Temporal Networks and the Activity Driven Framework

Nicolò Gozzi, **ISI Foundation**
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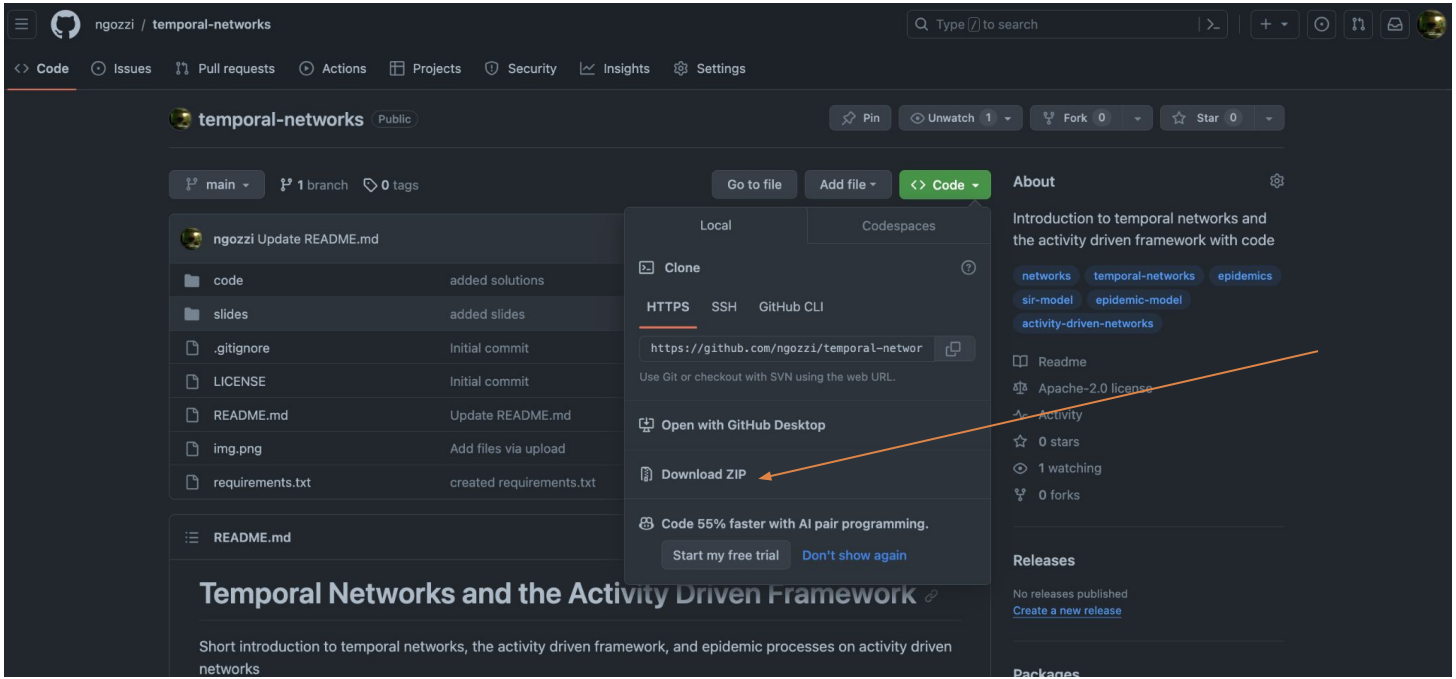
ISI Foundation Education

Download Code and Slides from Github (https://github.com/ngozzi/temporal-networks)

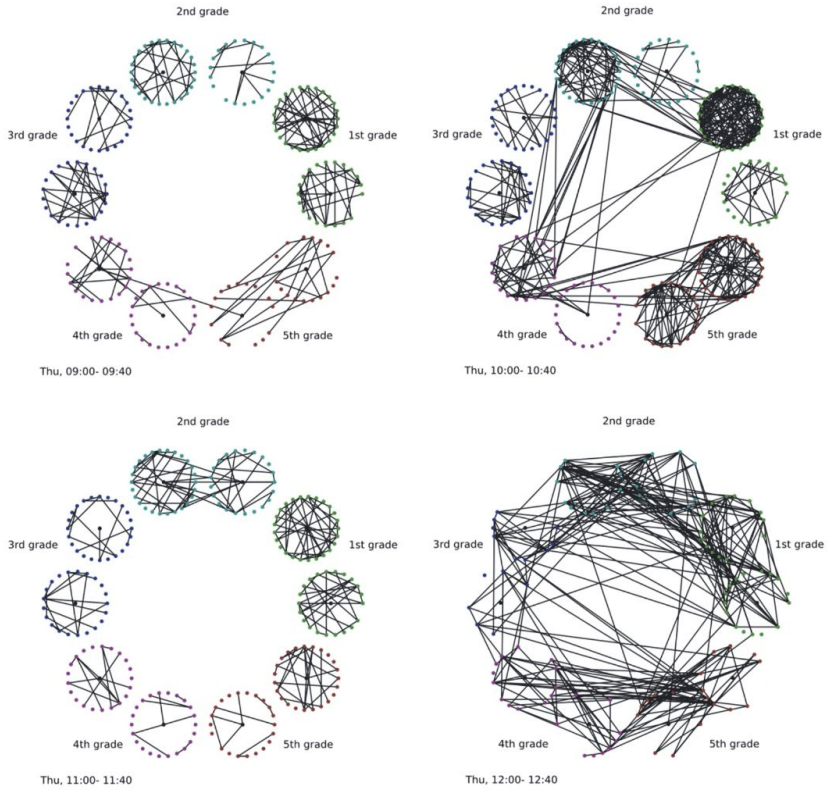
git clone https://github.com/ngozzi/temporal-networks.git

OR



What is a Temporal Network?

A temporal (or time-varying) network is a network whose links, or nodes, are **active only at certain times**



http://www.sociopatterns.org/gallery/dynamical-contact-patterns-in-a-primary-school/

Examples of Temporal Networks

- Person-to-person communication (emails, text messages, phone calls)
- Physical proximity (face-to-face interactions)
- Cell biology (protein interaction, gene-regulatory networks)
- Infrastructural networks (air-transport network)
- Neural and brain networks
- Ecological networks (seasonality, environmental changes)
- …

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→ The study of temporal network is profoundly related to the **study of dynamical phenomena** unfolding on such networks (e.g., epidemics)

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- When $t_N \sim t_P \rightarrow$ **Temporal Network**: the timescale of network evolution and of the dynamical process is comparable. It is convenient to use a time-varying network representation

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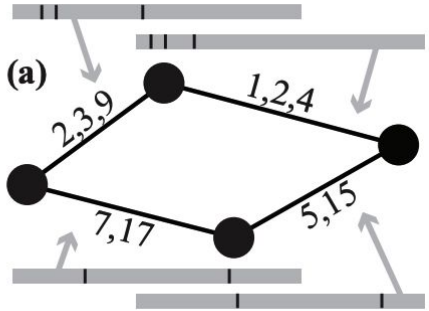
- When $t_N \ll t_P \rightarrow$ **Annealed Approximation**: the timescale of network evolution is much faster than the dynamical processes. It is convenient to use a time-aggregated (static) version of the network

Representation of Temporal Networks: Contact Sequences

Depending on their features, temporal networks can be represented as:

1. Contact Sequences:

- If **duration of interactions is negligible**, the network can be can be represented as a contact sequence *C* made of triples *(i, j, t)* where *i, j* $\in V$ and *t* denotes time.



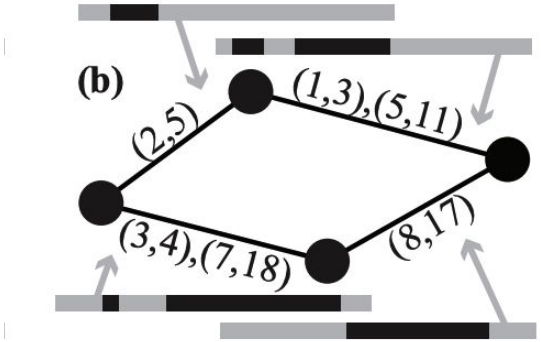
- Examples include communication data, and physical proximity data where the duration of the contact is negligible.
- Same time contacts are grouped into one graph the temporal network is presented as a **sequence of static graphs**

Visualization from: https://arxiv.org/pdf/1108.1780.pdf

Representation of Temporal Networks: Interval Graphs

Depending on their features, temporal networks can be represented as:

2. Interval Graphs:



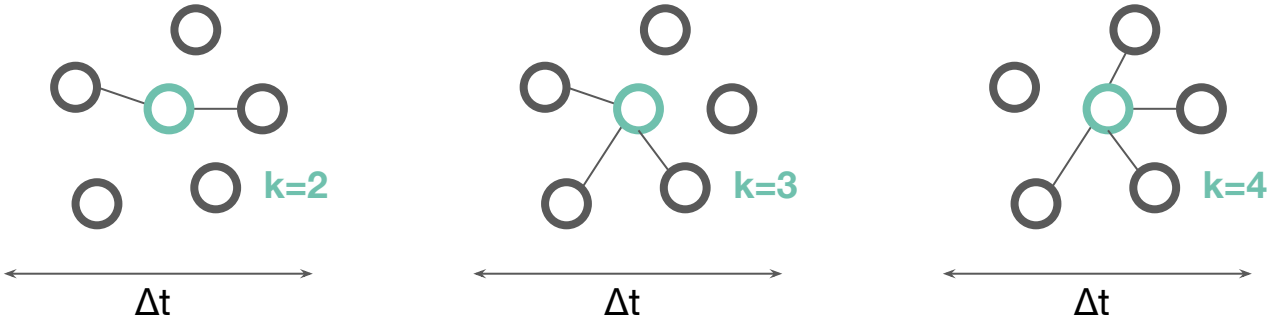
- in this case, the edges are active over a set of intervals time intervals $T_e = \{(t_1, t'_1), \ldots (t_n, t'_n)\}$
- Examples include proximity contact networks
- Similarly to static graph, it can be defined an adjacency index:

$$a(i, j, t) = \begin{cases} 1 & \text{if } i \text{ and } j \text{ are connected at time } t \\ 0 & \text{otherwise} \end{cases}$$

Visualization from: https://arxiv.org/pdf/1108.1780.pdf

Topological Measures for Temporal Network

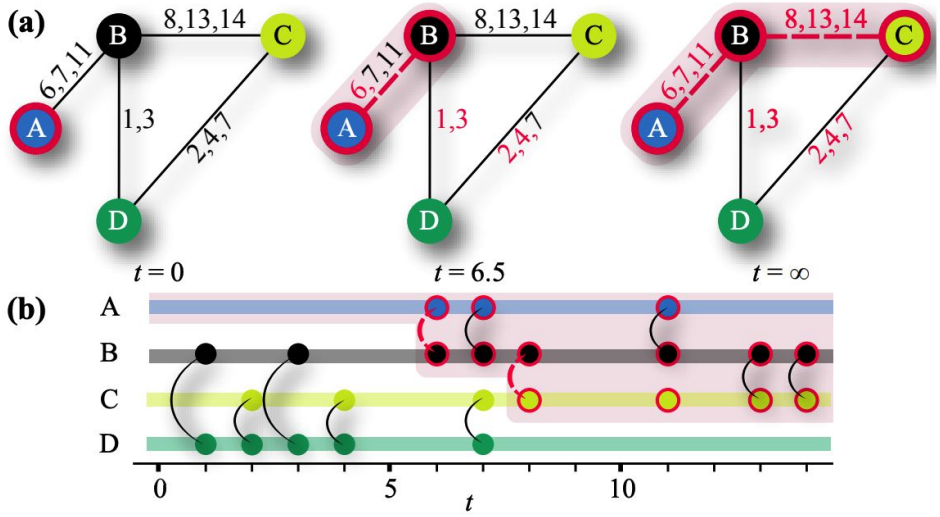
- Many of the metrics developed for static networks can still be applied to temporal networks
- These measures can be computed on the **aggregated network** over a certain time interval or over regular time steps
- In doing so, we can compute, for example, the **time-dependent degree** of a node



- However, other properties are directly influenced by the order of link activations

Time-respecting paths and reachability

- In a static graph, a path is simply a sequence of sequential edges
- In temporal networks, **paths are sequences of link ordered in time**



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Time-respecting paths and reachability

- In a static graph, a path is simply a sequence of sequential edges
- In temporal networks, **paths are sequences of link ordered in time**
- More formally, **time-respecting paths** are defined as sequences of contacts with **non-decreasing times**
- The set of vertices that can be reached by time-respecting paths from node *i* within an observation window is called the **set of influence** of *i*
- The average fraction of nodes in the sets of influence of all vertices as the **reachability ratio**

Connectivity and components

- Connectivity measures if a **pair of nodes is connected by a path**
- Connectivity is **not a symmetric relation for temporal graphs** (*i* may be reachable by time-respecting paths from *j*, but not the opposite)
- We can define:
  - two nodes *i* and *j* of a temporal network are **strongly connected** if there is a directed, time-respecting path connecting *i* to *j*
  - two nodes *i* and *j* are **weakly connected** if there are undirected time respecting paths from i to *j* and *j* to *i* (i.e. the directions of the contacts are not taken into account)
- Based on this, we can define **strongly or weakly connected components** of the temporal graph

Distances, Latencies, and Fastest Paths

- For static networks, the **distance between two nodes** is defined as the length of the shortest path joining them (in terms of n. of edges)
- For temporal network, one can consider the fastest time-respecting path(s) between two nodes
- The shortest time within which *i* can reach *j* is called their **latency** (also temporal distance)

The Activity Driven Framework

The Activity Driven Framework

Classic Network Growth Models (Erdös-Rényi, preferential attachment model) are **connectivity-driven models:**

- Network's topology is at the core of the models' definition
- Well-suited to capture the features of network systems whose links among nodes are long-lived elements
- However, in some systems interactions may rapidly change on a very short time scale

The activity-driven model is a **temporal network model** that can be used to describe those systems

The Activity Driven Framework

The core assumption of the activity driven model is that each node *i* has an **activity potential** a_i defined as the **probability per unit time to create new interactions**

Network Initialization:

- Consider *N* disconnected nodes
- Each node is assigned an activity sampled from a distribution *F(a)*
- To avoid divergences of *F(a)* close to the origin we assume $\varepsilon \leq a \leq 1$

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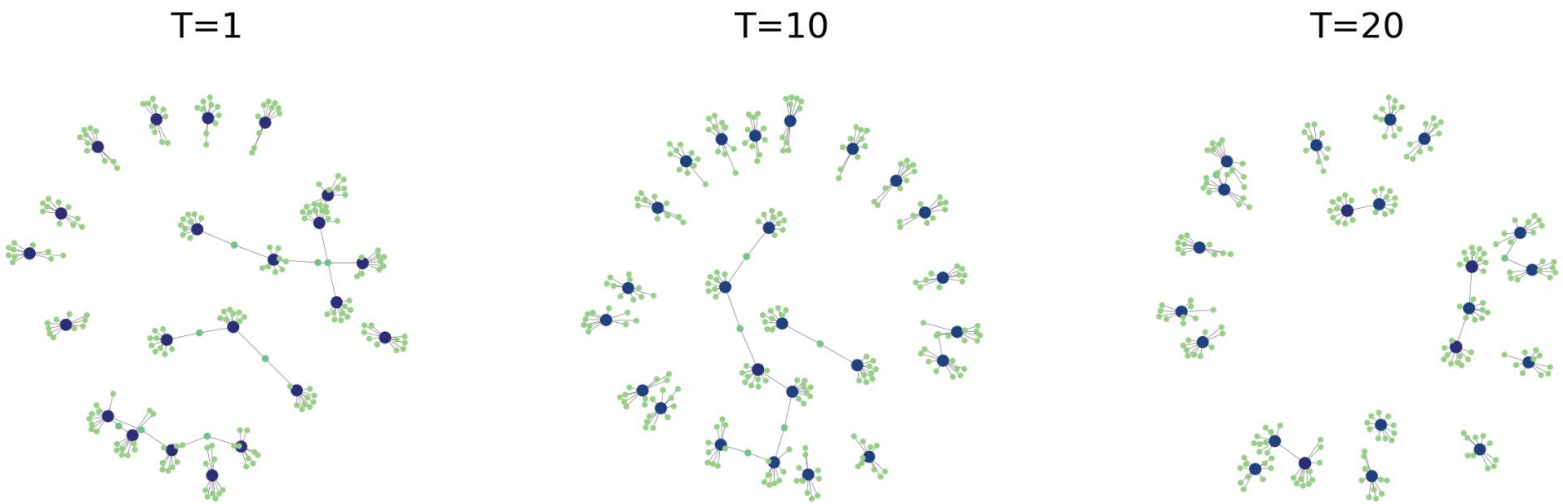
ADN - Example

We consider $F(a) \sim a^{-\gamma}$, with $\gamma = 2.1$ and $m = 10$



At each time step, the instantaneous network will be composed by a **set of stars around the nodes that were active** at that time step

ADN - Time-aggregated Network

We define the integrated network as the union of all the networks obtained in each previous time step:

$$G_T = \bigcup_{t=0}^{t=T} Gt$$

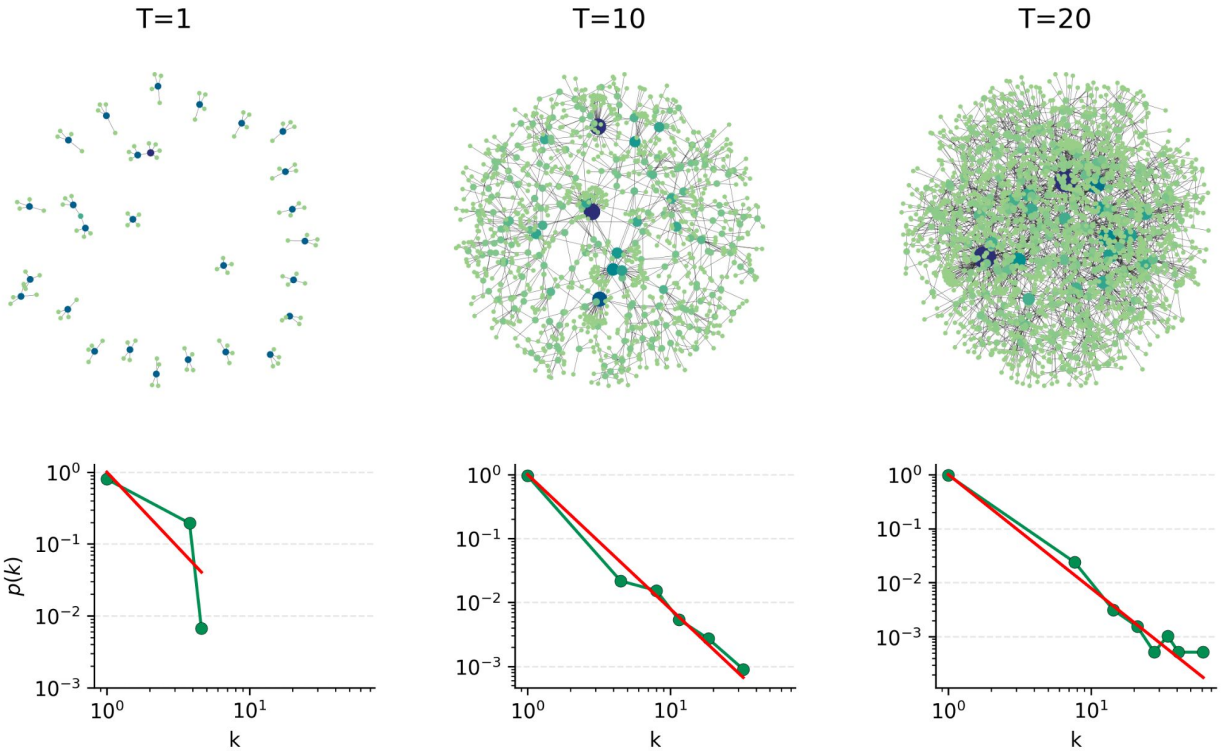
It can be shown that node *i* will have at time *T* a degree in the integrated network given by:

$$k_i(T) = N\left(1 - e^{-Tmpx_i/N}\right)$$

And the degree distribution $P_T(k)$ of the integrated network at time *T* is:

$$P_T(k) \sim F[k / (T \cdot m)]$$

ADN - Time-aggregated Network



The **degree distribution** in the time-aggregated network follows the **distribution of the activity**

Hence, heterogeneous activity patterns induce the **formation of hubs** (i.e., highly active nodes engaging over and over in social interactions)

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- Pros: The full dynamics of the network and its ensuing structure is thus completely encoded in the activity potential distribution F(x)
- Cons: since links are created at random, the distribution of **links' weights** in the time-integrated network **is homogeneous** and thus very far from observations in real networks

ADN - Extension to Communities

- Real complex networks are organised into tightly connected groups → **communities** (e.g., circles of friends)
- As a result, the vast majority of **connections takes place within communities** rather than across them
- The ADN framework can be extended to go **beyond random partner selection** and include also communities

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ADN - Extension to Communities

The parameter **η regulates the modularity** of the emerging network:

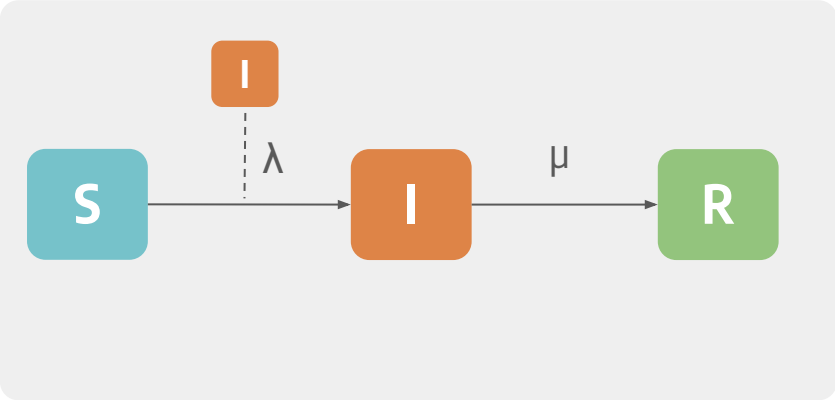
- For $\eta = 0$ (and in case of community sizes $s \ll N$) the network unfolds very similarly to the random partner selection case
- Instead for $\eta = 1$ the network will be formed by completely disconnected communities.

Epidemic Spreading on ADN

Epidemic Spreading on ADN - SIR Model

SIR compartmental model:

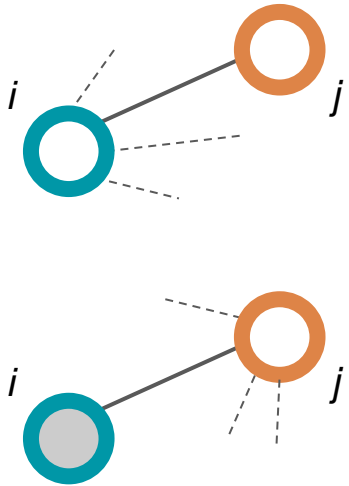
- Nodes are divided into 3 groups: susceptible, infected, and recovered
- By interacting with the infected, susceptibles may get infected at rate λ
- Infected nodes recover spontaneously at rate μ



Epidemic Spreading on ADN - SIR Model

Nodes can become infected in two ways at each time step:

1. Node *i* is **active**, establish a connection with an infected node *j* and acquire the infection from *j*
2. Node *i* is **inactive**, but is it contacted by infected and active node *j* that infects *i*



Epidemic Spreading on ADN - SIR Model (Equations)

$$d_t S_a = -m\lambda S_a a \int da' \frac{I_{a'}}{N} - m\lambda \int da' \frac{I_{a'} a'}{N}$$

$$d_t I_a = -\mu I_a + m\lambda S_a a \int da' \frac{I_{a'}}{N} + m\lambda \int da' \frac{I_{a'} a'}{N}$$

$$d_t R_a = \mu I_a$$

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Number of susceptible nodes that are active and become infected contacting an infected node

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Number of susceptible nodes that are inactive and become infected when contacted by an active infected node

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Number of infected nodes that spontaneously recover at rate μ

SIR Model on ADN - Epidemic Threshold

Using a mean-field approach, we can derive the epidemic threshold of the SIR model on memory-less activity driven networks:

$$\frac{\lambda}{\mu} > \frac{1}{m} \frac{1}{\langle a \rangle + \sqrt{\langle a^2 \rangle}}$$

And it follows that the Basic Reproduction Number is:

$$R_0 = m \frac{\lambda}{\mu} \left(\langle a \rangle + \sqrt{\langle a^2 \rangle} \right)$$

- If $R_0 > 1$ the epidemic will be able to spread
- if $R_0 < 1$ the initial outbreak will not result in a macroscopic epidemic

References

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Extra

SIR Model on ADN - Epidemic Threshold

We consider the evolution of the number of infected node of activity class *a*:

$$d_t I_a = -\mu I_a + m\lambda S_a a \int da' \frac{I_{a'}}{N} + m\lambda S_a \int da' \frac{I_{a'} a'}{N}$$

Since $N_a = S_a + I_a + R_a$ we can substitute $S_a = N_a - I_a - R_a$:

$$d_t I_a = -\mu I_a + m\lambda (N_a - I_a - R_a) a \int da' \frac{I_{a'}}{N} + m\lambda (N_a - I_a - R_a) \int da' \frac{I_{a'} a'}{N}$$

SIR Model on ADN - Epidemic Threshold

In early stage assumption we have that $R_a \sim 0$ and $I_a \sim 0$. Therefore, we drop all the second order terms obtaining:

$$d_t I_a = -\mu I_a + m\lambda N_a a \int da' \frac{I_{a'}}{N} + m\lambda N_a \int da' \frac{I_{a'} a'}{N}$$

By integrating both sides over all activity classes we have:

$$d_t I = -\mu I + m\lambda \langle a \rangle I + m\lambda \Theta$$

where $\Theta = \int da I_a a$ and $\langle a^n \rangle = \int da\, F(a) a^n$

SIR Model on ADN - Epidemic Threshold

To characterise the evolution of I(t) we then need to derive an equation for Θ. In particular, multiplying both sides of previous equation by *a* and integrating across all activities we get:

$$d_t\Theta = -\mu\Theta + m\lambda\langle a^2\rangle I + m\lambda\langle a\rangle\Theta$$

The epidemic threshold can be obtained studying the stability of the system of differential equations defined by:

$$d_t I = -\mu I + m\lambda\langle a\rangle I + m\lambda\Theta$$

$$d_t\Theta = -\mu\Theta + m\lambda\langle a^2\rangle I + m\lambda\langle a\rangle\Theta$$

SIR Model on ADN - Epidemic Threshold

Indeed, the disease will be able to spread only if the largest eigenvalue of the Jacobian matrix *J* of the system is larger than zero. Here, *J* can be written as:

$$\begin{pmatrix} -\mu + m\lambda\langle a\rangle & m\lambda \\ m\lambda\langle a^2\rangle & -\mu + m\lambda\langle a\rangle \end{pmatrix}$$

By solving the eigenvalue problem for this matrix, and imposing positivity of largest eigenvalue, we get the threshold:

$$\frac{\lambda}{\mu} > \frac{1}{m}\frac{1}{\langle a\rangle + \sqrt{\langle a^2\rangle}}$$

And therefore the R0 reads:

$$\boxed{R_0 = m\frac{\lambda}{\mu}\left(\langle a\rangle + \sqrt{\langle a^2\rangle}\right)}$$