Phylogenetic Biology Week 13

Biology 1425
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Front matter...

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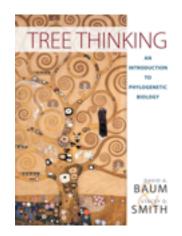


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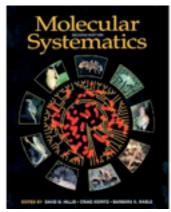
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Sources

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



INFERRING PHYLOGENIES

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

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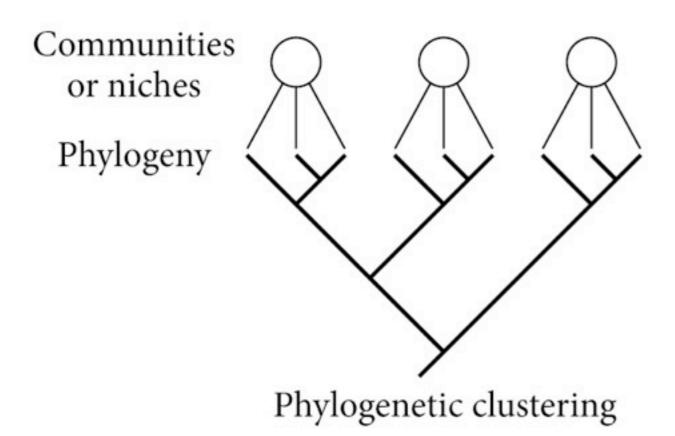
Phylogenies in community biogeography Cyanea coriacea 100 Clermontia arborescens Delissea subcordata Brighamia insignis Invasion of Hawaii Trematolobella macrostachys Lobelia gloria-montis Invasion of the Pacific L. hypoleuca 100 53 L. niihauensis Society Schlerotheca jayoram Islands 57 Bonin L. boninensis Islands L. giberroa 100 steps L. organensis 68 98 L. columnaris 81 L. petiolata 46 Continental L. nicotianifolia 70 Isotoma axillaris L. excelsa Burmeistera gutierrezii 100

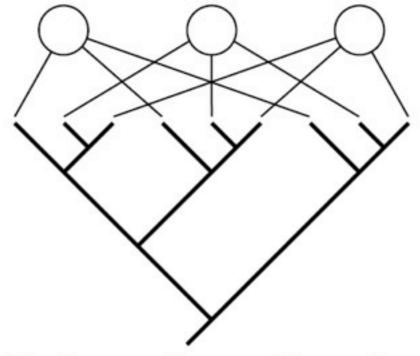
Centropogon crispiloba

L. cardinalis

Baum and Smith 2012, Figure 11.1

Phylogenies in community ecology





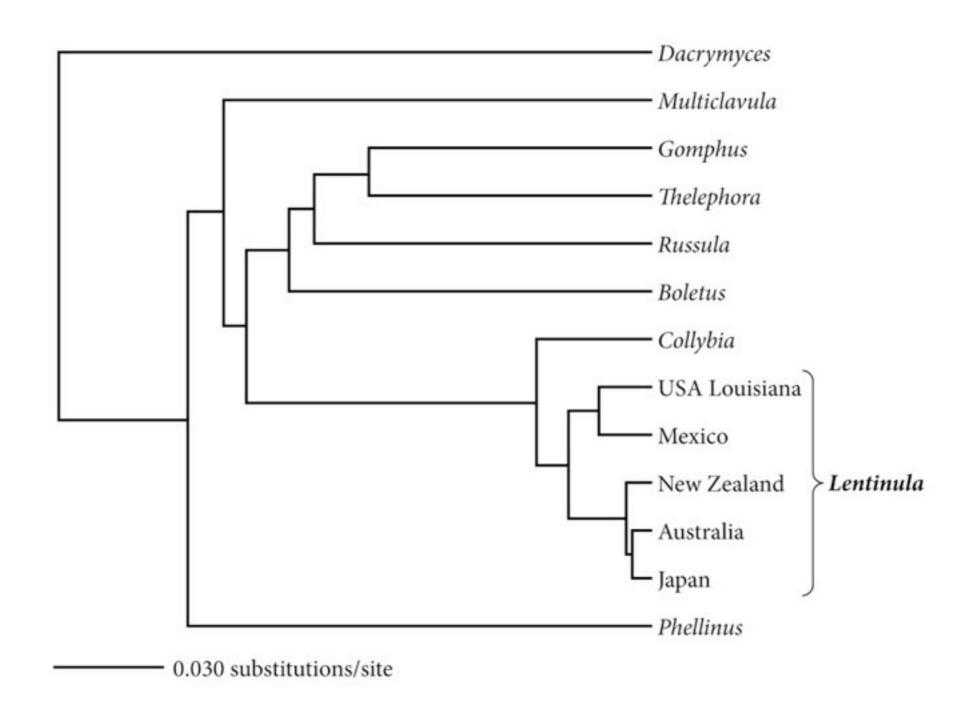
Phylogenetic overdispersion

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...