Lifemapper

Phylogeography and MetaCommunity

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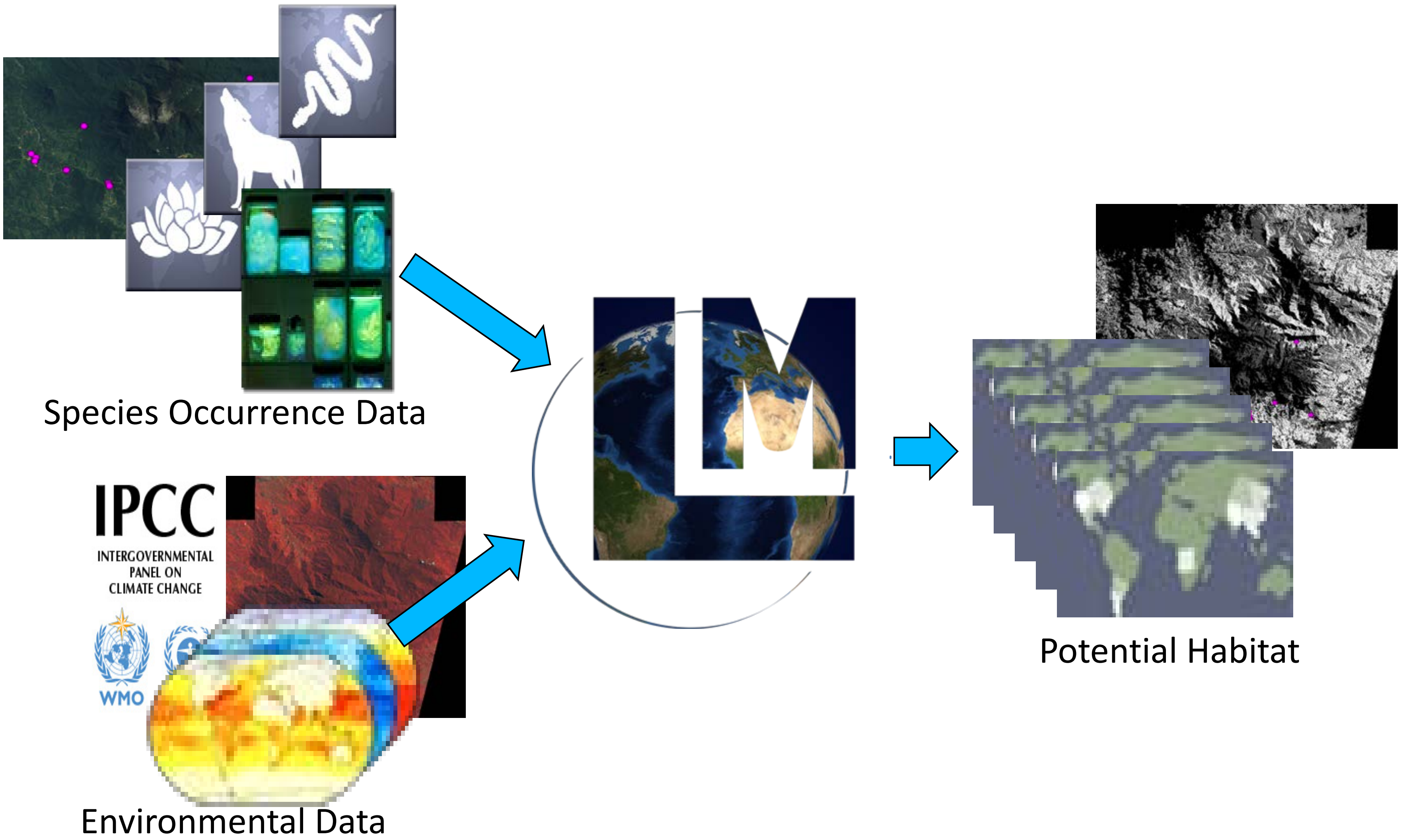
Lifemapper

LmSDM: Species Distribution Modelling



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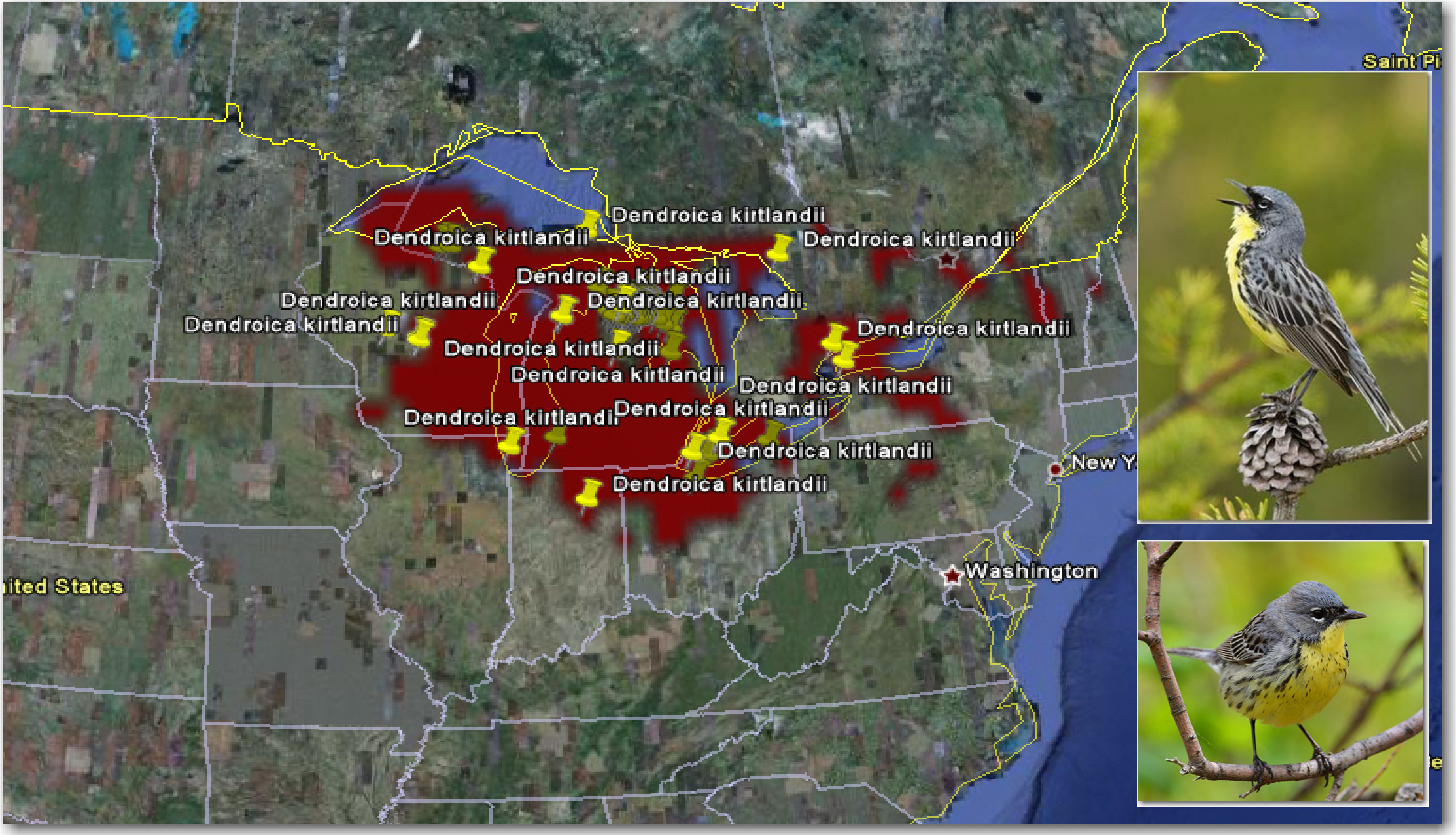
Kirtland's Warbler Range



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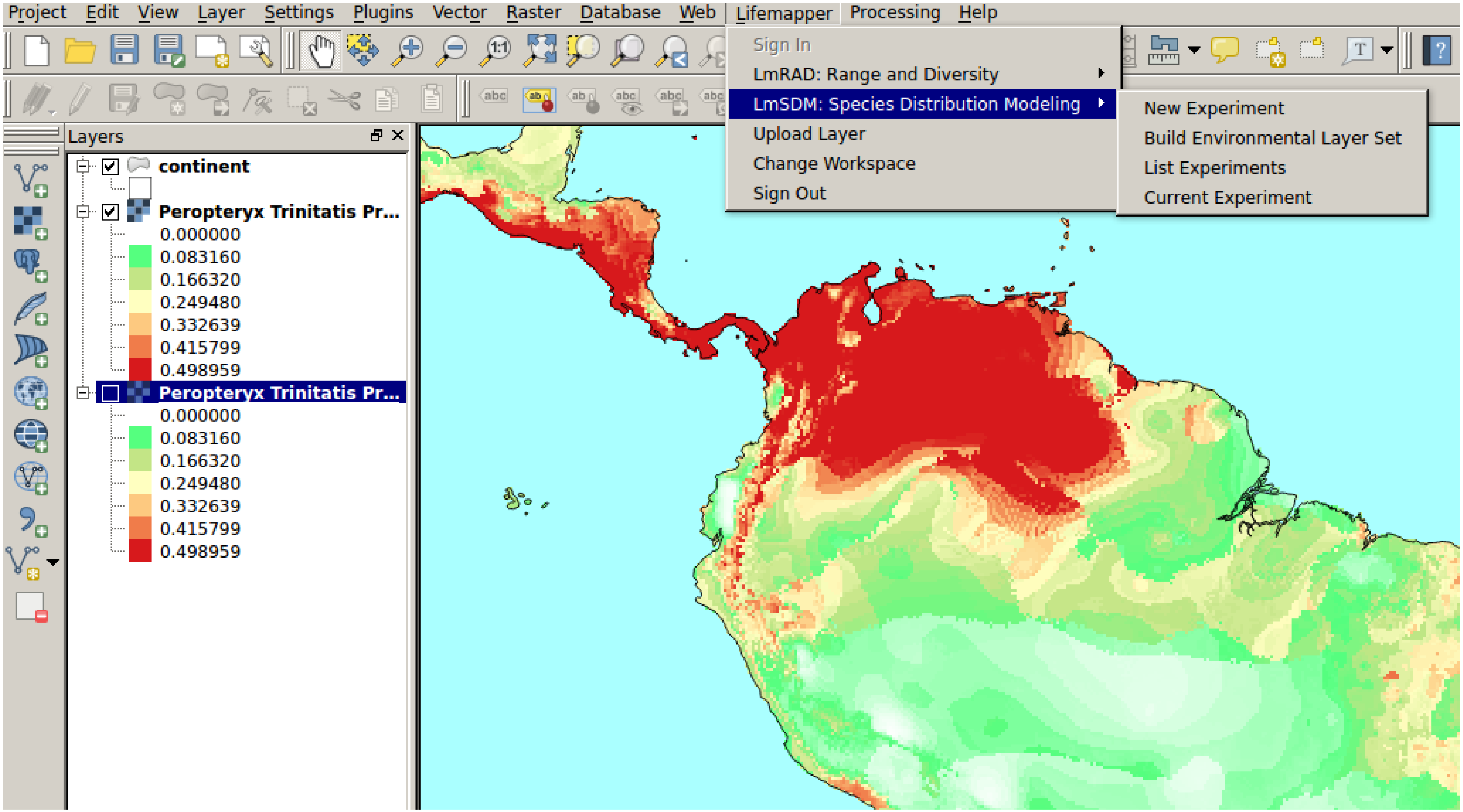
Lifemapper Qgis plugin



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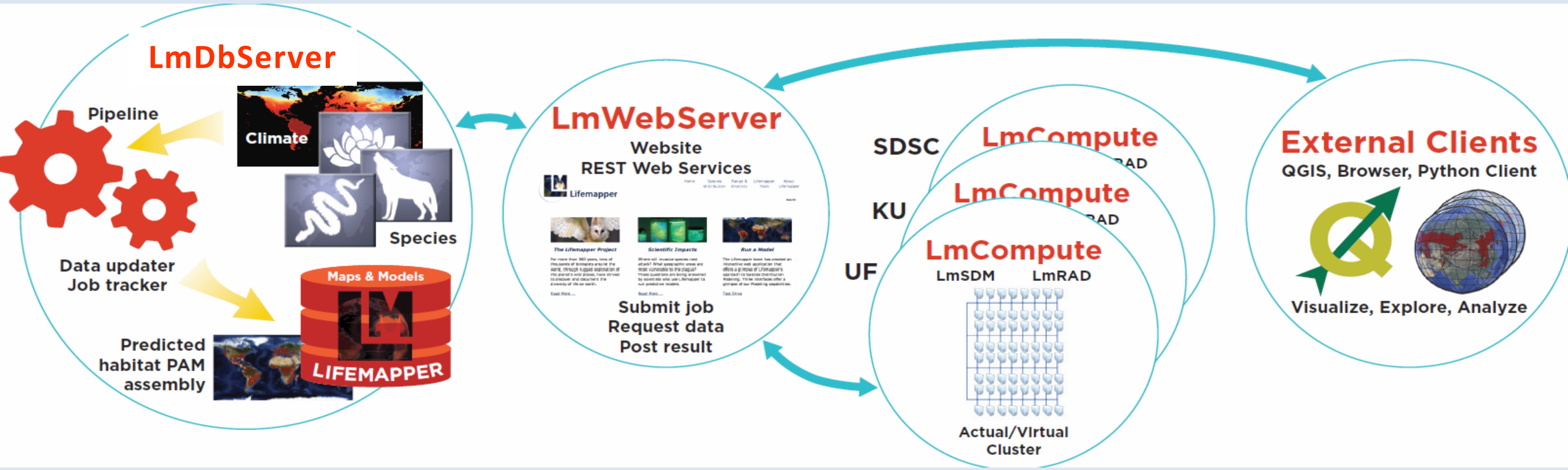
Component Design



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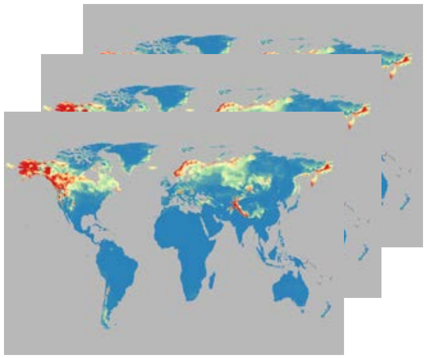
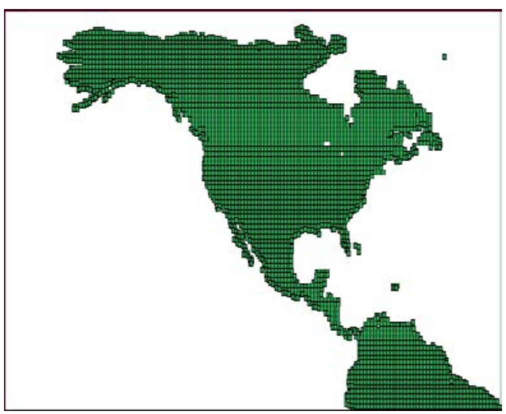
LmRAD: Presence Absence Matrix (PAM)



Species

Sites



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

Multi-species analyses and visualizations

It's that moment they told us about when matrix algebra would save our lives

$$\begin{pmatrix} a_{11} & a_{12} & & \\ a_{21} & a_{22} & \cdots & \\ & \vdots & & \\ & & & a_{nm} \end{pmatrix} * \begin{pmatrix} b_{11} & b_{12} & & \\ b_{21} & b_{22} & \cdots & \\ & \vdots & & \\ & & & b_{mj} \end{pmatrix} = \begin{pmatrix} \sum_{k=1}^{m} a_{1k} * b_{k1} & \sum_{k=1}^{m} a_{1k} * b_{k2} & & \sum_{k=1}^{m} a_{1k} * b_{kj} \\ \sum_{k=1}^{m} a_{2k} * b_{k1} & \sum_{k=1}^{m} a_{2k} * b_{k2} & \cdots & \\ & \vdots & & \\ \sum_{k=1}^{m} a_{nk} * b_{k1} & \sum_{k=1}^{m} a_{nk} * b_{k2} & & \sum_{k=1}^{m} a_{nk} * b_{kj} \end{pmatrix}$$

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	NAME	ALGEBRAIC DEFINITION	LINEAR ALGEBRA
1	Whittaker's multiplicative beta	$\beta_W = \frac{1}{\overline{\omega}^*}$	$\beta_W = \frac{SN}{Trace(\mathbf{\Omega})}$
2	Lande's additive beta	$\beta_A = S(1 - 1/\beta_W)$	$\beta_A = S[1 - \frac{Trace(\mathbf{\Omega})}{SN}]$
3	Legendre's beta	$\beta_L = SS(\mathbf{X}) = SN/\beta_W - \left(\sum_{j=1}^{s} \omega_j^2\right)/N$	$\beta_L = Trace(\mathbf{\Omega}) - \boldsymbol{\varphi}^T \mathbf{1}_N$
4	Range-richness of a species	$\psi_i = \sum_{j=1}^{N} \delta_{i,j}\alpha_j$	$\boldsymbol{\psi} = \mathbf{X}\boldsymbol{\alpha} = \mathbf{\Omega}\mathbf{1}_S$
5	Per-site range size of a locality	$\varphi_j = \sum_{i=1}^{S} \delta_{i,j}\omega_i$	$\boldsymbol{\varphi}^T = \boldsymbol{\omega}^T\mathbf{X} = \mathbf{1}_N^T\mathbf{A}$
6	Matrix of covariance of composition of sites	$\mathbf{\Sigma}_{sites}(j,k) = \frac{1}{S}\sum_{l=1}^{S} \delta_{j,l}\delta_{k,l} - \frac{\alpha_j\alpha_k}{S^2}$	$\mathbf{\Sigma}_{sites} = \frac{1}{S}\mathbf{A} - \boldsymbol{\alpha}^*(\boldsymbol{\alpha}^*)^T$
7	Matrix of covariance of ranges of species	$\mathbf{\Sigma}_{sps}(h,i) = \frac{1}{N}\sum_{j=i}^{N} \delta_{i,j}\delta_{h,j} - \frac{\omega_i\omega_h}{N^2}$	$\mathbf{\Sigma}_{species} = \frac{1}{N}\mathbf{\Omega} - \boldsymbol{\omega}^*(\boldsymbol{\omega}^*)^T$
8	Mean composition covariance	$\alpha_j^* = \frac{\tau_j}{\overline{\varphi}_j^* - \beta_W^{-1}}$	$\overline{\boldsymbol{\tau}} = \frac{1}{NS}\boldsymbol{\varphi} - \beta_W^{-1}\boldsymbol{\alpha}^*$
9	Mean range covariance	$\omega_i^* = \frac{\overline{\rho}_i}{\overline{\psi}_i^* - \beta_W^{-1}}$	$\overline{\boldsymbol{\rho}} = \frac{1}{NS}\boldsymbol{\psi} - \beta_W^{-1}\boldsymbol{\omega}^*$
10	Schluter sites-composition covariance	$V_{sites} = \frac{\overline{\varphi}^* - S/\beta_W^2}{1/\beta_W - \overline{\psi}^*/N}$	$V_{sites} = \frac{\mathbf{1}^T\mathbf{\Sigma}_{sites}\mathbf{1}}{Trace(\mathbf{\Sigma}_{sites})}$
11	Schluter species-ranges covariance	$V_{sps} = \frac{\overline{\psi}^* - N/\beta_W^2}{1/\beta_W - \overline{\varphi}^*/S}$	$Vsps = \frac{\mathbf{1}^T\Sigma_{sps}\mathbf{1}}{Trace(\Sigma_{sps})}$
12	Wright & Reeves' nestedness	$N_C = \frac{1}{2}\sum_{j=1}^{S} \omega_j(\omega_j - 1)$ $= \frac{1}{2}(N\overline{\varphi} - \frac{S}{N}\frac{1}{\beta_W})$	$N_C = \frac{1}{2}(N\boldsymbol{\varphi}^T\mathbf{1} - \frac{S}{N}\frac{1}{\beta_W})$
13	Stone & Roberts C-score	$C = \frac{2}{S(S-1)}\left[\sum_{i=1}^{S}\sum_{h<i}(\omega_i - \omega_{i,h})(\omega_h - \omega_{i,h})\right]$	$C' = \mathbf{1}^T\left[(\frac{ns}{\beta_W})^2 - 2\boldsymbol{\omega}^T\boldsymbol{\psi} - \mathbf{\Omega}\odot\right]$

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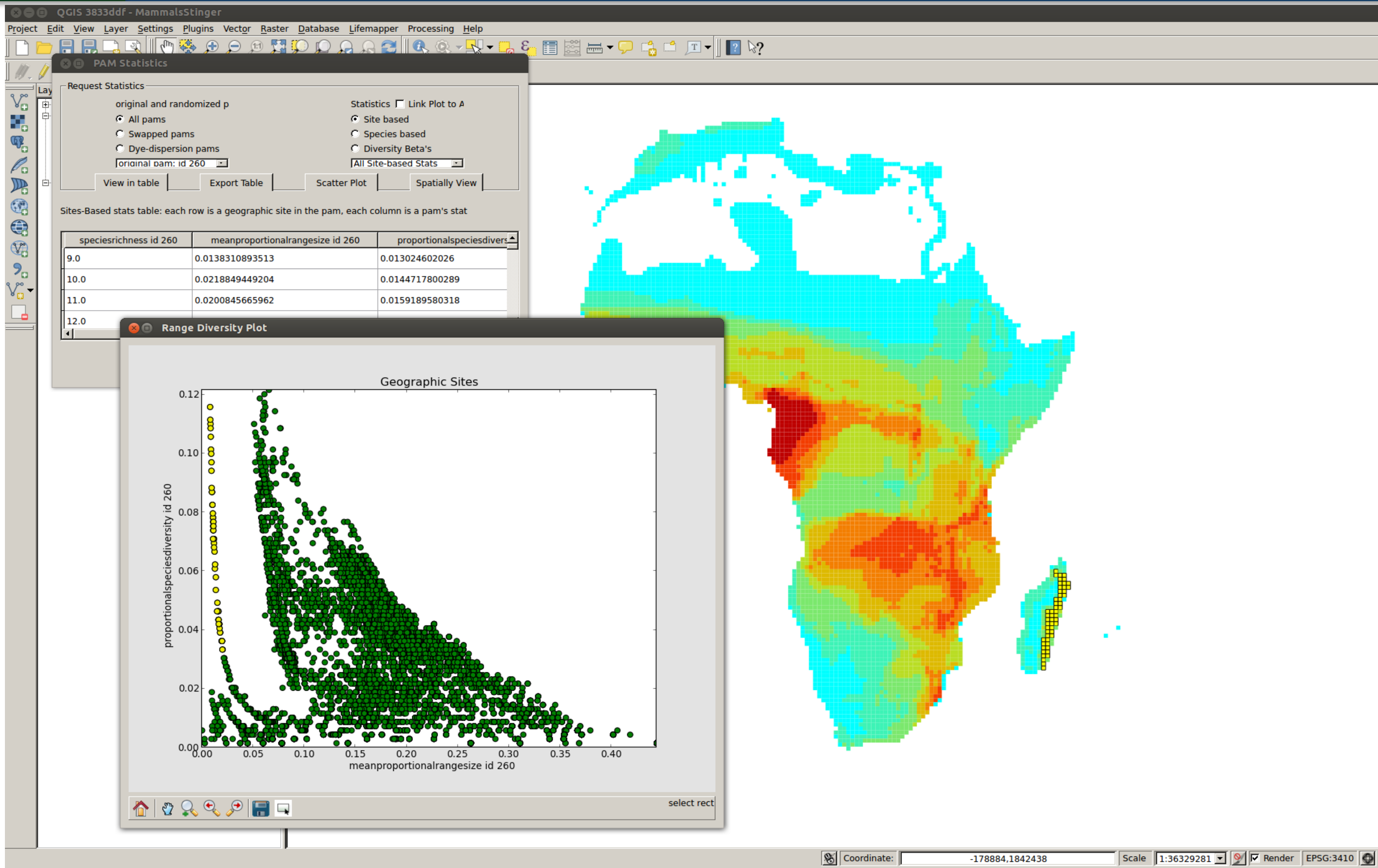
Covariance in interactive plot show biogeographic patterns



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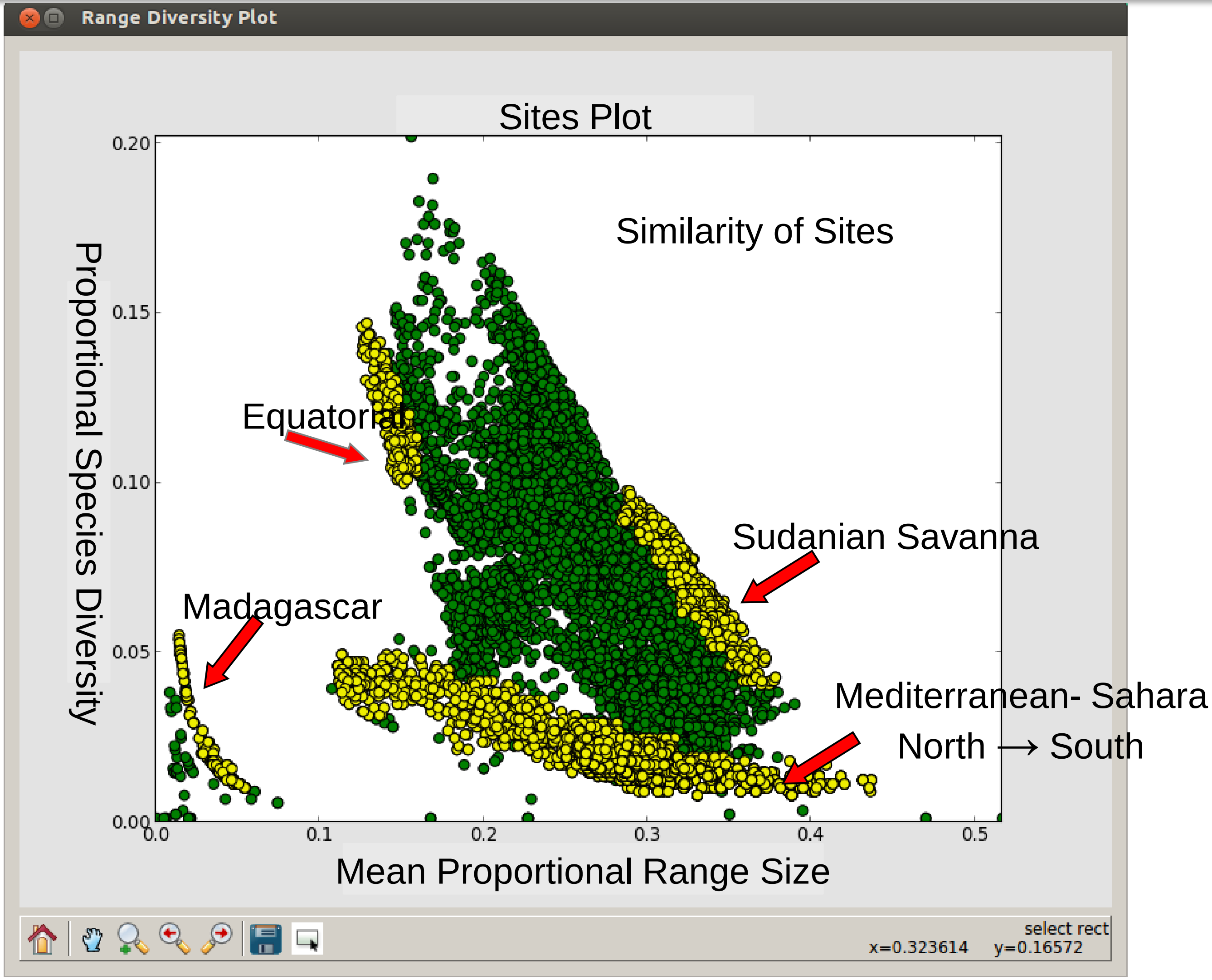
Similarity of Sites



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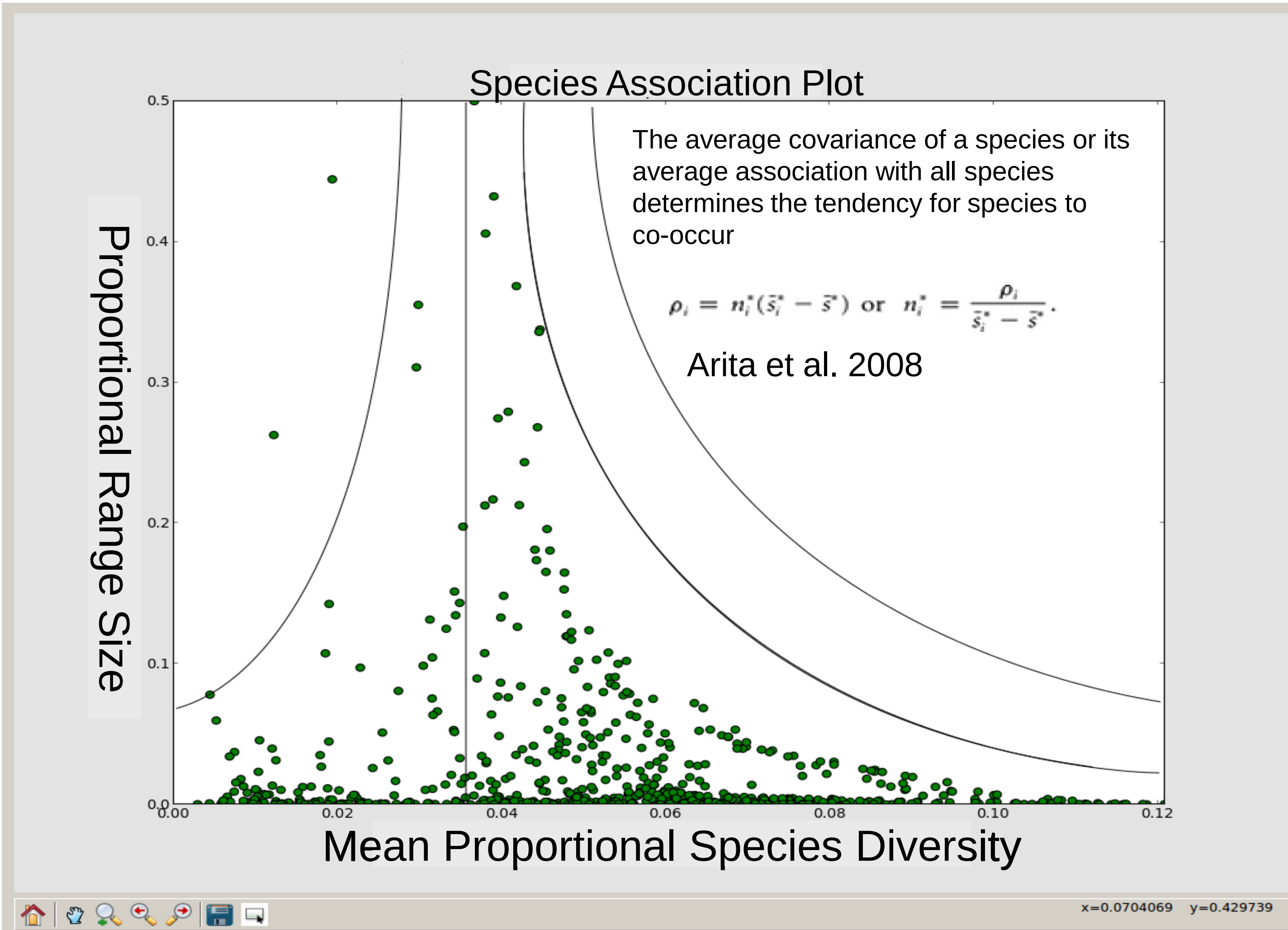
Degree of Co-Occurrence



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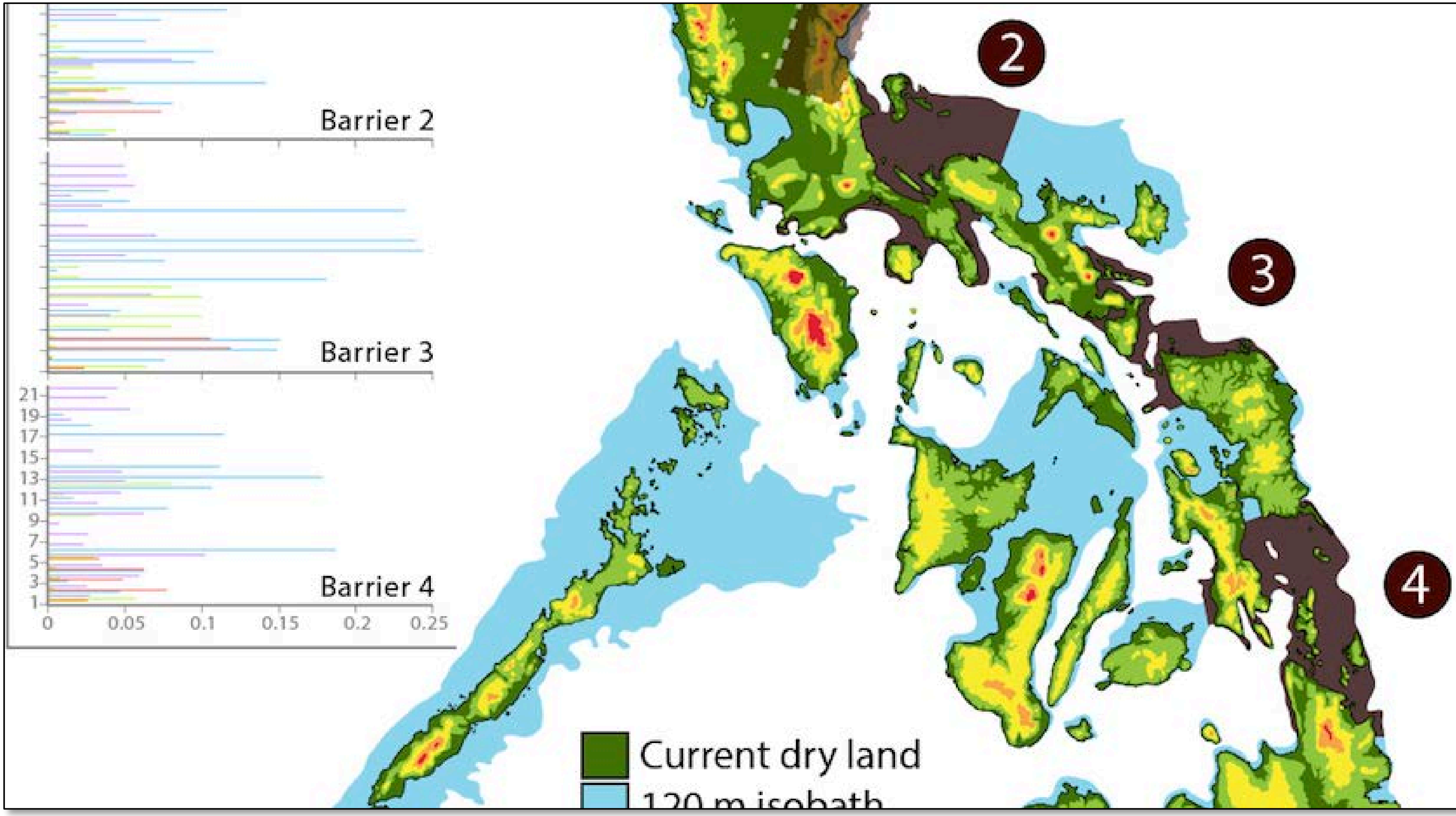
Phylogenetic Diversity Across Transition Zones



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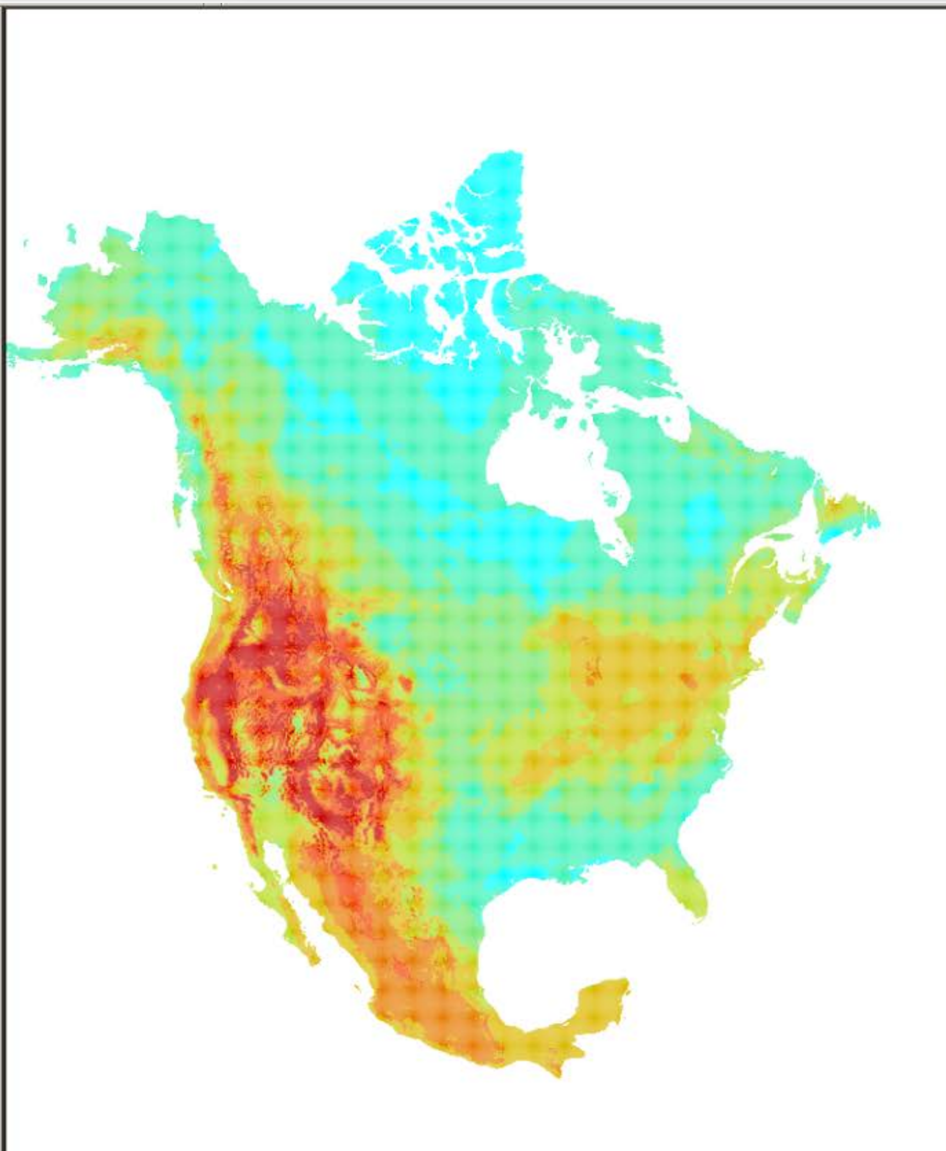
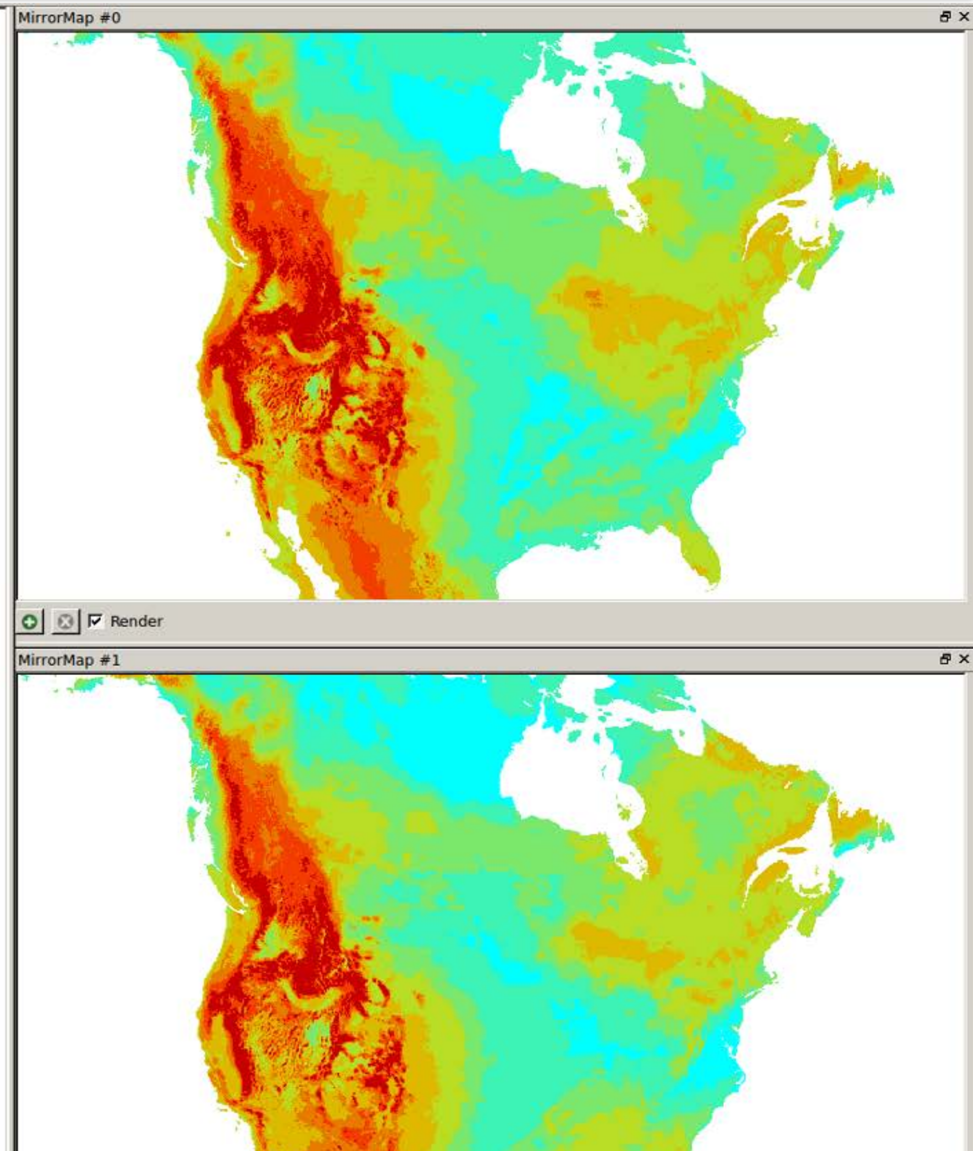
Using PAMs for Predicting Patterns of Diversity





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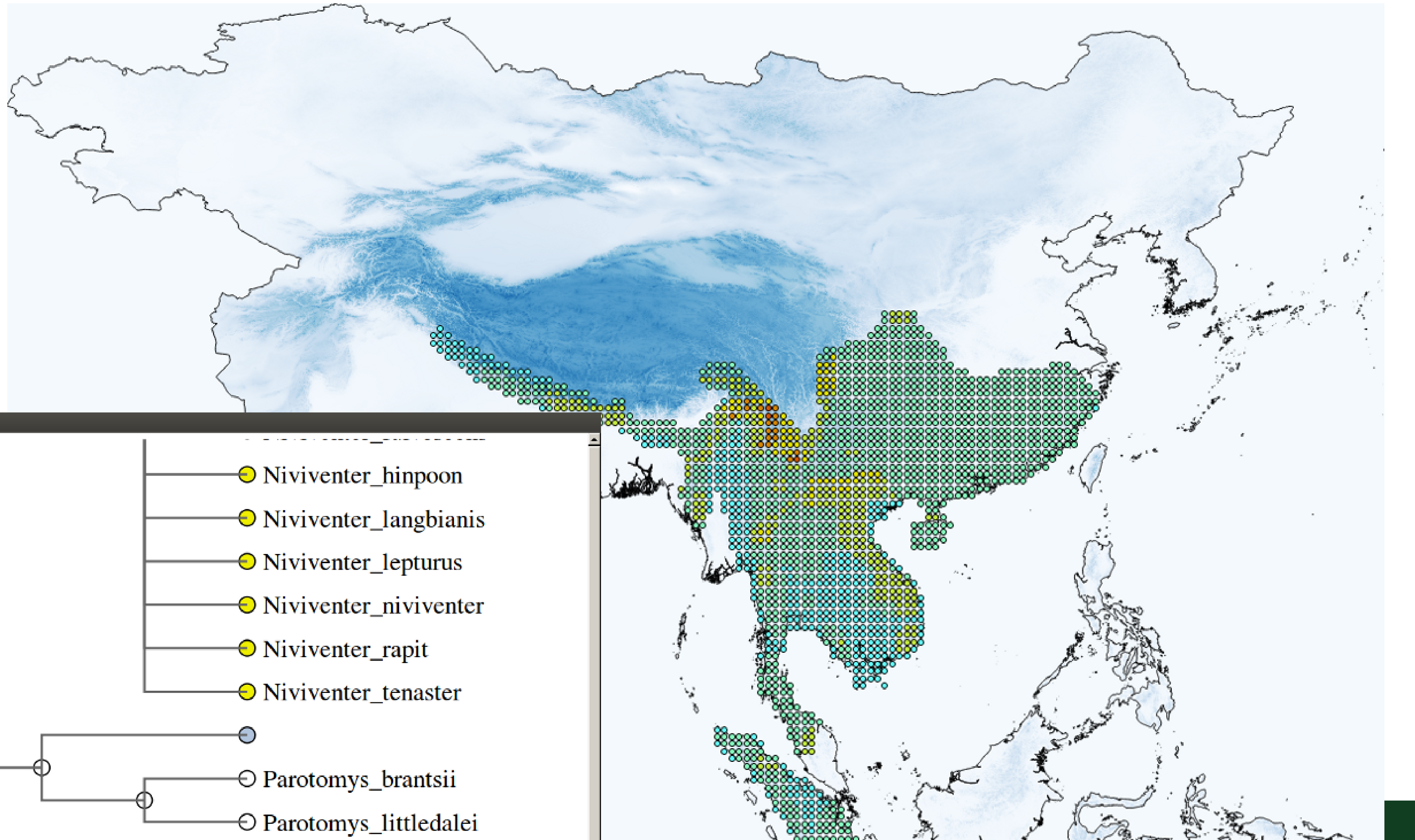
Mapping Diversity across a Species' Range



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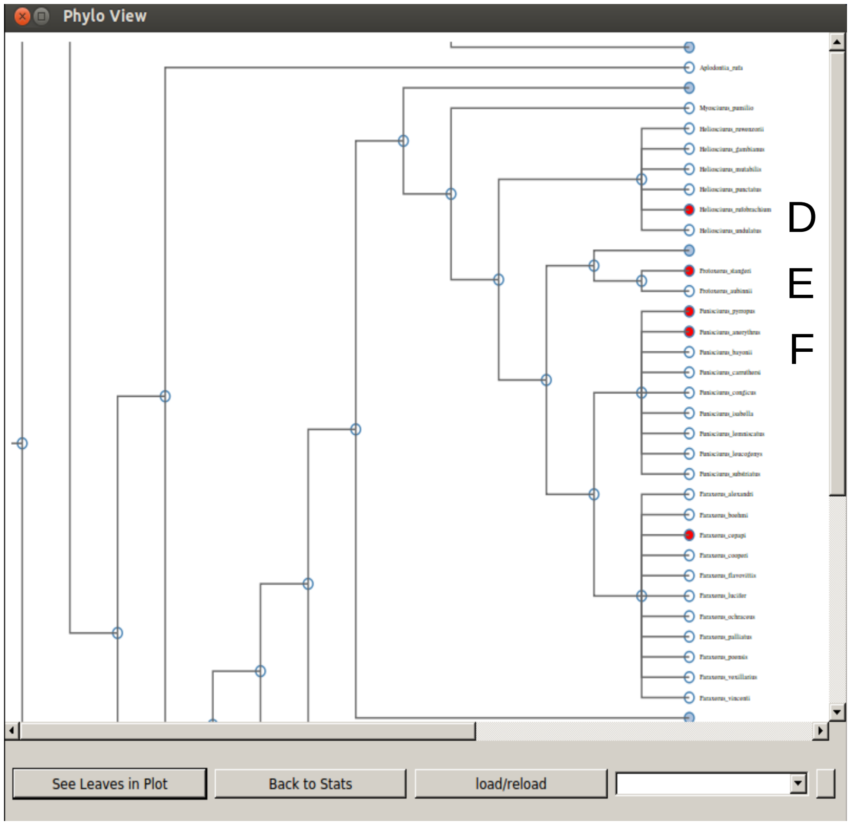
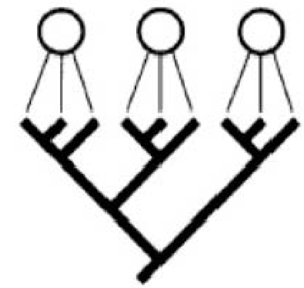
Phylogenetic Diversity P(D)Community Assembly



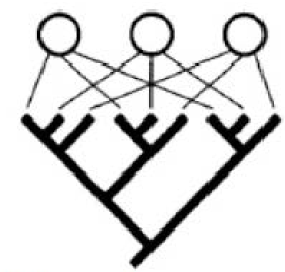
Phylogenetic Distances

	D	E	F
D	0.00	0.05	0.16
E	0.05	0.00	0.16
F	0.16	0.16	0.00

Community



Phylogenetic clustering



Phylogenetic evenness

Mean pair-wise distance between all species in a community

Mean distance to nearest taxon for each species in the community

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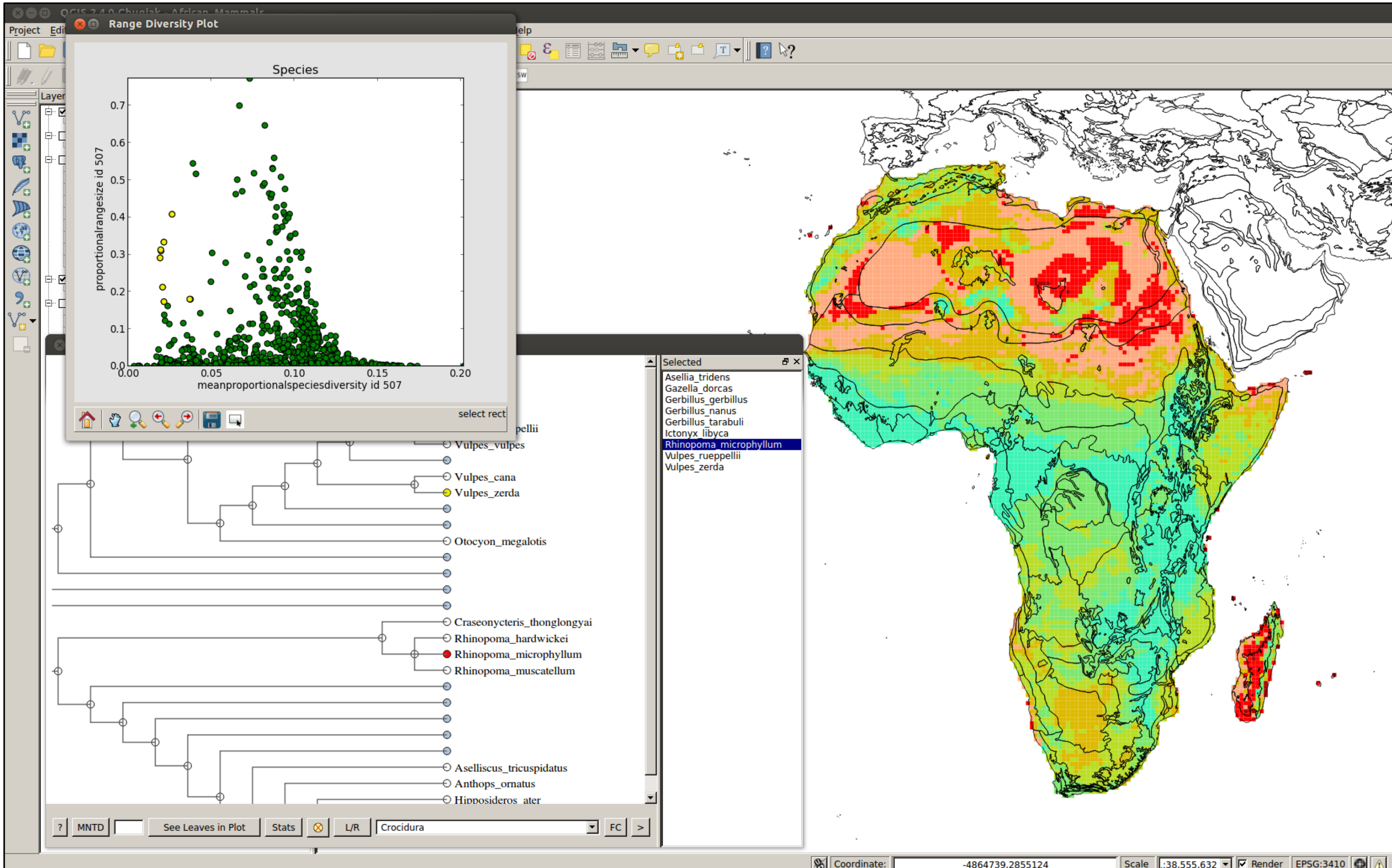
Grand Integration: Phylogeny, Biogeography, Diversity



Finish