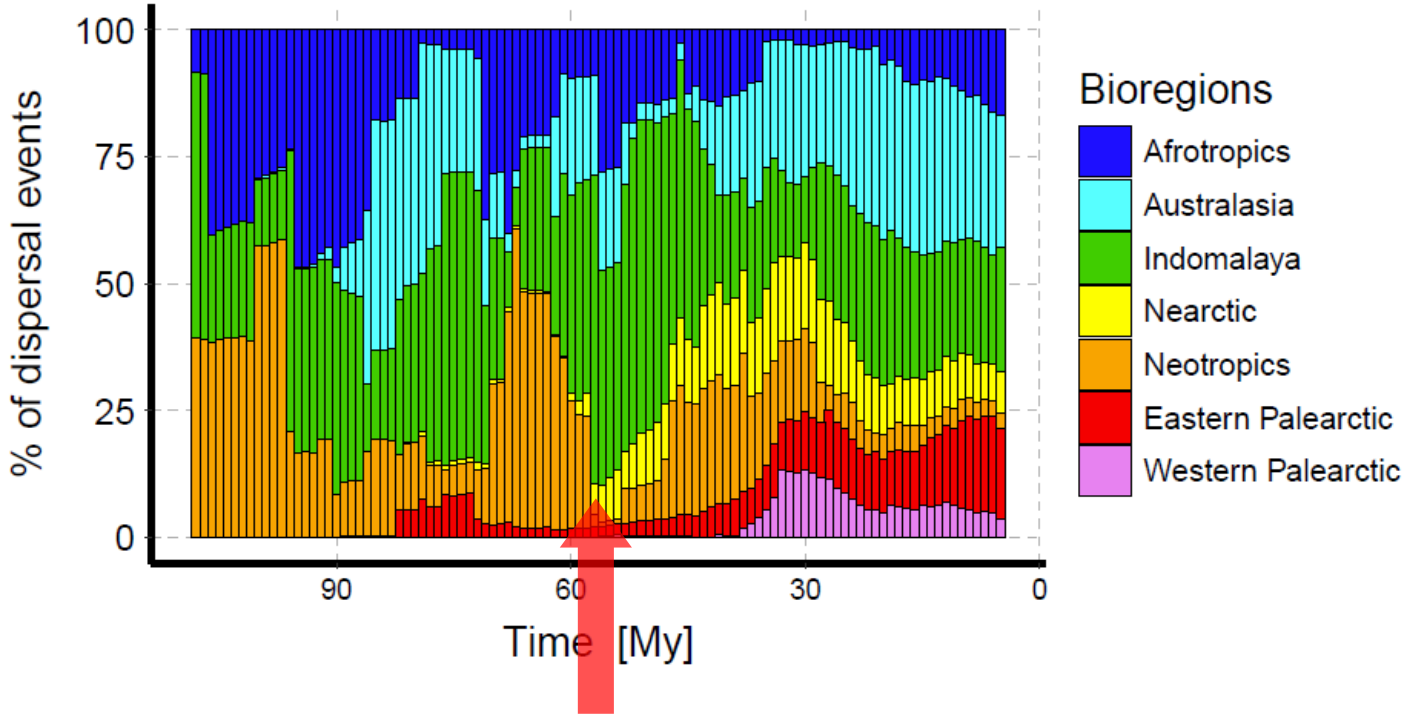

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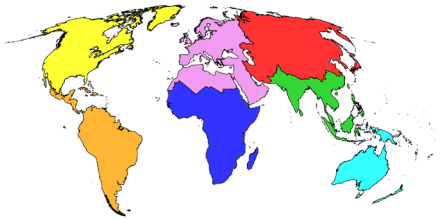

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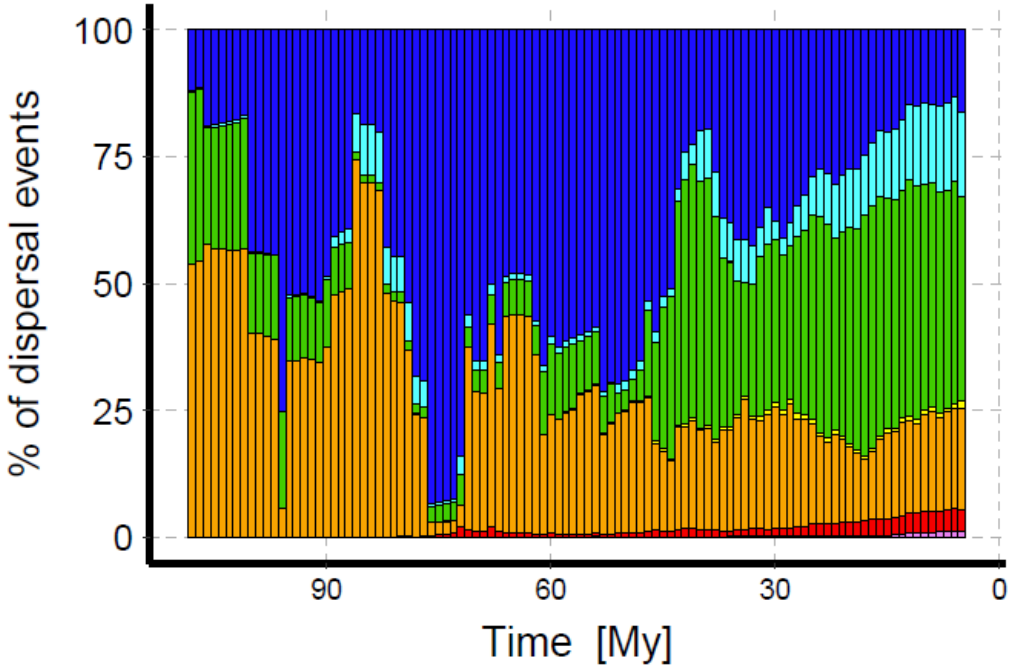

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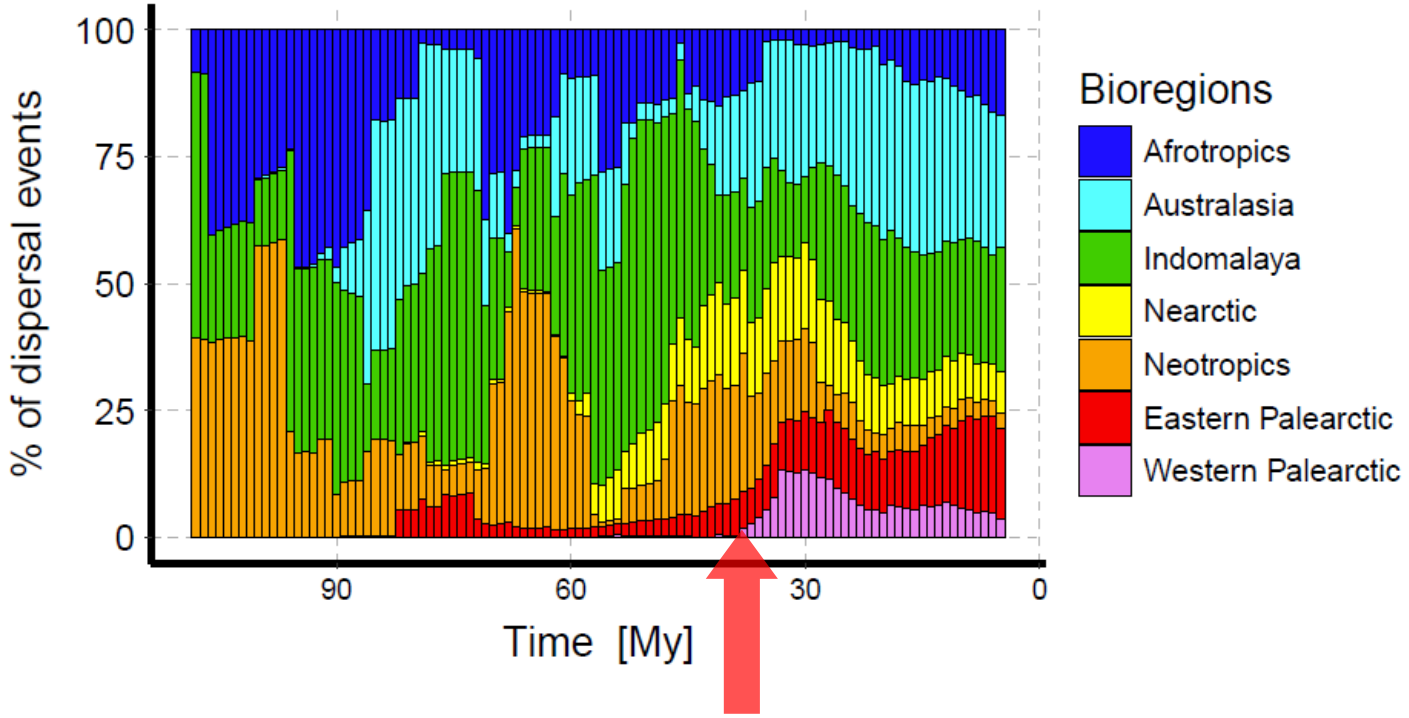

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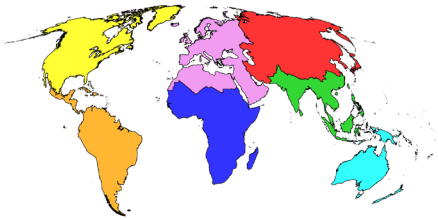
Macroevolutionary sources & sinks



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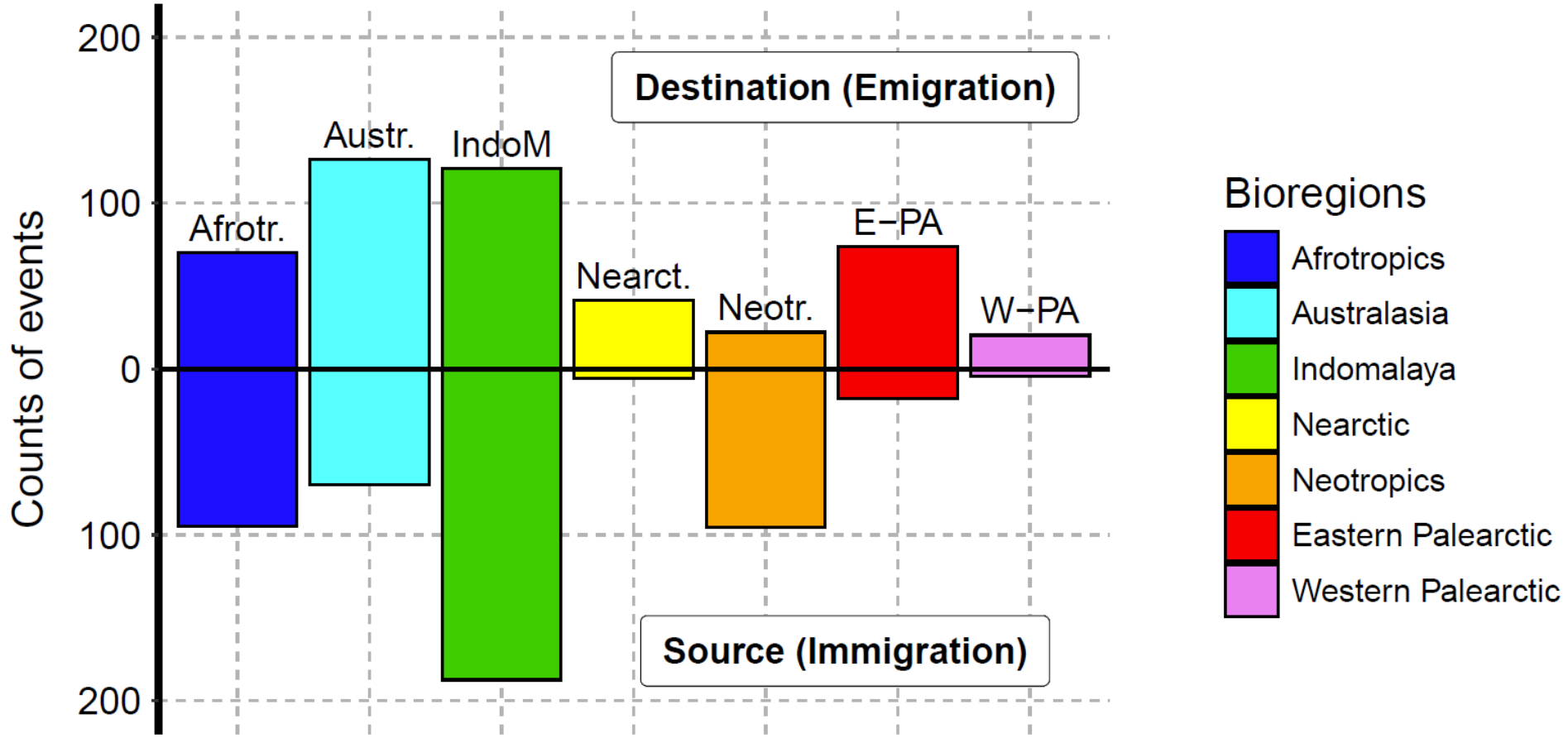

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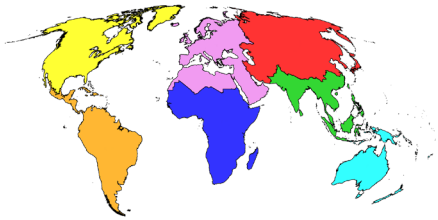

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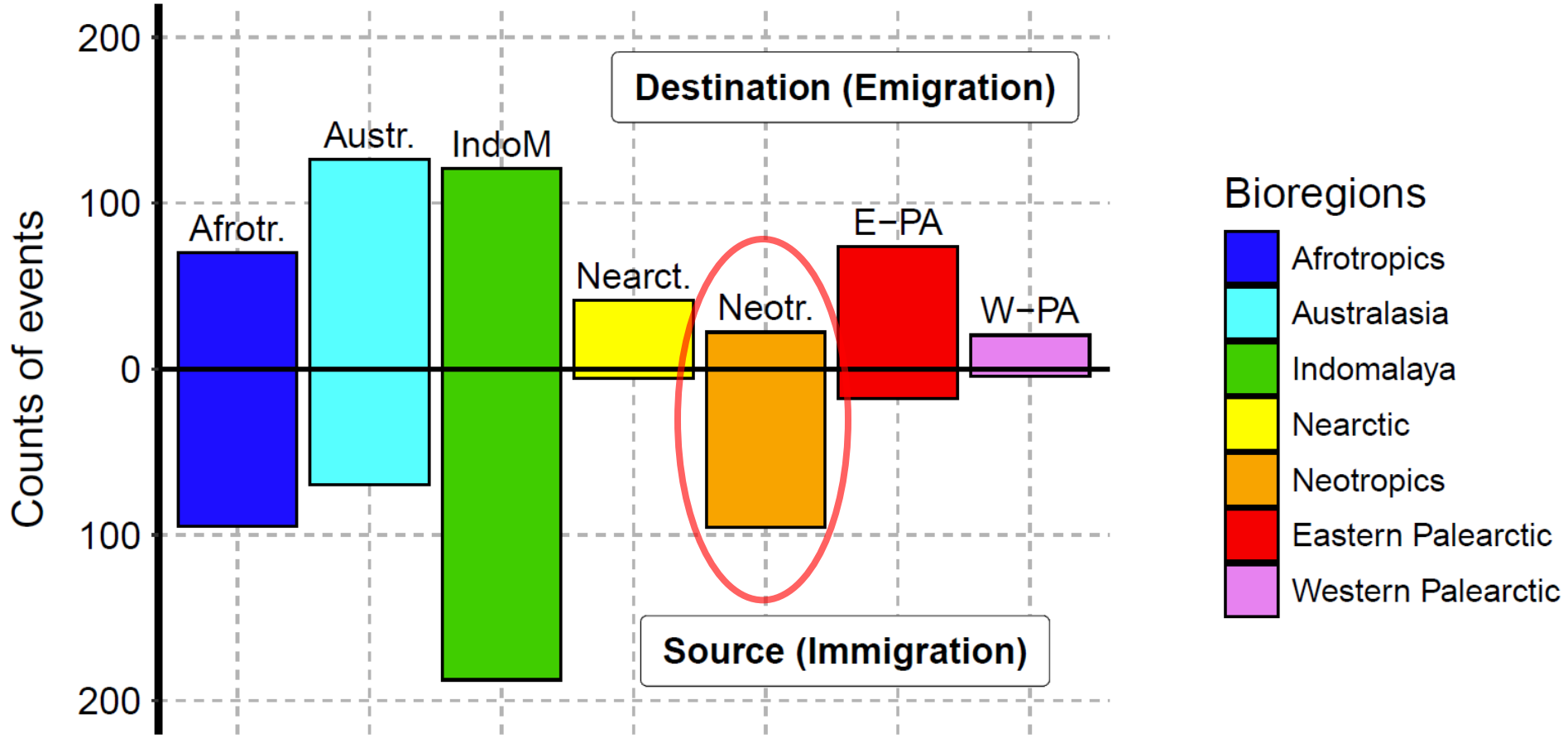

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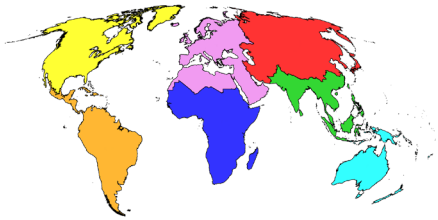

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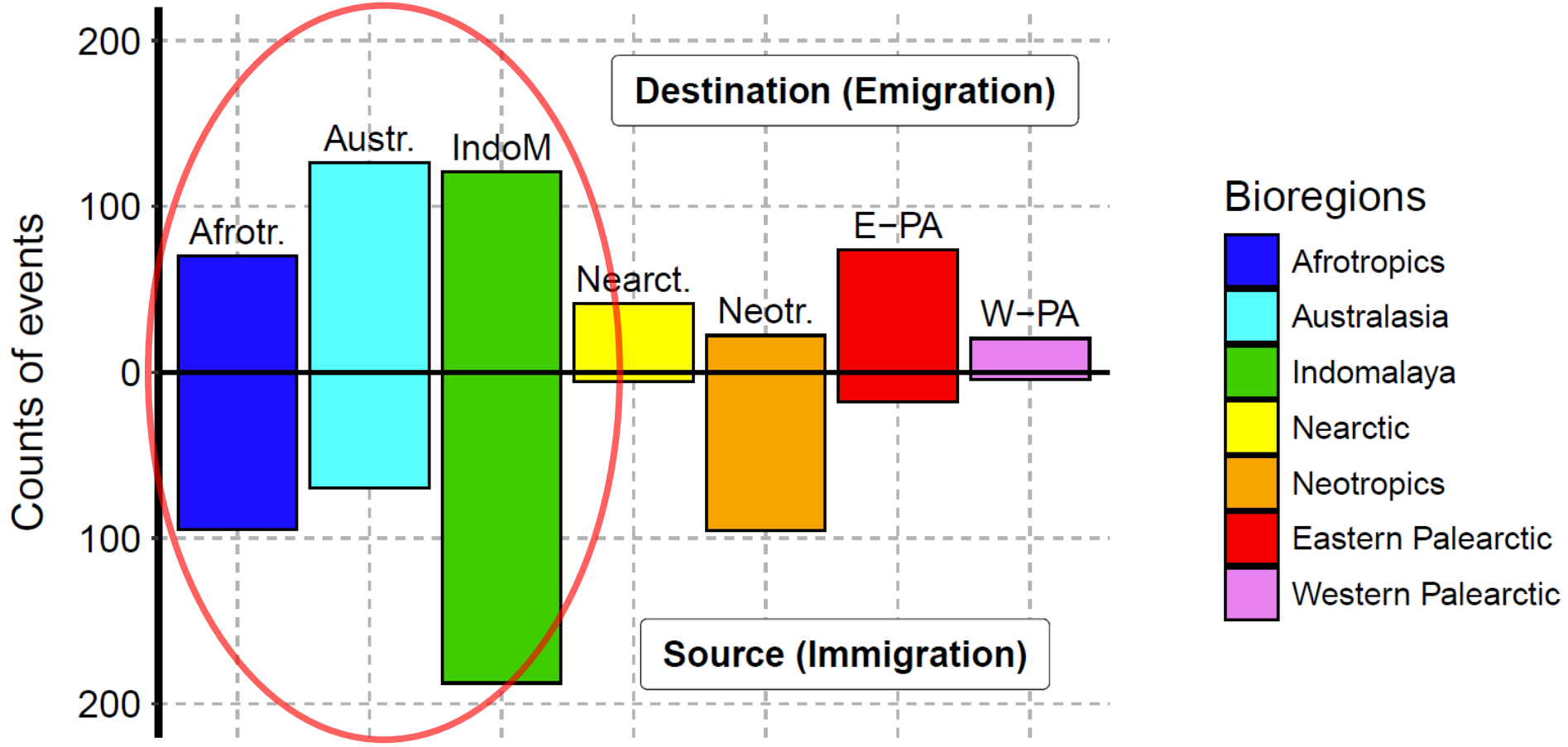

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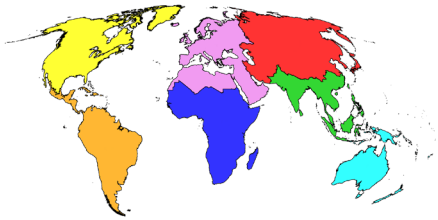

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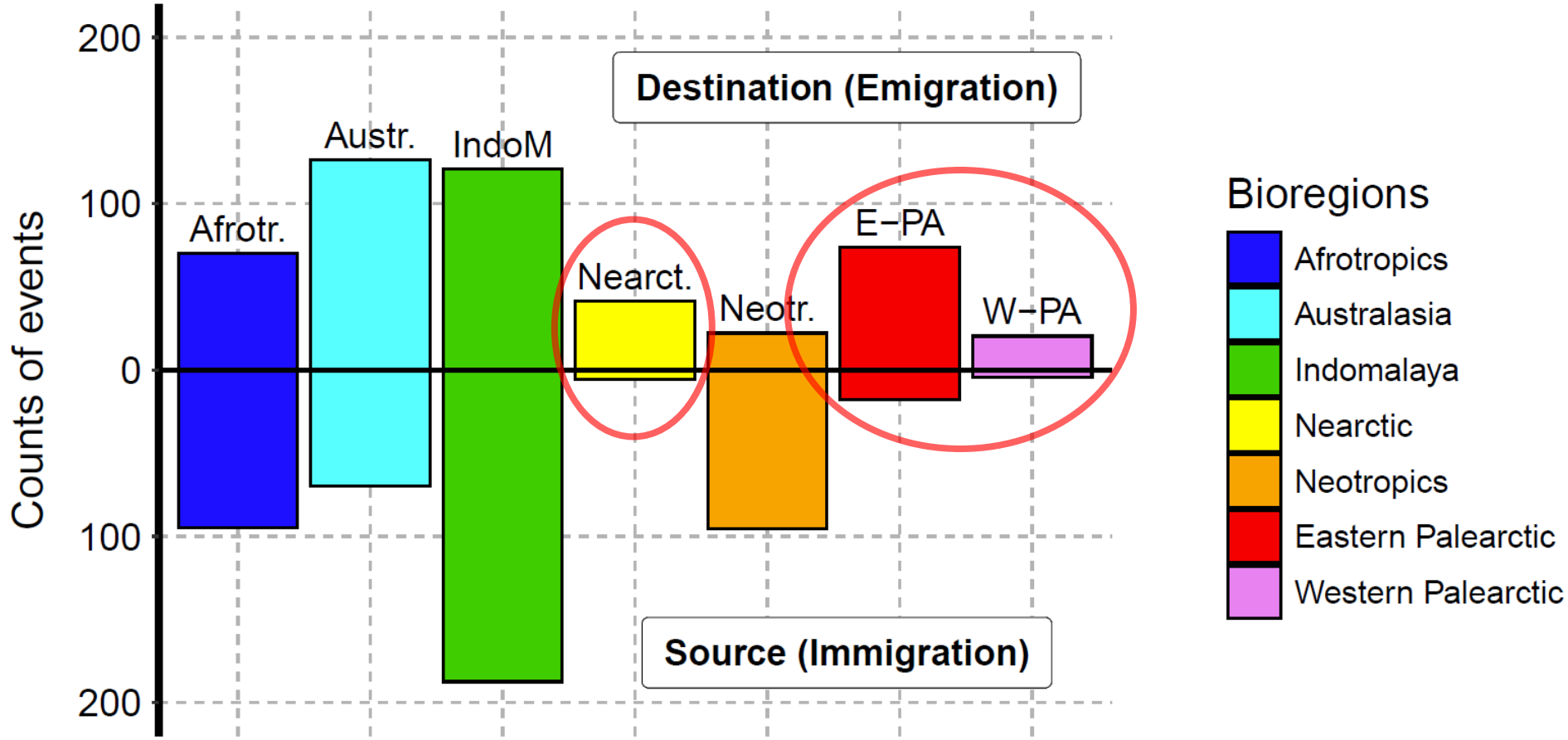
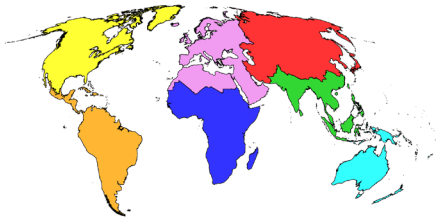
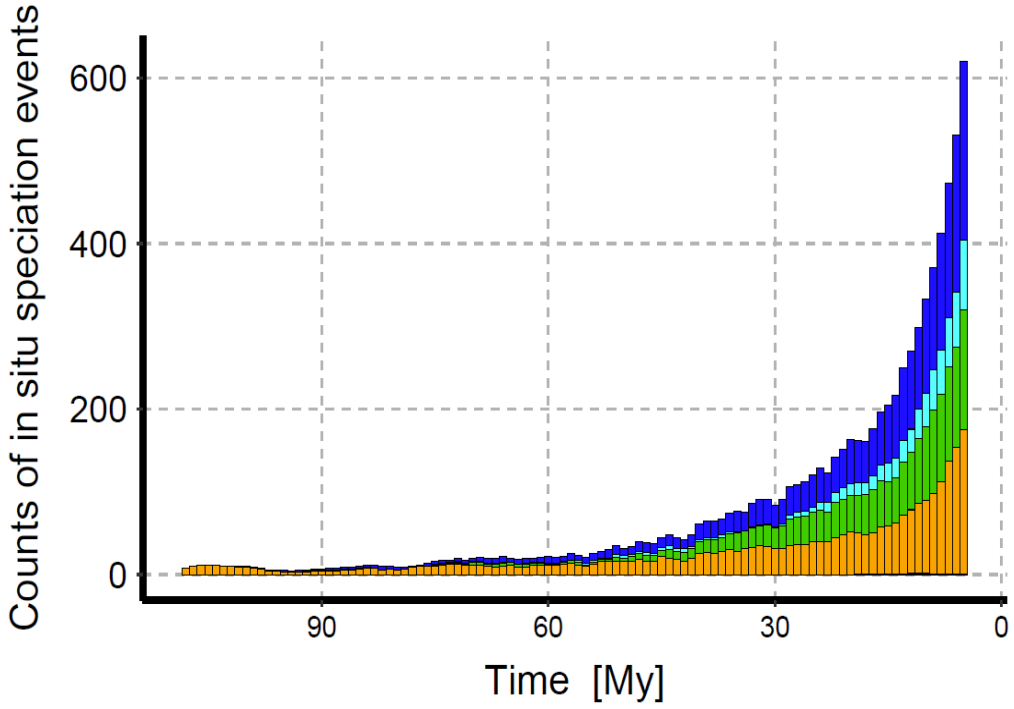


Doré et al., *in prep.*

In situ diversification in time



Counts
in situ speciation events
per Bioregions



Percentages
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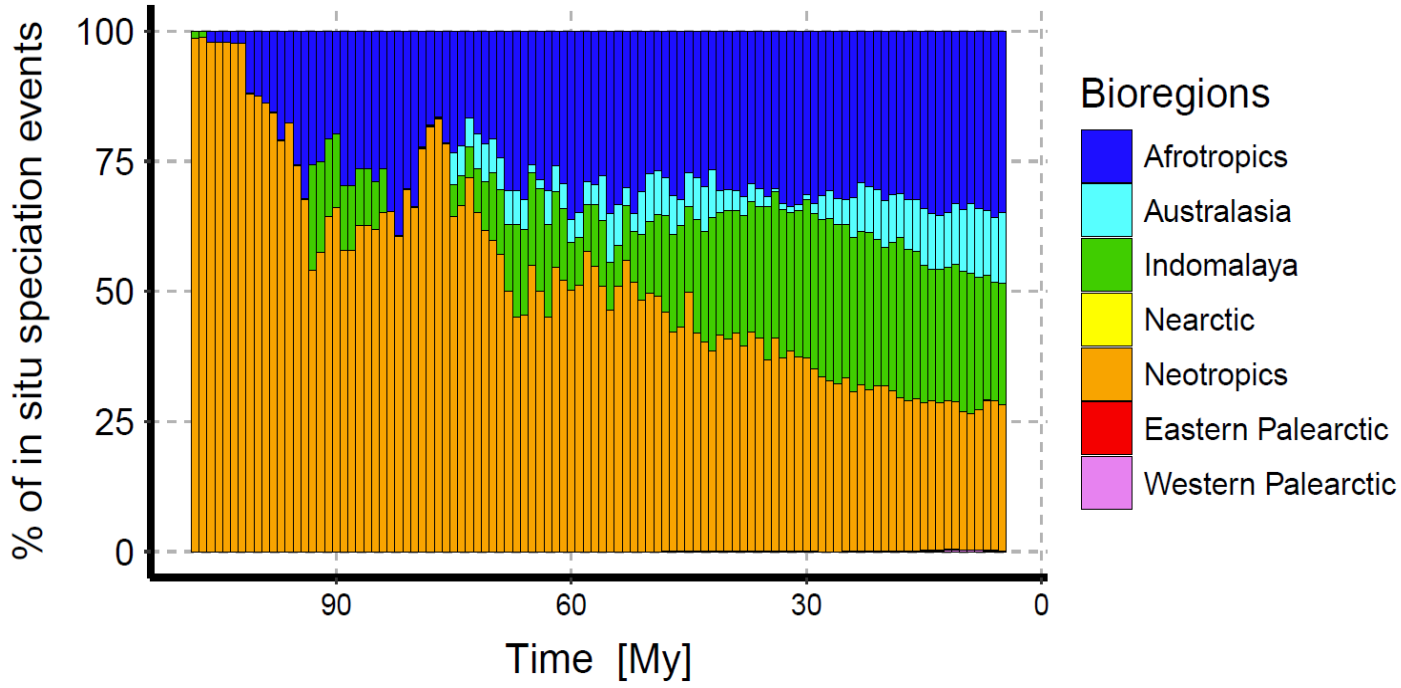

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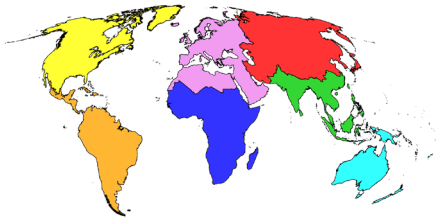

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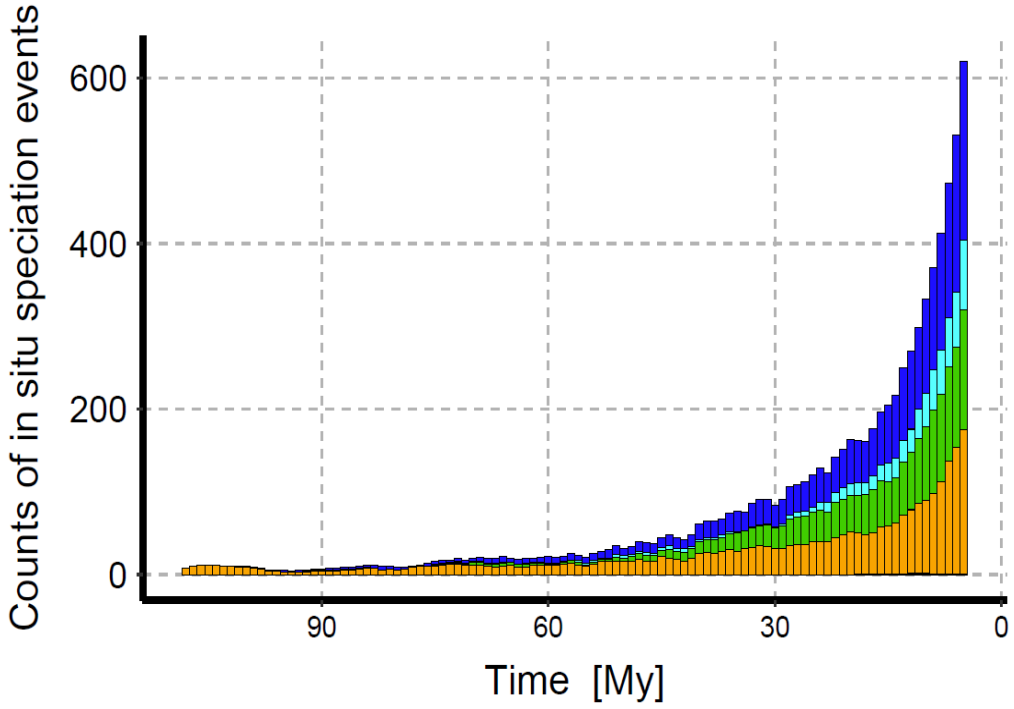

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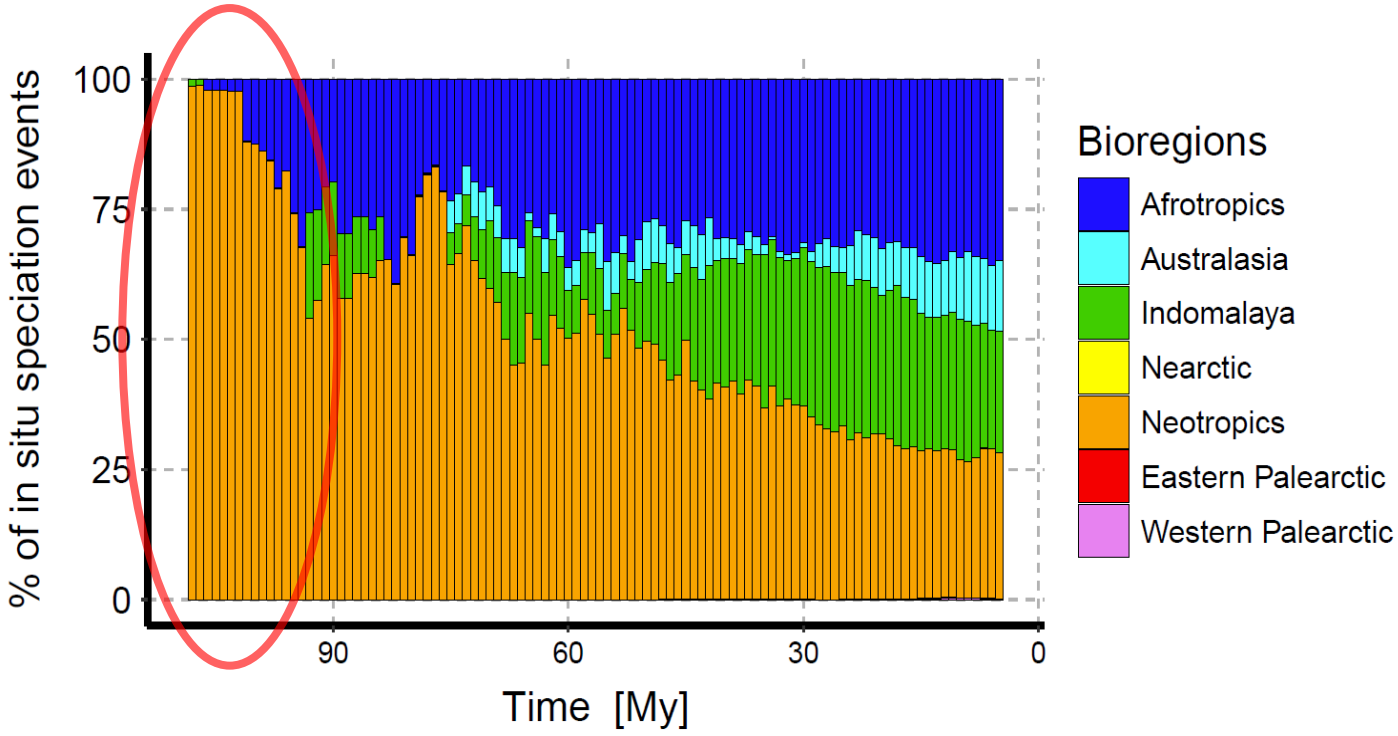

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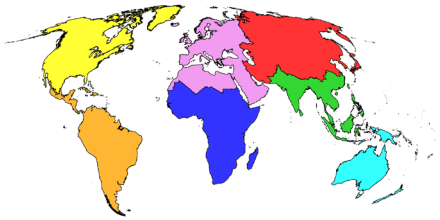

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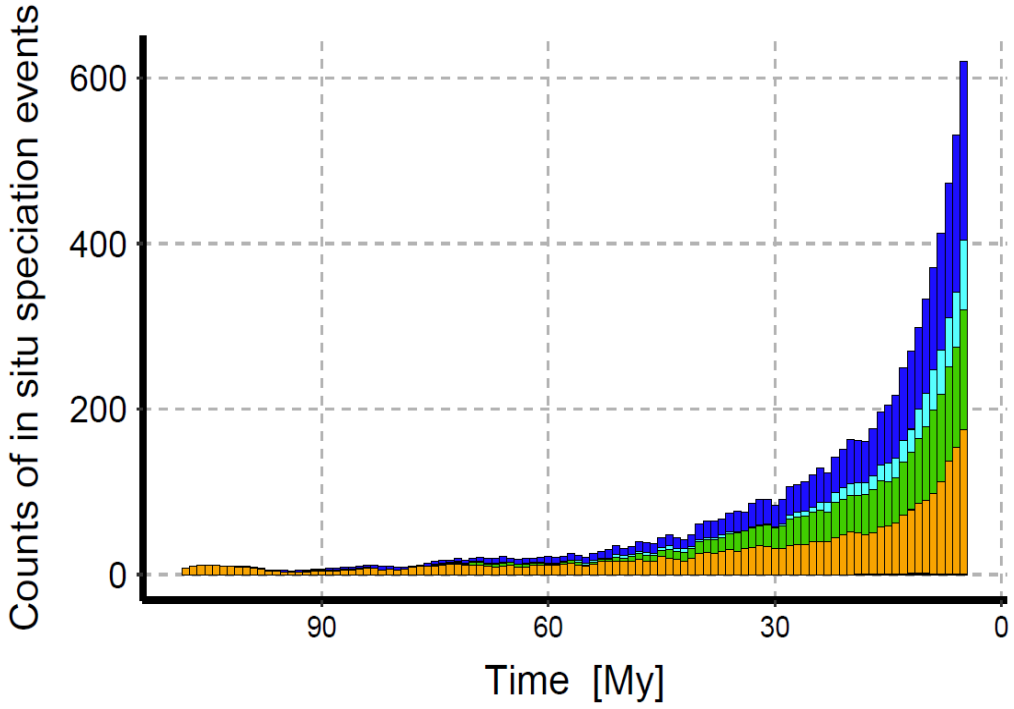

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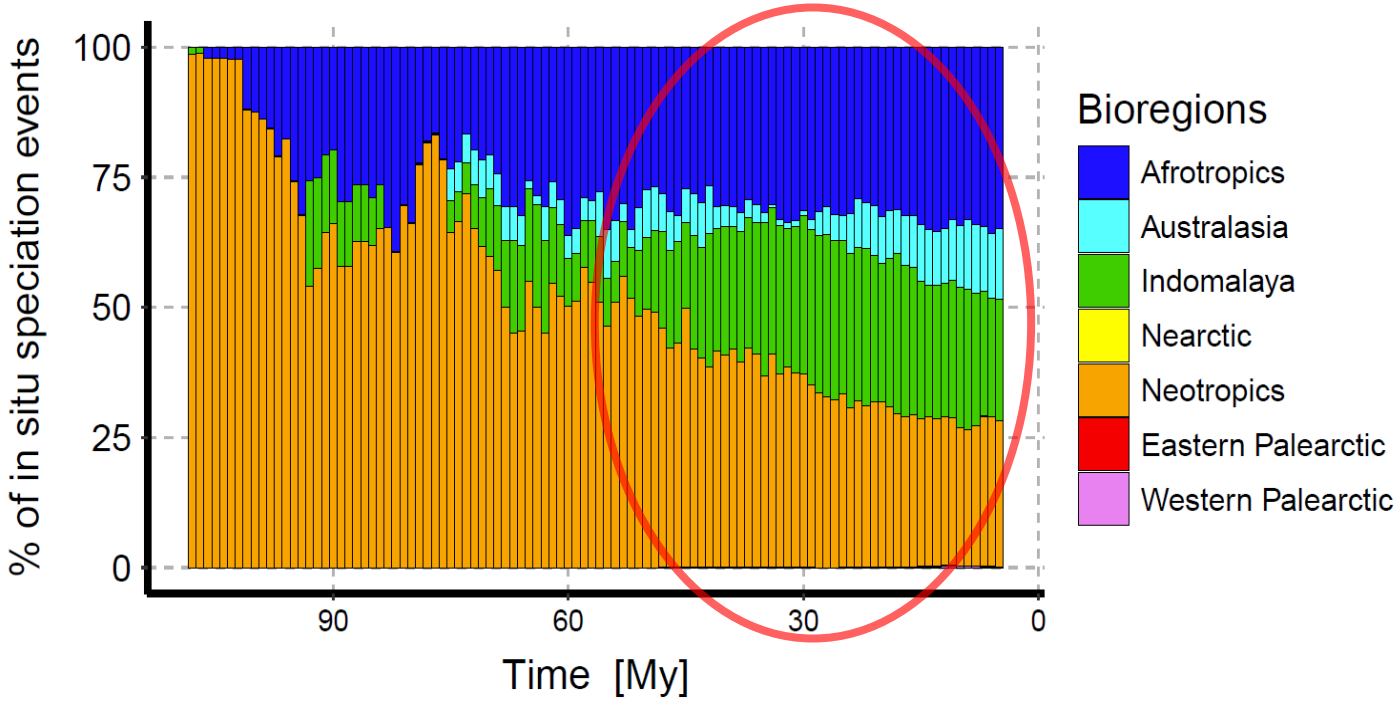

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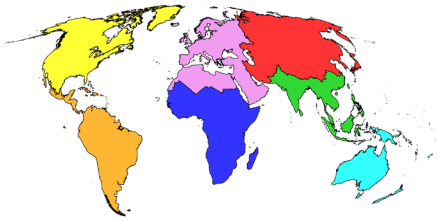
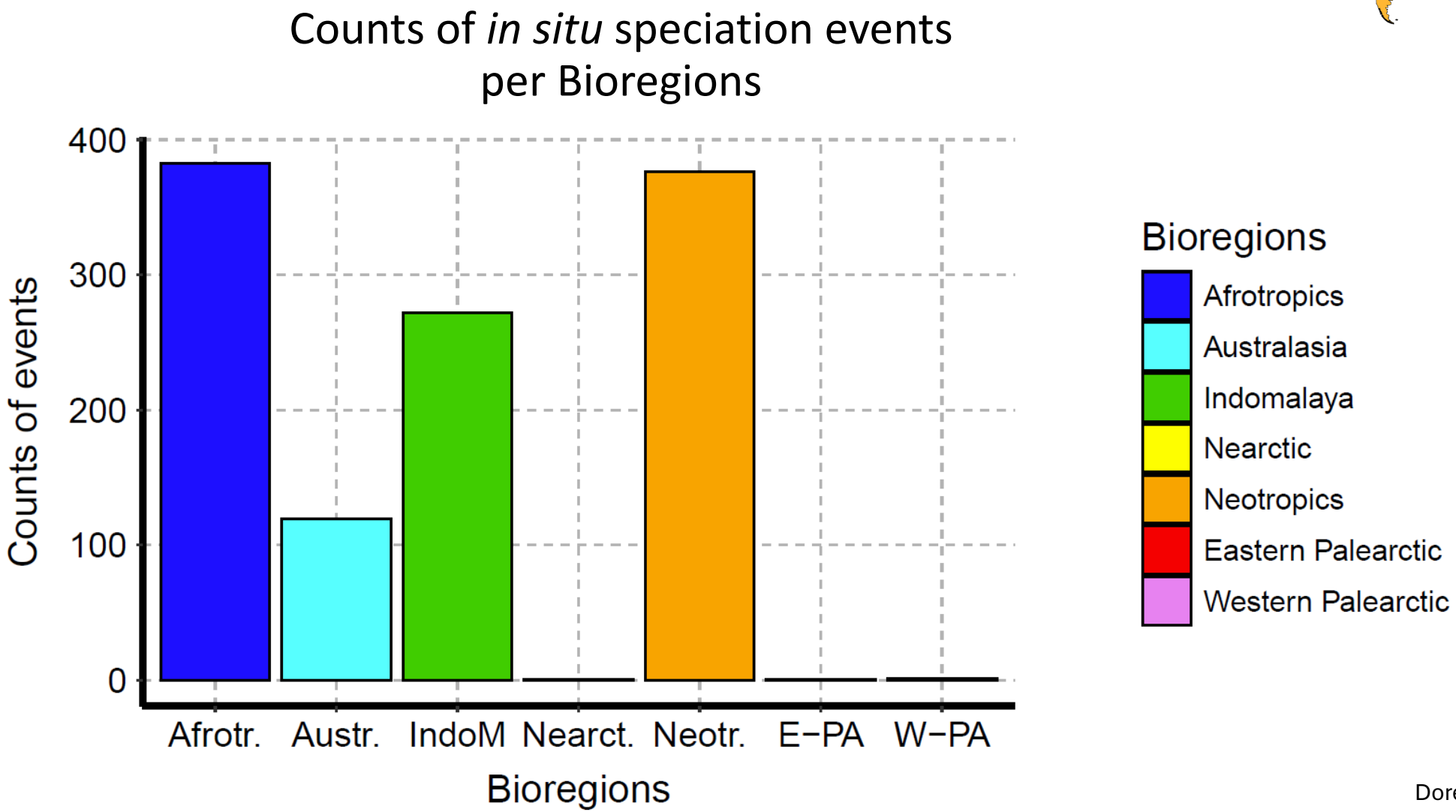
Overall *in situ* diversification





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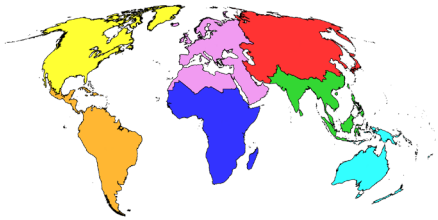
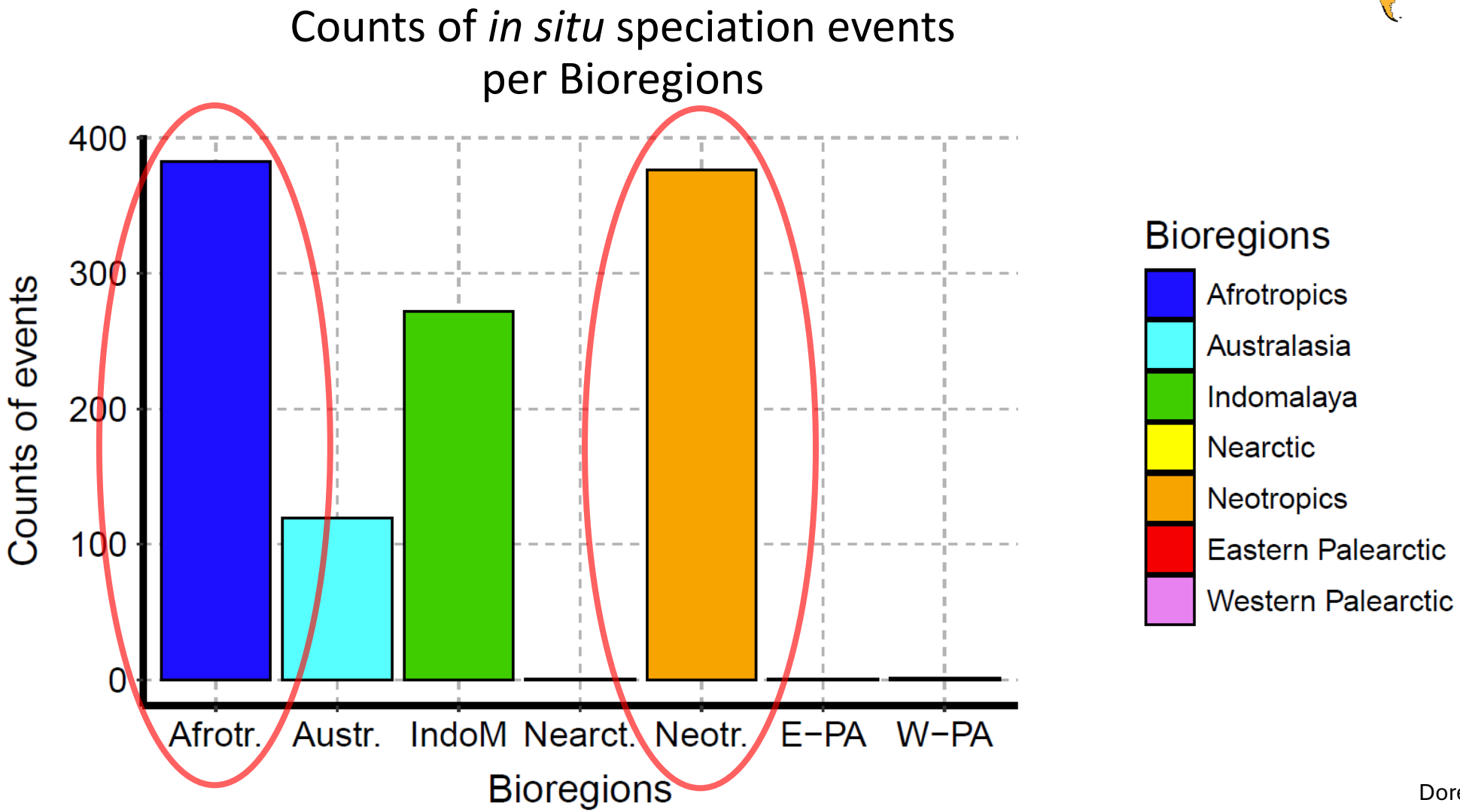
Overall *in situ* diversification





Doré et al., *in prep.*

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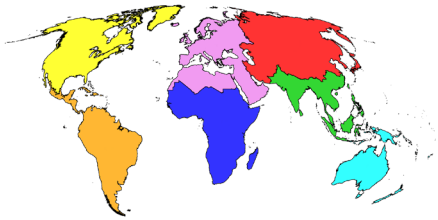

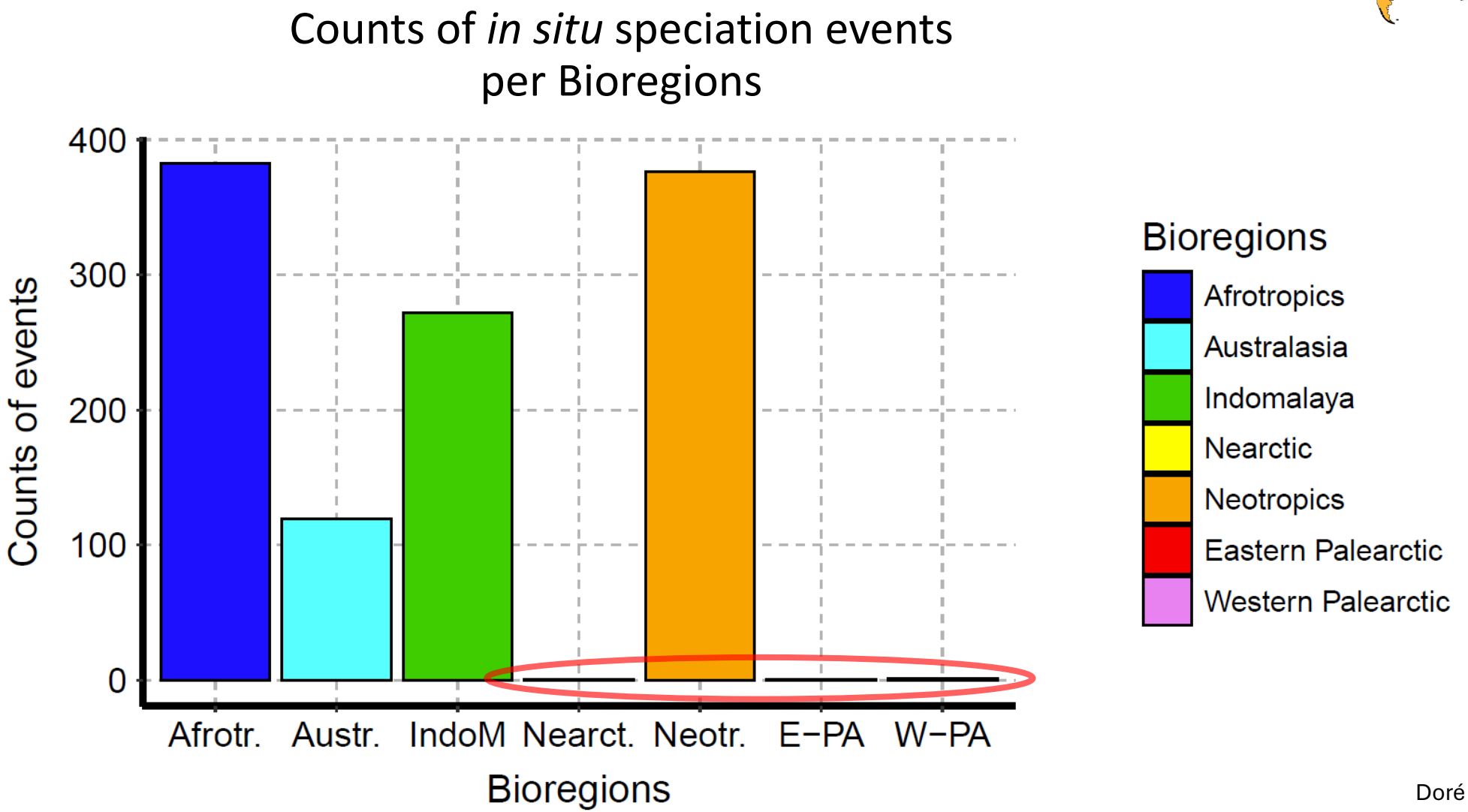

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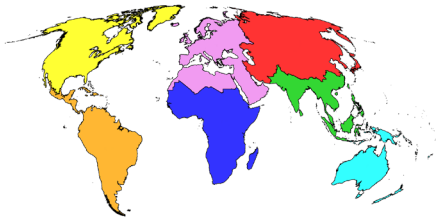
Conclusions



Origin in **Gondwana** ≈ 110-120 My

Timing of **first colonizations**:

- **Australasia** from Neotropics = **90 My**
- **Eastern Palearctic** from (Indo)Malaya = **80 My**
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Dispersal dynamics:

- Early sources: **Neotropics** + **Afrotropics**
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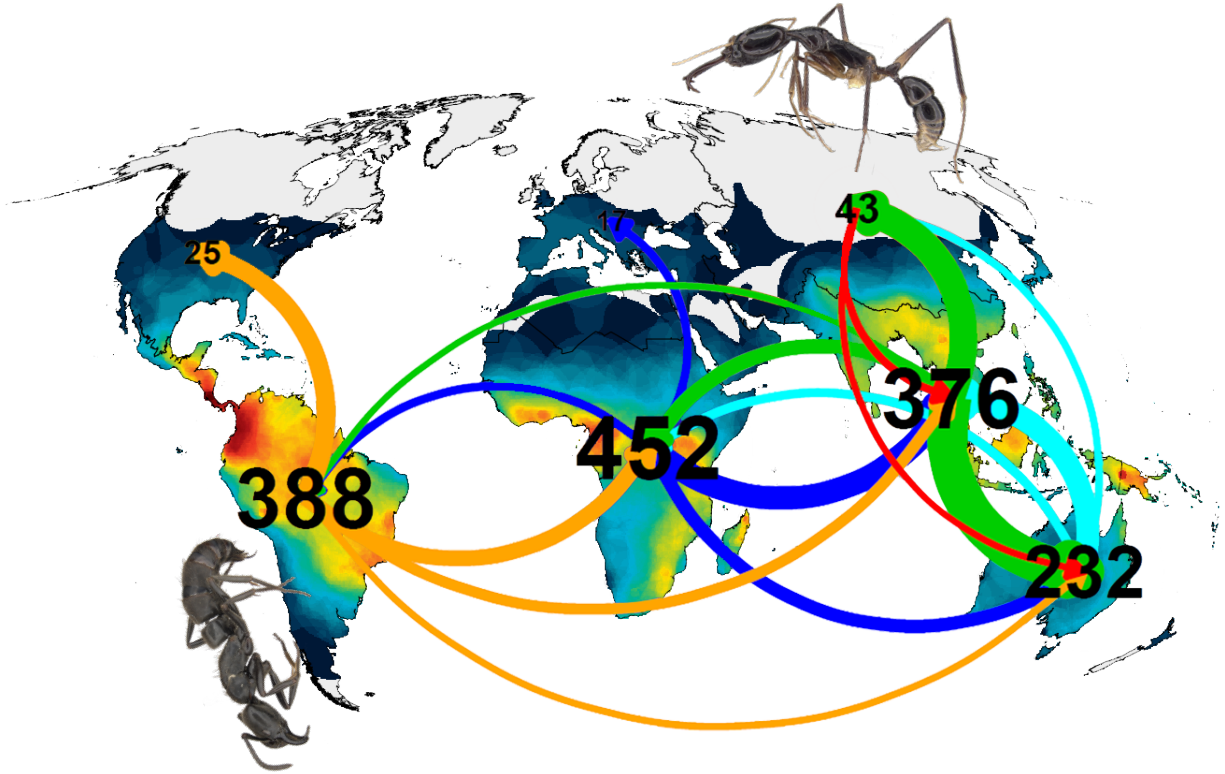

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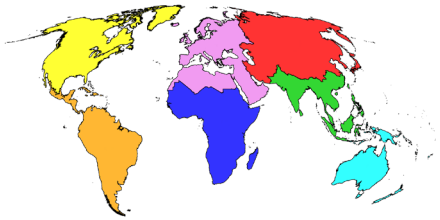

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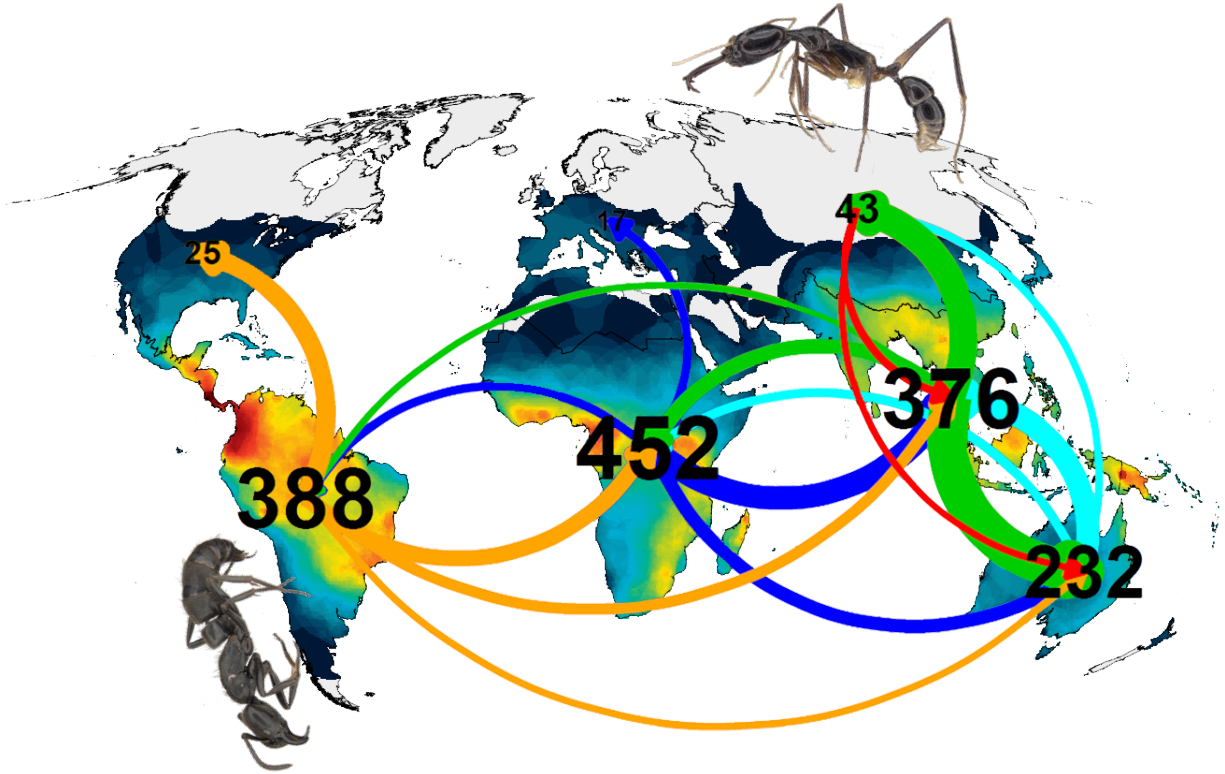

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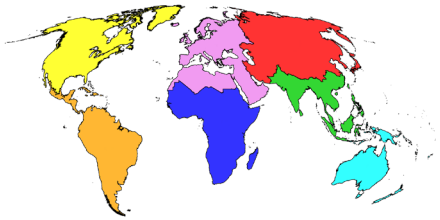

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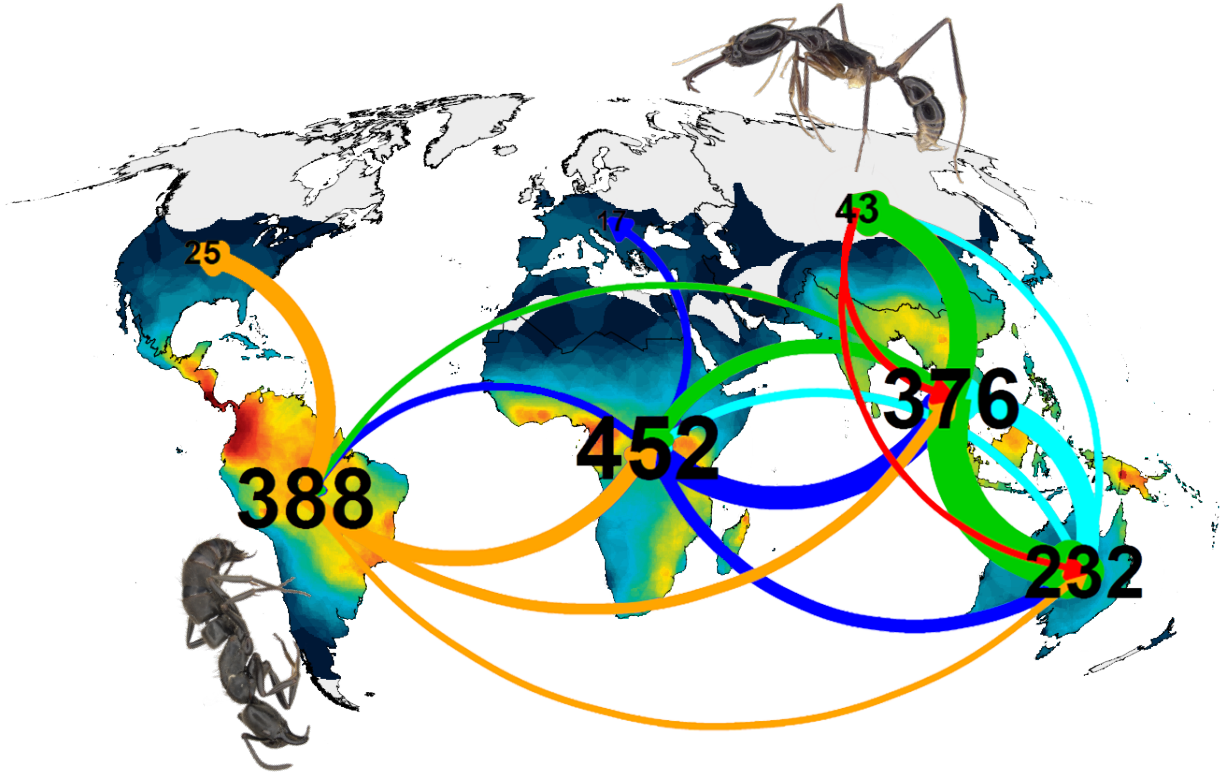

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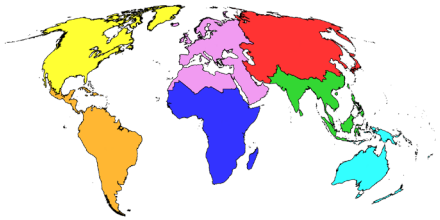

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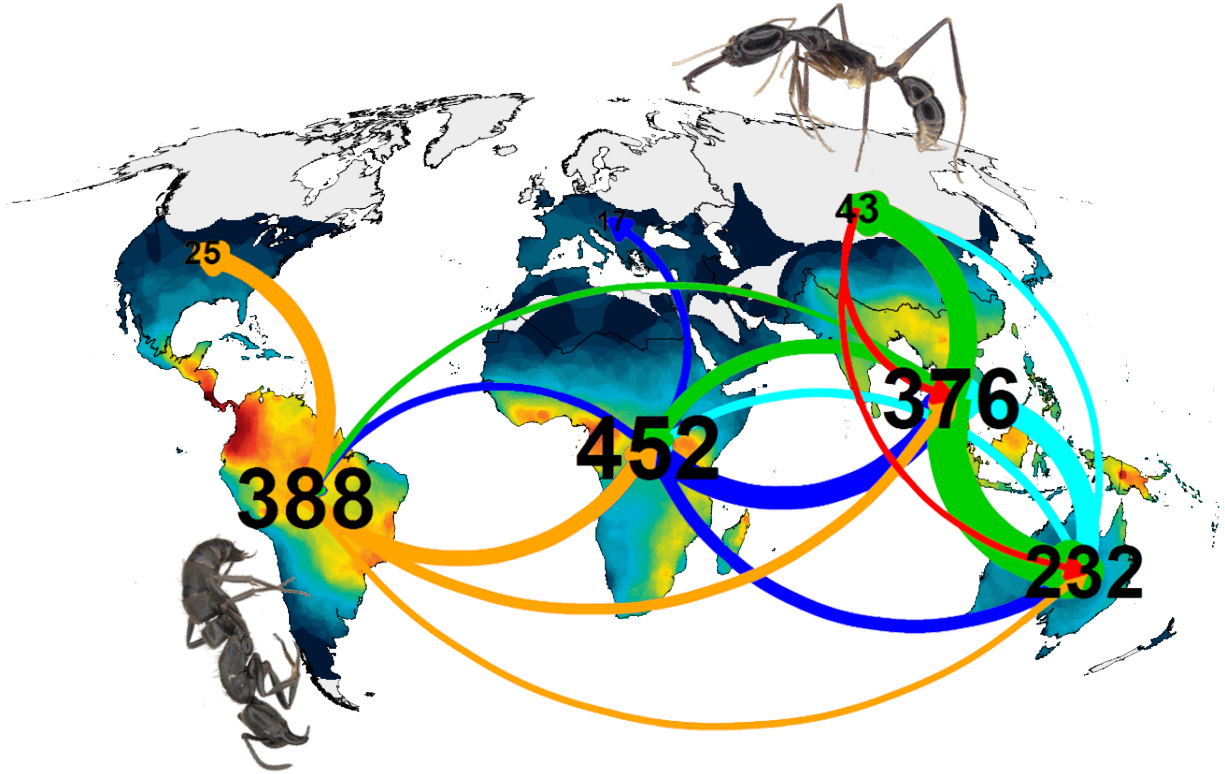

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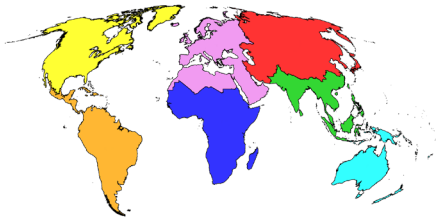

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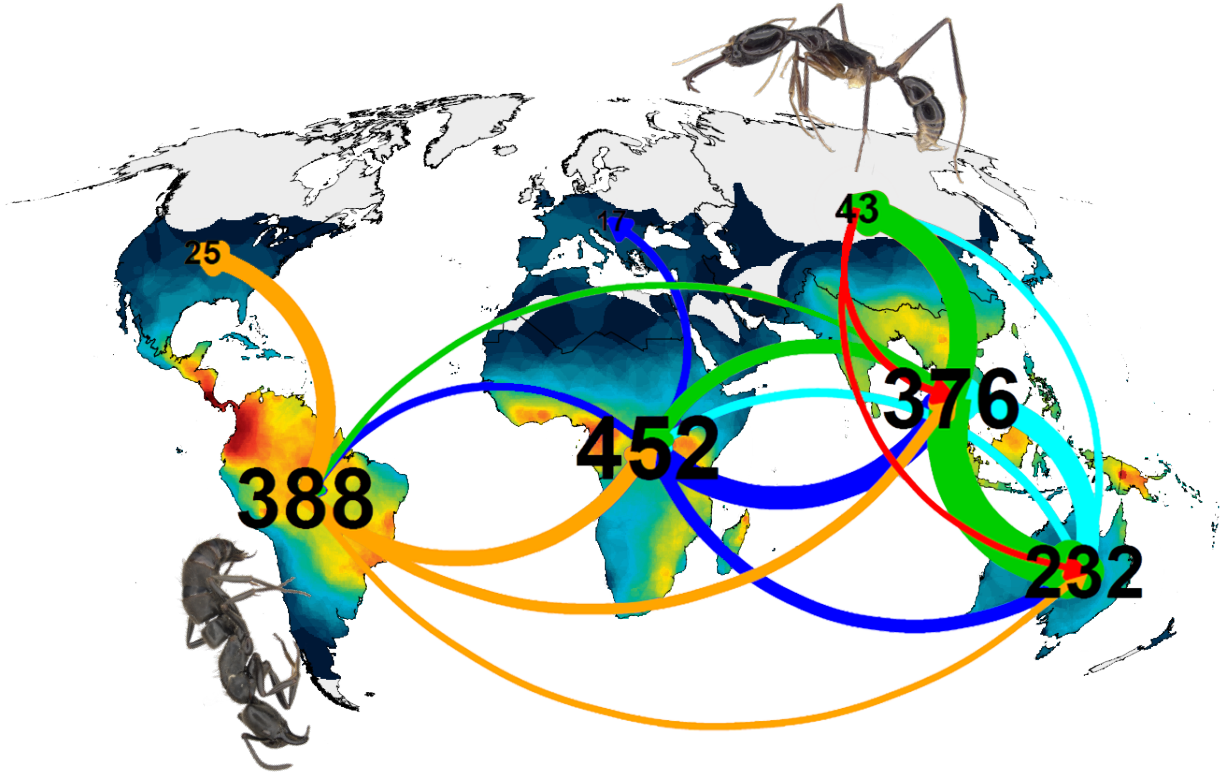

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- Tropical **niche conservatism**
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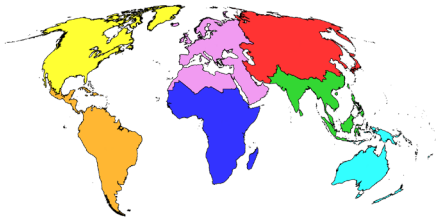

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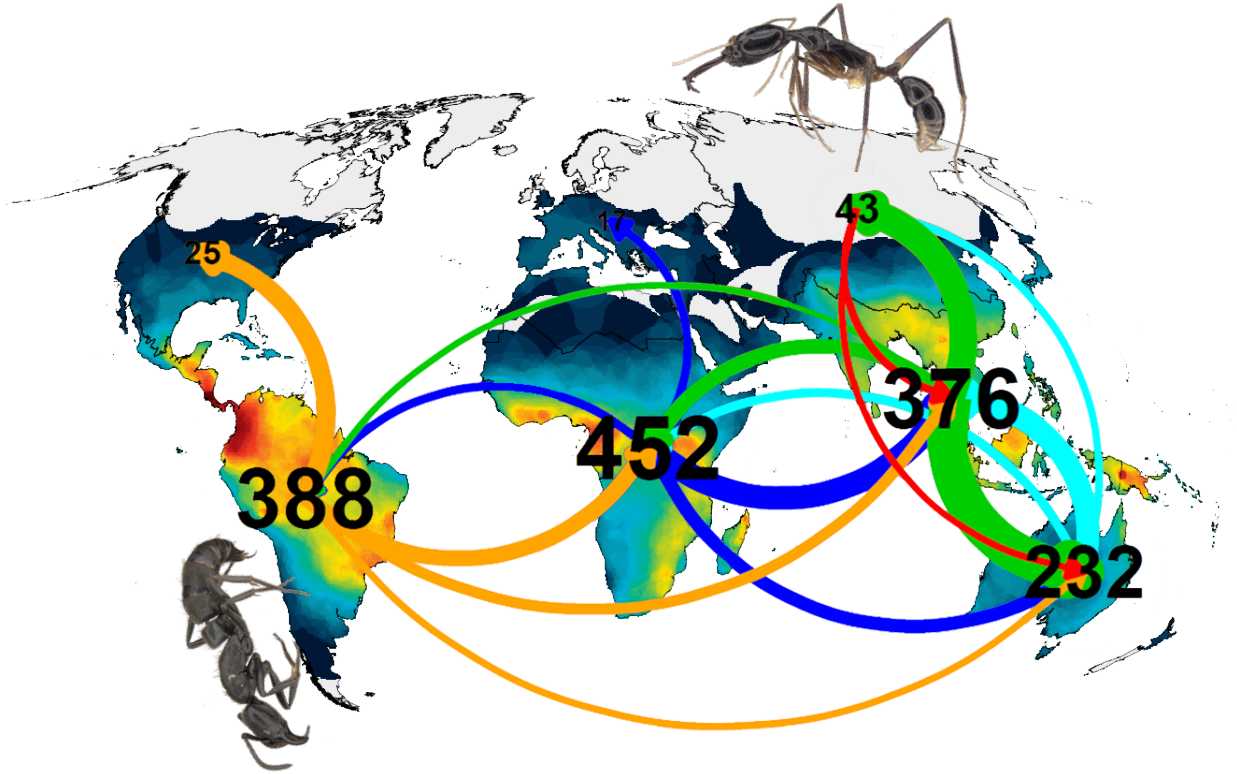

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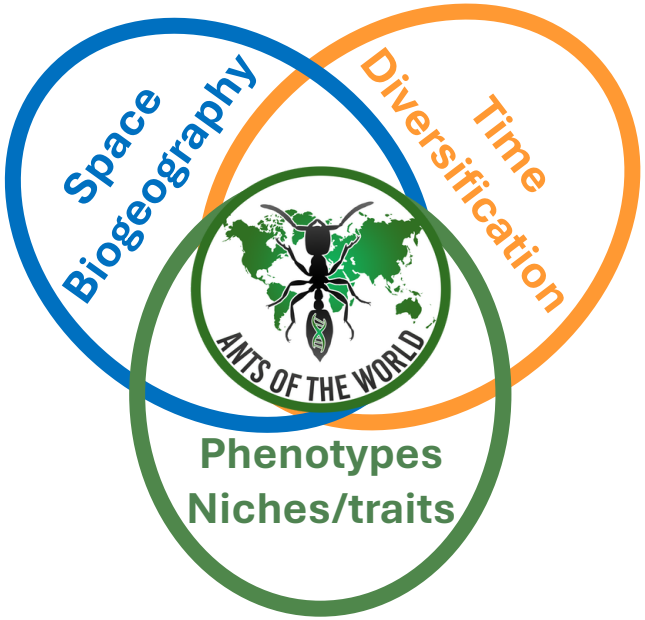
Perspectives



Climatic niche evolution:

- Is evolution repeating itself? Compare the **filling of the niche** across bioregions

Morphology & **Diversification**:

- Do **key morphological innovations** trigger diversification uplifts?

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CIBD Center for Integrative Biodiversity Discovery

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UCDAVIS UNIVERSITY OF CALIFORNIA


Applicant for
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SCAN ME
Questions?
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