Phylogenetic Biology
Week 13

Biology 1425

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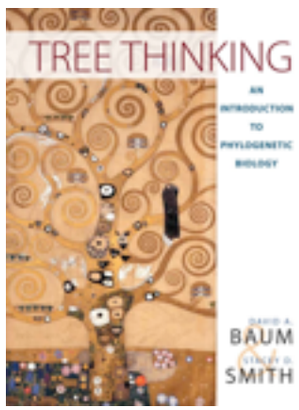
Brown University

2013

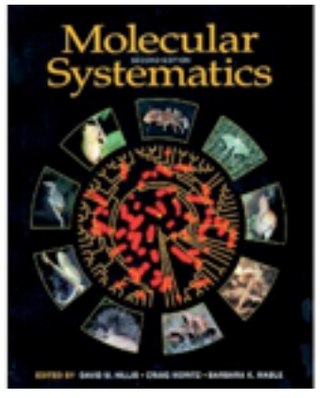
Front matter...

Sources

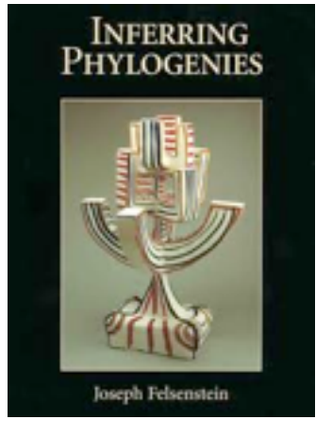
Some non-original content is drawn from:



Baum, D and S. Smith (2012) Tree Thinking: and Introduction to Phylogenetic Biology. Roberts and Company Publishers. ISBN 9781936221165



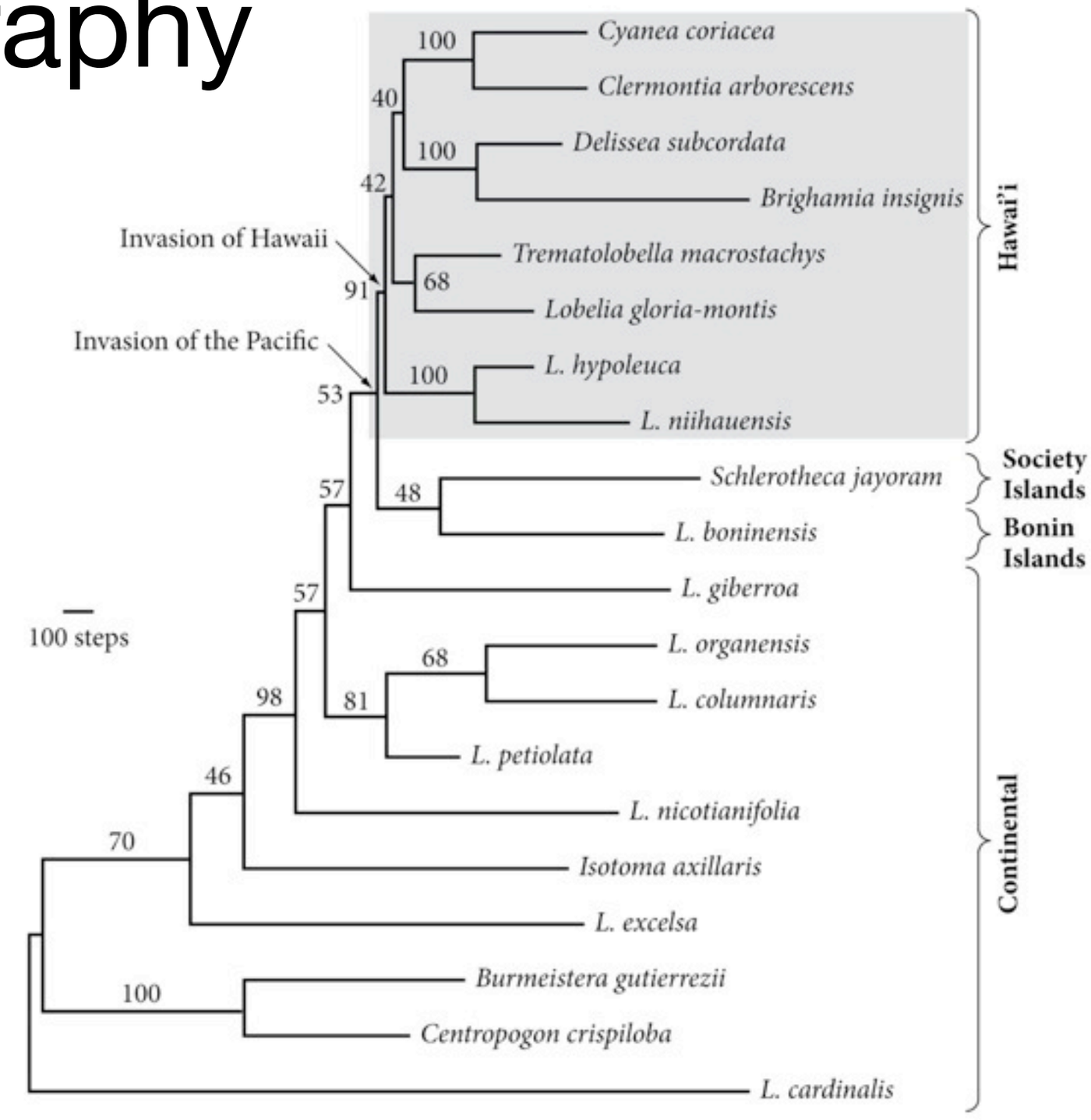
Swofford, D. L., Olsen, G. J., Waddell, P. J., & Hillis, D. M. (1996). Phylogenetic inference. In: Molecular Systematics, Second Edition. eds: D. M. Hillis, C Moritz, & B. K. Mable. Sinauer Associates. ISBN 9780878932825



Felsenstein, J. (2003) Inferring Phylogenies. Sinauer Associates. ISBN 978-0878931774

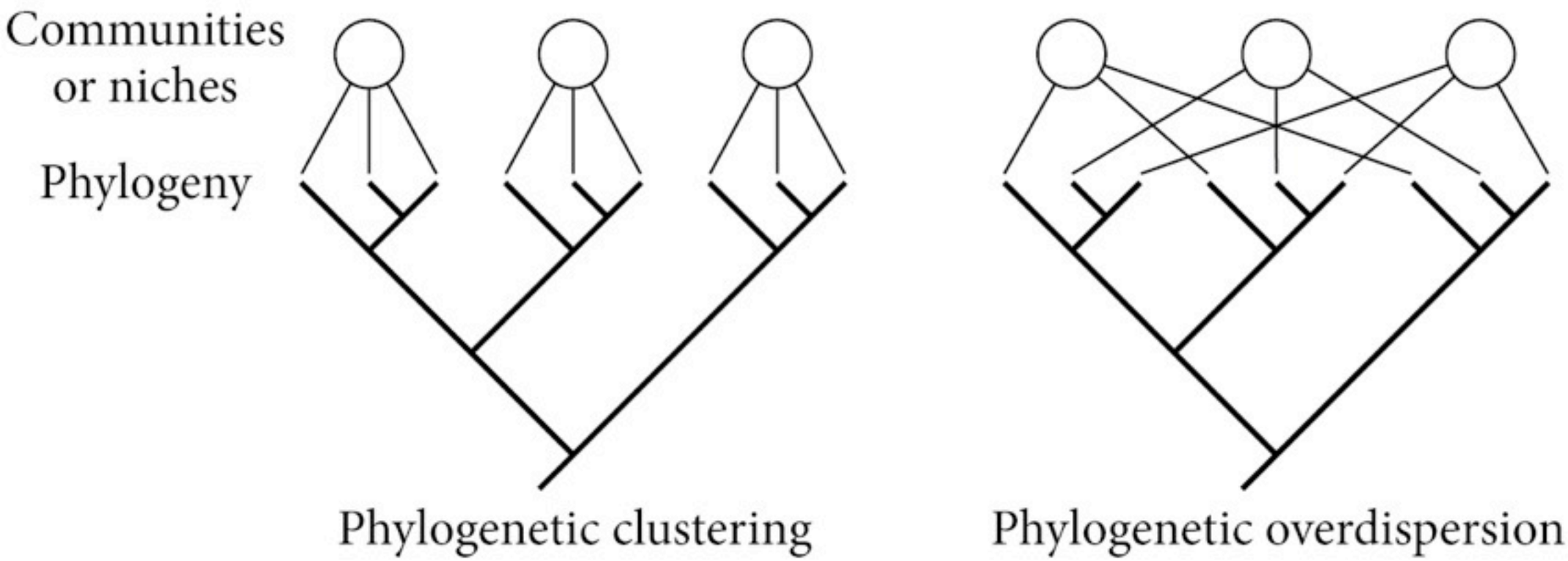
Other non-original content is referenced by url.

Phylogenies in community biogeography



Baum and Smith 2012, Figure 11.1

Phylogenies in community ecology



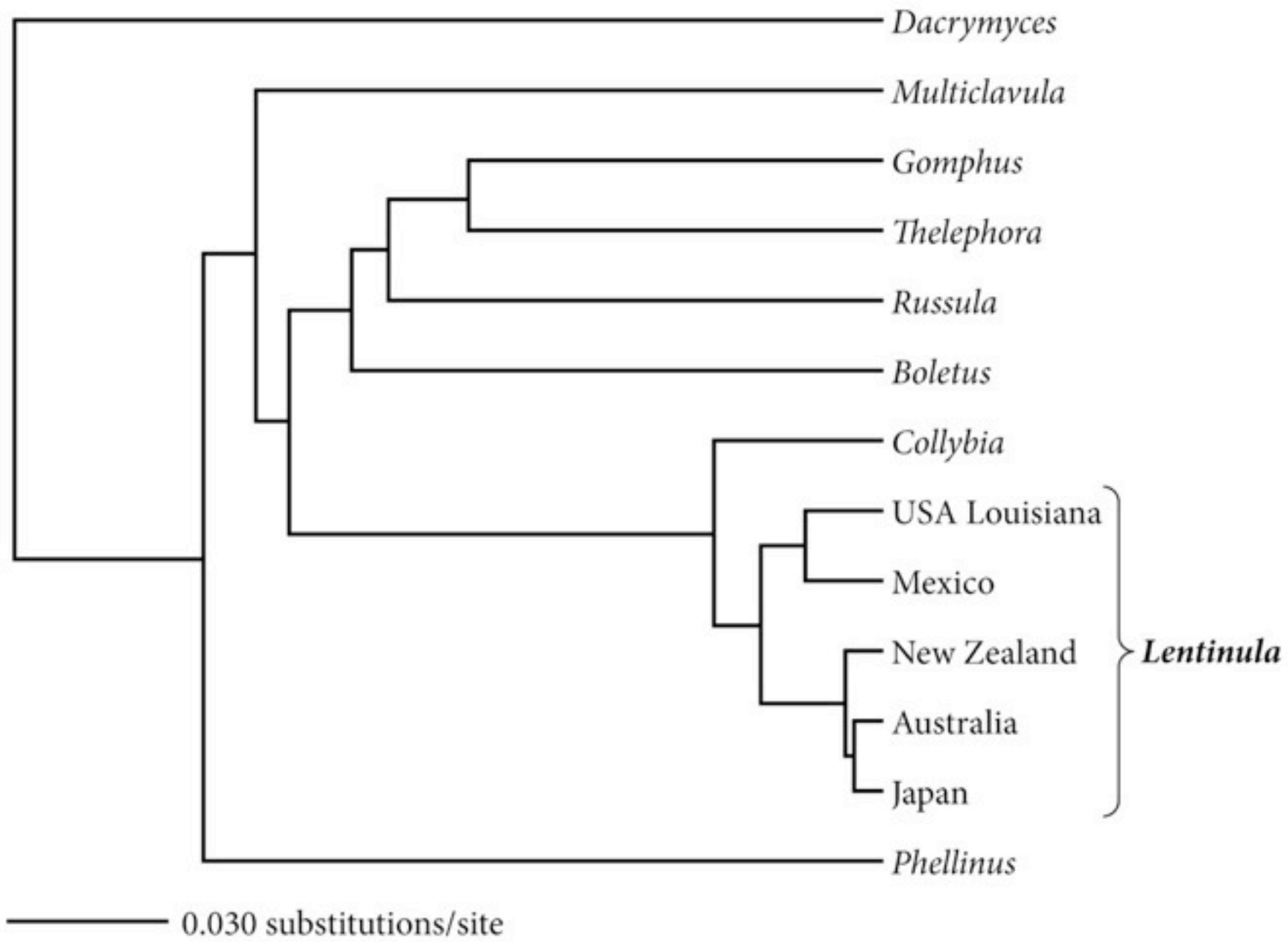
Baum and Smith 2012, Figure 11.9

When searching for a tree under a molecular clock, can just apply the additional constraint that the tree is ultrametric.

Clock models use node depth as a parameter, there are n-1 internal nodes.

Non-clock models use branch length as a parameter. There are 2n-3 branches

So clock models are actually simpler.



Baum and Smith 2012, Figure 11.13

Clock models are often found to be violated - there really are changes in rates.

Relaxed clock models can accommodate these rate changes.

To determine actual node ages, need fossils...