

# New High Performance Solutions for the Multiple Genetic Sequence Alignment Problem

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**Abstract**—The main goal of this PhD work is to propose and evaluate a novel multiple sequence alignment algorithm that obtains accurate results, in computationally reasonable times, for the alignment of hundreds of sequences of sizes that can reach thousands of bases, genes or proteins. As part of this investigation, parallelization techniques must be identified that exploit the characteristics of parallel computing architecture models currently available nowadays and in the near future.

