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Visualisation of PET data in the Fly Algorithm

Z. Ali Abbood[1,2], J.-M. Rocchisani[3] and F. P. Vidal[1,2]

[1]School of Computer Science, Bangor University, LL57 1UT, United Kingdom
[2]Research Institute of Visual Computing, RIVIC
[3]Université Paris 13, Sorbonne Paris Cité, BPC, F-93430, Villetaneuse, France

Abstract

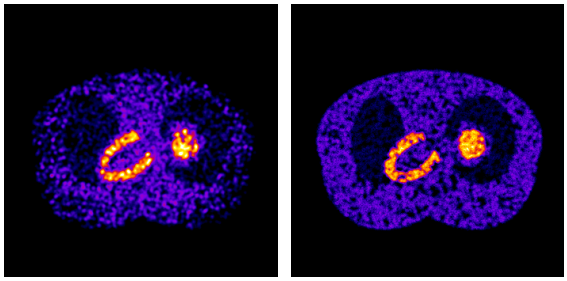
We use the Fly algorithm, an artificial evolution strategy, to reconstruct positron emission tomography (PET) images. The algorithm iteratively optimises the position of 3D points. It eventually produces a point cloud, which needs to be voxelised to produce volume data that can be used with conventional medical image software. However, resulting voxel data is noisy. In our test case with 6,400 points the normalised cross-correlation (NCC) between the reference and the reconstruction is 85.53%; with 25,600 points it is 93.60%. This paper introduces a more robust 3D voxelisation method based on implicit modelling using metaballs to overcome this limitation. With metaballs, the NCC with 6,400 points increases up to 92.21%; and up to 96.26% with 25,600 points.

Categories and Subject Descriptors (according to ACM CCS): I.3.8 [Computer Graphics]: Applications—Medical G.1.6 [Mathematics of Computing]: Optimization—Global optimization

1. Introduction

PET reconstruction using the Fly Algorithm is an artificial evolution strategy and it follows the iterative reconstruction paradigm. First, a random population of flies (3D points) is generated [Lou00]. Each fly emulates a radioactive emitter [VLLR11]. Genetic operators (here selection and mutation) are repeatedly applied to optimise the position of flies. The aim is to minimise the discrepancies between the data simulated by the flies and the input data from the scanner. The final concentration of flies will then be an estimate of the radioactive concentration.

To date, the final population of flies has always been considered as a point cloud. We demonstrate below that it is not the best representation to generate 3D voxel data.



(a) Reconstruction with 6,400 flies. (b) Reconstruction with 25,600 flies.

Figure 1: *Standard voxelisation: Each fly corresponds to a* δ *function.*

2. Noisy reconstruction

Each good fly is kept in the final 3D volume. We considered a fly as a Dirac delta function (δ): The value of each voxel is incremented for each fly it contains. The stochastic nature of the algorithm leads to noisy PET volumes (see Fig. 1(a)). To limit noise, more flies can be used in the reconstruction (see Fig. 1(b)). The reconstruction time significantly increases.

The reconstruction is then compared with the reference image (see Fig. 2). To quantify the similarities between a reference f and a test image t, the normalized cross-correlation (NCC) is used:

$$NCC(f,t) = \frac{1}{n}\Sigma_{x,y}\frac{(r(x,y)-\bar{r})\,(t(x,y)-\bar{t})}{\sigma_r\sigma_t}$$

with n the number of pixels, $\bar{r}$ and $\bar{t}$ the average values of f and t respectively, σ_r and σ_t the standard deviations of f and t respectively. $NCC(f,t)$ is equal to 100% when f and t are fully correlated; it is 0% when they are fully uncorrelated. Table 1 gives the NCC between Fig. 2 and the

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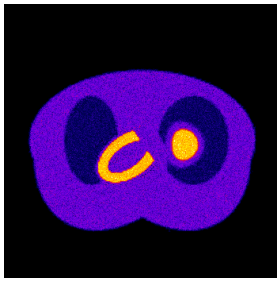


Figure 2: *Reference data (unknown).*

Table 1: *Normalised cross-correlation between the reference and reconstructed images.*

Image:	Fig. 1(a)	Fig. 1(b)	Fig. 4(a)	Fig. 4(b)
Method:	Noisy	Noisy	Metaballs	Metaballs
Flies:	6,400	25,600	6,400	25,600
NCC:	85.53%	93.60%	92.21%	96.26%

reconstructions. With 6,400 flies the NCC is 85.53%; with 25,600 flies it is 93.60%.

3. Density field

The aim of the fly algorithm is to estimate the radioactive concentration. As an output it produces a point cloud. This point cloud can be described as a density field. Instead of the δ function, an implicit function $(f(r))$ is used: A fly corresponds to a particle surrounded by a density field. The influence of the particle decreases with distance from the particle location. The final volume corresponds to:

$$V(x,y,z) = \Sigma_{i=0}^{N-1} f_i(\sqrt{(x-x_i)^2+(y-y_i)^2+(z-z_i)^2})$$

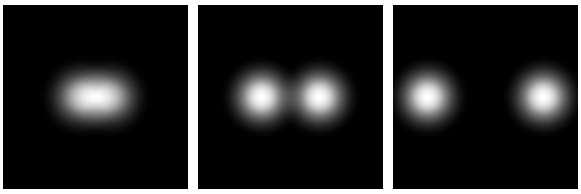
with V the voxel value at the location (x,y,z), and (x_i,y_i,z_i) the i-th particle's location. Metaballs are a well known type of implicit modelling technique [Bli82]. The density field can be modelled as:

$$f_i(r) = \begin{cases} a\left(1-\frac{3r^2}{b^2}\right) & \forall r \in [0;b/3] \\ \frac{3a}{2}\left(1-\frac{r}{b}^2\right) & \forall r \in [b/3;b] \\ 0 & otherwise \end{cases}$$

When two particles are close to each other, their density fields are combined in a smooth manner (see Fig. 3). When they are far from each other, their density fields remain separated. Fig. 4 shows the reconstruction results when implicit functions are used. The NCC with 6,400 flies is 92.21%; with 25,600 flies 96.26%.

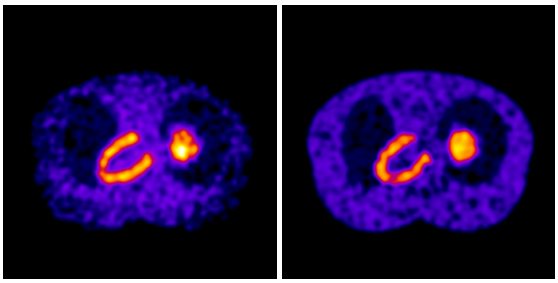
4. Conclusions

This poster focused on improving the voxel representation of PET images reconstructed using the Fly algorithm without increasing the computation time. The figures above show a significant improvement when implicit modelling is used. In our tests, 25,600 flies were initially needed to get a NCC value over 90%. With implicit modelling, only 6,400 flies produce comparable results.



(a) (b) (c)

Figure 3: *Illustration of density fields with two particles.*



(a) Reconstruction with 6,400 flies. (b) Reconstruction with 25,600 flies.

Figure 4: *New voxelisation: Each fly corresponds to a density field.*

Acknowledgements

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References

[Bli82] BLINN J. F.: A generalization of algebraic surface drawing. *ACM Trans. Graph. 1*, 3 (July 1982), 235–256. doi:10.1145/357306.357310. 2

[Lou00] LOUCHET J.: Stereo analysis using individual evolution strategy. In *Proc. ICPR'00* (2000), pp. 908–911. doi:10.1109/ICPR.2000.905580. 1

[VLLR11] VIDAL F., LUTTON E., LOUCHET J., ROCCHISANI J.-M.: Threshold selection, mitosis and dual mutation in cooperative co-evolution: Application to medical 3D tomography. In *Proc. PPSN XI* (2011), pp. 414–423. doi:10.1007/978-3-642-15844-5_42. 1