

Phylogenetic inferences in identifying the ancestral version of paralogs

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Abstract

Predicting common functionality between homologous genes/proteins has been a crucial effort for many biological studies. On the basis of general orthology conjecture, functions of orthologous proteins are likely to be closer to each other relative to of paralogs. On the other hand, extensive gene duplications and losses give rise to complex evolutionary patterns limiting our ability to interpret function-wise comparisons. Especially within co-orthologs, relationships cannot be specified further as lineage-specific events are independent of the neighboring clades. However, if a gene was essential for ancestral fitness, after duplication, one of the paralogs tends to remain preserved while the other copy often diverges. Here, I propose phylogeny-based methods to identify, if exists, the common ancestral version of paralogs with the aim of delineating functional equivalence between co-orthologous proteins.

References
