

Computational Methods for Spatial Transcriptomics in Cancer Research

Project description

Digital pathology is a cornerstone of cancer diagnosis and prognosis and involves the analysis of stained tissue slides, displaying millions of individual cells, their environments, and the overall tissue structure. Computational Pathology aims at providing Computer Vision tools to analyze these images, in view of supporting pathologists in their routine tasks or to provide models capable of predicting patient variables, such as overall survival or treatment response. Pathology datasets are usually very large, involving several hundreds, sometimes thousands of tissue slides.

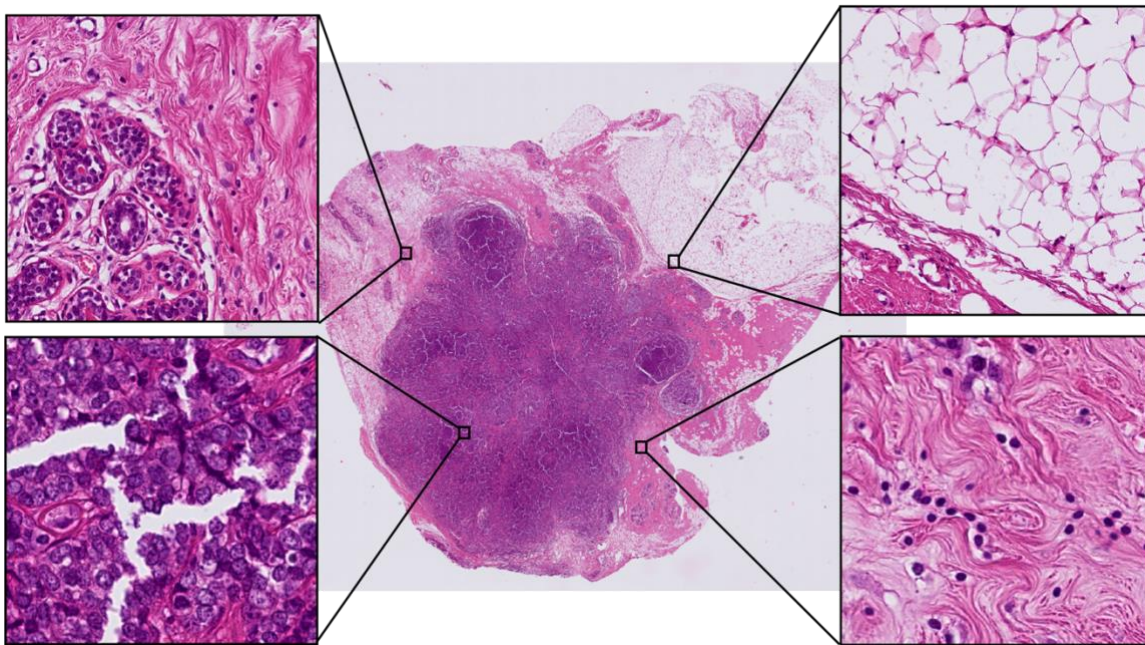


Figure 1 - Typical Whole Slide Image (WSI; here: breast cancer). Images are very large (Gigapixel range) and contain rich information on individual cells and the overall tissue architecture.

Spatial transcriptomics is a novel technique that allows to molecularly profile tissue types and cells in their spatial context. The technique comes in different flavors: image-based spatial transcriptomics (IST; expression of ~400 genes with subcellular resolution) and sequence-based spatial transcriptomics (SST; full transcriptome with a resolution of ~20 cells per spot). These data provide unprecedented insights into tissue architecture and multi-scale mechanisms

related to disease. Datasets are still scarce, as the acquisition is expensive, but our team is involved in several large-scale projects that generate large amounts of such data.

Spatial Transcriptomics comes with many interesting computational challenges. Indeed, from a computer vision perspective, spatial transcriptomics images are very large and feature a very large number of channels (hundreds to tens of thousands). Interesting questions are signal deconvolution for SST, spatial modeling of cell type arrangement. Another interesting aspect is the design of cross-modality models, allowing to reconstruct SST data from stained tissue slides, widely used in clinical practice.

The objective of this PhD project is to leverage Spatial Transcriptomics data (SST) and stained tissue slides to quantify intra-tumoral heterogeneity in bladder cancer and to investigate its relationship to outcome and treatment response. For this, the PhD student will work on a large cohort of bladder cancer, in close collaboration with experts in the fields of cancer biology and pathology.

Profile

We are looking for a highly motivated student holding a Master of Science (or an equivalent degree) in the field of Engineering, Mathematics or Informatics. Applicants should have some experience in Machine Learning, Artificial Intelligence or Computer Vision and a high degree of motivation to work in an interdisciplinary setting on biomedical applications.

Application

To apply for this position, please send your full application file to:

Thomas.Walter@minesparis.psl.eu. (subject: [PhD CBIO 2023])

The application file should contain:

- A cover letter explaining background, experience in AI / Computer Vision and the motivation to work on applications in life sciences
- Curriculum Vitae
- The name of at least one reference person (for instance the supervisor of the master thesis).

Research groups and institutions

Research group and collaborators

The project will take place at the Centre for Computational Biology (CBIO). The CBIO is a research center of Mines Paris, one of the major engineering schools for applied mathematics in France, and has an official partnership with INSERM, and the Institut Curie, a major hospital and research center dedicated to cancer. The project will be done in close collaboration with the pathology department at the Institut Curie. Our laboratory is located in the heart of Paris and we therefore benefit from an exceptional scientific and cultural environment.

Supervision

The project will take place under the supervision of Thomas Walter (<https://thomaswalter.github.io>), director of the CBIO, and Emmanuel Barillot (<https://curie.fr/personne/emmanuel-barillot>). We will further collaborate with Marvin Lerousseau (CBIO), François Radvanyi (Institut Curie) and Yves Allory (Institut Curie).