Coordinate Change Operators for Genetic Algorithms

Elizabeth F. Wanner
Departamento de Matemática
Universidade Federal de Ouro Preto
Minas Gerais, Brazil
efwanner@iceb.ufop.br

Eduardo G. Carrano
Centro Federal de Educação Tecnológica de Minas Gerais
CEFET-MG
Minas Gerais, Brazil
carrano@cpdee.ufmg.br

Ricardo H. C. Takahashi
Departamento de Matemática
Universidade Federal de Minas Gerais
Minas Gerais, Brazil
taka@mat.ufmg.br

ABSTRACT

This paper studies the issue of space coordinate change in genetic algorithms, based on two methods: convex quadratic approximations, and principal component analysis. In both methods, the procedure employs only the objective function samples that have already been obtained through the usual genetic algorithm operations, without the need of any additional function evaluation. The two procedures have been tested over a set of benchmark problems, and the data has been analyzed via a stochastic dominance analysis procedure. In both cases, the results suggest that in the transformed coordinates the genetic algorithm can able to deal with ill-conditioned problems in less iterations and with greater proportion of successful attempts, in comparison to the genetic algorithm without coordinate transformation.

Categories and Subject Descriptors

G.1.6 [**Mathematic of Computing**]: Numerical Analysis—*Optimization*

General Terms

Algorithms

Keywords

genetic algorithms, coordinate change, quadratic approximations, principal component analysis

1. INTRODUCTION

Coordinate change procedures have been applied in many optimization techniques. In the majority of the cases, an approximation for the function is built and is used to change the coordinates of the variable space. In the context of genetic algorithms, a previous work has already studied coordinate change, for enhancing the algorithm convergence properties: the paper [4] has proposed quadratic approximations for coordinate correction, inside the iterations of genetic algorithms, leading to coordinates in which the contour surfaces are maximally regular.

This paper presents a further refinement of the procedure proposed in [4], and proposes another possibility of employing coordinate change inside the iterations of genetic algorithms: the matrix of Principal Component Analysis of the current population is used for coordinate correction. Using the individuals, a Principal Component Analysis (PCA) procedure is employed and the coordinate change matrix of PCA is used to change the coordinates of the variable space. This leads to coordinates in which the variables are approximately uncorrelated.

The coordinate changes, based on the quadratic approximation and on the PCA, have been coupled to a real-coded GA and have been tested with some analytical functions found in the literature. A stochastic dominance analysis procedure has been employed on the results, suggesting that both methodologies of coordinate change, when coupled with GA, can outperform the simple GA.

GECCO'08, July 12–16, 2008, Atlanta, Georgia, USA.
ACM 978-1-60558-130-9/08/07.

2. COORDINATE CHANGE MATRIX

The quadratic approximation for the function is built using only the current population and the function evaluations over previous populations, in order to fit a convex quadratic approximated function for the objective function. In this way, no additional function evaluation is necessary. The coordinate change methodology intends to define new coordinates for the problem in such a way that the contour surfaces of the quadratic approximation become spheres. The Hessian matrix of this approximation is used in the coordinate change procedure. For more detailed information, see [4].

Principal Component Analysis (PCA) [1] is a procedure that is employed to transform a set of correlated variable into a new set (sometimes smaller) of uncorrelated variables. The procedure of PCA is employed here with the purpose of re-scaling the space directions, reducing the difference between the data variances in the different directions (the data variance becomes similar in all space directions). The elimination of some dimensions is not employed here.

3. COORDINATE CHANGE OPERATION

Consider the nonlinear unconstrained problem where $f(\cdot)$ is a real-valued nonlinear function. The coordinate change methodology intends to define new coordinates that are favorable for the application of further algorithm operations. In both cases of quadratic-approximation and PCA coordinate change, the variable transformation becomes:

$$\begin{aligned} \tilde{x} &= Vx \\ x &= V^{-1}\tilde{x} \end{aligned} \qquad (1)$$

The coordinate change is expected to enhance the motion of the GA population toward the point of minimum of the objective function, by performing an operation that becomes favorable in an "average" sense, over the regions of the space that have been already visited by the GA populations. It is worthwhile to notice that the coordinate change only affects the coordinates of the population. The objective function is always evaluated in the original coordinates. The proposed methodology, in any case, is very simple and can be included in the iteration cycle of any genetic algorithm.

4. RESULTS

The comparison approach proposed is an adaptation of the multiobjective procedure for evaluation of evolutionary algorithms described in [3]. An algorithm is evaluated by two different cost factors:(i) the number of function evaluations needed to reach a stopping criterion; and (ii) the value of the objective function that is found after the optimization procedure. The algorithm is run until the objective value is not enhanced after 100 generations. When this condition occurs, the number of function evaluations that is assigned to the algorithm as a cost function is the number of function evaluations that was necessary for reaching *at the first time* such objective function value. If the algorithm exceeds a maximum of 100 generations without reaching a stable objective function value, then the function evaluation cost factor becomes $100 \times popsize$, and the algorithm stops.

The pair of merit functions (i) and (ii) makes possible the comparison of algorithms when some of them are not able, at all, to find the best solutions, up to a reasonable number of function evaluations. Such comparison makes sense under the assumption that an algorithm that does not find the best solution is still useful if it can find a sub-optimal "good solution" with a reasonable computational effort. Such merit factors, instead of being evaluated via their average values, are evaluated here via an approximation of the first-order *stochastic dominance* concept [2].

In order to implement the methodology, the experiments described in this section employ a simple version of a Genetic Algorithm with real encoding. The purpose of these experiments is to determine the effect of the coordinate change procedure on the performance of the simple GA. For brevity, the standard GA is denoted by sGA, the GA with coordinate change based on quadratic approximation is denoted by $qaGA$ and the GA with coordinate change based on principal component analysis is denoted by $pcaGA$

The three algorithms have been tested with quadratic functions with minimum at the space origin, with dimension equal to 2, 3 and 4, and different sets of eigenvalues (see Table 1). Such functions, although presenting a very particular structure, are suitable for evaluating the ability of the proposed methodologies for dealing with ill-conditioned problems. The algorithms have been tested also with a set of benchmark functions found in the literature (only the results with the Rastrigin function are commented here). For each test function, all algorithms (the sGA, the $qaGA$ and the $pcaGA$) have been executed 50 times, starting with the same basic parameters and the same initial population and the comparisons have been made following the approach discussed previously.

In all quadratic problems, the algorithms $qaGA$ and $pcaGA$ have outperformed the sGA in both merit functions considered (f_o and n_e). However, the algorithms $qaGA$ and $pcaGA$ are not ordered by a relation of "better than": the $qaGA$ has presented a smaller number of function evaluations up to the convergence, while the $pcaGA$ has presented a convergence

Table 1: Set of eigenvalues for the Hessian matrix, for quadratic problems of dimensions 2, 3 and 4.

Problem	Dimension	Eigenvalues
P1	2	1,100
P2	2	1,1000
P3	3	1,10,100
P4	3	1,100,1000
P5	4	1,10,100,1000

to better objective function values. It can be seen that, with the usage of the two coordinate change methodologies described in this work, the proposed algorithms $qaGA$ and $pcaGA$ become less sensitive to the condition number of the problem than the original GA.

In the case of the Rastrigin function, the $pcaGA$ dominates the $qaGA$, which in turn dominates the sGA.

5. CONCLUSIONS

The idea of transforming the coordinates of the decision variable vector for enhancing optimization procedures has been investigated in the context of a GA. This paper has proposed two methods for performing such transformation: (i) using the Hessian matrix of a convex quadratic approximation of the objective function, and (ii) using the *principal component analysis* coordinate transformation matrix, applied over the population of the GA. The results obtained here suggest that such coordinate transformation can be effective for dealing with ill-conditioned functions.

Acknowledgements

The authors would like to thank Capes, CNPq and Fapemig.

6. REFERENCES

[1] E. Oja. Neural networks, principal component, and subspaces. *International Journal of Neural Systems*, 1:61–68, 1989.

[2] S. Pemmaraju and S. Skiena. *Computational Discrete Mathematics: Combinatorics and Graph Theory with Mathematica* . Cambridge, 2003.

[3] R. H. C. Takahashi, J. A. Vasconcellos, J. A. Ramirez, and L. Krahenbuhl. A multiobjective methodology for evaluation genetic operators. *IEEE Transactions on Magnetics*, 39:1321–1324, 2003.

[4] E. F. Wanner, F. G. Guimarães, R. H. C. Takahashi, and P. F. Fleming. Quadratic approximation-based coordinate change in genetic algorithms. In *Proceedings of the IEEE Congress on Evolutionary Computation*, Vancouver, CA, 2006. IEEE Press.