Evolutionary Algorithms for Cardiovascular Decision Support

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Abstract. *The extraction of information from cardiovascular models may improve the diagnosis and treatment of cardiovascular diseases. Retrieving information on the dynamics of the cardiovascular system is done by identifying the structure, order and parameters of various type of models, traditionally lumped parameter and ARMA models, which provide a way to extract knowledge on the overall state of the cardiovascular system. There are specific system identification techniques developed for specific cardiovascular models. Our method is general, easily applicable to various model variations. The identification of structure, order and parameters is considered as a multi-objective optimization problem, which we solve with Genetic Algorithms (GAs). The paper deals with the comparison of variants of GAs for the task, and introduces a novel multi-level GA approach (muleGA), which, in this particular application, is preferable over the more traditional Pareto-based and aggregating fitness techniques.*

Keywords: Cardiovascular Modelling, Parameter Estimation, Genetic Algorithms

1. Introduction

Non-invasive continuous-time beat-to-beat measurement and estimation of highly informative cardiovascular parameters such as arterial blood pressure, cardiac output and stroke volume is becoming more available since the introduction of devices such as Portapres or Finapres based on the Penaz method, making the signal acquisition available outside the intensive care unit (ICU). Invasive beat-to-beat measurement of arterial blood pressure is carried out in the intensive care or high-dependency unit as a key monitoring technique of real-time hemodynamic monitoring systems. Both invasive and non-invasive measurements are used mainly for monitoring purposes, no sophisticated data-mining and time-series analyzing and forecasting algorithms are exploited in present day medical practice.

Advanced techniques for modeling the dynamics of the cardiovascular system however exist [1, 2 ,3], although these are mostly used for research purposes [4, 5]. By the means of high performance generic methods, employing the search and optimization capabilities of Genetic Algorithms [6], real-time estimation of hard-to-measure cardiovascular parameters is possible to some extent. Encouraging results were presented on the application of evolutionary search methods for model identification [7] and for cardiovascular modeling [8]. Zaid et al. reports basic results on simulating the cardiovascular state with a model whose parameters are adjusted according to the patient's easily measureable vital signals [9, 10]. This topic was further researched by Heldt et al. [11]. The latter system not only executes model identification but runs pattern recognition and physiologic reasoning tasks to comprehensively form a modern ICU device. As Zaid et al [9], we also use the 9-compartment CVSIM model [12] both for the simulation of cardiovascular signals (virtual patient), and for adjusting the model's configuration to have its outputs match the outputs of the virtual patient's (see Fig.1).

2. Subject and Methods

We used and extended the GALib [13] GA-library with multi-objective [14] and multi-level functionality. Four type of GAs were tested against each other in our single-level test configurations, Steady-State-GA [13], micro-GA [15], NSGA-II[16] and SPEA-II [17]. For the multi-level experiments, we used our published multi-level algorithm [18] fine-tuned for the current application. In short, the multi-level GA (muleGA) works the same way as any other GA, with the main difference being the individuals of the populations, as in our multi-level case, the information represented by individuals are functions of so-called lower level GAs, which the individuals encompass. So, each individual runs few GAs in itself. When these lower-level GAs are evolved is detailed in our previous research paper [18]. Each GA in the multi-level structure can be of any type. In our multi-level tests, at each level, we use the Simple-GA, provided by the GALib library [13]

Our problem statement was: for the given output (virtual patient) signals find the input parameters that would be difficult to measure otherwise. The simulator at our disposal (CVSIM) did an excellent job at the forward calculation, and we tried to find the most suitable input vector to the simulator by using single- and multi-level genetic algorithm structures. The search space was 28-dimensional (of which 10 were held constant) and we considered four output signals (x0 - Left Ventricle Pressure, q1 - Arterial Flow, q3 - Right Ventricle Flow, v5 - Pulmonary Venous Volume). Each time a candidate input vector evaluated we programmed the simulator with it and ran the simulator until we got 700 samples for the output signals our experiment was concerned with. Then for each signal we calculated the absolute difference from the reference over all samples and normalized the result. The objective of the optimization was to minimize the average of the differences.

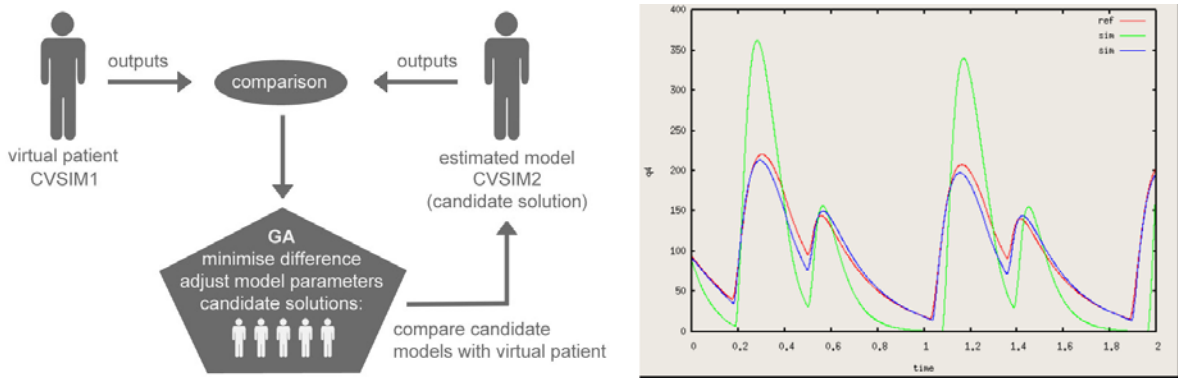

Fig. 1. The figure on the left shows our test configuration. The parameter sets evolved by the Genetic Algorithm(GA) are run in candidate models which are compared to the virtual patient's output. The absolute difference of the output signals are taken into account by the GA's fitness function. The figure on the right shows one output from the virtual patient (red) and one output from the best candidate solution plotted 2 times, at the first (green) and at the last iteration (blue). Note, that in the last iteration, the output of the virtual patient and the output of the estimated model are virtually the same.

Input vectors were represented by 28-gene genomes. The initial value of the genes was chosen randomly from a specific range. The genome mutated by randomly shifting all of its genes which weren't kept constant, while ensuring they don't fall out of bounds.

In the multi-level case, bottom-level GAs encoded full input vectors in order to be able to feed the simulator, but only aimed to optimize for two output signals out of four. Genomes of the top-level GA were constructed such that each of them had two subordinate GAs, one of them optimizing for one pair of the output signals, and the other for the rest. During the

evaluation, a top-level individual will fed the simulator (CVSIM2 on Fig.1) with the average of the input vectors represented by the current best solutions of its subordinate GAs. On the top-level, all output signals of the simulator is considered for evaluation.

3. Results and Discussion

First we tested the traditional single level GAs. Results show (see Fig.2) that there is no significant difference in the goodness of solutions regardless of GA type, however the Steady-State GA running an aggregating fitness function had significantly better running time (10-20 times faster) than the Pareto-based approaches.

	MicroGA	SPEA-II	SState	NSGA-II
MicroGA		TT: $0 \rightarrow p = 0.20$ KS: $0 \rightarrow p = 0.55$	TT: $0 \rightarrow p = 0.54$ KS: $0 \rightarrow p = 0.79$	TT: $0 \rightarrow p = 0.98$ KS: $0 \rightarrow p = 0.79$
SPEA-II			TT: $0 \rightarrow p = 0.55$ KS: $0 \rightarrow p = 0.55$	TT: $0 \rightarrow p = 0.23$ KS: $0 \rightarrow p = 0.55$
SState				TT: $0 \rightarrow p = 0.53$ KS: $0 \rightarrow p = 0.67$
NSGA-II				
Mean	-3.914	-3.723	-3.818	-3.917
Div	1.094	1.115	1.057	1.227

Fig. 2. The results of comparison of four GAs. Mean values are close to the theoretically optimal -4 (problems specific) value. Paired T (TT) and Kolmogorov-Smirnov (KS) tests fail to reject the null-hypothesis (that the expected values of the compared results are identical) at 5% significance level. We can conclude, that no single-level GA is performing better than the others in this particular problem, as far as the quality of the solution is concerned.

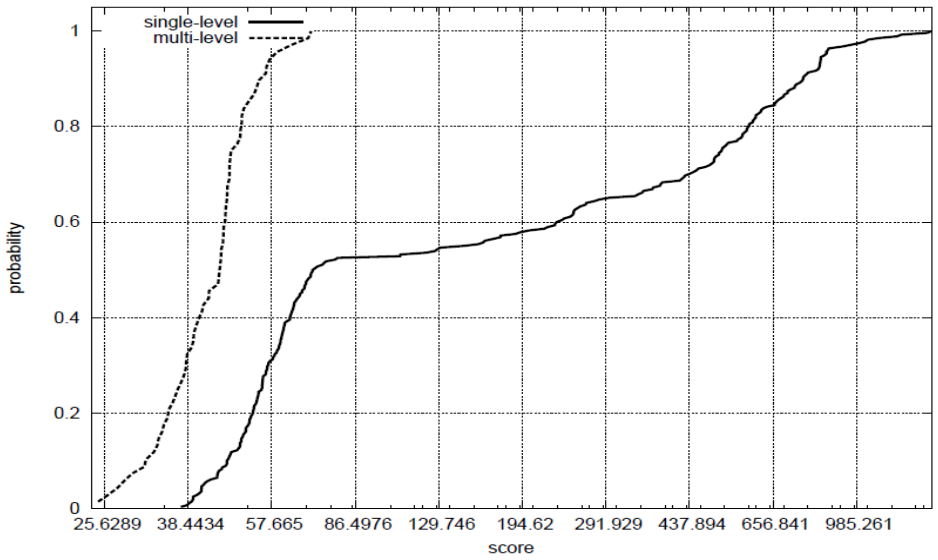

Fig. 3. The probability of solutions found by single-level and multi-level GAs are lower than a specific score (low-is-best) is shown on the figure. For this problem domain, the multi-level GA approach is clearly more powerful considering the quality of the solutions.

We repeated the CVSIM experiment a several times and examined the performance and the objective score distribution of the algorithms. Single-level and multi-level configurations were run more than 300 times to calculate average running time for the different methods. The multi-level technique is 2 to 5 times slower, but still faster than the Pareto-based algorithms. Considering the quality of the solutions, the best results of the single-level

algorithm achieved worse scores much frequently. Computing the Kolmogorov-Smirnov test (KS=5.052) confirms the two distributions indeed different (see Fig.3)

4. Conclusion and Future Work

We showed that GAs are capable of estimating the parameters of a lumped parameter cardiovascular model such that it mimics the outputs of the reference signals. As our reference signals were synthesized with the same CVSIM model, future work is needed to test the method with real signals. Our first tests show that for real signals, the 9-compartment CVSIM model is insufficient, so the 21-compartment counterpart needs to be used. Because of this, the efficiency of our multi-level GA is emphasized, as it is capable to perform better in high dimensional search spaces than any of the single-level GA variants tested.

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