# Single Cell Analysis

Bioinformatics

# About Us:

| Name | Role | Email | Part 1 | Part 2 |
|---|---|---|---|---|
| Brian Yee | Bioinformatician | bay001@ucsd.edu | 6/30 - 7/2 | |
| Shashank Sathe | Bioinformatician | shsathe@ucsd.edu | 6/30 - 7/2 | |
| Noorsher (Noor) Ahmed | Biomedical Sciences graduate student | noa001@ucsd.edu | 6/30 - 7/5,7/7 | 7/9 - 7/12 |
| Yan Song | Project Scientist | yasong@ucsd.edu | | 7/9 - 7/12 |
| Gene Yeo | Principal Investigator | geneyeo@ucsd.edu | 6/29 - 7/10 | |

# About You:

- Pair programming
- Slack channel: cshlsinglecell19.slack.com
- Own datasets?

## What best describes your level of programming experience?
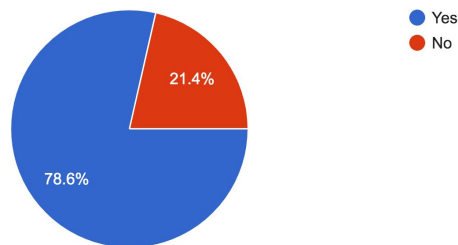14 responses
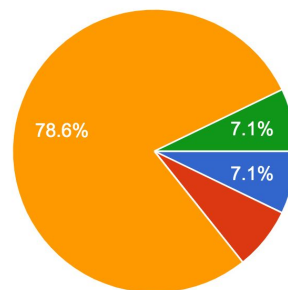


- None
- I have done "omics" experiments but someone else has processed my data
- I have played around with one or more programming languages
- I am fluent in at least one programming language
- I am fluent in one or more languages and am fully capable of processing my own data
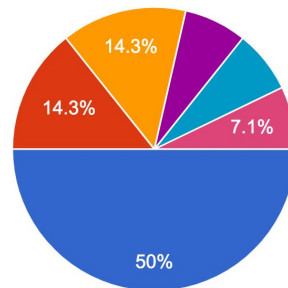
## What best describes your level of single-cell analysis experience?



- I have no hands-on experience with single-cell data
- I have worked with a bioinformatician to process data and interpret results
- I have processed and analyzed my own data
- I have analyzed lots of single-cell d…
- I have reanalyzed other people's (pr…
- I am processing and analyzing my o…
- I have begun to process my own da…

## Do you have your own scRNA dataset that you would like to look at?
14 responses



- Yes
- No

# Bioinformatics schedule - 2 parts

Part 1 (6/30 - 7/2): Basic processing and QC of scRNA datasets

- Intro to TSCC/python
- Process scRNA datasets from [Haber et al. 2017](#), and [Macosko et al. 2015](#) using Cellranger and DropSeqTools
- Start QC methods

Part 2 (7/9 - 7/12): Analysis!

- Finish QC methods
- Basic analysis
- Future directions

"Office hours": 8:30pm - zzz most nights

# Logging into TSCC

**ssh ucsd-trainXY@tscc-login2.sdsc.edu**

Or

**ssh -i /path/to/id_rsa ucsd-trainXY@tscc-login2.sdsc.edu**

(Replace "XY" with your assigned number)

# Onboarding

```
                    cd ~

git clone https://github.com/YeoLab/cshl_2019
```

# Onboarding

1. `jupyter notebook --ip=$(hostname --ip-address) --no-browser`
2. copy/paste the provided link and navigate to the cshl_2019 folder
3. Work through notebooks 1-3 (4 is optional if you have time)
4. Will continue with single-cell data processing tomorrow after lunch