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Research Abstract

**Solver for Sparse Symmetric Positive Definite Linear
Equations using Parallel Genetic ordering**

Verma Abhishek

Undergraduate Student (Computer Science)
National Institute of Technology, Tiruchirapalli

Several direct methods have been devised for solving sparse symmetric and positive definite linear systems. Finding an ordering of the matrix to minimize the height of elimination tree is crucial for effectively computing the Cholesky factor on parallel systems. This problem is known to be NP-hard. The height of the elimination tree is an indication of the number of parallel elimination steps. Though many effective heuristics have been proposed, the problems of how good these heuristics are near optimal and how to further reduce the height of elimination tree remain unanswered. This project is an effort to this investigation.

A parallel genetic algorithm customized to optimize this parallel ordering problem is devised. It is characterized by two novel genetic operators, adaptive merge crossover and tree rotation mutation. The genetic algorithm is parallelized in order to utilize high performance of clustered computing and tested on a three node Beowulf cluster.

It has been observed that without seeding a heuristic, the population requires a large number of iterations to evolve into an optimal solution. There is no overhead involved for generating the heuristic. The overhead of generating the heuristic cannot be justified for the improvements achieved presently.

Mentor: *Professor Phalguni Gupta, Department of Computer Science & Engineering*