Internship proposition 2025-2026

(One-page max)

Master 2 GP Medicine 4R (Repair, Replace, Regenerate, Reprogram)

Lab: Inserm U1229 Regenerative Medicine and Skeleton (RMeS)
Team: REJOINT, group StratOA

Name and position of the supervisor: Marie-Astrid Boutet, CRCN, group leader; and co-supervisor Anaïs Cardon, postdoc.

Email of the supervisor: marie-astrid.boutet@univ-nantes.fr; anais.cardon@univ-nantes.fr

Candidate (if internship filled): /

Title of the internship: Profile and spatial distribution of innate lymphoid cells in osteoarthritis synovial tissues.

Summary of the internship proposal:

Osteoarthritis (OA) is the most common rheumatic disease affecting over 500 million people worldwide. OA is an incurable and debilitating joint disease that leads to cartilage degradation, bone remodeling, and synovial tissue inflammation (synovitis).

Synovitis has been shown to play an important role in OA initiation and progression. Although the contribution of macrophage to the pathogenesis of OA is well appreciated, the contribution of other innate immune cells, and particularly innate lymphocytes to synovial inflammation in OA is poorly understood. Innate lymphoid cells (ILC) are innate lymphocytes having an important role in orchestrating immune responses and maintaining tissue homeostasis. Our preliminary results showed that ILC can be found in the synovium of both OA patients and mouse models of the disease. ILC accumulation correlated with synovial inflammation, suggesting a role for ILC in regulating synovial immune cell responses. It now appears crucial to **decipher the diversity and spatial distribution of ILC in joint tissues**, with respect to the clinical features of the patients and the histopathological features of the synovial tissues.

This project will be integrated in the framework of the international ANR project "OLYMPiC2024" (collab. I. Mattiola, Berlin, Germany), we propose to:

- Investigate **ILC gene signatures in bulk RNAseq datasets** already available, generated from 94 synovial tissues collected in end-stage OA patients;
- Analyze a new set of **spatial transcriptomic data** (Xenium, 10X Genomics) generated from FFPE synovial tissues of end-stage OA patients.
- According to the results obtained, participate in the establishment of **in vitro assays** aimed at validating the hypothesis generated by in sillico analyses.

Overall, these data will help **better understand OA physiopathology and will strongly contribute to the development of novel therapeutic strategies**.

<u>Profile(s) linked to the project:</u>

☐ Experimental Biology *(Recherche expérimentale)*
☐ Clinical Research *(Recherche clinique)*
☒ Research in data analysis (Recherche en analyse de données)