**Statistical modeling of gene expression profiles in spatial transcriptomics**

Spatial transcriptomics is a groundbreaking technology that allows the measurement of the activity of thousands of genes in a tissue sample and maps where the activity occurs. This technology has enabled the study of the spatial variation of the genes across the tissue. Comprehending gene functions and interactions in different areas of the tissue might lead to a deeper understanding of several key biological mechanisms, such as cell-cell communication or tumor-microenvironment interaction. In this talk, I will discuss some computational and statistical issues concerning three main research questions: i) the clustering of the areas of the tissue sample according to the spatial variation of the genes; ii) the existence of clusters of genes that are spatially variable only in some of the areas discovered from i); iii) the highly variable genes in the areas discovered from i) net of any spatial effect.