

Phylogenetic approaches to understanding the evolution of genome function

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There is considerable interest in comparing functional genomic data across species. One goal of such work is to provide an integrated understanding of genome and phenotype evolution. Most comparative functional genomic studies have relied on multiple pairwise comparisons between species, an approach that does not incorporate information about the evolutionary relationships among species. The statistical problems that arise from not considering these relationships can lead pairwise approaches to the wrong conclusions, and are a missed opportunity to learn about biology that can only be understood in an explicit phylogenetic context. Our recent phylogenetic reanalyses of comparative functional genomics studies that were originally based on pairwise comparisons concretely demonstrate the inadequacy of pairwise comparisons for analyzing functional genomic data across species. It will be critical to adopt phylogenetic comparative methods in future functional genomic work. Fortunately, phylogenetic comparative biology is also a rapidly advancing field with many methods that can be directly applied to functional genomic data.