Asynchronous Parallel Evolutionary Algorithms: Leveraging Heterogeneous Fitness Evaluation Times for Scalability and Elitist Parsimony Pressure

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Project Objective

- Empirically study the performance gain of Asynchronous Parallel Evolutionary Algorithms (APEAs) versus Synchronous Parallel Evolutionary Algorithms (SPEAs) as a function of the number of nodes in a master-slave model.
- Analyze the unique "elitist" parsimony pressure resulting from employing APEAs on global populations with significantly varying fitness evaluation times, and describe its beneficial effects for promoting more efficient solutions with equal solution quality.

Background

- Evaluation times that are consistent for each individual in a population are labelled as homogeneous, where varying times are considered heterogeneous. In the case of heterogeneous evaluation times, computation cycles will be wasted if the EA requires a synchronization step. Figure 1 indicates the idle cycles in red.
- The number of slave nodes utilized by SPEAs is limited by the number of offspring (λ) in a given generation as seen in Figure 2. APEAs sends individuals to all *n* slave nodes (Figure 3).
- In SPEAs, slave nodes that are assigned quickly evaluated individuals must wait for all other nodes to complete their tasks before the population can be synchronized and the next generation can be distributed. These wasted cycles will accumulate through each generation. APEAs do not need to wait, which eliminates the wasted cycles at each node.

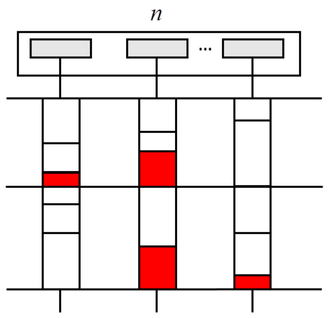

Figure 1: SPEA $n \leq \lambda$

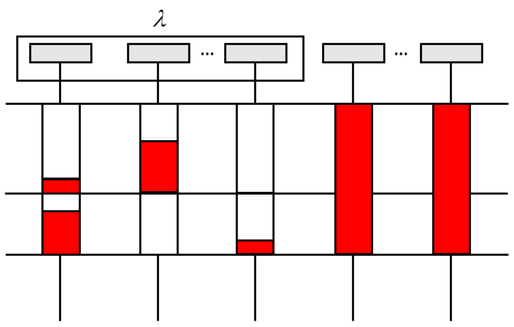

Figure 2: SPEA $n > \lambda$

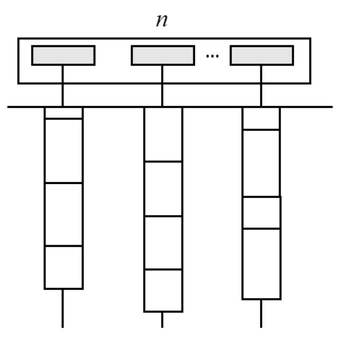

Figure 3: APEA

Approach

- *Experiment 1*: Compare the results for APEAs and SPEAs when the evaluation time of an individual is randomly assigned at each evaluation. This technique is used in related works.
- *Experiment* 2: Perform the same comparison when the time is inherited from the parents and remains as an attribute of that particular individual. This is similar to realistic problems

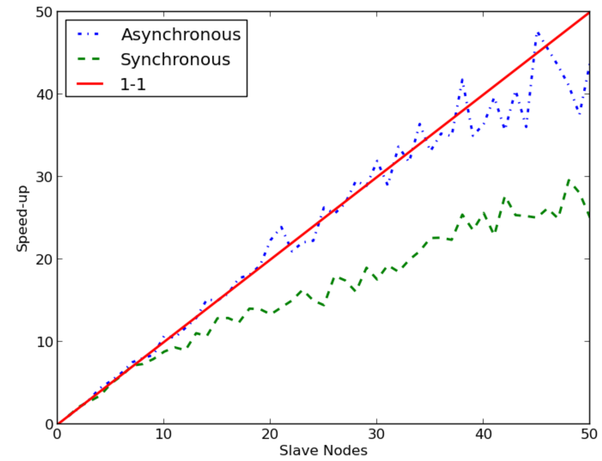

Figure 4: Plot of speed-up of convergence time vs number of slave nodes

Discussion

- Figure 4 indicates the performance in Experiment 1 when an individual is randomly assigned a time at evaluation, and Figure 4 illustrates the second experiment when the evaluation time is gene-based, or an inherited attribute. The superlinear improvement of the APEA in Figure 5 over the linear performance in Figure 4 demonstrates the existence and influence of "elitist parsimony pressure."
- The individuals with shorter evaluation times are considered more often for survival than those that take longer to process. This pressures the population to include faster solutions without an explicit objection or penalty for solution size or evaluation time. Figure 6 describes the evaluation times of the individuals in the final population.

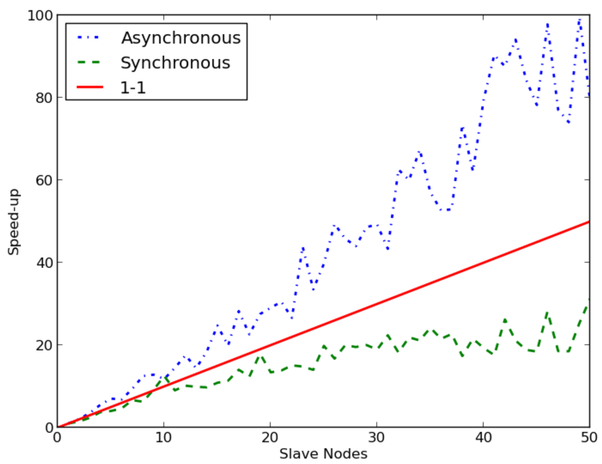

Figure 5: Plot of speed-up of convergence time vs number of slave nodes with gene-based heterogeneous evaluation time

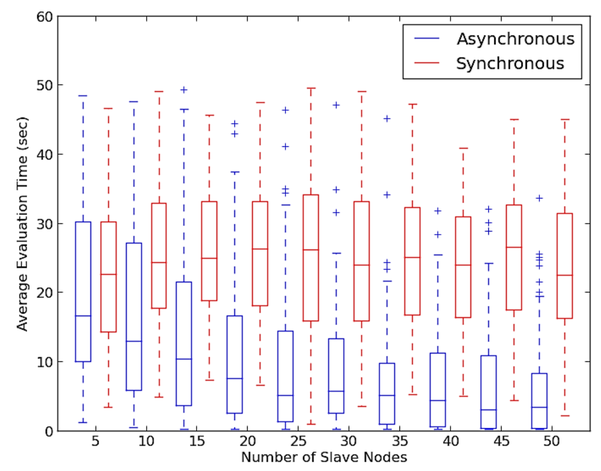

Figure 6: Box plot of average evaluation time of the final population of each run. The results are paired in increments of five slave nodes where blue indicates the results of the asynchronous runs and red indicates the results of the synchronous runs.

Future Work

- Consider the effects of other population mechanics for the APEA.
- Rather than provide an explicit encoding of the evaluation time into an individual, allow for implicit encodings in the simulation.
- Remove the assumption that each node will have the same processing speed to better understand how the hardware also influences the results.

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