Spatial FluxVis- a dashboard for simplifying spatial fluxomics

Brandon Coke[1], Annalisa Occhipinti[1]
1 Health Data Research UK, 2 Teeside University

Introduction- What is fluxomics and why is it important?

Fluxomics is means of **measuring how fast cells break down and make** the chemicals the need to grow and survive. This rate of break down and creation of chemicals are referred to as **metabolic fluxes**. Fluxomics has been used to:

- Understand **cancer metabolism** to better understand chemotherapy resistance and **develop more powerful treatments.**
- Untangle the **mechanisms of complex diseases** such as Alzheimers where abnormal metabolism may play a role in the development of the disease.
- **Tackle antimicrobial resistance**- by understanding how disease-causing bacteria (pathogens) develop resistance to our therapies.

A **major hurdle** in fluxomics is getting down to the **resolution of individual cells**. Single cell metabolomics is in its infancy- there are no mature platforms for researchers to use. In contrast, **single cell proteomics and RNA-seq**- which measures protein and RNA levels respectively are **mature 'omics platforms** where we can **reliably get accurate metabolic fluxes** by estimating levels using enzyme expression levels.

To ease this process- in this project aims to **develop a pipeline** to download, process and finally visualise single cell spatial fluxomics by leverging **matched transcriptomic and histological data** from the HEST-1K database- a database which stores spatial single cell (sc) RNA-seq data- i.e. the expression of genes of individual cells as well as their position from images of the tissues.

Objectives

1) Develop a pipeline that download, process and normalise RNA-seq data from the HEST-1K database
2) Leverage scFEA to convert the spatial transcriptomics data into fluxomics data.
3) Match the coordinates in the RNA-seq spot data to the imaging data.
4) Create Spatial FluxVis- a python dashboard that is able to visualise the transcriptomic and fluxomics data.

Methods and results

To process the raw data from the HEST-1K database I used the python package **scanpy to normalise and correct** for artefacts in the scRNA-seq data. Once normalised I feed this data into **scFEA to estimate the metabolic fluxes**. This package uses enzyme expression levels to estimate rate of metabolism for a given pathway in groups called modules.

I then used **pandas to extract the coordinates** for each spot in the data using the json files included with each entry in the database. Alongside this I used **scikit-image and PIL to downscale** and convert the images to mesh array in order to **generate interactive spot plots using Altair**.

Finally, I used **dash to create an interactive dashboard** to visualise the spatial data via the Spatial FluxVis dashboard. Altogether other users can use this pipeline to visualise their own spatial fluxomic data starting from raw transcriptomics data.

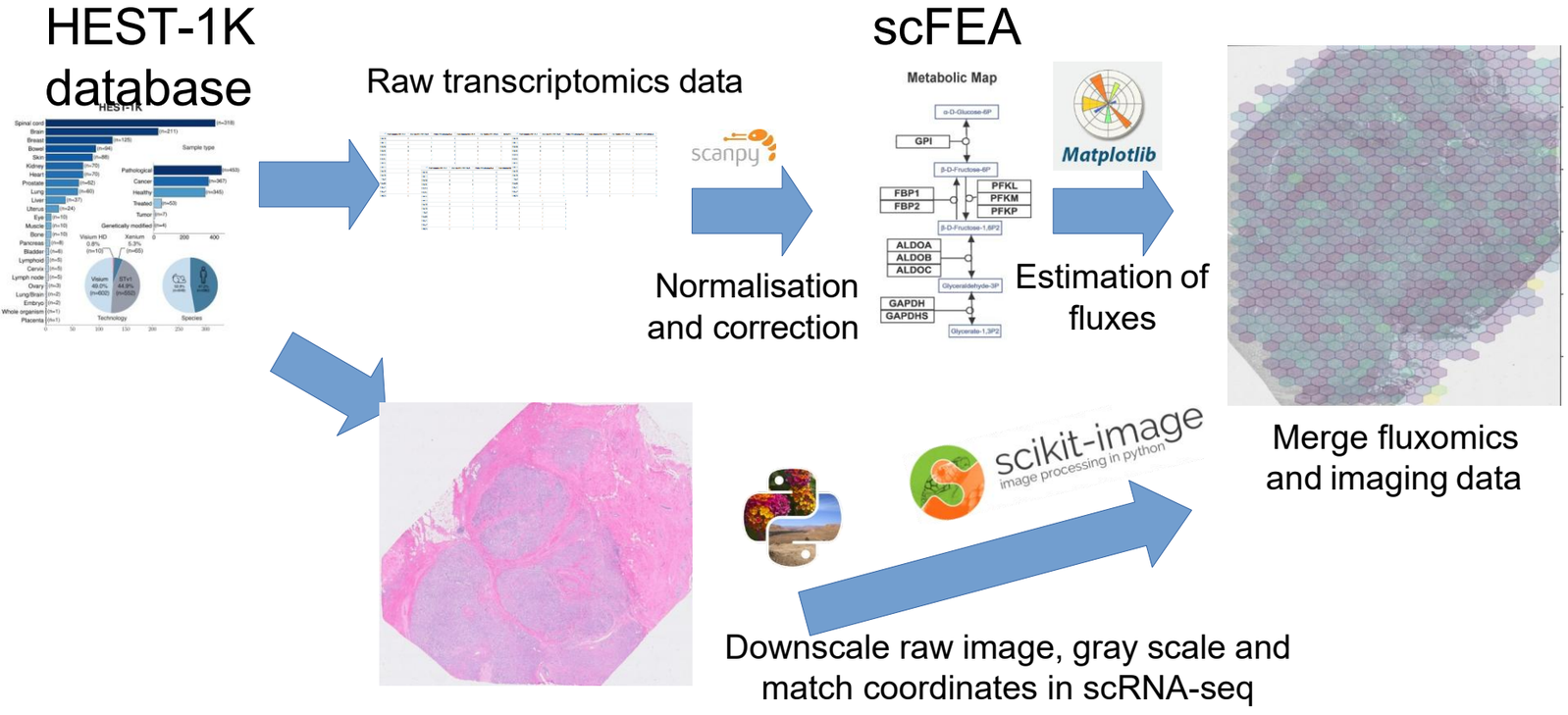

Figure 1- Overview of project- data processing

Discussion

This project has developed an easy-to-use pipeline to go from **raw scRNA-seq data**, convert **into fluxomics data** and finally **visualise the spatial data** using an interactive dashboard- Spatial FluxVis.

This work is the first steps to make **fluxomics analysis more intuitive and approachable** for researchers less familiar with computational data analysis as well **leverage the wealth of transcriptomic data** we have available.

By visualising the spatial data researchers can identify whether there are regions of active growth in cancer and better understand how treat more advanced and complex cancer types.

Next steps...

- Optimise performance- remove support for multiple files or ability to upload files.
- Incorporate CellTypist to predict different cell types in the maps produced.
- Integrating processing step from HEST-1K database into application.
- Develop support for other organisms- enabling research to visualise fluxomics from pathogens i.e. disease causing bacteria.

Acknowledgements

- Dr Annalisa Occhipinti and her lab for their expertises during the project in fluxomics.
- HDRUK for funding and training.
- Northern Health Futures (NorthFutures) Hub for sponsoring this project.

Citations

Email: bc7900@gmail.com

This work was supported by the Engineering and Physical Sciences Research Council [Grant EP/X031012/1]