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Evolution of eukaryotic gene structures

真核生物遺伝子構造の進化

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Genes on eukaryotic genomes are usually composed of multiple exons between which introns intervene. Computational prediction of exon-intron structures of genes from their genomic DNA sequences has been a long-standing problem, but even the most advanced gene-prediction pipelines still suffer from considerable amount of miss-predictions. We have recently developed a novel tool that can dramatically improve the accuracy of gene-structure prediction, where gene-structure-aware multiple protein sequence alignment (GSA-MPSA) of homologous (orthologous and paralogous) genes plays a crucial role. Evolutionary history of intron gains and losses inferred from the observed GSA-MPSAs will be discussed based on our results on two different categories of genes, a multiple gene superfamily and basically unique gene families.

Keywords: gene structure, evolution, exon theory, alternative splicing, gene prediction

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