

Comp790-166: Computational Biology

Lecture 2

January 21, 2021

Today

- Linear algebra background/review (content from SLMT)
 - Matrix Rank and Low Rank Approximations
 - SVD and singular values
- Graphs
 - Notation, Basic Properties
 - Paths and Diffusion
 - Graph Laplacian
- Building Graphs from Data
 - k-d trees and random projection trees
 - LargeVis

Notation

I will be using the following notation throughout these notes.

- \mathbf{X} is a matrix
- \mathbf{x}_i is column i of \mathbf{X} , so a column vector
- X_{ij} is the ij th entry of \mathbf{X}

Matrix Rank

Definition: A rank 1 matrix can be expressed as the outer product of two vectors, $\mathbf{u}\mathbf{v}^T$, where u and v are column vectors. Similarly, a matrix \mathbf{M} is at most rank k if it can be written as the sum of k rank 1 matrices,

$$\mathbf{M} = \sum_{j=1}^k \mathbf{u}_j \mathbf{v}_j^T \quad (1)$$

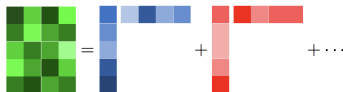


Figure 2.1: Decomposition of a matrix $M \in \mathbb{R}^{5 \times 4}$ as sum of the rank-1 components. Note that each component is the product of a column vector u_j and a row vector v_j^T .

Figure: (From SLMT (Janzamin *et al.*) A matrix can often be determined by a small number of *factors*, where each factor is a rank 1 matrix.

A Rank-2 Matrix Toy Example

	Math.	Classics	Physics	Music		Verbal	Quantitative
Alice	19	26	17	21	$= \begin{pmatrix} 4 \\ 3 \\ 2 \\ 5 \\ 6 \end{pmatrix} \begin{pmatrix} 1 \\ 5 \\ 2 \\ 3 \end{pmatrix}^\top + \begin{pmatrix} 3 \\ 1 \\ 1 \\ 2 \\ 5 \end{pmatrix} \begin{pmatrix} 5 \\ 2 \\ 3 \\ 3 \end{pmatrix}^\top$		
Bob	8	17	9	12			
Carol	7	12	7	9			
Dave	15	29	16	21			
Eve	31	40	27	33			

Figure 2.2: Score Matrix M is an example for the scores of students (indexing the rows) in different tests on distinct subjects (indexing the columns). A corresponding low rank decomposition is also provided where the rank is two in this example.

Figure: (From SLMT (Janzamin *et al.*) Write the student \times subject score matrix as a sum of verbal and quantitative ability.

$$\text{Score}(\text{student}, \text{test}) = \text{student}_{\text{verbal ability}} \times \text{student}_{\text{test verbal}} + \text{student}_{\text{quant ability}} \times \text{student}_{\text{test quant}}$$

Matrices in Real Life are Not Exactly Low Rank

Some reasons why a matrix could deviate from low rank structure:

- Noisy entries (common in biology, entries could even be missing)
- The low rank components (factors) may not interact linearly
- Several prominent factors and many small factors.

However, a matrix can still be *approximately* low rank and we can use SVD to find the low rank matrix that is closest, or best approximates the observed matrix.

- If you find yourself fascinated by low rank structure of data matrices, check this out <https://arxiv.org/abs/1705.07474>.

Matrix Norms, for Quantifying when Matrices are Close

Frobenius Norm is the simplest example and is just L_2 norm,

$$\|\mathbf{M}\|_F = \sqrt{\sum_{i=1}^n \sum_{j=1}^m M_{ij}^2} \quad (2)$$

We seek the matrix \mathbf{N} that makes $\|\mathbf{M} - \mathbf{N}\|_F$ as small as possible for some particular rank k .

Singular Value Decomposition (SVD)

The SVD of a matrix, \mathbf{M} with $\mathbf{M} \in \mathbb{R}^{n \times m}$ is defined as,

$$\mathbf{M} = \mathbf{U}\mathbf{D}\mathbf{V}^T = \sum_{j=1}^{\min\{m,n\}} \sigma_j \mathbf{u}_j \mathbf{v}_j^T \quad (3)$$

- $\mathbf{U} = [\mathbf{u}_1 | \mathbf{u}_2 | \dots | \mathbf{u}_n] \in \mathbb{R}^{n \times n}$ (left singular vectors),
 $\mathbf{V} = [\mathbf{v}_1 | \mathbf{v}_2 | \dots | \mathbf{v}_n] \in \mathbb{R}^{n \times n}$ (right singular vectors).
- \mathbf{U} and \mathbf{V} are orthonormal ($\mathbf{U}^T \mathbf{U} = \mathbf{I}, \mathbf{V}^T \mathbf{V} = \mathbf{I}$).
- \mathbf{D} is a diagonal matrix with diagonal entries
 $\sigma_1 \geq \sigma_2 \geq \dots \geq \sigma_{\min\{m,n\}} \geq 0$ (σ_i s are singular values)

Truncated SVD

Here is how you can construct a rank k approximation for your matrix, $\mathbf{M} \in \mathbb{R}^{n \times m}$. Assuming that $\mathbf{M} = \mathbf{U}\mathbf{D}\mathbf{V}^T$ is the SVD of \mathbf{M} , then you can compute the rank k truncated SVD of \mathbf{M} as,

$$\mathbf{M}_{(k)} = \mathbf{U}_{(k)}\mathbf{D}_{(k)}\mathbf{V}_{(k)}^T \quad (4)$$

- entries of \mathbf{D} are sorted in descending order on the diagonal and $\mathbf{D}_{(k)}$ is the first $k \times k$ submatrix of \mathbf{D}
- $\mathbf{U}_{(k)}$ is the first k columns of $\mathbf{U} \in \mathbb{R}^{N \times N}$
- $\mathbf{V}_{(k)}$ is the first k columns of $\mathbf{V} \in \mathbb{R}^{M \times M}$

An Application of SVD in Something You Use All of the Time

The Moore Penrose Pseudo Inverse can approximate the inverse of a matrix, \mathbf{M} . Suppose $\mathbf{M} = \mathbf{U}\mathbf{D}\mathbf{V}^T$ is the rank- k truncated SVD. Then the pseudo inverse of \mathbf{M} is defined as,

$$\mathbf{M}^{-1} = \mathbf{V}\mathbf{D}^{-1}\mathbf{U}^T \quad (5)$$

PCA Using what we just learned about SVD

Consider n datapoints, $\mathbf{x}_1, \mathbf{x}_2 \dots \mathbf{x}_n \in \mathbb{R}^d$, such that the data are centered with $\sum_i \mathbf{x}_i = \mathbf{0}$. Then the covariance matrix can be computed as,

$$\mathbf{M} = \frac{1}{n} \sum_{i=1}^n \mathbf{x}_i \mathbf{x}_i^T \quad (6)$$

\mathbf{M} is positive semi-definite (PSD) and SVD on PSD matrices always has symmetric structure such that the left and right singular vectors are the same so,

$$\mathbf{M} = \mathbf{U} \mathbf{D} \mathbf{U}^T = \sum_{j=1}^d \sigma_j \mathbf{u}_j \mathbf{u}_j^T \quad (7)$$

The Top Singular Vector is the Direction with the Most Variance

Geometrically, the covariance matrix can be viewed as an ellipsoid and \mathbf{u}_1 corresponds to the longest axis.

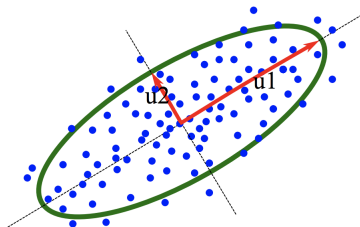


Figure 2.4: Geometric representation of principle components u_1 and u_2 for the covariance matrix of data points x_i 's.

Figure: (From SLMT (Janzamin *et al.*))

A very exciting application of linear algebra \rightarrow graphs.

Graphs

A graph is a collection of nodes joined by edges. Or generally, a data structure for capturing relational information.

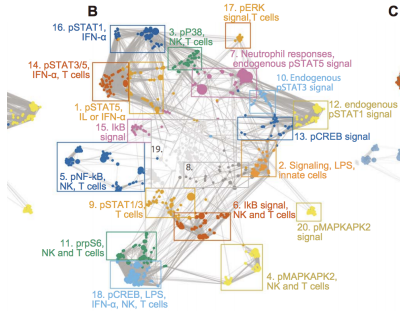


Figure: Figure from Aghapeeour *et al.* Science Immunology. 2018. A graph of function and frequency features immune cell-types (nodes), with edges representing strong correlation across patients.

Mathematical Representations of Graphs

Consider an undirected, unweighted network with N nodes. Then its adjacency matrix (**A**) is defined as,

$$A_{ij} = \begin{cases} 1 & \text{there is an edge between nodes } i \text{ and } j \\ 0 & \text{otherwise} \end{cases}$$

In practical situations, you will want to use a sparse representation of your adjacency matrix or define an edgelist also known a $|E| \times 2$ matrix of 'source' (column 1) and 'target' (column 2) node indices.

Encoding the Strength of Connection Between Nodes

Sometimes we have a notion about how similar pairs of nodes are. For example, correlation, or other similarity measure. This extra information can be helpful in our analysis and interpretation of graph structure. The adjacency matrix of an undirected, weighted graph with N nodes is similarly defined as,

$$A_{ij} = \begin{cases} w_{ij} & \text{there is an edge between nodes } i \text{ and } j \\ 0 & \text{otherwise} \end{cases}$$

Here w_{ij} represents the strength of the connection between nodes i and j .

- The adjacency matrix can be used to quickly gain intuition about properties of the graph, which we will see as a coming attraction.

Example

Consider the adjacency matrix for an undirected graph with $N = 3$ nodes,

$$\mathbf{A} = \begin{bmatrix} 0 & 2 & 1 \\ 2 & 0 & 0.5 \\ 1 & 0.5 & 0 \end{bmatrix}$$

Here, nodes 1 and 2 have twice as strong of a connection as nodes 1 and 3. This graph is also **complete graph** in that there exists an edge connecting every pair of nodes.

The Simplest Node Ranking Strategy: Degree

Let **A** be the adjacency matrix for a graph with N nodes. The **degree** of a node of node i (k_i) counts the number of nodes that node i is connected to or,

$$k_i = \sum_{j=1}^N A_{ij} \quad (8)$$

Every edge has two ends. So, for m edges in a graph, there are $2 \times m$ ends of edges. Therefore, the total sum of edges in the graph can be written as,

$$2m = \sum_{i=1}^n k_i \quad (9)$$

Paths in a Graph

- **Path:** A path in a graph is a sequence of nodes such that every consecutive pair of nodes in the sequence is connected by an edge. This is also known as a route across the graph.
- **Path Length:** The path length between nodes i and j is the number of edges that need to be traversed to reach node j from node i .
- **Geodesic Path:** The geodesic path or shortest path is the shortest network distance between a pair of nodes.
 - There are a lot of beautiful shortest path algorithms for doing this efficiently that we will not cover here.

Example

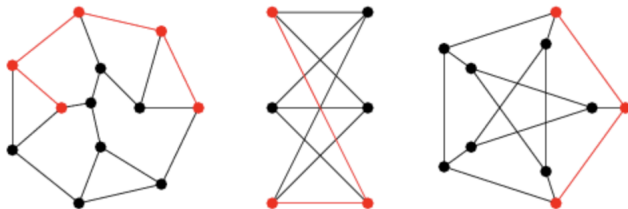


Figure: There could be multiple paths between a pair of nodes, but we are interested in the path that is the shortest.

Diffusion on Graphs

Suppose we have some quantity that will spread or *diffuse* across a graph, given the graph's connectivity. Suppose there is a quantity of ψ_i at node j , that flows to an adjacent node i at a rate of $C(\psi_j - \psi_i)$. The rate at which ψ_i is changing is given as,

$$\frac{d\psi_i}{dt} = C \sum_j A_{ij}(\psi_j - \psi_i) \quad (10)$$

Splitting up terms, we can rewrite this as,

$$\frac{d\psi_i}{dt} = C \sum_j A_{ij}\psi_j - C\psi_i \sum_j A_{ij} = C \sum_j A_{ij}\psi_j - C\psi_i k_i \quad (11)$$

Diffusion continued

$$\frac{d\psi_i}{dt} = C \sum_j A_{ij} \psi_j - C \psi_i \sum_j A_{ij} = C \sum_j A_{ij} \psi_j - C \psi_i k_i \quad (12)$$

further simplifies to,

$$\frac{d\psi_i}{dt} = C \sum_j (A_{ij} - \sigma_{ij} k_i) \psi_j. \quad (13)$$

Here, k_i is the degree of node i and $\sigma_{ij} = 1$ if $i = j$ and is 0 otherwise.

Diffusion and Connection with the Graph Laplacian

$$\frac{d\psi_i}{dt} = C \sum_j (A_{ij} - \sigma_{ij} k_i) \psi_j. \quad (14)$$

can be expressed in matrix form as,

$$\frac{d\psi}{dt} = C(\mathbf{D} - \mathbf{A})\psi. \quad (15)$$

Here, \mathbf{D} is an $N \times N$ diagonal matrix where k_i is the i th diagonal element and represents the degree of node i .

- The **Graph Laplacian** is the matrix $\mathbf{L} = \mathbf{D} - \mathbf{A}$, and satisfies $\frac{d\psi}{dt} + C\mathbf{L}\psi = 0$ (aka the diffusion equation).

Laplacian Matrix in More Detail

The elements of the Laplacian matrix are defined as follows for an undirected, unweighted matrix.

$$L_{ij} = \begin{cases} k_i & \text{if } i = j \\ -1 & \text{if } i \neq j \text{ and there is an edge } (i, j) \\ 0 & \text{otherwise} \end{cases}$$

The Graph Laplacian Has Many Nice Linear Algebraic Properties

- In a network with c components, the number of zero eigenvalues is equal to the number of components, (c).

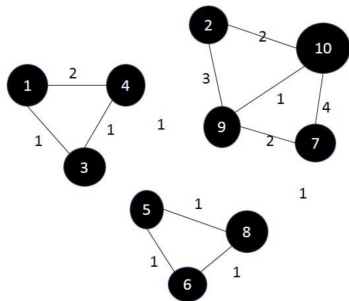


Figure: Each group of nodes makes a component.

Building graphs from data

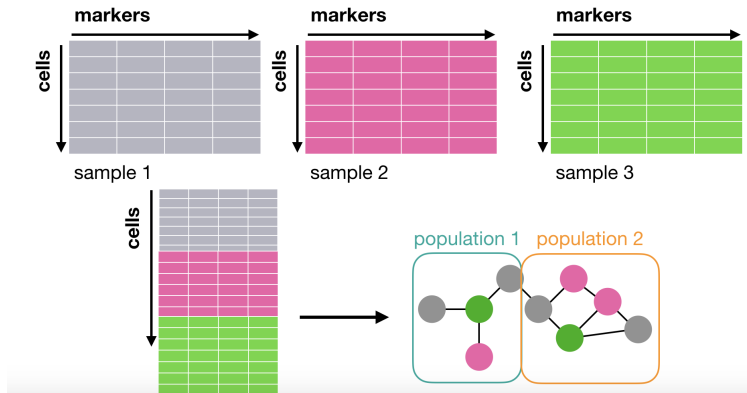


Figure: The task is to compute distances between all pairs of cells, and connect each cell with their nearest neighbors

k-Nearest Neighbor Graphs

- Suppose our dataset, \mathcal{X} is defined as $\mathcal{X} = \{\mathbf{x}_i\}_{i=1\dots N}, \mathbf{x}_i \in \mathbb{R}^d$.
- The general idea is to connect each node with its k nearest neighbors
 - Compute all pairwise similarities between all pairs of nodes
 - For a node, i , find the k nodes that are closest and draw edges.
- Computing all pairwise distances quickly becomes expensive ($O(N^2d)$).

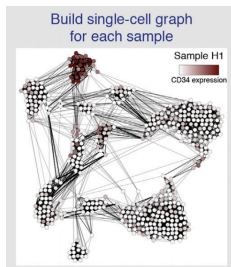


Figure: from Levine *et al.* Cell. 2015. Each cell is connected to its k -nearest

Randomized Trees for Nearest Neighbor Search

People have come up with clever ways to compute k -NN graphs much faster. A popular approach is k -d trees and most recently random projection trees.

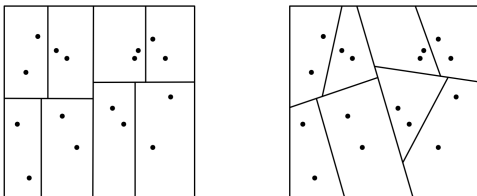


Figure: from Dasgupta *et al.* JMLR. 2013. k - d tree (left), random projection tree (right).

k -d tree

This is a partition of \mathbb{R}^d hyper-rectangular cells based on the datapoints.

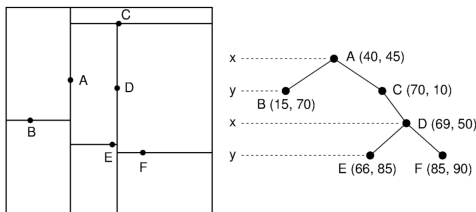


Figure: Alternate between splitting according to the 'x' and 'y' dimensions. For a nearest-neighbor query, q , move q down to its appropriate leaf and return neighbors in that subspace of the leaf node.

Random Projection Trees

Instead of doing axis parallel splits, split directions and split points are randomly selected.

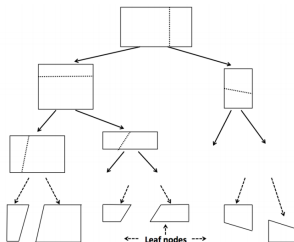
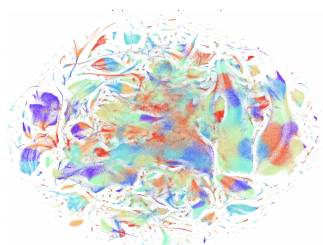


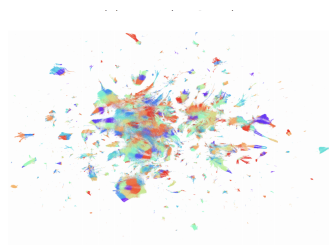
Figure: Random projection tree. (see <https://cseweb.ucsd.edu/~dasgupta/papers/exactnn-colt.pdf> for a discussion on randomized partition trees.)

One Application of k -NN Graph is Visualization (LargeVis)

Using random projection trees, LagreVis creates an embedding for a set of points with a probabilistic model.



(c) WikiDoc (t-SNE)



(d) WikiDoc (LargeVis)

Figure: from Tang *et al.* The Web Conference (WWW). 2016. tSNE and 'string behavior' from being designed to preserve super local similarities.

A Probabilistic Model for Graph Embedding

For some nodes, i and j , let y_i and y_j be their embedding coordinates such that $y_i, y_j \in \mathbb{R}^d$ (for visualization purposes, $d = 2$). We can model the probability that an edge exists between nodes i and j as a function ($f(\cdot)$) of their learned embedding coordinates, or,

$$P(e_{ij} = 1) = f(\|y_i - y_j\|) \quad (16)$$

- An important criterion to be satisfied is that $f(\cdot)$ must ensure a high probability when i and j are close, and low otherwise.
- For example: $f(x) = \frac{1}{1+ax^2}$

Writing Down the Likelihood of the Observed Graph

The authors define a similarity measure between pairs of nodes where there is an edge, based on the original data, \mathbf{x}_i and \mathbf{x}_j . Our probability of an edge existing between nodes i and j can be modified from the previous slide to incorporate edge weights as,

$$P(e_{ij} = w_{ij}) = P(e_{ij} = 1)^{w_{ij}} \quad (17)$$

The likelihood of the graph can be written as,

$$\begin{aligned} O &= \prod_{(i,j) \in E} P(e_{ij} = 1)^{w_{ij}} \prod_{(i,j) \in \tilde{E}} (1 - P(e_{ij} = 1))^\gamma \\ &\propto \sum_{(i,j) \in E} w_{ij} \log P(e_{ij} = 1) + \sum_{(i,j) \in \tilde{E}} \gamma \log(1 - P(e_{ij} = 1)) \end{aligned}$$

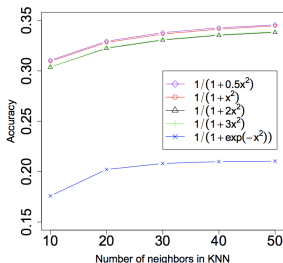
\tilde{E} represents pairs of nodes with no edge.

Brief Overview of Optimization of Parameters

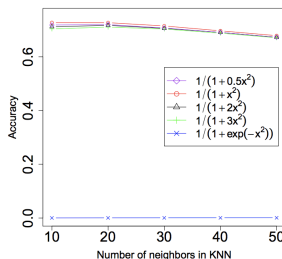
- Since these graphs are very sparse, there are a lot of ‘negative edges’ or edges $\in \tilde{E}$. So the authors used a smart negative sampling approach to only consider a subset of negative node pairs
 - For each node, i , consider sample some pair nodes, j .
 - A node j to pair with i as a negative example is sampled with probability $\propto d_j^{0.75}$. Here d_j is the degree of node j .
 - Optimize parameters with asynchronous stochastic gradient descent (<https://papers.nips.cc/paper/2011/file/218a0aefd1d1a4be65601cc6ddc1520e-Paper.pdf>)

Choice of $f(\cdot)$

The authors tested how choice of $f(\cdot)$ affected the quality of their embedding. Looks like there is one bad choice, but overall, does not make a huge difference.



(a) WikiDoc



(b) LiveJournal

Figure: from Tang *et al.* The Web Conference (WWW). 2016.

More Practical Reasons to Use LargeVis: Scales better than tSNE

Nothing would ever be as fast as PCA. But, if you need to understand more local types of similarities between data points, perhaps it's worth the wait....

Table 2: Comparison of running time (hours) in graph visualization between the t-SNE and LargeVis.

Algorithm	20NG	MNIST	WikiWord	WikiDoc	LiveJournal	CSAuthor	DBLP Paper
t-SNE	0.12	0.41	9.82	45.01	70.35	28.33	18.73
LargeVis	0.14	0.23	2.01	5.60	9.26	4.24	3.19
Speedup Rate	0	0.7	3.9	7	6.6	5.7	4.9

Figure: from Tang *et al.* The Web Conference (WWW). 2016. Comparison in run-time between tSNE and LargeVis.

Recap

- Matrix Rank and SVD
- Graphs: Properties, Laplacian
- LargeVis: An example of using a graph-based representation of data that was computed efficiently for visualization.

Next time:

Graph partitioning and ranking nodes (in a way that is more sophisticated than just node degree....)