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Gene structure prediction by transcript mapping and multiple sequence alignment

転写産物マッピングと多重配列アラインメントによる遺伝子構造予測

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Multiple sequence alignment (MSA) and gene structure prediction have been major research themes in bioinformatics. Today, MSA plays central roles in predictive research on many areas, including higher-order structural prediction of proteins and RNAs, prediction of functional sites in proteins, DNAs and RNAs, and phylogenetic analyses. However, MSA has not been seriously used so far in relation to gene structure prediction. In the first half of the lecture, I will quickly review current status of the methods for MSA and gene prediction. The second half will be devoted to our on-going study that tries to combine these two areas to access and improve the quality of gene prediction. Some results obtained from real data will be presented.

Keywords: Gene structure prediction, splicing, multiple sequence alignment, genome mapping, new generation sequencer