



Mathematical Biology Seminar



Monday, September 27, 2010

3 pm – 657 CAB

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Inferring the past for traits that alter speciation and extinction rates

I will describe BiSSE, a likelihood-based approach to infer how speciation and extinction rates depend on the state of a particular character. The phylogenetic tree of a group of species contains information about character transitions and about diversification: higher speciation rates, for example, give rise to shorter branch lengths. The likelihood method that we have developed uses the information contained in a phylogeny and integrates over all possible evolutionary histories to infer the speciation and extinction rates for species with different character states. Our method can be used to provide more detailed information than previous methods, allowing us to disentangle whether a particular character state is rare because species in that state are prone to extinction, are unlikely to speciate, or tend to move out of that state faster than they move in.

Join us for refreshments in CAB 549 immediately following the Seminar