

A.1 a) Convert this into an adjacent matrix:

1	0	0
1	1	1
0	1	0
0	0	1

Each column represent an edge, and the rows are nodes.

Edge 1 connects Node 1 & Node 2

Edge 2 connects Node 2 & Node 3

Edge 3 connects Node 2 & Node 4

0	1	0	0
1	0	1	1
0	1	0	0
0	1	0	0

b) B - Erdős-Rényi (Random Network) Model

In this model, each possible edge between a pair of nodes is formed independent with equal probability.

c) C - Nash Equilibrium.

A Nash equilibrium occurs when each player's strategy is optimal given the strategies of all other players, thus no one can improve their outcome by changing their strategy alone.

d] B - Assortative Mixing.

This refers to the tendency of nodes to connect to others that are similar in some way like age, degree etc.

e] D - Because it quantify how often a node lies on the shortest paths between other nodes.

- Betweenness certainly focuses on how critical a node is for connecting others, especially when information has to pass along shortest path unlike degree centrality, which just counts immediate connections.

f] C - The presence of many nodes with very high degree (hubs) that maintain connectivity.

- Scale-free networks have a few highly connected hubs. Random failure usually hit low-degree nodes, so the network survives. But if the hub fails, it can break the whole structure, making it vulnerable to targeted attacks.

g] A - The number of intra-community edge is significantly higher than degree sequence.

- High modularity means most connections are within communities, and very few are between them - more than what you'd expect in a random setup.

h) B - 2/5

- Neighbours of X : A, B, C, D

Neighbours of Y : C, D, E

Intersection : C, D \rightarrow 2 nodes

Union : A, B, C, D, E \rightarrow 5 nodes

$$\therefore \text{Jaccard coefficient} = \frac{2}{5}$$

i) A - 4CM uses edge probability independent;

LTM uses a weight of active -- threshold.

- 4CM - each active neighbour gets one independent chance to activate a node.

LTM - a node becomes active only when the sum of influence from its neighbours crosses a threshold.

j) B - Because aggregating feature from dissimilar neighbours can blur the node's -- harder.

- In heterophilic networks, pulling in feature from neighbours can actually confuse the model.

The GCN ends up including unrelated info which reduces classification accuracy.

A-2 To effectively reduce the spread of a novel influenza strain modeling by the SIR framework, and with the constraint of vaccinating only 5% of the population, we can use a combination of network analysis technique to identify the most strategic individual for vaccination. The goal is to maximize impact with minimal resource by targeting those

most critical to the virus potential spread.

- Using two network concepts.

1. Degree centrality - This metric identifies individuals with the highest number of direct connections in the network. These people interact with many others and are more likely to become infected and pass the disease to several others.

Why it works - Vaccinating individuals with high degree centrality can prevent a large number of initial infections.

Sort nodes by degree - Like a person who interacts with 30 people daily poses a high risk of spreading the virus. So, vaccinating them early cuts off multiple potential transmission chains.

- 2. Between centrality - This metric highlights nodes that frequently lie on the shortest path between other nodes. These people serve as a bridge between the parts of the network, enabling the disease to jump between groups or communities.

Vaccinating high-betweenness individuals can stop the spread from moving across communities which is critical in keeping the outbreak localized.

Compute betweenness scores and flag nodes that take risk highly especially those not already chosen by degree critical.
Like even if someone doesn't have a lot of

connections, they may be the only link between two large groups. So, if disease reaches them it could suddenly infect the entire new section.

- To maximize effectiveness - Rank all individuals by both degree & betweenness centrality. Then identify the score high on both, as they are both highly connected and act as critical bridges.

Select the top 5% from this prioritized list for vaccination. This ensures that we are vaccinated not just the socially active individuals, but also the structural 'gatekeepers' of the network.

- To justify this - Using just degree centrality might ignore structurally important nodes with lower connections but high strategic placement.

Using only betweenness might ignore 'super-spreading' with many contacts.

Combining both ensures a balance strategy blocking both high frequency and high impact paths.

A.3 To enhance the suggested collaborations feature for academic researchers we can combine link prediction algorithms with node embedding techniques like Node2Vec, using data from co-citation and co-authorship networks. This would identify meaningful, research-driven connections.

that are both relevant and novel.

1 Using Link Prediction + Node Embedding.

So, link prediction helps forecasting which pairs of researchers are likely to collaborate in the future based on existing network patterns.

Like - Jaccard coefficient, Adamic-Adar, etc.

However these methods are mostly rely on local network structure and may miss deeper patterns.

Node embedding technique like Node2Vec solves this by learning a vector representation of each researcher based on their position in the network. These vectors captures both structural & semantic similarities.

By combining the two - Node2Vec provides dense embedding capture the researcher's role & context. Link prediction uses these embeddings to predict future or potential links.

- Role of Homophily in collaboration - This is a tendency for similar individual to collaborate more often.

In practice: A computer scientist is more likely to co-author with another CS than with a biologist.

Effect on Recommendation: Node2Vec embedding's

naturally captures homophily, since co-authorship and citation networks often group researchers with similar interests.

- While homophily is useful, it can also reinforce academy silos. To encourage cross-disciplinary collaboration we can tweak our system to highlight 'bridge' opportunities.

Add a diversity penalty or bonus to the recommended score:

For example, suggest a data scientist to a climate researcher if they have both co-authored with someone in environmental modeling.

This promotes novel and interdisciplinary connections without compromising on quality.

A.4 a) The Girvan-Newman algorithm is a method for community detection that works by progressively removing edges to reveal the underlying community structure of a network. Think of it like cutting the weakest link between groups to let natural clusters emerge.

- b - At each step compute edge betweenness for all edges and remove the edge with the highest value. Repeat this until desired community structure emerges.

C- Computing edge betweenness Centrality is expensive per calculation, making the algorithm slow for large networks.

d- The Louvain method is a popular, fast & scalable algorithm that detects communities by optimizing modularity. This allows it to efficiently find the high-modularity partitions in very large networks, often with millions of nodes, much faster than the Girvan - Newman.

A.5 a) Intuition behind Page Rank Algorithm -

PageRank models the importance of the node as probability that makes a random walker land on it considering both direct link and importance of linking nodes.

b) Damping factor role - The damping factor is (typically 0.85) represents probability that a random walker flows a link, $1-d$ is the probability of jumping to a random node, ensuring the process does not give stuck.

c) Dangling nodes are nodes with no outgoing link to any other node. If the random surfer lands on a dangling node, there's nowhere to go, which can cause the PageRank score to 'leak' and algorithm may not converge properly.

A common solution to redistribute the Page Rank of dangling nodes evenly to all nodes in the network. This trick ensures that the Page Ranks ~~are~~ continue to sum to 1 and that the algorithm converges smoothly, even with dangling nodes present.

A.6 a) A strategy pairs where ~~neither~~ ~~can~~ improve their payoff by ~~the~~ changing their strategy.

- check each pair:

(U, A) : Pay off $(3, 2)$

- player 1: switch to $L \rightarrow 2 < 3$, no improv
- player 2: switch to $B \rightarrow 1 < 2$, "
- Nash equilibrium.

(U, B) Payoff $(0, 1)$

- Player 1: switch $L \rightarrow 2 > 0$, improv
- Not Nash.

(L, B) , pay off $(2, 3)$:

- Player 1: switch to $U \rightarrow 0 < 2$, No improvement.
- player 2: switch to $A \rightarrow 0 < 3$, "
- Nash equilibrium.

There are two ~~new~~ strategy Nash equilibria
 (U, A) & (L, B)

b) player 1 plays U with probability P , L with probability $1-P$.
 Player 2's strategy:

Expected pt payoff for player 2 in choosing strategy A:

$$E[A] : p \times 2 + (1-p) \times 0 = 2p$$

Expected payoff for player 2 in choosing strategy B:

$$E[B] = p \times 1 + (1-p) \times 3$$

$$= p + 3(1-p)$$

$$= p + 3 - 3p = 3 - 2p$$

c) For player 2

$$E[A] = 2p = 2 \times 0.7 = 1.4$$

$$E[B] = 3 - 2p = 3 - 2(0.7) = 1.6$$

Since $E(B) > E(A)$, player 2 would choose strategy B.

For player 1, (0.7 U, 0.32)

$$\text{Expected payoff} = 0.7 \times 0 + 0.3 \times 2$$

$$= 0.6 \text{ (when player 2 choose B)}$$

The expected outcome for player 1 receive a payoff of 0.6 & player 2 receive a payoff of 1.6.

A-7 Given:

Directed edges $A \rightarrow B$

$C \rightarrow B$

$D \rightarrow B$

weighted matrix $w = \begin{bmatrix} 0.5 & 0 \\ 0.1 & 0.2 \end{bmatrix}$

a) Aggregate neighbours -

$$h_n^{(0)} = \frac{1}{3} h_a^{(0)} + h_c^{(0)} + h_o^{(0)} = \left(\begin{bmatrix} 1 \\ 1 \end{bmatrix} + \begin{bmatrix} 0 \\ 3 \end{bmatrix} + \begin{bmatrix} 2 \\ 2 \end{bmatrix} \right) \frac{1}{3}$$

$$= \frac{1}{3} \begin{pmatrix} 3 \\ 6 \end{pmatrix} = \underline{\underline{\frac{1}{2}}}$$

b) Transform -

$$W \cdot h_n^{(0)} = \begin{bmatrix} 0.5 & 0 \\ 0.1 & 0.2 \end{bmatrix} \cdot \begin{pmatrix} 1 \\ 2 \end{pmatrix}$$

$$= \begin{bmatrix} 0.5(1) + 0(2) \\ 0.1(1) + 0.2(2) \end{bmatrix}$$

$$= \underline{0.5} \begin{bmatrix} 0.5 \\ 0.5 \end{bmatrix}$$

c) Apply ReLU Activation.

Applying ReLU

$$h_B^{(1)} = \text{ReLU} \left(\begin{bmatrix} 0.5 \\ 0.5 \end{bmatrix} \right)$$

~~= 0~~

$$= \begin{bmatrix} 0.5 \\ 0.5 \end{bmatrix}$$

$$\text{Final Answer } h_B^{(1)} = [0.5, 0.5]$$