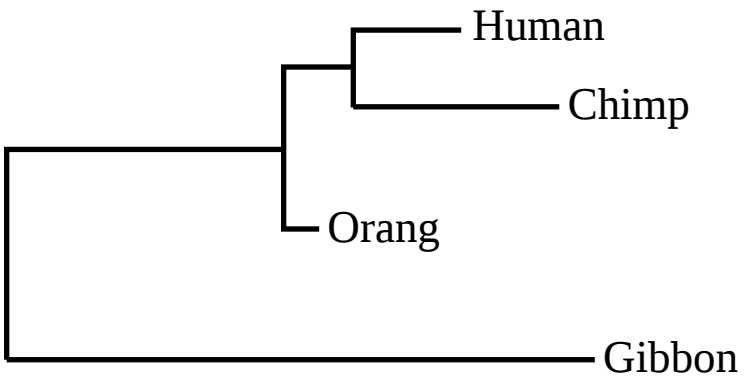
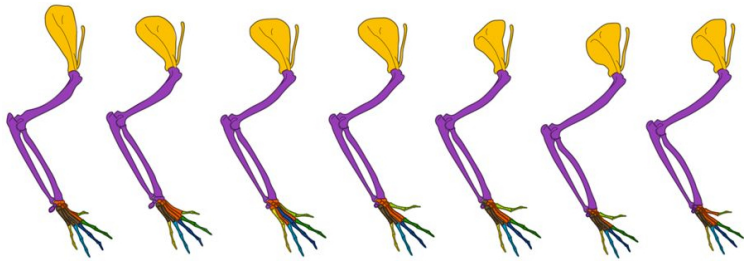
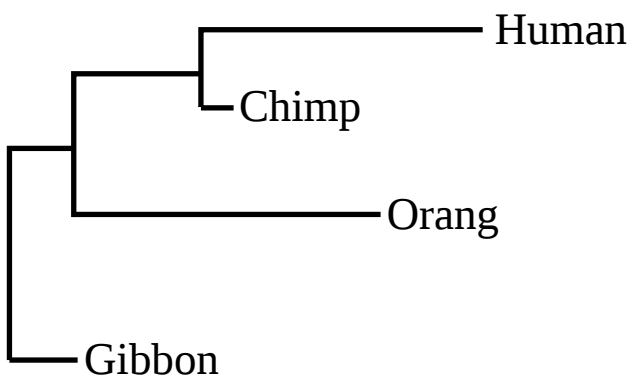
Discovering Mosaic Patterns: Phylogenies and Quantitative Traits

Caroline Parins-Fukuchi
Dept. of Ecology and Evolutionary Biology
University of Michigan

- Phenotypic traits may differ in their patterns of divergence

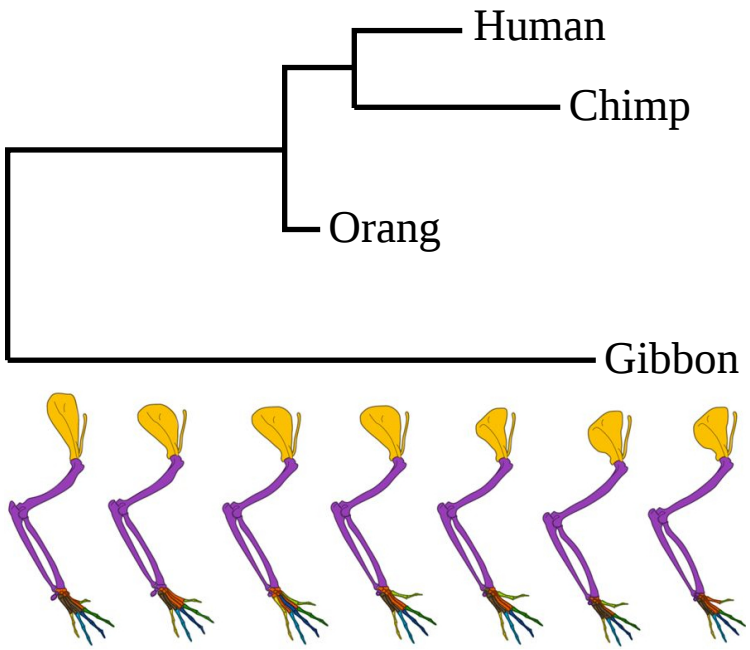


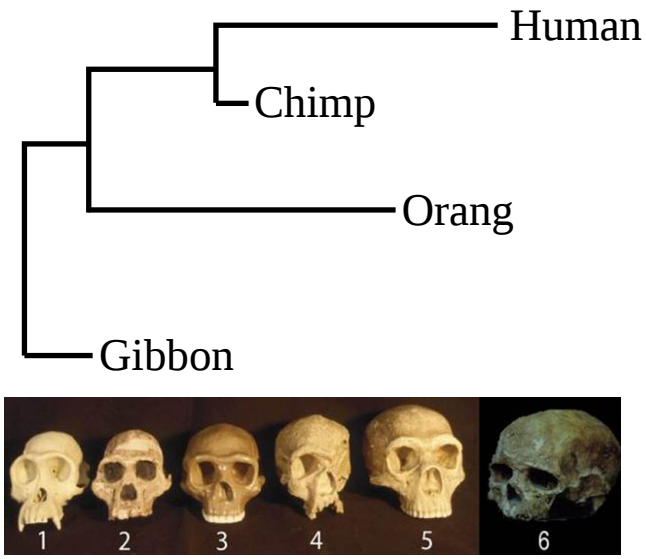




*Branch lengths = evolutionary rate

- Phenotypic traits may differ in their patterns of divergence
- These patterns may be biologically interesting





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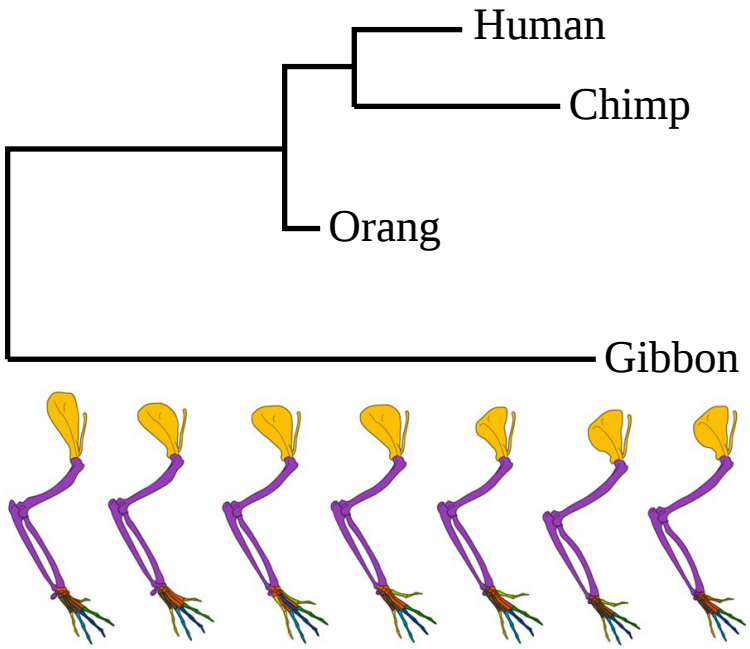
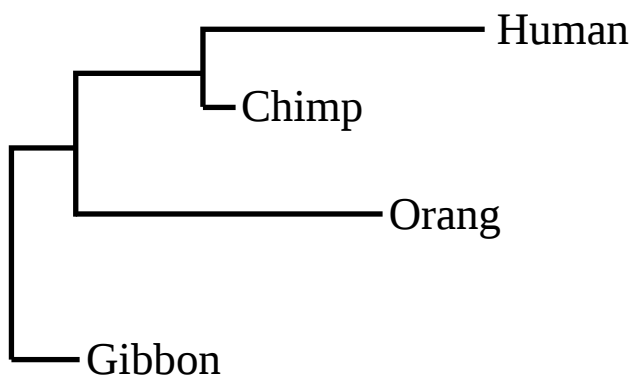
- These patterns may be biologically interesting
- Frame in terms of 'mosaic' evolution





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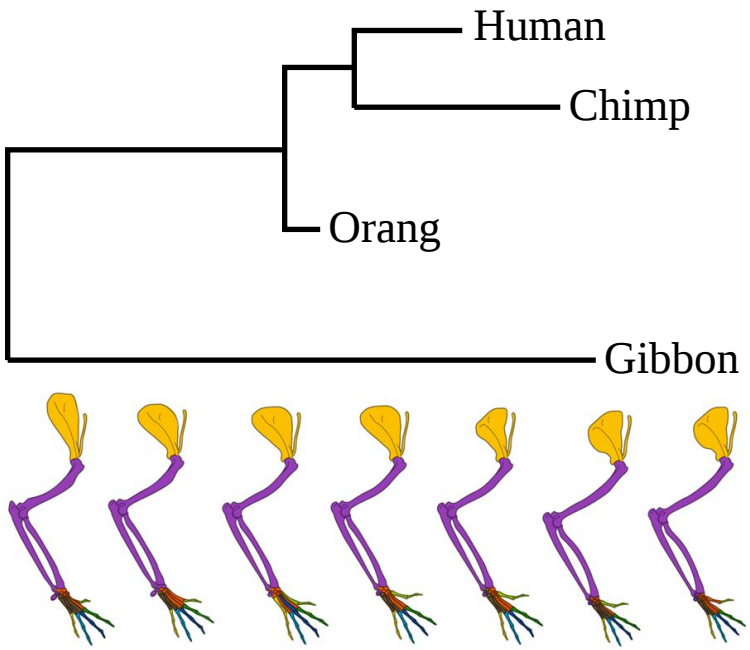
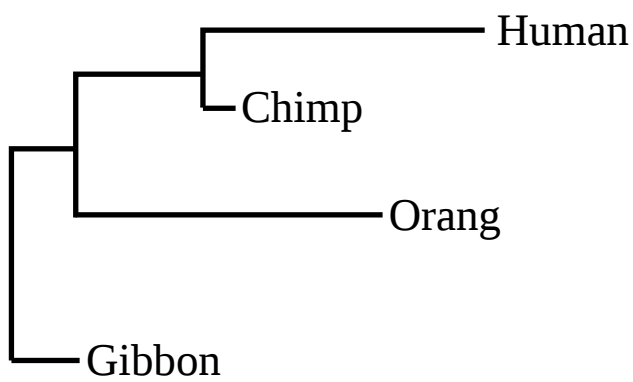
- Frame in terms of 'mosaic' evolution
- We want to delimit 'evolutionary' modules of traits





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PNAS

Developmental origins of mosaic evolution in the avian cranium

Ryan N. Felice[a,b,1] and Anjali Goswami[a,b,c]

[a]Department of Genetics, Evolution, and Environment, University College London, London WC1E 6BT, United Kingdom; [b]Department of Life Sciences, The Natural History Museum, London SW7 5DB, United Kingdom; and [c]Department of Earth Sciences, University College London, London WC1E 6BT, United Kingdom

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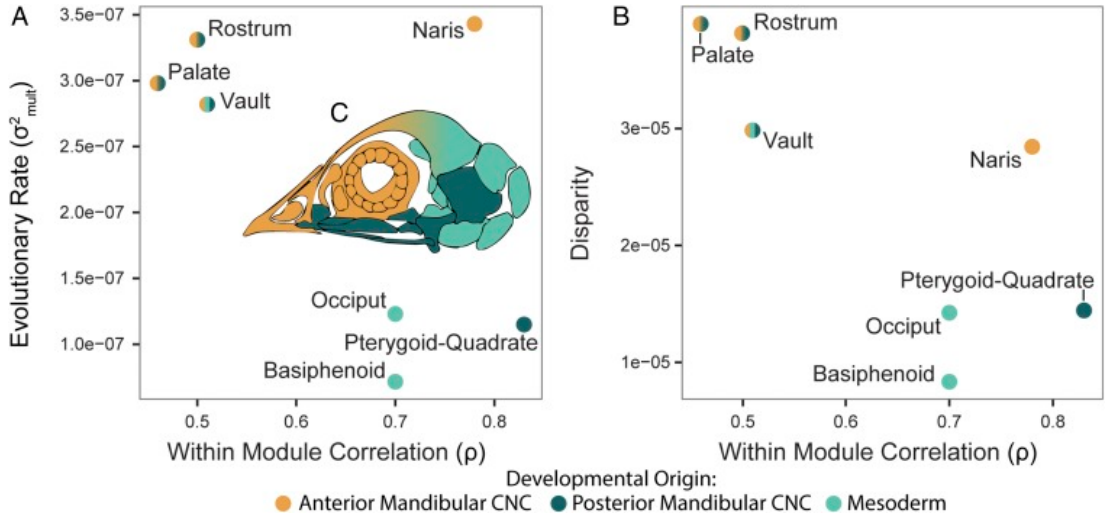
SEE COMMENTARY

Mosaic evolution, which results from multiple influences shaping genes. For example, manipulating the expression of *Fgf8* generates



PNAS

Evolutionary mode routinely varies among morphological traits within fossil species lineages

Melanie J. Hopkins[a,b,1] and Scott Lidgard[a]

[a]Department of Geology, Field Museum of Natural History, Chicago, IL 60605; and [b]Museum für Naturkunde, Leibniz Institute for Research on Evolution and Biodiversity at the Humboldt University Berlin, 10115 Berlin, Germany

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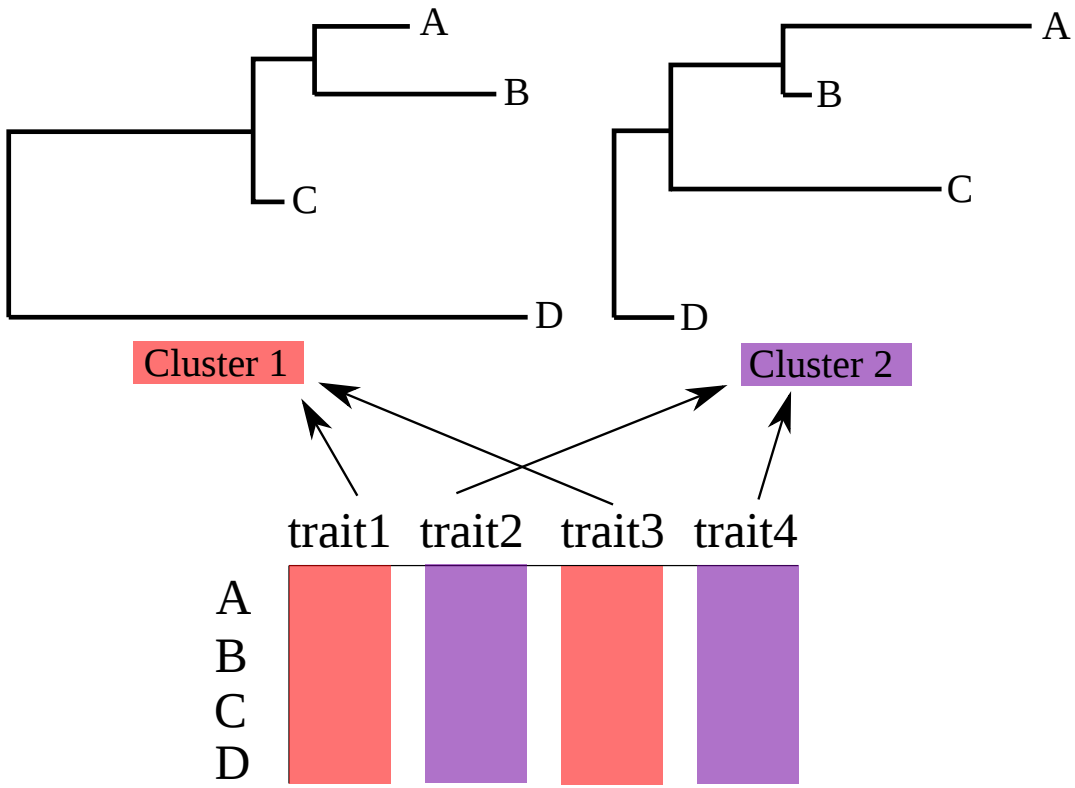
Recent studies have revitalized interest in methods for detecting evolutionary modes in both fossil sequences and phylogenies. seen in the overall species morphology captured in discriminant analysis of the same set of traits. It is notable that these traits

Mosaic evolution

- Mosaic evolution treats suites of traits as modules
- Previous studies statistically test known hypothetical modules
- Might want to discover new modules

Recast as a (phylogenetic) clustering problem:

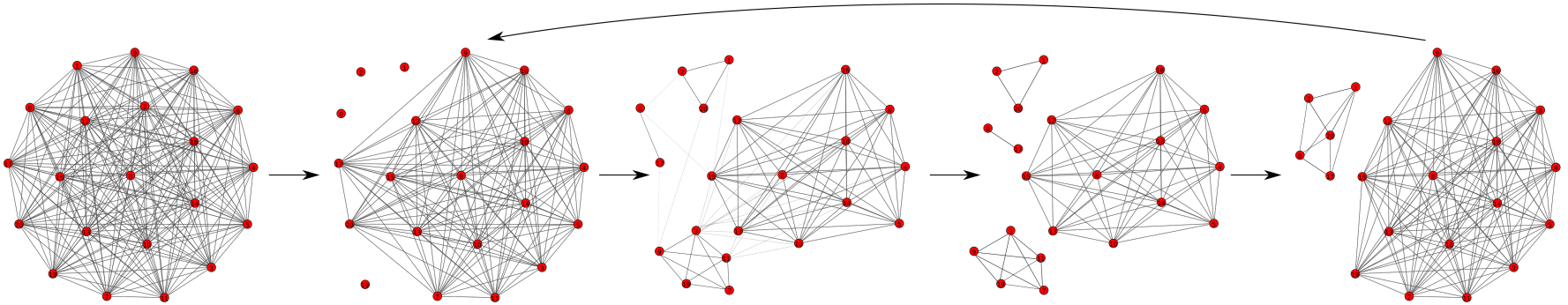
- Clusters as modules
- Each module is defined by a model
- Model = tree with branch lengths



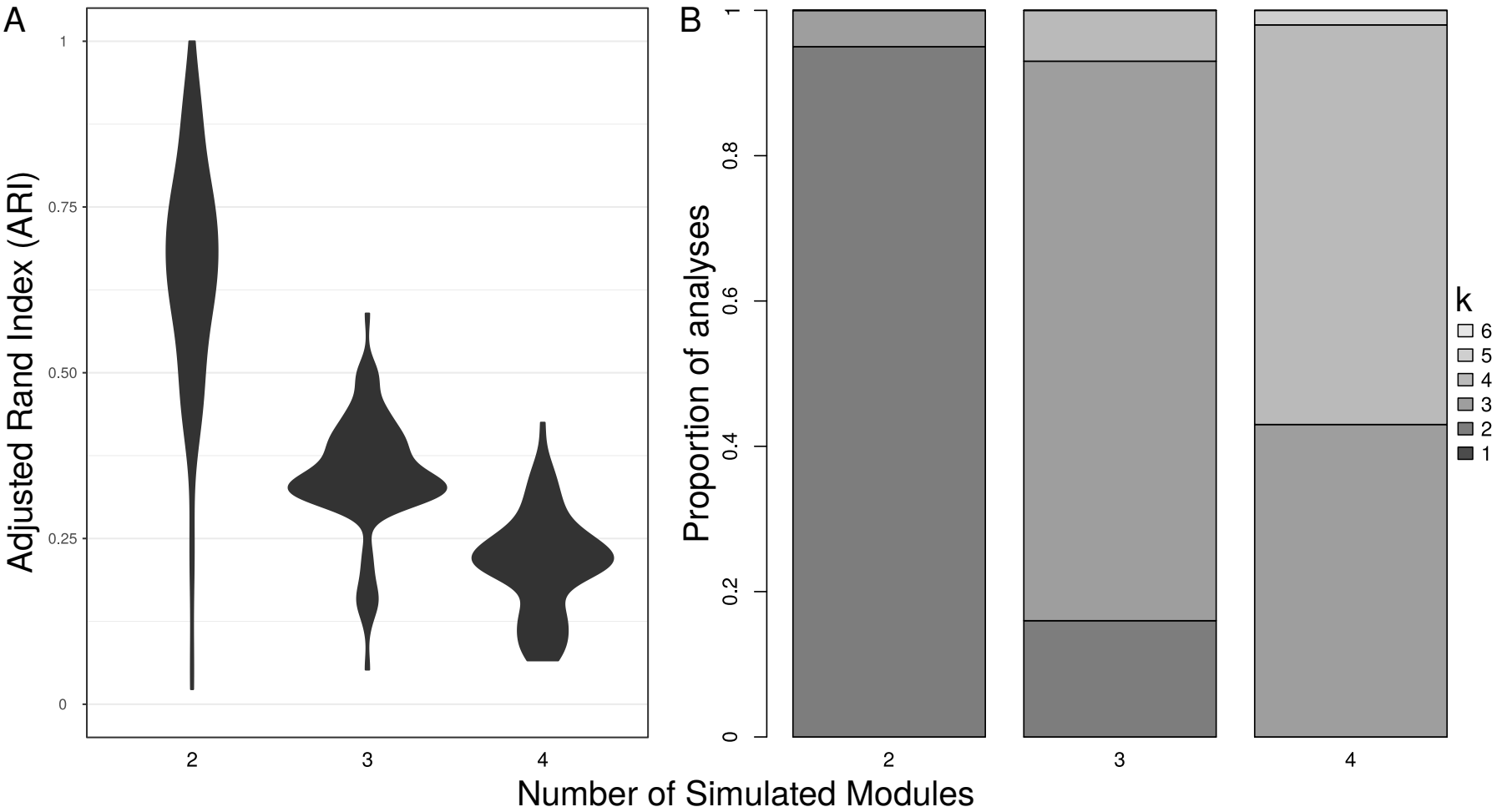
Algorithm

Parametric unsupervised learning of evolutionary modules

- Greedy heuristic search of module space using AIC/BIC
- Iterative merging and splitting
- Implemented in Golang program *greedo*



Simulations perform pretty well



Search Limitations

- Method performs very well when # of components (K) are small
- Performs passably well as K increases, but accuracy decreases a lot
- Heuristic search is limited (gets stuck)– solutions?
  - genetic algorithms?

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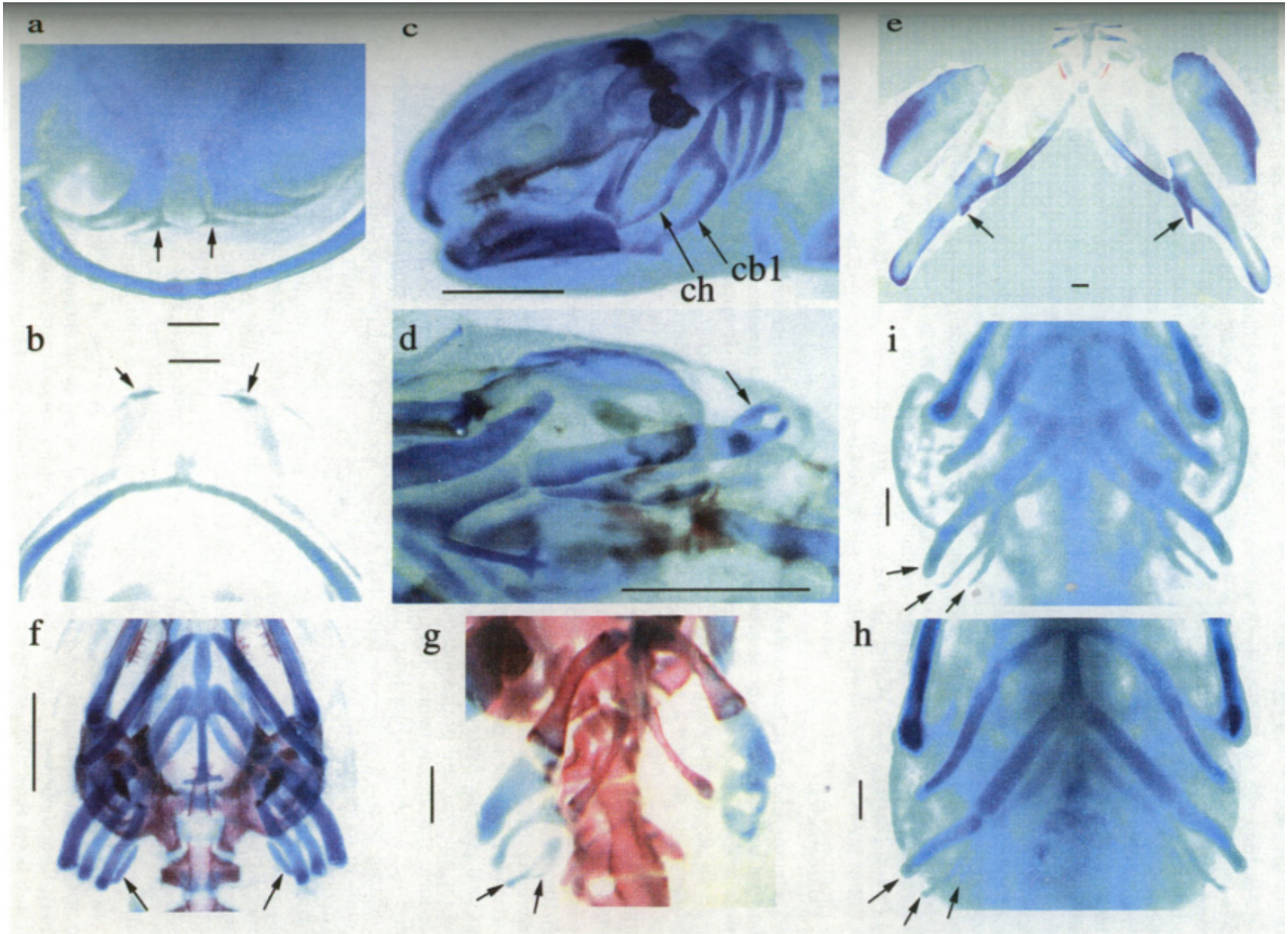
  - genetic algorithms?
  - simulated annealing?
  - **random restarts + model averaging**

Amphibian Skull Development



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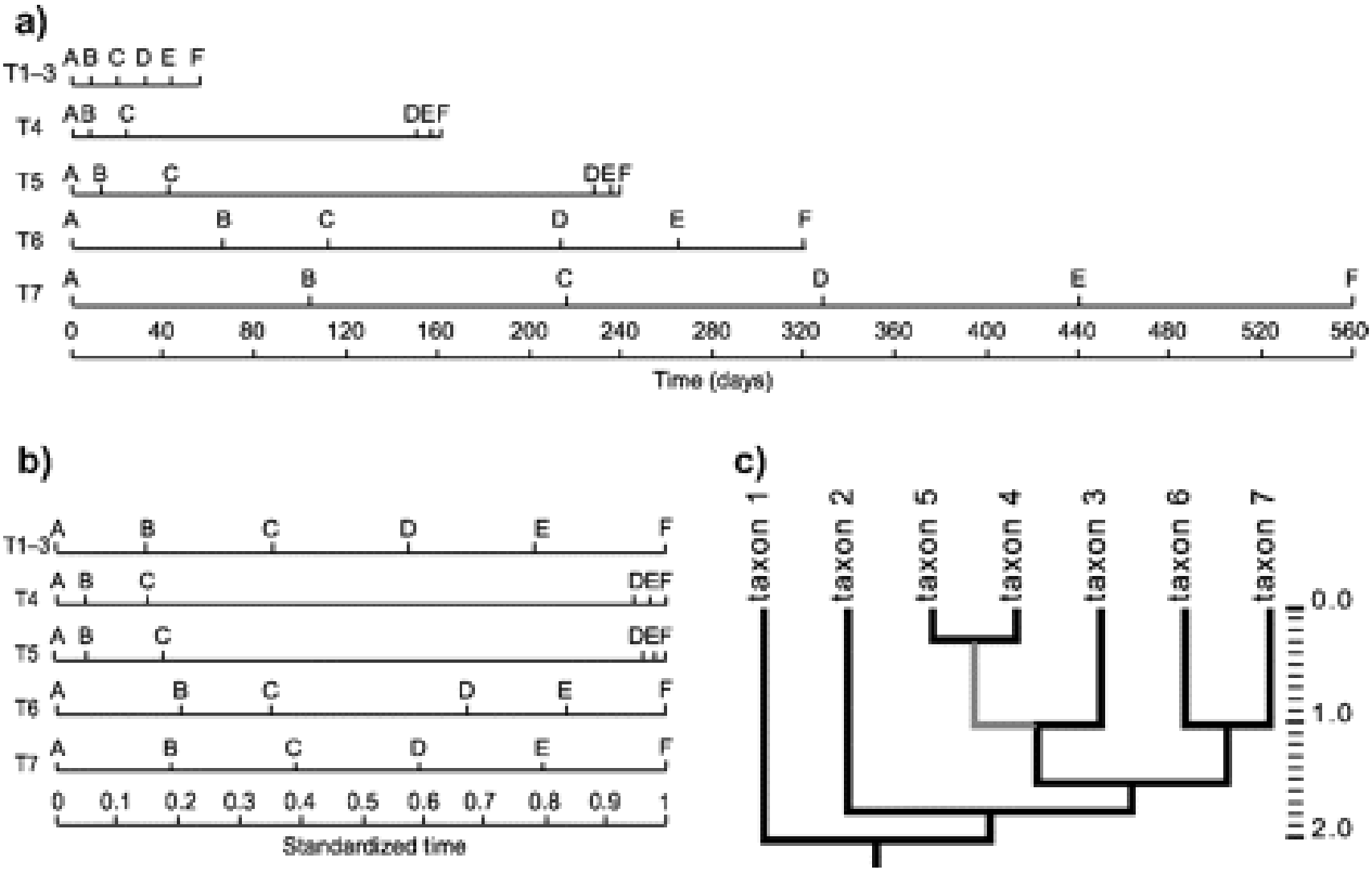
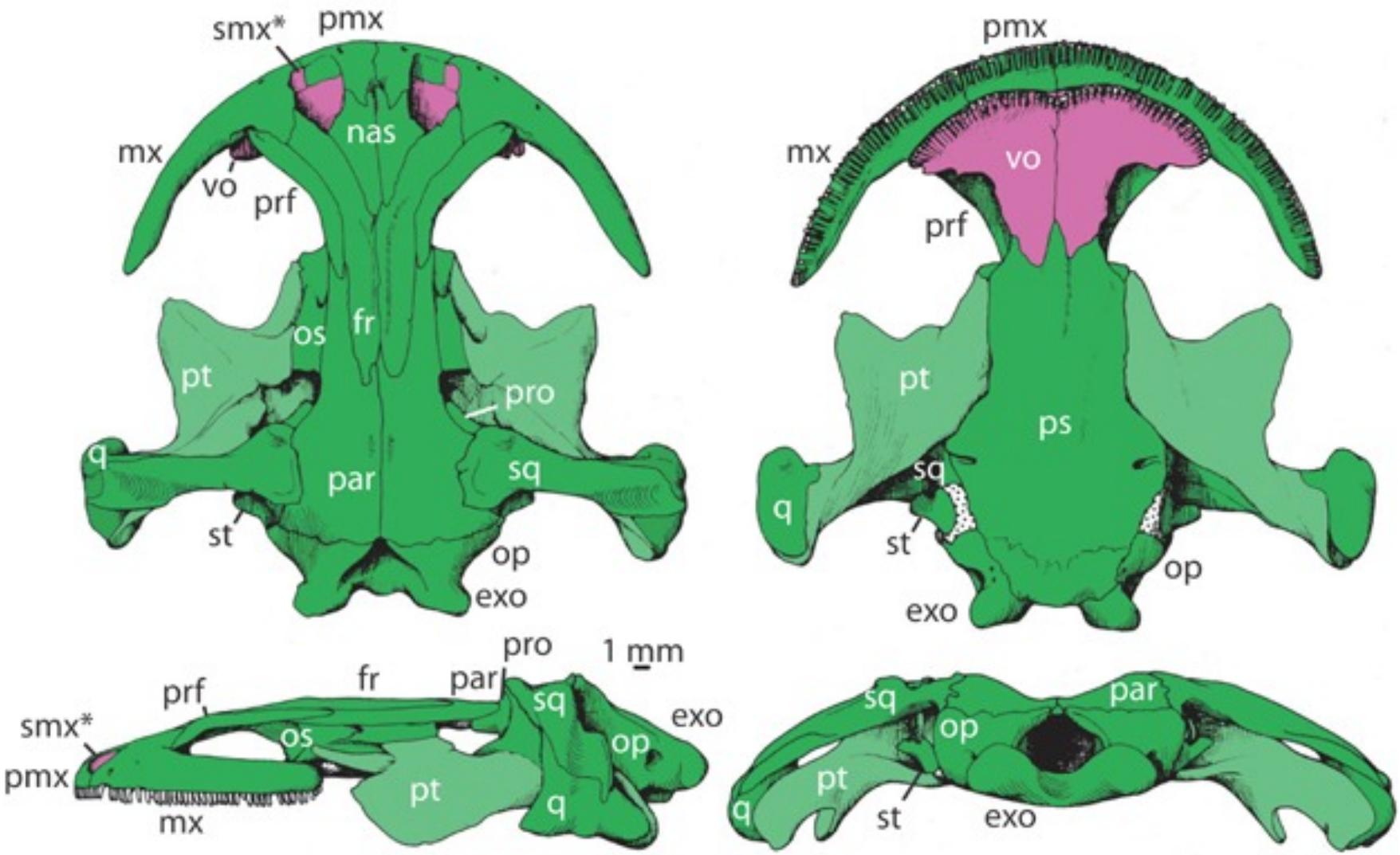


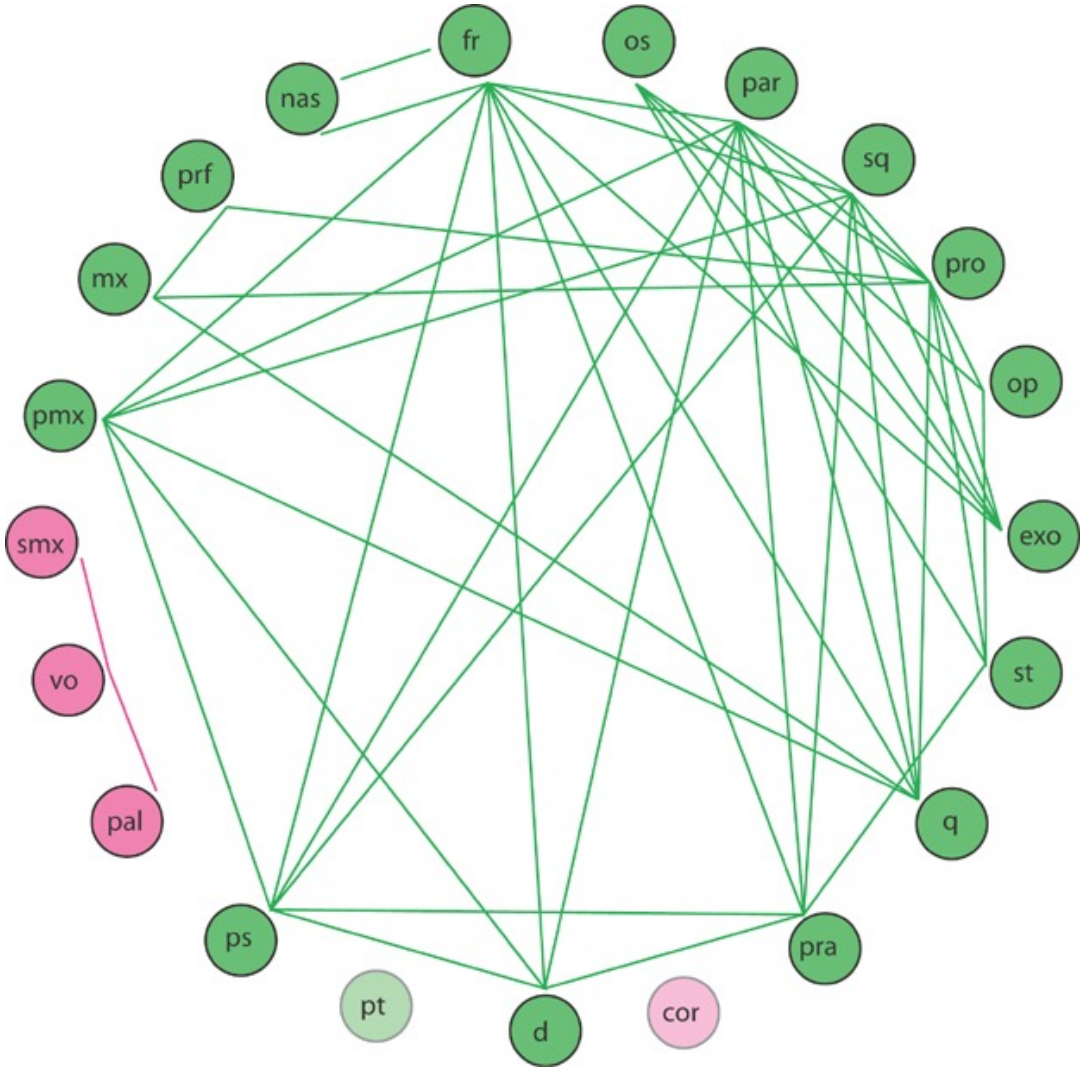
Continuous recodings of developmental sequences in phylogenetics (Laurin and Germain 2009, 2011)

Amphibian Skull Development



Lissamphibian skull development has previously been analyzed for modularity using PCA (Laurin 2014)

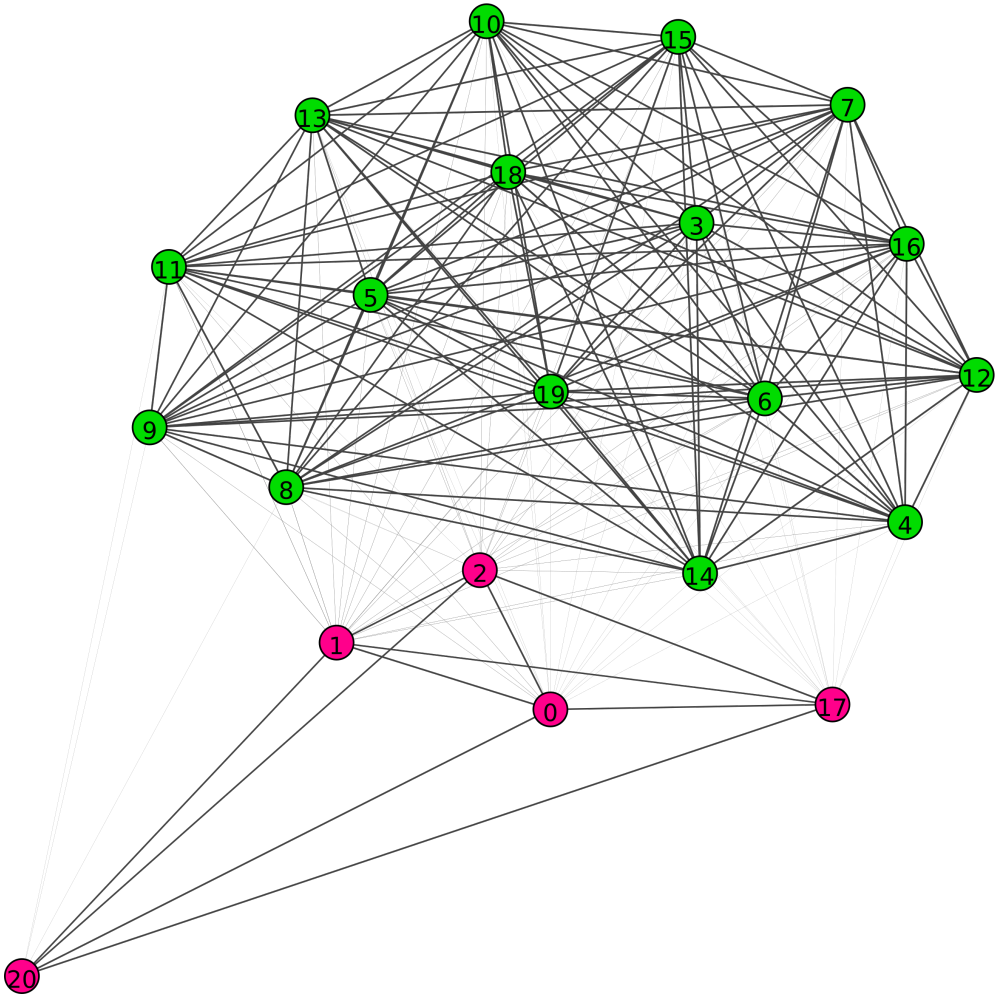
Amphibian Skull Development



Laurin 2014

Amphibian Skull Development

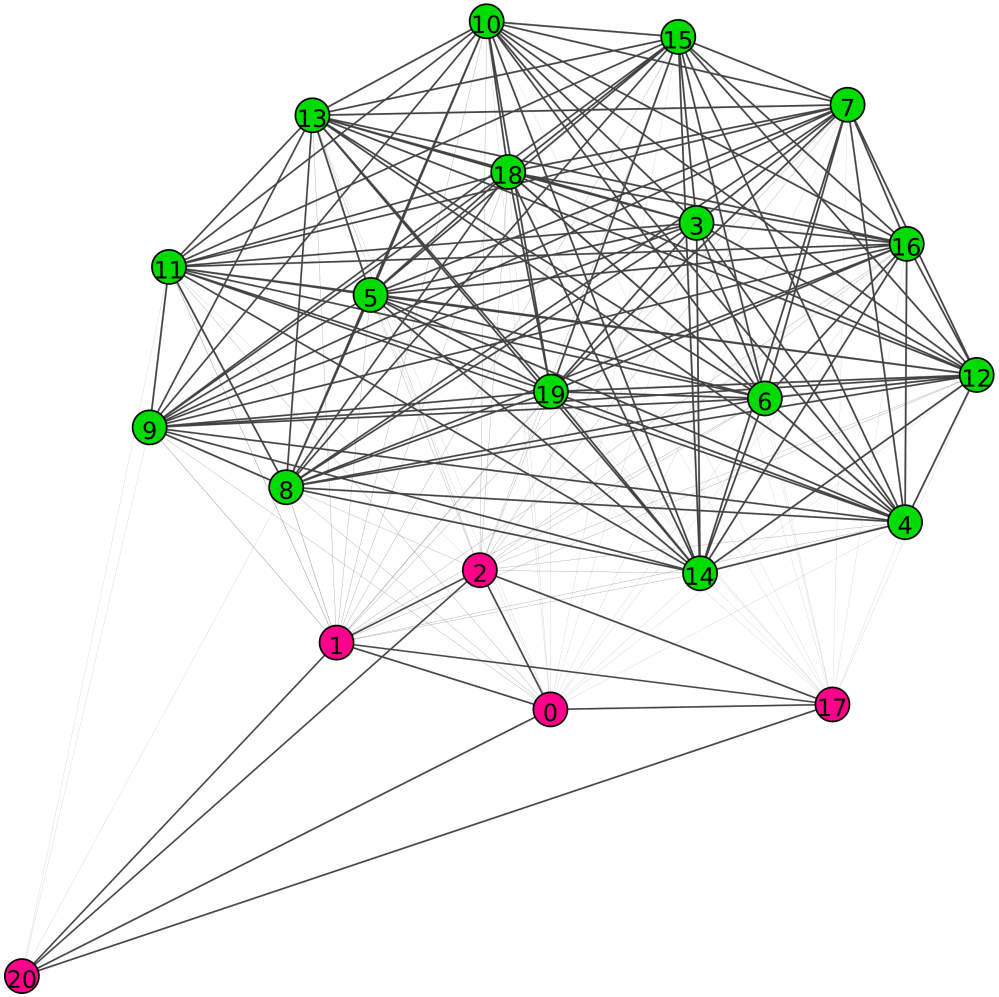
- Want to recapitulate Laurin's result
- Module assignment differs from Laurin's slightly



Amphibian Skull Development

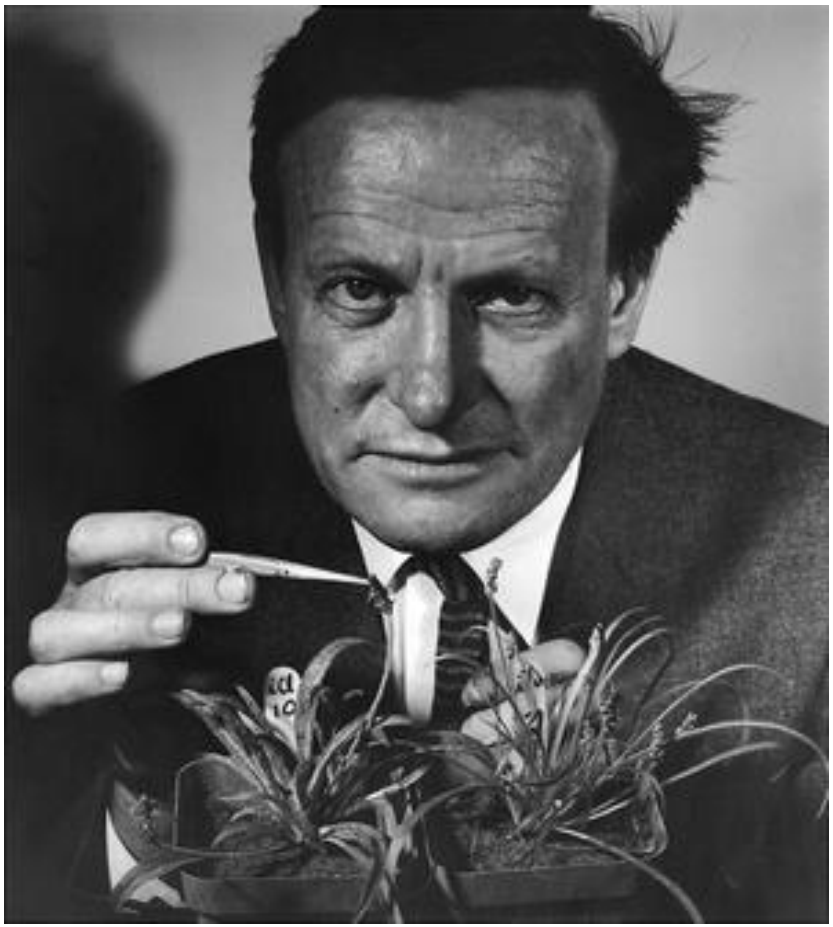
Different questions between two approaches:

- Laurin is examining statistical covariance
- *greedo* explicitly models shared evolutionary patterns



Vitaceae morphology

- Mosaic evolution in angiosperms is an old, under-explored idea
- Stebbins spent much of his later years working on this (Stebbins 1983, 1984)

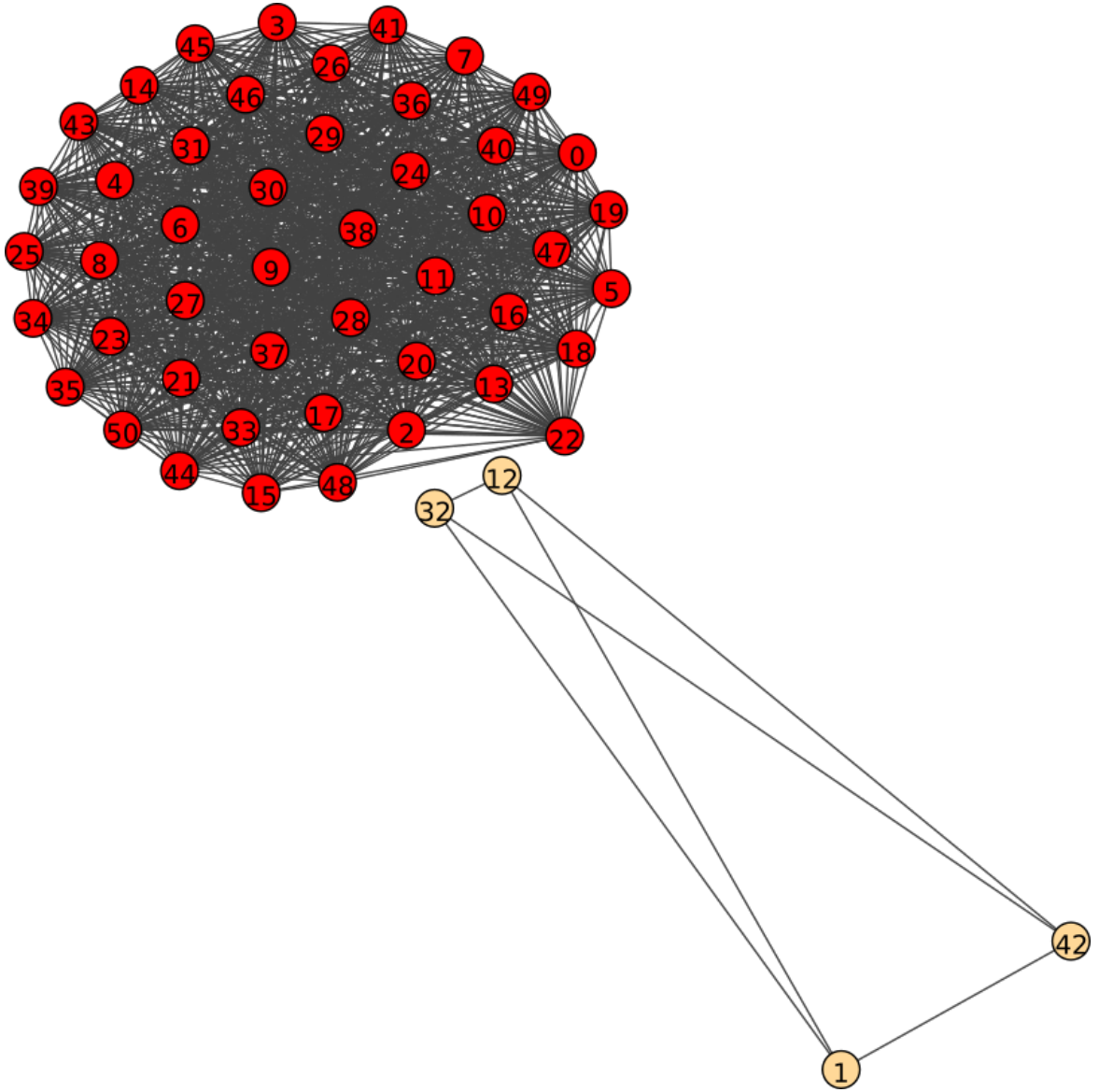


Vitaceae morphology

- Test for mosaic evolutionary dynamics in Vitaceae (grapes)
- Dataset of 52 continuous reproductive traits (Chen 2009)
- Living and fossil taxa




Vitaceae morphology



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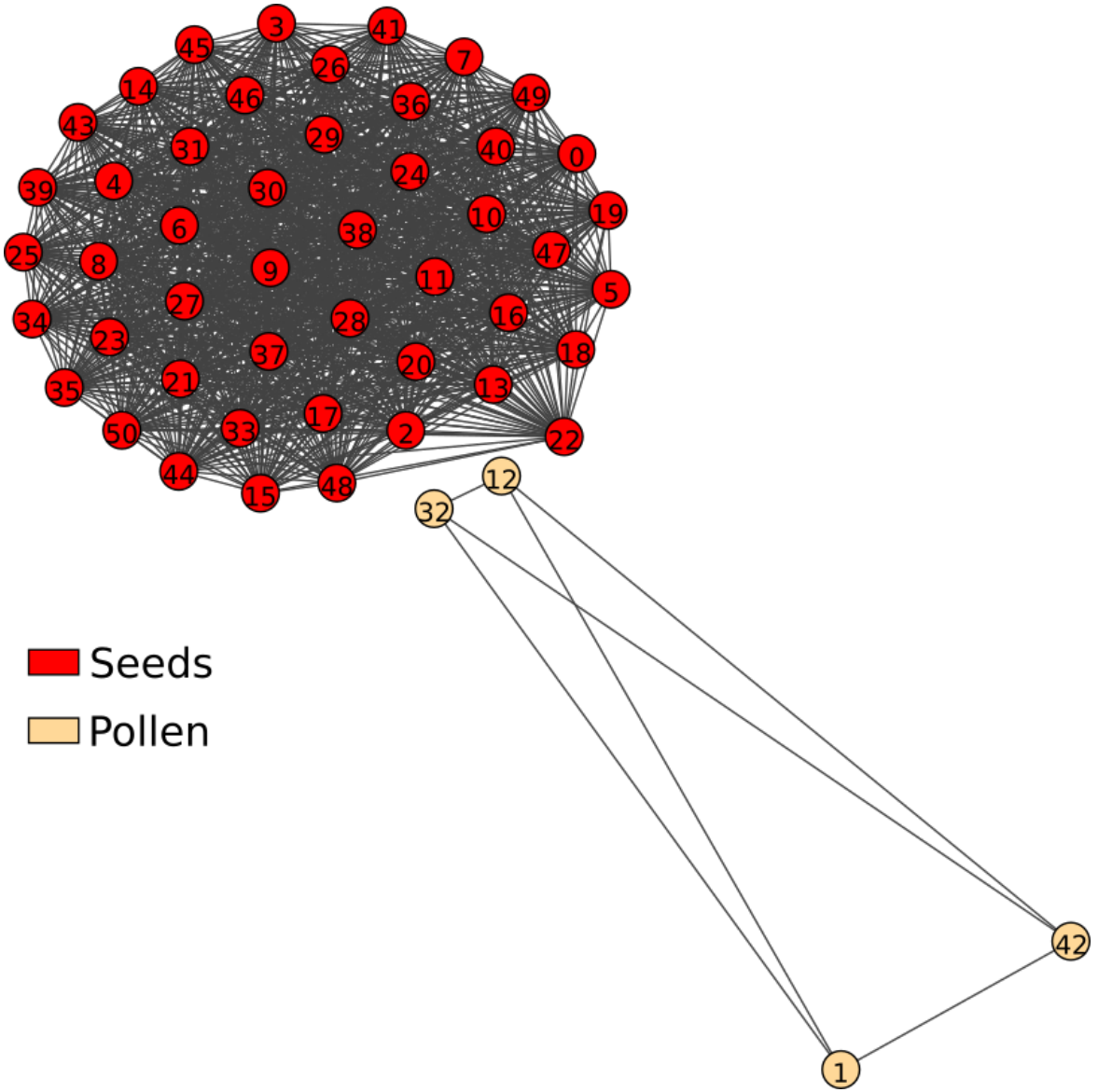
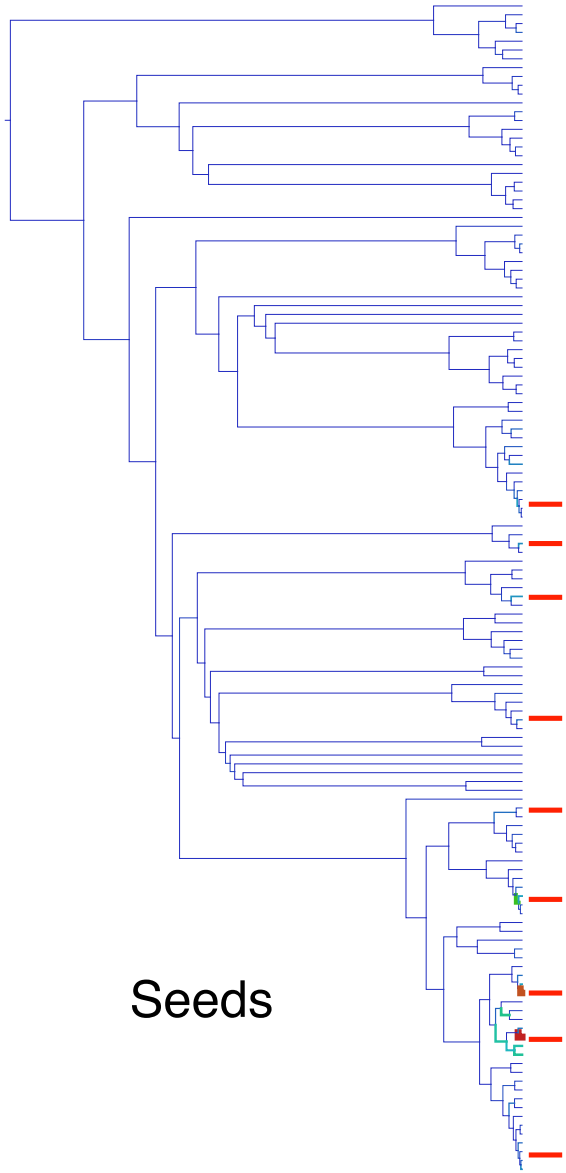
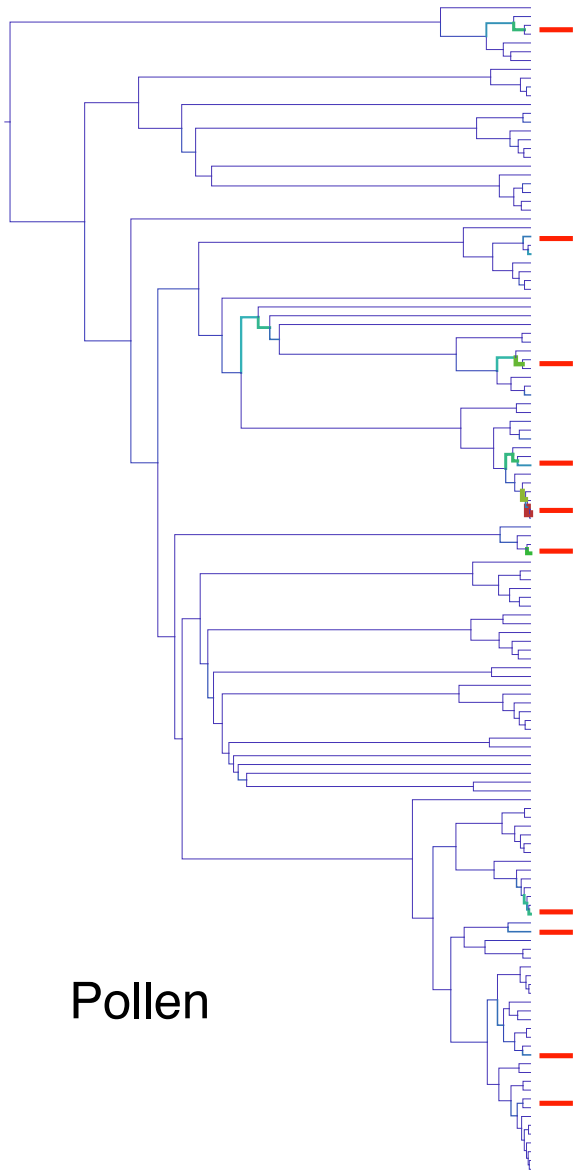


Vitaceae morphology





Vitacaceae morphology

- Mosaic reproductive evolution in grapes
- Environmental and genomic drivers?
- Changes in modularity through time?

Future applications

- Gene expression?
- Phylogenetic reconstruction?

Acknowledgements

- Greg Stull
- Michel Laurin
- Stacey Smith
- Chris Dick

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