About the research centre or Inria department

Inria, the French National Institute for computer science and applied mathematics, promotes "scientific excellence for technology transfer and society". Graduates from the world's top universities, Inria's 2,700 employees rise to the challenges of digital sciences. With its open, agile model, Inria is able to explore original approaches with its partners in industry and academia and provide an efficient response to the multidisciplinary and application challenges of the digital transformation. Inria is the source of many innovations that add value and create jobs.

Team presentation

Multidimensional and multimodal light microscopy combined with GFP (Green Fluorescence Protein) tagging has taken a prominent role in life science research due to its ability to study in vitro and in vivo biomolecules in the cell compartments and cell domains.

The main objective of SERPICO team is to decipher the dynamic coordination and organization of molecular complexes at the single cell level. Our first aim is to foster dedicated technological and methodological developments to build an integrated imaging approach that bridges the resolution gaps between the molecule and the whole cell, including their temporal behavior. While we will focus on particular biological models of endo-membrane biogenesis and trafficking in the endosomal-recycling pathway of specialized cells, most of results and developments will apply in different fields of cell and integrative biology. A global and pluridisciplinary (applied mathematics, computer science, statistics and biology) approach is necessary to identify the molecular processes resulting in pathological situations (cancer, degenerative diseases ...), as well as to validate future therapeutic agents.

In collaboration with UMR 144 CNRS Institut Curie ("Subcellular Structure and Cellular Dynamics" Unit and PICT (Cell and Tissue Imaging Facilities) -IBiSA), SERPICO team provides computational methods and mathematical models to automatically extract, organize and model information present in temporal series of images as they are obtained in multidimensional light microscopy.

Research themes

To link accurately all data information rising from different imaging modalities, further developments in image analysis, multiscale modeling and statistics are required. We address the following themes:

- Image superresolution and image denoising to preserve cell integrity (photo-toxicity versus exposure time)
- Information extraction from images and videos in multidimensional microscopy for molecular interaction analysis
- Spatio-temporal organization modeling of molecular species and multiscale architectures
- Computational simulation and modeling of membrane transport at different spatial and temporal scales

Context

Within the framework of a partnership (you can choose between)

- collaboration between Institut Curie teams and Max Planck Institute (Martinsried, Germany)

Assignment

Cryo-electron tomography (cryo-ET) allows to capture 3D images of cells in a close to native state, at sub-nanometer resolution. However, noise and artifact levels are such that heavy computational processing is needed to access the image contents. In the Serpico group, we currently investigate the deep learning framework to accurately and jointly localize multiple classes of 3D macromolecules in cryo-electron tomograms. We compared this framework to the current state of the art, namely template matching on both synthetic and experimental data. We show that our DL framework is faster, produces less ambiguous results and shows superior performance on synthetic data. On experimental data we achieved 86% overlap with expert annotations and show that our method detections are complementary to these annotations. Nevertheless, the DL framework require an huge amount of labeled image data for training a given macromolecule (e.g. ribosome, proteasome). This labeling is very consuming and expensive.

In the PhD project, we plan to exploit simulators combined to a macromolecule data bank in order to generate any training set for any macromolecule. Transfer learning will be then used to matched experimental data we achieved 86% overlap with expert annotations and show that our method detections are complementary to these annotations. Nevertheless, the DL framework require an huge amount of labeled image data for training a given macromolecule (e.g. ribosome, proteasome). This labeling is very consuming and expensive.

Main activities

- Analyze the state-of-the-art methods in deep learning and cryo-electron tomography
- Innovate and develop detection and classification methods and algorithms for macromolecule localization
- Design experimental protocols in collaboration with experts in optics and biology
- Test, change up until validation
- Write papers and reports
- Dissiminate and distribute software

Conditions for application

Thank you for applying online.

Please submit your CV, cover letter and any recommendations.
Skills
Technical skills and level required: biomedical image analysis, statistics, machine learning, computer science
Languages: English
Relational skills: willingness to cross boundaries and learn new concepts in machine learning and biology
Other valued appreciated: open-minded

Benefits package
- Subsidised catering service
- Partially-reimbursed public transport
- Social security
- Sports facilities

Remuneration
Gross salary: 1982 euros (1st year) and 2085 euros

Defence Security:
This position is likely to be situated in a restricted area (ZRR), as defined in Decree No. 2011-1425 relating to the protection of national scientific and technical potential (PPST). Authorisation to enter an area is granted by the director of the unit, following a favourable Ministerial decision, as defined in the decree of 3 July 2012 relating to the PPST. An unfavourable Ministerial decision in respect of a position situated in a ZRR would result in the cancellation of the appointment.

Recruitment Policy:
As part of its diversity policy, all Inria positions are accessible to people with disabilities.

Warning: you must enter your e-mail address in order to save your application to Inria. Applications must be submitted online on the Inria website. Processing of applications sent from other channels is not guaranteed.