Multiobjective VLSI Cell Placement using Distributed Genetic Algorithm

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ABSTRACT

Genetic Algorithms have worked fairly well for the VLSI cell placement problem, albeit with significant run times. Two parallel models for GA are presented for VLSI cell placement where the objectives are optimizing power dissipation, timing performance and interconnect wirelength, while layout width is a constraint. A Master-Slave approach is mentioned wherein both fitness calculation and crossover mechanism are distributed among slaves. A Multi-Deme parallel GA is also presented in which each processor works independently on an allocated subpopulation followed by information exchange through migration of chromosomes. A pseudo-diversity approach is taken, wherein similar solutions with the same overall cost values are not permitted in the population at any given time. A series of experiments are performed on ISCAS-85/89 benchmarks to show the performance of the Multi-Deme approach.

Categories and Subject Descriptors

D.1.3 [**Programming Techniques**]: Concurrent Programming—*Parallel programming*

General Terms

Algorithm, Performance

Keywords

Parallel Genetic Algorithms, Cluster Computing, Fuzzy Logic, Genetic Crossover.

1. INTRODUCTION

Genetic Algorithms have been extensively used for solving NP-hard problems such as VLSI cell placement [2, 3]. Parallelization of these algorithms has increasingly become an attractive option for accelerating performance, especially due to the consistent growth in performance to cost ratios of cluster computing environments. Two parallel GA strategies are described here that target the optimization of width-constrained, multi-objective placement.

2. PARALLELIZATION OF GENETIC ALGORITHMS

Prior to developing parallelization strategies, a profiling analysis of the serial GA was carried out to determine computation intensive functions and routines. It was seen that the runtime intensive operations are fitness calculation and the parent crossover. The first parallel model is a 'Global Selection' approach where the population is divided among slave processors, which then carry out individual crossover followed by fitness evaluation of generated offsprings. Selection of the new population is done at the Master, which collects the cumulative offsprings from the slave processors. The performance results of this approach were poor with very low speedup for small circuits. However, with increasing circuit size, which translates into higher complexity and larger search space, there is more potential with distributing the fitness calculation and the crossover. In the case of smaller circuits, any gains achieved by such a distribution would be lost due to communication overheads.

The second approach - the Multi-Deme parallel GA, has often been favored over simplistic data distribution as in the earlier model. In this strategy, the population is distributed among all processors, which independently run their own GA for a predefined number of generations. An extensive study of the parameters governing the performance of this model was done by Cantú-Paz [1]. The pseudo-code of the algorithm is presented in Figure 1.

The initial population constructor runs on the master processor, which then distributes the solutions among all the slave processors. Following this, all nodes, including the root execute the serial GA on their allocated population for a predefined number of iterations called the Migration Frequency (MF). Then each node sends a certain number of its best solutions to the root. The number of solutions sent is controlled by the Migration Rate (MR) parameter. The root determines the MR best solutions from the collective $MR*(N)$ solutions and broadcasts it to all processors. These migrants if not already present on the processors, are then absorbed into the existing population by weeding out and replacing the weakest solutions. Each processor then continues with the serial GA for another MF number of generations. Every interval between migrations, i.e., the length of time defined by MF number of generations is called

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as *Epoch*. The stopping criteria is a predefined number of Epochs.

It is important to note that the migrant absorption policy dictates the replacement of worst solutions with incoming migrants only if the migrants already do not exist within the population. Also, logically this model could represent a fully connected topology of non-hierarchical processing elements which cooperate to determine the best MR solutions among themselves and absorb these into their existing populations.

3. RESULTS AND DISCUSSION

The parallel architecture used in this work is a dedicated eight-node cluster connected via a low-latency network. Each of these nodes is a general purpose stand-alone Pentium4 workstation running at 2.0GHz with 256MB memory and running the RedHat Linux distribution. The cluster runs over a Fast-Ethernet switch. Communication between nodes is achieved using the MPICH implementation of the Message Passing Interface.

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ALGORITHM Multi − Deme_Parallel_GA
NOTATION
RANK : ROOT= Root Processor designated by Rank=0
RANK : NON − ROOT= All other Processors designated by rank>0
RANK : ANY= All processors, including Root
MF= Migration Frequency
MR= Migration Rate
N= Number of Processors
Epoch = Instances of Migration
EPOCH_MAX = Maximum Number of Migrations Stopping Criteria
Begin
(Multi − Deme_Parallel_GA)

FOR RANK:ROOT
Initial Population Constructor
Distribute Initial Population
ENDFOR RANK:ROOT

FOR RANK:ANY
  Receive Allocated Population
ENDFOR RANK:ANY

LOOP-A
  FOR RANK:ANY
    LOOP-B
      Serial GA on Allocated Population:
        Choice of Parents
        Crossover and Offspring Generation
        Fitness Calculation
        New Population Selection
    END LOOP-B IF [Num_Iterations >= MF]
    Send MR Best Solutions and Costs to ROOT
  ENDFOR RANK:ANY

  FOR RANK:ROOT
    Collect the best MR*N solutions
    Determine best MR distinct solutions
    Broadcast MR solutions
  ENDFOR RANK:0

  FOR RANK:ANY
    Receive MR Best Solutions
    IF [Received Migrants not present in existing Population]
      Replace Worst Solutions with Received Solutions
    ENDIF
  ENDFOR RANK:ANY

END LOOP-A IF [Epoch >= EPOCH_MAX]

FOR RANK:0
  Return Best solution.
ENDFOR RANK:0

End (Multi − Deme_Parallel_GA)
```

Figure 1: Structure of the Multi-Deme Parallel GA.

Results for the Multi-Deme Parallel GA are documented in Table 1. The Migration Frequency and Migration Rate are twenty and one respectively, i.e., all processors run the GA on their allocated sub-population for twenty generations, followed by migration of one chromosome between them. The GA parameters are the same as used for the serial Genetic Algorithm. Figure 2 gives the speedup performance for the s386 circuit.

Table 1: Multi-Deme Parallel GA: Runtime to reach a target fitness with increasing number of processors.

Circuit	Target Fitness	Time taken to reach target fitness							
		P=1	P=2	P=3	P=4	P=5	P=6	P=7	P=8
s298	0.73	219	116	79	62	48	42	37	36
s386	0.63	314	171	109	89	71	62	52	52
s832	0.54	569	306	199	155	122	105	89	88
s953	0.54	1004	549	354	280	222	191	162	162
s641	0.64	2734	1439	933	730	589	520	425	424
s1196	0.54	1538	876	549	439	348	299	247	248
s1494	0.53	1679	942	597	460	367	319	263	268
s1488	0.54	1672	913	592	459	368	316	266	268
s3330	0.50	6818	3959	2584	1933	1523	1317	1090	1094

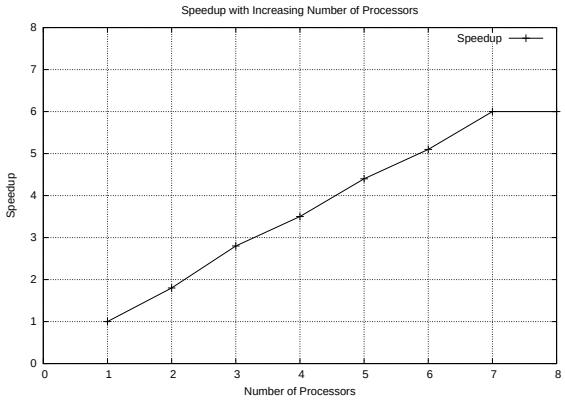

Figure 2: Speedup for circuit s386. The speedup pattern is almost identical for all circuits

4. CONCLUSION

This paper primarily serves as a demonstration of documented GA parallelization strategies to multiobjective optimization problems. The first approach was a variation of the canonical Master-Slave parallel GA, with both fitness and crossover distributed among processors. Only Selection was implemented by the Master. Performance gains in terms of reduced run-time were seen only for larger circuits. On the other hand, the Multi-Deme approach reported consistent performance gains independent of problem complexity and size of the search space.

5. ACKNOWLEDGMENT:

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