

Variance Reduction in Meta-EDA

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ABSTRACT

We study the benefit of measurement replication when using the Relevance Estimation and Value Calibration method to calibrate a genetic algorithm. We find that replication is not essential to REVAC, which makes it a strong alternative to existing statistical tools which are computationally costly.

Categories and Subject Descriptors G.3 [Probability and statistics]: experimental design, I.2.8 [Artificial Intelligence]: heuristic methods

General Terms Algorithms, Experimentation

Keywords EDA, UMDA, parameter control

1. DESCRIPTION OF WORK

The Relevance Estimation and Value Calibration (REVAC) method has been offered as a tool to calibrate the parameters of an evolutionary algorithm in a robust way [3]. REVAC is a Univariate Marginal Distribution Algorithm [2], where only one solution is replaced between updates of the distribution estimator, and not the entire population. REVAC uses the Shannon entropy of the estimated marginal distribution over each parameter to estimate the relevance of that parameter.

Reliable calibration of a non-deterministic EA requires measurements (outcomes of runs) with low variance. The most common way to reduce variance is to repeat the measurement several times and use the averages. Instead, REVAC bases averages on distributed measurements. We investigate whether the replication of measurements improves speed and quality when using REVAC.

For the EA to calibrate and for the objective function to solve we rely on [1], but we calibrate 3 instead of 2 parameters: p_m , p_c , and the population size s . The performance of parameter vector $\langle p_m, p_c, s \rangle$ is the negative computational cost of solving the objective function, i.e., negative population size times the number of generations needed to maximize the function. Execution is aborted if the computational cost reaches an upper threshold. The associated relevance estimation is based on the entropy of each marginal distribution. The settings of REVAC are identical to those in [3]. We evaluate 5 different levels of replications: 1, 2, 3, 5, and 10 replications. For each level or replication we calibrate

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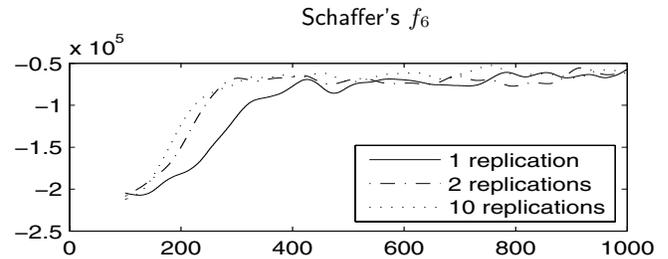


Figure 1: x -axis: no. of evaluated parameter vectors; y -axis: avg performance of parameter vectors chosen through the current distribution.

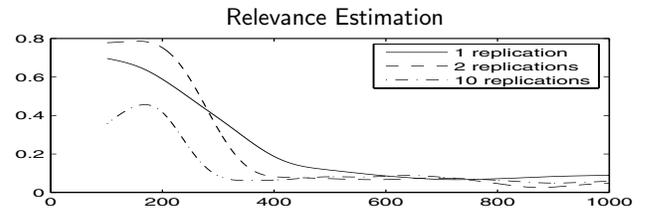


Figure 2: y -axis: mean squared error of the achieved relevance prediction with respect to the "practical optimum" (being the average over a large number of independent experiments)

each test function 10 times. Because of space limitation we only report results on one objective function, Schaffer's f_6 .

2. CONCLUSION

Using REVAC with only a single replication per parameter vector is sufficient to calibrate an evolutionary algorithm and to estimate the relevance of each parameter. If resources permit more evaluations, it is more advisable to run REVAC several times to increase the robustness of the results.

3. REFERENCES

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