In the context of an FIL funded, collaborative project we are looking for an

M2 student

for the **implementation and optimization of a workflow for the reconstruction and denoising of tomograms from CryoEM data**. Cryo electron tomography (cryo-ET) is a rapidly evolving imaging field for the determination of in situ (ultra-) structures. Acquired tilt series need to be aligned and corrected for technical aberrations to optimize the quality of the tomographic reconstruction. However, even under optimal conditions, cryo electron tomograms suffer from a low signal to noise ratio, resulting in significant challenges for subsequent data interpretation. Hence, optimized workflows and denoising approaches are needed to facilitate result interpretation. As part the AIsyCryo funded project, we will be developing new algorithms to improve the SNR after tomogram reconstruction for better data visualization. The internship aims are 1) preparing a dataset that will be used for benchmarking our new and state-of-the-art algorithms, 2) benchmarking the algorithms using several quality metrics and distributed computational resources and 3) integrating the selected algorithms in a user-friendly software environment.

We are looking for a team player with a strong interest in image processing, tools benchmarking and implementation of user-friendly interfaces.

The successful candidate will work under the supervision of Christophe Combet and co-supervision by Valentin Debarnot in the CIRI's StruVir team. This emerging team is headed by Christiane Riedel and interested in the host factor requirements of animal viruses and the structure of their interactions. The CIRI is an internationally renowned research centre focusing on viral and bacterial pathogen as well as the host immune system.

Expected starting date: **January 2026**.

Please send your CV and a letter of motivation to christophe.combet@cnrs.fr and get in touch in case you would like to obtain further information concerning the project, the teams involved and the application procedure.

References:

Advances in cryo-ET data processing: meeting the demands of visual proteomics. Watson AJI and Bartesaghi A. *Curr Opin Struct Biol*, **2024**. https://doi.org/10.1016/j.sbi.2024.102861.

Cryo-electron tomography: A long journey to the inner space of cells. Baumeister W. *Cell*, **2022**, https://doi.org/10.1016/j.cell.2022.06.034.

Current data processing strategies for cryo-electron tomography and subtomogram averaging. Pyle E and Zanetti G. *Biochem J*, **2021**, https://doi.org/10.1042/BCJ20200715.