

- This homework is due at 11:59pm on April 22, 2022. Please submit by email to natalies@cs.unc.edu+comp790.
- There are a few files provided:
 - Protein-Protein Interaction Network 1, with edges determined according to co-expression in `Coexpress_Edges.csv`
 - Protein-Protein Interaction Network 2, with edges determined according to experimental information given in `Experimental_Edges.csv`
- You are welcome to consult with other colleagues, but please write up your own independent solution.
- You are welcome to use Python, Julia, or R here.
- You are welcome to write up your assignment using the `HW2_790-166.tex` template, or write up the solutions in the method of your choice.
- This homework is worth 62 points total.
- Please submit your final writeup as a PDF. Please try not to end me pages of output from Jupyter notebooks :) I simply want to see the few lines of code you used to answer each sub-question.
- Make sure to comment and elaborate on your answers in places where you are asked to comment!

Problem 1

Understanding the Rayleigh Ritz Theorem (12 points)

Here we will empirically explore the Rayleigh Ritz Theorem which says the following.

- Let $\mathbf{A} \in \mathbb{R}^{N \times N}$ be a square symmetric matrix with eigenvalues $\lambda_1 \leq \lambda_2 \leq \dots \leq \lambda_n$ and corresponding eigenvectors $\{\mathbf{v}_1, \mathbf{v}_2, \dots, \mathbf{v}_n\}$. Defining $R_{\mathbf{A}}(\mathbf{x}) = \frac{\mathbf{x}^T \mathbf{A} \mathbf{x}}{\mathbf{x}^T \mathbf{x}}$, then the minimum value of $R_{\mathbf{A}}(\mathbf{x})$ is λ_1 and occurs when $\mathbf{x} = \mathbf{v}_1$.
- Obviously, this is a nice property to understand, as $\mathbf{x}^T \mathbf{A} \mathbf{x}$ represents the quadratic form that we are often trying to minimize.
- This property can be extended to find the matrix \mathbf{X} that minimizes $\text{trace}(\mathbf{X}^T \mathbf{L} \mathbf{X})$. Specifically, the k -dimensional matrix, \mathbf{X} that minimizes $\text{trace}(\mathbf{X}^T \mathbf{L} \mathbf{X})$ is the first k eigenvectors of \mathbf{L} (e.g. those corresponding to the k smallest eigenvalues) and the minimum value obtained for $\text{trace}(\mathbf{X}^T \mathbf{L} \mathbf{X})$ will be $\lambda_1 + \lambda_2 + \dots + \lambda_k$.

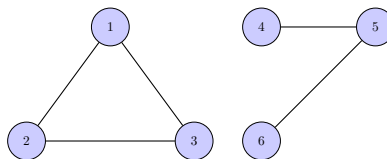


Figure 1: The graph, \mathcal{G} that we already met in homework 1.

1. **Problem Setup 1** (1 point) Create the adjacency matrix, \mathbf{A} for \mathcal{G} and compute the graph Laplacian matrix, \mathbf{L} for this graph. Note that you already did this in homework 1. Just copy it here!

2. **Problem Setup 2** (1 point) Find the eigenvalues and eigenvectors of \mathbf{L} . Note that you also have done this in homework 1.
3. **Eigenvalue Sorting** (2 points). We first need to order the eigenvalues of \mathbf{L} from largest to smallest. That is, you need to return the indices of eigenvalues that would sort them from smallest to largest.
4. **What Won't Be the Minimum** (2 points). Find the fourth smallest eigenvalue, λ_4 and its corresponding eigenvector \mathbf{v}_4 . Evaluate $\mathbf{v}_4 \mathbf{L} \mathbf{v}_4^T$ and write down the number that you get.
5. **Compare to the Following, which will be smaller** (2 points). Find the first smallest eigenvalue, λ_1 and its corresponding eigenvector \mathbf{v}_1 . Evaluate $\mathbf{v}_1 \mathbf{L} \mathbf{v}_1^T$ and write down the number that you get. Comment on this wrt what you got using the fourth eigenvalue/eigenvector.
6. **Forming the Non-Optimal 2d Embedding** (2 points). Now we will use the eigenvectors that minimize $\text{trace}(\mathbf{X}^T \mathbf{L} \mathbf{X})$. Form a matrix with two columns where the first column is the third eigenvector \mathbf{v}_3 and the second column is the fourth eigenvector \mathbf{v}_4 . Define the embedding matrix, \mathbf{E} as the matrix that horizontally concatenates \mathbf{v}_3 and \mathbf{v}_4 as $\mathbf{E} = [\mathbf{v}_3 | \mathbf{v}_4]$.
 - Compute $\text{trace}(\mathbf{E}^T \mathbf{L} \mathbf{E})$. Record what you get.
 - Compute $\lambda_3 + \lambda_4$ and comment about what you get with respect to the trace you just computed.
7. **Forming the Optimal 2 Embedding** (2 points) Now we will use the eigenvectors that minimize $\text{trace}(\mathbf{X}^T \mathbf{L} \mathbf{X})$. Form a matrix with two columns where the first column is the first eigenvector \mathbf{v}_1 and the second column is the second eigenvector \mathbf{v}_2 . Define the embedding matrix, \mathbf{E} as the matrix that horizontally concatenates \mathbf{v}_1 and \mathbf{v}_2 as $\mathbf{E} = [\mathbf{v}_1 | \mathbf{v}_2]$.
 - Compute $\text{trace}(\mathbf{E}^T \mathbf{L} \mathbf{E})$. Record what you get.
 - Compute $\lambda_1 + \lambda_2$ and comment about what you get with respect to the trace you just computed.

Problem 2

(50 Points Total) Protein-Protein Interaction (PPI) Graph Alignment

Two protein-protein interaction networks for Humans were downloaded from the string database <https://string-db.org/> and pre-processed to produce sufficiently large but not too large subgraphs. In the first graph, edges were determined according to co-expression information `Coexpress_Edges.csv`. In the second graph, edges were determined according to validated, experimental information. Our challenge is to apply a graph alignment technique to see if the same proteins map to each other between these two graphs. Recall REGAL alignment <https://arxiv.org/pdf/1802.06257.pdf>. The following homework sub-problems will walk us through implementing the REGAL graph alignment approach.

1) **Constructing Node Features (5 points):** The first part of REGAL is to create a feature vector for each node that helps to summarize something about its context. We will use a simple k -hop method to construct a feature vector for each node. Recall that for a node, i , its ' k -hop subgraph' can be obtained by considering nodes that are within k hops from i . (Hint: you may find the following useful https://networkx.org/documentation/stable/reference/generated/networkx.generators.ego.ego_graph.html).

We will consider k -hop networks for $k = 1, 2, 3, 4$. Write a function, where for a particular k , you collect the set of neighboring nodes within k hops of each node and summarize the degree distribution of these collective ' k -hop neighbors' with 4 statistics : {min degree, median degree,

mean degree, max degree}. After doing this for each value of k , you should ultimately be able to represent each node with 16 features (4 considered hops \times 4 summary statistics per hop). As an example, assuming Graph 1 has N_1 nodes, define its node feature matrix, $\mathbf{X}_1 \in \mathbb{R}^{N_1 \times 16}$ matrix.

2) **Intuition Building (5 points):** Use your new function to build the described feature vectors for Supragingival Plaque Network (Network 1). Assuming this network has N_1 nodes, **project these N_1 nodes into two dimensions using your dimensionality reduction method of choice**, based on the 16 computed features ($\mathbf{X}_1 \in \mathbb{R}^{N_1 \times 16}$).

3) **Choosing Landmarks (5 points):** Recall that REGAL constructs an embedding for each node by specifying landmark nodes that have been collected across both of the graphs being aligned. Choose a set of d landmark nodes **collectively** across Graphs 1 and 2. You can play with d later, but considering the total number of nodes is < 200 between graphs 1 and 2, perhaps $d = 30$ is a good place to start. You can choose the set of d landmarks at random, or use a more sophisticated approach. **Explain your choice of landmarks and write a function to return these landmark nodes.**

4) **Computing Similarities to Landmarks (5 points):** In part 1), you wrote a function to compute feature vectors for each node. Assuming Graph 1 has N_1 nodes and Graph 2 has N_2 nodes, **write a function that computes a similarity measure in this 16-dimensional space between each of the nodes in Graph 1 and Graph 2 to each of the d landmarks.** So, you should end up with a matrix, $\mathbf{C} \in \mathbb{R}^{(N_1+N_2) \times d}$.

5) **Extract Landmark \times Landmark Matrix (5 points):** As you know, the \mathbf{C} that you constructed contains the d landmark nodes! Write a function to construct $\mathbf{W} \in \mathbb{R}^{d \times d}$ submatrix of \mathbf{C} where the similarities between the landmarks were stored.

6) **Embedding via Landmarks (5 points):** Given Theorem 3.1 in <https://arxiv.org/pdf/1802.06257.pdf>, we can compute the collective node embedding matrix (across Network 1 and Network 2), $\tilde{\mathbf{Y}} \in \mathbb{R}^{(N_1+N_2) \times d}$, as

$$\tilde{\mathbf{Y}} = \mathbf{C}\mathbf{U}\mathbf{\Sigma}^{1/2}$$

Recall that here, \mathbf{U} and $\mathbf{\Sigma}$ are obtained through an SVD on the pseudo inverse (\mathbf{W}^{pinv}) of the (landmark \times landmark) similarity matrix, $\mathbf{W} \in \mathbb{R}^{d \times d}$ extracted from \mathbf{C} .

$$\mathbf{W}^{\text{pinv}} = \mathbf{U}\mathbf{\Sigma}\mathbf{V}^T$$

Hints: These are useful for pseudoinverse (<https://numpy.org/doc/stable/reference/generated/numpy.linalg.pinv.html>) and SVD (<https://numpy.org/doc/stable/reference/generated/numpy.linalg.svd.html>).

Given this information, write a function to compute $\tilde{\mathbf{Y}}$.

7) **Putting it All Together Visualization 1 (5 points):** You have now defined an embedding for all nodes in Networks 1 and 2 in some d -dimensional space through $\tilde{\mathbf{Y}}$. **Use your favorite dimensionality reduction method of choice to project the collective set of nodes in Networks 1 and 2 into two dimensions. Color the nodes by which network they are from. Comment on any observations.**

8) **Alignment Between Graphs (5 points):** Given $\tilde{\mathbf{Y}}$, calculate a similarity score (your choice) between each node in Network 1 and every node in Network 2.

9) **Creativity (5 points):** Now that you have the entire pipeline in place, play around with it a bit. For example, considering changing how you define the features for nodes in part 1), changing the value of d , changing how you choose landmarks, or anything else that is interesting to you! **Re-run steps 1-7 with your modification and comment on how it changes the interpretation of alignment between Network 1 and Network 2 given in \tilde{Y} .**

10) **Creativity Part 2 (5 points):** Imagine a collaborator dropped these two networks on your desk. They are paying you from their grant, so you need to produce something to give them. **Create a visualization of your choice that reflects something about the similarity between Network 1 and Network 2** (in terms of node alignment, clustering structure, etc).

Congratulations! You implemented REGAL from scratch!