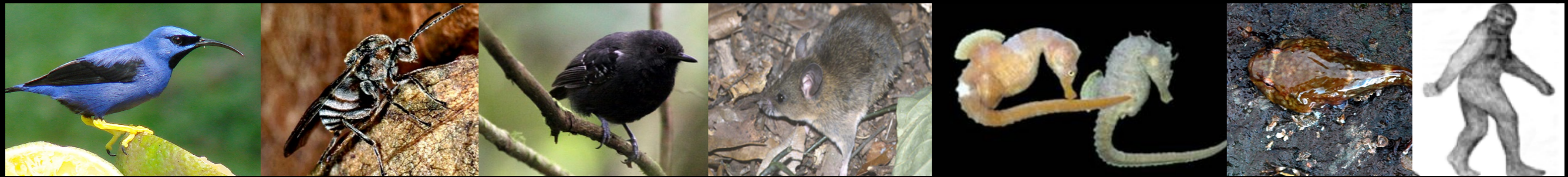


Welcome to CompPhylo 2019



Michael Hickerson
City University of New York
City College of New York
American Museum of Natural History

The comparative
phylogeographic
pipe dream

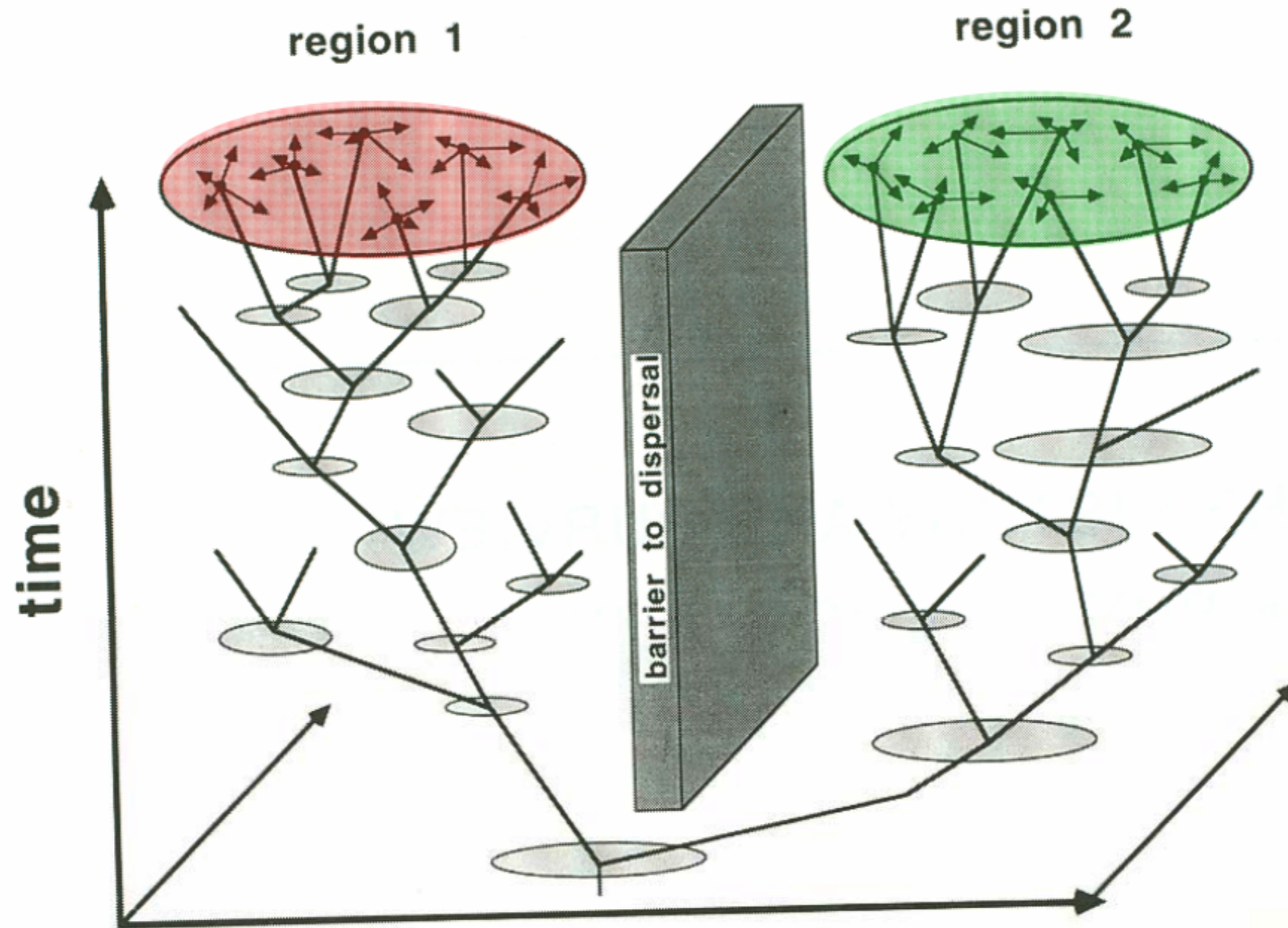


John Avise



Godfrey Hewitt



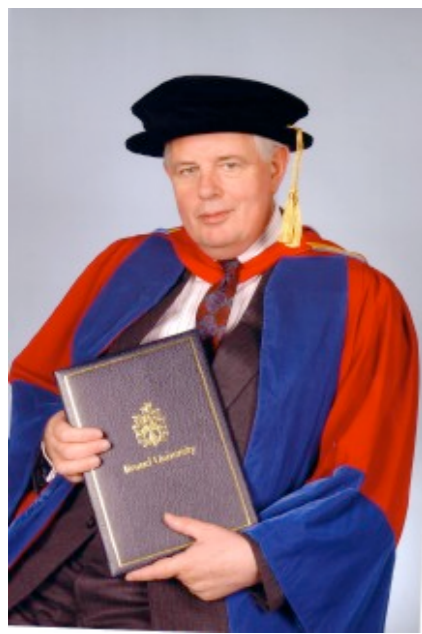


~1987 Avise coins “**phylogeography**”



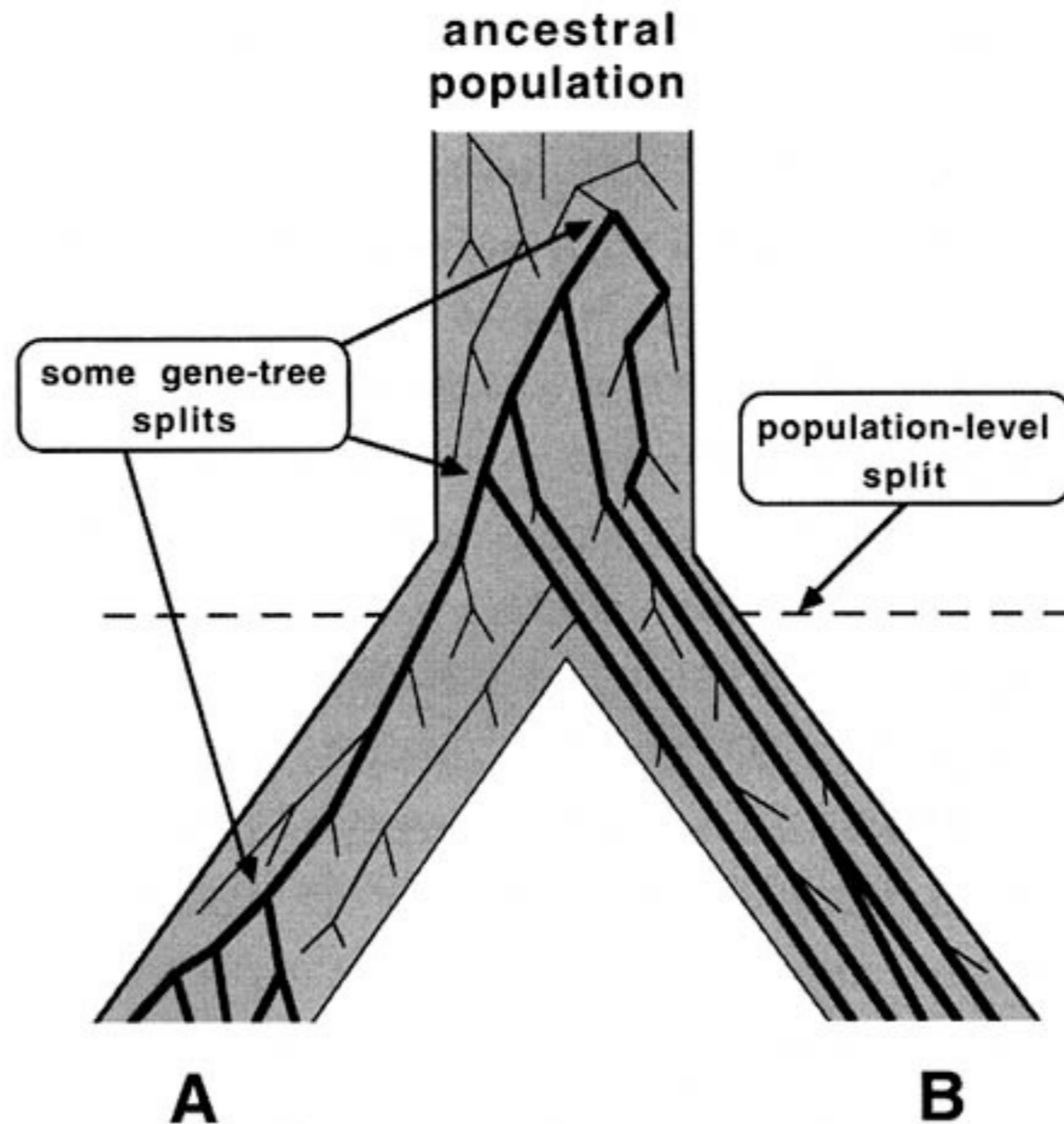
J. Avise

mtDNA Gene trees carry signature of species **demographic histories** (outgrowth of PCR revolution)



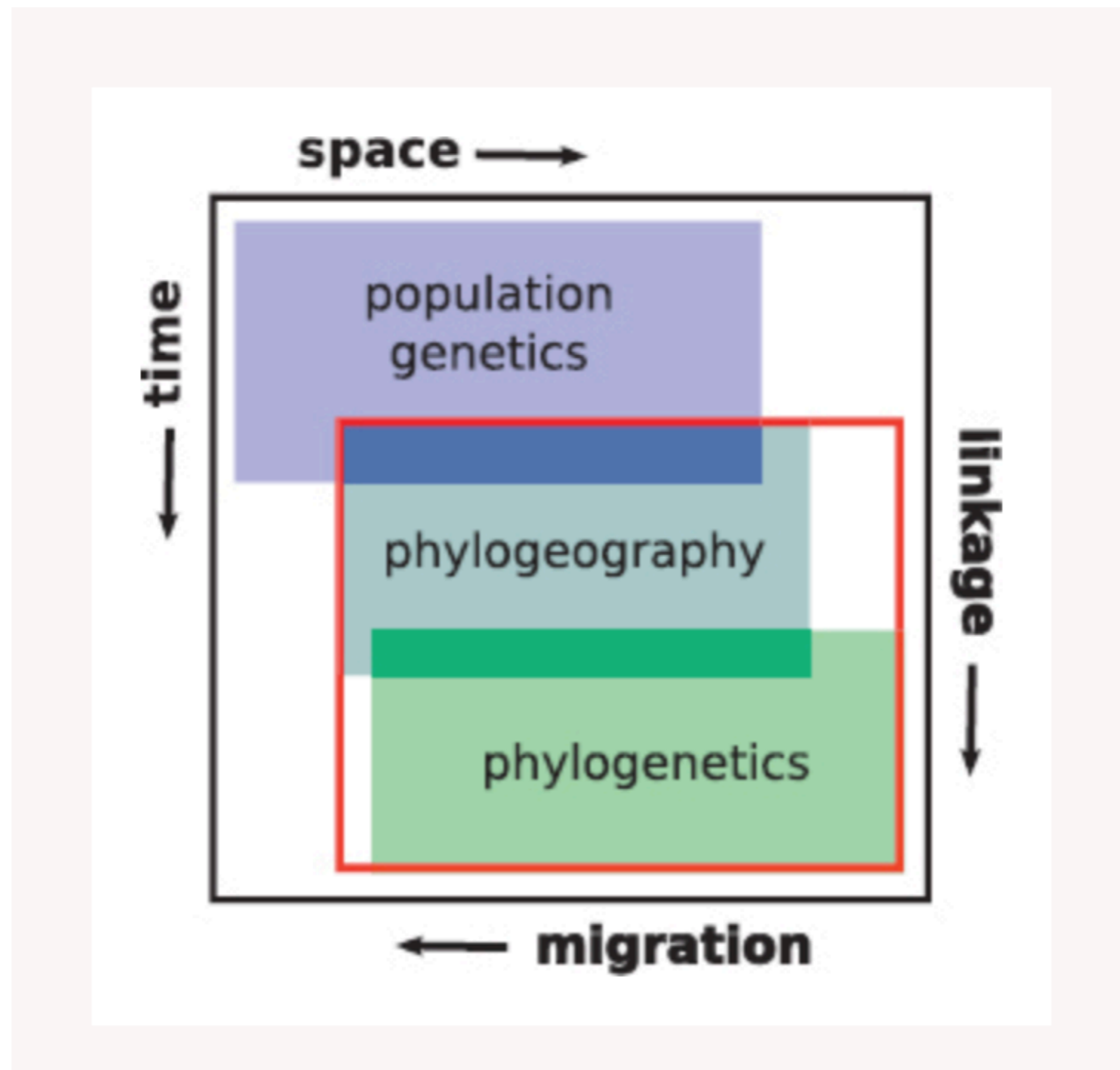
Kingman

$$P_c(t) = \left(1 - \frac{1}{2N_e}\right)^{t-1} \left(\frac{1}{2N_e}\right).$$

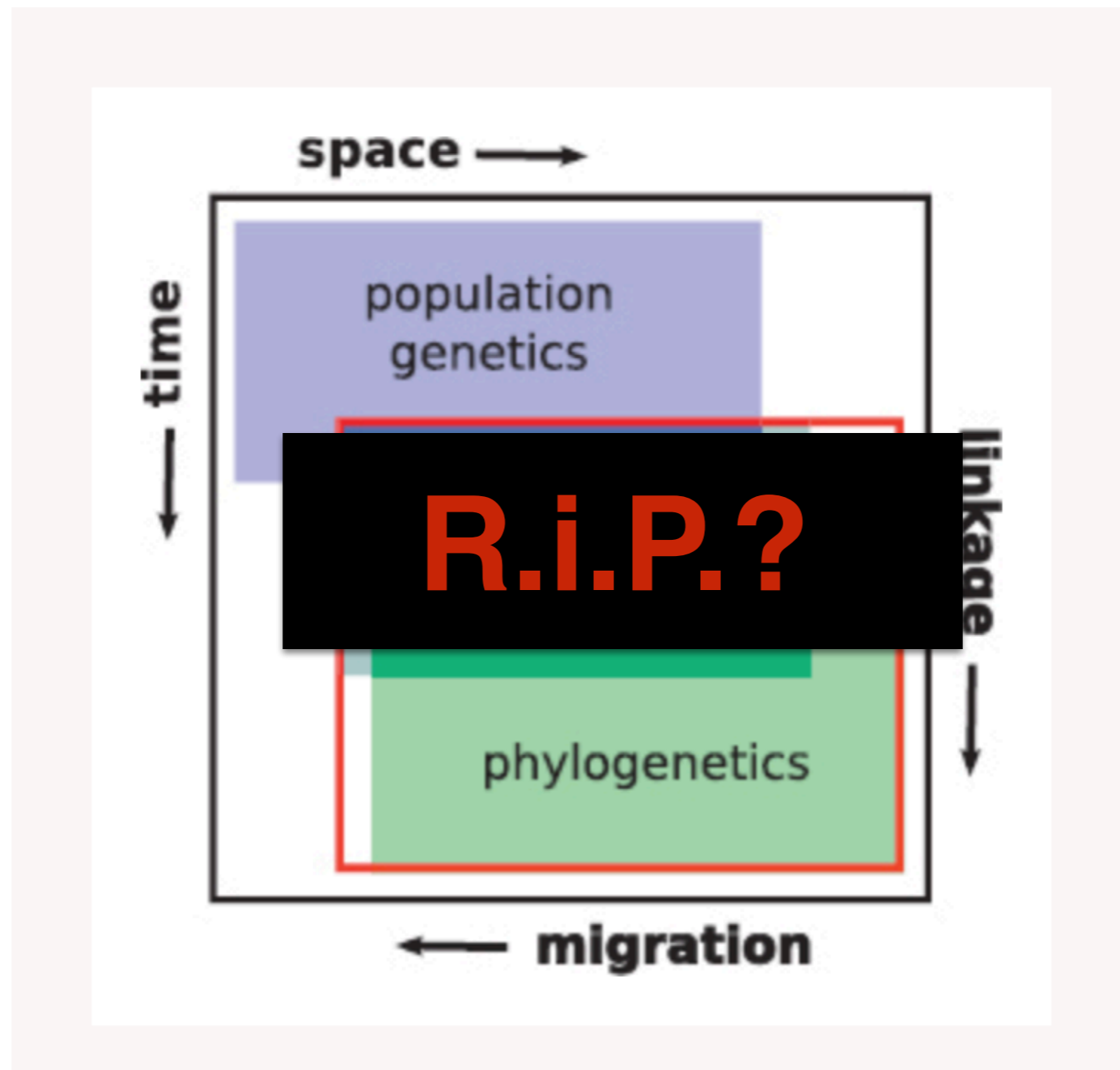


Tajima

Coalescent Theory (1983) slowly percolates into phylogeography and later into phylogenetics (working statistical model)

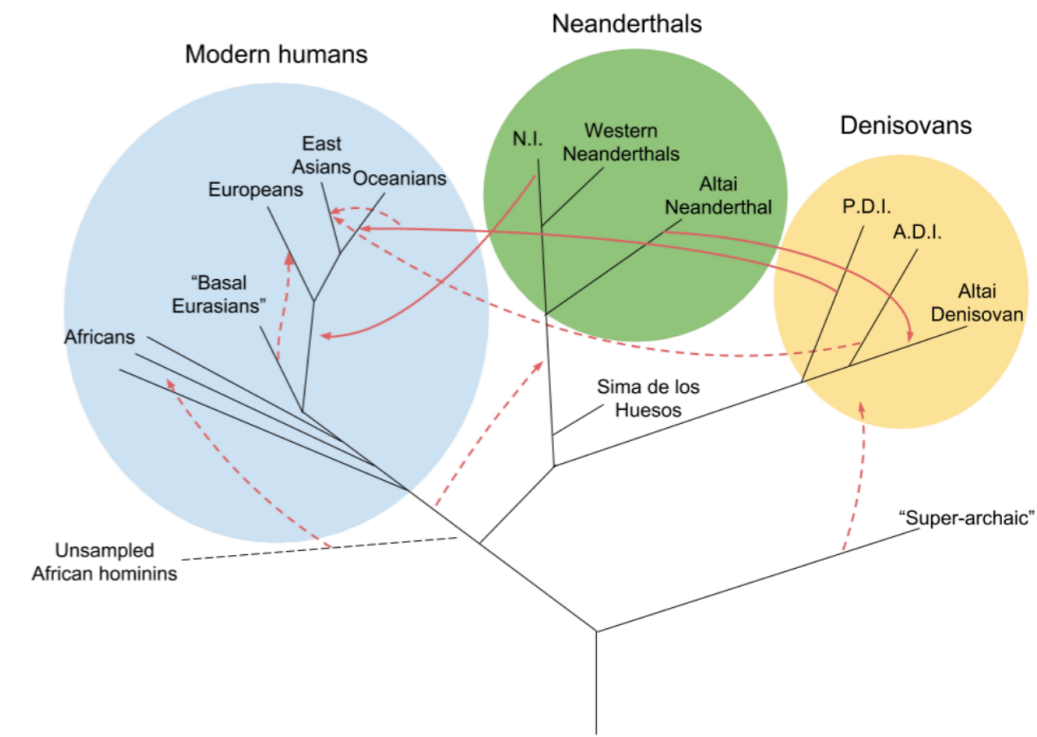
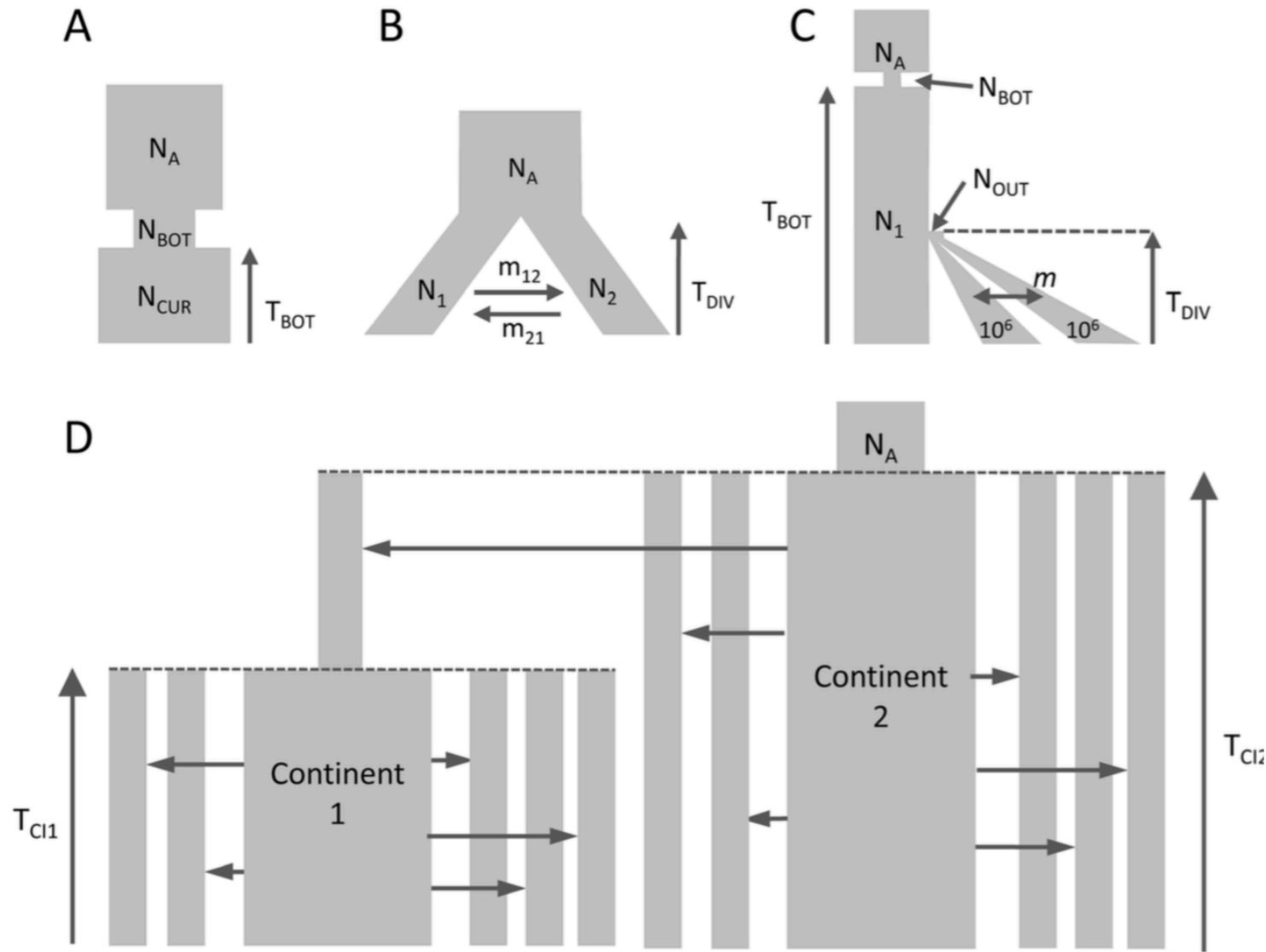


Avise et al. 1987 —————→ *Edwards et al. 2016*

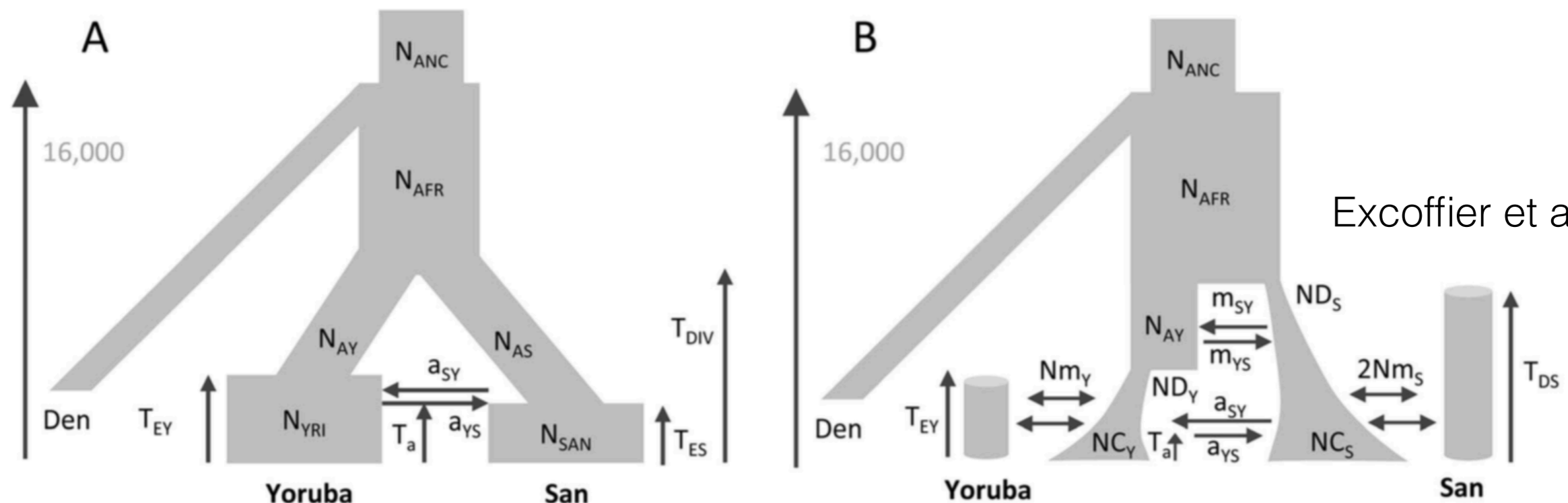


Edwards et al. 2016

phylogeography \approx demographic historical inference

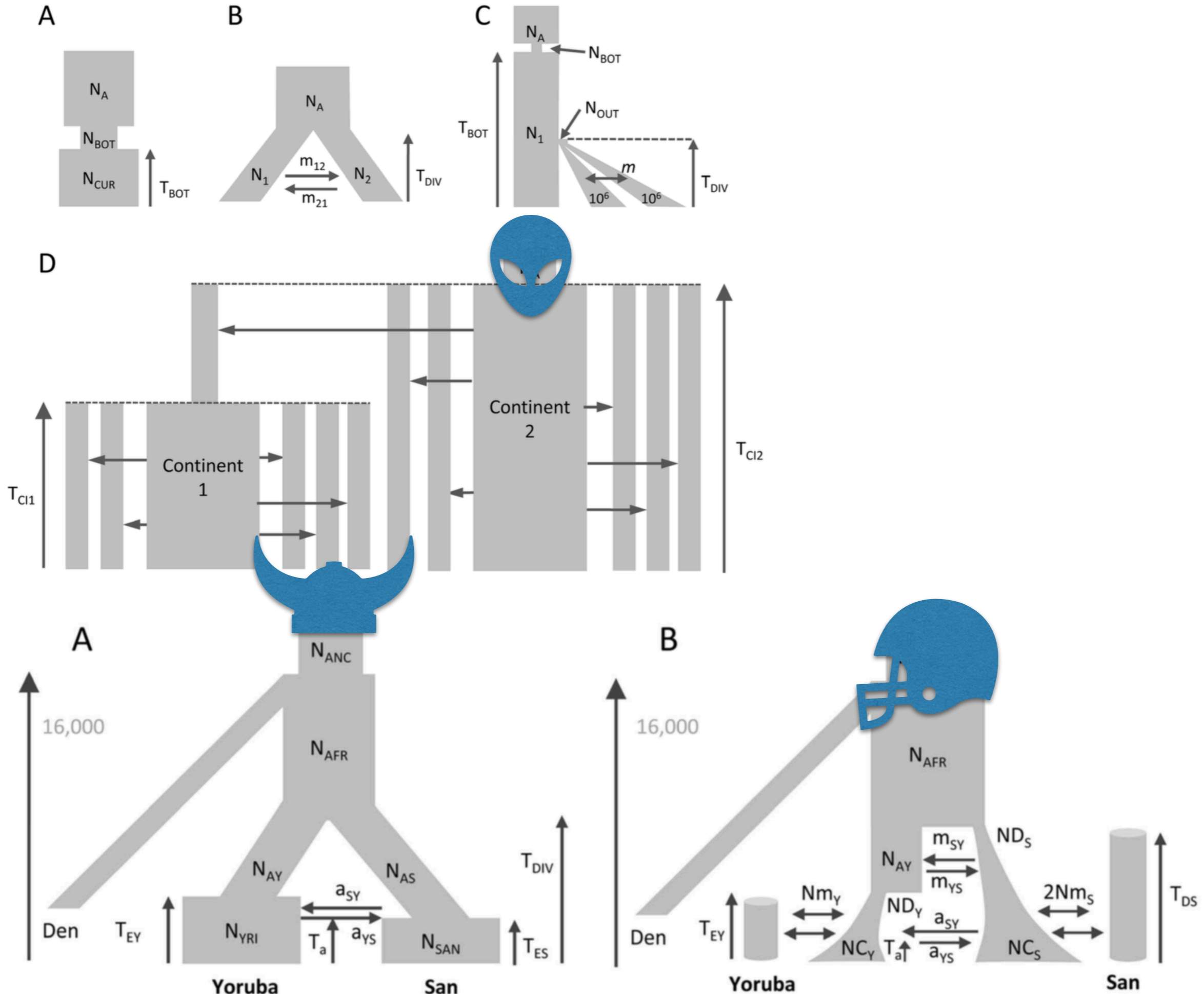


Dannemann & Racimo 2018



Excoffier et al. 2015

phylogeography = demographic historical inference



The comparative
phylogeographic
pipe dream
lives!



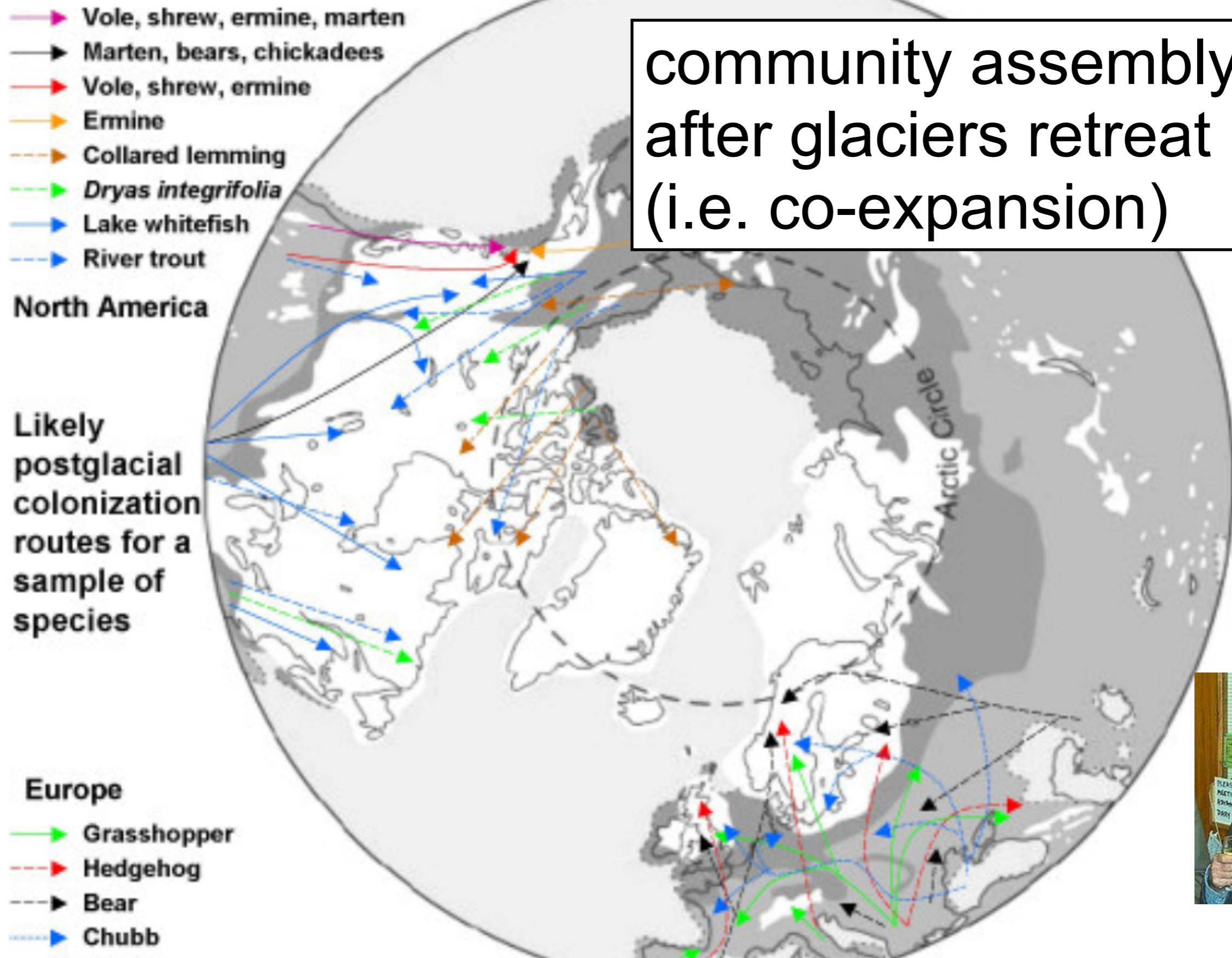
John Avise



Godfrey Hewitt

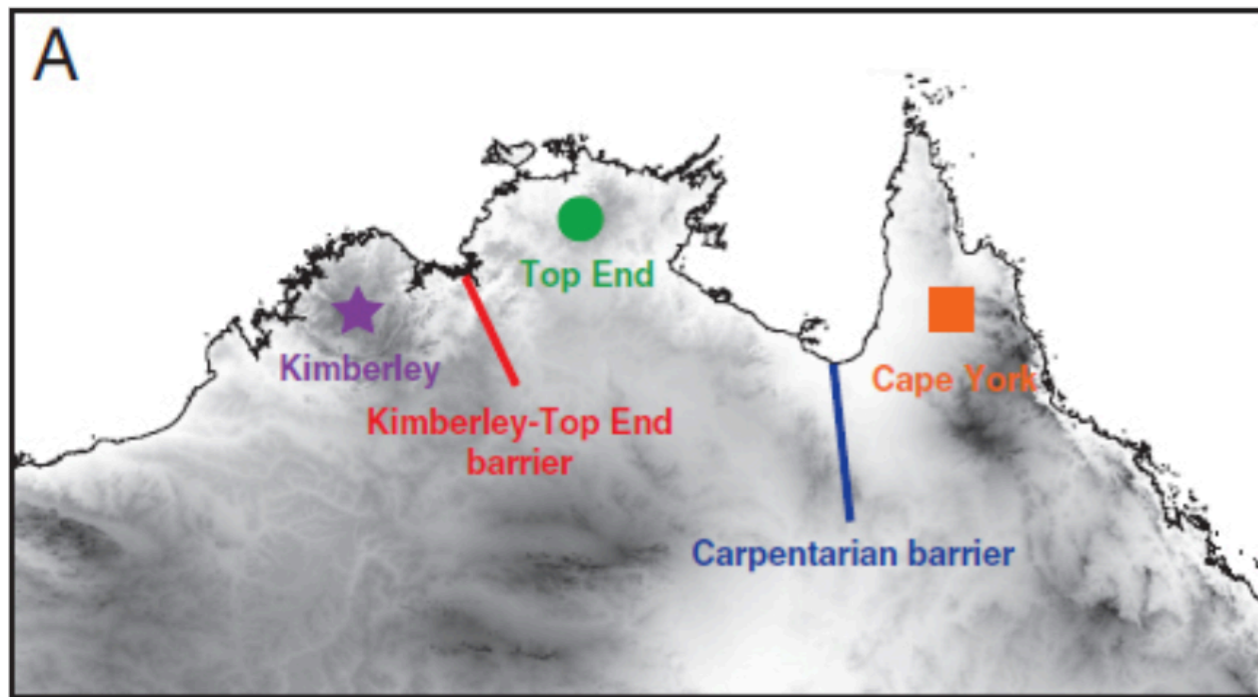
leveraging inferences from multiple species
demographic histories

community assembly
after glaciers retreat
(i.e. co-expansion)

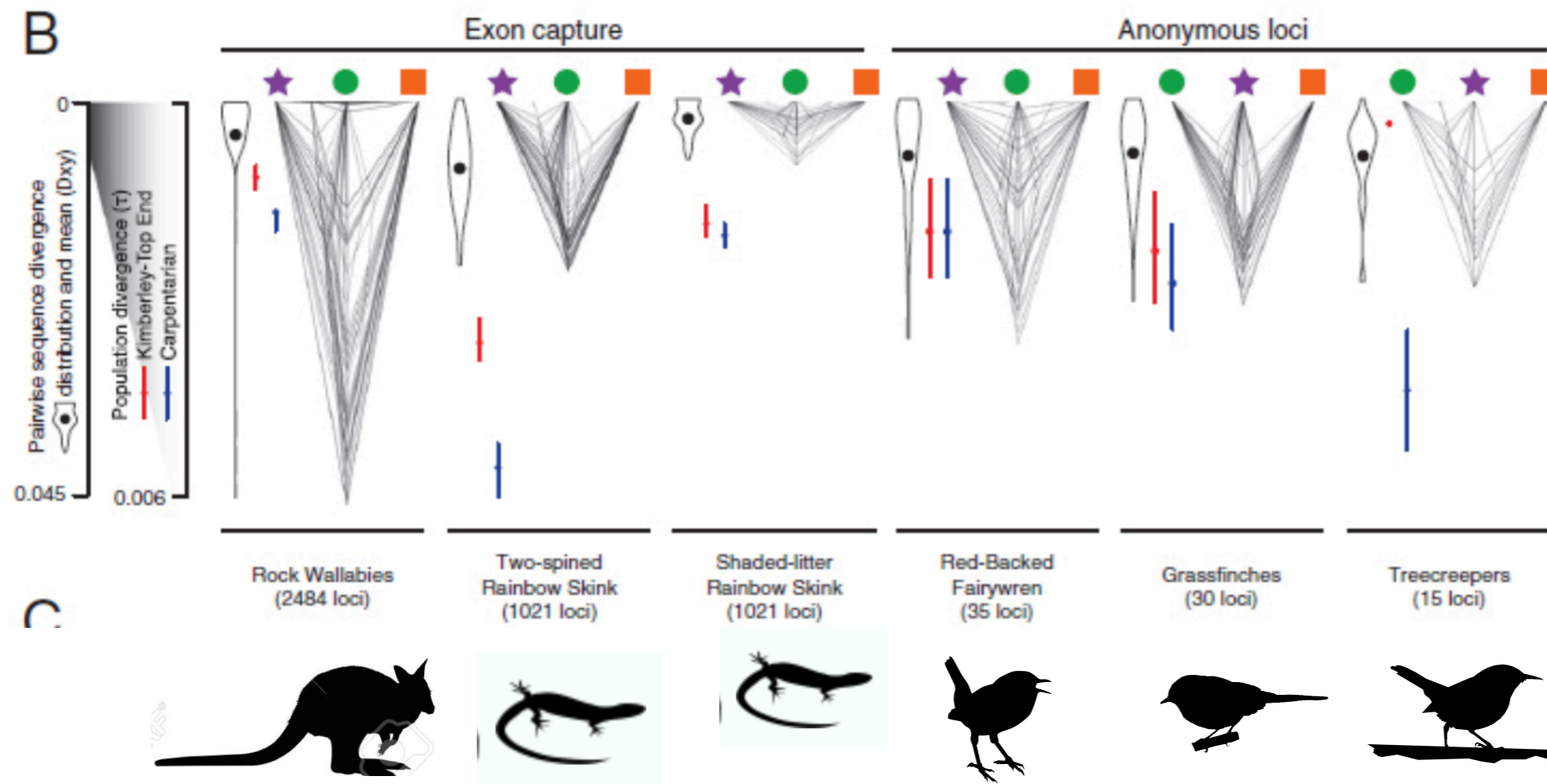


Hewitt 2004

i.e. stepping back and looking at the combined
results of multiple phylogeographic studies



regional
diversification
i.e. co-
diversification

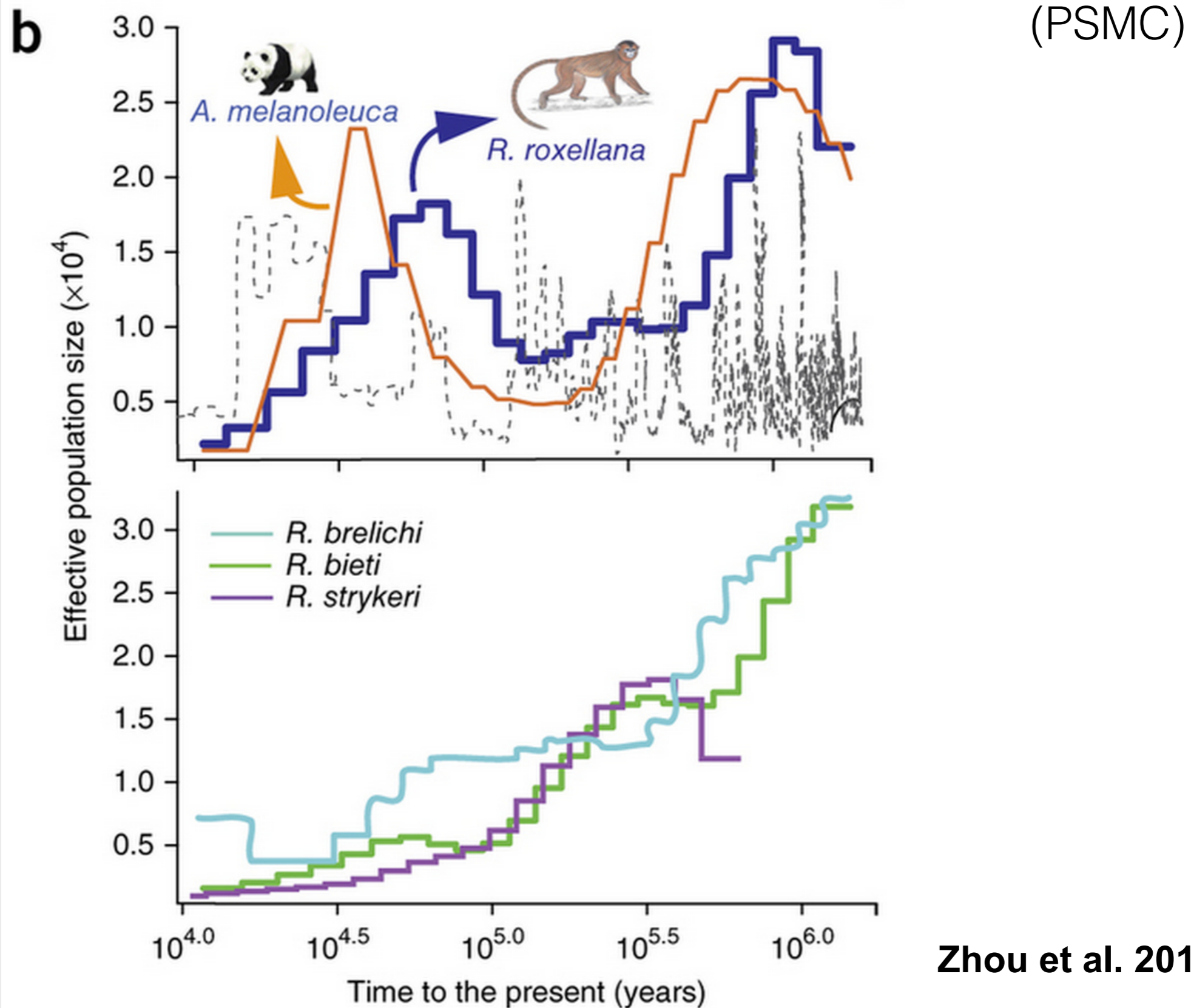


Edwards et al. 2016

i.e. stepping back and looking at the combined
results of multiple phylogeographic studies

whole genome approach

Comparative population genomics w/genomes



Zhou et al. 2014

blast from the past 1998 - 2006

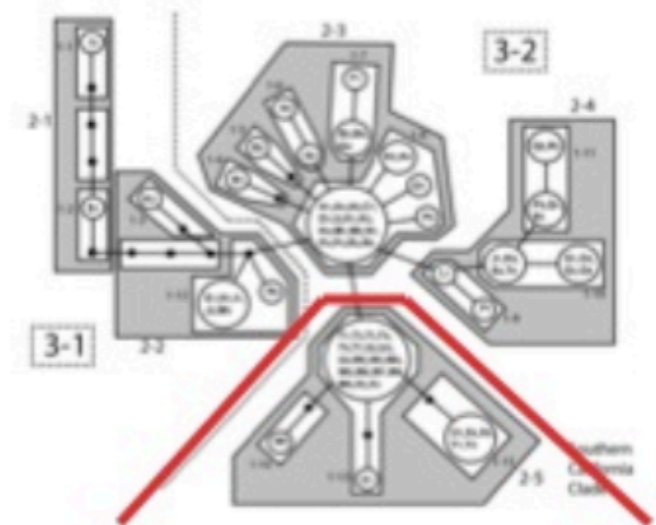
Wrentit



California Thrasher



White-headed Woodpecker



Nested Clade Analysis 1998 - 2006

Wrentit



California Thrasher



White-headed Woodpecker



co-demographic
/assemblage
history

**Coalescent
Model**

Prediction

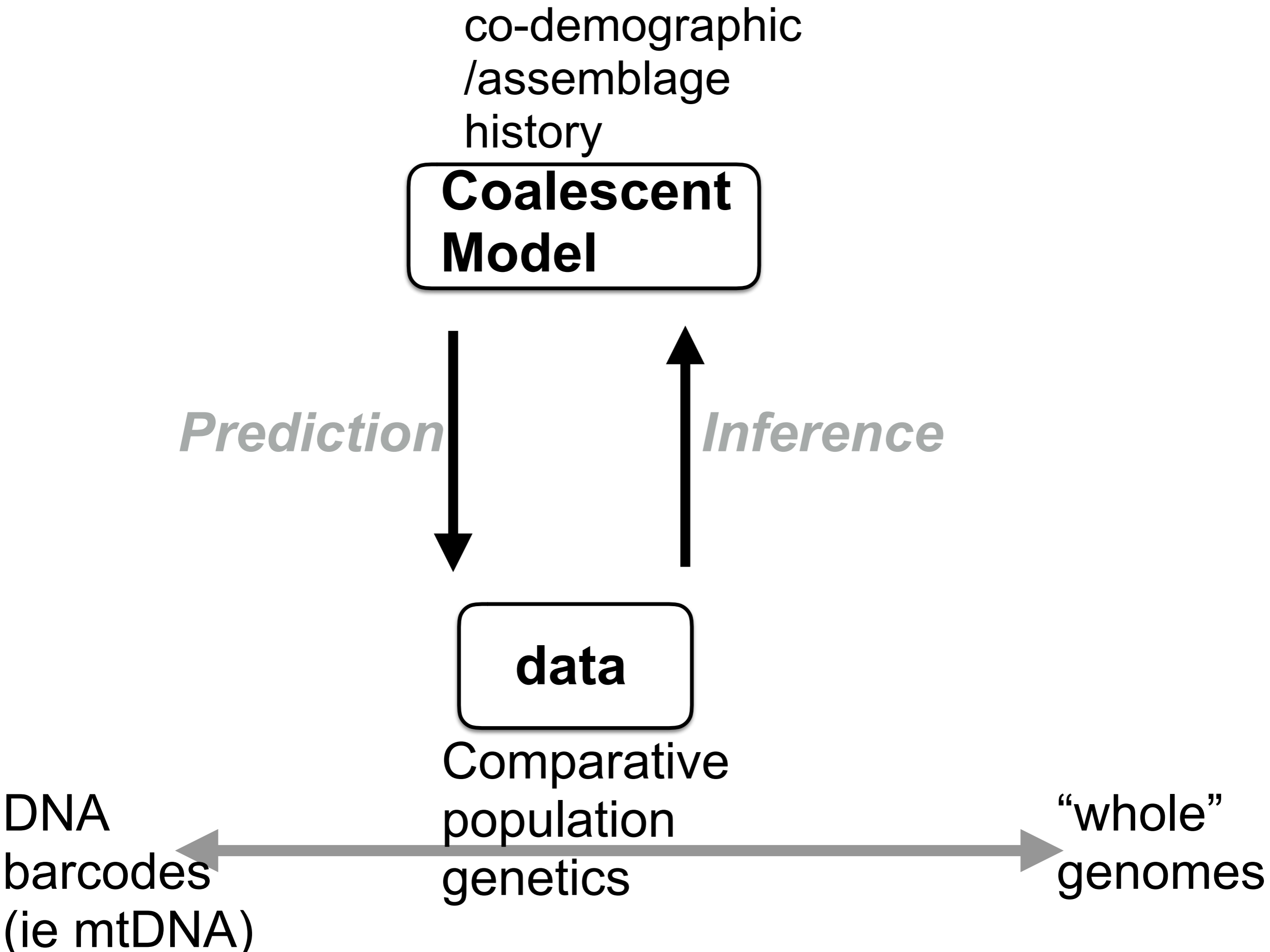
Inference

data

Comparative
population
genetics

DNA
barcodes
(ie mtDNA)

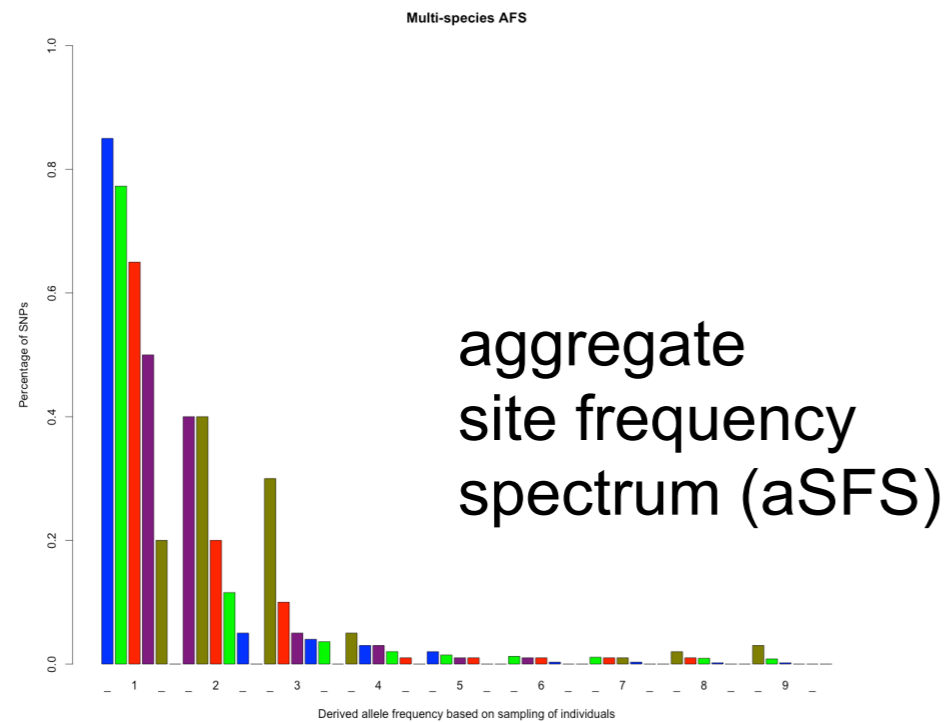
“whole”
genomes



Central Questions of Comparative Phylogeography

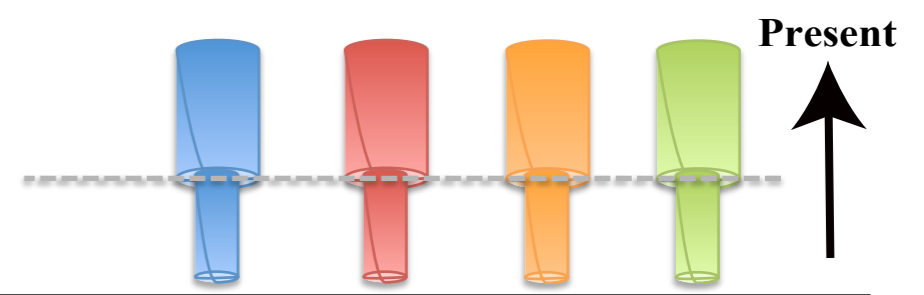
1. vicariance or dispersal?
- 2. synchronous demographic histories?**
- 3.

fitting models of co-expansion, co-contraction with SNP data

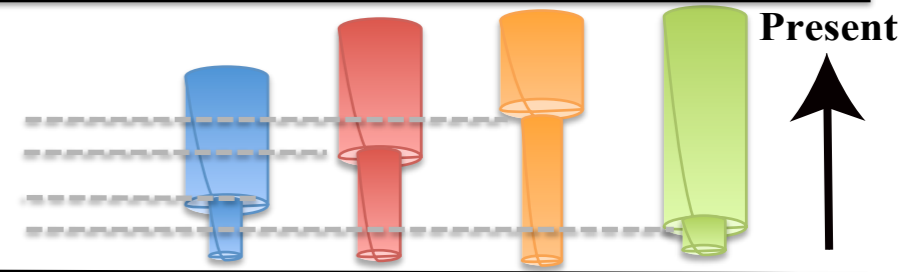


Alexander Xue

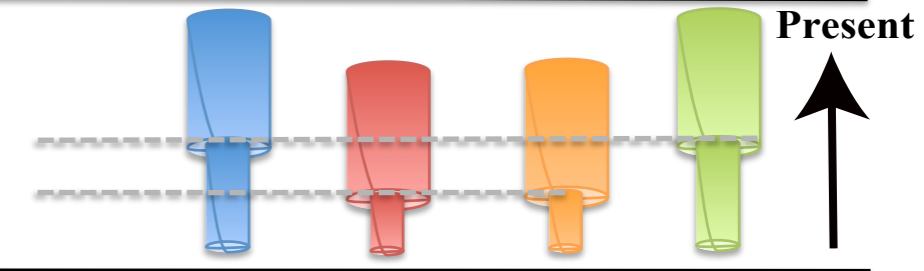
A) Synchronous
expansion



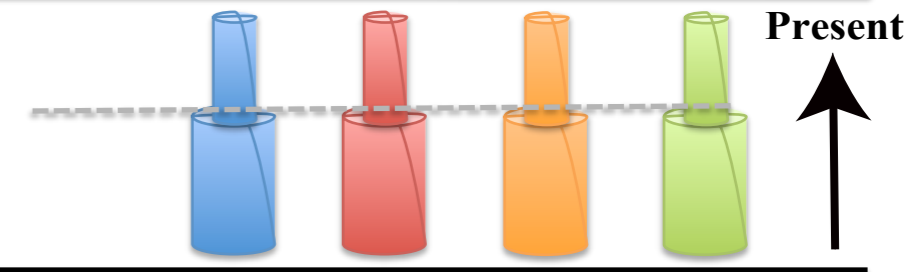
B) Asynchronous
expansion



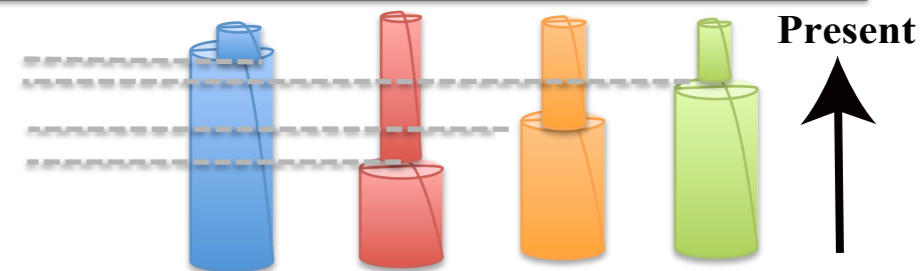
C) Expansion mixture:
asynchronous
&
synchronous



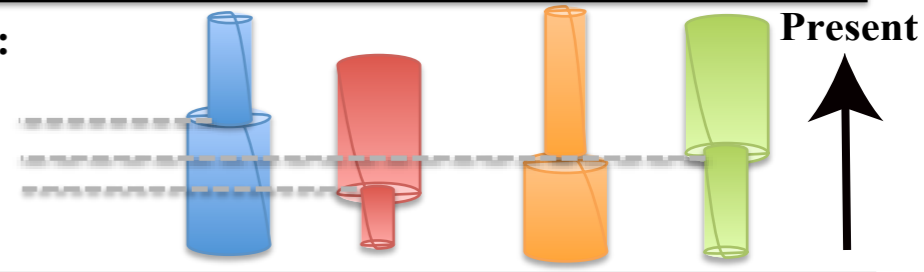
D) Synchronous
contraction



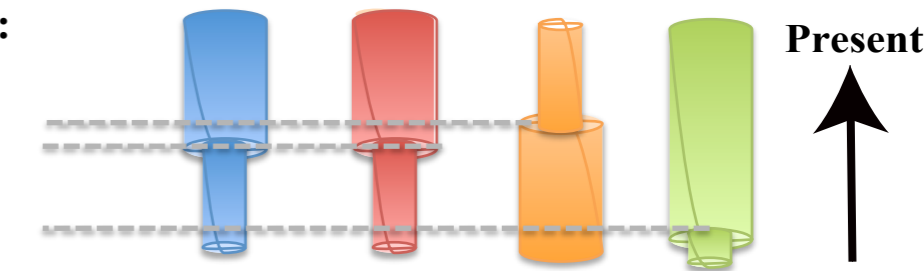
E) Asynchronous
contraction



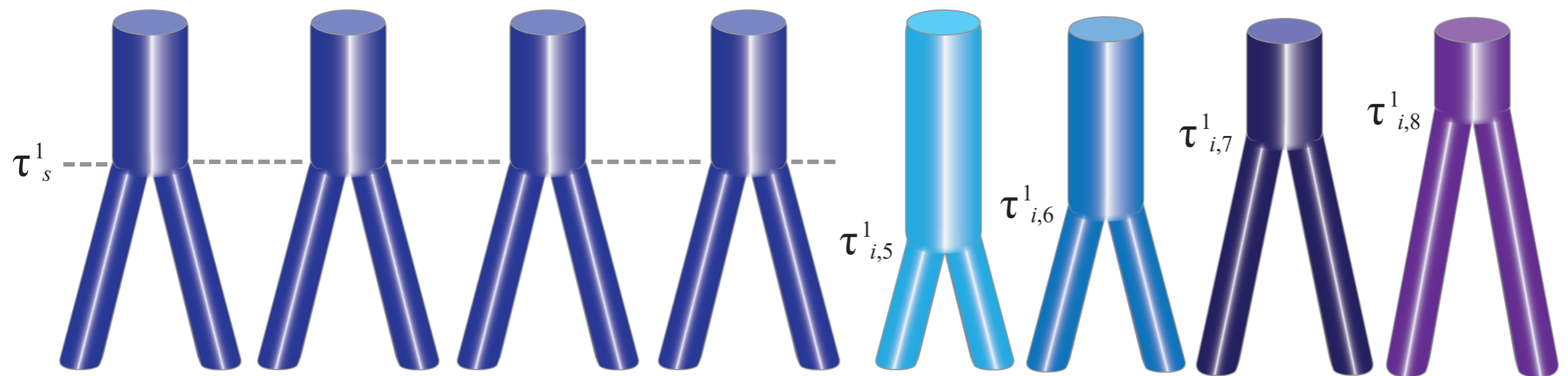
F) Trajectory mixture I:
asynchronous
expansion
&
contraction



G) Trajectory mixture II:
synchronous &
asynchronous
expansion
&
contraction



fitting models of co- divergence with SNP data



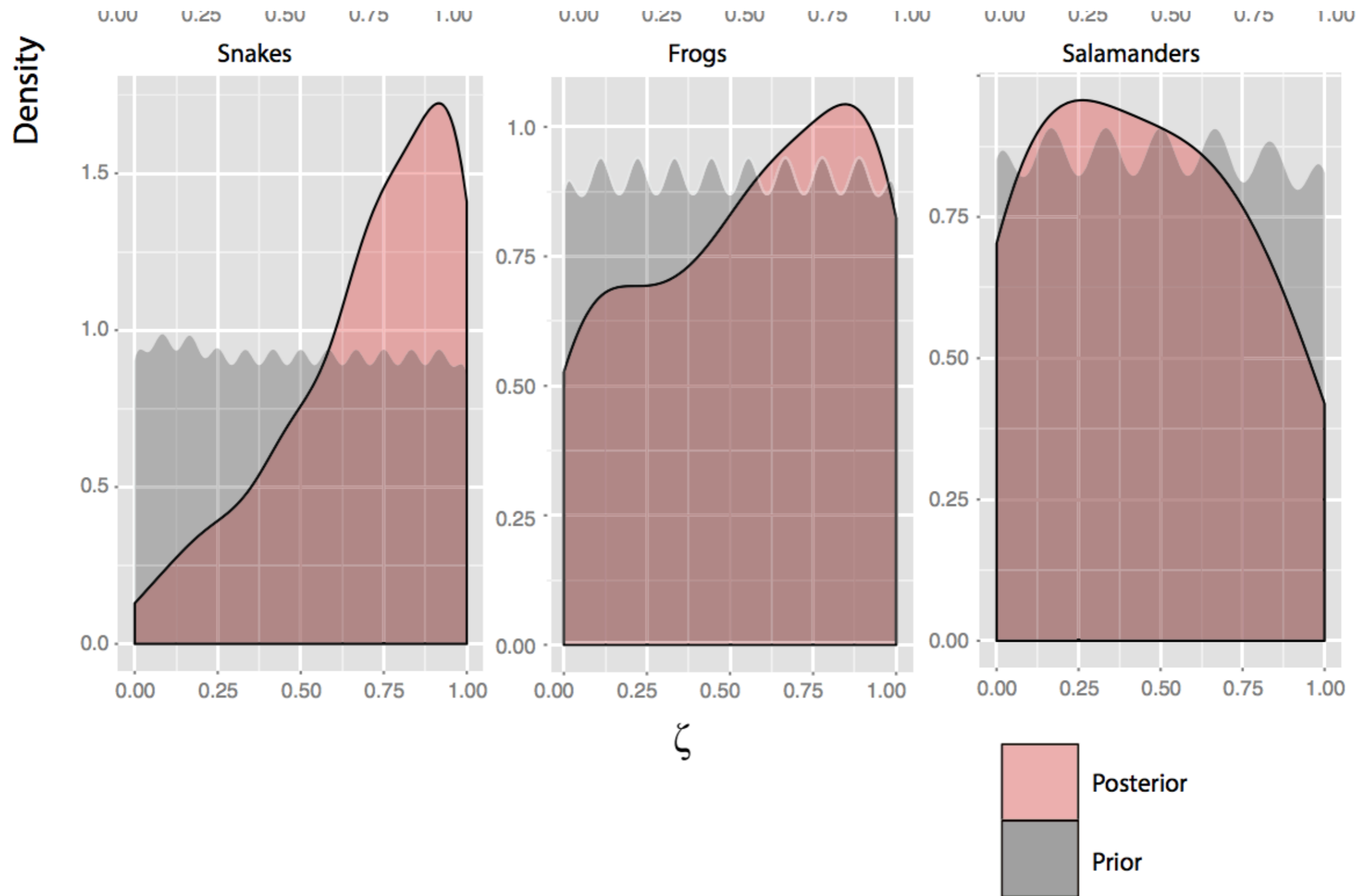
Alexander Xue

fitting co-demographic models is not easy

		Mean model posterior probabilities				
		$\zeta = 0.0$	$\zeta = 0.4$	$\zeta = 0.6$	$\zeta = 0.8$	$\zeta = 1.0$
Tolerance level of accepted simulations = 0.001						
True model	$\zeta = 0.0$	0.624	0.204	0.113	0.044	0.015
	$\zeta = 0.4$	0.172	0.421	0.254	0.113	0.040
	$\zeta = 0.6$	0.112	0.274	0.352	0.186	0.077
	$\zeta = 0.8$	0.053	0.100	0.192	0.410	0.244
	$\zeta = 1.0$	0.008	0.036	0.088	0.219	0.649

$\zeta = \% \text{ of taxa co-expanding}$

fitting co-demographic models is not easy



ζ = % of taxa co-expanding




Burbrink et al 2016

Co-expansion & Co-contraction

ORIGINAL ARTICLE

WILEY MOLECULAR ECOLOG

Long-term in situ persistence of biodiversity in tropical sky islands revealed by landscape genomics

Alicia Mastretta-Yanes¹  | Alexander T. Xue^{2,3}  | Alejandra Moreno-Letelier⁴ | Tove H. Jorgensen⁵ | Nadir Alvarez^{6,7} | Daniel Piñero⁸ | Brent C. Emerson^{9,10} 



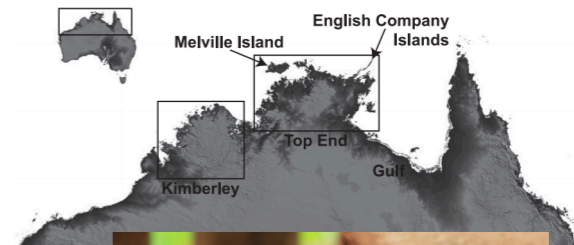
Co-expansion

ORIGINAL ARTICLE

WILEY MOLECULAR ECOLOG

Pleistocene climatic changes drive diversification across a tropical savanna

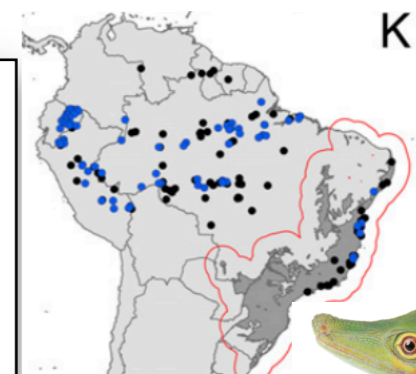
Sally Potter^{1,2}  | Alexander T. Xue^{3,4}  | Jason G. Bragg^{1,2} | Dan F. Rosauer^{1,2} | Emily J. Roycroft^{5,6} | Craig Moritz^{1,2}



asynchronous expansion

Inferring responses to climate dynamics from historical demography in neotropical forest lizards

Ivan Prates^{a,b,1}, Alexander T. Xue^{a,b}, Jason L. Brown^{a,c}, Diego F. Alvarado-Serrano^{a,d}, Miguel T. Rodrigues^e, Michael J. Hickerson^{a,b,f}, and Ana C. Carnaval^{a,b}



Shortcomings (plenty)

too much inferential uncertainty?

model is too simple?

not spatially explicit

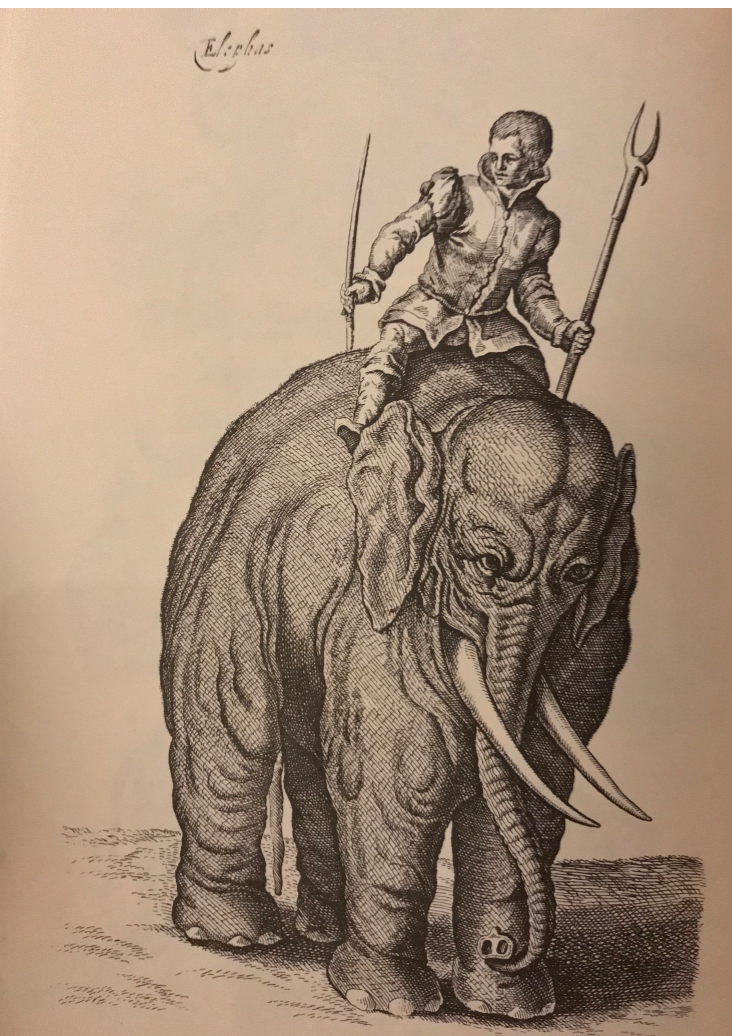
Shortcomings (plenty)

too much inferential uncertainty?

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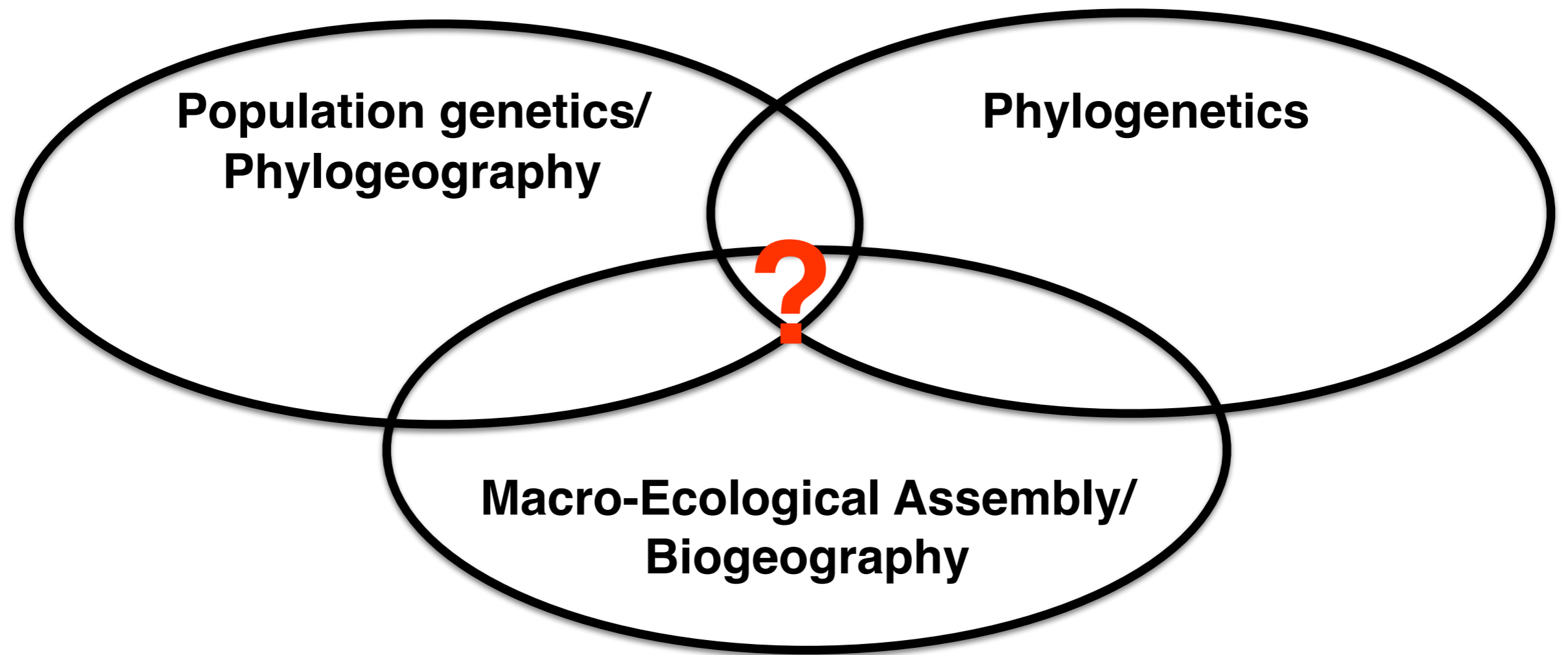
not spatially explicit

models not well-grounded in ecological theory



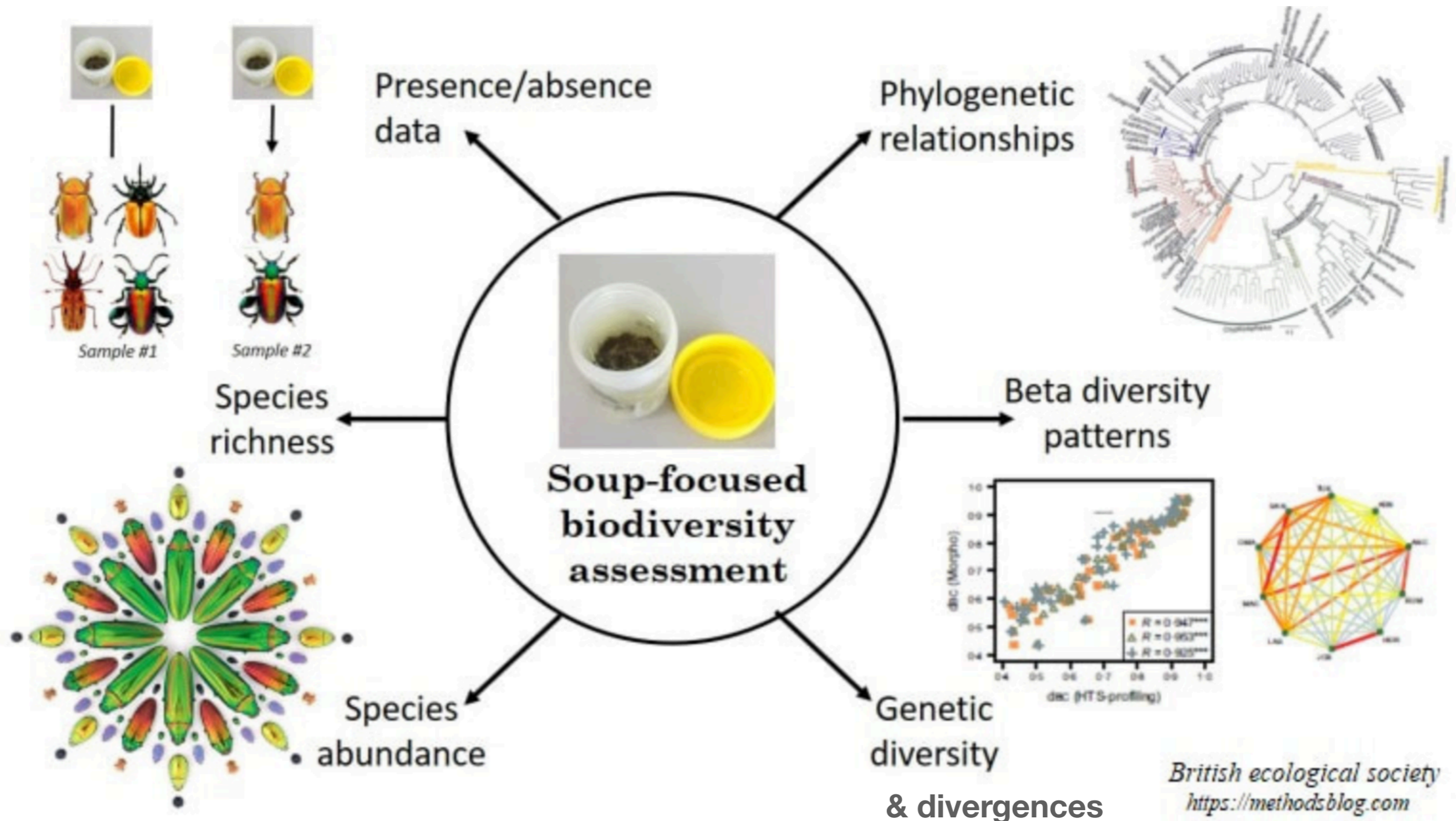
Central Questions of Comparative Phylogeography

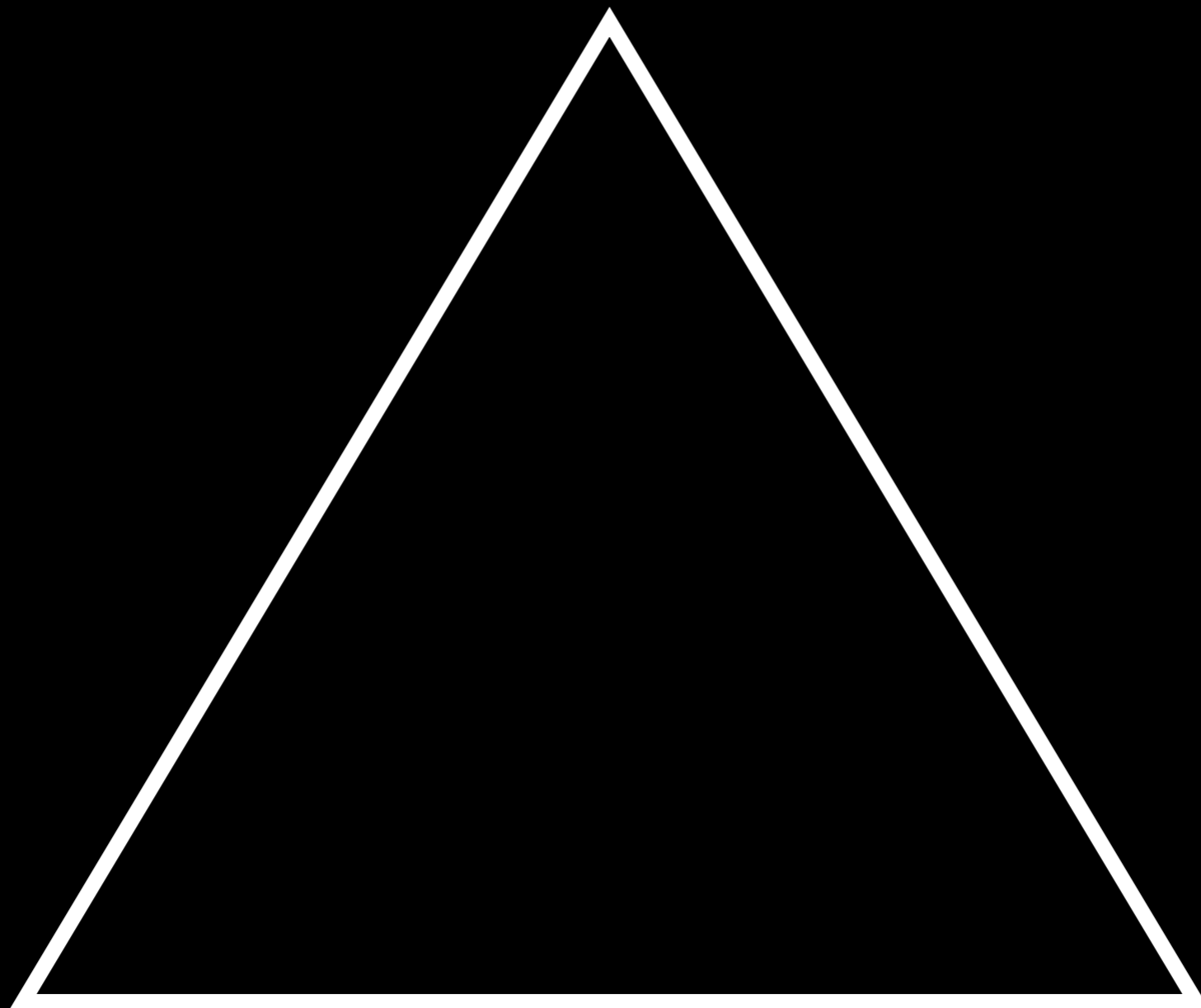
1. vicariance or dispersal?
2. synchronous demographic histories?
- 3. how deterministic is assembly and/or co-demography? (e.g. do traits matter?)**



how about the whole enchilada ?

a comparative phylogeographic model that predicts all 6 axes of the data hyper-cube





**Biodiversity
Metrics**

Species abundance spectra

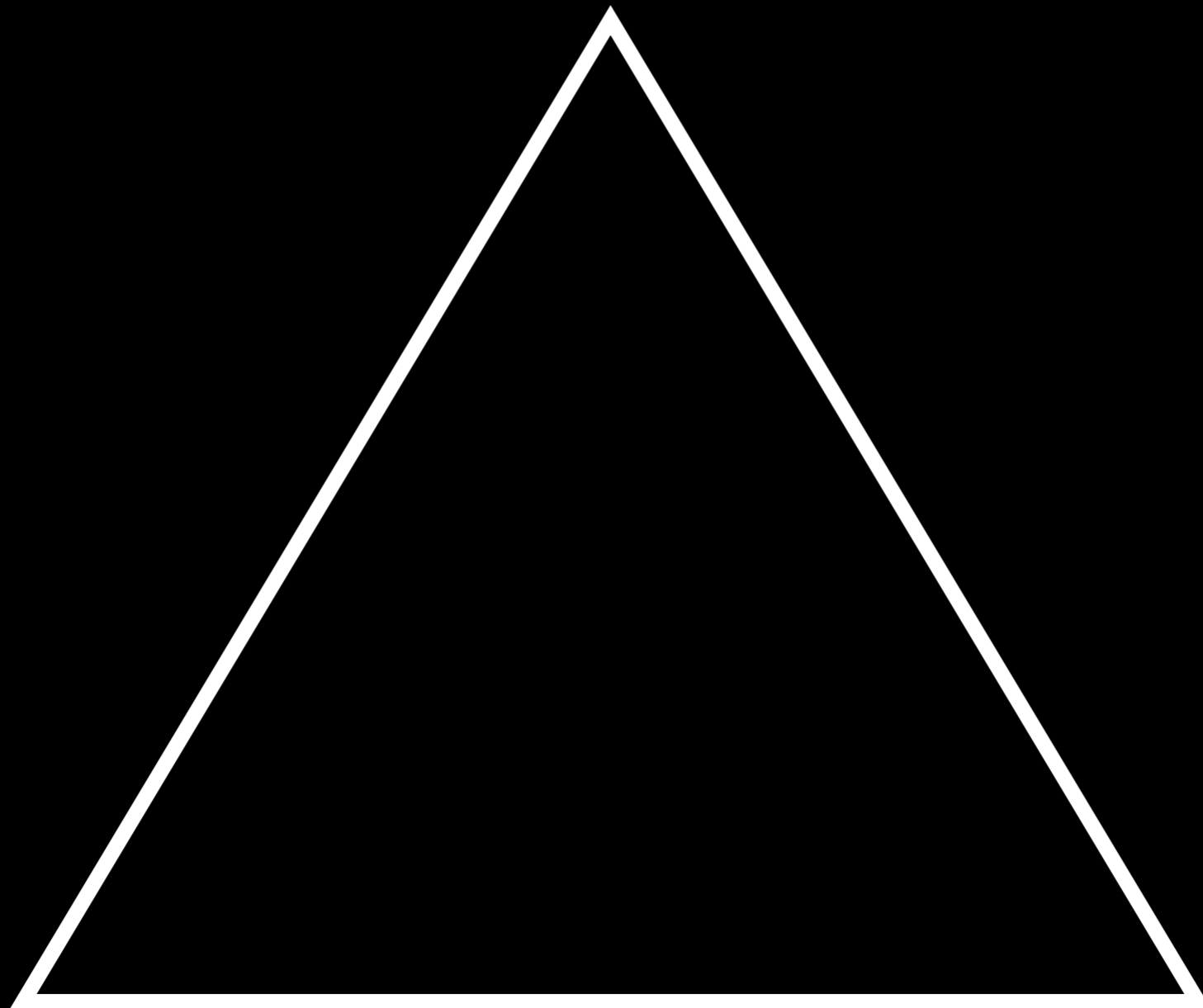
Genetic diversity spectra

Trait diversity spectra

abiotic variables

bioclimatic variables

remote sensing products



**Biodiversity
Metrics**

Species abundance spectra

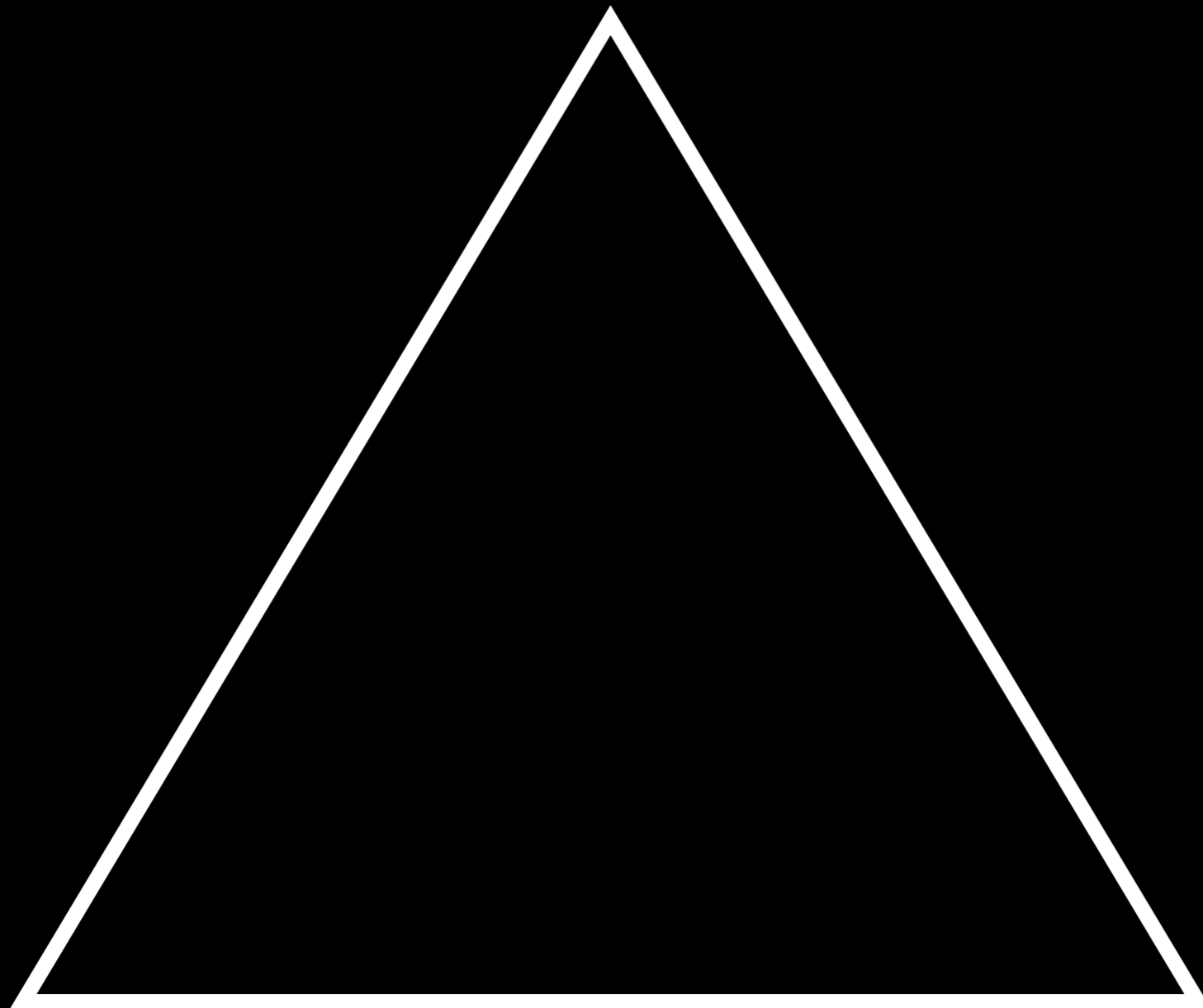
Genetic diversity spectra

Trait diversity spectra

abiotic variables

bioclimatic variables

remote sensing products



**Historical-Biogeographic
Processes**

**Biodiversity
Metrics**

Species abundance spectra

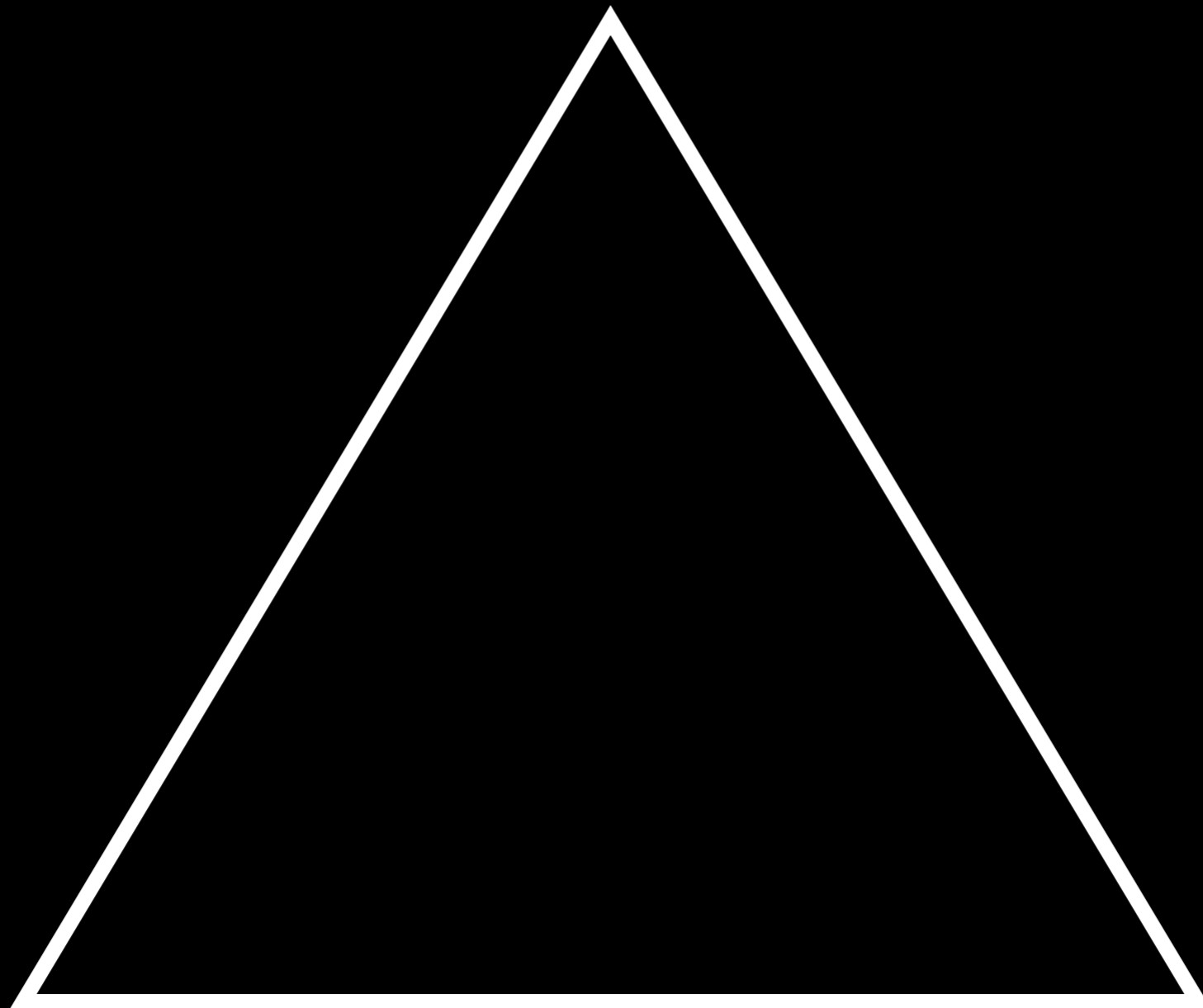
Genetic diversity spectra

Trait diversity spectra

abiotic variables

bioclimatic variables

remote sensing products



**Biodiversity
Metrics**

Species abundance spectra

Genetic diversity spectra

Trait diversity spectra

**Historical-Biogeographic
Processes**

estimation



Isaac Overcast
CUNY

can we bridge models of population genetics
and abundance under a unified model of
biogeographic assembly?



abiotic variables

bioclimatic variables

remote sensing products

prediction

Biodiversity Metrics

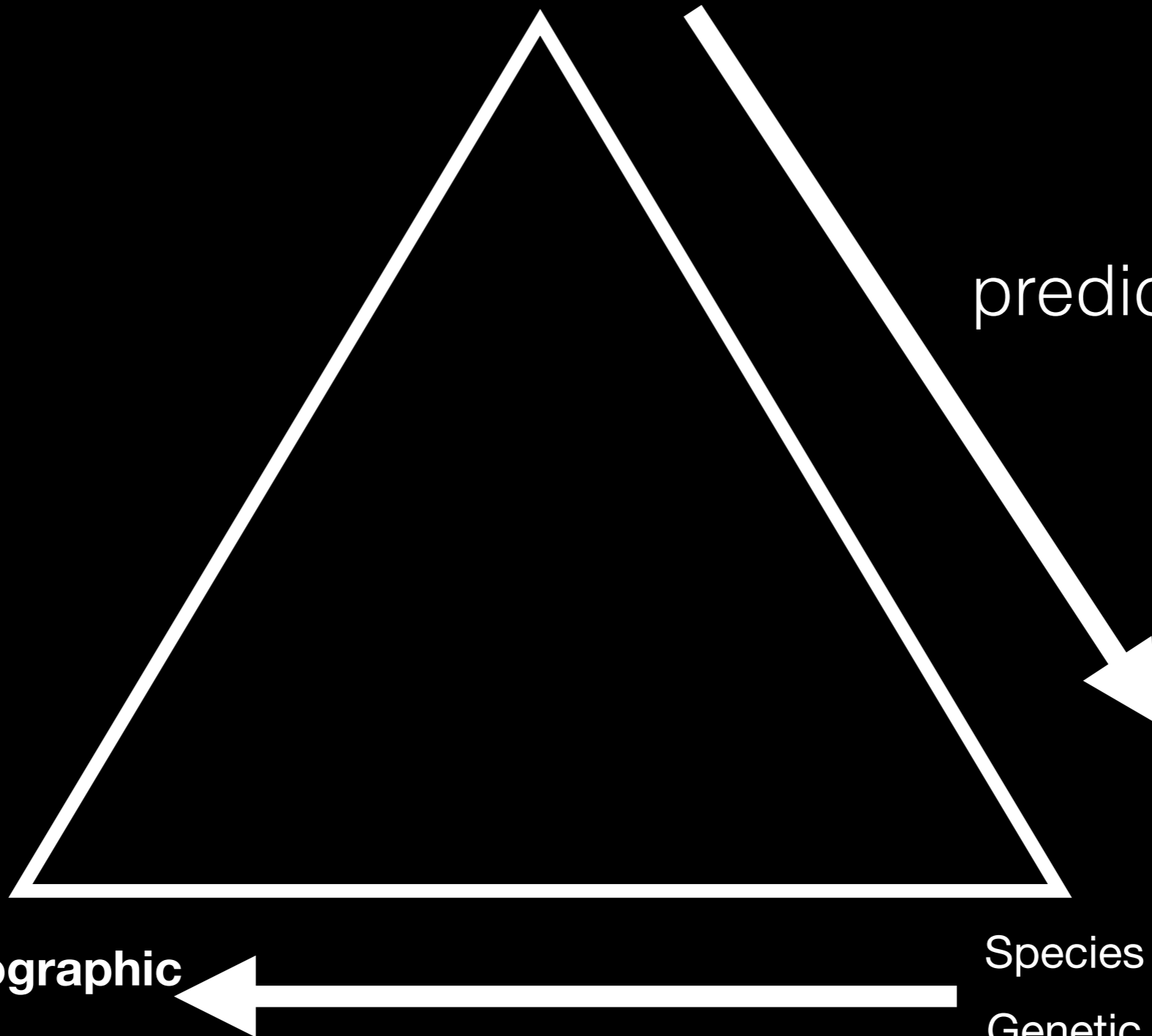
Species abundance spectra

Genetic diversity spectra

Trait diversity spectra

Historical-Biogeographic Processes

estimation

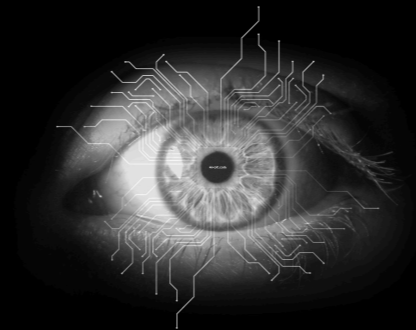


abiotic variables

bioclimatic variables

remote sensing products

prediction



Biodiversity Metrics

Species abundance spectra

Genetic diversity spectra

Trait diversity spectra

estimation

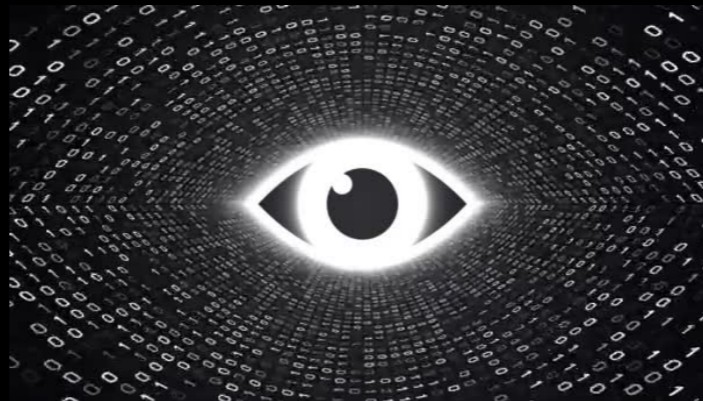
Historical-Biogeographic Processes

abiotic variables

bioclimatic variables
remote sensing products

yeah,
right

prediction



Biodiversity Metrics

Species abundance spectra
Genetic diversity spectra
Trait diversity spectra

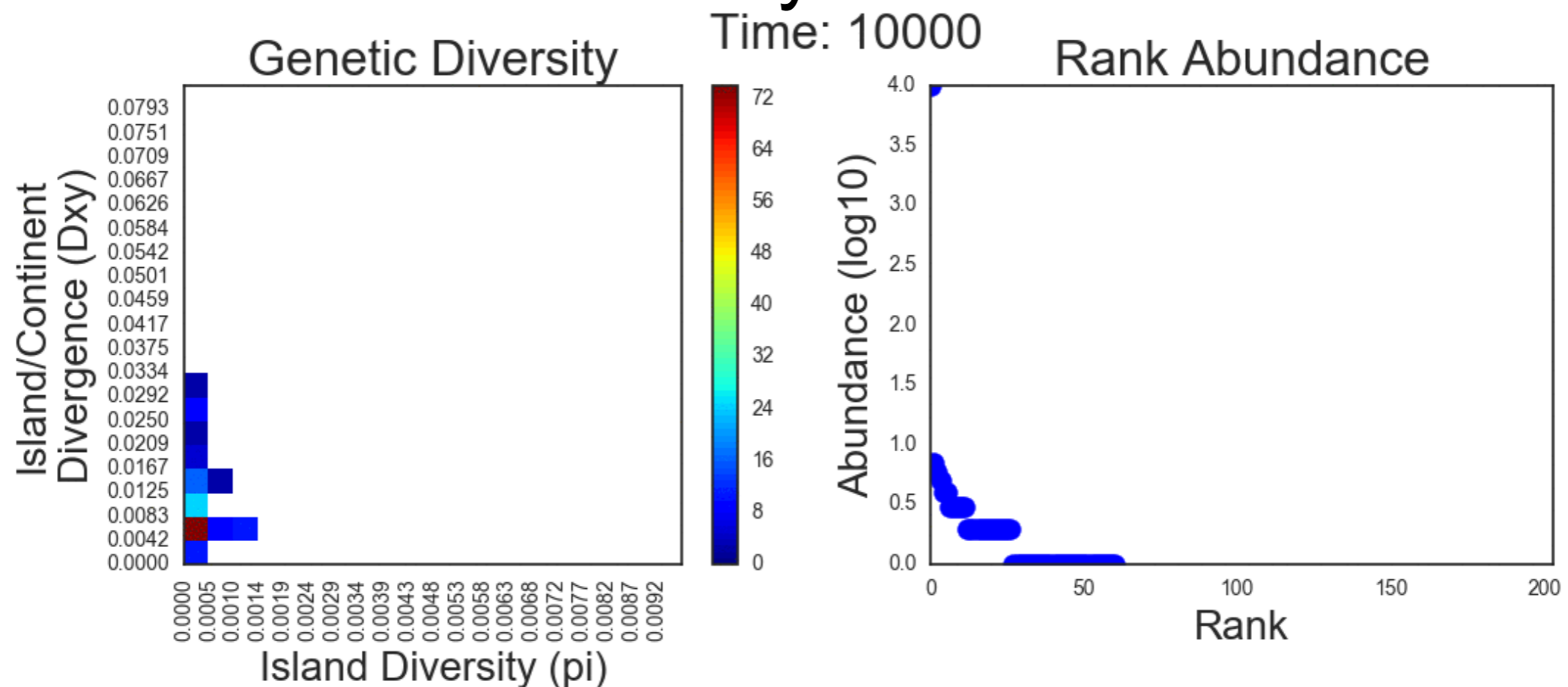
Historical-Biogeographic Processes

estimation



Isaac Overcast
CUNY

JOINT ASSEMBLY MODEL: co-generates richness, distributions of abundance and genetic diversity across island/mainland community

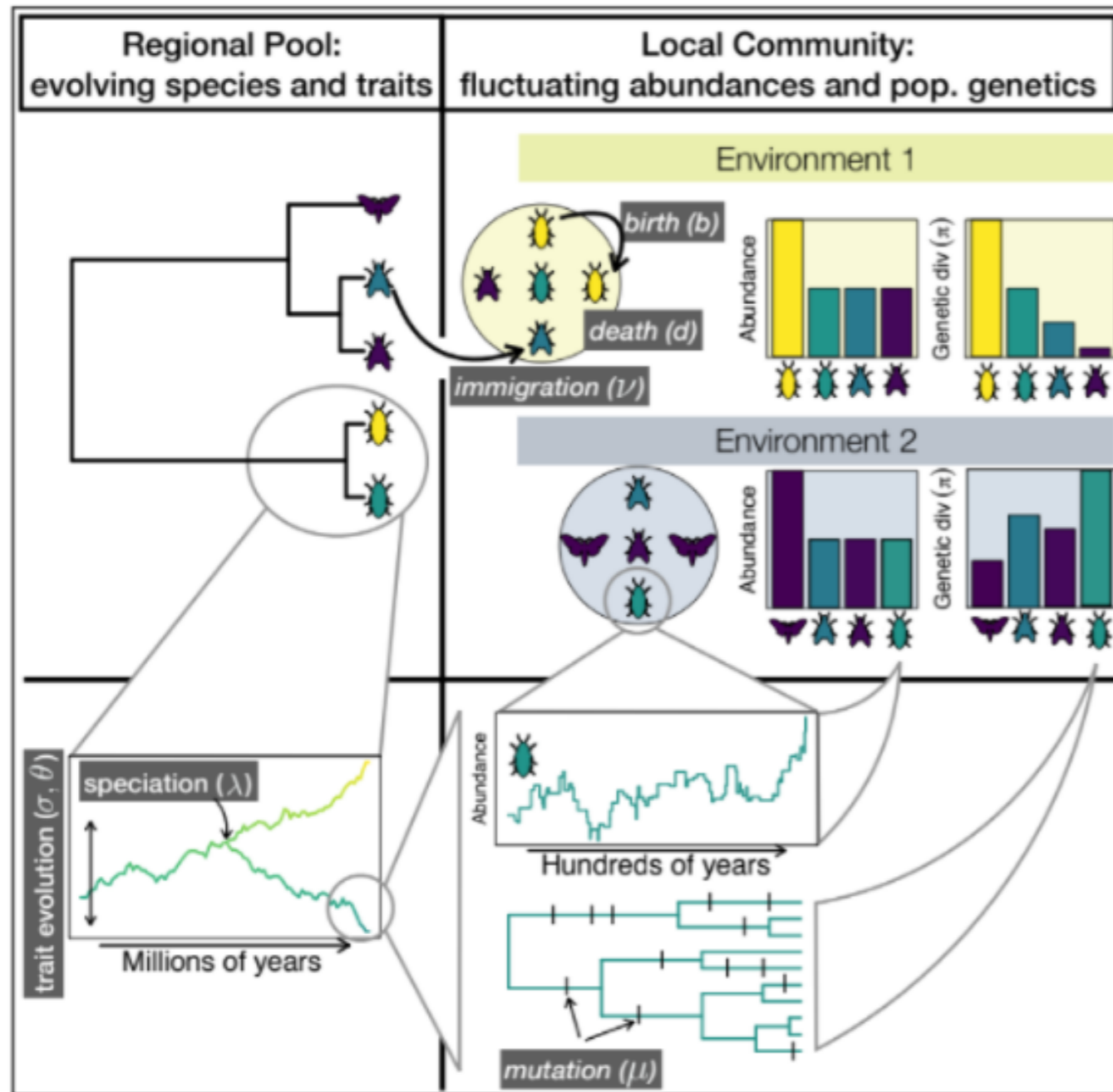


sEcoEvo Working



Neutral & non-neutral
community-wide
predictions of:

- **Abundances**
- **Genetic diversity/
divergence**
- **Phylogenies**
- **Trait values**



Massive
Eco-
Evolutionary
Synthesis
Simulations



**Andy Rominger
(SFI)**

MESS DAG

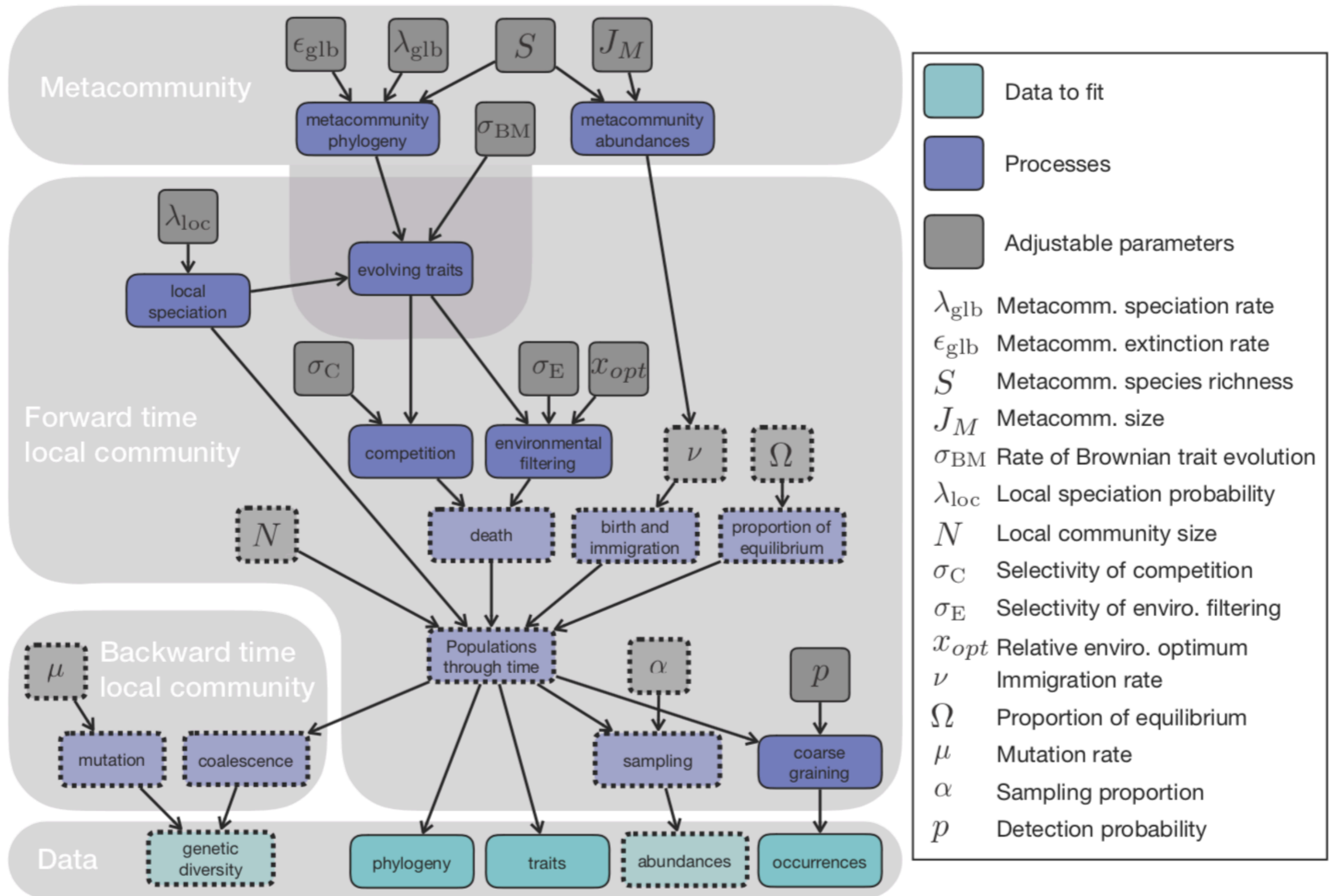
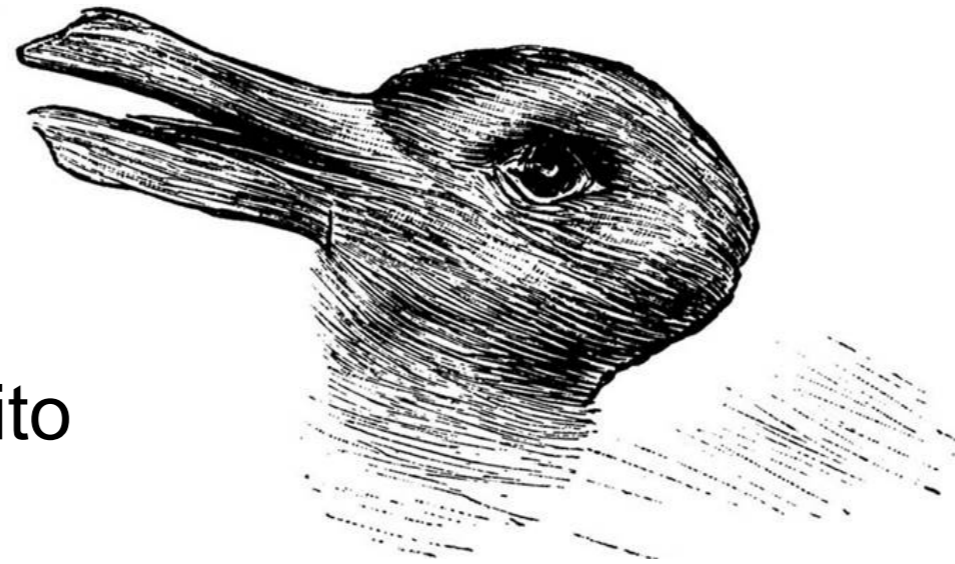


Figure 2: Directed Acyclic Graph showing how each free parameter in the RoLE model feeds into modeled biological

HickerLab

Laura Bertola
Alexander Xue*
Diego Alvarado*
Melina Giakoumis
Connor French
Andrea Calderon Brito
Case Sniffin
Isaac Overcast



*alumni

sEcoEvo- MESS Team

Isaac Overcast
James Rosindell
Andy Rominger
Luke Harmon
Megan Ruffley
Bob Week



iDiv

German Centre for Integrative
Biodiversity Research (iDiv)
Halle-Jena-Leipzig



SANTA FE
INSTITUTE

MESS Data

Brent Emerson Henrik Krehenwinkel
Christine Parent Rosemary Gillespie
Chris Meyer

Support

The **City** College
of New York



**THE
GRADUATE
CENTER**
CITY UNIVERSITY
OF NEW YORK

Thank you!

