# Modelling epidemics on networks with cliques

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## THE PLAN

• An introduction to modeling epidemics.

O Modeling epidemics on regular tree graphs.

Modeling epidemics on networks with cliques.

## AN INTRODUCTION TO MODELING EPIDEMICS HISTORY

- 1920s: Reed-Frost model investigated the number of individuals infected and immune for certain periods of time
- I927: Kermack and McKendrick's SIR model with 3 states Susceptible, Infectious and Removed
- **3** 2005: Keeling and Eames's contact networks

#### AN INTRODUCTION TO MODELING EPIDEMICS Modeling through graphs

- Each vertex denotes an individual.
- Edges denote possible paths of infection.



Figure: In this network, pink vertices represent females, blue vertices represent males, and stars represent the origins of infection.

#### Definition

A **tree** is an undirected graph in which any two vertices are connected by exactly one path, and a **rooted tree graph** is a tree in which one vertex has been designated the root. A **regular tree graph** is a tree graph in which every nonterminal vertex has the same number of edges connected to it. The **height**  $\lambda$  is the largest distance between any node and root, and the **degree** d is the number of nodes connected to the root by an edge.



Figure: An example of a tree graph of degree d = 3 and height  $\lambda = 2$ .

# MODELING EPIDEMICS ON REGULAR TREE GRAPHS IONTW PLATFORM



#### Figure: From [Seibold-Callender]

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MODELING EPIDEMICS ON REGULAR TREE GRAPHS

**R**ELATIONS BETWEEN PARAMETERS

Proposition (Seibold-Callender)

Let N denote the number of nodes in a regular tree graph. Then





#### Figure: From [Seibold-Callender]

#### Definition

For each node,  $P_{inf}$  is the probability of infection, while  $P_{rec}$  is the probability of recovery.

#### Definition

We denote by  $\delta$  the number of edges in the outbreak duration.  $\delta_{\lambda}$  is the expected average outbreak duration, given by  $\sum_{i=1}^{\lambda+1} i \cdot P_i$ , where  $P_i$  is the probability the duration spans *i* edges.

• Duration when  $P_{rec} = 1$  and  $P_{inf} = 1$ 

$$\flat \ \lambda + 1 \le \delta \le 2\lambda + 1$$

- Consider  $P_{inf} \neq 1$ . A specific node getting infected has probability  $P_{inf}$ . Then,
  - Both adjacent nodes remain uninfected with probability  $(1 P_{inf})^2$ .
  - One becomes infected with probability  $2P_{inf} \cdot (1 P_{inf})$ .
  - Both become infected with probability  $P_{inf}^2$ .

#### Theorem (Seibold-Callender)

#### Let $P_i$ denote the probability that the outbreak duration is i. Then

$$P_1 = (1 - P_{inf})^d$$

$$P_{2} = \sum_{r=1}^{d} {d \choose r} P_{inf}^{r} (1 - P_{inf})^{d-r} (1 - P_{inf})^{d\cdot r}$$

$$P_{\lambda+1} = 1 - (P_1 + P_2 + \dots + P_{\lambda}).$$

(*Recall*  $\lambda$  *is the maximum distance, in edges, a node can exist from the root)* 

**Question:** How can we model outbreaks in more general types of graphs, to account for symmetries appearing, for example, from family structures?

How to extend these results to better encompass real networks?

- Irregular tree graphs
- Additional variables such as age, weight, and race
- Cliques in graphs



# EPIDEMICS ON NETWORKS WITH CLIQUES

#### Definition

A clique is a subset S of a graph such that all pairs of vertices in S are connected by an edge. A clique with c vertices is called a c-clique. A maximum clique is the clique of largest size in a graph. The clique number, denoted as  $\omega(G)$ , is the number of vertices in a maximum clique of G.



Figure: Clique number  $\omega(G) = 4$ .

**Question:** How can we bound the clique number to understand the duration of outbreaks in terms of  $P_{rec}$  and  $P_{inf}$  in this new setting?

# EPIDEMICS ON NETWORKS WITH CLIQUES

#### Theorem (Nikiforov)

If G does not contain a complete subgraph of k + 1 vertices, then

$$\lambda \leq \sqrt{\frac{2(k-1) \cdot e}{k}},$$

where e denotes the number of edges.

From there, we can deduce:

Proposition

The number  $\omega(G)$  is bounded by

$$\frac{1}{1-\frac{\lambda^2}{2e}} \le \omega(G).$$

#### **EPIDEMICS ON NETWORKS WITH CLIQUES** Regular tree graphs with induced cliques

Theorem (Turan)

If G does not contain a complete subgraph of k + 1 vertices, then

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$$e < rac{k-1}{2k} \cdot n^2,$$

where n is the number of vertices of G.

From there, we can deduce:

Proposition

In terms of n, we bound  $\omega(G)$  by

$$\frac{n}{n-\lambda} \le \omega(G).$$

#### EPIDEMICS ON NETWORKS WITH CLIQUES ROOT PLACEMENT

Question: How does the origin of infection affect outbreak duration?

• Case 1: When the root is outside all cliques



• Case 2: When the root is in a clique and connected to the "body" of G



• Case 3: When the root is a vertex inside a clique



#### EPIDEMICS ON NETWORKS WITH CLIQUES Safe zones

**Question:** How can one remove a given number of links or nodes of a network so that an outbreak is contained within a subset of the graph?

#### Definition

The **safe zone** of a graph is defined as a subset of vertices that cannot be infected, and makes up one connected component. The number of vertices in the safe zone shall be denoted by **sz**.



We remove edges or vertices following the Optimal Link Removal (OLR) strategy of [Yang et al.].

# SUMMARY

We have studied epidemic outbreaks modeled on graphs:

- $(\star)$  We have studied [Seibold-Callender] approach for *regular tree graphs*.
- (\*) We have considered graphs with *cliques*, and bounded the clique number to understand the duraiton of outbreaks in terms of  $P_{rec}$  and  $P_{inf}$  in this new setting.
- $(\star)$  We have defined *Safe zones* and begun the study of their *sz* number.

# FURTHER WORK

In what remains of the year, we will do the following:

- $(\star)$  Bound duration depending on *root placement* in networks with cliques.
- $(\star)$  Expand to include *multiple roots* of infection.
- $(\star)$  Generalize when the removal of a vertex or edge forms a *safe zone*.
- $(\star)$  Determine how to *maximize sz.*

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# Thank you for listening! Any questions?