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Coarse-grained approaches for fast and memory-efficient comparison of biological sequences

粗視化に基づく配列比較の高速化と省スペース化

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Coarse graining is a well-known technique in the fields of image processing and structural analysis of biological macromolecules. Usually, this technique is employed when conventional method is too expensive in terms of computation time and/or memory. Although coarse-grained approaches have rarely been adopted in biological sequence analysis, such approaches might be useful to facilitate the analysis of the rapidly growing massive sequence data. In this lecture, I will discuss two cases in which coarse graining techniques may considerably improve the throughput of sequence analysis, i.e. fast similarity search and pairwise alignment of whole genomic sequences.

Keywords : Sequence comparison, coarse-grained approach, alignment, genome mapping, comparative genomics