3iA Côte d'Azur
Interdisciplinary Institute for Artificial Intelligence

Postdoctoral research topic

- **Title of the proposed topic**: Deep 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 vitæ including the list of the scientific publications
- Motivation letter
- Letter of recommendation of the thesis supervisor and/or post-doc supervisor.

- Keywords : Image and graph analysis, deep learning, graph convolution network, Statistical analysis, Extracellular matrix

- Description of the topic:

This research project aims to develop new AI methods and algorithms to analyse and extract valuable quantitative information to characterize the extracellular matrix (ECM), a molecular scaffold for cells in tissue. ECM is composed of fiber networks of different proteins such as fibronectin or collagen. The transformation of their structural properties in tumour tissue contributes to cancer progression, spread and treatment resistance. Usually tumours are analysed from the cell point of view, rarely from the angle of their ECM, although it provides important complementary information. The goal of this project is to analyse quantitatively and statistically the topological and geometrical changes in fiber networks of the tumor ECM. Work in progress, based on confocal images of fibronectin (one ECM component) networks, uses graph modelling, graph matching and optimal transport to define distances, which captures the dynamics of topological and geometrical structures of the graphs from confocal microscopy images [1,2,3]. Recent technological advances in fluorescence microscopy allow high-resolution multispectral imaging of ECM in large tumor samples, thus providing information for several markers (fibronectin, collagen,...). The ECM in some regions can be

modelled by graphs which will be extracted from each spectral band to model the different components of ECM ; their homogeneity and inter-correlation will be analysed using the distance between graphs already defined. In other regions, the organization of ECM proteins is not clearly defined and structural biomarkers need to be established. As the slide scanner and multispectral imaging system produces high-resolution images at high throughput, a major goal of the post-doc will be to develop deep learning methods on multispectral images to discriminate between healthy and tumoral environments and to quantify the geometrical structure of the ECM. Where fibers are organized in networks, Deep learning methods on graphs [4] such as graph convolution network will be considered. 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 prediction of treatment response.
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).

[1] A. Grapa, G. Efthymiou, R. Meunier, S. Schaub, A. Radwanska, L. Blanc-Féraud, X. Descombes, E. Van-Obberghen-Schilling " Classification of the Fibronectin variants with curvelets " Proc. IEEE International Symposium on Biomedical Imaging (ISBI), Washington DC, USA, April 2018.
[2] A. Grapa, L. Blanc-Féraud E. Van Obberghen-Schilling and X. Descombes "Optimal Transport vs Many-to-many assignment for Graph Matching" Colloque GRETSI sur le traitement du signal et des images, Lille, France, août 2019.
[3] G. Efthymiou, A. Radwanska, A. Grapa, S. Beghelli-de la Forest Divonne, D. Grall, S. Schaub, M. Hattab, S. Pisano, M. Poet, D. Pisani, L. Counillon, X. Descombes, L. Blanc-Feraud, and E. Van Obberghen-Schilling "Fibronectin Extra Domains tune cellular responses and confer topographically distinct features to fibril networks" Journal of Cell Science, 2021.
[4] Z Zhang, P Cui, W Zhu “Deep learning on graphs: A survey” IEEE Transactions on Knowledge and Data Engineering, 2020.