

## **Title: Multiscale spatial data analysis to decipher responses to cancer treatment**

Over the past ten years, the world of biomedical research has undergone a fast digital transformation, representing both a challenge and an opportunity. Recent advances in sequencing- and imaging-based approaches have led to a new era of spatial profiling, enabling the unbiased quantification of genes, proteins and morphological features throughout a given tissue. Health researchers and clinicians can now characterize patient samples at unprecedented depth and resolution in space and time, leading to new insights. These insights will improve diagnoses, treatments, and patient health outcomes. Despite their extraordinary potential, spatial data present significant challenges from the point of view of data analysis. Experiments generate large, complex, and multimodal datasets requiring specialized computational tools.

The Gottardo lab specializes in the development of computational tools and methods for the analysis of high-dimensional spatial and single-cell data. Our proposed project aims to integrate different spatial and single-cell data modalities generated from FFPE tissue to dissect responses to cancer treatment. Our primary objective is to create innovative machine-learning techniques that integrate morphological features extracted from digital pathology, spatial transcriptomics, proteomics, and single-cell RNA-seq data. The aim of this integration is to enhance our understanding of the tumor microenvironment by inferring cellular features and interactions between cells. Our hypothesis is that the integration of data across different modalities will lead to the discovery of new and reliable biomarkers for identifying the response to cancer treatment.

We are seeking individuals who possess a robust computational background and a keen interest in creating and utilizing novel machine learning and AI tools for spatial and single-cell data. The ideal candidate will be able to work with state-of-the-art technologies, such as spatial transcriptomics data (Visium and Xenium), FLEX single-cell RNA-seq, and Lunaphore Comet. Additionally, they will have the chance to work alongside pathologists, cancer researchers, and clinicians to apply the tools they create to cutting-edge data obtained from patient samples at Lausanne University Hospital. This will provide opportunities for translational research.