

Dimensions US-BIOTA: A multidisciplinary framework for biodiversity prediction in the Brazilian Atlantic forest hotspot



Photo by Mauro Teixeira Jr.

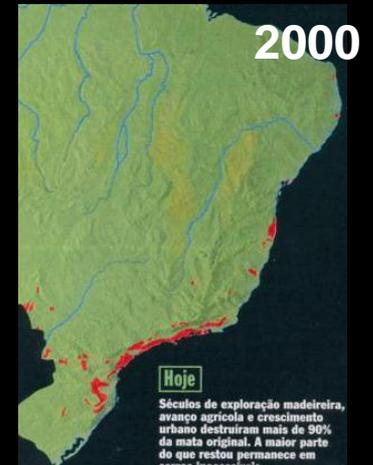
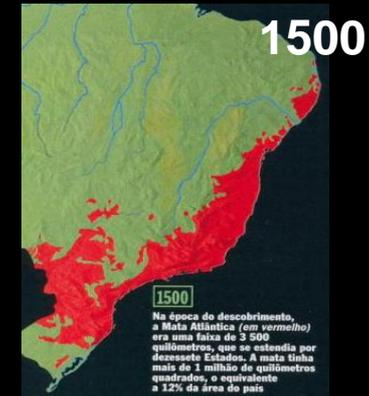


Workshop Dimensions US-BIOTA São Paulo
10/02/2014

Ana Carolina Carnaval (CUNY), Cristina Miyaki (USP)

Predicting geographical patterns of diversity is relevant in the face of rapid environmental shifts;

The Atlantic Forest of Brazil is a case in point.



BIODIVERSITY PATTERNS



**HISTORICAL
(EVOLUTIONARY)
PROCESSES**

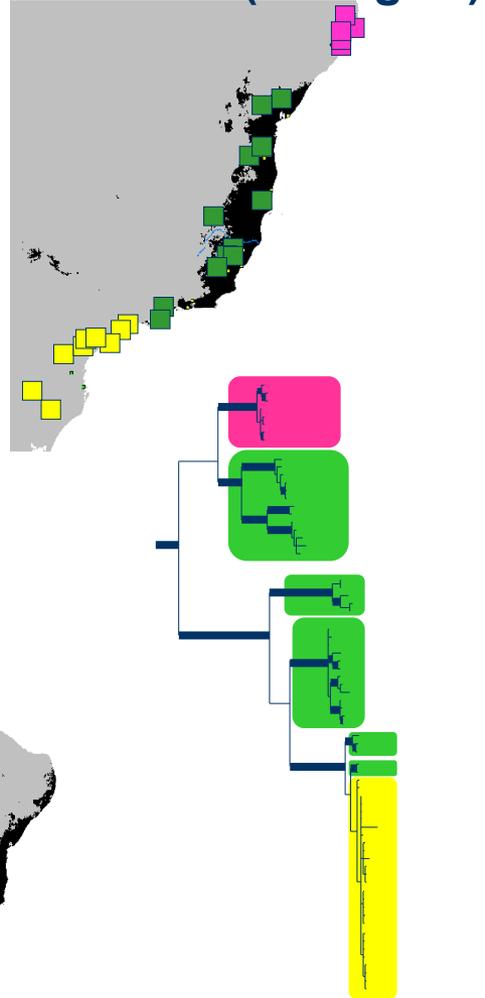
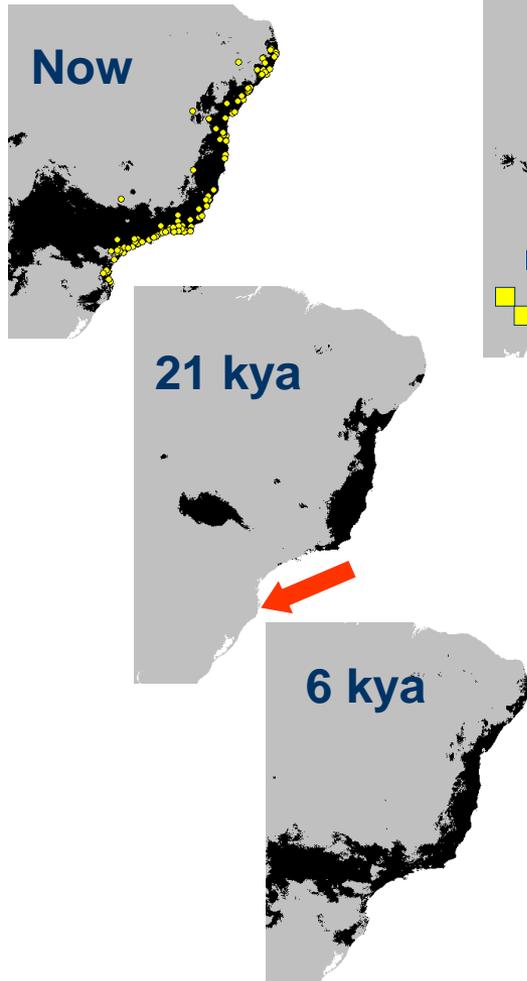


Photo by Agustin Camacho

Genetic data from widespread (mostly lowland) AF species suggest important role of Late Quaternary climate change in defining genetic diversity patterns

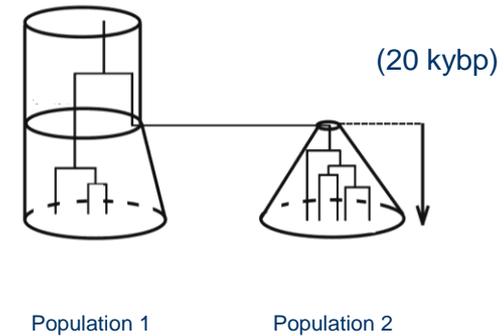


Intersection (“refugia”)

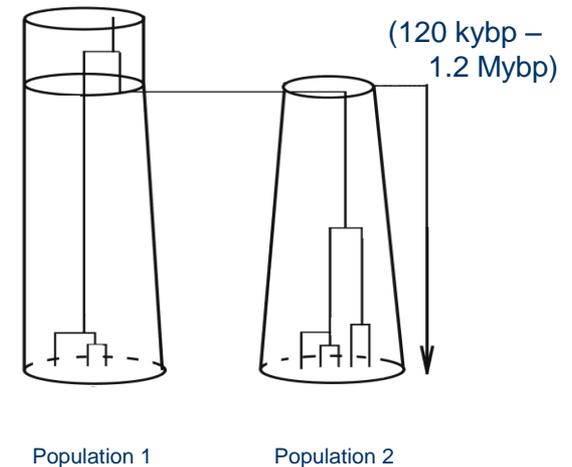


DNA data support

Post-LGM colonization of S lowland forests, explaining lower levels of genetic diversity in the S



Long-term persistence in isolated refugial areas



Carnaval et al. 2009

Genetic data from multiple montane (mostly southern) AF species suggest climatic stability in the south



Caparaonia itaiquara



Heterodactylus imbricatus



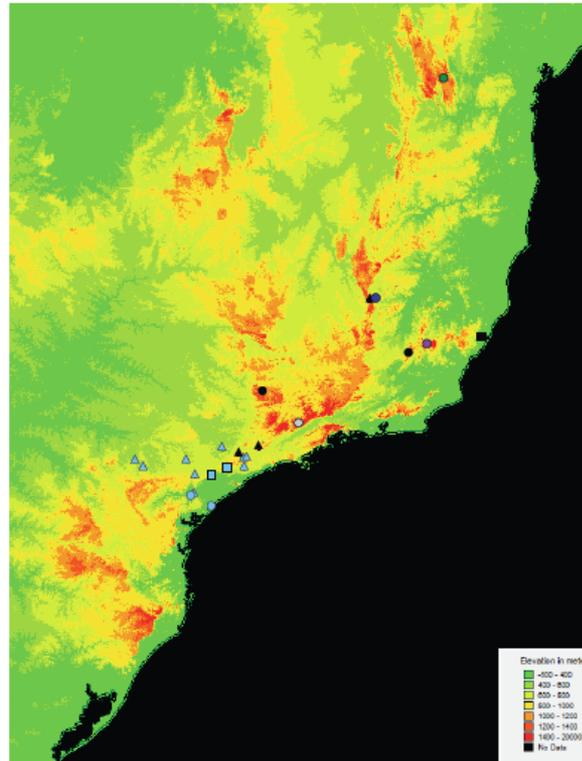
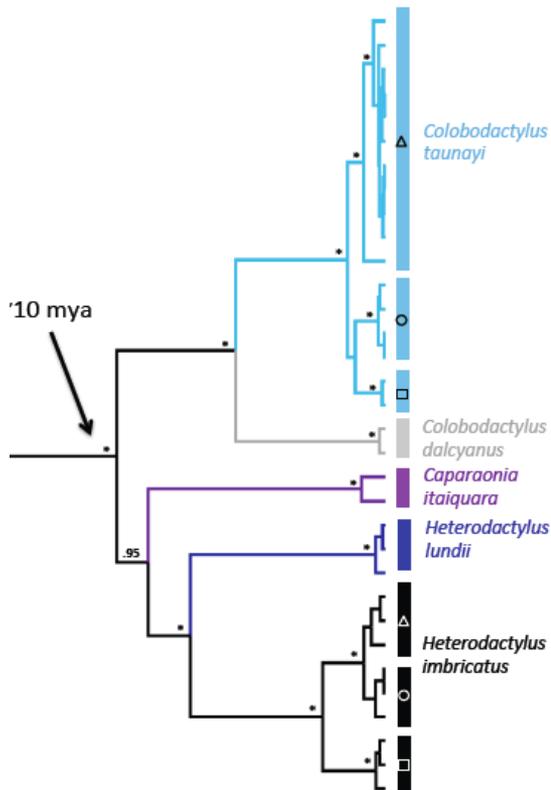
Heterodactylus lundii



Colobodactylus taunayi

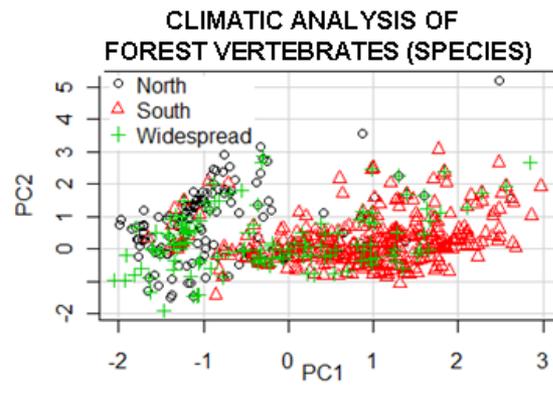
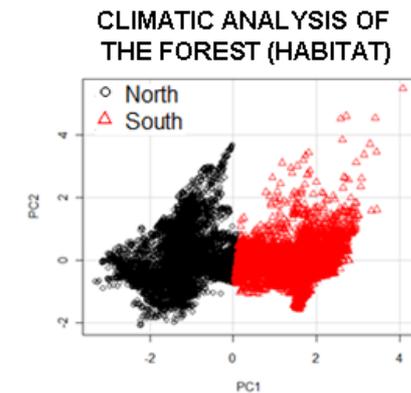


Colobodactylus dalcyanus

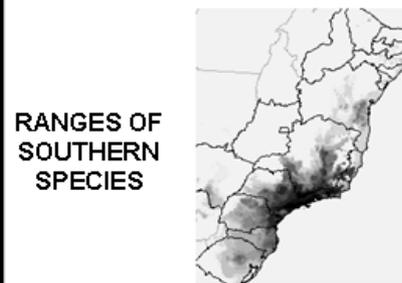
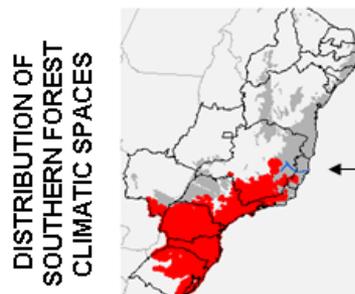
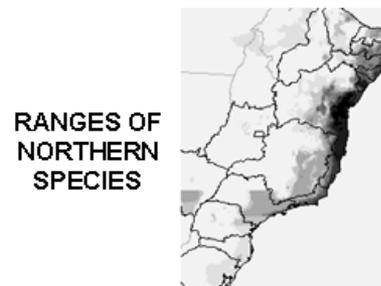
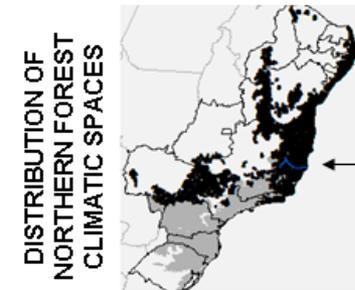


How many forests are there in our forest?

(Slightly) increasing complexity of correlative AF models



Left: PCA-based identification of two climatically distinct spaces within the Atlantic rainforest (top), and their respective northern (black) and southern (red) geographical ranges (bottom).

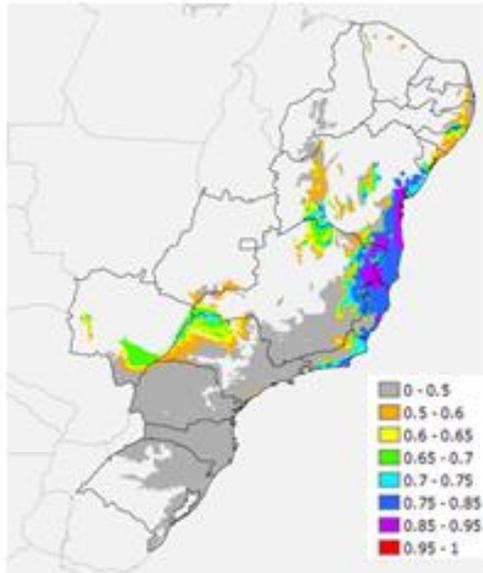


Right: PCA-based identification of species assemblages along the climatic axes of the Atlantic forest (top) depicting their northern (black), southern (red), or widespread (green) distributions.

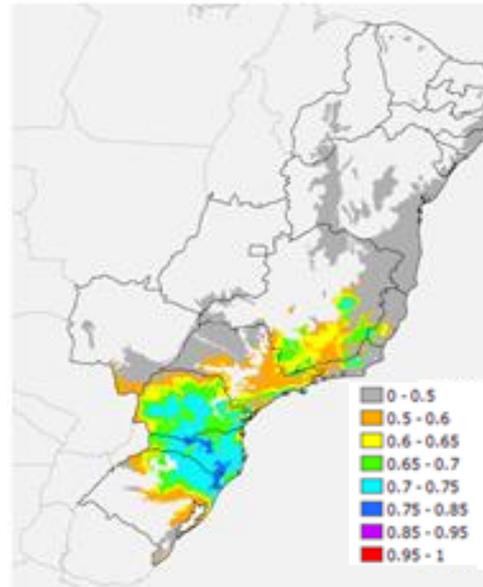
Mapping historical climatic stability – shifting refugia models (allowing forest dispersal across time slices)

PALEOSTABILITY
LAST 120 KYR

NORTHERN CLIMATIC
SPACE



SOUTHERN CLIMATIC
SPACE



Legend depicts suitability values, calculated as the sum of negative log probabilities of forest occurrence in each time period.

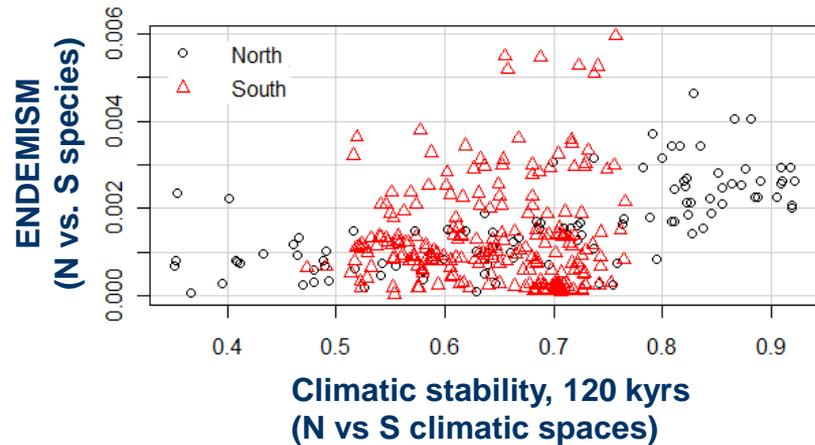
Higher stability still found in N vs S when we incorporate forest dispersal over time
Models over last 21kyr not that different from over 120kyr

If this movie works, we can review some of these ideas under a different perspective



And thank Jason Brown for the flight

Correlates of lineage endemism differ between the N and S (and we wouldn't see it by modeling the forest as a single entity)



phylogeographic endemism	variables	r	p	
overall	area	-0.243	0.033	*
	NPP	0.415	0.001	*
	120 kyr stability	0.387	0.007	*
	21 kyr stability	0.265	0.033	*
north	area	0.097	0.595	
	NPP	0.076	0.670	
	120 kyr stability	0.677	0.019	*
	21 kyr stability	0.642	0.04	*
south	area	-0.397	0.01	*
	NPP	0.467	0.001	*
	120 kyr stability	0.069	0.733	
	21 kyr stability	-0.001	0.995	

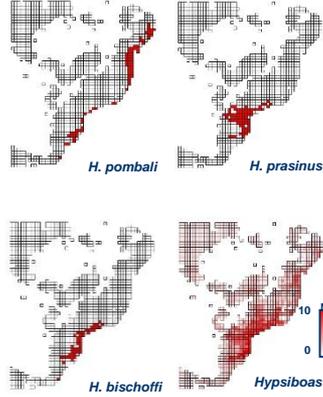
Assessing the spatial structure of phylogenetic turnover in the Brazilian Atlantic Rainforests: A First Step

Jason L. Brown¹, Mariana Lyra, Paula Valdujo, Dan Rosauer, and Ana Carnaval²

We employ phylogenetic generalized dissimilarity modelling (Phylo-GDMs), to characterize spatial phylogenetic turnover in the AF.

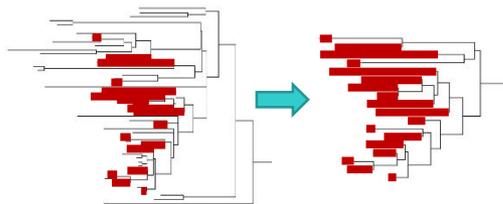
A case study on *Hypsiboas* Frogs

1. Occurrence Data



Occurrence data were collected for 18 species that occur in the AF and used to generate species distribution models with MAXENT.

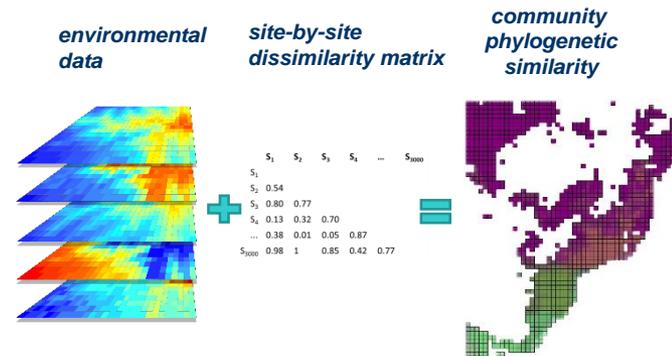
2. Phylogenetic Data



A phylogenetic hypothesis of all *Hypsiboas* species sequenced to date. Red branches depict species that inhabit the AF.

A trimmed phylogeny of the *Hypsiboas* species that inhabit the AF

Generalized dissimilarity modelling is a statistical technique for modelling changes in species composition between sites as a function of environmental and geographical attributes. More recently, it was extended to incorporate phylogenetic relationships into biodiversity analyses in ways not previously possible. This provides an intuitive way to model phylogenetic turnover across landscapes.

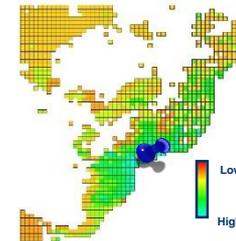


Correlations between the input spatial data (i.e. climate and vegetation) and a site-by-site distance matrix of phylogenetic dissimilarity are input into a GDM. A visualization of the Phylo-GDM depicts color space, where similar colors depict phylogenetically similar areas. The greater the difference in color space, the greater the differences in phylogenetic composition of the community.

3. Generate a matrix of the phylogenetic dissimilarity between each study locality

Phylogenetic Sorenson Index:
 $1 - \frac{2A}{(2A+B+C)}$
 where A is the length of shared branches and B and C are the length of branches found only in neighbor sets 1 & 2

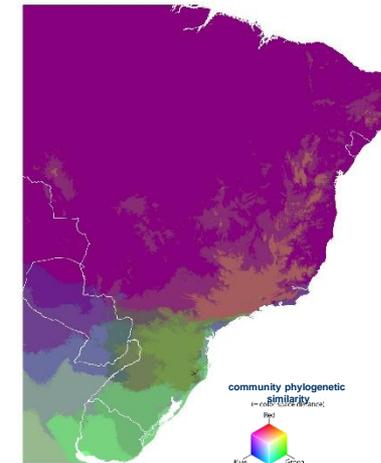
A visual depiction of Phylogenetic Sorenson Indexes for *Hypsiboas* spp. relative to one site



Output is a N dimensional site-by-site dissimilarity matrix, where N equals the number of sites included in analyses

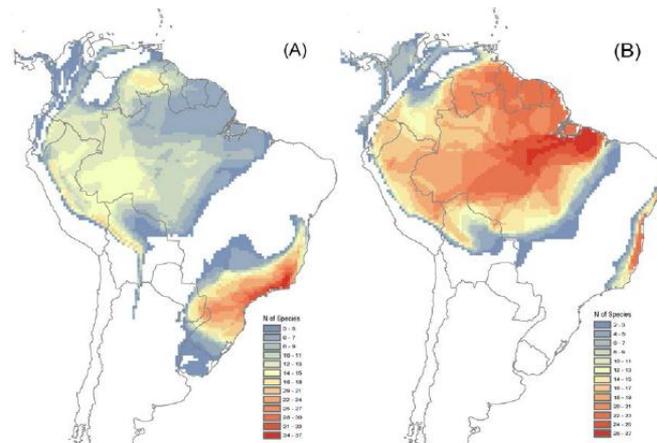
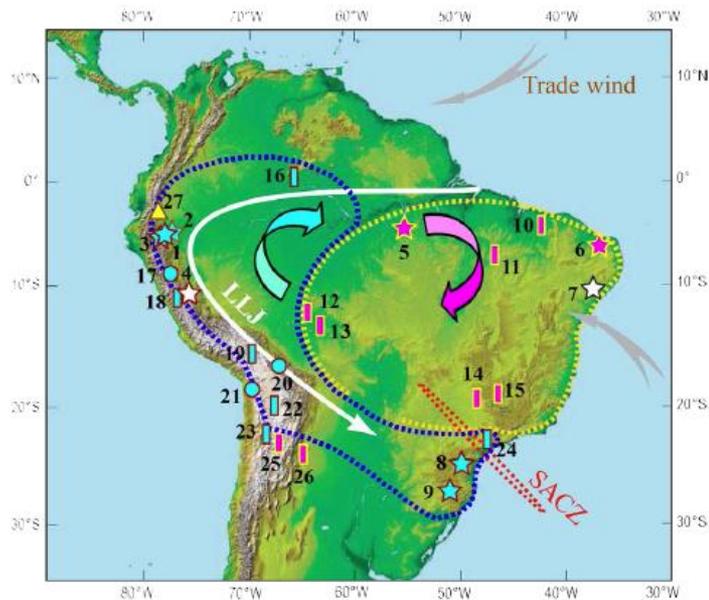
5. Project the Phylo-GDM into climate space

Once a GDM is properly parameterized, the model can be projected in high resolution climate space to depict turnover across the entire landscape. In addition, it can be projected into novel climates (i.e. future and paleo-climates).



To understand (and model) the MECHANISMS that explain this difference between the N and S biota, and AF environments, we can

- Describe the dynamics of moisture transport in the AF now and in the past
- Link past dynamics of moisture transport with biogeographical connections between the AF and other South American biomes



Records of past climate dynamics and richness patterns of forest bird species shared by the Amazonian and Andean forests with the SAF (A) or NAF (B) (from Cheng et al. 2013). Blue tones represent low richness; red depicts high richness.

To understand (and model) the MECHANISMS that explain this difference between the N and S biota, and AF environments, we can

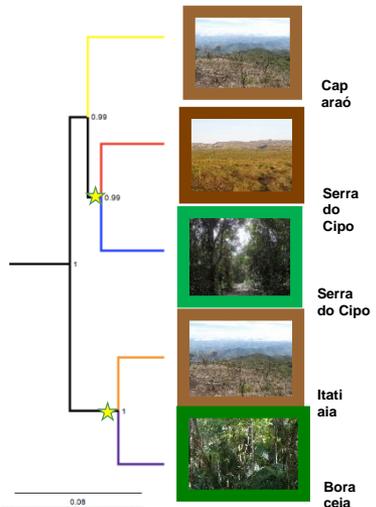
- Study the physiological limits of AF species and how they are linked to local microhabitats and diversity patterns



Maria Strangas
MT Rodrigues,
AC Carnaval

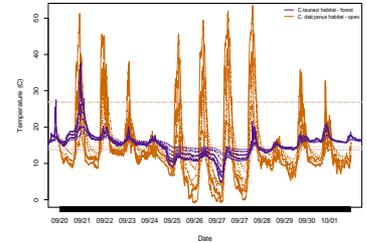
Understanding niche evolution: morphology and physiology of Heterodactylini lizards

Two pairs of closely related species occupy different environments (humid rainforest in green vs. open, high altitude fields in brown)

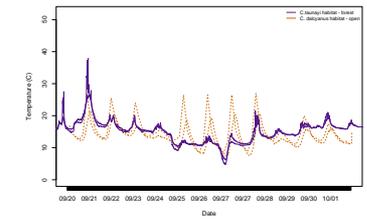


Microhabitat thermal environments of two closely related species differ. Coarse-grain data don't show these differences.

Microhabitat data suggest very different environments

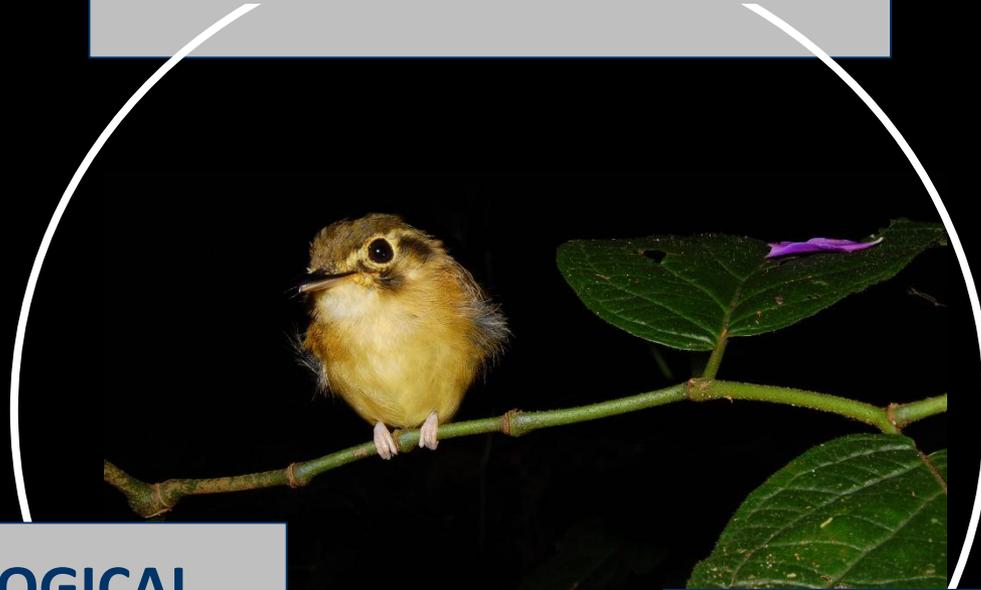


... even with behavioral thermoregulation



Dimensions US-BIOTA: A multidisciplinary framework for biodiversity prediction in the Brazilian Atlantic forest hotspot

BIODIVERSITY PATTERNS



**ECOLOGICAL
MECHANISMS,
CLIMATE &
VEGETATION
DYNAMICS**

**HISTORICAL
(EVOLUTIONARY)
PROCESSES**

Dimensions US-BIOTA: A multidisciplinary framework for biodiversity prediction in the Brazilian Atlantic forest hotspot

the taxonomic dimension of biodiversity



the functional dimension

the genetic dimension

Dimensions US-BIOTA: A multidisciplinary framework for biodiversity prediction in the Brazilian Atlantic forest hotspot

the taxonomic dimension of biodiversity



the functional dimension

the genetic dimension



the taxonomic dimension of biodiversity



the environmental dimension



the functional dimension



the genetic dimension



taxonomy

Diversity of plants

Diversity of invertebrates

Diversity of vertebrates

Diversity of bacteria

environment

Current climate, hydrology

Paleoclimates (speleothems oceanography)

Climatic data and modeling

Geology, tectonics

Paleoecology (fossil pollen)

function

Vegetation modelling

Ecosystem services

Animal physiology

Plant Ecology

Landscape Ecology

genetics

Pop. genetics

Genomics

Phylogeography



the taxonomic dimension of biodiversity



the functional dimension

the genetic dimension





the taxonomic dimension of biodiversity



the functional dimension

the genetic dimension



WORKSHOP US-BIOTA DIMENSIONS. FEB 10th 2014. OVERVIEW



1. The BIOTA-FAPESP Program; C. Joly
2. Dimensions US-BIOTA in the Atlantic Forest; A. Carnaval and C. Miyaki
3. Geomorphology and paleoclimates ; F. Cruz. C. Grohmann, S. Hiruma

BREAK, POSTERS

4. DNA, historical demography and communities past; M. Hickerson
5. Paleodiversity patterns, from the fossil record; M. Ledru
6. Historical biogeography, niche evolution in *Leandra*; M. Reginato

7. Landscape Ecology in the AF; M. C. Ribeiro
8. Climate modelling, INPE's projections, and distribution of Brazilian biomes; G. Sampaio
9. AF protected areas: vulnerability to climate change; R. Loyola

BREAK, POSTERS

10. The Global Biodiversity Observation Network; D. Faith

ROUNDTABLE

11. Final Remaks, Closing; C. Miyaki

taxonomy

Diversity of plants

Diversity of invertebrates

Diversity of vertebrates

Diversity of bacteria



environment

Paleoclimates (speleothems oceanography)

Climatic data and modeling

Geology, tectonics

Current climate, hydrology

Paleoecology (fossil pollen)

function

Vegetation modelling

Ecosystem services

Animal physiology

Plant Ecology

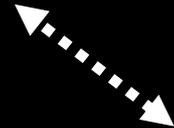
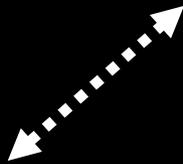
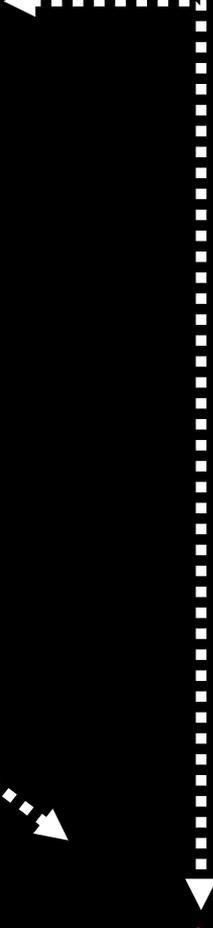
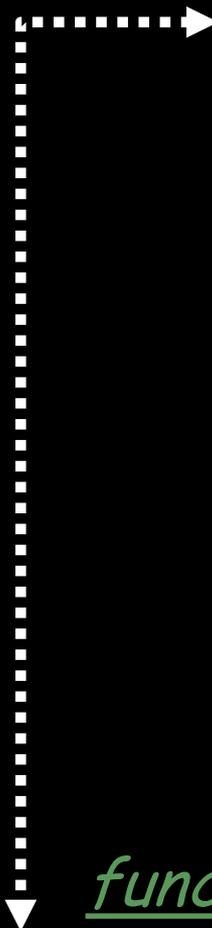
Landscape Ecology

genetics

Pop. genetics

Genomics

Phylogeography



To reflect and discuss at the end of the day:

1. What data or data analyses would YOU like to see generated by this initiative?

2. Which applications of the data would you see as important?

Strategies for conservation, links with policy

Public outreach

Professional preparation, student training, global science

3. How can the outcomes be greater than the sum of the parts (INTEGRATION)?

Synthesis, compendia, comparisons (new maps, data sets, digital archives)

Integration across fields under a hypothesis-testing framework, modeling and testing with independent data sets

One data set poses questions for others

Acknowledgements

FAPESP, NSF and NASA, “Dimensions US-BIOTA: A multidisciplinary framework for biodiversity prediction in the Brazilian Atlantic forest hotspot”

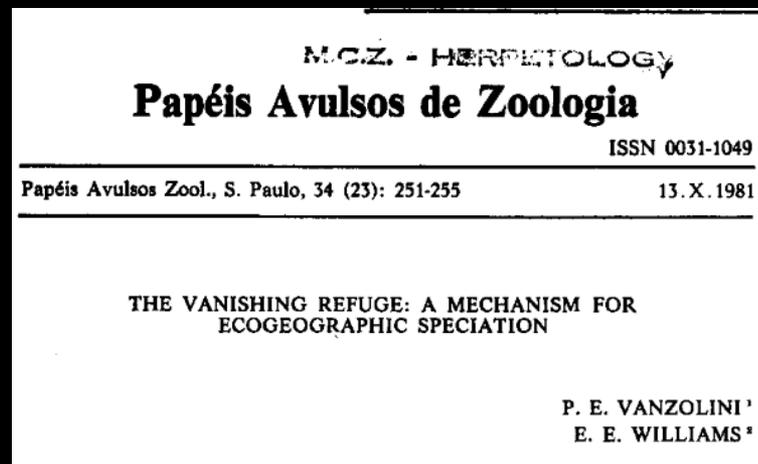
CNPq, CAPES, and NAP BioComp

FAPESP event planning team

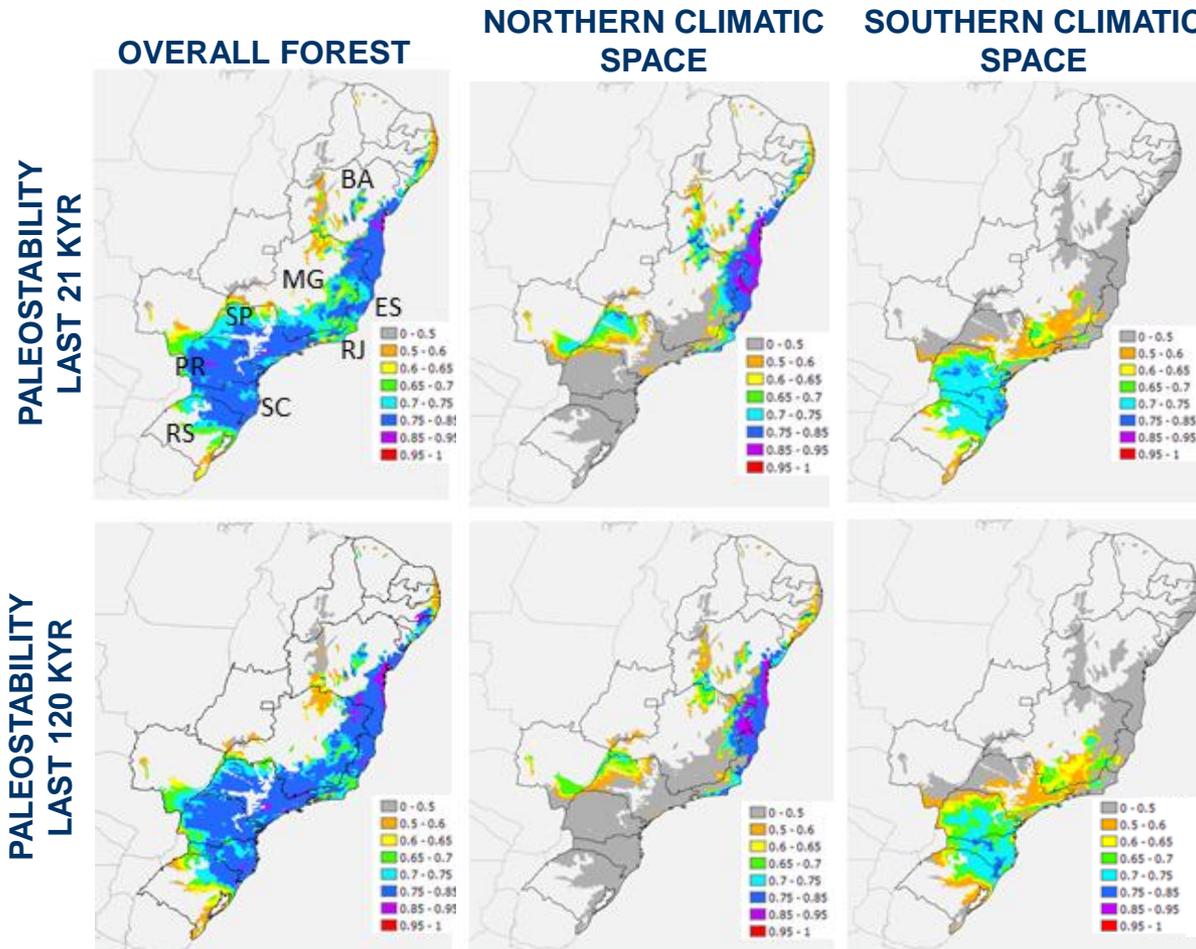
Project investigators, collaborators, and students



Paulo Vanzolini; Biogeographer and Composer († 2013)



Mapping historical climatic stability – shifting refugia models (allowing forest dispersal across time slices)



Legend depicts suitability values, calculated as the sum of negative log probabilities of forest occurrence in each time period.

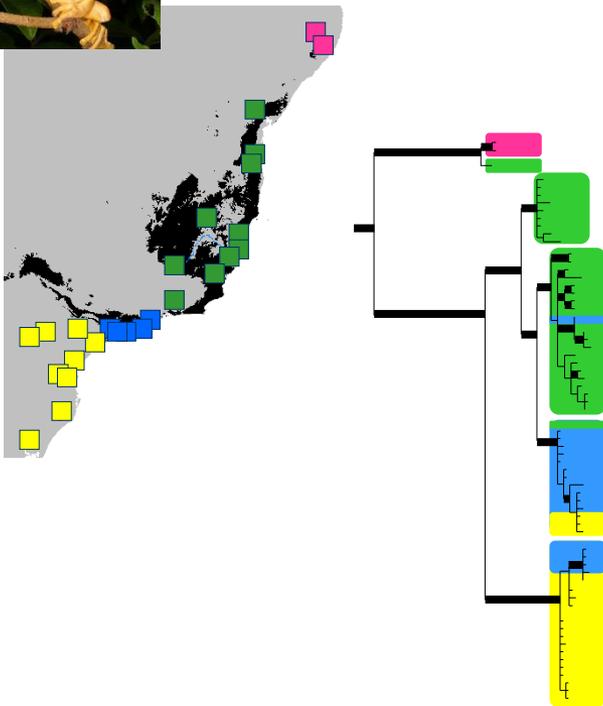
Higher stability still found in N vs S when we incorporate forest dispersal over time Models over last 21kyr not that different from over 120kyr

Can we use this climatic information to predict/model patterns of genetic (lineage) endemism?

Builds from the concept of Phylogenetic Endemism (Rosauer et al. 2009):

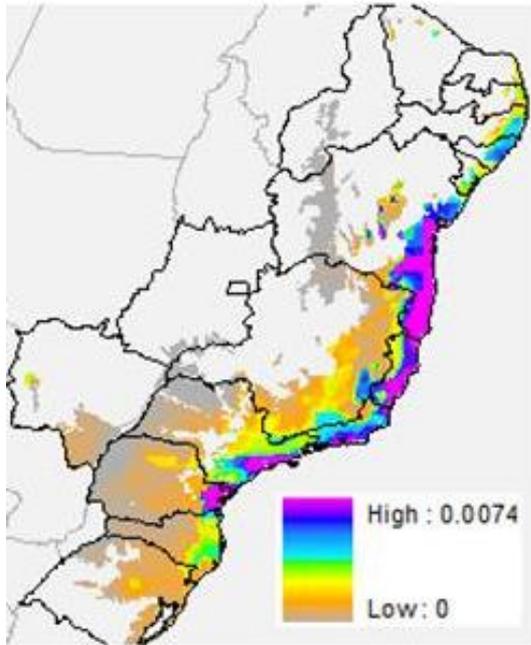
- The degree to which units of phylogenetic diversity are limited to the different portions of a target region.
- Reflects the concentration of evolutionary history in geographical space.

Exploring the usefulness of mapping Phylogeographic Endemism



- Particular focus in recent history (tree topology above species level is ignored)
- Interest in effects of Late Quaternary climate change on distribution of intra-specific genetic diversity
- Results from a combination of processes: lineage differentiation, lineage maintenance through time, and range restriction.

Does climate (both historically and now) predict patterns of genetic endemism?



PHYLOGEOGRAPHIC
ENDEMISM,
ALL SPECIES

- We combine DNA sequence data and correlative models of distribution for 25 spp of AF vertebrates to identify how major lineages are spatially restricted
- High scores are allocated to areas where a large component of genetic variation (within species) is restricted to a small area

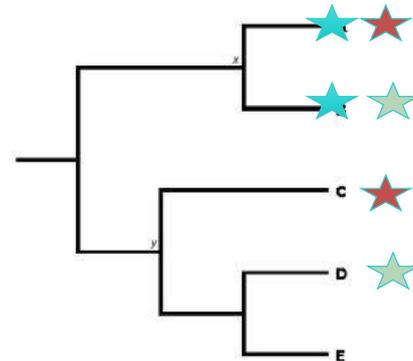
Phylogenetic Endemism = the amount of evolutionary history uniquely represented in a given area

Calculated by dividing the branch lengths uniting every possible pair of lineages by their combined ranges, then summing across all pairs of lineages...

$$PE = \sum_{\{c \in C\}} \frac{L_c}{R_c}$$

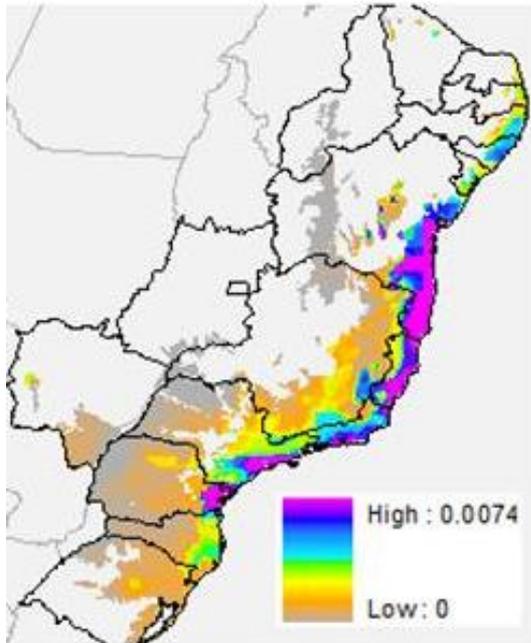
Length of branch (c)

The clade range (the union of the combined ranges of the taxa descended on the phylogeny from branch)



... so high scores are allocated to areas where a large component of phylogenetic variation is restricted to a small area

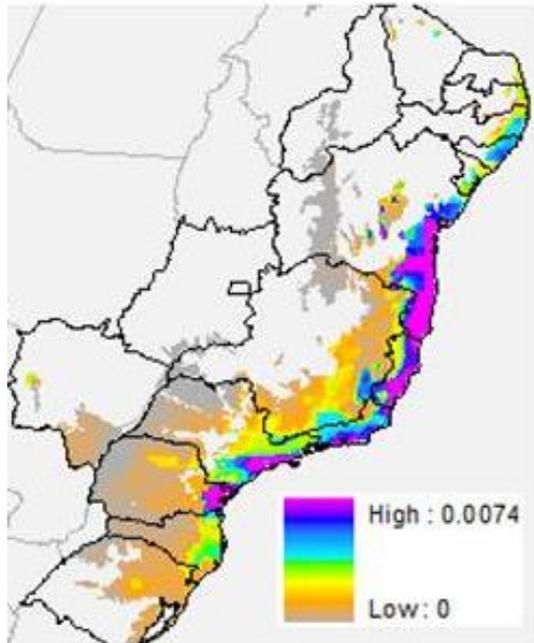
Does climate (both historically and now) predict patterns of phylogeographic endemism?



PHYLOGEOGRAPHIC
ENDEMISM,
ALL SPECIES

- We combine mtDNA sequence data and SDMs for 25 spp of AF tetrapods to identify how major intraspecific lineages are spatially restricted
- We use BIODIVERSE (Laffan et al. 2010) to map phylogeographic endemism (PgE)
- High scores are allocated to areas where a large component of phylogeographic variation is restricted to a small area

Does climate (both historically and now) predict patterns of phylogeographic endemism?



PHYLOGEOGRAPHIC
ENDEMISM,
ALL SPECIES

- PgE reflects the degree to which the evolutionary history of each major intra-specific lineage (as opposed to each taxon) is spatially restricted.

Hence it depends on

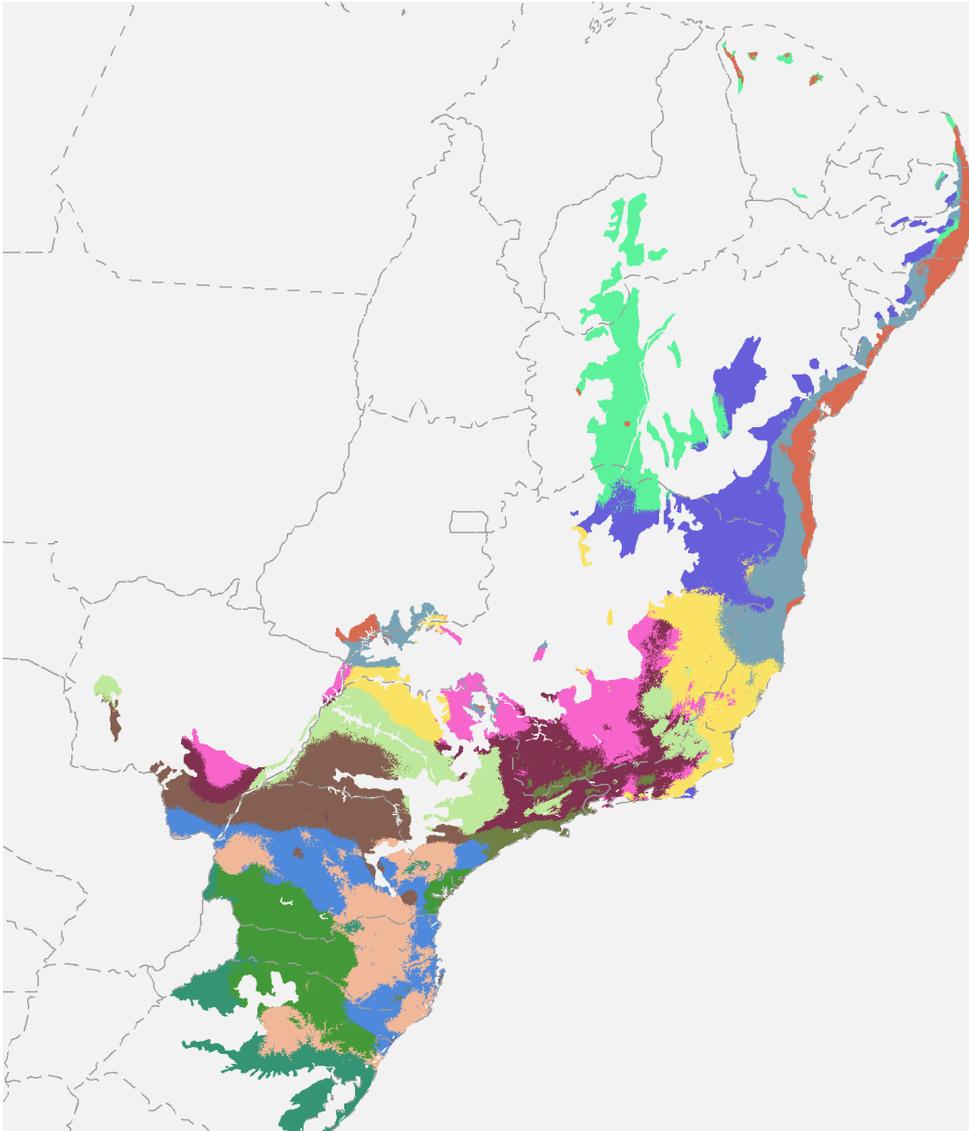
- the range of that lineage
- how much of its history is shared with closely related lineages
- how widespread those lineages are.

Does climate (both historically and now) predict patterns of phylogeographic endemism?

Using SAM (Spatial Analyses in Macroecology; Rangel et al. 2010), we ran correlations and partial regressions between PgE and

1. Historical climate: an estimate of climatic stability of the forest over the last 21 kyr (1kyr intervals) and 120 kyr (4kyr intervals) based on shifting refugia models from snapshot simulations using the Hadley Center Climate model (Fuchs et al. 2013)
2. Present-day climate: NPP and a proxy of climate heterogeneity (area of uniquely defined climatic spaces, as per k-means clustering)

Mapping contemporary climates



Discrete climatic spaces within the Atlantic Forest under present-day climates given K-clustering analysis ($K = 14$).

Table 2. Partial Least Squares Regressions of phylogeographic endemism against historical stability (proxy for lineage maintenance through time) and the geographic extent (area) of unique, contemporary climatic spaces (proxy for present-day range restriction) across across A) the entire Atlantic Forest, B) only the northern climatic space of the forest, and C) only the southern climatic space of the forest.

Response variable	Predictor variables	r ²	AIC weights
A. Overall phylogeographic endemism (Atlantic forest-wide, all species pooled)	120 kyr stability & current climate	0.208	1
	120 kyr stability	0.15	<0.001
	current climate	0.059	<0.001
	shared 120 kyr stability & current climate	0.01	
	21 kyr stability & current climate	0.141	1
	21 kyr stability	0.07	<0.001
	current climate	0.059	<0.001
	shared 21 kyr stability & current climate	-0.002	
B. Phylogeographic endemism, northern species only	120 kyr stability & current climate	0.459	0.273
	120 kyr stability	0.458	0.727
	current climate	0.009	<0.001
	shared 120 kyr stability & current climate	<0.001	
	21 kyr stability & current climate	0.414	0.286
	21 kyr stability	0.412	0.714
	current climate	0.001	<0.001
	shared 21 kyr stability & current climate	<0.001	
C. Phylogeographic endemism, southern species only	120 kyr stability & current climate	0.162	0.389
	120 kyr stability	0.005	<0.001
	current climate	0.157	0.611
	shared 120 kyr stability & current climate	0.003	