

Assessing co-evolution among discrete traits.



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Co-occurring evolutionary events usually point to complex adaptive phenomena, sometimes implicating epistasis. While a number of methods have been developed to account for co-occurrences of events on the same branch of an evolutionary tree, there is a need to account for the larger diversity of possible relative positions of events in a tree. We propose a method to quantify to what extent two or more evolutionary events are associated on a phylogenetic tree. The method is applicable to any discrete character, like substitutions, anatomical modifications or any gains/losses/changes of a biological function. Our method uses a general approach to statistically test for significant associations between events along the tree, which encompasses both co-occurrences in the same branch, and chronologies in different branches. We address this problem using two different complementary methods: a moment-based method and a likelihood framework. The strengths and weaknesses of the methods were assessed via simulated controlled scenarii. We illustrated the versatility of the approach on two biological cases: the loss of cell motility in intracellular pathogens and the coevolution of nucleotides in the bacterial 16S RNA.