

Abstract

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Multiple sequence alignment using massively parallel mathematics of arrays.

The aim of this research is to investigate the potential of the Mathematics of Arrays (MoA) partitioning scheme in high dimensional scientific computational problems, such as Multiple Sequence Alignment (MSA) in Computational Biology. This work aims to deliver a unified partitioning scheme that works invariant of the dataset shape (dimension and lengths), and is portable among different high performance machines, cluster architectures, and potentially Grids.