



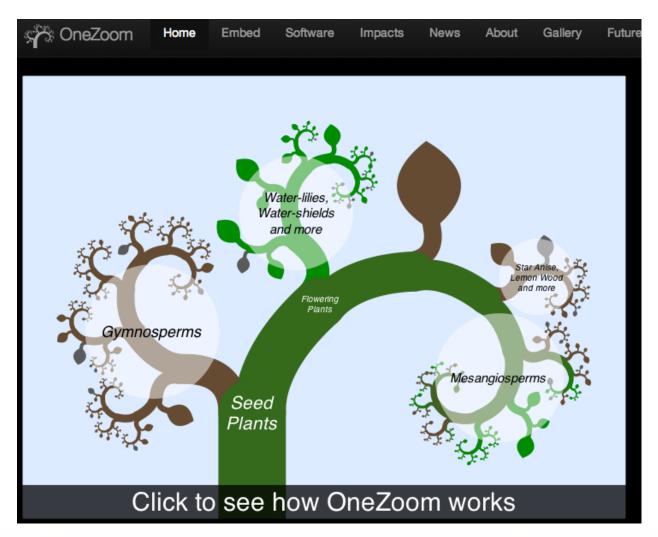
Pamela S. Soltis Florida Museum of Natural History University of Florida







# **Linking to Phylogeny**





# **PhyloJIVE**

Links biodiversity data to trees Joe Miller & Garry Jolley-Rogers phylojive.ala.org.au/



## **Phylojive**

PhyloJive (Phylogeny Javascript Information Visualiser and Explorer) is a web based application that places biodiversity information aggregated from many sources onto compact phylogenetic trees.

The project is the brainchild of Garry Jolley-Rogers and Joe Miller and was developed by Temi Varghese and Garry Jolley-Rogers as part of the Taxonomy Research & Information Network (TRIN) – see the original project page, original code repository and ALA code repository. The ALA has contributed to the PhyloJive codebase to integrate a number of web services: occurrence data, maps and character data from Identify Life. This work has been undertaken with help and advice from Joe Miller.

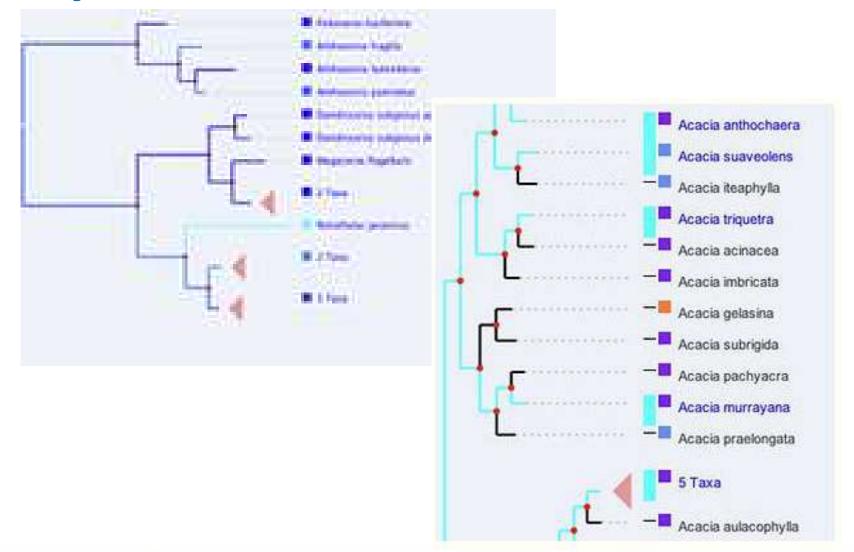
The getting started page outlines the steps for creating a new phylogenetic tree and contains demo data sets that can be used to get up and running.



A. buxifolia
Source: Australian Plant
Image Index Image by: Macd

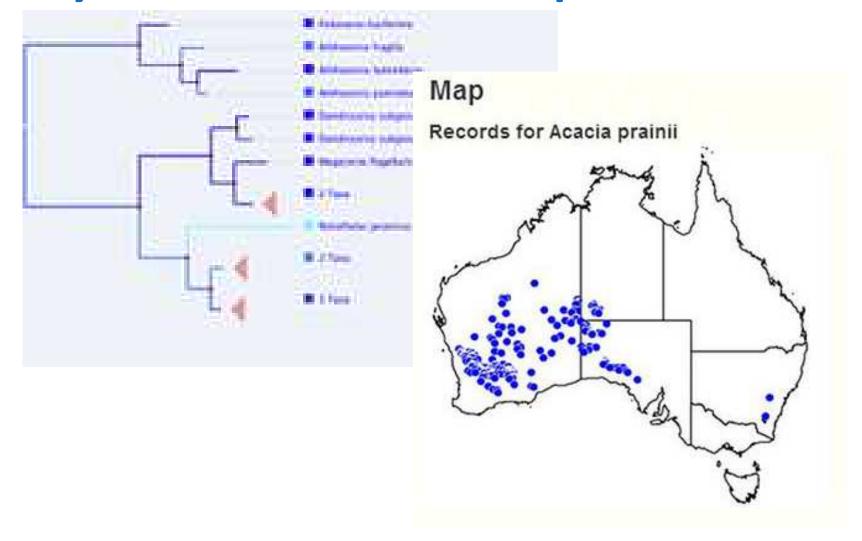


# **PhyloJIVE: trees and traits**



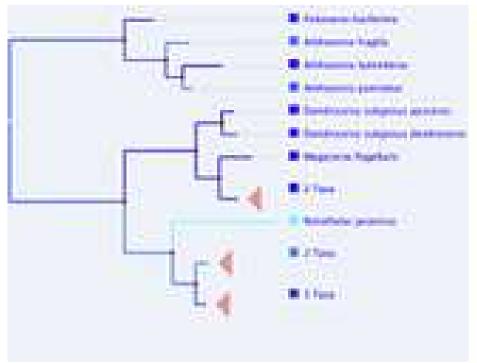


# **PhyloJIVE: trees and maps**

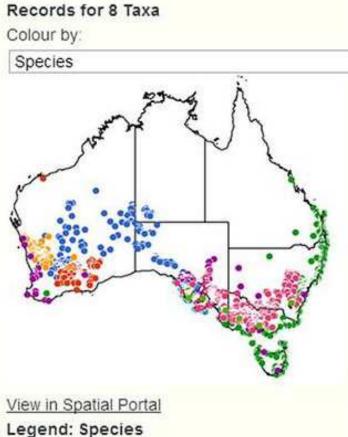




# PhyloJIVE: trees and maps



Combine traits and distributions



Мар

Acacia prainii

Acacia camptoclada



# **PhyloJIVE**





# **PhyloJIVE**

Learn about research directions



Learn how your collection can

benefit from our work



Download lesson plans about using

digitized specimens

## **Next-Generation Biodiversity Research**

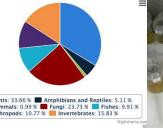
- How are processes such as speciation and extinction associated with niche divergence?
- How have traits and ecological niches changed through time as a function of changes to geographic range and fluctuations in climate and geology?
- How is the evolution of phenotype correlated with changes in ecological niche at deep time scales?
- How is the phylogenetic diversity of a given area related to evolution of phenotype in that area?
- How have diversification processes interacted with climate and geology to shape modern biotas?
- How can fossil locality data inform our understanding of range and ecological niche evolution?
- How do traits change over time? Can within-species phenotype variation with respect to climate and ecology inform our understanding of trait lability and evolution at deep time scales?

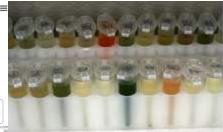


## **Specimen Data & the Big Data Challenge**

- Not just volume of data
- But integration of diverse data types
- For novel applications









**EXAMPLE WORKFLOWS: RESOURCES:** Lifemapper Arbor · ecological niche modeling evolutionary models · biodiversity and range · comparative methods analysis visualization visualization 1 select clade taxon names Open Tree of Life iDigBio phylogenies · taxonomy / names specimen data / images visualization • fossil data / images 2 run ecological niche modeling 3 analyze ENM data (ENM) for all tips and tree to calculate: · shifts in ecological niche for a pruned subtree of occurrence species in phylogenetic constraints data on niche evolution taxon names 3 analyze data to compute phylogenetic diversity (PD) analyze data to: 1 visualize · test hypotheses of "dark parts" of review specimens, character evolution score morphology for clade—species select area of interest. · reconstruct ancestral species without it with missing query global presence/absence trait data matrix (PAM) to get species subset 1 select clade analyze data to: estimate rates and test hypotheses of diversification {T3, T4, T5, T7} 2 upload new trees to improve phylogenetic resolution 1 select occurrence data sampling proportions (from taxonomy) 2 analyze data to quantify and qualify biodiversity

and co-visualize maps, trees, and geospatial stats

















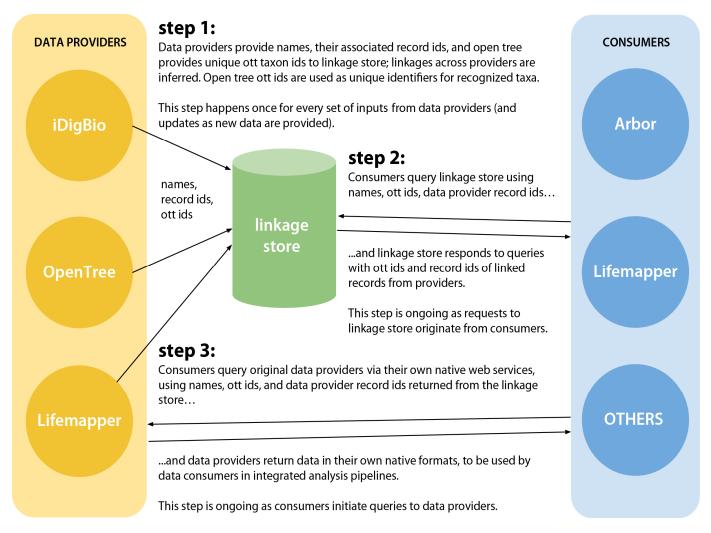














## **RESOURCES:**



## Lifemapper

- · ecological niche modeling · biodiversity and range
- analysis
- visualization

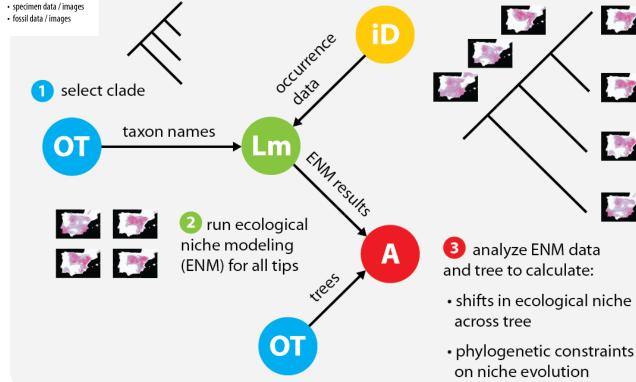


- · evolutionary models
- comparative methods visualization



## Open Tree of Life phylogenies

- · taxonomy / names · visualization
- iDigBio · trait data





## **RESOURCES:**



## Lifemapper

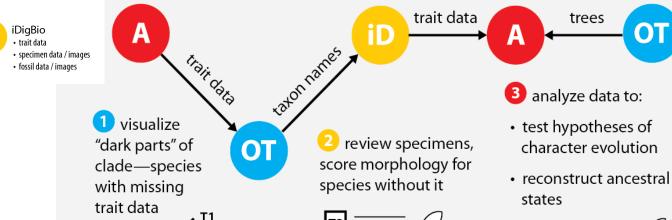
- · ecological niche modeling · biodiversity and range
- analysis
- visualization

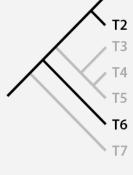


## Open Tree of Life

- · taxonomy / names
- visualization

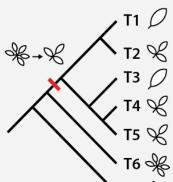






{T3, T4, T5, T7}





trees

OT



## **RESOURCES:**



## Lifemapper

- ecological niche modelingbiodiversity and range
- analysis
- visualization



## Arbo

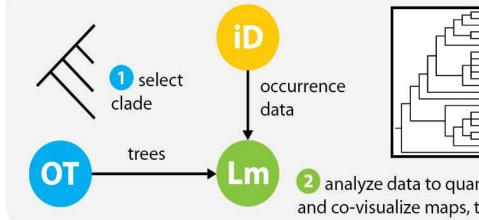
- evolutionary modelscomparative methods
- visualization

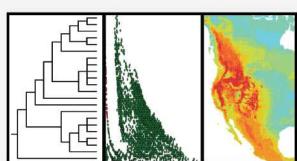
- Open
  - Open Tree of Life
     phylogenies
  - taxonomy / namesvisualization



## iDigBio

- trait data
- specimen data / images
- · fossil data / images





analyze data to quantify and qualify biodiversity and co-visualize maps, trees, and geospatial stats



**EXAMPLE WORKFLOWS: RESOURCES:** Lifemapper Arbor · ecological niche modeling evolutionary models · biodiversity and range · comparative methods analysis visualization visualization 1 select clade taxon names Open Tree of Life iDigBio phylogenies · taxonomy / names specimen data / images visualization • fossil data / images 2 run ecological niche modeling 3 analyze ENM data (ENM) for all tips and tree to calculate: · shifts in ecological niche for a pruned subtree of occurrence species in phylogenetic constraints data on niche evolution taxon names 3 analyze data to compute phylogenetic diversity (PD) analyze data to: 1 visualize · test hypotheses of "dark parts" of review specimens, character evolution score morphology for clade—species select area of interest. · reconstruct ancestral species without it with missing query global presence/absence trait data matrix (PAM) to get species subset 1 select clade analyze data to: estimate rates and test hypotheses of diversification {T3, T4, T5, T7} 2 upload new trees to improve phylogenetic resolution 1 select occurrence data sampling proportions (from taxonomy) 2 analyze data to quantify and qualify biodiversity and co-visualize maps, trees, and geospatial stats



# **Integrating Phylogenetics and Plant Trait Data**



# **Plant Trait Database**

PhotosyntheticPathway

Respiration LeafArea NfixationCapacity

SLA Regeneration Capacity Growth Form

PhenologyType LeafN

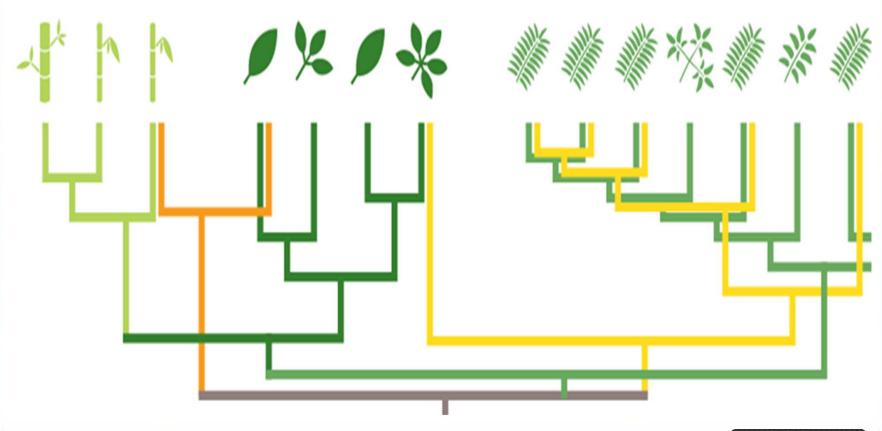
LeafP LeafLongevity PhotosyntheticCapacity

MaxPlantHeight SeedMass





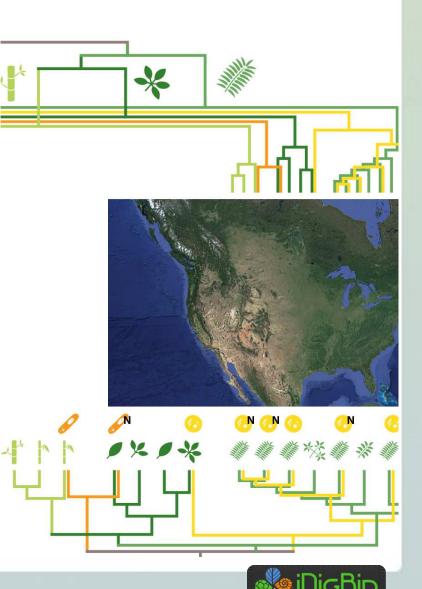
# **Plant Trait Database**





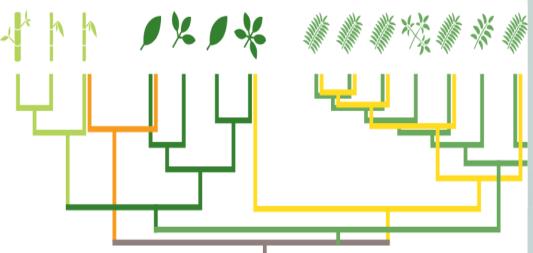
## **Integrating Phylogenetics and Plant Trait Data**

- Community-level phylogenies
  - Comparisons of phylogenetic diversity across spatial scales
  - Correlation of plant functional traits
  - Over- and underdispersion of traits:
    - Are traits phylogenetically constrained or broader properties of communities?
    - Implications for long-term health of communities









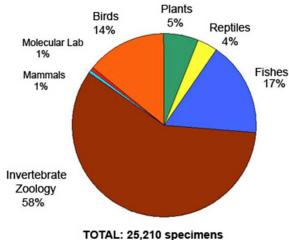
# **Linking Collections to Genomics**

- Link specimens to GenBank records
- Use of specimens for genetics/genomics
- National network of genetic resources









FLMNH GRR: the Genetic Resources Repository Florida Museum of Natural History





## **GenBank Records**



## Welcome to NCBI

The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.

About the NCBI | Mission | Organization | Research | NCBI News

## Examples of the /specimen\_voucher information:

```
/specimen_voucher="UAM:Mamm:52179"
/specimen_voucher="AMCC:101706"
/specimen_voucher="USNM:field series 8798"
/specimen_voucher="personal:Dan Janzen:99-SRNP-2003"
/specimen_voucher="99-SRNP-2003"
```



## **Herbarium DNA and NGS**

- Fresh leaf material hard to obtain for many taxa
- DNA from available herbarium material often degraded – Is this a problem?
- Often yes for PCR, but not for NGS
  - Small DNA fragments (e.g., 200-400 bp) required for most NGS protocols!
- Using herbarium material extensively for NGS in Icacinaceae
  - Herbarium samples as old as 80 years have worked fine

G. Stull 1955



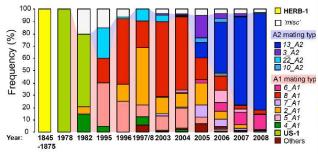


## **Pearls**

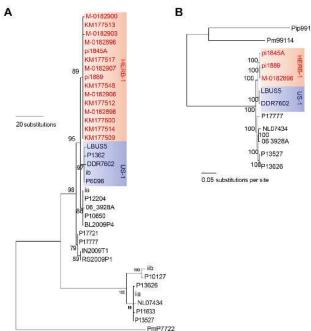
Mining Herbaria for Plant Pathogen Genomes: Back to the Future

Kentaro Yoshida<sup>1</sup>, Hernán A. Burbano<sup>2</sup>\*, Johannes Krause<sup>3</sup>, Marco Thines<sup>4,5,6,7</sup>, Detlef Weigel<sup>2</sup>\*, Sophien Kamoun<sup>1</sup>\*

















# **Linking Collections to Genomics**

- Participated in NSF-sponsored workshop on DNA banks at Missouri Botanical Garden, Jan. 2013
- Assembled a file of national DNA and tissue banks
- Developed a common web portal to these collections
- DNA resources ultimately connected to specimen data in iDigBio





## **Grant Godden**













## iDigBio Links DNA Banks and Genetic Resource Repositories with New Web Feature, Requests Community Input

Natural history collections have always played a crucial role in organismal biology, serving both as repositories for biological specimens that document biodiversity in space and time and sources of materials for scientific study.

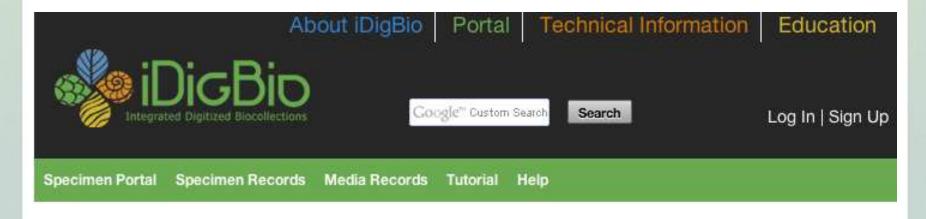


## My Top Resources

- Contact Us
- Digitization

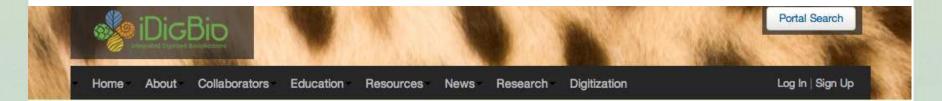


https://www.idigbio.org/genetic-resources



DNA Banks and Genetic Resource Repositories in the United States





## DNA Banks and Genetic Resource Repositories in the United States

iDigBio is actively compiling a list of DNA banking facilities and genetic resource repositories in the United States that maintain collections of nucleic acid extracts (DNA or RNA) or preserved tissues suitable for genetic and genomic studies of biodiversity.

The following resources (listed alphabetically by institution) represent collections currently known by or reported to iDigBio. Each entry includes the name of the institution, the date listed on iDigBio, a brief description, an institutional link, and searchable keywords: e.g., fields of study; repository type; storage type (cryogenic, ultra-cold, etc.); and resources available (nucleic acid extracts, frozen tissues, silica-dried tissues, etc.).

To report the availability of genetic resources at your institution, or to revise or update an existing entry, please contact Grant Godden.

iDigBio thanks the participants of the DNA Banking Workshop hosted by the Missouri Botanical Garden (January 2013) and Breda Zimkus (Museum of Comparative Zoology, Harvard University), in particular, for assistance in compiling these resources.

	Abstract	URL
Academy of Natural Sciences	The Laboratory for Molecular Systematics and	http://www.ansp.org/research/systematics-evolution/resources/molecular-biology/facilities/



## My Top Resources

- Contact Us
- Digitization
   Documentation
- iDigBio Forums
- iDigBio Resources
- iDigBio Specimen Portal
- · iDigBio Wiki

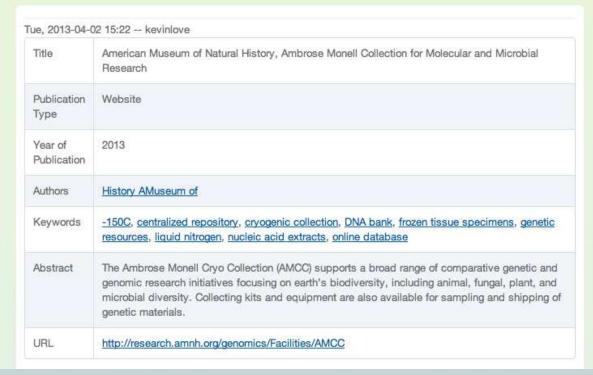
## **Upcoming Events**



# Index to DNA Banks in US: an example



## American Museum of Natural History, Ambrose Monell Collection for Molecular and Microbial Research





- iDigBio Forums
- iDigBio Resources
- · iDigBio Specimen Portal
- · iDigBio Wiki

**Upcoming Events** 



## Summary

- Specimens continue as foundation for systematics
- Emerging tools and infrastructure to link phylogenies with specimens – multitude of applications for diverse research questions
- Multiple connections to molecular data:
  - GenBank records
  - Specimens as sources of genomic data
  - Index to DNA Banks
- Exciting time now integrating phylogenetic, genetic, and ecological data in basic and applied research – and into the future!



# Acknowledgments

- Joe Miller, PhyloJIVE
- Open Tree of Life, Arbor, Lifemapper collaborators
- D. Soltis, J. Xiang, M. Mack, J. Lichstein –
   phylogenies, plant traits, specimens
- Grant Godden & Kevin Love for Index to DNA Banks

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