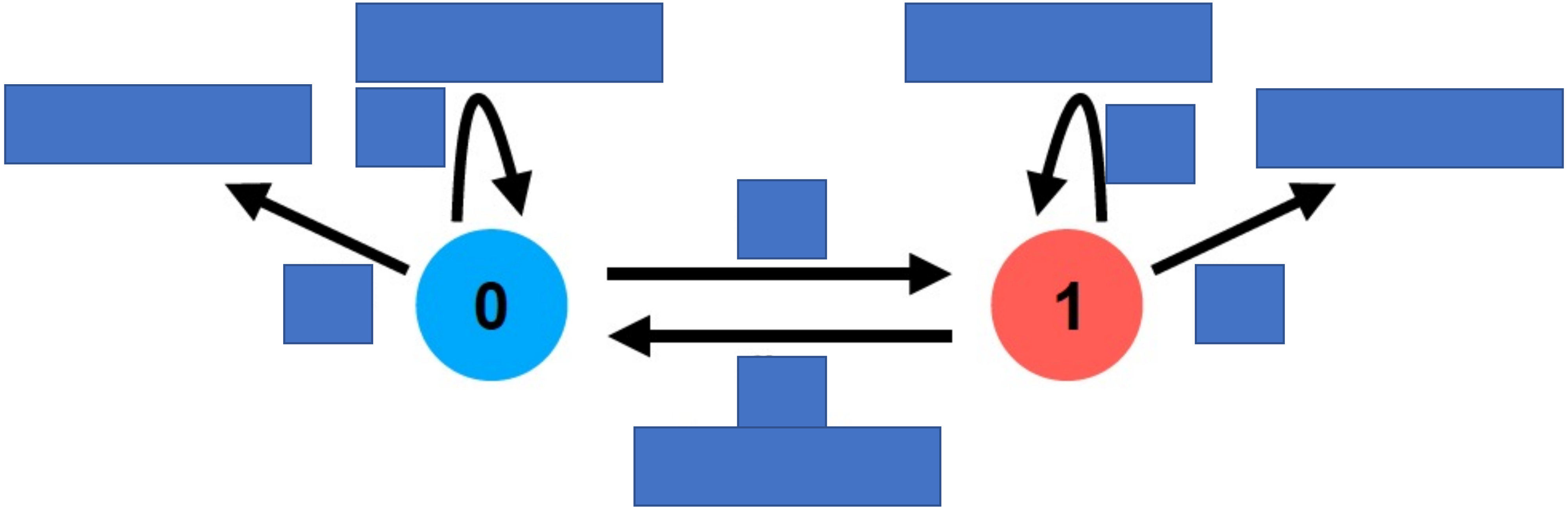
BiSSE

Maddison et al., 2007;
Systematic Biology



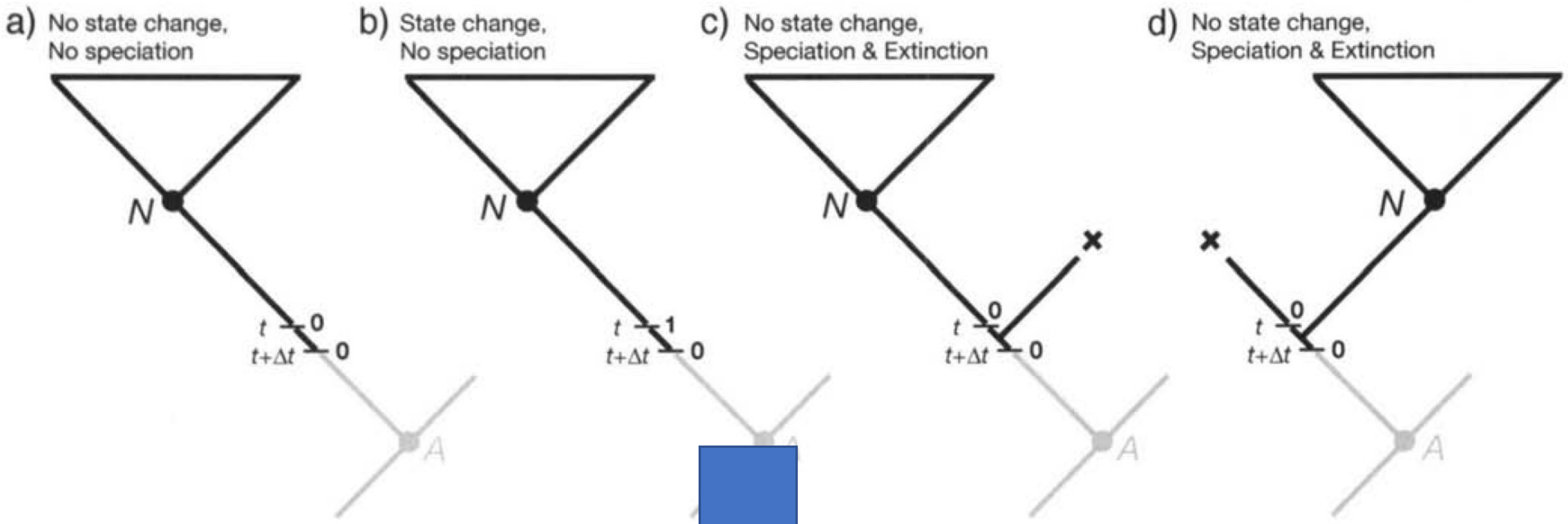
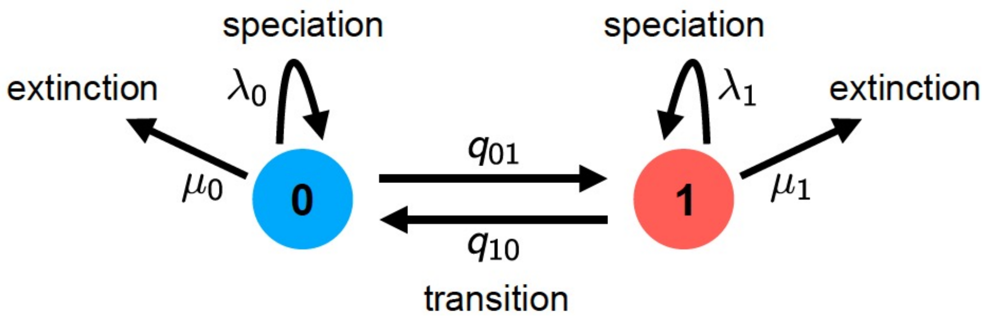

a) No state change,
No speciation
b) State change,
No speciation
c) No state change,
Speciation & Extinction
d) No state change,
Speciation & Extinction
N
t
t+Δt
0
1
A

FIGURE 2.


speciation
speciation
extinction
extinction
λ0
λ1
μ0
μ1
q01
q10
0
1
transition

Geographic state speciation and extinction (GeoSSE)

Introducción a la Biogeografía Paramétrica

Semana 2

Dra. Karen López y Dra. Marysol Trujano

Ventajas y limitaciones

- Integran la dimensión temporal
- Se incorpora el error asociado
- Se puede disc entre escenar métodos esta (LRT, Bayes Fa
- Pueden integrar diferentes fuentes de evidencia

- Costosos computacionalmente
- do por el número as aunque...
- de parámetros
- erencia entre de dispersion aunque...

Limitaciones conceptuales

JOURNAL ARTICLE

Phylogenetic Inference of Reciprocal Effects between Geographic Range Evolution and Diversification

Emma E. Goldberg ✉, Lesley T. Lancaster, Richard H. Ree   Author Notes

Systematic Biology, Volume 60, Issue 4, July 2011, Pages 451–465, https://doi.org/10.1093/sysbio/syr046

Published: 05 May 2011   **Article history** ▾

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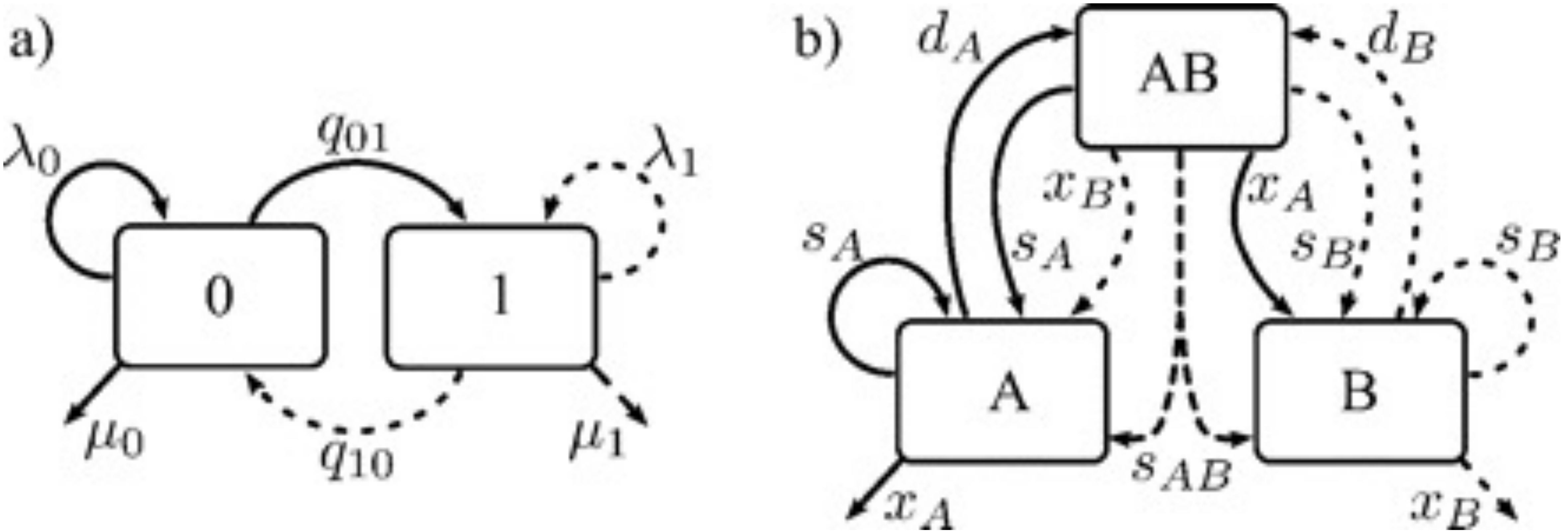
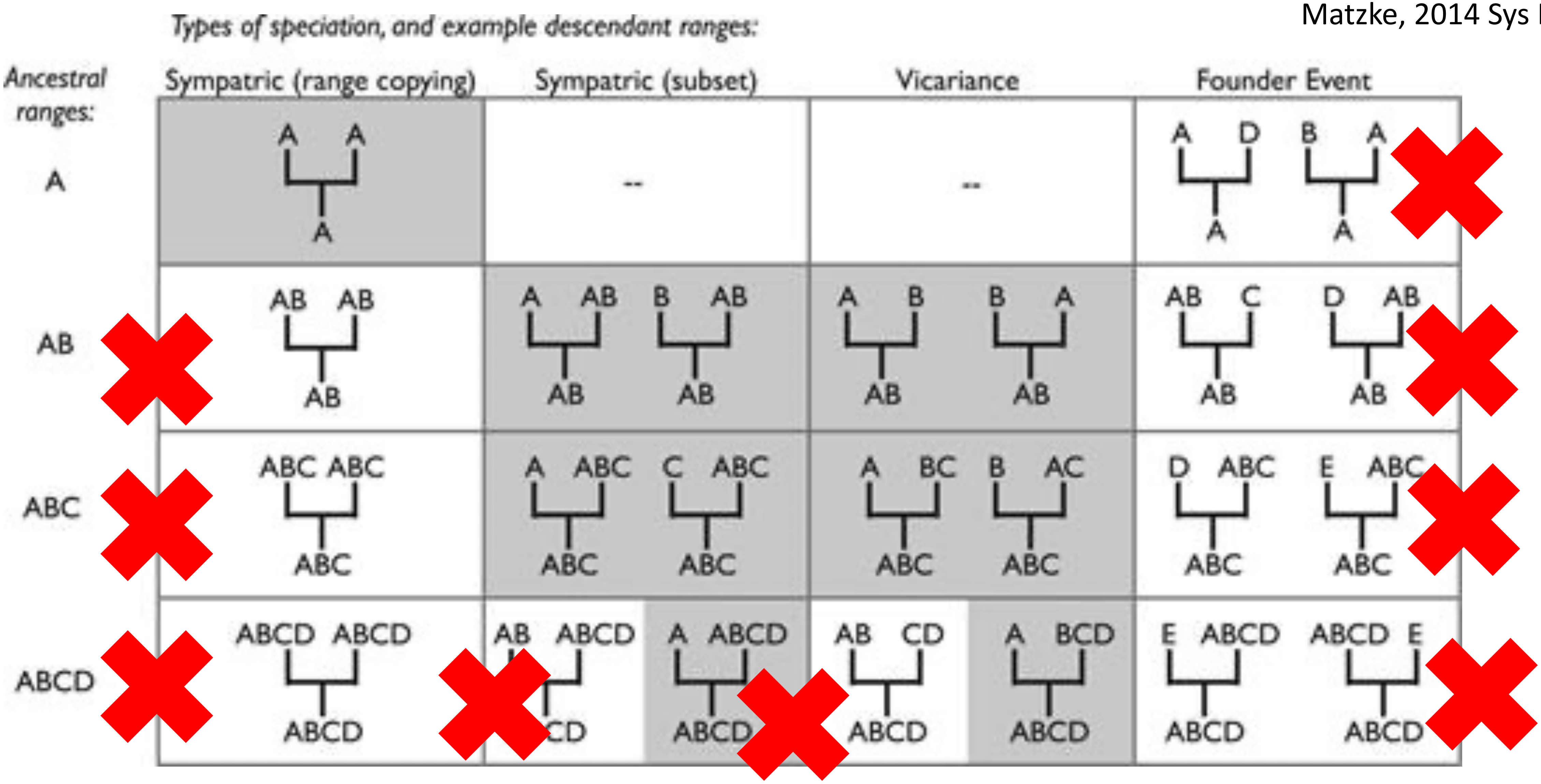
Abstract

Geographic characters—traits describing the spatial distribution of a species—may both affect and be affected by processes associated with lineage birth and death. This is potentially confounding to comparative analyses of species distributions because current models do not allow reciprocal interactions between the evolution of ranges and the growth of phylogenetic trees. Here, we introduce a



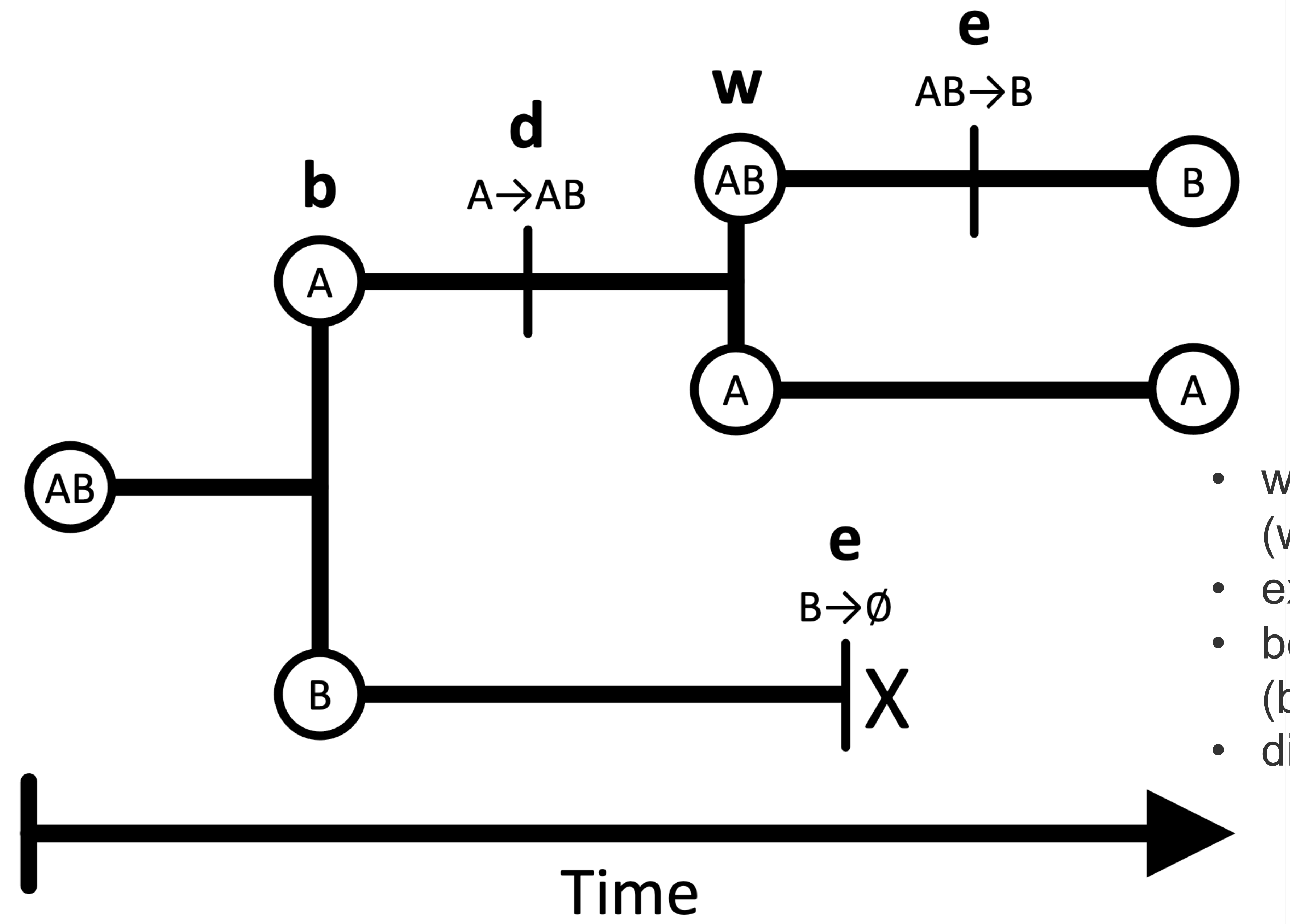
Syst Biol, Volume 60, Issue 4, July 2011, Pages 451–465, https://doi.org/10.1093/sysbio/syr046

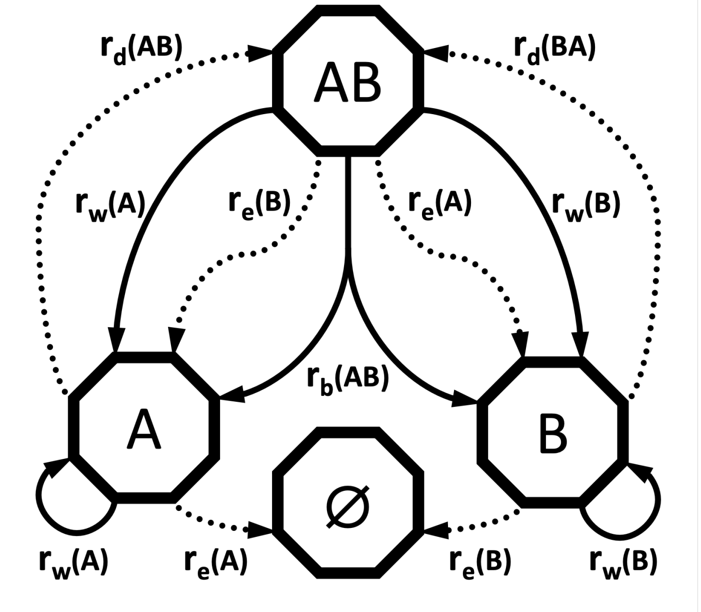
Matzke, 2014 Sys Bio



DEC

DEC+J

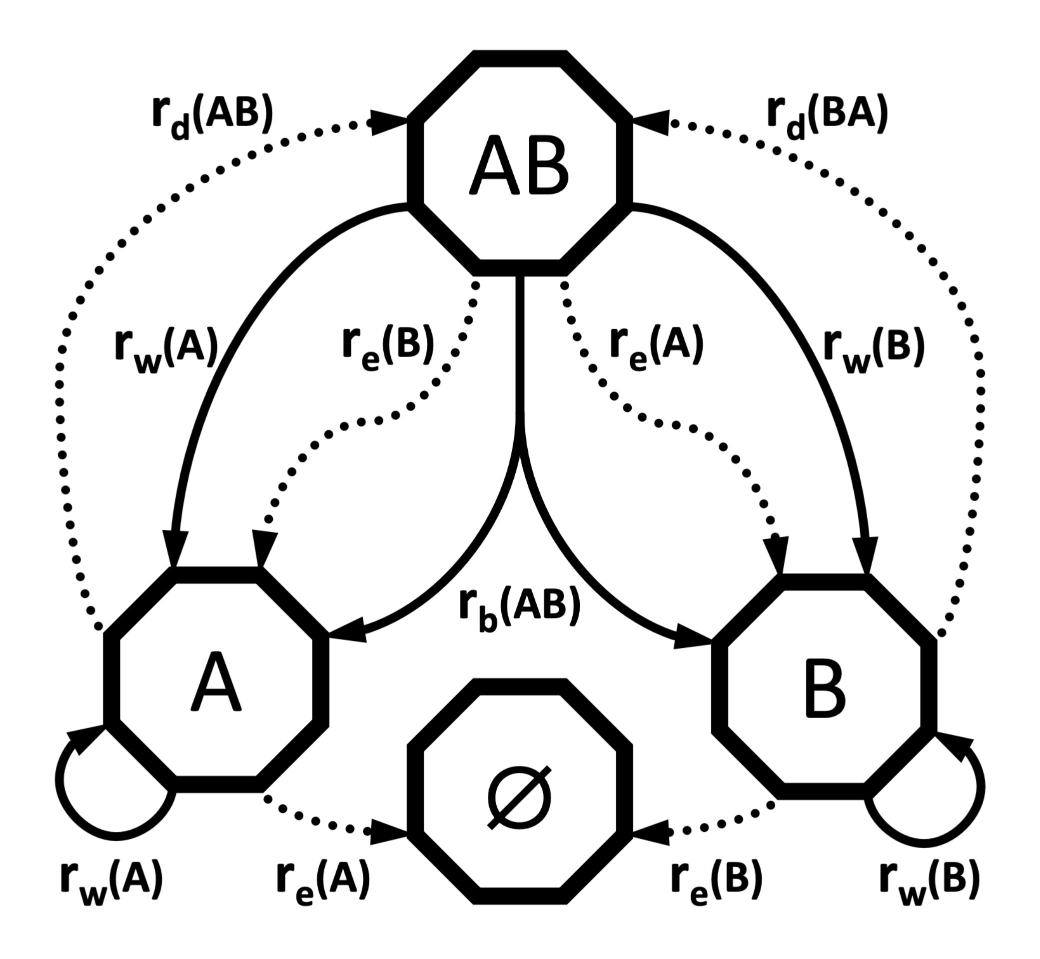




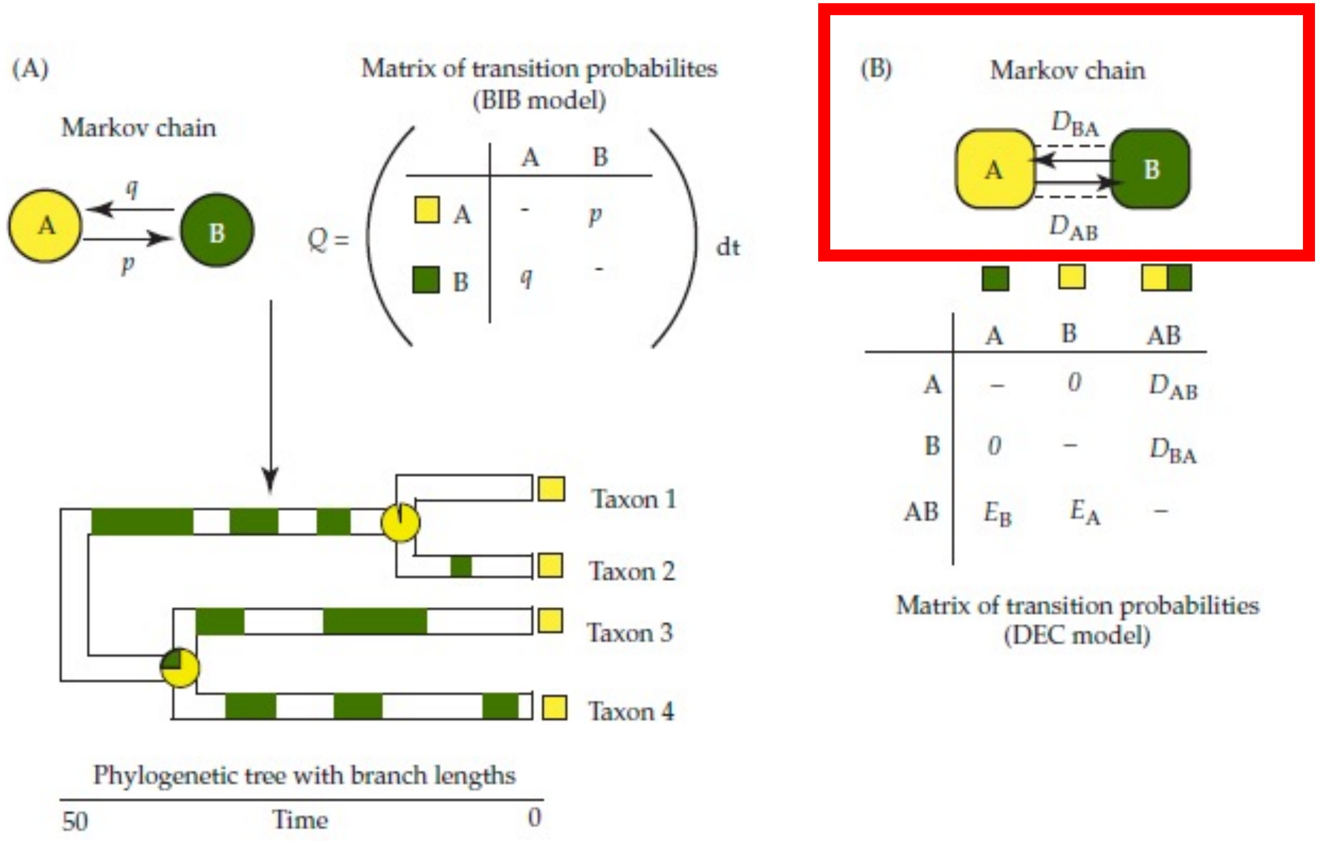
- within-region speciation (w)
- extinction (e)
- between-region speciation (b)
- dispersal (d).

Image from: https://revbayes.github.io/tutorials/geosse/

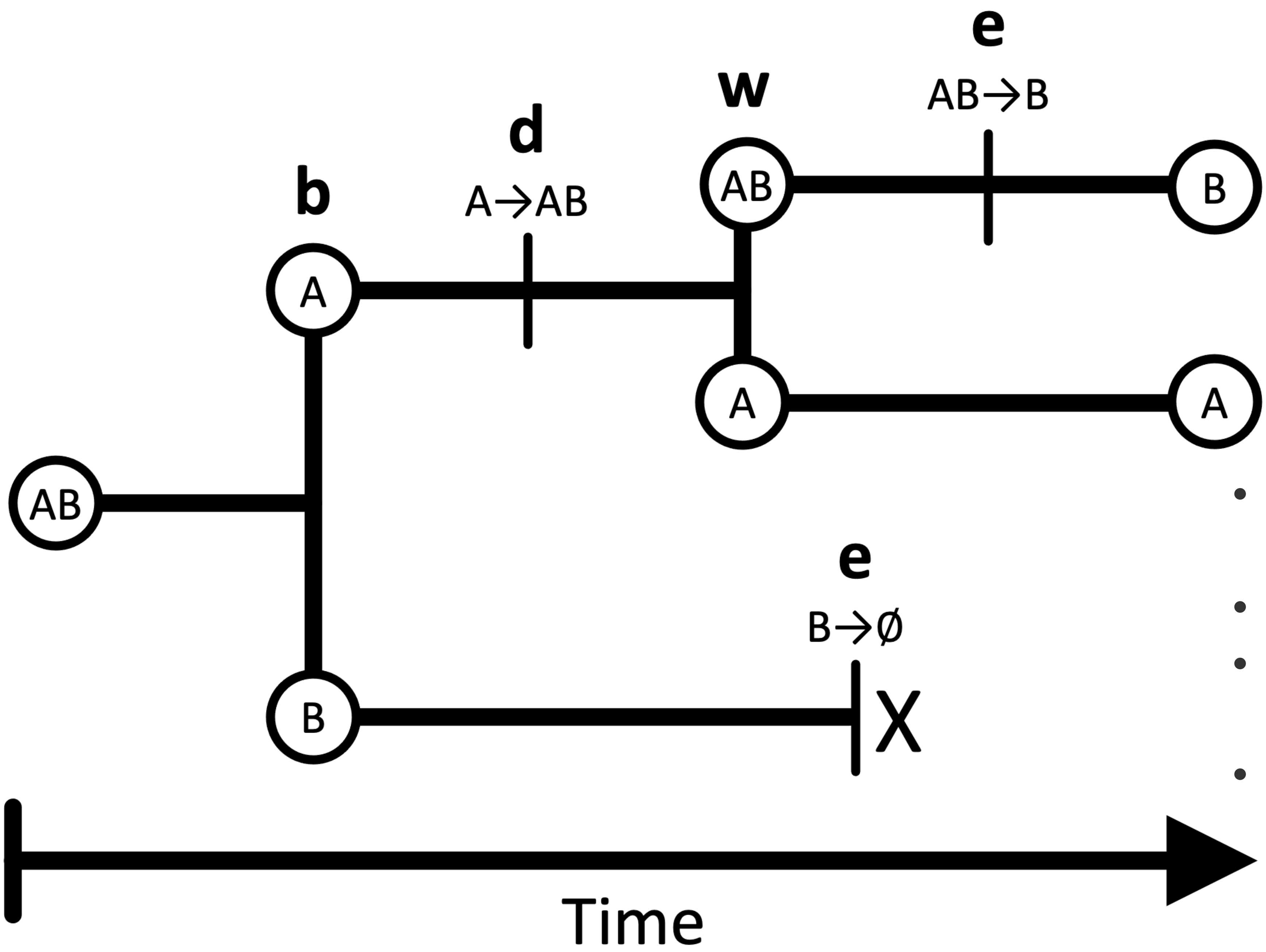
Transition diagram for the GeoSSE model with two regions, based on Figure 1 from (Goldberg et al. 2011). Anagenetic processes are represented with dashed arrows, while cladogenetic processes are represented with solid arrows.

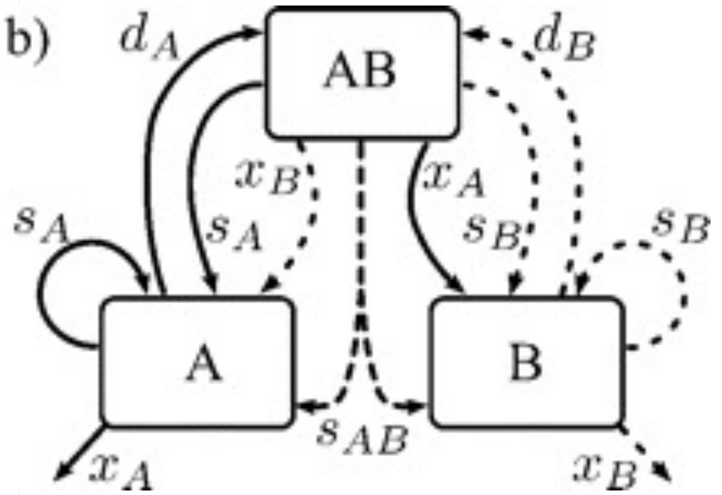


DEC



(A)
Markov chain
A
B
q
p
Matrix of transition probabilites
(BIB model)
Q =
A
B
-
p
q
-
dt
Taxon 1
Taxon 2
Taxon 3
Taxon 4
Phylogenetic tree with branch lengths
50
Time
0
(B)
Markov chain
D_{BA}
D_{AB}
A
B
AB
A – 0 D_{AB}
B 0 – D_{BA}
AB E_B E_A –
Matrix of transition probabilities
(DEC model)





- within-region speciation (w)
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- dispersal (d).

Image from: https://revbayes.github.io/tutorials/geosse/

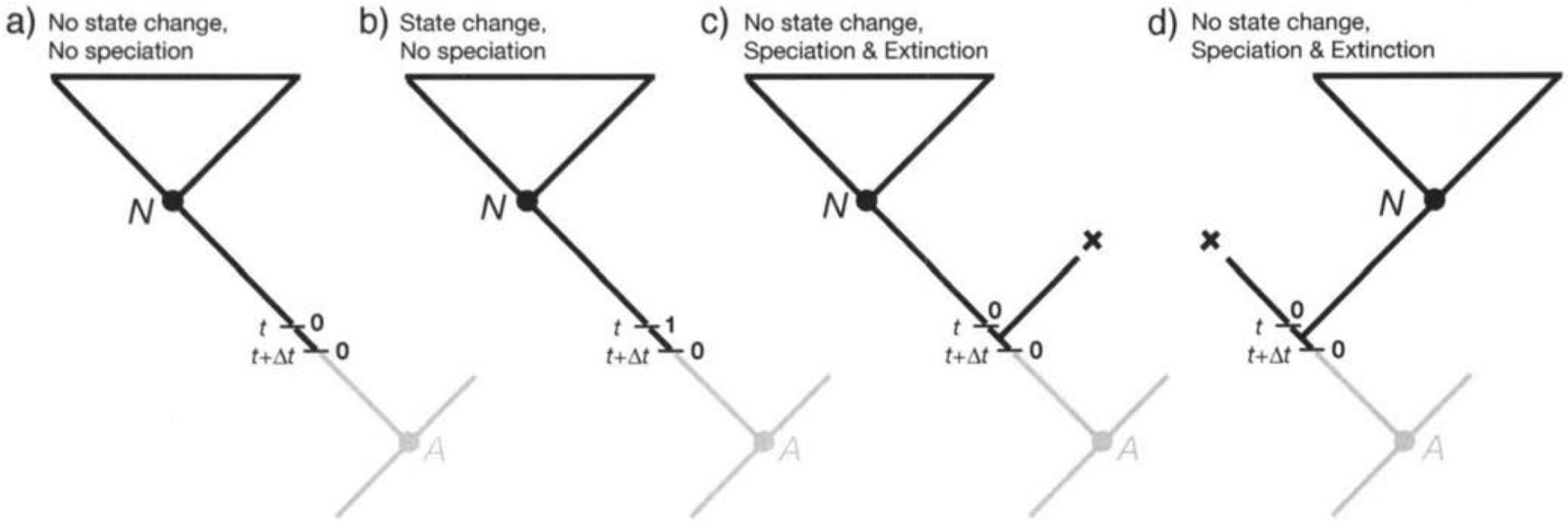


FIGURE 2. Alternative scenarios by which a lineage with state 0 at time $t+\Delta t$ on the branch might yield clade decended from node N but no other living descendants.

Limitaciones

Limitaciones

Areas:

A B C

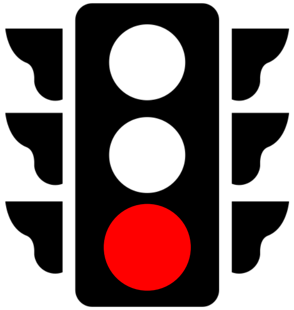
$\mathbf{Q} =$

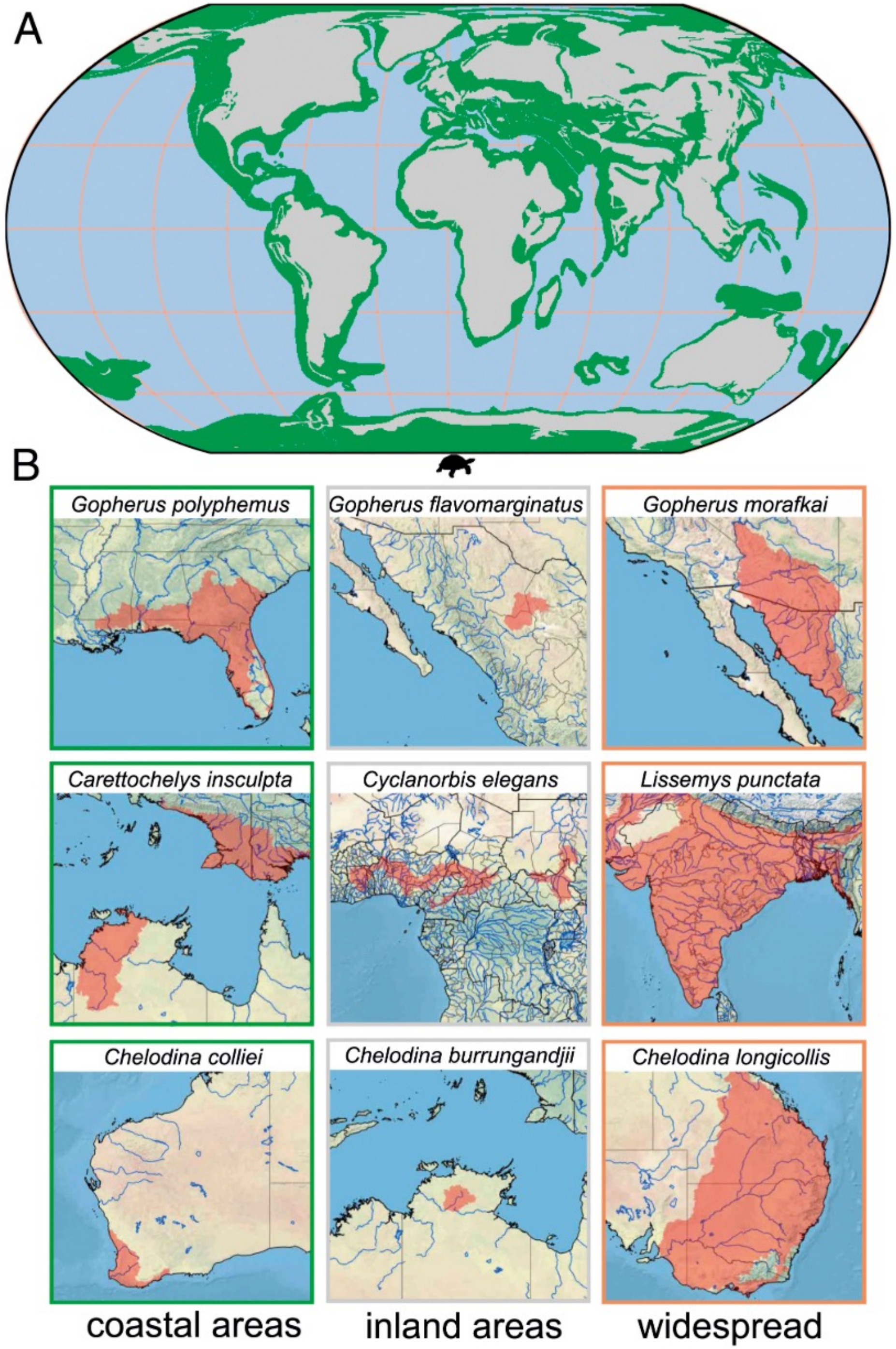
	$\emptyset$	A	B	C	AB	AC	BC	ABC
$\emptyset$	$-$	0	0	0	0	0	0	0
A	e_A	$-$	0	0	d_{AB}	d_{AC}	0	0
B	e_B	0	$-$	0	d_{BA}	0	d_{BC}	0
C	e_C	0	0	$-$	0	d_{CA}	d_{CB}	0
AB	0	e_B	e_A	0	$-$	0	0	$d_{AC} + d_{BC}$
AC	0	e_C	0	e_A	0	$-$	0	$d_{AB} + d_{CB}$
BC	0	0	e_C	e_B	0	0	$-$	$d_{BA} + d_{CA}$
ABC	0	0	0	0	e_C	e_B	e_A	$-$

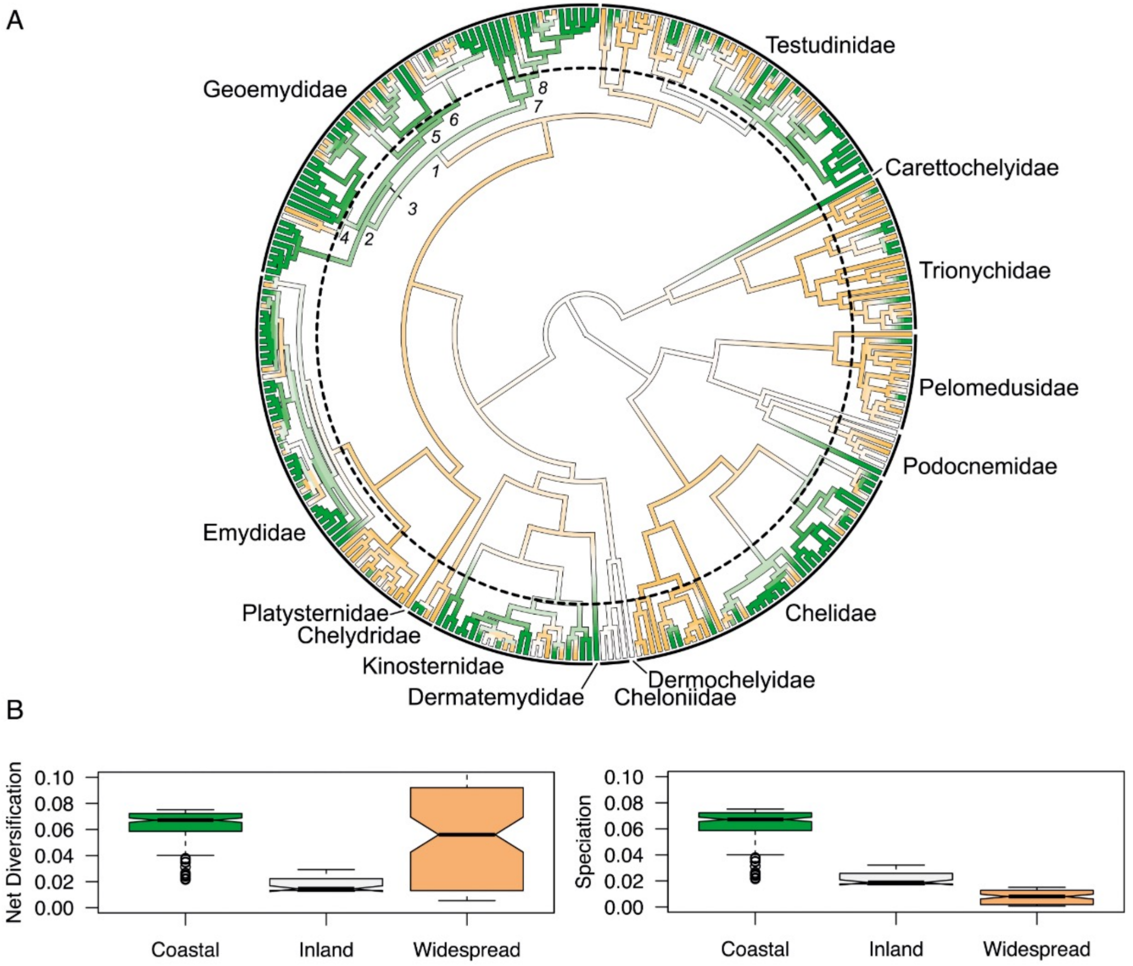
The number of possible states *s* is 2^r, where *r* is the number of regions .

$2^4 = 16$
$2^5 = 32$
$2^6 = 64$

$2^7 = 128$
$2^8 = 256$
$2^9 = 512$

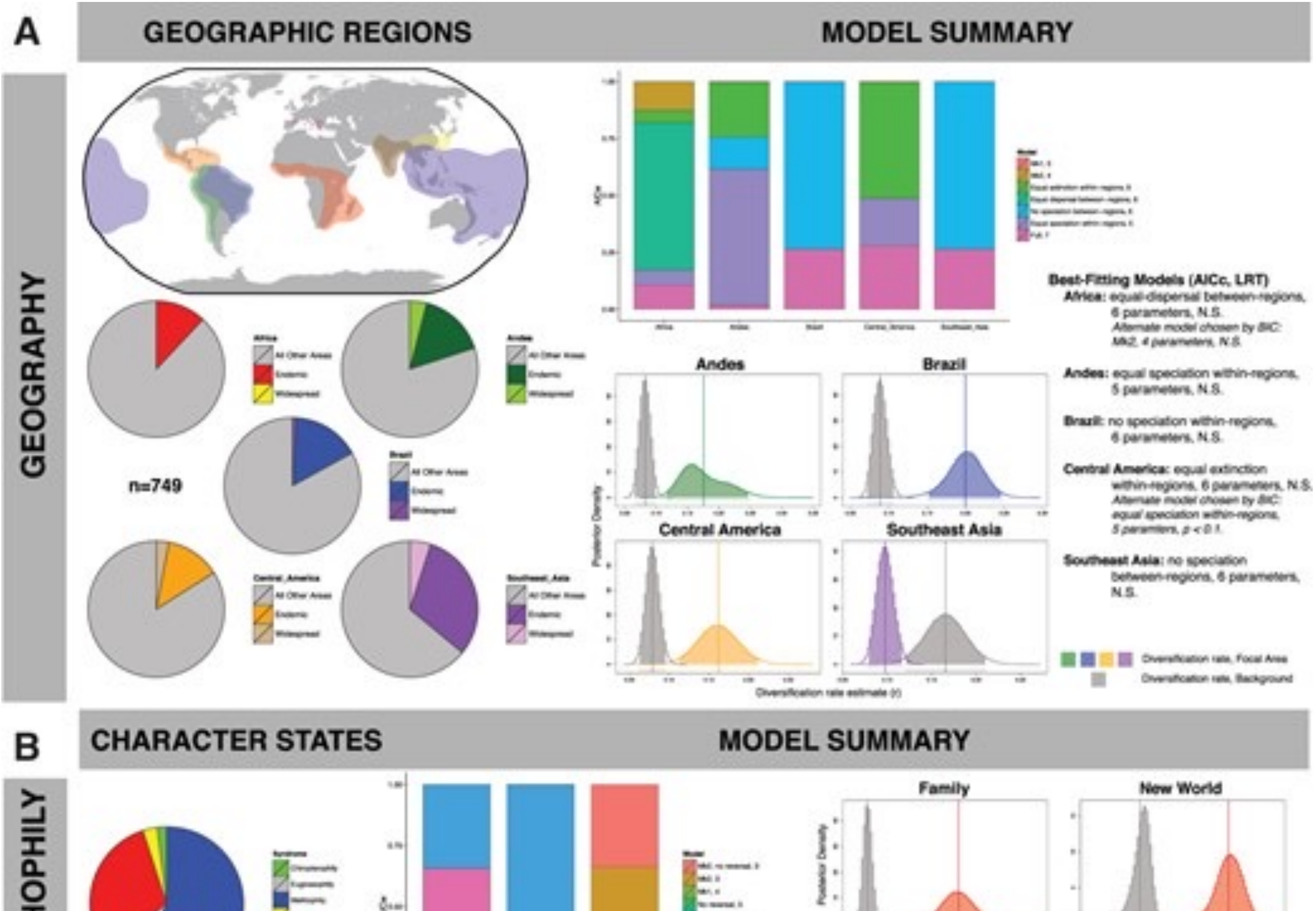






Thomson et al., 2021; PNAS

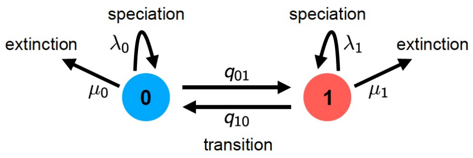
Roalson & Roberts, 2016; Syst Bio



Limitaciones

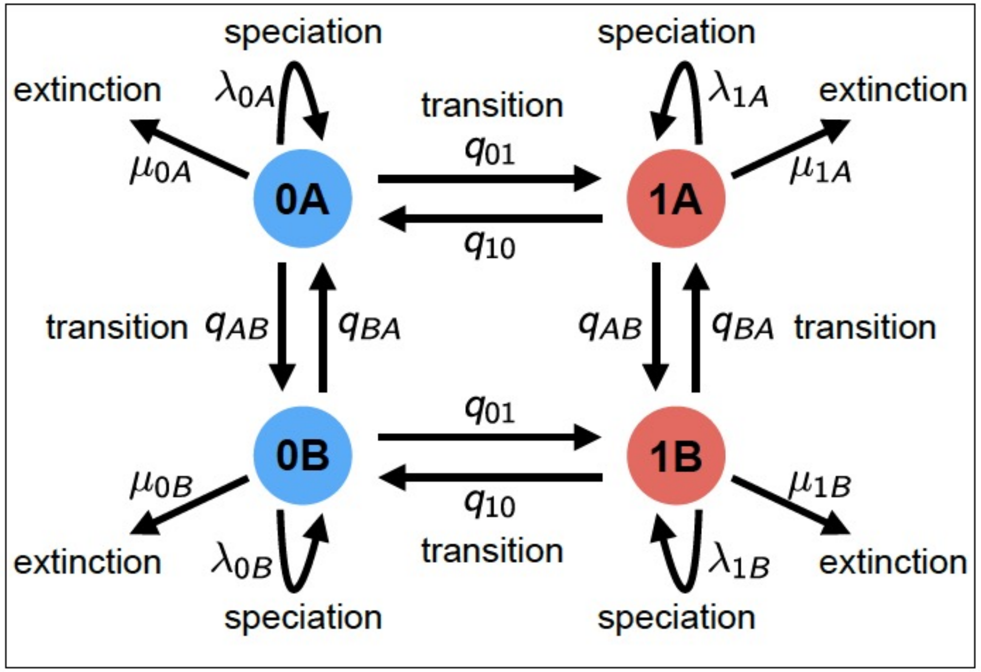
BiSSE

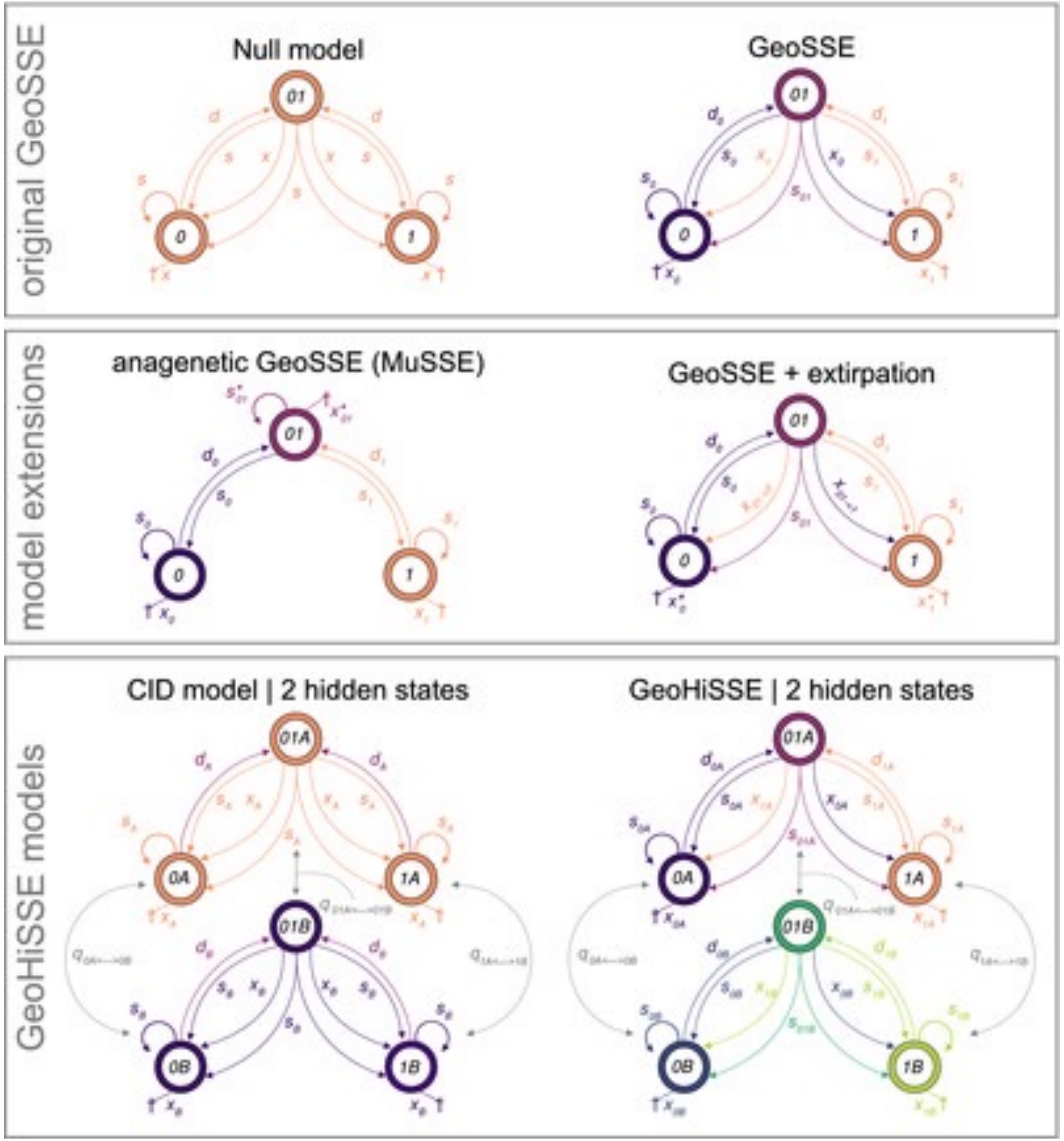
Maddison et al., 2007;
Systematic Biology



HiSSE

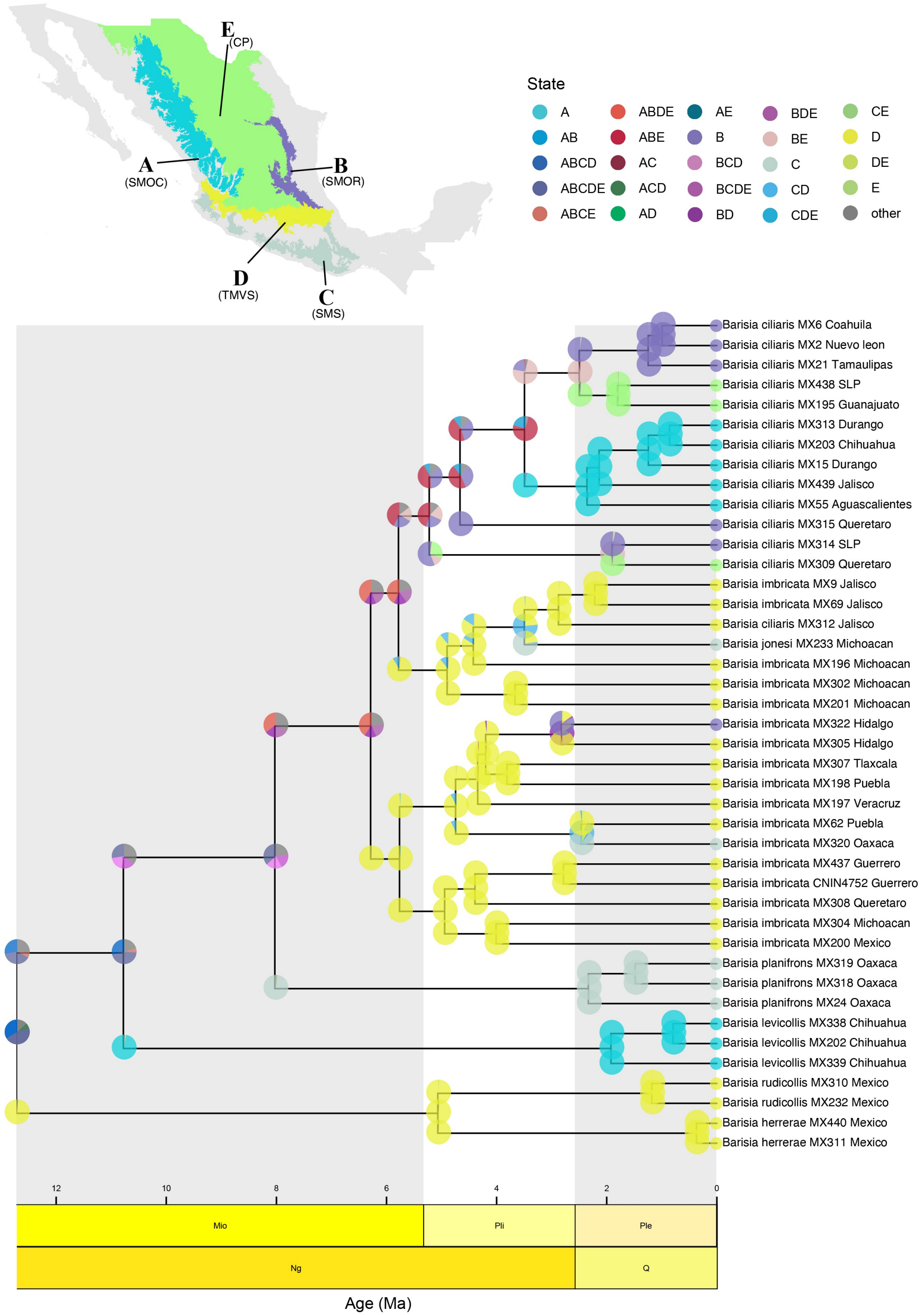
Maddison and FitzJohn 2015;
Systematic Biology





Caetano et al., 2018; Evolution

Zaldivar-Riverón et al., In prep



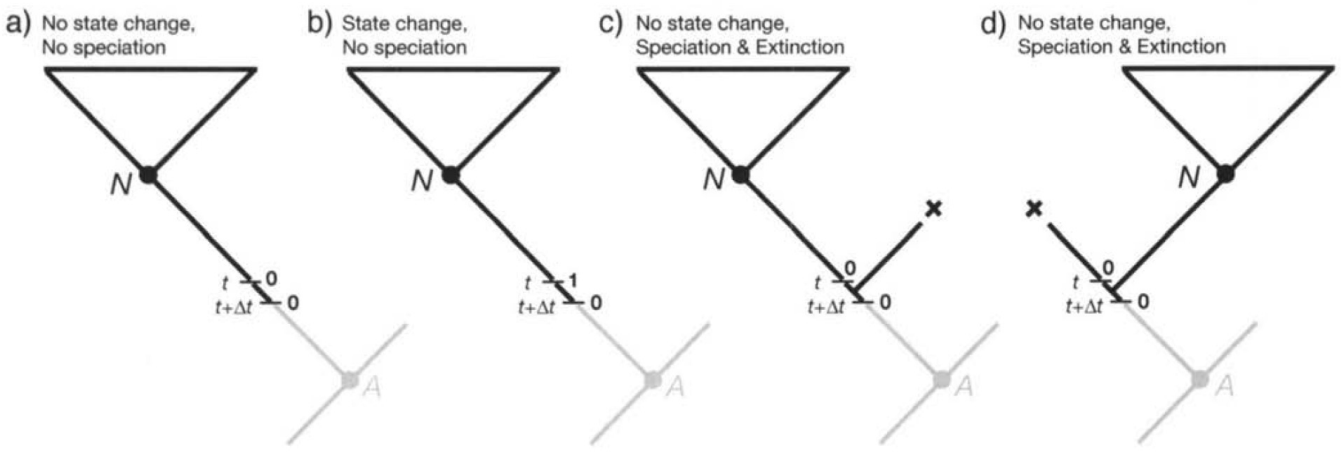


FIGURE 2. Alternative scenarios by which a lineage with state 0 at time $t+\Delta t$ on the branch might yield clade decended from node N but no other living descendants.

Cladogenetic State change Speciation and Extinction (ClaSSE)

Introducción a la Biogeografía Paramétrica

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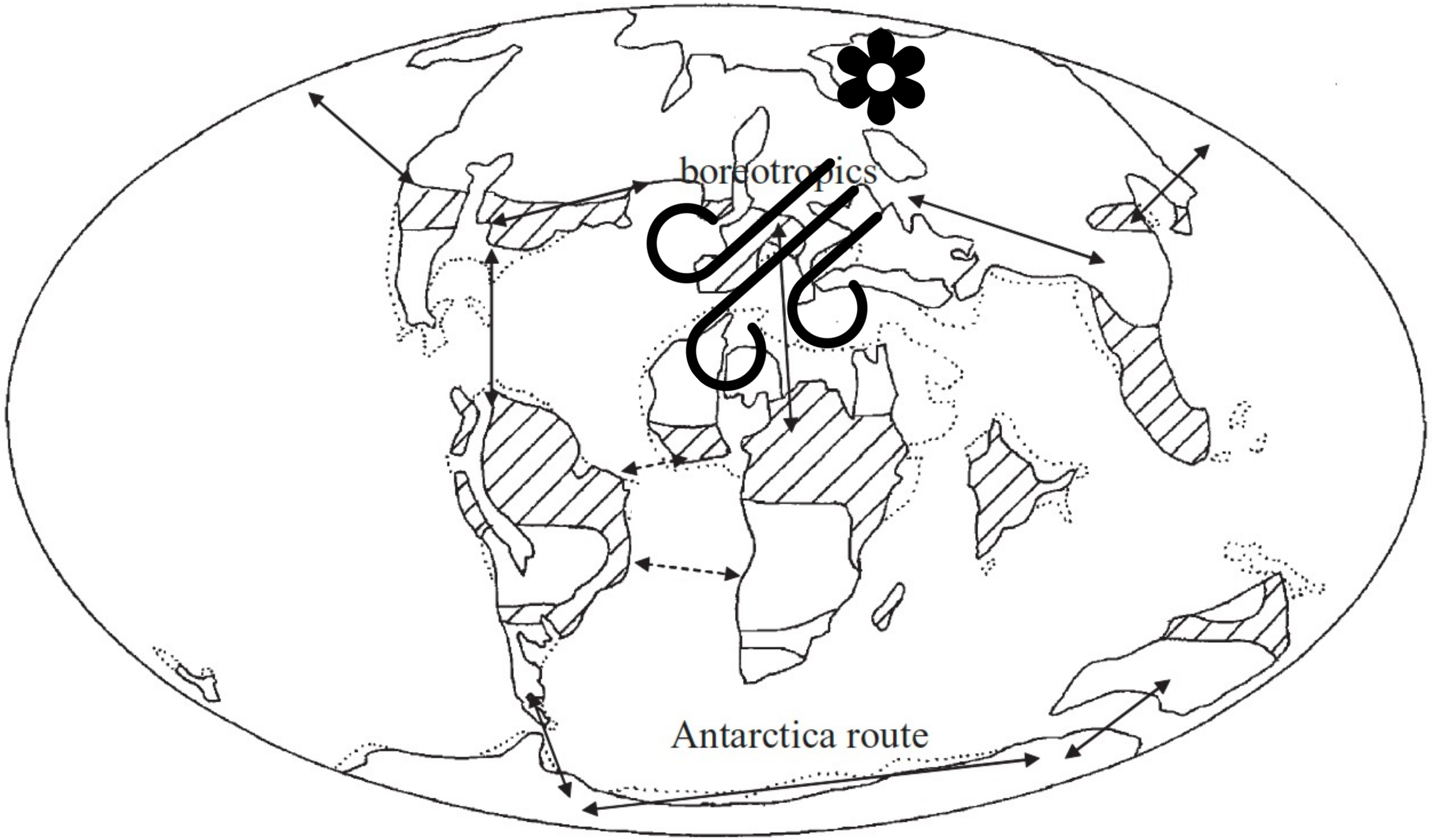
Ventajas y limitaciones

- Integran la dimensión temporal
- Se incorpora el error asociado
- Se puede discriminar entre escenarios con métodos estadísticos (LRT, Bayes Factor, AIC)
- Pueden integrar diferentes fuentes de evidencia

- Costosos computacionalmente
- Limitado por el número de áreas aunque...
- Coste de parámetros
- No diferencia entre tipos de dispersion aunque…

Pennington & Dick, 2004



JOURNAL ARTICLE

TEMPO AND MODE IN PLANT BREEDING SYSTEM EVOLUTION

Emma E. Goldberg, Boris Igić

Evolution, Volume 66, Issue 12, 1 December 2012, Pages 3701–3709, https://doi.org/10.1111/j.1558-5646.2012.01730.x

Published: 01 December 2012 **Article history** ▾

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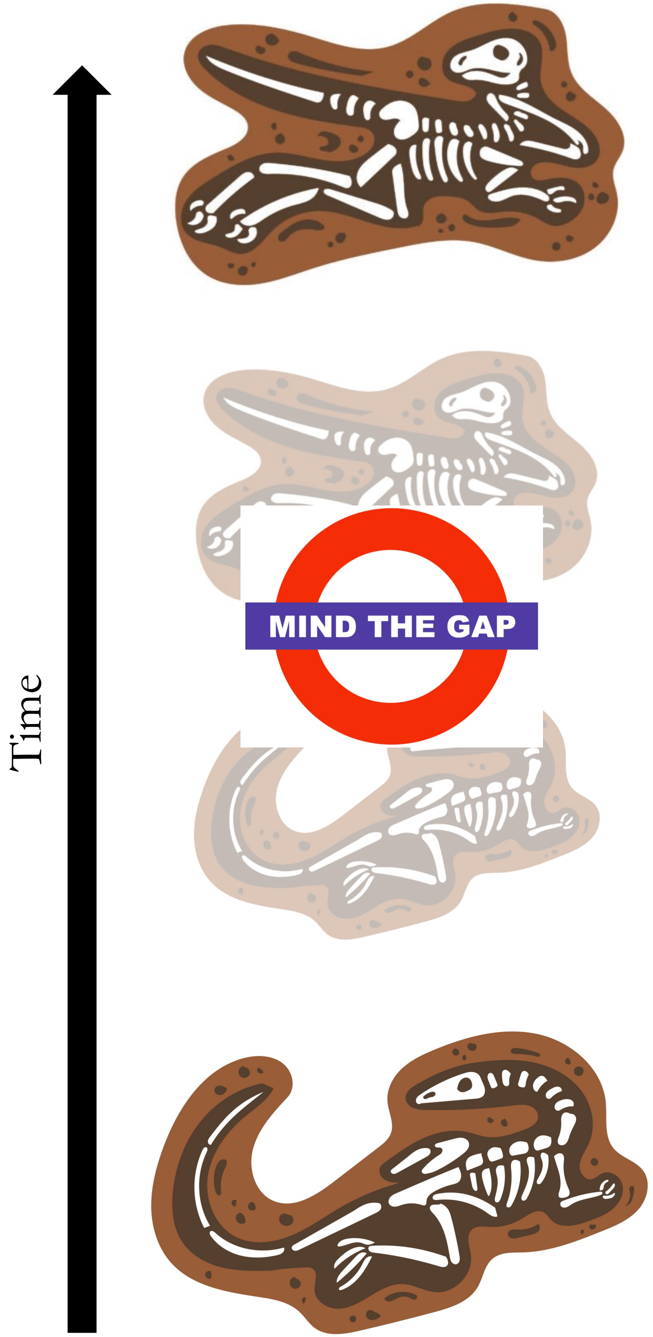
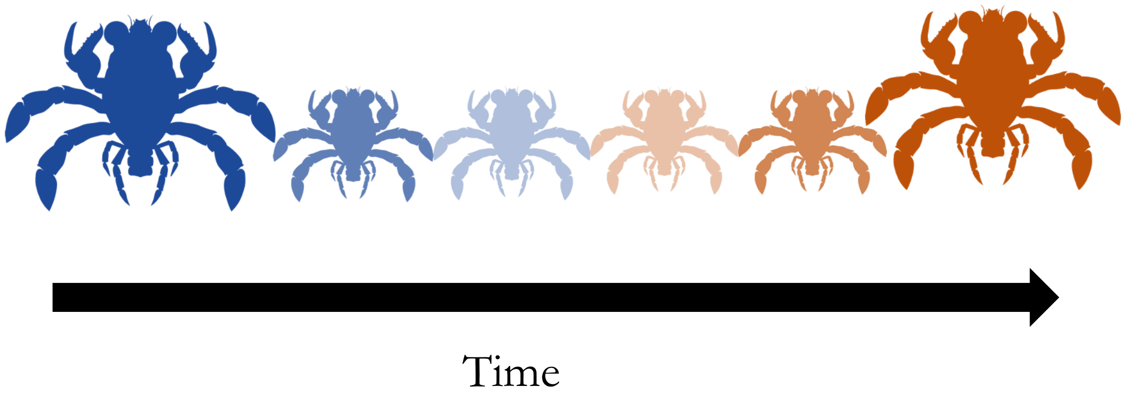
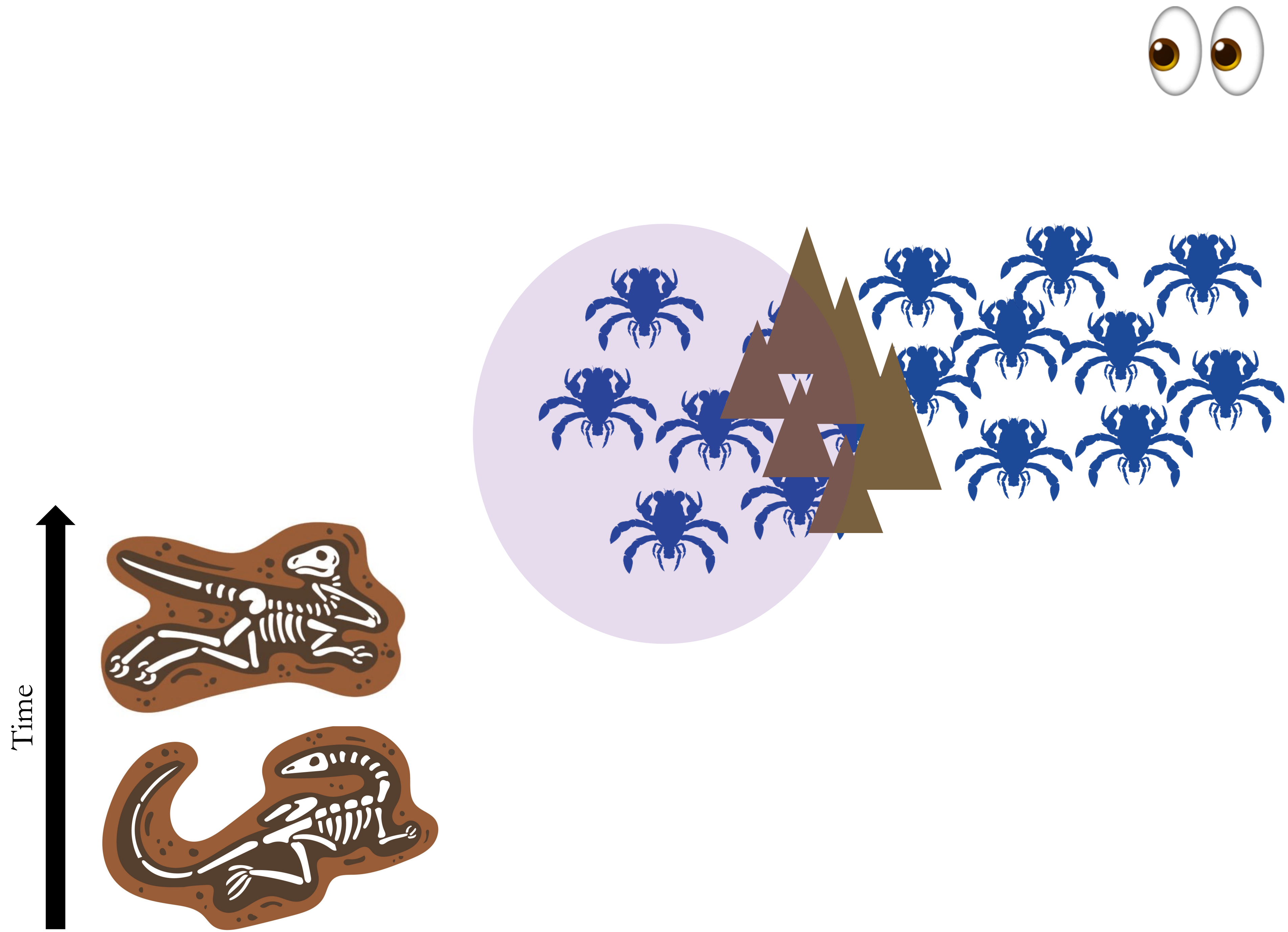
Abstract

Classic questions about trait evolution—including the directionality of character change and its interactions with lineage diversification—intersect in the study of plant breeding systems. Transitions from self-incompatibility to self-compatibility are frequent, and they may proceed within a species ("anagenetic" mode of breeding system change) or in conjunction with speciation events ("cladogenetic" mode of change). We apply a recently developed phylogenetic model to the nightshade family Solanaceae, quantifying the relative contributions of these two modes of evolution along with the

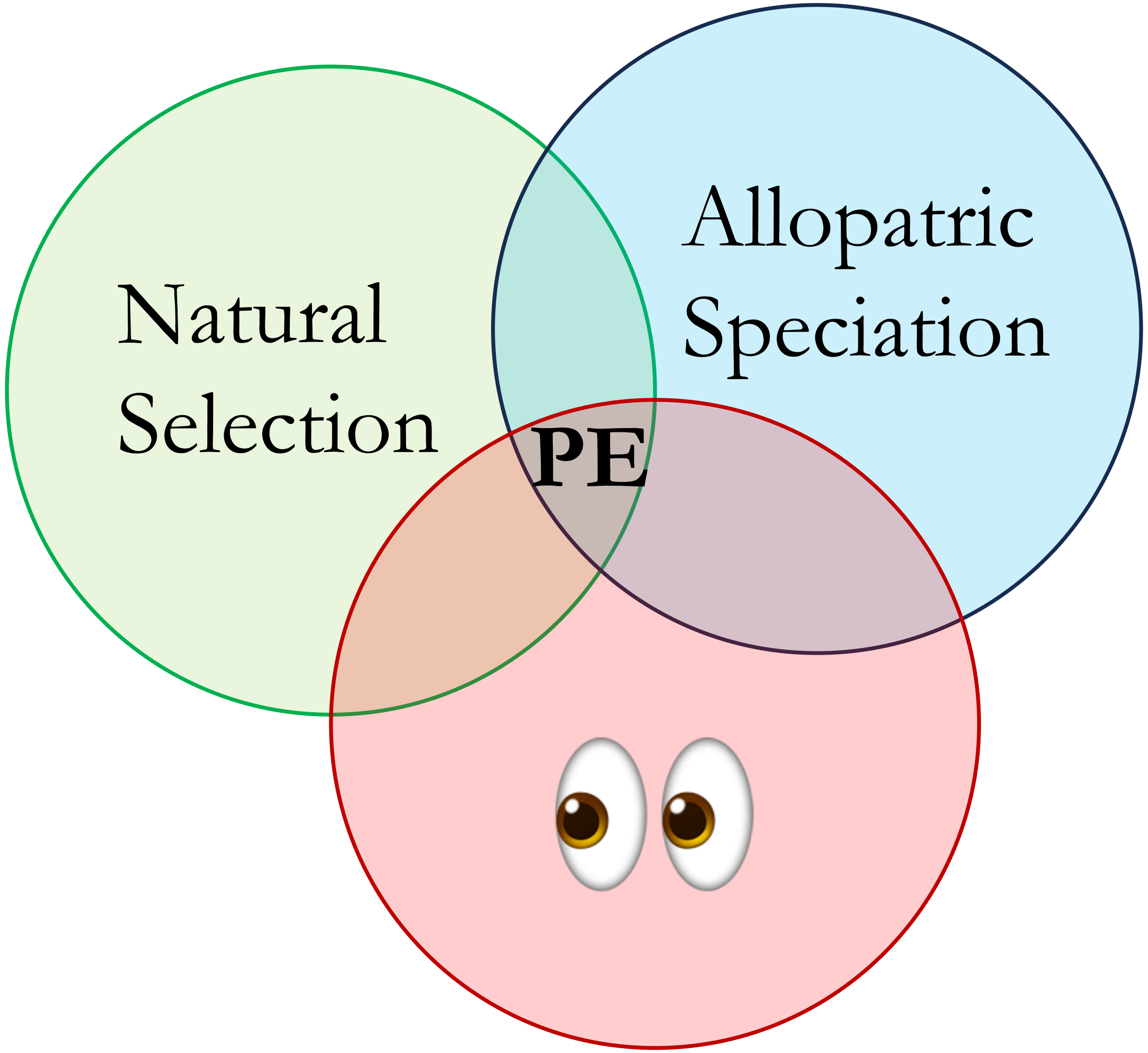

Time
MIND THE GAP

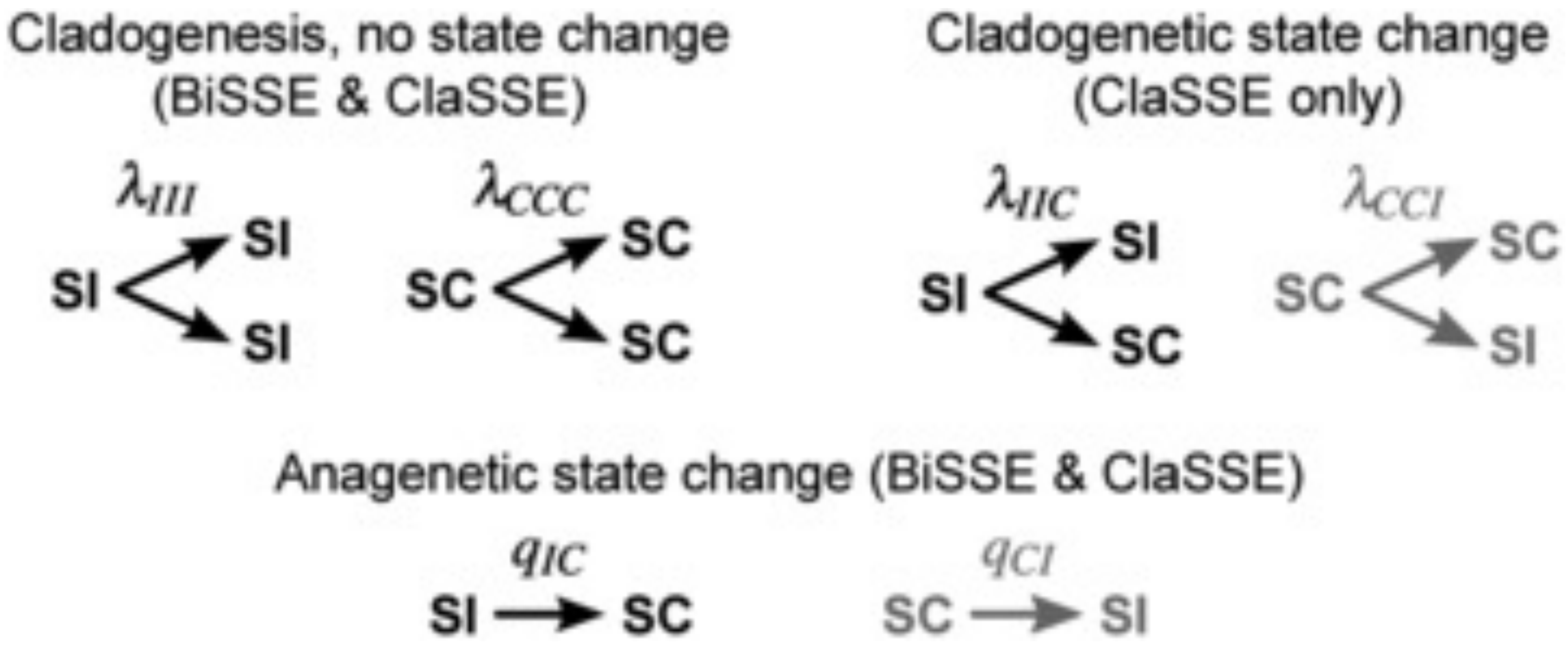

Time


Time

Punctuated Equilibria (PE)

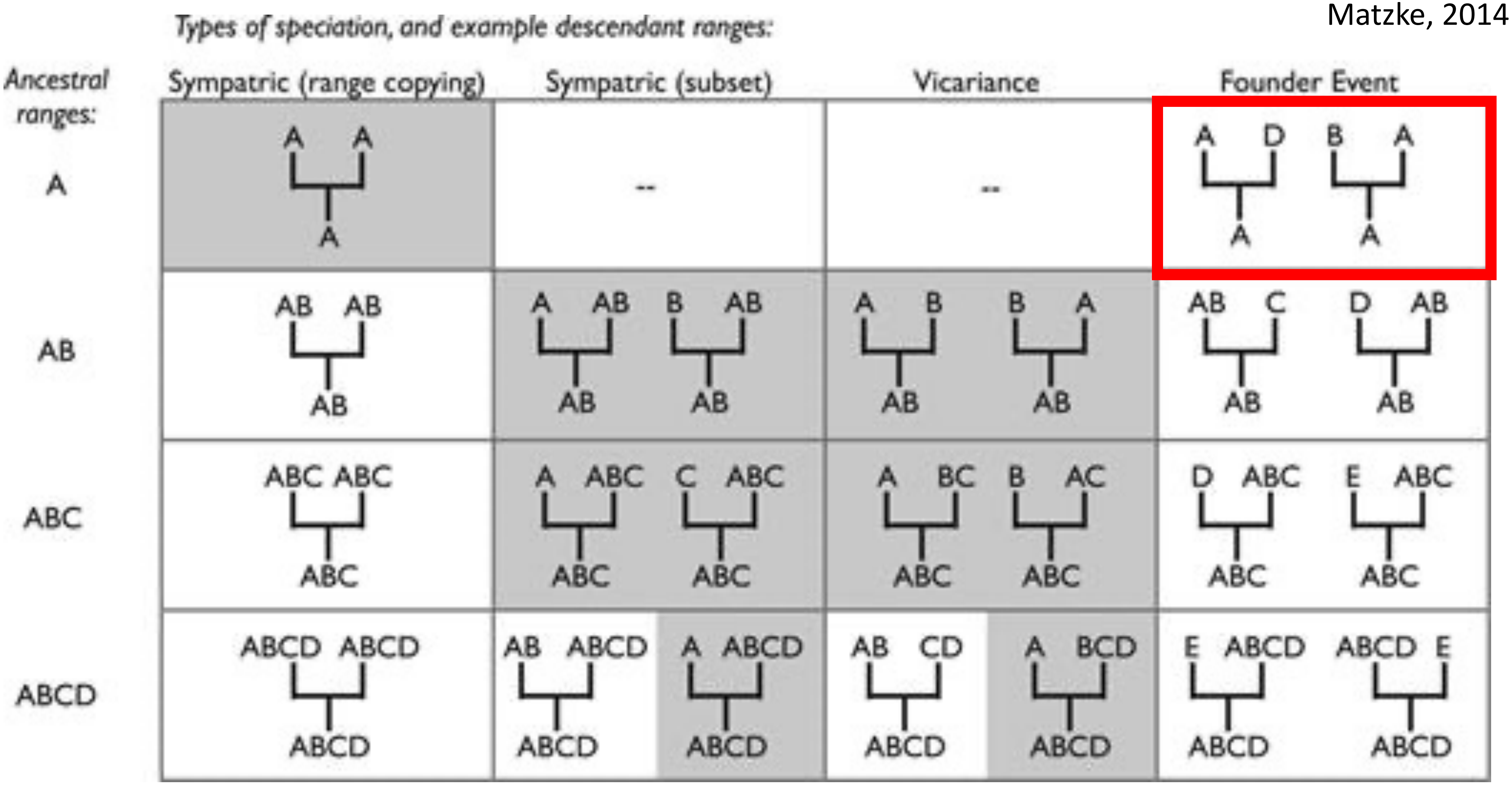
1970s by Eldredge
and Gould





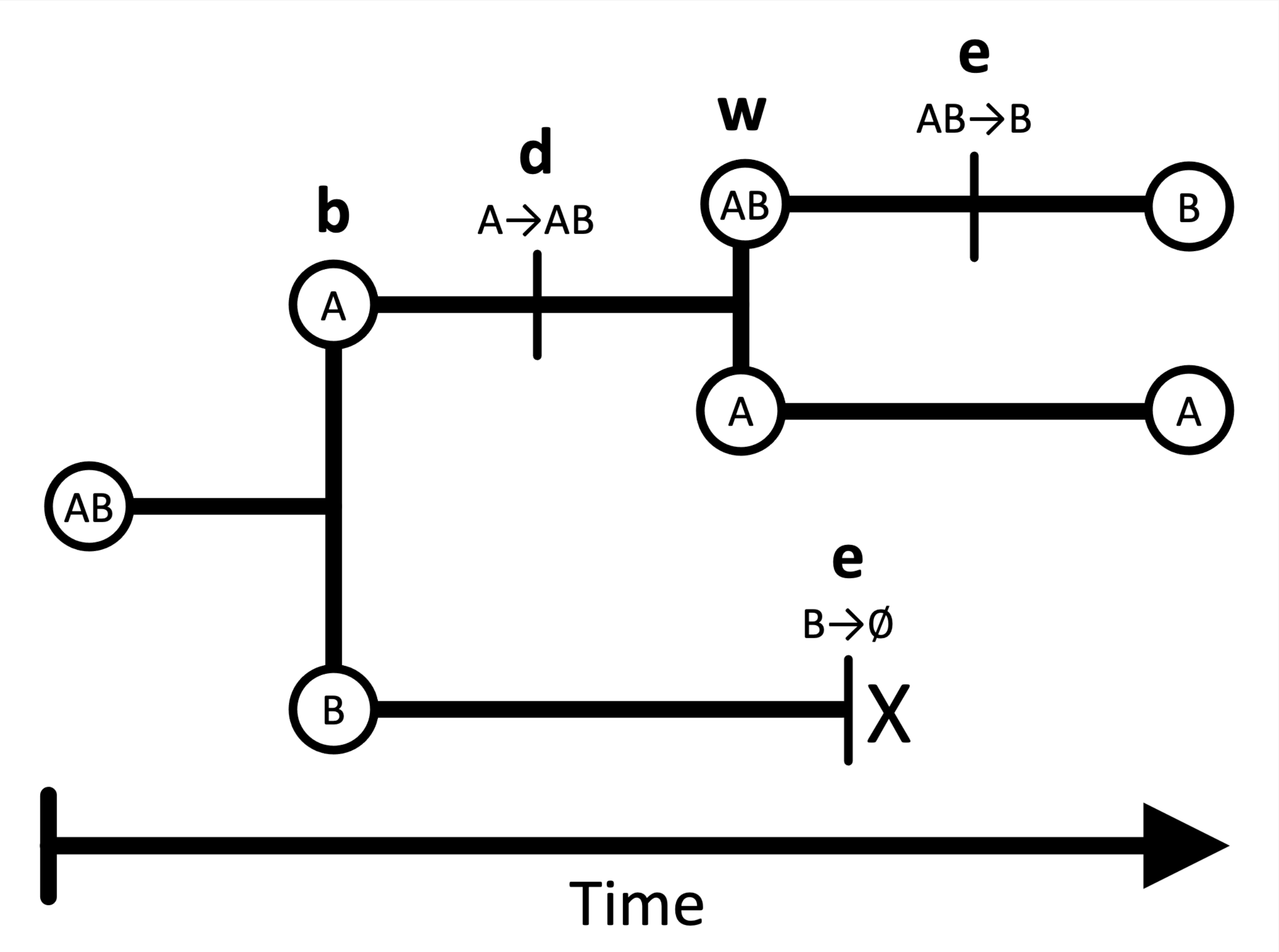
Cladogenesis, no state change
(BiSSE & ClaSSE)
λ_{III}
SI
SI
SI
λ_{CCC}
SC
SC
SC
Cladogenetic state change
(ClaSSE only)
λ_{IIC}
SI
SI
SC
λ_{CCI}
SC
SC
SI
Anagenetic state change (BiSSE & ClaSSE)
q_{IC}
SI
SC
q_{CI}
SC
SI

Matzke, 2014 Sys Bio

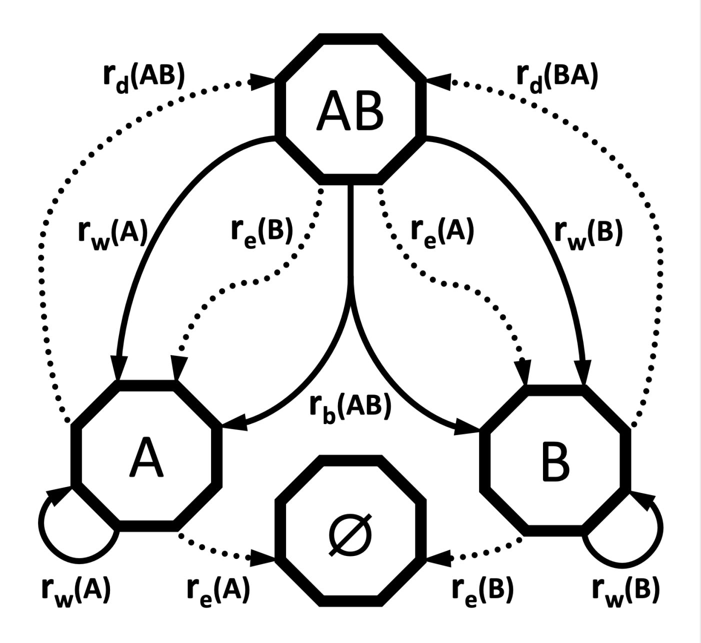


DEC

DEC+J

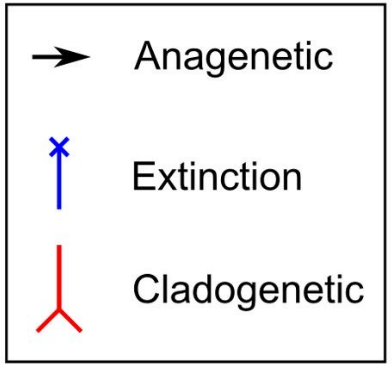


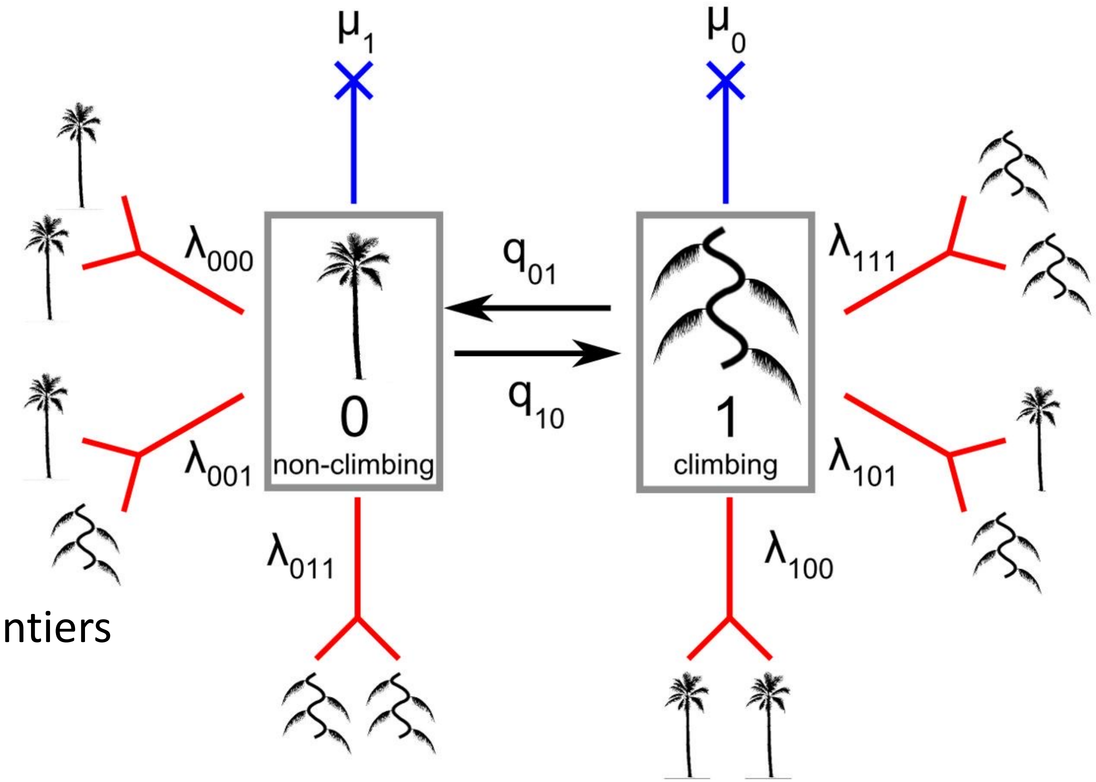
e
AB→B
w
d
A→AB
b
AB
B
A
A
A
AB
e
B→Ø
B
X
Time



$r_d(AB)$
$r_d(BA)$
AB
$r_w(A)$
$r_e(B)$
$r_e(A)$
$r_w(B)$
$r_b(AB)$
A
B
Ø
$r_w(A)$
$r_e(A)$
$r_e(B)$
$r_w(B)$

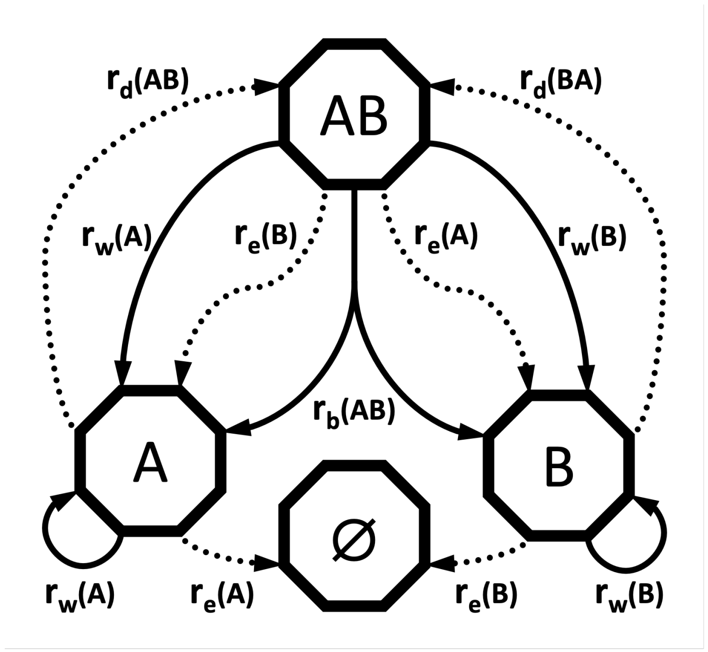
ClaSSE

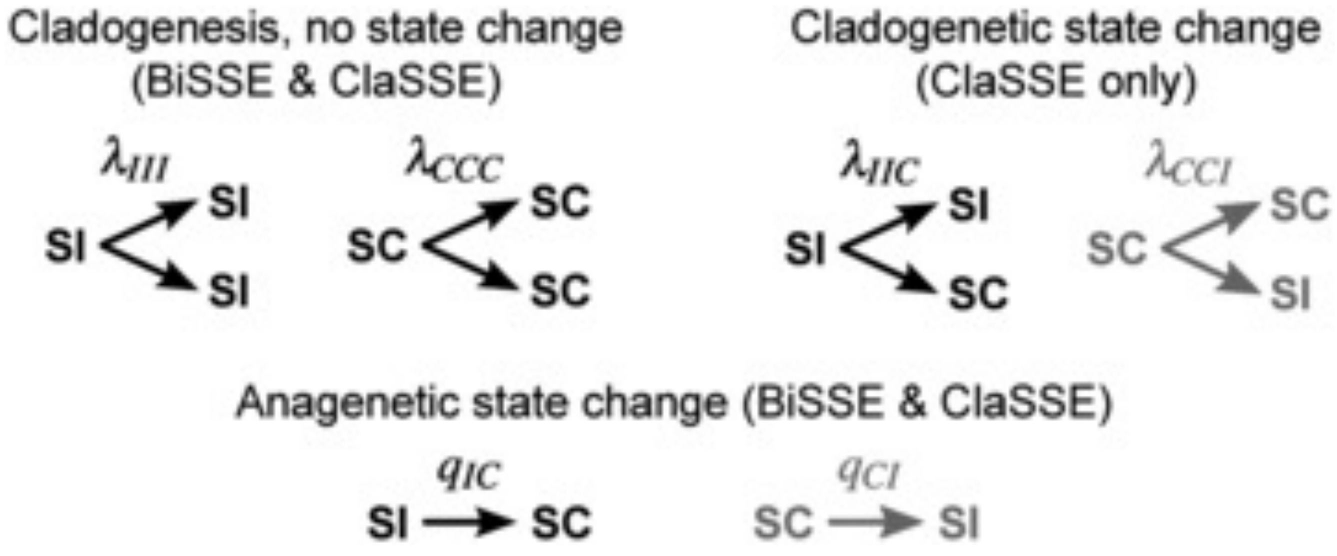


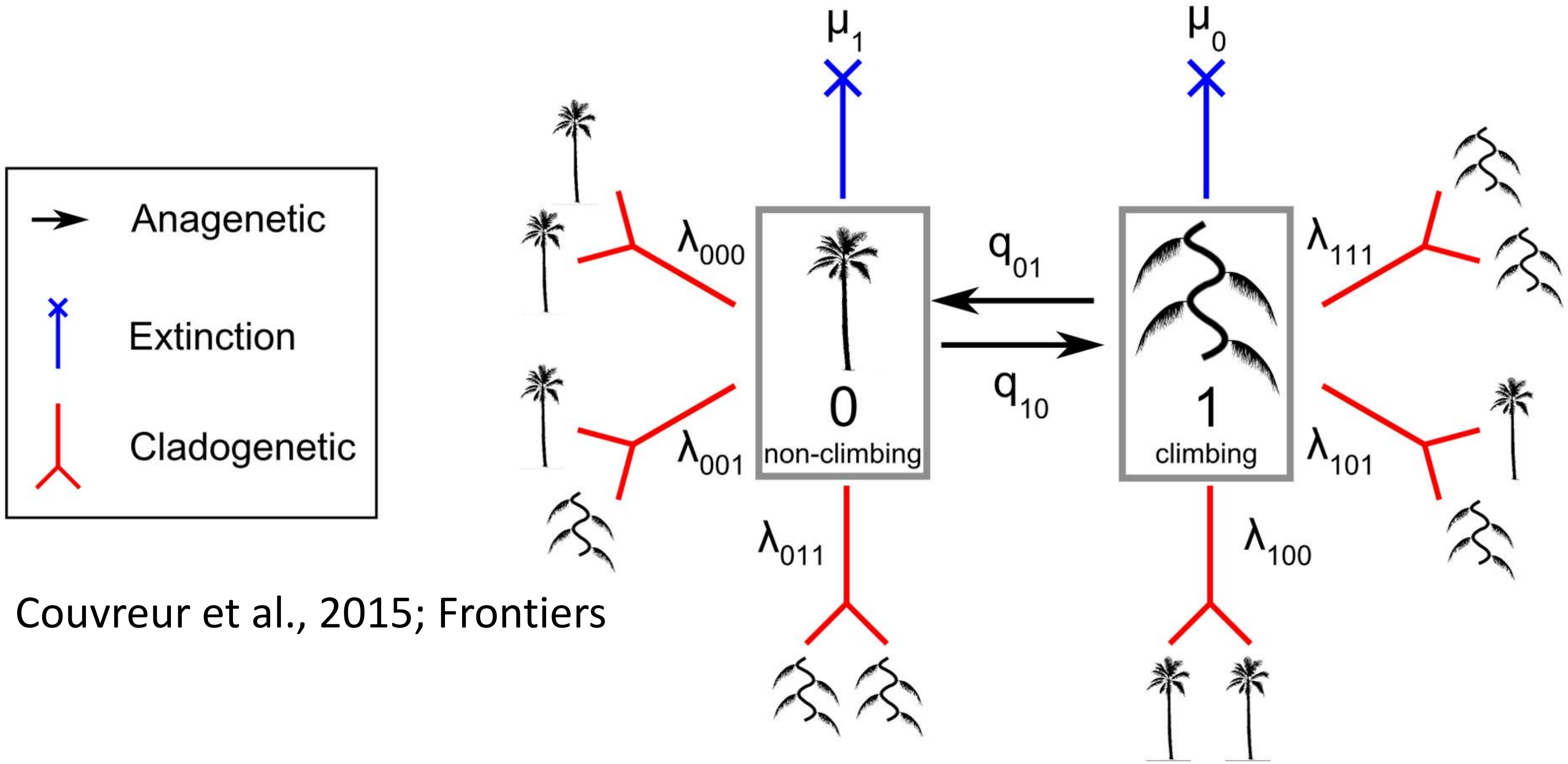


Couvreur et al., 2015; Frontiers

GeoSSE







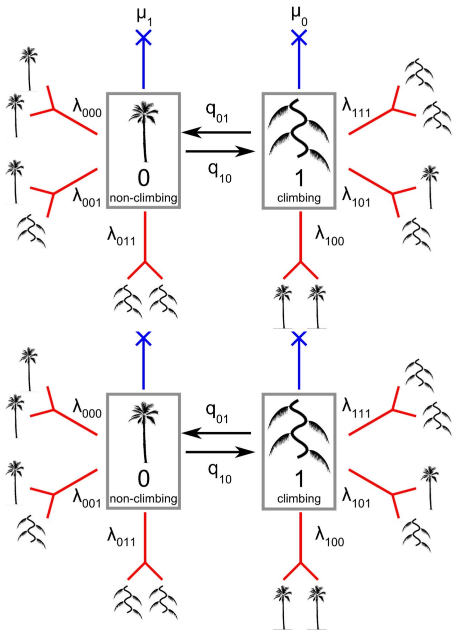
Couvreur et al., 2015; Frontiers

0 = 00 = the null state with no range

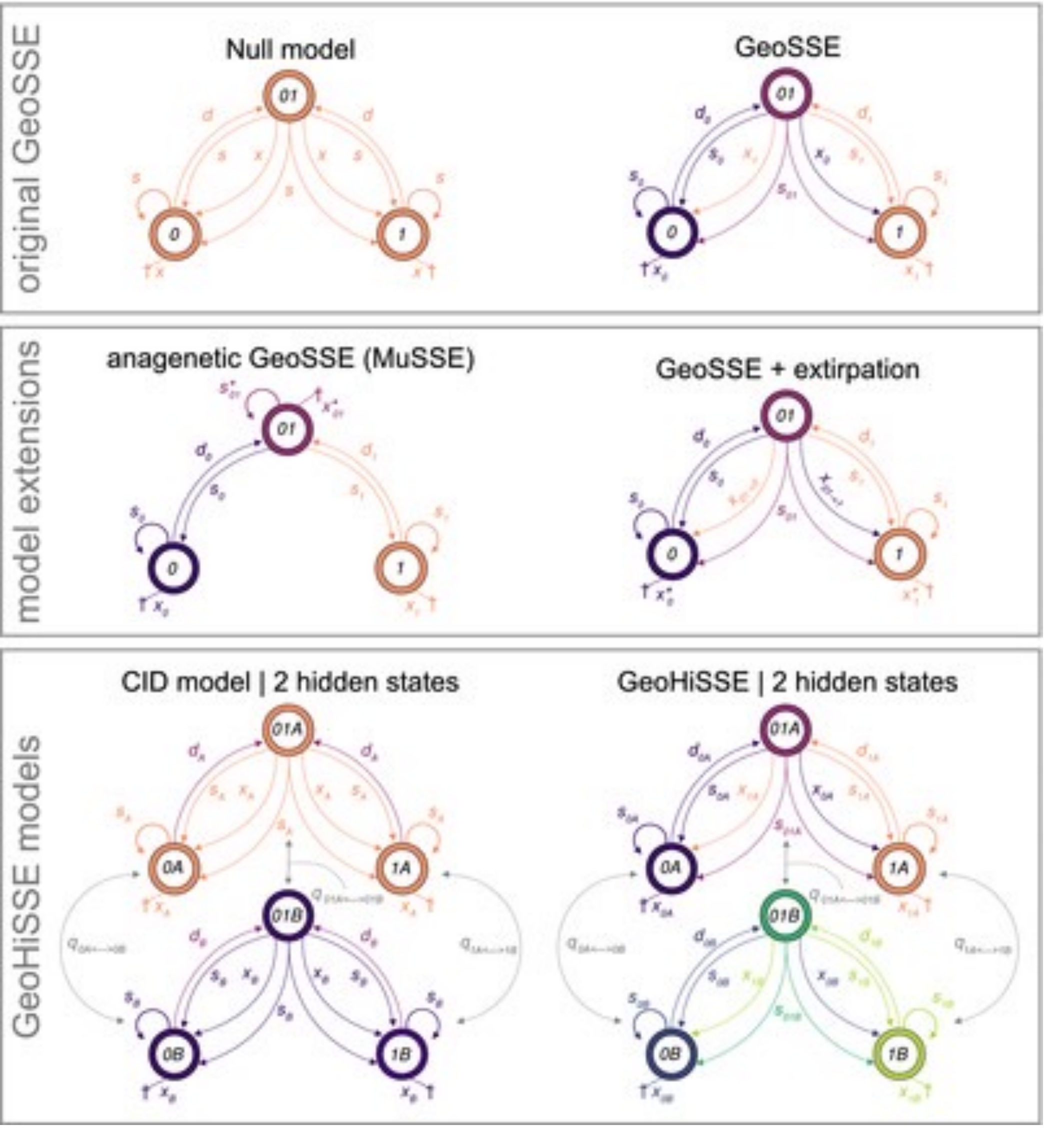
1 = 01 = Area A only

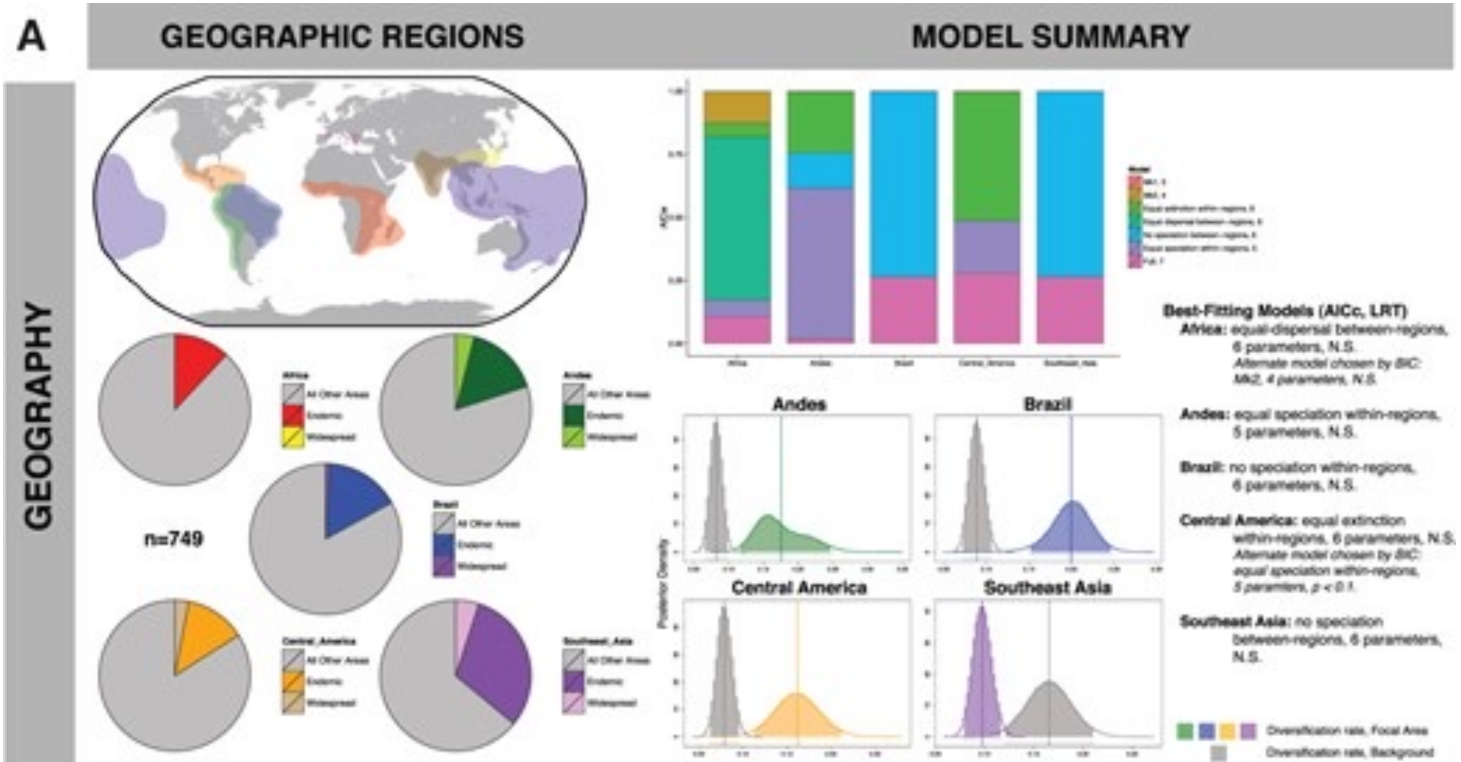
2 = 10 = Area B only

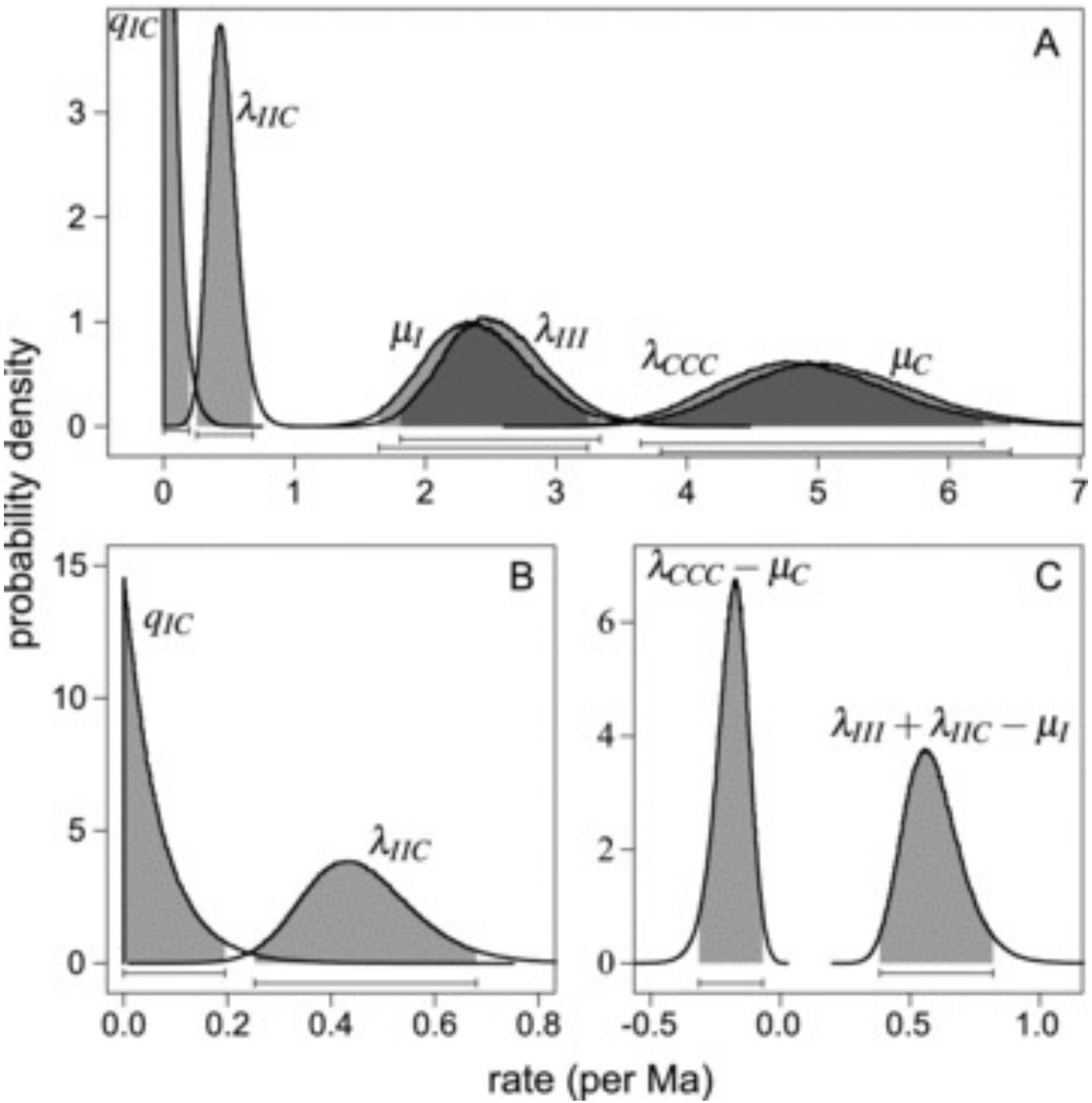
3 = 11 = both areas AB



state,range
0,0000
1,1000
2,0100
3,0010
4,0001
5,1100
6,1010
7,0110
8,1001
9,0101
10,0011
11,1110
12,1101
13,1011
14,0111
15,1111


original GeoSSE
Null model
GeoSSE
model extensions
anagenetic GeoSSE (MuSSE)
GeoSSE + extirpation
GeoHiSSE models
CID model | 2 hidden states
GeoHiSSE | 2 hidden states


A
GEOGRAPHIC REGIONS
MODEL SUMMARY
GEOGRAPHY
n=749
Andes
Brazil
Central America
Southeast Asia
Best-Fitting Models (AICc, LRT)
Africa: equal-dispersal between-regions, 6 parameters, N.S. Alternate model chosen by BIC: Mk2, 4 parameters, N.S.
Andes: equal speciation within-regions, 5 parameters, N.S.
Brazil: no speciation within-regions, 6 parameters, N.S.
Central America: equal extinction within-regions, 6 parameters, N.S. Alternate model chosen by BIC: equal speciation within-regions, 5 parameters, p < 0.1.
Southeast Asia: no speciation between-regions, 6 parameters, N.S.
Diversification rate, Focal Area
Diversification rate, Background



A
q_{IC}
λ_{IIC}
μ_I
λ_{III}
λ_{CCC}
μ_C
B
q_{IC}
λ_{IIC}
C
$\lambda_{CCC} - \mu_C$
$\lambda_{III} + \lambda_{IIC} - \mu_I$
probability density
rate (per Ma)