Abstract

The BLAST heuristic algorithm is one of the widely used algorithms for finding similar sequences in sequence databases. The paper acquires importance as traditional approaches to sequence homology searches using BLAST have proven to be too slow to keep up with the current rate of sequence acquisition. The use of the BLAST application on a single processor has become too costly, inefficient, and time-consuming for many life science laboratories. An obvious improvement that has already been suggested is the use of database segmentation to speedup BLAST. A two master method to improve the performance of the parallel BLAST algorithm is presented here. It is found that the two master method has performed better than the single master method.

References

Parallel Two Master Method to Improve BLAST Algorithm’s Performance

Sequences". Journal of Molecular Biology, 147, 195-197.

**Index Terms**

- Computer Science
- Parallel Processing

**Keywords**

- Sequence alignment
- BLAST
- Database segment
- Query segment
- Efficiency
- Speedup