to obtain elemental maps of elements having energy loss values higher than 400eV, such as oxygen and iron.
The principles of electron tomography, as well as the new approaches for the samples observation, volume alignment and EFTET will be illustrated by several biological examples. In particular, by: (i) the study of melanosome morphogenesis, these organelles are implied in the synthesis and storage of melanine and are implicated in several skin pigmentation diseases and cancers; (ii) the analysis of the centriolar structure on basal bodies, which plays a substantial role in the cellular motility and are similar to the centrioles of centrosomes which are responsible for the cellular division; and (iii) the study, by EFTET, of granular metal inclusions in bacteria which represents an adaptive mechanism to extreme media.

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17H30-17H55 Spline-based approach to orientation assignment for three-dimensional electron microscopy

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In our previous work, we have developed a volume-to-image registration algorithm for a continuous *a posteriori* assignment of the parameters of orientation and position to Electron Cryo-Microscopy (cryo-EM) single particle images for a high-resolution Three-Dimensional (3D) particle reconstruction [1]. To determine these parameters, our algorithm employs a Levenberg-Marquardt gradient-based iterative minimization of a least-squares measure of dissimilarity between the two-dimensional Fourier Transform (FT) of the particle image and the extracted corresponding central slice of the 3D particle model FT relying on the central-slice theorem.

The algorithm that is the most similar to ours is FREALIGN [2] which also computes continuous parameters of the particle orientation. While FREALIGN minimizes the phase dissimilarity between the experimental image and its model weighted by the amplitude of the FT of the experimental image, our algorithm minimizes both the amplitude dissimilarity and the phase dissimilarity. Also, contrary to FREALIGN which uses nearest-neighbour interpolation, our algorithm uses cubic B-splines to interpolate the data accurately. Our optimization algorithm is faster than Powell's method of FREALIGN since we have access to the gradient of the cost function. To improve the robustness of the algorithm, we use a frequency-domain weighting of the cost function.

As all iterative algorithms, our method is sensitive to the choice of the initial parameters. To improve the robustness to the initial parameters, we have developed a strategy for the assignment based on the minimum final value of the dissimilarity measure for several different initializations. In this paper, we show the performance of our algorithm when using this strategy based on three starting points. A generalization to any number of points is straightforward.

We validate the algorithm in a fully controlled simulation environment where the ground-truth solution is known *a priori*. We assess the assignment accuracy in terms of the warping index that is commonly used in the area of image registration. We synthesize a set of images at known poses using a 3D model of a protein from the PDB (Protein Data Bank). We first show the performance of our algorithm when initialized using the assignment by only one of the three standard quantized-parameter methods [3,4,5]. Then, we present the result of their joint use for initialization. We show that the "mixed" strategy can be used to refine the assignment obtained by the standard algorithms. In these experiments, we achieved the assignment with the warping index smaller than 2 voxel. At the end, we present the performance of our approach in refining a 3D model of a GroEL chaperonin using real cryo-EM data with no ground-truth solution. We observe that this method improves the consistency of the volumes from the previous iteration.

Our algorithm is available in the Xmipp package [6]. In the future work, we will apply the techniques described here on other cryo-EM particles and macromolecular assemblies

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18H00-18H25 Mouse single photon scintigraphy

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Mouse became the model of choice for number of human pathologies. This is due to several factors including small size, high prolificity and capability of easy production of transgenic animals. The need for longitudinal studies that is to say following disease evolution in the same animal over time leeds to the development of special imaging devices. All modalities are involved in this technological gap : the small size of the animal explain the difficulties of developping adapted systems. Due to the idea that scintigraphy is inherently of poor spatial resolution, attempt to use it for mouse imaging began with a delay relative to other imaging modalities (eg MRI, CT, PET and echography).
We used a dedicated Anger type rotating gamma camera with 1 to 1.5 mm pinhole, 170 mm x 170 mm field of view and 25 photomultiplicators (Gaede Medizinsysteme Gmbh, Freiburg, Germany). Various tracers aimed at assessment of different physiological functions were used. One difficulty is that the radioactive tracer should be injected strictly intravenously, through a femoral catheter to avoid extravasation and changes in blood volume of mice under gaseous anesthesia. Depending on the tracers properties, dynamic, planar and tomographic data were acquired. We used medical software designed for analysis of human data to exploit the results and build a normal dtabase for mouse scintigraphy

Posters

1 Monte Carlo simulation of F18 disintegration in biological matter. Application to tumour volume reconstruction in PET

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The imaging by positron emission (called PET for Positron Emission Tomography) gives *functional* information of tumours. Nevertheless, it is still difficult to get accurate *anatomical* data from this kind of images, essentially due to the fact that a phenomenological seuillage is needed to extract a visualization of the tumor zones from the PET data. That's why mixed apparatus appeared, especially PET-CT, which combines PET with Computer Tomodensitometry (CT). In this way, functional and anatomical data can be obtained and tumors can be more precisely positioned. However, the spatial resolution of the PET images remains limited (of the order of 5 mm for human) and depends strongly of the radiopharmaceutical injected. In order to solve this problem, we have developed a complete Monte Carlo simulation to study in details the track of the positron and of the post-annihilation photons in biological matter in order to obtain the real energetic cartography induced by all the charged particles created. This energetic image will be compared to the