Entropic and Real-Time Analysis of the Search with Panmictic, Structured, and Parallel Distributed Genetic Algorithms

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SUMMARY

It has been a well-known fact that genetic algorithms (GAs) get part of their success from the efficient exploration/exploitation balance. This equilibrium is related to the population diversity decreasing rate. This rate is not the same for all GAs, but it depends on the reproductive cycle being used. In particular, steady-state $(\mu+1)$-GAs (ssGA) have a larger convergence rate than traditional (genGA) generational (μ,μ)-GAs. Also, decentralized GAs are still not well known, and this is the reason for studying two of their most popular models: cellular, and distributed GAs (cGA & dGA, respectively).

We have analyzed the diversity decreasing rates of the mentioned algorithms by computing the mean bit entropy H of the population $P(t)$ at time t. Our goal is to compare and better understand the models. The distributed GA runs in every node a nodal ssGA/genGA/cGA, performing isolated migrations of a random string in a ring topology.

We have studied many problems but we only show the results for the generalized sphere problem (16 vars. encoded in 32 bits each one: SPH16-32), and the subset sum (SSS128). For the tests we used a global population of $512/n_{proc}$ individuals, proportional selection, double point crossover, and bit-flip mutation (100 runs).
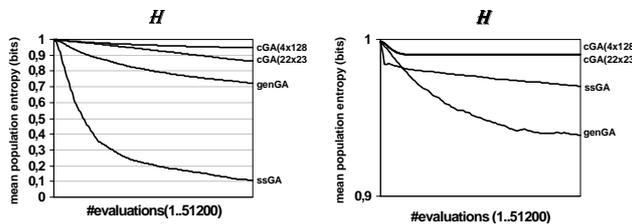
Figure 1: SPH16-32 (left) & SSS128 (right); non-distributed GAs.

In Figure 1 left we can appreciate that ssGA losses diversity quickly (as expected), and genGA shows a moderate loss rate; cGA is the best in preserving diversity: in this GA the diversity is related to the shape of the grid containing the population. For the SSS128 (Figure 1 right) diversity is quite high for all the models. When distributed in 8 islands (SPH16-32), they all lose diversity since every island has a smaller population.

Notice the influence of the migration frequency: a high coupling provokes quick convergence (Figure 2 right), while loosely coupled islands show sharp increments in the diversity when migrations occur (Figure 2 left).
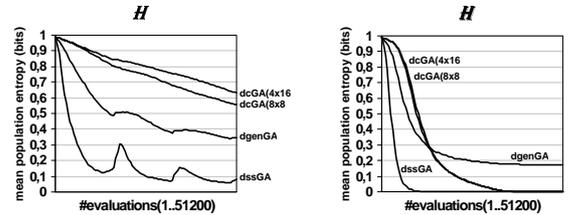

Figure 2: SPH16-32 with dGAs: freq. 32 (left) and 1 (right).

The models using a cGA have sustained high levels of diversity in all the tests. The migration frequency greatly affects the diversity level (Figure 3), while the synchronism seems not to alter the diversity spectrum for the tested problems (homogeneous hardware). However, the execution time shows clear advantages -even superlinear speedup- for asynchronous models (Figure 4).
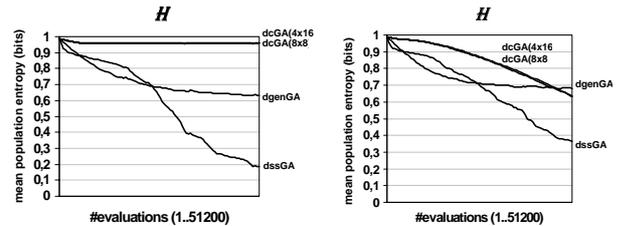

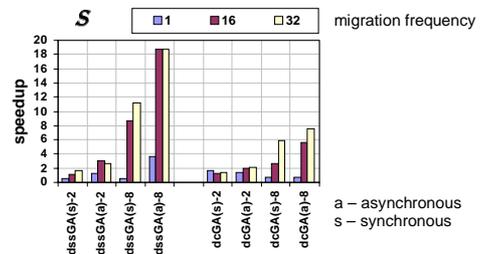Figure 3: SSS128 with a/sync dGAs freq. 32 (left) and 1 (right).

Figure 4: Speedup in SSS128 (1-2-8 processors, freqs. 1-16-32).

REFERENCES

E. Alba, C. Cotta, J. M. Troya (1999). "Entropic and Real-Time Analysis of the Search with Panmictic, Structured, and Parallel Distributed Genetic Algorithms". Tech. Rep., LCC ITI 99/07.