

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),

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

- **The laboratory and research group:** I3S laboratory, MORPHEME group, joint INRIA SAM, I3S, iBV team.
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Apply by sending an email directly to the supervisor.

The application will include:

- **Letter of recommendation of the supervisor indicated above**
 - Curriculum vitæ including the list of the scientific publications
 - Motivation letter
 - Letter of recommendation of the thesis supervisor and/or post-doc supervisor.
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- **Keywords :** Image and graph analysis, deep learning, graph convolution network, Statistical analysis, Extra-Cellular 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. Their structural properties are transformed in presence of tumour to prevent immune cells to penetrate. Usually tumours are analysed from the cell point of view, rarely by their environment such as ECM, while it gives important complementary information. The goal of this project is to analyse quantitatively and statistically the topological and geometrical changes in fiber networks of the ECM in presence of cancer.

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 allows to capture the dynamics of topological and geometrical structures from confocal microscopy images of fibronectin [1,2,3]. Recent technological advances in microscopy allow acquiring high-resolution multispectral imaging of large samples, thus providing information

from several markers (fibronectin, collagen,...). Graphs will be extracted from each spectral band to model the different components of ECM and their homogeneity and inter-correlation will be analysed using the distance between graphs already defined. As the scanner 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 graphs [4] such as graph convolution network to discriminate and classify between healthy and tumoral environment. These studies will provide insights into the tumoral 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 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 .