PET Reconstruction Using a Cooperative Coevolution Strategy

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Introduction and Motivations: Fully 3D tomographic reconstruction in nuclear medicine requires high computing power and leads to many challenges. The trend today is to use more general methods that can integrate more realistic models (application-specific physics and data acquisition system geometry). To date, the use of such methods is still restricted due to the heavy computing power needed. Evolutionary algorithms have proven to be efficient optimisation techniques in various domains, including medicine and medical imaging. However the use of evolutionary computation in tomographic reconstruction has been largely overlooked. In previous work, we showed that an artificial coevolution strategy (also called "Parisian evolution") based on the "fly algorithm" can be used to reconstruct the 3D distribution of radioactive emitters in Single Photon Emission Computed Tomography (SPECT) [1,2]. In this abstract, we propose a computer-based algorithm for fully 3D reconstruction in Positron Emission Tomography (PET) based on the same approach and evaluate its relevance. Realistic models describing the physics of PET could be integrated in the reconstruction loop while taking advantage of artificial evolution to reduce the computing time.

Material and Methods: A cooperative coevolution strategy scheme based on the fly algorithm is proposed to optimise the position of radioactive emitters with respect to the input data. Each fly represents a point of the patient 3D space and acts as a radioactive emitter. The final population of flies corresponds to the tracer density in the patient being scanned, i.e. the reconstructed data. In SPECT, the input data corresponds to raw 2D projections at successive angles around the patient that can be formated into a sinogram format. Each time a new fly is created, a simulation is done in order to calculate its illumination pattern. In PET, the input data corresponds to a set of lines of response (LORs) that correspond to annihilation events. In the simulation, each fly is producing an adjustable number of annihilation events. The result of this simulation consists of a list of pairs of detector identification numbers that correspond to LORs.

A "marginal fitness" metrics based on the "leave-one-out cross-validation" method is used to evaluate the contribution of each fly. The fitness metrics corresponds to a distance measurement between simulated data and the actual data given by the imaging system. It gives the contribution (positive or negative) of a given fly with respect to the whole population. This fitness calculation method is then integrated into an evolution strategy scheme to optimise the position of flies.

We have developed a phantom model to assess the reconstruction algorithm. It is made of nine cylinders having two different radius (1 cm and 2.5 cm) and with four different radioactivity concentrations (C1 = 18,300 count/ml, C2 = 11,500 count/ml, C3 = 1,800 count/ml, and C4 = 115,000 count/ml). For each annihilation event, two coincidence photons are emitted. If they both hit a detector, a LOR is recorded. LORs are directly used by the reconstruction algorithm as input data. The central slice (512×512 pixels – pixel size 1.7 mm) through the cylinders is reconstructed. To evaluate the algorithm, profiles at the centre of each cylinder in the reconstructed slice are compared to the simulated profiles. In addition, we measure the full width at half maximum (FWHM) for each cylinder and we compare reconstructed and simulated values.

Results: Figure 1 shows the simulated and reconstructed slices. The reconstructed image appears to be visually similar to the reference image. Figure 2 presents the profiles extracted from Figure 1 (as the profiles of the upper bright areas will be symmetrically similar to those of the lower areas, they are not plotted here). These profiles appear to be relatively close. On Figure 2, the radius of each cylinder seems to match the corresponding radius in the reference slice. Also, the difference of radioactivity concentration is preserved in the reconstructed slice.

However, FWHM values (see Table 1) and the reconstructed slice show that the edge of cylinders are blurred, yielding to relative difference between simulated and reconstructed FWHM values up to 36%. This could be due to the fact that each fly contribute in the same way to the reconstructed slice, independently of their contribution metrics (marginal fitness). In other words, a fly with a low marginal fitness (i.e. a low contribution) and a fly with a high marginal fitness (i.e. high contribution) have an equal intensity.

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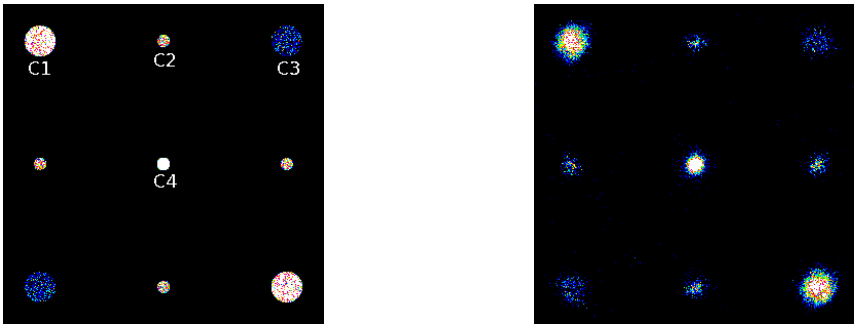
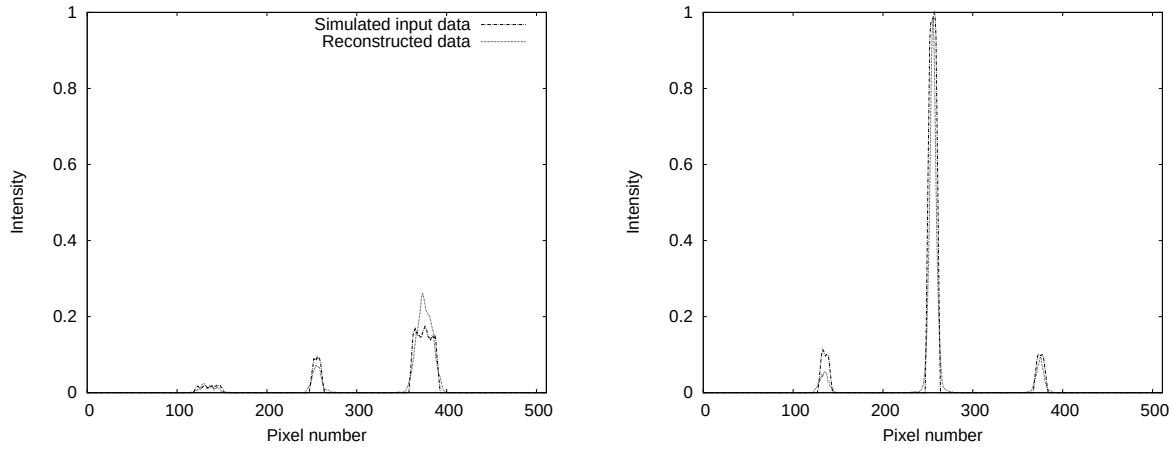


(a) Simulated input data. (b) Reconstructed data.

Figure 1: Example of PET reconstruction.



(a) Lower bright areas. (b) Middle bright areas.

Figure 2: Profiles extracted from Figure 1.

Radiotracer concentration (in count/ml)	FWHM from simulated slice (in mm)	FWHM from reconstructed slice (in mm)	relative difference (in %)
C1 = 18,300	48.4	35.0	28
C2 = 11,500	18.3	18.3	0
C3 = 1,800	51.7	40	23
C4 = 115,000	18.3	11.7	36

Table 1: FWHM values obtained from reconstructed and simulated profiles.

Conclusion: We have presented a novel method for reconstructing tomographic data in PET using evolutionary computation. This tomographic reconstruction approach gives promising results that are still open to further refinement, such as the visualisation of flies with respect to their fitness value, and the use of more realistic input data.

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Related Publications:

1. J. Louchet: “Stereo analysis using individual evolution strategy”. In *Proceedings of the International Conference on Pattern Recognition (ICPR ’00)*, page 1908, 2000.

2. A. Bousquet, J. Louchet, J.-M. Rocchisani: “Fully three-dimensional tomographic evolutionary reconstruction in nuclear medicine”. In *Artificial Evolution (EA ’07)*. Volume 4926 of Lecture Notes in Computer Science, pp. 231–242, 2007.