

Leveraging High Throughput Ecology and Population Genetics for Biogeographic Inference and Prediction

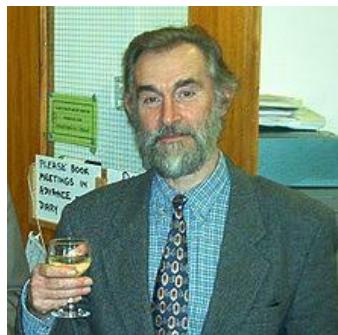


Michael Hickerson
City University of New York
City College of New York
American Museum of Natural History

The comparative phylogeographic pipe dream

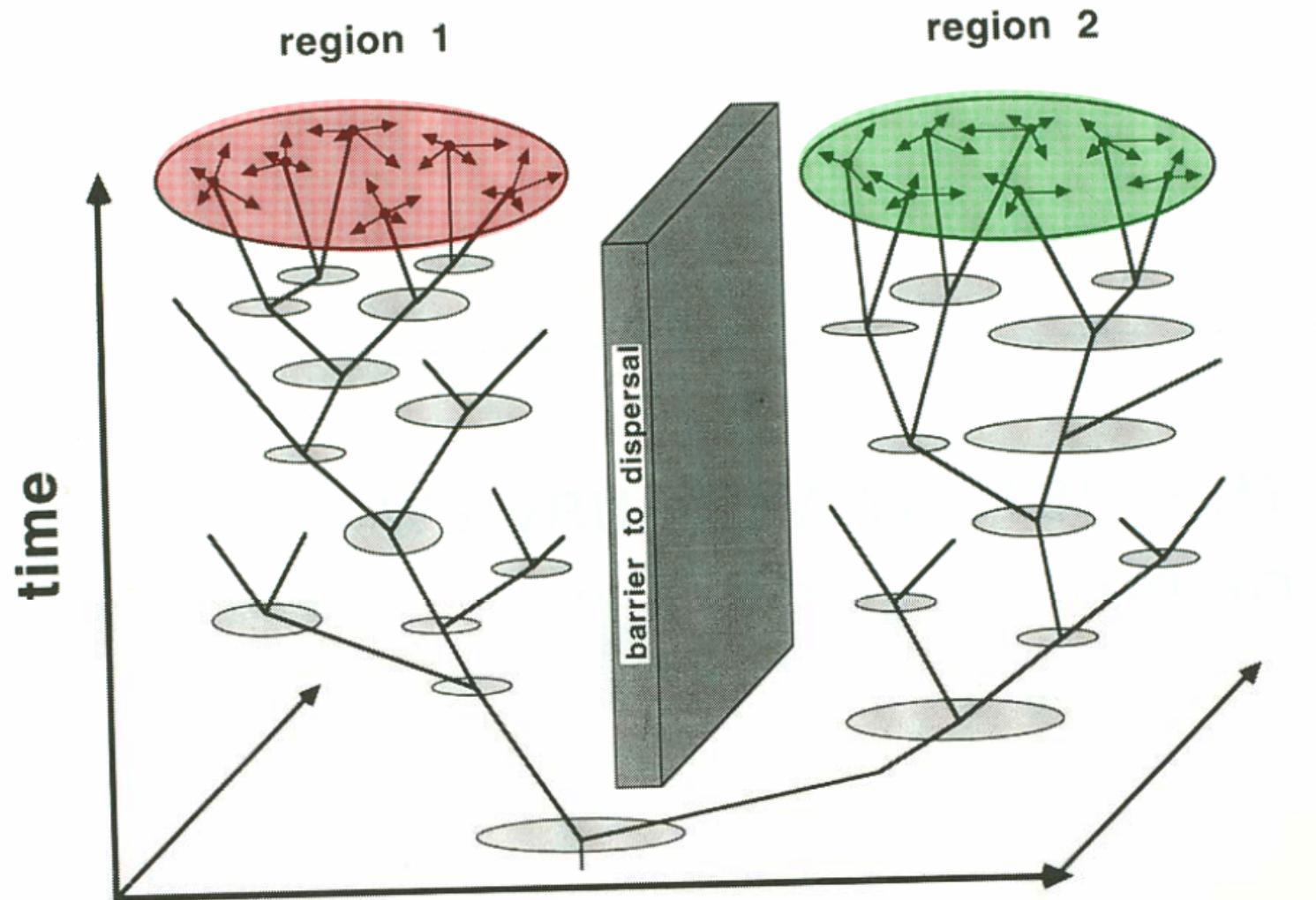


John Avise



Godfrey Hewitt



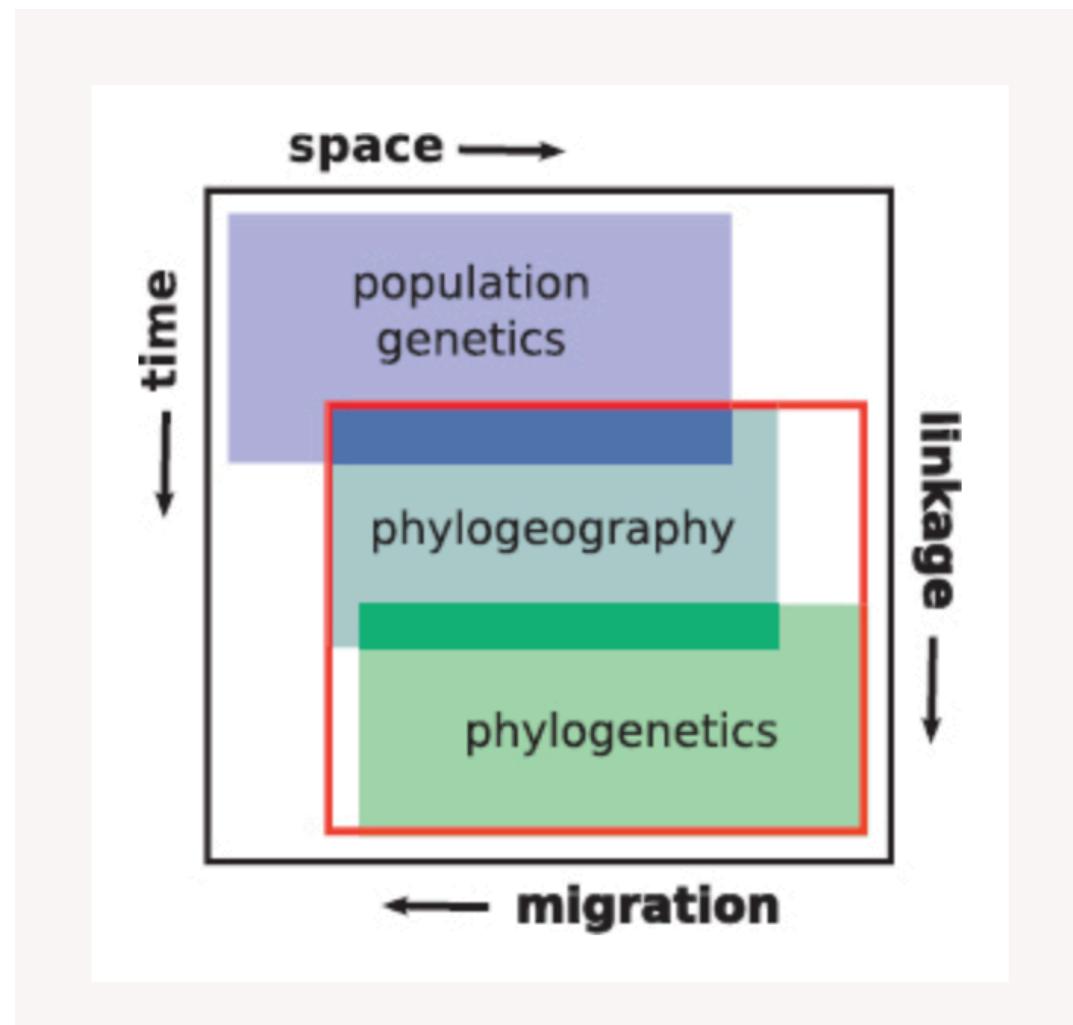


~1987 Avise coins “**phylogeography**”

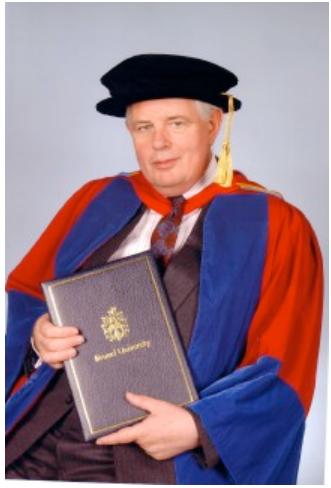


J. Avise

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

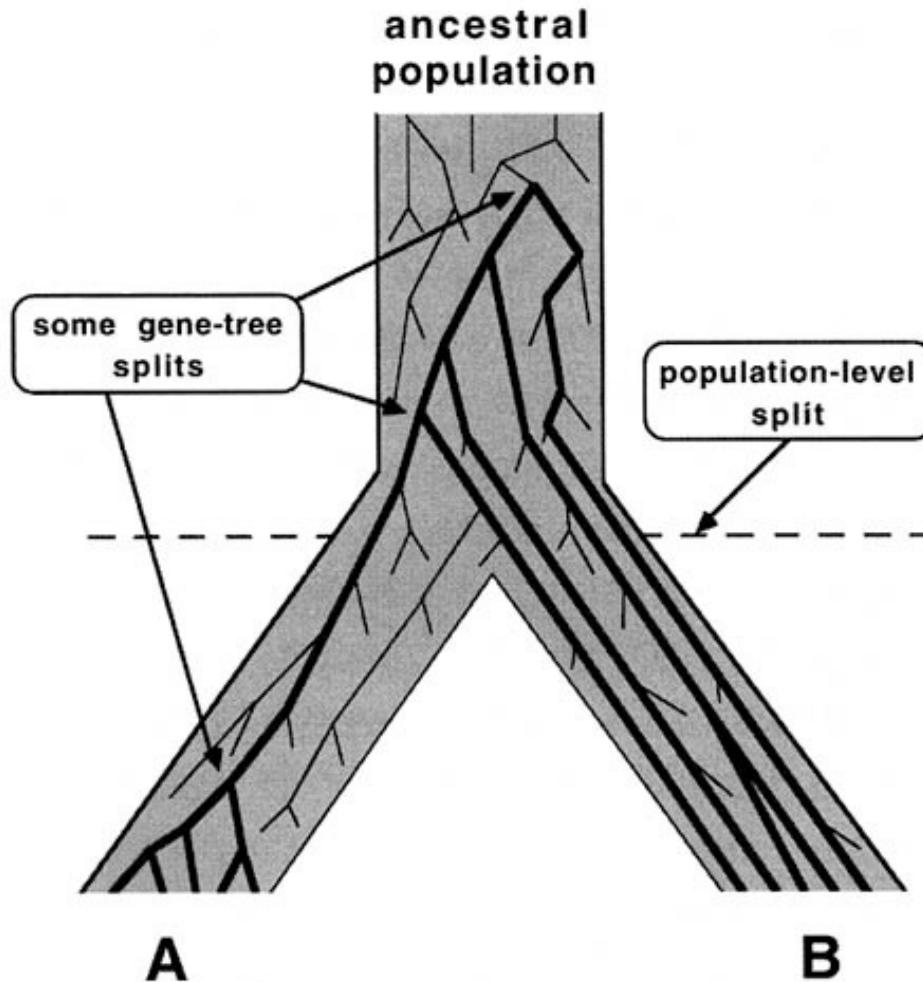


Edwards et al. 2016



Kingman

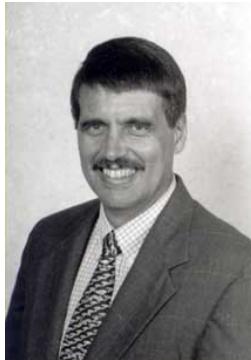
$$P_c(t) = \left(1 - \frac{1}{2N_e}\right)^{t-1} \left(\frac{1}{2N_e}\right).$$



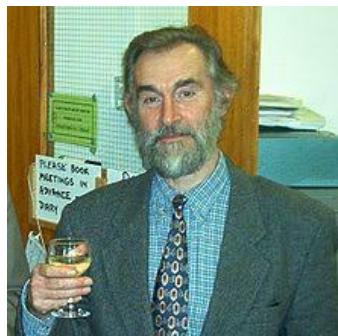
Tajima

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

The comparative phylogeographic pipe dream



John Avise



Godfrey Hewitt



leveraging inferences from multiple species histories

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

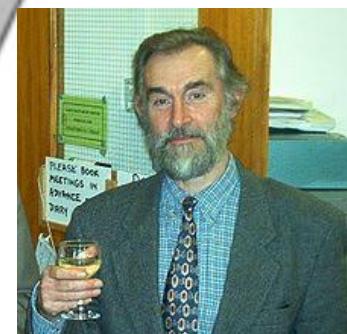
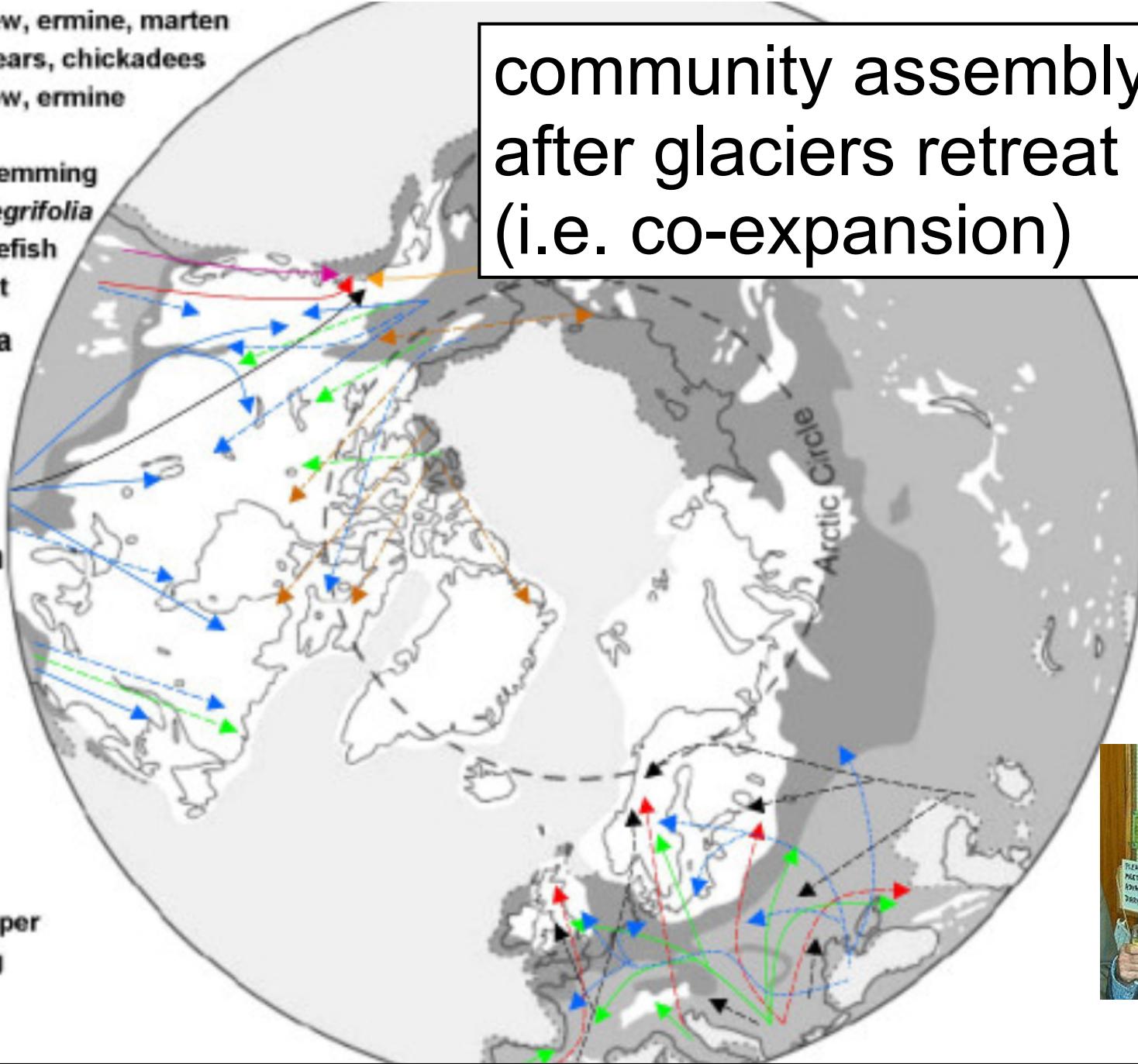
North America

Likely postglacial colonization routes for a sample of species

Europe

- Grasshopper
- Hedgehog
- Bear
- Chubb

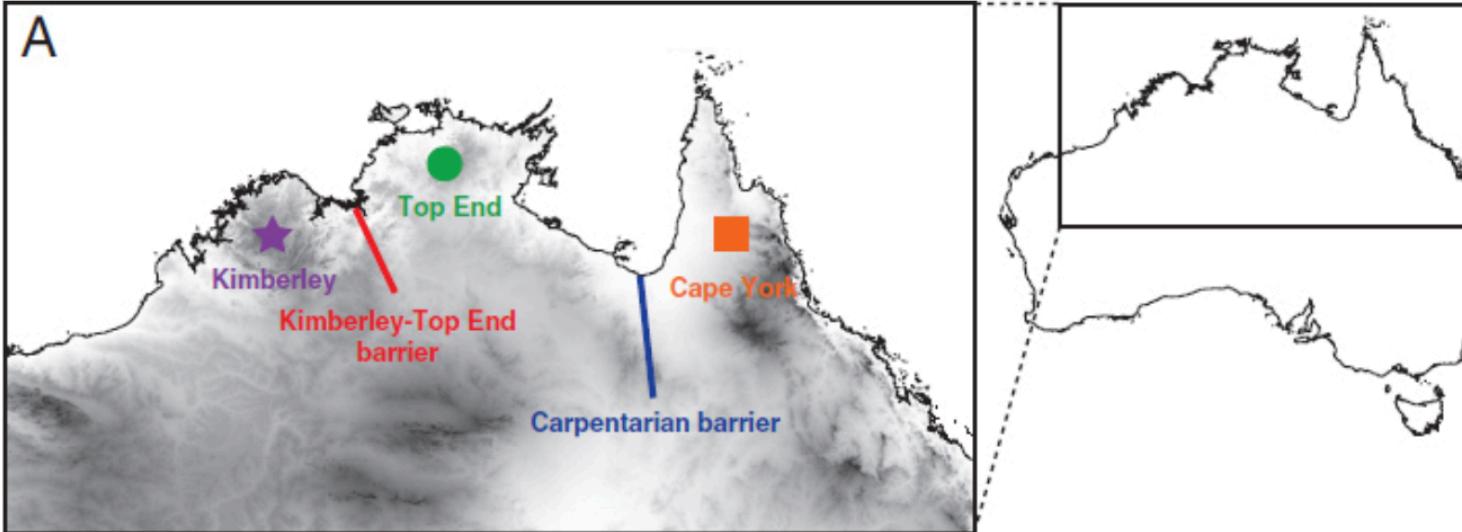
community assembly after glaciers retreat (i.e. co-expansion)



Hewitt 2004

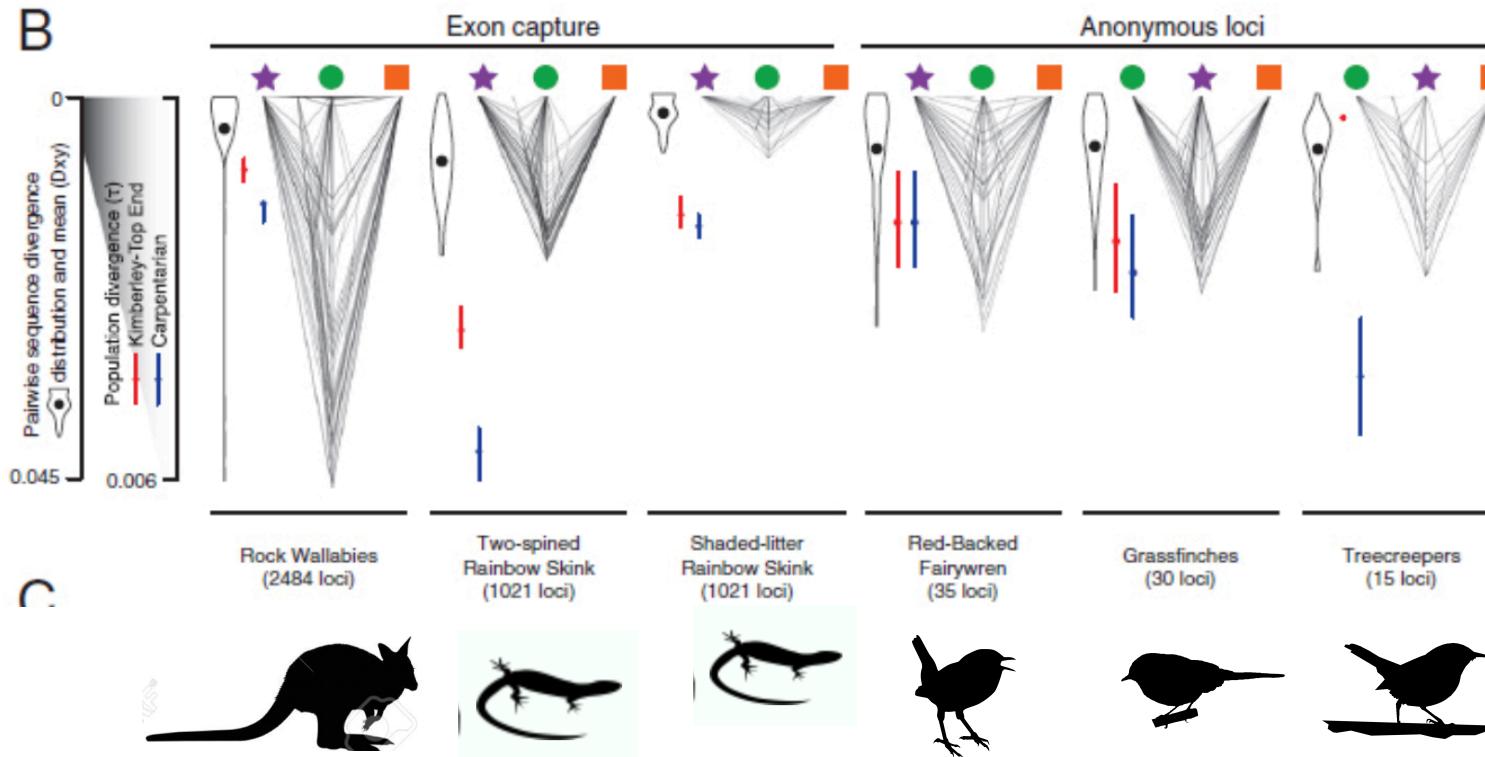
i.e. stepping back and looking at the combined results of multiple phylogeographic studies

A



regional
diversification
i.e. co-
diversification

B



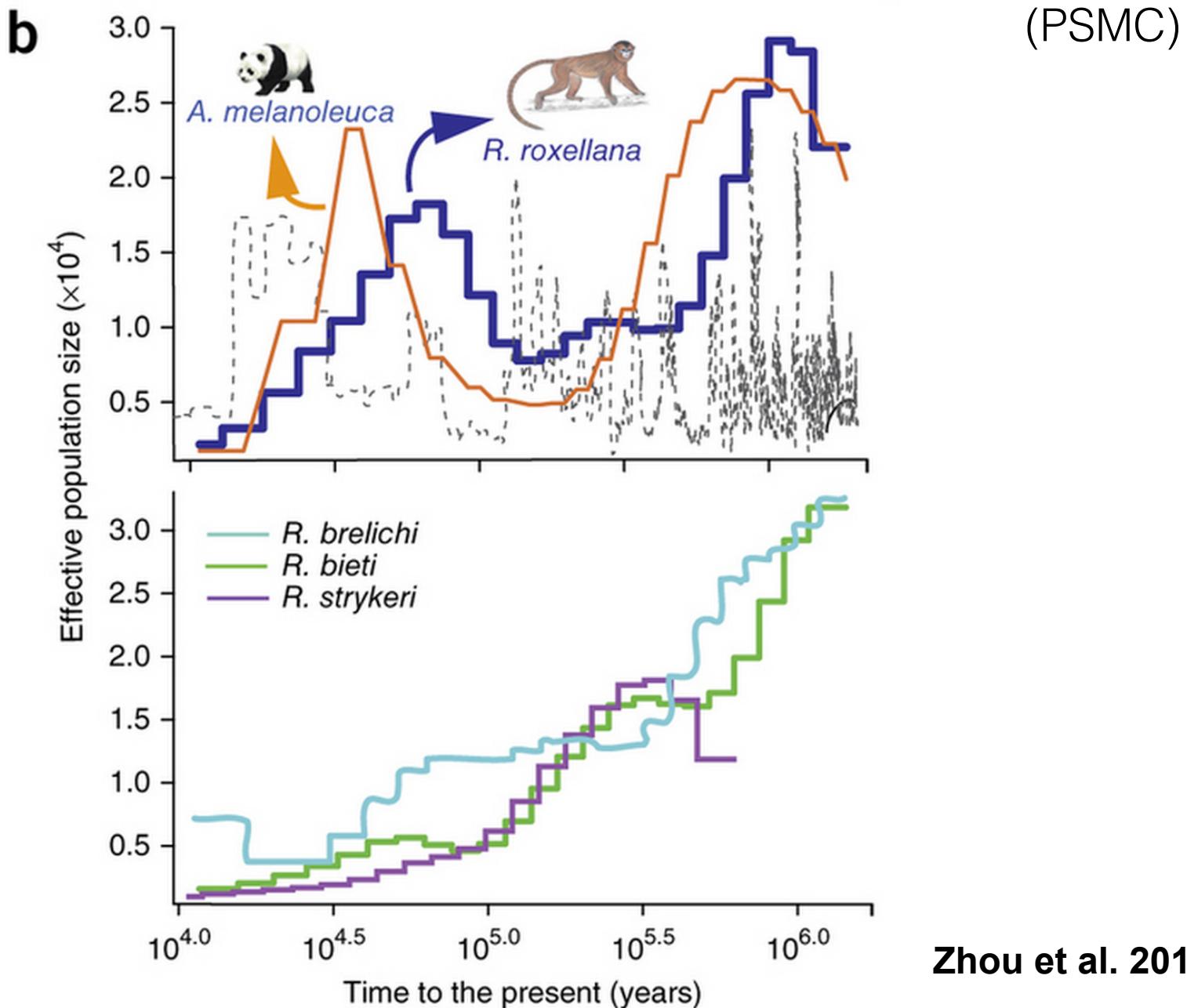
C



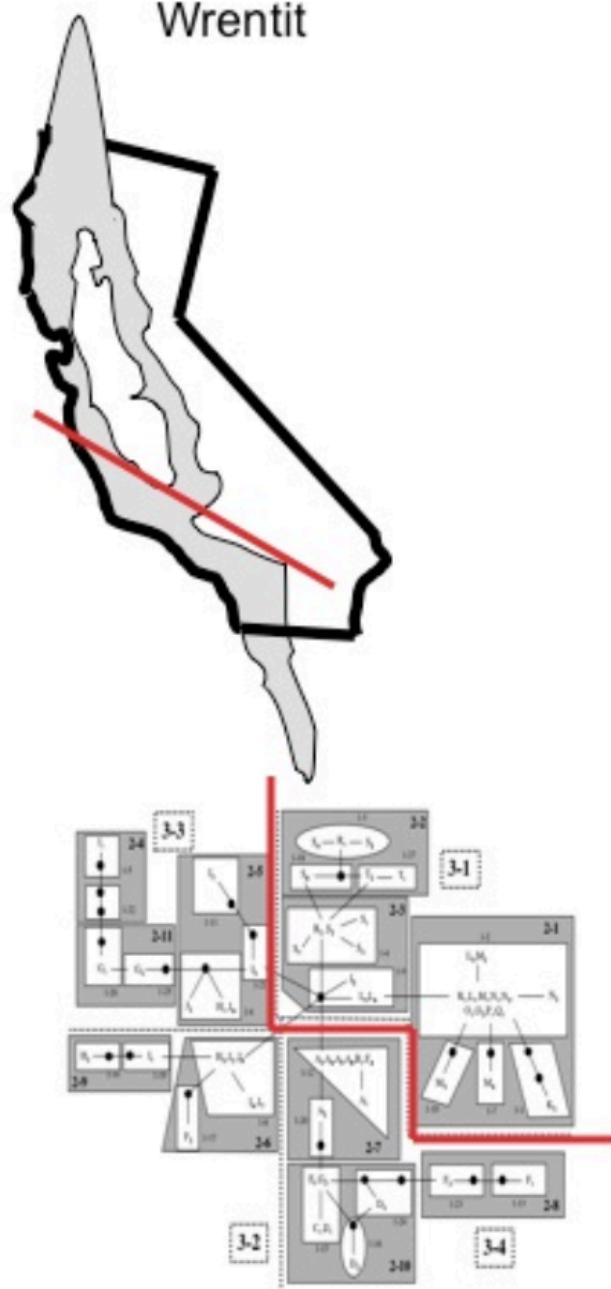
i.e. stepping back and looking at the combined
results of multiple phylogeographic studies

whole genome approach

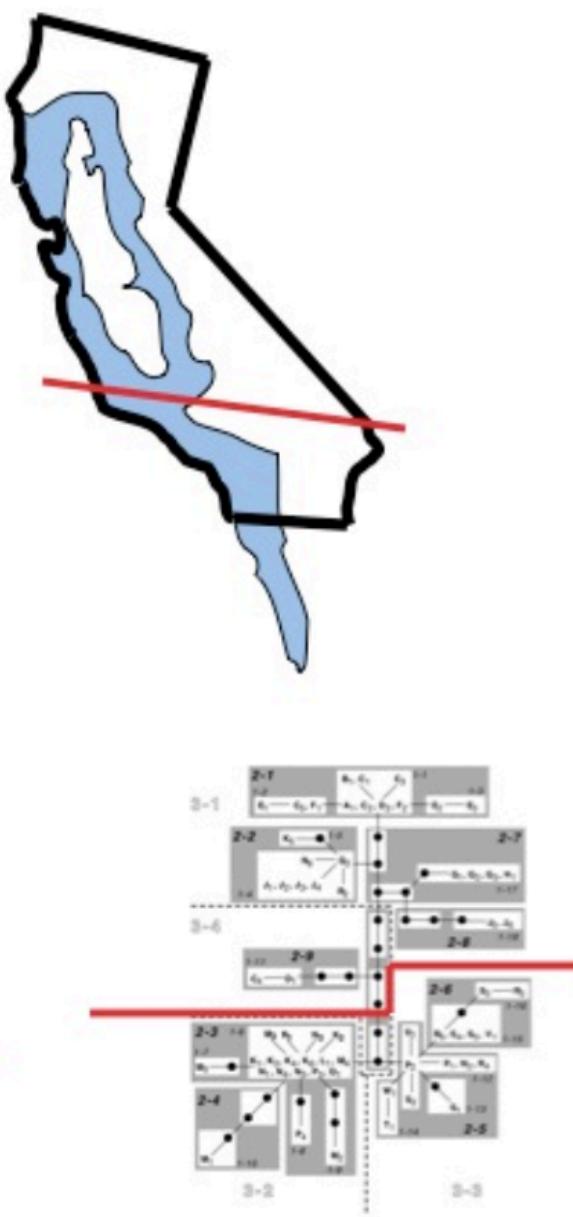
Comparative population genetics w/genomes



Wrentit



California Thrasher



White-headed Woodpecker

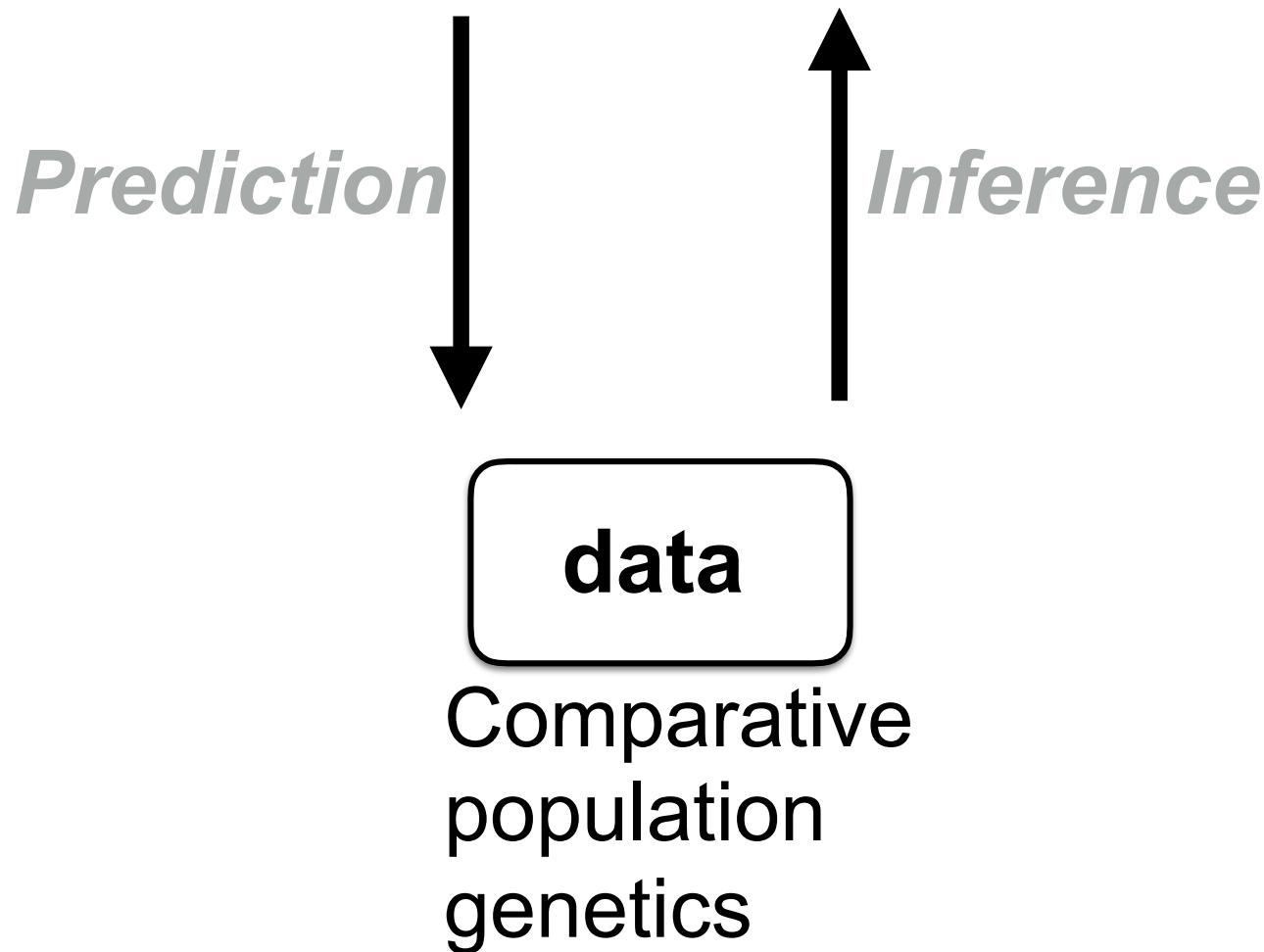




Comparative Phylogeography of California Avifauna, from Burns et al. (2007)

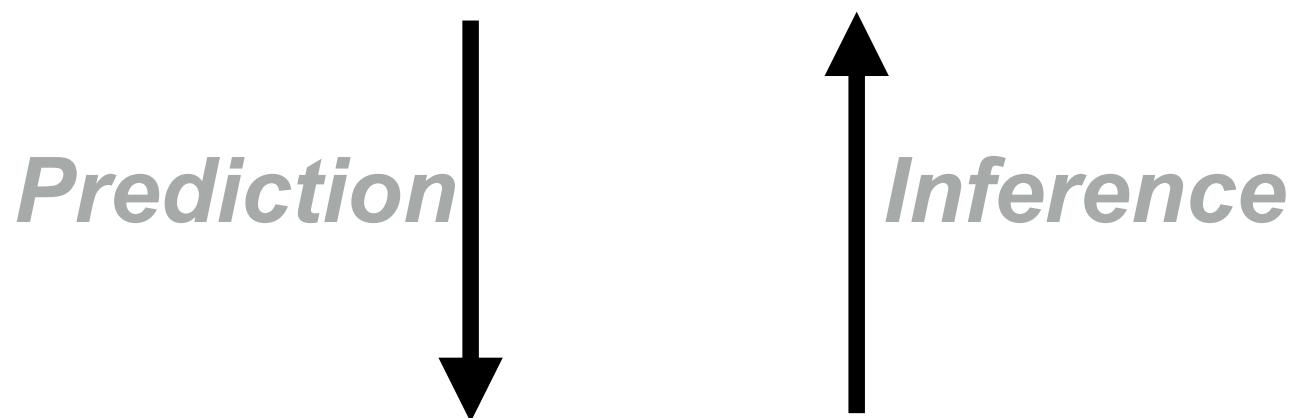
assemblage
history

Coalescent Model



assemblage
history

Coalescent Model



Comparative
population
genetics

DNA
barcodes
(ie mtDNA)

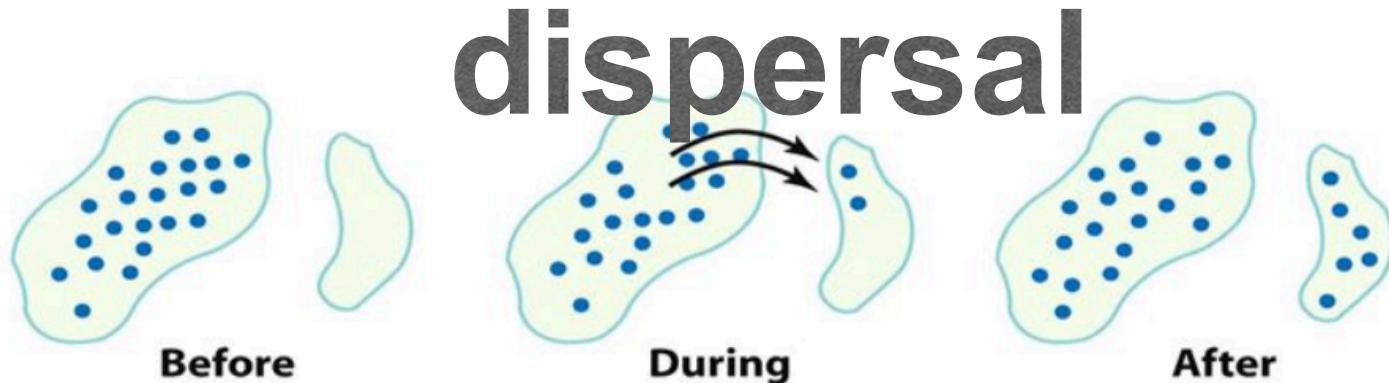
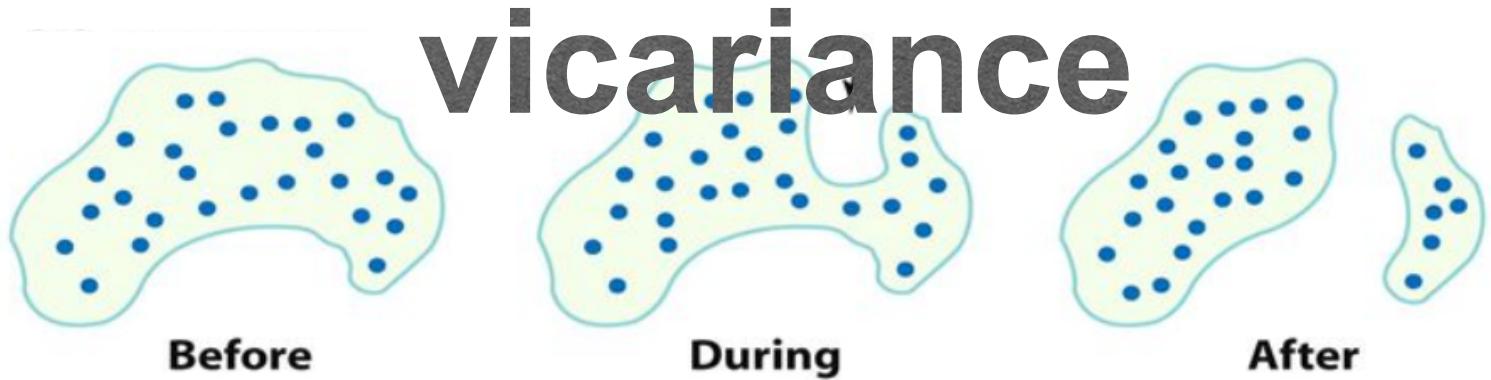
“whole”
genomes

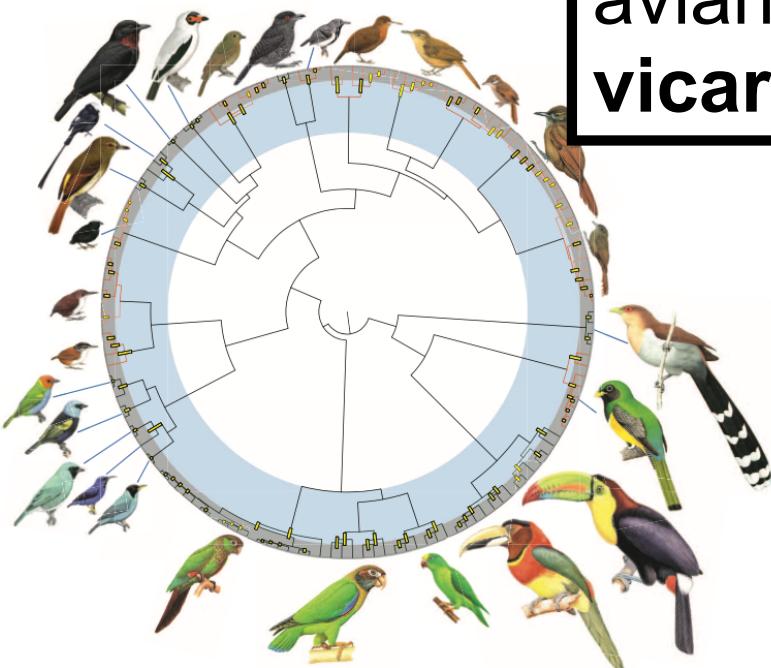
Central Questions of Comparative Phylogeography

1. vicariance or dispersal?

2.

3.





avian diversification from
vicariance or dispersal?

The drivers of tropical speciation

Brian Tilston Smith, John E. McCormack, Andrés M. Cuervo, Michael J. Hickerson, Alexandre Aleixo, Carlos Daniel Cadena, Jorge Pérez-Emán, Curtis W. Burney, Xiaou Xie, Michael G. Harvey, Brant C. Faircloth, Travis C. Glenn, Elizabeth P. Derryberry, Jesse Prejean, Samantha Fields & Robb T. Brumfield ✉

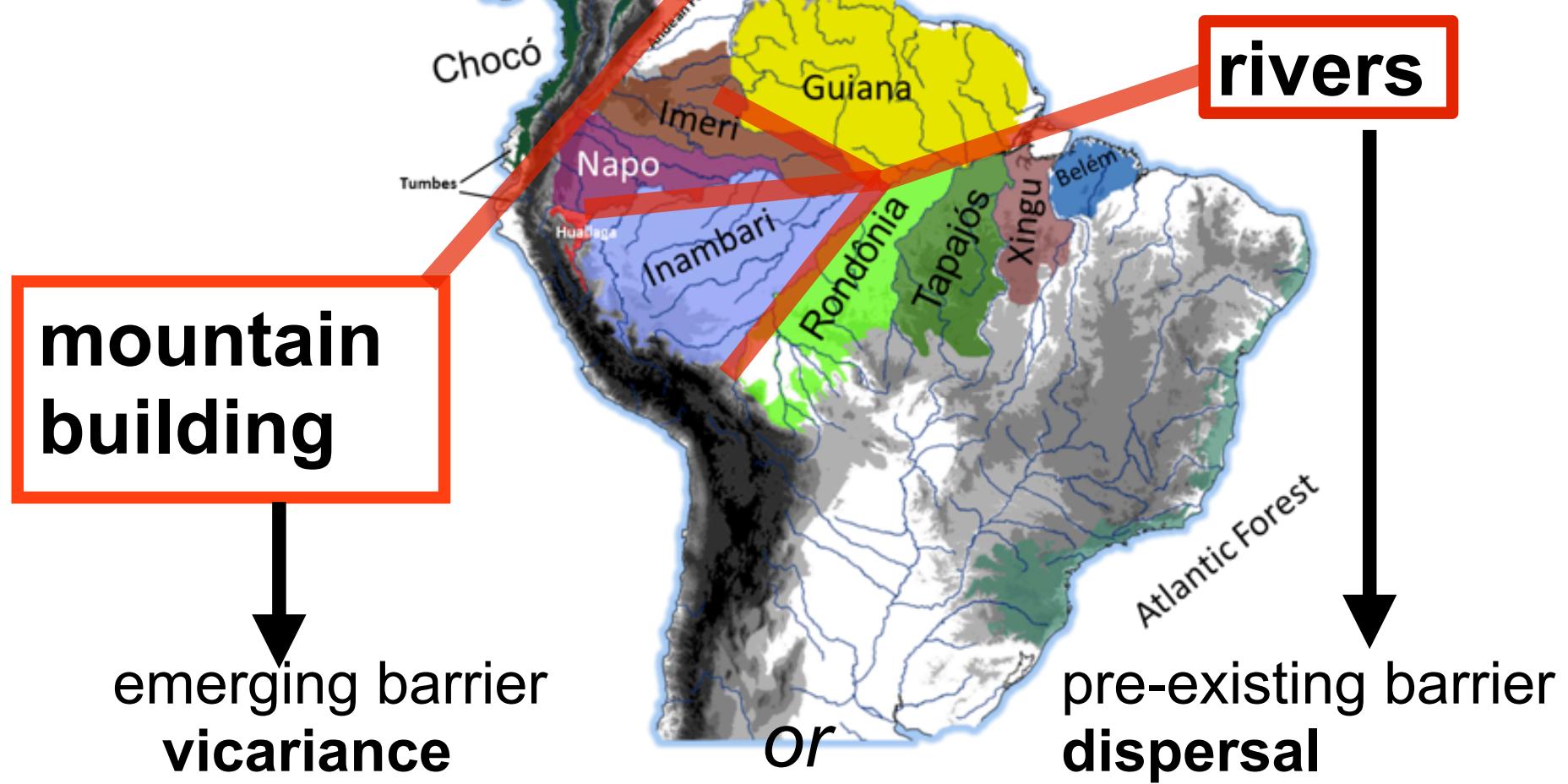
Nature 515, 406–409 (20 November 2014) | Download Citation ↴

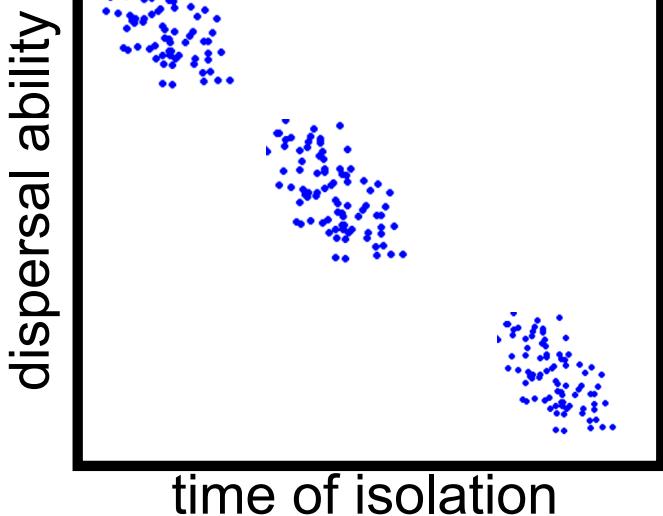
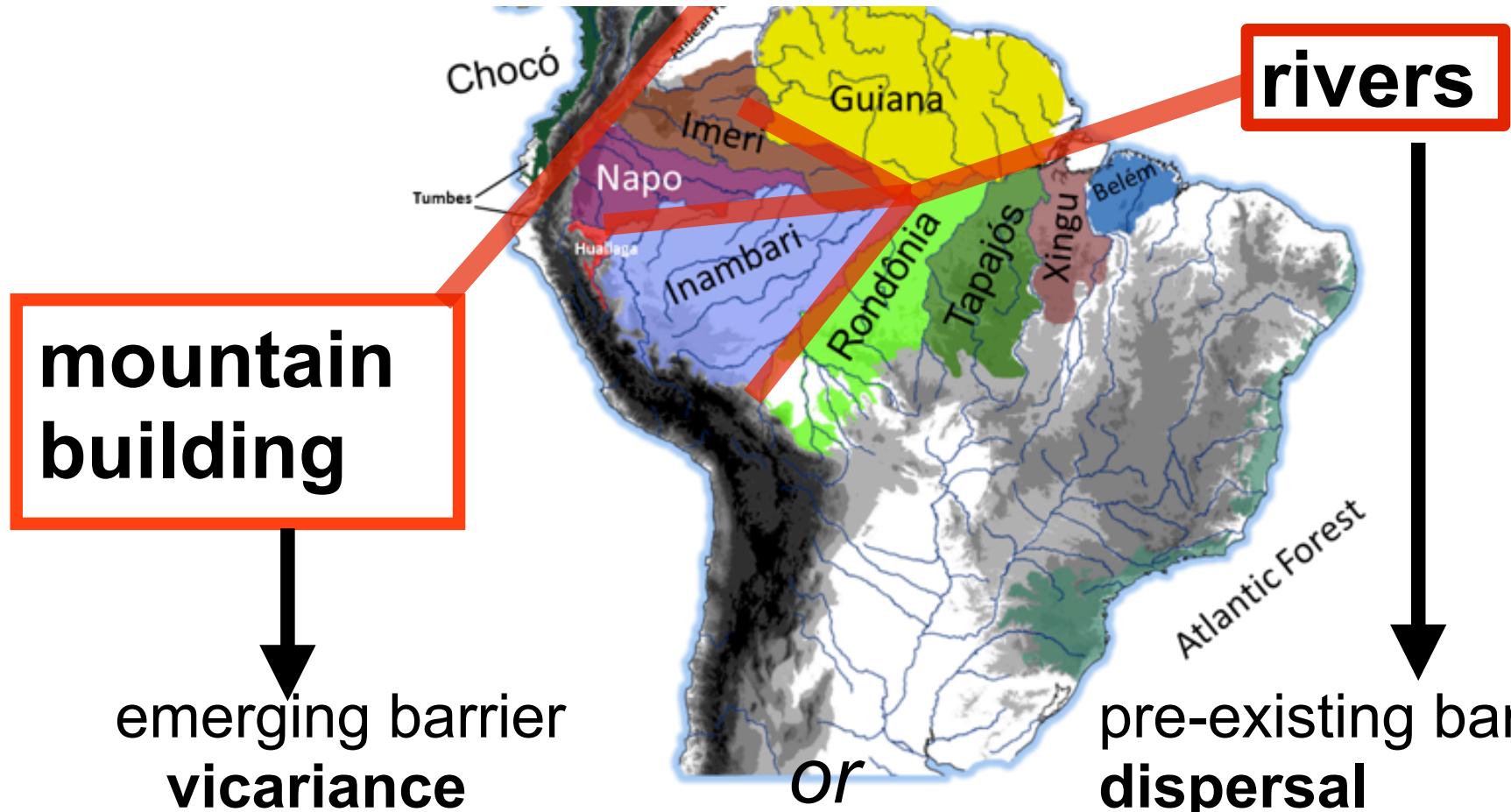


Robb Brumfield - LSU

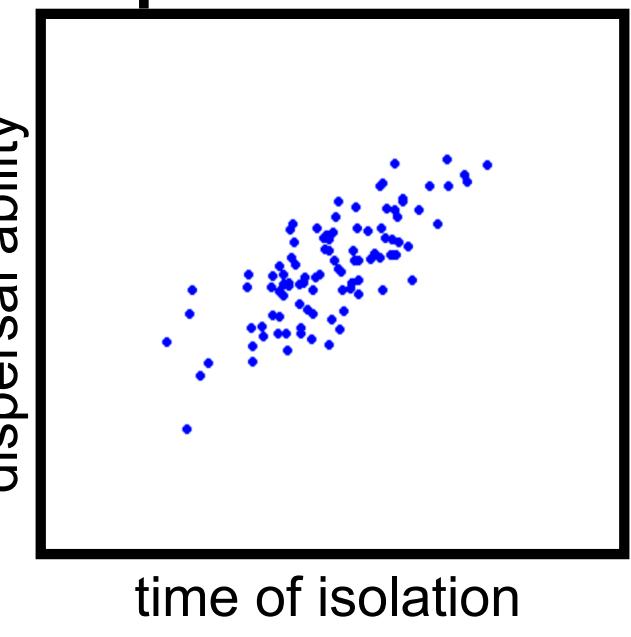


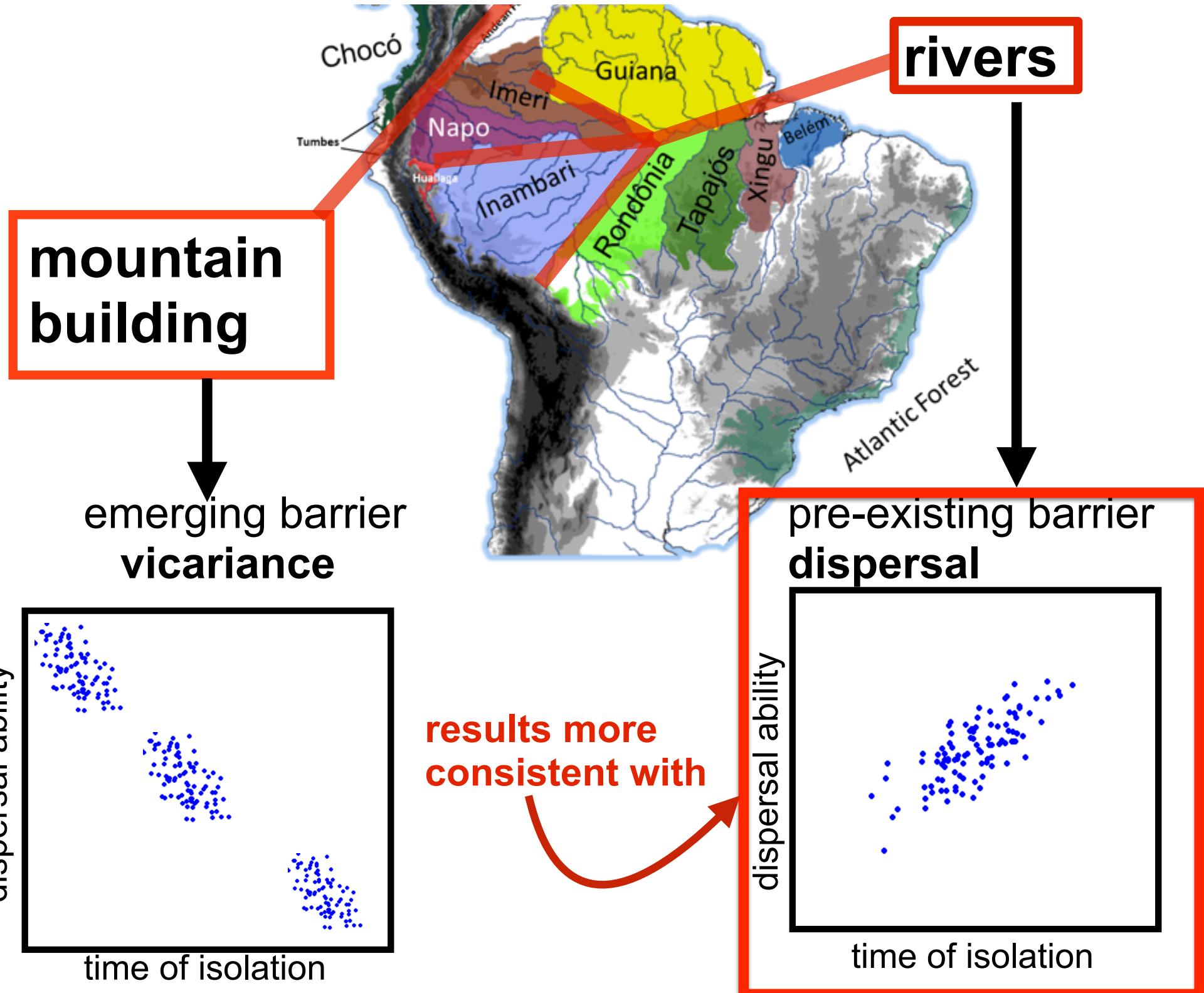
Brian Smith - AMNH





predictions

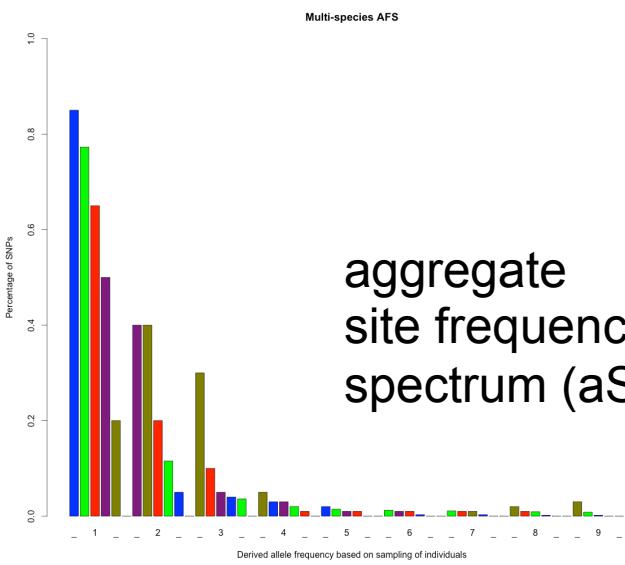




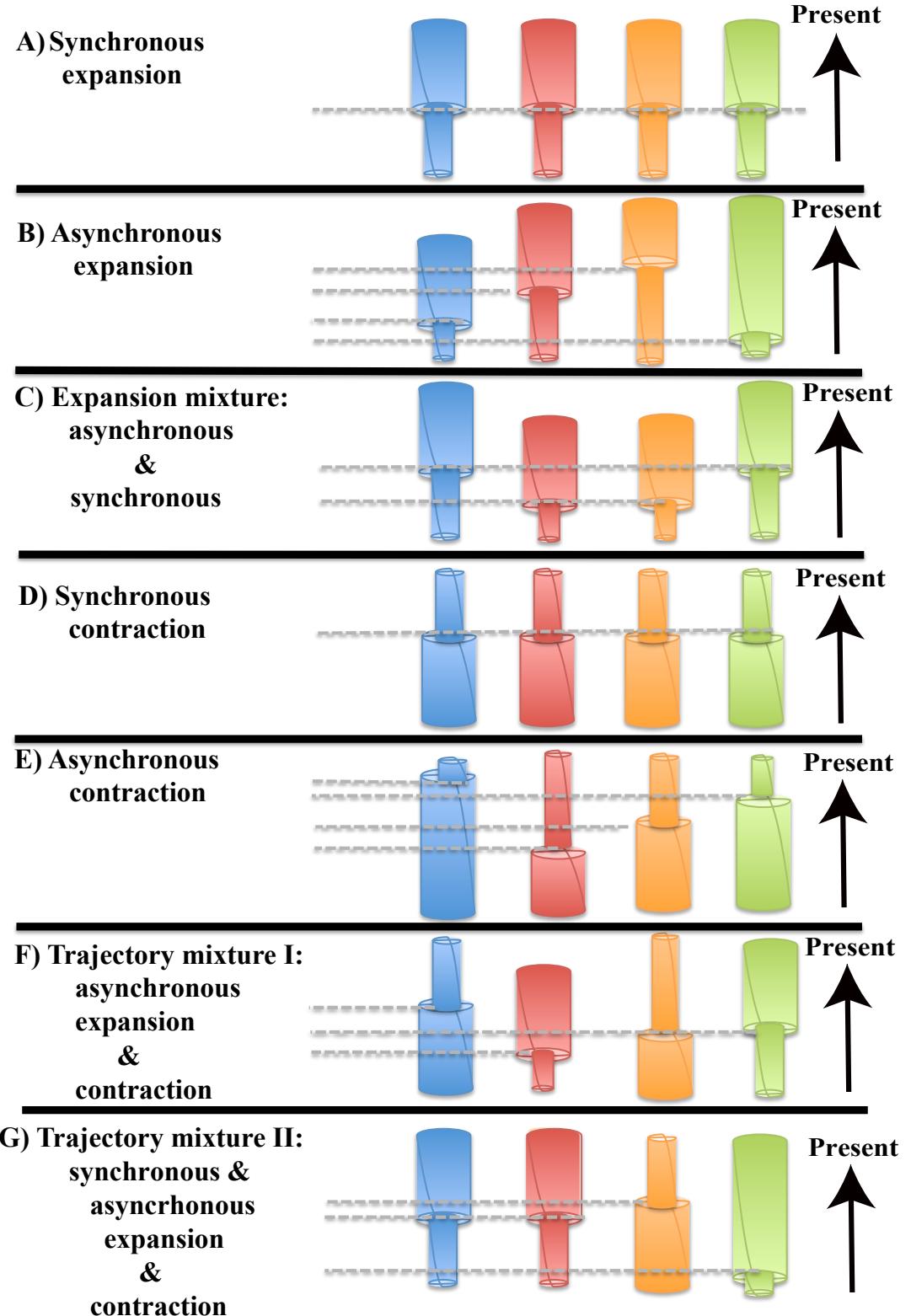
Central Questions of Comparative Phylogeography

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

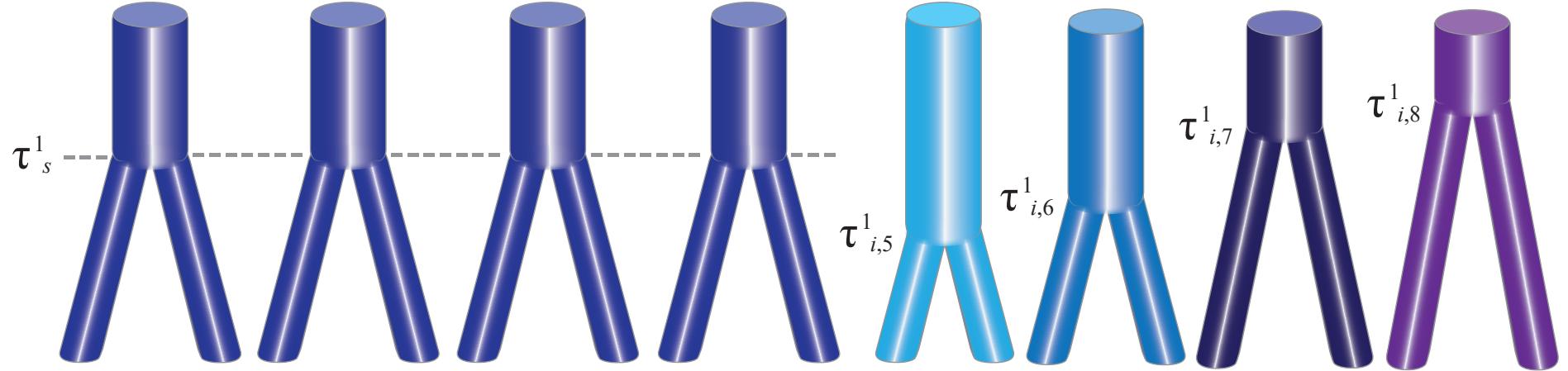
fitting models of co-expansion, co-contraction with SNP data



Alexander Xue



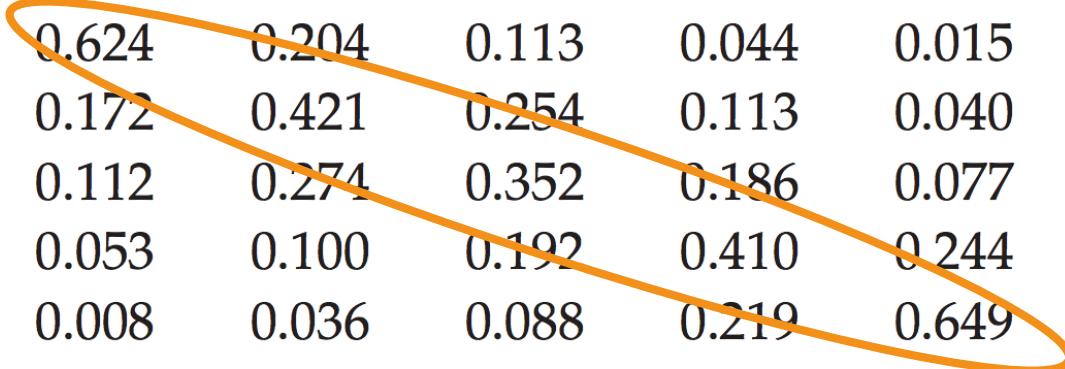
fitting models of co-divergence with SNP data



Alexander Xue

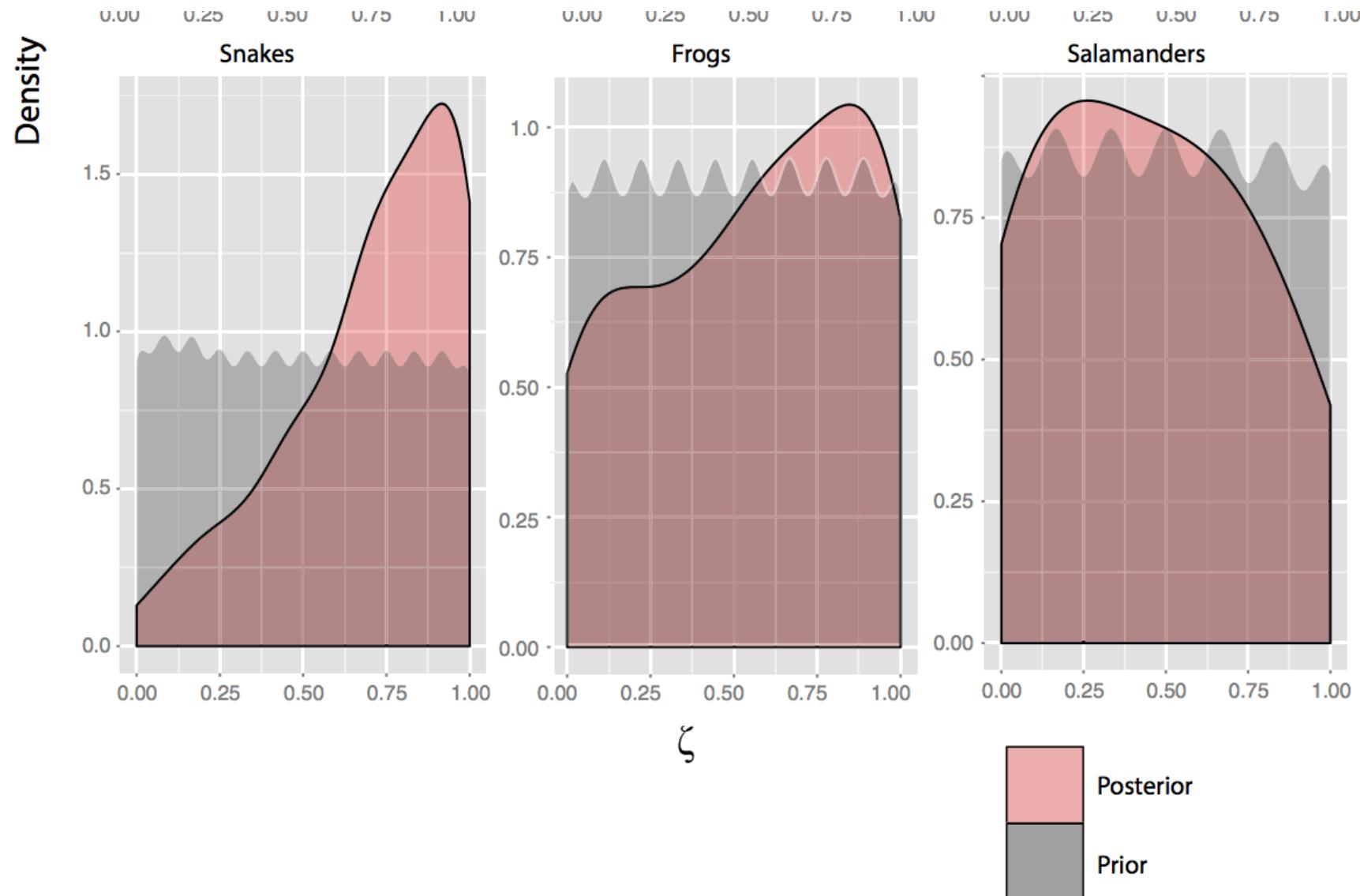
fitting co-demographic models is not easy

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



ζ = % 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-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

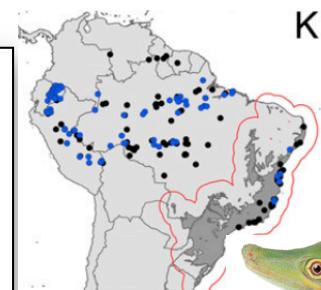
Sally Potter^{1,2} | Alexander T. Xue^{3,4} | Jason G. Bragg^{1,2} | Dan F. Rosauer^{1,2} | Emily J. Roycroft^{5,6} | Craig Moritz^{1,2}



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}



K



Shortcomings (plenty)

too much inferential uncertainty?

model is too simple?

not spatially explicit

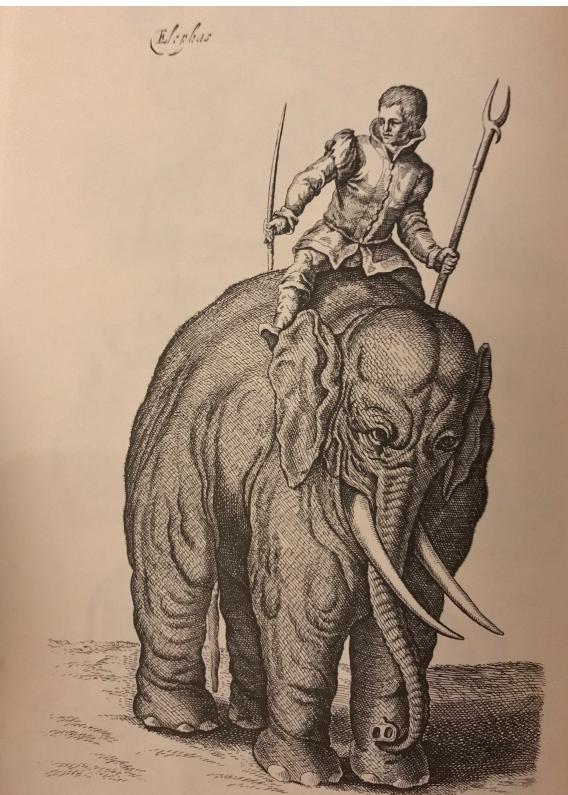
Shortcomings (plenty)

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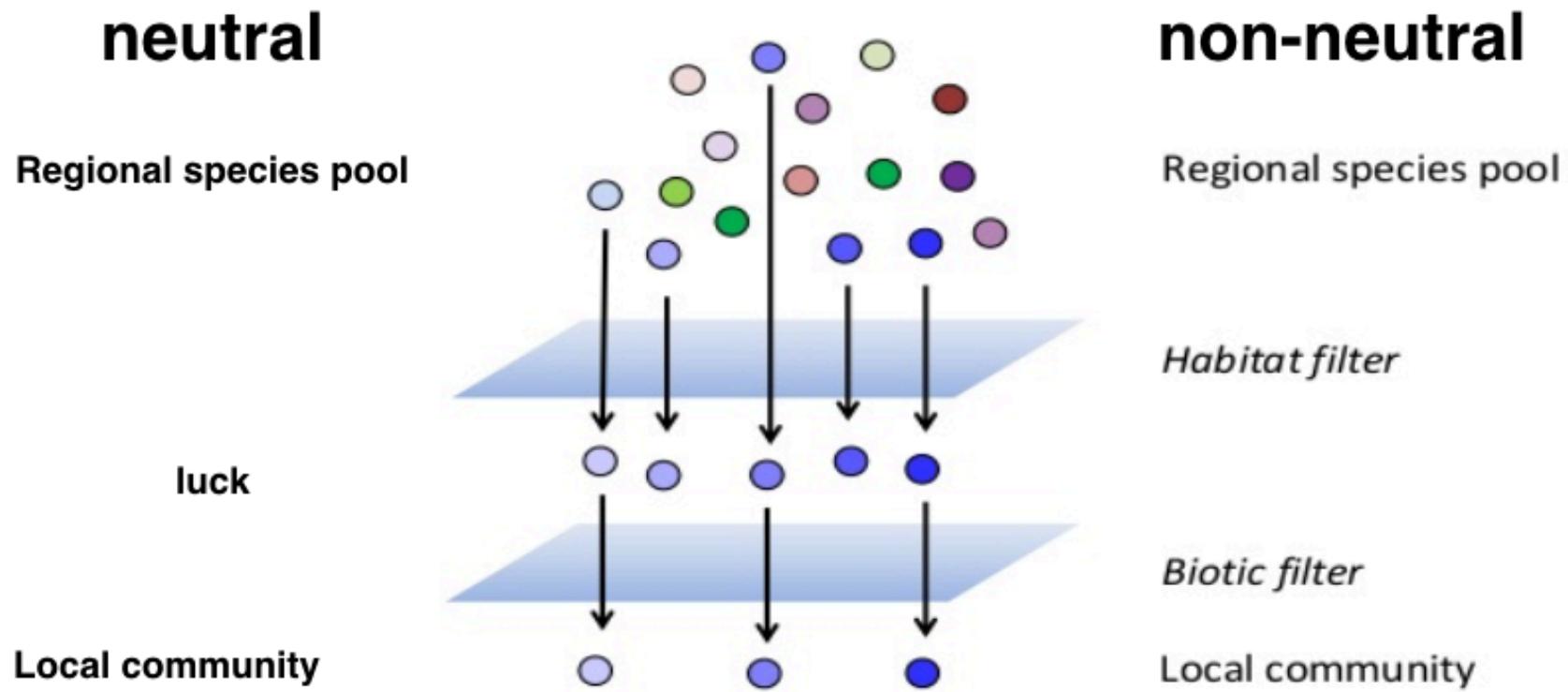
models not grounded in ecological theory



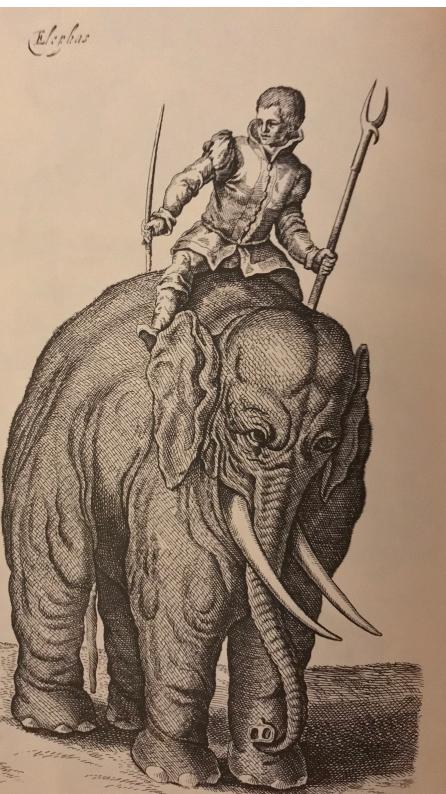
Central Questions of Comparative Phylogeography

1. vicariance or dispersal?
2. synchronous demographic histories?
3. **how deterministic is assembly and/or demographic histories? Do traits matter?**

merging comparative phylogeography & biogeographic assembly theory(ies)



Build Comparative Phylogeography models with ecological theory(ies)??



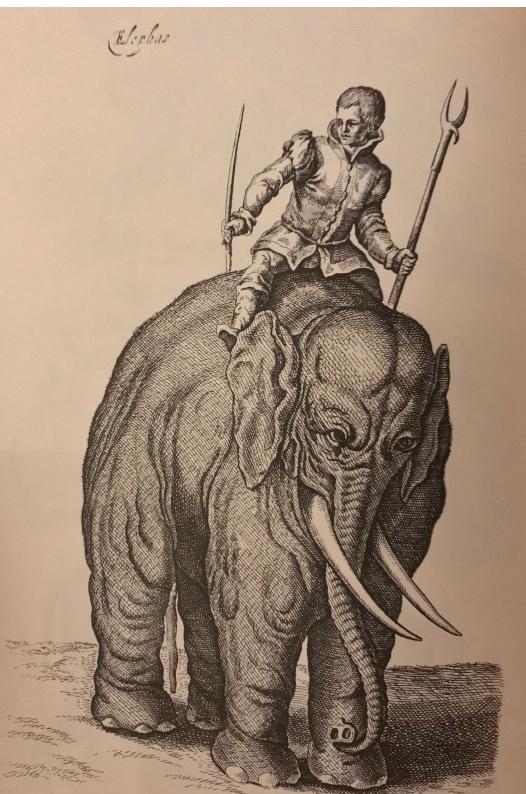
Build Comparative Phylogeography models with ecological theory(ies)??

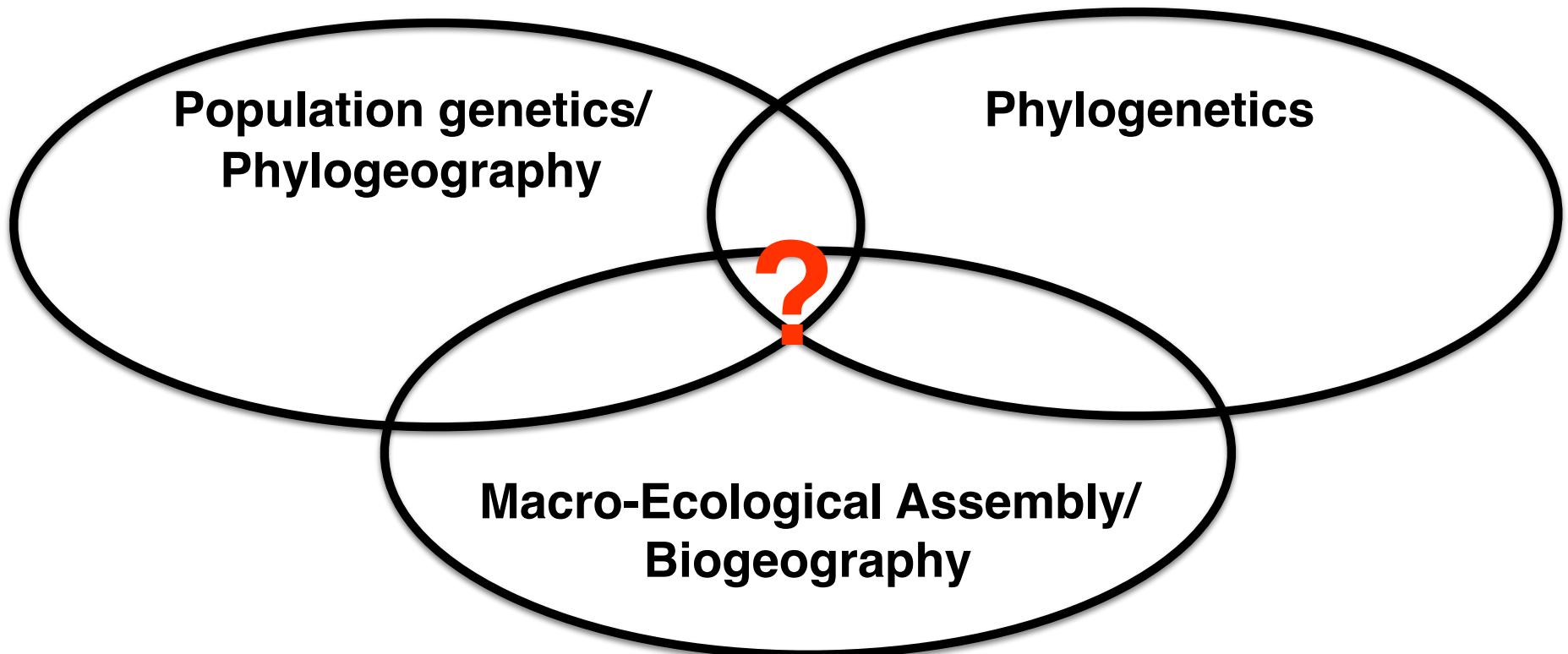
Toward Community Genetics

Janis Antonovics

The Theory of
Ecological Communities

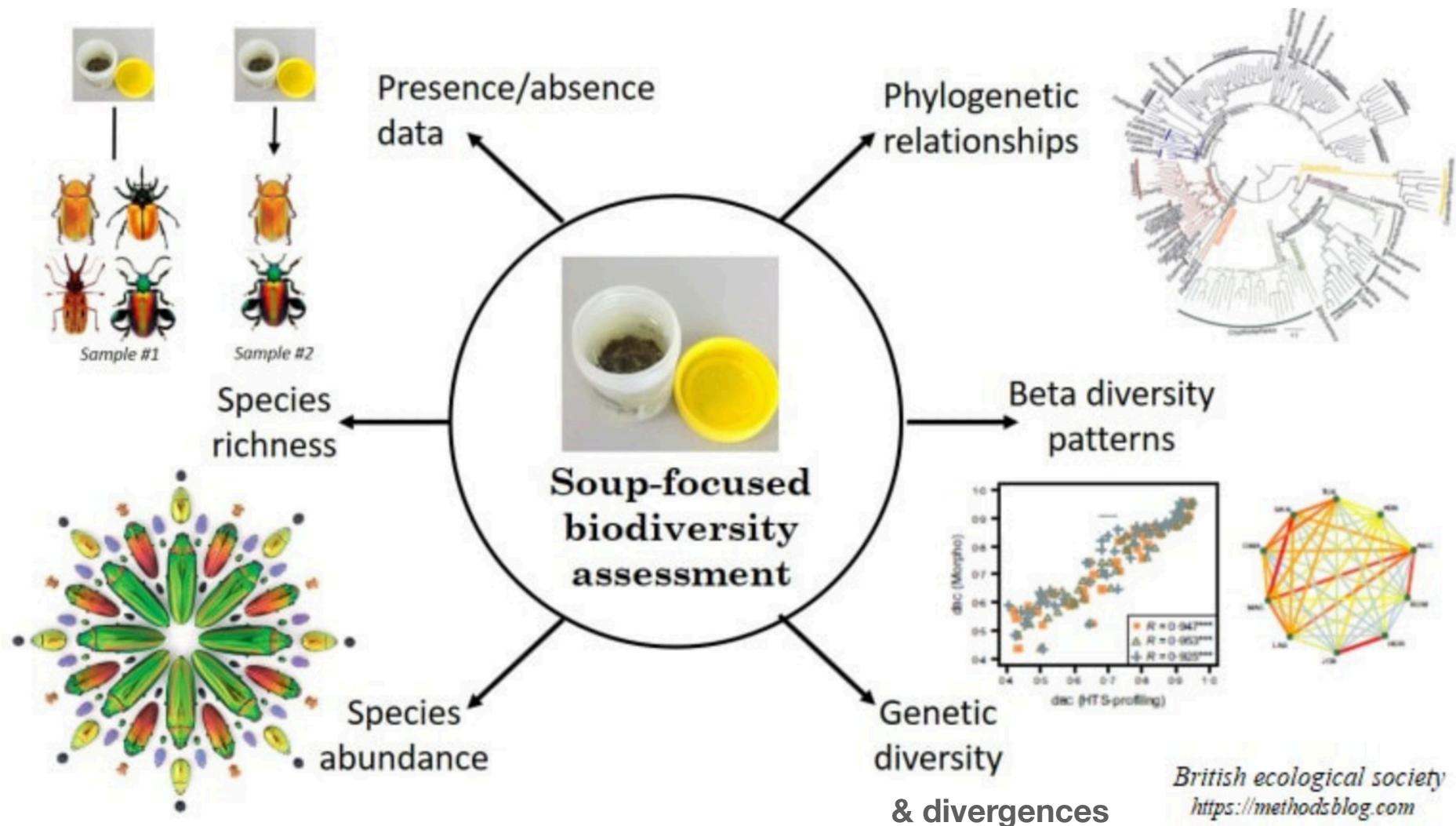
Mark Vellend

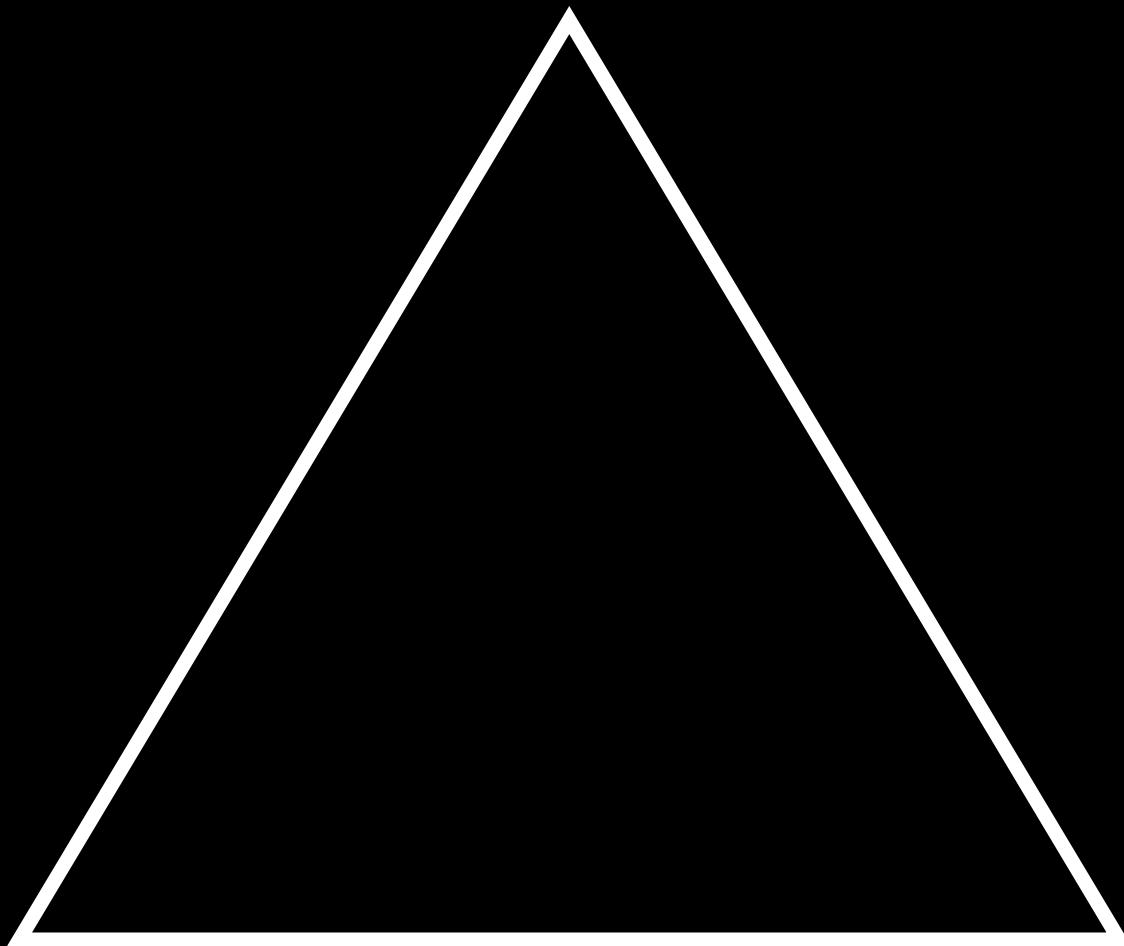




how about the whole enchilada ?

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





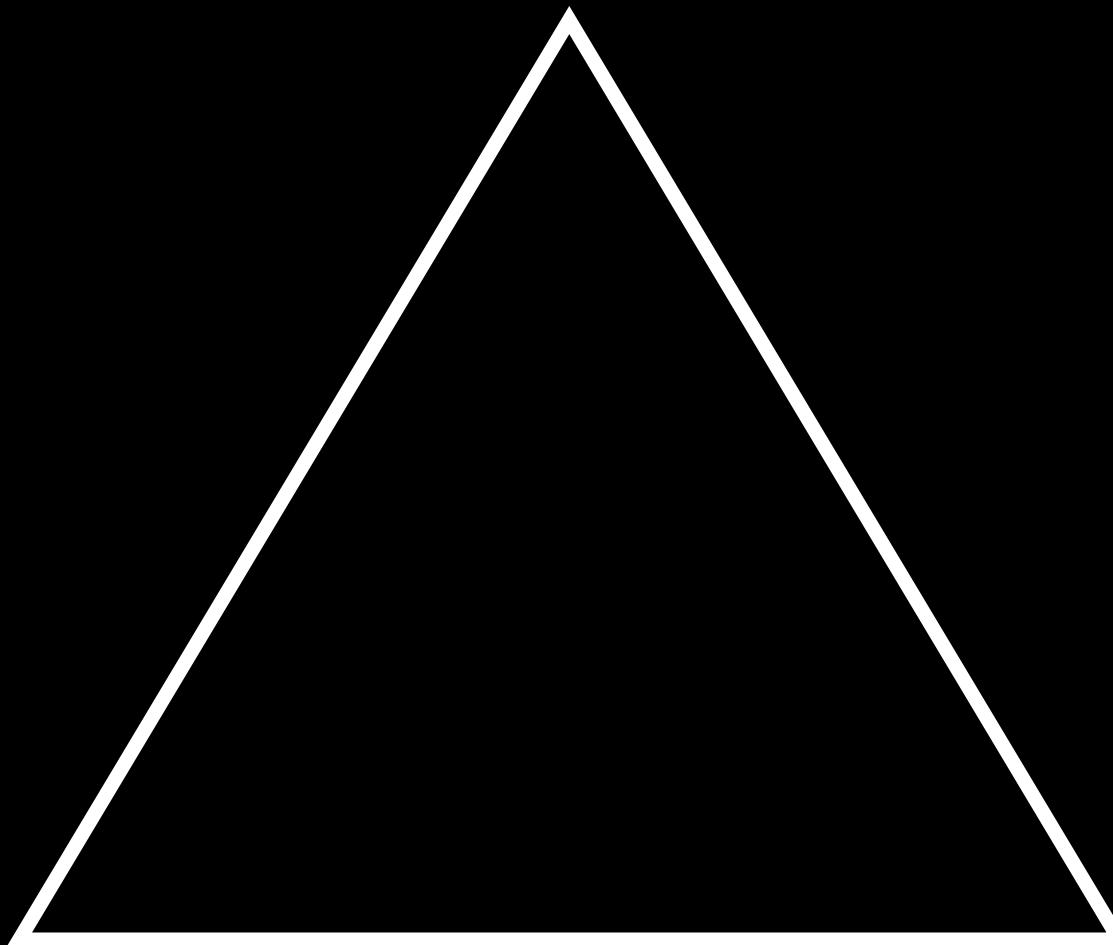
Biodiversity Metrics

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

abiotic variables

bioclimatic variables

remote sensing products



Biodiversity Metrics

Species abundance spectra

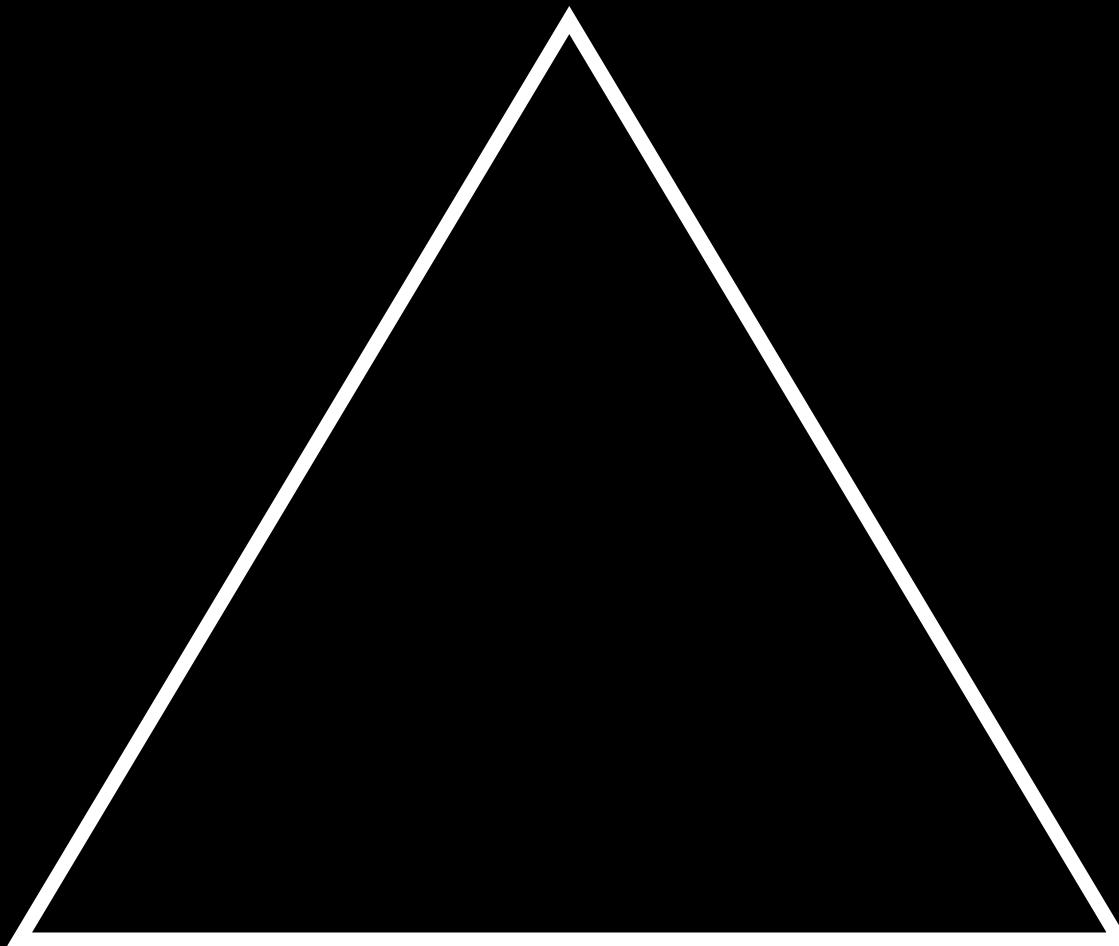
Genetic diversity spectra

Trait diversity spectra

abiotic variables

bioclimatic variables

remote sensing products



**Historical-Biogeographic
Processes**

**Biodiversity
Metrics**

Species abundance spectra

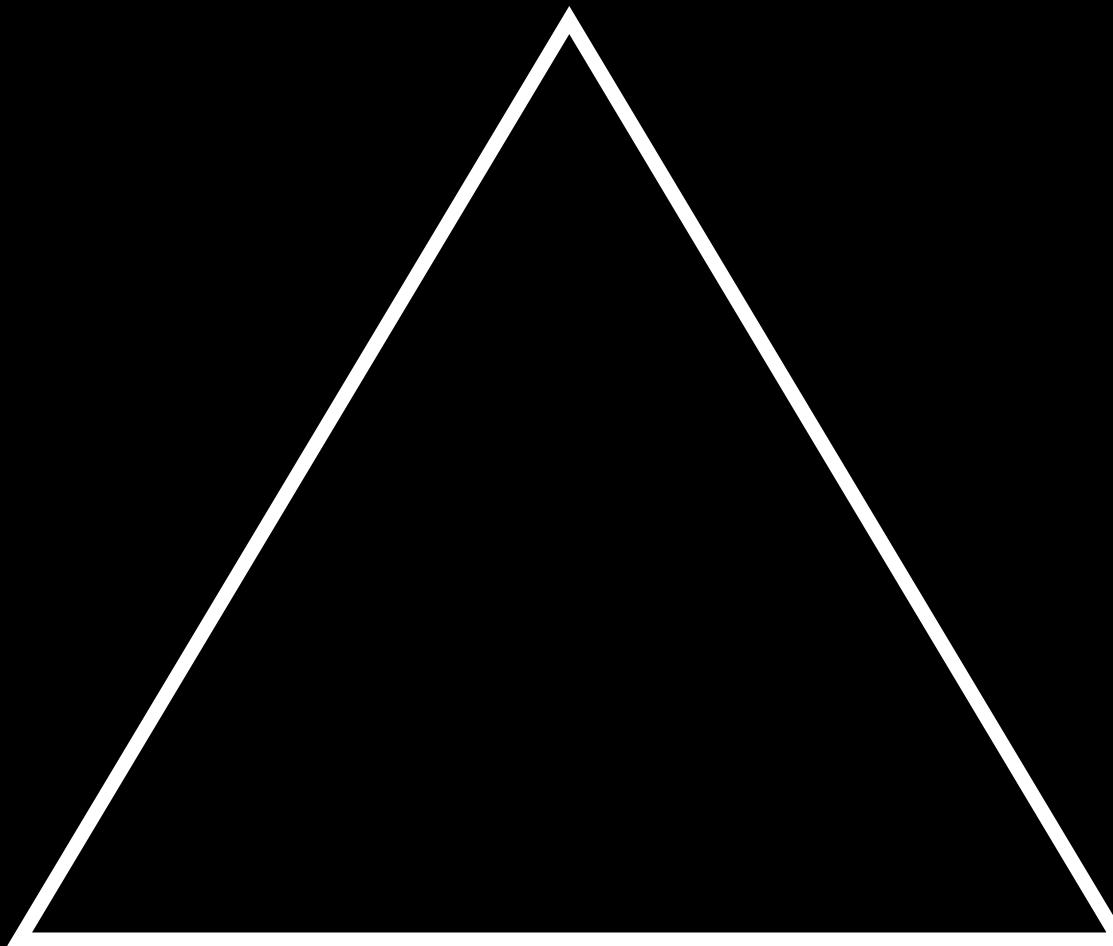
Genetic diversity spectra

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



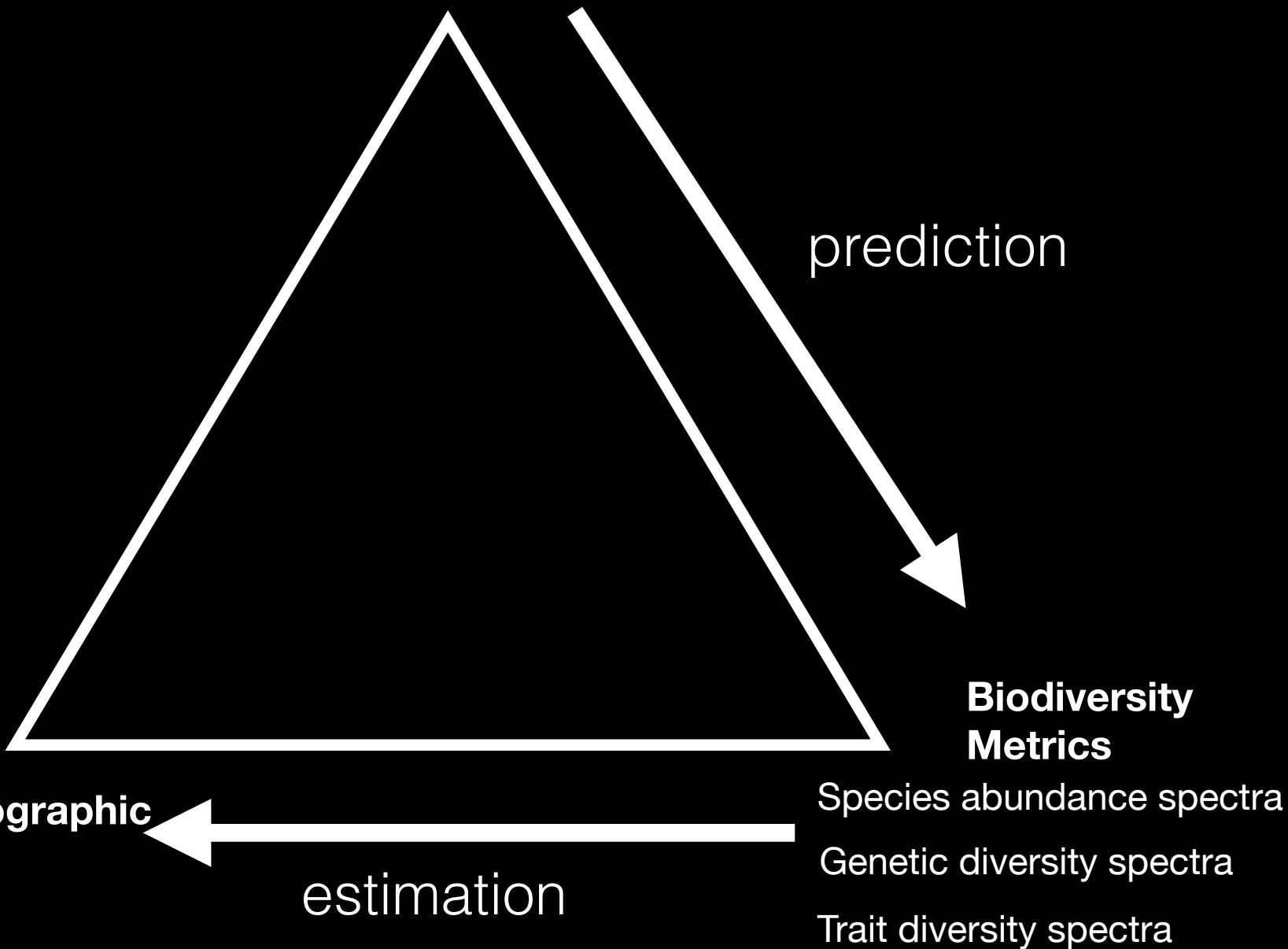
Isaac Overcast
CUNY

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



abiotic variables

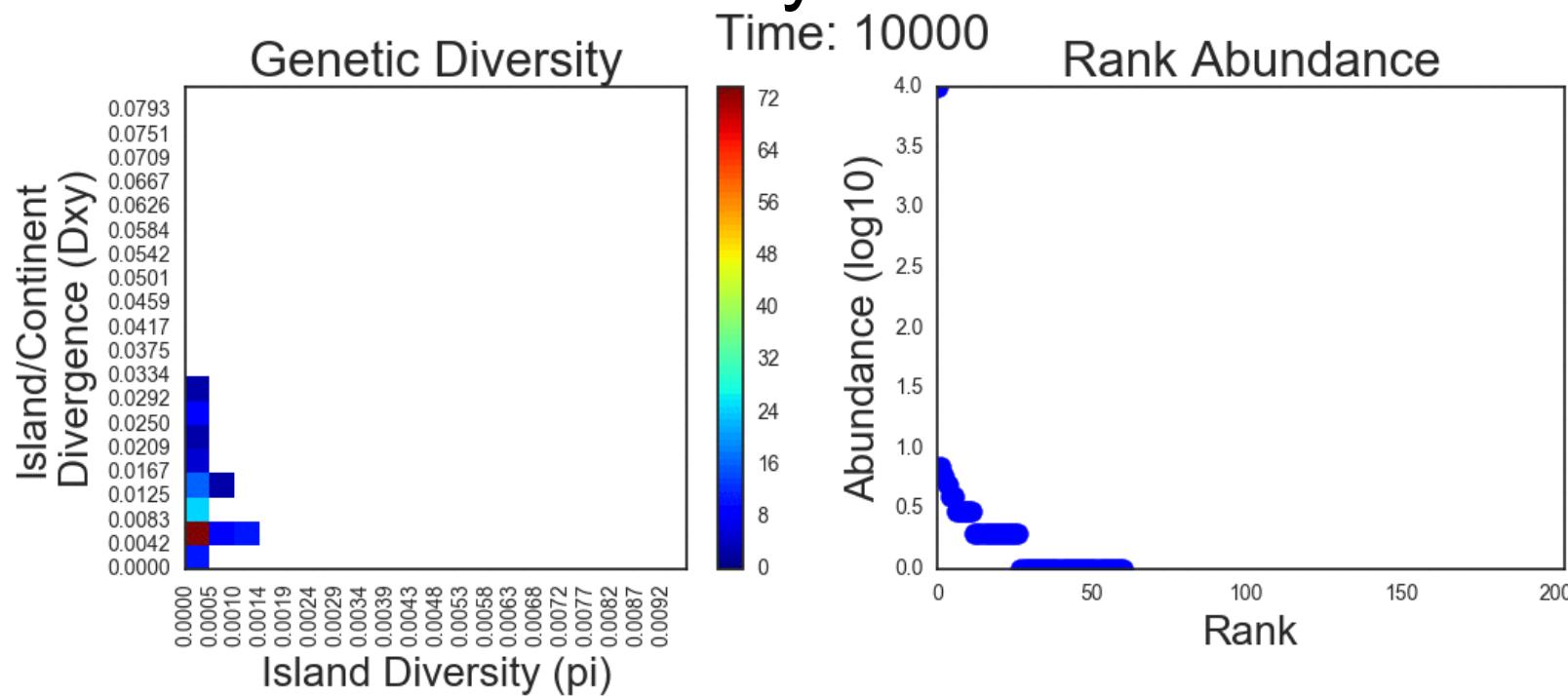
bioclimatic variables
remote sensing products



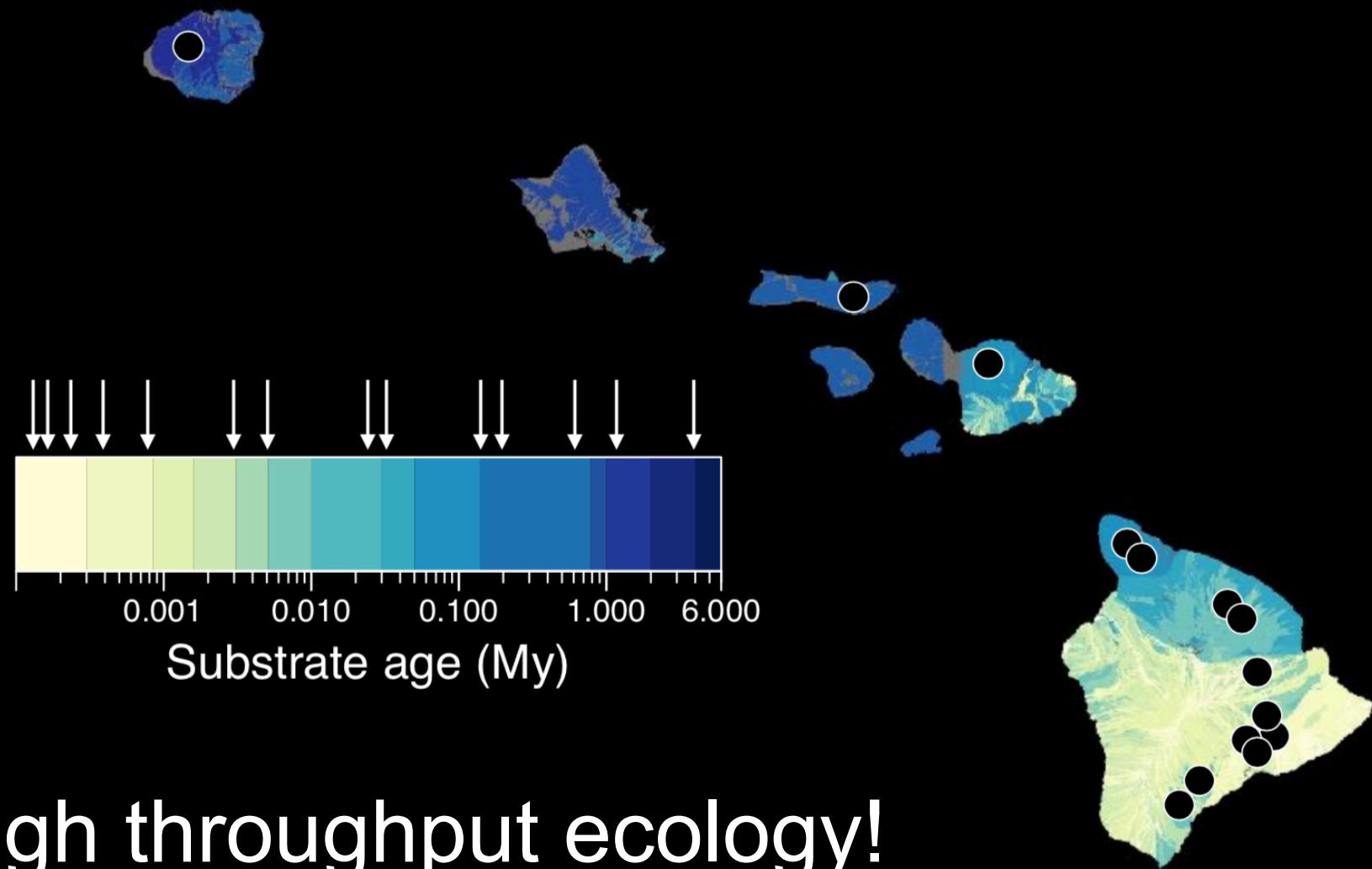


Isaac Overcast
CUNY

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



community scale data??
(richness, abundance, pop genetics and
traits?)



high throughput ecology!

High throughput pipeline



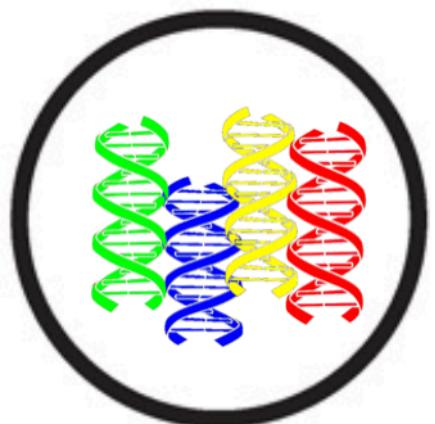
Specimen sorting



Measuring & photographing



DNA extraction



Multiplex PCR



Illumina sequencing

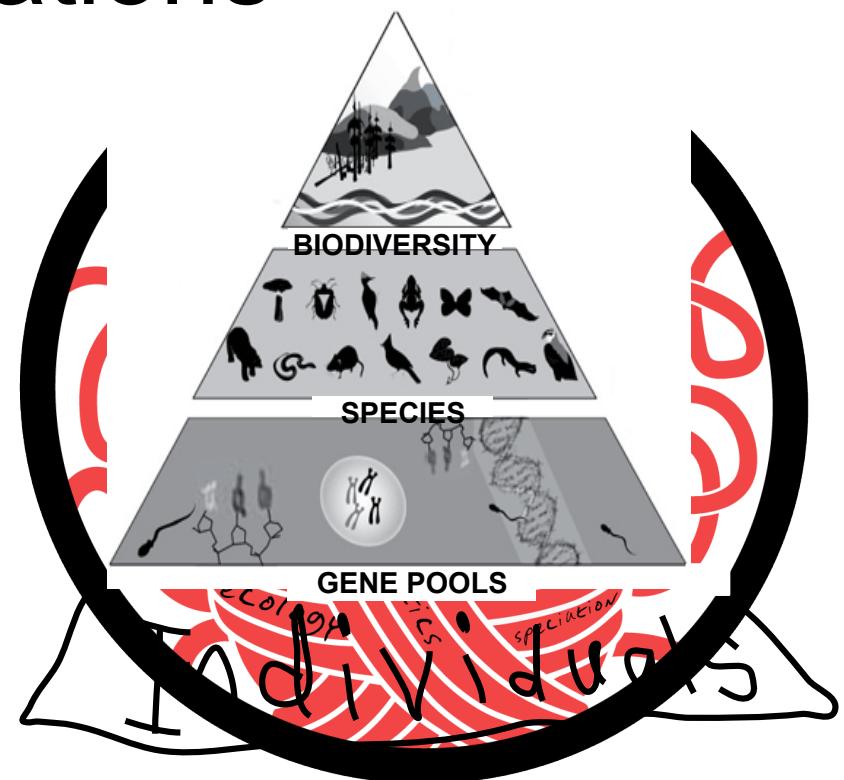


Computational analysis

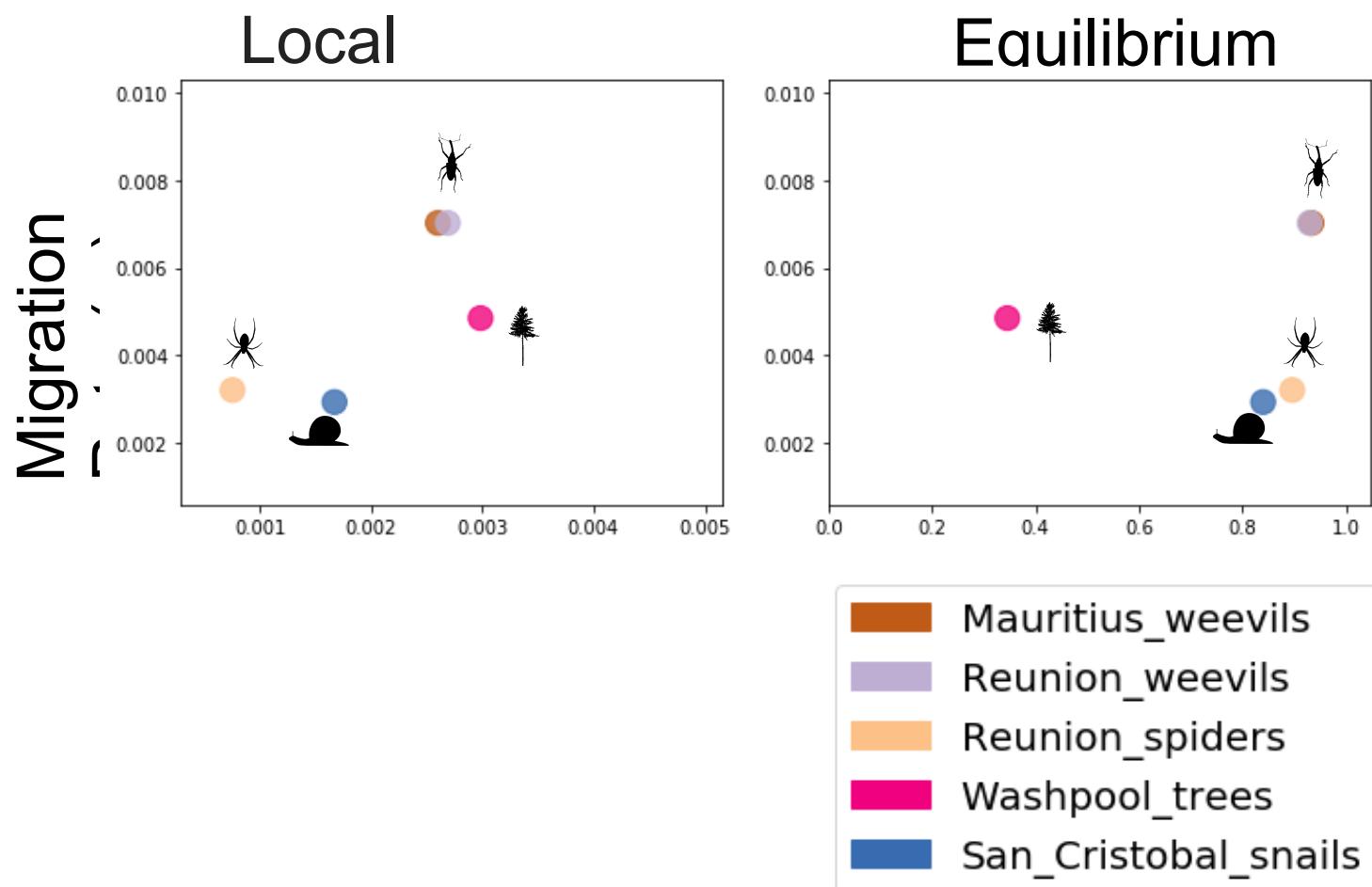
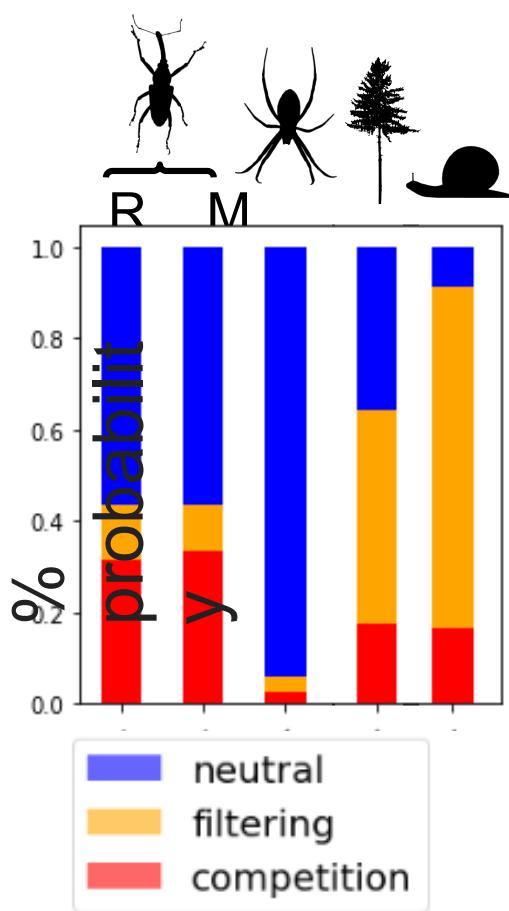
Ccdb.ca, Illumina.com, dna-barcoding.blogspot.com

Histograms Massive Eco-evolutionary Synthesis integrated Simulations joint community- scale predictions of: **MESS**

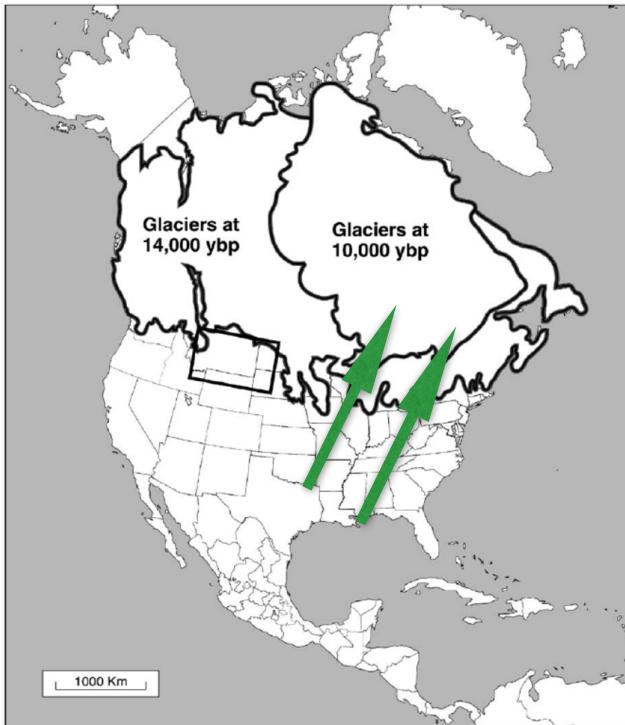
- Abundances
- Genetic diversities
- Phylogenies
- Trait values



MESS Empirical Inference



ABC - how simple can it be?



- How did a temperate assemblage respond to Holocene warming?

Ecology Letters, (2016)

doi: 10.1111/ele.12695

LETTER

Asynchronous demographic responses to Pleistocene climate change in Eastern Nearctic vertebrates

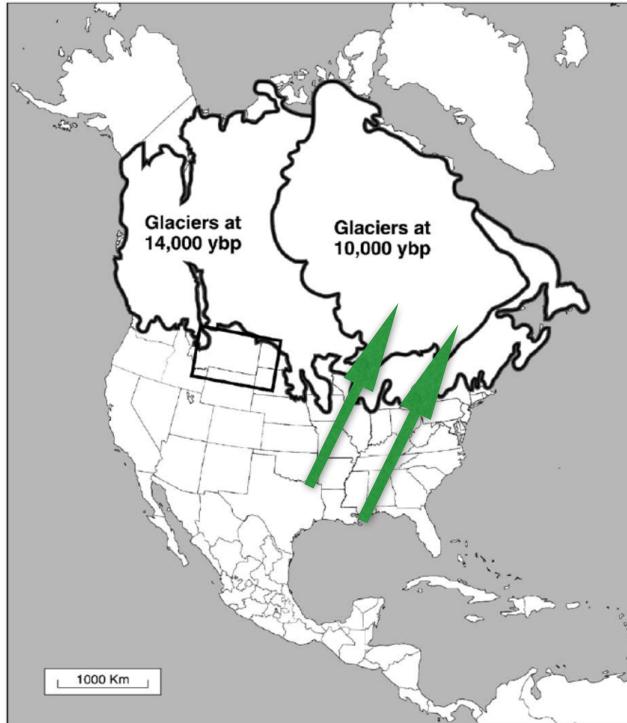
Frank T. Burbrink,^{1*} Yvonne L. Chan,² Edward A. Myers,^{3,4} Sara Ruane,⁵ Brian Tilston Smith⁶ and Michael J. Hickerson^{4,7,8}



Yvonne Chan - U.Hawaii



Brian Smith - AMNH



Frank Burbrink - AMNH

- How did a temperate assemblage respond to Holocene warming?

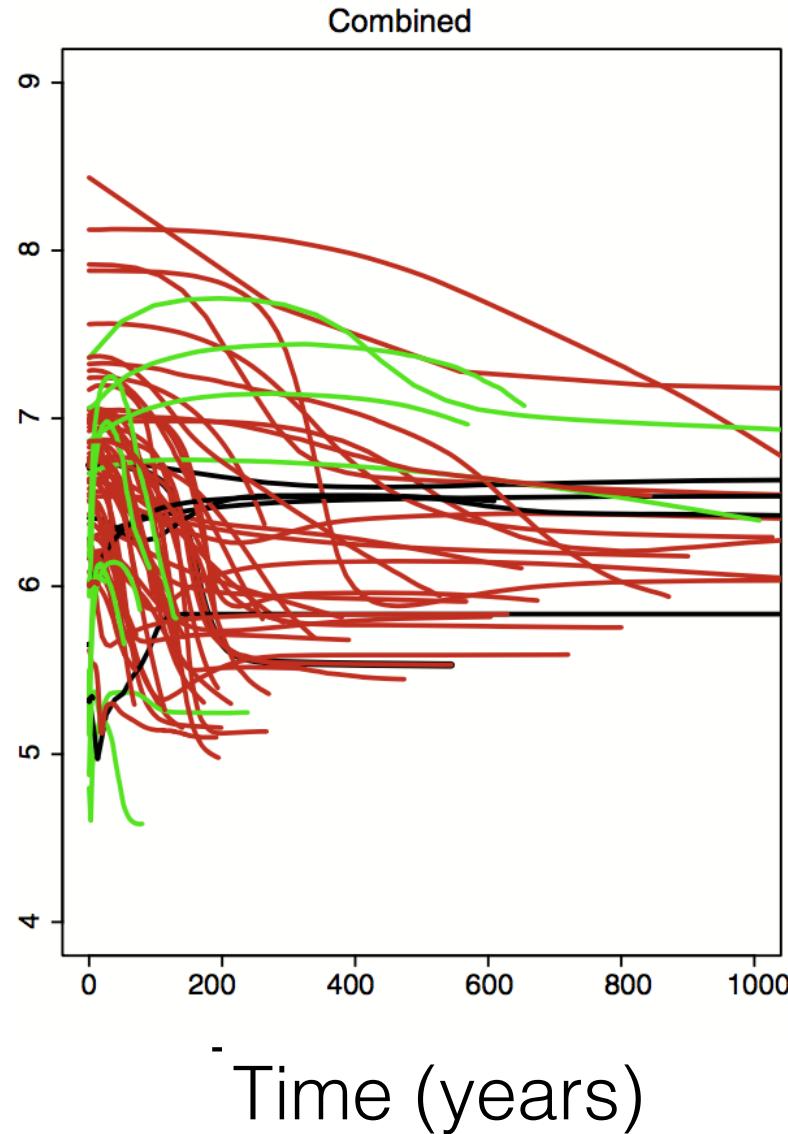
90 lineages:

birds
mammals
frogs
salamanders
lizards
snakes

mtDNA
10 - 400 individuals per taxon
hierarchical Bayesian model

> 90 Skyline plots (eastern Nearctic - w/ mtDNA)

Effective
Pop Size

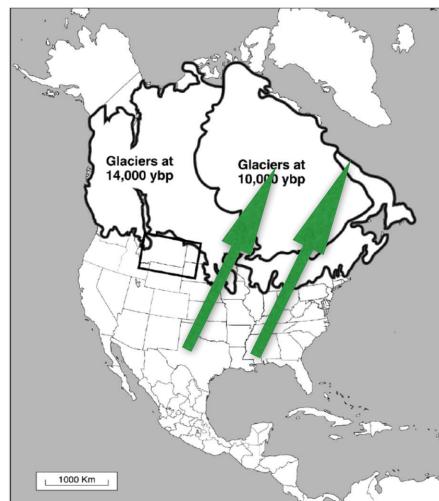


- Impractical for large number of species
- Difficult to statistically compare results

hierarchical Bayesian model

$$P(\zeta, \tau, \phi \mid \text{Data}) \propto p(\text{Data} \mid \zeta, \tau, \phi) = p(\text{Data} \mid \phi, \tau) p(\phi) p(\tau \mid \zeta) p(\zeta)$$

flexible
within species uncertainty
across species estimates



Chan et al. 2014

Xue and Hickerson 2014

Xue and Hickerson 2017

hierarchical Bayesian model

$$P(\zeta, \tau, \phi \mid \text{Data}) \propto p(\text{Data} \mid \zeta, \tau, \phi) = p(\text{Data} \mid \phi, \tau) p(\phi) p(\tau \mid \zeta) p(\zeta)$$

hyperparameters

ζ = Co-expansion Proportion

τ_s = Co-expansion time



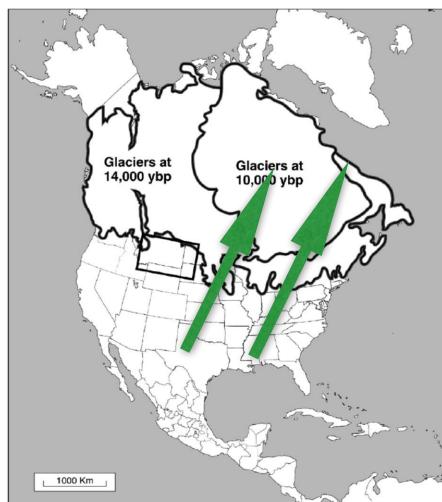
species-specific parameters (ϕ, τ)

τ = expansion times

$\{\tau_1, \dots, \tau_n\}$

$\phi = N$, expansion magnitudes (independent)

$\{\phi_1, \dots, \phi_n\}$ $\{N_1, \dots, N_n\}$



Chan et al. 2014

Xue and Hickerson 2014

hierarchical Bayesian model

$$P(\zeta, \tau, \phi \mid \text{Data}) \propto p(\text{Data} \mid \zeta, \tau, \phi) = p(\text{Data} \mid \phi, \tau) p(\phi) p(\tau \mid \zeta) p(\zeta)$$

hyperparameters

ζ = Co-expansion Proportion

τ_s = Co-expansion time

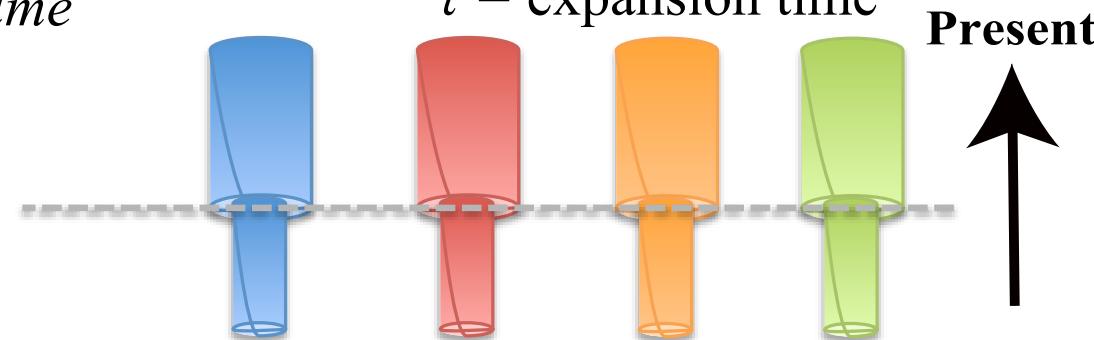
A) Synchronous expansion

$\zeta = 1.0$

species-specific parameters (ϕ, τ)

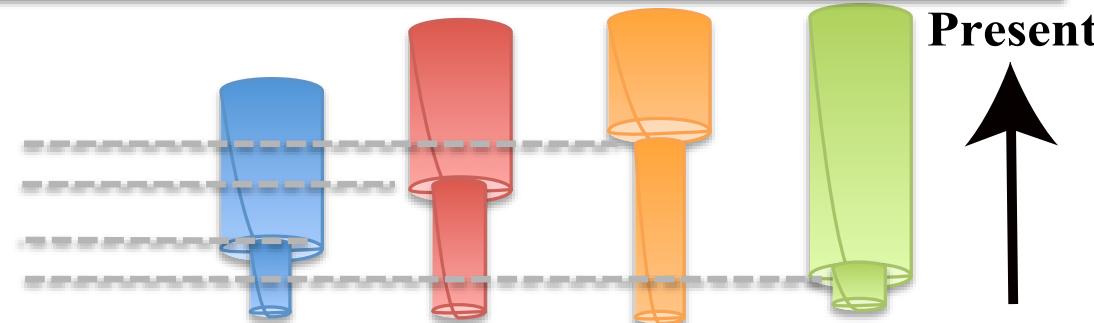
$\phi = N$, expansion magnitude

$\tau =$ expansion time



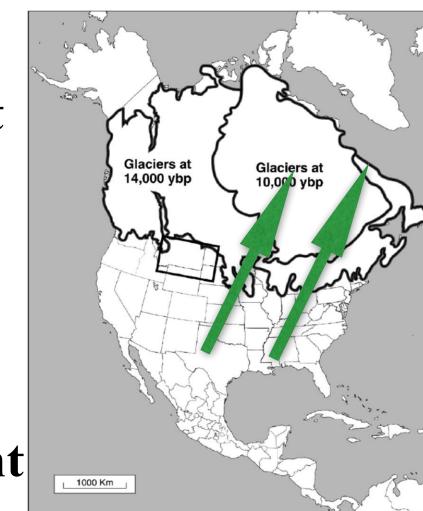
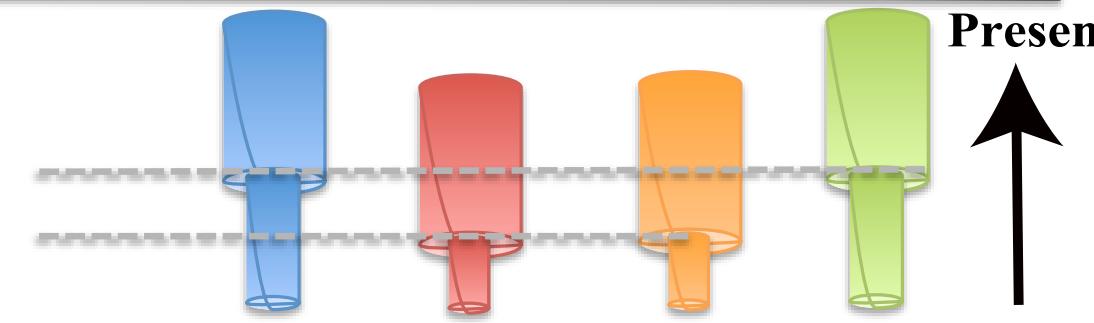
B) Asynchronous expansion

$\zeta = 0.0$



C) Expansion mixture:
asynchronous
&
synchronous

$\zeta = 0.5$



Chan et al. 2014

Xue and Hickerson 2014

$$P(\zeta, \tau, \phi \mid \text{Data}) \propto p(\text{Data} \mid \zeta, \tau, \phi) = p(\text{Data} \mid \phi, \tau) p(\phi) p(\tau \mid \zeta) p(\zeta)$$

hard to solve analytically (and we want flexibility)

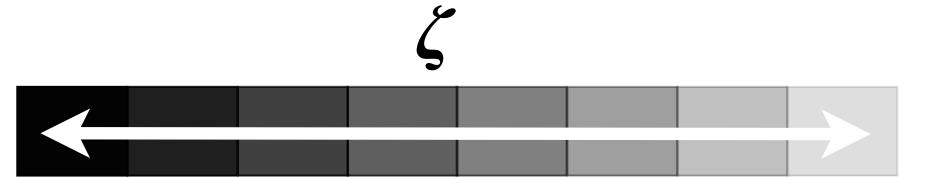


Approximate Bayesian Computation - ABC

Likelihood of HyperParameter
value is inversely proportional to
the difference $\text{Data}_{\text{simulated}} - \text{Data}_{\text{observed}}$

Approximate Bayesian Computation - ABC

Simulate Genetic **Data** from random values from the hyperprior $p(\phi) p(\tau | \zeta) p(\zeta)$



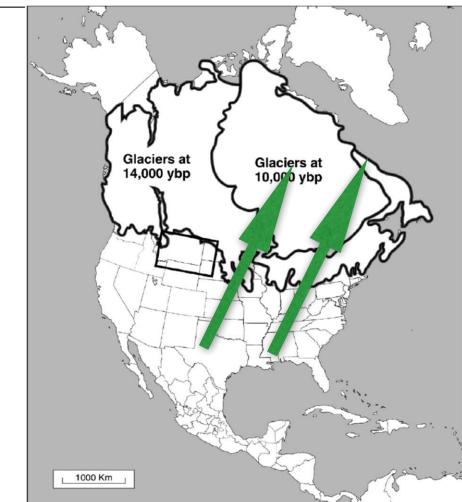
INCONGRUENCE

CONGRUENCE

Compress **Data** (summary statistics)

simulate coalescent & mutation across assemblage

Compare Compressed Simulated **Data** to Compressed Observed **Data**



Keep if the Match is Close Enough

$$Data_{simulated} - Data_{observed} \approx 0 ?$$

Approximate Bayesian Computation - ABC

Simulate Genetic **Data** from
random values from the
hyperprior $p(\zeta)$

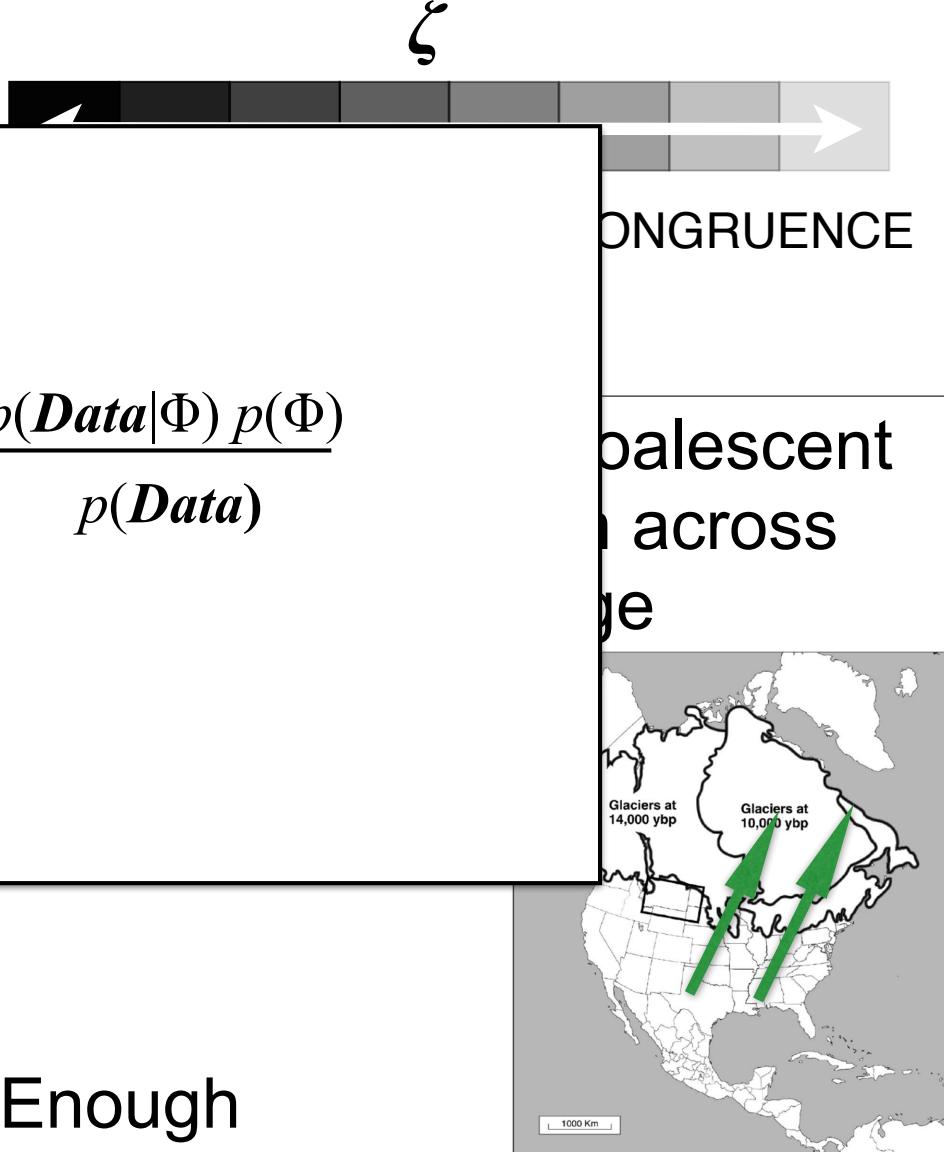
Compress Data

$$P(\Phi | \text{Data}) = \frac{p(\text{Data}|\Phi) p(\Phi)}{p(\text{Data})}$$

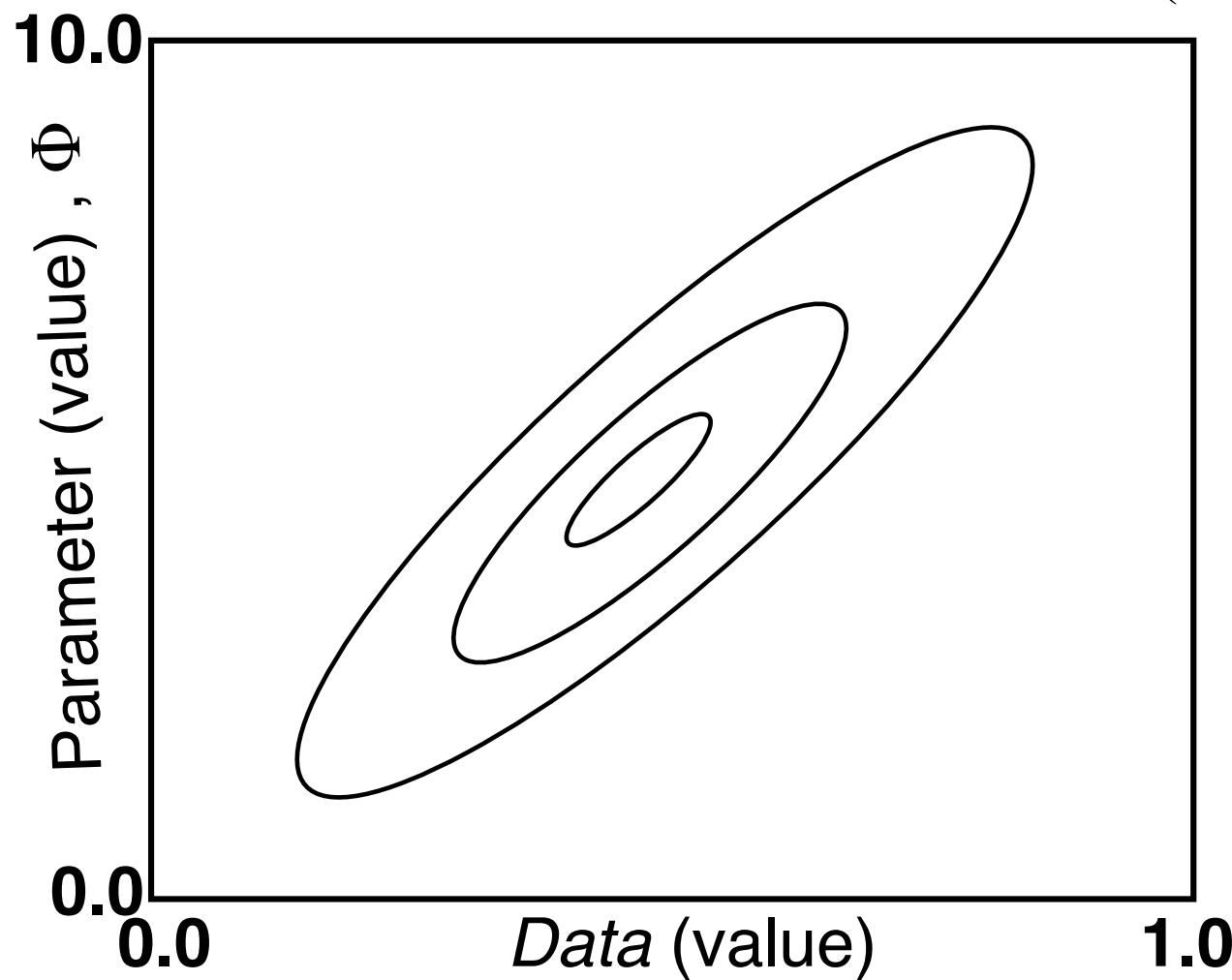
Compare Compressed
to Compressed Observed

Keep if the Match is Close Enough

$$\text{Data}_{\text{simulated}} - \text{Data}_{\text{observed}} \approx 0 ?$$



$$P(\Phi \mid Data) = \frac{p(Data \mid \Phi) p(\Phi)}{p(Data)}$$

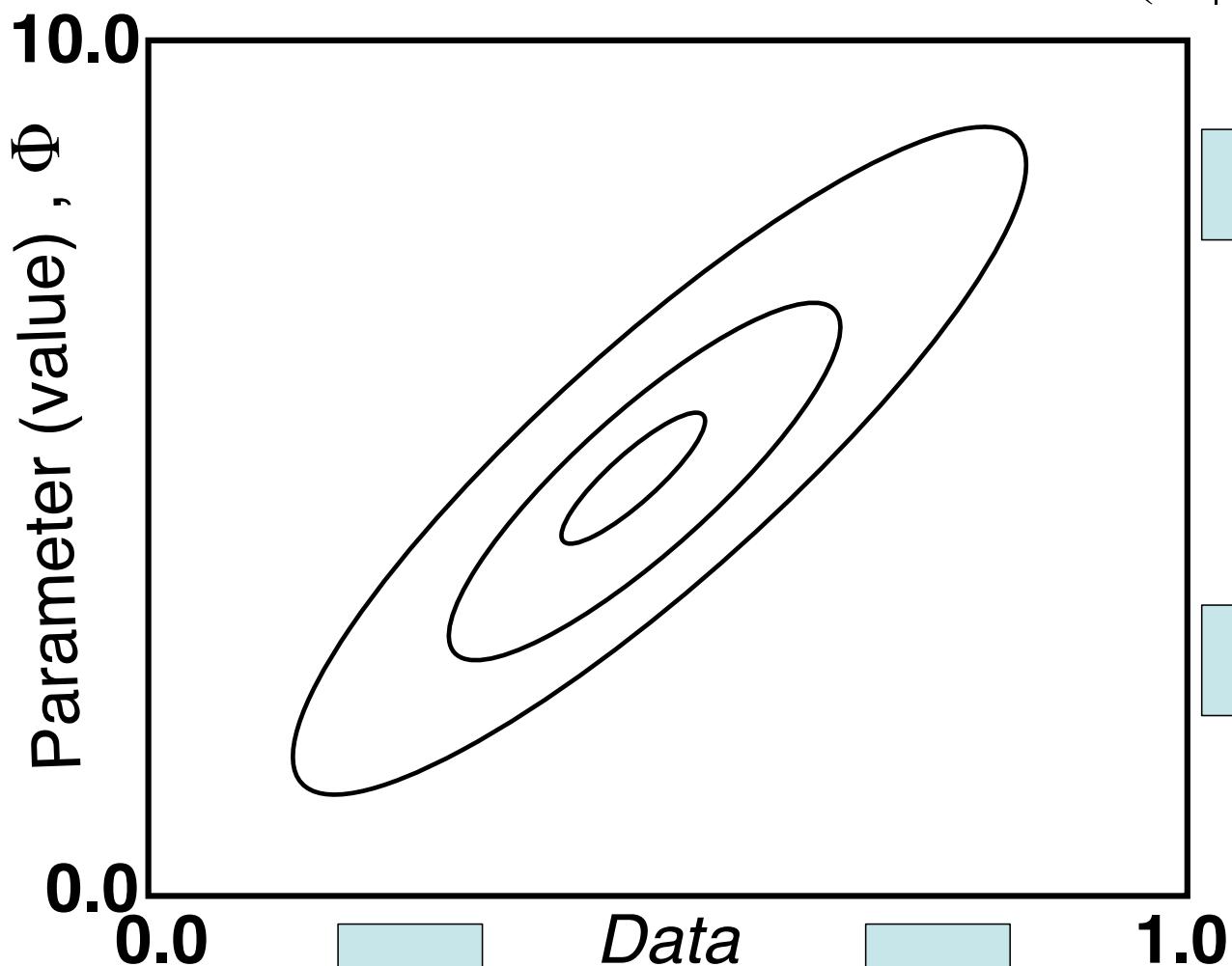


Mark Beaumont's
ABC schematic

if $Data_{simulated} - Data_{observed} \approx 0 ?$

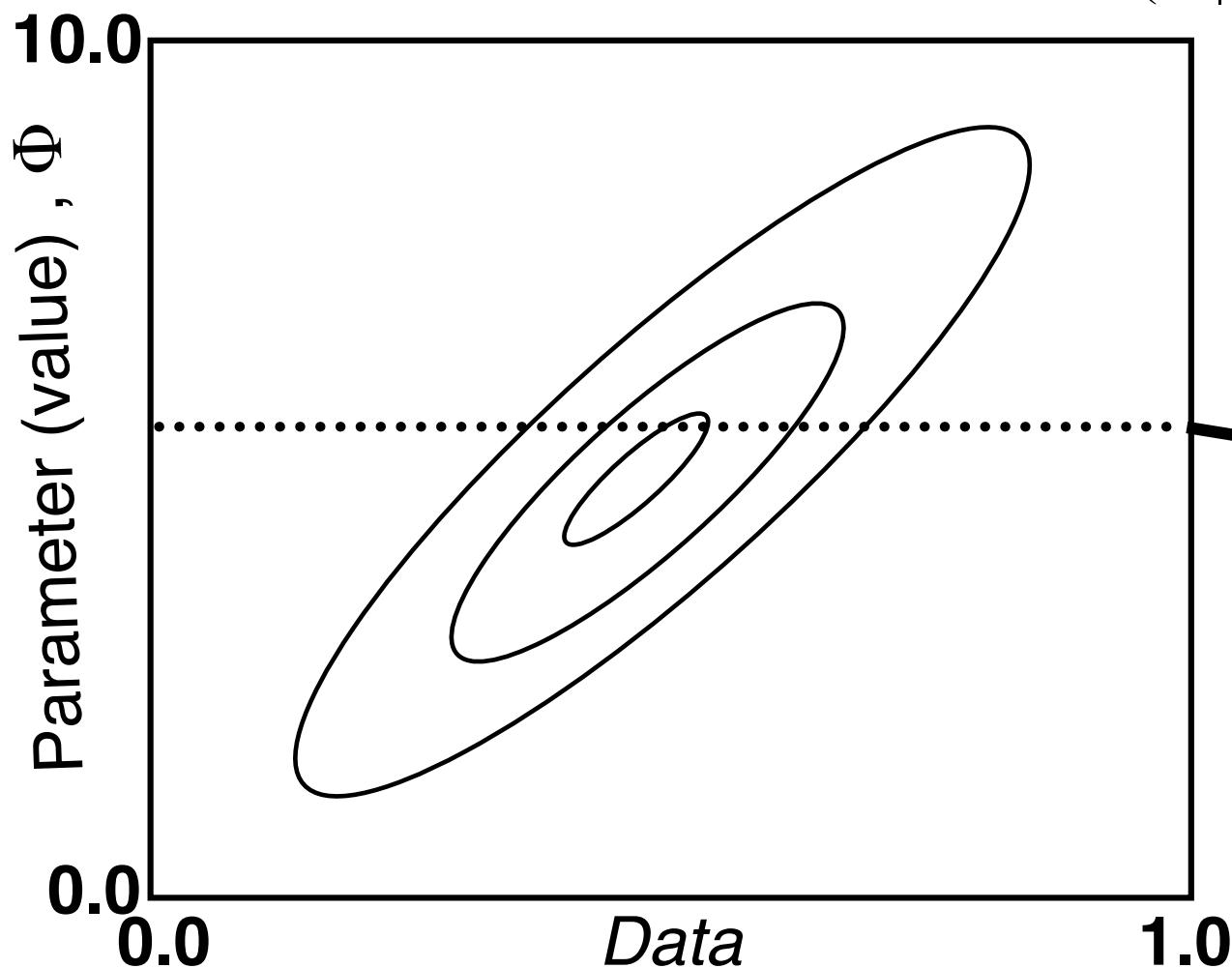
then $\Phi_{simulated} \approx \Phi_{observed}$

$$P(\Phi \mid Data) = \frac{p(Data \mid \Phi) p(\Phi)}{p(Data)}$$

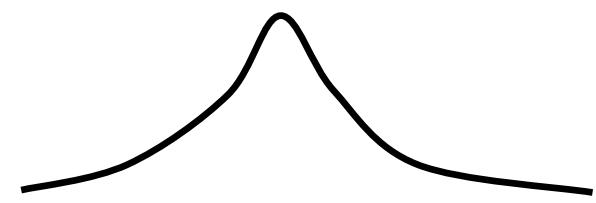


Prior – $p(\Phi)$

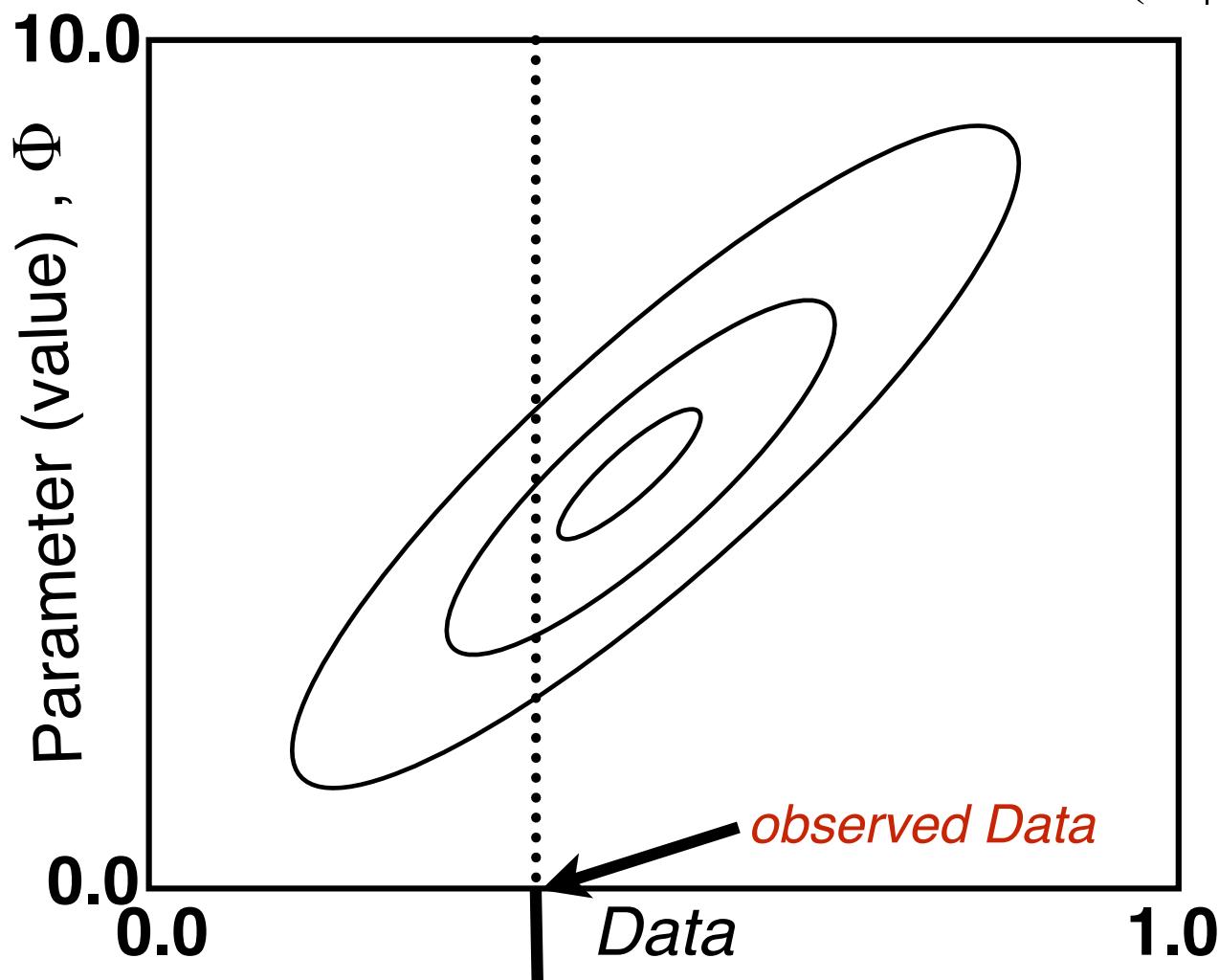
$$P(\Phi \mid \text{Data}) = \frac{p(\text{Data} \mid \Phi) p(\Phi)}{p(\text{Data})}$$



Likelihood-
 $P(\text{Data} \mid \Phi)$

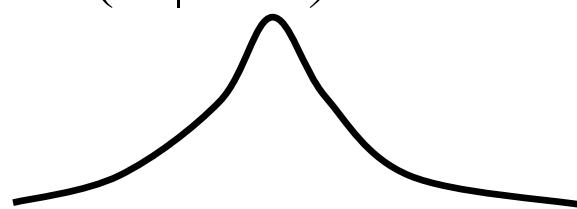


$$P(\Phi \mid Data) = \frac{p(Data \mid \Phi) p(\Phi)}{p(Data)}$$

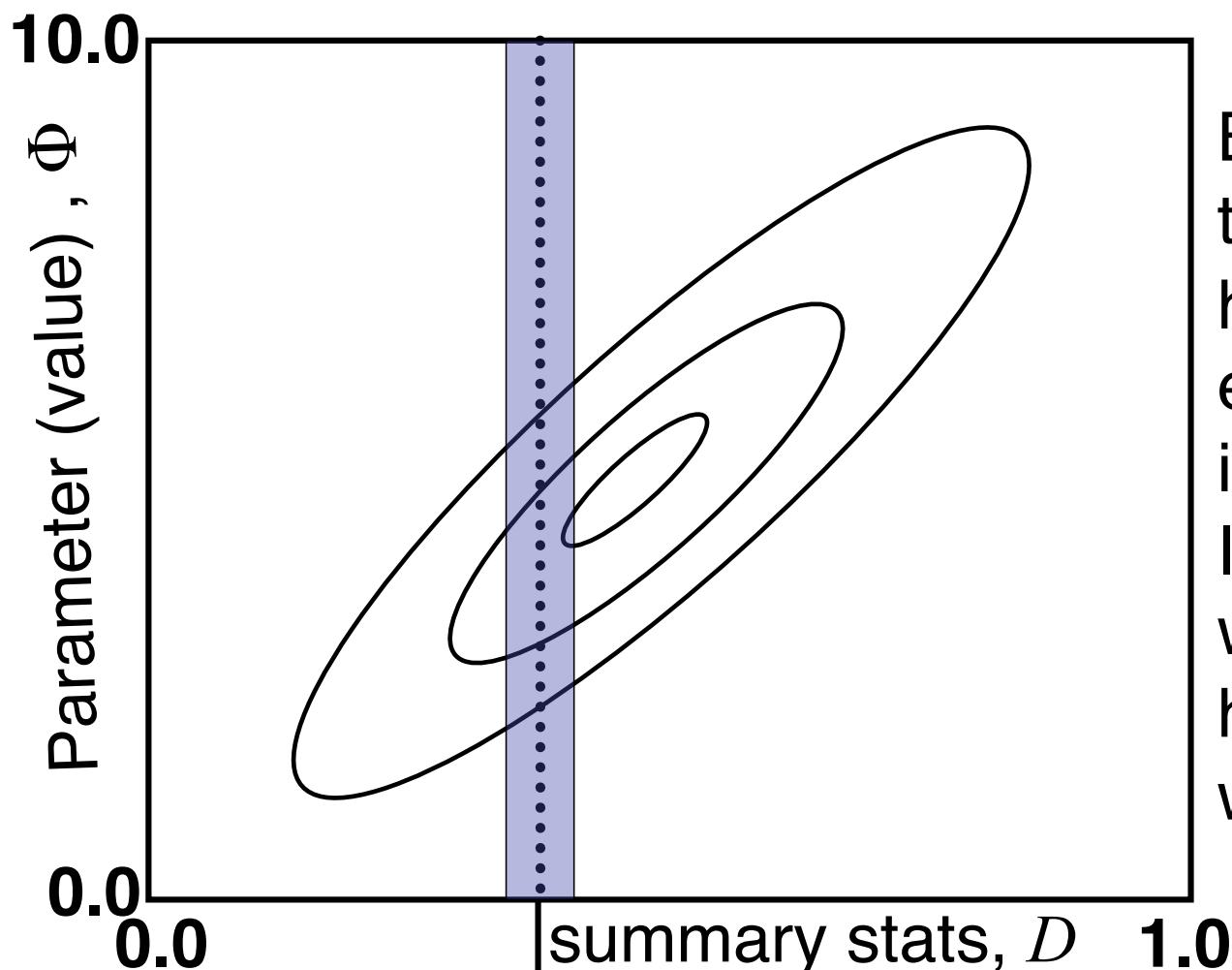


Posterior distribution –

$$P(\Phi \mid Data)$$



$$P(\Phi \mid \text{Data}) = \frac{p(\text{Data} \mid \Phi) p(\Phi)}{p(\text{Data})}$$



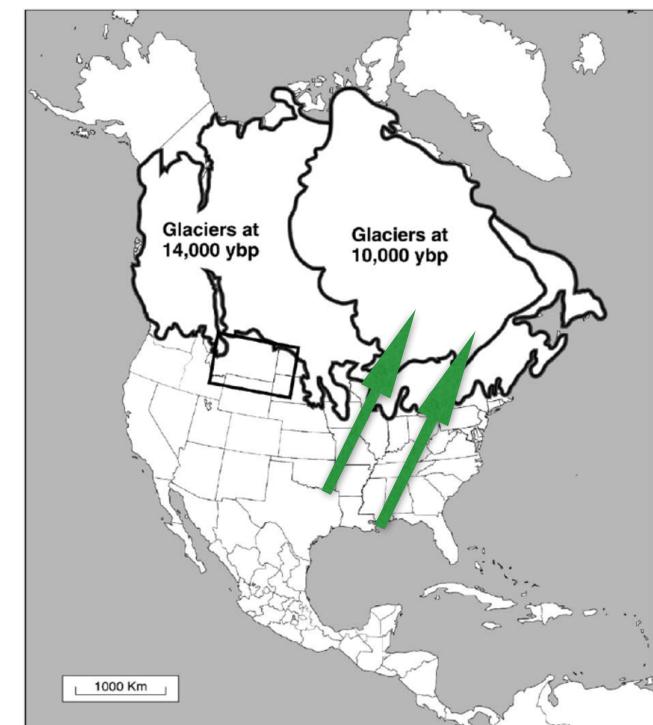
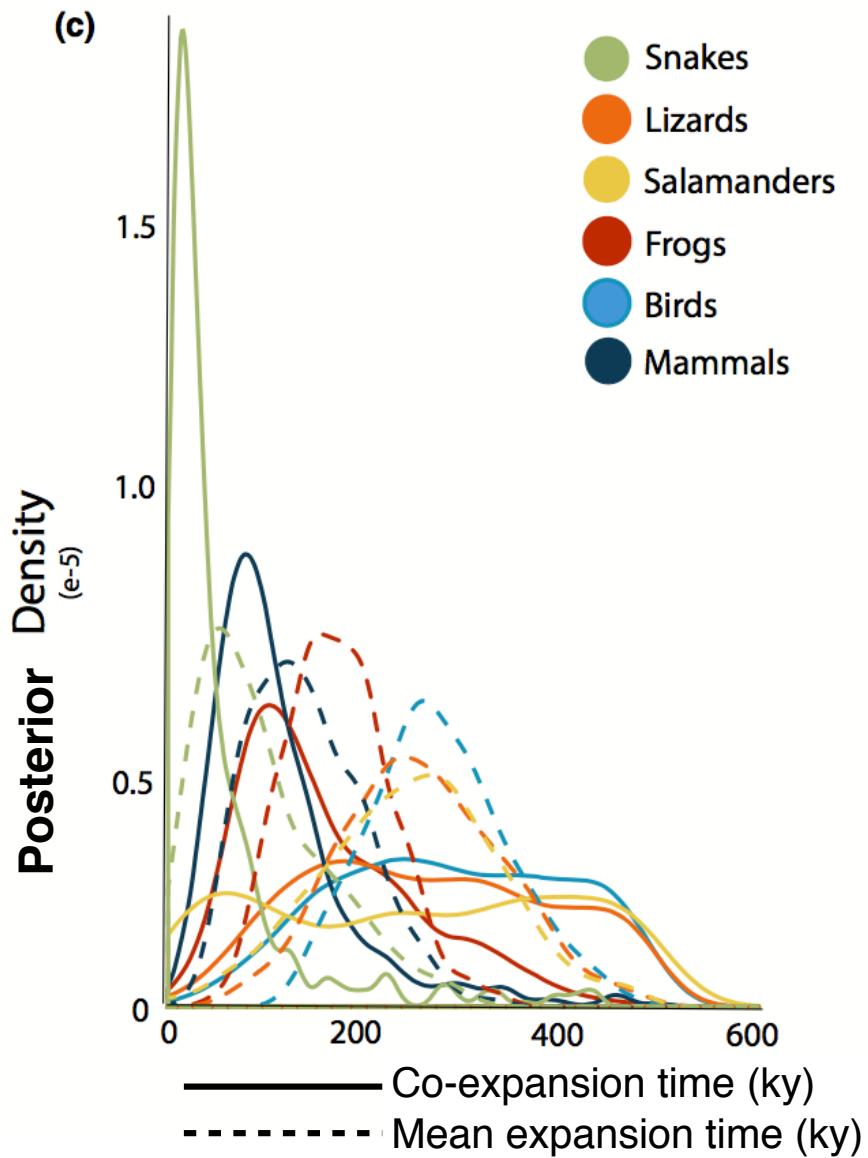
By converting Data to summary stats D , hitting the data exactly is not required. Instead we we need to only hit $\|D_i - D_{obs}\| < \varepsilon$ within a “threshold”

Posterior distribution –

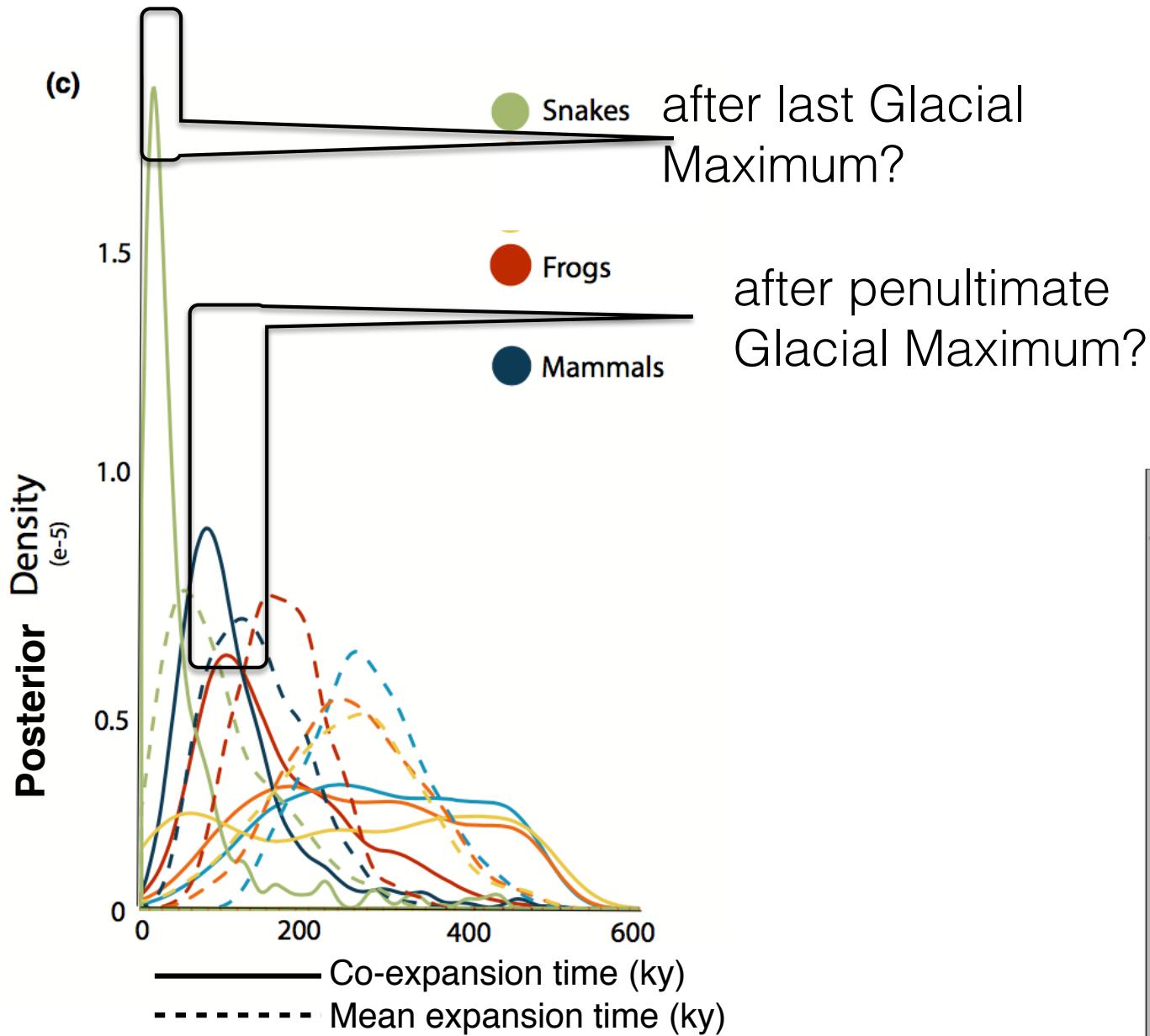
$$P(\Phi \mid \text{Data})$$

Results (hABC)

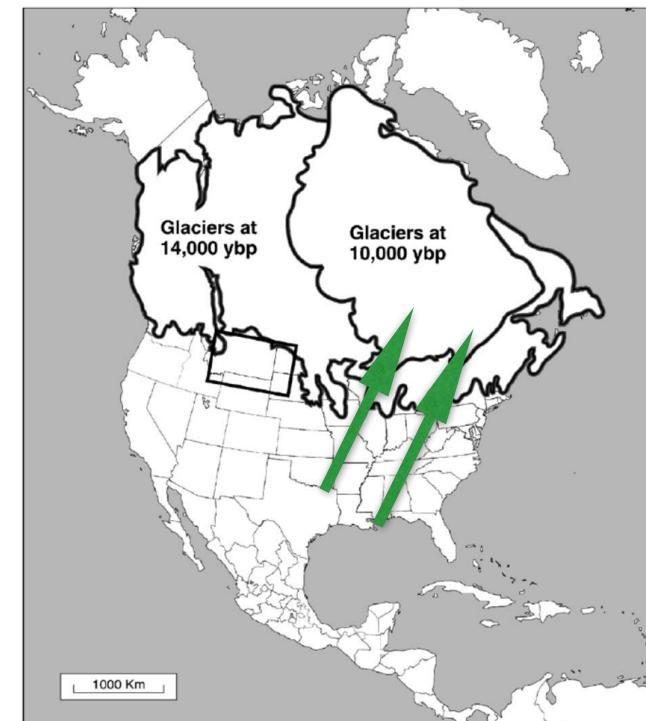
overall, extremely asynchronous, but



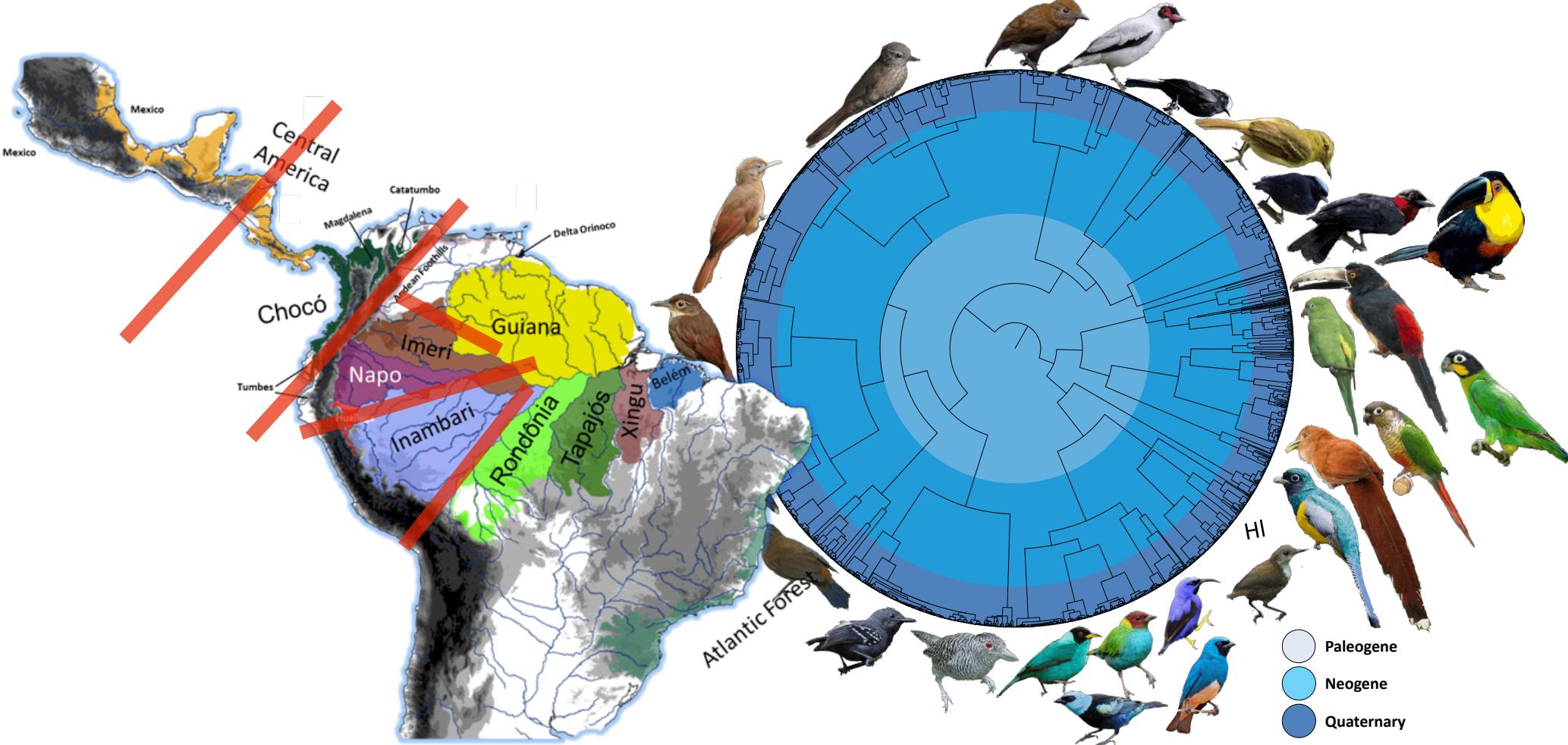
Results (hABC)



Strong to moderate recent co-expansion in **Snakes, Frogs and Mammals**



Bird Speciation in the Neo-tropics during the Quaternary



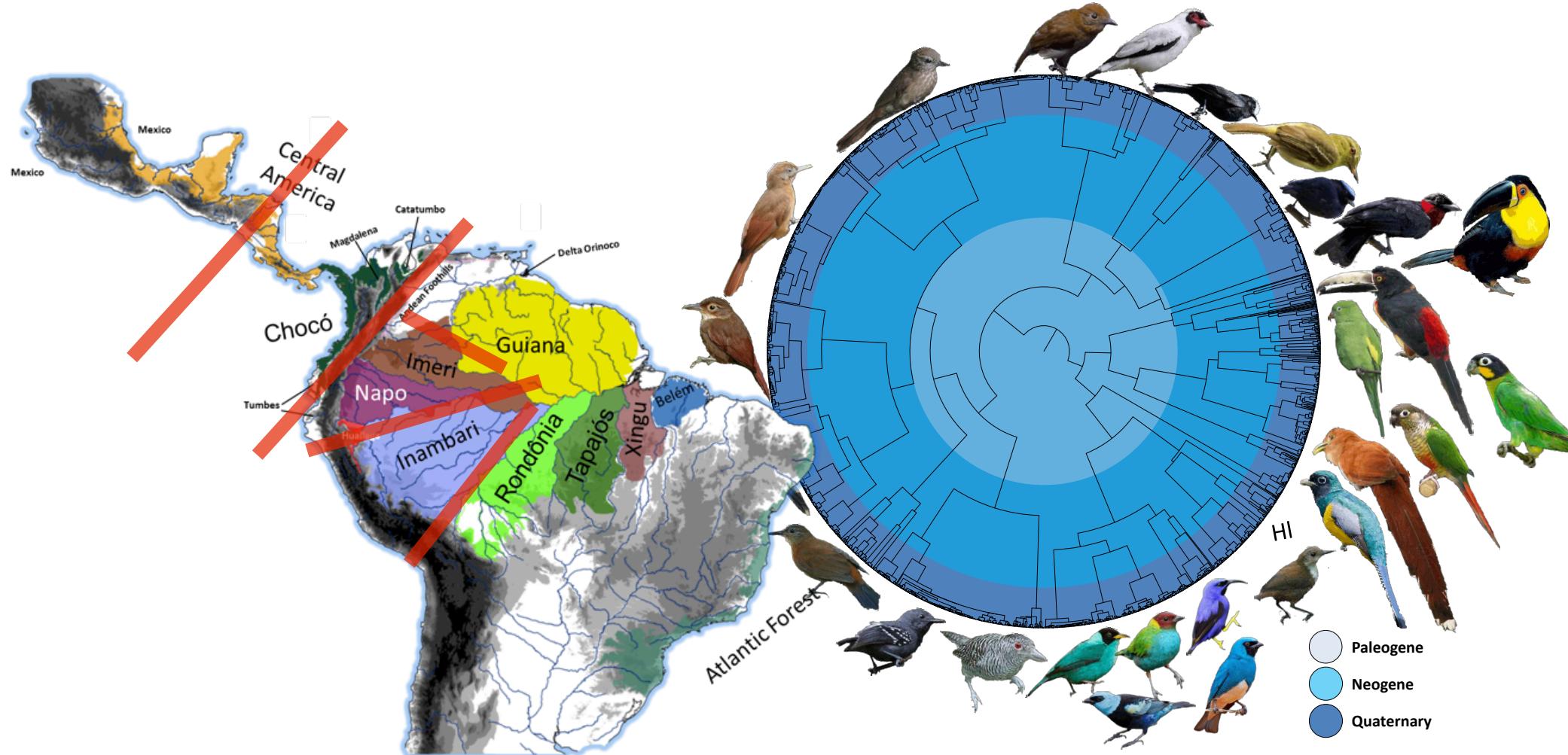
colonization or Vicariance?

predictions

random times

simultaneous

Bird Speciation in the Neo-tropics during the Quaternary



Φ

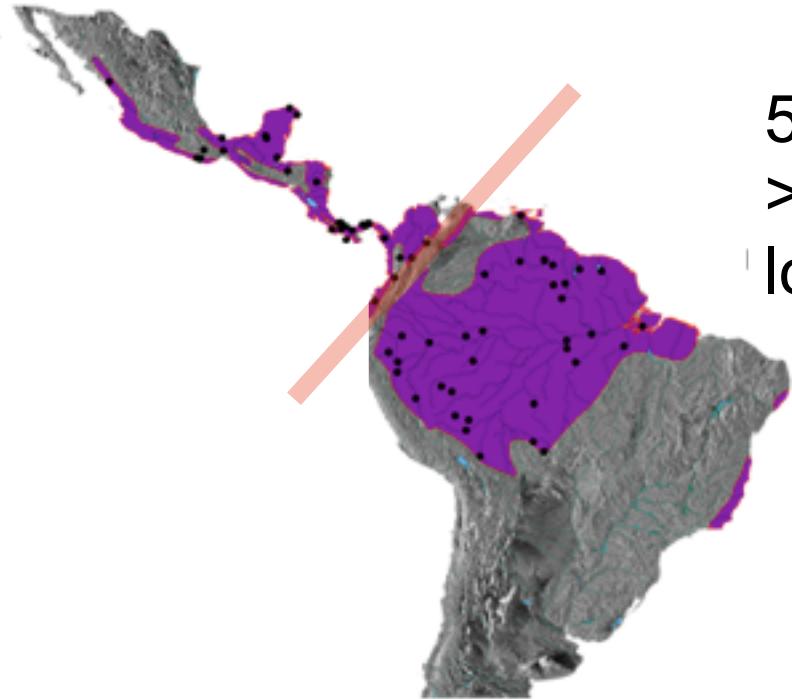


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CONGRUENCE

Development of ABC inferential strategy

- 1. Summary statistic Selection**
- 2. Prior Selection & Model Checking**
- 3. Estimator Validation with PODS
(pseudo-observed data sets)**
- 4. Estimation**



5 sister species pairs
> 150 “ultra-conserved element loci” (UCEs)

1. Summary statistic Selection

π

θ_w

π_{net}

$SD(\pi - \theta_w)$

(per species-pair mean across > 150 UCE loci)

correlates with variability in divergence times

Development of ABC inferential strategy

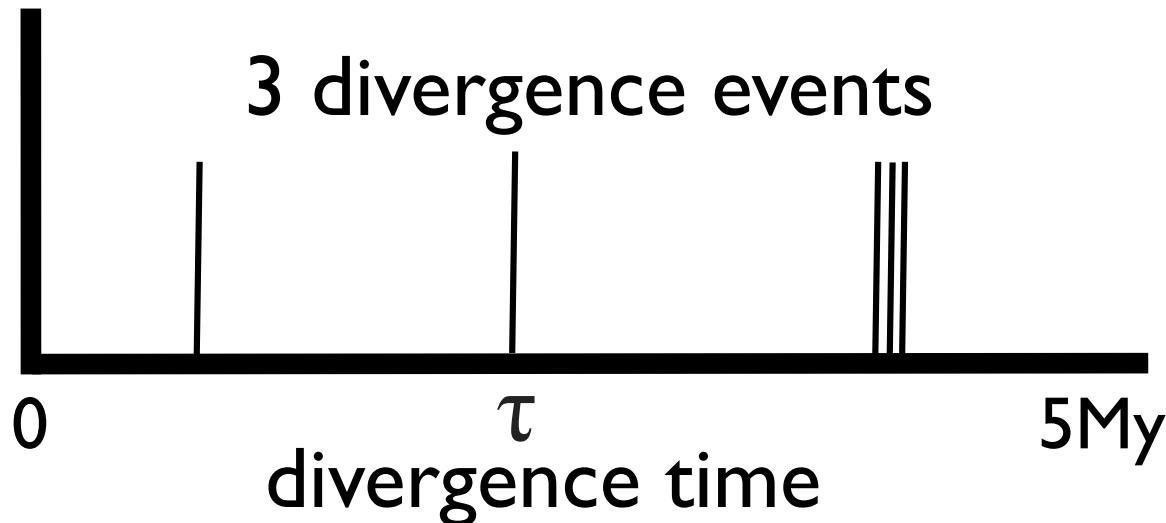
1. Summary statistic Selection
- 2. Prior Selection & Model Checking**
3. Validation
4. Estimation

2. Prior Selection

hyperparameter Ψ = number of divergence times

5 species pairs arose at 1 - 5 different “events”

“event” = a single or tightly clustered grouping of divergence times (ie $\text{Var}(\tau) \approx 0.0$)



2. Prior Selection

5 species pairs arose at 1 - 5 different times ($\Psi = 1 - 5$)

$\Psi = 1$ single clustered pulse of divergence)

$\Psi = 2; 1\&4, 4\&1, 3\&2, 2\&3$)

$\Psi = 3; 1\&2\&2, 2\&1\&2, 2\&2\&1, 3\&1\&1, 1\&3\&1, 1\&1\&3$)

$\Psi = 4; 1\&1\&1\&2, 1\&1\&2\&1, 1\&2\&1\&1, 2\&1\&1\&1$)

$\Psi = 5; 1\&1\&1\&1\&1$)

2. Prior Selection

$\Pr(\Psi)$ = discrete uniform prior (1,2,3,4 and 5 times all equally likely)

$\Psi = 1$ single clustered pulse of divergence)

$\Psi = 2; 1\&4, 4\&1, 3\&2, 2\&3)$

$\Psi = 3; 1\&2\&2, 2\&1\&2, 2\&2\&1, 3\&1\&1, 1\&3\&1, 1\&1\&3)$

$\Psi = 4; 1\&1\&1\&2, 1\&1\&2\&1, 1\&2\&1\&1, 2\&1\&1\&1)$

$\Psi = 5; 1\&1\&1\&1\&1)$

2. Prior Selection

Model / HyperParameter space



INCONGRUENCE
(random colonization)

CONGRUENCE
(vicariance)

$\Psi = \text{high}$

HyperParameter

$\Psi = \text{low}$

Species-Specific Parameters

$$\Theta = \begin{cases} \mu & \text{mutation rates} \\ N\mu=\theta & (\theta_{\text{anc}} \& \theta_D) \text{ population mutation parameters} \\ \tau & \text{divergence times} \end{cases}$$

2. Prior Selection

Species-Specific Parameters

$$\Theta = \begin{cases} \mu \\ N\mu=\theta \text{ } (\theta_{\text{anc}} \& \theta_{\text{D}}) \\ \tau \end{cases}$$

Prior

$\Pr(\mu) = \text{gamma } (1/\alpha \text{ with mean 1.0})$
flexible locus specific scaling

$\Pr(\theta) = \sim U(0, \theta_{\max})$

$\Pr(\tau) = \sim U(0, \tau_{\max})$

2. Prior Selection

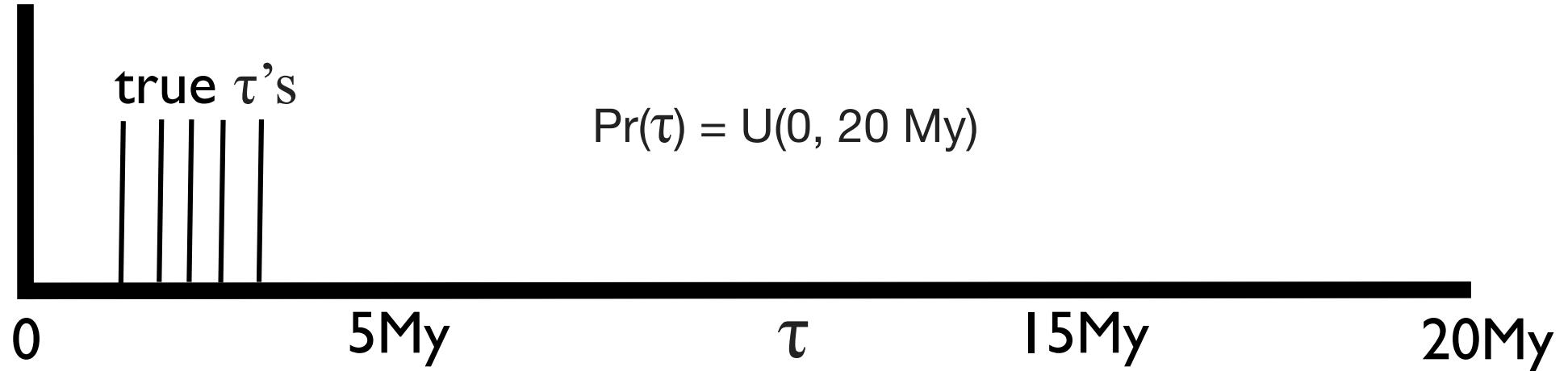
τ divergence times

$$\Pr(\tau) = U(0, \tau_{\max})$$

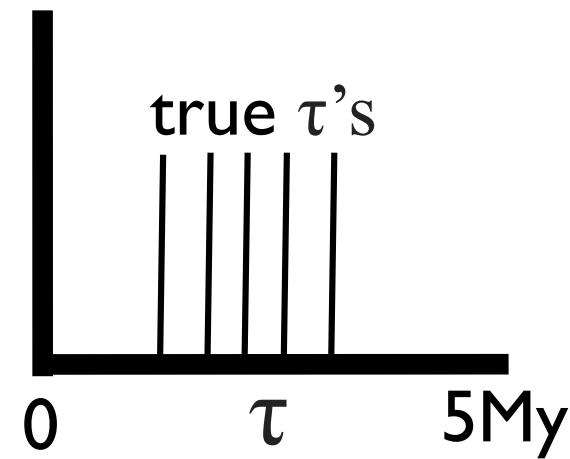
important to choose prior $\Pr(\tau)$ with good sampling properties

2. Prior Selection

How do we choose the prior?



VS

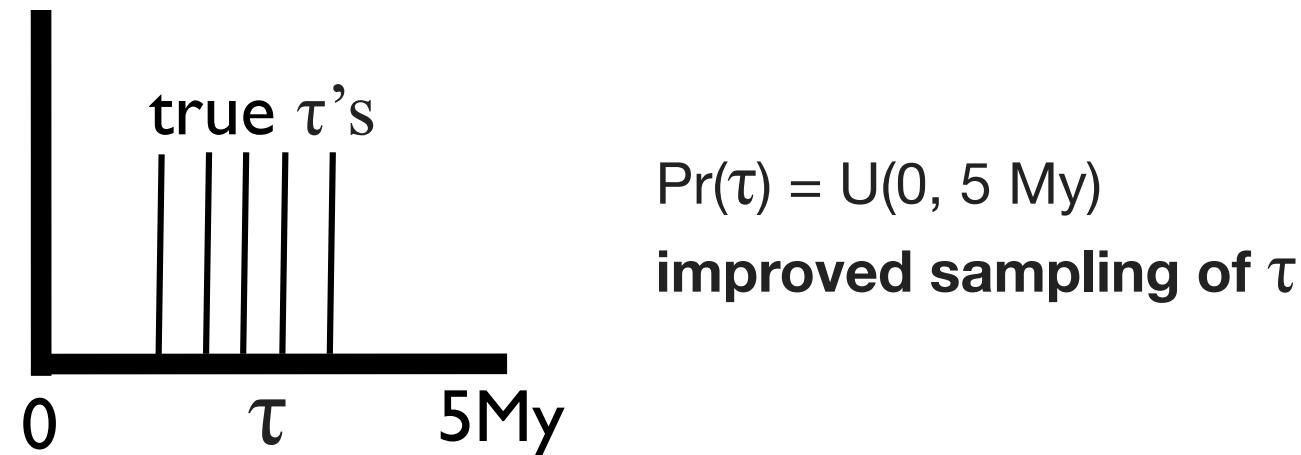
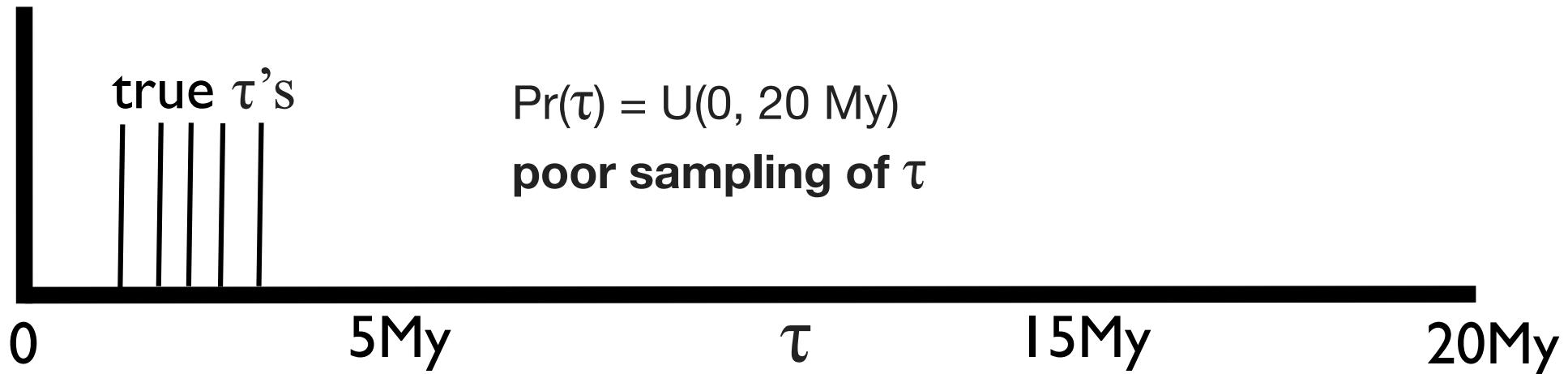


2. Prior Selection

important to choose prior $\Pr(\tau)$ with good sampling properties

Poor Sampling: if the 5 real τ 's are within 1-3 My, and $\Pr(\tau) = U(0, 20 \text{ My})$, then the chance of randomly drawing of 5 plausible times ($\Psi = 5$) is < 0.1%.

Leads to downward bias in Ψ



2. Prior Selection

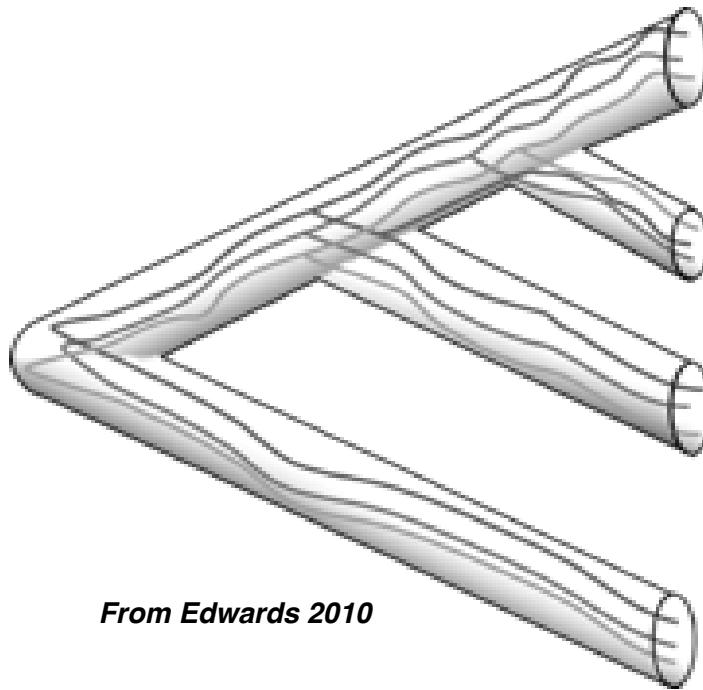
How do we choose the prior?

1. look at the data
2. graphical checks from trial runs
3. Bayesian model averaging

2. Prior Selection

How do we choose the prior?

1. look at the data

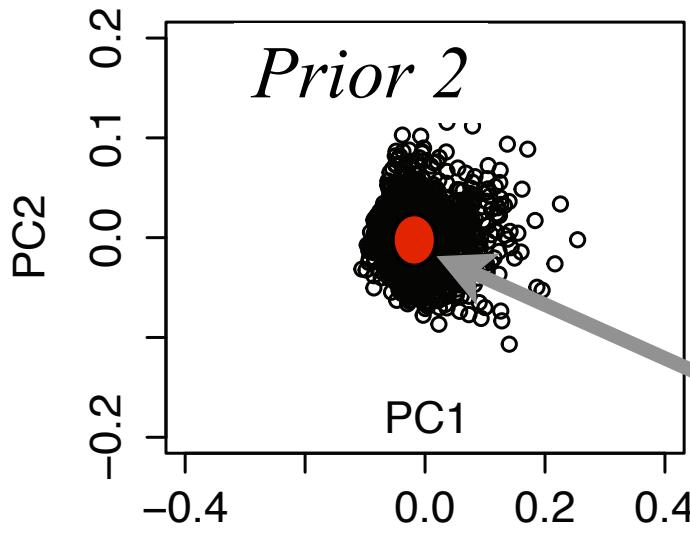


**use gene tree divergences as the maximum
(population divergence < gene divergence)**

2. Prior Selection

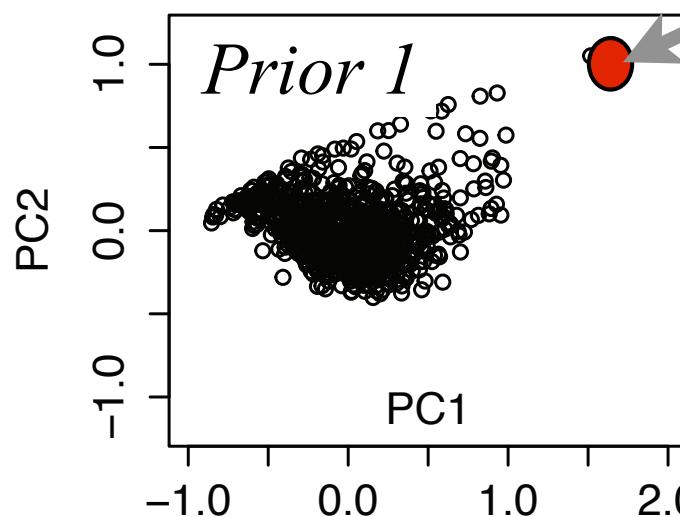
How do we choose the prior?

2. graphical checks from trial runs (small prior samples)



well sampled prior

observed
data



poorly sampled prior

(Hickerson et al. 2014)

2. Prior Selection

How do we choose the prior?

3. Bayesian model averaging

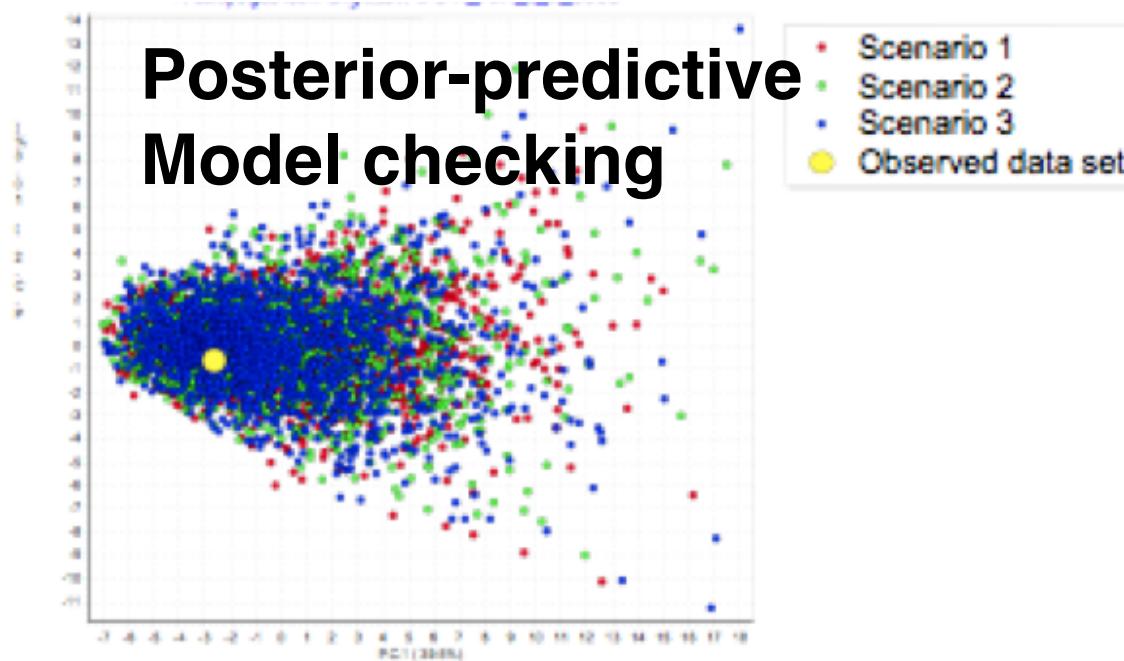
Sample from **multiple** candidate priors

$$\{M_1, \dots, M_8\}$$

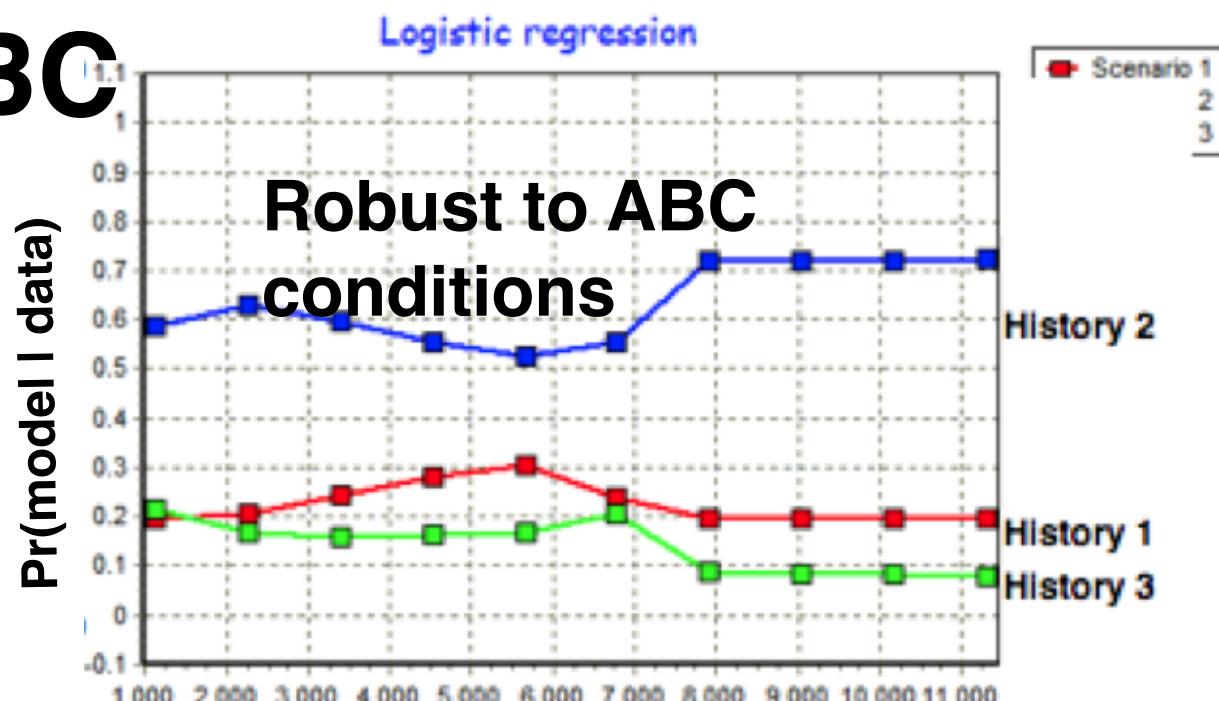
Do regular ABC estimation

ABC posterior estimate is weighted by posterior strength
of each prior

Posterior-predictive Model checking



DIY-ABC



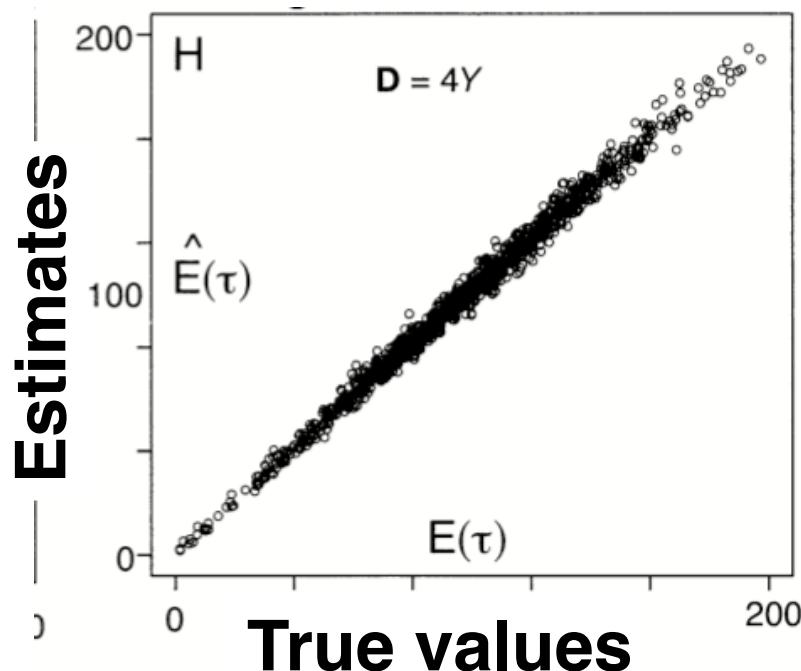
Proportion of accepted simulations

Development of ABC inferential strategy

1. Summary statistic Selection
2. Prior Selection and Model Checking
- 3. Estimator Validation with PODS
(pseudo-observed data sets)**
4. Estimation

3. Estimator Validation with PODS (pseudo-observed data sets)

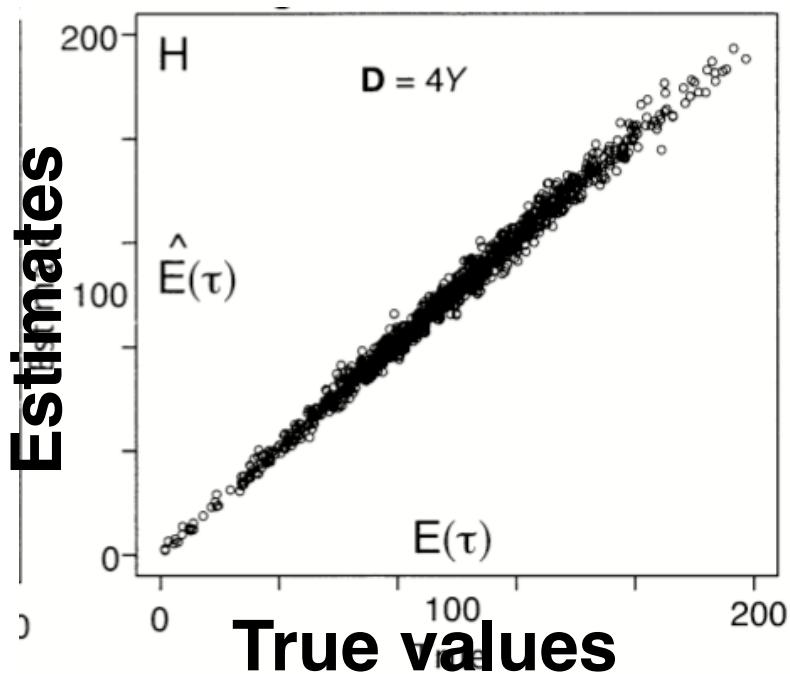
- 1 simulate “reference table” (the prior sample)
- 2 simulate PODS (pseudo-observed data sets with recorded parameter values)
- 3 make ABC estimates from the PODS



requires CPU

CUNY high
performance computing
facility

Simulation validation of ABC



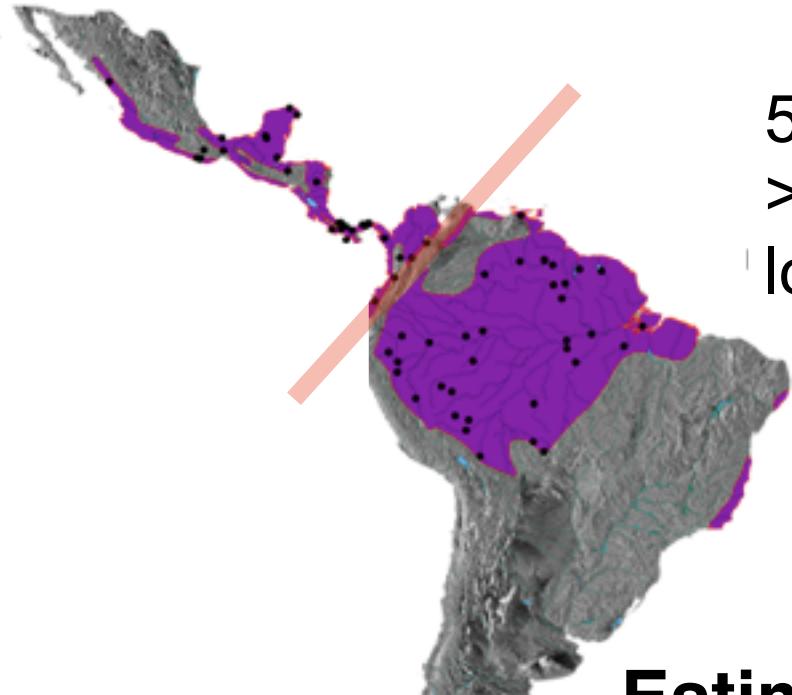
> 300,000 Credit card
numbers later

Beware
www.citibank.com



Development of ABC inferential strategy

- 1. Summary statistic Selection**
- 2. Prior Selection and Model Checking**
- 3. Estimator Validation with PODS
(pseudo-observed data sets)**
- 4. Estimation**



5 sister species pairs
> 150 “ultra-conserved element loci” (UCEs)

Estimation

INCONGRUENCE
(random colonization)



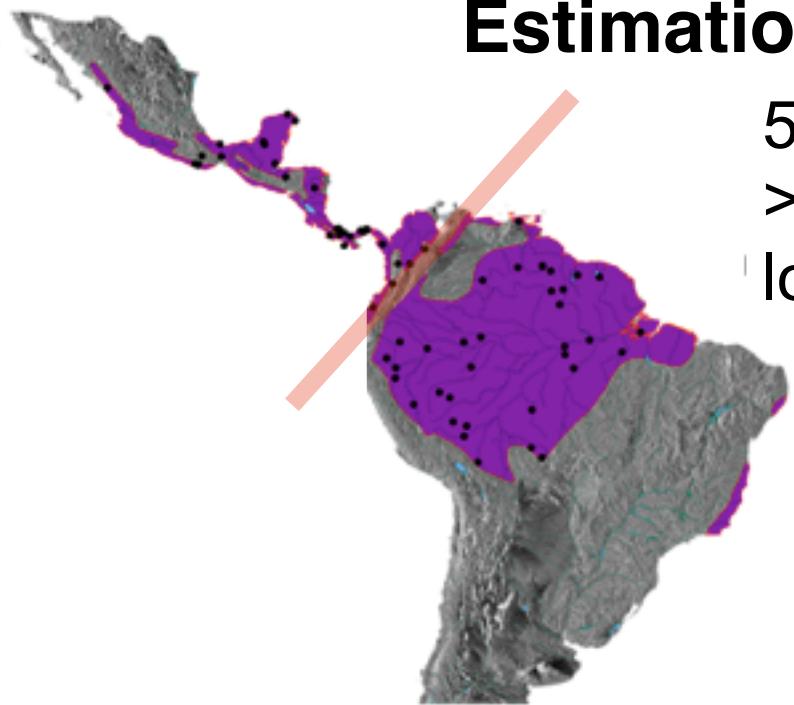
CONGRUENCE
(vicariance)

HyperParameter

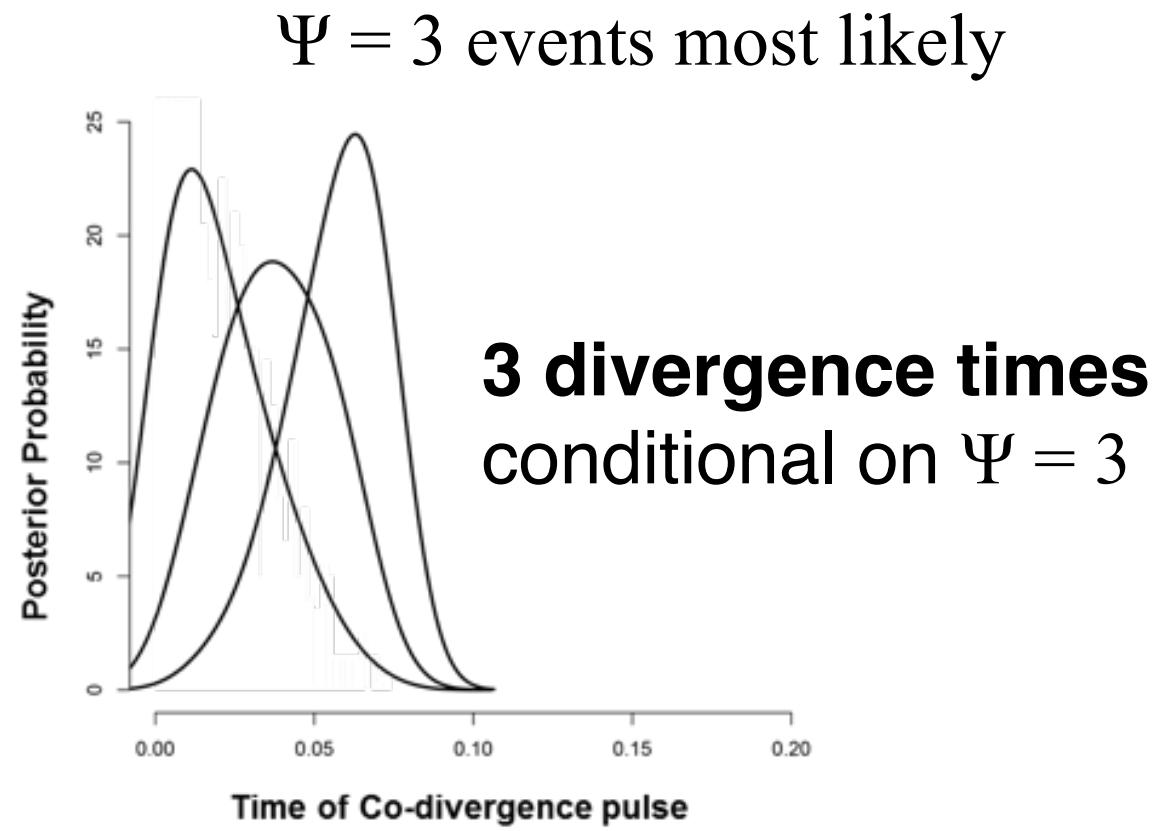
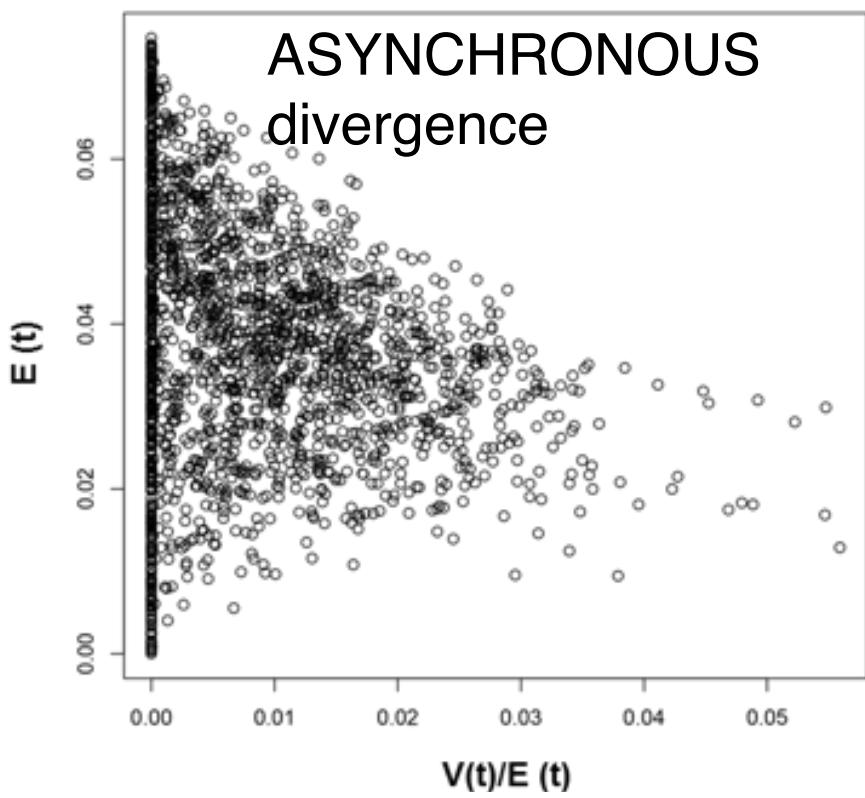
1 simulate “reference table”

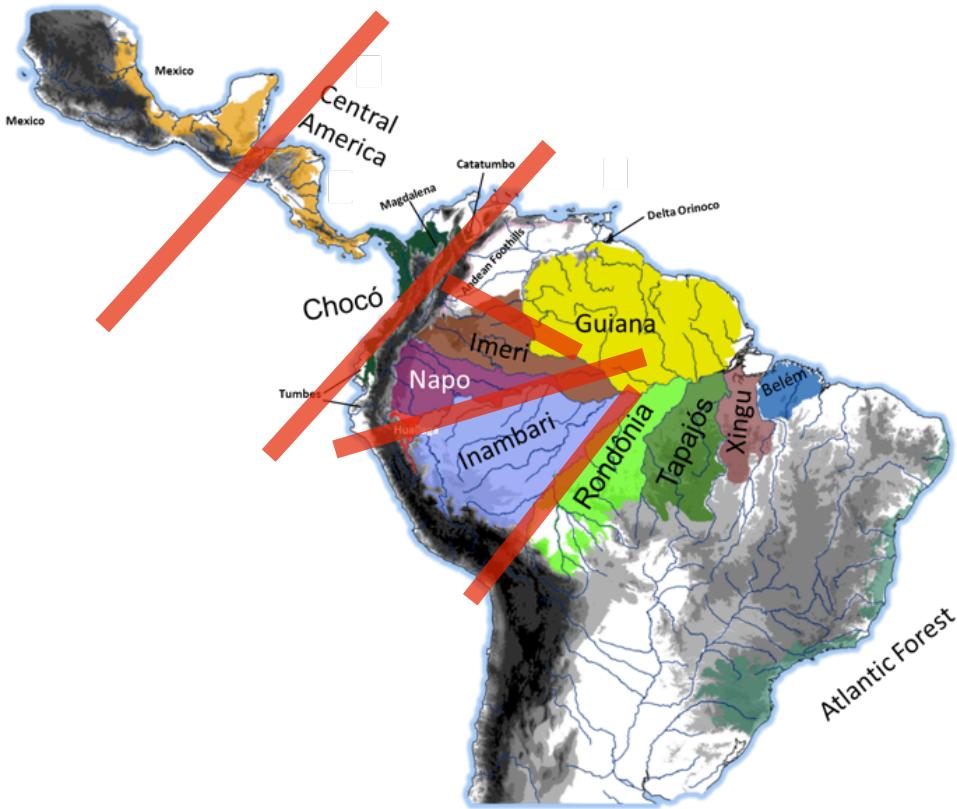
2 make ABC estimates (comparing Data with simulated data in reference table)

Estimation



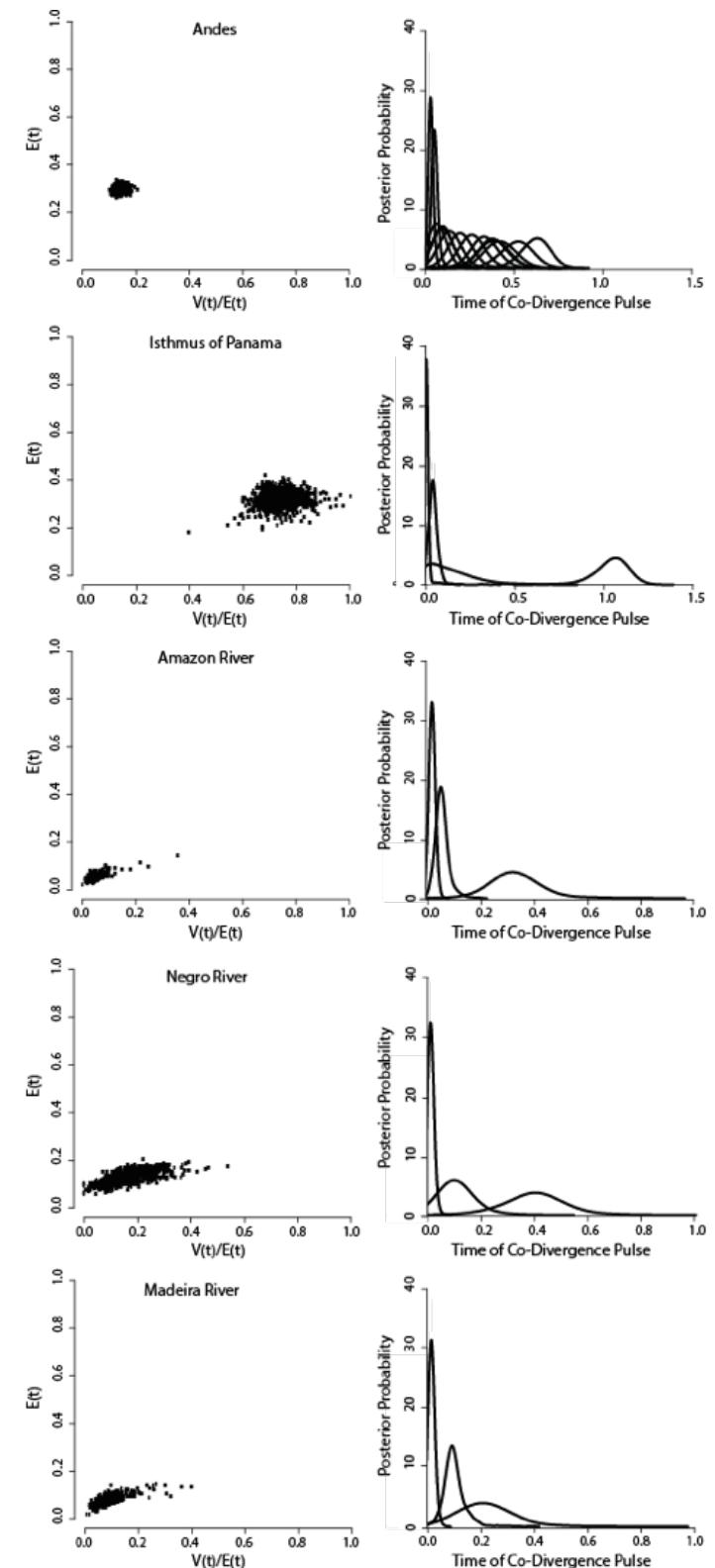
5 sister species pairs
> 150 “ultra-conserved element loci” (UCEs)





**5 breaks (30 - 50 mtDNA pairs
across each break)**

**ASYNCHRONOUS divergence at all 5
breaks**



Software - MTML - msBayes

- 1. Format data files (FASTA or IM file for each species-pair)**
- 2. Convert data to summary statistic vector**
- 3. prior selection & checking**
- 4. Simulate the reference table (samples from the prior)**
- 5. ABC filtering**
- 6. PODS validation and/or power analysis**

Software - MTML - msBayes

1. Format data files (FASTA or IM file for each species-pair)

data = 5 species pairs, >150 loci each (not all the same loci)

```
$convertIM.pl andes_UCE.list
```

Software - MTML - msBayes

2. Convert data to summary statistic vector

```
$obsSumStats.pl -T obsSSUCE.table  
batch.masterIn.fromIM > obsSSUCE.txt
```

```
emacs obsSSUCE.table  
emacs obsSSUCE.txt
```

makes
vector file (computer-readable)
&
summary statistic table (human-readable)

Software - MTML - msBayes

3. prior selection & checking

check prior settings:

emacs batch.masterIn.fromIM

simulate ‘small’ samples of candidate priors

candidate prior 1

```
msbayes.pl -c batch.masterIn.fromIM -r 1000 -o  
prior_UCEs_TtauAncT0.01_1.0_0.25_candidate1
```

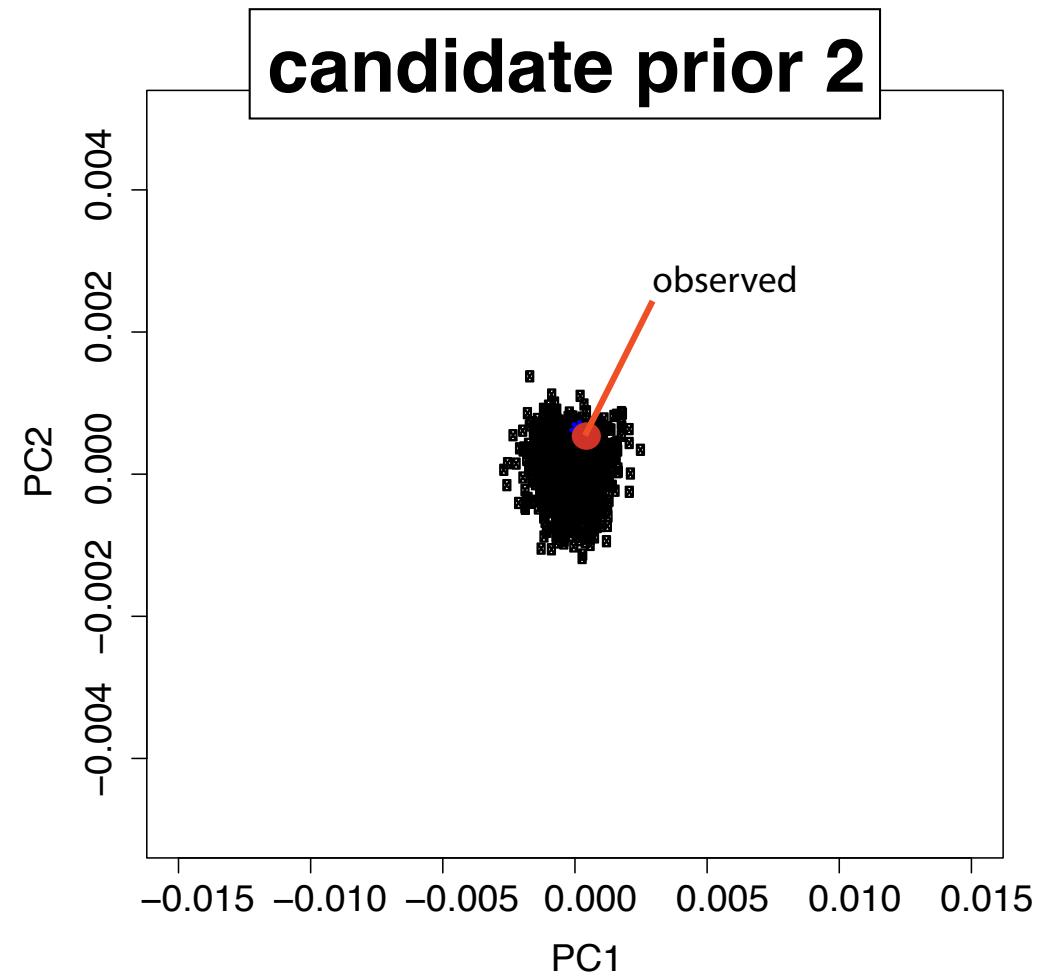
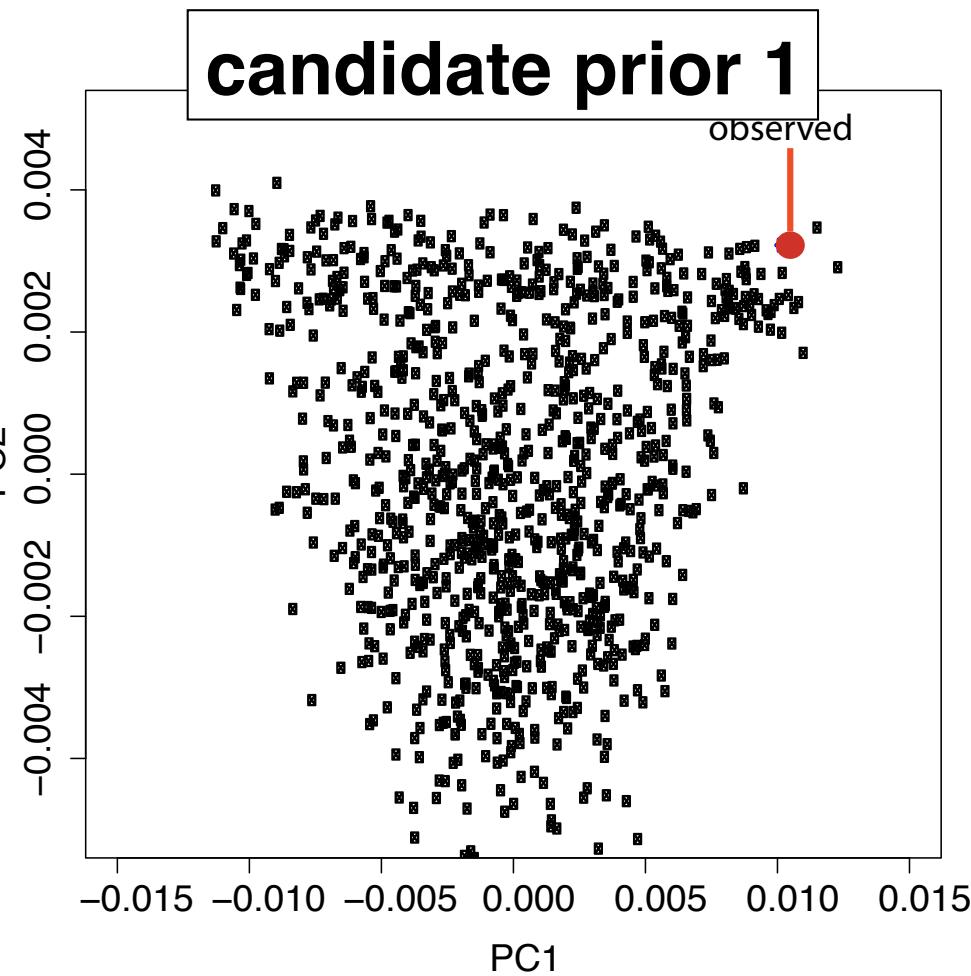
candidate prior 2

```
msbayes.pl -c batch.masterIn.fromIM -r 1000 -o  
prior_UCEs_TtauAncT0.01_0.075_0.25_candidate2
```

Software - MTML - msBayes

3. prior selection & checking

plot the first 2 PCAs of the sumstats (from both prior samples)



Software - MTML - msBayes

4. Simulate the reference table (samples from the prior) once or in parallel

```
./msbayes.pl -c batch.masterIn.fromIM -r 1000000 -o  
prior_UCEs_TtauAncT0.01_1.0_0.25
```

number of simulations
name of reference table (large prior sample)

Software - MTML - msBayes

1. initial filter

```
rm PosteriorUCEs_3Mpsi_any  
.msReject obsSSUCE.txt  
prior_UCEs_TtauAncT0.01_1.0_0.25 0.001 6 7 8 9 10 >  
PosteriorUCEs_3Mpsi_any
```

2. post-rejection transformation on accepted set (abc.r)

3. plot posterior

4. calculate Bayes factors or odds ratios

5. ABC filtering (rejection sampling)

Software - MTML - msBayes

6. PODS validation and/or power analysis

Software - MTML - msBayes

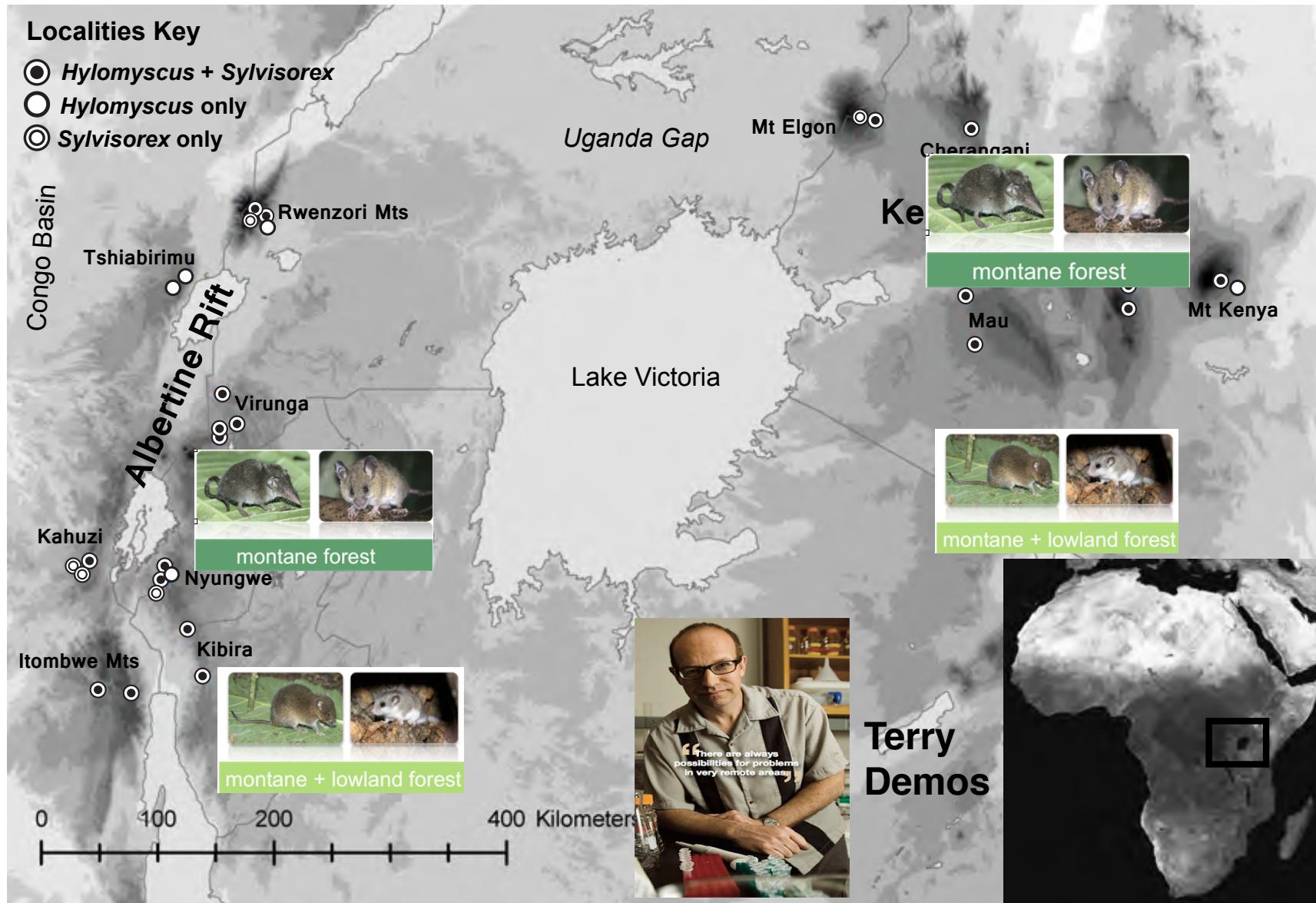
***a posteriori* analysis**

model averaging - how to represent uncertainty in number of divergence times (Ψ)

example 4 species pairs of African rodents

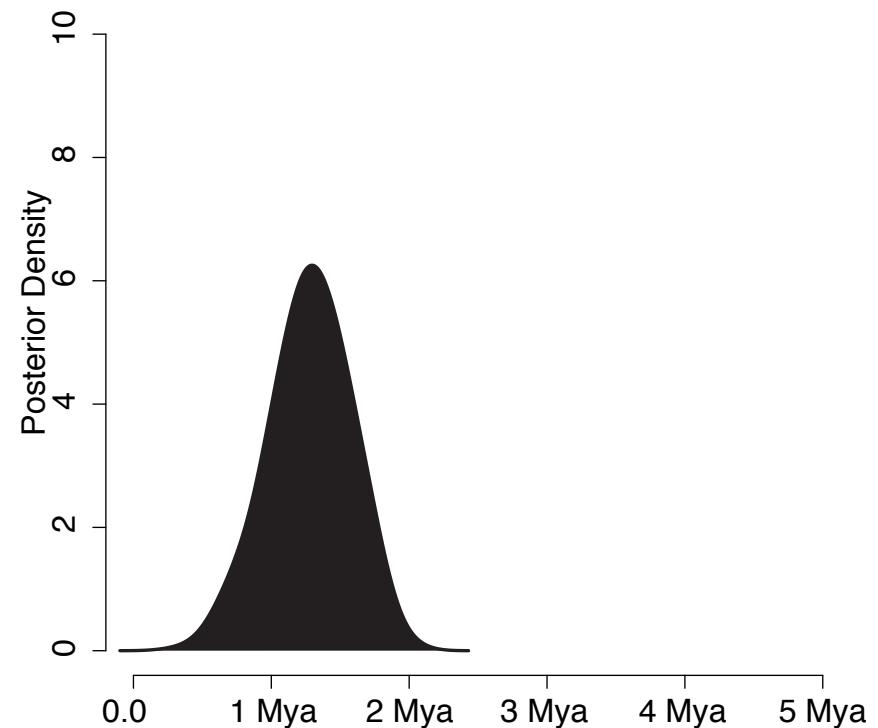
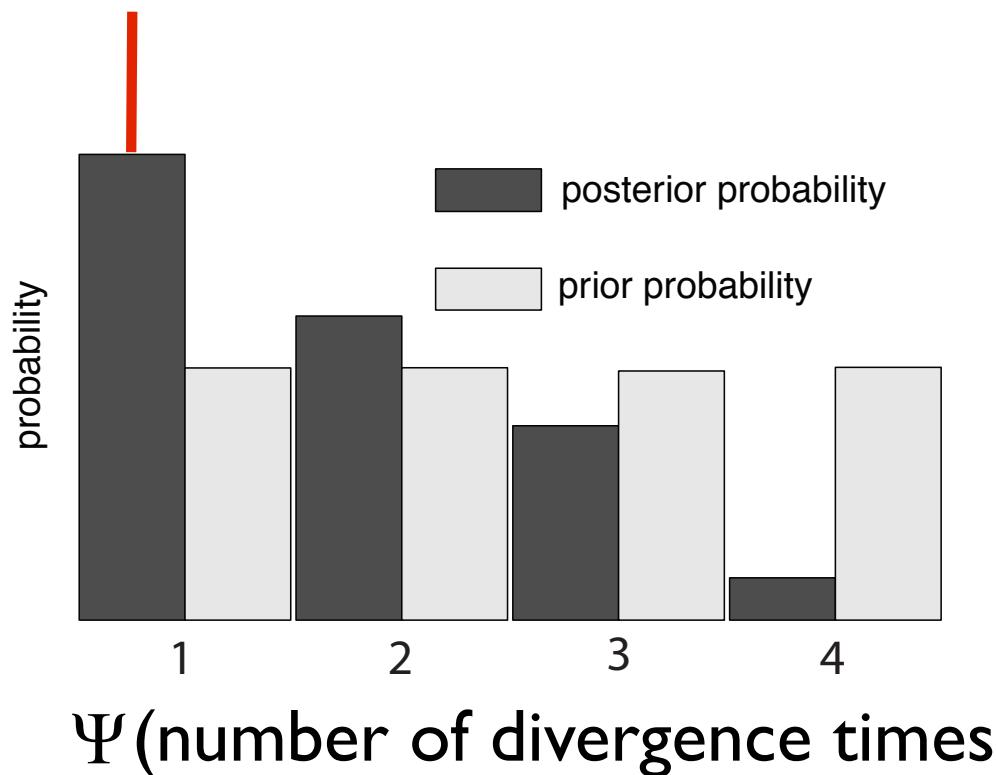
Software - MTML - msBayes

example - 4 East/West species pairs of African rodents



Software - MTML - msBayes

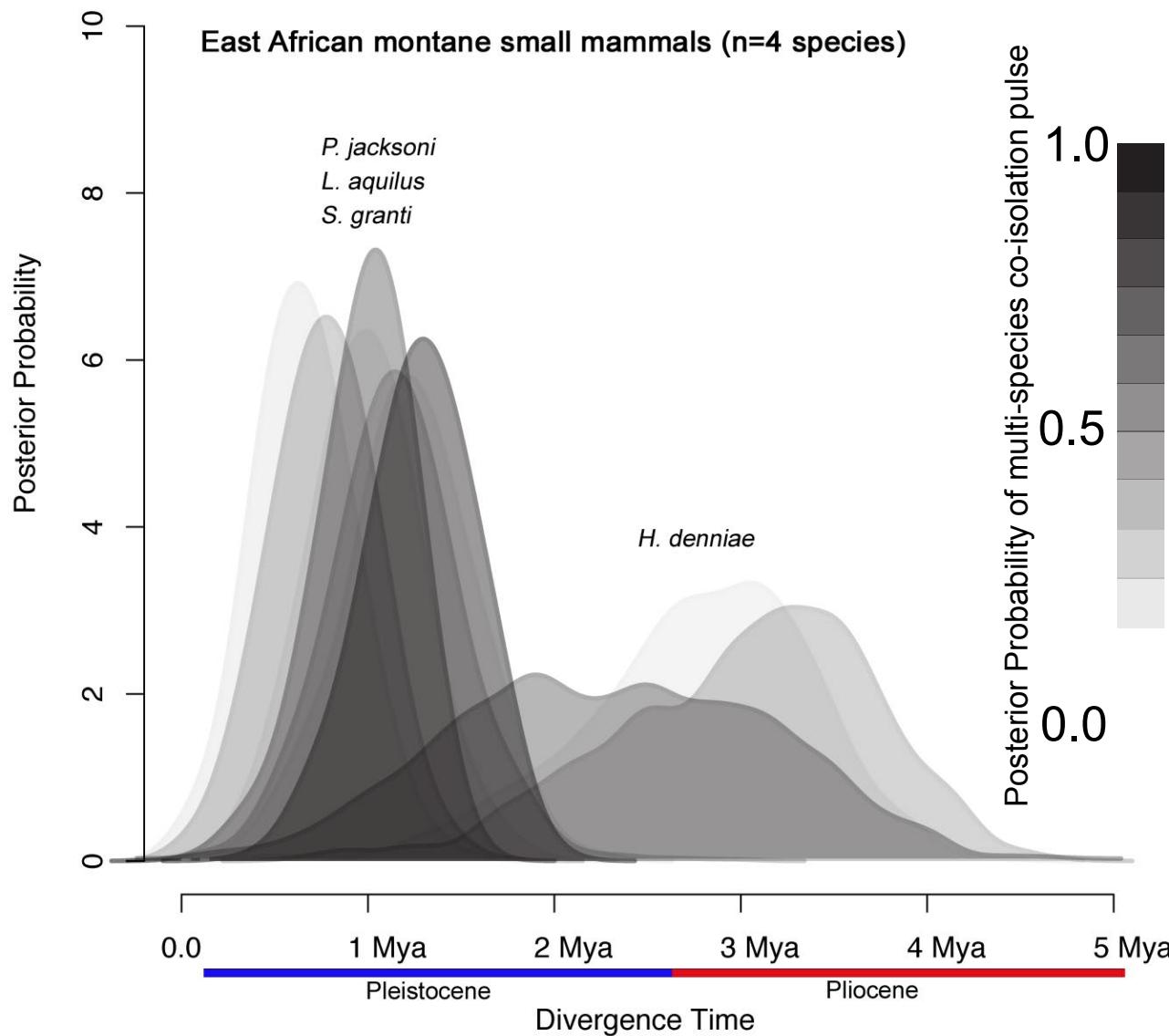
divergence times conditional on Ψ with
highest posterior probability ($\Psi=1$ in this case)



“simultaneous” divergence time
for 4 pairs

Software - MTML - msBayes

estimate divergence times averaged across posterior for number of times (Ψ)

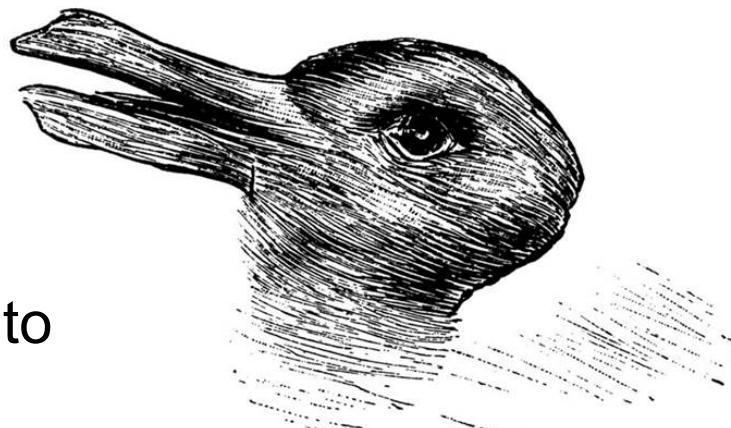




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Biodiversity Research (iDiv)
Halle-Jena-Leipzig



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INSTITUTE

The **City** College
of New York



THE GRADUATE CENTER
CITY UNIVERSITY
OF NEW YORK



MESS Data

Brent Emerson Henrik Krehenwinkel
Christine Parent Rosemary Gillespie
Chris Meyer

Thank you!



