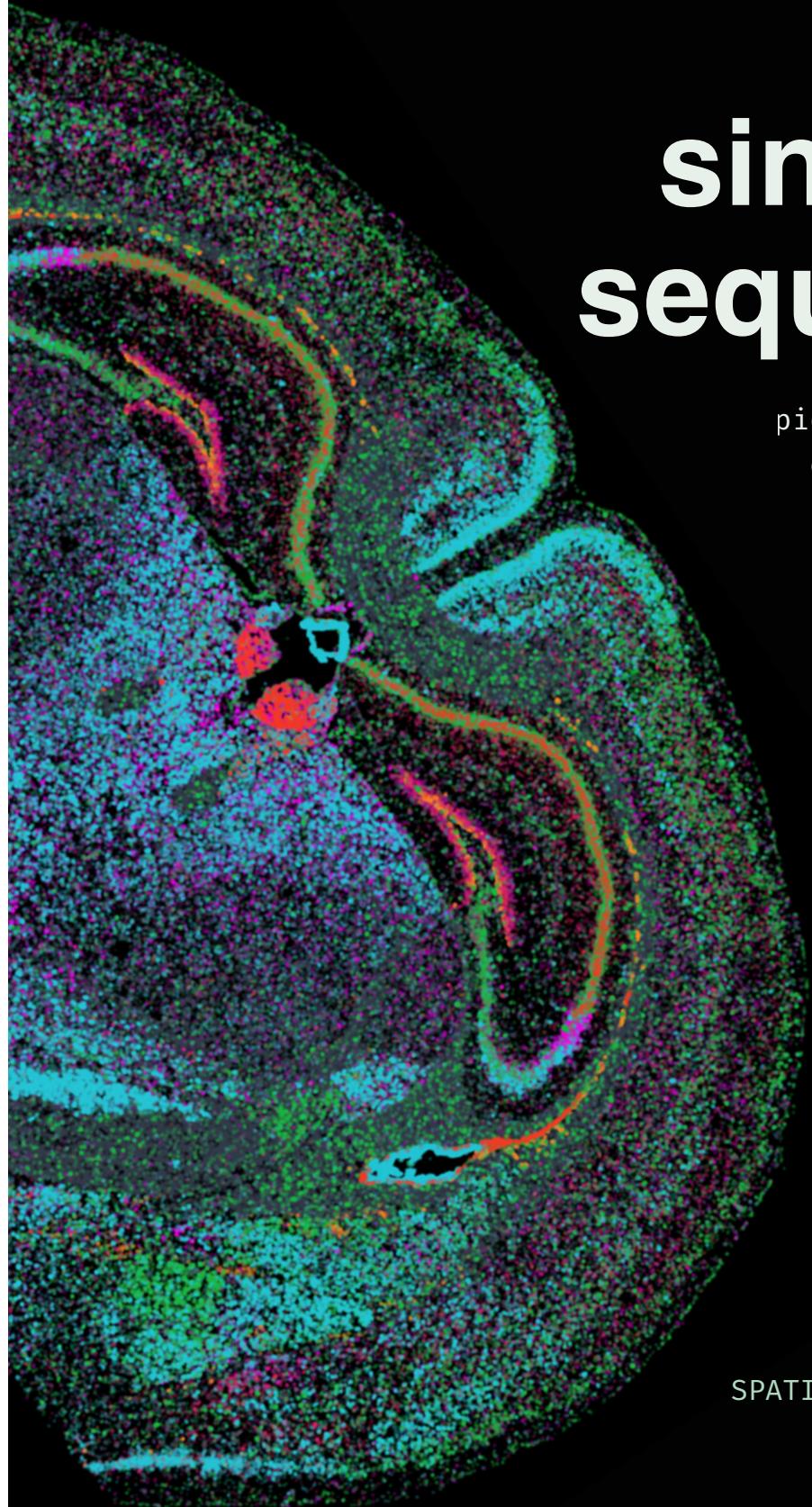


spatial single-cell sequencing

piecing together the puzzle
of cellular heterogeneity



SOCIETY NEWS

MEET THE TEAM

SPATIAL SINGLE-CELL SEQUENCING

CODE YOUR WAY

Society News



BINFSOC

Recent Events.

-- Discord Games Night

Upcoming Events.

-- Paint & Sip Term 2 Week 2

-- Barbeque Term 2 Week 3

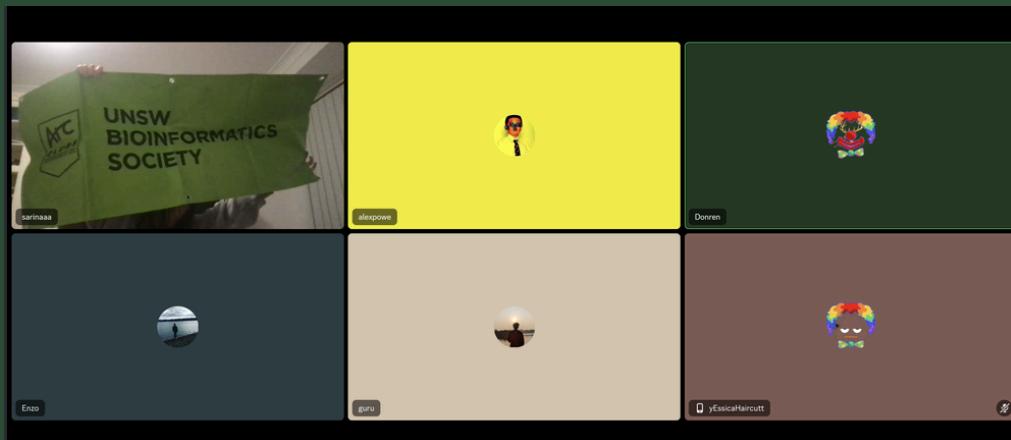
-- Networking Night Term 2 Week 4

B

DISCORD GAMES NIGHT



During Week 9 of Term 1, BINFSOC hosted its much-anticipated online event - Discord Games Night, bringing together bioinformatics students for an evening of fun and jollity. Within the span of one hour, participants bonded over a variety of engaging activities like Skribbl.io, Gartic Phone and Bobble League, sharing laughter and creating memories with fellow members of their cohort. The friendly competitions and lively interactions between students served as the perfect opportunity to unwind and relax right before the exam period, providing a well-deserved and much-needed break from their academic endeavours. Overall, the event was a resounding success, and we wish to continue fostering such enjoyable experiences for bioinformatics students in the future.



Meet the team

BINF SOC TEAM 2024



Donren Leung

president_

fun fact: I accidentally fell asleep in BINF2010 and extended the lecture recording by 1 hour



Anish Sanghvi

vice president_

fun fact: I have seen 'Madagascar 3' 31 times



Albert Tan

general secretary_

fun fact: I have multiple food allergies



Simon Wu

treasurer_

fun fact: I love listening to people argue in their native language - yes, even if I don't understand them



Education

executive:

**NADIL
KUMBUKAGE**

subcom members:

- Max
- Dragon

Pubs/IT

executive:

**YVONNE
HUANG**

subcom members:

- Gavin
- Rubin



HR

executive:

**ALEX
CHIN**

subcom members:

- | | |
|------------|----------|
| -- Lorenzo | -- Jake |
| -- Hannah | -- Jaime |

Sponsorships

executive:

DONREN
LEUNG

subcom members:

-- Jessica L -- Jessica P
-- Jaime



Events

executive:

SARINA
CHAI

subcom members:

-- Stanley -- Martina -- Jessica L
-- Guru -- Arijq



Marketing

executive:

SIMON
WU

subcom members:

-- Julian -- Emaan
-- Geoni -- Lipda

piecing together the puzzle of cellular heterogeneity

Author: Rubin Roy Compiled: Rubin Roy Edit: Yvonne Huang



spatial single-cell sequencing

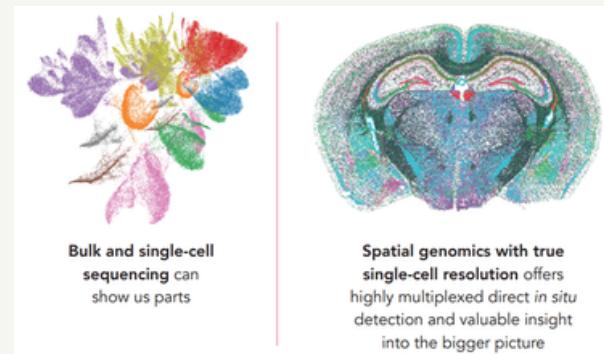
Following on from our last article on [single-cell sequencing \(scRNA-seq\)](#) featured in BINFsights22, we will now be looking into the next wave of single cell analysis - [spatially resolved transcriptomics \(SRT\)](#), which was crowned Nature's method of the year in 2020.

Over the past decade, single-cell sequencing has become a staple in the field of biomedical research for obtaining high-resolution transcriptomes of individual cells. Conventional scRNA-seq techniques do not provide contextual information regarding the positions of these cells in a sample, which can be useful in informing their identity and function. This is where spatially resolved transcriptomics proves useful: a single-cell sequencing technique that preserves spatial information.

Why is spatial context important?

Cell biology is all about the context surrounding the complex network of interactions that take place between cells - the smallest building blocks of living organisms. Accordingly, the ability to decipher the spatial organisation of cells within tissues can be highly valuable in providing information regarding the cells' states, identities, phenotypes, as well as the signals they are exposed to.

This is why spatial single-cell sequencing is a key technological advancement in helping to further our knowledge on the complex organisation of cells and tissues, ultimately unveiling important biological functions.



Visual comparison between regular single cell sequencing and spatial single cell sequencing which fits the parts found using the latter together. Image: Vizgen

How does spatially resolved transcriptomics work?

To understand spatial single-cell sequencing we need to delve into the workflows that are currently available. There are currently two main approaches: [imaging-based](#) and [sequencing-based](#) technologies.

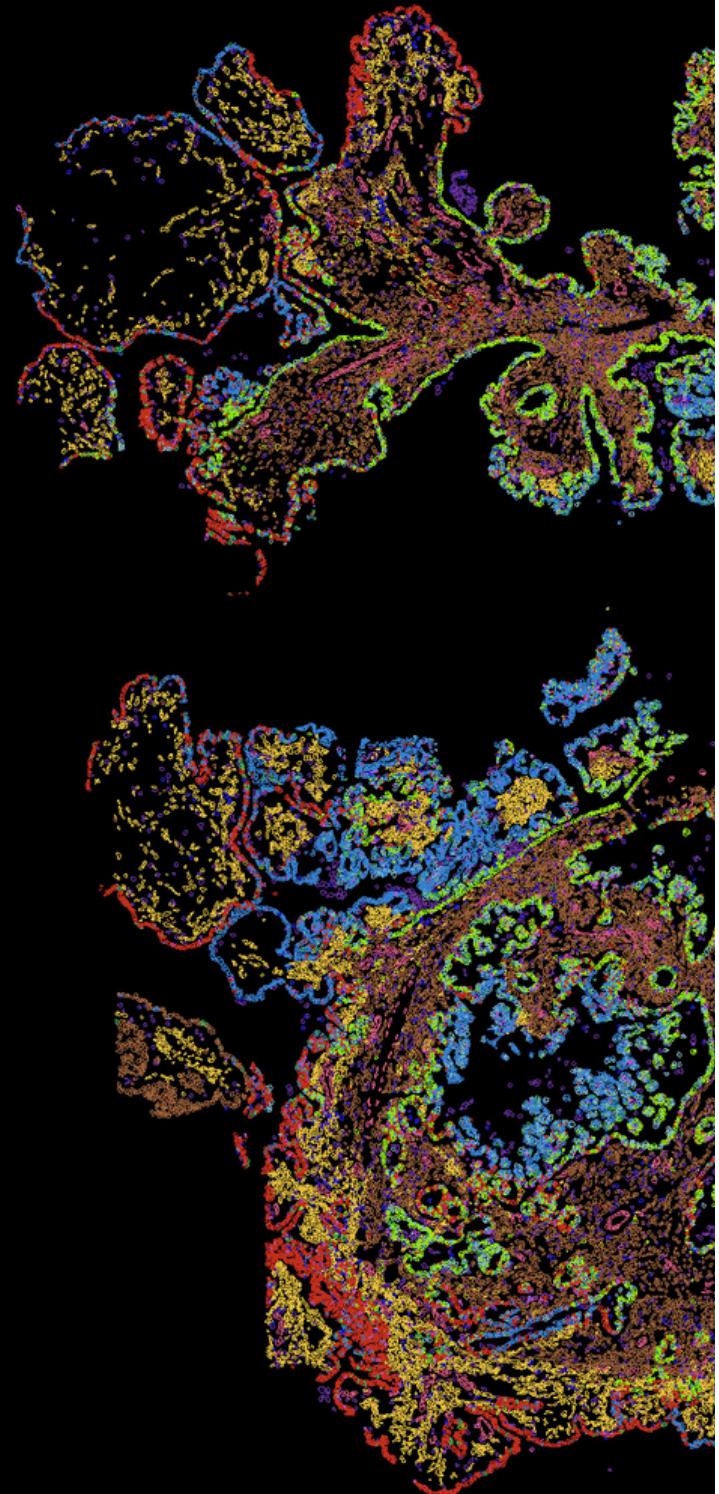
Imaging-based techniques involve *in situ* measurements of mRNA expression through [in situ hybridisation \(ISH\)](#) or [in situ sequencing \(ISS\)](#). The [single-molecule FISH \(smFISH\)](#) method is the current gold standard for transcript detection. This combines fluorescence [in situ hybridisation \(FISH\)](#) with digital imaging

microscopy, where fluorochrome-labelled probes are hybridised to target mRNAs *in situ* and then imaged using microscopy. On the other hand, sequencing-based technologies involve the extraction and subsequently profiling of mRNAs *in vitro* via next-generation sequencing (NGS) techniques, preserving spatial information through direct recording of location or through spatially-barcoded microarray probes.

Once the data has been collected, bioinformatics tools are extremely useful in conducting downstream analyses of the huge volumes of sequencing data, computationally reconstructing the spatial organisation of cells within the tissue to uncover meaningful insights. Some utility packages that have been developed for this purpose include [Giotto](#), [STUtility](#), [Seurat](#) in R and [scapy](#), [stLearn](#), [squidpy](#) in Python. Major insights include the architecture of tissues consisting of cellular arrangements within anatomical regions. In addition, cell interactions within their microenvironment can also be studied to unveil factors that influence cellular behaviour.

Potential applications

The application of spatial single-cell sequencing has the potential to impact a range of biomedical sub-disciplines including neuroscience, immunology, and developmental biology. In studying complex diseases such as cancer, the ability to



FFPE human ovarian cancer sample was analysed by MERSCOPE. Image: Vizgen

capture spatial information enables researchers to gain insights into tumour heterogeneity and identify rare cell populations that have the potential of functioning as targets for treatment via precision medicine. Furthermore, using spatial single-cell sequencing to study embryonic development can enhance understanding of tissue patterning in the formation of organs and anatomical structures. In the field of neuroscience, spatial mapping can prove useful in understanding the distribution of neuronal subtypes and their connections with each other, which combine to form neural circuits. This aids our ability to comprehend neurological disorders and brain signalling. Finally, spatial single-cell sequencing enables further investigation into the spatial interactions of immune cells which can shed light on immune responses and their association with autoimmune diseases.

Current challenges

The evident promise of spatial single-cell sequencing unfortunately faces several challenges including technical limitations, data integration and accessibility. Currently, limited spatial resolution, low capture efficiency and high background noise make it difficult to ensure reliable and accurate capturing of spatial data. While high throughput methods are available, they are often quite expensive and hence are inaccessible for smaller

labs or those in lower socioeconomic regions. Another challenge faced by SRT is the integration of spatial information with single-cell sequencing data, which is computationally demanding due to the large scale and high dimensionality of spatial datasets. Hence, developing improved bioinformatics tools that are scalable and capable of processing this data is essential for advancing this field.

Conclusion

In conclusion, spatial single-cell sequencing presents itself as the next chapter in the development of single-cell sequencing technology which will deepen our understanding of biological systems. This revolutionary technology bridges the gap between single-cell genomics and spatial biology to provide more insights that will drive the development of new medications and research. As we strive to further our understanding within the field of biology the advent of spatial single-cell sequencing will undoubtedly propel scientific discovery in the future.

References and further reading:

- nature.com/articles/s41592-020-01033-y
- genomemedicine.biomedcentral.com/articles/10.1186/s13073-022-01075-1
- ncbi.nlm.nih.gov/pmc/articles/PMC9891446

Code Your Way



Welcome back to "Code Your Way"

In this issue, the BINFSOC team is pleased to bring you another installment featuring select shell, Python, Perl or R commands. These will be further illustrated with examples that are relevant to Bioinformatics, be it data retrieval, manipulation, or visualisation. We hope you enjoy learning or refreshing your memory.

Your feedback is crucial to us – if you would like us to cover something, please do write to us at the address shared on the last page.

Author: Gavin Li Compiled: Gavin Li Edit: Yvonne Huang



Git pt. 2

Set-up Environment

To set up your Git environment for the first time, follow these steps:

Configuration Levels:

Git configuration variables are stored in 3 places:

- System-wide:
`~/.gitconfig` or `~/.config/git/config`
- User-specific:
`.git/config`
- Repository-specific:
`[path]/etc/gitconfig`

Viewing Configuration:

To view all configuration settings that are in effect for your Git environment, along with their origins:

```
$ git config --list  
--show-origin
```

Setting Your Identity:

Set your username and email address (please use your own name and email)

- Username:
`$ git config --global user.name "John Doe"`
- Email:
`$ git config --global user.email johndoe@example.com`

Configuring Your Editor:

- Set your default text editor (e.g., Emacs):
`$ git config --global core.editor emacs`
- On Windows, specify the full path to the executable file.

Git pt. 2

What is GitLab?



If you have read all the way up to here, you might know quite well what GitHub is. However, this section delves on a relative of GitHub's - GitLab.

GitLab is a web-based platform offering comprehensive DevOps capabilities, including project planning, source code management, CI/CD automation, monitoring, and security features. Similar to GitHub, GitLab is built on Git for version control but provides a single application for the entire software development lifecycle. It integrates project management tools like issue tracking and kanban boards, streamlining collaboration. GitLab's CI/CD pipeline automates testing, building, and deployment processes directly from the

repository, ensuring rapid and consistent delivery of code changes. Monitoring tools enable teams to track application performance and health within the GitLab interface.

Additionally, GitLab incorporates security features like SAST, DAST, and dependency scanning, identifying and addressing vulnerabilities early in the development cycle. While GitHub focuses primarily on code hosting and collaboration, GitLab's integrated approach offers a comprehensive solution for teams looking to optimise their DevOps workflows and improve productivity.

Git pt. 2

GitLab vs. GitHub?

SIMILARITIES

Git-Based Version Control:

Both platforms are based on Git, providing developers with version control capabilities such as branching, merging, and commit history tracking. This common foundation manage code changes efficiently and seamless collaboration.

Collaboration Features:

Both platforms offer issue tracking, pull requests, and review tools. These features means developers can communicate, review code changes, and address issues, enhancing teamwork and code quality.

Community Engagement:

Both platforms have vibrant open-source projects, and organisations sharing code and contributing on projects.

DIFFERENCES

Business Model:

GitLab employs an open-core model, with core features open-source and enterprise features under a commercial license. GitHub mainly hosts Git repositories, bundling extras like issue tracking and project management.

Feature Set:

Both platforms offer core functionalities like version control and collaboration tools. However, GitLab stands out with its comprehensive suite covering the entire DevOps lifecycle, including CI/CD pipelines, monitoring, and security features, streamlining workflow management.

Focus on DevOps:

GitLab integrates project planning, source code management, CI/CD, monitoring, and security in its DevOps platform. GitHub focuses on code hosting and collaboration.

Git pt. 2

Basic commands (pt. 2)

> git add [file]	Add file changes to the staging area.
> git commit -m "[message]"	Commit staged changes with a descriptive message.
> git status	View the status of tracked and untracked files.
> git diff	Show the differences between the working directory and the staging area.
> git log	Display the commit history.
> git remote -v	List all remote repositories and their URLs.
> git fetch [remote]	Fetch changes from a remote repository without merging.
> git reset [file]	Unstage changes for a specific file.

Contact us



IF YOU HAVE ANY COMMENTS or feedback regarding BINFsights, please write to us at binfo@unswbinfsoc.com

We also encourage anyone to share with us anything you'd like us to take a look at, be it a bioinformatics tool that you have made or find useful; or news in the bioinformatics world that you'd like to see written about in future issues.



TO VIEW PAST AND PRESENT issues of BINFsights, check out our website at unswbinfsoc.com/binfo
Stay tuned on our Facebook page for updates regarding events and society news.

-- The BINFSOC Team

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