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Title:

A method to improve the performance of gene alignment

Abstract:

BLAST is the most popular algorithm for gene alignment. The technique for gene alignment is used to measure how similar two DNA sequences are. Thus, it is very important for genetics or for studying the evolution of organisms. However, the performance of BLAST is usually limited by the size of RAM of the CPU if the lengths of DNA sequences are too long. Thus, we develop a method to lower the memory usage in order to improve the performance of BLAST. Meanwhile, the method is also much more efficient than the old BLAST algorithm. In this talk, I will give a short brief about gene alignment and BLAST. Then, I will give an introduction to our method.