

# Course Introduction

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## Arguments for Phylogenetic and Functional Analyses in Ecology

**SESYNC**  
**1 Feb 2017**

- ## Introductions
- Quickly around the room
    - Name
    - Institution
    - One brief statement on general research interests

## General Course Info

- Thanks to:
  - SESYNC for (tons of) help organizing, space, funding
  - The funding gods (NSF Div. Biol. Infra.):
    - Advances in Biological Informatics (Swenson)
      - Funded research developing/testing phylogenetic methods
      - Funded this workshop
    - SESYNC/Univ. of Maryland
      - Doubled size of workshop
      - People & infrastructure

## General Course Info

- Mixture of:
  - Lectures to build understanding of concepts and to discuss concepts and existing literature
    - I think it is most interesting and productive to discuss topics as I present them instead of just me lecturing
    - **Cautionary note: lectures are the outcome of my perspective on the field and therefore are biased towards my opinion**
      - In some instances I will raise counter opinions
      - In other words, there may be (many?) alternative routes/perspectives that I don't present due to my biases that may be useful for you to use and I am happy to discuss them if you like.

## General Course Info

- Mixture of:
  - R examples
    - Some data handling
    - Some data structure
    - Examples of how to build existing or ‘new’ functions
      - I do this so you know what is actually being done, how it is done (important for your development of new code if you have a new idea), and so you can see how code might be improved
      - Depending on your R abilities this aspect of the course may be very hard to understand, but stay with us.
  - Simply using existing/‘new’ functions
    - Useful particularly for those that don’t understand R code very well and just want to know how to plug in data and get an ‘answer’

## General Course Structure

- Wednesday (Today)
  - Morning
    - Why use phylogenetic and function information in ecology?
    - Phylogenetic terminology and structure
    - Phylogenetic data in R
    - Trait data in R
    - Community data in R
  - Afternoon
    - Alpha Diversity

## General Course Structure

- Thursday
  - Morning
    - Null Models
    - Integrating Species Abundance Distributions & Traits (Phylogenies)
      - Lead by Maria Natalia Umana
  - Afternoon
    - Beta Diversity

## General Course Structure

- Friday
  - Morning
    - Phylogenetic Non-Independence
    - Quantifying Phylogenetic Signal & Trait Evolution
  - Afternoon
    - A Primer of Comparative Methods

## General Course Structure

- Saturday
  - 1/2 to 1/3 day
  - Talking to other programs
  - Splitting and speeding up code
  - Wrangling data
  - Student specific queries

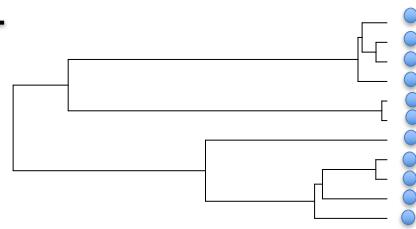
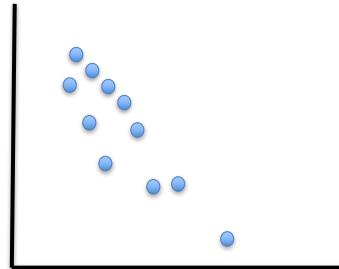
Why phylogenies and function in  
ecology

## Problem with Traditional Correlation Tests

### Central Assumptions in Statistics

-Normally distributed data (parametric statistics)

-Independent observations  
- Points are independent

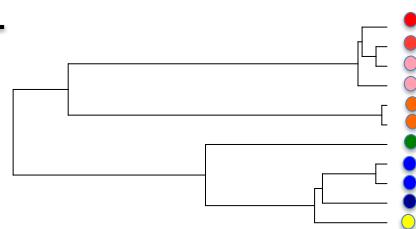
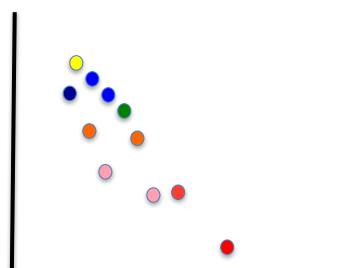


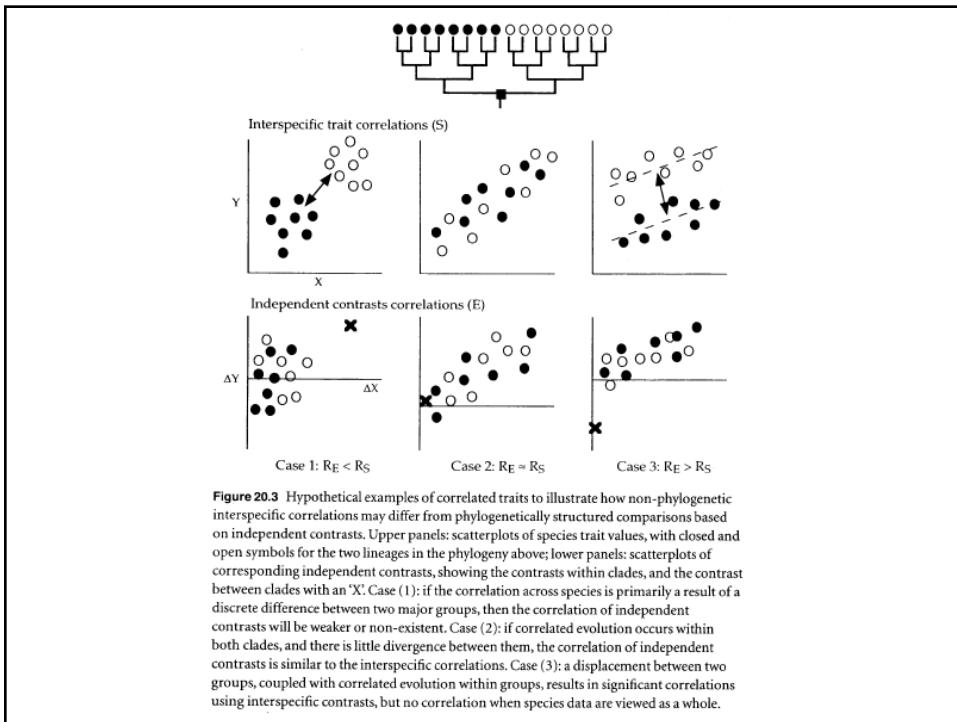
## Problem with Traditional Correlation Tests

### Central Assumptions in Statistics

-Normally distributed data (parametric statistics)

-Independent observations  
- Points are independent





# The Questions

- How can so many species co-exist?
- Why are there so many species in the first place and where did they come from?
- What determines the assembly of communities?

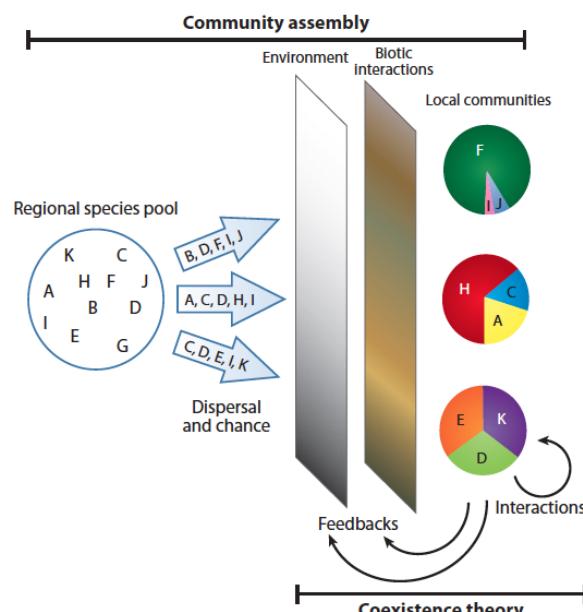
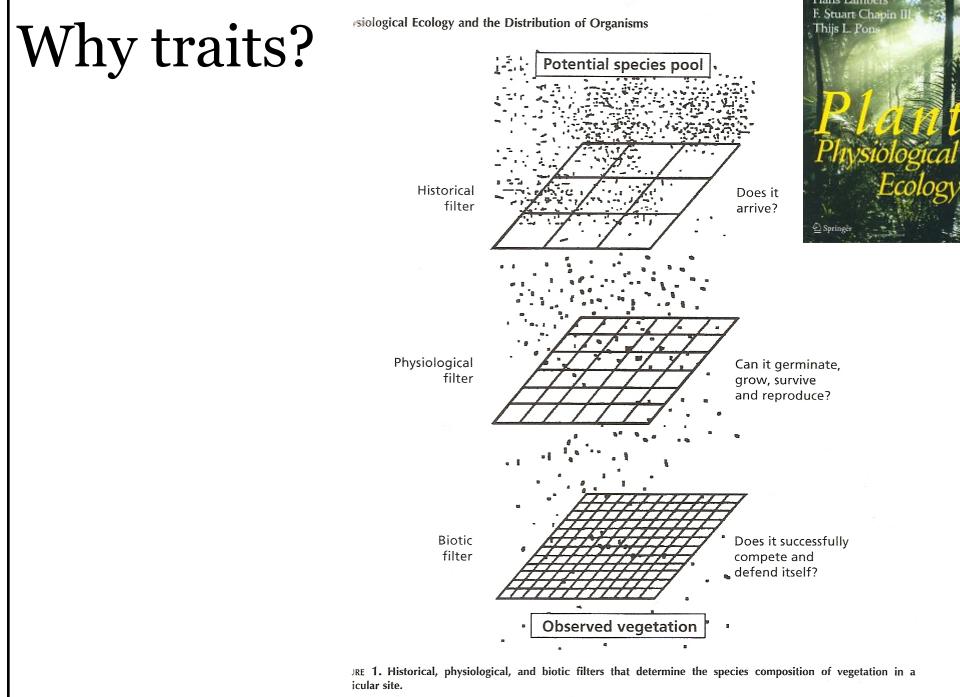
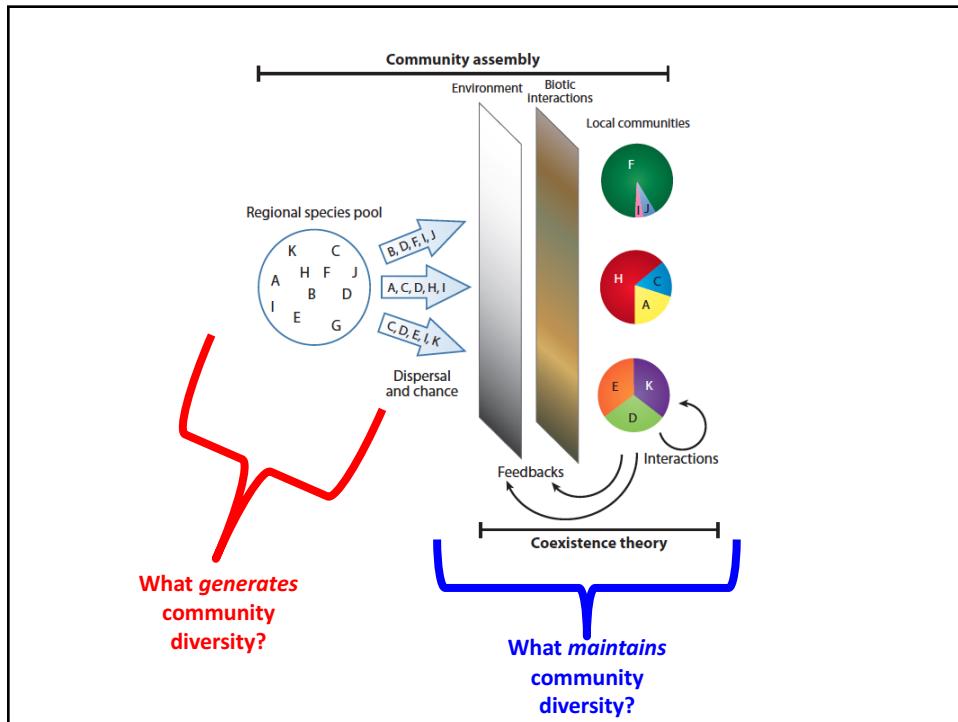


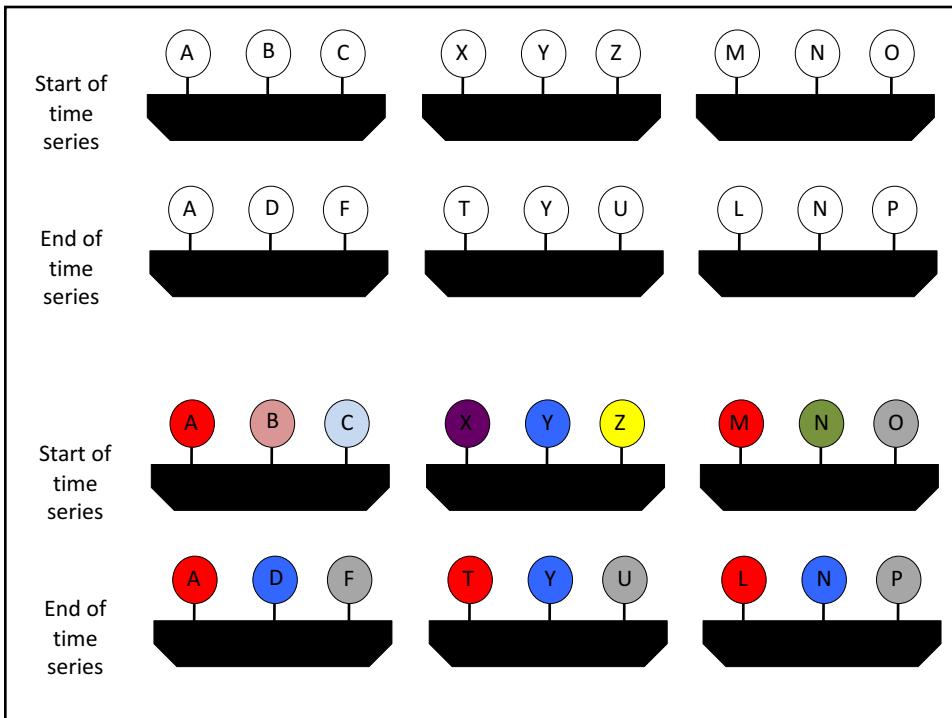
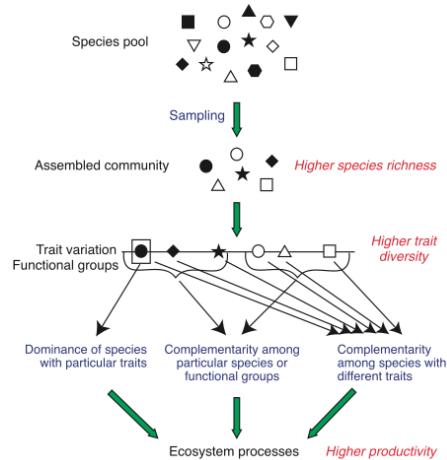
Figure 1

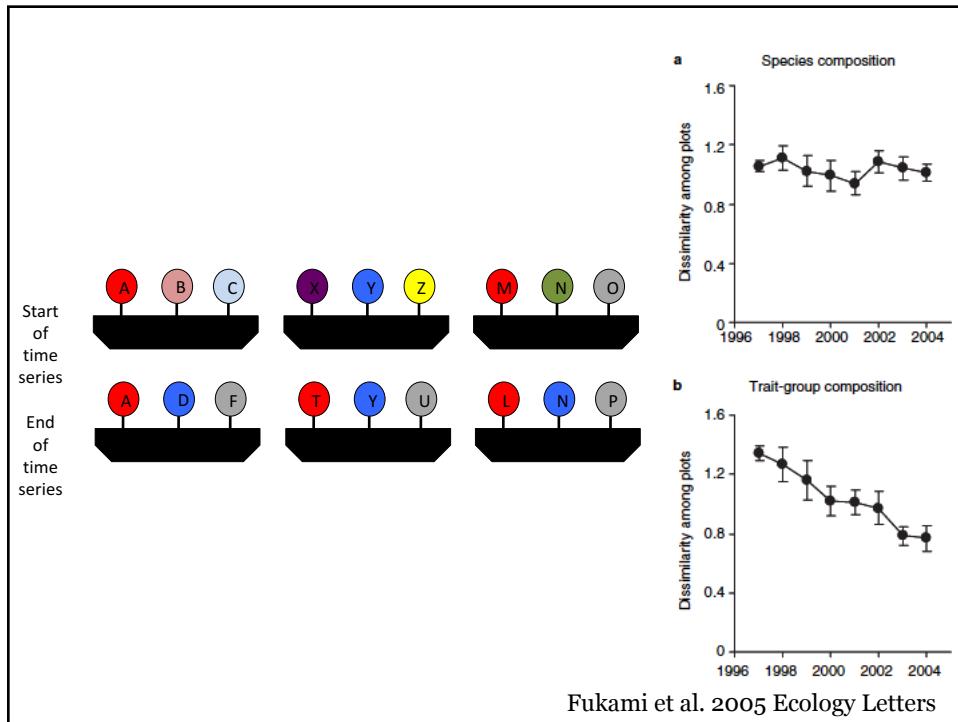
HilleRisLambers et al. 2012 A.R.E.S.



## Why traits?

- Functional diversity is generally the dimension of biodiversity that is most closely linked to ecosystem processes
- Investigations that ignore function may often incorrectly infer process





## A Case Study: The Temporal Turnover of Tropical Tree Assemblages – Why Traits Matter



## What Do We Know About Tropical Tree Communities?

- Tropical tree assemblages are diverse
  - 0.5 km<sup>2</sup> of Panamanian rain forest has as many tree species as eastern North America
- Tropical tree assemblages are surprisingly dynamic
  - 7 censuses over 30yrs on Barro Colorado Island, Panama
    - 391,278 individuals counted
    - 174,435 tree deaths
    - 155,955 recruits



## Determinism vs Stochasticity

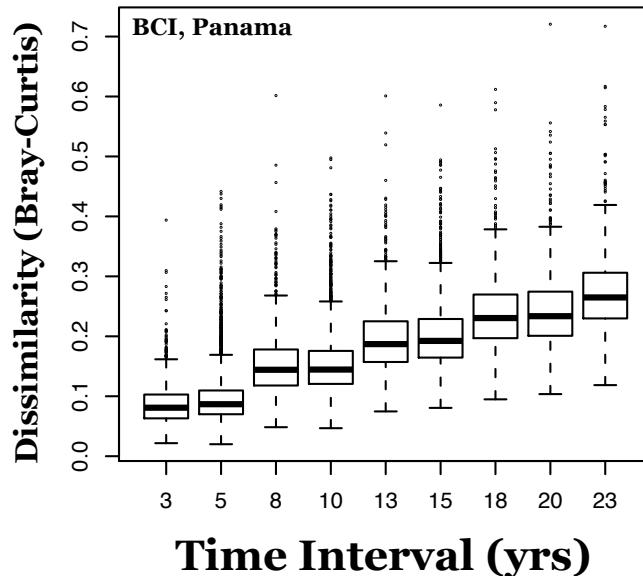
- Tropical tree assemblages present a substantial challenge for community ecologists
  - Niche vs Neutral
- Strong tests of niche and neutral predictions require information regarding the similarity of species
  - Direct measurements of functional similarity
  - Phylogenetic proxies of similarity?

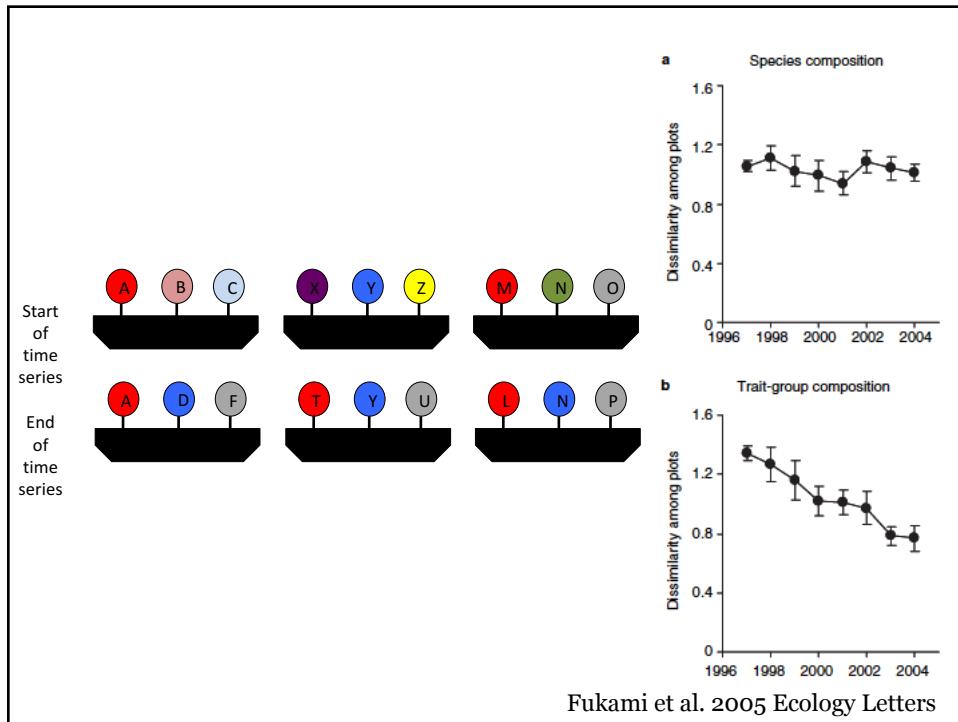


## Function, Phylogeny and Tropical Trees

- Non-random phylogenetic and functional structure within forest plots
  - e.g. Webb 2000; Kembel & Hubbell 2006; Swenson et al. 2006, 2007; Swenson & Enquist 2007; Kraft et al. 2008; Swenson & Enquist 2009; Kraft & Ackerly 2010, Paine et al. 2011...
  - Scale dependency
- Non-random spatial turnover in the phylogenetic and functional composition
  - Swenson 2011; Swenson et al. 2011, 2012; Hardy et al. 2012; Zhang et al. 2013
- Temporal turnover and dynamics?
  - Neutral drift ?

## Tropical Tree Temporal Turnover





# Niche & Neutral Predictions

- **Neutral Theory**
  - Functional & phylogenetic turnover no different than that expected **given** the observed species and individual turnover (**think drift**)
  
- **Deterministic Turnover**
  - Luquillo (successional) functional & phylogenetic turnover should be faster than that expected **given...**(**think directional selection**)
  - BCI (less disturbed) functional & phylogenetic turnover should be slower than that expected **given...**(**think stabilizing selection**)

# Trait Data

- “Functional traits”
  - Leaf %C, %N, %P
  - Specific Leaf Area ( $\text{cm}^2/\text{g}$ )
  - Maximum Height
  - Seed Mass
  - Wood Density
  - C & N Stable Isotopes
  - Root:Shoot
  - Amax (Photosynthetic Rate)
  - Hydraulic Conductance
  
- Mass-based traits
  - Generally best predictors of demographic rates in these forests
  
- Multivariate similarity



**Joe Wright**  
STRI

# Molecular Phylogenies

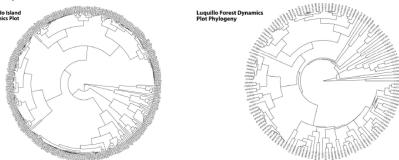
## Specimen Vouchering

- 3-4 Individuals for vouchering
- Tagged individuals within plots
- Deposited in US (Smithsonian)



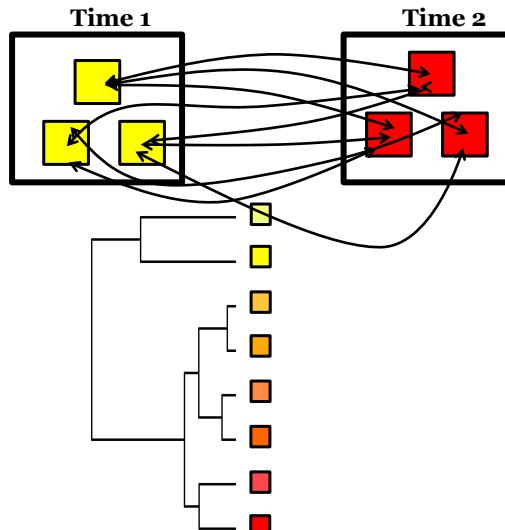
## Sequencing and Alignment (Kress & Erickson SI)

- DNA Regions (*rbcL*, *matK*, *trnH-psbA*)
- Global and taxonomically-informed alignment
- Kress et al. 2009 PNAS, 2010 PLoS One



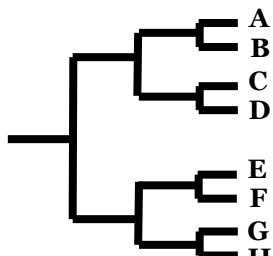
# Phylogenetic & Functional Turnover

- Phylogenetic and Functional Turnover
- Between each time interval within each subplot
  - 20x20m

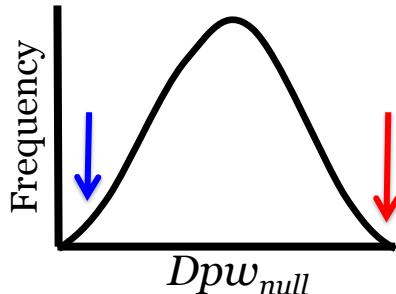
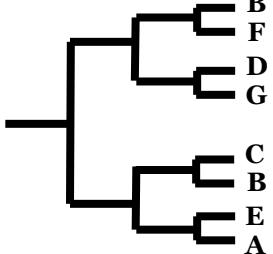


$$D_{PW} = f_A \sum_{i=1}^{S_A} f_i \bar{\delta}_{ib} + f_B \sum_{j=1}^{S_B} f_j \bar{\delta}_{ja}$$

## Null Models



Shuffle Names



Does not randomize community data

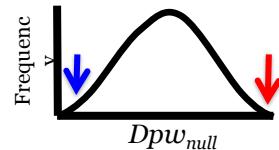
Maintains:

- species alpha and beta diversity
- community and species abundances
- levels of spatial contagion within a species (ie 'dispersal limitation')

Randomizes:

- functional similarity and relatedness of species

## Predictions



- **Neutral Theory**

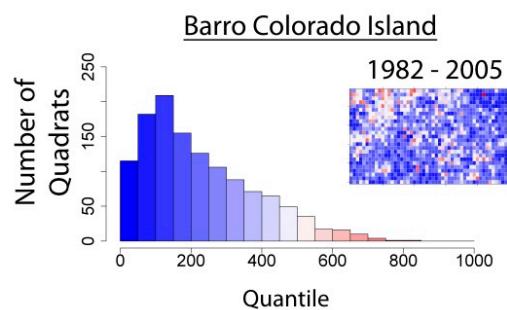
- Functional & phylogenetic turnover no different than that expected **given** the observed species and stem turnover

- **Deterministic Turnover**

- Luquillo (successional) functional & phylogenetic turnover should be faster than that expected **given...**
- BCI (less disturbed) functional & phylogenetic turnover should be slower than that expected **given...**

## Part 1: BCI Results

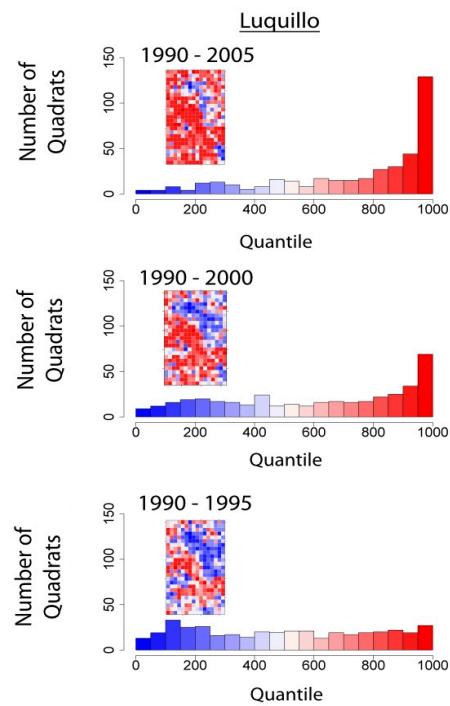
- *Lower than expected functional turnover through time*
- Phylogeny = Random
  - Habitat differences



Swenson et al. *Ecology* 2012

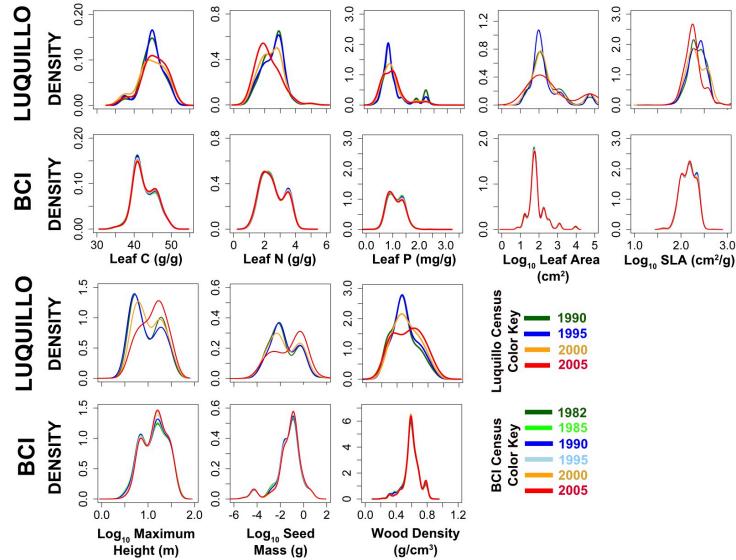
## Part 1: LUQ Results

- *Higher than expected functional turnover through time*
- Phylogeny = Random
  - No habitat differences



Swenson et al. *Ecology* 2012

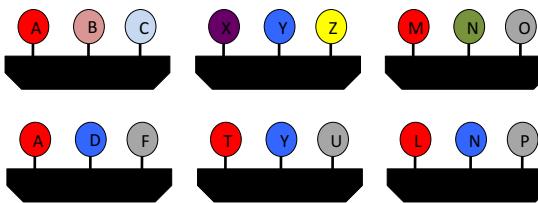
# Function Through Time



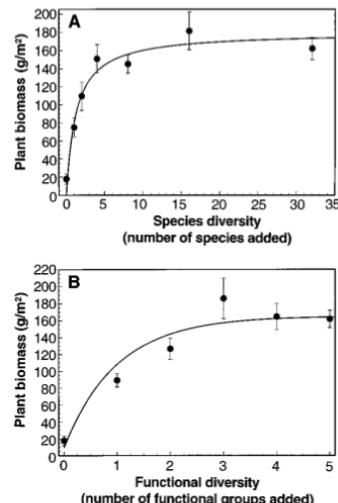
Swenson et al. *Ecology* 2012

## Part 1: Summary

- Neutral Theory & Temporal Turnover
  - Can we predict which *species* will colonize?
    - Probably not, but we may be able to predict what type of *functional strategy* will colonize.
- BCI Functional Stasis with Drifting Binomials
  - 391,278 individuals
  - 174,435 tree deaths
  - 155,955 recruits



## Functional Diversity

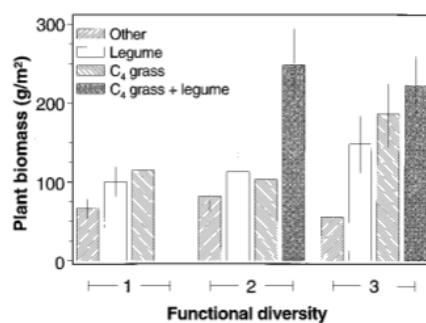


Tilman et al. 1997 Science

**Fig. 1.** (A) Dependence of 1996 aboveground plant biomass (that is, productivity) (mean and SE)

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## Functional Diversity



**Fig. 2.** Effects of functional composition on 1996 aboveground plant biomass (productivity) in plots containing at least one legume species (Legume), at least one C<sub>4</sub> grass species (C<sub>4</sub> grass), at least one of each (C<sub>4</sub> grass plus legume), or only species from other functional groups (Other). Mean and SE are shown, using all plots containing 1, 2, or 3 functional groups.

Tilman et al. 1997 Science

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**ECOLOGY LETTERS**

*Ecology Letters*, (2012) 15: 637–648

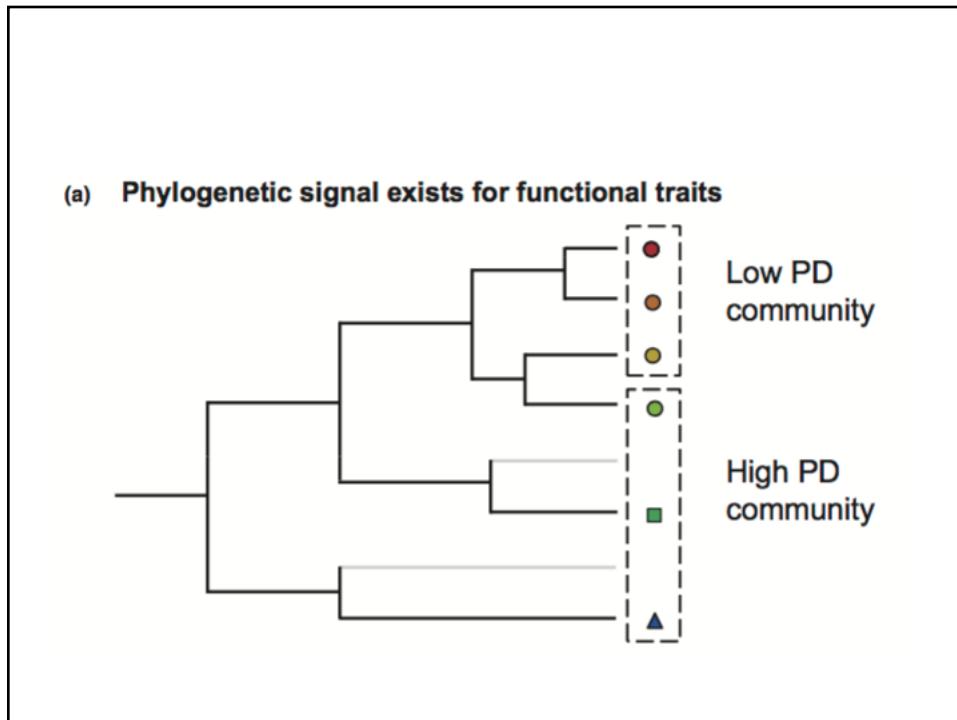
doi: 10.1111/j.1461-0248.2012.01795.x

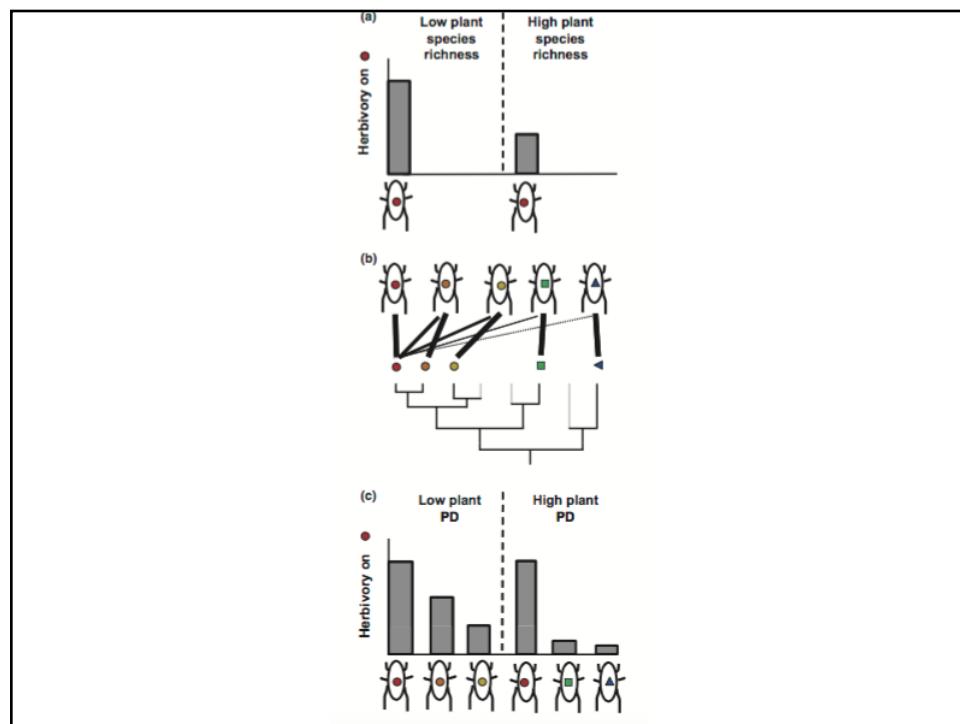
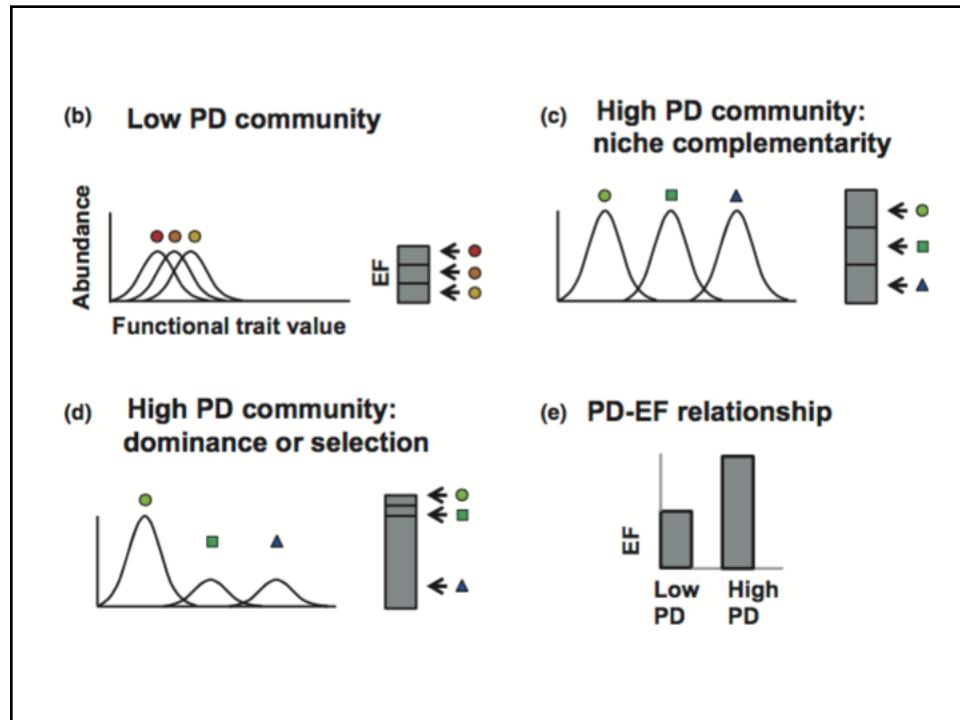
**IDEA AND PERSPECTIVE**

**Phylogenetic diversity and the functioning of ecosystems**

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**Abstract**  
 Phylogenetic diversity (PD) describes the total amount of phylogenetic distance among species in a community. Although there has been substantial research on the factors that determine community PD, exploration of the consequences of PD for ecosystem functioning is just beginning. We argue that PD may be useful in predicting ecosystem functions in a range of communities, from single-trophic to complex net-





# Phylogenetic Diversity

## Evolutionary history and the effect of biodiversity on plant productivity

Marc W. Cadotte<sup>a,b,1</sup>, Bradley J. Cardinale<sup>b</sup>, and Todd H. Oakley<sup>c</sup>

<sup>a</sup>National Center for Ecological Analysis and Synthesis, University of California, 735 State Street, Santa Barbara, CA 93101; <sup>b</sup>Department of Biological Sciences, University of Toronto, 1265 Military Trail, Scarborough, ON, Canada M1C 1A; and <sup>c</sup>Department of Ecology, Evolution, and Marine Biology, University of California, Santa Barbara, CA 93106

Edited by Michael J. Donoghue, Yale University, New Haven, CT, and approved September 10, 2008 (received for review June 20, 2008)

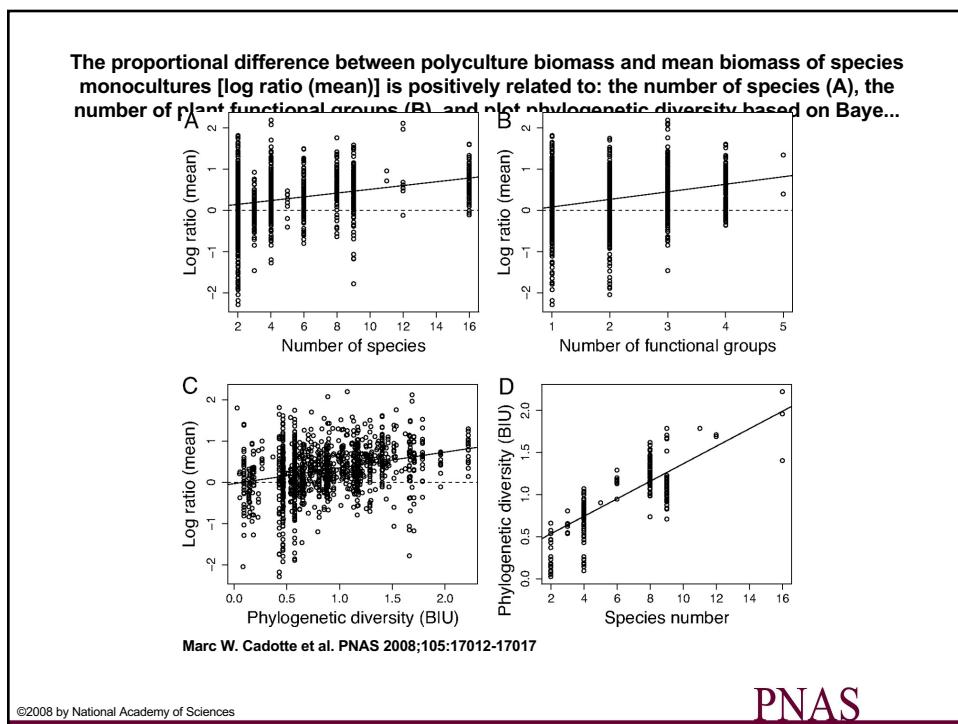
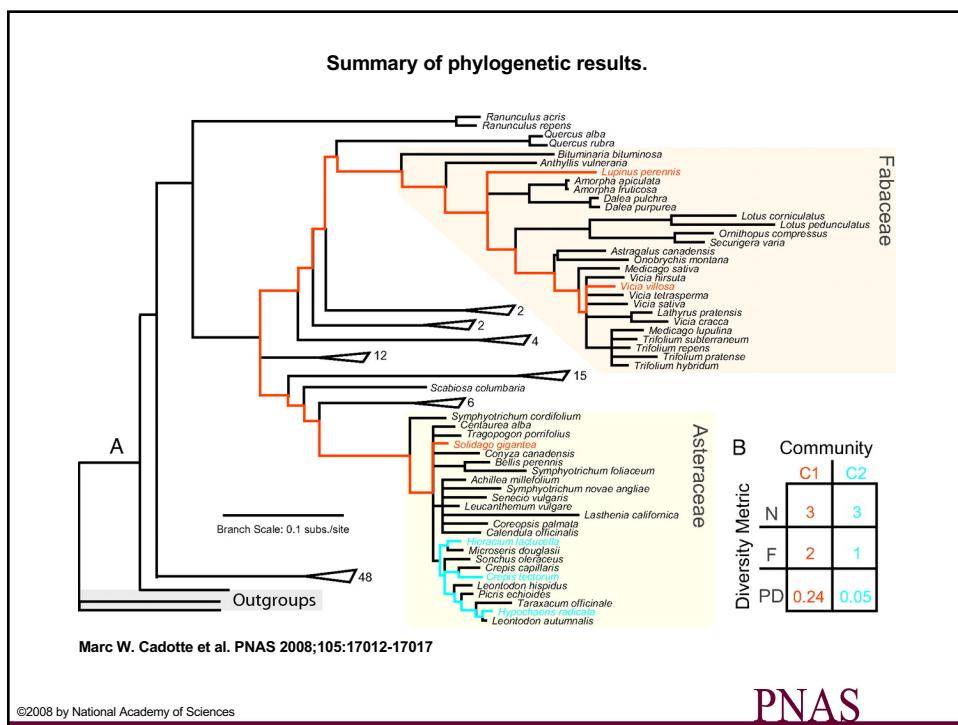
**Loss of biological diversity because of extinction is one of the most** Here, we present results from a formal metaanalysis of

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# Temperate Grasslands



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**Phylogenetic vs Functional Diversity**

OPEN  ACCESS Freely available online

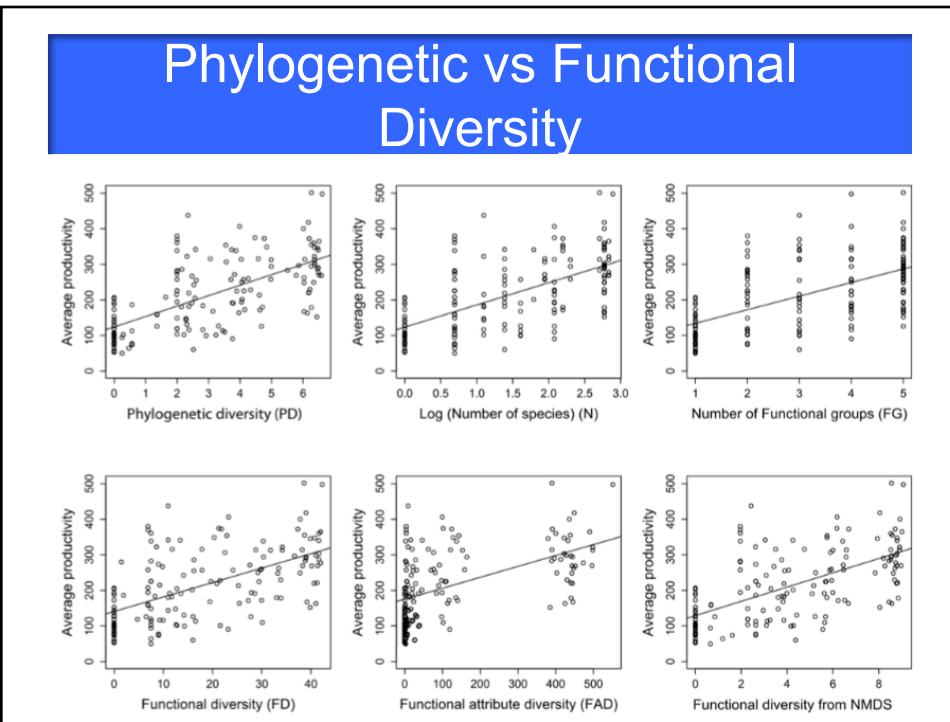


**Using Phylogenetic, Functional and Trait Diversity to Understand Patterns of Plant Community Productivity**

**Marc W. Cadotte<sup>1,2\*</sup>, Jeannine Cavender-Bares<sup>3</sup>, David Tilman<sup>3</sup>, Todd H. Oakley<sup>4</sup>**

1 National Center for Ecological Analysis and Synthesis, University of California Santa Barbara, Santa Barbara, California, United States of America, 2 Department of Biological Sciences, University of Toronto - Scarborough, Scarborough, Ontario, Canada, 3 Department of Ecology, Evolution and Behavior, University of Minnesota, St. Paul, Minnesota, United States of America, 4 Department of Ecology, Evolution and Marine Biology, University of California Santa Barbara, Santa Barbara, California, United States of America

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## Phylogenetic vs Functional Diversity

**Table 3.** Comparison of multivariate predictor models from the stratified all subsets routine.

Variable	DF	Pvalue	AIC	R <sup>2</sup>	AW
PD	149	<0.001	1752.78	0.415	$3.92 \times 10^{-20}$
PD/Nfix	148	<0.001	1722.18	0.529	$1.72 \times 10^{-13}$
PD/SW	148	<0.001	1701.54	0.589	$5.24 \times 10^{-09}$
PD/SW/PA	147	<0.001	1683.04	0.641	$5.43 \times 10^{-05}$
PD/SW/Nfix	147	<0.001	1683.75	0.640	$3.82 \times 10^{-05}$
PD/SW/PA/Nfix	146	<0.001	1667.04	0.682	$1.62 \times 10^{-01}$
PD/SW/PA/LPA	146	<0.001	1680.46	0.652	$1.98 \times 10^{-04}$
PD/SW/PA/Nfix/LPA	145	<0.001	1664.53	0.691	$5.68 \times 10^{-01}$
PD/SW/PA/Nfix/FG	145	<0.001	1666.02	0.688	$2.70 \times 10^{-01}$

doi:10.1371/journal.pone.0005695.t003

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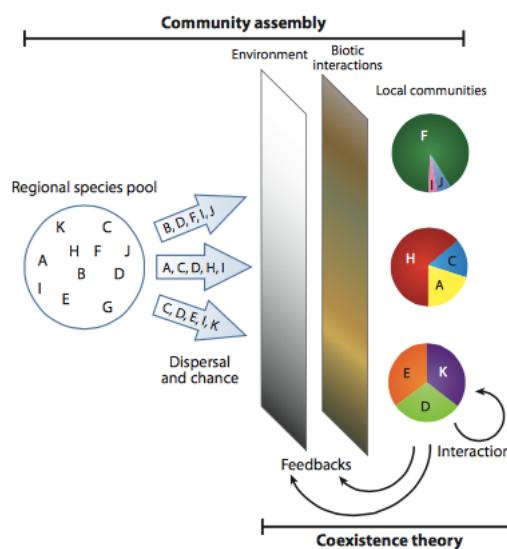
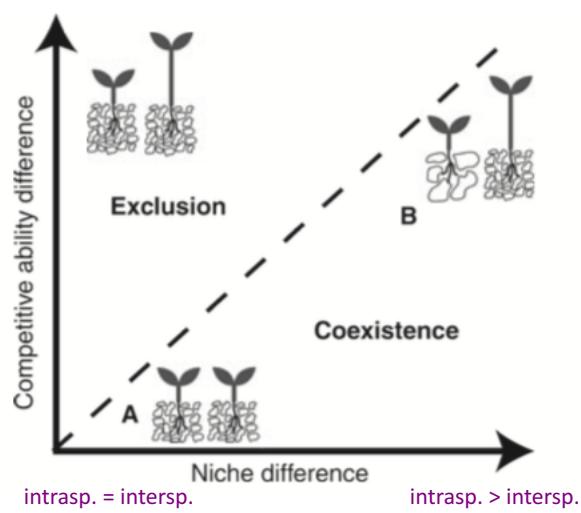
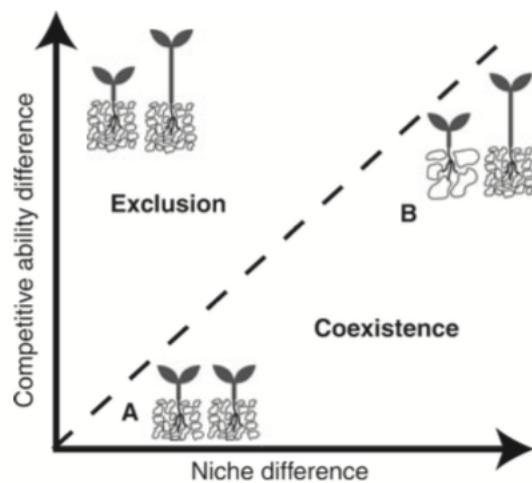
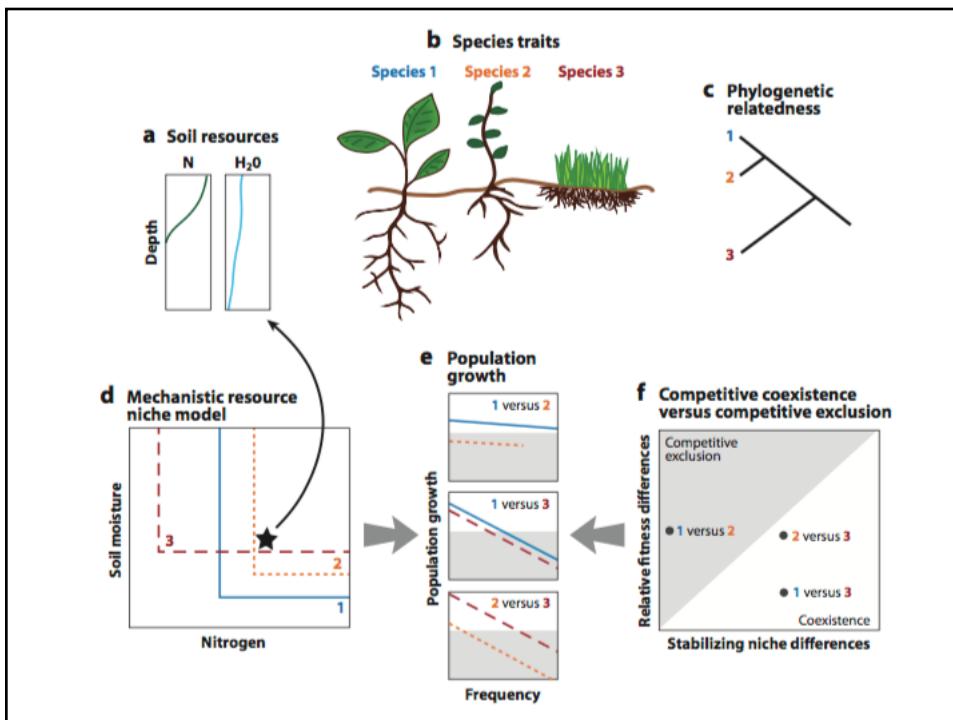
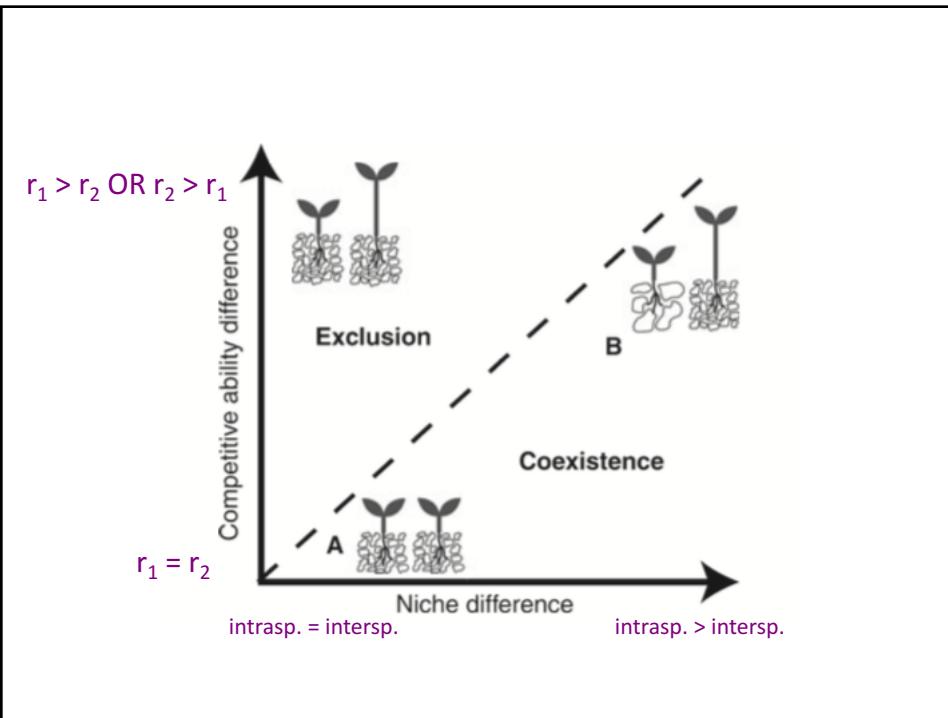
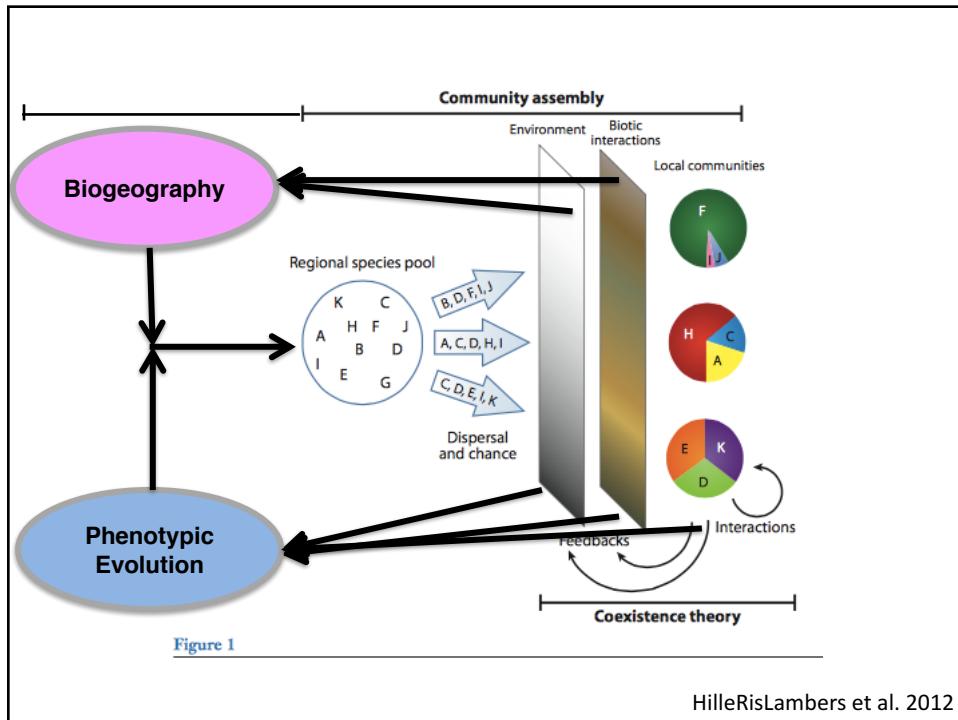


Figure 1

HilleRisLambers et al. 2012







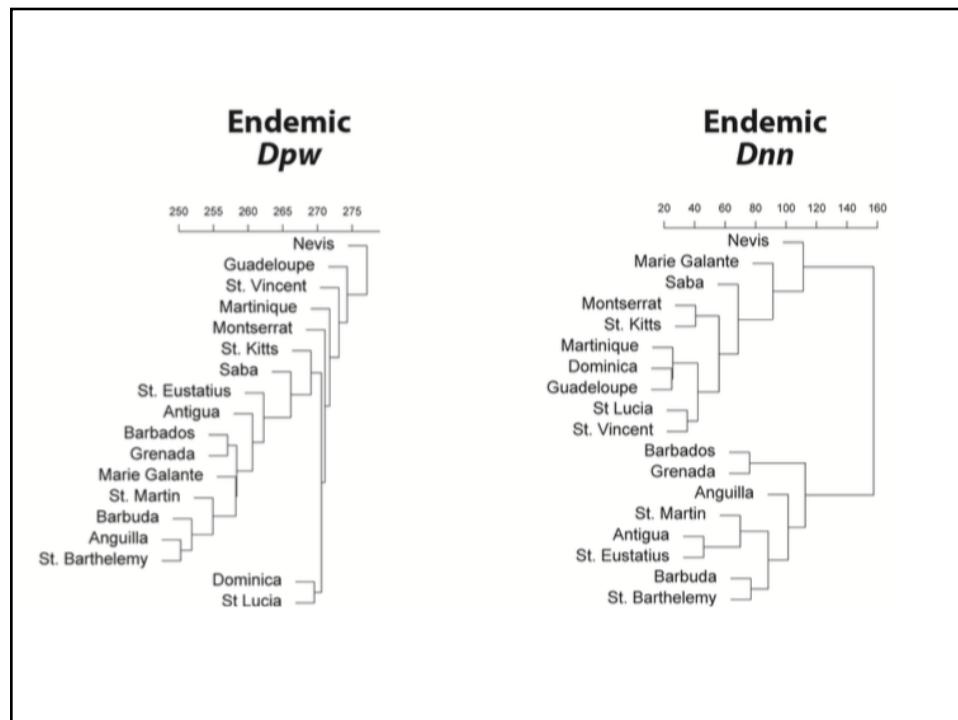
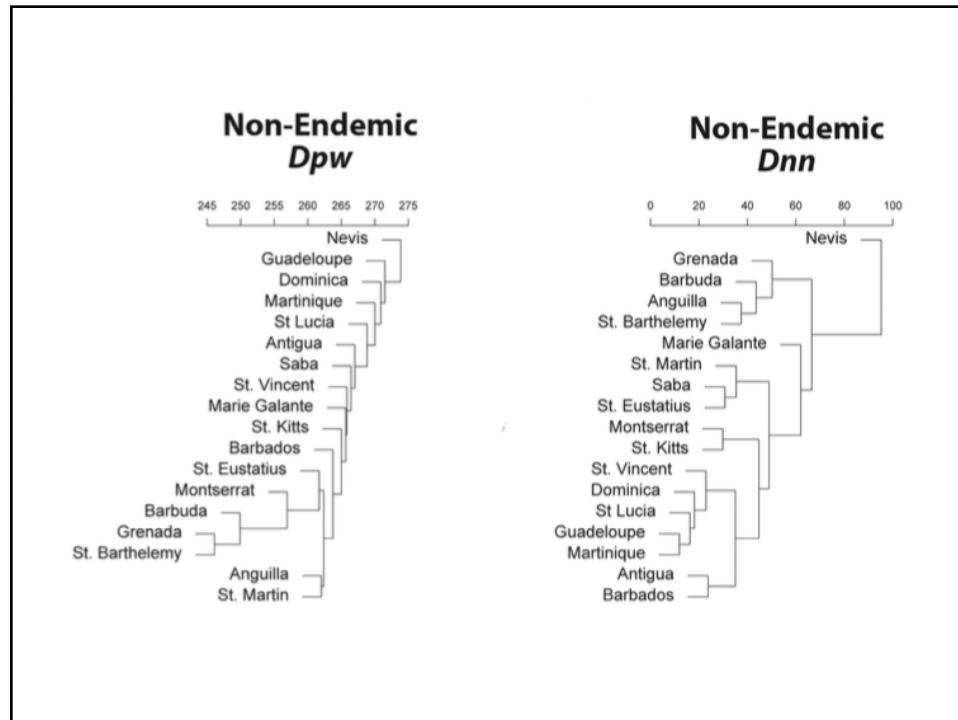
## Phylogenetic Backbones Not Proxies

Relative Contribution of Lineages to Assemblages



Phylofloristics: an example from the Lesser Antilles

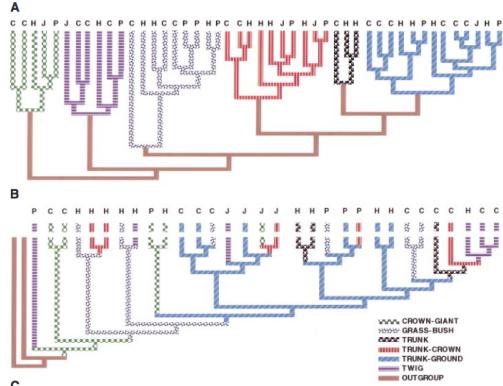
Nathan G. Swenson\* and María N. Umaña



# Phylogenetic Backbones Not Proxies

## Contingency and Determinism in Replicated Adaptive Radiations of Island Lizards

Jonathan B. Losos,\* Todd R. Jackman, Allan Larson,  
Kevin de Queiroz, Lourdes Rodríguez-Schettino



Tempo & Mode  
of Phenotypic  
Evolution

## Contingency and Determinism in Replicated Adaptive Radiations of Island Lizards

Jonathan B. Losos,\* Todd R. Jackman, Allan Larson,  
Kevin de Queiroz, Lourdes Rodríguez-Schettino

**A = Trait dendrogram (aka *Anolis* ecomorphs)**

**B = Phylogeny**

**C= Phylogeny on each island**

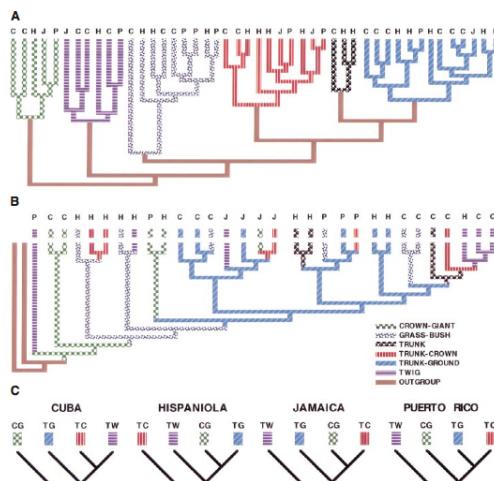


Fig. 1. (A) UPGMA phenogram showing that members of the same ecomorph class cluster in morphology.

