

SIR Model

SIR model:

- In addition to the **I** and **S** states, a recovery state **R** is present
- Individuals get infected and some recover
- Once hosts recover (or are removed) they can no longer get infected and are not susceptible



SIR Model, Equations

$$I + S + R = N$$

$$\frac{dS}{dt} = -\beta IS,$$

$$\frac{dI}{dt} = \beta IS - \gamma I,$$

$$\frac{dR}{dt} = \gamma I.$$

γ defines the recovering probability of an infected individual at a time stamp

SIR Model, Equations, Cont.

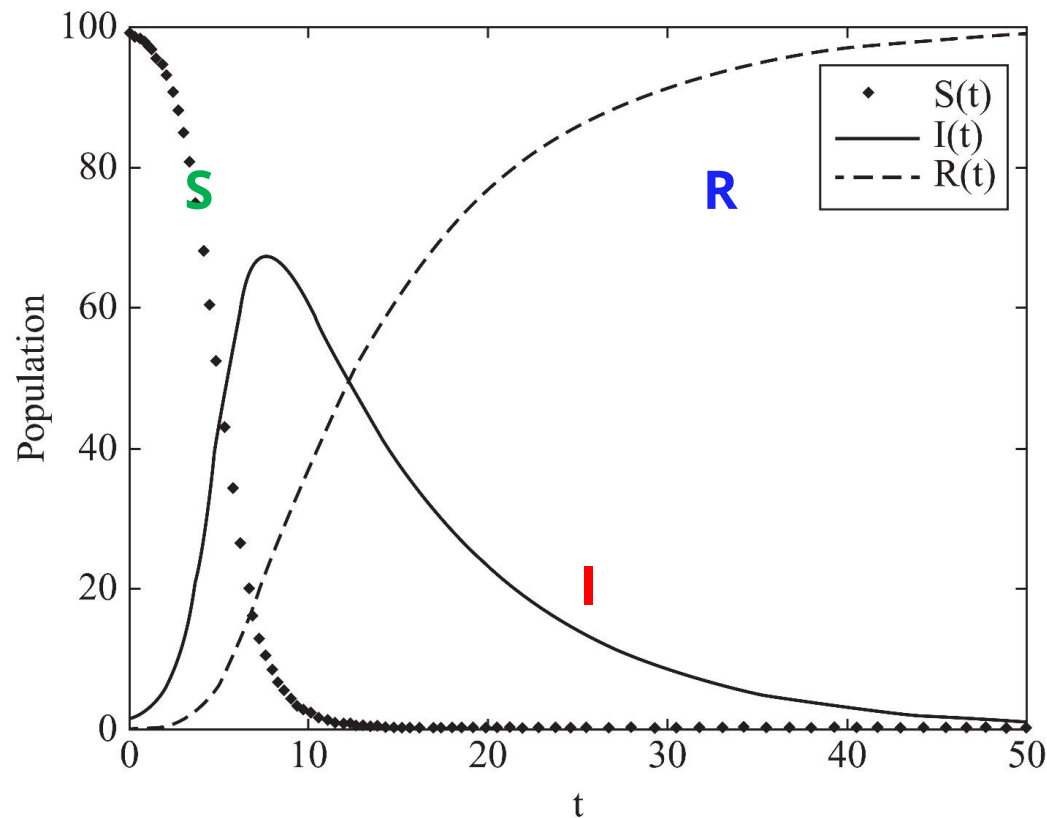
$$\begin{aligned}\frac{dS}{dt} &= -\beta IS, & \longrightarrow & \frac{dS}{dR} = -\frac{\beta}{\gamma} S \\ \frac{dI}{dt} &= \beta IS - \gamma I, \\ \frac{dR}{dt} &= \gamma I. & \longrightarrow & \log \frac{S_0}{S} = \frac{\beta}{\gamma} R \quad (R_0 = 0)\end{aligned}$$

$$\frac{dR}{dt} = \gamma(N - S - R)$$

$$\frac{dR}{dt} = \gamma(N - S_0 e^{-\frac{\beta}{\gamma} R} - R) \quad \longrightarrow \quad t = \frac{1}{\gamma} \int_0^R \frac{dx}{N - S_0 e^{-\frac{\beta}{\gamma} x} - x}$$

There is no closed form solution for this integration and only numerical approximation is possible.

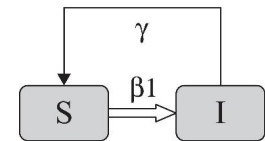
SIR Model: Example



SIR model simulated with $S_0 = 99$, $I_0 = 1$, $R_0 = 0$, $\beta = 0.01$, and $\gamma = 0.1$

SIS Model

- The **SIS** model is the same as the **SI** model with the addition of infected nodes recovering and becoming susceptible again



$$\frac{dS}{dt} = \gamma I - \beta IS, \quad \frac{dI}{dt} = \beta IS - \gamma I$$

$$\Rightarrow \frac{dI}{dt} = \beta I(N - I) - \gamma I = I(\beta N - \gamma) - \beta I^2$$

$$\frac{dI}{dt} = \beta I(N - I) - \gamma I = I(\beta N - \gamma) - \beta I^2$$

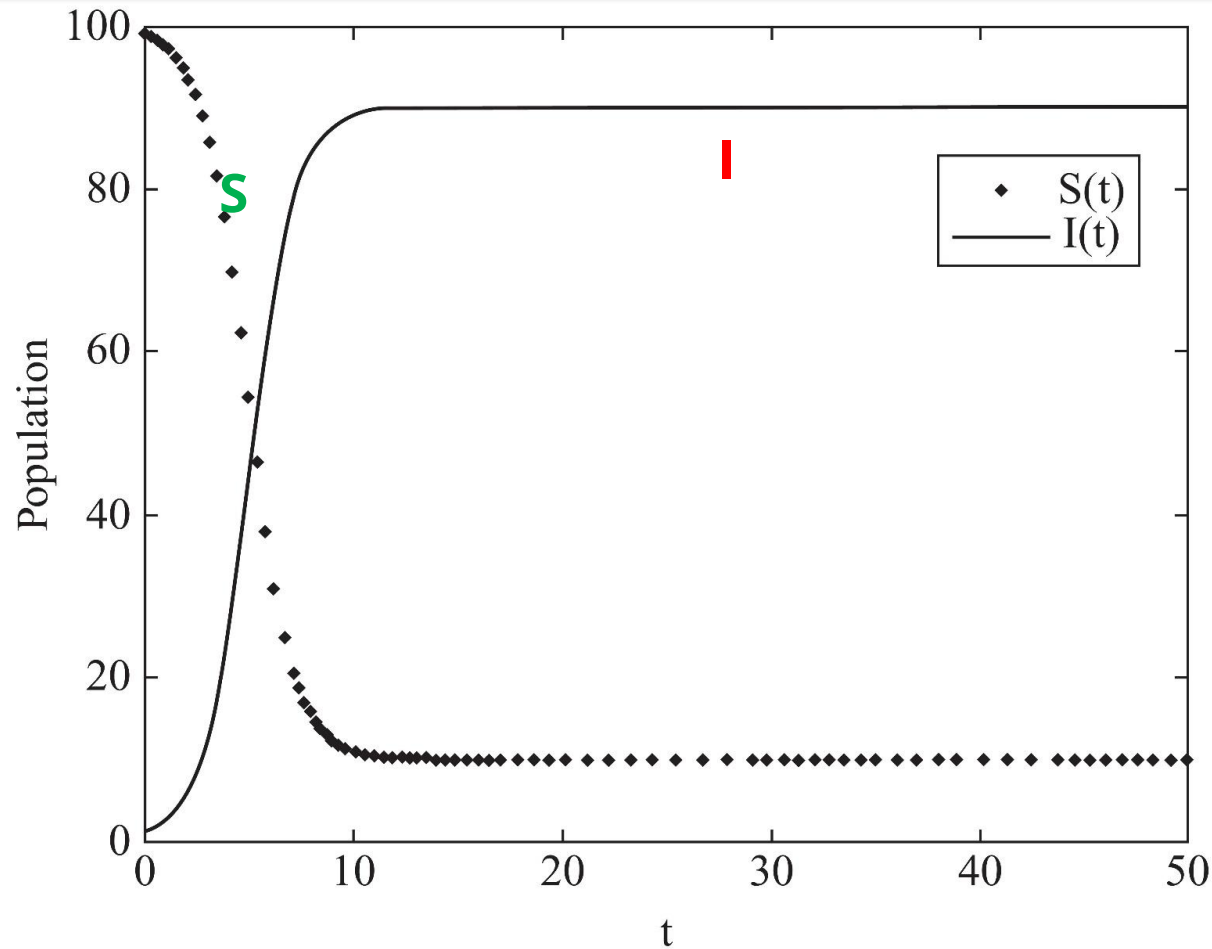
Case 1: When $\beta N \leq \gamma$ (or when $N \leq \frac{\gamma}{\beta}$):

- The first term will be at most zero or negative
- The whole term becomes negative
- In the limit, $I(t)$ will decrease exponentially to zero

Case 2: When $\beta N > \gamma$ (or when $N > \frac{\gamma}{\beta}$):

- We will have a logistic growth function like the **SI** model

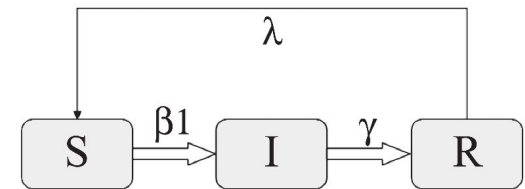
SIS Model



SIS model simulated with $S_0 = 99$, $I_0 = 1$, $\beta = 0.01$, and $\gamma = 0.1$

SIRS Model

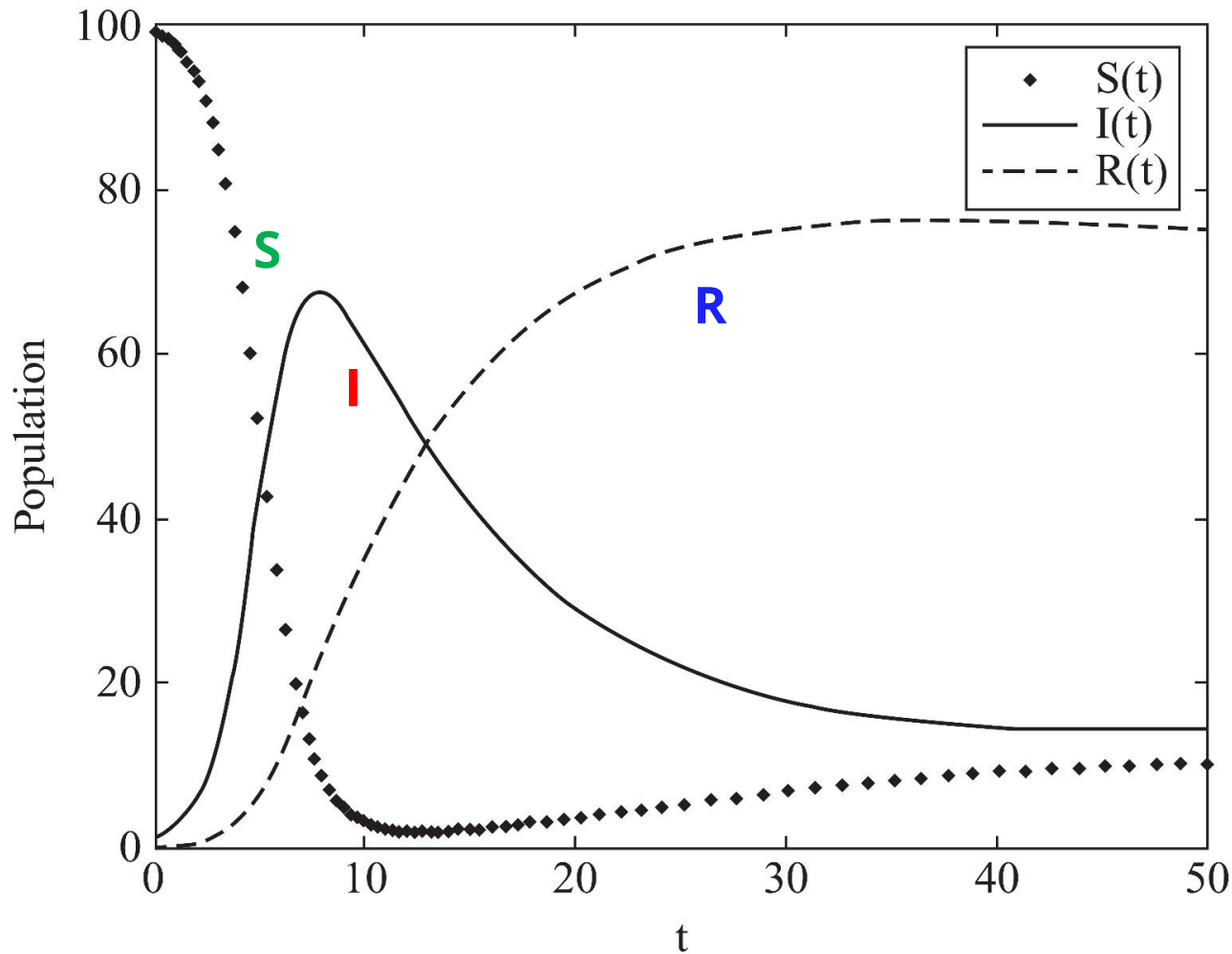
The individuals who have recovered will lose immunity after a certain period of time and will become susceptible again



$$\begin{aligned}\frac{dS}{dt} &= \lambda R - \beta IS, \\ \frac{dI}{dt} &= \beta IS - \gamma I, \\ \frac{dR}{dt} &= \gamma I - \lambda R.\end{aligned}$$

Like the SIR, model this model has no closed form solution, so numerical integration can be used

SIRS Model



SIRS model simulated with $S_0 = 99$, $I_0 = 1$, $R_0 = 1$, $\beta = 0.01$, $\lambda = 0.02$, and $\gamma = 0.1$

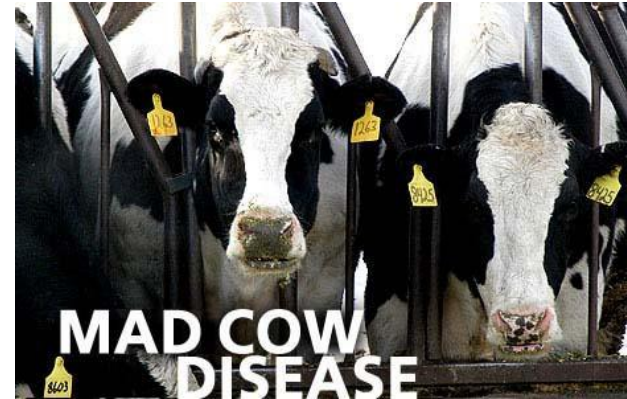
Epidemic Intervention

- Suppose that we have a susceptible society and want to prevent more spread by vaccinating the most vulnerable individuals
- What is the best way to vaccinate a population?

Randomly pick some nodes and ask them who is the most popular from their point of view, then vaccinate those individuals!

Epidemic Intervention: *Mad Cow Disease*

- Jan. 2001
 - First case observed in UK
- Feb. 2001
 - 43 farms infected
- Sep. 2001
 - 9,000 farms infected



In the mad cow disease case, we have weak ties

- Animals being bought and sold
- Soil from tourists, etc.

How to stop the disease:

- Banned movement (make contagion spread more difficult, or quarantine)
- Killed millions of animals (remove weak ties)

CS 579: Online Social Network Analysis

Influence and Homophily

Kai Shu

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Social Forces

- **Social Forces** connect individuals in different ways
- When individuals get connected, we observe distinguishable patterns in their connectivity networks.
 - **Assortativity**, also known as *social similarity*
- In networks with assortativity:
 - Similar nodes are connected to one another more often than dissimilar nodes.
- Social networks are *assortative*
 - A high similarity between friends is observed
 - We observe similar behavior, interests, activities, or shared attributes such as language among friends

Why are connected people similar?

Influence

- The process by which a user (i.e., influential) affects another user
- The influenced user becomes more similar to the influential figure.
 - **Example:** If most of our friends/family members switch to a cellphone company, we might switch [i.e., become influenced] too.

Homophily

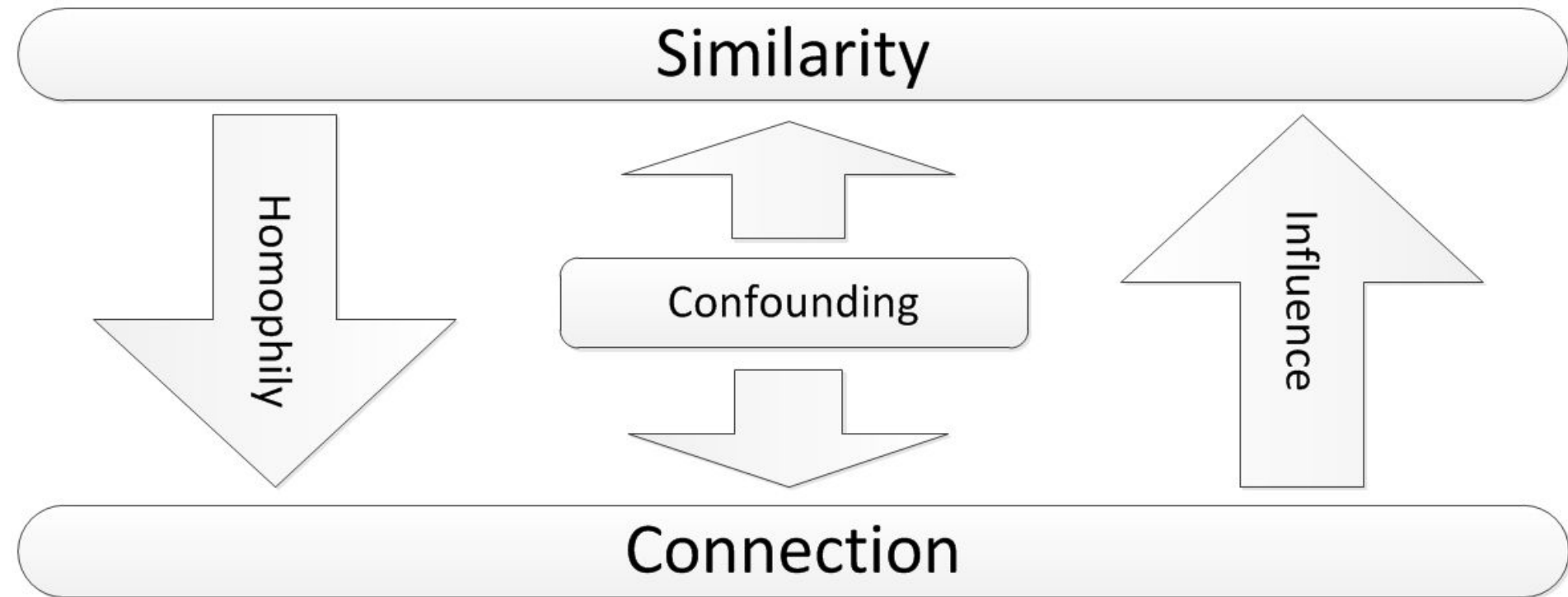
- Similar individuals becoming friends due to their high similarity
 - **Example:** Two musicians are more likely to become friends.



Confounding

- The environment's effect on making individuals similar
 - **Example:** Two individuals living in the same town are more likely to become friends than two random individuals

Influence, Homophily, and Confounding

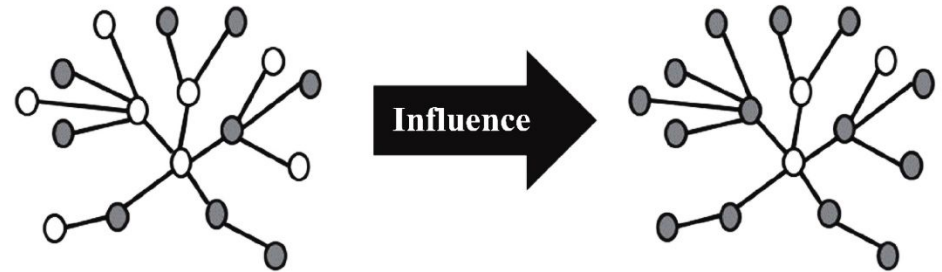


Source of Assortativity in Networks

Both influence and Homophily generate similarity in social networks

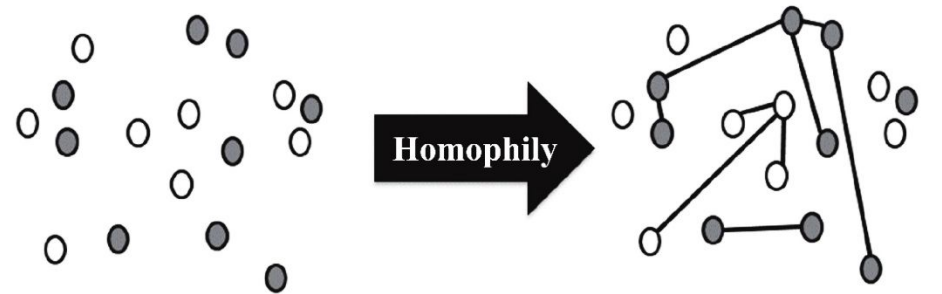
Influence

Makes connected nodes similar to each other



Homophily

Selects similar nodes and links them together



Assortativity Example

The city's draft tobacco control strategy says more than 60% of under-16s in Plymouth smoke regularly

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Patches for Plymouth's young smokers

By Jo Irving
BBC Devon website



More than 60% of Plymouth's under-16s smoke

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Plymouth NHS Trust Stop Smoking Service

Why?

- Smoker friends influence their non-smoker friends

Influence

- Smokers become friends
 - Can this explain smoking behavior?

Homophily

- There are lots of places that people can smoke

Confounding

Our goal

1. How can we measure assortativity?
2. How can we measure influence or homophily?
3. How can we model influence or homophily?
4. How can we distinguish between the two?

Measuring Assortativity

Assortativity: An Example

- The friendship network in a US high school in 1994
- Colors represent races,
 - : Whites
 - **Grey**: Blacks
 - **Light Grey**: Hispanics
 - **Black**: others
- High assortativity between individuals of the same race



Measuring Assortativity for **Nominal** Attributes

- Assume **nominal** attributes are assigned to nodes
 - Example: race
- Edges between nodes of the same type can be used to measure assortativity of the network
 - Same type = nodes that share some attribute value(s)
 - Node attributes could be nationality, race, sex, etc.

$$\frac{1}{m} \sum_{(v_i, v_j) \in E} \delta(t(v_i), t(v_j)) = \frac{1}{2m} \sum_{ij} A_{ij} \delta(t(v_i), t(v_j))$$

$t(v_i)$ denotes type of vertex v_i

$$\delta(x, y) = \begin{cases} 0, & \text{if } x \neq y \\ 1, & \text{if } x = y \end{cases}$$

Kronecker delta function

Assortativity **Significance**

- **Assortativity significance**

- The difference between **measured assortativity** and **expected assortativity**
- The higher this difference, the more significant the assortativity observed

Example

- In a school, 50% of the population is **White** and the other 50% is **Hispanic**.
- We expect 50% of the connections to be between members of different races.
- If all connections are between members of different races, then we have a significant finding

Assortativity **Significance**

Assortativity

Expected assortativity
(according to configuration model)

$$Q = \frac{1}{2m} \sum_{ij} A_{ij} \delta(t(v_i), t(v_j)) - \frac{1}{2m} \sum_{ij} \frac{d_i d_j}{2m} \delta(t(v_i), t(v_j))$$
$$= \frac{1}{2m} \sum_{ij} \left(A_{ij} - \frac{d_i d_j}{2m} \right) \delta(t(v_i), t(v_j)).$$

This is **modularity**

Normalized Modularity [**Finding the Maximum**]

The maximum happens when all vertices of the same type are connected to one another

$$\begin{aligned} Q_{\text{normalized}} &= \frac{Q}{Q_{\max}} \\ &= \frac{\frac{1}{2m} \sum_{ij} (A_{ij} - \frac{d_i d_j}{2m}) \delta(t(v_i), t(v_j))}{\max[\frac{1}{2m} \sum_{ij} A_{ij} \delta(t(v_i), t(v_j)) - \frac{1}{2m} \sum_{ij} \frac{d_i d_j}{2m} \delta(t(v_i), t(v_j))]} \\ &= \frac{\frac{1}{2m} \sum_{ij} (A_{ij} - \frac{d_i d_j}{2m}) \delta(t(v_i), t(v_j))}{\frac{1}{2m} 2m - \frac{1}{2m} \sum_{ij} \frac{d_i d_j}{2m} \delta(t(v_i), t(v_j))} \\ &= \frac{\sum_{ij} (A_{ij} - \frac{d_i d_j}{2m}) \delta(t(v_i), t(v_j))}{2m - \sum_{ij} \frac{d_i d_j}{2m} \delta(t(v_i), t(v_j))} \end{aligned}$$

Modularity: **Matrix Form**

- Let $\Delta \in \mathbb{R}^{n \times k}$ denote the **indicator matrix** and let k denote the number of types

$$\Delta_{x,k} = \begin{cases} 1, & \text{if } t(x) = k; \\ 0, & \text{if } t(x) \neq k \end{cases}$$

- The **Kronecker delta** function can be reformulated using the indicator matrix

$$\delta(t(v_i), t(v_j)) = \sum_k \Delta_{v_i,k} \Delta_{v_j,k}$$

- Therefore,

$$(\Delta \Delta^T)_{i,j} = \delta(t(v_i), t(v_j))$$

Normalized Modularity: **Matrix Form**

Let Modularity matrix be

$$B = A - dd^T / 2m$$

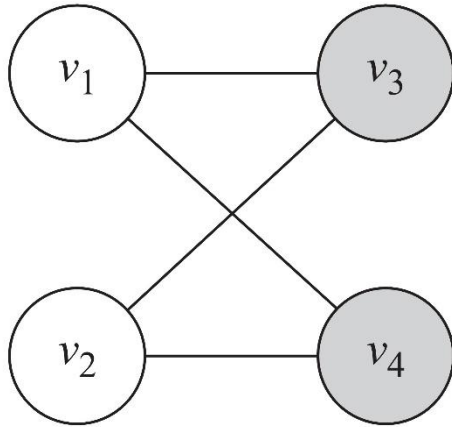


$d \in \mathbb{R}^{n \times 1}$ is the degree vector

Modularity can be reformulated as

$$\begin{aligned} Q &= \frac{1}{2m} \sum_{ij} \underbrace{\left(A_{ij} - \frac{d_i d_j}{2m} \right)}_{B_{ij}} \underbrace{\delta(t(v_i), t(v_j))}_{(\Delta \Delta^T)_{i,j}} = \frac{1}{2m} \text{Tr}(B \Delta \Delta^T) \\ &= \frac{1}{2m} \text{Tr}(\Delta^T B \Delta) \end{aligned}$$

Modularity Example



$$A = \begin{bmatrix} 0 & 0 & 1 & 1 \\ 0 & 0 & 1 & 1 \\ 1 & 1 & 0 & 0 \\ 1 & 1 & 0 & 0 \end{bmatrix}, \quad \Delta = \begin{bmatrix} 1 & 0 \\ 1 & 0 \\ 0 & 1 \\ 0 & 1 \end{bmatrix}, \quad \mathbf{d} = \begin{bmatrix} 2 \\ 2 \\ 2 \\ 2 \end{bmatrix}, m = 4$$

$$B = A - \mathbf{d}\mathbf{d}^T/2m = \begin{bmatrix} -0.5 & -0.5 & 0.5 & 0.5 \\ -0.5 & -0.5 & 0.5 & 0.5 \\ 0.5 & 0.5 & -0.5 & -0.5 \\ 0.5 & 0.5 & -0.5 & -0.5 \end{bmatrix}$$

$$Q = \frac{1}{2m} \text{Tr}(\Delta^T B \Delta) = -0.5$$

The number of edges between nodes of the **same color** is less than the **expected** number of edges between them