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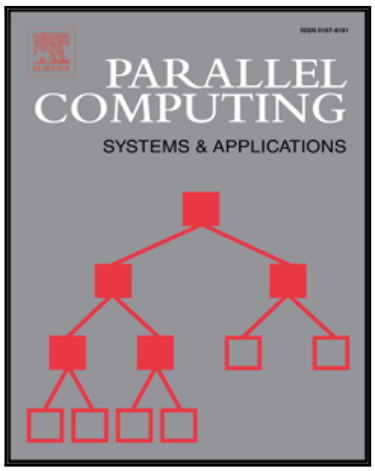

Searching for common patterns on protein sequences by means of a parallel hybrid Honey-Bee Mating Optimization algorithm

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Highlights

- A hybrid (OpenMP/MPI) parallel multiobjective approach based on HBMO is proposed.
- We use as benchmark an important bioinformatics problem, the motif discovery problem.
- We conduct executions by using different number of cores to a maximum of 128 cores.
- Comparisons with parallel biological tools demonstrate the quality of our approach.
- Besides good parallel results, it also makes good biological predictions.

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