

# Overview of single-cell RNA-seq

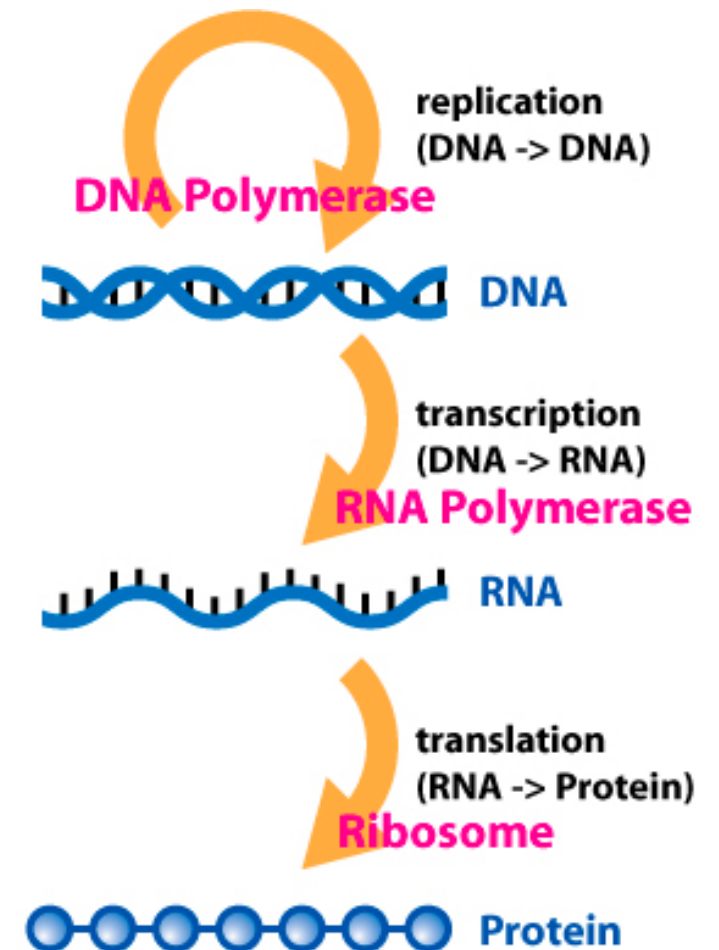
Biocomputing Bootcamp Day 5

Hyun Min Kang  
University of Michigan

# DNA, RNA, and protein...

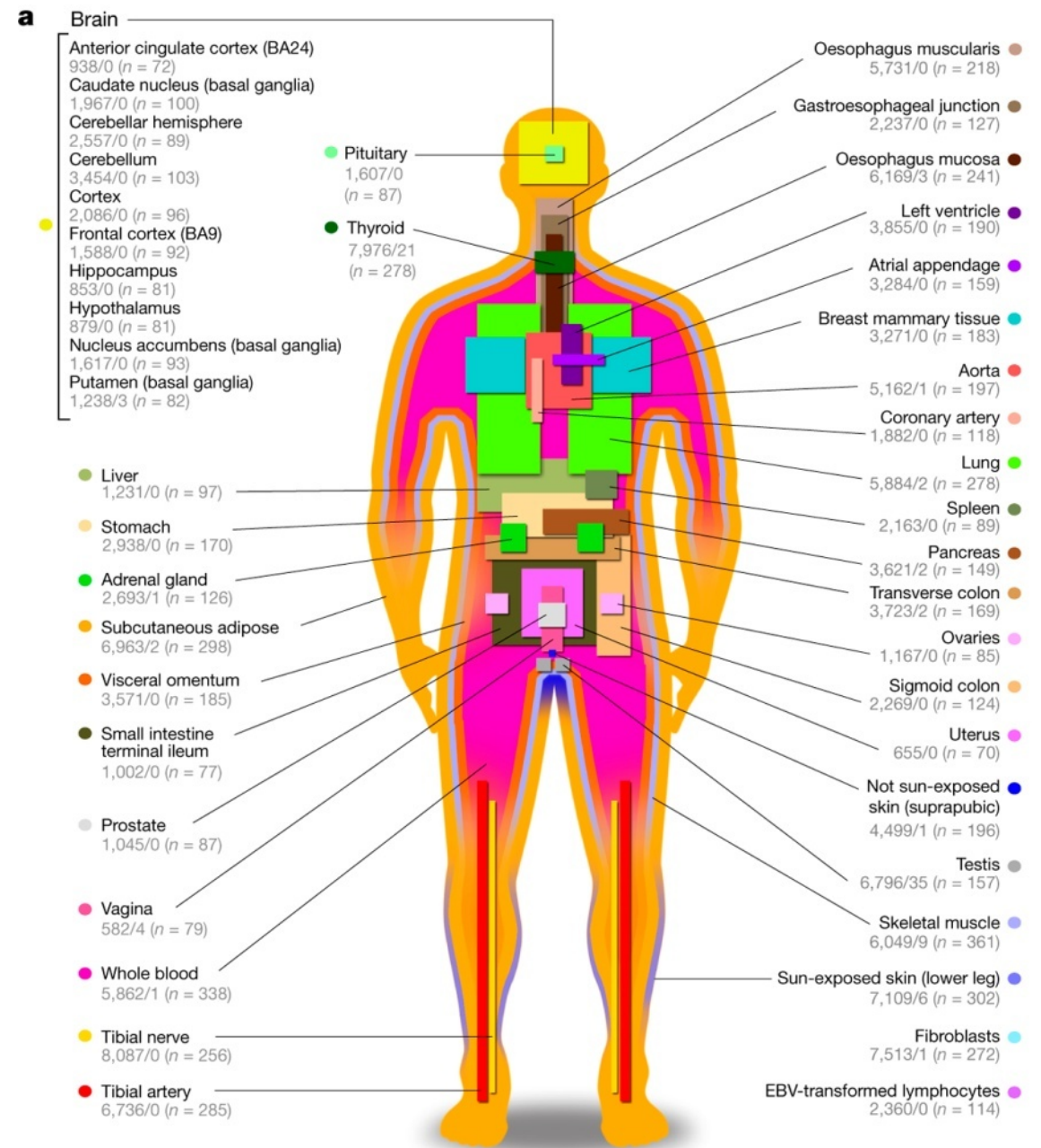
*(Warning: very simplified view)*

- DNA encodes the same information across all the cells (if somatic mutations are ignored).
- **RNAs** are transcribed from DNA, at different levels by cell types, environment, or individuals,
- Proteins are product of RNAs, representing *genes*.



# Why sequence RNAs?

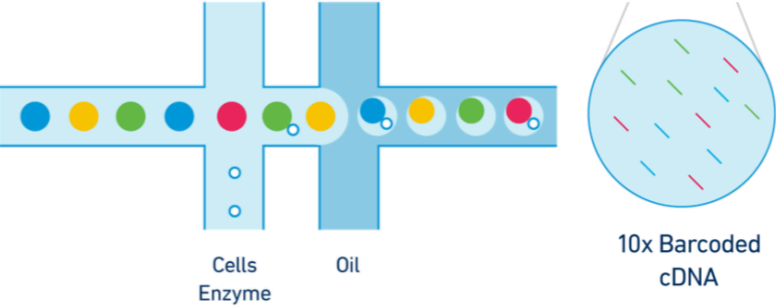
- Different tissues **express** various genes at different levels.
- RNA expression **quantifies** the relative abundance of each transcribed genes.
- Understanding how RNA levels change across conditions, individuals, and cell types is extremely **important**.



# Entering **single cell** RNA-seq...



# Standard scRNA-seq analysis workflow



scRNA-seq experiment

**Droplet Barcode**    **UMI**    **mRNA read (50-100bp)**

AGCTGACGGCAT TTACGCGG ATGCGC...  
 AGCTGACGGCAT TTACGCGG AGCGTA...  
 AGCTGACGGCAT AGCTTAGC CTAGCT...  
 CGAAGTAGCTAG GCCTGAAT GTAGCC...  
 CGAAGTAGCTAG GCCTGAAT GTAGCC...

Raw sequence reads (FASTQ)

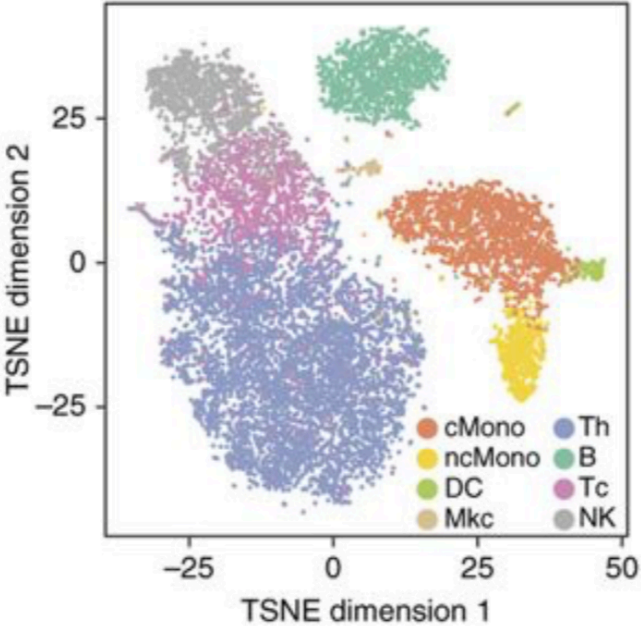
*STAR aligner*

Aligned Reads



each record contains extra tags representing barcode & UMI

*cellRanger, DropseqTools*



*Seurat*

Digital Expression Matrix

	Gene 1	Gene 2	...	Gene 20,000
Droplet 1	10	0		1
Droplet 2	0	1		0
...				
Droplet 5,000	1	5		0

# Digital expression matrix

Droplet Barcode	<i>CD3G</i>	<i>CD8A</i>	<i>CST3</i>	<i>MS4A7</i>	<i>LYZ</i>	<i>GNLY</i>	<i>S100A4</i>	<i>MS4A1</i>	<i>IL7R</i>
<b>ACGTCATGCATA</b>	0	0	0	0	1	0	3	0	3
<b>AGTCATATACTA</b>	0	0	1	0	3	0	0	6	2
<b>CTAGATCGATTA</b>	0	1	1	0	2	1	5	0	1
<b>GCTAGTAGTTCA</b>	0	0	22	3	24	0	16	0	0
<b>CCGATCGATCTG</b>	0	0	0	0	0	3	5	0	0
<b>TGAGCTAGCTTG</b>	1	1	0	0	1	0	9	0	0
<b>AGATAGATCGAT</b>	0	0	0	0	1	0	2	0	2
<b>CGATCGQATCGT</b>	0	0	0	0	1	0	0	0	3
<b>TGATGCTAGCTA</b>	0	0	0	0	0	1	3	1	0

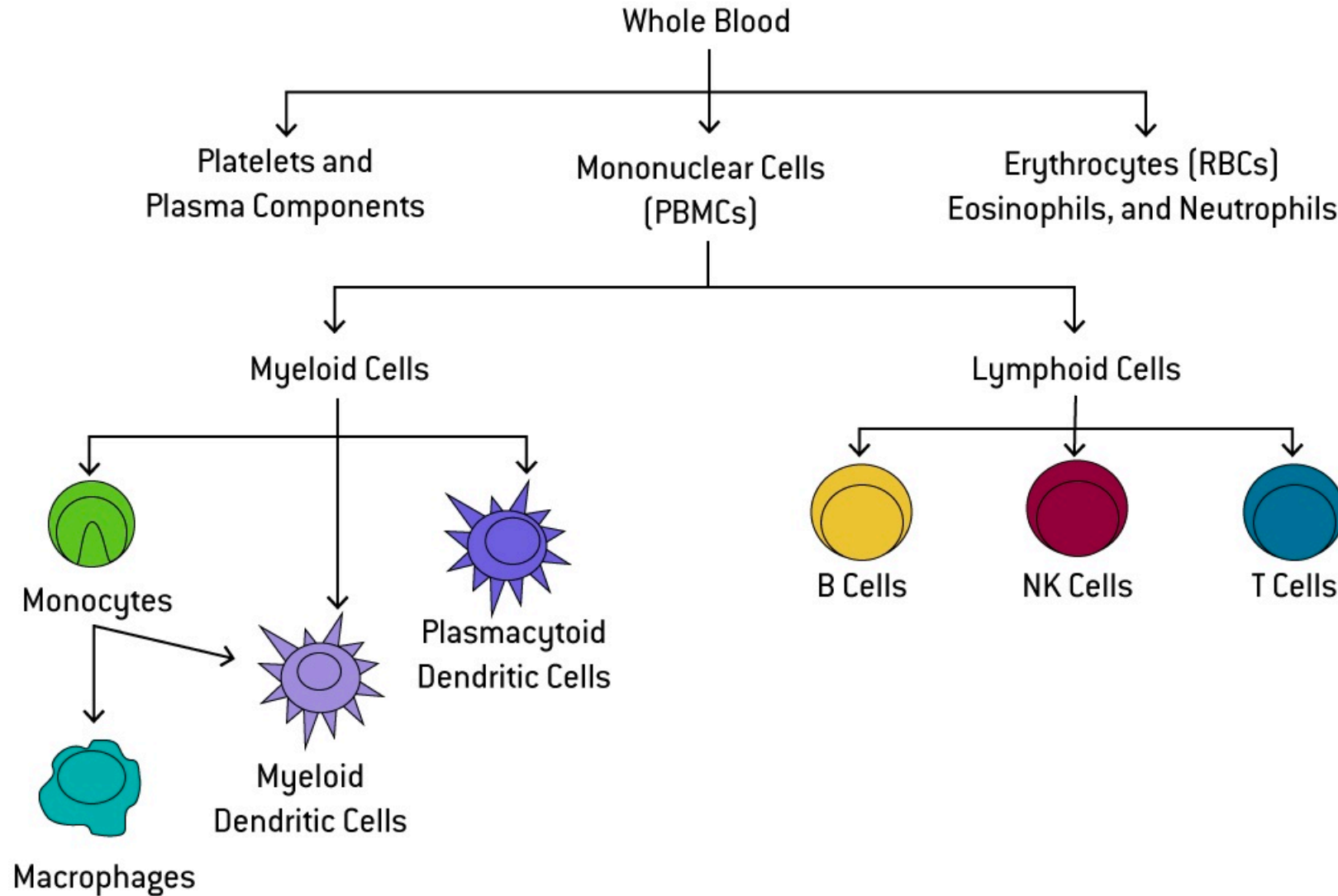
# Sparse representation of digital expression

Index	Droplet Barcode
1	<b>ACGTCATGCATA</b>
2	<b>AGTCATATACTA</b>
3	<b>CTAGATCGATTA</b>
4	<b>GCTAGTAGTTCA</b>
5	<b>CCGATCGATCTG</b>
6	<b>TGAGCTAGCTTG</b>
7	<b>AGATAGATCGAT</b>
8	<b>CGATCGQATCGT</b>
9	<b>TGATGCTAGCTA</b>

Index	Genes
1	<b><i>CD3G</i></b>
2	<b><i>CD8A</i></b>
3	<b><i>CST3</i></b>
4	<b><i>MS4A7</i></b>
5	<b><i>LYZ</i></b>
6	<b><i>GNLY</i></b>
7	<b><i>S100A4</i></b>
8	<b><i>MS4A1</i></b>
9	<b><i>IL7R</i></b>

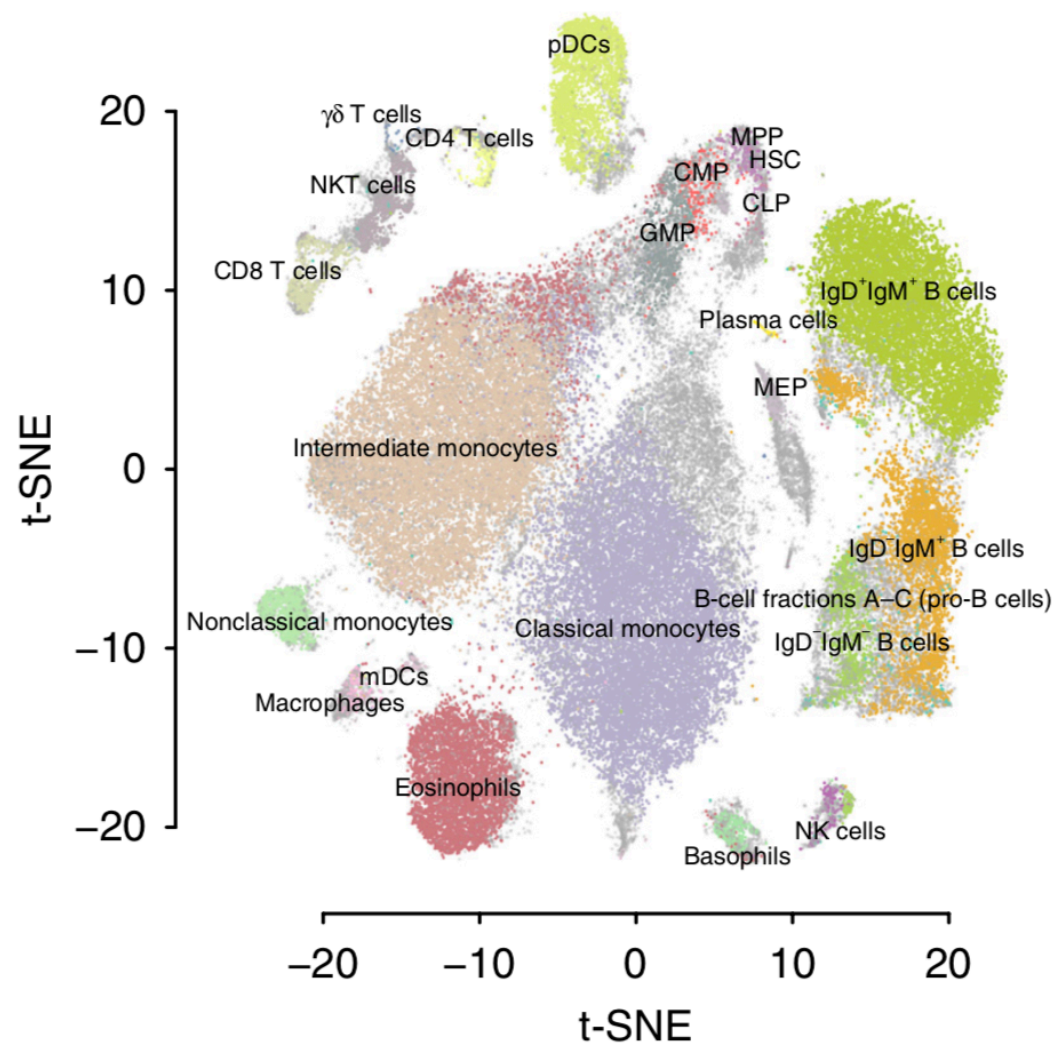
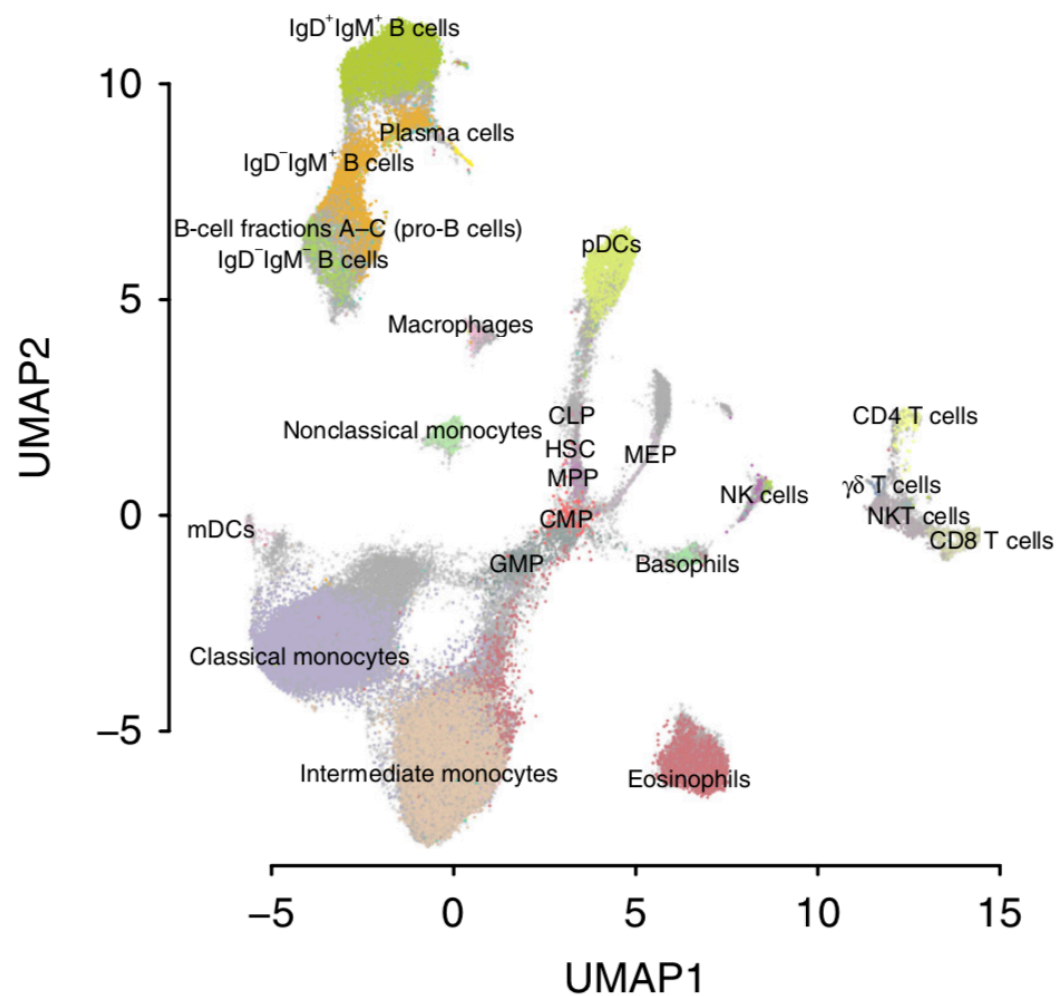
iGene	iBarcode	Count
1	6	<b>1</b>
2	3	<b>1</b>
2	6	<b>1</b>
3	2	<b>1</b>
3	3	<b>1</b>
3	4	<b>22</b>
4	3	<b>3</b>
5	1	<b>1</b>
5	2	<b>3</b>
5	3	<b>2</b>
5	4	<b>24</b>
...	...	...

# Cell types in PBMCs





# Manifold learning of single cells



# Goal of today

- Learn how to read large data files using python and R
- Learn how to summarize the data and ask questions on them.
- Learn how to summarize the data visually.
- Learn how to apply existing methods on a large dataset.
- Learn how to perform statistical tests on a large dataset.