Seminar/Talk

Phylogenomics and the Procrustean bed of the species tree

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Phylogenomics has largely succeeded in its aim of accurately inferring species trees, even when there are high levels of discordance among individual gene trees. These resolved species trees can be used to ask many questions about trait evolution, including the direction of change and number of times traits have evolved. However, the mapping of traits onto trees generally uses only a single representation of the species tree, ignoring variation in the gene trees used to construct it. Recognizing that genes underlie traits, these results imply that many traits follow topologies that are discordant with the species topology. As a consequence, standard methods for character mapping will incorrectly infer the number of times a trait has evolved. In this talk I give examples from our work on wild tomatoes, bats, and mosquitoes of how discordant genealogies can lead to misleading inferences about the frequency of convergent evolution.

Wednesday, May 17, 2017 12:30pm - 01:30pm

I22 Lakeside View (I22.01)

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