IntronBase: A new resource for mining gene structure of orthologous genes from nine metazoa.

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Today there are many species for which a fully sequenced genome is available, and a wide range of approaches and algorithms to compare these genome sequence have been developed. The identification of clusters of othologous genes, for example, has turned out to be an important component of many comparative genome analyses. When integrated with additional information such as gene structure, e.g. the exon-intron structure, sets of orthologs can be a powerful resource for research in biology and evolution.

IntronBase combines this information for 447 clusters of orthologous genes from nine metazoan species. For each of the gene clusters, it provides information about exon-intron structure of all family members, as well as their intron sequences and flanking exon sequences.

Genes of interest can be searched by their corresponding protein ID or using GeneOntology IDs. It is also possible to search for introns or clusters based on taxon representation. IntronBase was recently used to evaluate the phyolgenetic signal in the gene structure of the nine taxa by Hill *et al*.

IntronBase can be used via the internet at http://bioinformatics.uni-potsdam.de/projects/intronbase or installed locally.

References:

Hill *et al.*, Analysis of phylogenetic signal in protostomal intron patterns using Mutual Information; under review