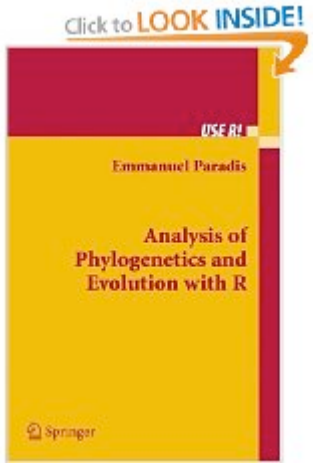
Useful Resources

Website: www.r-phylo.org

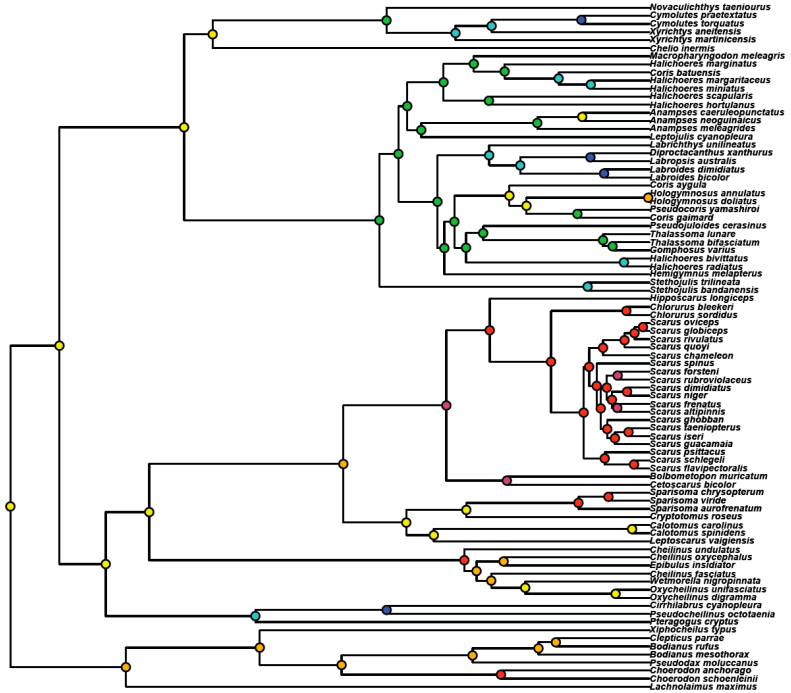
Listserve: r-sig-phylo@r-project.org

Book

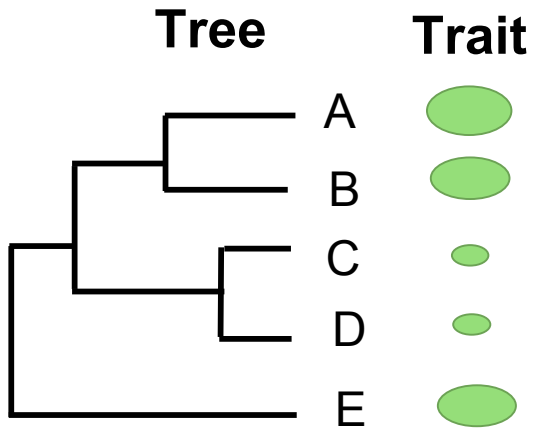


Paradis (2006) Analysis of phylogenetics and evolution with R. Springer (Use R! series)

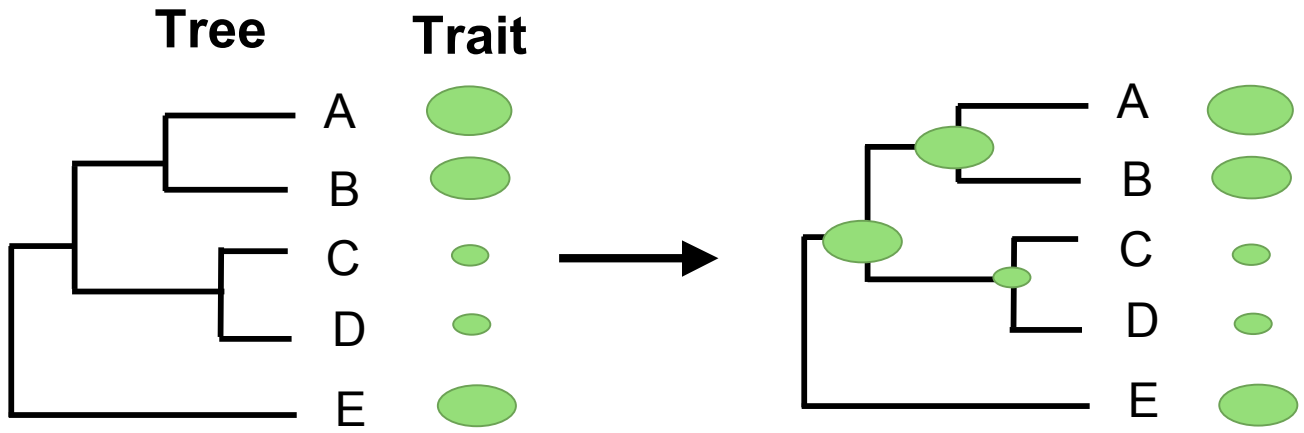
Ancestral State Reconstruction
or
Ancestral State Estimation



Ancestral State Reconstruction

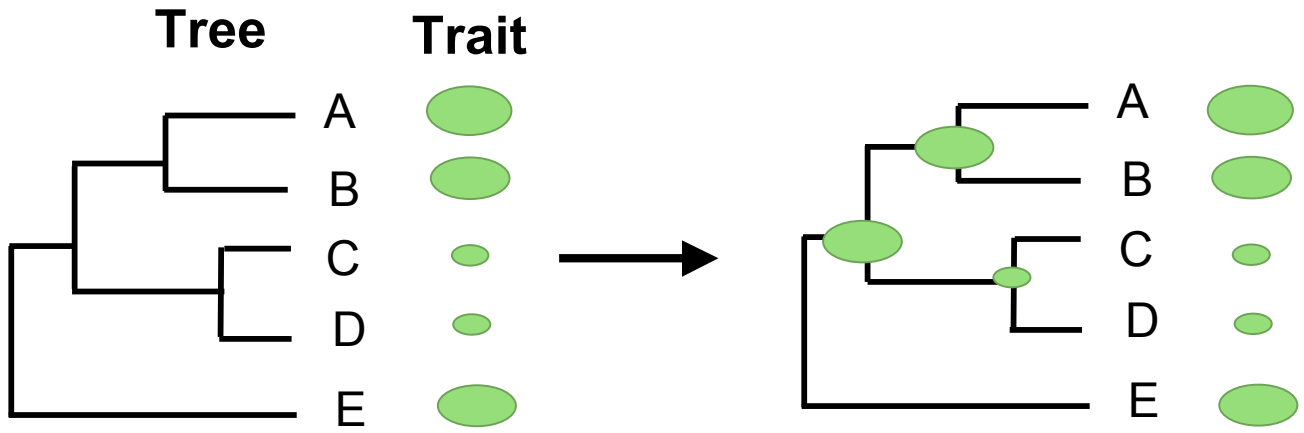


Ancestral State Reconstruction



Infer how traits have changed through time

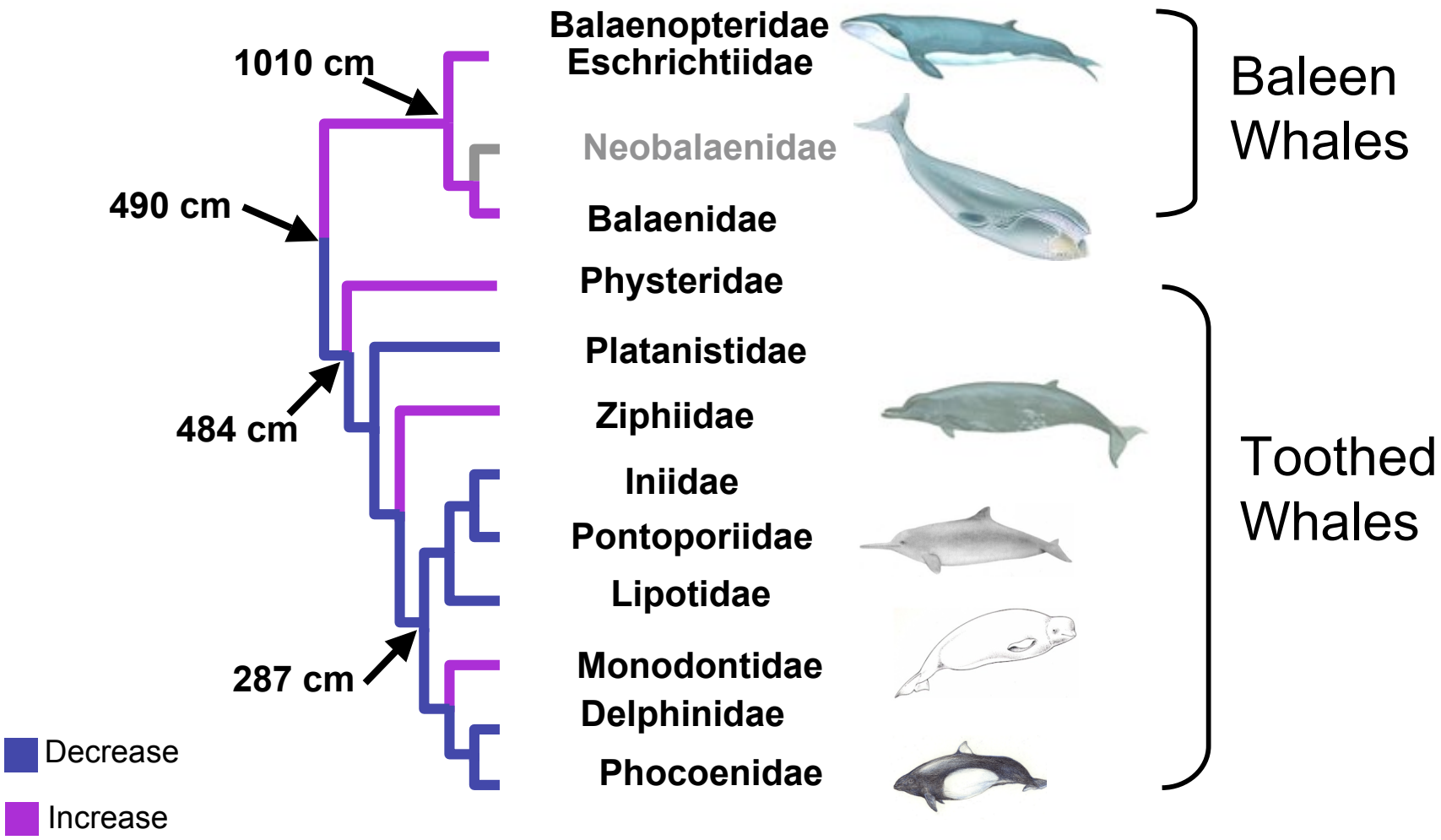
Ancestral State Reconstruction



Infer how traits have changed through time

Visualize/identify complex macroevolutionary/macroecological patterns

Evolution of Size in Whales



Ancestral State Reconstruction

- Reconstruction methods
  - Squared-change parsimony
    - Weighted or unweighted
  - Maximum likelihood
  - Generalized least squares (GLS)
  - Bayesian

Ancestral State Reconstruction

- Reconstruction methods
  - Squared-change parsimony
  - Maximum likelihood
  - GLS
  - Bayesian

Ape package
ace function

Ancestral State Reconstruction

- Reconstruction methods
  - Squared-change parsimony
  - Maximum likelihood
  - GLS

ace method="GLS"

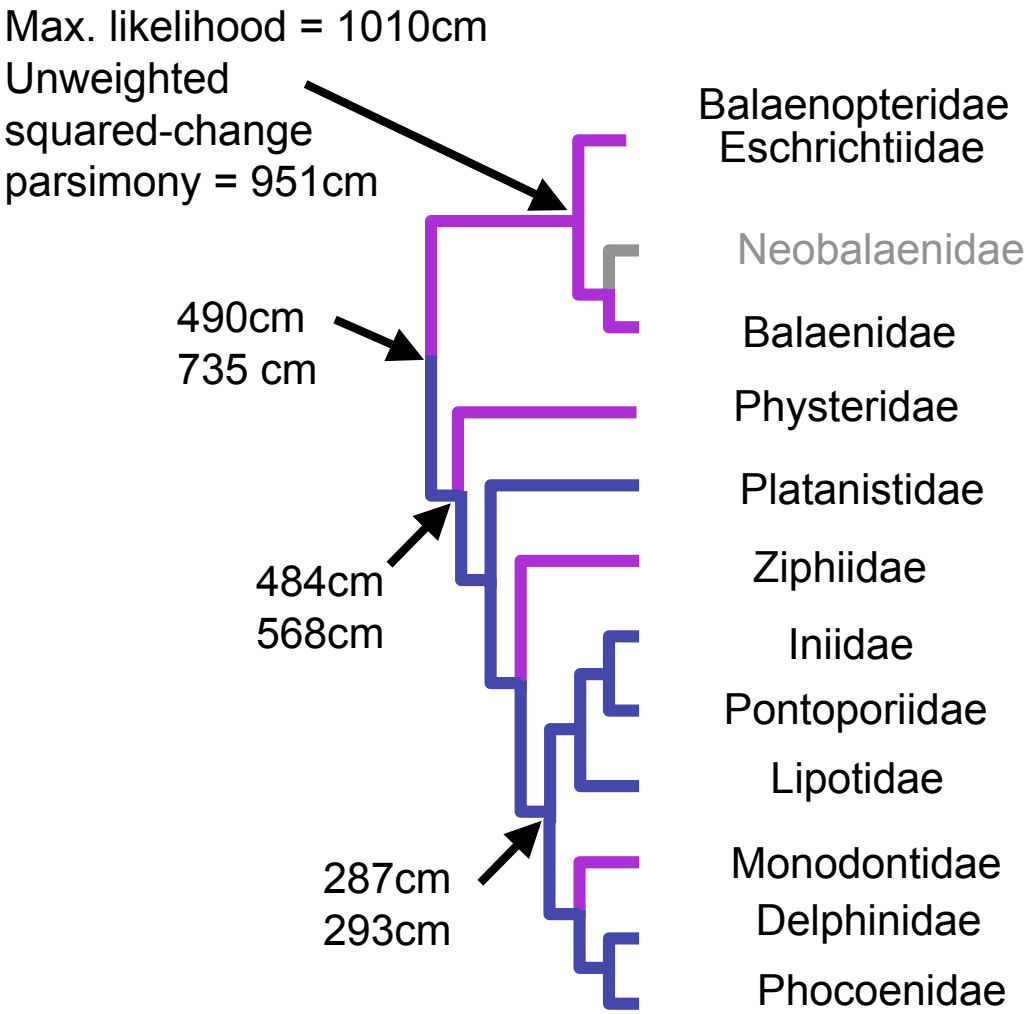
Caveat this method is unstable and can generate unusual error messages. Use at your own risk!

Ancestral State Reconstruction

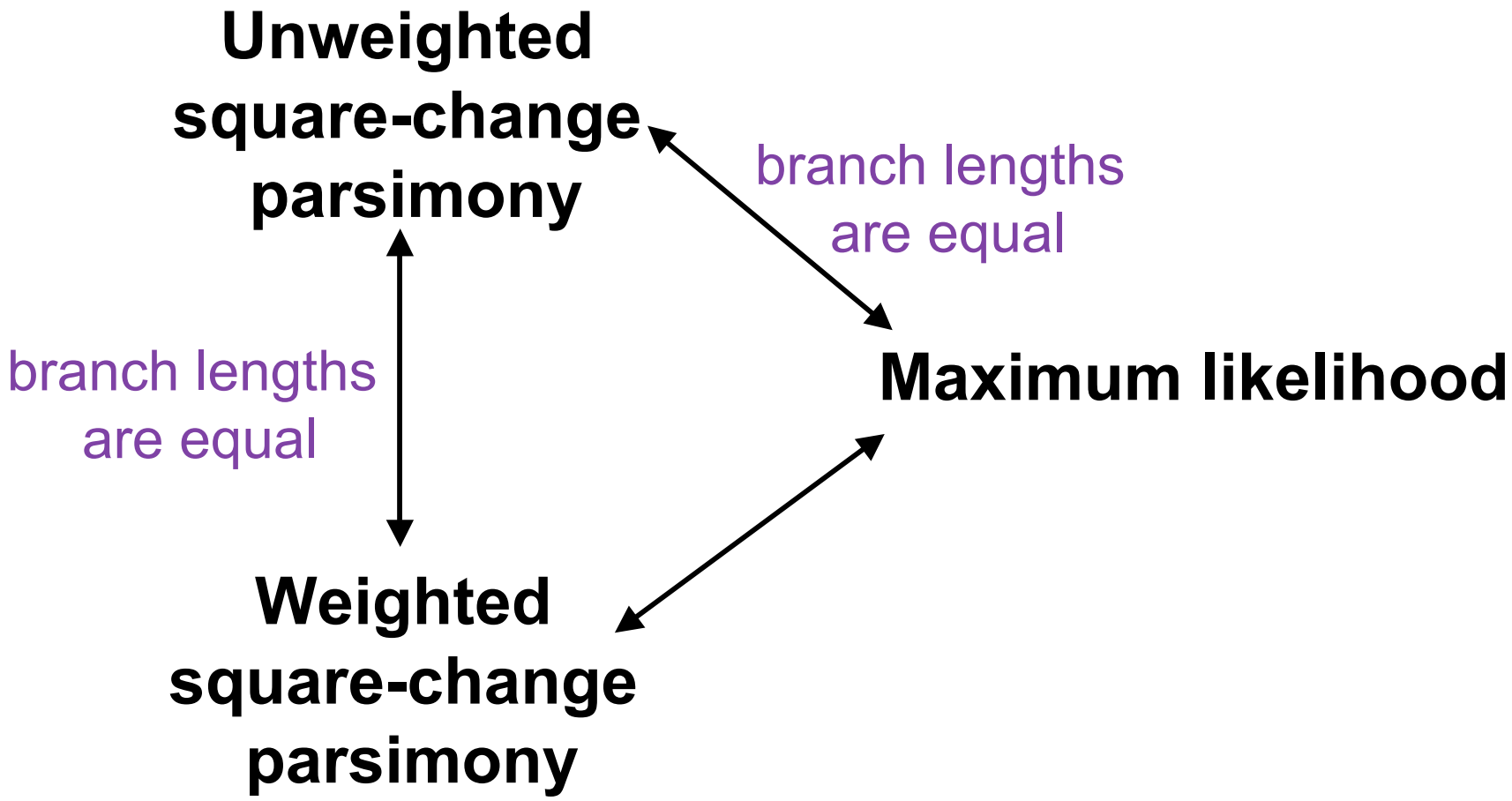
- **Squared-change parsimony**
  - Minimizes evolutionary change across the tree
  - Unweighted ignores branch length information
  - Weighted incorporates branch length information
- **Maximum likelihood**
  - Most likely set of ancestral states when whole phylogeny is considered
  - Incorporates branch length information
  - Evolutionary model to estimate rate of evolution

    (Brownian motion currently implemented in R)

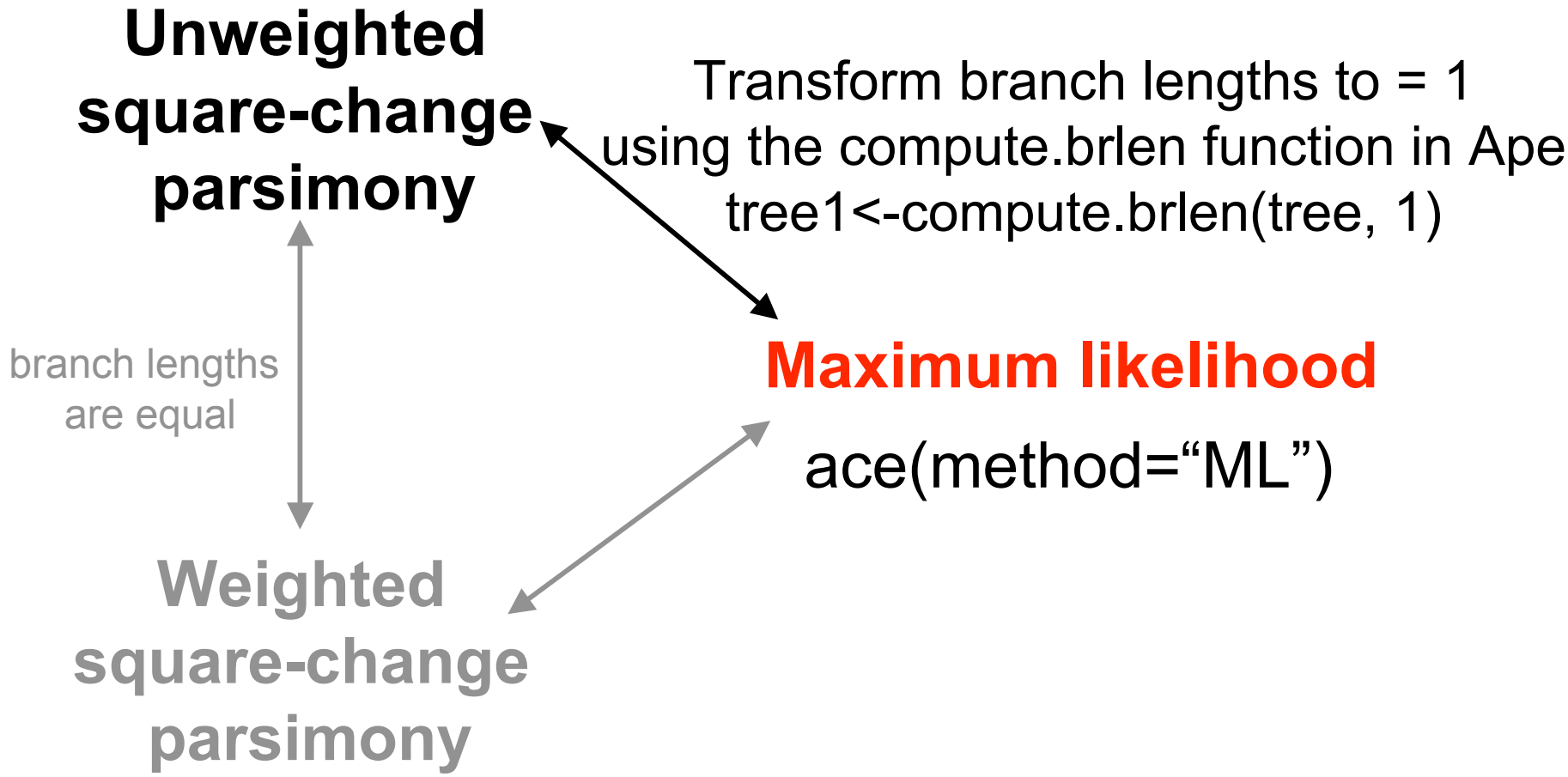
Evolution of Size in Whales



Ancestral State Reconstruction



Implementation



Ancestral State Reconstruction

Discrete traits in

- Maximum likelihood used to fit Markovian models of discrete character evolution.

  ace(type=discrete)

Ancestral State Reconstruction

Discrete traits in

- Maximum likelihood used to fit Markovian models of discrete character evolution. ace(type=discrete)

Equal

Character states	1	2	3
1	0	1	1
2	1	0	1
3	1	1	0

Symmetrical

	1	2	3
1	0	1	2
2	1	0	3
3	2	3	0

All-rates different

	1	2	3
1	0	1	2
2	3	0	4
3	5	6	0

Ancestral State Reconstruction

Discrete traits in

- Maximum likelihood used to fit Markovian models of discrete character evolution.

Equal

Character states	1	2	3
1	0	1	1
2	1	0	1
3	1	1	0

ace(type=discrete, model="ER")

Symmetrical

	1	2	3
1	0	1	2
2	1	0	3
3	2	3	0

ace(type=discrete, model="SYM")

All-rates different

	1	2	3
1	0	1	2
2	3	0	4
3	5	6	0

ace(type=discrete, model=ARD")

Disparity

Measure of morphological diversity

Disparity

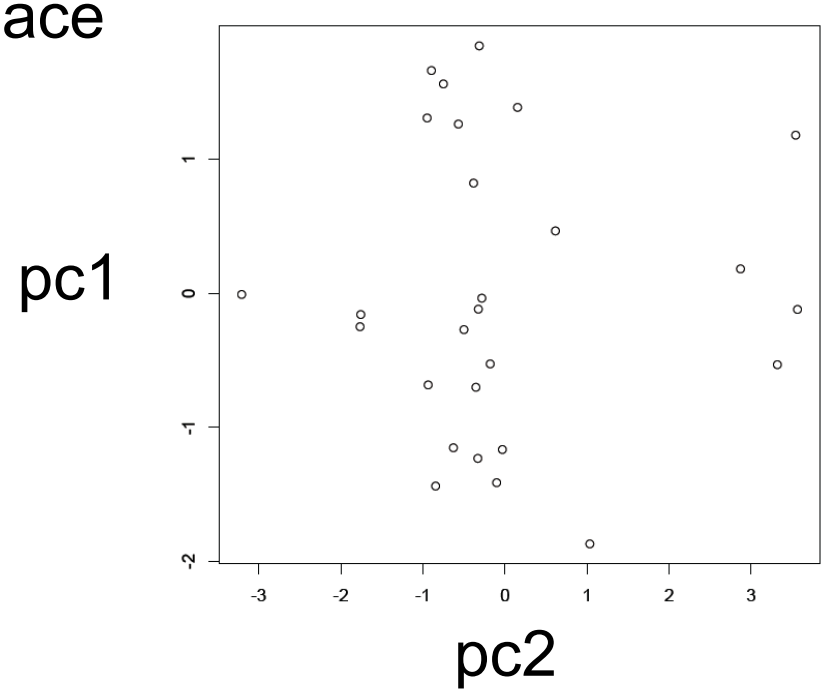
Evolution of diversity --> species richness --> morphological richness

- Are taxonomically rich clades also morphologically diverse?
- How does morphological diversity relate to ecological differences?

Disparity

Measure of morphological diversity

- Sample-size independent
  - Average pair-wise distance between points in morphospace



Disparity

Measure of morphological diversity

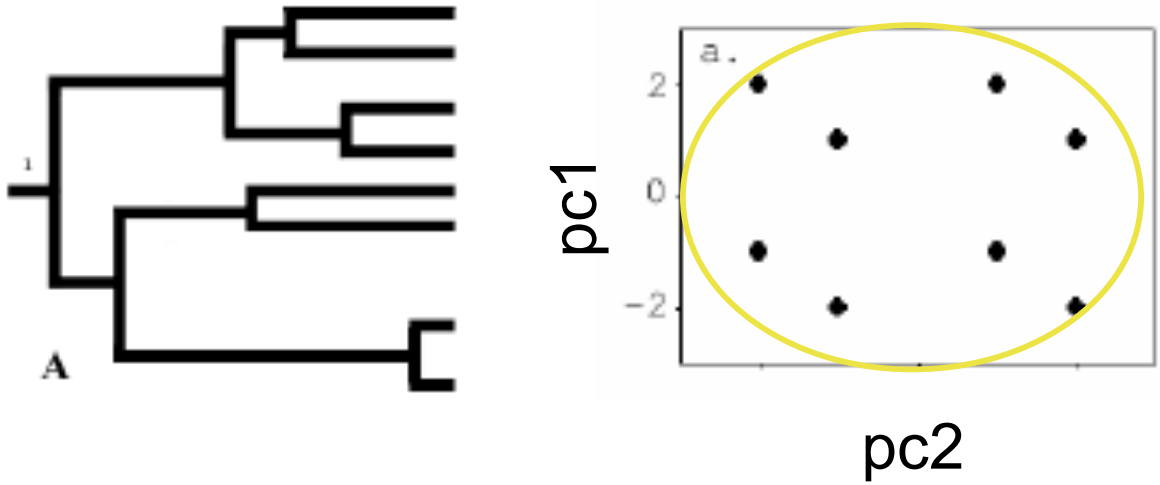
- Sample-size independent
- Geiger package
  - Average-squared Euclidean distance, if all axes are in the same units.
  - Average-Manhattan distance (sum of the absolute differences of their coordinates)

Harmon et al. 2003, Science 301: 961-964

Disparity

Geiger package

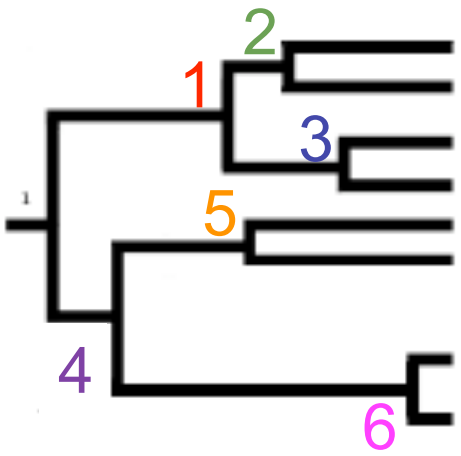
1. Disparity across the whole tree (compare to other clades).
   – Average pair-wise distance in morphospace between all species in the dataset

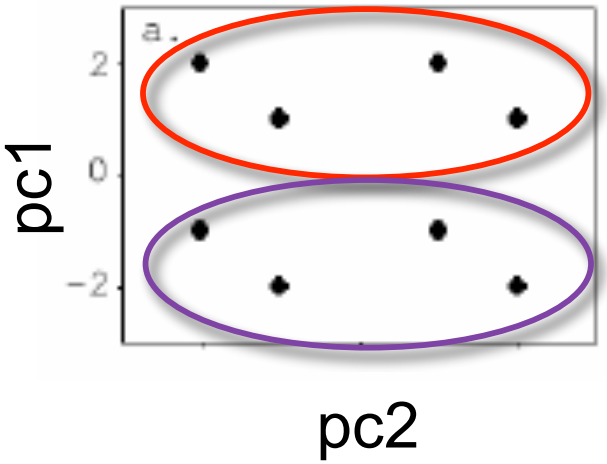


Disparity

Geiger package

1. Disparity across the whole tree (compare to other clades).
2. Disparity for every clade in the phylogeny
   - Average pair-wise distance in morphospace between all species in the clade





Disparity

Geiger package

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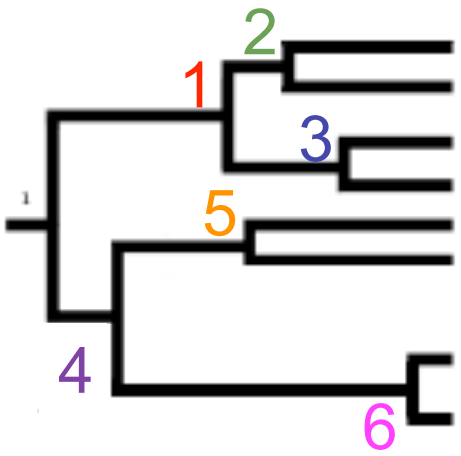
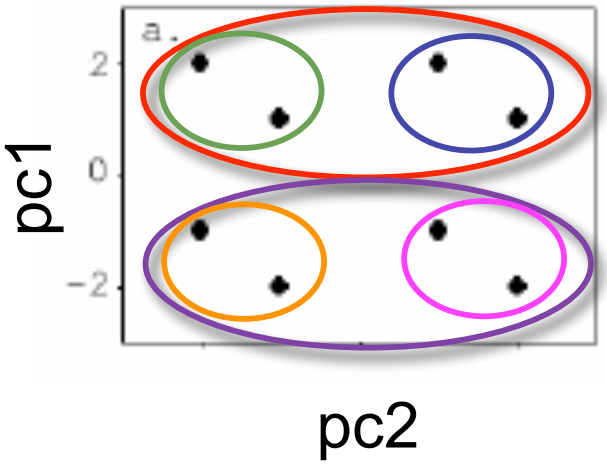


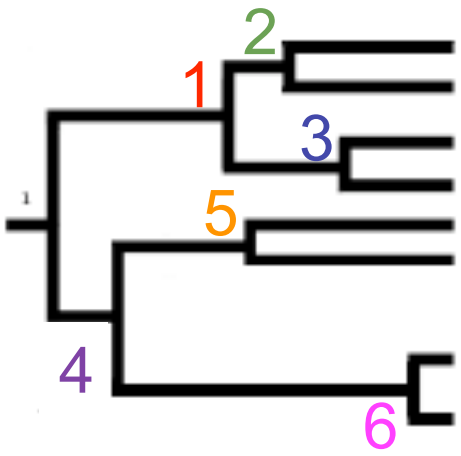


Disparity

Geiger package

1. Disparity across the whole tree (compare to other clades).
2. Disparity for every clade in the phylogeny
3. Disparity through time

   Does disparity correspond to clade differences?



Disparity

Geiger package

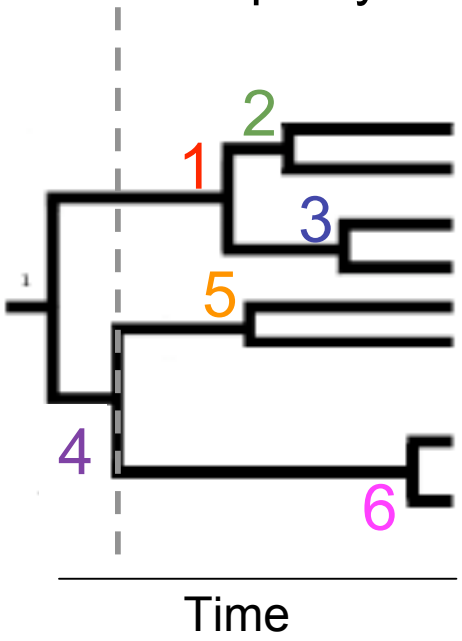
1. Disparity across the whole tree (compare to other clades).
2. Disparity for every clade in the phylogeny
3. Disparity through time
   - Relative disparity for each node

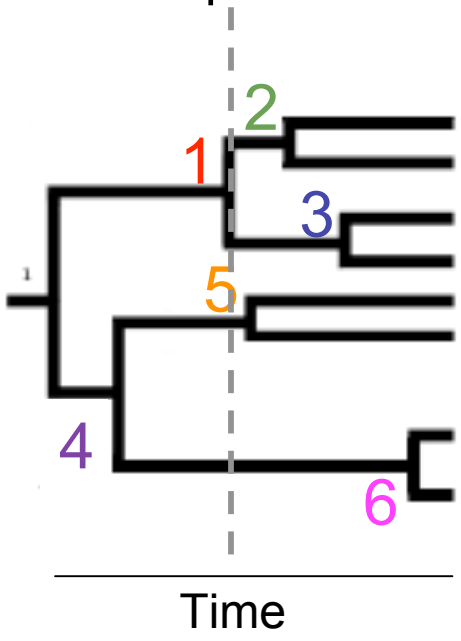
     (disparity for clade/whole tree disparity)
   - Calculate at each divergence event average relative disparity for each sub-clade present at that time period.

Disparity

3. Disparity through time

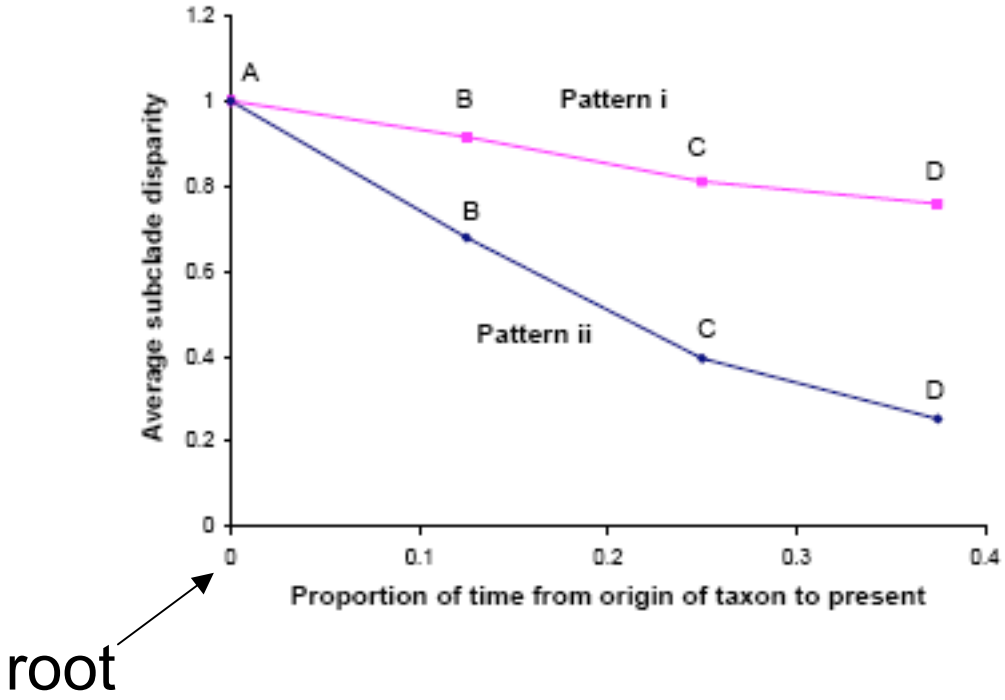
- Relative disparity for each node
  (disparity for node/whole tree disparity)
- Calculate at each divergence event average relative disparity for each sub-clade present at that time period.





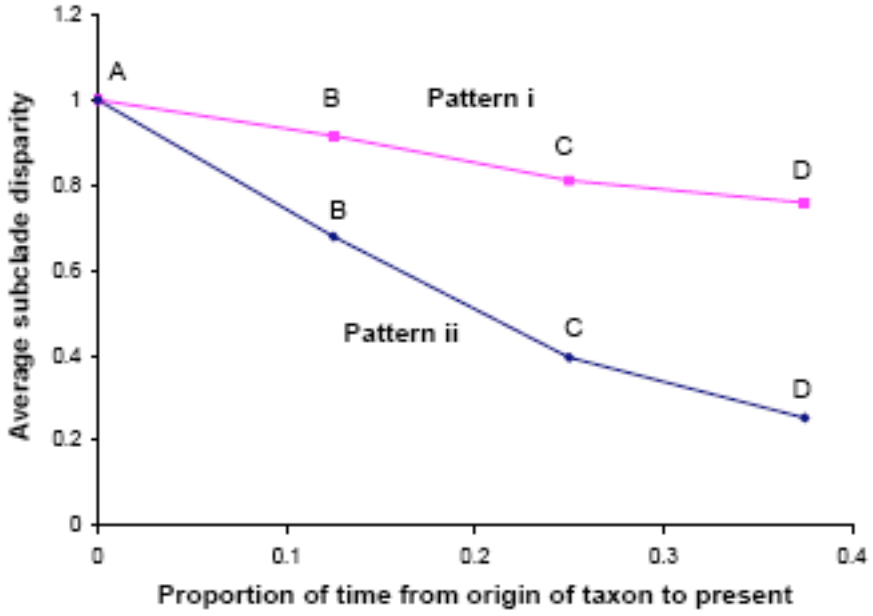
Disparity

3. Disparity through time plots



Disparity

3. Disparity through time

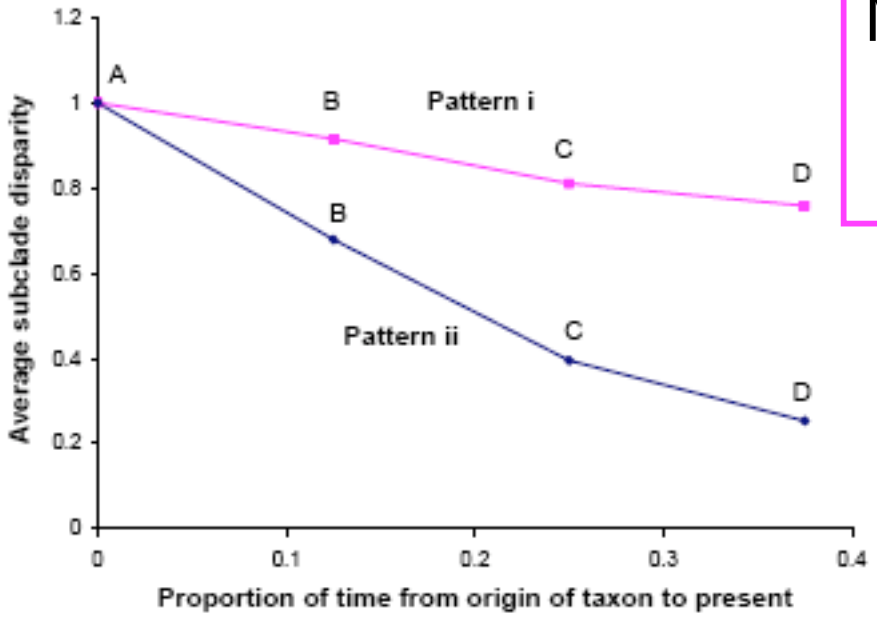


High average disparity through time = variation within sub-clades

Decreasing average disparity through time = variation between sub-clades

Disparity

3. Disparity through time

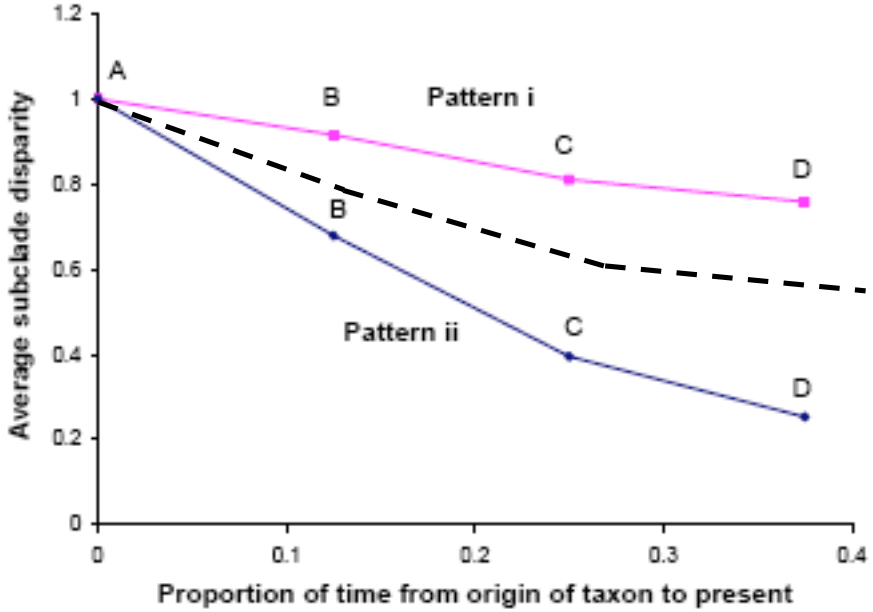


Morphological convergence. Sub-clades overlap each other in morphospace

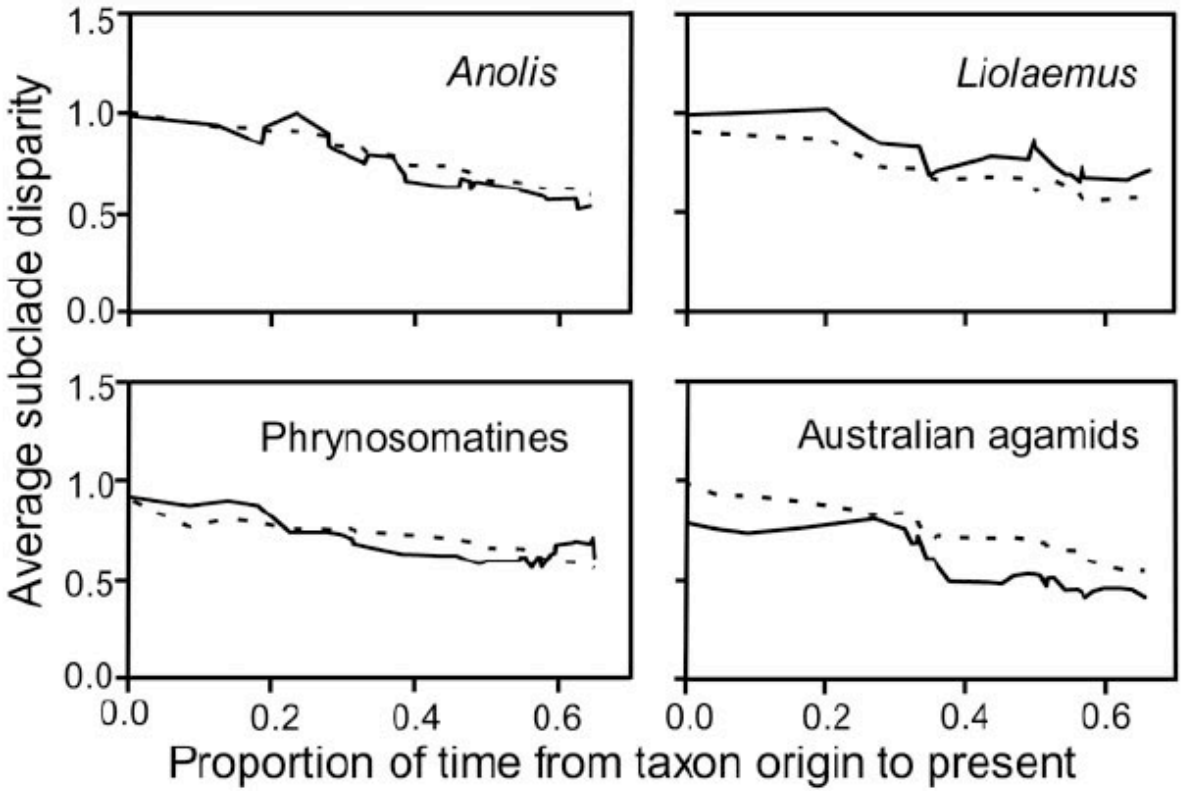
No morphological convergence - sub-clades occupy different morphospaces

Disparity

3. Disparity through time



Null expectation (morphological datasets simulated on the phylogeny)

Disparity

3. Disparity through time - Iguanian lizards