Artificial evolution for PET and SPECT reconstruction

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Flies for PET: an Artificial Evolution Strategy for Image Reconstruction in Nuclear Medicine

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We present an **iterative algorithm** based on an **evolutionary approach** for **image reconstruction** in **nuclear medicine**. Our method is based on a **cooperative coevolution** strategy (also called **Parisian evolution**): the "**fly algorithm**". Each fly is a 3D point that mimics a positron emitter. The flies' position is progressively optimised using **evolutionary computing** to closely match the data measured by the imaging system. The population of flies approximates the radioactivity concentration. We have developed **new genetic operators** that have been proven to be more efficient than state-of-the-art operators used in evolutionary computing[5]. To speed-up computations, the reconstruction is automatically performed at **progressive resolution**.

Introduction

Image reconstruction in tomography is an ill-posed inverse problem. This problem can be solved as an optimisation problem, and on such cases, evolutionary algorithms (EAs) have been proven efficient in general, and in particular in medical imaging. We focus here on tomographic reconstruction in PET.

Artificial Evolution

Evolutionary computing is a family of optimisation algorithms relying on Darwin's principles. In particular, it makes use of operators based on the biological mechanisms of natural evolution.

Standard PET reconstruction algorithms

Reconstruction methods in nuclear medicine are often divided into two classes:

    i) analytical methods, and
    ii) iterative statistical methods.

Analytical methods are based on continuous modeling and the reconstruction process consists in the inversion of measurement equations. The most frequently used algorithm is the filtered back-projection (FBP).

Iterative method model.
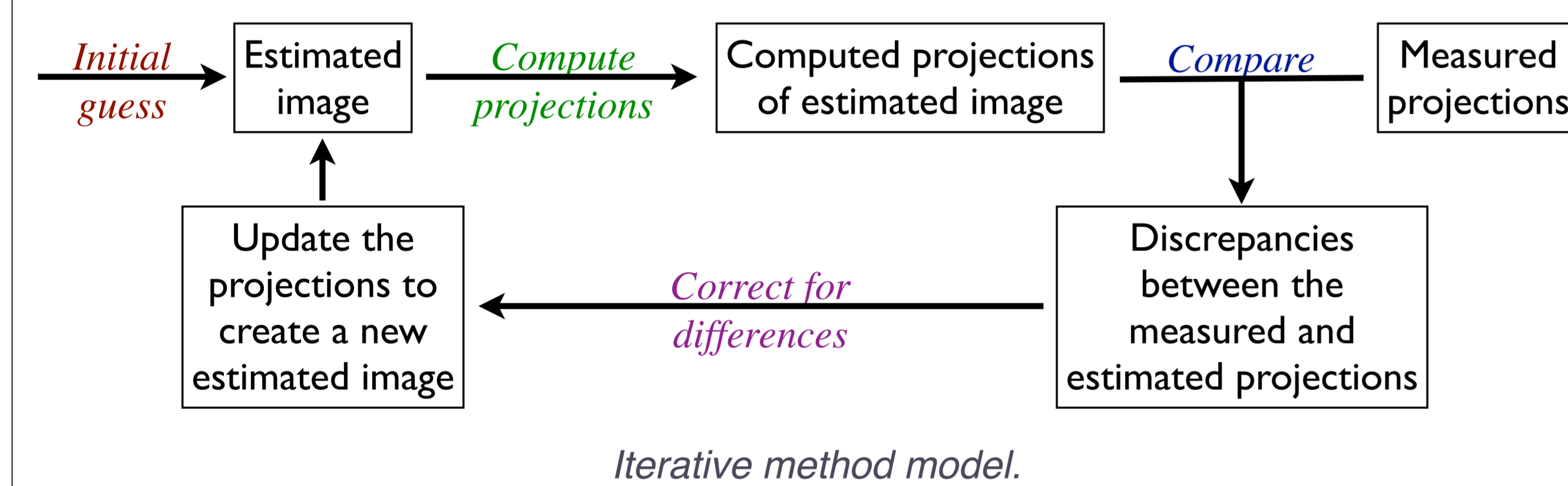
Statistical methods are based on iterative correction algorithms. These methods are relatively easy to model:

1. the reconstruction starts using an initial estimate of the image (generally a constant image),
2. projection data is computed from this image,
3. the estimated projections are compared with the measured projections,
4. corrections are made to correct the estimated image, and
5. the algorithm iterates until convergence of the estimated and measured projection sets.

There are different ways to implement these iterative methods. The main differences are about the computation of the projections, how the physics corrections (scattering, random, attenuation, etc.) are applied, and how the error corrections are applied in the estimated projections. Iterative methods include the most widely used techniques in SPECT and PET, such as the maximum-likelihood expectation-maximization method (ML-EM) and its derivative, the ordered subset expectation-maximization algorithm (OS-EM).

PET reconstruction using the fly algorithm

The algorithm that we present here follows the iterative algorithm paradigm. In preliminary studies, we introduced a cooperative coevolution strategy (or "Parisian evolution") called "fly algorithm" to minimize errors between the estimated projection data and the measured data. We showed that this approach can be used in SPECT reconstruction [1] and PET reconstruction [2,3,4]. Here, the searched distribution of radionuclides is modeled as a sample set of 3D points, the population of "flies". Each fly emits either photons or positrons depending on the image modality. The evolutionary algorithm evolves the position of flies using genetic operators to match reconstructed data with measured data.

The steps of the iterative method can be described as follows:

• Start with an **initial guess**. Initially, the flies' position is **uniformly distributed** within the volume defined by the scanner, or distributed depending on an **initial estimate reconstructed** using a fast **simple back projection** (SBP) performed on GPU using OpenGL. Each individual, or fly, corresponds to a 3D point.
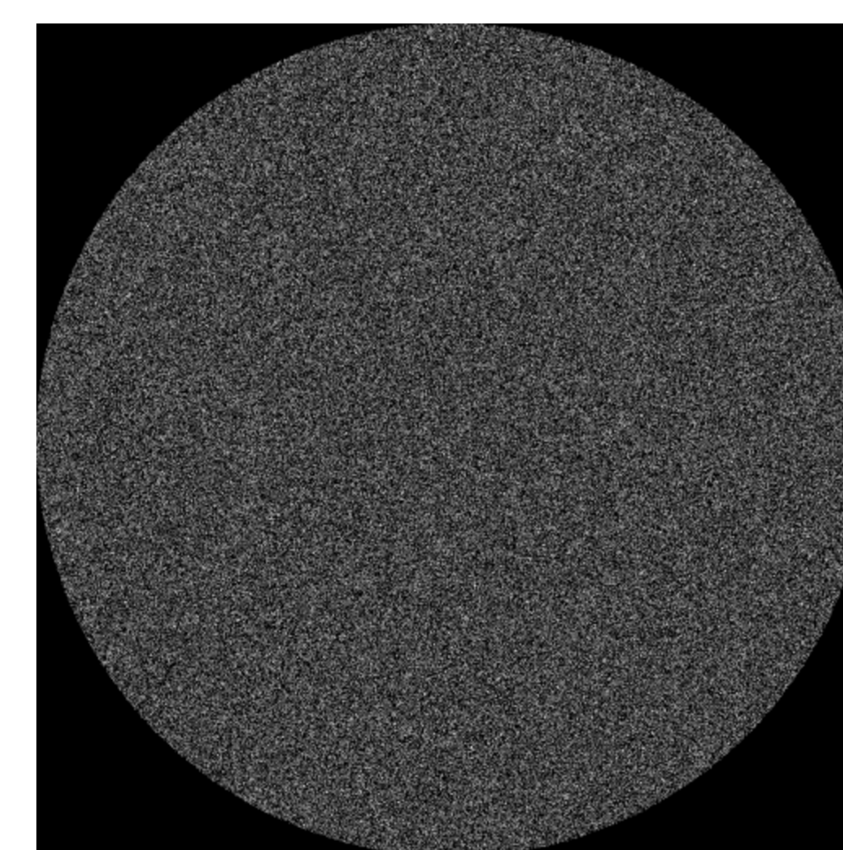
Uniform initialization using 5^5 flies.
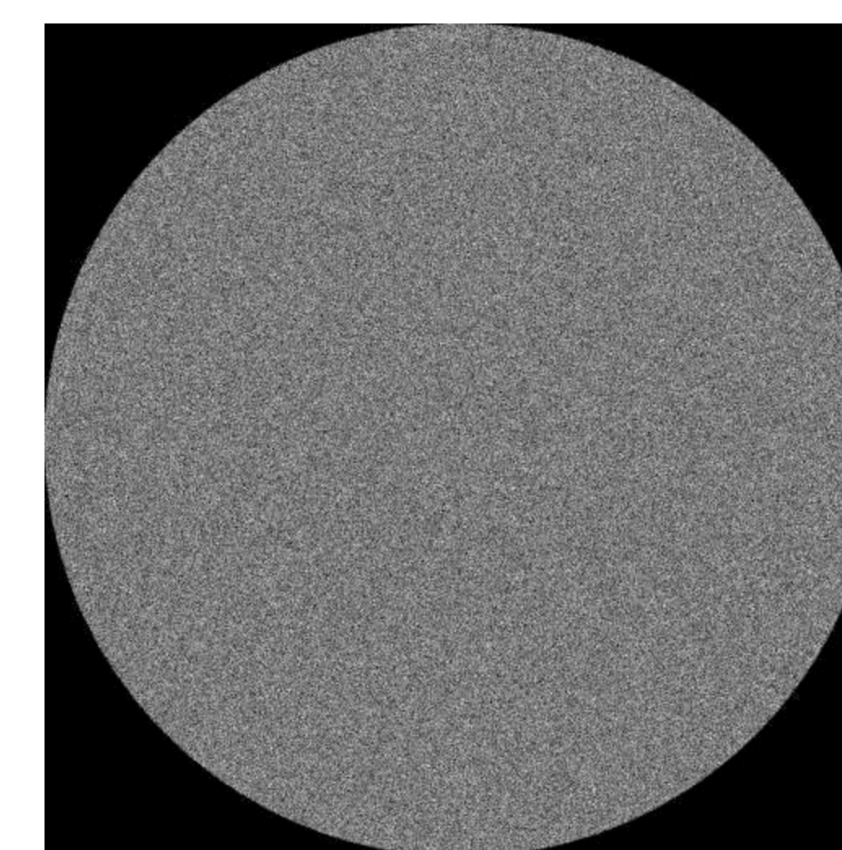
Uniform initialization using 3^6 flies.
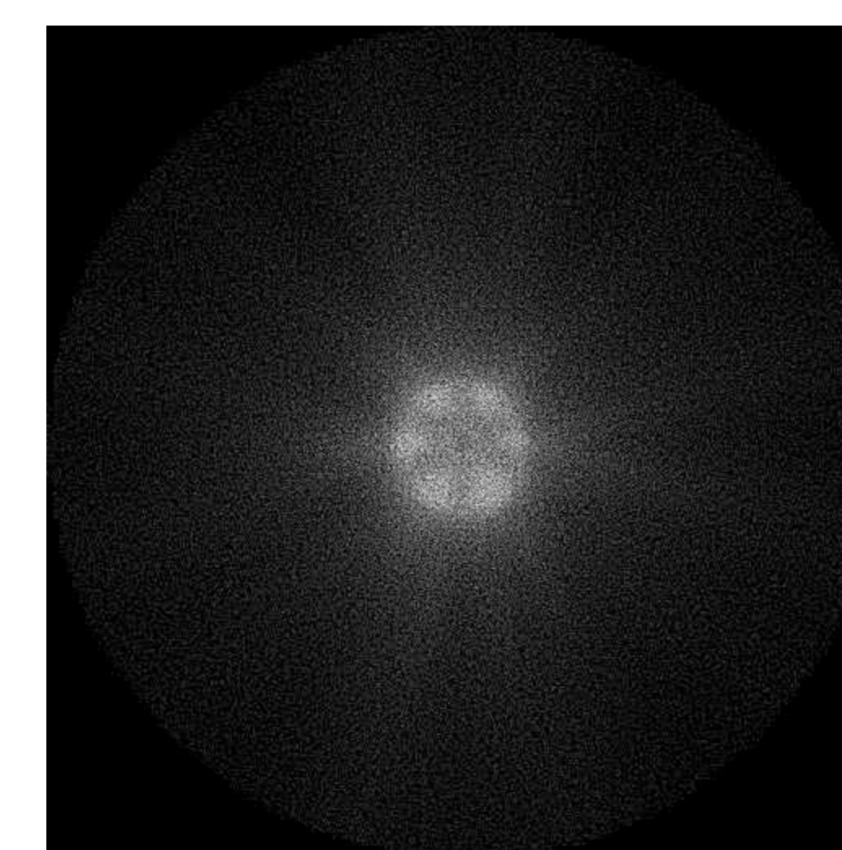
Initialization using SBP and 5^5 flies.
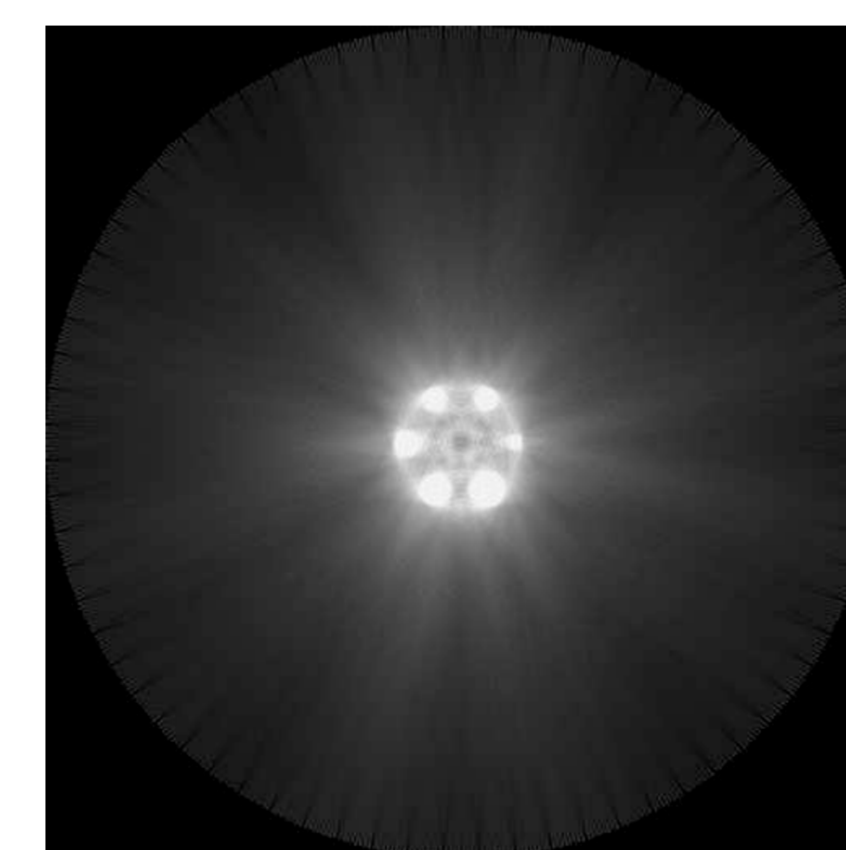
Simple back projection.
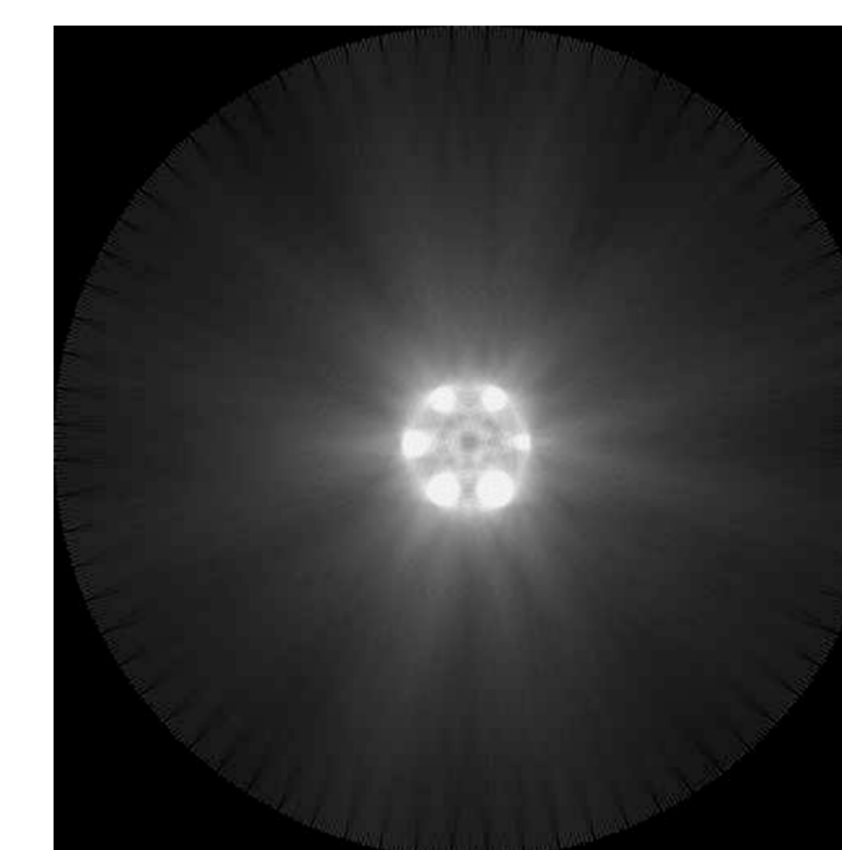
Initialization using SBP and 3^6 flies.

• To **produce estimated projection data**, **each fly mimics a radioactive emitter**, i.e. a stochastic simulation of annihilation events is performed. For each annihilation event, a photon is emitted in a random direction. A second photon is then emitted in the opposite direction. If both photons are detected by the scanner, the corresponding LOR is recorded. The scanner properties (e.g. detector blocks and crystals positions) are modeled, and each fly is producing an adjustable number of annihilation events.
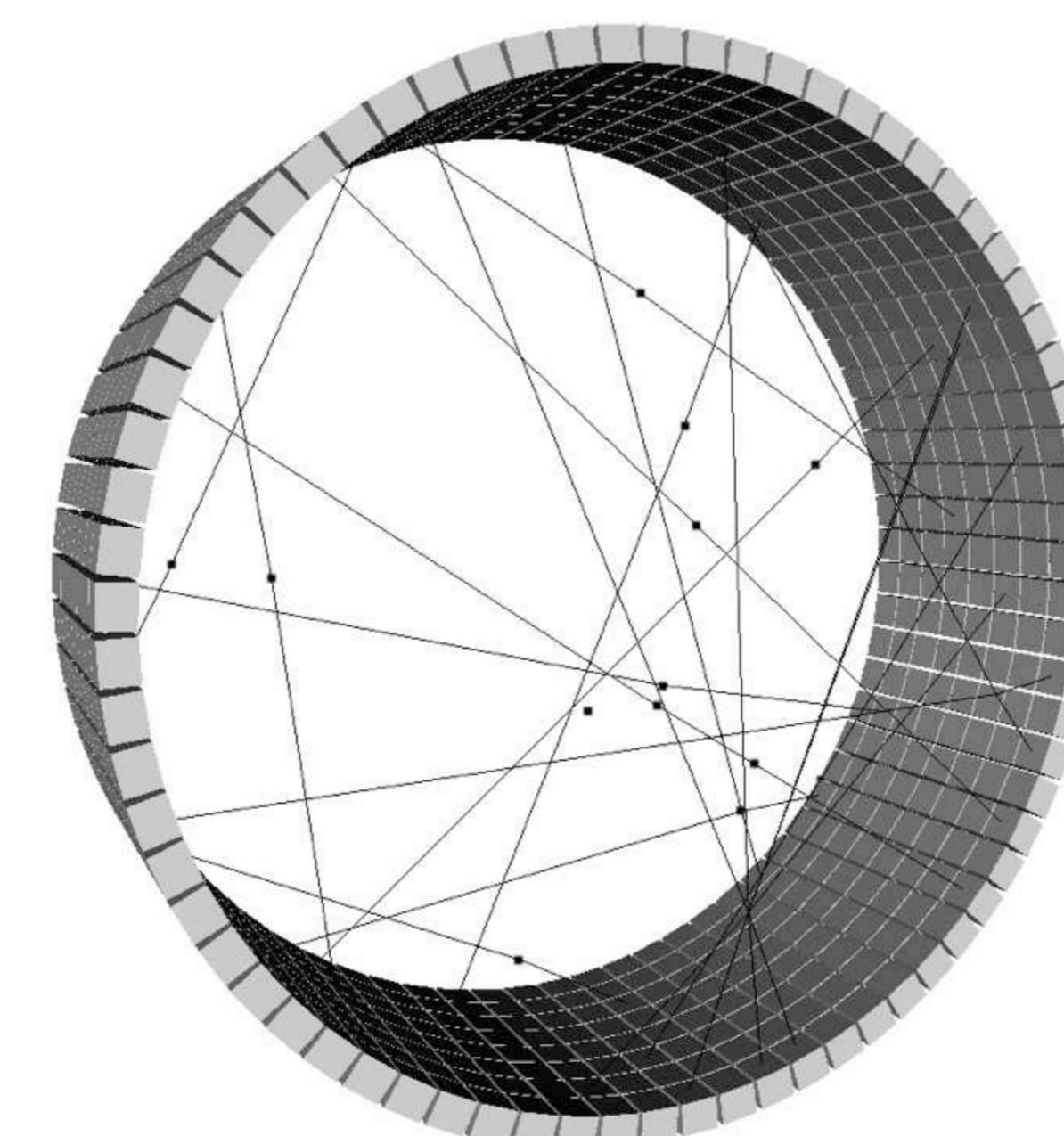
Each Fly Represents an Emitting Point.

• The **optimisation** is performed **using genetic operations**. The fitness function used during the selection operation takes into account the discrepancies between the estimated projections and the measured projections (see [4] for details about the fitness metric). The **regularization** is taken care by the **mutation operator**. **Multi-resolution** is achieved thanks to our **mitosis operator**. When the reconstruction is optimum at the current resolution, an automatic mitosis is triggered to double the population size, hence improve the resolution (see [4,5] for details about our specific genetic operators).

• The algorithm iterates until the convergence of the estimated data with the measured data, i.e. the spacial concentration of flies will correspond to an estimate of the radionuclides' concentration.

Results

In [2,3], we showed the ability of the early version of the algorithm (i.e. without taking advantage of some specific genetic operators we designed in [4,5]) to reconstruct simple 2D objects at low resolution. In [4], results at higher resolution are presented, as well as the fully-3D reconstruction of an object with a complex shape. This section presents new results, obtained using our specific genetic operators, with more sophisticated numerical phantoms of growing complexity.

Reference image. *Reconstructed data.* *Reference image.* *Reconstructed data.*
Hot sphere. *Jaszczak cold sphere.*

Reference image. *Reconstructed data.* *Reference image.* *Reconstructed data.*
Jaszczak hot rodes. *Jaszczak cold rodes.*
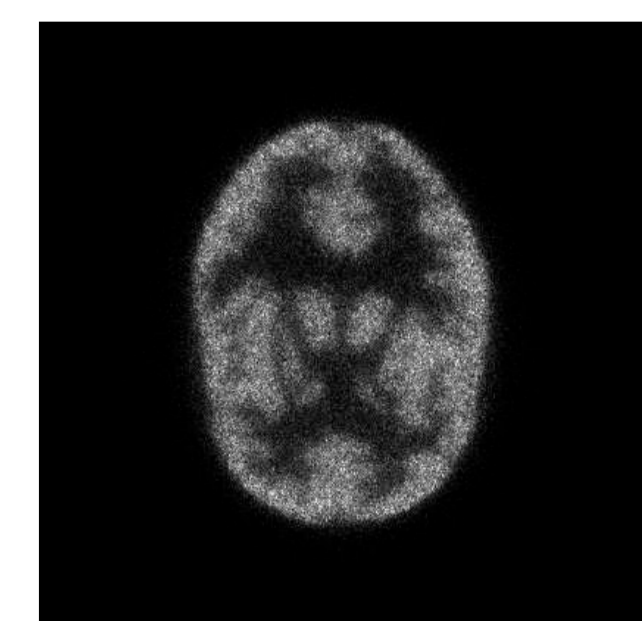
Reference image. *Reconstructed data.* *Reference image.* *Reconstructed data.*
Cardiac example. *Hoffman phantom.*

Conclusion

New results of positron emission tomographic reconstruction using a specific cooperative co-evolution scheme based on the fly algorithm have been presented. It demonstrated the ability of the algorithm to reconstruct images using input data that corresponds to standard phantom models (the Standard Jaszczak phantom) and anatomically realistic models (cardiac and brain). However, the reconstruction of hot regions seems better than the reconstruction of cold areas; this needs to be addressed. Further work will include a concurrent study with the OS-EM algorithm and a quantitative analysis of the results. Further work will also include the correction of photon attenuation and Compton scattering in the modeled system matrix.
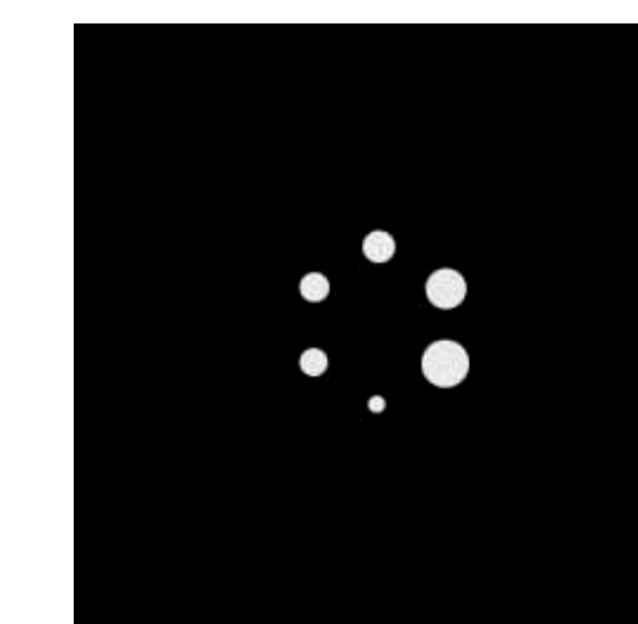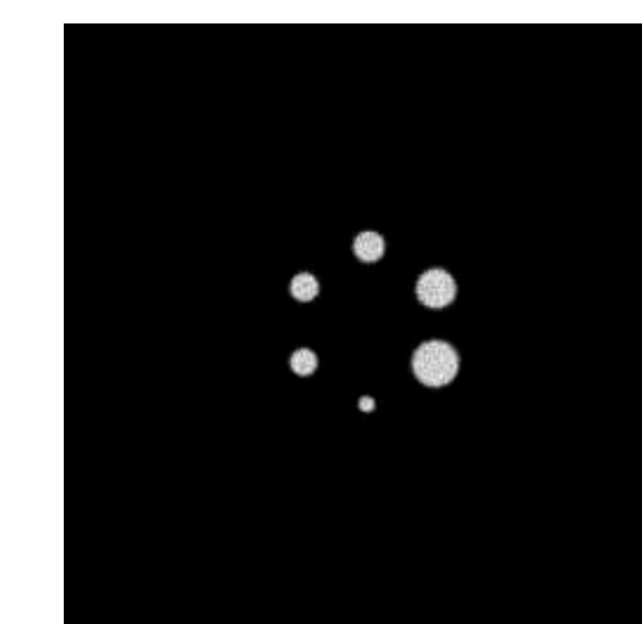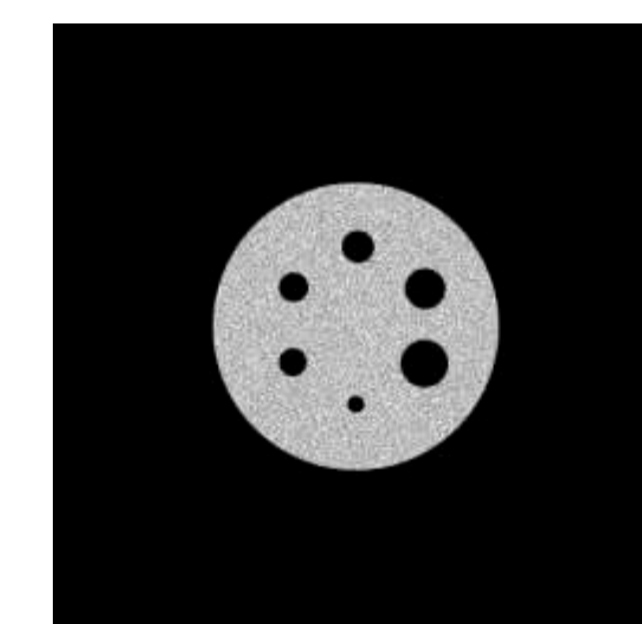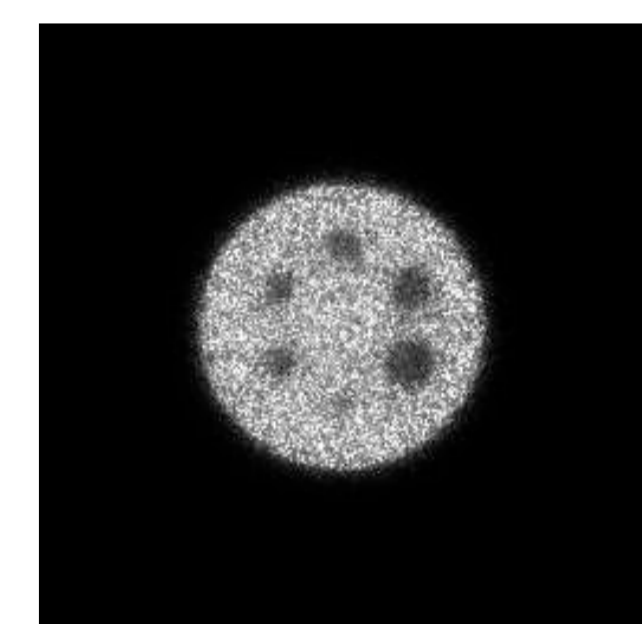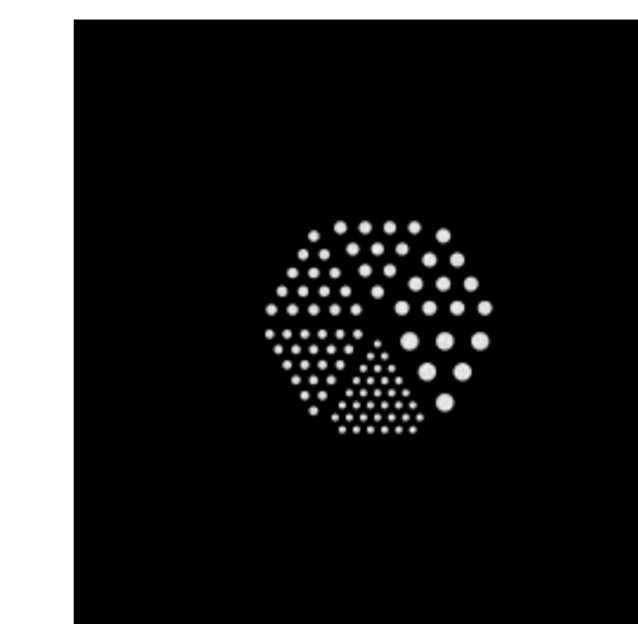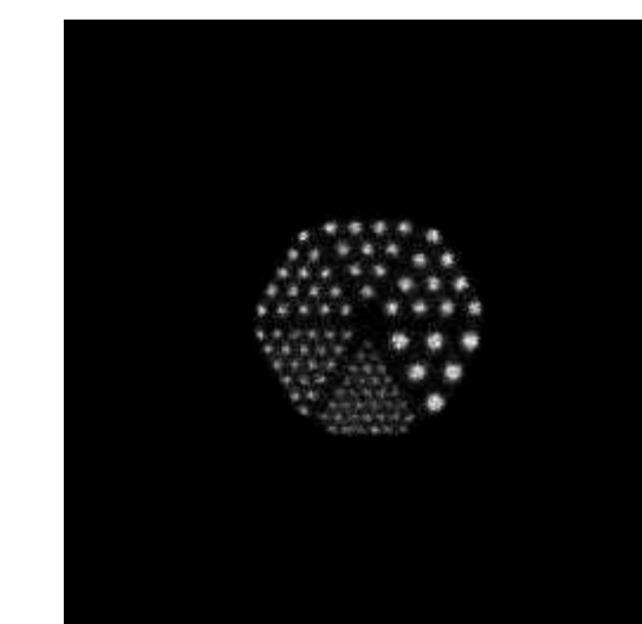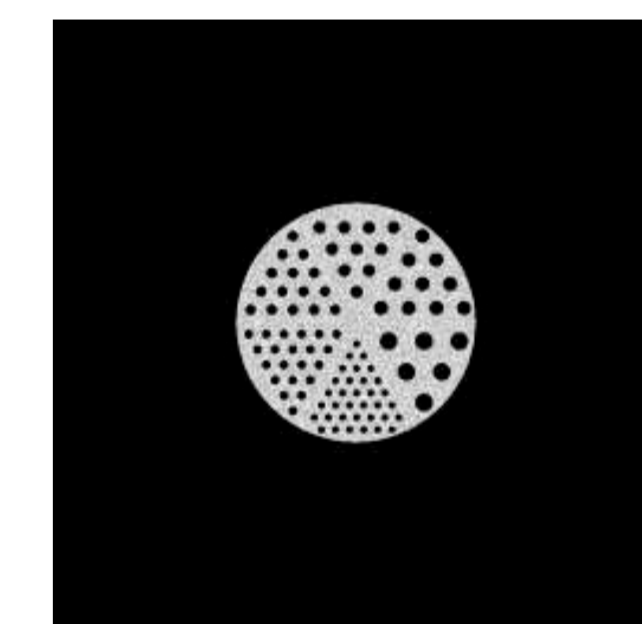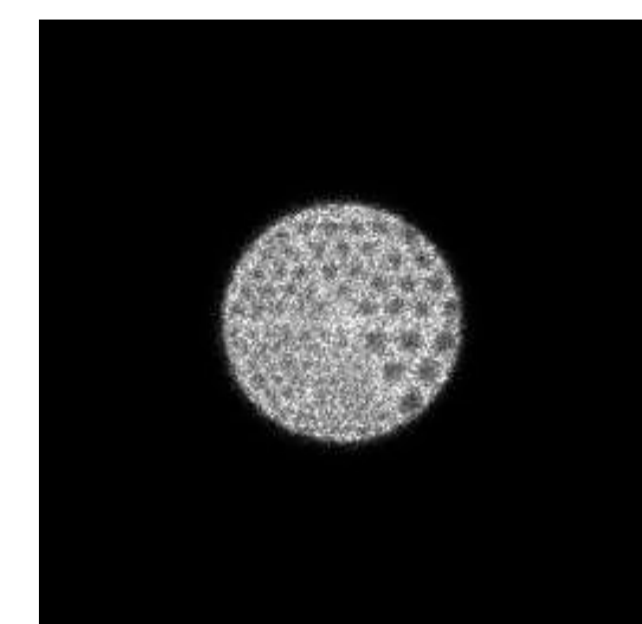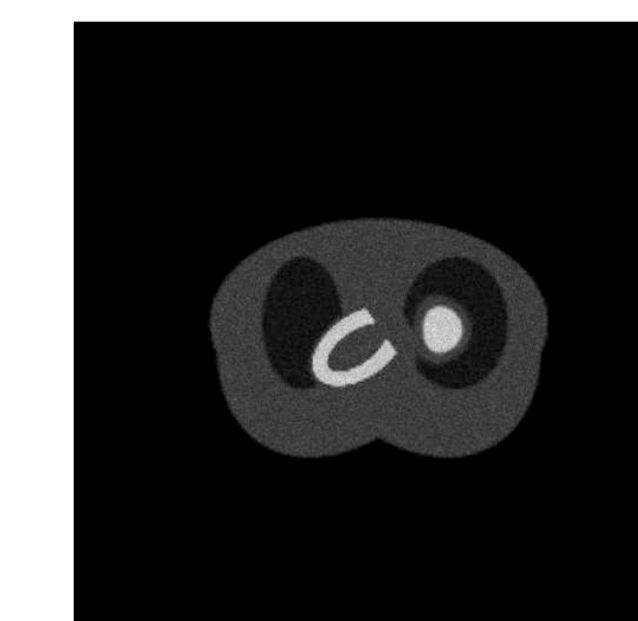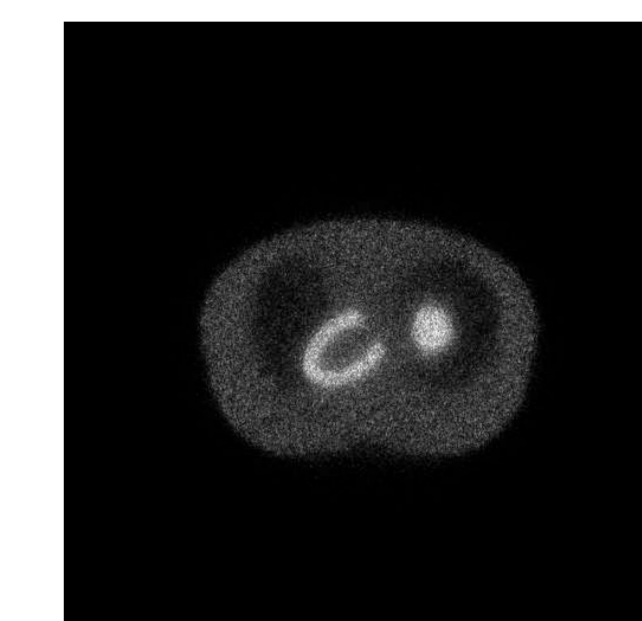
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