

CSHL Single Cell Analysis

2022 - Day 1

Schedule

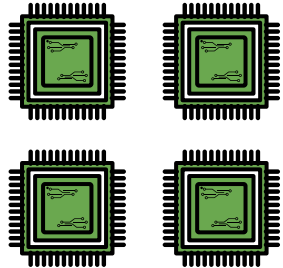
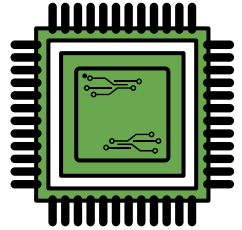
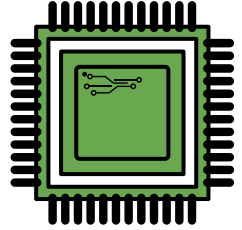
1	2	3	5
Intro	RNAseq	ATACseq Multi-OME	Spatial Transcriptome
July-3/4	July 5/6	July 11/13	July 14/15
Python Pandas Bash Jupyter	Statistics Cellranger Scanpy	Cellranger-arc MUON	Squidpy Bento
Brian Yee Norah Al-azzam	Clarence Mah Shashank Sathe	Andres Vallejo	Noorsher Ahmed Deepak Pant

Your TAs - About & Contact Info

Name	Dates on site	Email
Brian Yee	July 2 - 5	bay001@health.ucsd.edu
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Single cell processing often requires use of multiple processors or nodes

- To analyze **data**, use a computer or node.
- To analyze **more data**, use multiple processors within the node.
- To analyze tons of data, use a cluster of multiple nodes.



We will be using a variety of tools and resources throughout this course

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TSCC

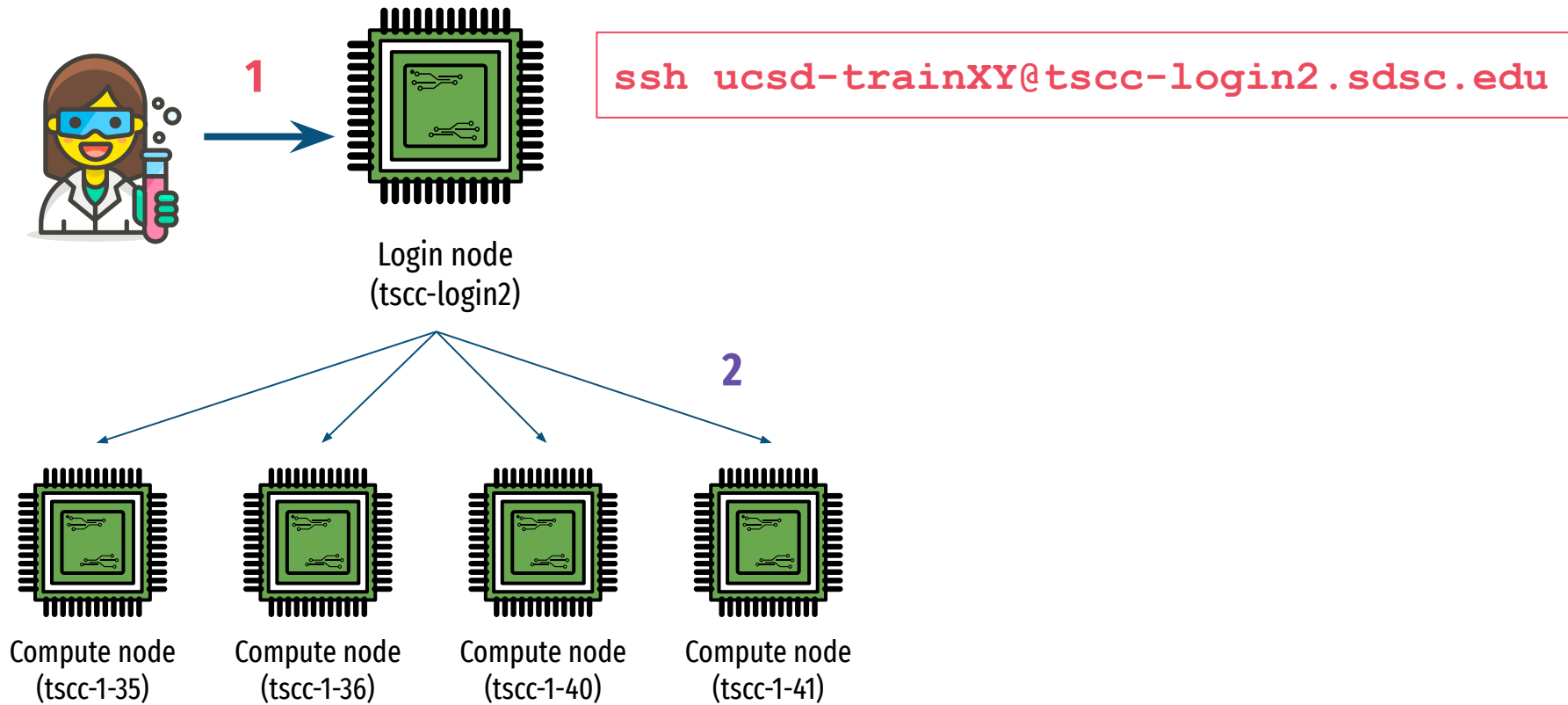
cellranger
cellranger-arc

2

Jupyterhub

Scanpy
MUON
Squidpy
Bento

Logging into the Triton Shared Computing Cluster (TSCC)



```
qsub -I -q home-yeo -l nodes=1:ppn=4 -l walltime=8:00:00
```

Logging into Jupyterhub



1



<https://stratushub-dev.sdsc.edu/jhub/>