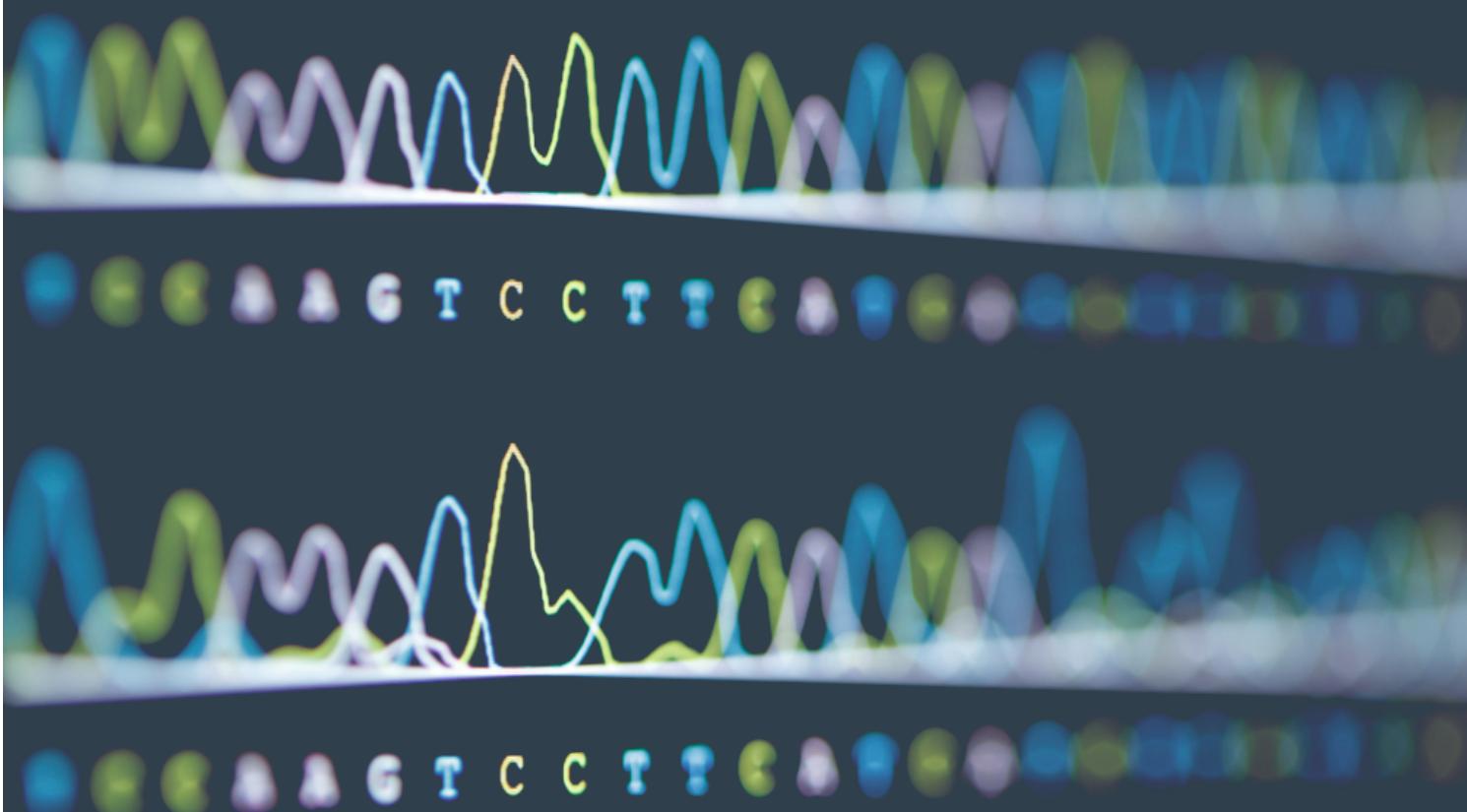


# single-cell omics

# unveiling the mysteries of cellular heterogeneity



SOCIETY NEWS

## PRESIDENT'S ADDRESS RECENT EVENT ROUND-UP

SINGLE-CELL OMICS

IMAGE SOURCE:  
Turtle Rock Scientific/Science Photo Library

# Society News



BINF  
SOC

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## Recent Events.

- Hackathon
- Meet Your Cohort Lunch
- Subcommittee Induction
- Peer Mentoring
- Escape Room

## Upcoming Events.

- |                        |                         |
|------------------------|-------------------------|
| -- Discord Games Night | 12th April, 19:30-20:30 |
| -- Paint & Sip         | Term 2                  |
| -- Networking Night    | Term 2                  |

# President's Address



## Welcome to the first BINFsights issue for 2024!

It's a thrill to be back as we leap into another year brimming with ideas and boundless passion. Reflecting on our journey since our inception in 2021, our resolve has never been stronger to foster meaningful connections, broaden education, and ignite inspiration to create a vibrant and supportive space within bioinformatics.

A big thank you to everyone's unwavering support which has made our growth and successes possible — undeniably we would not be where we are without each of you.

Looking back, 2023 was a flourishing year where we witnessed the launch of our Education portfolio, and our venture into the booming world of TikTok. For the first time, we held our flagship Annual Industry Networking Night in the Ainsworth Design Studio, gathering the highest attendance we'd ever seen. We joined forces with COMBINE and SPDSC to host a Bioinformatics Analysis Hackathon as our first inter-university event ever, and had plenty of other inter-society collaborations like the Amazing Race last term.

As we navigate through the rest of Term 1, we have been delighted to see record-shattering engagement in our Peer Mentoring program and Subcommittee recruitment drive. It has also been heart-warming to meet so many new faces at the O-Week stall, Meet your Cohort Lunch, Paint Bears, and Escape Room challenge — truly a testament to the warm and tight-knit community we are nurturing at BINFSOC.

So what's on the horizon?

Get ready to mark your Term 2 calendar with Paint and Sip with BABSOC, the highly-anticipated Annual Industry Networking Night, and many more inter-society projects we can't wait to announce. Plus watch out for your chance to rep BINFSOC in style with our upcoming yearly merch release!

Here's to higher heights as the rest of 2024 unfolds for us. Together, let's make this year one for the history books!



**DONREN LEUNG**

BINFSOC PRESIDENT 2024

# B

# Hackathon



The inaugural COMBINE x BINFSOC x SPDSC Hackathon, held in September last year, marked a historic moment as our society's first ever inter-university event, bringing together 27 students from UNSW and USYD to delve into the innovative world of bioinformatics.

Seven teams were challenged to perform bioinformatics analysis in the areas of RNA-Seq, Proteomics and Spatial Transcriptomics, culminating in a spectacular showcase of presentations aided by aesthetic and compelling and visualisations. All groups performed exceptionally well, producing a high quality of analysis in a single day!

We would like to extend a huge thank you to the [UNSW Engineering Faculty](#), [COMBINE](#) and the [Sydney Precision Data Science Centre](#) for making this event possible.

— The 2023 BINFSOC Team



# B

# SUBCOM INDUCTION

We are thrilled to kick off 2024 by welcoming a record-breaking 19 subcommittee members across our 6 portfolios: Marketing, Events, Human Resources, Publications/IT, Sponsorships, and Education.

For many, Induction Day on Week 4 Saturday marked their first time coming together as a team. The event balanced formalities such as briefings over roles and responsibilities, with ample casual opportunities for team bonding. Activities ranged from human bingo, a heartwarming Pizza Hut lunch, and a lively karaoke session that tore our voices and ears apart. The evening brought us closer with a group dinner, after which we meandered through the city before calling it a day.

These moments of shared laughter have not only laid the foundation for cohesive teamwork, but also hold the promise of a memorable journey ahead. As we move forward, this sense of camaraderie will undoubtedly serve as a catalyst for our collective success in BINFSOC.



*Welcome aboard, 2024 BINFSOC team!*

# B

# PEER MENTORING

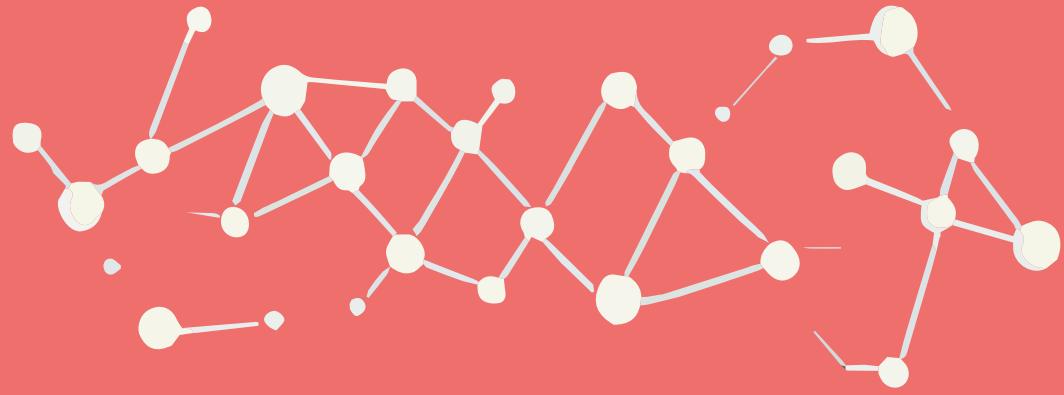
An annual tradition that we are glad to continue this year is our Peer Mentoring program. We recruited senior students as mentors who are willing to share their experiences as they near the end of their academic journeys. Having completed the UNSW Peer mentoring training, these mentors are grouped up with mentees who, still in their early years of university, are eager to gain insights that can help them navigate through their programs.



From painting keychains to weekly catch-ups on the latest BINFSOC updates, our Peer Mentoring program has seen success in socially engaging students as they immerse themselves in a bigger cohort, make newfound connections as well as stay informed of all the events and opportunities that BINFSOC has to offer. We can't wait to witness the diverse range of experience that the Peer Mentoring program will bring forth in the upcoming weeks.



*Experts at hand, painting the bears.*



# unveiling the mysteries of cellular heterogeneity

*Author: Rubin Roy      Compiled: Rubin Roy*

# single-cell omics

In the realm of biological research, the advent of **single-cell omics** has sparked a revolution, illuminating the intricate world of individual cells and unravelling the complexities of cellular heterogeneity. This cutting-edge technology has transcended traditional bulk analysis methods, allowing scientists to delve deep into the molecular landscape of single cells and gain unprecedented insights into cellular functions and interactions. Single-cell omics has opened new frontiers in understanding the fundamental building blocks of life and as such is bound to revolutionise medicine.

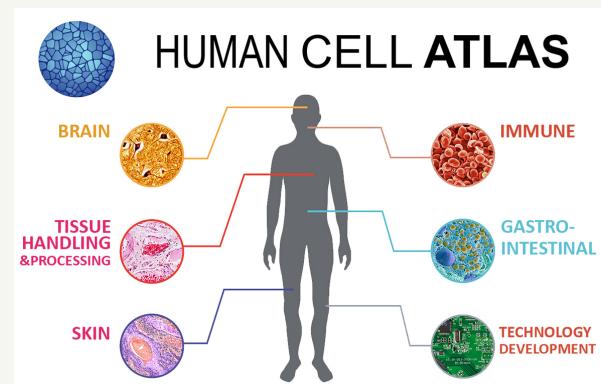
## What is single-cell omics and scRNA-seq?

So what is single-cell omics? Put simply, it is the study of biological molecules at the single cell level and encompasses different areas such as genomics, transcriptomics, proteomics, metabolomics and other such approaches. A key technique within this area of study is known as single-cell sequencing which is used to sequence the DNA or RNA of individual cells. Take for example a blood sample, which is a complex mixture of different cell types from which we want to see the gene expression of a single cell.

This can be analogised to trying to identify the taste of a blueberry in a fruit smoothie composed of various other fruits. Clearly, it sounds like a tricky task, however using **single cell RNA sequencing (scRNA-seq)** we are now able to measure the expression levels of thousands of genes within individual cells.

## How is it useful?

Now you may be wondering, how is this useful? Well, there are 37.2 trillion cells in the human body and the ability to analyse individual cells enables us to hence build our understanding of the different cell types that make up the human body, as well as how subpopulations of these cells respond to stimuli. Projects like the **Human Cell Atlas** utilise single cell RNA sequencing to create a complete map of all the cell types in the human body.



Different areas of research that drive the Human Cell Atlas project, including various cell types. Image: Human Cell Atlas

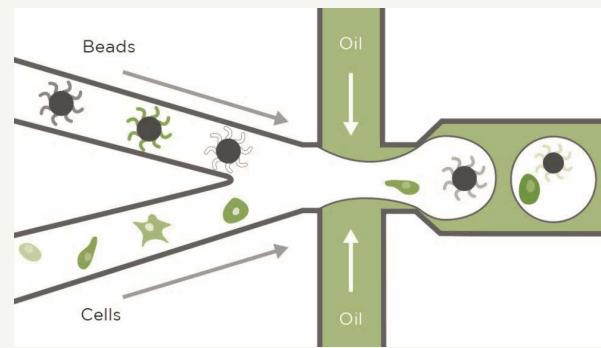
By examining the transcriptome at a single-cell level, we are able to study the molecular characteristics and functional importance of millions of cells. This provides a high-resolution view of the cellular dynamics within a tissue or organism.

A few prospective developments include personalised medicine that is more suitable and effective for different individuals, and targeted treatments that can work on a single cell basis, for example only targeting cancerous cells. Branching out of the field of medicine, single cell sequencing can also be used to explore microbial systems, agricultural systems and environmental processes which can lead to improvements in ecosystem management, crop yields and support our efforts against environmental challenges such as climate change and pollution.

### Single-cell RNA technology

Let's now take a detailed look into how single cell RNA sequencing works. The first step requires cells to be isolated from the sample of interest which can be accomplished using a variety of methods including **fluorescence-activated cell sorting (FACS)**, **microfluidics-based techniques**, or **manual isolation** under a microscope.

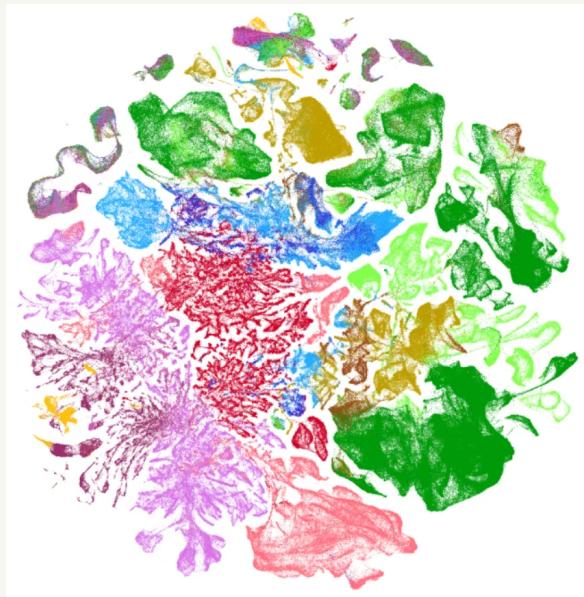
Next, the individual cells are lysed to release their RNA content mainly in the form of **messenger RNA (mRNA)** molecules which are then purified and reverse transcribed into **complementary DNA (cDNA)**. The cDNA is then amplified using **polymerase chain reaction (PCR)** and tagged with sequencing adapters in preparation for sequencing.



Droplet-based microfluidics technique for single-cell RNA sequencing. Isolated cells are co-encapsulated with beads that are uniquely barcoded with oligonucleotides in oil micro-droplets. The cells are lysed after mixing to allow for hybridisation and reverse transcription. Image: Dolomite Bio.

Adapters contain **unique molecular identifiers (UMIs)** or **barcodes** that enable the identification of these cells' origin once they are pooled together into libraries. Then, the libraries are subjected to high-throughput sequencing via platforms such as Illumina. The sequence data generated can be analysed and involves the alignment or mapping of sequencing reads to a reference genome or transcriptome, as well as the quantification and identification of different gene expressions between cells.

Finally, computational methods are employed to cluster cells based on their gene expression profiles which can then be visualised in two or three dimensions to identify distinct cell populations and explore their relationships with each other.



UMAP representation of ~4 million single-cell transcriptomes from an adult mouse brain, labelled by source brain region.  
Image: Yao Z. et al. 2023, Nature.

## Conclusion

Single-cell omics mark a pivotal advancement in the field of bioinformatics. Its ability to unravel cellular heterogeneity via a granular approach to cellular analysis establishes it as a driving force for future drug discoveries and precision drug delivery — the gateway for personalised medicine.

With the help of bioinformatics to effectively manage, analyse and interpret the vast and complex scRNA-seq data, the future potential for single-cell omics is immense as we strive to deepen our understanding of life at its most fundamental level.

## References and further reading:

- <https://www.humancellatlas.org/>
- <https://www.nature.com/articles/s41580-023-00615-w>
- <https://img1.17img.cn/17img/files/201711/attachment/bcda0535-3742-4c84-b064-8ea3abb24cdd.pdf>
- <https://www.nature.com/articles/s41586-023-06812-z>

# Code Your Way



Welcome back to "Code Your Way"

The BINFSOC team is pleased to bring you another installment of our section discussing some 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.

If you want us to cover something, please do write to us at the address shared on the last page.

*Author: Gavin Li   Compiled: Yvonne Huang*



# Git

## What is Git?



# git

Git, the cornerstone of modern version control systems, revolutionises the management of project development by fundamentally altering how data is stored and tracked. Unlike traditional systems such as SVN or CVS, Git eschews the conventional approach of storing file-based changes in favour of capturing snapshots of the entire project at various points in time.

Git's snapshot-based approach provides several key advantages. Firstly, it offers a more intuitive and comprehensive view of the project's evolution, allowing users to visualise and understand changes more effectively. Secondly, it enhances data integrity by rigorously check-summing all content, ensuring that any alterations are immediately detected and accounted for.

This robust integrity check mechanism, based on SHA-1 hashes, instils confidence in the system's ability to safeguard against corruption or loss. Additionally, Git's design philosophy prioritises local operations, minimising the need for network communication and reducing latency. With the entire project history stored locally, most operations can be performed instantaneously without relying on remote servers. This local-centric approach not only enhances speed and efficiency but also enables uninterrupted productivity even when offline or disconnected from a network.

Conceptually, Git organises files into three distinct states: modified, staged, and committed. This organisational framework mirrors the process of preparing a photograph - users make modifications to files, selectively stage those changes for inclusion in the next snapshot (commit), and ultimately solidify them into the project's history.

# Git

## Set-up

To install Git on various platforms, follow these steps:

### Installing on Linux:

Use the package management tool of your distribution.

- For Fedora-based systems  
\$ sudo dnf install git-all
- For Debian-based systems:  
\$ sudo apt install git-all

### Installing on Windows:

- Download the official Git for Windows installer from:  
<https://git-scm.com/download/win>.
- Alternatively, use the Git Chocolatey package, available from:  
<https://gitforwindows.org/>.

### Installing on macOS:

Install the Xcode Command Line Tools, or download the macOS Git installer from:  
<https://git-scm.com/download/mac>.

### Installing from Source:

#### 1. Install dependencies:

- For Fedora:

```
$ sudo dnf install dh-autoreconf curl-devel expat-devel gettext-devel openssl-devel perl-devel zlib-devel asciidoc xmlto docbook2X
```

- For Debian:

```
$ sudo apt-get install dh-autoreconf libcurl4-gnutls-dev libexpat1-dev gettext libbz-dev libssl-dev asciidoc xmlto docbook2x install-info
```

#### 2. Additional steps for Fedora/RHEL systems:

```
$ sudo dnf install getopt
$ sudo ln -s /usr/bin/db2x_docbook2texi /usr/bin/docbook2x-texi
```

#### 3. Get the latest release from kernel.org or GitHub.

#### 4. Compile and install:

```
$ tar -zxf git-2.8.0.tar.gz
$ cd git-2.8.0
$ make configure
$ ./configure --prefix=/usr
$ make all doc info
$ sudo make install install-doc
install-html install-info
```

#### 5. Optionally, clone the Git repository for updates:

```
$ git clone https://git.kernel.org/pub/scm/git/git.git
```

# Git

## Basic commands

> **git init** Initialize a new Git repository in the current directory.

> **git clone [url]** Clone a remote repository into a new directory.

> **git branch** List all branches in the repository.

> **git checkout [branch]** Switch to a different branch.

> **git merge [branch]** Merge changes from one branch into the current branch.

> **git pull** Fetch the latest changes from a remote repository and merge them into the current branch.

> **git push** Push local commits to a remote repository.

# Contact us



IF YOU HAVE ANY COMMENTS or feedback regarding BINFsights, please write to us at [binfo@unswbinfsoc.com](mailto: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](http://unswbinfsoc.com/binfo)  
Stay tuned on our Facebook page for updates regarding events and society news.

-- The BINFSOC Team

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