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Lecture 12 - Random network dynamics epidemic models

Examples of network dynamics
ECE 5260 – ORIE 5735

Anna Scaglione

Cornell Tech

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Content

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Outline

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Summary of network processes discussed

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- **Random walk**: At each t:
  1. $\boldsymbol{x}^{\text{rw}}(t) = \boldsymbol{e}_{v_t}(t)$, where v_t is the vertex chosen at random and $\boldsymbol{e}_v(t)$ is the $v$thcoordinate vector
  2. The probability mass of the vertex being chosen is the vector such that $\boldsymbol{\pi}(t+1) = \boldsymbol{W}\boldsymbol{\pi}(t)$, where $\boldsymbol{W}$ is the transition probability matrix ($\boldsymbol{W} = \boldsymbol{I} - \boldsymbol{L}^{\text{rw}}$ for the uniform random walk)
  3. $\lambda_2(\boldsymbol{W}) < 1$ implies that $\boldsymbol{\pi}(t) = \boldsymbol{\pi}^* + O(\lambda_2^t(\boldsymbol{W}))$
- **Consensus Gossiping**: At each t:
  1. The state is updated **synchrounously** $\boldsymbol{x}(t+1) = \boldsymbol{W}\boldsymbol{x}(t)$,
  2. The $\|\boldsymbol{x}(t) - x^{\text{ave}}\mathbf{1}\| = O(\lambda_2^t(\boldsymbol{W}))$
  3. The state is updated **asynchrounously** $\boldsymbol{x}(t+1) = \boldsymbol{W}(t)\boldsymbol{x}(t)$,
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Ordinary Differential Equation (ODE)

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- Often these processes are described in terms of (possibly stochastic) ODE
- Basically, $\dot{x}(t) = \frac{dx(t)}{dt}$ is used in lieu of the finite difference (the change) of states $(x(t+1) - x(t))$
- Note that for the processes we defined $W = I -$ **Laplacian** - i.e. either L^{rw} or αL or $L(t)$
- Let us take for example the synchronous average consensus. Subtracting at both sides $x(t)$

$$\overbrace{x(t+1) - x(t)}^{\approx dt\dot{x}(t)} = \overbrace{(I - \alpha L)}^{W} x(t) - x(t) = x(t) - \alpha L x(t) - x(t) = -\alpha L x(t)$$

$$\approx \dot{x}(t) = -\frac{\alpha}{dt} L x(t)$$

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Ordinary Differential Equation (ODE)

- We can call $\alpha/dt = \gamma$. For the discrete time dynamics ODEs are very reasonable approximations when changes are relatively small:

$$\approx \dot{\boldsymbol{x}}(t) = -\gamma \boldsymbol{L}\boldsymbol{x}(t)$$

- Assume the eigenvalue decomposition of $\boldsymbol{L} = \boldsymbol{U}\boldsymbol{\Lambda}\boldsymbol{U}^{-1}$ and denote by $\boldsymbol{\xi}(t) = \boldsymbol{U}^{-1}\boldsymbol{x}(t)$:

$$\dot{\boldsymbol{\xi}}(t) = \boldsymbol{U}^{-1}\dot{\boldsymbol{x}}(t) = -\gamma \boldsymbol{U}^{-1}\boldsymbol{L}\boldsymbol{x}(t) = -\gamma \boldsymbol{U}^{-1}\boldsymbol{U}\boldsymbol{\Lambda}\boldsymbol{U}^{-1}\boldsymbol{x}(t)$$

$$= -\gamma \overbrace{\boldsymbol{U}^{-1}\boldsymbol{U}}^{=\boldsymbol{I}}\boldsymbol{\Lambda}\overbrace{\boldsymbol{U}^{-1}\boldsymbol{x}(t)}^{=\boldsymbol{\xi}(t)} = -\gamma\boldsymbol{\Lambda}\boldsymbol{\xi}(t)$$

Solution

- Since $\boldsymbol{\Lambda}$ is diagonal, $\dot{\boldsymbol{\xi}}(t) = -\gamma\boldsymbol{\Lambda}\boldsymbol{\xi}(t)$ this is a set of $N = |\mathcal{V}|$ decoupled first order ODEs that have as a solution an exponential trend. Given $\boldsymbol{\xi}(0) = \boldsymbol{U}^{-1}\boldsymbol{x}(0)$:

$$\dot{\xi}_k(t) = -\gamma\lambda_k\xi_k(t) \quad \Rightarrow \quad \xi_k(t) = \lambda_k e^{-\gamma\lambda_k t}\xi_k(0)$$

- Denote by $\boldsymbol{u}_k$ the columns of $\boldsymbol{U}$ and by $\boldsymbol{v}_k^\top$ the rows of $\boldsymbol{U}^{-1}$.

- From the solution for $\boldsymbol{\xi}(t)$, we can get back the solution for $\boldsymbol{x}(t)$, since $\boldsymbol{\xi}(t) = \boldsymbol{U}^{-1}\boldsymbol{x}(t) \ \Rightarrow \boldsymbol{x}(t) = \boldsymbol{U}\boldsymbol{\xi}(t)$

$$\boldsymbol{x}(t) = \boldsymbol{U}\boldsymbol{\xi}(t) = \sum_{k=1}^{N} \boldsymbol{u}_k\xi_k(t) = \sum_{k=1}^{N} \boldsymbol{u}_k\lambda_k e^{-\gamma\lambda_k t}\xi_k(0)$$

and since $\xi_k(0) = \boldsymbol{v}_k^\top\boldsymbol{x}(0)$:

$$\boldsymbol{x}(t) = \sum_{k=1}^{N} \lambda_k e^{-\gamma\lambda_k t}\boldsymbol{u}_k\boldsymbol{v}_k^\top\boldsymbol{x}(0)$$

Summary for linear homogenous ODE

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- We can call $\alpha/dt = \gamma$. The ODE approximation for the discrete time dynamics is:

$$\approx \dot{\boldsymbol{x}}(t) = -\gamma \boldsymbol{L}\boldsymbol{x}(t)$$

- Assuming $\xi_k(0) = \boldsymbol{v}_k^\top \boldsymbol{x}(0)$, with $\boldsymbol{x}(0)$ the initial state, the solution of these network ODEs is, in general:

$$\boldsymbol{x}(t) = \sum_{k=1}^{N} \lambda_k \xi_k(0) e^{-\gamma\lambda_k t}\boldsymbol{u}_k = \sum_{k=1}^{N-1} \lambda_k \xi_k(0) e^{-\gamma\lambda_k t}\boldsymbol{u}_k$$

where here the second equation is because, for the Laplacian, $\lambda_N = 0$

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1 Review

2 General models for network dynamics

3 Conclusions

General non-linear models for network dynamics

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- They are often studied in the form of ODEs, particularly to analyze if the system becomes stable.
- We omit the index t for simplicity. The mathematical form is:

$$\dot{x}_i = f_i(x_i) + \sum_{j \in \mathcal{N}_i} w_{ij} g_{ij}(x_i, x_j) \quad \forall i \in \mathcal{V}$$

and w_{ij} are the edge weights, which are zero if $(i, j) \notin \mathcal{E}$

- Note that in general a dynamical system is $\dot{x}_i = g(x_1, \ldots, x_N)$, not generally a mixture of pairwise interactions. Yet, in many case it is a good model.
- Often, in models, the two functions $f_i(x_i)$ and $g_{ij}(x_i, x_j)$ are the same for all nodes, i.e. they are $f(x_i)$ and $g(x_i, x_j)$

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Example: susceptible-Infected (SI) Epidemic model

- An example of such models is the so called SI model, where $x_i(t)$ represents the probability of infection
- In this case $\dot{x}_i(t)$ is a stochastic ODE that models the change in probability of infection for node i due to random contact with its set of peers $\mathcal{N}_i$

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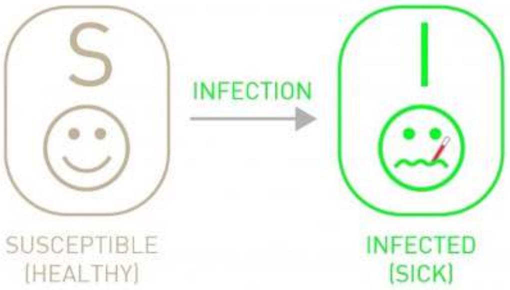

Probability of node i catching the disease

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- The SI model depends on a parameter β capturing the probability of contact of two neighbors per unit time.
- The dynamics of the probability are based on the infection event probability for node i is the probability that node i catches the disease from any of its neighbors in an interval dt.
- Let $I_i(t)$=infection event for node i at time t. Clearly

$$I_i(t+dt) = \text{node } i \text{ is sick already or it infected by a neighbor}$$

- Let $I_{ij}(t)$=node i catches the disease from node j at time t, then:

$$I_i(t+dt) = I_i(t) \cup_j I_{ij}(t)$$

Infection event

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We need to characterize the probability of each event I_{ij}

- The probability of the event I_{ij} this node is a specific neighbor $j \in \mathcal{N}_i$ the intersection of three events:
  - **Infection event** I_{ij}: Node i catches the disease from node j:

    1. $I_j =$ node j must be already infected (the probability is $x_j(t)$) and
    2. $S_i =$ node i must be suscetible (the probability of being suscepible $1 - x_i(t)$) and
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Probability of node i catching the disease

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- The probability $P(I_{ij})$ can be written as the following probability calculation:

$$\begin{aligned} P(I_{ij}) &= P(I_j \cap S_i \cap M_{ij}) \\ &= P(I_j) \times P(S_i) \times P(M_{ij}) \\ &= x_j(1 - x_i)\beta dt \end{aligned}$$

- Hence the probability that node i is infected at time $t + dt$ is:

$$x_i(t + dt) = P(I_i \cup_{j \in \mathcal{N}_i} I_{ij}) = \underbrace{P(I_i)}_{x_i(t)} + \sum_{j \in \mathcal{N}_i} \underbrace{P(I_{ij})}_{x_j(1-x_i)\beta dt}$$

because either node i is infected or one of the neighbors will infect i and because these events are mutually exclusive, their probabilities add up.

Dynamics of the Susceptible-Infected (SI) model

- Hence, the rate of change in probability $\frac{x(t+dt)-x(t)}{dt} = \dot{x}$ is:

SI model $$\dot{x}_i = \sum_{j\in\mathcal{N}_i} \beta x_j(1-x_i) \equiv \beta(1-x_i)\sum_{j\in\mathcal{N}_i} x_j$$

- Note that it has exactly the structure as:

$$\dot{x}_i = f(x_i) + \sum_{j\in\mathcal{N}_i} w_{ij} g(x_i, x_j)$$

where $f(x_i) = 0$, the weights are all the same $w_{ij} = \beta,\ (i,j) \in \mathcal{E}$ and $w_{ij} = 0$ else, and $g(x_i, x_j) = (1-x_i)x_j$, which is non linear.

- All the stuff we said about linear dynamics cannot be applied to study global convergence properties...

SI model meanfield analysis

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- Let us call by $X = \sum_{i=1}^{N} x_i$, which is the expected size of the population of infected people. Note that:

$$x^{\text{ave}} = \frac{1}{N}\sum_i x_i \quad \Rightarrow \quad X = N x^{\text{ave}}$$

- The expected number of **susceptible people** is $S = N - X$
- It is interesting (and often easier) to explore the dynamics of x^{ave} to gain insight on the average infection rate across a network
- The study of the dynamics of x^{ave} is called the meanfield analysis.

Logistic differential equation

- Next, we find a closed-form expression for $x^{\text{ave}}(t)$, under the simplifying assumption of the fully connected case, i.e. $\forall i, \ \mathcal{N}_i = \mathcal{V}$ (i.e. an invidual can meet anyone)
- Note that in this case, on average, a susceptible individual meets an infected one is $\frac{\beta S X}{N}$. This value can be written as:

$$\frac{\beta(N-X)X}{N} = \beta(1-x^{\text{ave}})Nx^{\text{ave}}$$

- Therefore

$$\dot{X} = N\dot{x}^{\text{ave}} = \beta(1-x^{\text{ave}})Nx^{\text{ave}} \quad \Rightarrow \quad \dot{x}^{\text{ave}} = \beta(1-x^{\text{ave}})x^{\text{ave}}$$

- This equation in red is called Logistic Equation.

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- In general the solutions of non-linear ODEs are difficult to obtain in closed form.
- However, the solution of the Logistic Equation is known in closed-form and is:

$$x^{\mathsf{ave}}(t) = \frac{x^{\mathsf{ave}}(0)e^{\beta t}}{1 - x^{\mathsf{ave}}(0) + x^{\mathsf{ave}}(0)e^{\beta t}}$$

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Logistic differential equation trend

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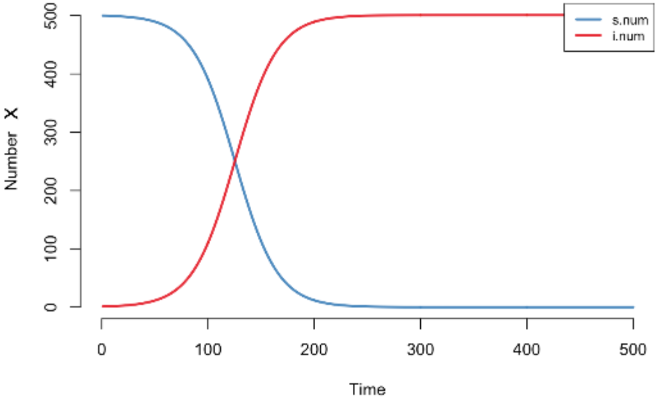
- The trend of the curve is a sigmoid. The rate at which the susceptible agents decrease is $s^{\text{ave}}(t) = 1 - x^{\text{ave}}(t)$



Network dynamics in the SI model

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- There is no clean closed form solution when we analyze the dynamics of $x_i(t)$ instead of the meanfield $x^{\text{ave}}(t)$.
- As you can imagine, the dynamics are not that hard to simulate.
- The trick to gain insight is to analyze the spread at its onset, when $x_i(t) \approx 0$
- In this case, denoting by $\boldsymbol{A}$ the adjacency matrix of the network:

$$\dot{x}_i = \beta(1 - x_i) \sum_{j \in \mathcal{N}_i} x_j \approx \beta \sum_{j \in \mathcal{N}_i} x_j, \quad \Rightarrow \quad \dot{\boldsymbol{x}} \approx \beta \boldsymbol{A} \boldsymbol{x}$$

because we are approximating $(1 - x_i) \approx 1$.

Network dynamics in the SI model

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Logistic differential equation

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- As we have seen, assuming that $\boldsymbol{A} = \boldsymbol{U}\boldsymbol{\Lambda}\boldsymbol{U}^{-1}$, denoting by $\boldsymbol{\xi}(0) = \boldsymbol{U}^{-1}\boldsymbol{x}(0)$, for linear ODEs

$$\boldsymbol{x}(t) \approx \sum_{k=1}^{N} \xi_k(0) e^{\beta\lambda_k t}\boldsymbol{u}_k, \quad t \text{ small}$$

  hence at the onset the curve grows exponentially

- Naturally this happens in the first portion, close to the beginning. After that the curve cannot do anything else but saturate to value 1, so it cannot continue exponentially growing.
- Note that if there is only one infected individual j^* then $\xi_k(0) = [\boldsymbol{v}_k]_{j^*}$, the j^* component of the rows of $\boldsymbol{U}^{-1}$.

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Limitations of the SI model

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- An obvious criticism of this model is that it does not capture the fact that some individuals either recover or, sadly, die.
- Because they can no-longer infect others they should be **removed** from the population that can infect people
- This is an obvious extension, we discuss next.
- Another extension (we are not going to cover) is the case where people become susceptible again, for instance, to a variant.

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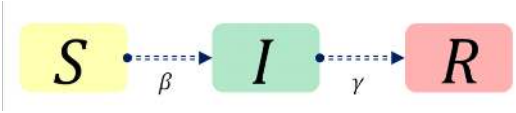
Susceptible-Infected-Removed (SIR) model



- A better model for epidemic spread is the so called SIR model
- As the name suggests accounts for the fact that some nodes in the network shall be removed, if they become immune or are dead due to the disease
- Let $r_i(t)$ represent the probability that the node is removed and γ the probability that a node infected recovers. I must be:

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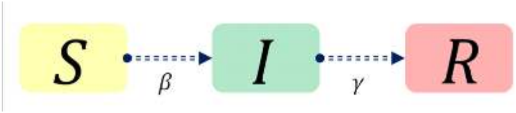

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Solving the SIR model approximately

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- As done for the SI model we can attempt to first analyze the meanfield solution in the case where everyone can meet any other member of the population $\mathcal{V}$
- In this case the equation does not have a close-form solution
- Some insight is gained noting that relationship of $s^{\text{ave}} = 1 - x^{\text{ave}}$ and $r^{\text{ave}} =$ the average percentage of removed nodes is:

$$\dot{s}^{\text{ave}} = -\beta s^{\text{ave}} x^{\text{ave}}, \quad \dot{r}^{\text{ave}} = \gamma x^{\text{ave}} \quad \Rightarrow \quad \frac{\dot{s}^{\text{ave}}}{s^{\text{ave}}} = -\frac{\beta}{\gamma} \dot{r}^{\text{ave}}$$

- The integral of $\frac{\dot{s}}{s}$ with respect to s, from $s^{\text{ave}}(0)$ to $s^{\text{ave}}(t)$ is $\ln s^{\text{ave}}(t) - \ln s(t)$. Hence, cosidering that $r^{\text{ave}}(0) = 0$:

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Solving the SIR model numerically

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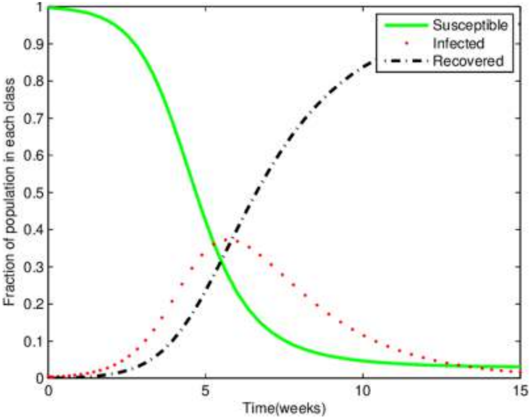
- In general the solution is calculated relatively easily numerically and looks as follows



Reproduction number R_o

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- A metric used often to characterize infection is the reproduction rate of infections. Let τ be the random time of recovery for a individual.
- During this time, the expected number of encounters is $\beta\tau$ and

$$R_o := \mathbb{E}[\beta\tau] = \beta\mathbb{E}[\tau]$$

- To compute R_o we need to compute the expected value of τ. Next we compute is probability density function (PDF) $p(\tau)$ of the recovery time.

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Reproduction number R_o for SIR model

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- $p(\tau)d\tau$ is the probability that an individual has recovered after at time τ, precisely in the interval $(\tau, \tau + d\tau]$.
- If the probability of recovering in an interval $d\tau$ is uniform and is $\gamma d\tau$, the probability that the individual has not recovered yet at time τ is:

$$\lim_{d\tau \to 0} (1 - \gamma d\tau)^{\frac{\tau}{d\tau}} = e^{-\gamma\tau}$$

- Hence, that the probability of recovery in the interval $(\tau, \tau + d\tau]$ is the product of the probability of not recovering until τ, we computed above, times the probability of recovering in $(\tau, \tau + d\tau]$, which is $\gamma d\tau$:

$$p(\tau)d\tau = e^{-\gamma\tau}\gamma d\tau \quad \Rightarrow \quad p(\tau) = \gamma e^{-\gamma\tau}, \tau \geq 0$$

which is an exponential PDF. Because for an exponential random variable $\mathbb{E}[\tau] = \frac{1}{\gamma}$, it follows that $R_o = \frac{\beta}{\gamma}$.

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Network dynamics for the SIR model

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- This case can be analyzed at its onset, along the lines we adopted to approximate they dynamics of the SI model

$$\dot{x}_i = \sum_{j\in\mathcal{N}_i} \beta(1-x_i)x_j - \gamma x_i \approx \sum_{j\in\mathcal{N}_i} \beta x_j - \gamma x_i, \;\Rightarrow \dot{\boldsymbol{x}} \approx (\beta \boldsymbol{A} - \gamma \boldsymbol{I})\boldsymbol{x}$$

- Therefore, once again, the solution is in the usual form that depends on the eigenvectors of the linear dynamics, which this time is $(\beta\boldsymbol{A} - \gamma\boldsymbol{I})$
- Given $\boldsymbol{A} = \boldsymbol{U}\boldsymbol{\Lambda}\boldsymbol{U}^{-1}$, then $(\beta\boldsymbol{A} - \gamma\boldsymbol{I}) = \boldsymbol{U}(\beta\boldsymbol{\Lambda} - \gamma\boldsymbol{I})\boldsymbol{U}^{-1}$.
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Outline

General analysis

- The dynamics can always be simulated, but we do not gain any insight.
- The idea of looking locally at the behavior of the dynamical equations is used often
- The starting point is a fixed point $\boldsymbol{x}^*$ for the equations, where $\dot{x}_i(t) = 0$ for all $i \in \mathcal{V}$

$$\forall i \in \mathcal{V} \quad f(x^*) + \sum_{j \in \mathcal{N}_i} g(x_i^*, x_j^*) = 0$$

- The approach is to look at the dynamics if one perturbs the state by a small amount $\boldsymbol{\epsilon}$, i.e. $\boldsymbol{x}(0) = \boldsymbol{x}^* + \boldsymbol{\epsilon}$ to understand if the fixed point is stable or the system goes somewhere else

Local dynamics and stability

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- The idea is to do a Taylor expansion of the dynamics around $\boldsymbol{x}^*$

$$
\begin{aligned}
\frac{\mathrm{d}x_i}{\mathrm{d}t} = \frac{\mathrm{d}\epsilon_i}{\mathrm{d}t} = f\left(x_i^* + \epsilon_i\right) + \sum_j A_{ij} g\left(x_i^* + \epsilon_i, x_j^* + \epsilon_j\right) \\
= f\left(x_i^*\right) + \epsilon_i \frac{\mathrm{d}f}{\mathrm{d}x}\bigg|_{x=x_i^*} + \sum_j A_{ij} g\left(x_i^*, x_j^*\right) \\
+ \epsilon_i \sum_j A_{ij} \frac{\partial g(u,v)}{\partial u}\bigg|_{u=x_i^*, v=x_j^*} + \sum_j A_{ij}\epsilon_j \frac{\partial g(u,v)}{\partial v}\bigg|_{u=x_i^*, v=x_j^*} \\
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\end{aligned}
$$

Local dynamics and stability

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- Defining:

$$\alpha_i = \frac{\partial f}{\partial x}\bigg|_{x=x_i^*}, \ \beta_{ij} = \frac{\partial g\left(u,v\right)}{\partial u}\bigg|_{u=x_i^*, v=x_j^*}, \ \gamma_{ij} = \frac{\partial g\left(u,v\right)}{\partial v}\bigg|_{u=x_i^*, v=x_j^*}$$

the equation becomes

$$\frac{d\epsilon_i}{dt} = \left[\alpha_i + \sum_j \beta_{ij} A_{ij}\right]\epsilon_i + \sum_j \gamma_{ij} A_{ij} \epsilon_j, \quad \Rightarrow \quad \dot{\boldsymbol{\epsilon}} \equiv \boldsymbol{M}\boldsymbol{\epsilon}$$

where $[\boldsymbol{M}]_{ij} = \left[\alpha_i \delta(i-j) + \sum_j \beta_{ij} A_{ij}\right] + \gamma_{ij} A_{ij}$ and $\delta(i)$ is the Kronecker delta.

Analysis

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- Once again, we find ourselves analyzing linear dynamics. The eigenvalues $\boldsymbol{M}$ determine if $\boldsymbol{\epsilon}(t)$ moves away from the fixed point, or if it dies out

- The solution depends on the EVD of $\boldsymbol{M} = \boldsymbol{U}\boldsymbol{\Lambda}\boldsymbol{U}^{-1}$. Calling $\boldsymbol{\varepsilon}(0) = \boldsymbol{U}^{-1}\boldsymbol{\epsilon}(0)$, like in the previous cases:

$$\boldsymbol{x}(t) \approx \boldsymbol{x}^* + \sum_{k=1}^{N} \varepsilon_k(0) e^{\lambda_k t} \boldsymbol{u}_k$$

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- While M depends on the adjacency matrix, the impact of the network is not crystal clear

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Two interesting cases

- One case where the dependency is clearer is when $\boldsymbol{x}^* = x^*\mathbf{1}$, i.e. the fixed point has all identical coordinates.
- We looked at this case for the SI and SIR models at the onset, where $\boldsymbol{x}^* = \mathbf{0}$, which is (an unstable) fixed point. In this case:

$$\alpha_i = \alpha = \left.\frac{\partial f}{\partial x}\right|_{x=x^*},$$

$$\beta_{ij} = \beta = \left.\frac{\partial g\,(u,v)}{\partial u}\right|_{u=x^*,v=x^*}$$

$$\gamma_{ij} = \gamma = \left.\frac{\partial g\,(u,v)}{\partial v}\right|_{u=x^*,v=x^*}$$

Two interesting cases

- In this case $\boldsymbol{M} = \alpha \boldsymbol{I} + \beta \text{diag}(\boldsymbol{A}\mathbf{1}) + \gamma \boldsymbol{A}$.
- Recall $\boldsymbol{d} = \boldsymbol{A}\mathbf{1}$ is the degree sequence, and $\boldsymbol{L} = \text{diag}(\boldsymbol{d}) - \boldsymbol{A}$
- If $\gamma = -\beta$, then $\boldsymbol{M} = \alpha \boldsymbol{I} + \beta \boldsymbol{L}$,
- This case is interesting because the stability of the fixed point is directly tied to the spectrum of $\boldsymbol{L}$

$$\alpha + \beta \lambda_k(\boldsymbol{L}) < 1$$

- Since $\lambda_N = 0$, it follows that for stability $\left.\frac{\partial f}{\partial x}\right|_{x=x^*} = \alpha < 1$
- This implies that for stability for stability to hold, if $\left.\frac{\partial g(u,v)}{\partial u}\right|_{u=x^*,v=x^*} = \beta$

$$\frac{1}{\lambda_1(\boldsymbol{L})} > -\frac{\alpha}{\beta}$$

Outline

Concluding remarks

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- In this lecture we introduced two network dynamics:
  - The random walk
  - The average consensus dynamics
  - General non-linear ODEs
- Next time we will finish the general case and talk about flow dynamics