Exploring MPI-Based Parallel Computing in Analyzing Very Large Sequences

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Abstract : The health industry is aiming towards personalized medicine. If the patient's genome needs to be sequenced it is important that the entire analysis be completed quickly. This paper explores use of parallel computing to analyze very large sequences. Two cases have been considered. In the first case, the sequence is kept constant and the effect of increasing the number of MPI-based processes is evaluated in terms of execution time, speed and efficiency. In the second case the number of MPI-based processes have been kept constant whereas, the length of the sequence was increased.