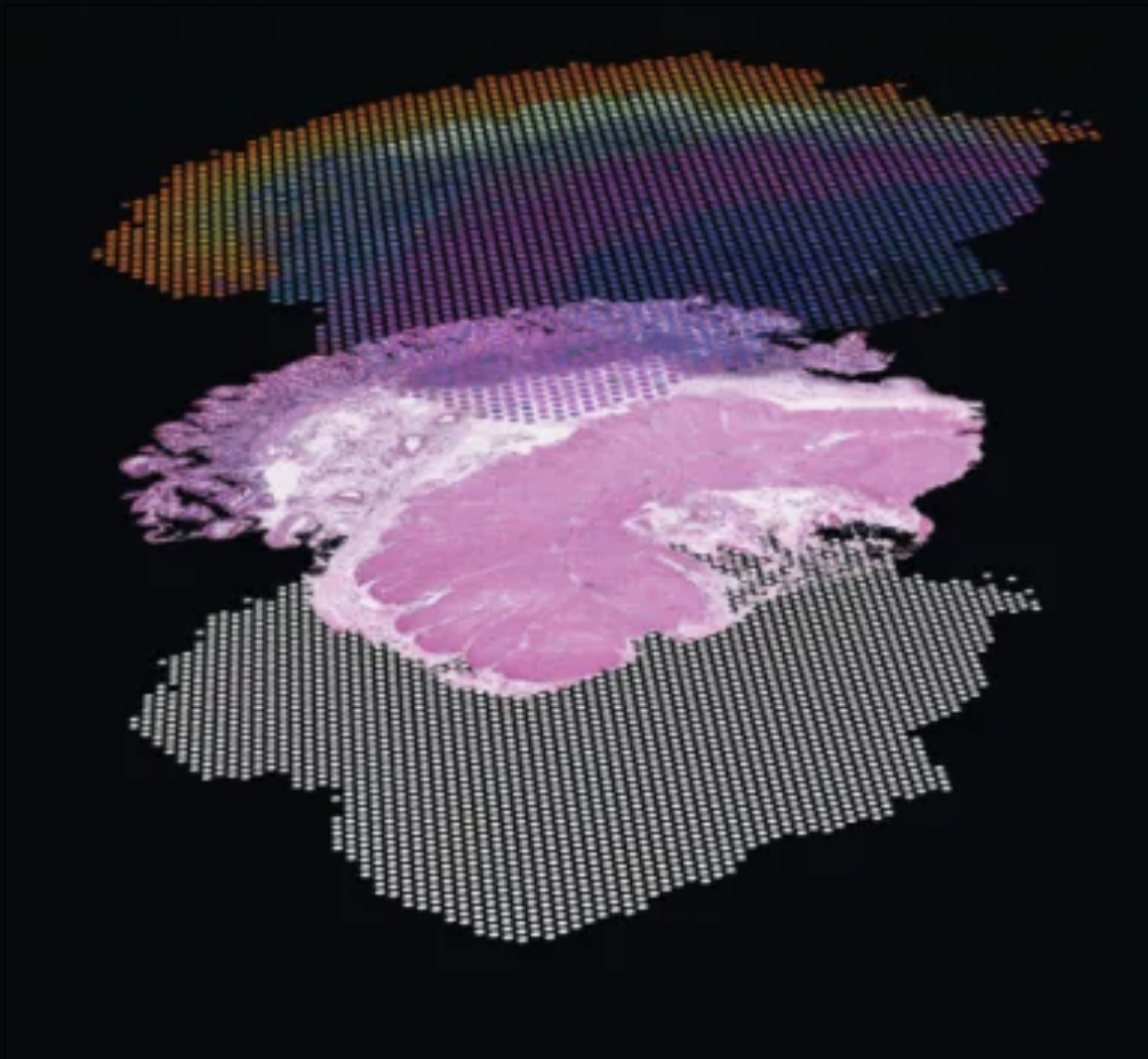# TranscriptomiC++

CSE201

Cover of Nature Methods Volume 18 Issue 1. Here spatially resolved transcriptomics has been nominated method of the year 2020 (Image: Ludvig Larsson, Natalie Stakenborg, Joakim Lundeberg and Guy Boeckxstaens Cover Design: Thomas Phillips)

MOTIVATION

• WHY CANCER AND GENOME?

It's clear nowadays that there's an important connection between cancer and human genome, but this correlation is a difficult thing to study because the gene expression of cancer cells has an high variability among people and among the tissues of the single person. Moreover, there can be many mutations developing over the time and if we want to understand and cure cancer is crucial to study the interactions between cancer cells and their neighbouring cells (to see how cancer cells are escaping the T-cells, for example). Because of that, we can't limit ourselves to the study of the DNA, but we need to study the RNA since it is the "instruction list" that guides the cells' behaviour/metabolism.

• WHAT IS THE POWER OF SPATIAL TRANSCRIPTOMICS?

Thoroughly characterising cells within the context of their relative locations within tissue is important for understanding both normal development and factors that underlie diseases.   Sequencing-based spatial analysis allows researchers to measure gene or protein expression while simultaneously determining where that activity occurs. **Here** you can find the video I showed you during my pitch and **here** you can find the paper about one technology of spatial transcriptomics showed in the video.

THE PROJECT

• WHAT HAVE BEEN DONE SO FAR?

This summer I tried to develop some algorithm to process these huge amount of data and tried to leverage the idea of *colocalization* to group genes acting in the same biological process. There's already some written code in Python that we will revise together. I would be more than happy to hear about new and different implementations and approaches.

• WHAT IS THE AIM OF THIS PROJECT?

The target would be to take as input the Spatial Transcriptomics data, process them and give as output of the pipeline the possibility to look at the spatial distribution on *any biological process* of interest. In other words, a biologist could use our tool and answer the questions like: "where is hypoxia happening in this clinical sample?", "What are T-Cells doing in this part of the tissue?", etc…

• WHO SHOULD JOIN THIS PROJECT?

Anyone interested in challenging him/herself with a state-of-the-art research project is welcome, but in particular it would be nice to have:

- At least 4/5 people in the **R&D team**: these people should be interested in mathematical modelling and biology. Big part of their work will be to research the available literature, adapt the methods and ideas found to our project and produce some "proof of work code" that if promising will be later implemented.
- At least 4/5 people in the **Backend/Algorithm Optimisation team**: these people should be relatively strong coders passionate about efficient memory/computational resources allocation and cloud computing. They will have the hard job to implement in an efficient way the ideas produced by the R&D team.
- At least 1/2 people in the **Database and API team:** these people will be also part of the Backend/ Algorithm Optimisation team, but in particular they will have the to figure out how to let our platform interact with some existing databases to retrieve some information needed for the analysis.
- At least 2/3 people in the **Frontend team**: as the name suggests, these people should be creatives and passionate about graphic design.They will work on the platform UX and general aesthetic. We want this to be an intuitive tool that any scientist without a coding background should be able to use.

Disclaimer: *No prior knowledge in any of these fields is required*. We will figure out all together how to do these things. Roles are not fixed and if we want we could also have some sort of "team rotations" so that everyone will have the chance do everything inside the group (or in general to participate in all the roles he/she likes)

• WHAT CAN YOU GET FROM THIS PROJECT?

This research project has the potential to give a meaningful contribution to state-of-the-art research. You will have the possibility to interact with real scientists and other experts, increasing your network. Moreover, if the methods developed are good enough this could also lead to a *paper publication* (this would really stand out in your CV for any research research position next summer and in the following years).