Postdoctoral research topic

• **Title of the proposed topic**: Machine Learning for extracellular matrix analysis from biological multispectral images

• **Research axis of the 3IA**: axis 3 AI for Computational Biology and Bio-inspired AI

• **Supervisor (name, affiliation, email)**: Laure Blanc-Féraud, CNRS, Morpheme team (I3S, INRIA SAM, iBV), laure.blanc-feraud@univ-cotedazur.fr

• **Potential co-supervisor** (name, affiliation): Xavier Descombes, INRIA, Morpheme team (I3S, INRIA SAM, iBV), Xavier.Descombes@inria.fr

  Ellen Van Obberghen-Schilling, INSERM, iBV, Ellen.VAN-OBBERGHEN@unice.fr

• **The laboratory and/or research group**: laboratoire I3S, équipe MORPHEME, commune INRIA SAM, I3S, iBV

**Apply by sending an email directly to the supervisor.**

**The application will include:**

• Curriculum vitae including the list of the scientific publications

• Motivation letter

• Letter of recommendation of the thesis supervisor and/or post-doc supervisor.

• **Description of the topic:**

This is an interdisciplinary research project, which aims to develop new AI methods and algorithms to analyze and extract valuable quantitative information regarding features of the extracellular matrix (ECM), a molecular scaffold for cells in tissue. This project concerns the analysis of high-content images of certain extracellular matrix components that are upregulated in disease tissue, such as cancer. It involves the development of image processing and machine learning tools for characterizing, modeling and classifying of ECM networks in tumors. Work in progress, based on confocal images of fibronectin (ECM component) networks, uses graph modeling and graph matching or optimal transport to define distances which allows to capture the dynamics of geometrical structures [1,2]. Recent technological advances in microscopy allow high resolution multiplexed imaging of large samples, using a combined scanner-multispectral imaging system. The analysis of ECM in multi-spectral whole-slide images presents several difficulties and raises image processing and machine learning issues that are yet to be resolved by currently available imaging software, including detection and modeling of multiple fibrillar structures, heterogeneity/correlation analysis of these non-cellular structures, feature extraction from massive data sets. Variable selection and learning methods will be developed in order to
define the quantitative characteristics of these fibre networks which allow discrimination and classification between healthy and tumoral environment. These studies will provide insights into the tumor ECM environment and, when confronted with results from immune/tumor cell biomarker analyses and clinical data, should assist in cancer diagnosis and treatment prediction.

The image processing tools involved in this research are segmentation/detection, graph modeling and analysis, graph correlation on multi-spectral images. In a second step, we will define a machine learning algorithm, embedding explicative properties, to characterize different states (e.g. normal, tumoral) from the defined graph representation. The project falls within the 3IA Chair of Laure Blanc-Féraud and within a digital pathology initiative in collaboration with the team of Ellen Van Obberghen-Schilling, iBV (biology lab).
