

Evolution of ecological communities through the lens of an island chronosequence

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NSF Dimensions of Biodiversity

nature.berkeley.edu/evolab

nature.berkeley.edu/hawaiiidimensions

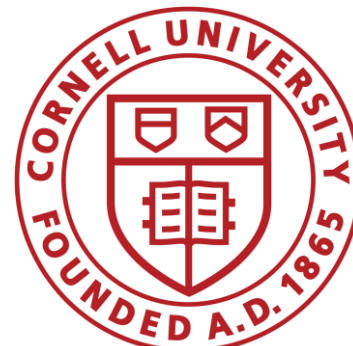
Evolution of ecological communities through the lens of an island chronosequence



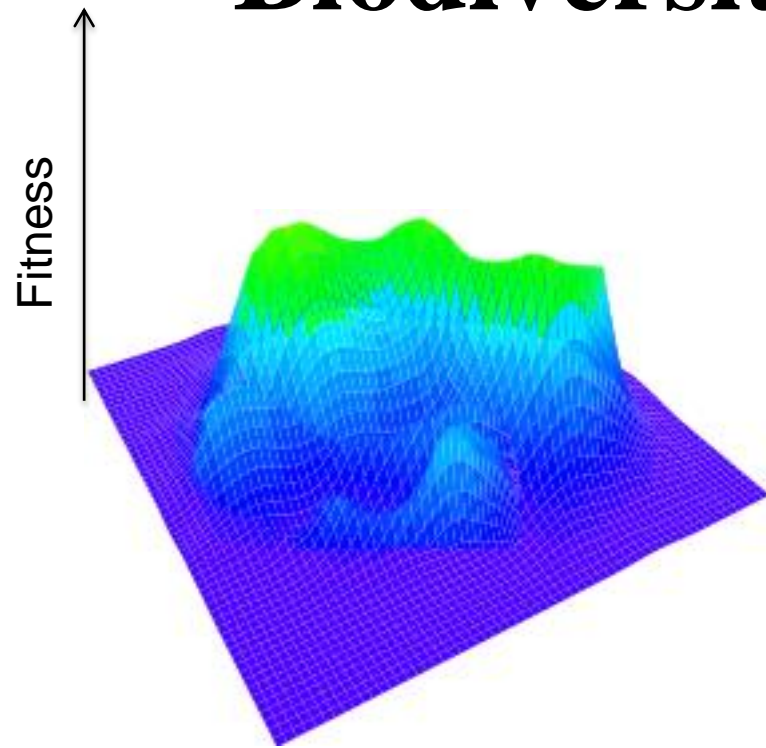
Andy Rominger, Henrik Krehenwinkel, Dan Gruner, Jun Ying Lim, Kari Goodman, Ellie Armstrong, Gordon Bennett, Michael Brewer, Darko Cotoras, Curtis Ewing, Diana Percy, Patrick O'Grady, Don Price, George Roderick, Kerry Shaw

Henrik

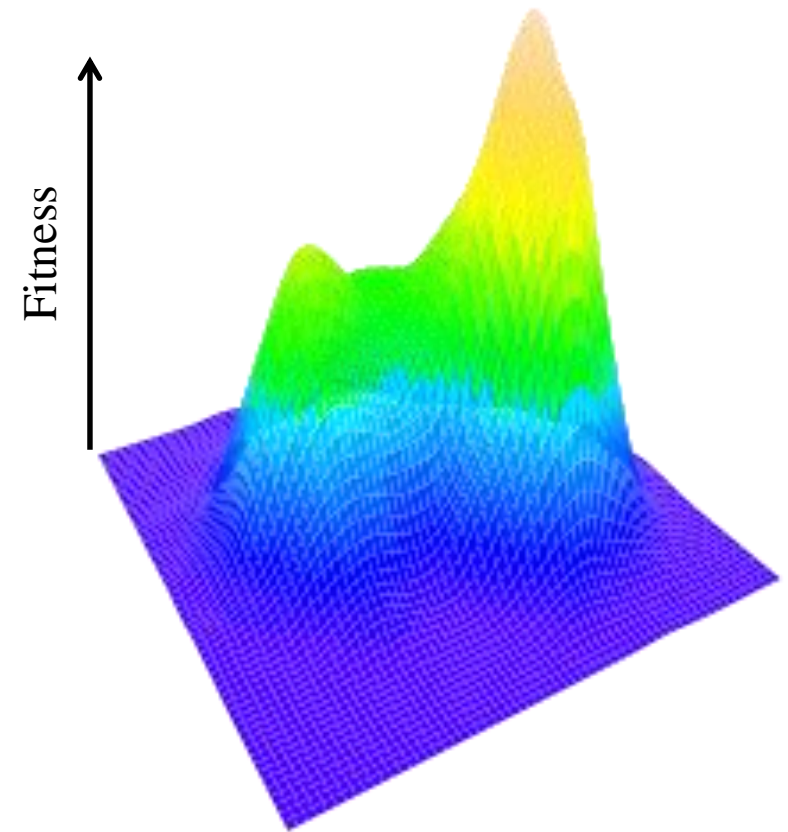
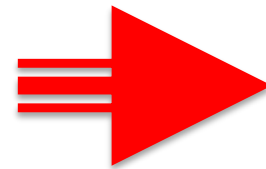
Krehenwinkel



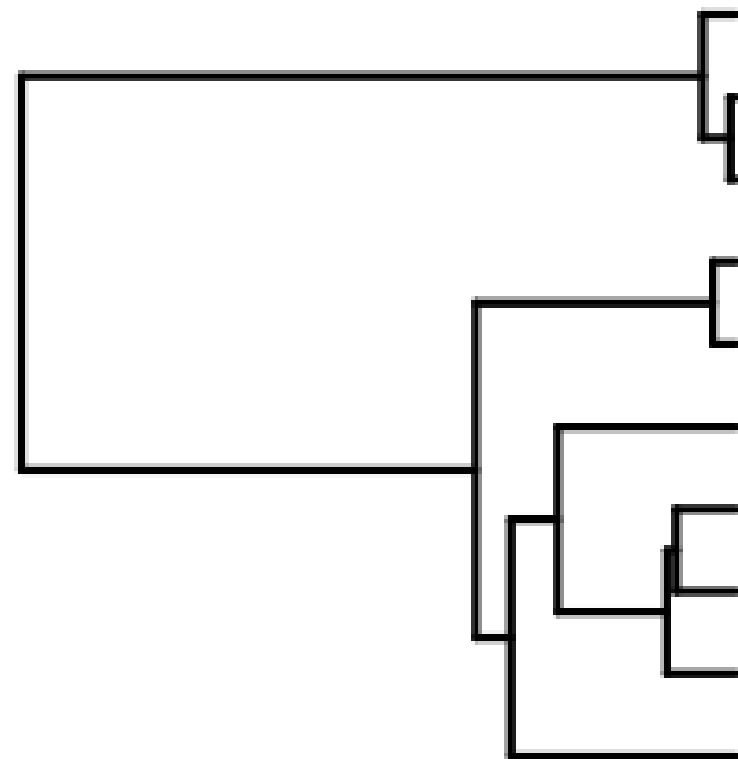
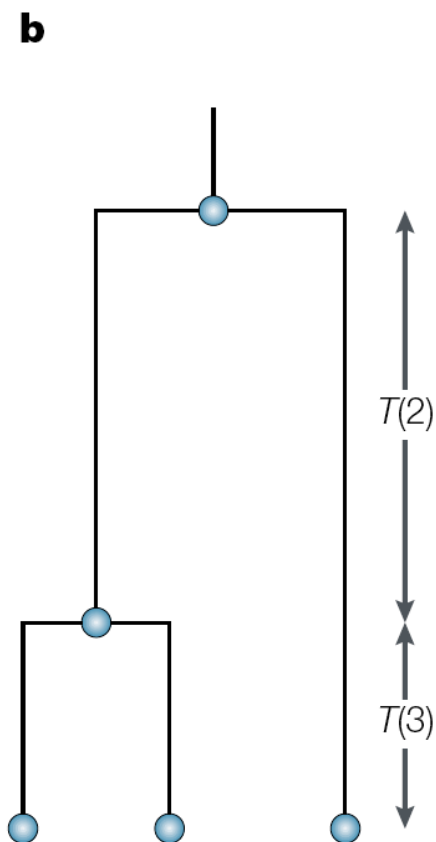
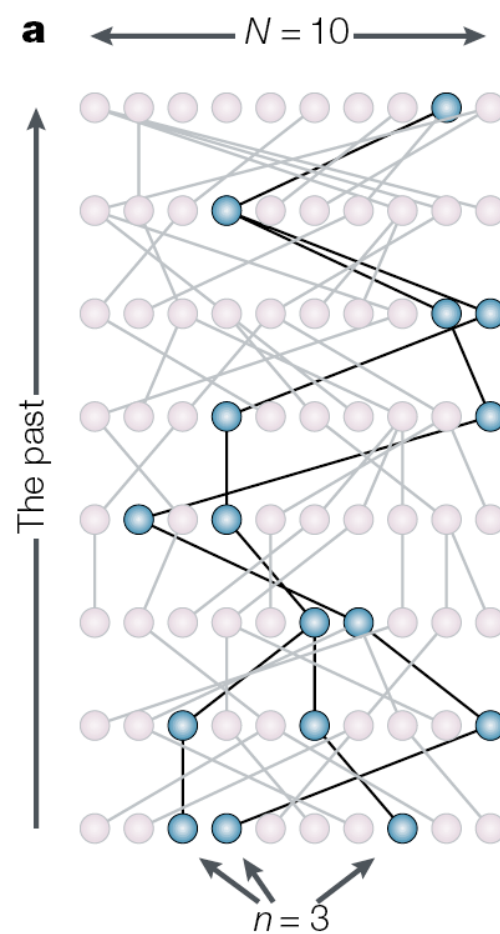
Biodiversity Dynamics

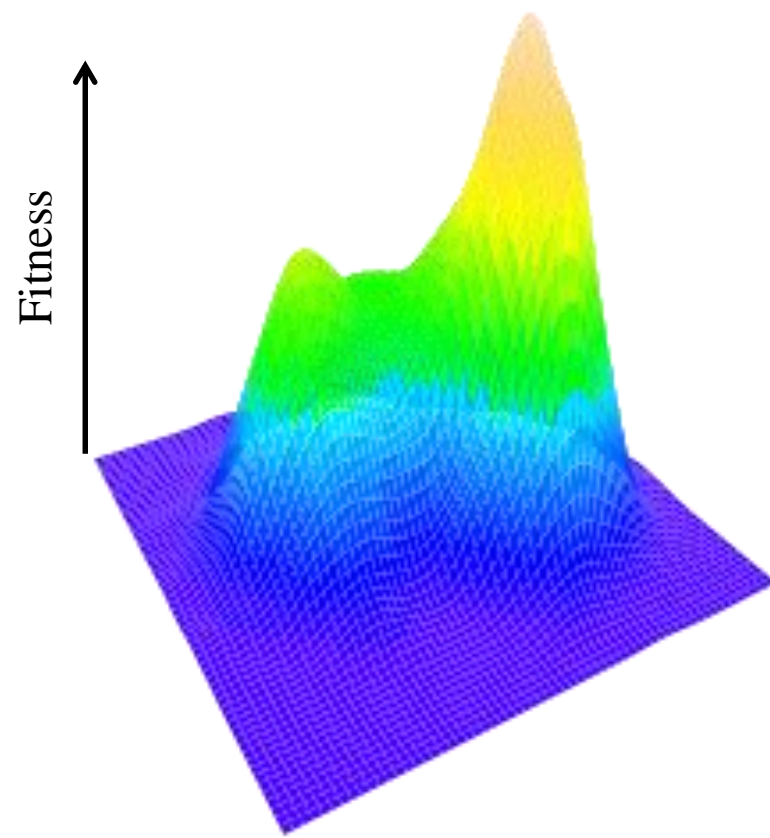


Microevolution

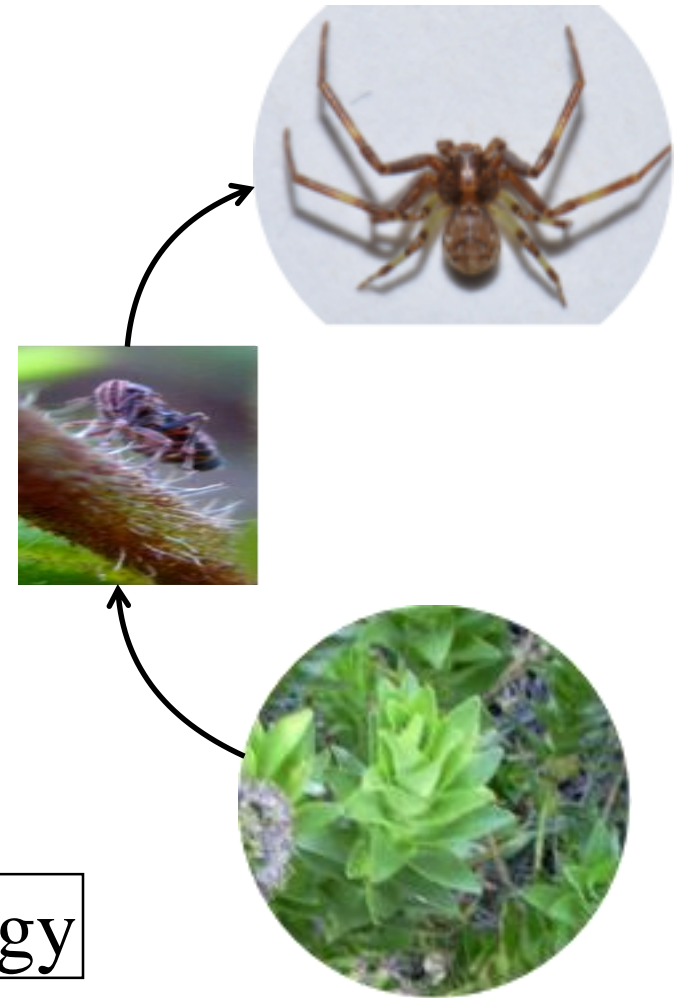
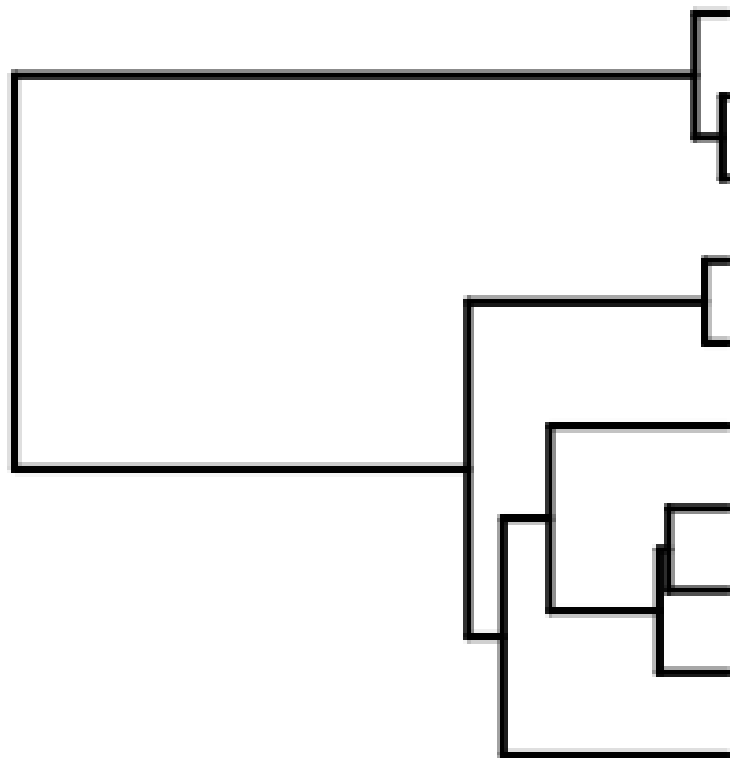


Macroevolution

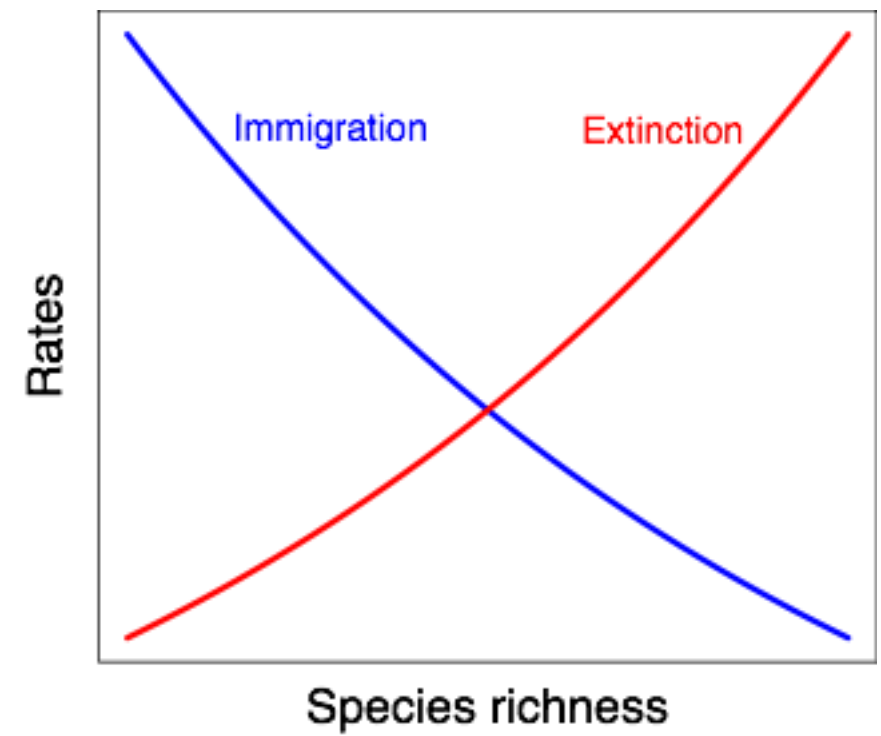


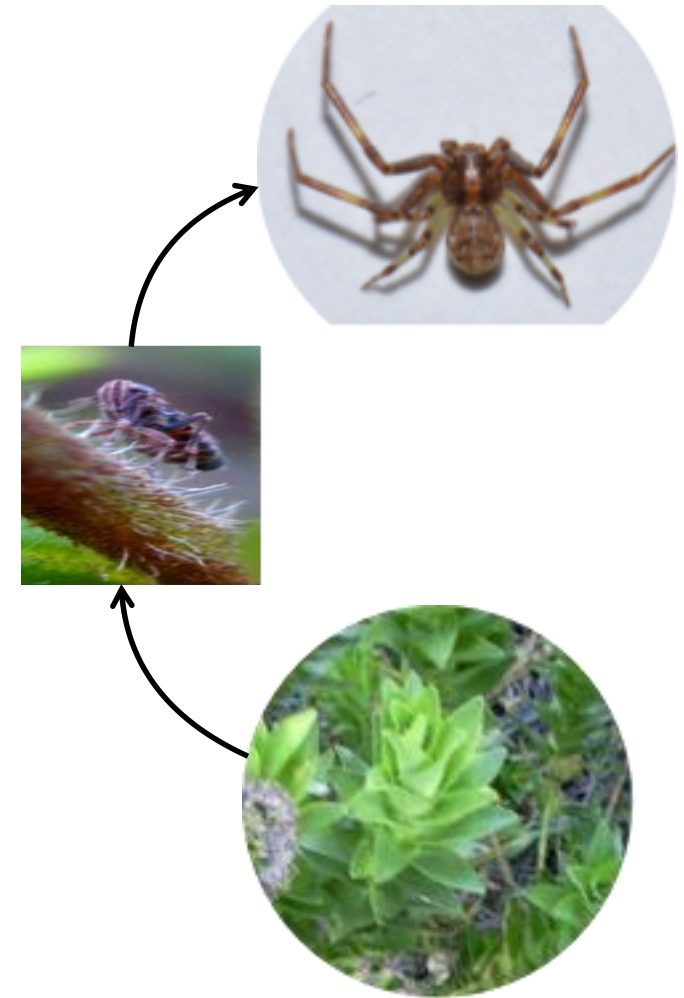
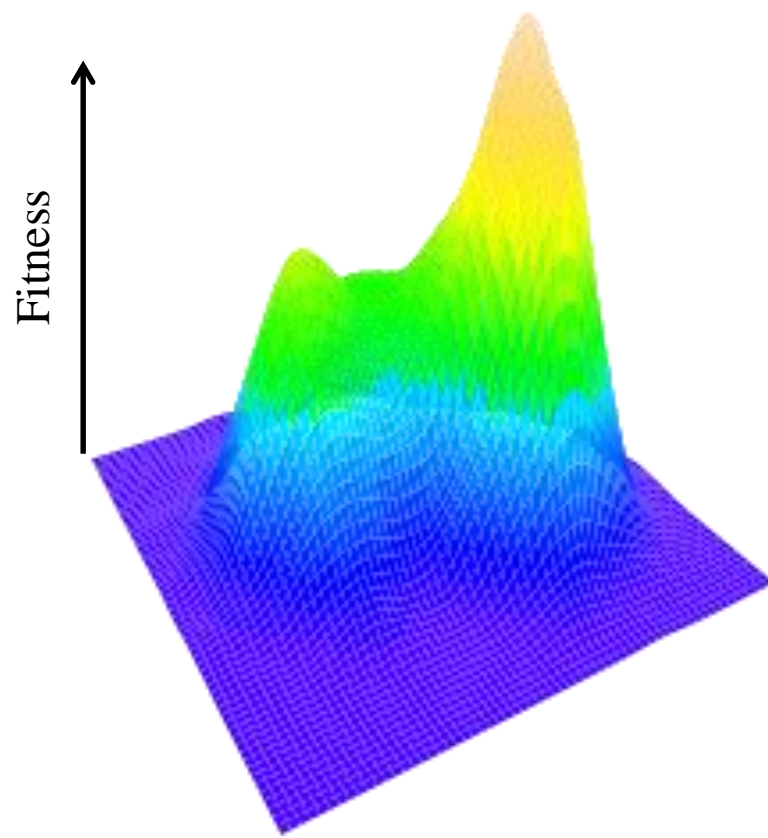


Evolution

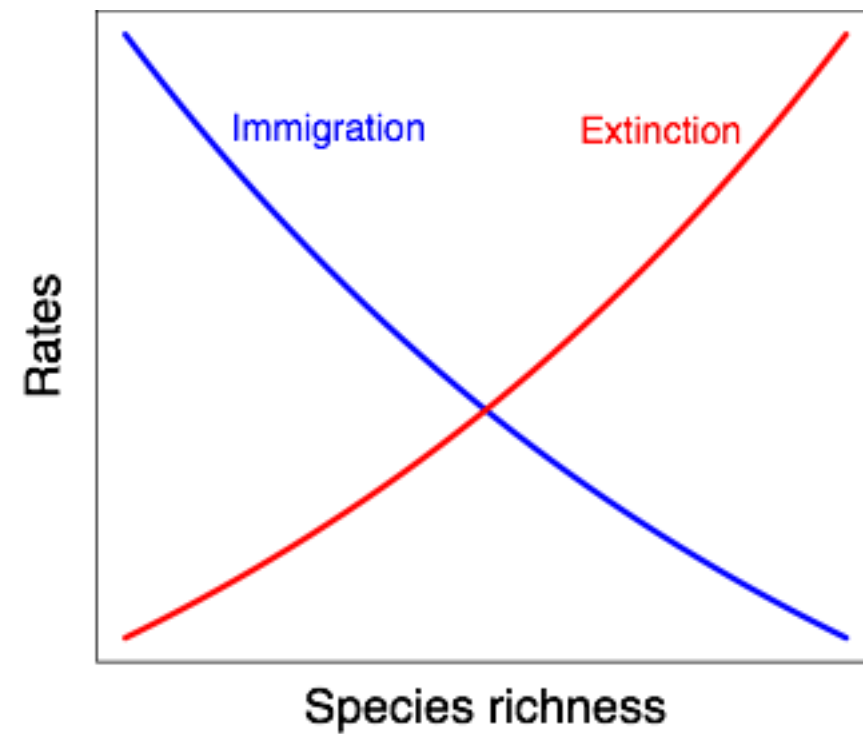
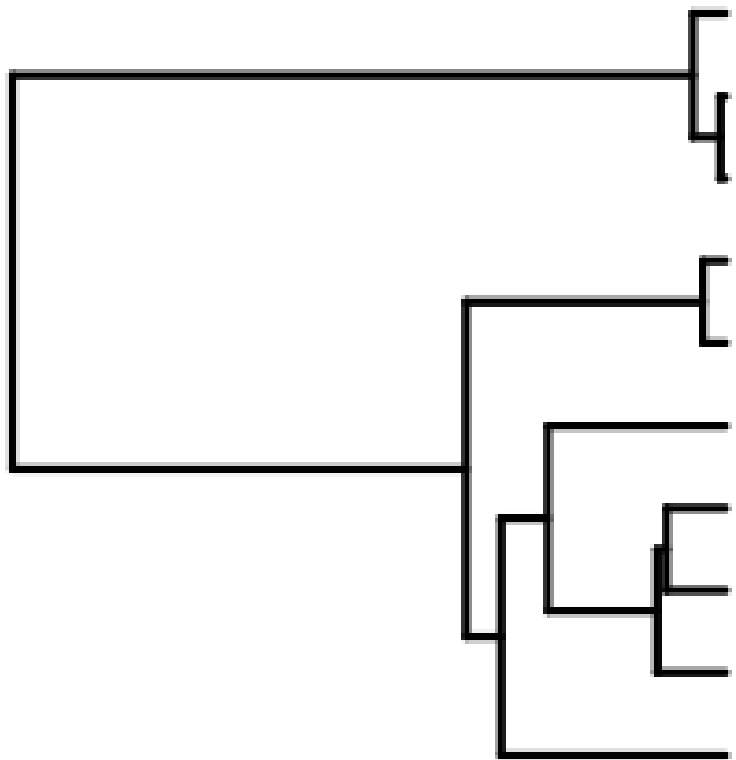


Ecology



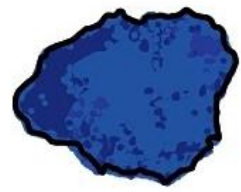


Biodiversity dynamics

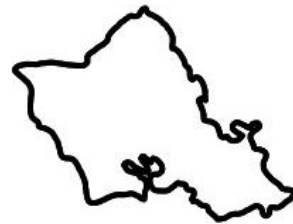


Processes occur over different scales, so how to assess dynamics?

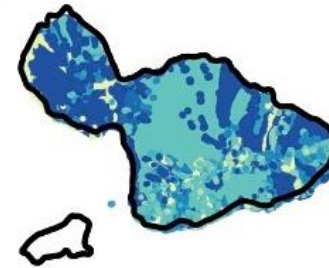
Island chronosequence



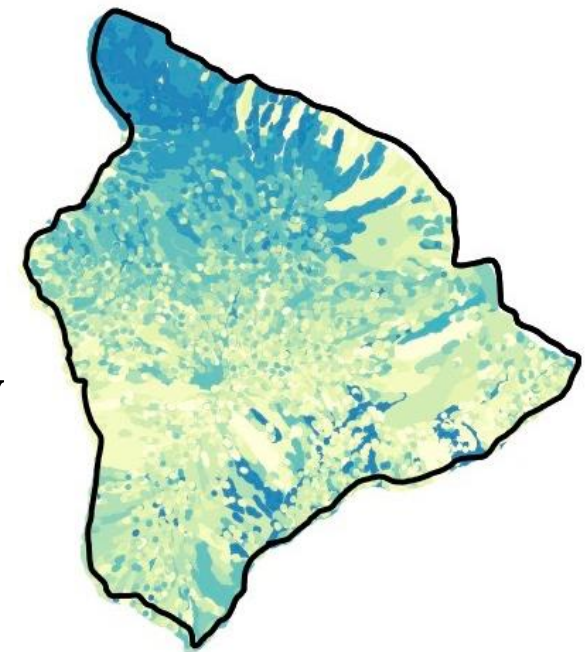
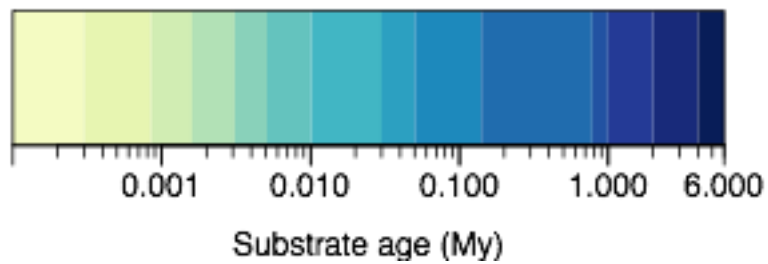
5.1 my



2.6-3.7 my

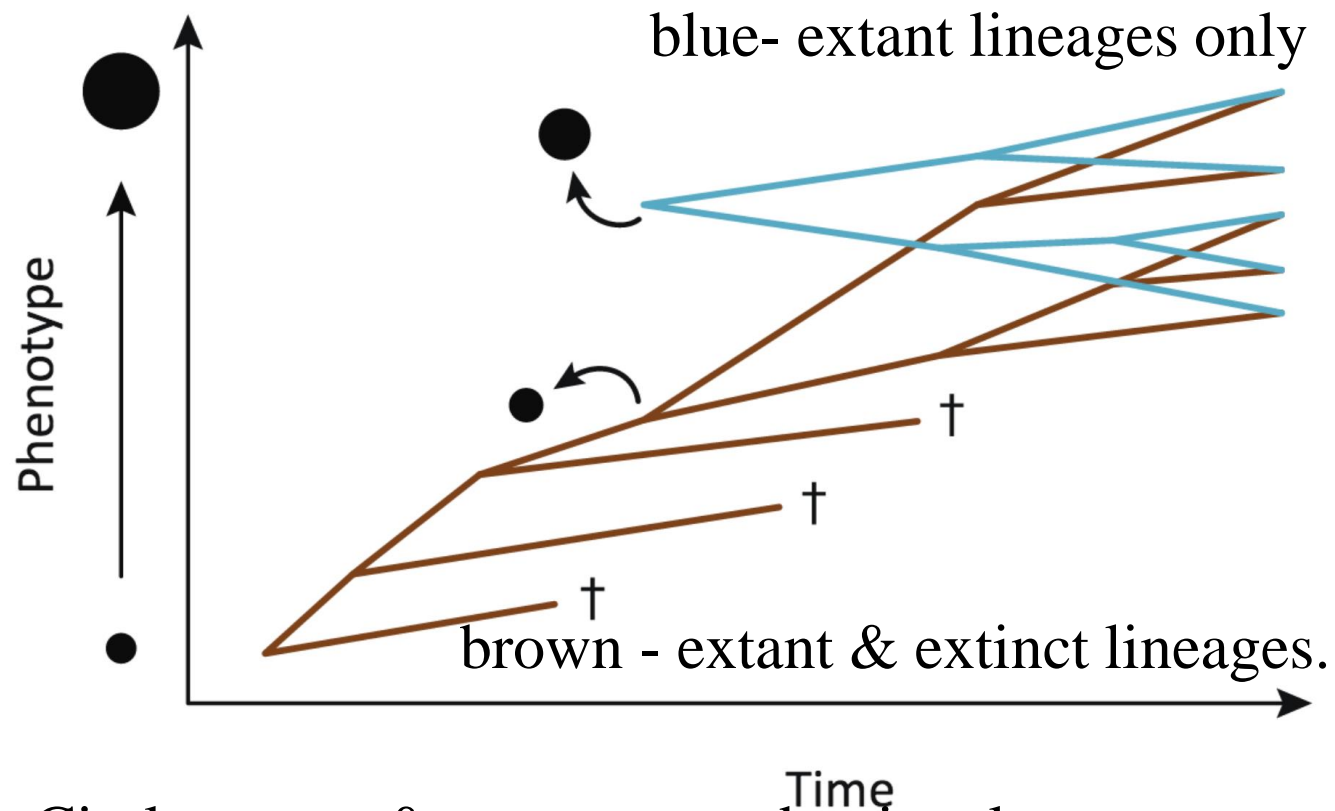


0.7-1.8 my



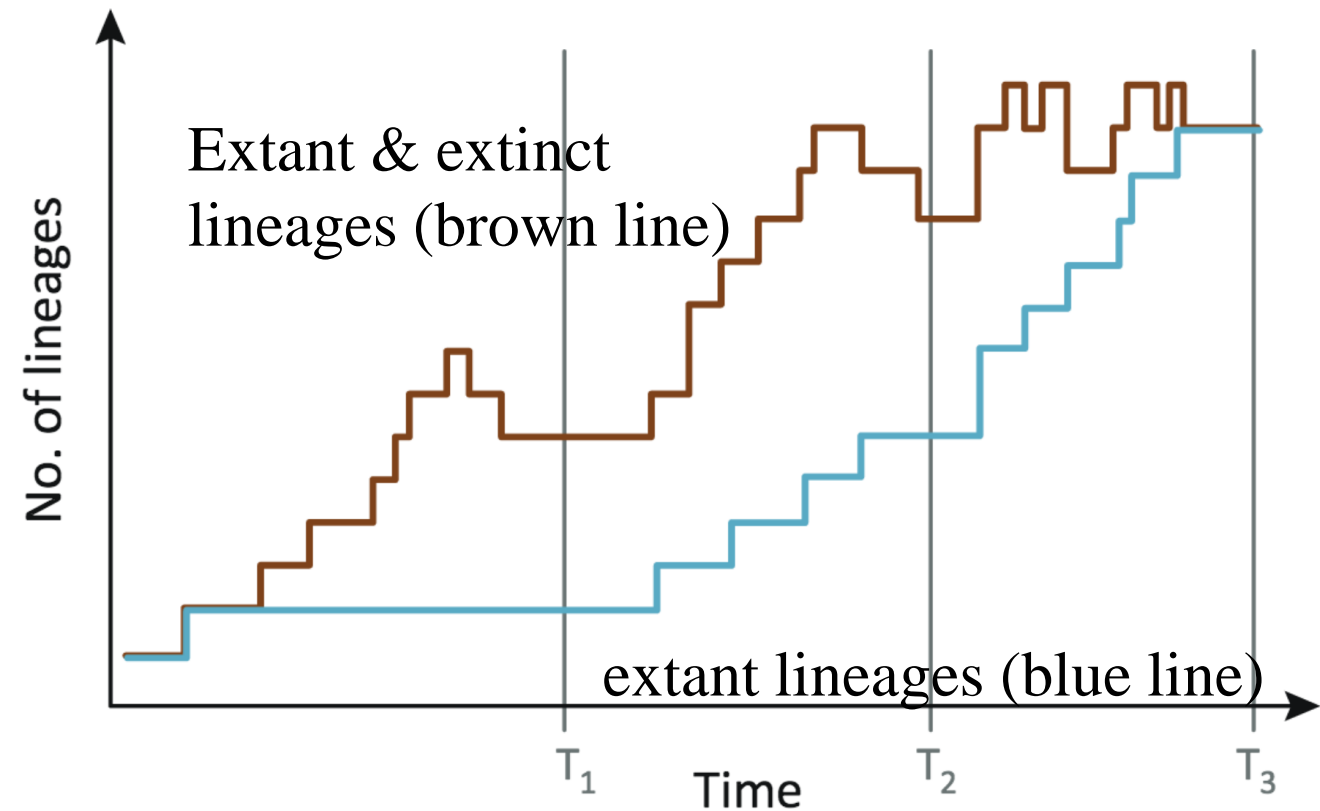
0-0.4 my

Dynamics of trait evolution



Circles - true & reconstructed trait value for the most recent common ancestor

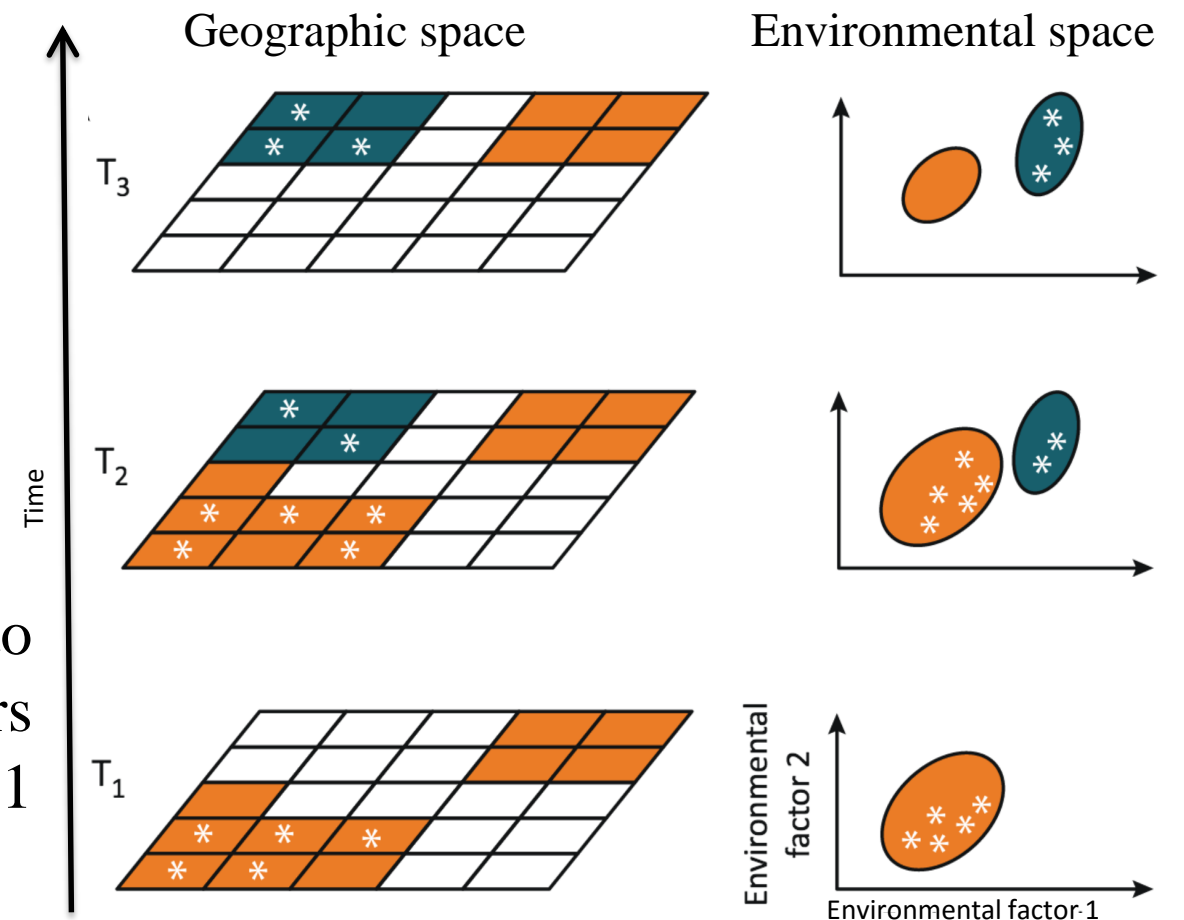
Species diversity through time



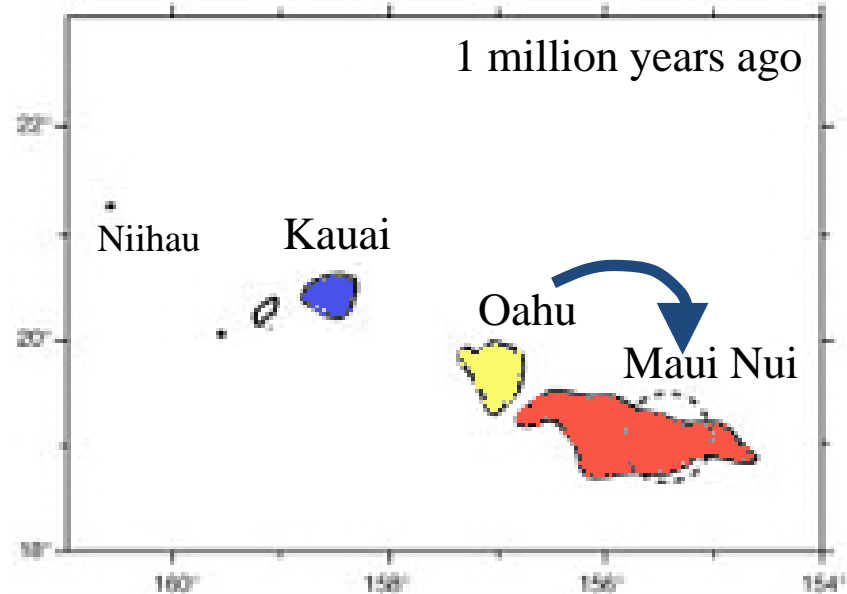
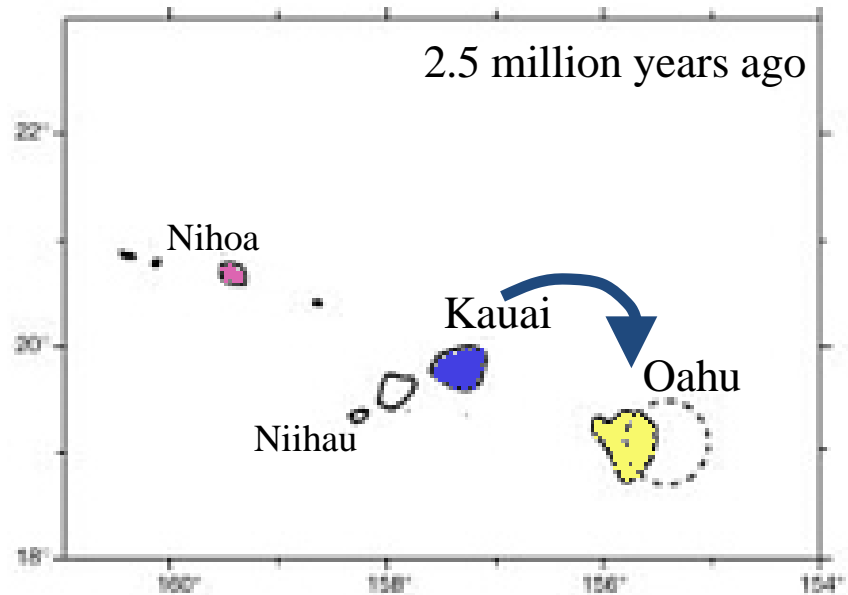
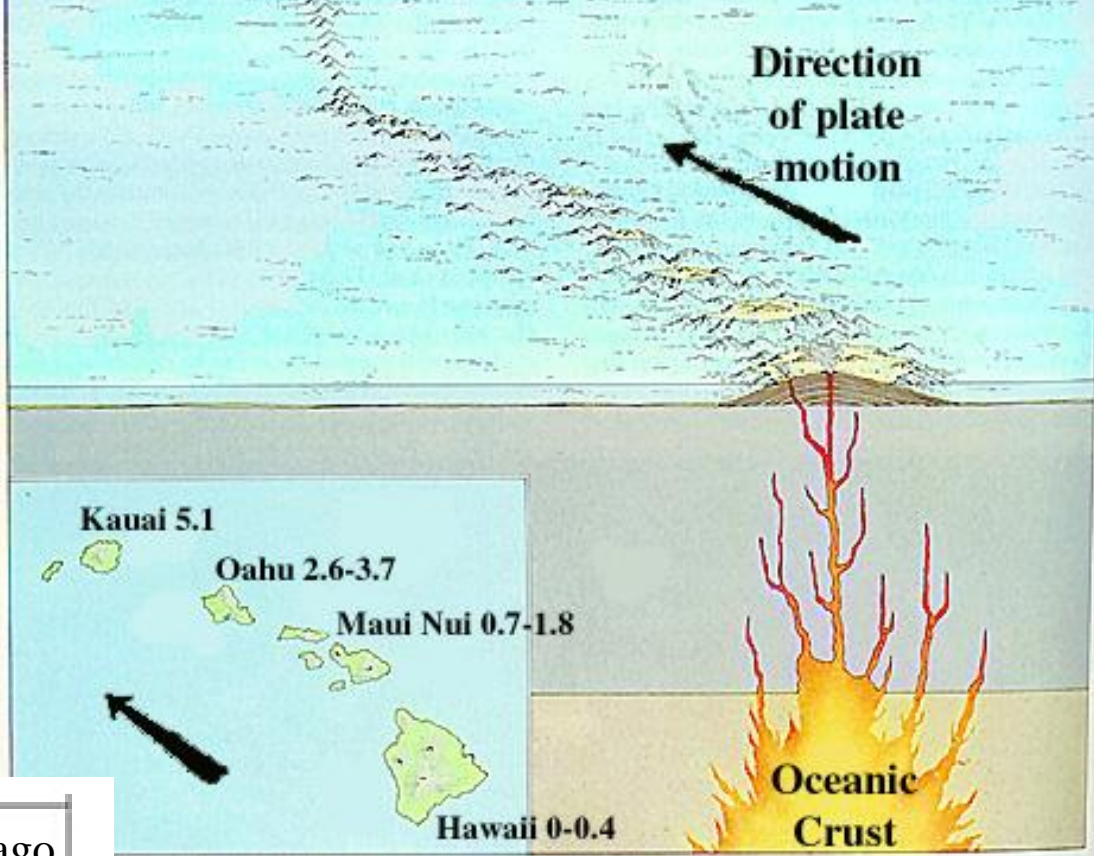
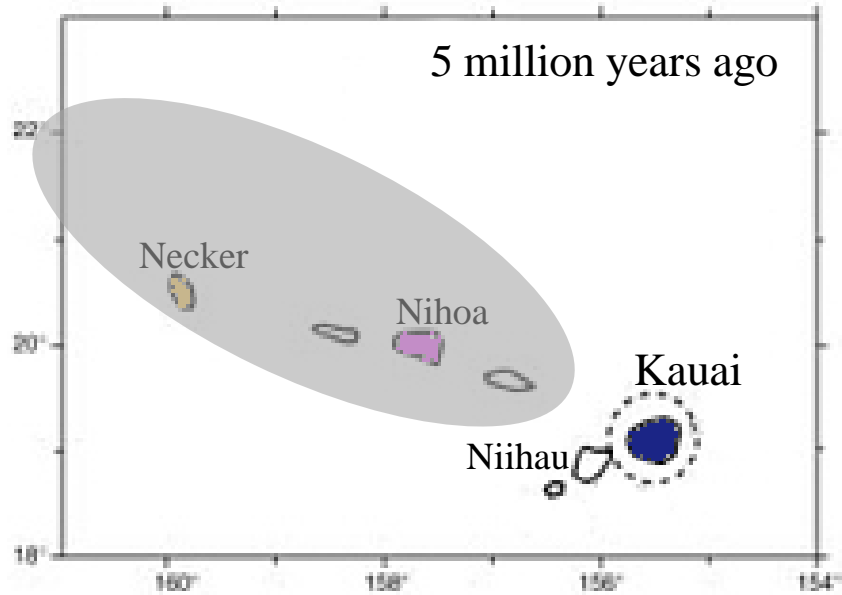
Temporal dynamics in niche interactions

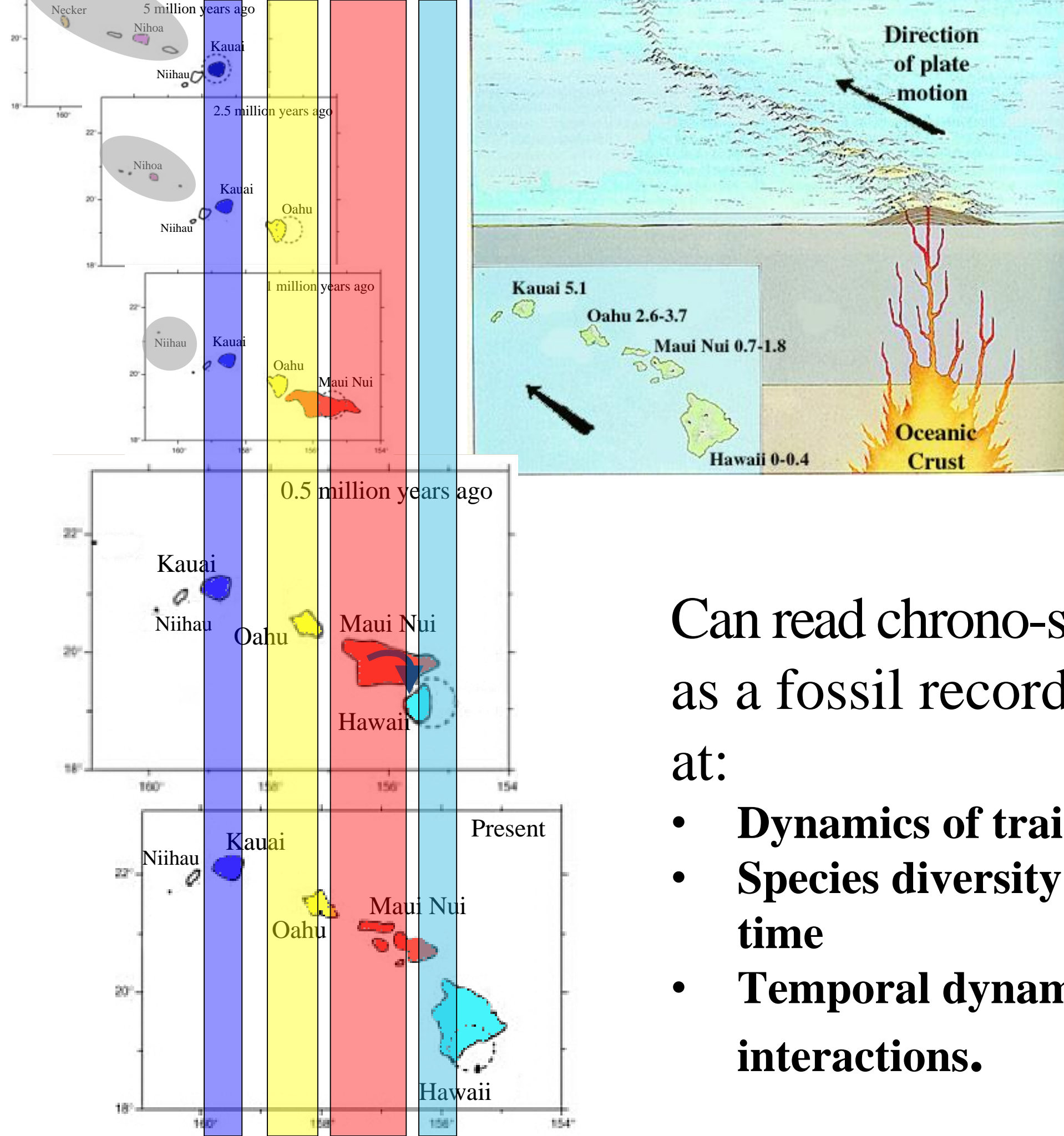
Neontological & paleontological data

Species shifts from orange to blue environment that appears only after T_1



Chronosequence





Can read chrono-sequence as a fossil record to look at:

- **Dynamics of trait evolution**
- **Species diversity through time**
- **Temporal dynamics in niche interactions.**

Island chronosequence

1. Microevolution 2 macroevolution

1. Evolutionary dynamics over time

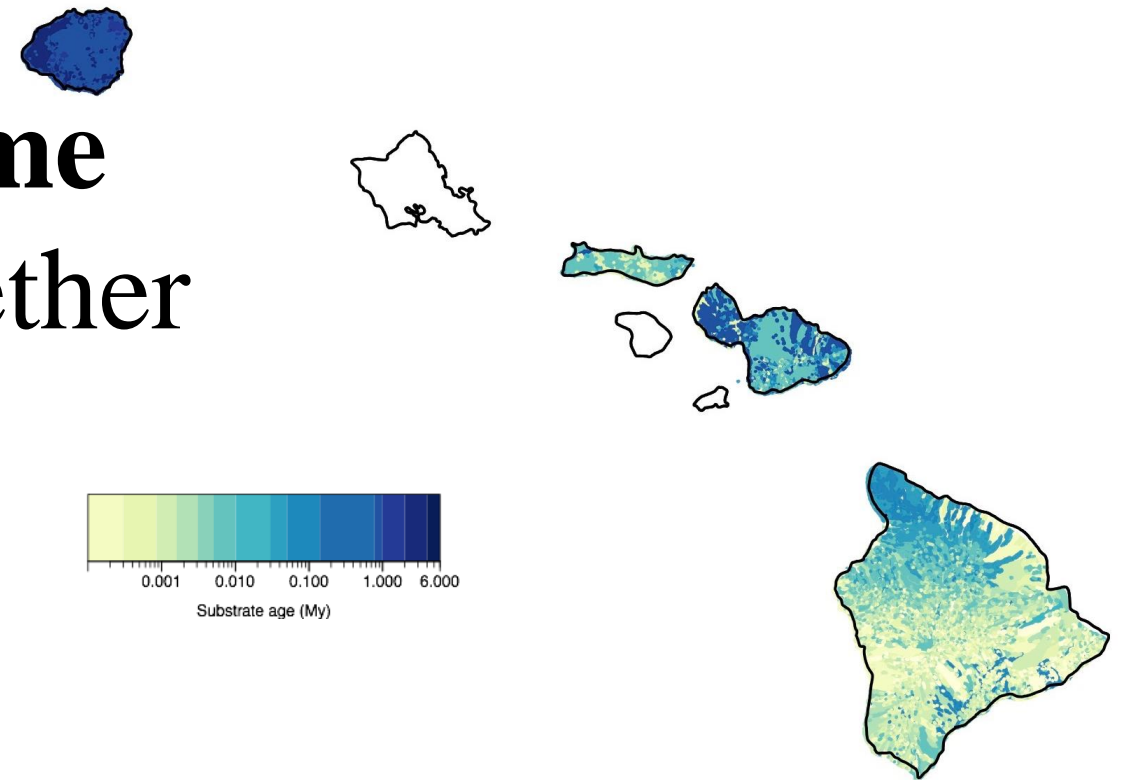
- Repetition of evolutionary process

2. Species diversity through time

- How communities come together over time

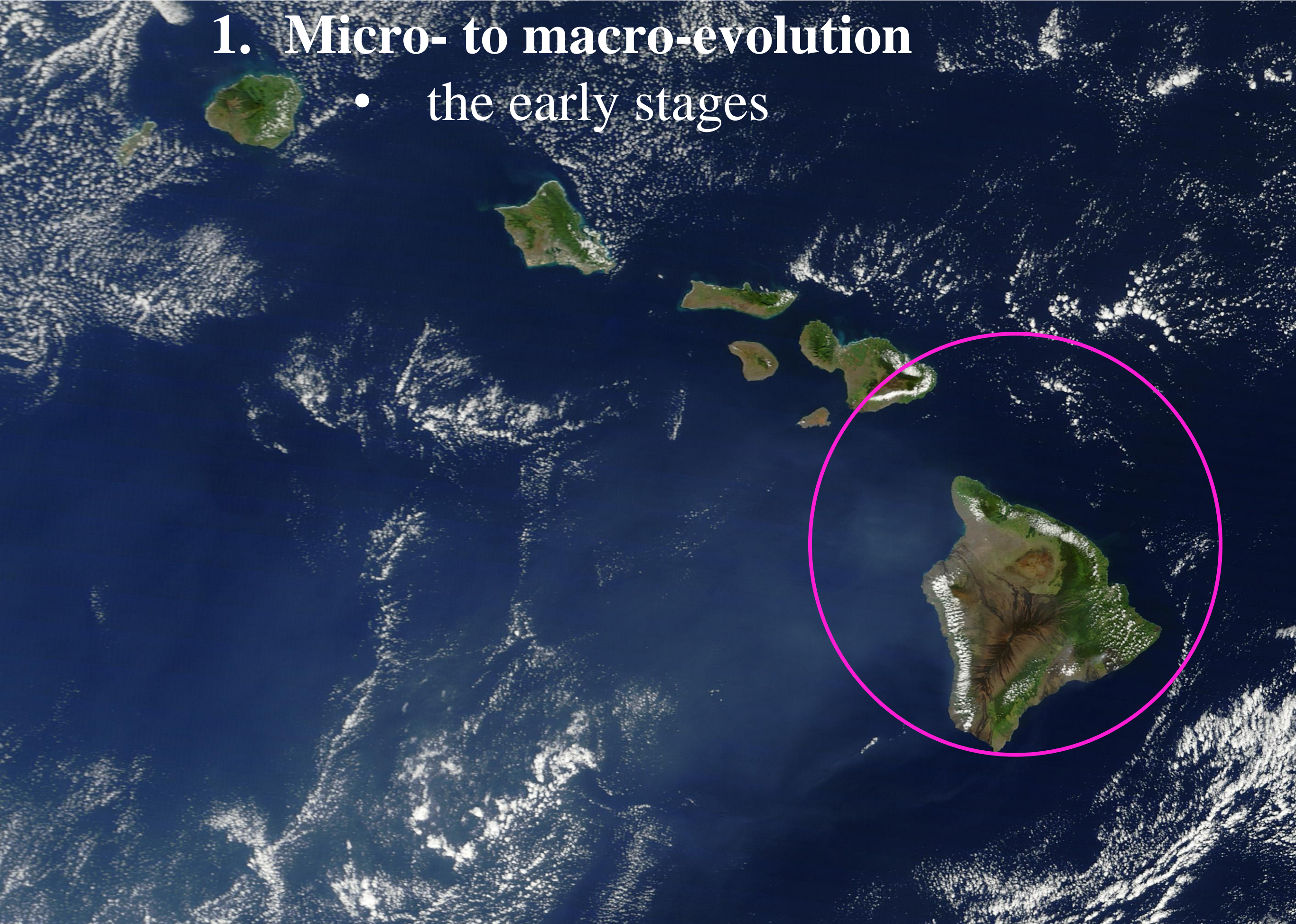
3. Ecological interactions

- Measurement of ecological metrics (space for time)

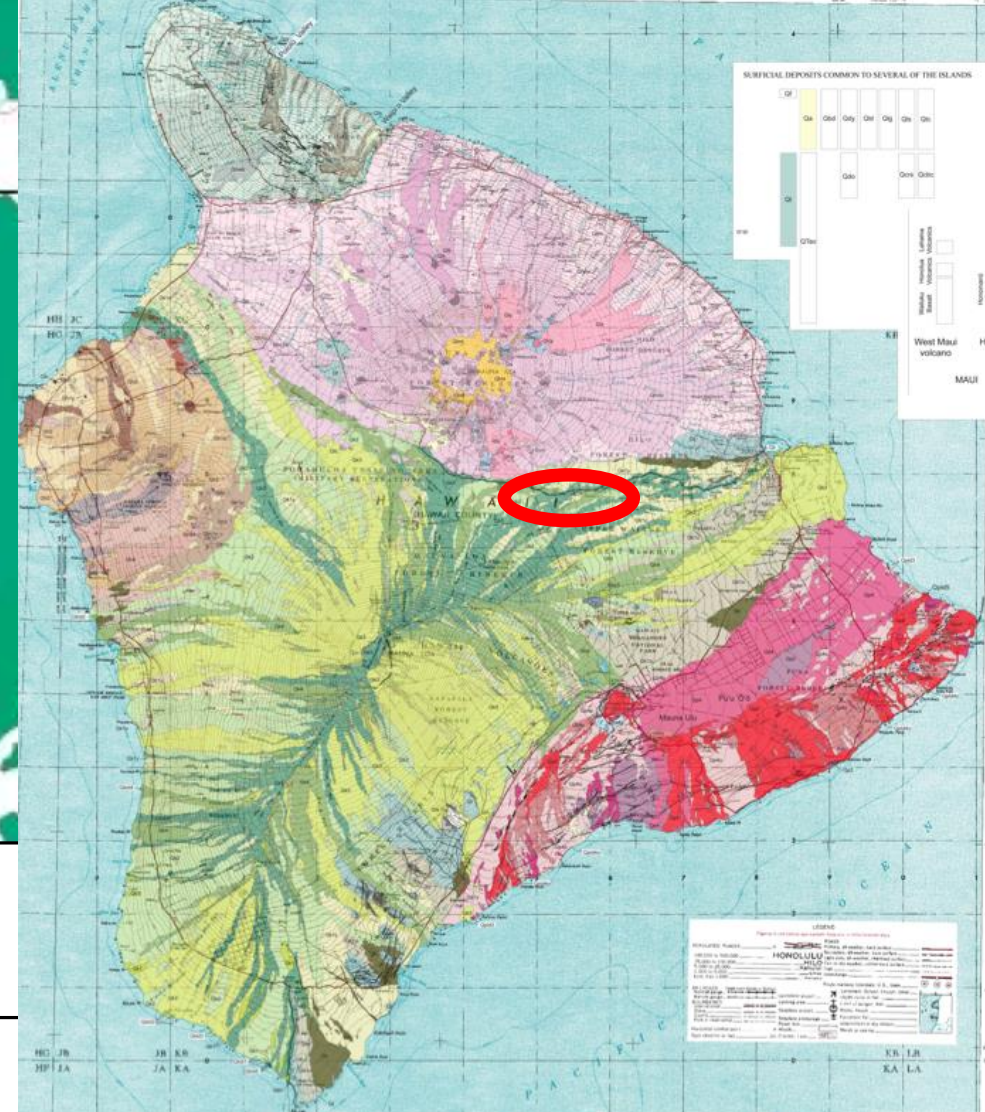
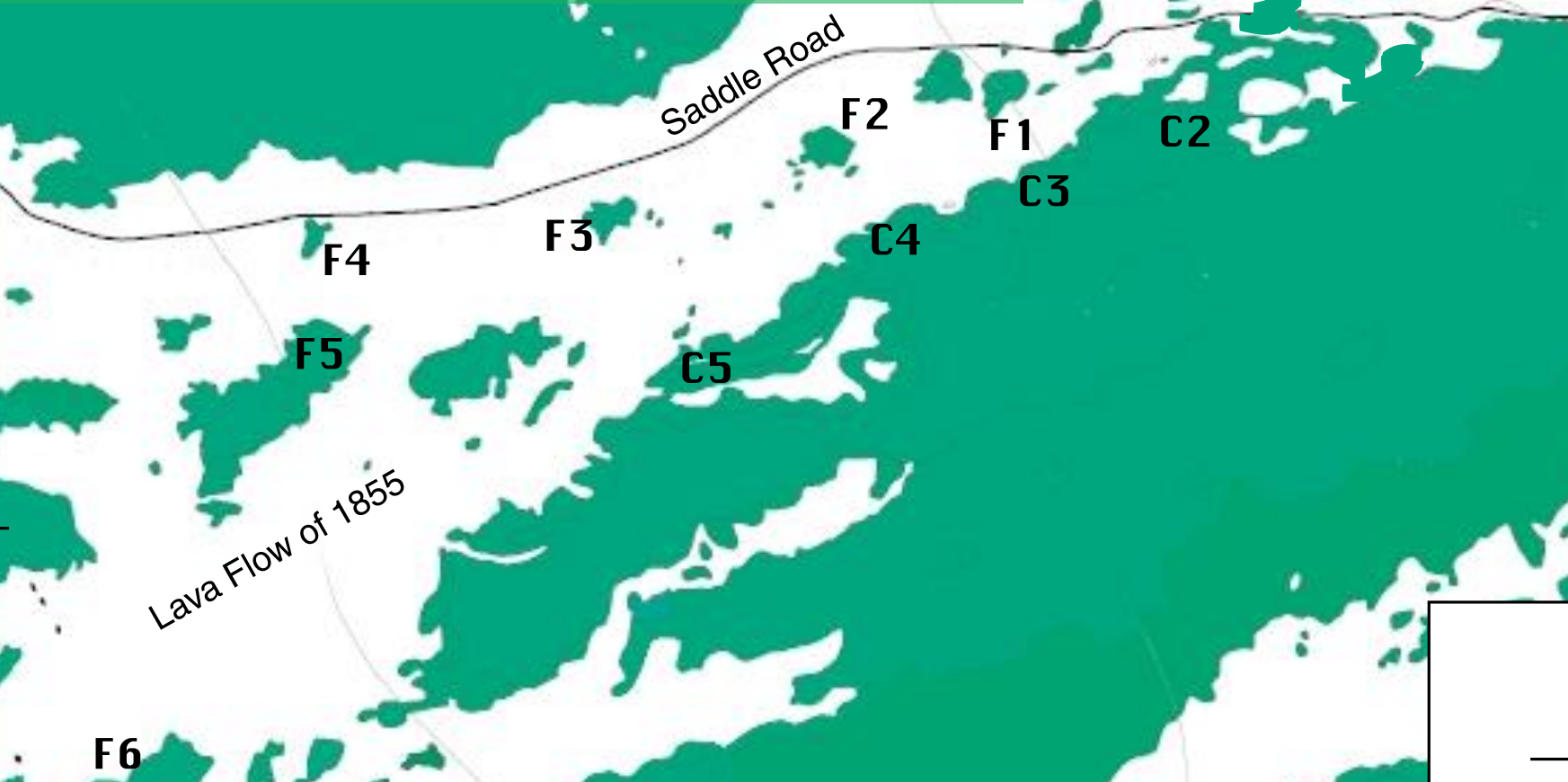


1. Micro- to macro-evolution

- the early stages



Youngest island

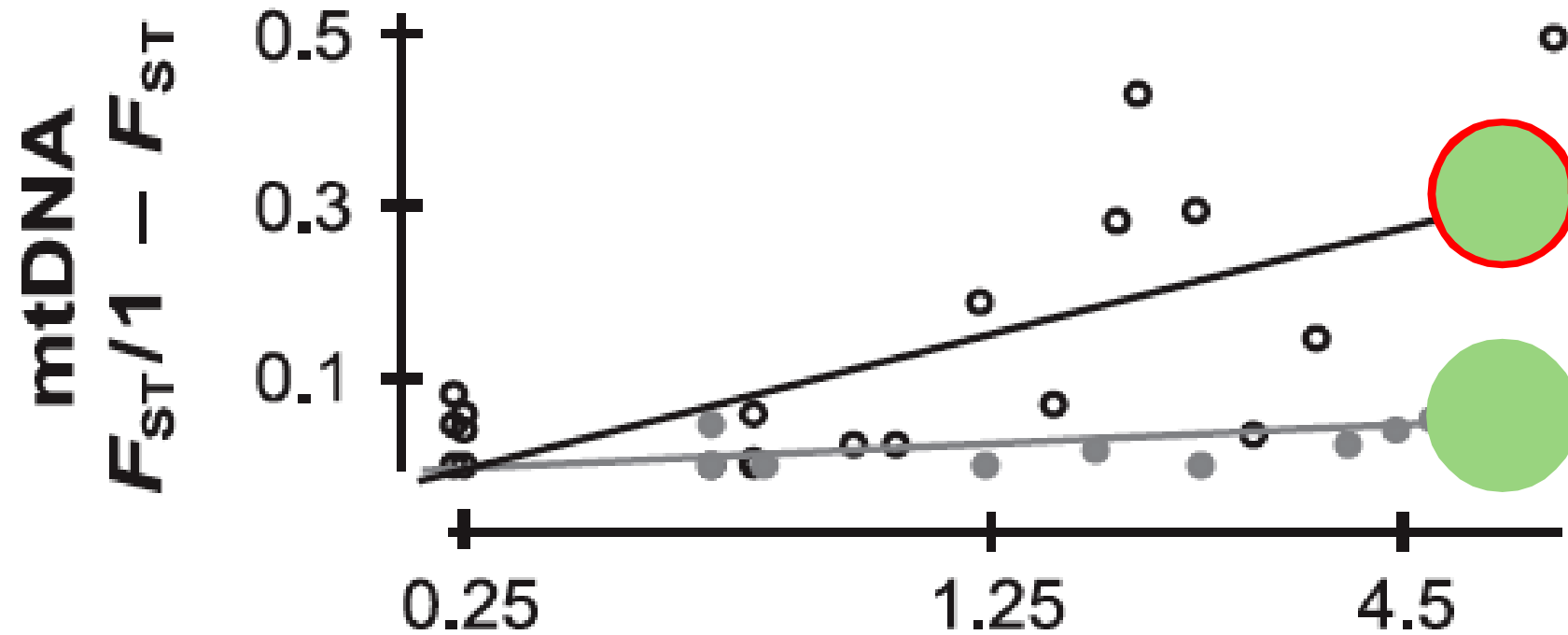


Dynamics on Hawaii Island as the “crucible of evolution”

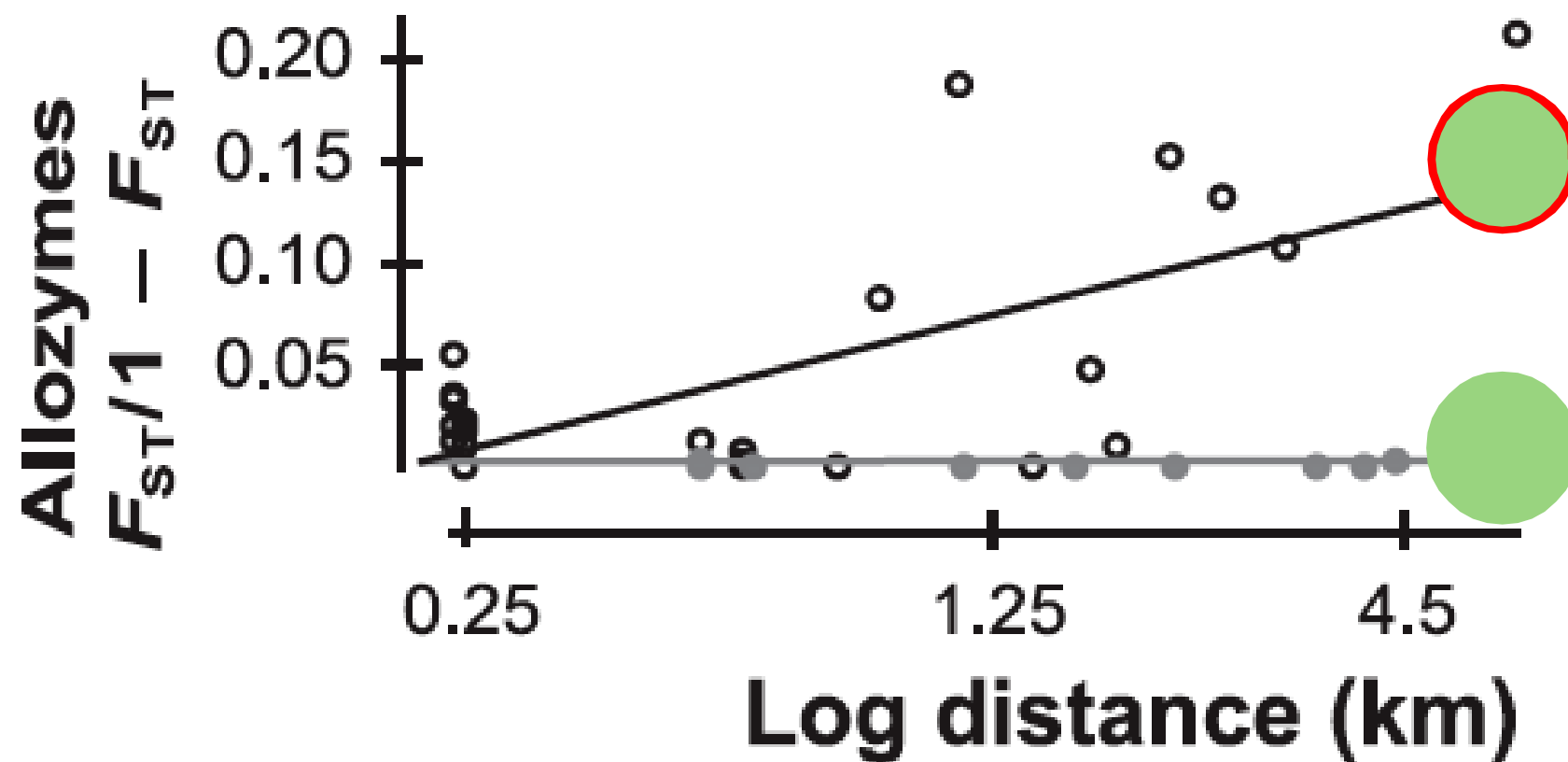
Carson et al. 1990 PNAS 87, pp. 7055-7057,

1. Micro-macro evolution 2. Evolutionary dynamics 3. Species diversity 4. Ecological interactions

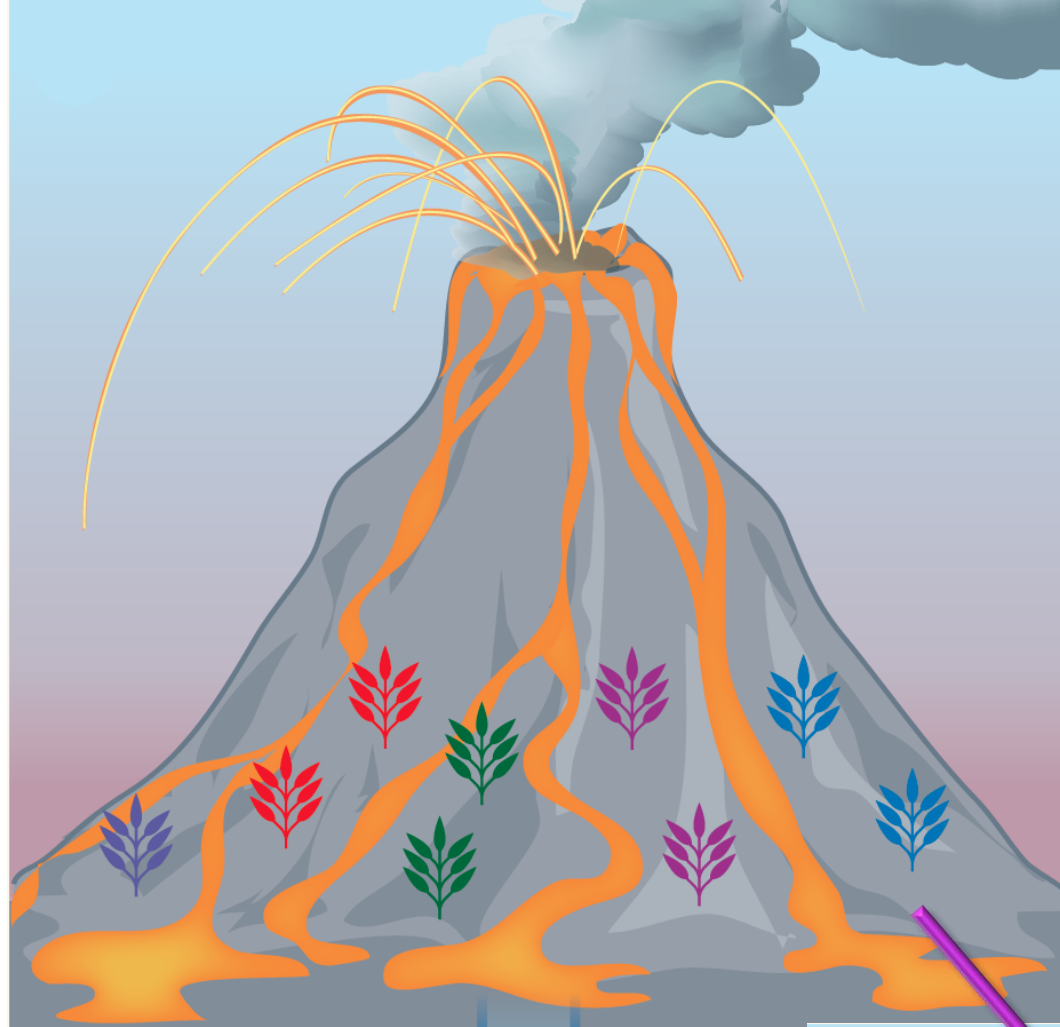
Tetragnatha brevignatha



Forest
habitat
specialist



Vandergast et al. 2004. *Mol Ecol* 13: 1729-1743

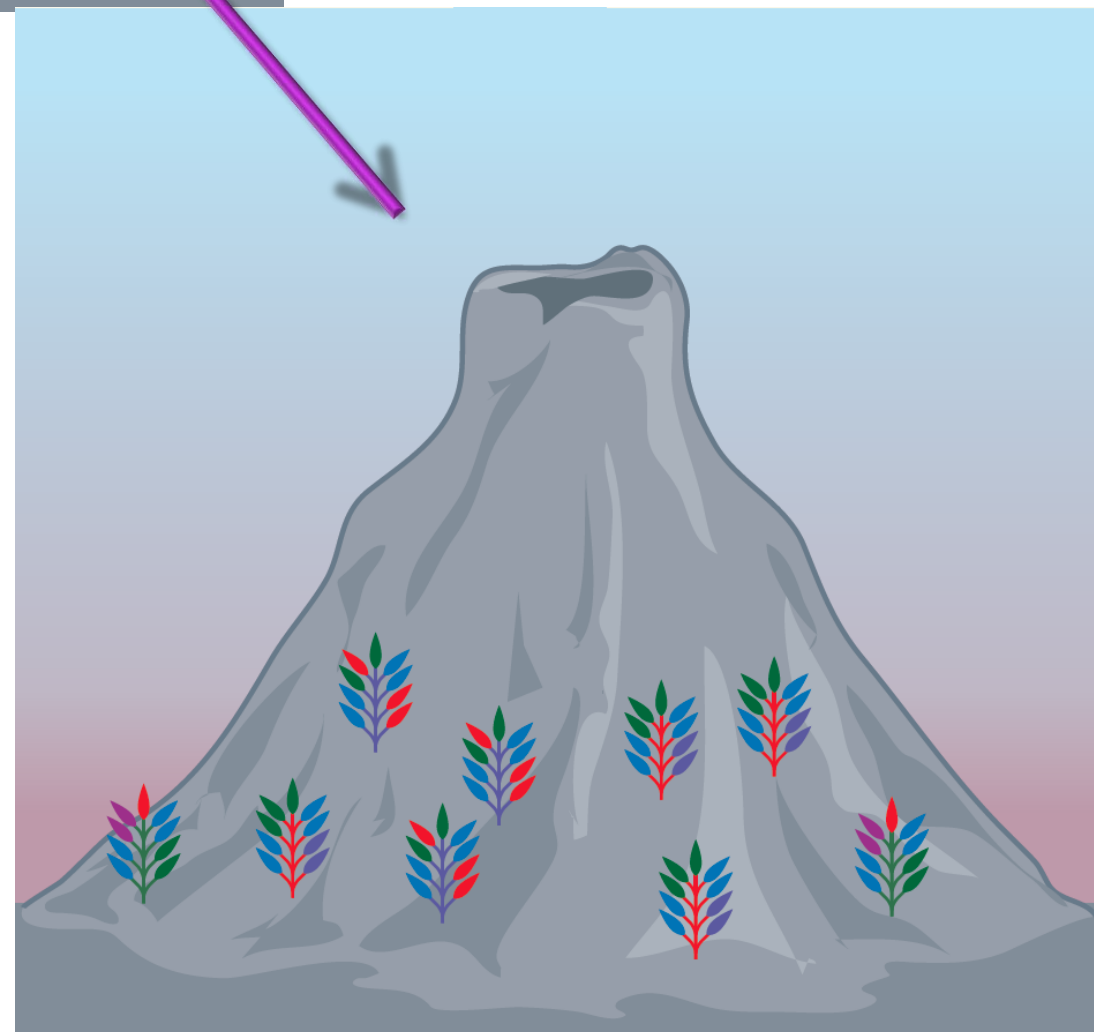


Balance between isolation & time

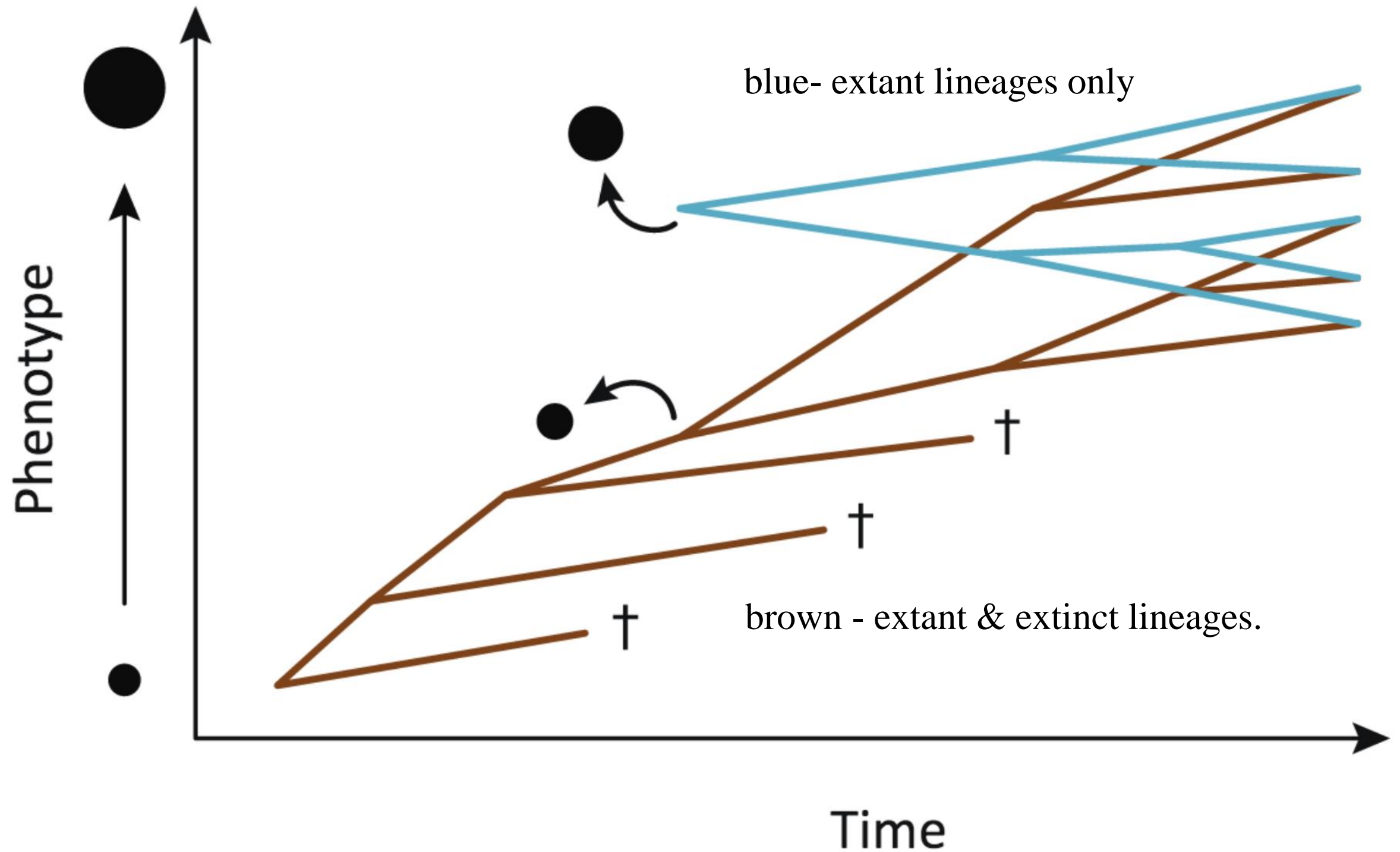
Isolation separates populations

Fusion injects diversity

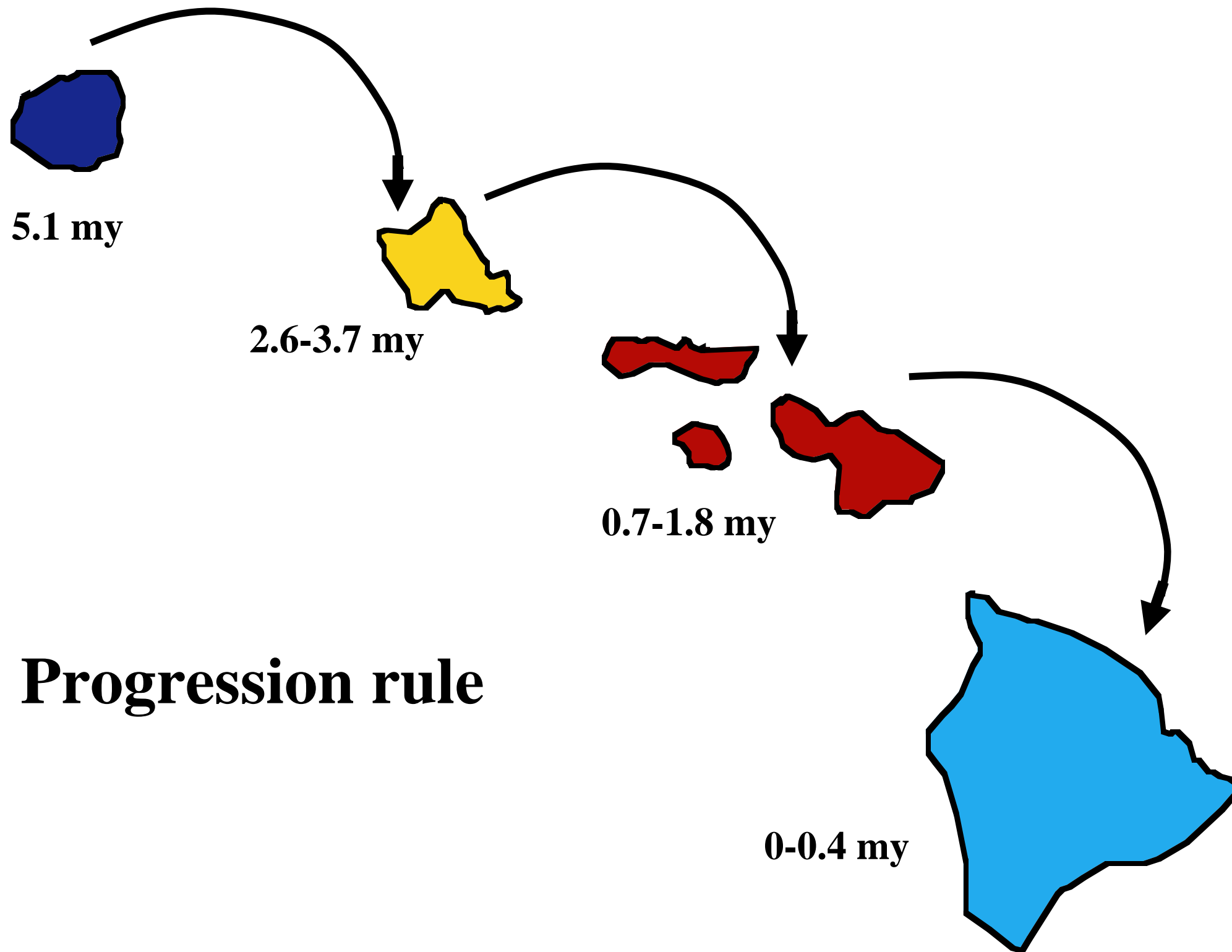
How does this play out over time?

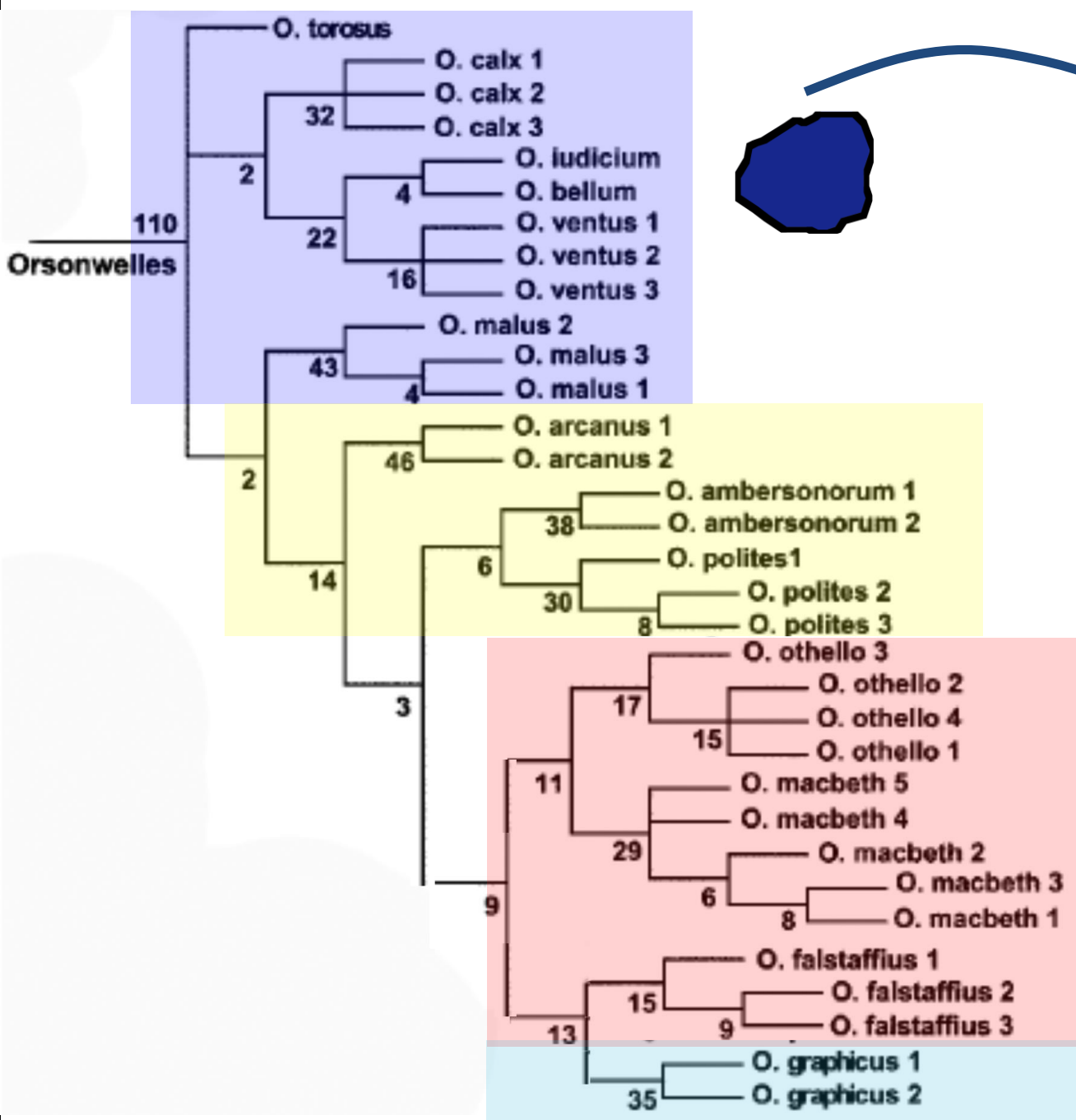


2. Evolutionary dynamics

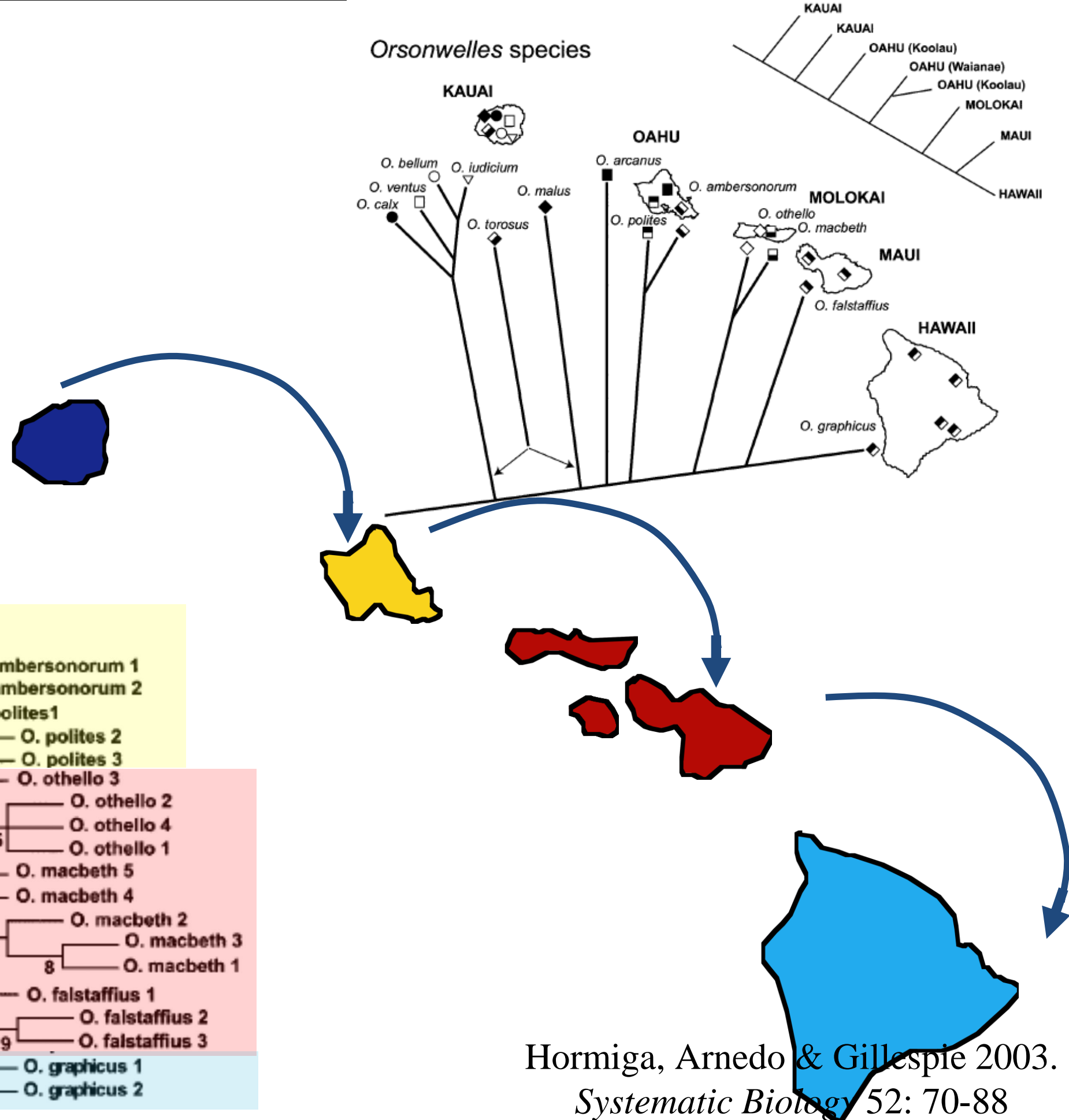


Evolutionary Dynamics





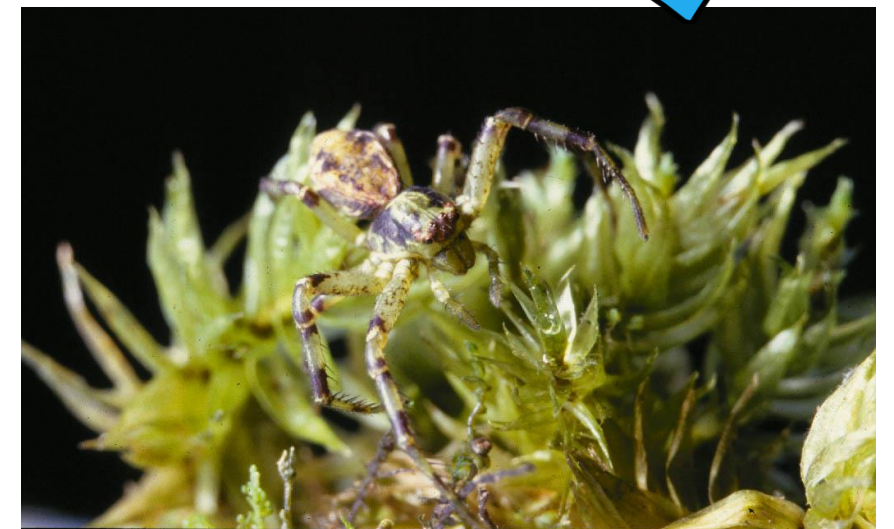
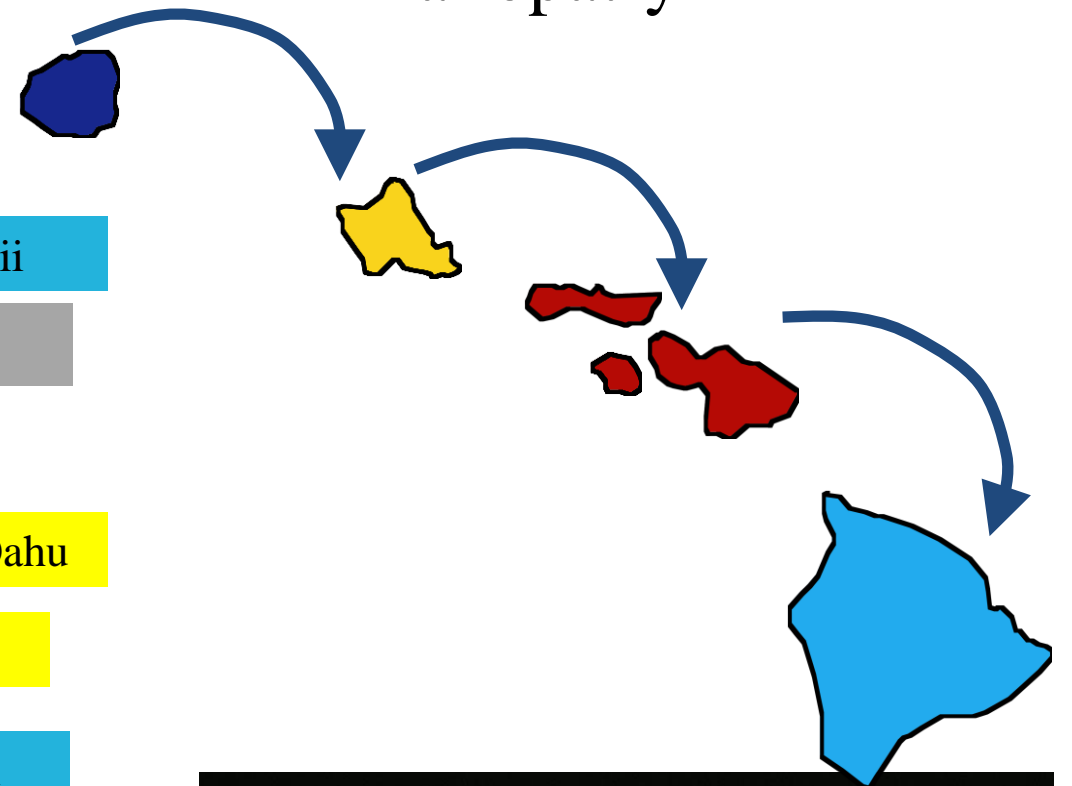
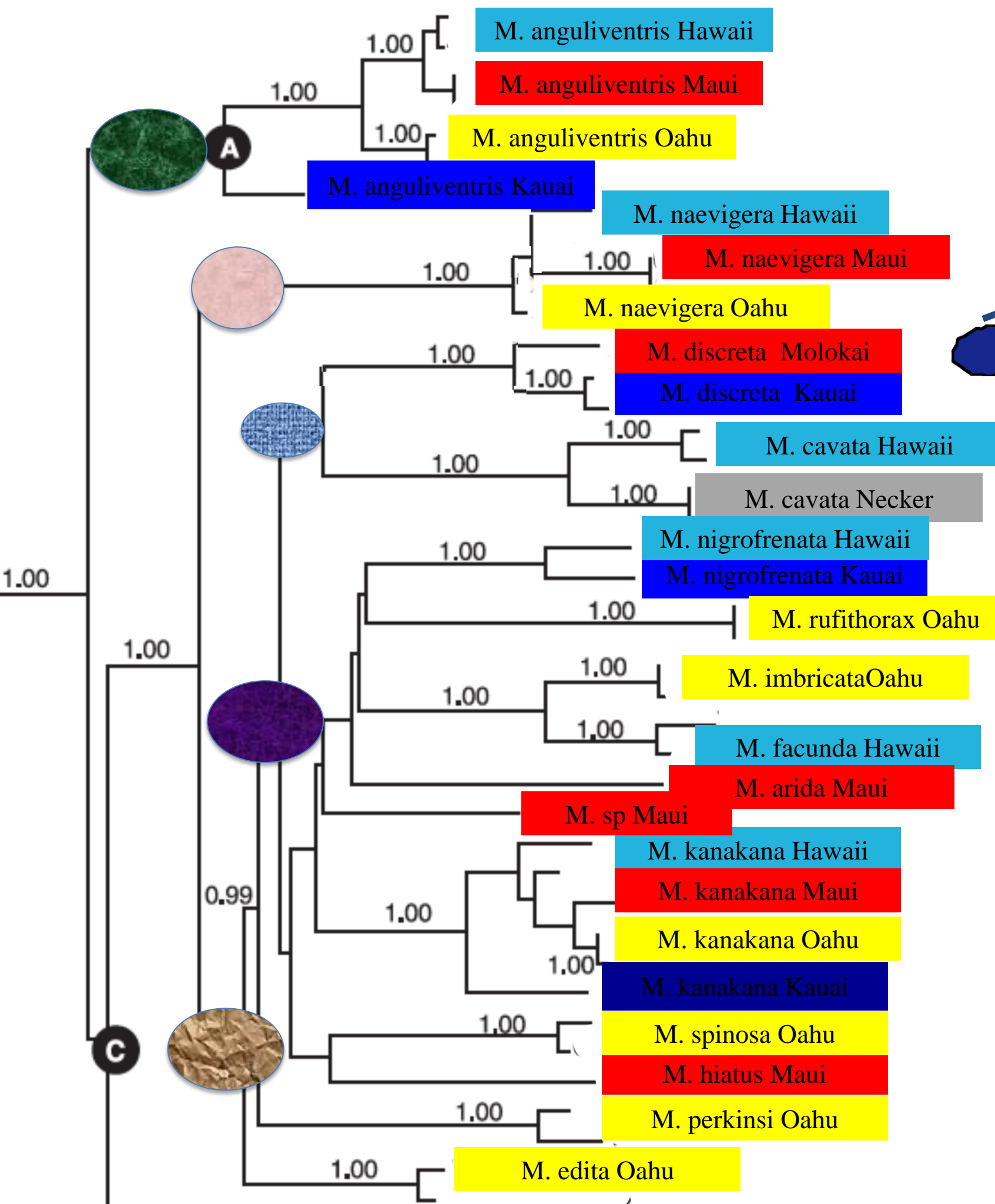
Orsonwelles species



Hormiga, Arnedo & Gillespie 2003.
Systematic Biology 52: 70-88

Diversification early in radiation

- Adaptive
- Populations diverge in allopatry

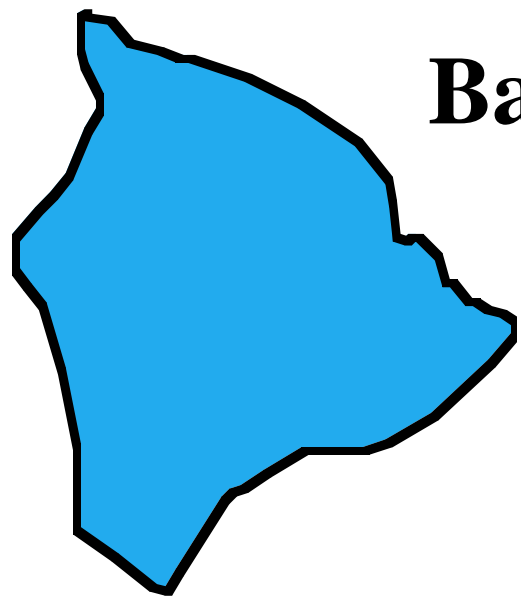


Garb & Gillespie, 2009.
Molecular Ecology



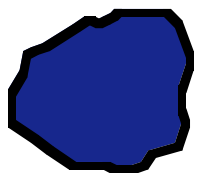
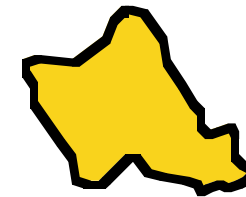
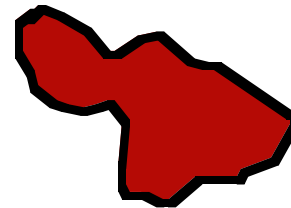
Radiation of long-jawed spiders, *Tetragnatha*, in Hawaii

1. Micro-macro evolution 2. Evolutionary dynamics 3 Species diversity 4. Ecological interactions



Based on mtDNA, minisatellites, & allozymes

..... general progression down island chain



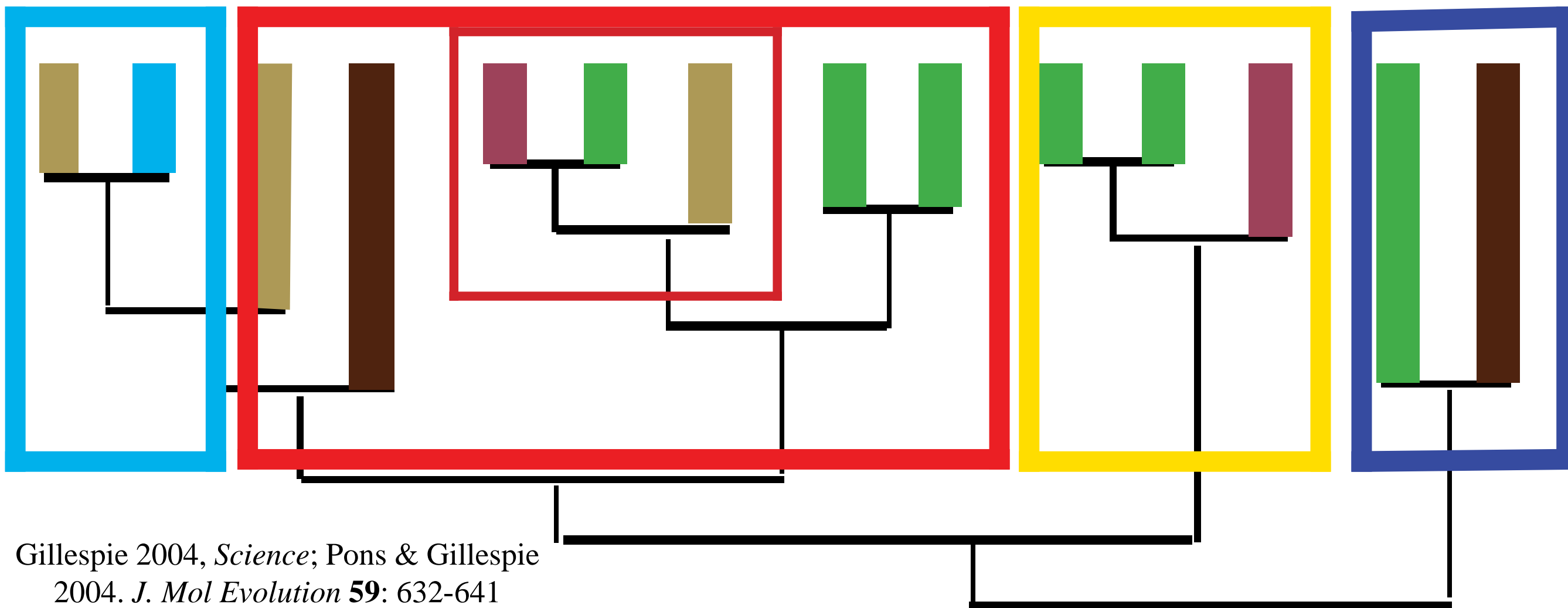
Independent evolution of ecomorphs

Hawaii

Maui Nui

Oahu

Kauai

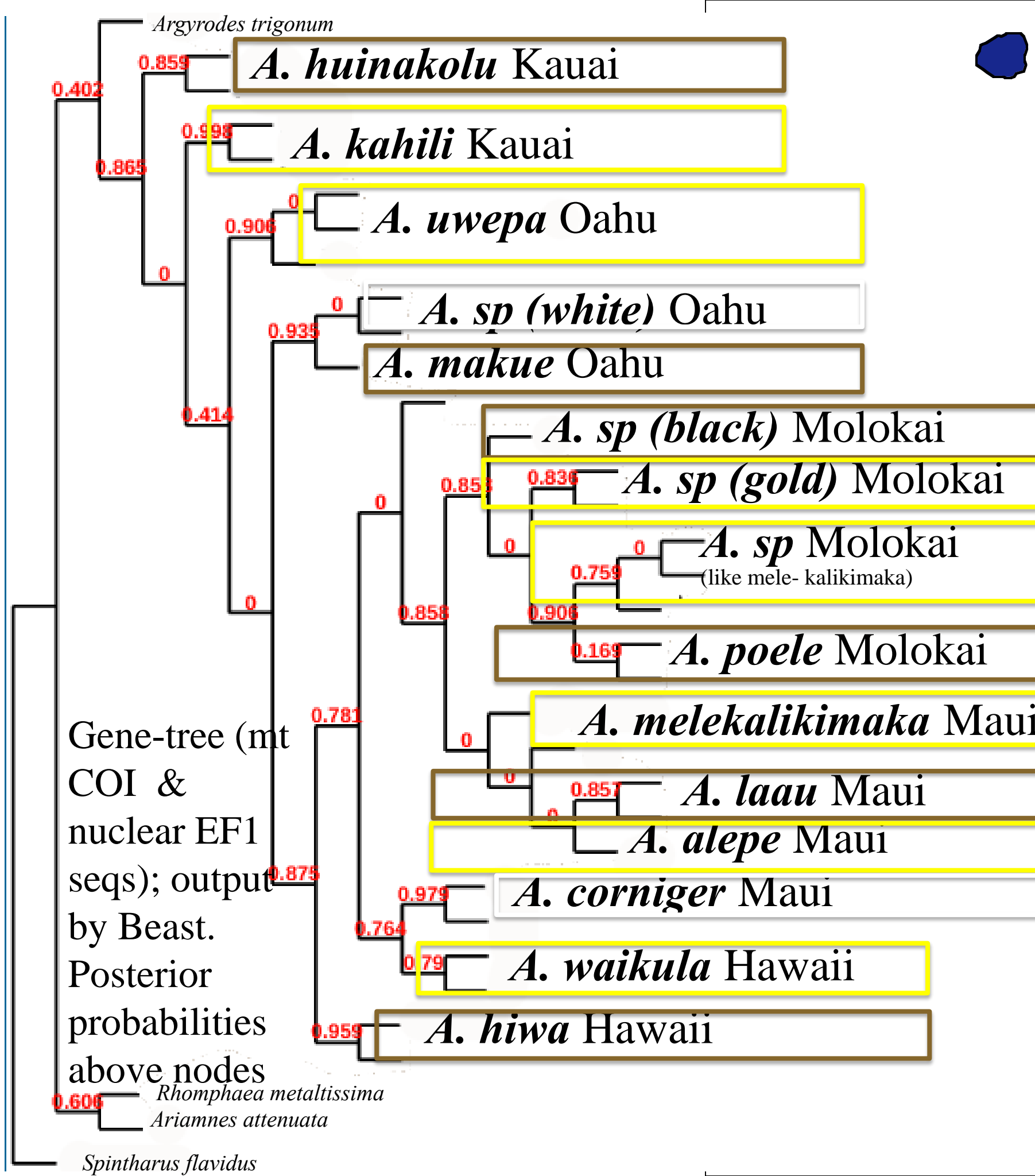


Gillespie 2004, *Science*; Pons & Gillespie
2004. *J. Mol Evolution* **59**: 632-641

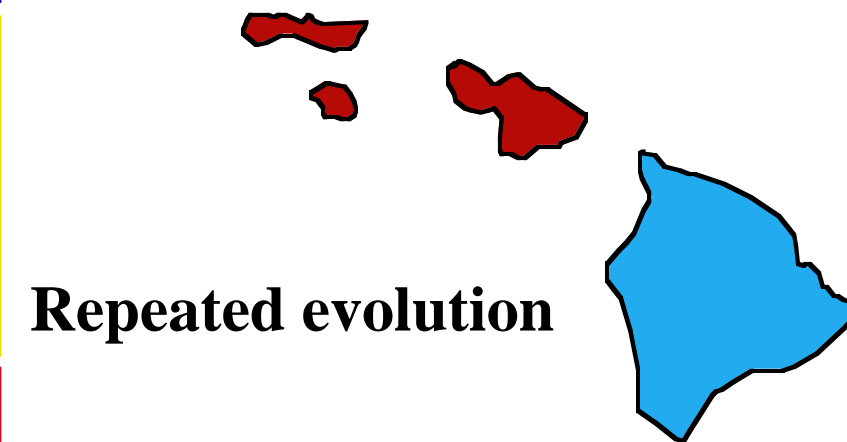
1. Micro-macro evolution 2. Evolutionary dynamics 3. Species diversity 4. Ecological interactions



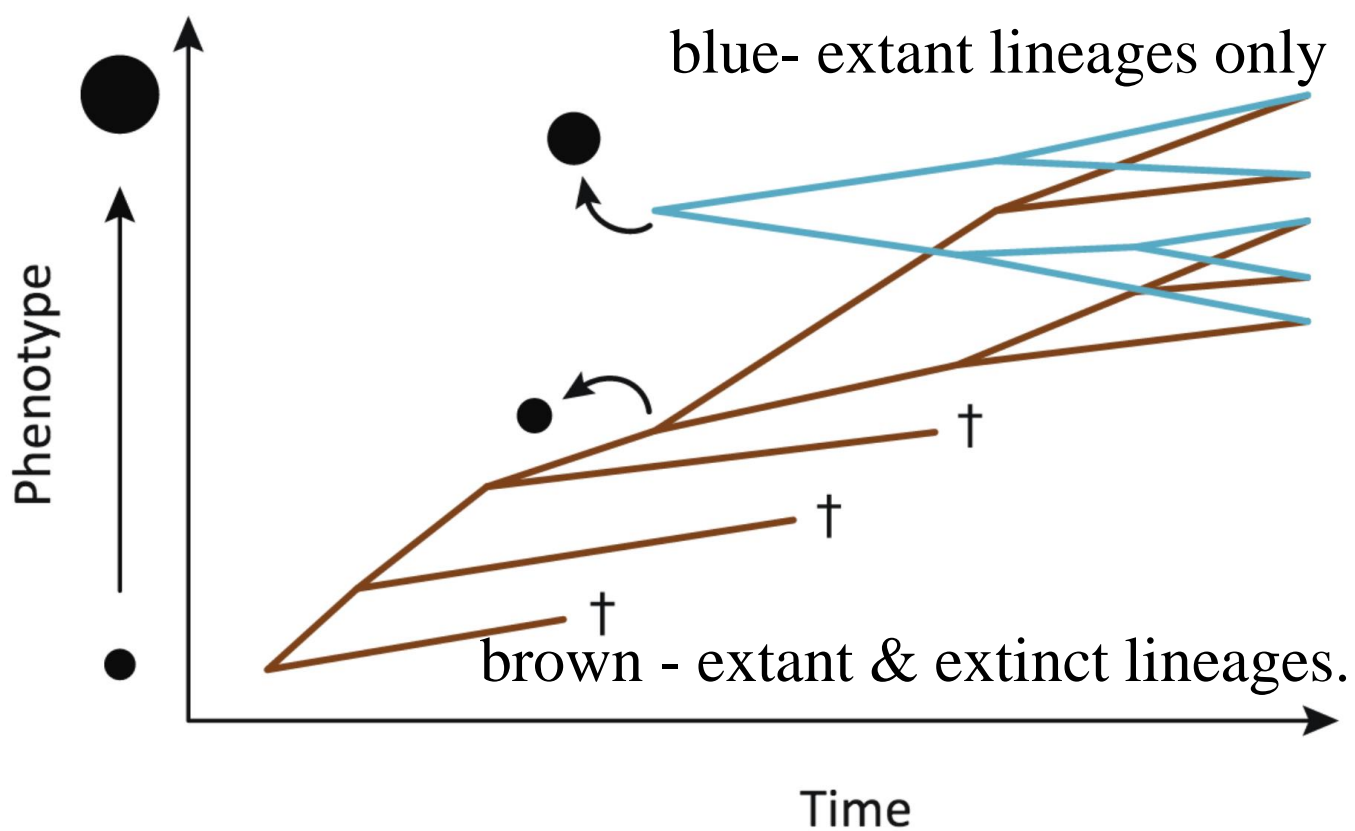
1. Micro-macro evolution 2. Evolutionary dynamics 3. Species diversity 4. Ecological interactions



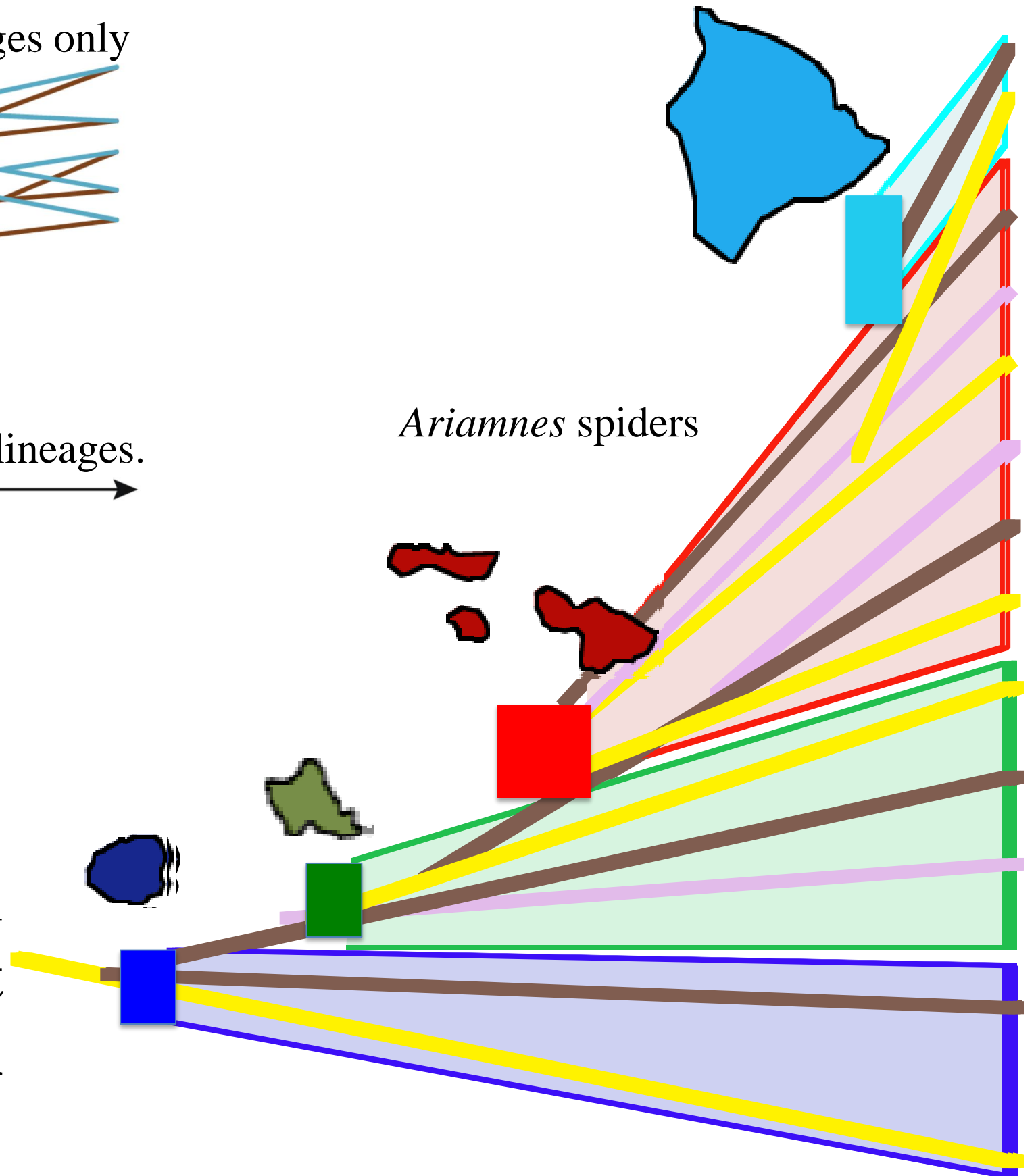
Evolution of “ecomorphs”



2. Evolutionary dynamics



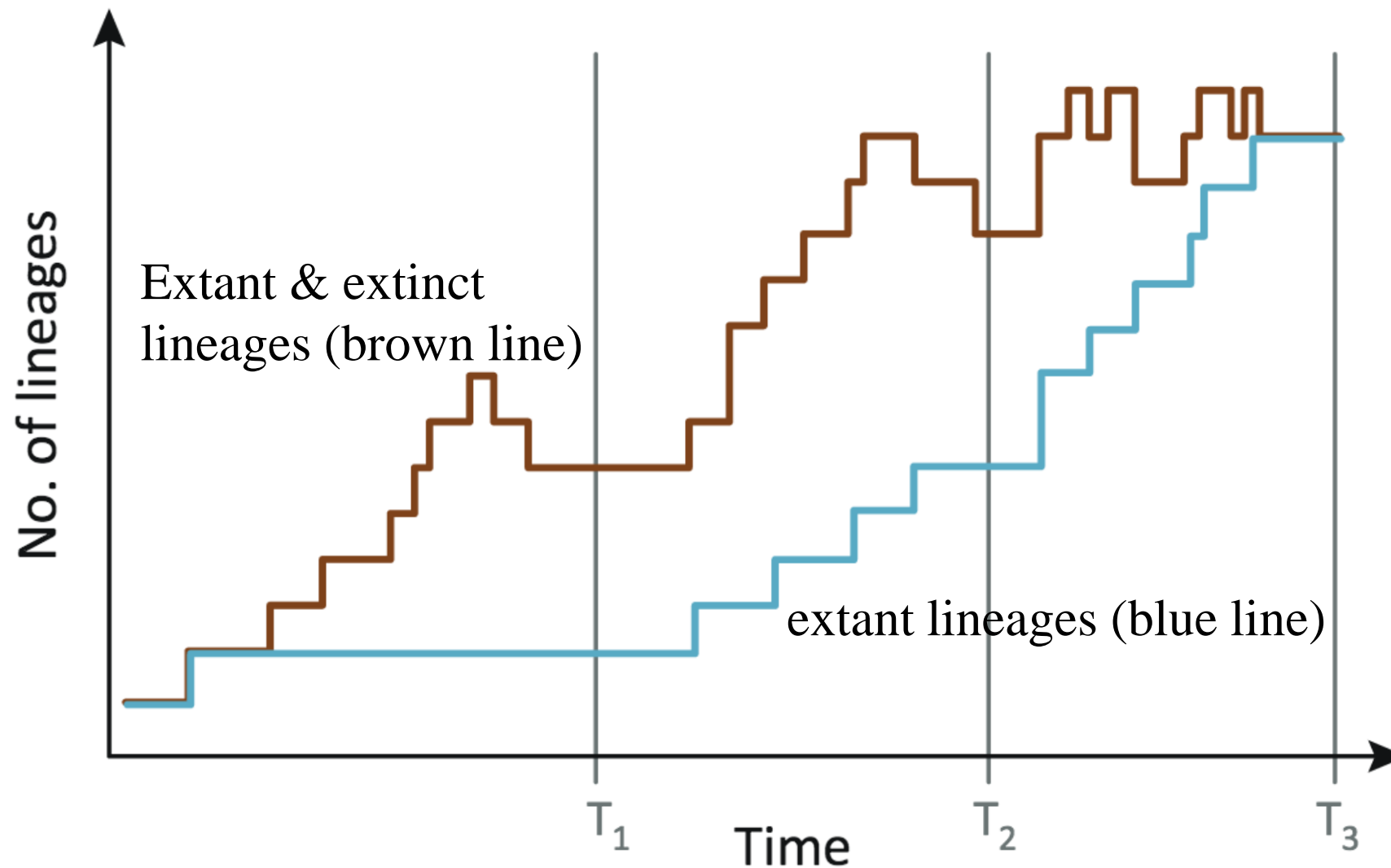
**“Onset” of diversification
in a given lineage is reset
on each island**



Therefore, we know that:

- **Taxa differ in**
 - The interplay between ecological & genetic shifts during diversification
- Can now look at patterns of diversity over time; whole communities

3. Species Diversity



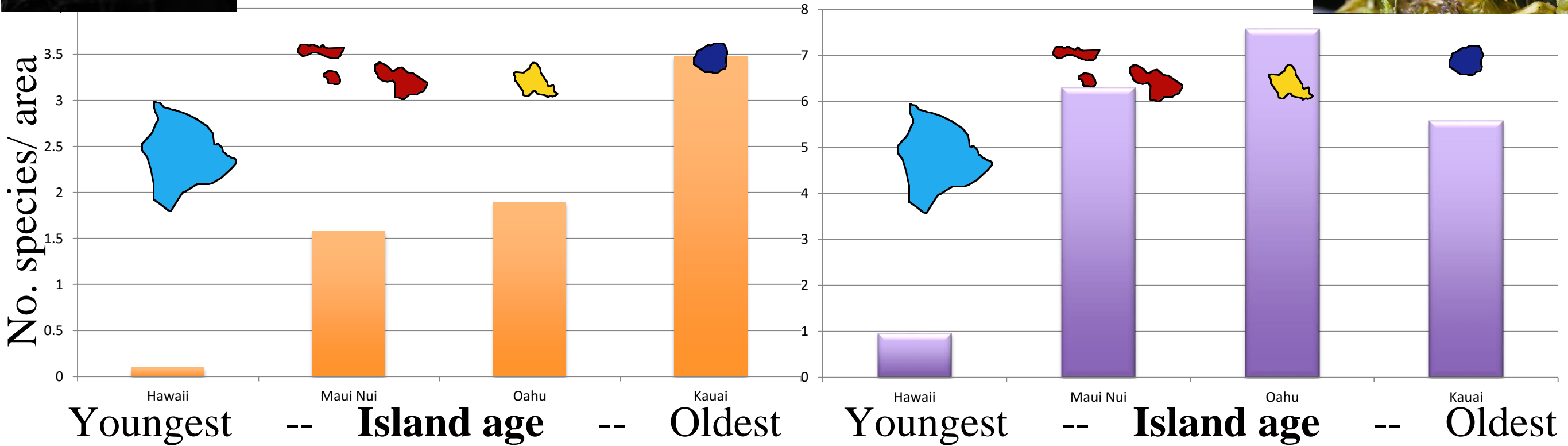


Insights from chronosequence

Orsonwelles



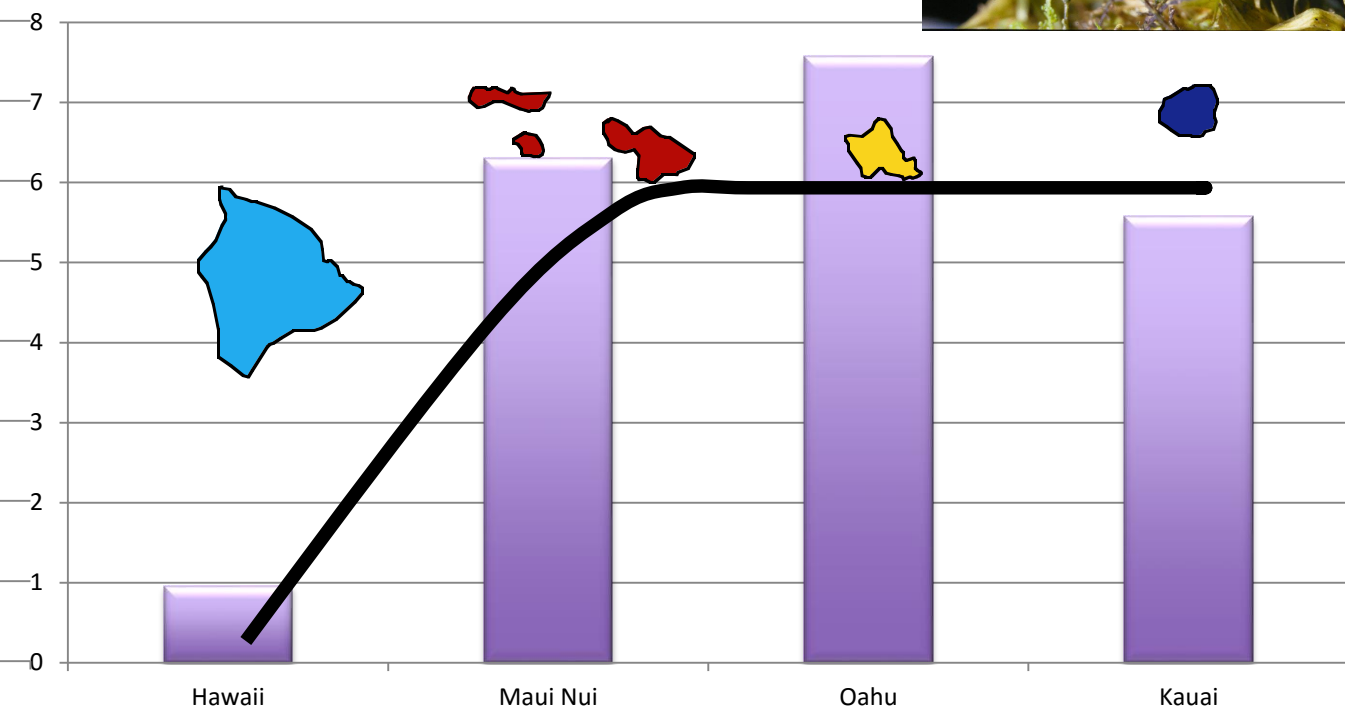
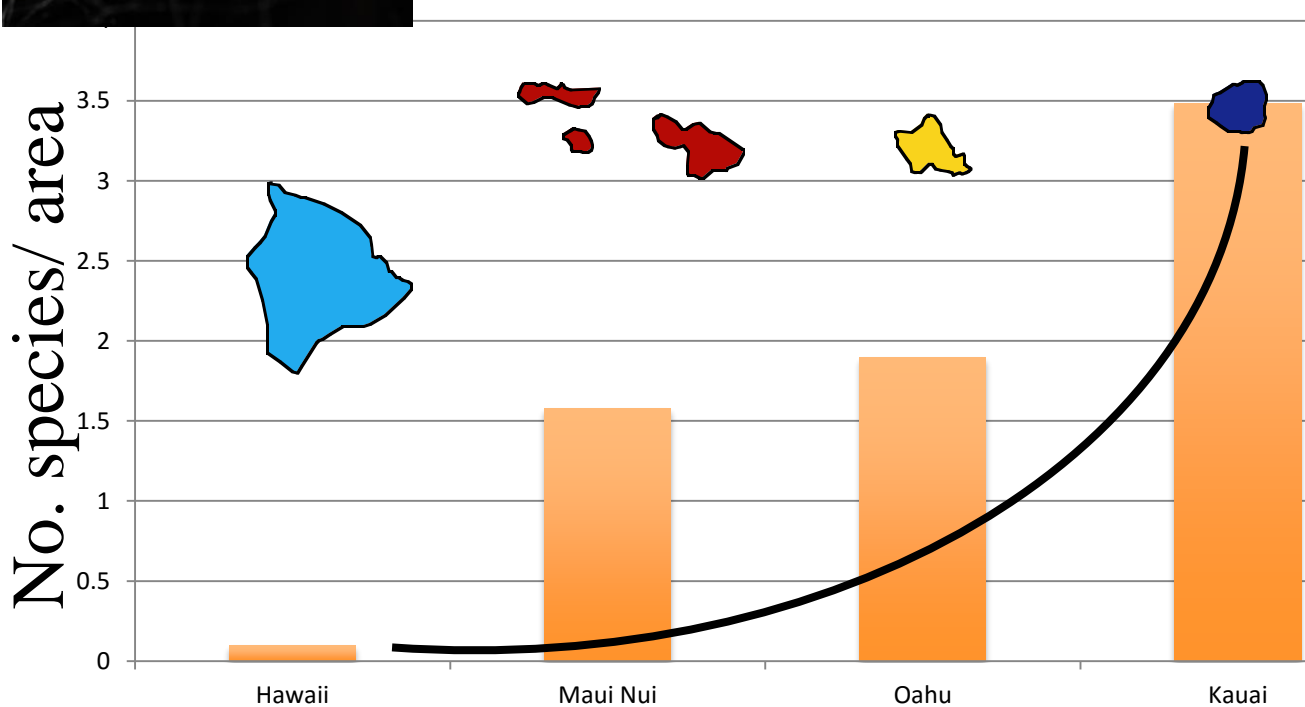
Mecaphesa



Insights from chronosequence

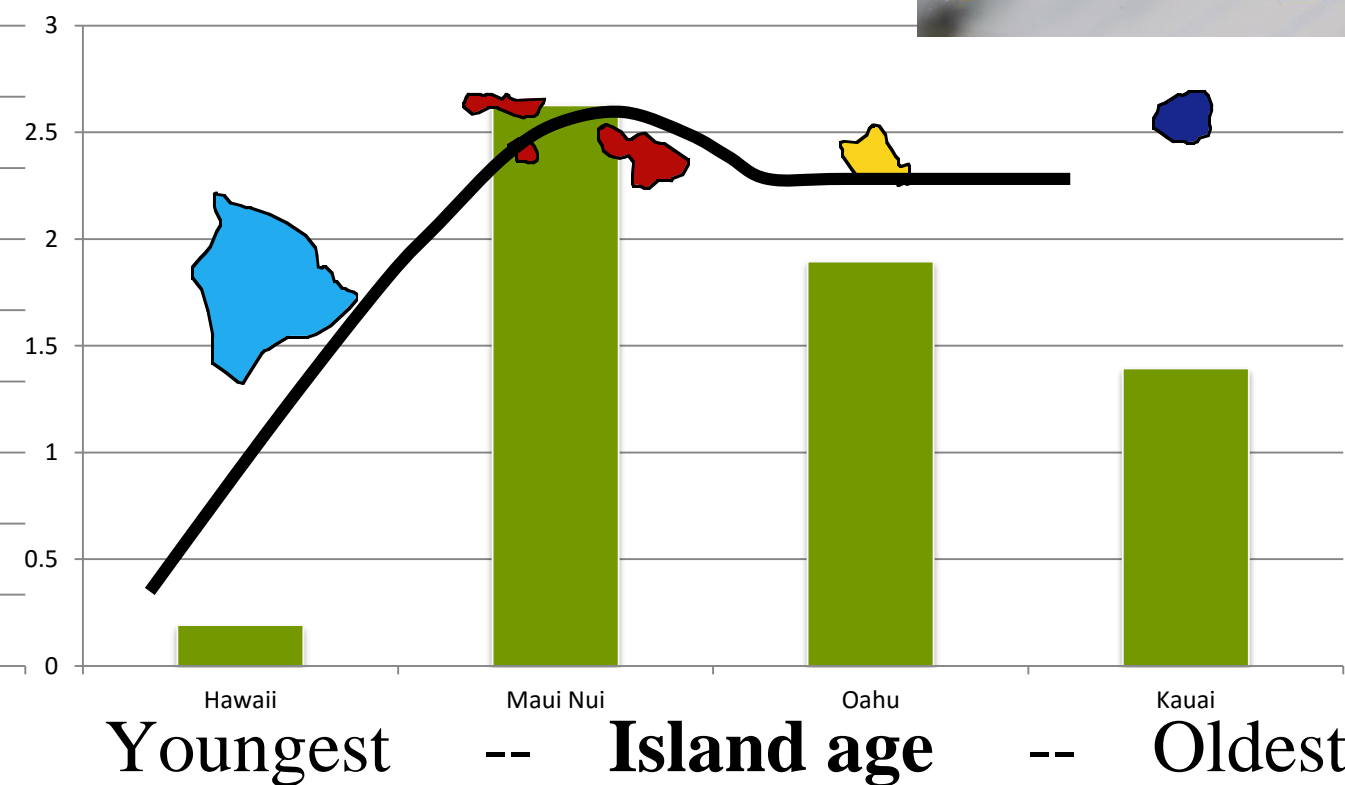
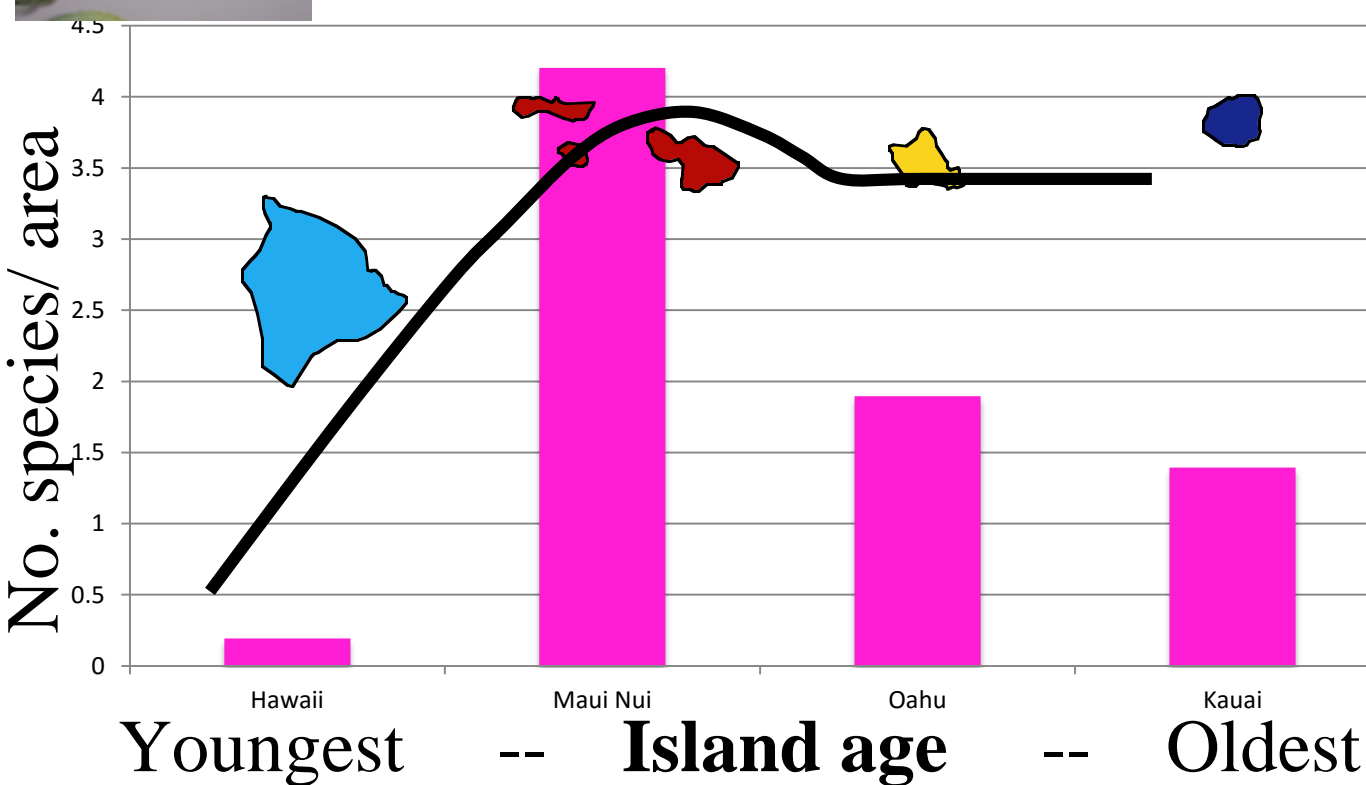
Orsonwelles

Mecaphesa

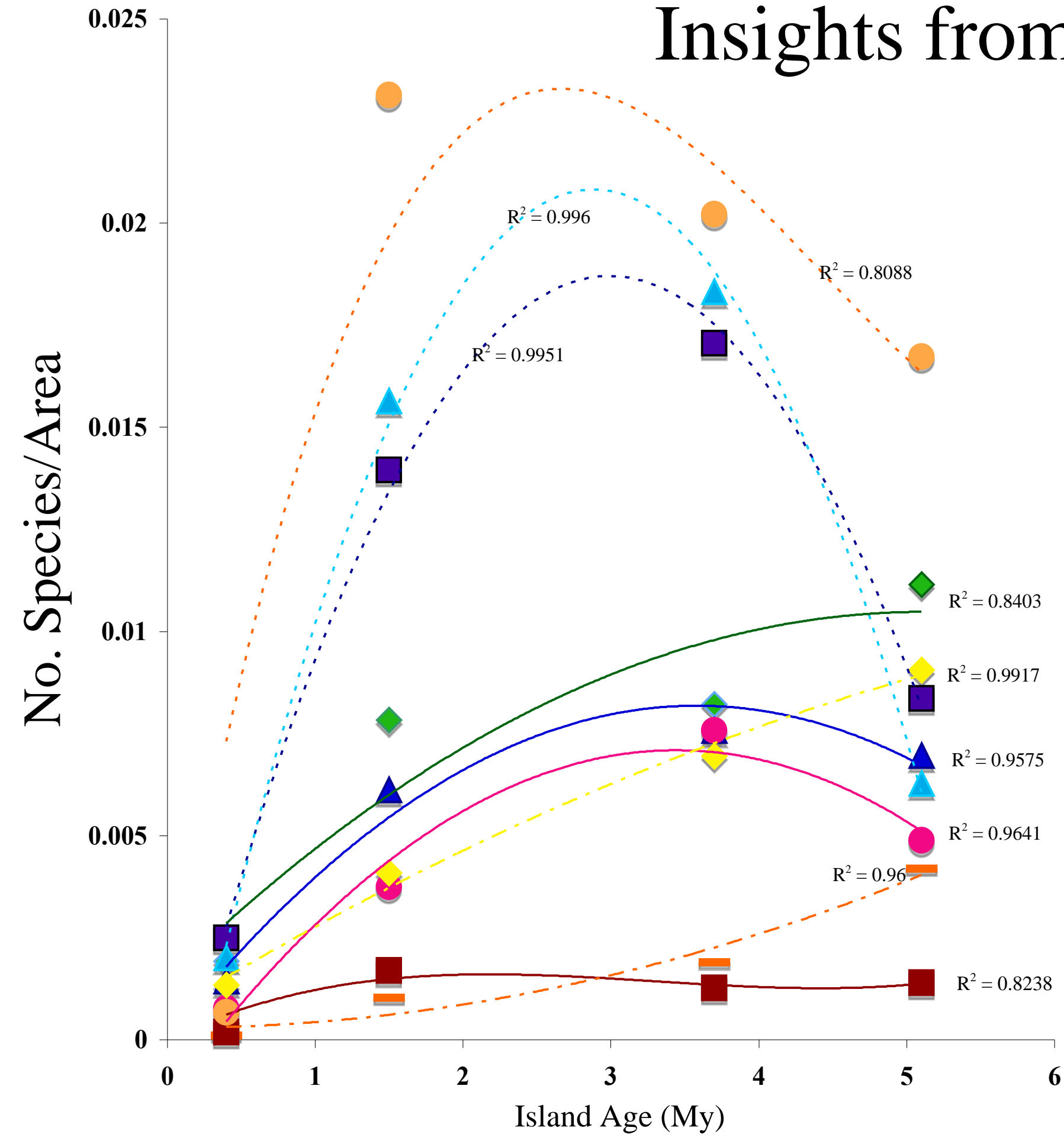


Ariamnes

Tetragnatha – spiny leg clade

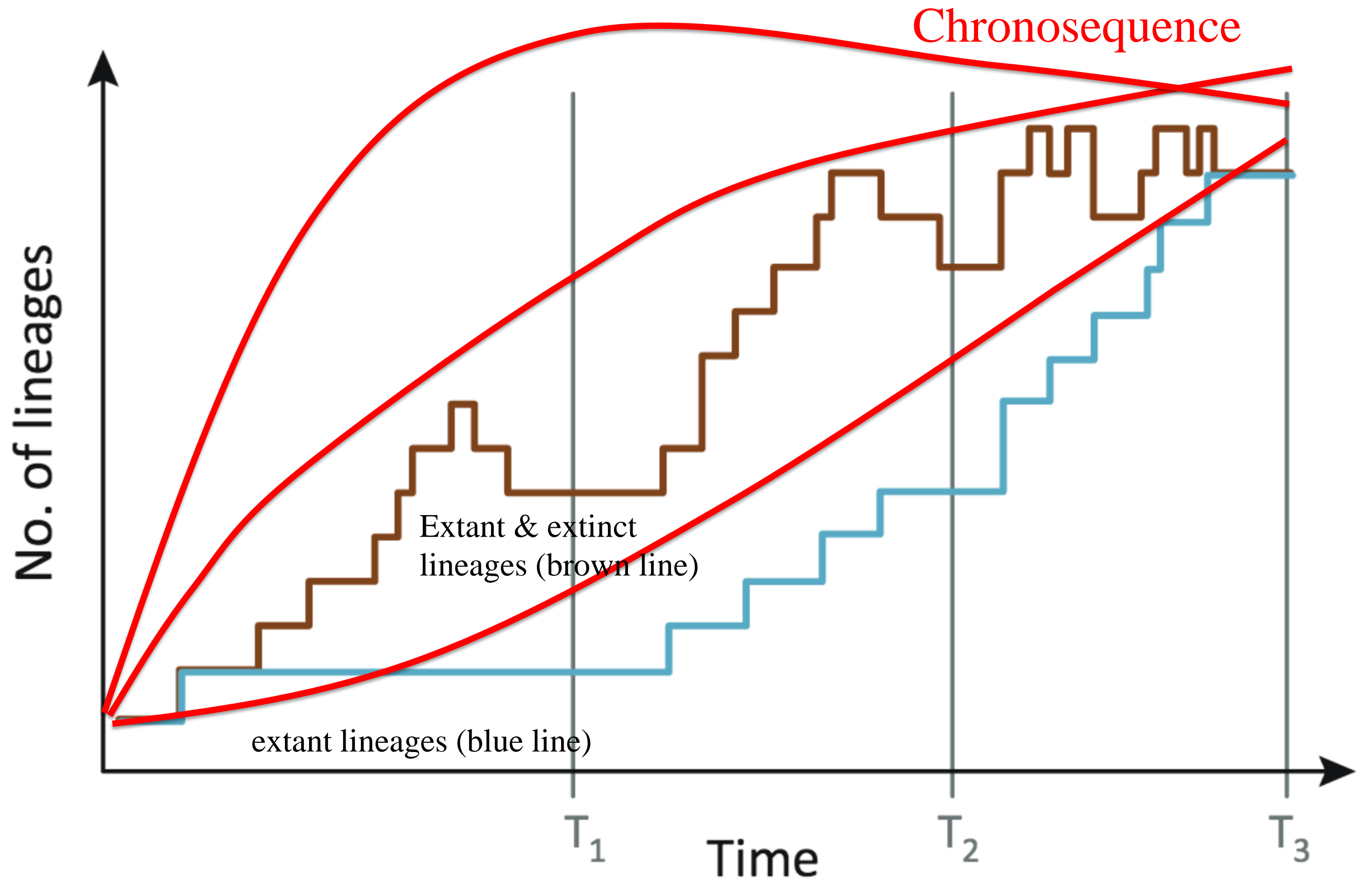


Insights from chronosequence



Gillespie & Baldwin 2009

Species diversity over time

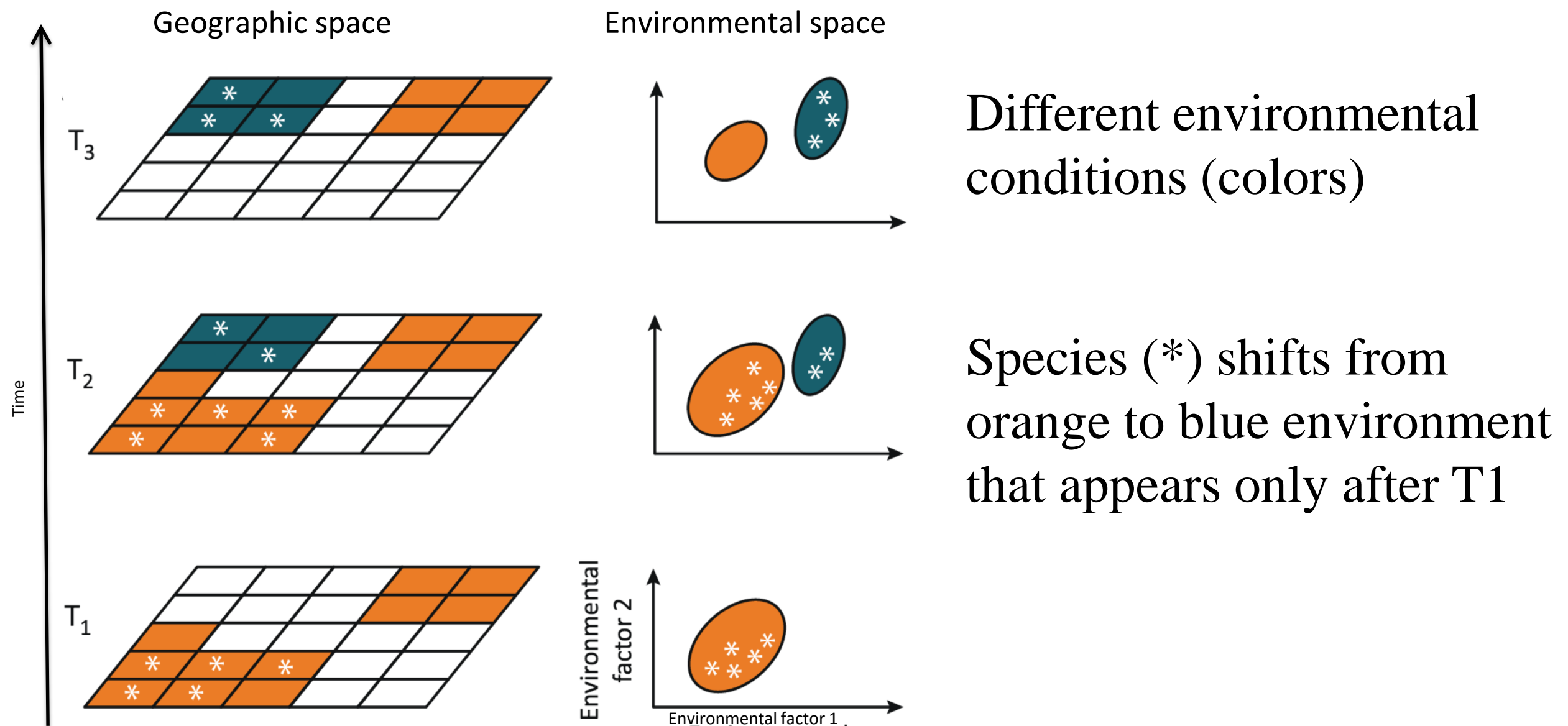


Therefore, we know that:

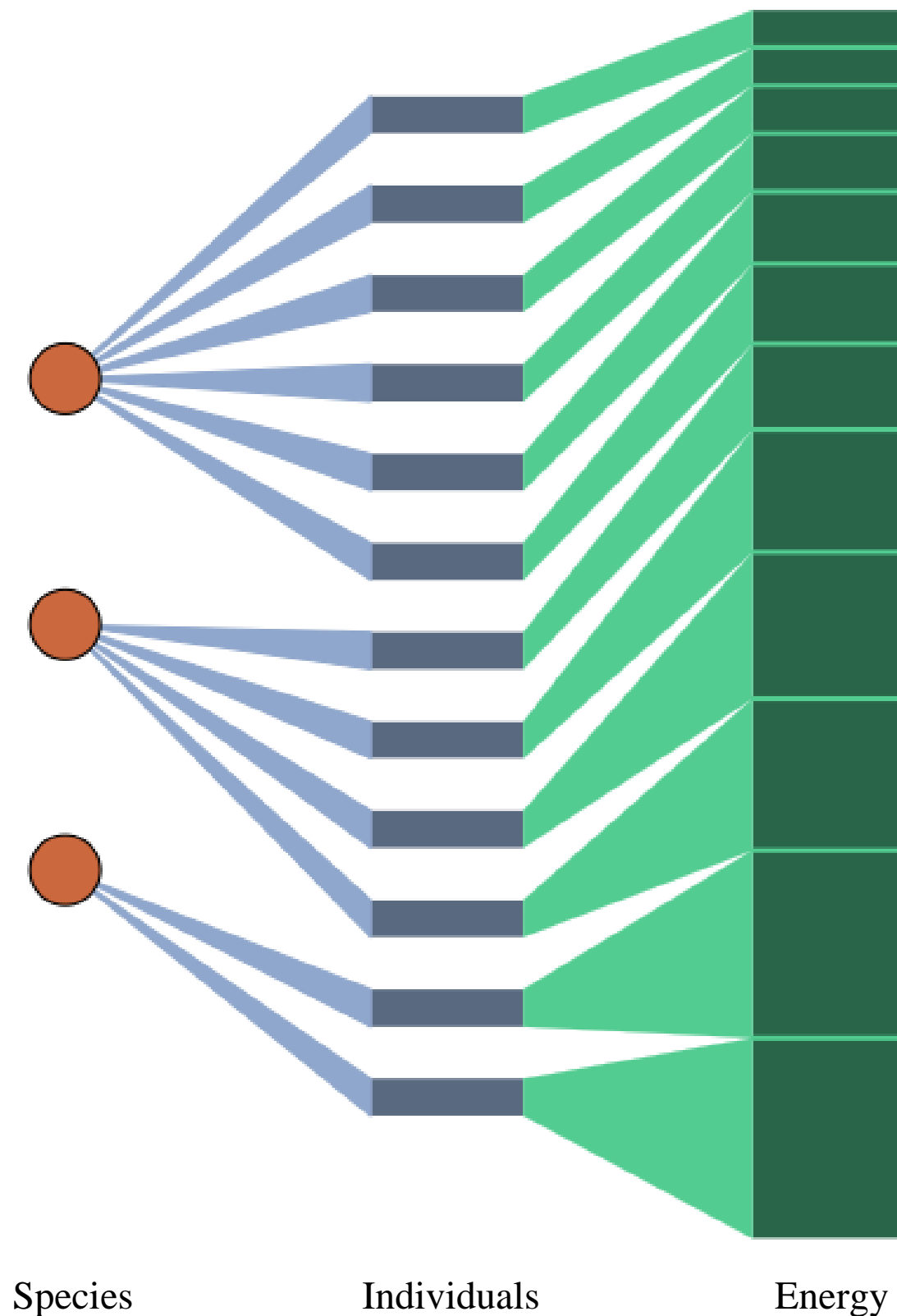
- **Taxa differ in**
 - The interplay between ecological & genetic shifts during diversification
 - **Rate of accumulation of species**
 - **Patterns of diversity over time**
 - Highlights how different groups perceive the chronosequence
 - and **ecological theory** can give us a guide as to what's novel

4. Ecological Interactions

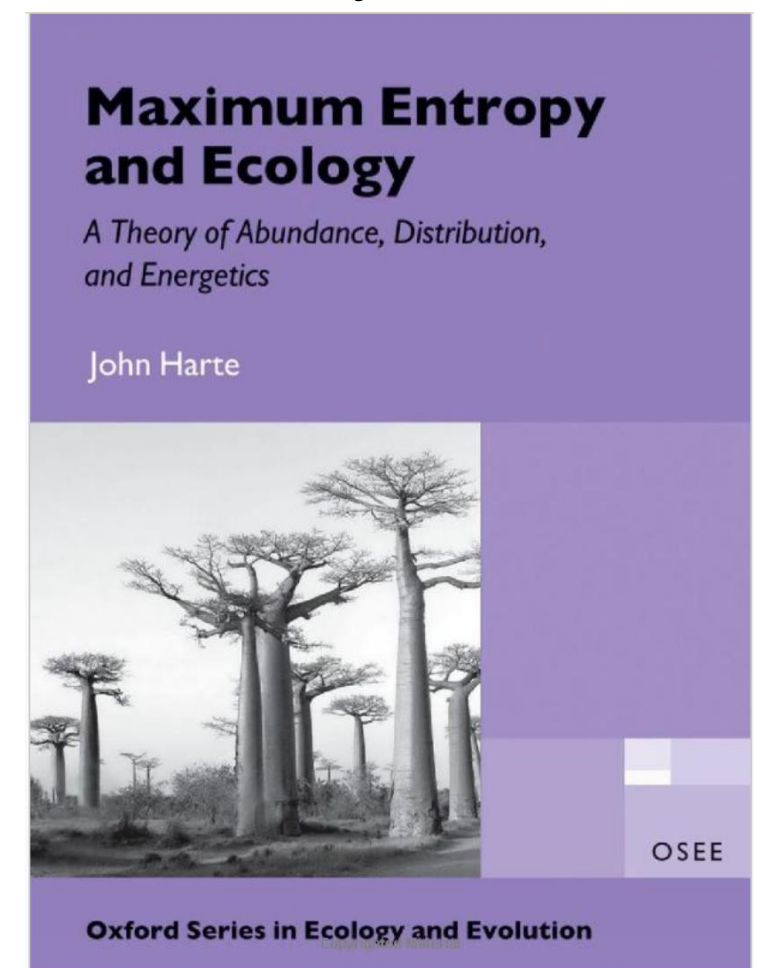
- Measurement of ecological metrics
- Space for time



Maximum Entropy Theory of Ecology

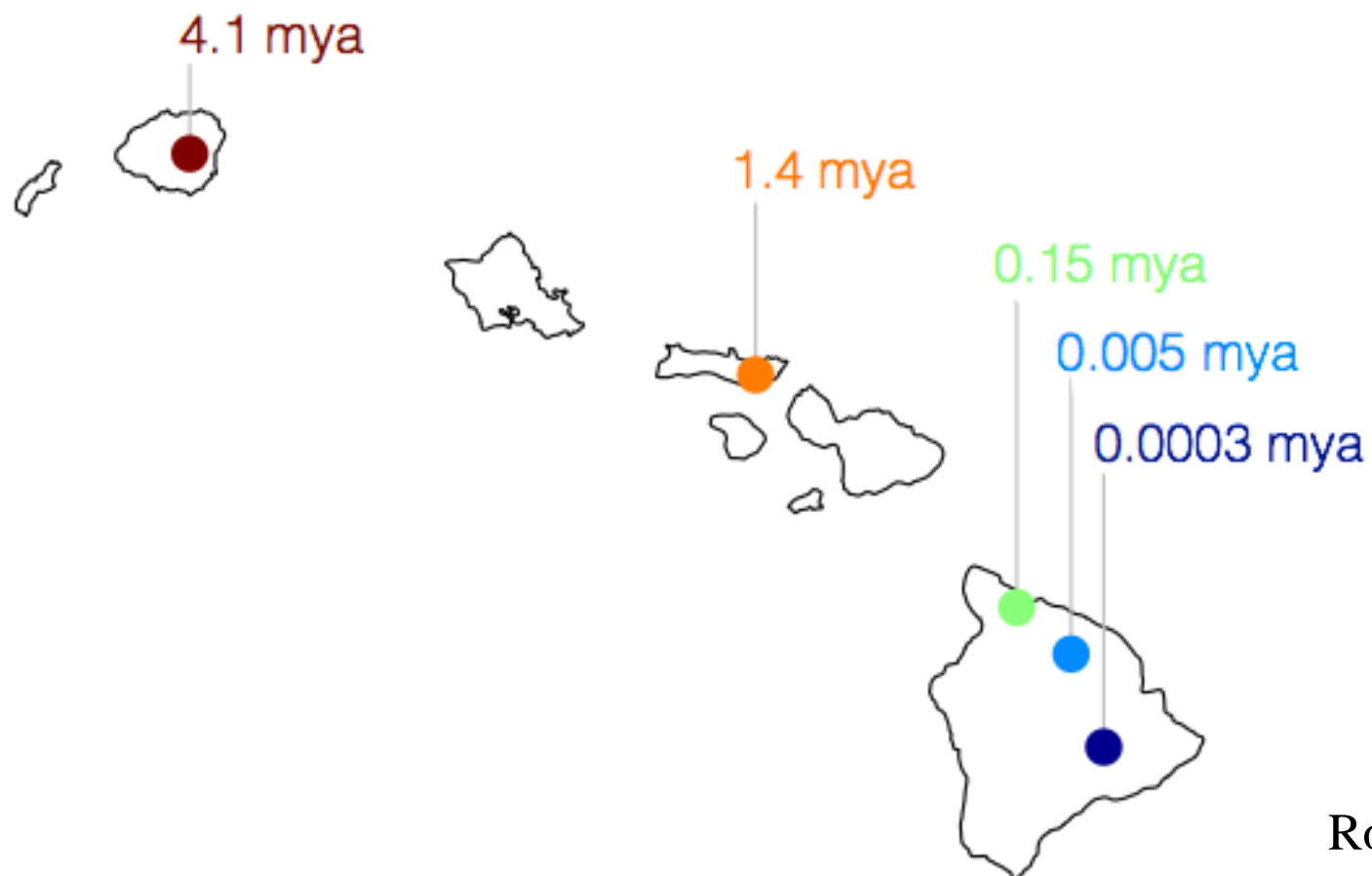
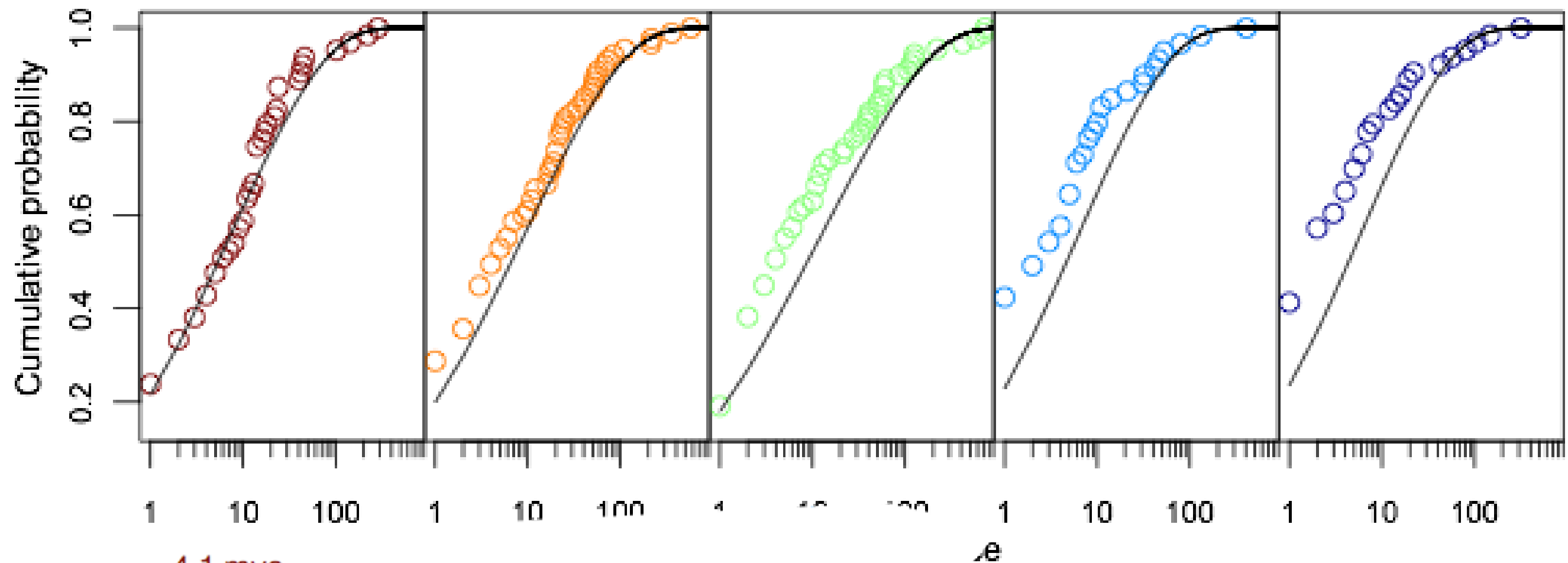


- Community-wide genetic divergence across space, environment and time (chronosequence)
- Testing novel theory



Harte (2011) Oxford University Press.

Fitting species abundance data to METE predictions

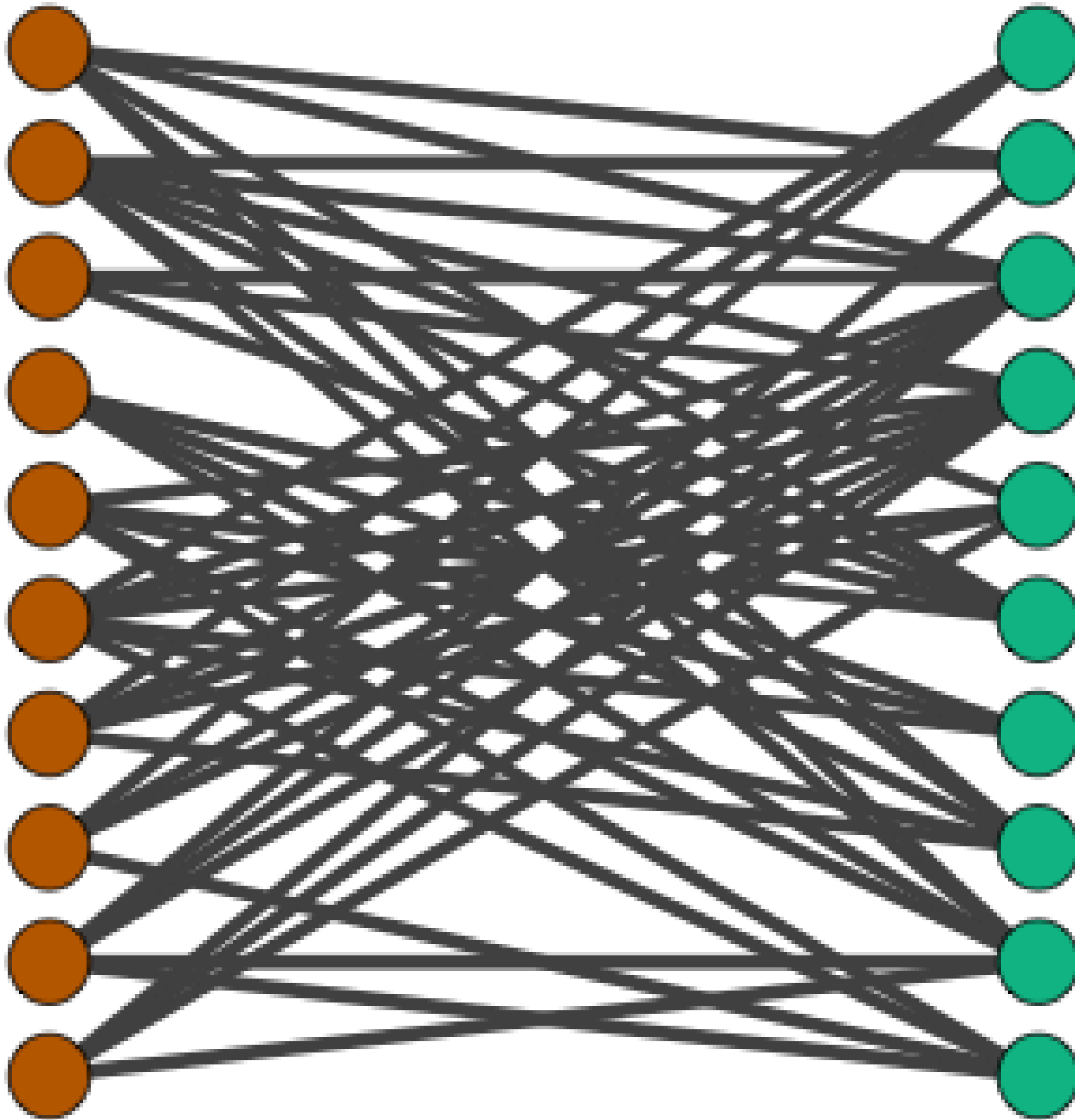


Deviation from predictions on youngest substrates may indicate that community has not yet reached steady state

Rominger *et al.* 2015 *Global Ecology and Biogeography*

1. Micro-macro evolution 2. Evolutionary dynamics 3. Species diversity 4. Ecological interactions

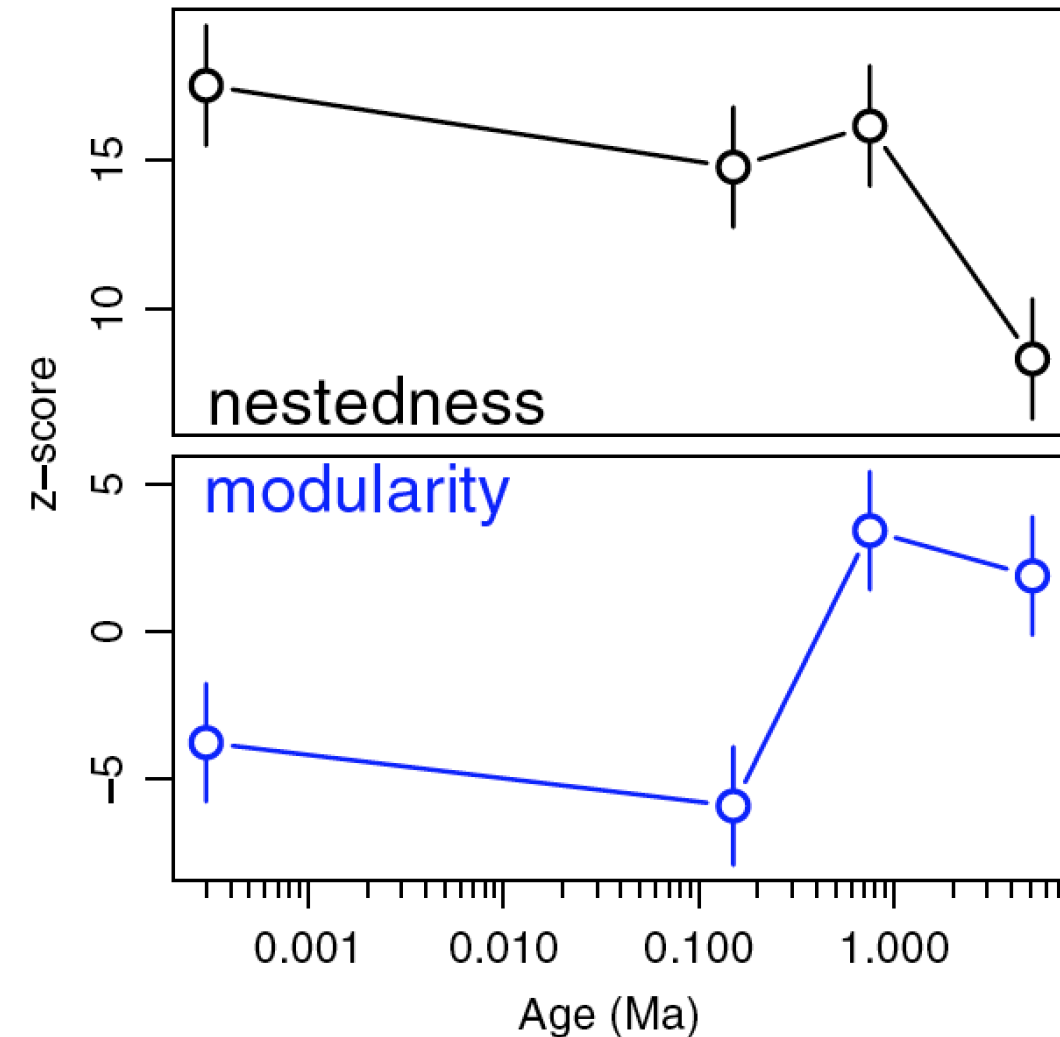
Interaction Networks



Modularity - degree to which species interact in semi-autonomous modules

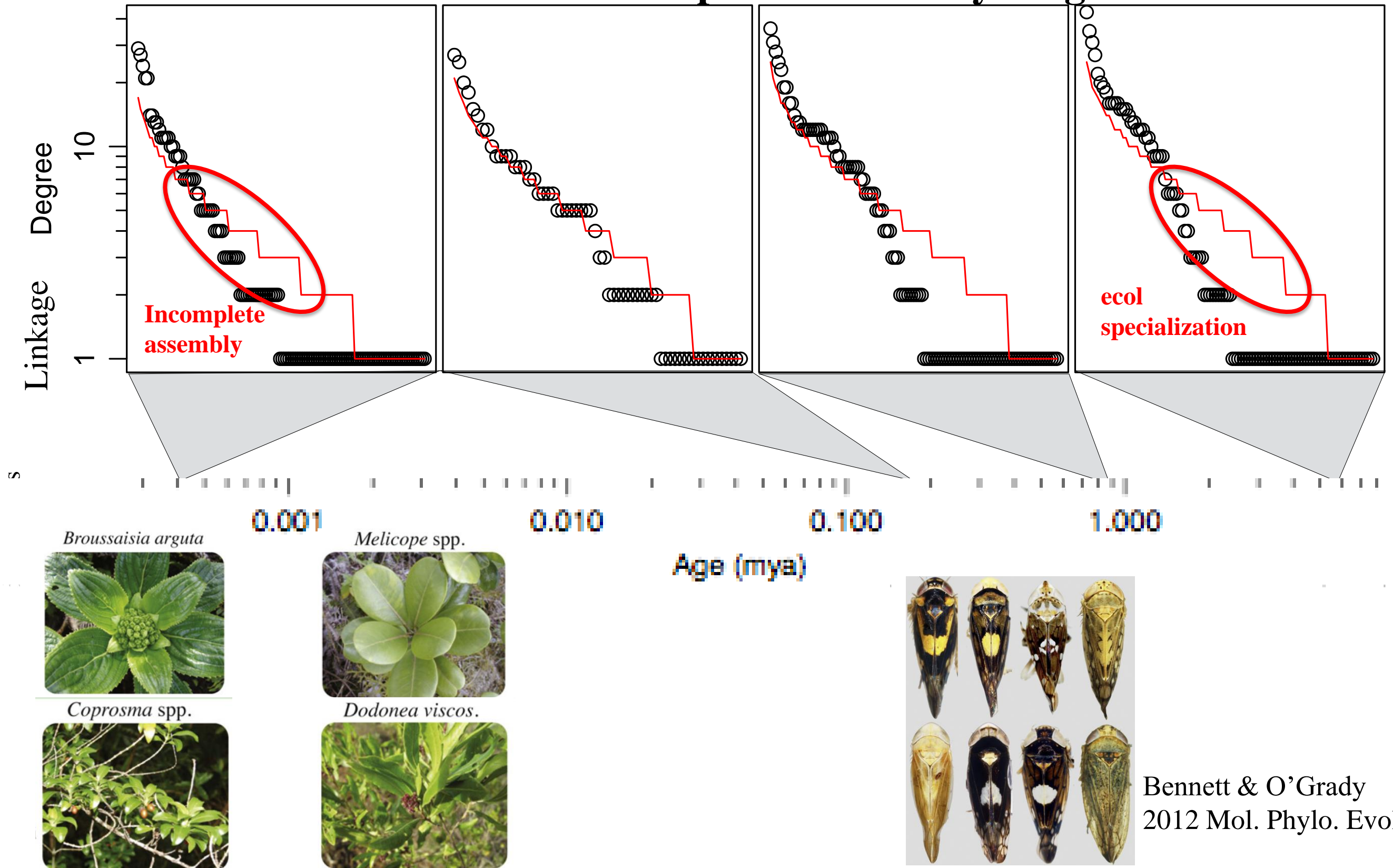
Nestedness - degree of asymmetry in interaction between specialists and generalists

- **Nestedness decreases** with site age. *Perhaps due to high immigration of new species with high probabilities to eat / be eaten by generalist species already present*



- **Modularity increases**, *likely due to coevolution*

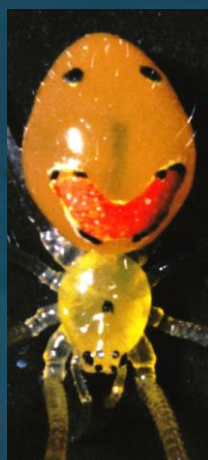
Networks deviate most from METE predictions on youngest & oldest sites



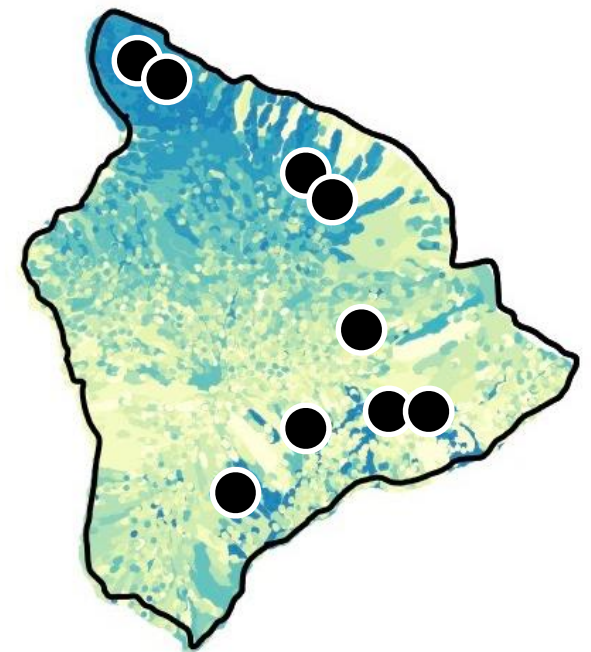
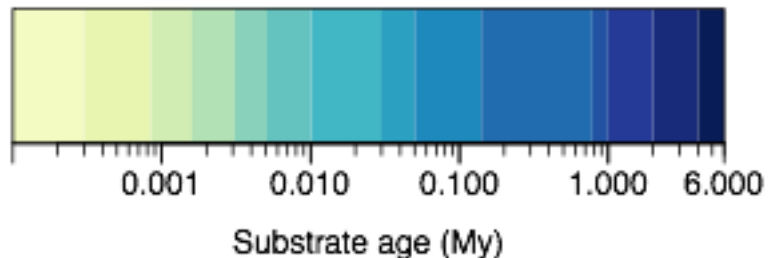
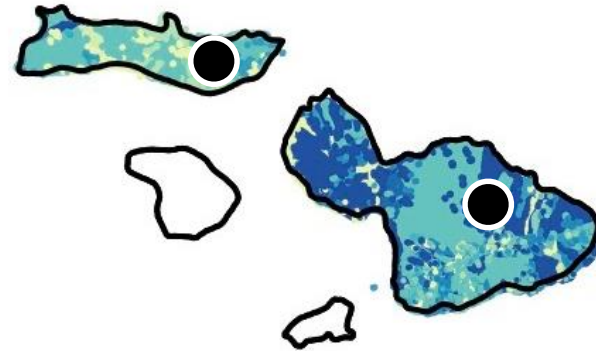
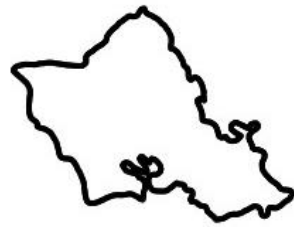
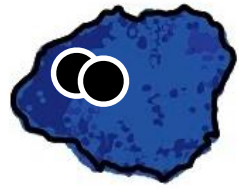
- ecological theory can give us a guide as to what's novel

Across the chronosequence we've found:

- Different arthropod groups perceive, colonize and diverge across evolving landscapes differently
- Results in different patterns of species accumulation over time
- Deviation from statistical steady state varies across groups and substrate ages.
- Interaction of ecological & evolutionary strategies, isolation & mixing, likely interact to produce patterns



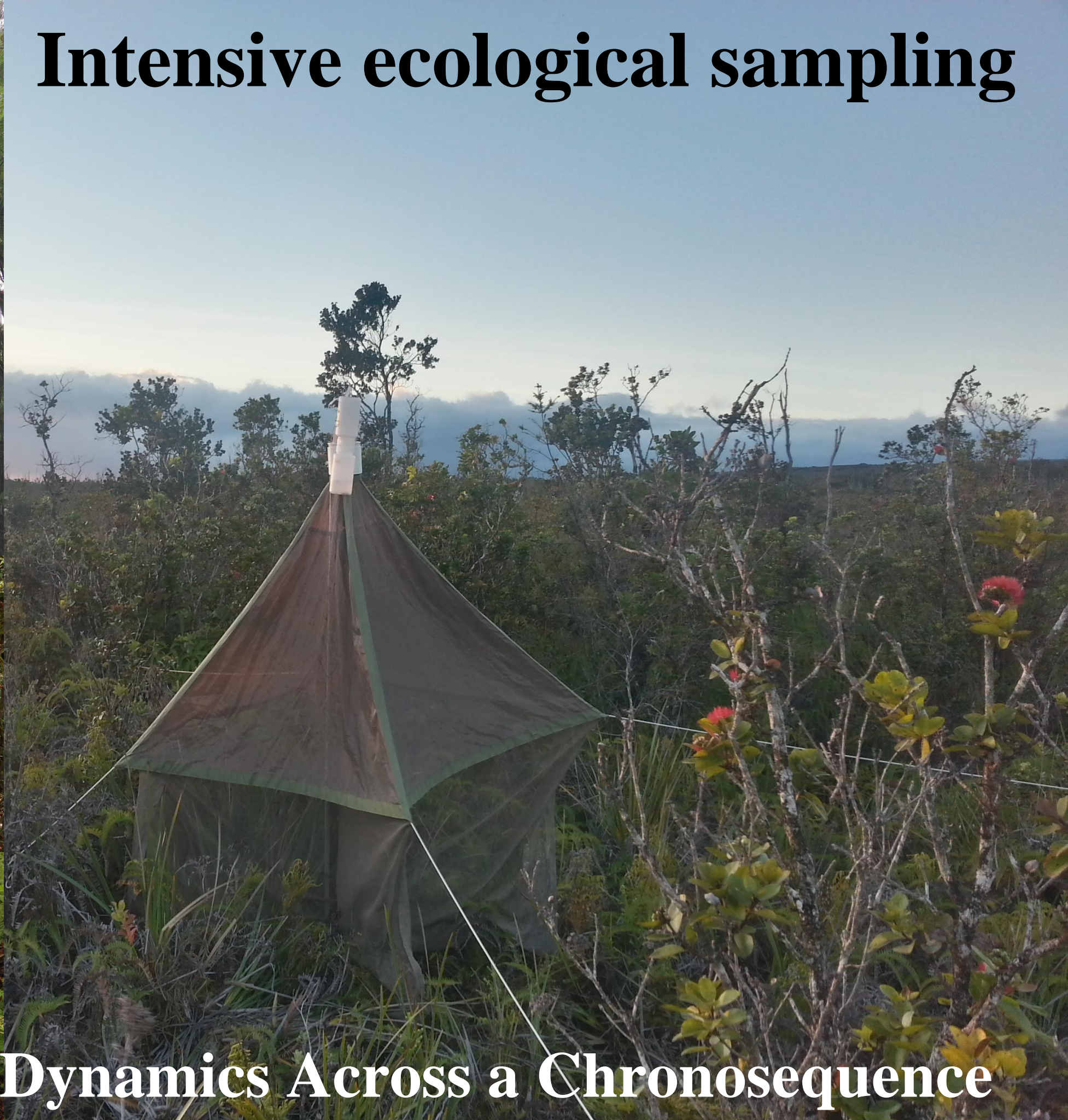
Research Underway



Looking at sites of similar **elevation**,
precipitation; all in *Metrosideros*
forest and accessible in **reserves**

Biodiversity Dynamics Across a Chronosequence

Intensive ecological sampling



Biodiversity Dynamics Across a Chronosequence

Metagenomics across the chronosequence

Changes in Evolutionary Dynamics

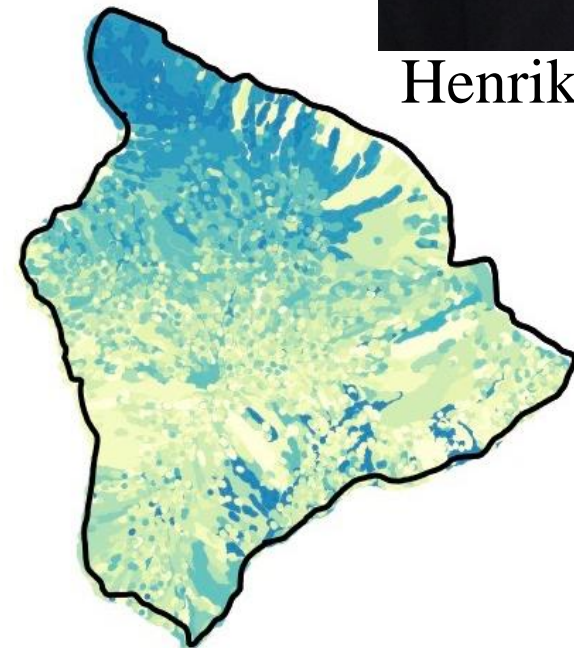
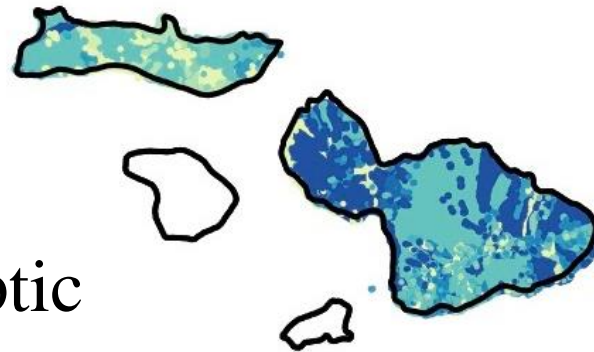
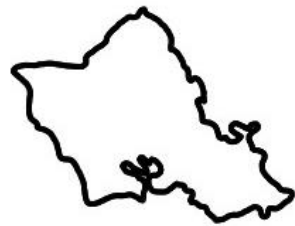
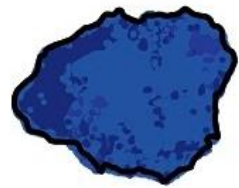
- Genetic structure of **all** lineages in the ecosystem
- Which factors drive divergence of lineages

Changes in Community Structure & Dynamics

- Rapid identification of taxa & cryptic diversity
- Relative abundances
- Using metabarcoding of whole predators to identify
 - prey-predator interactions
 - food plants of herbivores



Henrik Krehenwinkel

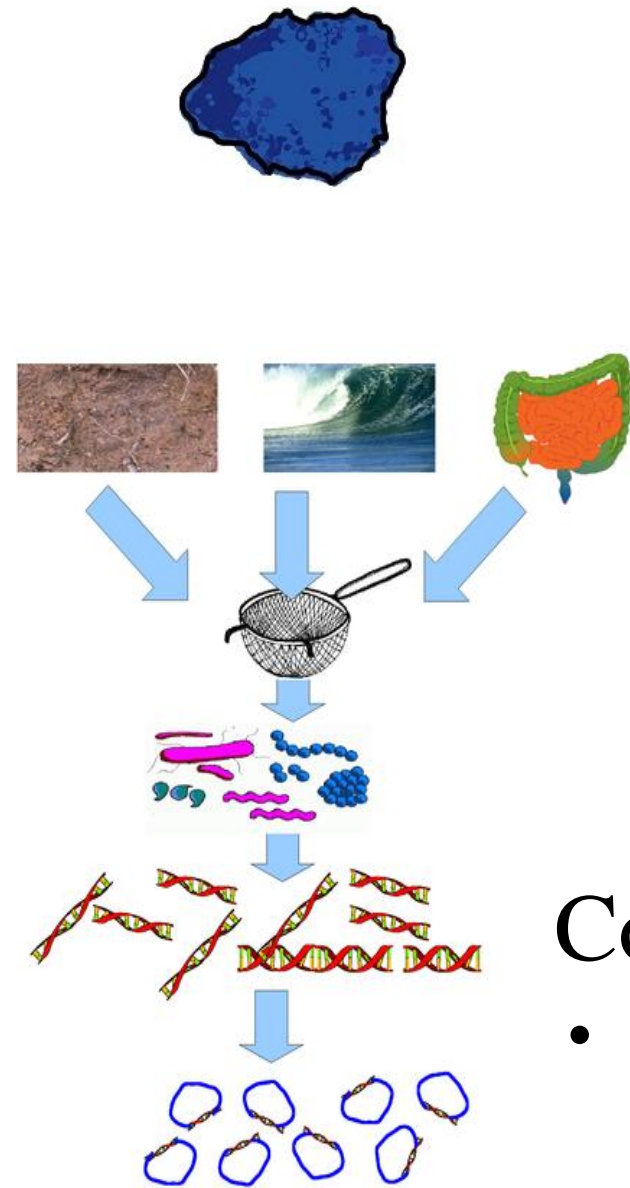


Zhou et al 2013. Ultra-deep sequencing enables high fidelity recovery of biodiversity for bulk arthropod samples without PCR amplification. GigaScience 2: 4.

Pinol, J. et al. 2013. A pragmatic approach to the analysis of diets of generalist predators Mol Ecol Resources 14: 18-26

Kozich et al. 2012 Applied & Environmental Microbiology

Metagenomics across the chronosequence

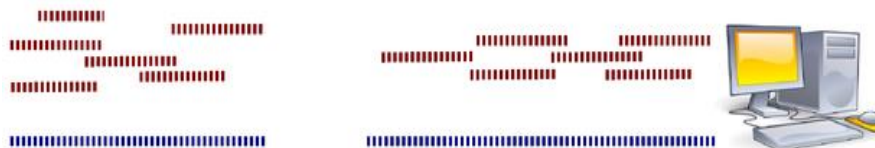
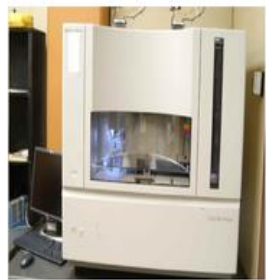


- 16s based taxon identification
- Molecular community studies
- Also functional genomic studies
- Initially on 454, now on MiSeq or HiSeq

- ITS in fungi
- COI in animals

Cost-effective mass-multiplexing

- MiSeq protocol developed for microbiome sequencing
- Applicable to any other PCR fragment; 400 microbiome samples /run; sequencing right after PCR



Gibson, J. et al. 2014 Simultaneous assessment of the macrobiome & microbiome in a bulk sample of tropical arthropods. PNAS 111: 8007–8012

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Leray, M. & Knowlton, N. 2014. DNA barcoding & metabarcoding PNAS

Mahalo! Thank you!



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