Genetic Algorithms for optimal intermittent measurements for tumor tracking

Antoine Aspeel[†1], Axel Legay[1] and Benoît Macq[1]

[1] *ICTEAM Institute, UCLouvain, Avenue Georges Lemaîtres 4-6, Louvain-la-Neuve, Belgium.*

Introduction

Radiotherapy is an essential tool in the arsenal of cancer treatment. Basically, it consists of irradiating the tumor while sparing healthy tissues. The zone that clinicians want to irradiate is called the clinical target volume, however the planning target volume is a larger zone that includes some margins. These margins compensate all treatment uncertainties, including the one on tumor position. In the case of mobile tumors, the position uncertainty leads to large margins. A tumor tracking method can reduce dramatically these margins. A classical approach is to acquire X-ray images in the treatment room that are used to estimate the tumor position. Unfortunately, X-ray imaging irradiates the patient. There is a trade-off on the number of such X-ray images: a large amount of them permits a precise tracking of the tumor but irradiates the healthy tissues; on the contrary, reducing the amount of X-ray images acquisition would better preserve healthy tissues from X-rays but would also require an increasing of the margins. Nowaday, the number of these images is fixed by a clinician on the basis of an acceptable induced X-ray dose. In clinical applications, these images are taken periodically, i.e. at constant rate. In [1], Aspeel *et al.* propose to relax this constraint by allowing variable rate imaging. Their optimal intermittent Kalman predictor for tumor tracking is a prediction method that takes the X-ray images, when they are the most useful. They present a combinatorial optimization problem to select the best measurement times and solve it with a genetic algorithm (GA). In this paper, different implementations of GAs are studied to efficiently solve this problem. A better GA could provide a better measurements repartition and then decrease the uncertainty on the estimated position.

Materials & Methods

The framework proposed in [1] is composed of 5 distinct steps that are recalled to make this article more selfcontained: **Step 1:** X-ray images are taken at constant rate, estimations of tumor positions are extracted with a home made algorithm. **Step 2:** These tumor locations are used to do a system idenfication, i.e, the tumor motion is modeled by a state space representation fitting the Kalman filtering formalism. **Step 3:** Knowing the model of the tumor motion, a GA is used to find the best set of measurement moments, it is $M = \{m_0, \dots, m_{N-1}\} \subset \{0, \dots, T-1\}$ such that $|M| = N$. They are chosen to minimize the sum of the prediction error covariance on the complete treatment. Such a quantity can be computed from the Kalman filtering equations. **Step 4:** Measurements are taken according to set M, the predictor begins but the treatment waits T_0 time steps that the quality of the prediction is sufficient. **Step 5:** The tumor treatment begins, measurements are still taken according to M.

In this paper, different variants of the GA are compared to solve the combinatorial optimizarion problem presented in step 3. The variable to optimize is the set $M = \{m_0, \dots, m_{N-1}\}$. The constraint $|M| = N$ makes the use of GA not trivial as shown by the following example with a 1-point crossover. Firstly, the variable M is encoded as a list of the measurement moments. It ensures that the number of measurements will not increase (as it could be the case if M is encoded in a binary vector of length T with t^{th} element equal 1 if $t \in M$ and 0 otherwhise). Other challenges are illustrated by the following example: let two parents $P_1 = 0\ 1\ 3\ |\ 5\ 6$ and $P_2 = 0\ 1\ 2\ |\ 3\ 5$ where | indicates the location of the crossover. The obtained offsprings are $O_1 = 0\ 1\ 3\ |\ 3\ 5$ and $O_2 = 0\ 1\ 2\ |\ 5\ 6$. One can do two observations, firstly O_1 contains a duplication of 3 which corresponds to take two times the same measurement, which corresponds to waste a possibility to

observe at another time step. Replacing one of the copy can only improve the objective function. The second observation is that O_2 does not contain a 3, while P_1 and P_2 both contain one. It means that some common genetic patrimony is lost which could slow down the convergence of the algorithm. Lets compare three different crossover. The first one is a *shuffle crossover* (SC) from [2]. It shuffles the order of vectors and then do a 1-point crossover. The second crossover method is a SC followed by a random replacement of duplicates, e.g. if the moment 3 appears two times in O_1, one of the duplicate is replaced by picking uniformly at random on all times not in O_1. This method is called *replaced crossover* (RC). The third method is the *count preserving crossover* (CPC) of [2]. It consists to do the crossover on subsets of $P_1 \backslash P_2$ and $P_2 \backslash P_1$. It permits to transmit the common time measurements $P_1 \cap P_2$ to both offsprings.

Results & Discussions

Three different crossovers have been tested on lung images and on synthetic examples. Figure 1 presents the evolution of the average and the minimum cost evaluation on the population for the three methods on a synthetic example. Firstly, one can observe that the SC and the RC give similar behaviors. The gap between the mean cost and the minimum cost does not decreases, meaning that the population does not converge to a single individual. On the contrary, this gap tends to vanish for the CPC, meaning that the population converges. This shows that the non-convergence is due to the lost of genetical patrimony and not to duplicates. Finally, the CPC gives a significantly smaller cost value.

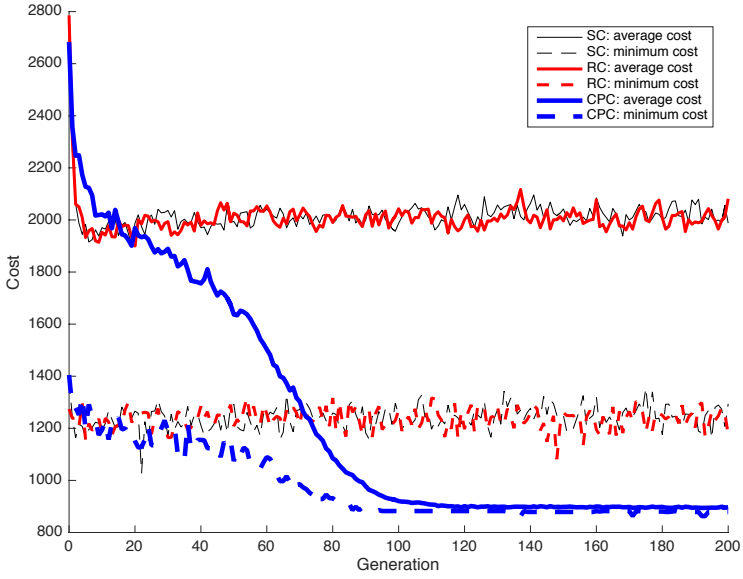

Figure 1: *Average and minimum cost on the population during generations for GA, with three different crossover: SC, RC and CPC.*

Conclusions

Numerical evidences look to show that a GA that implements CPC outperforms a GA with classic crossover, i.e. SC, or with RC. In addition, it has better convergence properties. This permits a better use of each X-ray image in case of tumor tracking with intermittent measurements.

References

[1] Aspeel, A., *et al.* (2019). Optimal intermittent measurements for tumor tracking in x-ray guided radiotherapy. In *Medical Imaging 2019: Image-Guided Procedures, Robotic Interventions, and Modeling*. SPIE. (Accepted).
[2] Umbarkar, A. J., *et al.* (2015). Crossover Operators in Genetic Algorithms: A Review. *ICTACT journal on soft computing*, *6*(1).
†Corresponding Author: antoine.aspeel@uclouvain.be