- "Donat el caràcter i la finalitat exclusivament docent i eminentment il·lustrativa de les explicacions a classe d'aquesta presentació, l'autor s'acull a l'article 32 de la Llei de propietat intel·lectual vigent respecte de l'ús parcial d'obres alienes com ara imatges, gràfics o altre material contingudes en les diferents diapositives"
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1

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Complex Networks

Albert Díaz Guilera
http://diaz-guilera.net
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COMPLEXITAT

2

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Dynamics on Networks

Albert Díaz Guilera
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3

Why dynamics?

- Nodes are entities that have dynamical properties
- Links represent the interaction patterns

4

Why dynamics?

- We know the topology: A_{ij}
- We know the dynamics of the units: $s_i(t+1)=f_i(s_i(t))$
- We know how they interact: $s_i(t+1)=f_{ij}(s_j(t))$

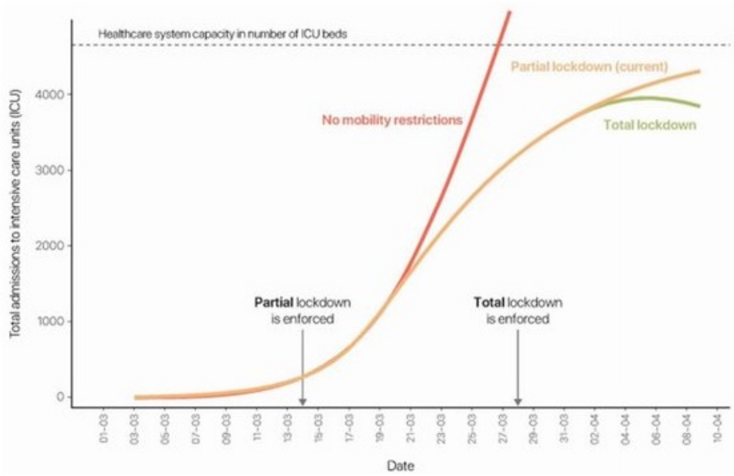
5

Emergence

- Can we predict the dynamical outcome?
- COMPLEX SYSTEMS: You cannot predict what will happen, but can say what could happen
- Scenarios

6

COVID-19



Previsió d'ingressos a les ucis pel Covid, sense col·lapse del sistema sanitari, publicada a 'The Lancet' el 27 de març pels científics que van augurar un col·lapse en un manifest del 21 de març. / **THE LANCET**

7

THE LANCET

CORRESPONDENCE | VOLUME 395, ISSUE 10231, P1193-1194, APRIL 11, 2020

Experts' request to the Spanish Government: move Spain towards complete lockdown

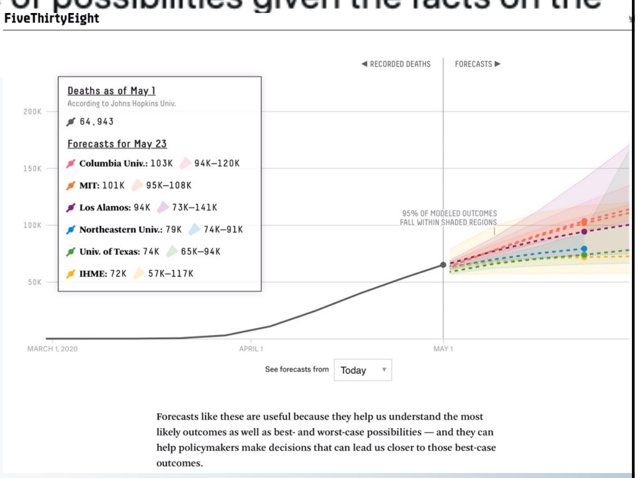
Oriol Mitjà • Àlex Arenas • Xavier Rodó • Aurelio Tobias • Joe Brew • José M Benlloch • et al. Show all authors •
Show footnotes

Published: March 27, 2020 • DOI: https://doi.org/10.1016/S0140-6736(20)30753-4

8

Alessandro Vespignani
@alexvespi

"COVID-19 models aren't made to be unquestioned oracles. They're not trying to tell us one precise future, but rather the range of possibilities given the facts on the ground"



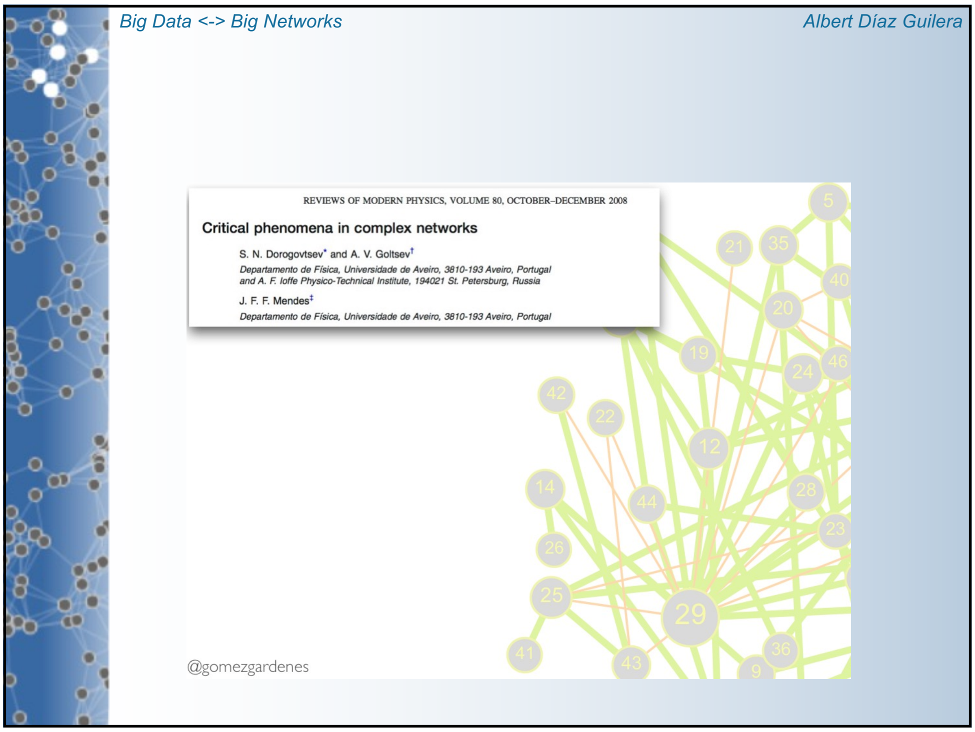
11

Big Data <-> Big Networks *Albert Díaz Guilera*

Main dynamical processes

- Cascades (Failures and Attacks)
- Simple diffusion & random walks
- Synchronization
- Contagion processes
- Evolutionary games
- Chaotic dynamics
- …………

15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S. N. Dorogovtsev* and A. V. Goltsev†
Departamento de Física, Universidade de Aveiro, 3810-193 Aveiro, Portugal
and A. F. Ioffe Physico-Technical Institute, 194021 St. Petersburg, Russia
J. F. F. Mendes‡
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@gomezgardenes

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Statistical physics of social dynamics
Claudio Castellano*
SMC, INFM-CNR and Dipartimento di Fisica, "Sapienza" Università di Roma, Piazzale A. Moro 2, 00185 Roma, Italy
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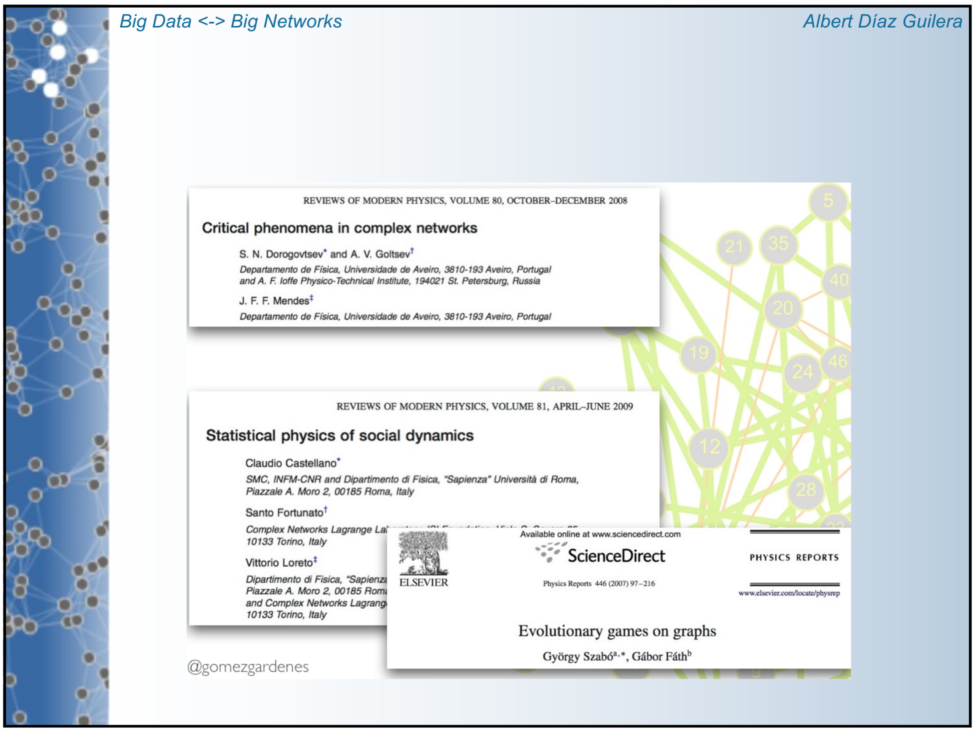
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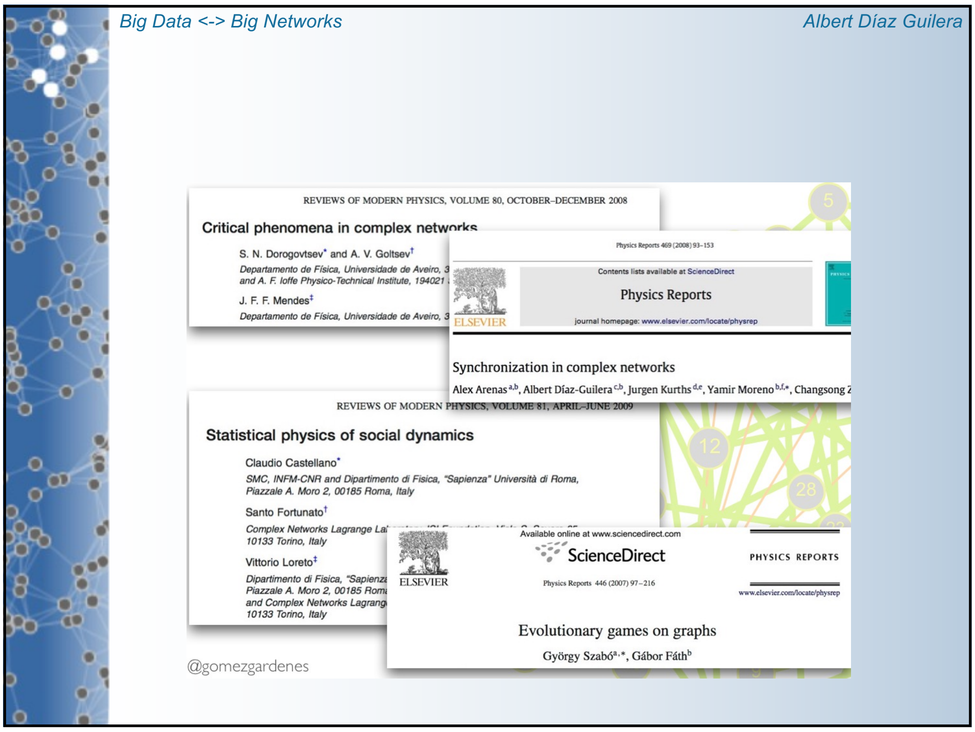
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Physics Reports 469 (2008) 93–153
Contents lists available at ScienceDirect
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Alex Arenas a,b, Albert Díaz-Guilera c,b, Jurgen Kurths d,e, Yamir Moreno b,f,*, Changsong Z
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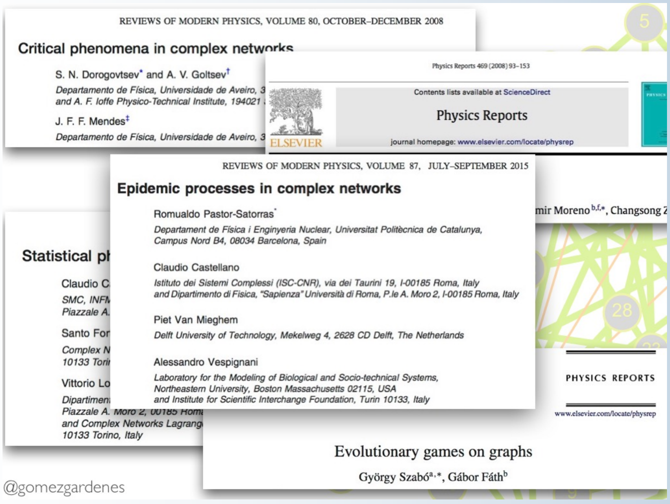

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Failures & attacks

- More related to static properties
- Percolation
- Damage propagation

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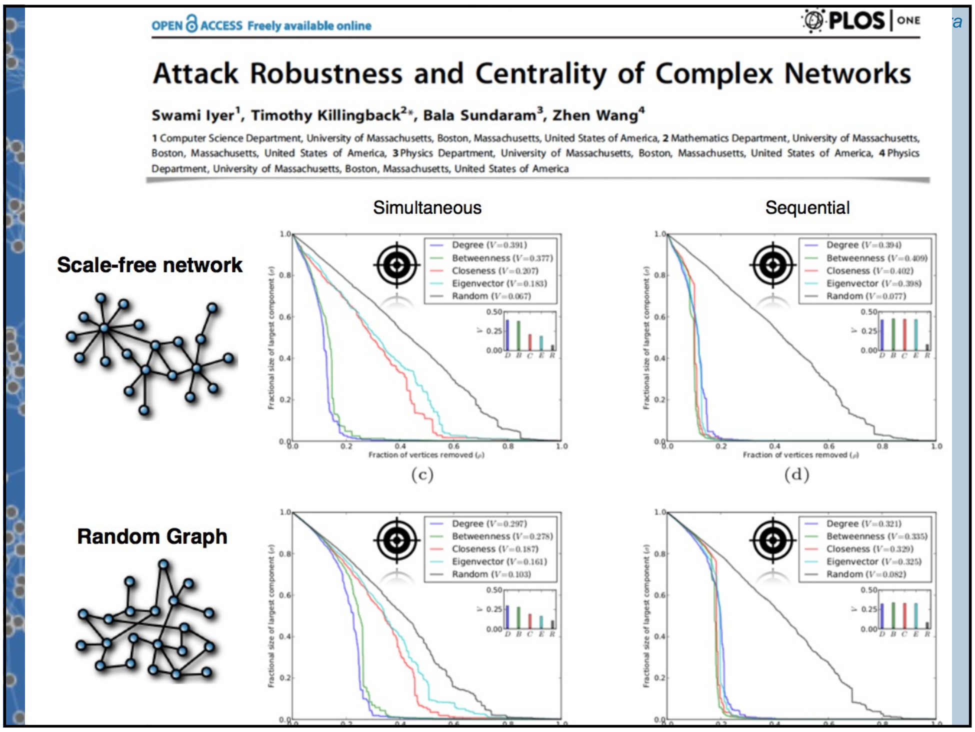
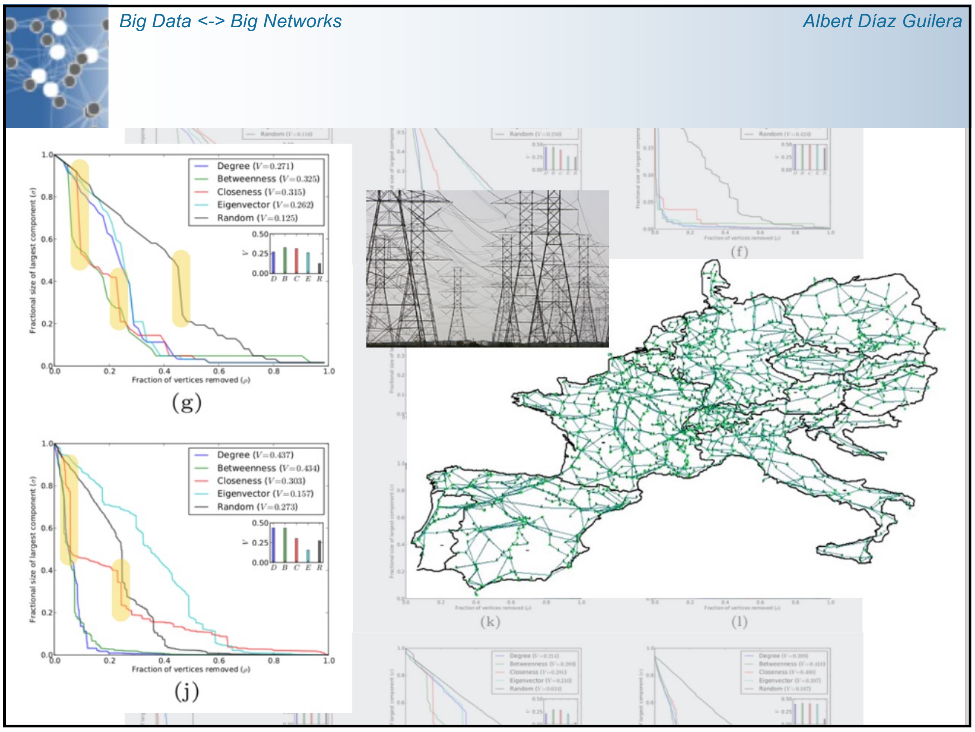

OPEN ACCESS Freely available online
PLOS ONE
Attack Robustness and Centrality of Complex Networks
Swami Iyer[1], Timothy Killingback[2*], Bala Sundaram[3], Zhen Wang[4]
1 Computer Science Department, University of Massachusetts, Boston, Massachusetts, United States of America, 2 Mathematics Department, University of Massachusetts, Boston, Massachusetts, United States of America, 3 Physics Department, University of Massachusetts, Boston, Massachusetts, United States of America, 4 Physics Department, University of Massachusetts, Boston, Massachusetts, United States of America
Simultaneous
Sequential
Scale-free network
Random Graph
Degree (V=0.391)
Betweenness (V=0.377)
Closeness (V=0.207)
Eigenvector (V=0.183)
Random (V=0.067)
Degree (V=0.394)
Betweenness (V=0.409)
Closeness (V=0.402)
Eigenvector (V=0.398)
Random (V=0.077)
Fraction of vertices removed (ρ)
Fractional size of largest component (σ)
(c)
(d)
Degree (V=0.297)
Betweenness (V=0.278)
Closeness (V=0.187)
Eigenvector (V=0.161)
Random (V=0.103)
Degree (V=0.321)
Betweenness (V=0.335)
Closeness (V=0.329)
Eigenvector (V=0.325)
Random (V=0.082)

22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Degree (V=0.271)
Betweenness (V=0.325)
Closeness (V=0.315)
Eigenvector (V=0.262)
Random (V=0.125)
Fraction of vertices removed (ρ)
Fractional size of largest component (σ)
(g)
Degree (V=0.437)
Betweenness (V=0.434)
Closeness (V=0.303)
Eigenvector (V=0.157)
Random (V=0.273)
(j)
(f)
(k)
(l)

23

Symulating dynamics ON networks

Because NetworkX adopts plain dictionaries as their main data structure, we can easily add states to nodes (and edges) and dynamically update them iteratively. This will be a simulation of dynamics *on* networks. This class of dynamical network models describe dynamic state changes taking place on a static network topology. Many real-world dynamical networks fall in this category, including:

- Regulatory relationships among genes and proteins within a cell, where nodes are genes and/or proteins and node states are their expression levels.
- Ecological interactions among species in an ecosystem, where nodes are species and node states are their populations.
- Disease infection on social networks, where nodes are individuals and node states are their epidemiological states (e.g., susceptible, infected, recovered, immunized, etc.).
- Information/culture propagation on organizational/social networks, where nodes are individuals or communities and node states are their informational/cultural states.

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Book

Introduction to the Modeling and Analysis of Complex Systems

Author(s): Hiroki Sayama

Keep up to date on *Introduction to Modeling and Analysis of Complex Systems* at http://bingweb.binghamton.edu/~sayama/textbook/!

Introduction to the Modeling and Analysis of Complex Systems introduces students to mathematical/computational modeling and analysis developed in the emerging interdisciplinary field of Complex Systems Science. Complex systems are systems made of a large number of microscopic components interacting with each other in nontrivial ways. Many real-world systems can be understood as complex systems, where critically important information resides in the relationships between the parts and not necessarily within the parts themselves. This textbook offers an accessible yet technically-oriented introduction to the modeling and analysis of complex systems. The topics covered include: fundamentals of modeling, basics of dynamical systems, discrete-time models, continuous-time models, bifurcations, chaos, cellular automata, continuous field models, static networks, dynamic networks, and agent-based models. Most of these topics are discussed in two chapters, one focusing on computational modeling and the other on mathematical analysis. This unique approach provides a comprehensive view of related concepts and techniques, and allows readers and instructors to flexibly choose relevant materials based on their objectives and needs. Python sample codes are provided for each modeling example.

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Typologies

- Time: continuous vs. discrete
- State: continuous vs. discrete

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Continuous state

$$x_t = F(x_{t-1}, t) \quad \text{(for discrete-time models), or}$$

$$\frac{dx}{dt} = F(x, t) \quad \text{(for continuous-time models),}$$

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Simple diffusion
(conservation law)

- Diffusion equation. Laplacian operator

$$\frac{dn(x,t)}{dt} = \nabla^2 n(x,t)$$

- Discrete Laplacian operator (1d)

$$\frac{dn_i(t)}{dt} = (n_{i+1}(t) - n_i(t)) - (n_i(t) - n_{i-1}(t))$$

$$\frac{dn_i(t)}{dt} = n_{i+1}(t) + n_{i-1}(t) - 2 \cdot n_i(t)$$

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- Discrete Laplacian operator (2d)

$$\frac{dn_{i,j}(t)}{dt} = n_{i+1,j}(t) + n_{i-1,j}(t) + n_{i,j+1}(t) + n_{i,j-1}(t) - 4 \cdot n_{i,j}(t)$$

- In general

$$\frac{dn_i(t)}{dt} = \sum_i^N a_{i,j} n_j(t) - k_i \cdot n_i(t) = -L_{ij} n_j(t)$$

- Where we have introduced the Laplacian matrix

$$L_{ij} = k_i \delta_{ij} - a_{ij}$$

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- Important in dynamical properties
- Discrete spectrum: eigenvalues and eigenvectors
- Ordered
  $0 = \lambda_1 \leq \lambda_2 \leq \ldots \leq \lambda_N$
- Number of 0 eigenvalues is equal to the number of (dis)connected components
- λ_2 is related to the time the system needs to be synchronized. Intuitively, when it is zero there are at least two disconnected components and the system will never synchronize

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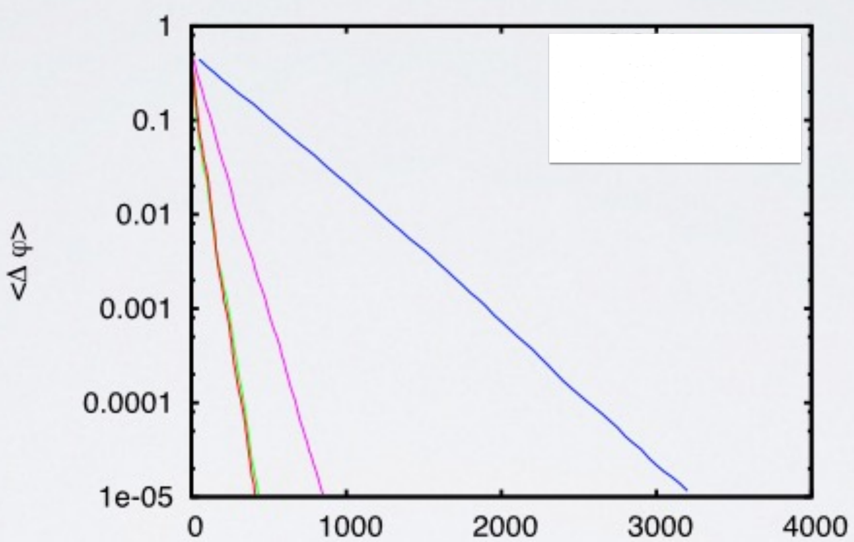

31

Eigenvalues and eigenvectors of the Laplacian matrix

$$\frac{d}{dt}\begin{pmatrix}\theta_1\\ \vdots \\ \theta_n\end{pmatrix} = -\sigma\begin{pmatrix}k_1 & -a_{12} & \cdots & -a_{1n}\\ -a_{21} & k_2 & \cdots & -a_{2n}\\ & & \vdots & \\ -a_{n1} & -a_{n2} & \cdots & k_n\end{pmatrix}\begin{pmatrix}\theta_1\\ \vdots \\ \theta_n\end{pmatrix}$$

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Linearized system

$$\frac{d\theta_i}{dt} = -\sigma\sum_j L_{ij}\theta_j \qquad i = 1, \ldots, N$$

whose solution is

$$\varphi_i(t) = \sum_j U_{ij}\theta_j(t) = \sum_j U_{ij}e^{-\lambda_j t}\theta_j(0) = \sum_{j,k} U_{ij}e^{-\lambda_j t}U^{-1}_{jk}\varphi_k(0)$$

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- This set of equations has to be verified at any time t
- Let's look now at the average of the square phase difference between any pair of oscillators:

$$\langle(\varphi_l(t)-\varphi_k(t))^2\rangle = \sum_{m,p}(U_{lm}-U_{km})(U_{lp}-U_{kp})e^{-\lambda_m t}e^{-\lambda_p t}\langle\theta_m(0)\theta_p(0)\rangle$$

$$\langle\theta_m(0)\theta_p(0)\rangle = \sum_{k,l}\langle U^\dagger_{mk}\varphi_k(0)U^\dagger_{pl}\varphi_l(0)\rangle = \sum_{k,l}U^\dagger_{mk}U^\dagger_{pl}\underbrace{\langle\varphi_k(0)\varphi_l(0)\rangle}_{2D\delta_{kl}} = 2D\delta_{mp}$$

- Since the eigenvector corresponding to the eigenvalue $\lambda_1 = 0$ has all its components identical, the sum runs $m = 2, \ldots, N$.

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- Then we get for the average squared phase difference

$$\langle(\varphi_l(t)-\varphi_k(t))^2\rangle = 2D\sum_{m=2}^{N}(U_{lm}-U_{km})^2e^{-2\lambda_m t}$$

This fact guarantees the final synchronization.

- Actually, we can define a characteristic time for each pair of oscillators

$$\tau_{lk}\ /\ \langle(\varphi_l(t)-\varphi_k(t))^2\rangle < \Theta\ ;\ \forall\ t > \tau_{lk}.$$

which depends only on the projections of the original nodes on the eigenvectors and on the eigenvalues.

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Consensus

2003 American Control Conference
http://www.cds.caltech.edu/~murray/papers/2002o_om03-acc.html

Consensus Protocols for Networks of Dynamic Agents

Reza Olfati Saber Richard M. Murray
Control and Dynamical Systems
California Institute of Technology
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Definition 2. (consensus) Let the value of all nodes x be the solution of the following differential equation:

$$\dot{x} = f(x), \quad x(0) = x^0 \in \mathbb{R}^n \tag{6}$$

In addition, let $\chi : \mathbb{R}^n \to \mathbb{R}$ be a multi-input single-output operation on $x = (x_1, \ldots, x_n)^T$ that generates a decision-value $y = \chi(x)$. We say all the nodes of the graph have reached consensus w.r.t. χ in finite time $T > 0$ if and only if all the nodes agree and $x_i(T) = \chi(x(0)), \forall i \in \mathcal{I}$. Similarly, let $x = x^*$ be a globally/locally asymptotically stable equilibrium of (6). We say all the nodes of the graph with initial values x_i^0 have *globally/locally asymptotically reached consensus regarding* χ if and only if $x_i^* = \chi(x(0)), \forall i \in \mathcal{I}$

...mputing examples

Example 1. Some of the common examples of the operation χ are given in the following:

$$\begin{aligned} \chi(x) &= Ave(x) = \frac{1}{n}\textstyle\sum_{i=1}^n x_i \\ \chi(x) &= Max(x) = \max\{x_1.x_2, \ldots, x_n\} \\ \chi(x) &= Min(x) = \min\{x_1.x_2, \ldots, x_n\} \end{aligned} \tag{7}$$

The corresponding consensus of these operations are referred to as the *average-consensus*, the *max-consensus*, and the *min-consensus*, respectively. This suggests a general name of χ*-consensus* for an agreement problem regarding the operation χ.

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Random walks

- In a regular lattice a set of random walkers is equivalent to diffusion
- Brownian particles: diffusion of probability
- PDE for random walk
- Stationary distribution? Homogeneous

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RW in a network

Random walks and diffusion on networks

Naoki Masuda

Department of Engineering Mathematics, University of Bristol, Bristol, UK

Mason A. Porter

Department of Mathematics, University of California Los Angeles, Los Angeles, USA

Mathematical Institute, University of Oxford, Oxford, UK

CABDyN Complexity Centre, University of Oxford, Oxford, UK

Renaud Lambiotte

Department of Mathematics/Naxys, University of Namur, Namur, Belgium

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$$p_{i \to j} = \frac{1}{k_i}$$

$$p_{i \to j} = \frac{1}{k^{\max}}$$

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Stationary distributions

- Proportional to degree
- Homogeneous

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Centrality measures

- Page Rank

$$PR(p_i) = \frac{1-d}{N} + d \sum_{p_j \in M(p_i)} \frac{PR(p_j)}{L(p_j)}$$

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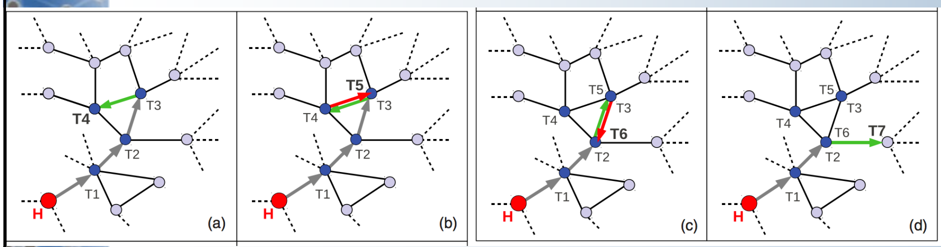
Search & exploration

PHYSICAL REVIEW E **86**, 066116 (2012)

Exploring complex networks by means of adaptive walkers

Luce Prignano,[1] Yamir Moreno,[2,3,4] and Albert Díaz-Guilera[1,2]



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Synchronization

- Continuously coupled
- Pulse-coupled

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Continuous coupling. Kuramoto model

$$\frac{d\theta_i}{dt} = \omega_i + \sigma \sum_j A_{ij} \sin(\theta_j - \theta_i) \qquad i = 1, \ldots, N$$

$$\frac{d\theta_i}{dt} = \sigma \sum_j A_{ij} \sin(\theta_j - \theta_i) \qquad i = 1, \ldots, N$$

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- http://mathinsight.org/applet/synchronizing_oscillators
- https://www.complexity-explorables.org/explorables/ride-my-kuramotocycle/

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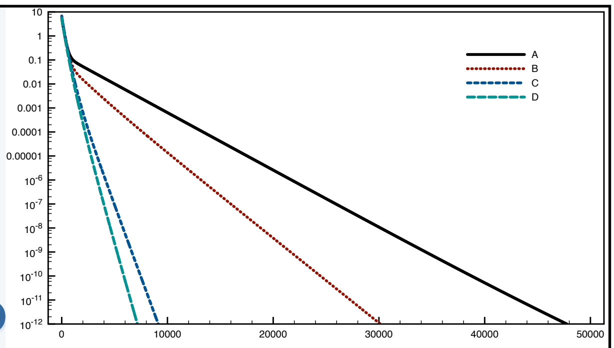
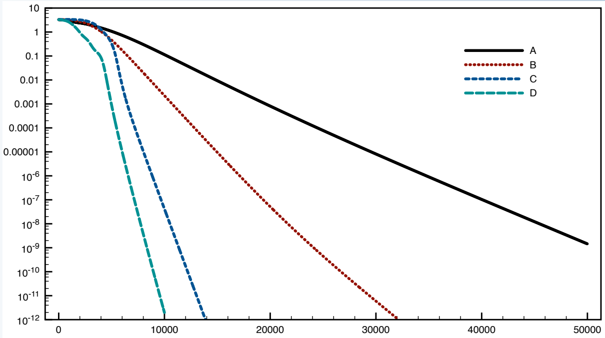
Kuramoto vs. linear





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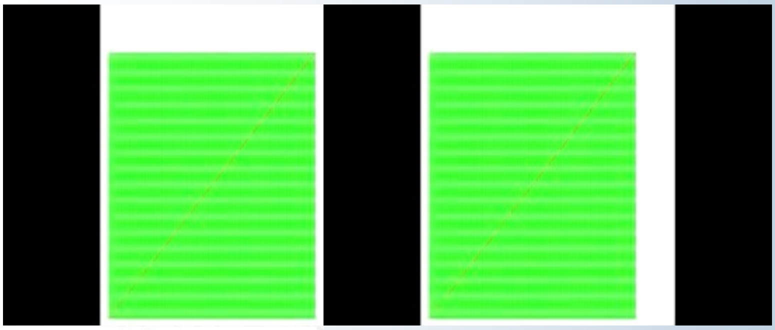
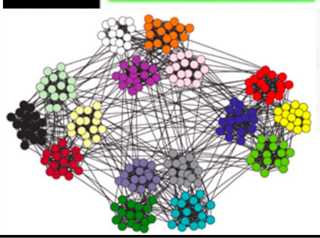
Time evolution of the correlation matrix





$$\rho_{ij}(t) = < cos(\theta_i(t) - \theta_j(t)) >$$

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Network symmetries

- Structural network
- Functional network

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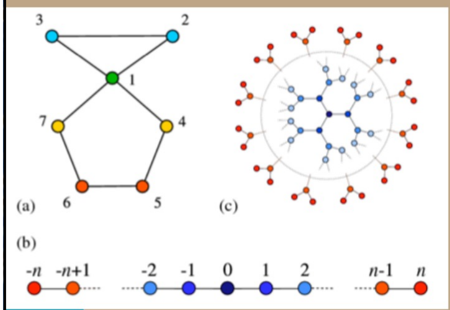
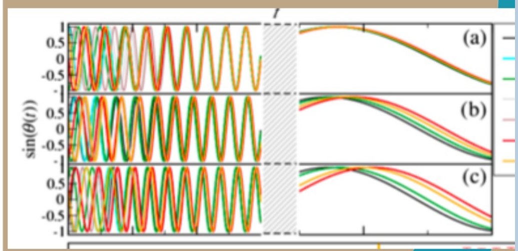
PRL 110, 174102 (2013) PHYSICAL REVIEW LETTERS week ending 26 APRIL 2013

Remote Synchronization Reveals Network Symmetries and Functional Modules

Vincenzo Nicosia,[1] Miguel Valencia,[2] Mario Chavez,[3] Albert Díaz-Guilera,[4] and Vito Latora[1,5]

$$\dot{\theta}_i = \omega + \lambda \sum_{j=1}^{N} a_{ij} \sin(\theta_j - \theta_i - \alpha).$$





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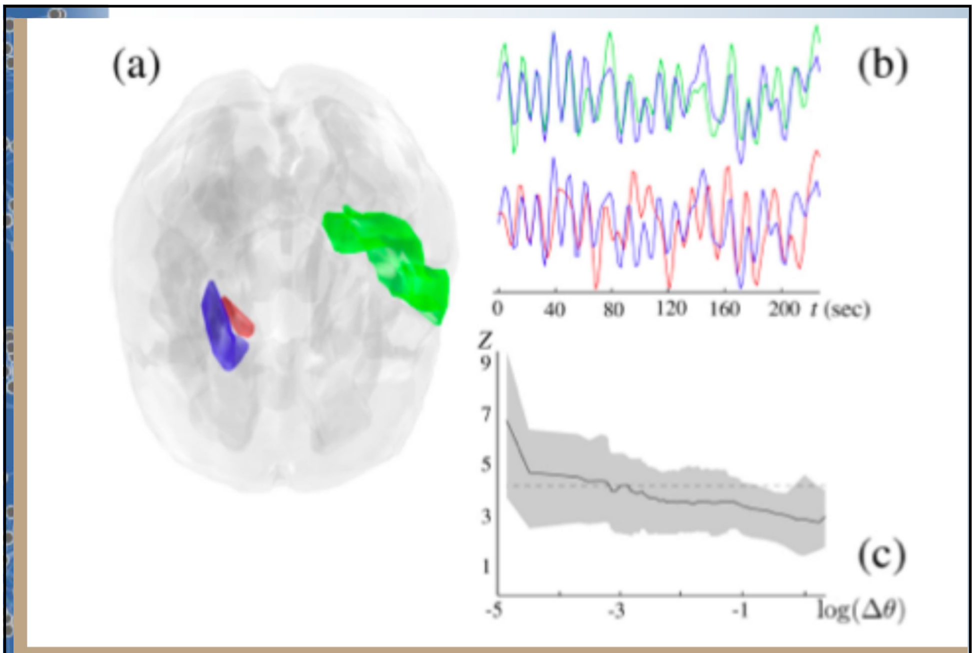

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Coding

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Code 15.8: net-kuramoto.py

Albert Díaz Guilera

```
import matplotlib
matplotlib.use('TkAgg')
from pylab import *
import networkx as nx

def initialize():
    global g, nextg
    g = nx.karate_club_graph()
    g.pos = nx.spring_layout(g)
    for i in g.nodes_iter():
        g.node[i]['theta'] = 2 * pi * random()
        g.node[i]['omega'] = 1. + uniform(-0.05, 0.05)
    nextg = g.copy()

def observe():
    global g, nextg
    cla()
    nx.draw(g, cmap = cm.hsv, vmin = -1, vmax = 1,
            node_color = [sin(g.node[i]['theta']) for i in g.nodes_iter()],
            pos = g.pos)

alpha = 1 # coupling strength
Dt = 0.01 # Delta t

def update():
    global g, nextg
    for i in g.nodes_iter():
        theta_i = g.node[i]['theta']
        nextg.node[i]['theta'] = theta_i + (g.node[i]['omega'] + alpha * ( \
            sum(sin(g.node[j]['theta'] - theta_i) for j in g.neighbors(i)) \
            / g.degree(i))) * Dt
    g, nextg = nextg, g

import pycxsimulator
pycxsimulator.GUI().start(func=[initialize, observe, update])
```

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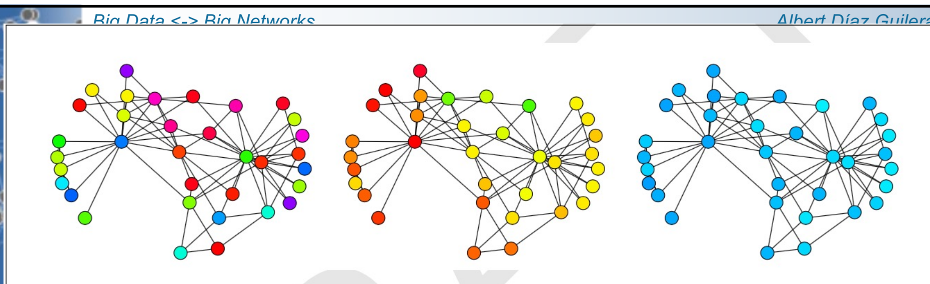
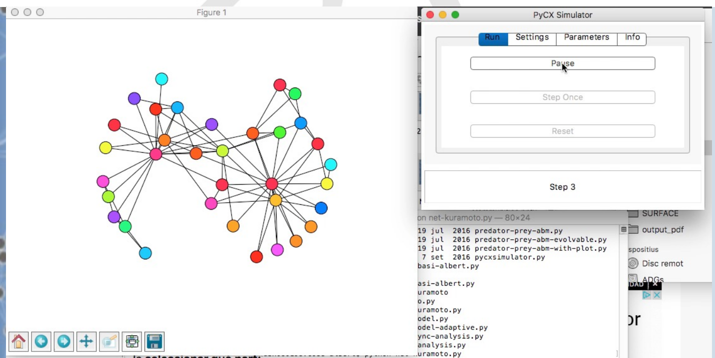


Figure 15.8: A visual output of Code 15.8. Time flows from left to right.



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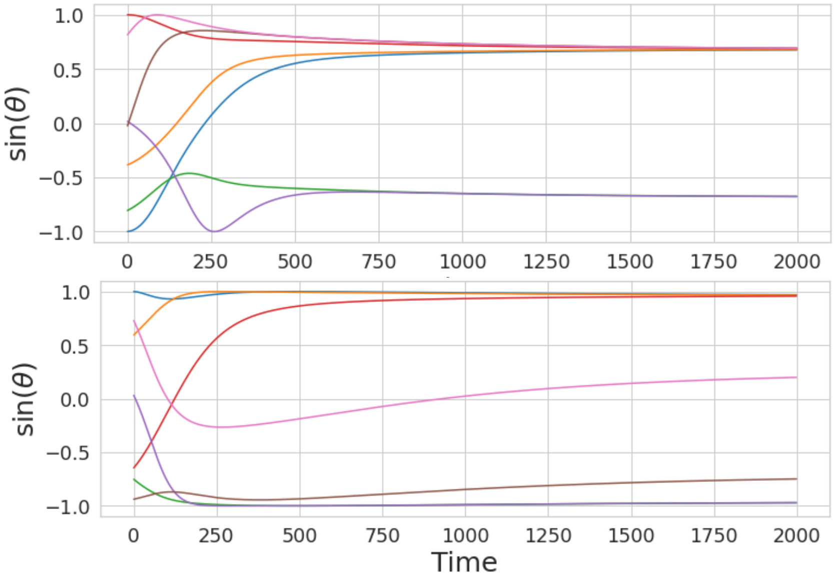
Opinion in signed networks



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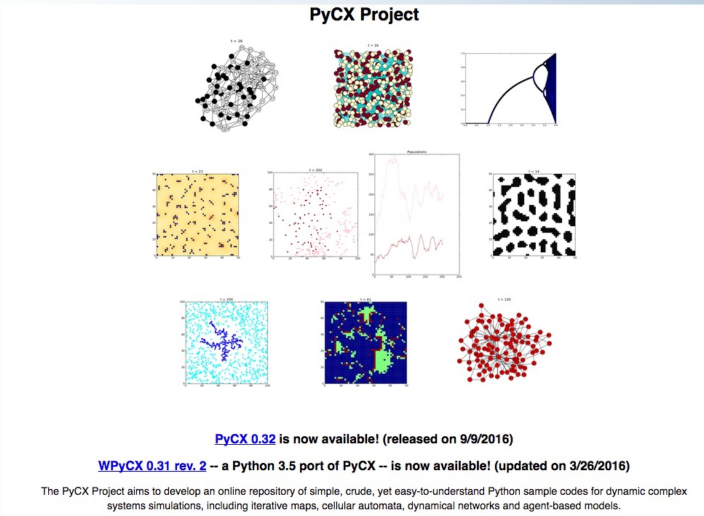
Pycx simulator

- http://pycx.sourceforge.net/



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Spreading

Phenomena	Agent	Network
Venereal Disease	Pathogens	Sexual Network
Rumor Spreading	Information, Memes	Communication Network
Diffusion of Innovations	Ideas, Knowledge	Communication Network
Computer Viruses	Malwares, Digital viruses	Internet
Mobile Phone Virus	Mobile Viruses	Social Network/Proximity Network
Bedbugs	Parasitic Insects	Hotel - Traveler Network
Malaria	Plasmodium	Mosquito - Human network

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Compartmentalization

Epidemic models classify each individual based on the stage of the disease affecting them. The simplest classification assumes that an individual can be in one of three *states* or *compartments*:

- *Susceptible (S)*: Healthy individuals who have not yet contacted the pathogen (Image 10.3).
- *Infectious (I)*: Contagious individuals who have contacted the pathogen and hence can infect others.
- *Recovered (R)*: Individuals who have been infected before, but have recovered from the disease, hence are not infectious.

The modeling of some diseases requires additional states, like *immune* individuals, who cannot be infected, or *latent* individuals, who have been exposed to the disease, but are not yet contagious.

Individuals can move between compartments. For example, at the beginning of a new influenza outbreak everyone is in the susceptible state. Once an individual comes into contact with an infected person, she can become infected. Eventually she will recover and develop immunity, losing her susceptibility to the the particular strain of influenza.

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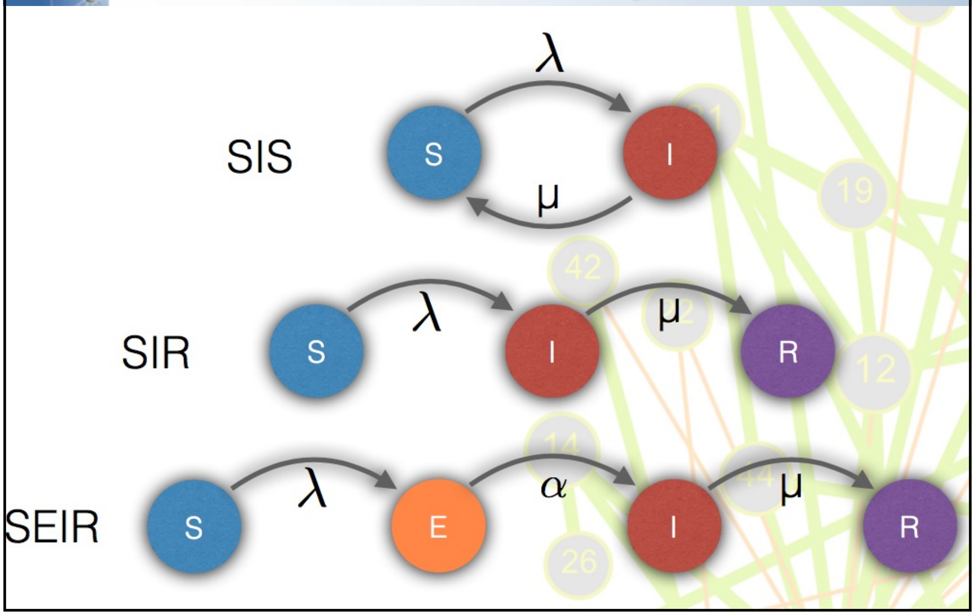
Some examples



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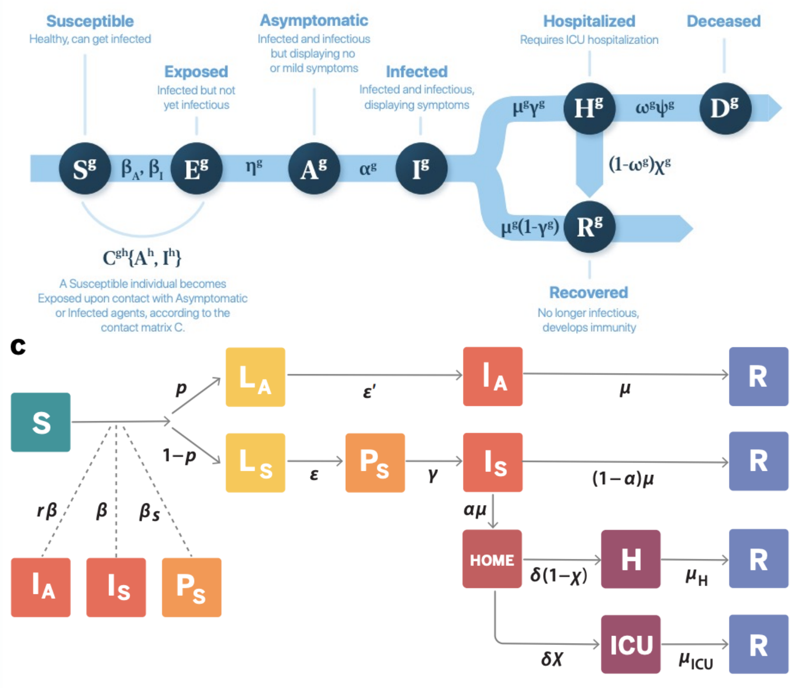
Big

CO VID



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Well mixed or mean field

- Rates of moving from one compartment to the other
- No network effects

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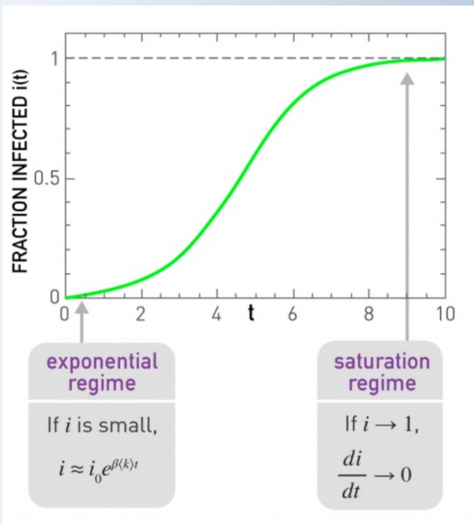
SI model

$$i(t) = I(t)/N$$

$$s(t) = S(t)/N$$

$$s(t) + i(t) = 1$$

$$\frac{di}{dt} = \lambda i(t) s(t)$$



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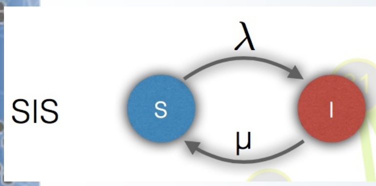
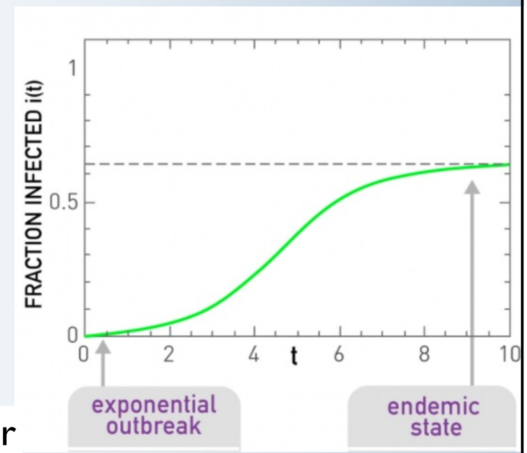
SIS model





$$R_0 = \lambda/\mu$$

Basic reproductive number

If $R_0 > 1$, the epidemic is in the endemic state.
If $R_0 < 1$ the epidemic dies out

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- **QUESTION:** What is the minimum value of λ for the epidemic outbreak to take place?

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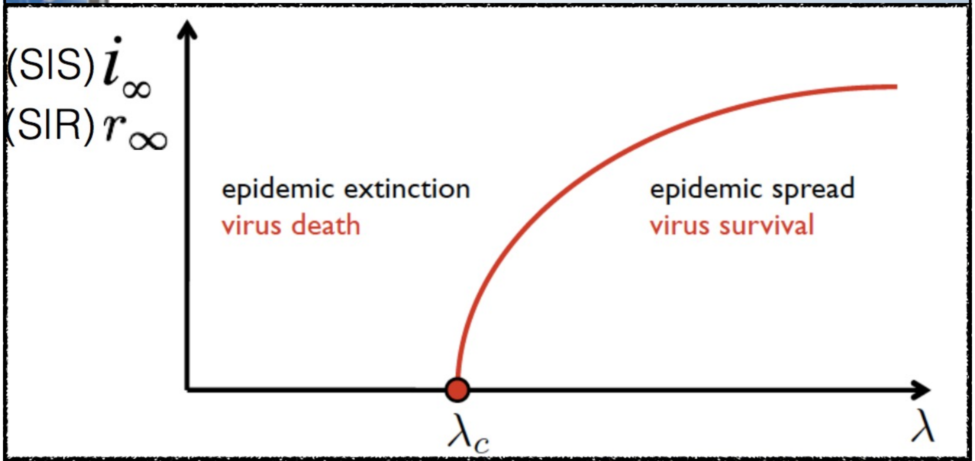
Epidemic threshold



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	SI	SIS	SIR
Exponential Regime: Number of infected individuals grows exponentially	$i=\frac{i_0 e^{\beta\langle k\rangle t}}{1-i_0+i_0 e^{\beta\langle k\rangle t}}$	$i=\left(1-\frac{\mu}{\beta\langle k\rangle}\right)\frac{Ce^{(\beta\langle k\rangle-\mu)t}}{1+Ce^{(\beta\langle k\rangle-\mu)t}}$	No closed solution
Final Regime: Saturation at t→=∞	$i(\infty)=1$	$i(\infty)=1-\frac{\mu}{\beta\langle k\rangle}$	$i(\infty)=0$
Epidemic Threshold: Disease does not always spread	No threshold	$R_0=1$	$R_0=1$

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Epidemics & Networks

14 PHYSICAL REVIEW LETTERS 2 APRIL 2001

Epidemic Spreading in Scale-Free Networks

Romualdo Pastor-Satorras[1] and Alessandro Vespignani[2]

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Network heterogeneity

- Not all nodes are statistically equivalent
- Assume that nodes with the same degree are statistically equivalent

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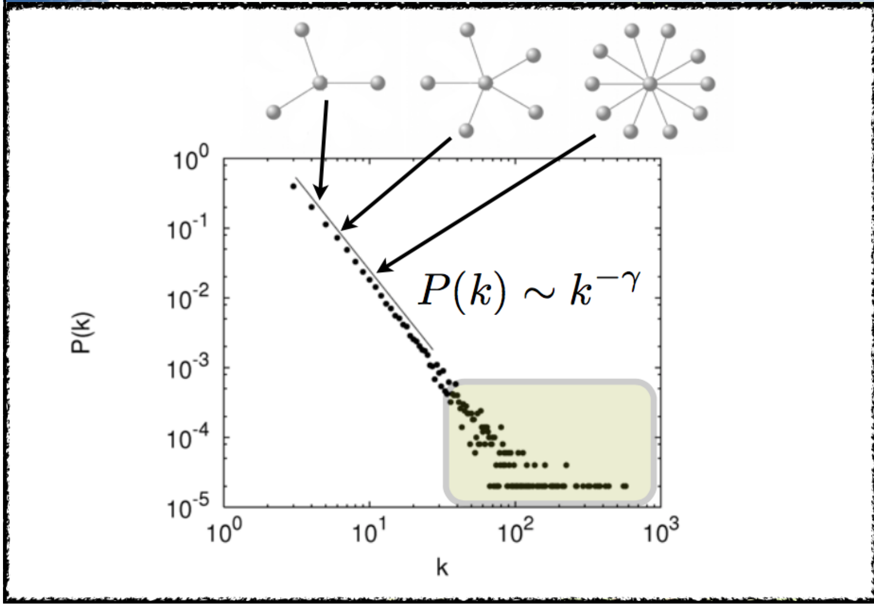

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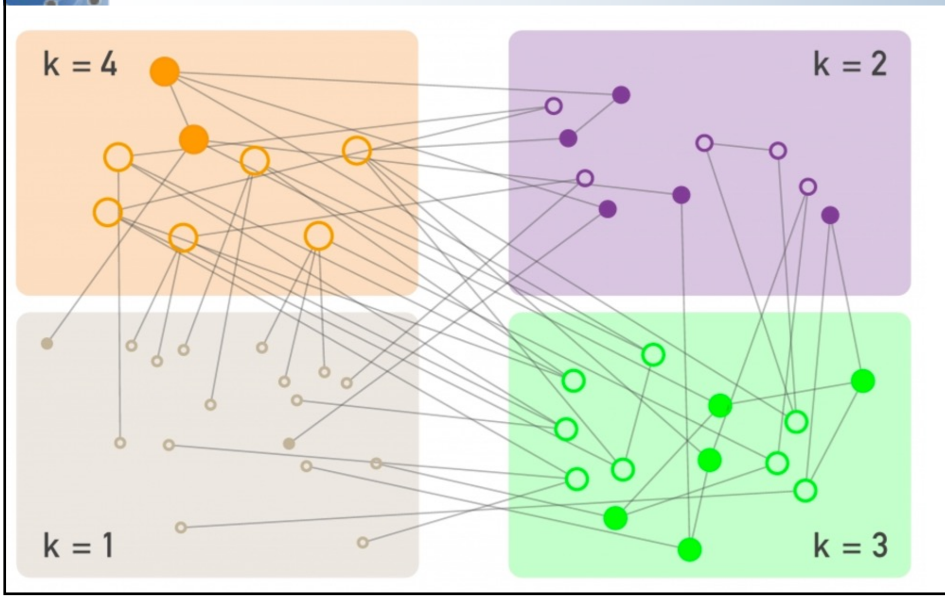
Degree Block approximation



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$$i_k = \frac{I_k}{N_k} \qquad s_k = \frac{S_k}{N_k}$$

$$i = \sum_k P(k) i_k \qquad s = \sum_k P(k) s_k$$

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Epidemics & Networks

$$\boxed{\lambda_c \sim \frac{\langle k \rangle}{\langle k^2 \rangle}}$$

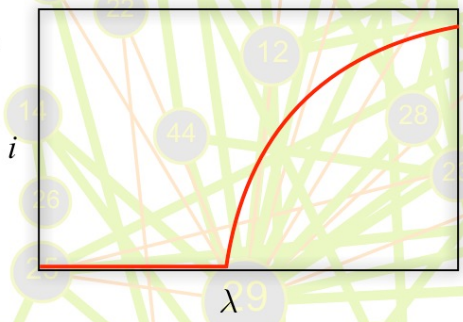
- in **Well-mixed** populations:

$$\langle k^2 \rangle = \langle k \rangle^2 \longrightarrow \lambda_c \sim \frac{1}{\langle k \rangle}$$

- in **Scale-Free** networks $P(k) \sim k^{-\gamma}$

if $2 < \gamma < 3$ then $\langle k^2 \rangle \to \infty$

$$\lambda_c \to 0$$



@gomezgardenes

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Epidemics & Networks

$$\boxed{\lambda_c \sim \frac{\langle k \rangle}{\langle k^2 \rangle}}$$

- in **Well-mixed** populations:

$$\langle k^2 \rangle = \langle k \rangle^2 \longrightarrow \lambda_c \sim \frac{1}{\langle k \rangle}$$

- in **Scale-Free** networks $P(k) \sim k^{-\gamma}$ i

if $2 < \gamma < 3$ then $\langle k^2 \rangle \to \infty$

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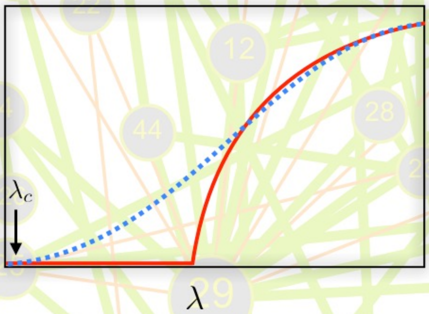

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Best seeds ???

Article | Open Access | Published: 28 February 2020

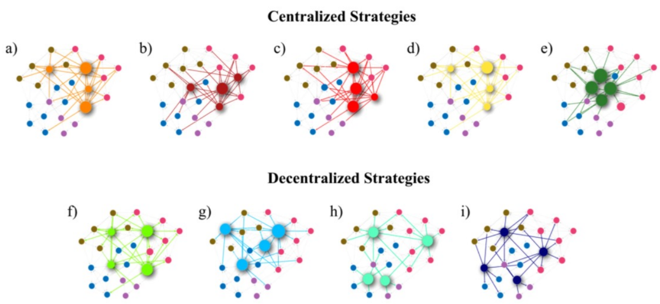
Benchmarking seeding strategies for spreading processes in social networks: an interplay between influencers, topologies and sizes

Felipe Montes, Ana María Jaramillo, Jose D. Meisel, Albert Diaz-Guilera, Juan A. Valdivia, Olga L. Sarmiento & Roberto Zarama

Scientific Reports **10**, Article number: 3666 (2020) | Cite this article

1367 Accesses | 18 Altmetric | Metrics

From: Benchmarking seeding strategies for spreading processes in social networks: an interplay between influencers, topologies and sizes



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Derivation of the effective reproduction number $\mathcal{R}$ for COVID-19 in relation to mobility restrictions and confinement

Alex Arenas[1*], Wesley Cota[2,3,4], Jesús Gómez-Gardeñes[2,3*], Sergio Gómez[1], Clara Granell[2,3], Joan T. Matamalas[5], David Soriano-Paños[2,3], Benjamin Steinegger[1]

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Alex Arenas[1*], Wesley Cota[2,3,4], Jesús Gómez-Gardeñes[2,3*], Sergio Gómez[1], Clara Granell[2,3], Joan T. Matamalas[5], David Soriano-Paños[2,3], Benjamin Steinegger[1]

- Mobility between áreas
- Contacts between age groups (different social patterns in countries)

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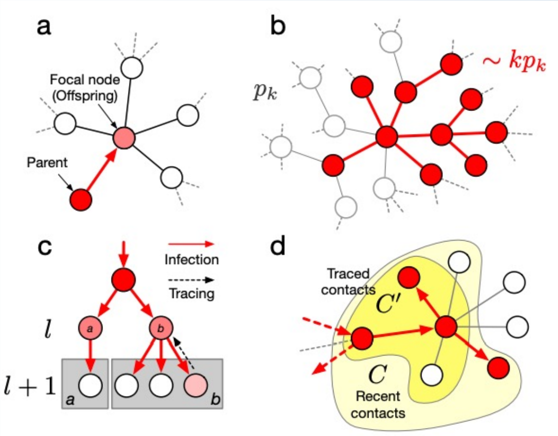
Contact tracing

The effectiveness of contact tracing in heterogeneous networks

Sadamori Kojaku,[1] Laurent Hébert-Dufresne,[2,3] and Yong-Yeol Ahn[1,4,*]



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Resources

- Network Epidemiology in the Time of Coronavirus
- https://www.youtube.com/watch?v=5NGFDnJKiKA

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Observables

- https://observablehq.com/@epichef

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Social models: agent based models (ABM)

- Voter model
- Opinion dynamics
- Language competition
- Cultural dynamics
- Naming game
- Evolutionary games

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Voter model

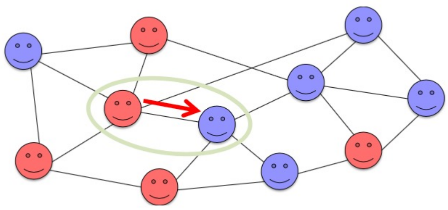

Figure 15.2: Schematic illustration of the voter model. Each time a pair of connected nodes are randomly selected (green circle), where the state of the speaker node (left) is copied to the listener node (right).

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Code 16.5: voter-model.py

Albert Díaz Guilera

```
import matplotlib
matplotlib.use('TkAgg')
from pylab import *
import networkx as nx
import random as rd

def initialize():
    global g
    g = nx.karate_club_graph()
    g.pos = nx.spring_layout(g)
    for i in g.nodes_iter():
        g.node[i]['state'] = 1 if random() < .5 else 0

def observe():
    global g
    cla()
    nx.draw(g, cmap = cm.binary, vmin = 0, vmax = 1,
            node_color = [g.node[i]['state'] for i in g.nodes_iter()],
            pos = g.pos)

def update():
    global g
    listener = rd.choice(g.nodes())
    speaker = rd.choice(g.neighbors(listener))
    g.node[listener]['state'] = g.node[speaker]['state']

import pycxsimulator
pycxsimulator.GUI().start(func=[initialize, observe, update])
```

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Language dynamics: AS model

$$P_i^{B\to A} = S\frac{1}{k_i}\sum_{j=1}^{N} A_{ij}\sigma_j$$

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Dynamics OF the links

- It is not the user that switches languages but the link that represent information exchange between users

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Axelrod model of cultural evolution

- One agent k (active) is selected at random.
- One of agent k's neighbours, denoted agent r (passive), is selected at random.
- Agents k and r interact with probability equal to their cultural similarity n_{kr}/f, where n_{kr} denotes the number of cultural features for which agents k and r have the same trait. The interaction consists in that active agent k selects at random one of the $f - n_{kr}$ features on which the two agents differ, and copies the passive agent r's trait. In this way, agent k approaches agent r's cultural interests.

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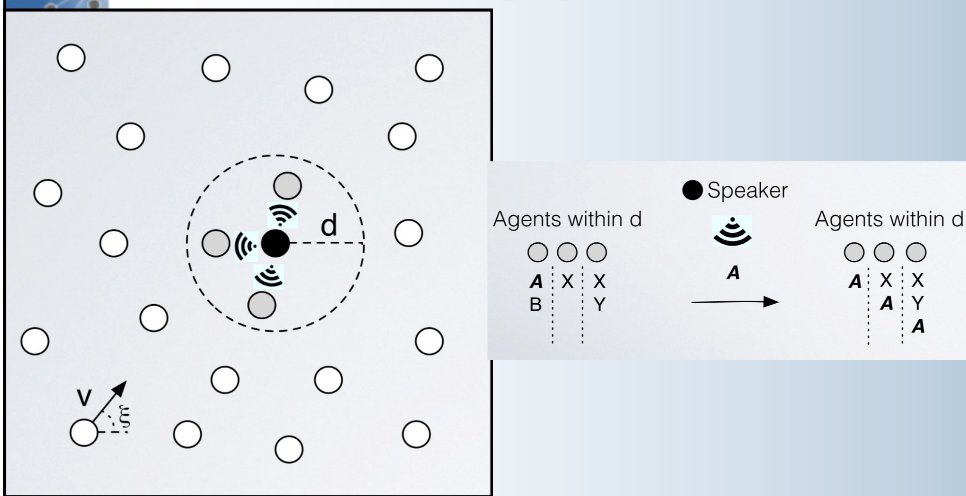
Naming games



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Evolutionary game theory

- Prisoner's dilemma

		Prisoner A: Silent	Prisoner A: Betray
Prisoner B	Silent	B: -1, A: -1	B: -3, A: 0
Prisoner B	Betray	B: 0, A: -3	B: -2, A: -2

Prisoner's dilemma payoff matrix

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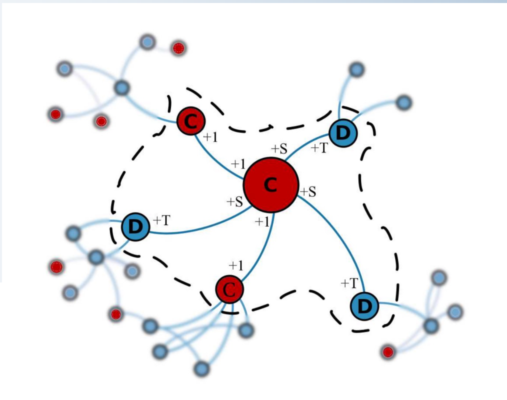
Payoff

$$
\begin{array}{c|cccc}
 & S_1 & S_2 & \dots & S_s \\
\hline
S_1 & P_{12} & P_{12} & \dots & P_{1s} \\
S_2 & P_{22} & P_{22} & \dots & P_{2s} \\
\dots & \dots & \dots & \dots & \dots \\
S_s & P_{s1} & P_{s2} & \dots & P_{ss}
\end{array}
$$

$$f_i = \sum_{j=1}^{N} A_{ij} P_{x_i x_j}$$



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Many applications

A Game Theory Based Congestion Control Protocol for Wireless Personal Area Networks

Chuang Ma,[1] Jang-Ping Sheu,[2] and Chao-Xiang Hsu[2]

[1]School of Computer and Information, Shanghai Second Polytechnic University, Shanghai 201209, China
[2]Department of Computer Science, National Tsing Hua University, Hsinchu 30013, Taiwan

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