Master 2 research internship in Integrated Structural & Cell Biology in Grenoble

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Host laboratory:
Lab: IBS

Host group/team:
MICA

Title of the M2 research internship:

Mapping protein complexes in their natural cellular environment using cryo-electron tomography.

Project summary

Cryo-electron tomography (cryo-ET) allows visualization of molecular structures within their native cellular environment. However, to fully exploit the advantages of this technique, a major challenge remains: accurately identifying and locating specific protein complexes within the crowded, noisy cellular landscape.

Our research objective is to develop a novel computational framework that represents protein complexes in cryo-ET data as graphs, naturally handling the irregular, incomplete, and non-uniform geometry present in biological scenarios. This can be achieved by combining two complementary approaches: density tracing and deep learning methods. The former draws from mathematical methods to produce a skeleton representation of the tomogram that can be naturally interpreted as a graph, while the latter enables the interpretation and analysis of the data within such a framework.

The M2 project will focus on establishing the graph construction pipeline, converting cryo-tomograms into graph representations for structural detection analysis. Working with synthetic and real cryo-ET data from microbial systems, the student will address important structural biology questions by characterizing their cellular context, morphology and ultrastructure. This foundational work will support future developments in graph neural networks for template-free protein identification and contribute to a deeper understanding of supramolecular organizations in cells.

Students will develop computational and analytical skills for interpreting biological image data, examining complex datasets to design strategies for extracting meaningful information. The project suits those interested in method development and how computational approaches are built and applied in biology; it can serve as a launchpad for a PhD in the structural biology of microbial systems and machine-learning analysis of nanoscale cellular architecture.

Keywords:
Cryo-electron tomography, computational methods, microbiology.