

Comp683: Computational Biology

Lecture 6

January 30, 2024

Today

- Finish probabilistic graph partitioning
 - Stochastic block model + application for spatial transcriptomics
 - Affiliation model
- Graph embedding
 - node2vec
- If time → single-cell
 - Intro to single-cell profiling and analysis

Review → Stochastic Block Model (SBM)

- **Intuition:** Members of a community should be connected to themselves and to members of other communities in the same way.
- **Model:** Assuming we have N nodes and K communities, we infer two main parameters
 - $\theta \in \mathbb{R}^{K \times K}$, a matrix of between-community edge probabilities
 - $z \in \mathbb{R}^{N \times 1}$, a vector of node-to-community assignments

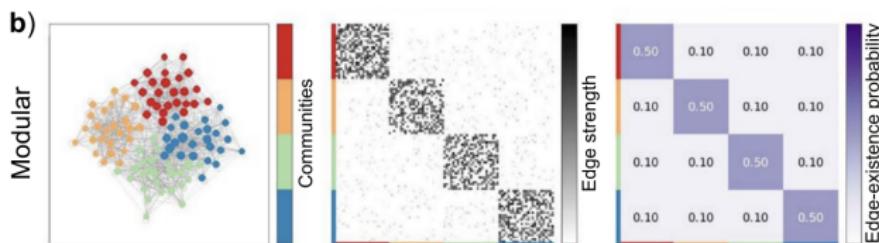


Figure: Notice the high within-edge probability on the diagonal of θ . from Fastkowitz *et al.* Scientific Reports. 2018.

SBM Complete Data Log Likelihood

$\sum_i \sum_q Z_{iq} \log \alpha_q + \frac{1}{2} \sum_{i \neq j} \sum_{q,l} Z_{iq} Z_{jl} \log b(A_{ij}, \theta_{ql})$ can be written completely as,

$$\sum_i \sum_q Z_{iq} \log \alpha_q + \frac{1}{2} \sum_{i \neq j} \sum_{q,l} Z_{iq} Z_{jl} \underbrace{[A_{ij} \log(\theta_{ql})]}_{\text{edges}} + \underbrace{(1 - A_{ij}) \log(1 - \theta_{ql})}_{\text{no edges}} \quad (1)$$

Fitting Parameters

- I will not go through it here, but you can either use expectation maximization (EM), belief propagation, or MCMC methods.
 - See → <https://arxiv.org/abs/1207.2328> for EM and BP
 - See → <https://journals.aps.org/pre/abstract/10.1103/PhysRevE.89.012804> for MCMC
- The fastest implementation of SBM model parameters that is most readily scalable to large graphs can be found in GraphTool → <https://graph-tool.skewed.de>

Issue

The presented approach is most appropriate for unweighted graphs. Currently, it is more challenging to accommodate edge-weights well without assuming some kind of a distribution on edge weights.

- Any ideas about this?

SBM Applied To Spatial Transcriptomics Dataset

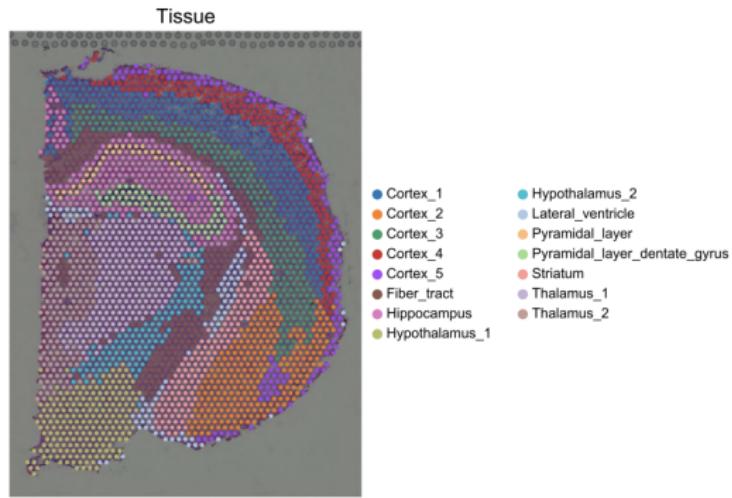
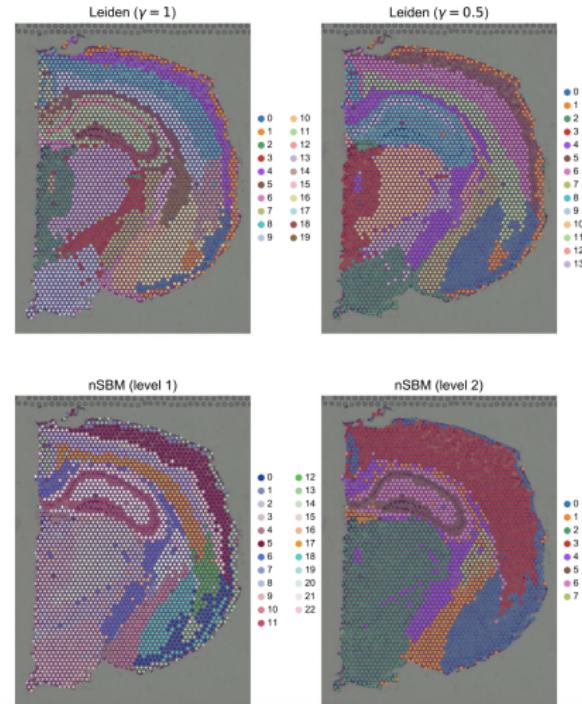


Figure: ground-truth annotation of cells within a coronal section of a mouse-brain from <https://link.springer.com/article/10.1186/s12859-021-04489-7>

Leiden vs SBM



SBM for the Human Microbiome

Nodes → microbial species, edges → interactions at bodysites. Infer multiple SBMs, where each SBM characterized several body sites according to similar microbial species interactions.

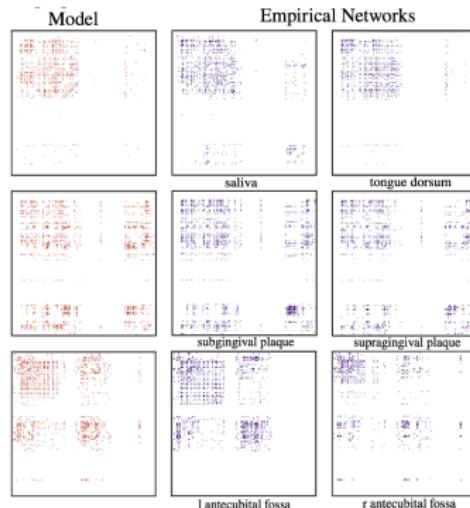


Figure: from Stanley *et al.* IEEE TNSE. 2016.

Affiliation Model for Community Structure

- This is a *soft* clustering approach where overlapping communities are allowed
- Instead of learning a hard node-to-community partition, we learn a node-to-community *propensity*

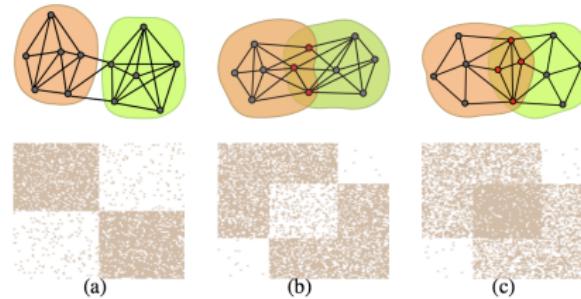


Figure: from Yang et al. ICDM. 2012

'BigClam' Approach to Overlapping Communities

Model the existence of an edge between nodes u and v based on the inner product of propensities, F_u and F_v .

DEFINITION 1. Let F be a nonnegative matrix where F_{uc} is a weight between node $u \in V$ and community $c \in C$. Given F , the BIGCLAM generates a graph $G(V, E)$ by creating edge (u, v) between a pair of nodes $u, v \in V$ with probability $p(u, v)$:

$$p(u, v) = 1 - \exp(-F_u \cdot F_v^T), \quad (1)$$

where F_u is a weight vector for node u ($F_u = F_{u\cdot}$).

Figure: from Yang and Leskovec. WSDM. 2013.

Finding the Optimal F_u

The log-likelihood of the graphs given the learned propensities, \mathbf{F}_u can be expressed as follows. The authors optimize each \mathbf{f}_u by fixing \mathbf{f}_v .

$$I(F_u) = \sum_{u \in \mathcal{N}_u} \log(1 - \exp(-F_u F_v^T)) - \sum_{v \notin \mathcal{N}(u)} F_u F_v^T \quad (2)$$

See their paper for more details. <https://cs.stanford.edu/people/jure/pubs/bigclam-wsdm13.pdf>.

Edge Probability vs Number of Shared Memberships

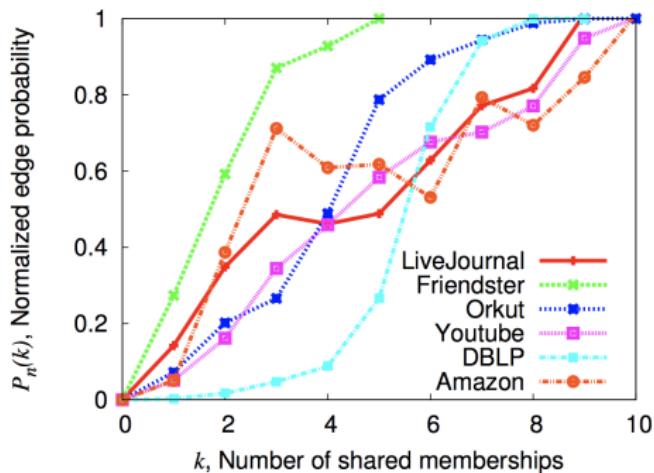


Figure: from Yang and Leskovec. WSDM. 2013.

Graph Representation Learning

- There is a lot of recent hype in the graph world about feature learning from graphs or learning a representation for each node in a continuous vector space
- For a particular node, u , the objective is to learn some representation in d dimensions, $f(u)$, with $f(u) \in \mathbb{R}^d$

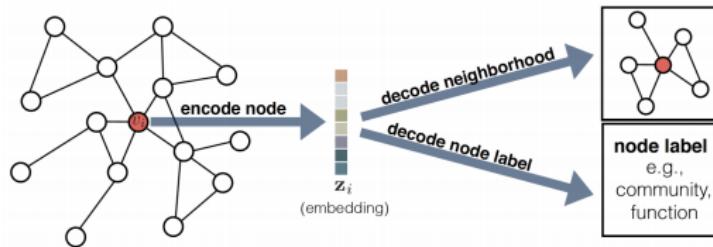


Figure: from Hamilton *et al.* ArXiv. 2018

Get Graph Partitioning for Free from Embedding

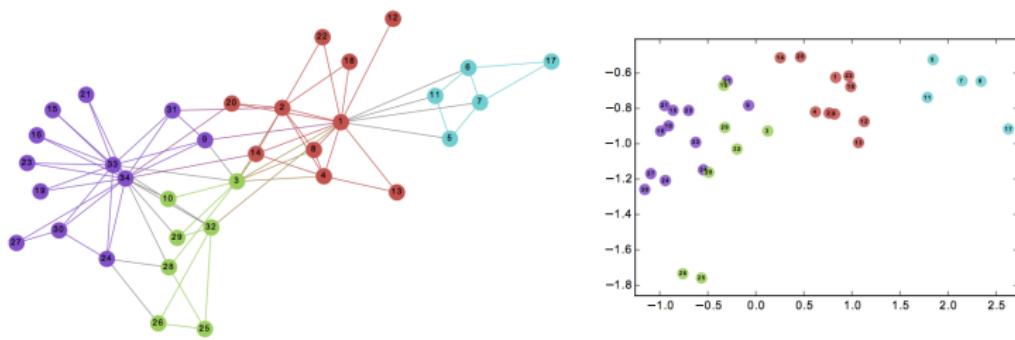
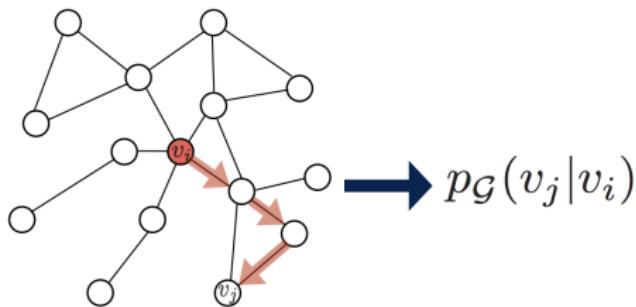
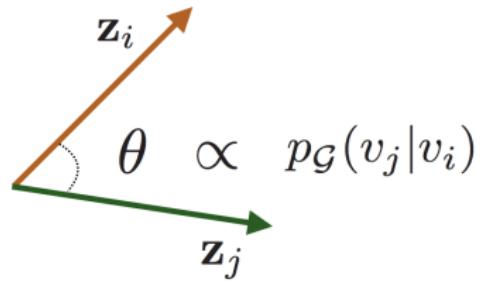


Figure: from Perozzi *et al.* KDD. 2014

The Random Walk Based Approach



1. Run random walks to obtain co-occurrence statistics.



2. Optimize embeddings based on co-occurrence statistics.

Figure: from Hamilton *et al.* ArXiv. 2018

Encoding the 'Role' of a Node with Node2Vec

- Node2Vec allows for control of whether the embedding captures between-node structural similarity (neighborhoods) or role (the types of nodes in connection with)

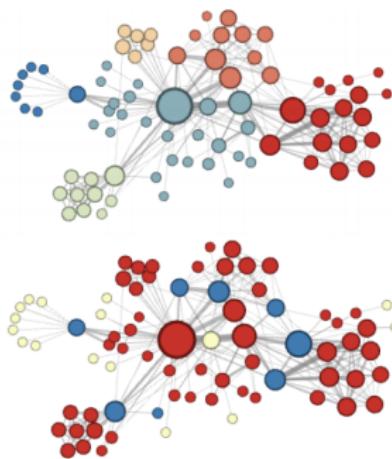


Figure: from Grover and Leskovec. KDD. 2016

Other Similar Approaches

- LINE → <https://arxiv.org/abs/1503.03578>
- DeepWalk → <https://arxiv.org/abs/1403.6652>
- Node2Vec → <https://arxiv.org/abs/1607.00653>
- Splitter → <https://arxiv.org/pdf/1905.02138.pdf>

Flexible Notion of Neighborhood (Breadth First)

When defining a neighborhood set N_s of some node u , there are two possible strategies. The following example assumes sampling $k = 3$ nodes.

- **Breadth-first Sampling:** Find the most immediate neighbors of node u and sequentially sample additional nodes according to their distance from u . In the image below, if we are selecting k neighbors, this selects s_1, s_2, s_3 .

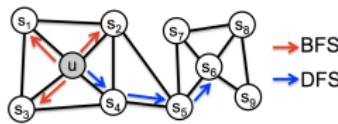


Figure 1: BFS and DFS search strategies from node u ($k = 3$).

Figure: from Leskovec and Grover. KDD. 2016

Flexible Notion of Neighborhood (Depth First)

- **Depth-first Sampling:** Select nodes sampled at sequentially further distances from the source node, u . According to the example below, nodes s_4, s_5, s_6 are selected.

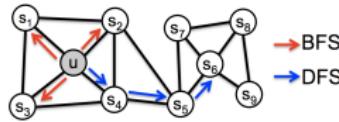


Figure 1: BFS and DFS search strategies from node u ($k = 3$).

Figure: from Leskovec and Grover. KDD. 2016

Node2Vec Objective

Starting with a graph, G with $G = (V, E)$, then the task is to learn a mapping function, f with $f : V \rightarrow \mathbb{R}^d$. Here, d is the number of dimensions of f . Ultimately, f is a matrix of size $|V| \times d$. $\mathcal{N}_s(u)$ is further defined as the nodes that are sampled in the walk from u . Then the objective is to find an f such that,

$$\sum_{u \in V} \log P(\mathcal{N}_s(u) | f(u)) \tag{3}$$

is as large as possible. Here, $\mathcal{N}_s(u)$ is conditioned on the feature representation of u , $f(u)$.

Conditional Independence Assumption

$$P(\mathcal{N}_S(u) | f(u)) = \prod_{n_i \in \mathcal{N}_s(u)} P(n_i | f(u)). \quad (4)$$

Conditional Likelihood for each Source, Neighborhood Pair

To model each source, neighborhood pair and given the conditional independence assumption introduced on the previous slide,

$$P(n_i \mid f(u)) = \frac{\exp(f(n_i) \cdot f(u))}{\sum_{v \in V} \exp(f(v) \cdot f(u))} \quad (5)$$

Varying Neighborhood According to DFS or BFS

As we have pointed out, $\mathcal{N}_S(u)$ is not restricted to the immediate neighbors of u . The authors define a flexible notion of a random walk on the graph that allows for sampling in either a DFS or BFS way. Assuming the random walk has just traversed edge (t, v) and now resides at node v . The transition probability from v to x (π_{vx}) can be written as,

$$\pi_{vx} = \alpha_{pq}(t, x) \cdot w_{vx} \quad (6)$$

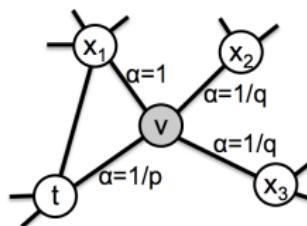


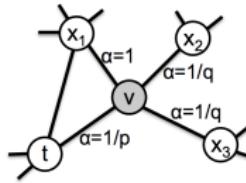
Figure: from Grover and Leskovec, KDD. 2016

Varying Neighborhood According to DFS or BFS

$$\pi_{vx} = \alpha_{pq}(t, x) \cdot w_{vx} \quad (7)$$

Here w_{vx} is the edge weight between nodes v and x or simply $\{0, 1\}$ if the graph is unweighted. d_{tx} denotes shortest path distance between t and x (we are at v). A user can specify p or q .

$$\alpha_{p,q}(t, x) = \begin{cases} 1/p & \text{if } d_{tx} = 0 \\ 1 & \text{if } d_{tx} = 1 \\ 1/q & \text{if } d_{tx} = 2 \end{cases}$$



Intuition Behind p

- p controls the likelihood of immediately revisiting a node in the walk.
 - A **low** value of p would keep the walk local, close to the starting node, u . A low value of p would encourage local walks next to a source node, u .

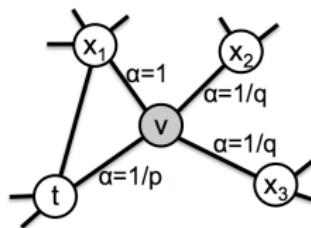


Figure: from Grover and Leskovec, KDD. 2016

Intuition Behind q

item q allows for differentiation between inward and outward nodes

- For $q < 1$, the walk is inclined to visit nodes that are further from node t . (Depth First)

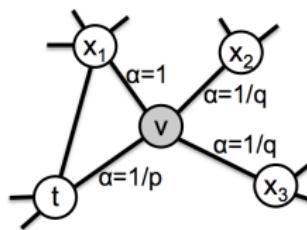
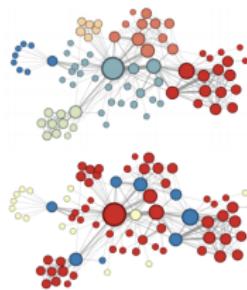


Figure: from Grover and Leskovec, KDD. 2016

Allow for Variation in What Defines Nodes as Being Similar

- **Application of Capturing Local Similarities:** Identify proteins involved in a common pathway. Or parts of the brain that are correlated to each other.
- **Usefulness of Capturing More Global Similarities:** Identify proteins that are regulators of many other proteins but are not related extensively among them selves.
- Validating a graph representation (**project idea!!!**).



Embedding as a Tool for a Variety of Tasks on Graphs

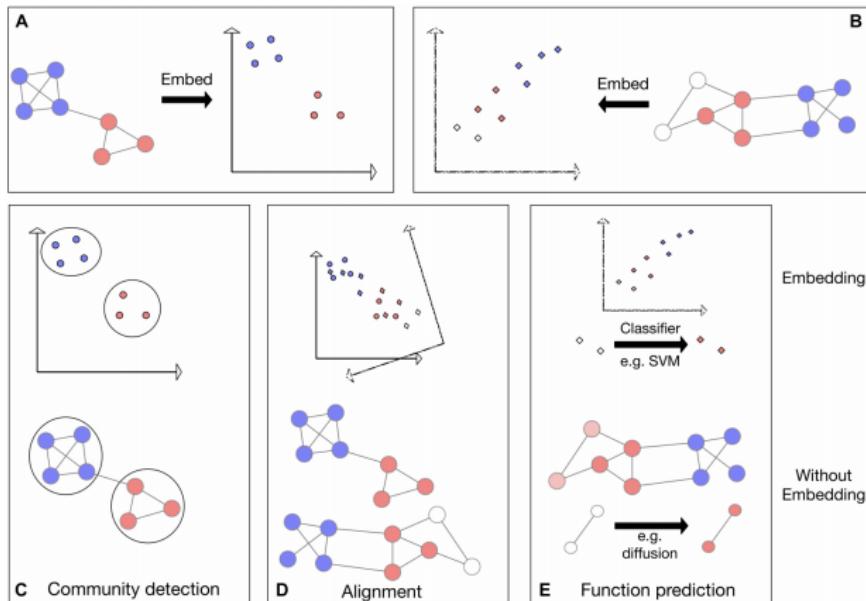


Figure: from Nelson *et al.* Frontiers in Genetics. 2019. Protein families (C). Cross-Species Alignment (D), Function Prediction (E)

Recap of Why we Love Graphs in Biology

- Graphs are useful for representing relational information
 - Cells, Patients, etc.
- There are a lot of well-defined tasks on graphs that we can use to answer our questions
 - Graph partitioning
 - Diffusion for smoothing (which we will see later), and partitioning if we were to work with Graph Laplacian
 - Visualization- connecting visualization with the scientific problem
 - Other tasks not discussed: link prediction, collaborative filtering, label propagation.

Single Cell Intro Day

- What are single-cell assays?
- Mass Cytometry (CyTOF) Bioinformatics
- Automating Human Gating with Spade
 - What is a gate?
- Practical Considerations (normalization, batch effects)

What is a Single-Cell Assay?

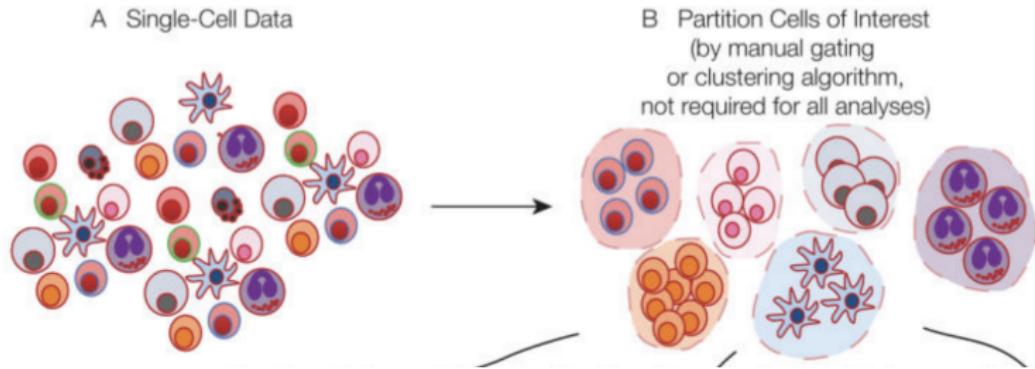


Figure: from Spitzer *et al.* Cell. 2016. In general, we are taking a biological sample (blood, tissue, etc.) and measuring properties of individual cells. We then seek to track and understand entire cell-populations.

What Level of Biology do You Want to Measure?

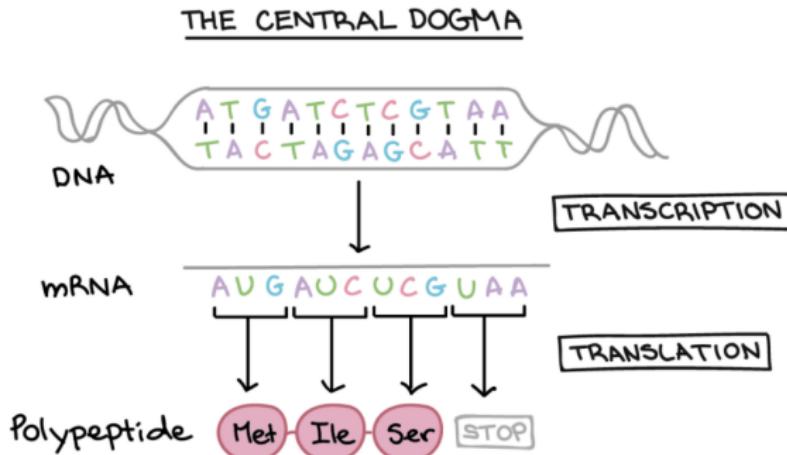


Figure: Remember, DNA → RNA → protein

scRNA seq for measuring gene expression

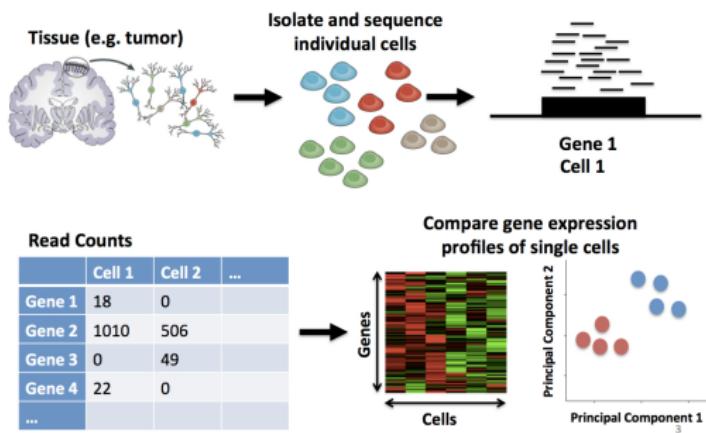


Figure: from <https://learn.genecore.bio.nyu.edu/single-cell-rnaseq/>. Measure the expression of 10s of thousands of genes in 10s of thousands of cells.

Disclaimer

Here we will discuss analysis of single-cell **proteomics** assays because they are useful for **immunophenotyping**, or identifying, tracking, and characterizing the diverse immune cell-types.

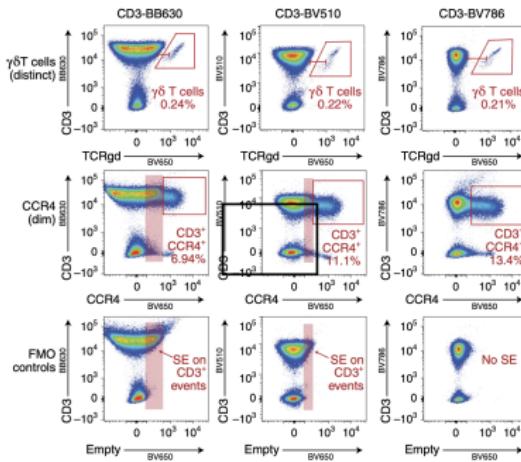


Figure: from Nature Immunology. 2021. We use protein expression in cells to figure out what they are.

Why Do we Care About Immune Profiling?

Example 1: The immune system adapts during pregnancy. We can use it to predict someone's likelihood of pre-mature birth.

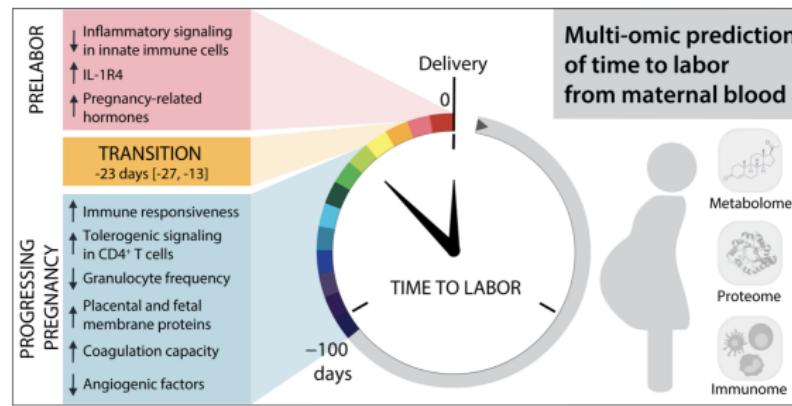


Figure: from Science Translational Medicine. 2021.