

# Welcome to CompPhylo 2019

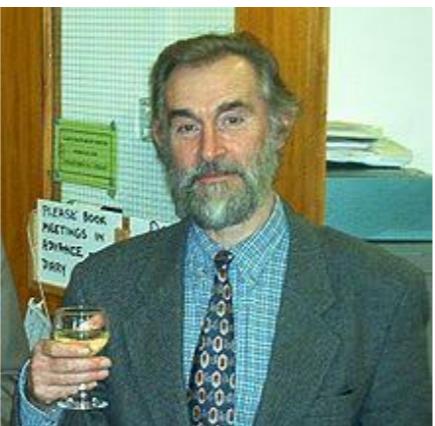


Michael Hickerson  
City University of New York  
City College of New York  
American Museum of Natural History

# The comparative phylogeographic pipe dream

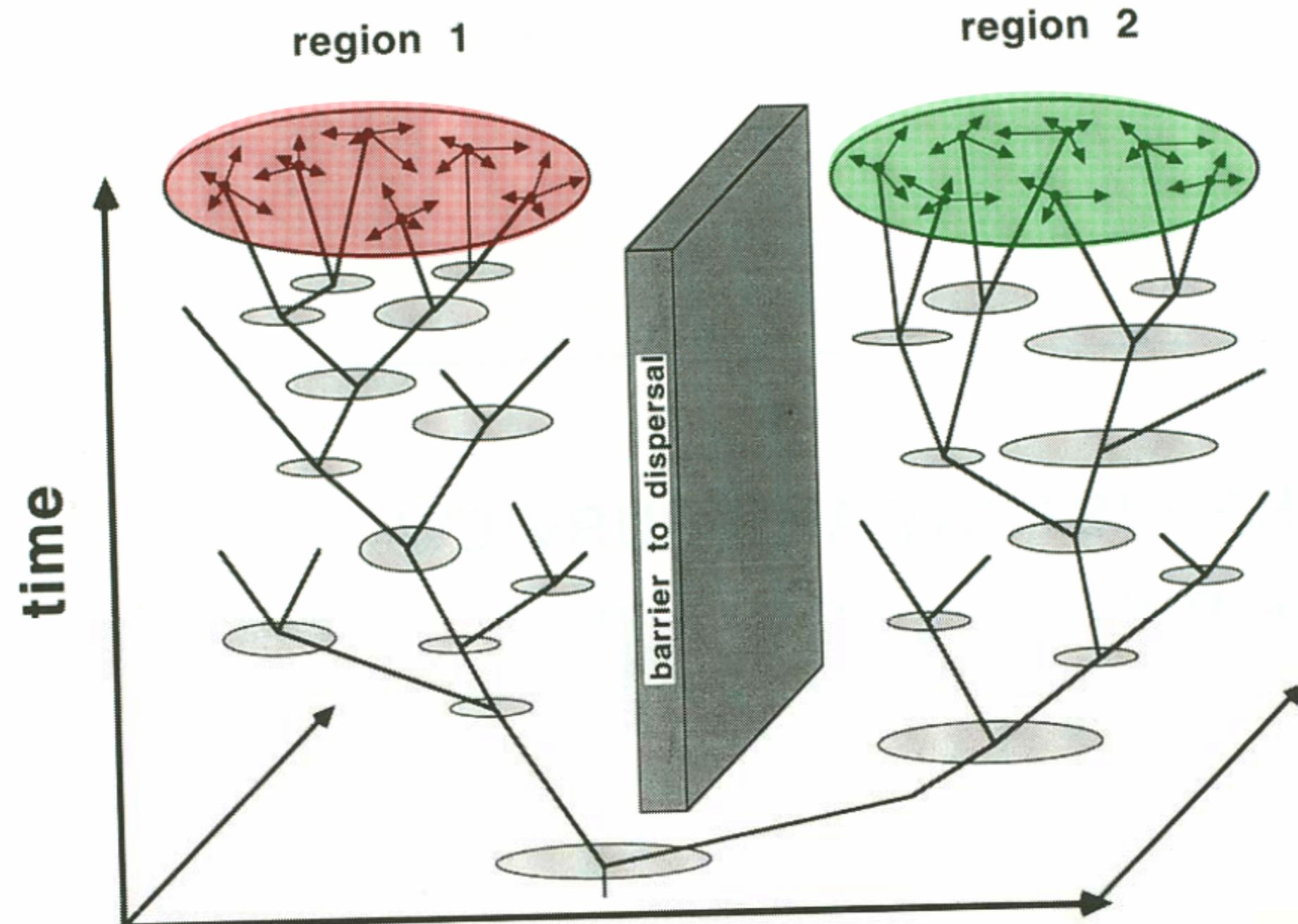


**John Avise**



**Godfrey Hewitt**



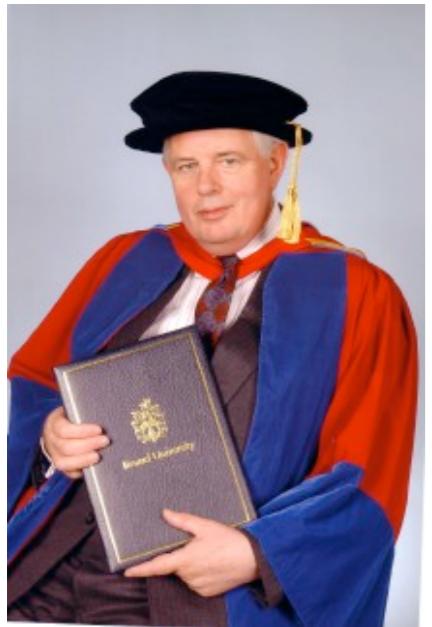


~1987 Avise coins “**phylogeography**”



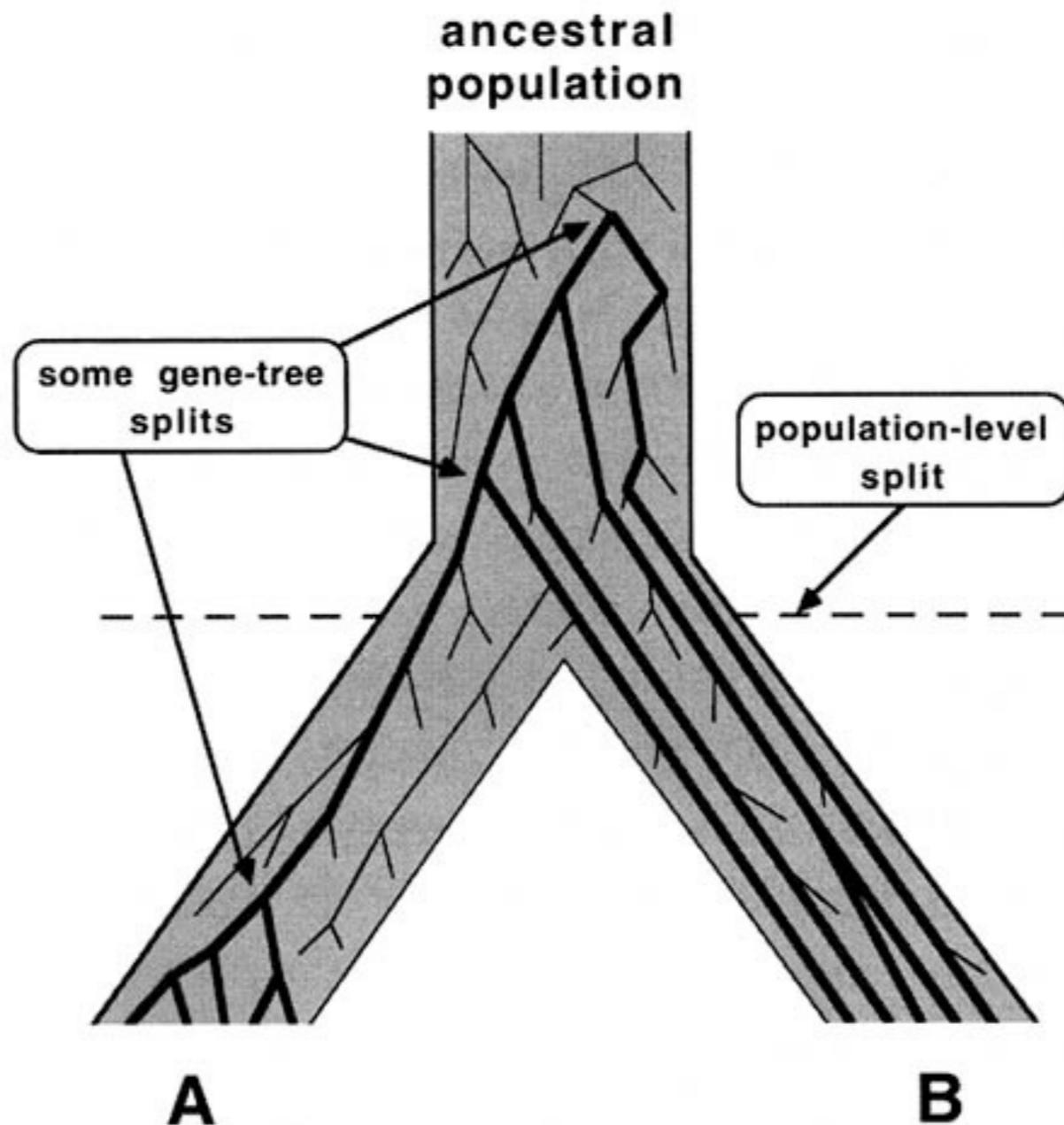
J. Avise

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



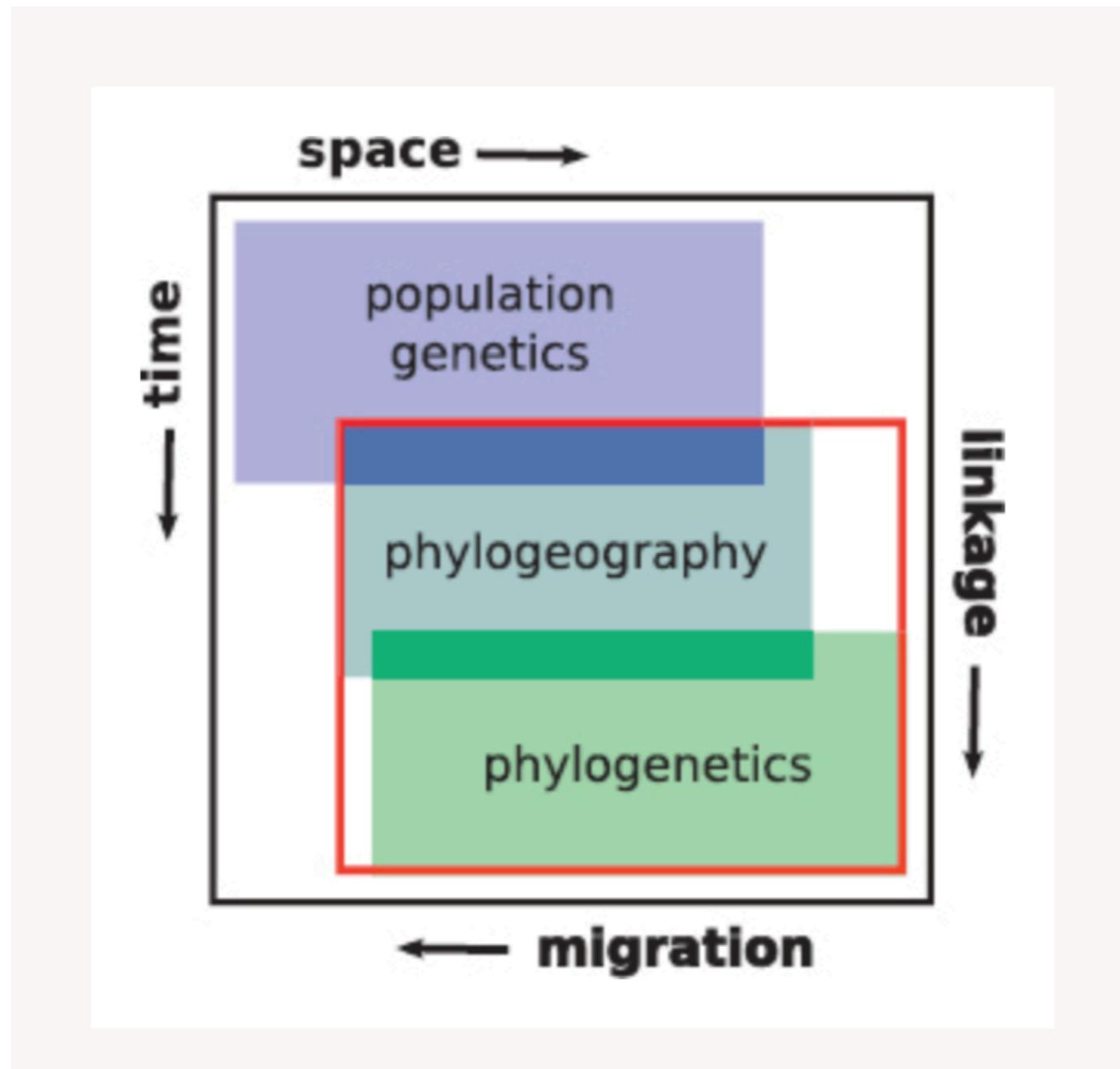
Kingman

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

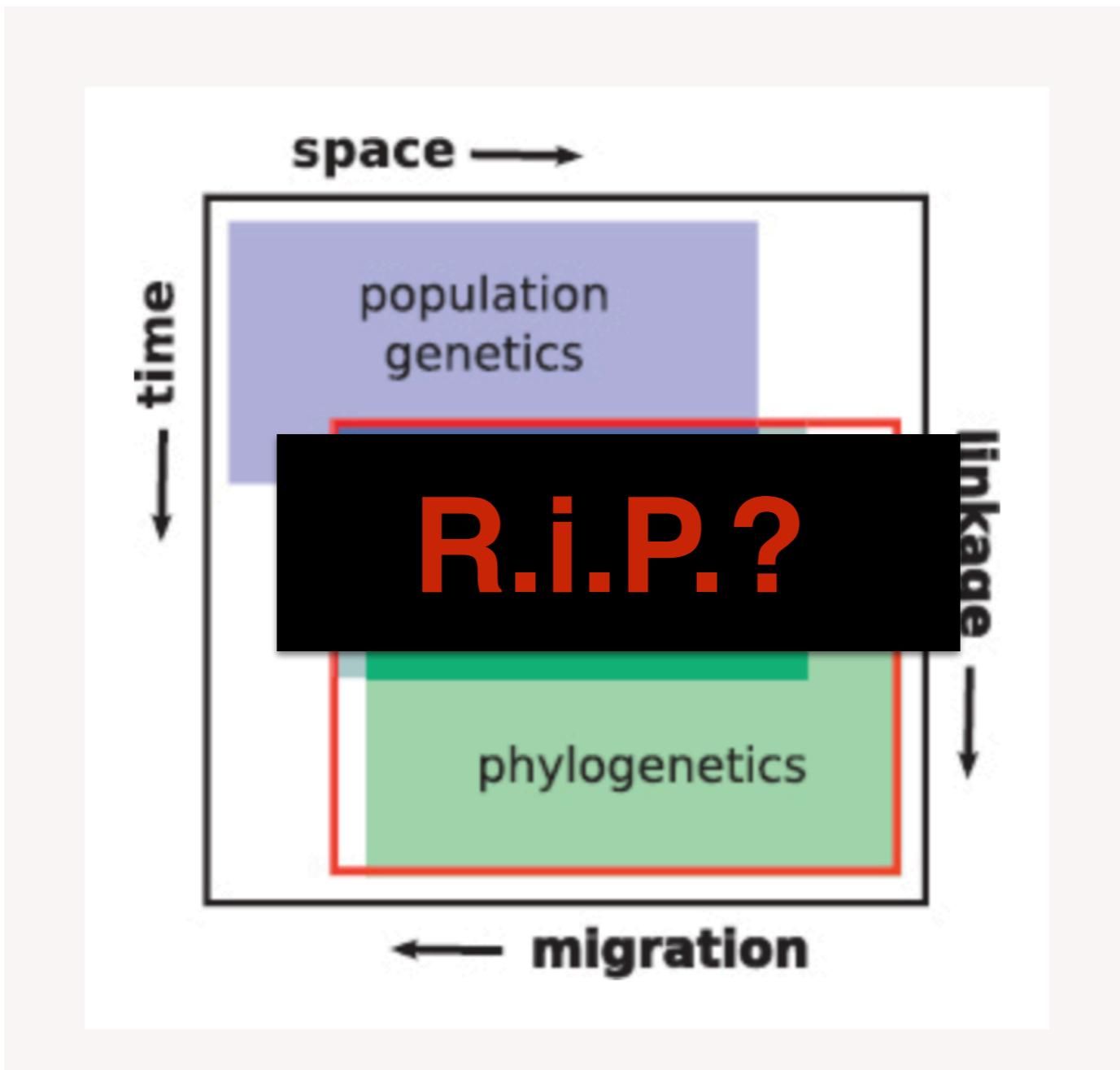


Tajima

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



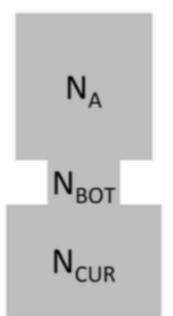
Avise *et al.* 1987 → Edwards *et al.* 2016



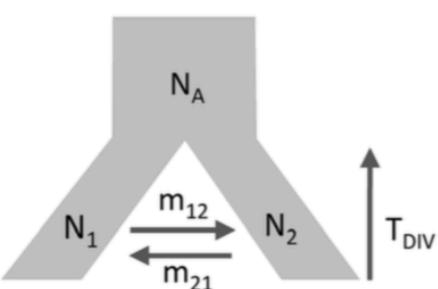
*Edwards et al. 2016*

# phylogeography ≈ demographic historical inference

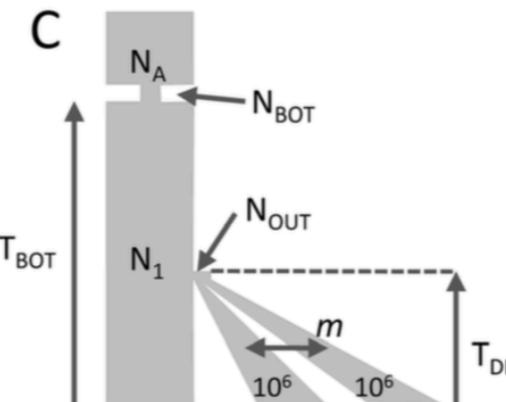
A



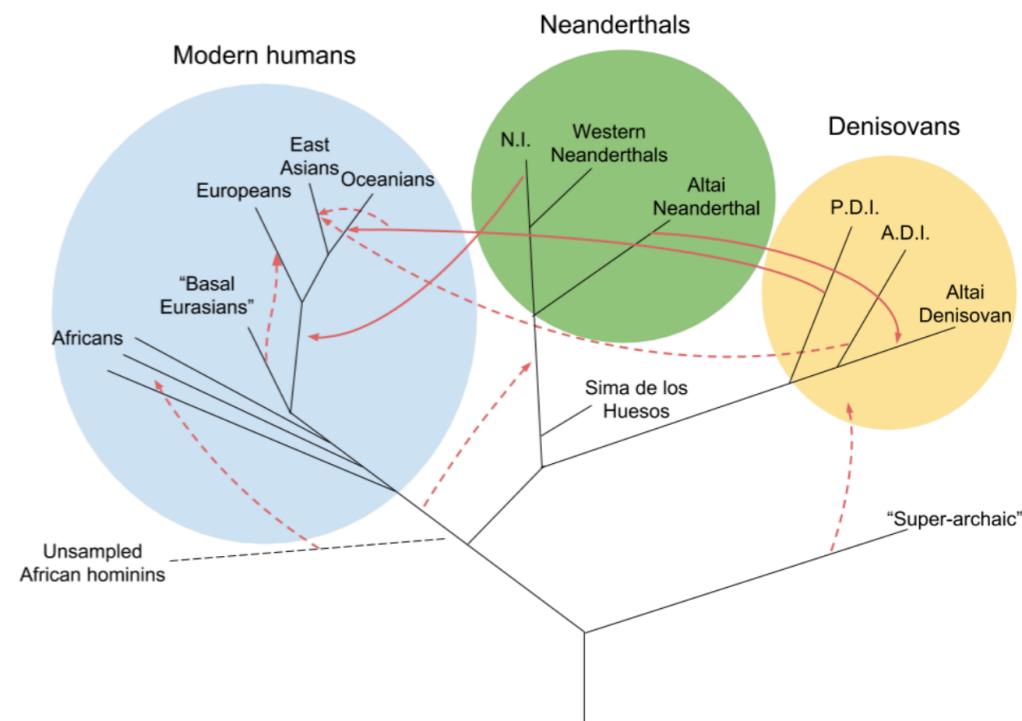
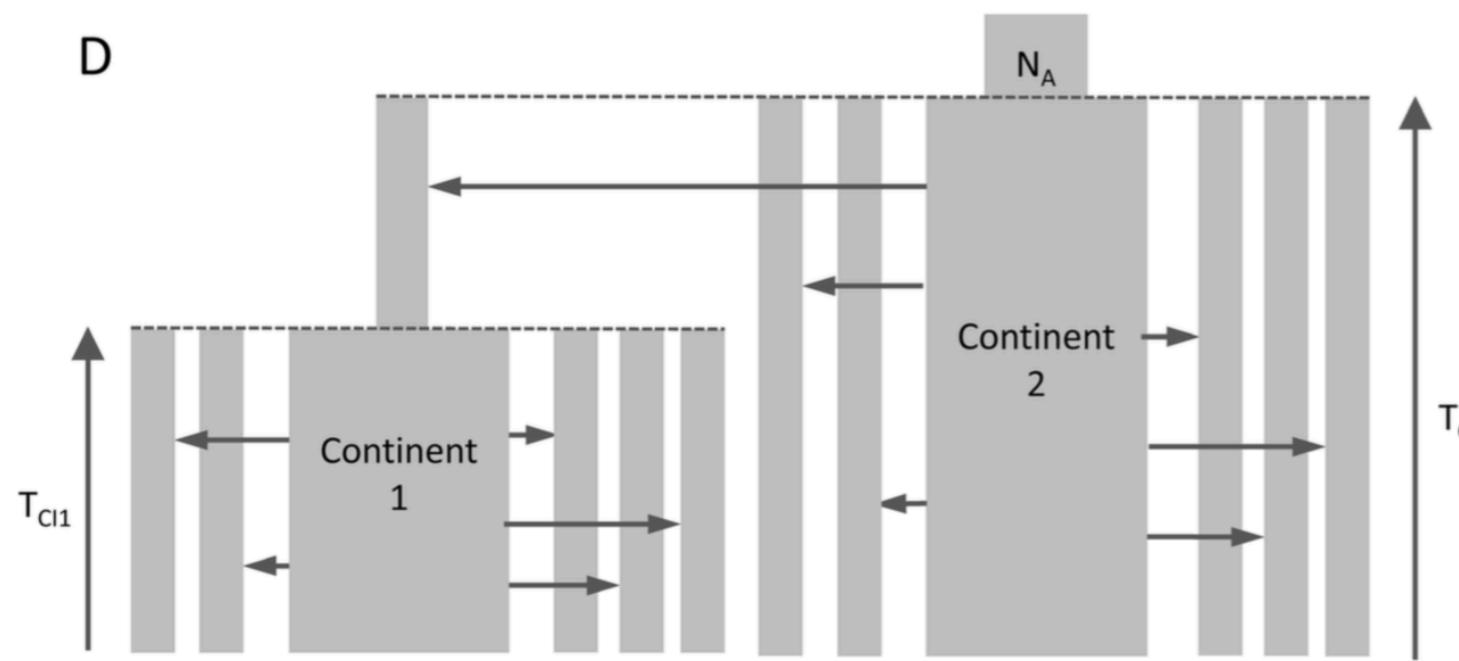
B



C

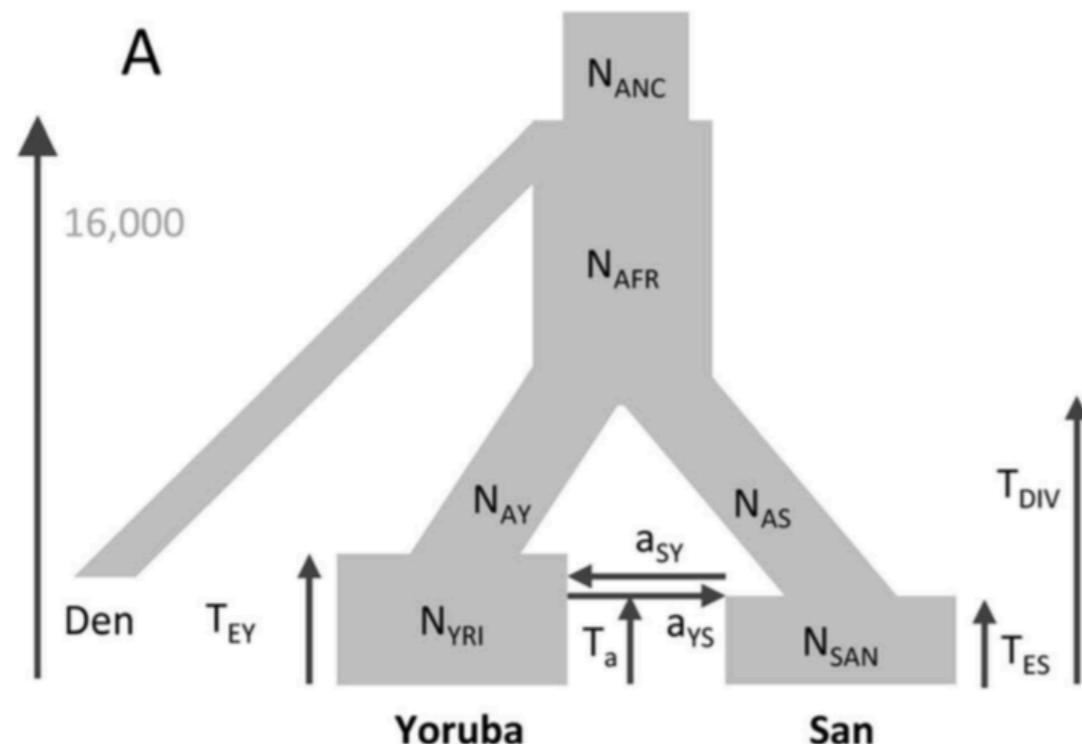


D

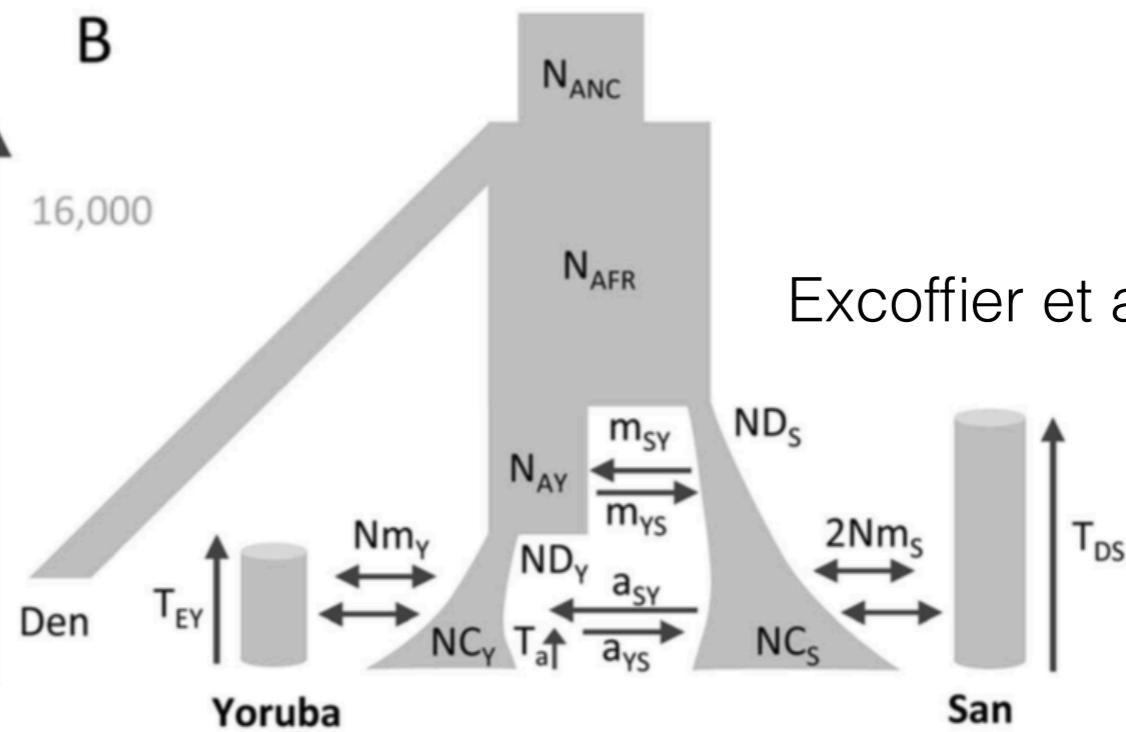


Dannemann & Racimo 2018

A



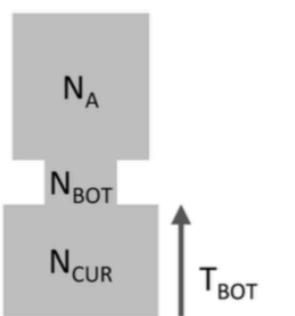
B



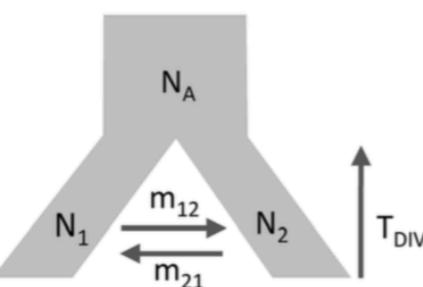
Excoffier et al. 2015

# phylogeography = demographic historical inference

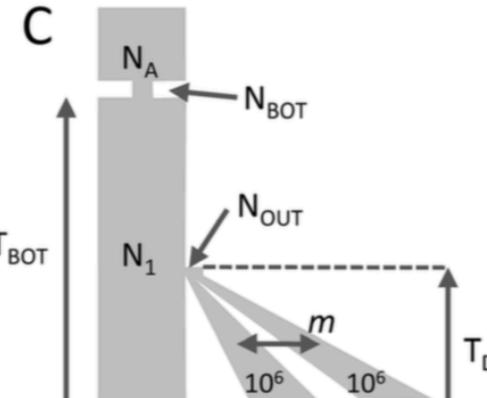
A



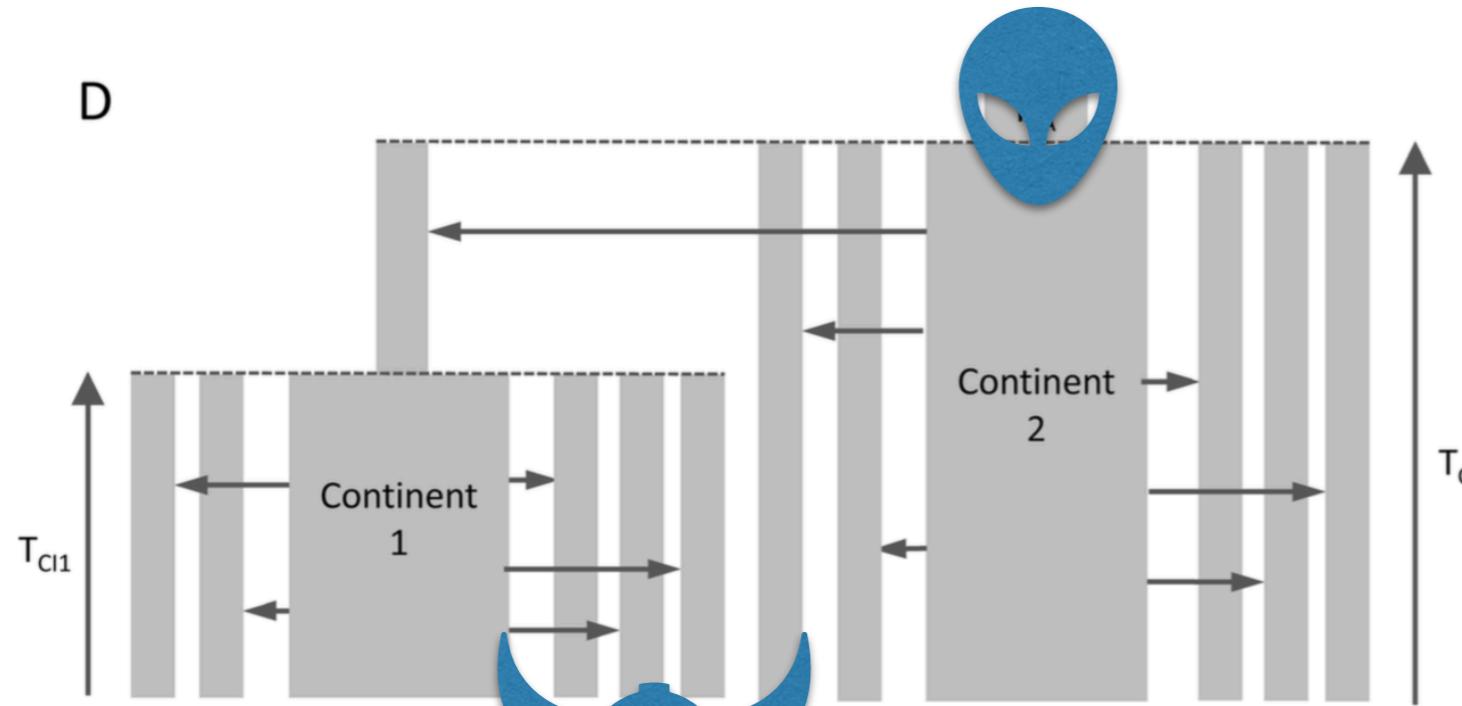
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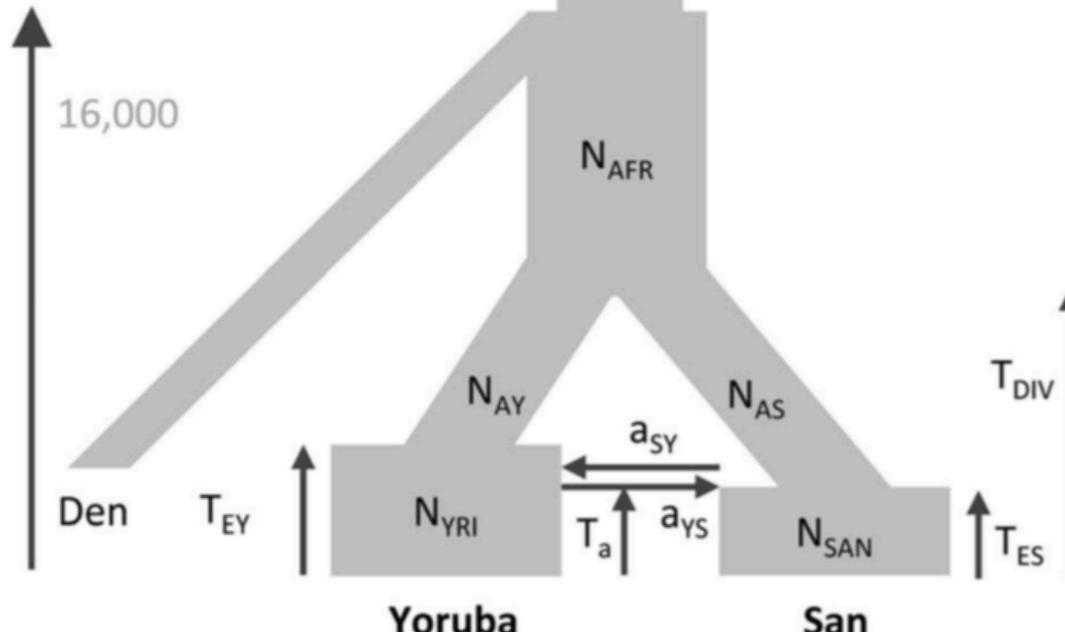
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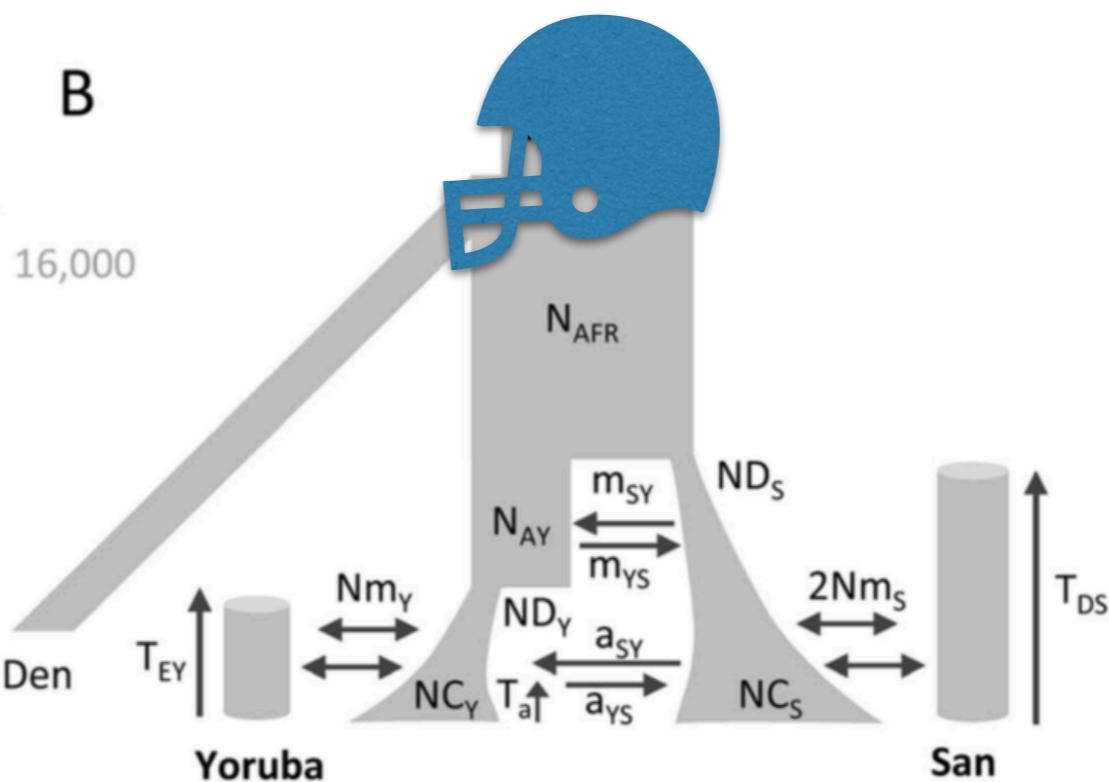
D



A



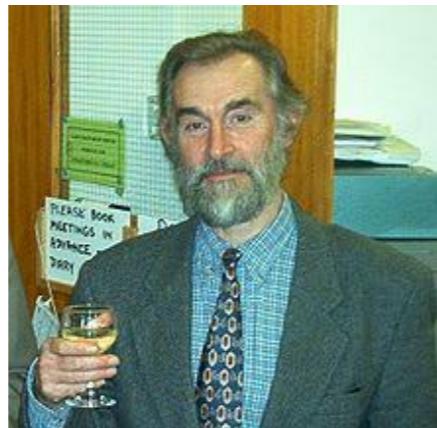
B



The comparative  
phylogeographic  
pipe dream  
lives!



John Avise



Godfrey Hewitt



leveraging inferences from multiple species  
demographic histories

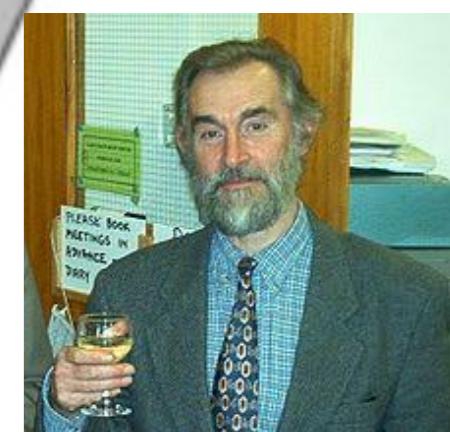
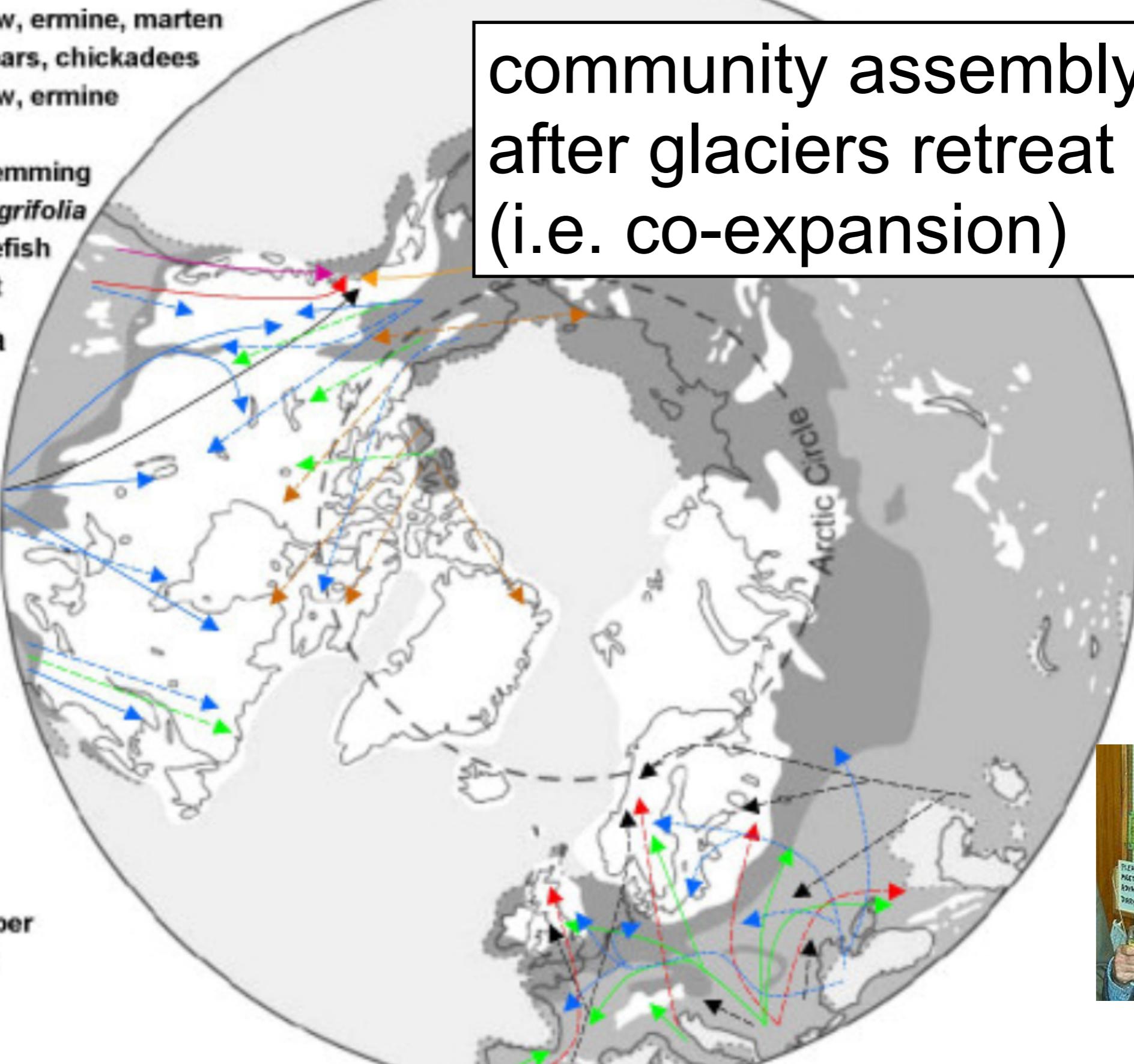
- Vole, shrew, ermine, marten
- Marten, bears, chickadees
- Vole, shrew, ermine
- Ermee
- Collared lemming
- *Dryas integrifolia*
- Lake whitefish
- River trout

North America

Likely postglacial colonization routes for a sample of species

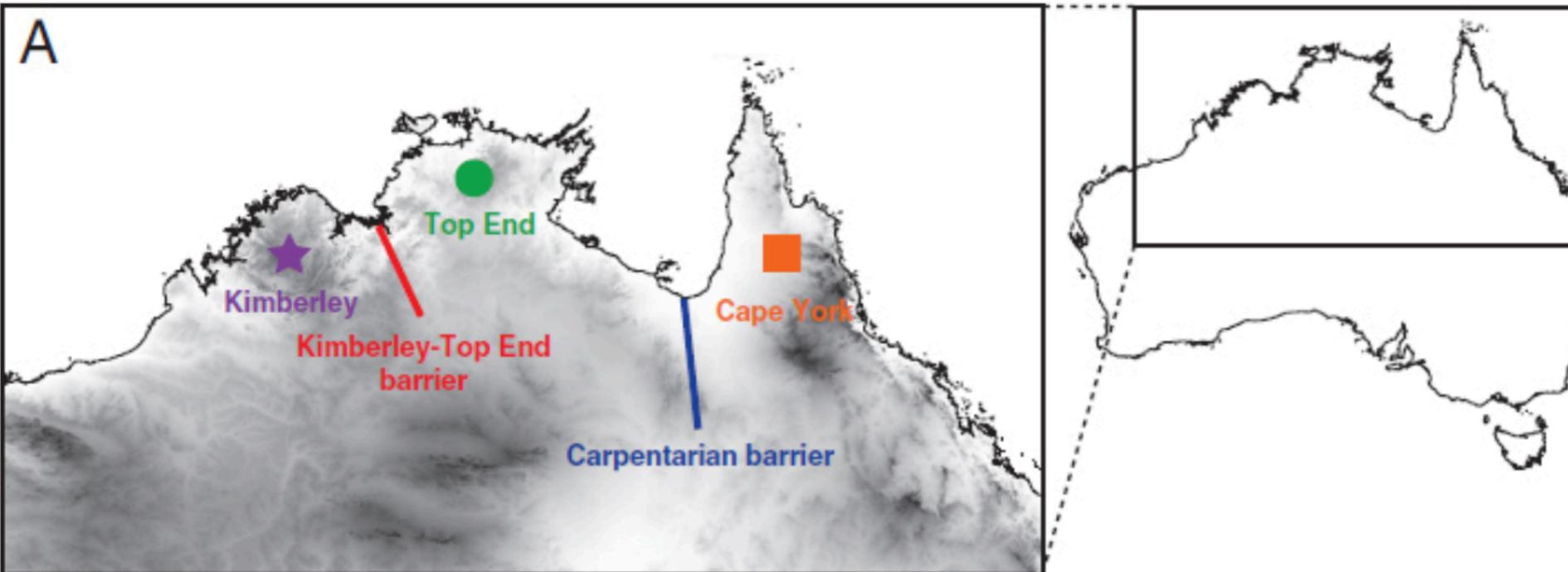
Europe

- Grasshopper
- Hedgehog
- Bear
- Chubb

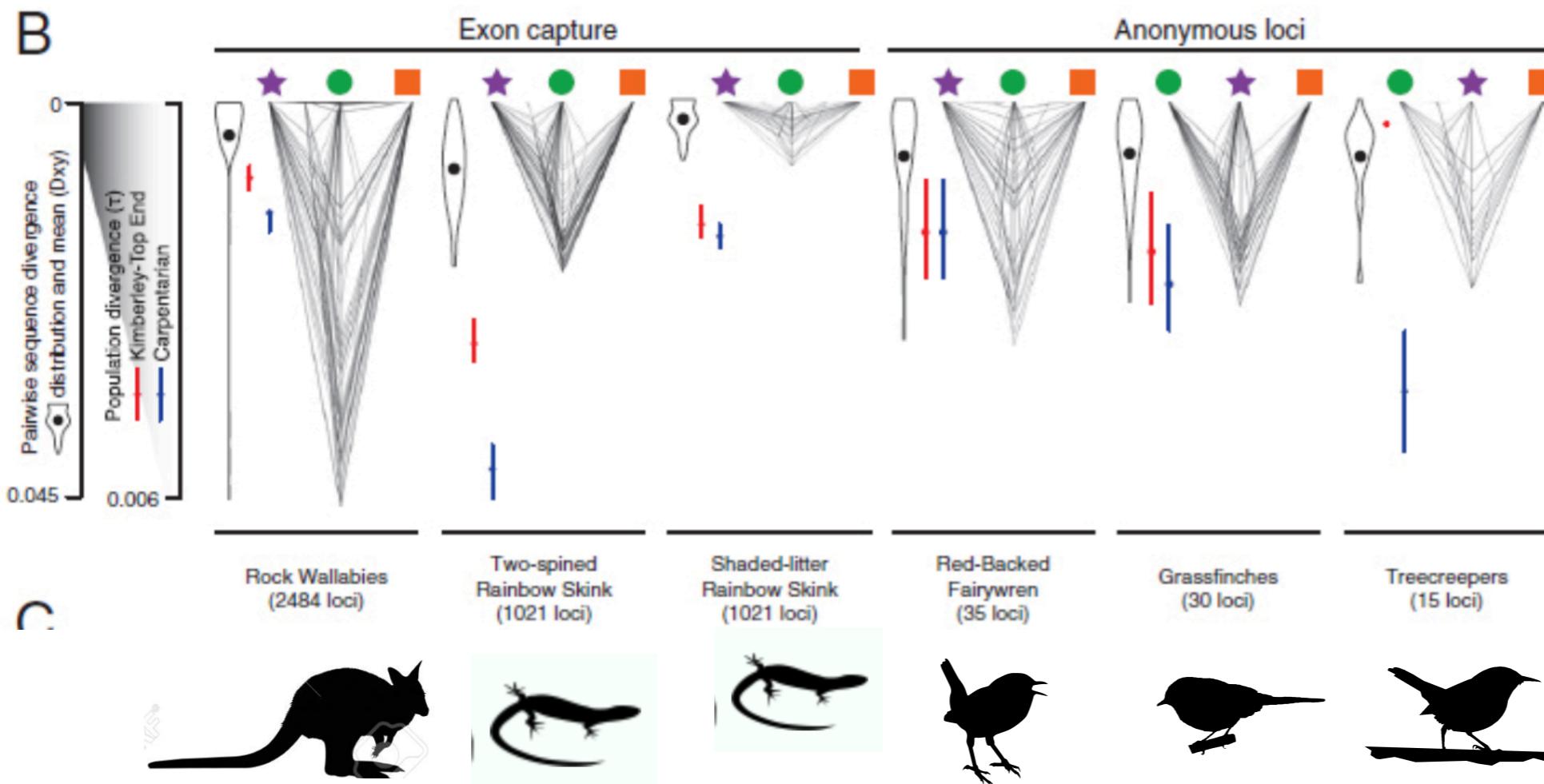


Hewitt 2004

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

**A**

regional  
diversification  
i.e. co-  
diversification

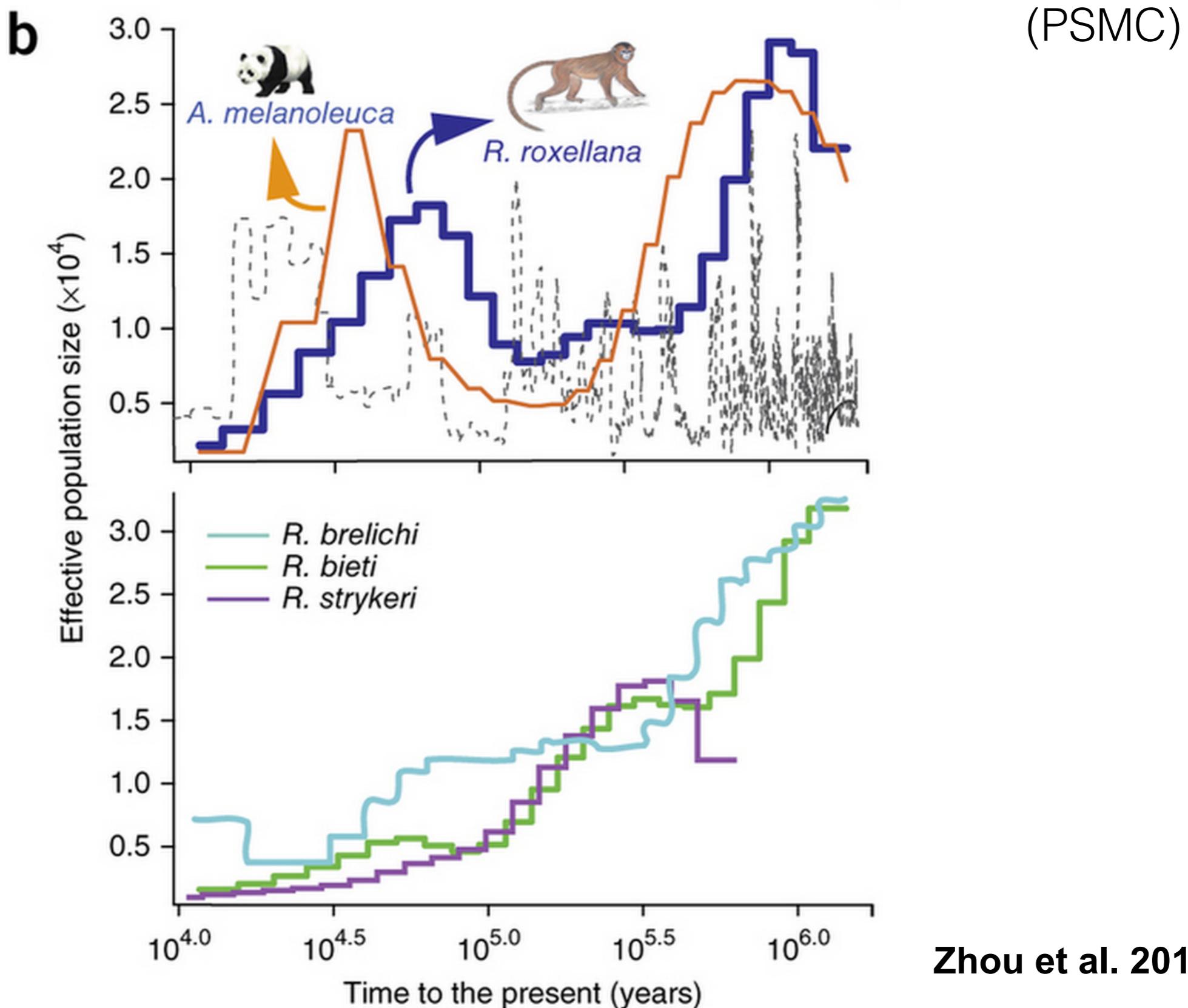
**B****C**

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



# blast from the past 1998 - 2006

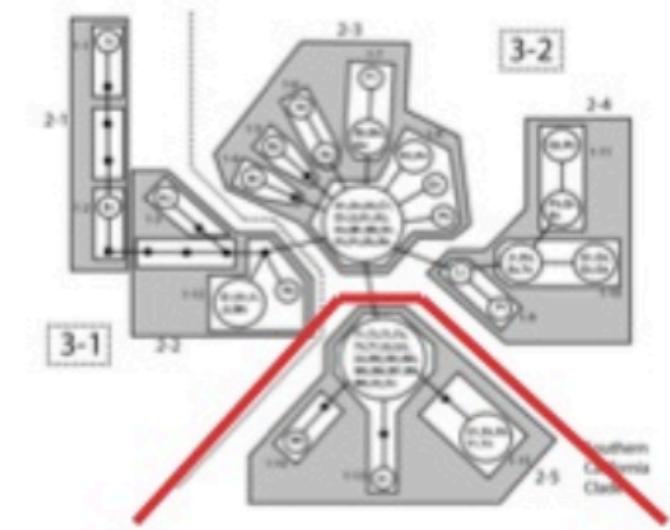
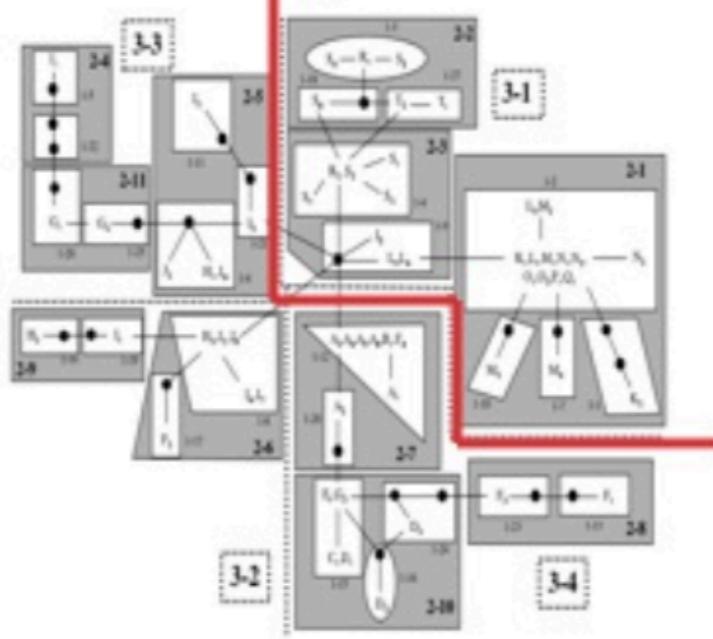
Wrentit



California Thrasher

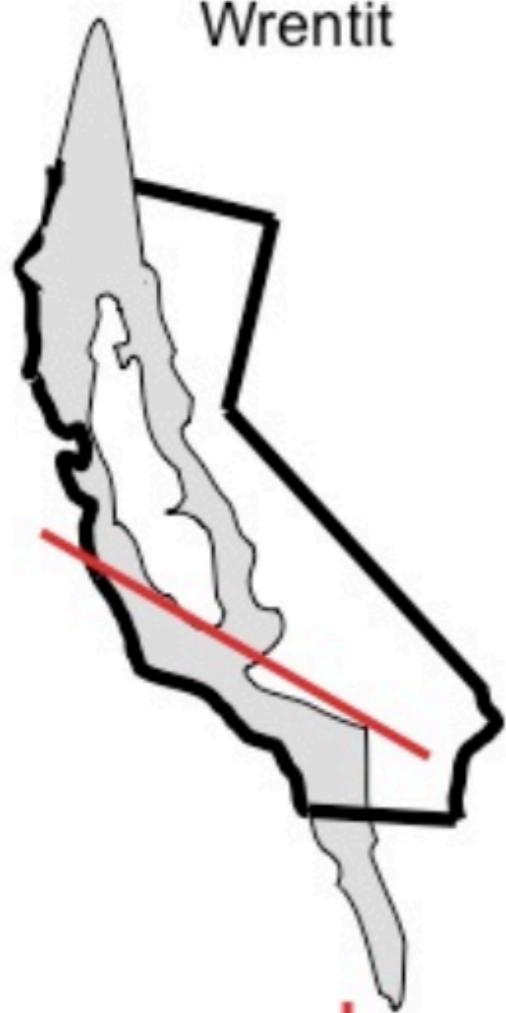


White-headed Woodpecker



# Nested Clade Analysis 1998 - 2006

Wrentit



California Thrasher

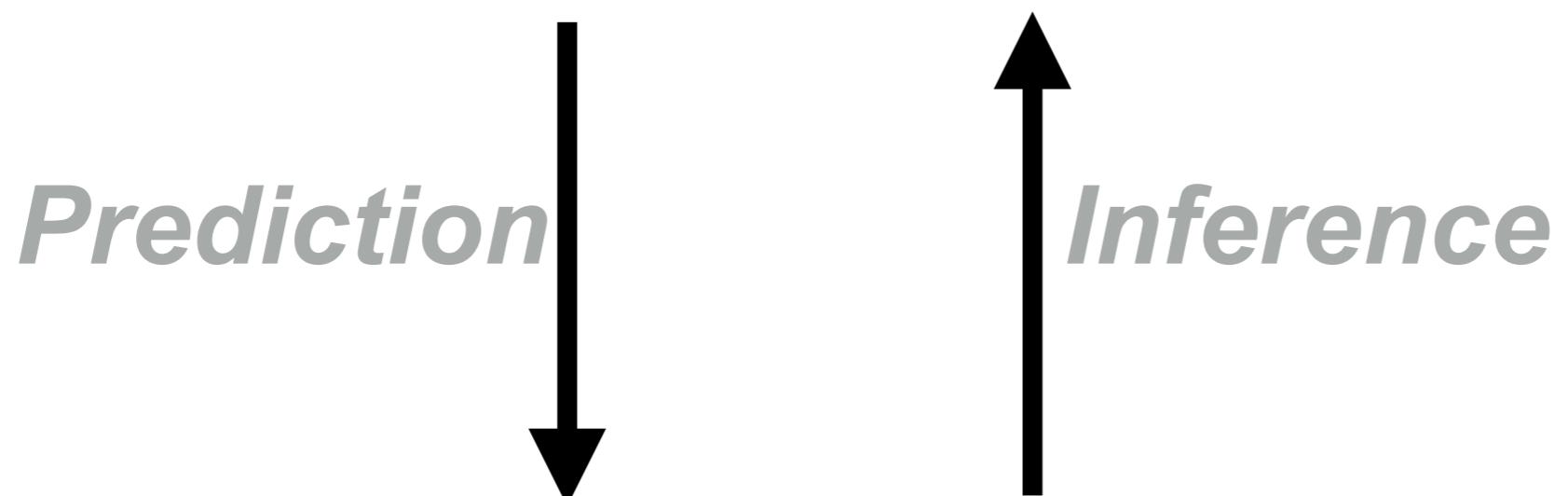


White-headed Woodpecker



co-demographic  
/assemblage  
history

## Coalescent Model



DNA  
barcodes  
(ie mtDNA)

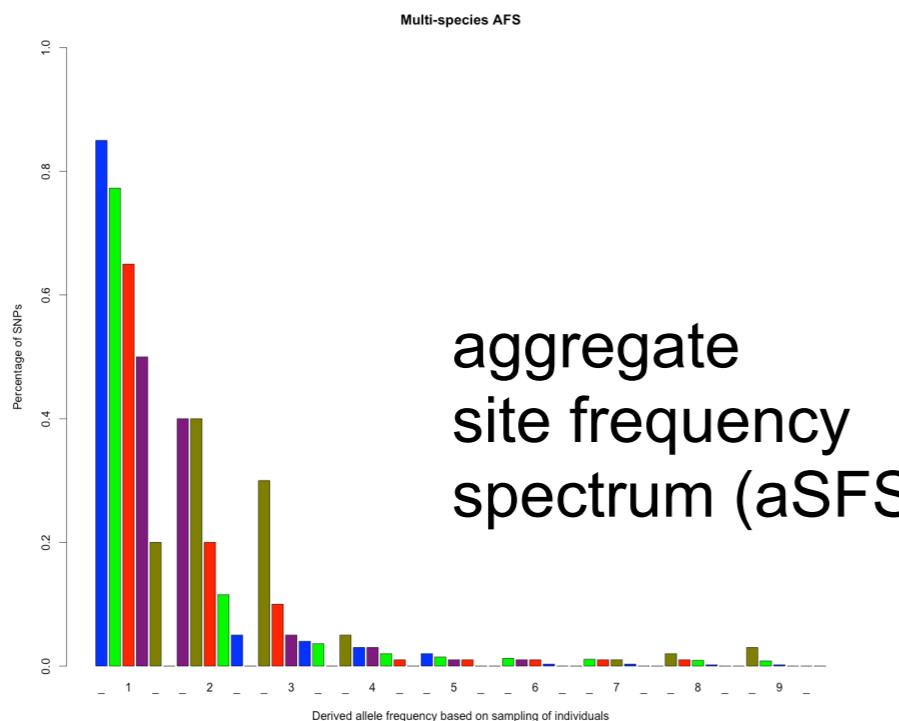
Comparative  
population  
genetics

“whole”  
genomes

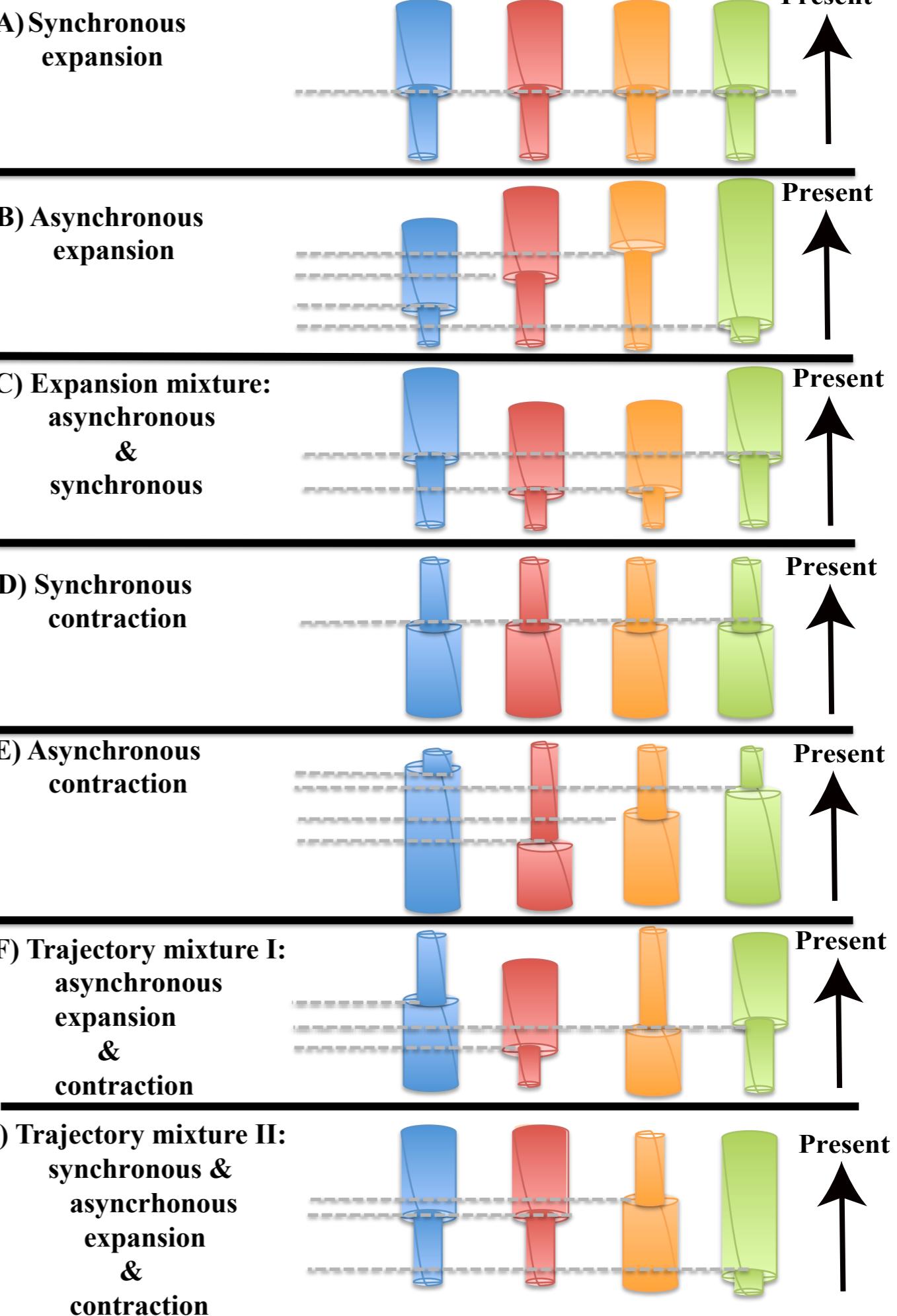
# **Central Questions of Comparative Phylogeography**

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

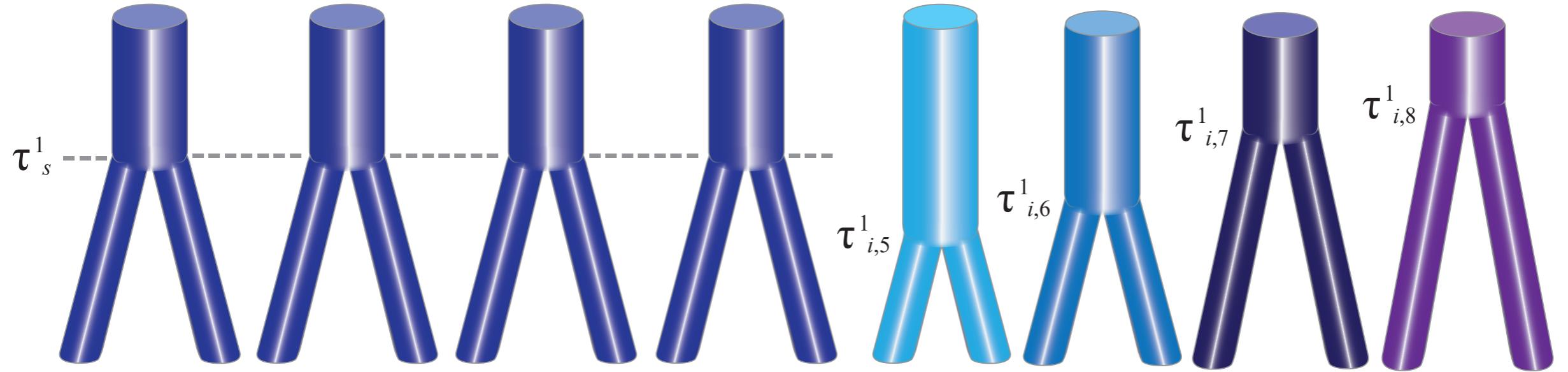
# fitting models of co-expansion, co-contraction with SNP data



Alexander Xue



# fitting models of co-divergence with SNP data



Alexander Xue

# fitting co-demographic models is not easy

## Mean model posterior probabilities

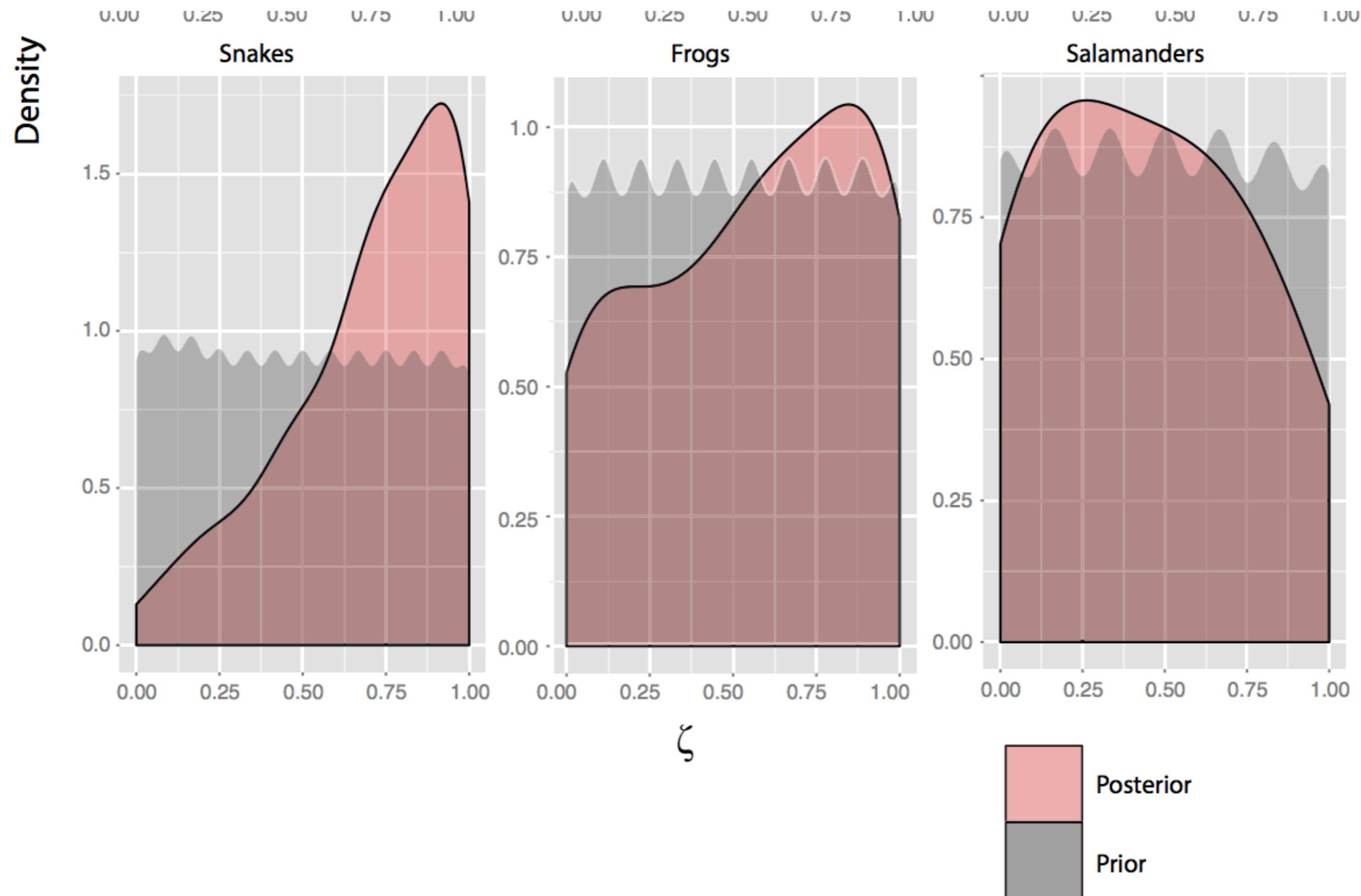
	$\zeta = 0.0$	$\zeta = 0.4$	$\zeta = 0.6$	$\zeta = 0.8$	$\zeta = 1.0$
--	---------------	---------------	---------------	---------------	---------------

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

$\zeta$  = % of taxa co-expanding

# fitting co-demographic models is not easy



$\zeta = \%$  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-Yanes<sup>1</sup>  | Alexander T. Xue<sup>2,3</sup>  | Alejandra Moreno-Letelier<sup>4</sup> | Tove H. Jorgensen<sup>5</sup> | Nadir Alvarez<sup>6,7</sup> | Daniel Piñero<sup>8</sup> | Brent C. Emerson<sup>9,10</sup> 



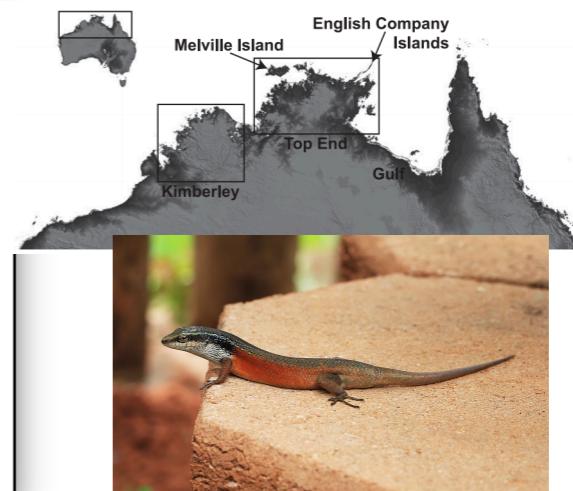
## Co-expansion

ORIGINAL ARTICLE

WILEY MOLECULAR ECOLOG

## Pleistocene climatic changes drive diversification across a tropical savanna

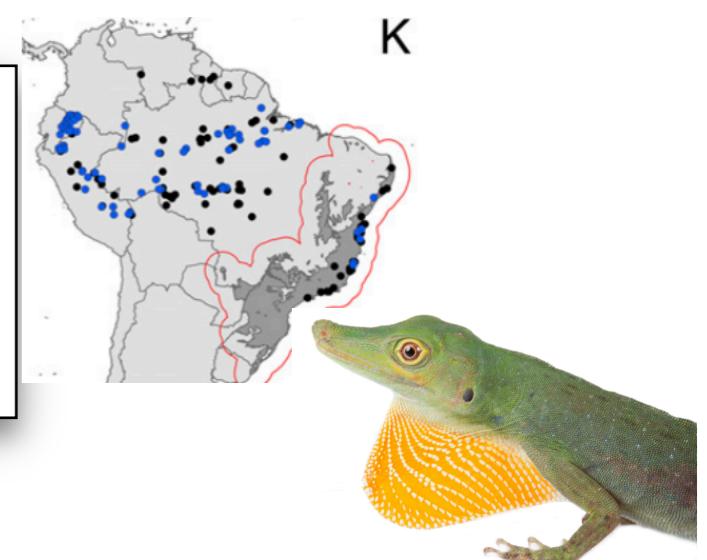
Sally Potter<sup>1,2</sup>  | Alexander T. Xue<sup>3,4</sup>  | Jason G. Bragg<sup>1,2</sup> | Dan F. Rosauer<sup>1,2</sup> | Emily J. Roycroft<sup>5,6</sup> | Craig Moritz<sup>1,2</sup>



## asynchronous expansion

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

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



## **Shortcomings (plenty)**

too much inferential uncertainty?

model is too simple?

not spatially explicit

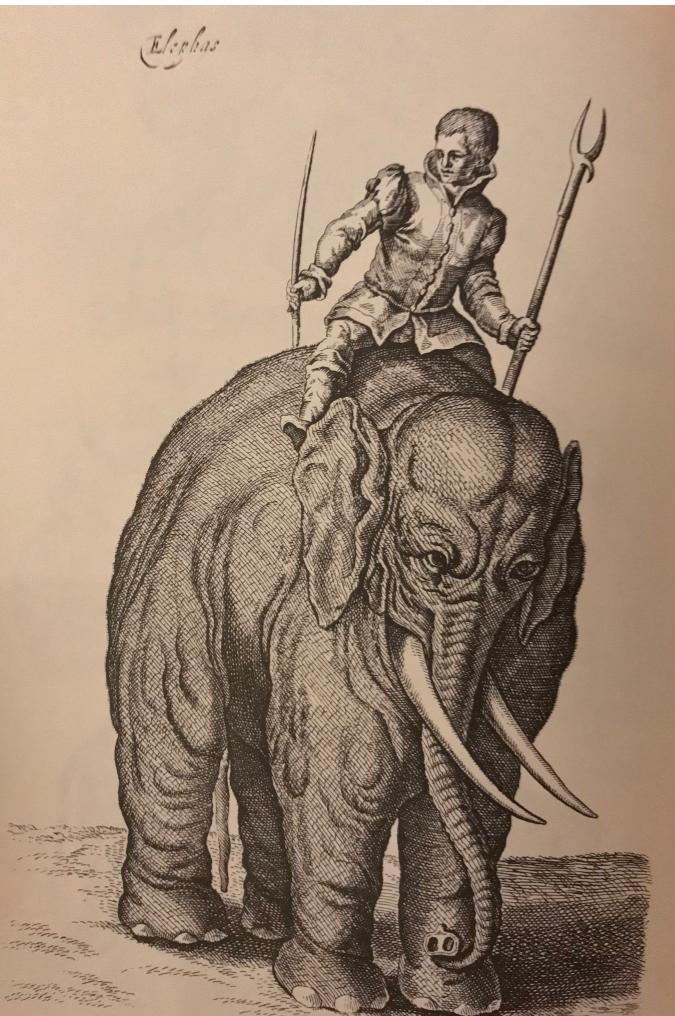
# **Shortcomings (plenty)**

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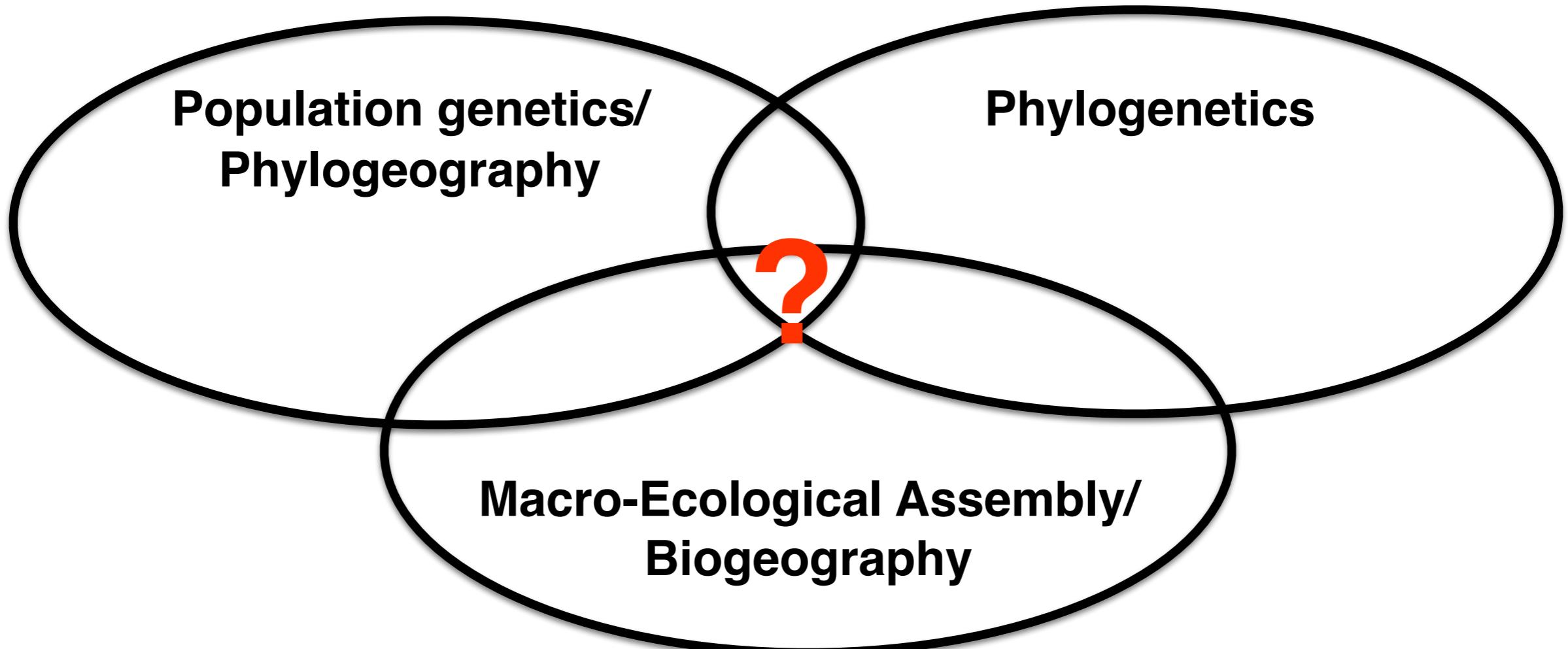
not spatially explicit

**models not well-grounded in ecological theory**



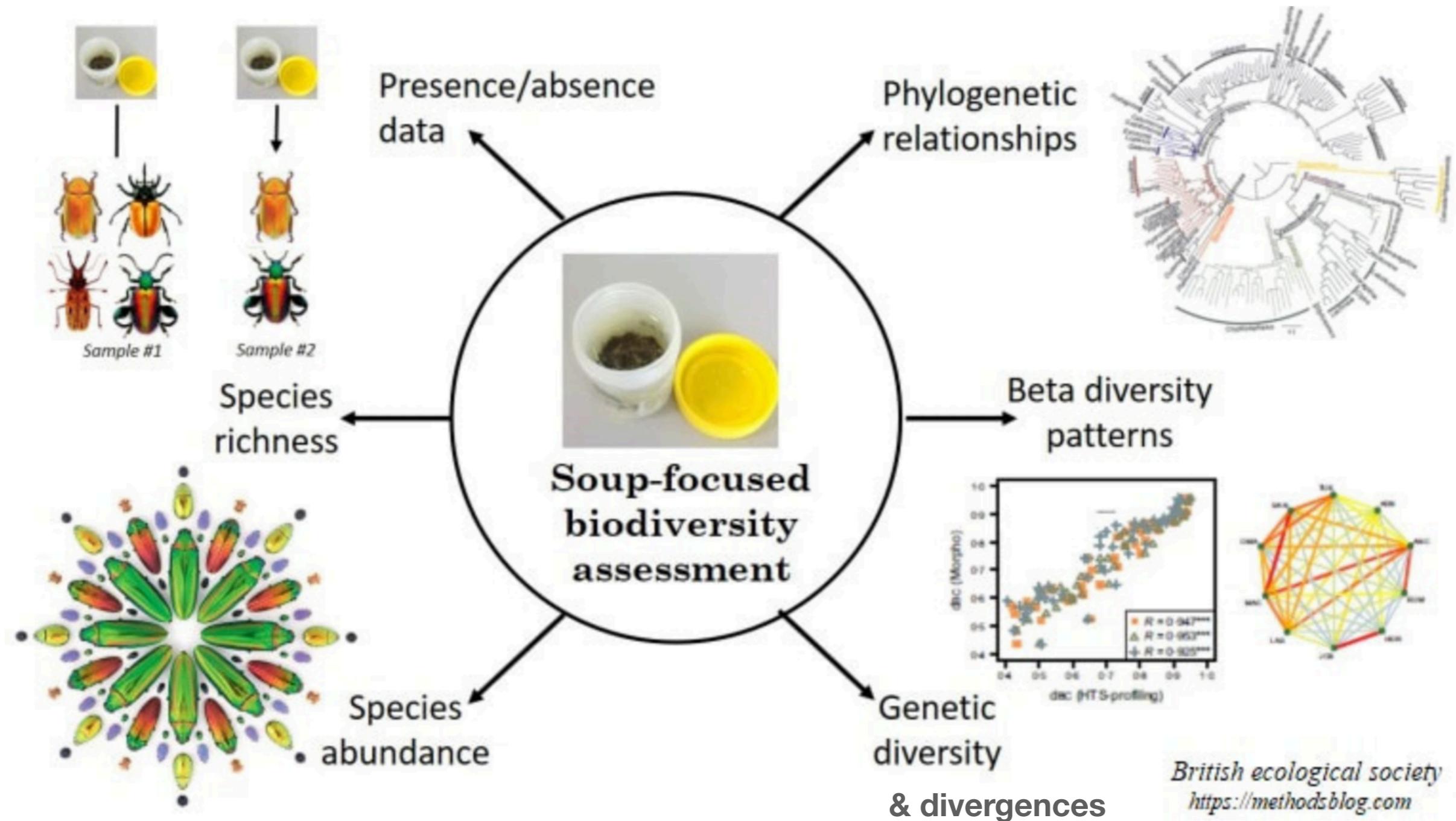
# **Central Questions of Comparative Phylogeography**

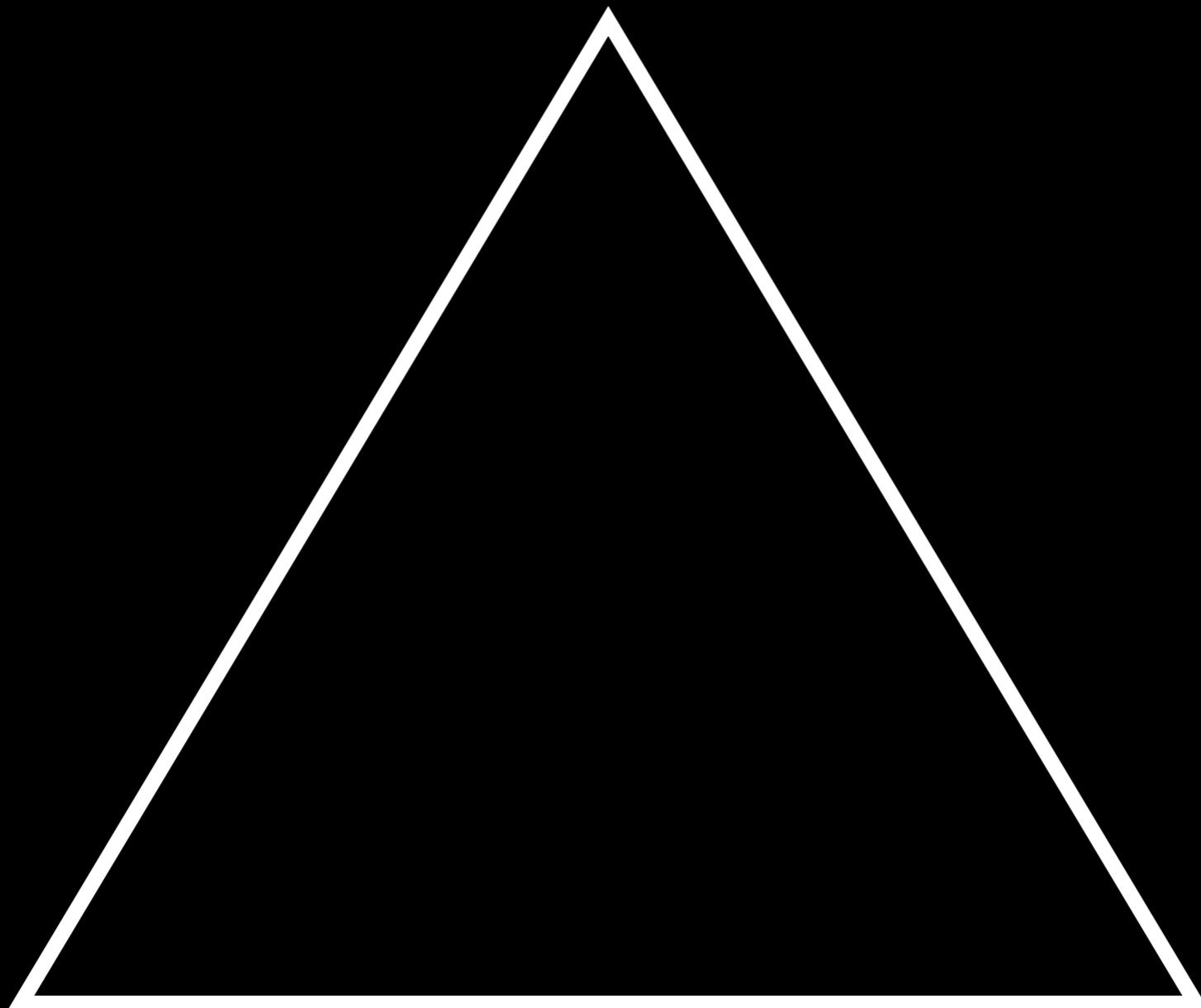
- 1. vicariance or dispersal?**
- 2. synchronous demographic histories?**
- 3. how deterministic is assembly and/or co-demography? (e.g. do traits matter?)**



# how about the whole enchilada ?

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





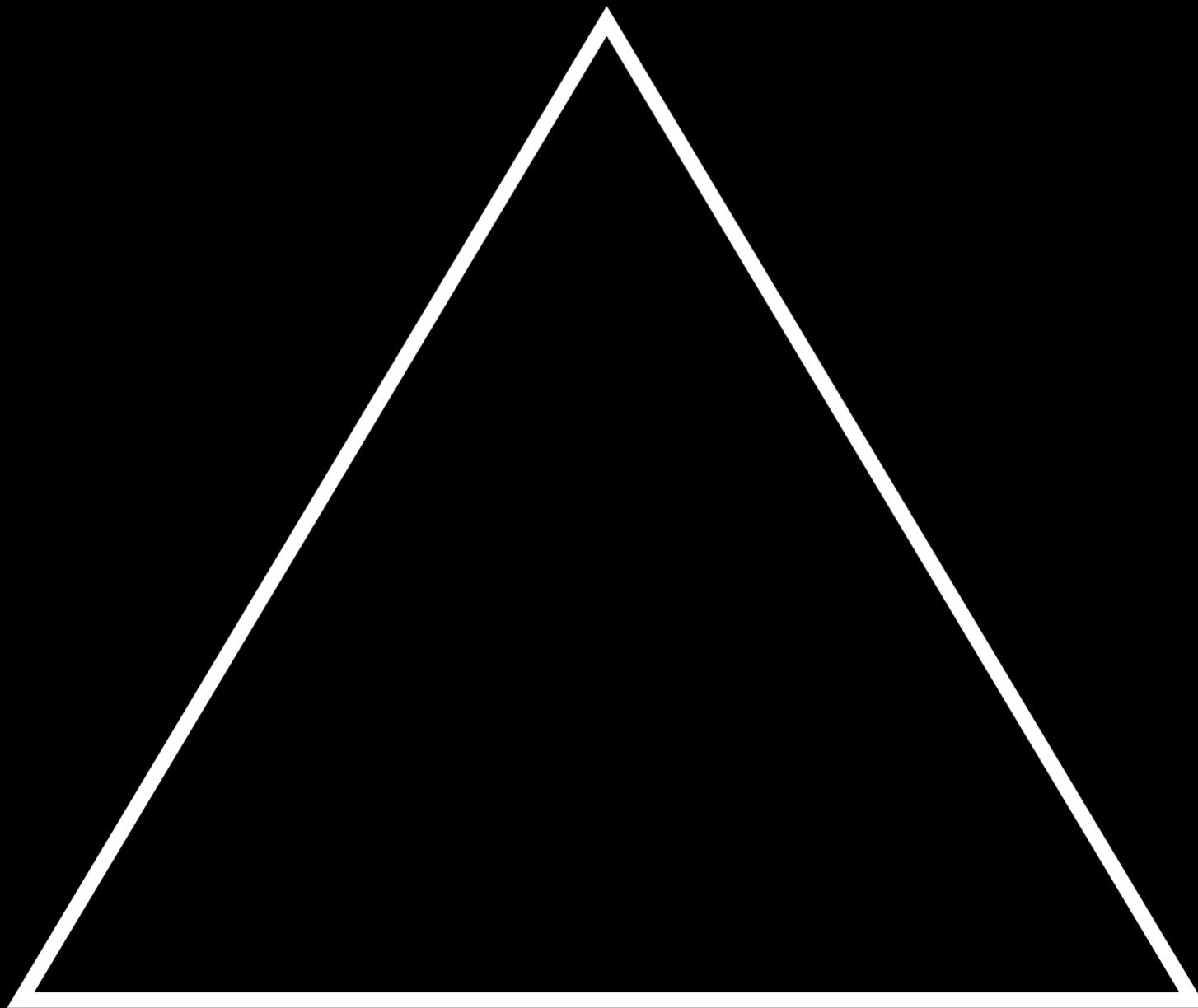
## **Biodiversity Metrics**

- Species abundance spectra
- Genetic diversity spectra
- Trait diversity spectra

# abiotic variables

bioclimatic variables

remote sensing products



## Biodiversity Metrics

Species abundance spectra

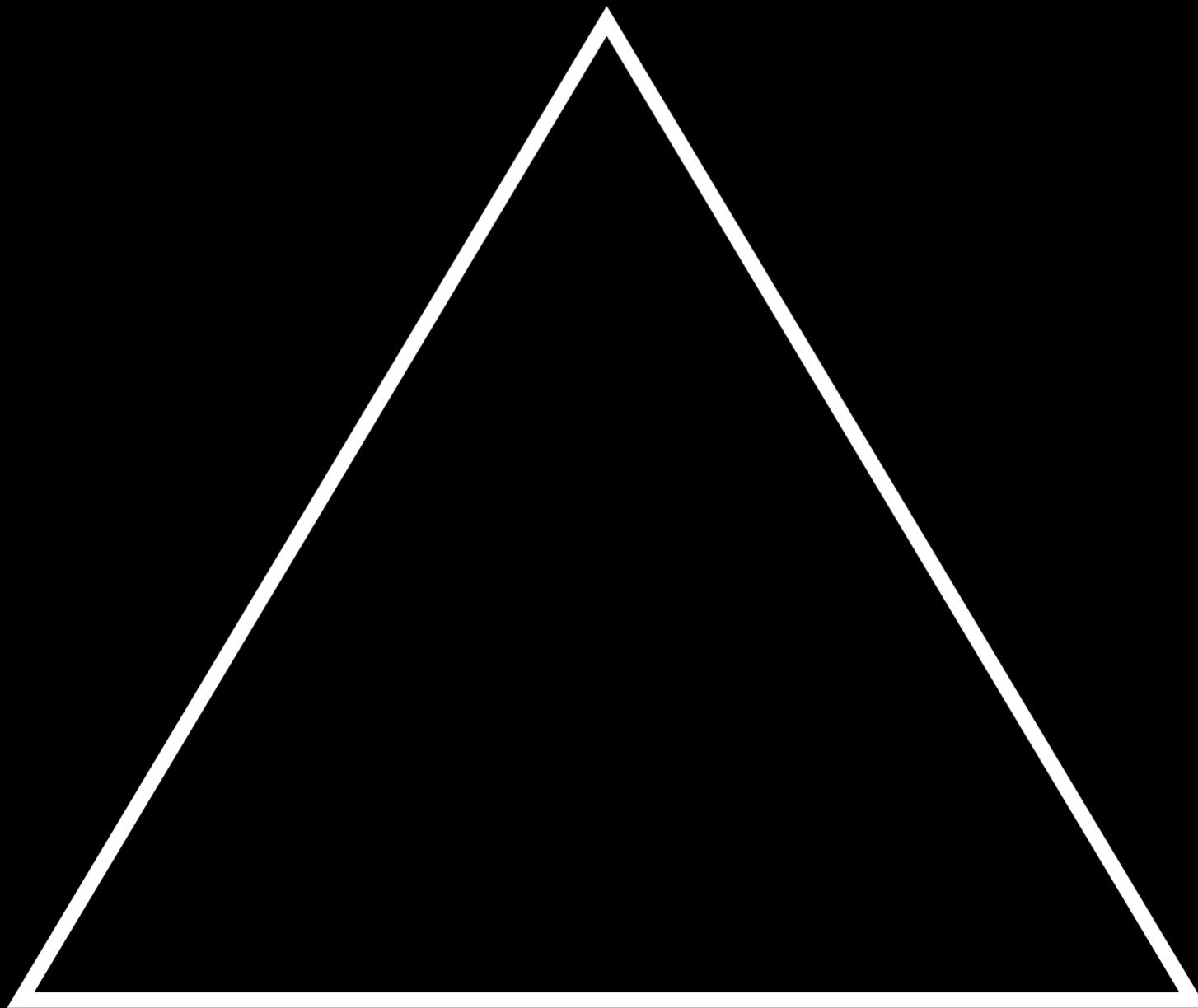
Genetic diversity spectra

Trait diversity spectra

## **abiotic variables**

bioclimatic variables

remote sensing products



**Historical-Biogeographic  
Processes**

**Biodiversity  
Metrics**

Species abundance spectra

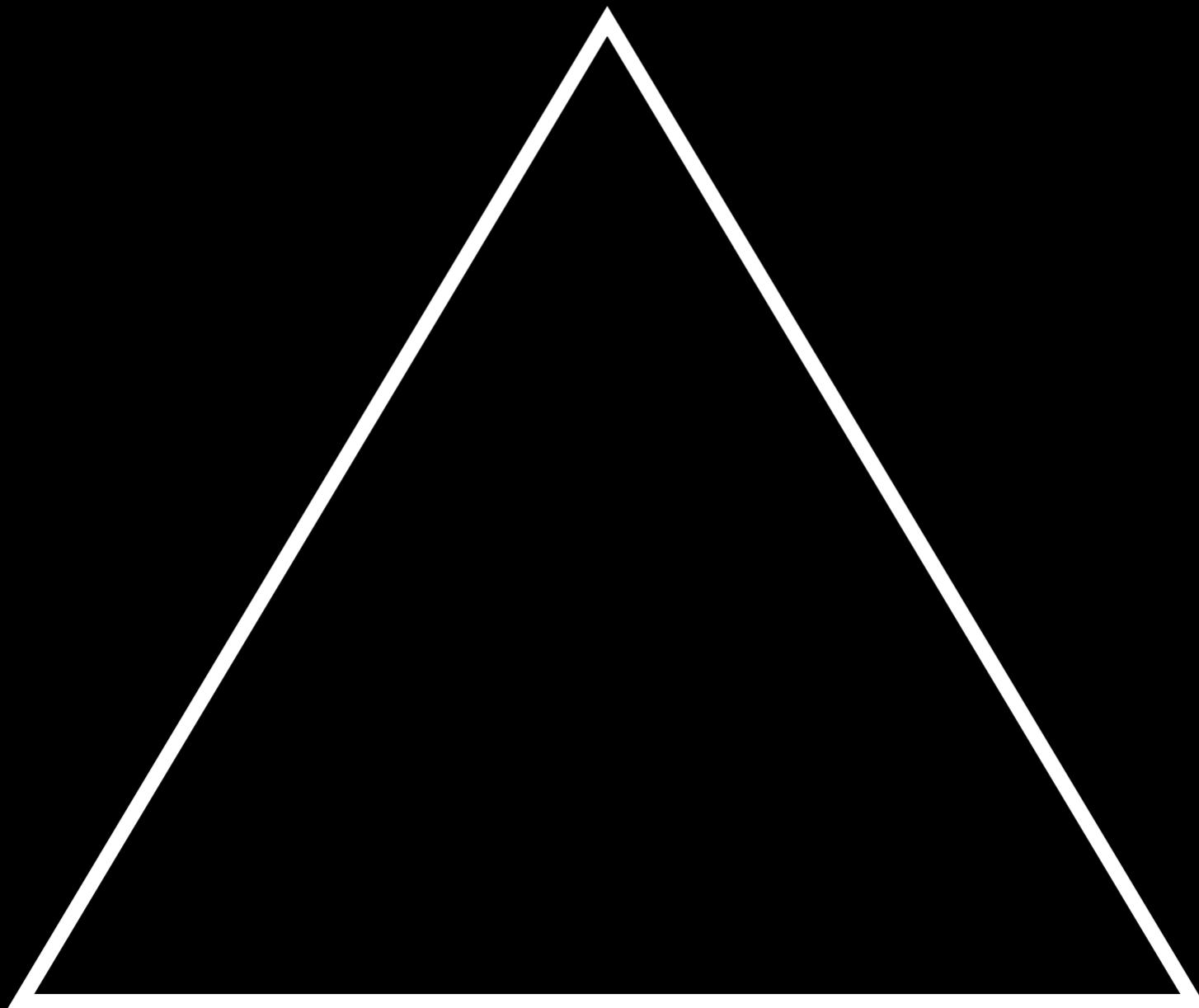
Genetic diversity spectra

Trait diversity spectra

## abiotic variables

bioclimatic variables

remote sensing products



**Historical-Biogeographic  
Processes**



estimation

**Biodiversity  
Metrics**

Species abundance spectra

Genetic diversity spectra

Trait diversity spectra



Isaac Overcast  
CUNY

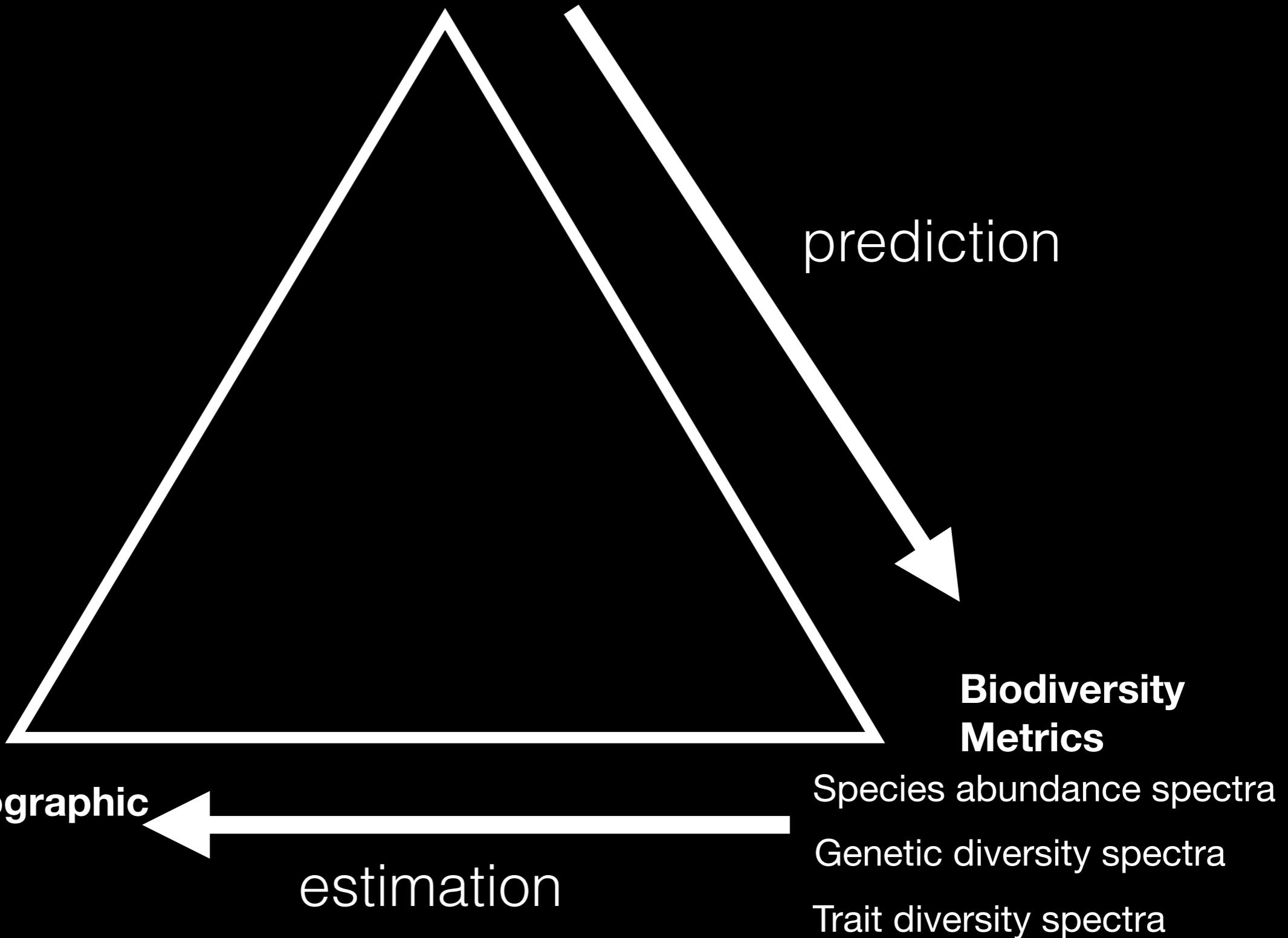
can we bridge models of population genetics  
and abundance under a unified model of  
biogeographic assembly?



## abiotic variables

bioclimatic variables

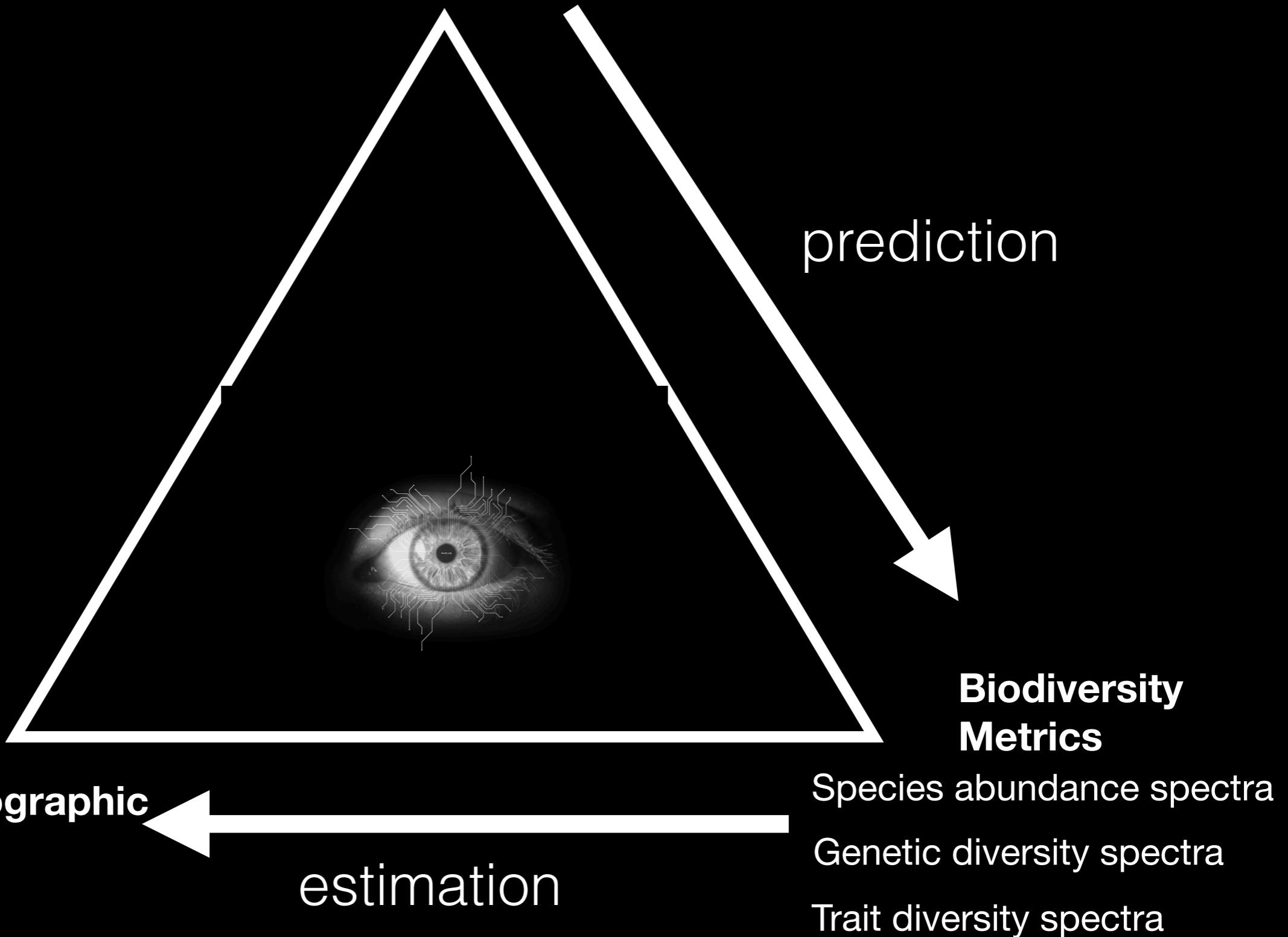
remote sensing products



## abiotic variables

bioclimatic variables

remote sensing products

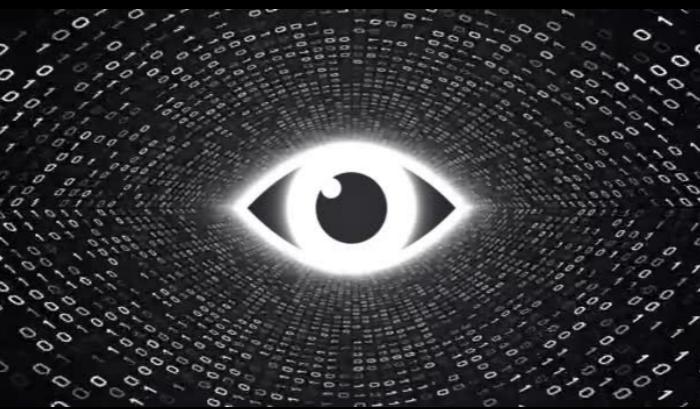


## abiotic variables

bioclimatic variables

remote sensing products

yeah,  
right



prediction

## Biodiversity Metrics

Species abundance spectra

Genetic diversity spectra

Trait diversity spectra

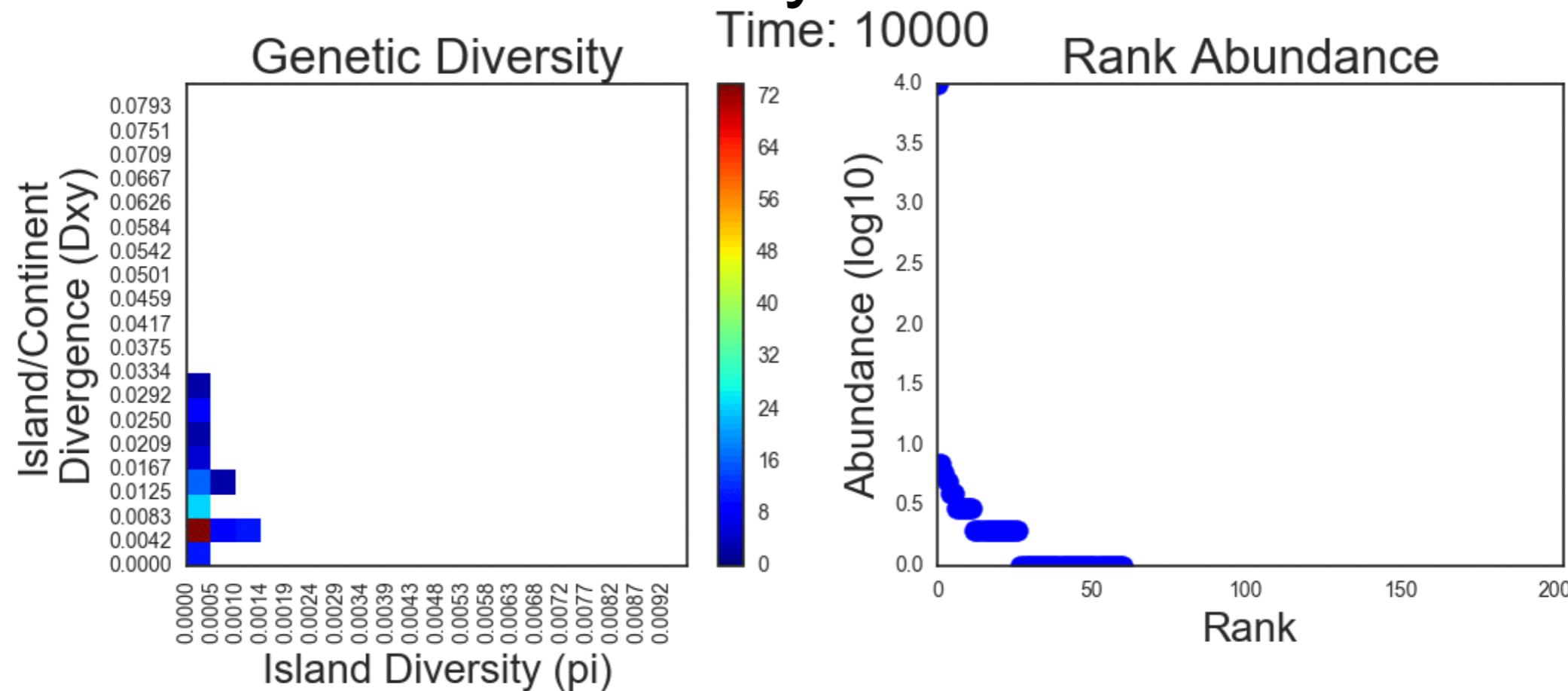
## Historical-Biogeographic Processes

estimation

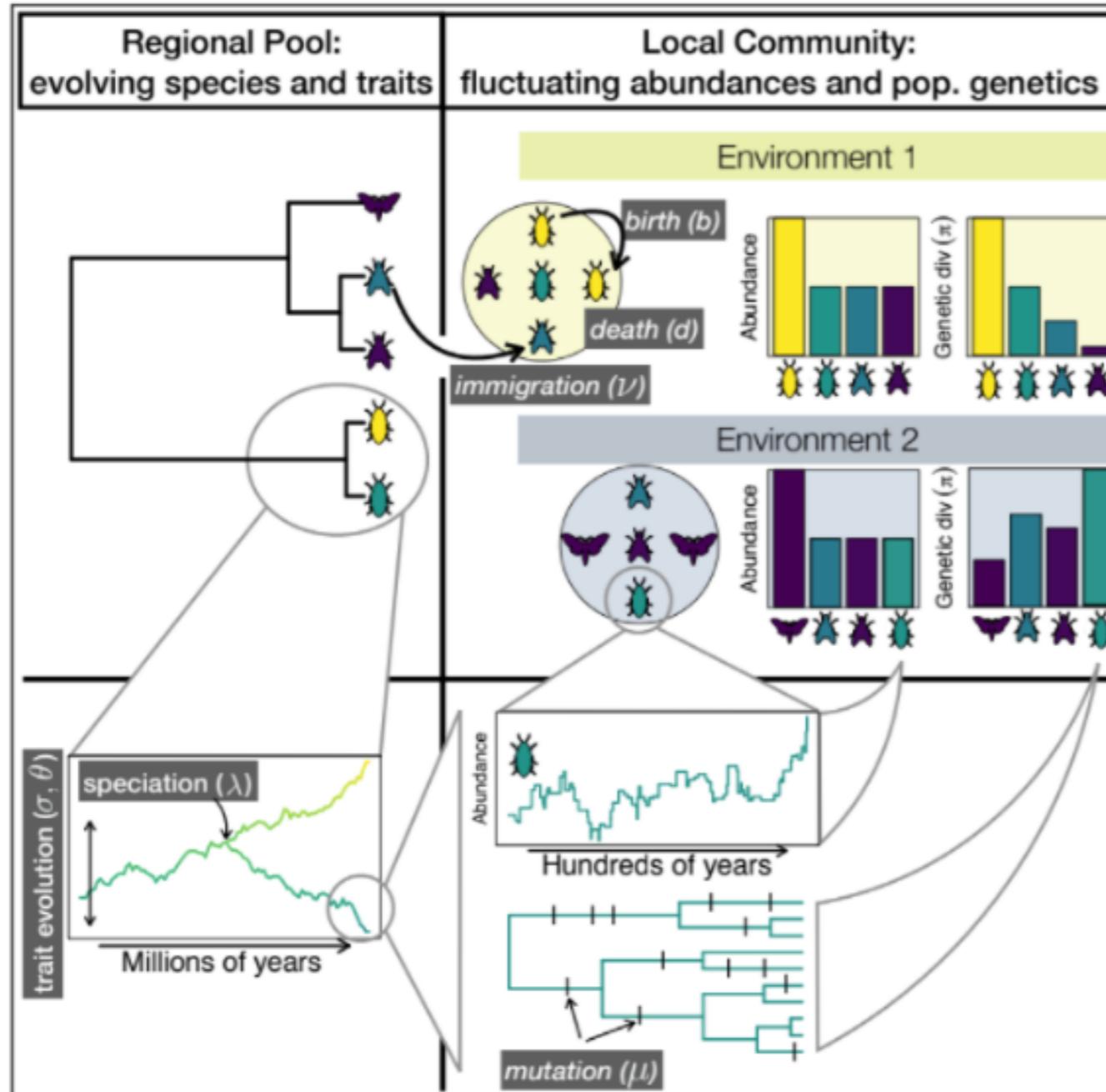


Isaac Overcast  
CUNY

**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**

**M**assive  
**E**co-  
Evolutionary  
**S**ynthesis  
**S**imulations



Andy Rominger  
(SFI)

# MESS DAG

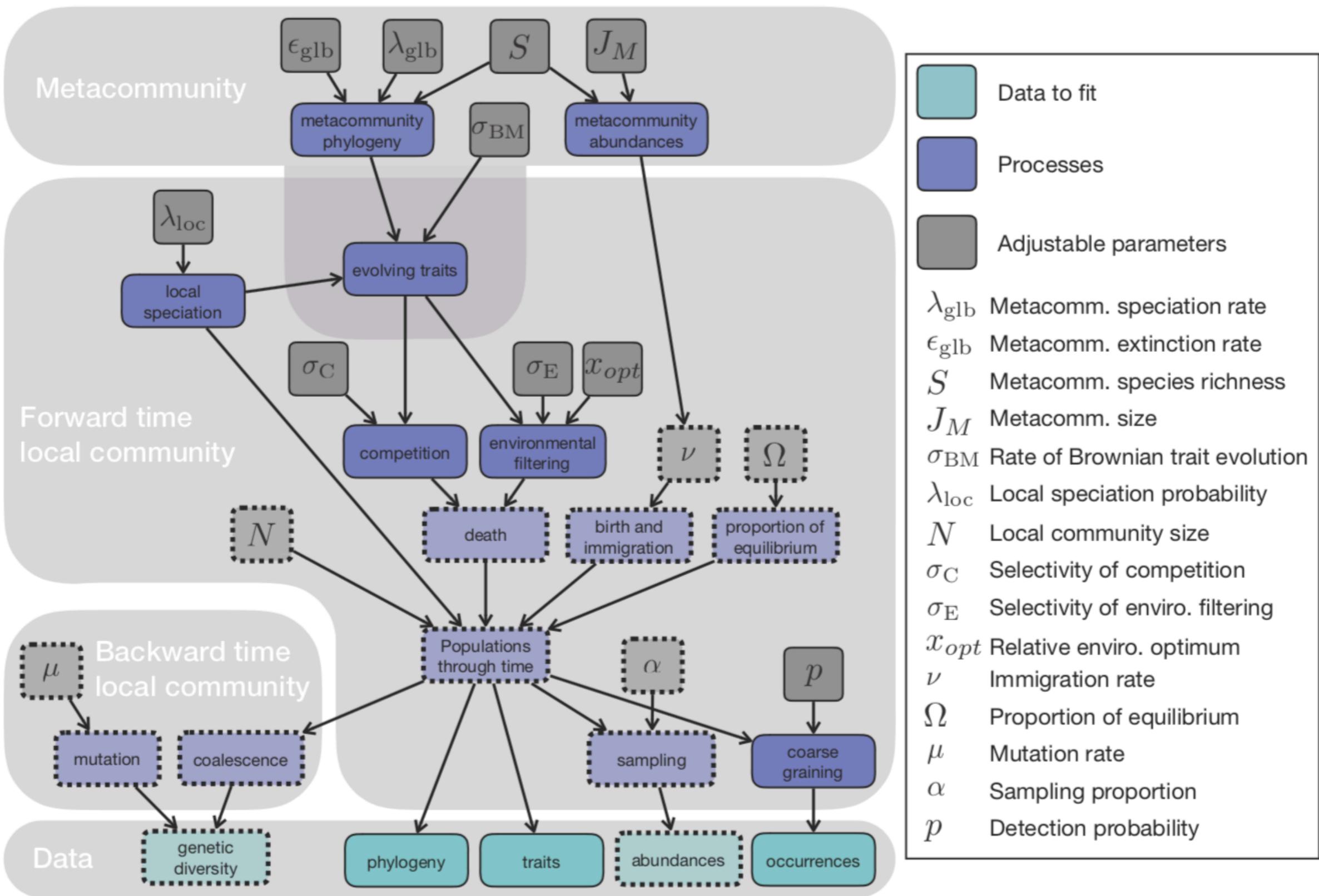


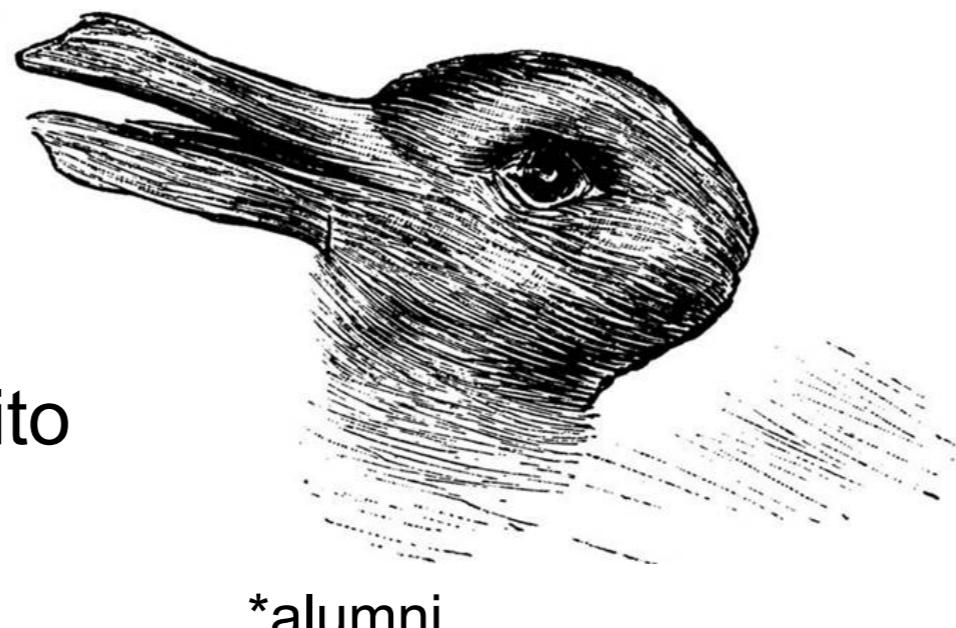
Figure 2: Directed Acyclic Graph showing how each free parameter in the RoLE model feeds into modeled biological



@\_hickerson\_

# HickerLab

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



\*alumni

## Support

The City College  
of New York



THE GRADUATE  
CENTER  
CITY UNIVERSITY  
OF NEW YORK



iDiv

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



SANTA FE  
INSTITUTE

## sEcoEvo- MESS Team

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

## MESS Data

Brent Emerson    Henrik Krehenwinkel  
Christine Parent    Rosemary Gillespie  
Chris Meyer

# Thank you!

