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Multiple sequence alignment and evolutionary analysis

多重配列アラインメントと進化解析

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Multiple sequence alignment (MSA) enables the inference of correspondences of residues in three or more biological sequences that share an evolutionary history. In this lecture I will explain several MSA methods implemented in the MAFFT multiple sequence alignment program. MSA has a wide range of applications in bioinformatics analysis, such as function prediction, structure prediction and organismal classification. As a representative application of MSA, I will discuss phylogenetic tree inference and the interpretation of such a tree, using the opsin gene family as an example. A web-based tool, aLeaves, which can be used to prepare a biologically relevant dataset from animal genomes will also be introduced.

Keywords: Sequence analysis, Progressive method, Iterative refinement method, Phylogenetic tree