PRAGMA VBE

Lifemapper

Lifemapper Evolves

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http://lifemapper.org

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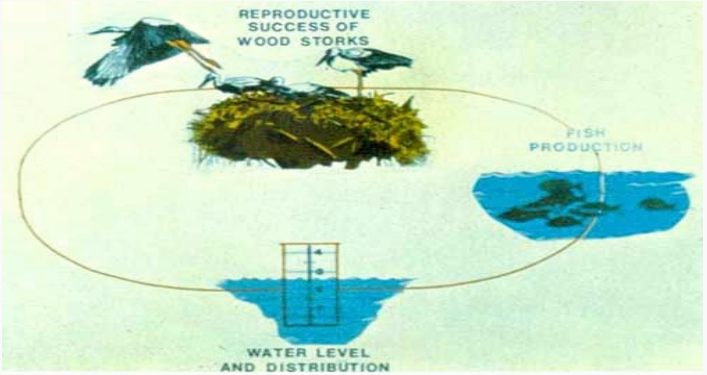
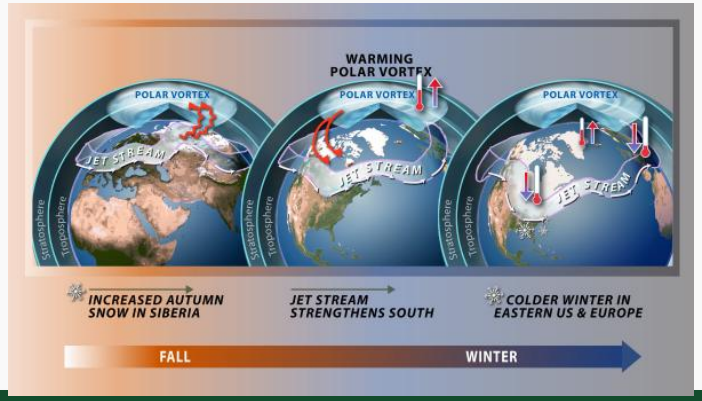
Lifemapper brings together …

Biodiversity Inventory

Macro-Ecological Modeling



Global Climate Change



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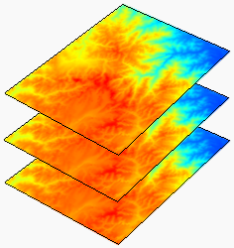
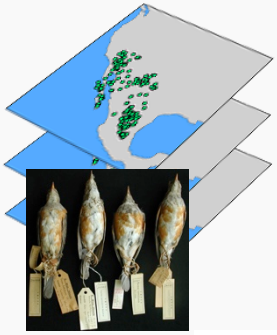
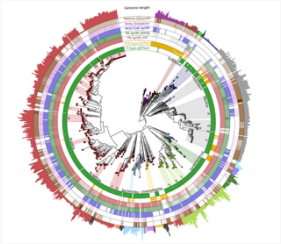
Lifemapper Analyses





- Inputs
  - Environmental
  - Specimen occurrence points
  - Phylogenetic tree
- Tools
  - Species Distribution Modeling (SDM)
  - Macro-Ecological Analyses
  - Meta-Community Phylogenetic Analyses (MPCA)
- Results
  - Potential species habitat maps
  - Biodiversity / Phylogenetic Maps and Analyses



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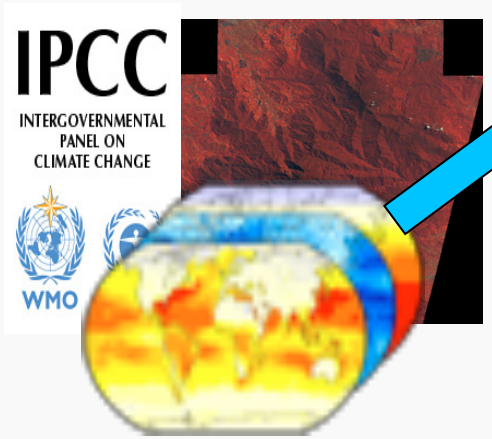
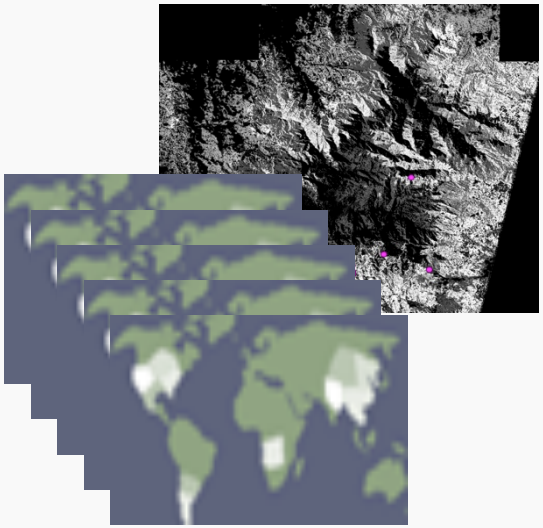
Species Distribution Modeling

Species Occurrence Data



Environmental Data



Potential Habitat

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Demo

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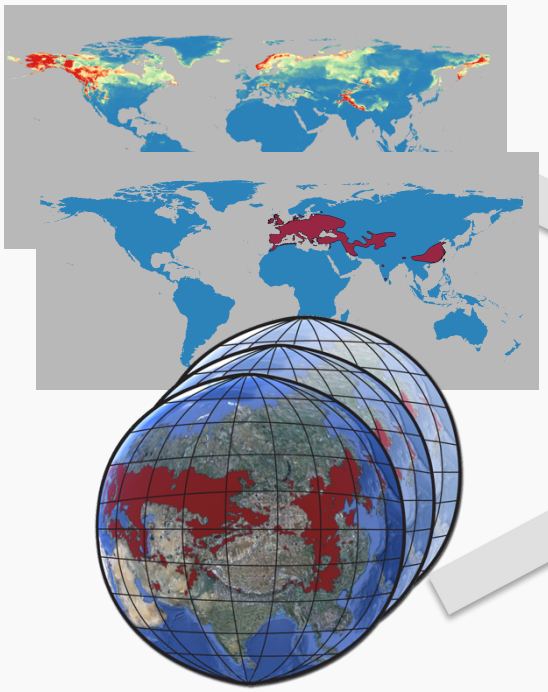
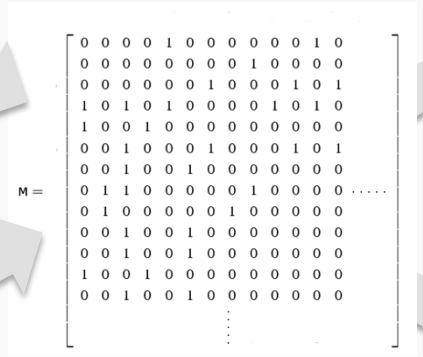
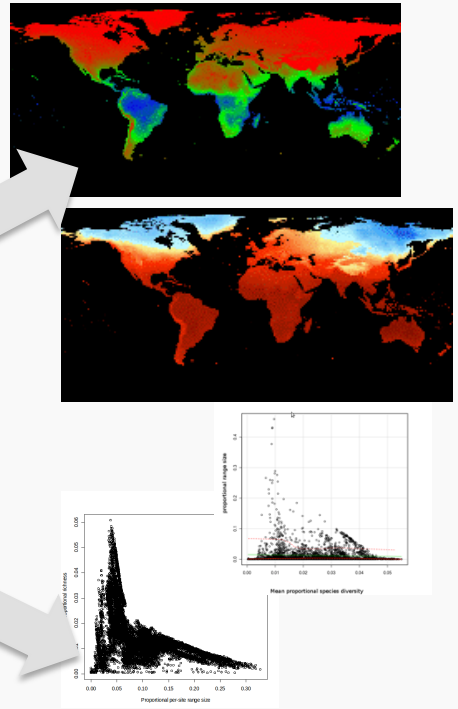
Macro-ecological Analyses



Species Habitat Data



Presence Absence Matrix (PAM)



Multi-species analyses

Range and Diversity Quantifications

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How to create a PAM

- What species group?
  - Subset by species in a study area
  - Subset by taxonomic or phylogenetic tree
- Define the area
  - Region bounding box
  - Site / cell size
- For every species, find presence/absence for every site
  - Lifemapper automates using input SDMs and thresholds
  - Calculate presence based on coverage and values in site

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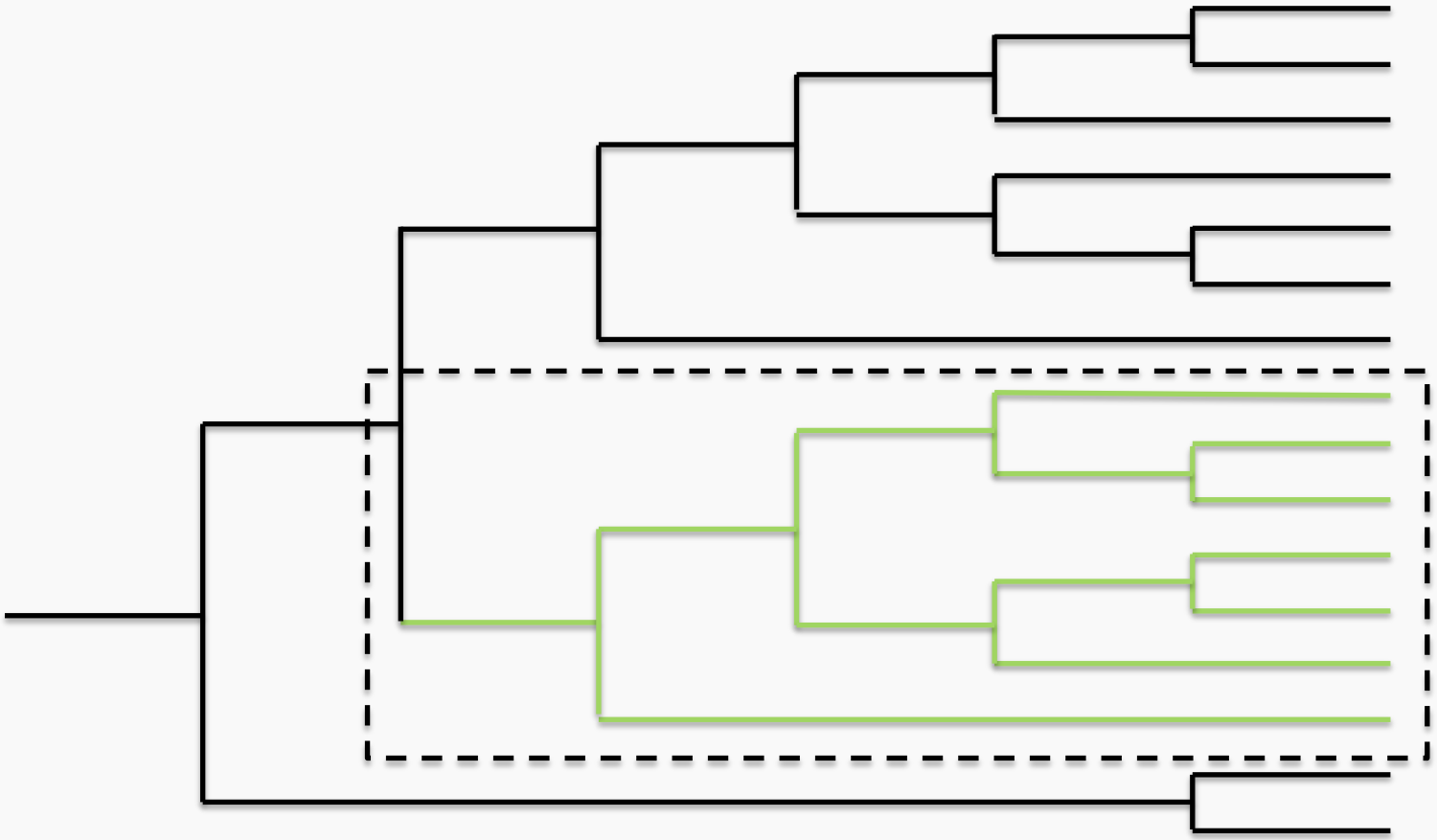
Select a species pool



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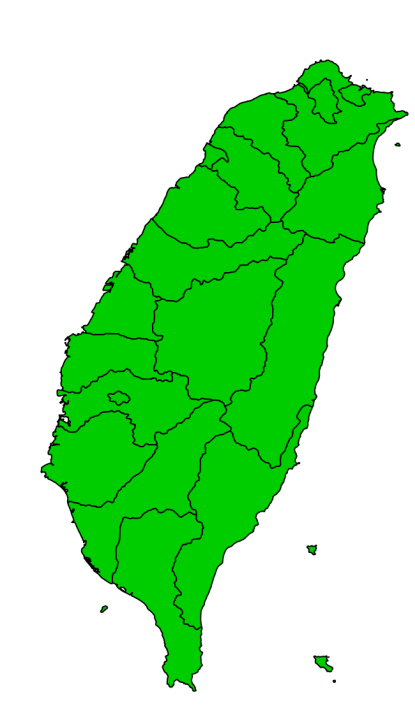
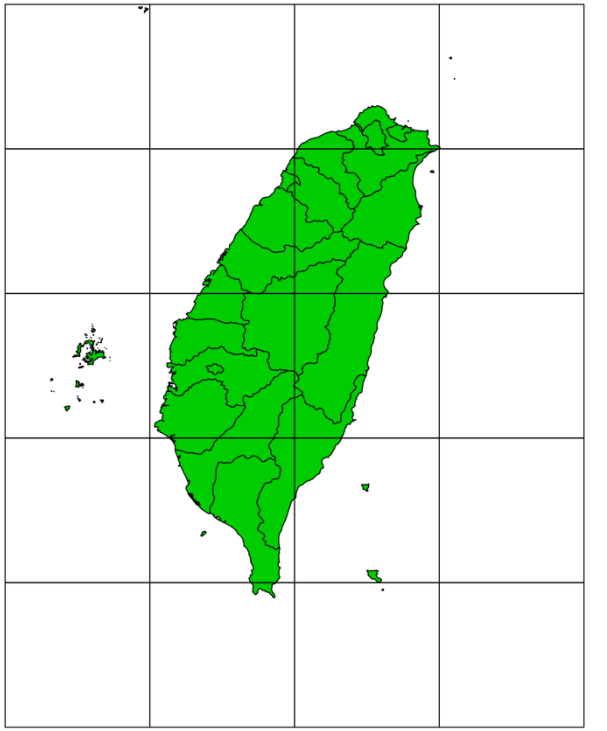
Create the grid





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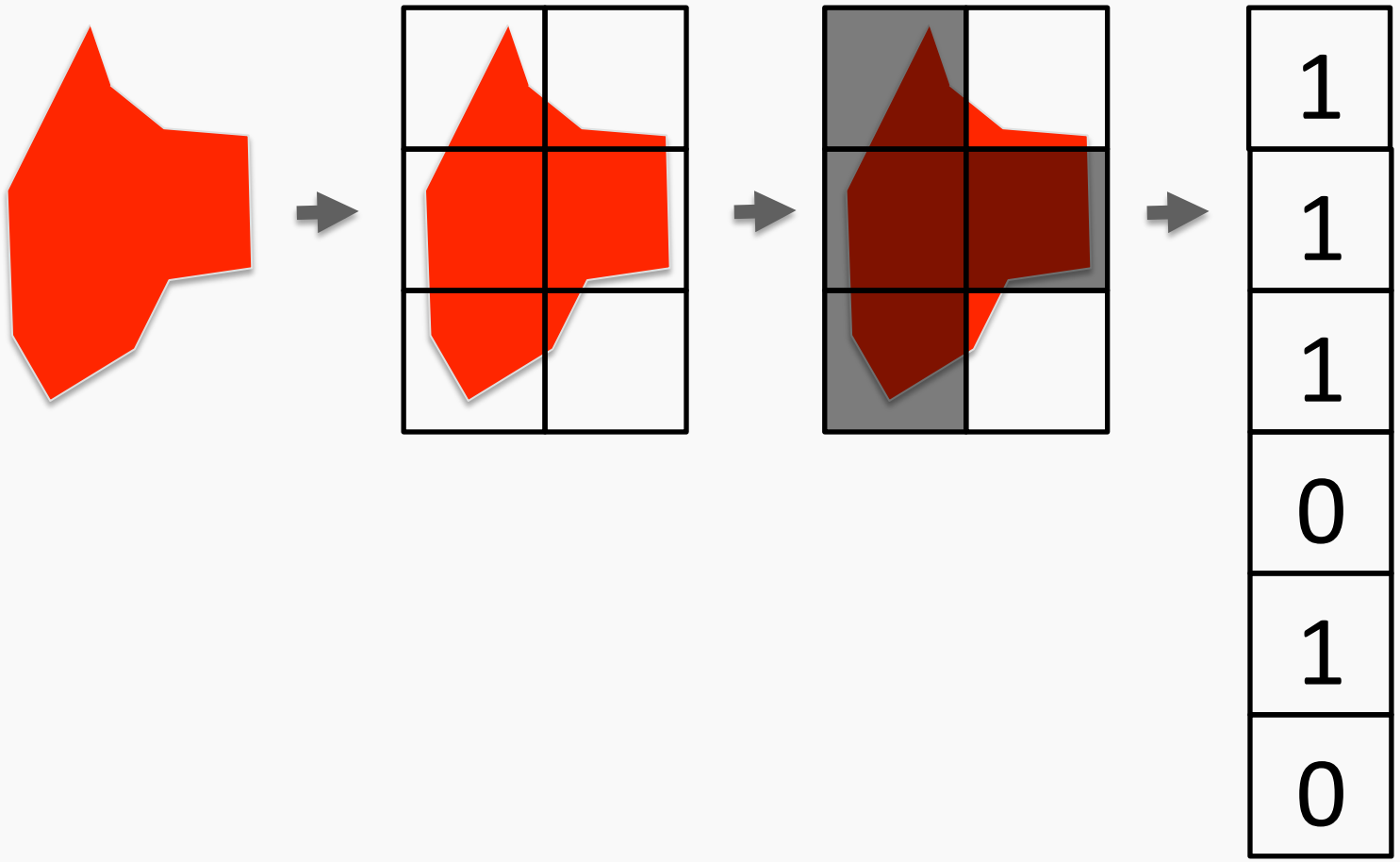
Determining presence



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Site Statistics

- Species richness
  - The number of species present at each site
- Proportional species richness
  - The proportion of the number of species present at each site compared to the total number of species in the species pool
- Total range size
  - The sum of the range sizes of all of the species present at each site
- Proportional species range size
  - The proportion of the sum of the range sizes of all species at a site compared to the sum of the range sizes for all species in the species pool

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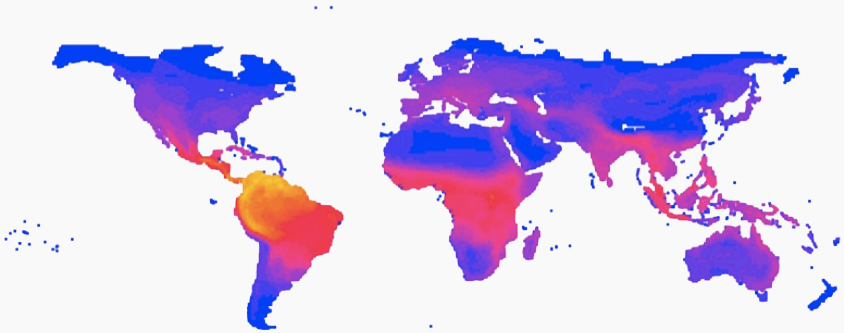
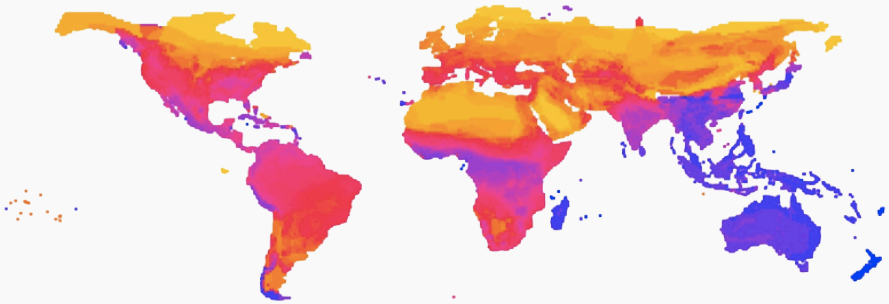
Terrestrial Mammals



Proportional Species Richness

High	
Yellow	
Moderate	Red
Low	Blue



Per-site Range Size

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Global PAM and subsetting

- Lifemapper creates a "**Global PAM"** for all species in a dataset
- Subsets of the Global PAM may be requested for analyses. Subset by:
  - Species
  - Geography
  - Time
- Study the effects of scale and time
  - Do patterns remain the same?

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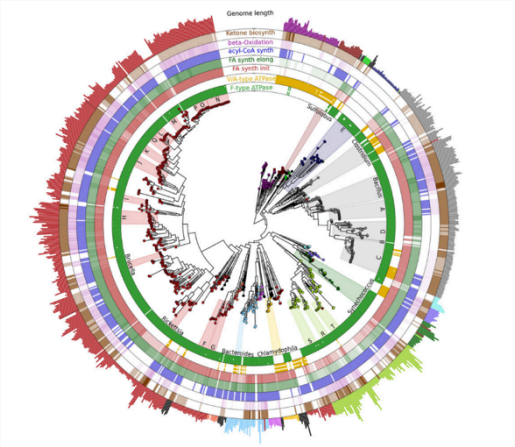
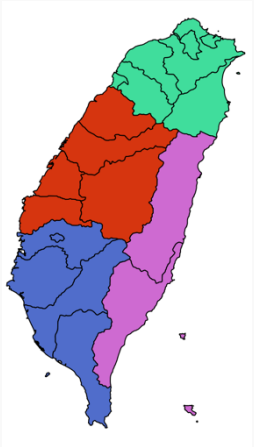
Meta-Community Phylogenetic Analyses (MCPA)



$$M = \begin{bmatrix} 0&0&0&0&1&0&0&0&0&0&0&1&0 \\ 0&0&0&0&0&0&0&0&1&0&0&0&0 \\ 0&0&0&0&0&0&1&0&0&0&1&0&1 \\ 1&0&1&0&1&0&0&0&0&1&0&1&0 \\ 1&0&0&1&0&0&0&0&0&0&0&0&0 \\ 0&0&1&0&0&0&1&0&0&0&1&0&1 \\ 0&0&1&0&0&1&0&0&0&0&0&0&0 \\ 0&1&1&0&0&0&0&0&1&0&0&0&0 \\ 0&1&0&0&0&0&0&0&1&0&0&0&0 \\ 0&0&1&0&0&1&0&0&0&0&0&0&0 \\ 0&0&1&0&0&1&0&0&0&0&0&0&0 \\ 1&0&0&1&0&0&0&0&0&0&0&0&0 \\ 0&0&1&0&0&1&0&0&0&0&0&0&0 \\ & & & & & & \vdots & & & & & & \end{bmatrix}$$



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MCPA

Evaluates the interaction between

- phylogenetic structure
- historical biogeographic events
- environmental filtering

in driving species distributions in a community

Inputs

- PAM – inputs can be SDMs or range maps
- Phylogenetic tree
  - Must be binary
  - If it has branch lengths, the tree must be ultrametric
  - Encoded into a species X node matrix
- Environmental predictors
  - Intersected with sites to create a matrix matching PAM
- Biogeographic hypotheses (barriers or corridors for species distribution)
  - Encode all into a single matrix as (-1, 0, 1)

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Lifemapper

Demo

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Virtualization Technologies

- Runs on Linux on x86 hardware
- Ideal to run on clusters
- Advantages in VBE
  - Can create bigger instance
  - Can have long running instance
  - Dynamic input data
  - Intended for use by multiple external clients

- Runs on Linux, Windows, OSX
- Ideal for laptops but
  - Must setup networking
  - Instance size/memory is limited by laptop hardware
- Advantages in VBE
  - Can special-purpose instance
  - Can have short-lived instance
  - Pre-defined stable input data
  - Intended for field work (with no network connection) and teaching tool

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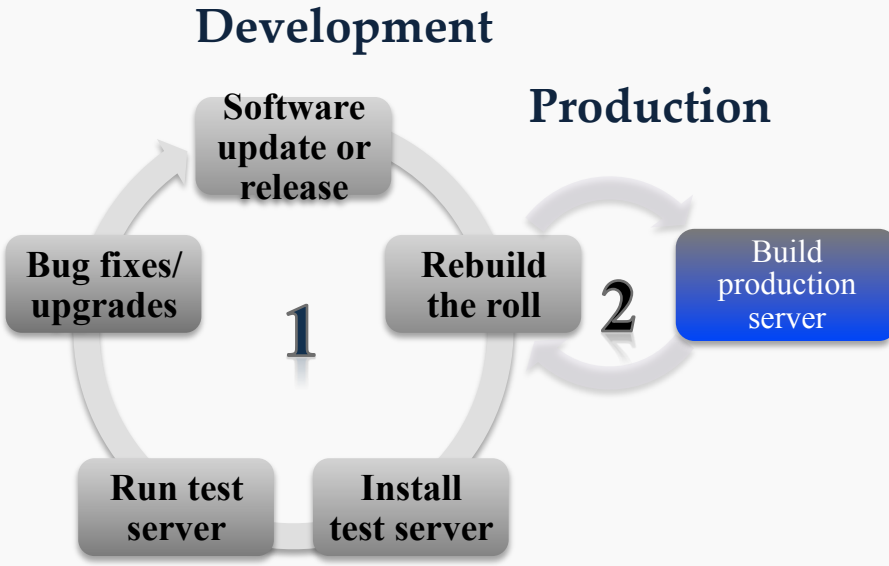
Virtualization Advantages

- **Increase availability and flexibility of Lifemapper**
  - Reduce cost of installing/configuring/ replicating
  - Ease burden of hardware and software integration
- **Reduce time from software update to server availability:**
  - Minimize time spent on build and configuration
  - Automate most hands-on tasks.
  - Implement tests components and configuration
- **Prepare for larger, high quality data and increased computational complexity:**
  - low resolution climate data → high resolution satellite imagery
  - single-species SDM experiments → multi-species macro-ecology experiments



Lifemapper

http://lifemapper.org

https://github.com/lifemapper/

Rocks

http://www.rocksclusters.org

PRAGMA

https://github.com/pragmagrid/lifemapper-compute

https://github.com/pragmagrid/lifemapper-server

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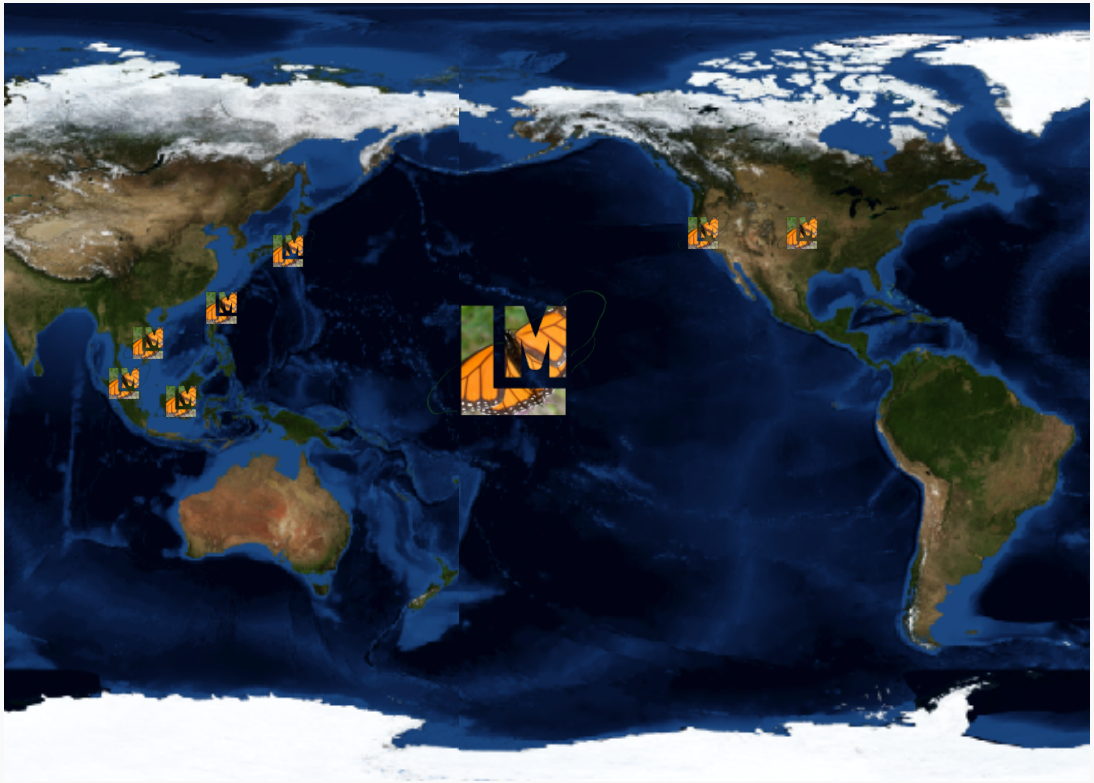
Distributed Lifemapper

- Support focused and comparative studies
  - Taiwan at NCHC
  - Workshop for researcher introduction
  - Follow up with Taiwanese museums and researchers



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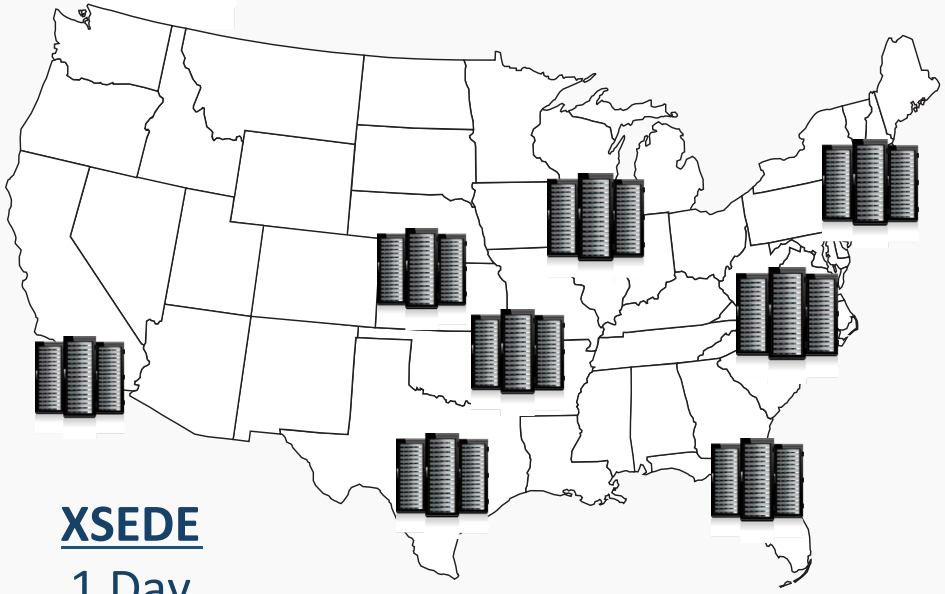
Scaling Computation from Desktop to National Grid

Inputs
500,000 species
4 climate scenarios
3 model algorithms
(= 6 million models)

Desktop
1.8 Years

KUBI Cluster
104 Days

KU ACF
5 Days



XSEDE
1 Day

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US NSF

OCI-1234983

BIO-1458422

BIO-1356732

USGS

BIP-G14AC00285

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Biodiversity Expedition Next Steps

- Regional installations
- Move to HPC challenges – scaling
  - management / computational resources
  - Tune Notre Dame's workflow tools + compute resources
- UI changes allowing display through SAGE2
  - Replaced QGIS with generic browser-based UI
  - Works on dynamic web service calls OR local data
- Next steps:
  - Create/populate then move VC?
  - Containers? Virtual frontend + containers for computations?
  - Live connection b/w iDigBio and OpenTree (Biotaphy)
  - Marine models with NMMST (CENTRA)