

Propagation patterns of contagion processes on networks and hypernetworks

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<http://www.sociopatterns.org>

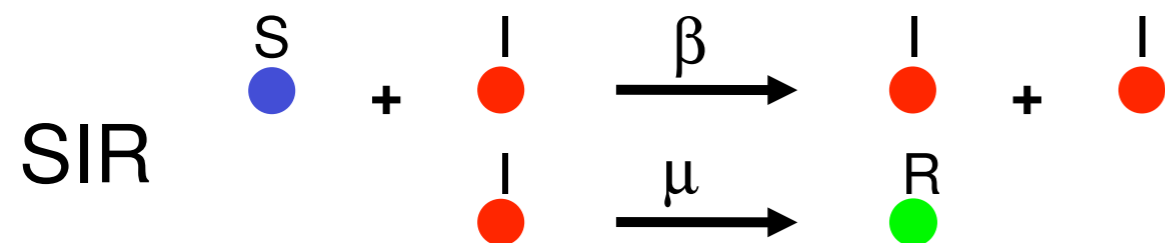
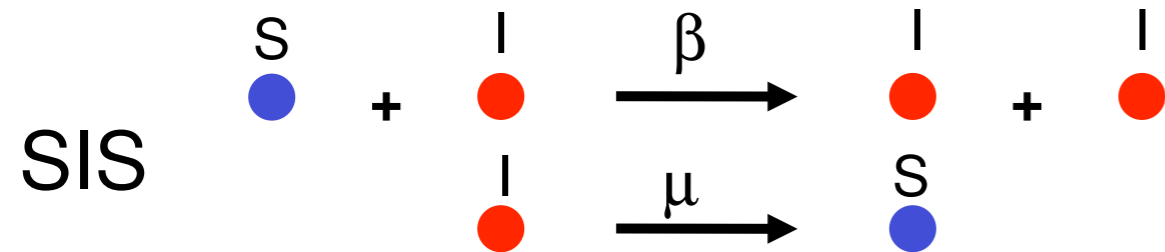
<http://dataredux.weebly.com>

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Modeling spreading processes

Propagation of infectious diseases: standard simplified epidemic modelling

- Disease evolution: discrete states of the host S, I, R, etc...
- Contagion events: result from single exposures (“simple contagion”)



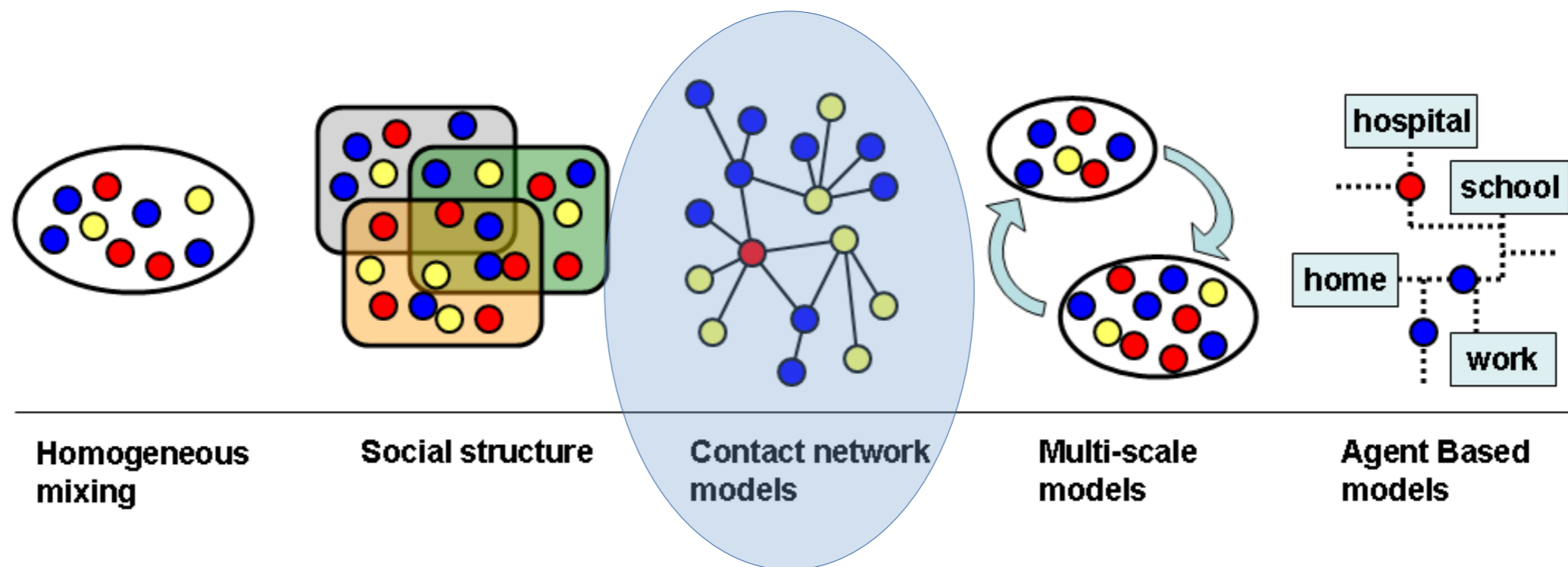
Modeling spreading processes

Propagation models

Simple contagion: Epidemic-like, single exposure (SI, SIS, SIR,...)

Structure of interactions

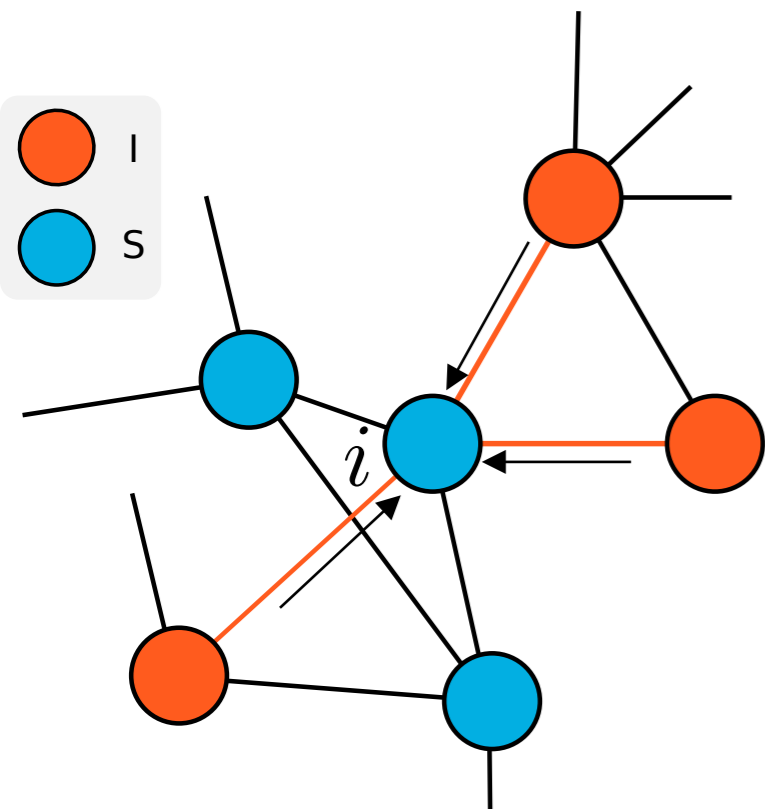
From extremely simplified (mean-field) to extremely detailed (ABMs)



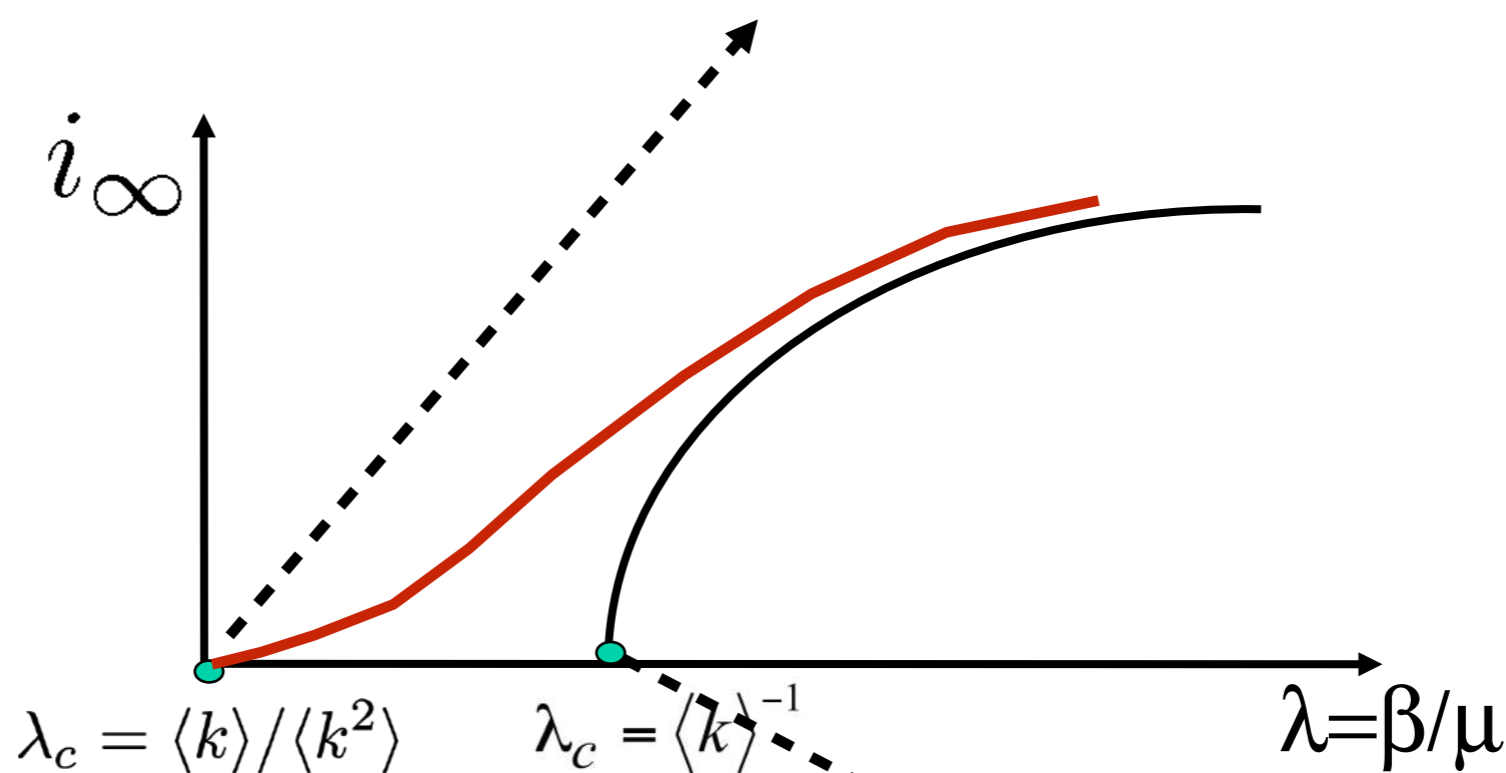
Individuals=nodes of a network

Interactions=along edges of the network

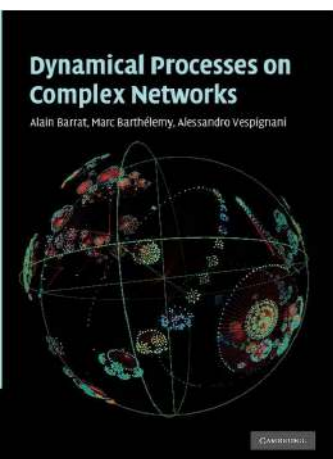
Simple contagion on networks



- Heterogeneous structure
- => Epidemic threshold going to 0
- => relevance of hubs and cores
- => cascading dynamics from hubs to low degree nodes



Homogeneous contact structure
 (e.g., random graph)
 => Finite epidemic threshold



REVIEWS OF MODERN PHYSICS

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Epidemic processes in complex networks

Romualdo Pastor-Satorras, Claudio Castellano, Piet Van Mieghem, and Alessandro Vespignani
 Rev. Mod. Phys. **87**, 925 – Published 31 August 2015

However (I):
simple contagion
is not enough

Complex contagion

Multiple sources needed for a transmission event

“a contagion is complex if its transmission requires an individual to have contact with two or more sources of activation”, i.e. if a “contact with a single active neighbor is not enough to trigger adoption”

(Centola & Macy, Am. J. Socio. 2007)

REPORT

The Spread of Behavior in an Online Social Network Experiment

Damon Centola

+ See all authors and affiliations

Science 03 Sep 2010:
Vol. 329, Issue 5996, pp. 1194-1197
DOI: 10.1126/science.1185231

“Individual adoption was much more likely when participants received social reinforcement from multiple neighbors in the social network.”

 PLOS ONE

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RESEARCH ARTICLE

Evidence of complex contagion of information in social media: An experiment using Twitter bots

Bjarke Mønsted , Piotr Sapieżyński , Emilio Ferrara , Sune Lehmann  

Published: September 22, 2017 • <https://doi.org/10.1371/journal.pone.0184148>

“We provide experimental evidence that the complex contagion model describes the observed information diffusion behavior more accurately than simple contagion.”

Structural diversity in social contagion

Johan Ugander, Lars Backstrom, Cameron Marlow, and Jon Kleinberg

PNAS April 17, 2012 109 (16) 5962-5966; <https://doi.org/10.1073/pnas.1116502109>

Edited by Ronald L. Graham, University of California at San Diego, La Jolla, CA, and approved February 21, 2012

“We find that the probability of contagion is tightly controlled by the number of connected components in an individual's contact neighborhood, rather than by the actual size of the neighborhood.”

Complex contagion

A simple model of global cascades on random networks

Duncan J. Watts

PNAS April 30, 2002 99 (9) 5766-5771; <https://doi.org/10.1073/pnas.0820904>

A particularly simple binary decision rule with externalities that captures the essential features outlined above is the following: An individual agent observes the current states (either 0 or 1) of k other agents, which we call its *neighbors*, and adopts state 1 if at least a threshold fraction ϕ of its k neighbors are in state 1, else it adopts state 0.

PRL 115, 218702 (2015)

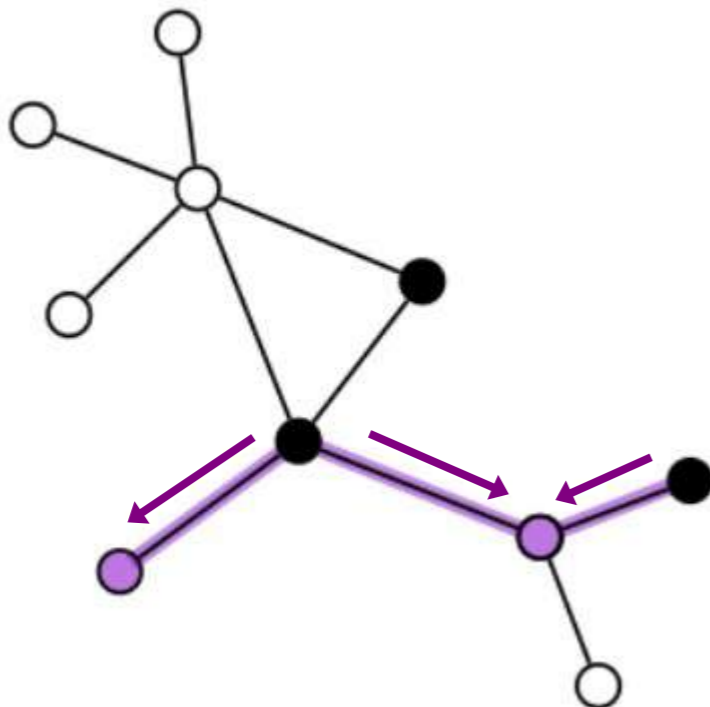
PHYSICAL REVIEW LETTERS

week ending
20 NOVEMBER 2015

Kinetics of Social Contagion

Zhongyuan Ruan,^{1,2} Gerardo Iñiguez,^{3,4} Márton Karsai,⁵ and János Kertész^{1,2,4,*}

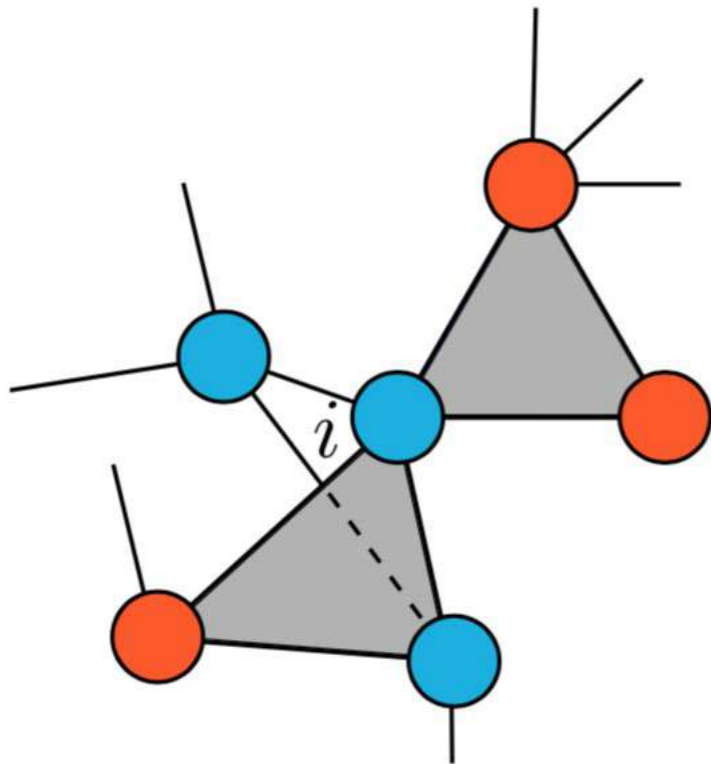
different kinetics behind them (Fig. 1). Motivated by empirical observations [24], we extend Watts' threshold model by considering *blocked* nodes immune to social influence and discuss their effect on cascade formation. In



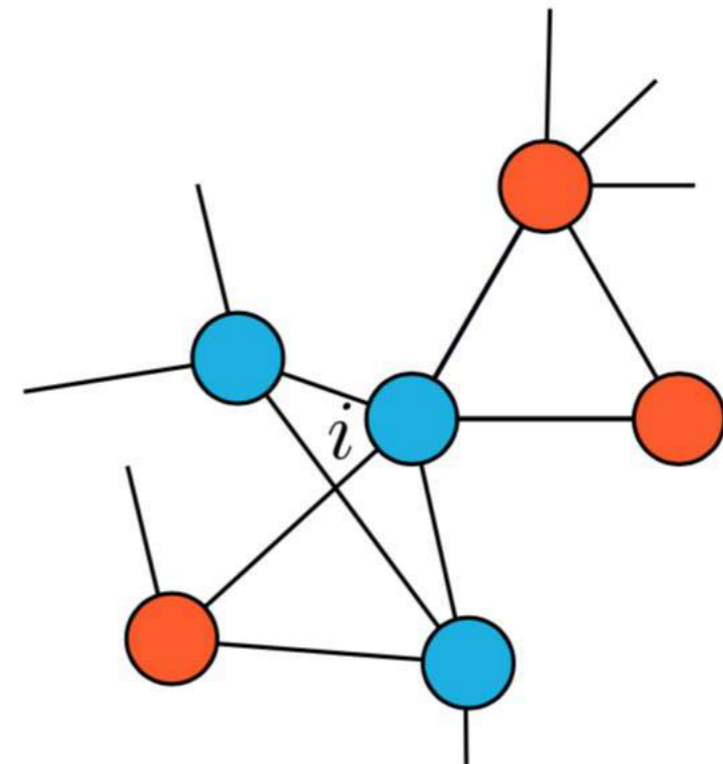
Parameter: fraction of neighbours I needed to change state $S \rightarrow I$

However (II):
the network representation
is not enough

Social structure:
group interactions

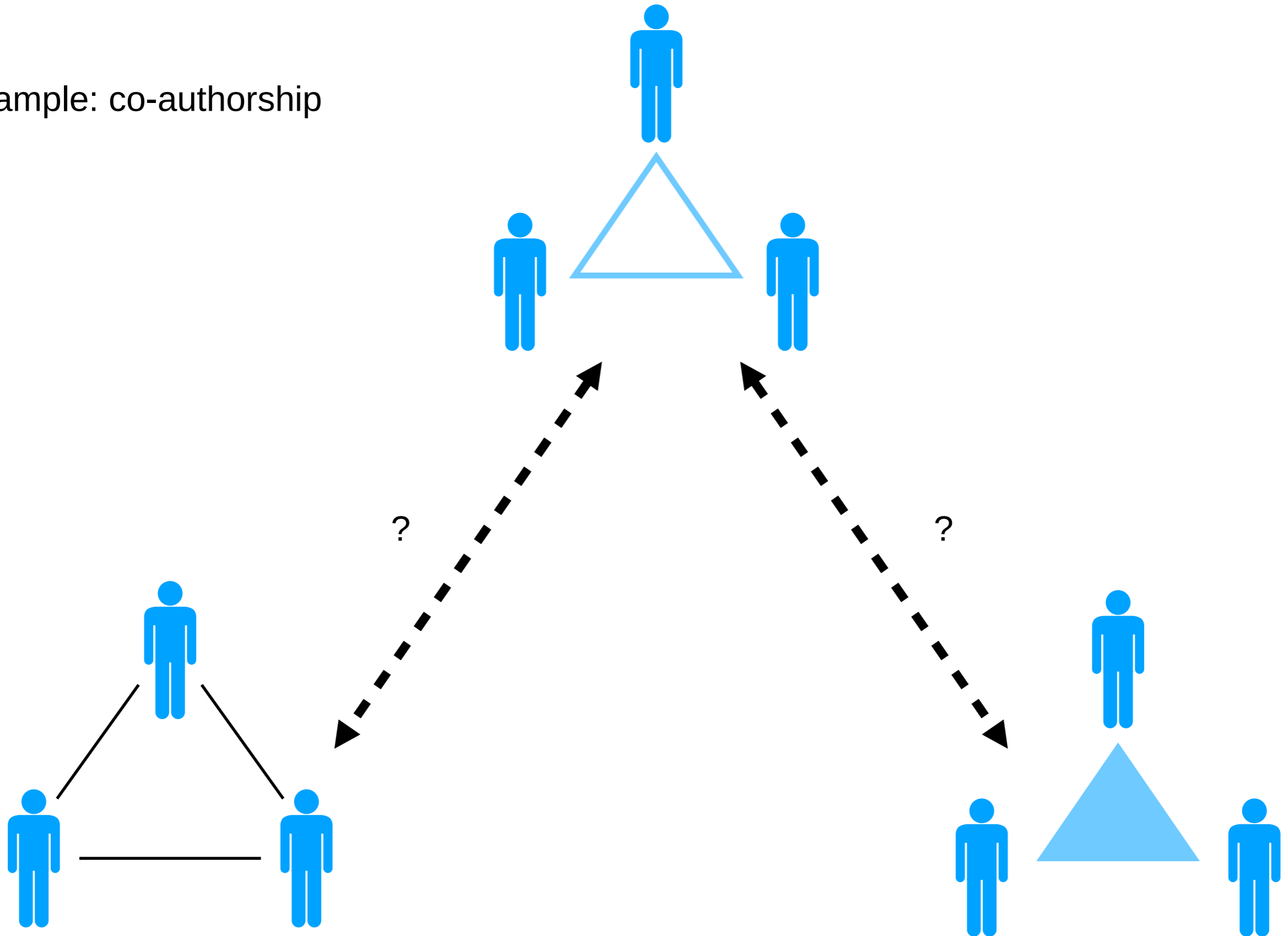


Network representation:
limited to pairwise interactions



Networks are not enough

Example: co-authorship

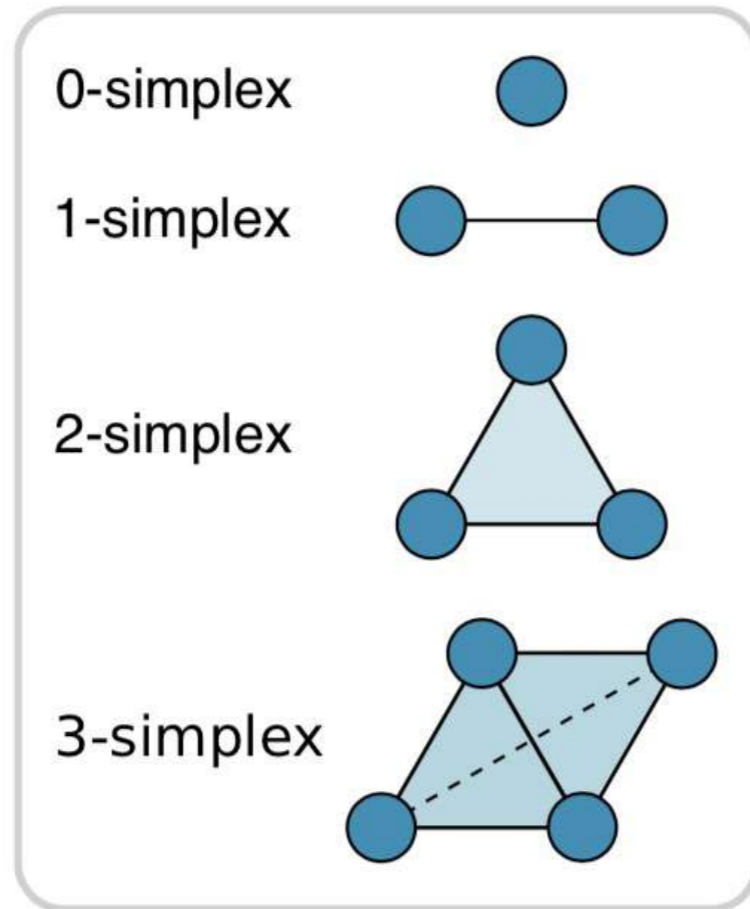


Three binary interactions / three papers

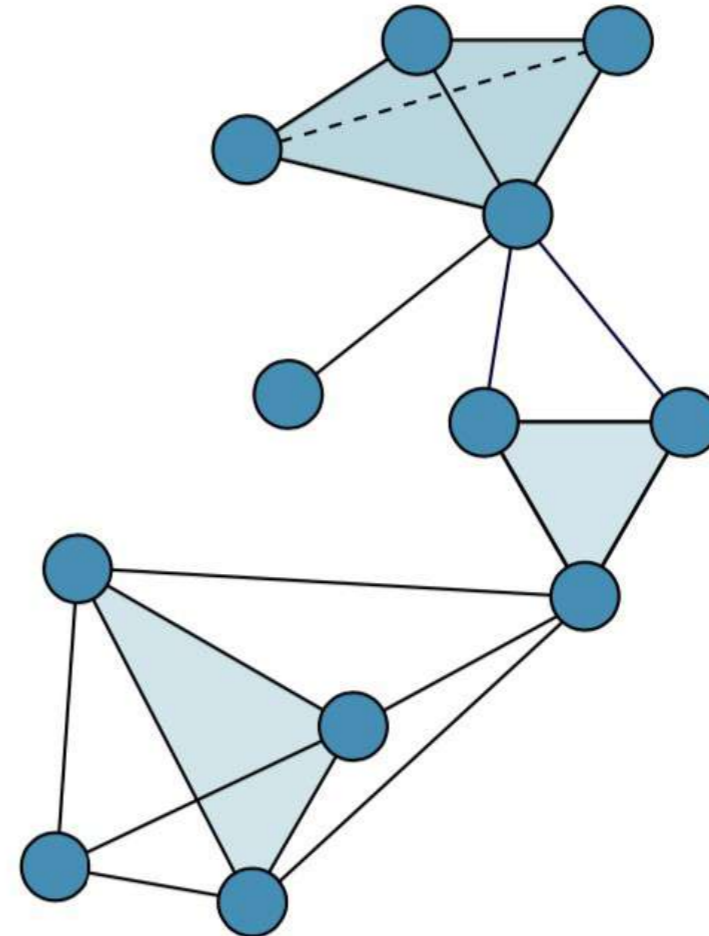
One group interaction / one paper

Going beyond networks: Hypergraphs, simplicial complexes

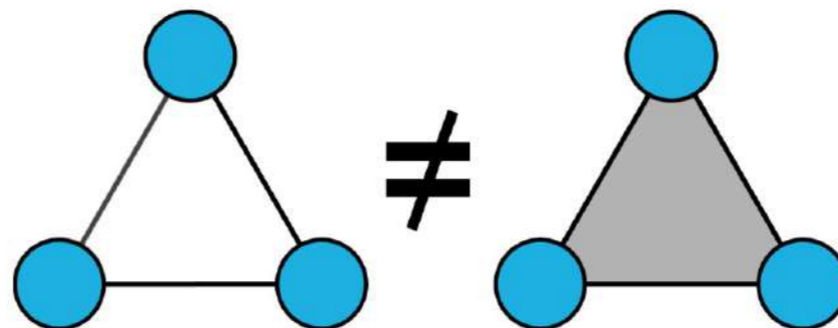
d-dimensional
group interactions



Social structure:
simplicial complex



clique simplex



Mixing simple and complex contagion: epidemic-like models on simplicial complexes

“Simplagion”






ARTICLE

<https://doi.org/10.1038/s41467-019-10431-6>

OPEN

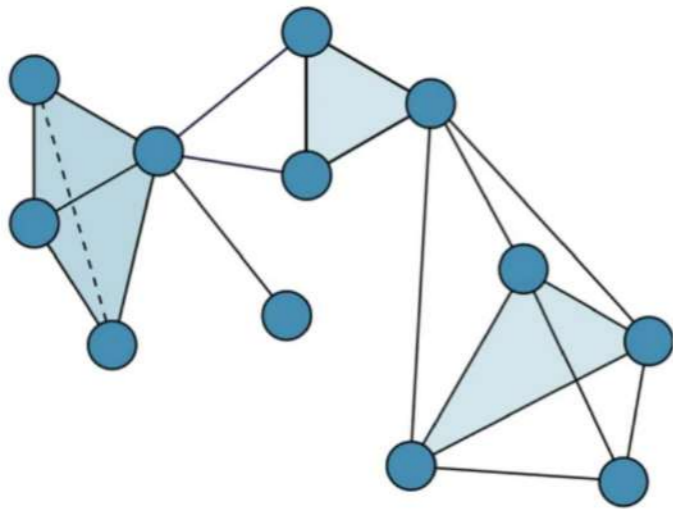
Simplicial models of social contagion

Iacopo Iacopini ^{1,2}, Giovanni Petri^{3,4}, Alain Barrat ^{3,5} & Vito Latora ^{1,2,6,7}

Nat Commun 10, 2485 (2019)

Simplicial contagion model

Social structure: (static) simplicial complex, dimension D

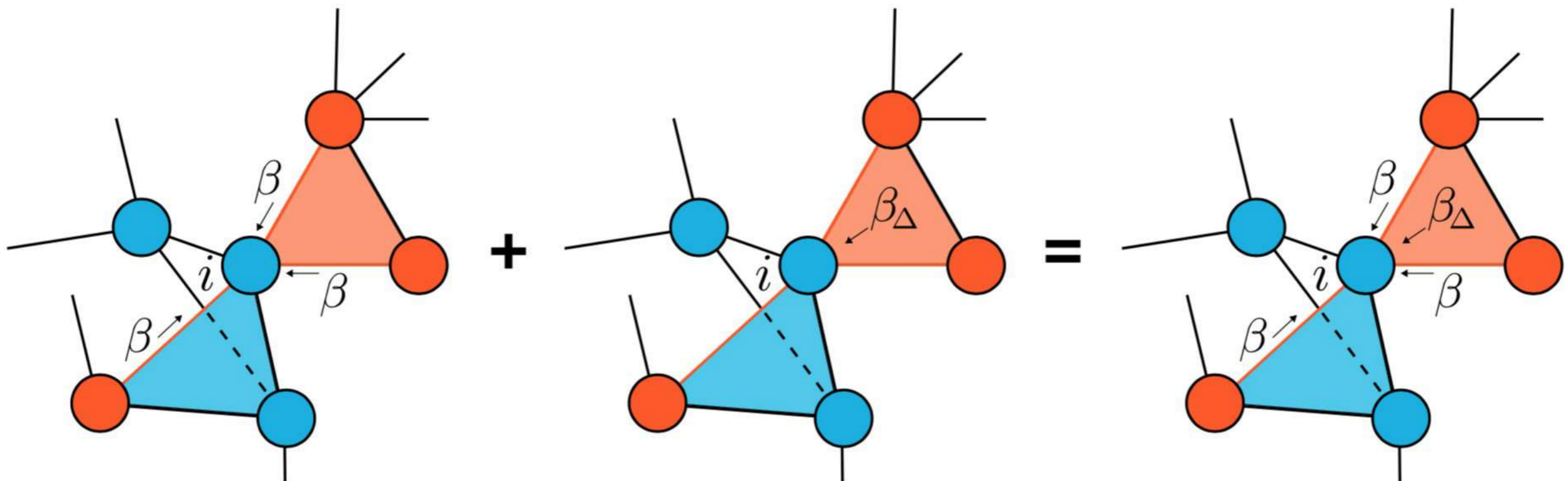


SIS - like



Contagion parameters: β , β_Δ

β_Δ proba per unit time that a S node in a simplex of dimension d becomes I if all the other nodes in the simplex are I



1-simplices (links)
Simple contagion events

2-simplices (triangles)
group effect (synergy)
Complex contagion events

Small β_Δ : continuous SIS-like transition

Large β_Δ :

- Transition becomes discontinuous
- Dependency on initial conditions

ARTICLE

<https://doi.org/10.1038/s41467-019-10431-6>

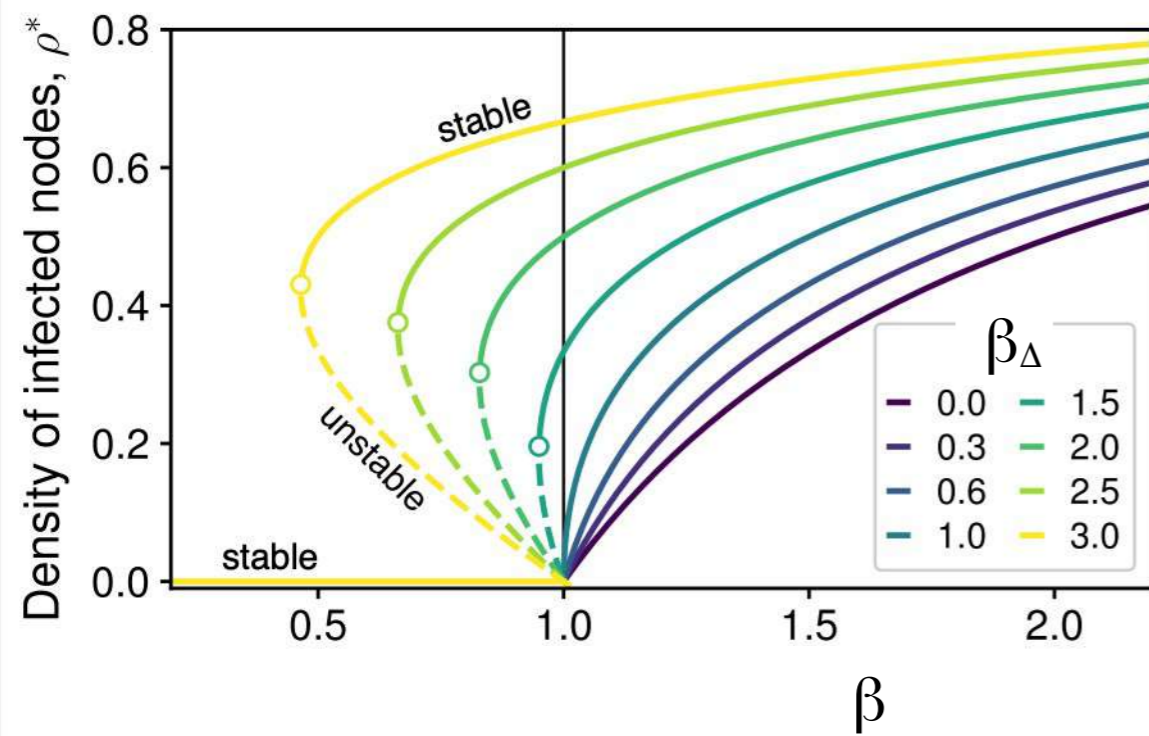
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Simplicial models of social contagion

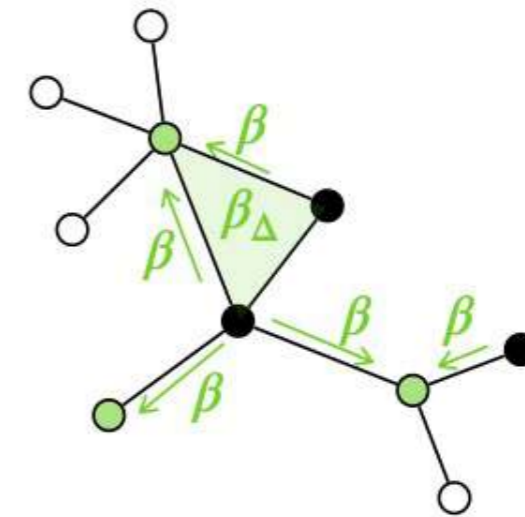
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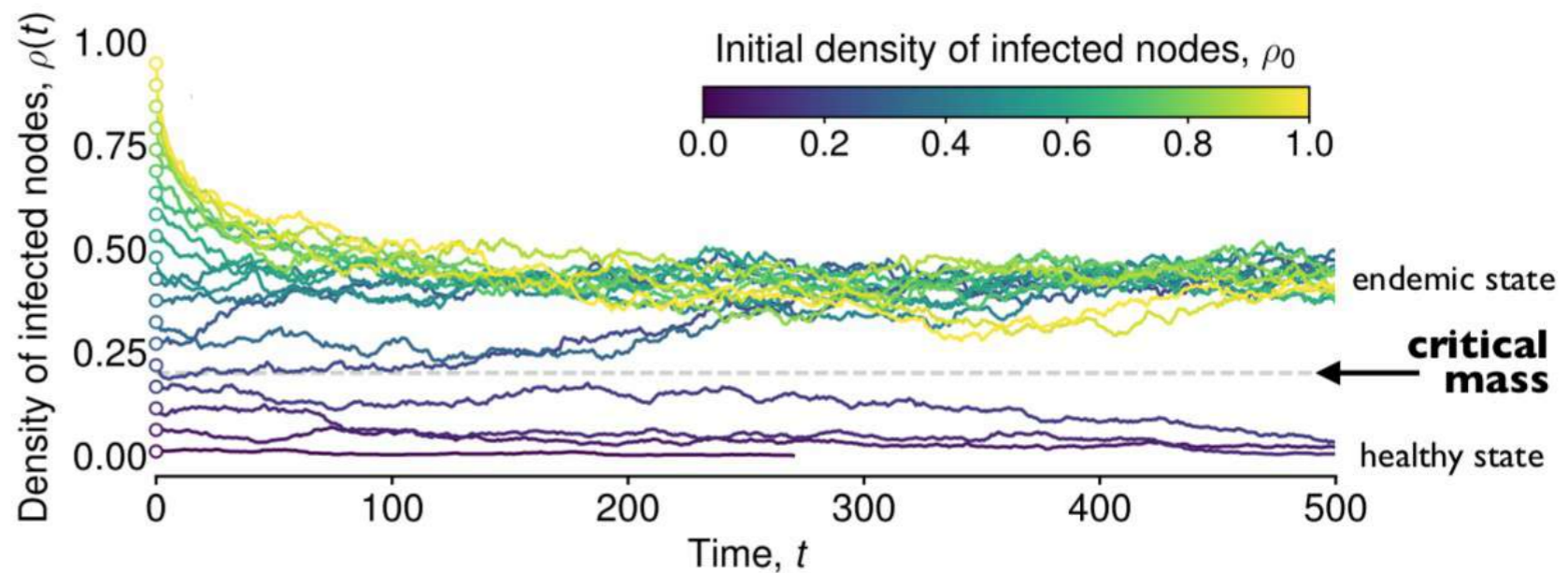
a



Simplicial



Role of initial conditions, Critical mass effect



Non-linear higher order contagion model



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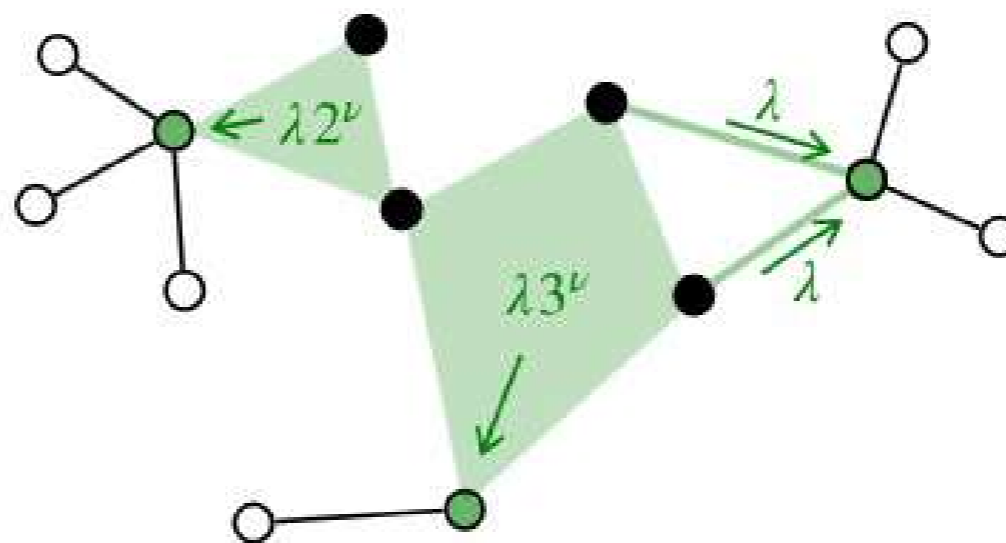
Influential groups for seeding and sustaining nonlinear contagion in heterogeneous hypergraphs

[Guillaume St-Onge](#) , [Iacopo Iacopini](#), [Vito Latora](#), [Alain Barrat](#), [Giovanni Petri](#), [Antoine Allard](#) & [Laurent Hébert-Dufresne](#) 

[Communications Physics](#) 5, Article number: 25 (2022) | [Cite this article](#)

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$$\beta(n, i) = \lambda i^\nu$$



Simple contagion
Cascading complex contagion
Higher-order complex contagion



Propagation patterns ?

More specifically

- Are the propagation patterns similar or different for different models and types of contagion processes (on a given network)? (Similarity is often implicitly assumed in theoretical works)
- From an observed propagation, can we deduce the type of contagion process (simple, cascade, higher-order)?

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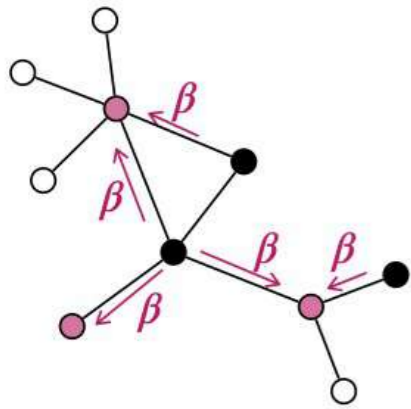
Propagation patterns

Infection patterns in simple and complex contagion processes on networks

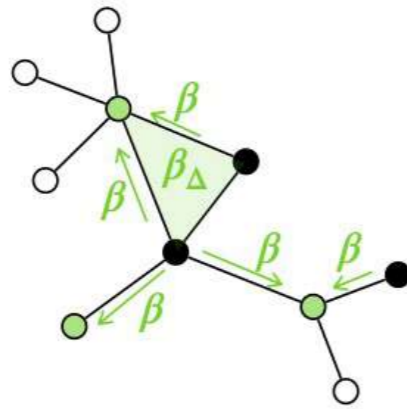
Diego Andrés Contreras , Giulia Cencetti , Alain Barrat

Version 2 Published: June 10, 2024 • <https://doi.org/10.1371/journal.pcbi.1012206>

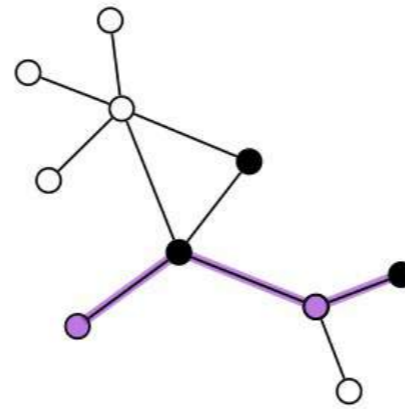
Simple



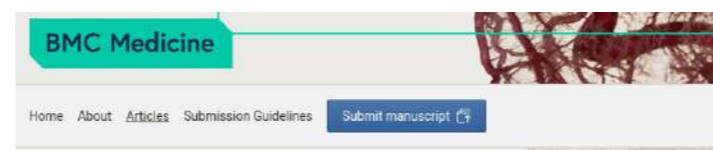
Simplicial



Threshold



Infection patterns = C_{ij} : probability that node i infects node j in a run
non-symmetric
correlated with weights of connections



Research article | [Open access](#) | Published: 21 November 2007

Predictability and epidemic pathways in global outbreaks of infectious diseases: the SARS case study

Vittoria Colizza , Alain Barrat, Marc Barthélemy & Alessandro Vespignani

BMC Medicine 5, Article number: 34 (2007) | [Cite this article](#)

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END NOTE

The infection tree of global epidemics

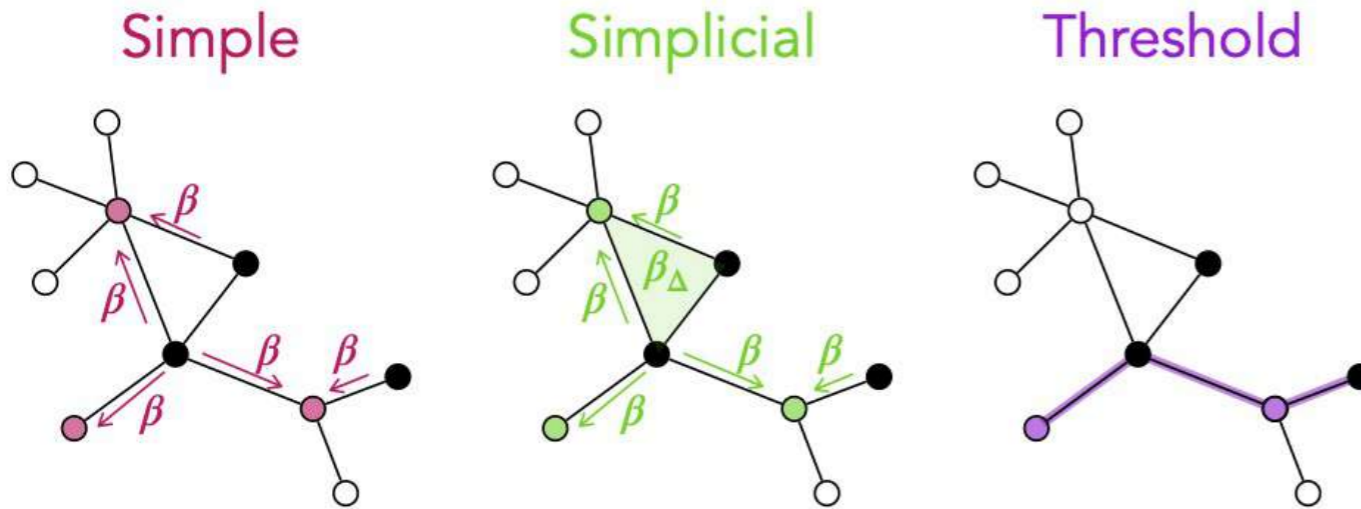
ANA PASTORE Y PIONTTI, MARCELO FERREIRA DA COSTA GOMES, NICOLE SAMAY, NICOLA PERRA and ALESSANDRO VESPIGNANI

Propagation patterns

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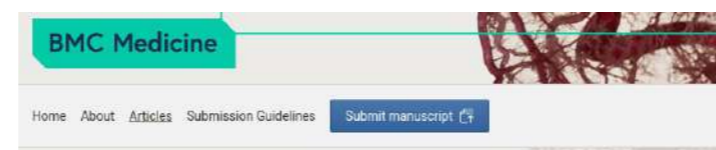
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Version 2 Published: June 10, 2024 • <https://doi.org/10.1371/journal.pcbi.1012206>



Infection patterns = C_{ij} : probability that node i infects node j in a run
non-symmetric
correlated with weights of connections

Usual question: for a **given spreading process** (often: SI, SIR) how do the infection patterns depend on a network's properties?



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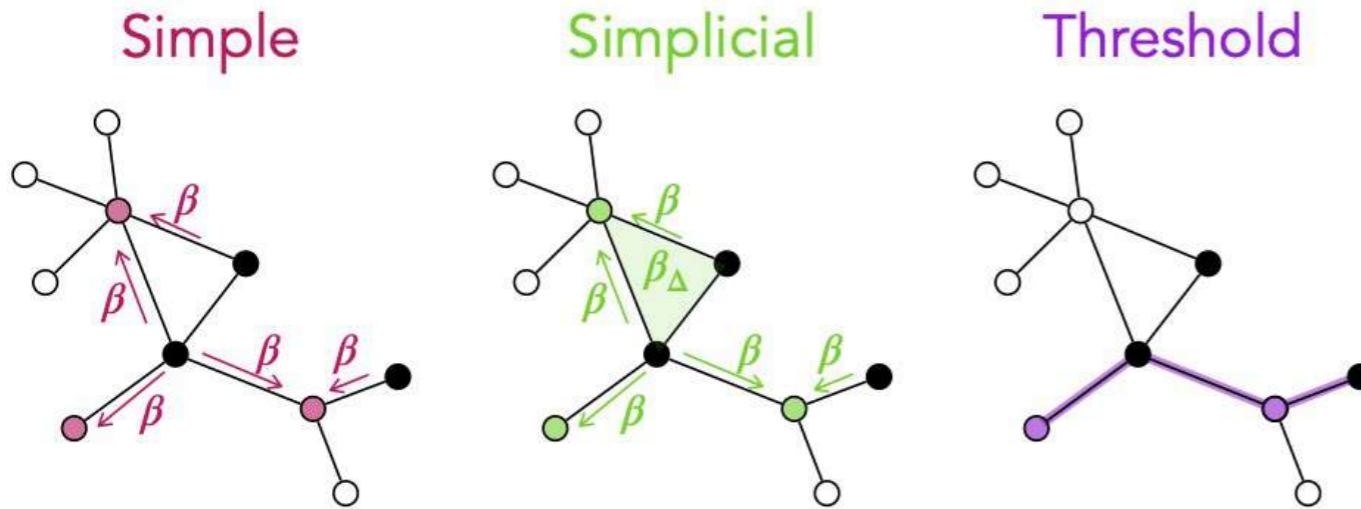
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Propagation patterns

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Diego Andrés Contreras, Giulia Cencetti, Alain Barrat

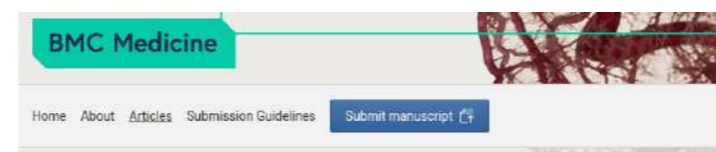
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Infection patterns = C_{ij} : probability that node i infects node j in a run
non-symmetric
correlated with weights of connections

Usual question: for a given spreading process (often: SI, SIR) how do the infection patterns depend on a network's properties?

Here: For a **given network**, how do the infection patterns depend on the parameters of a spreading model?
the details of the simple contagion model?
the nature of the contagion model (simple/simplicial/threshold)?



Research article | [Open access](#) | Published: 21 November 2007

Predictability and epidemic pathways in global outbreaks of infectious diseases: the SARS case study

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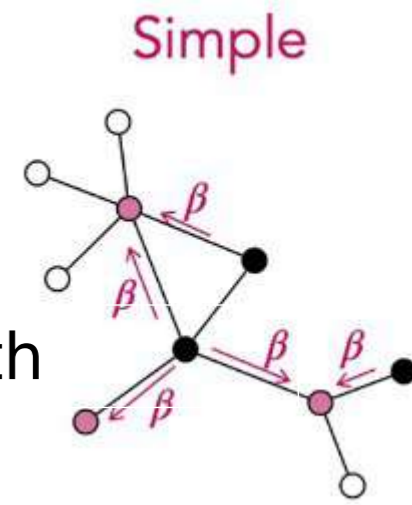
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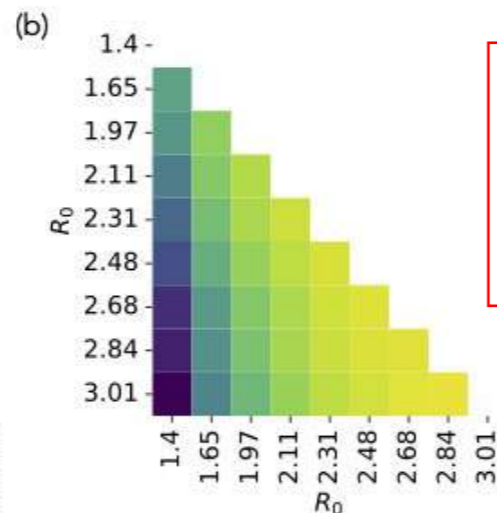
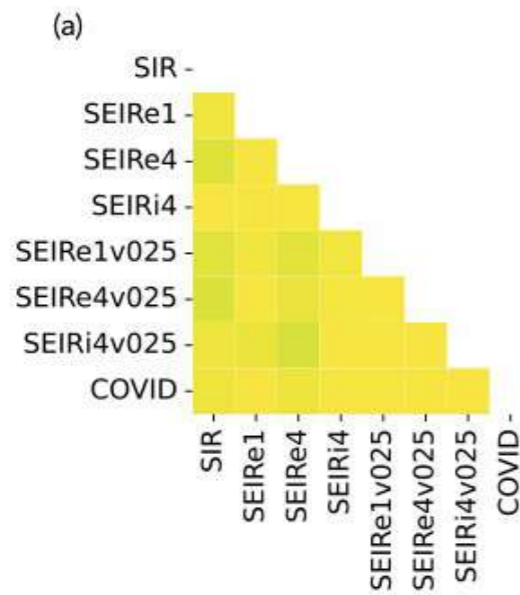
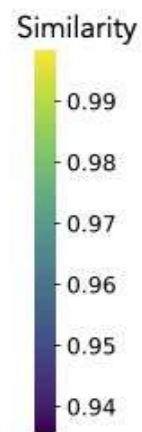
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Propagation patterns

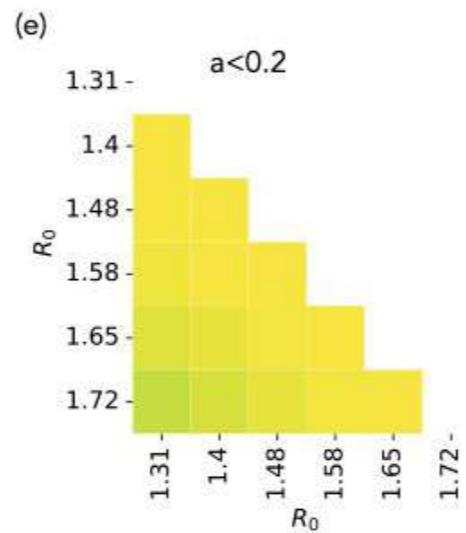
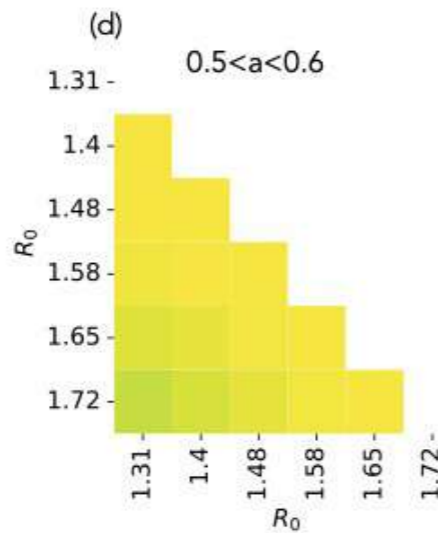
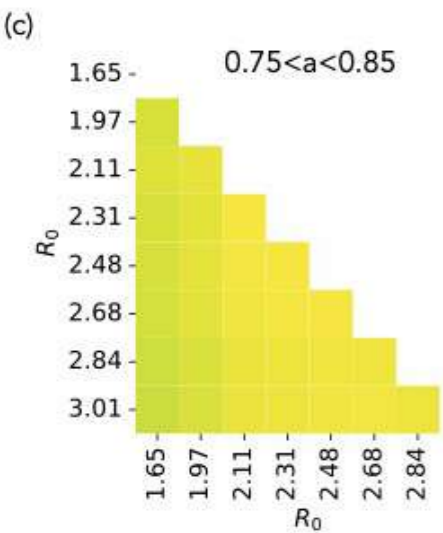


Similarity between infection patterns of **simple contagion** models with

- different compartments
- Markovian vs non-Markovian dynamics
- different timescales



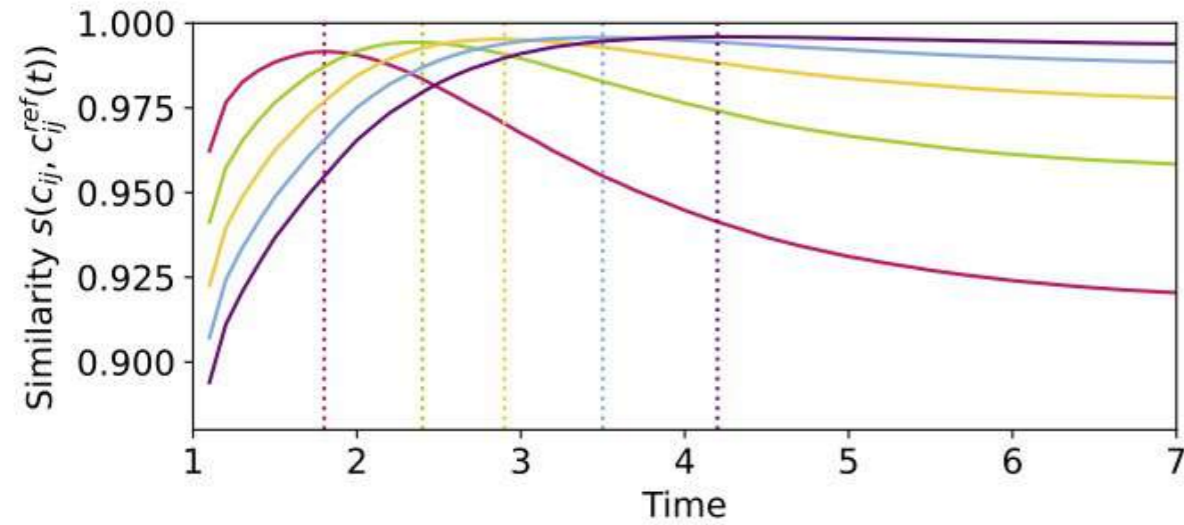
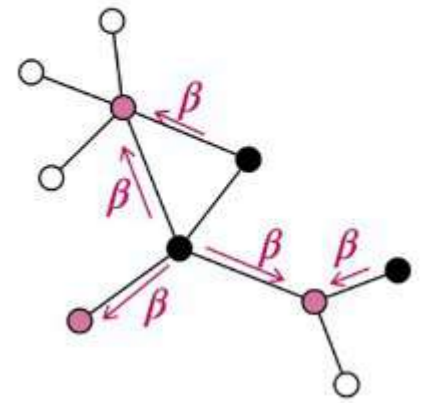
Very high similarity for different models
Slight dependence on R_0
Fixed if attack rate is given



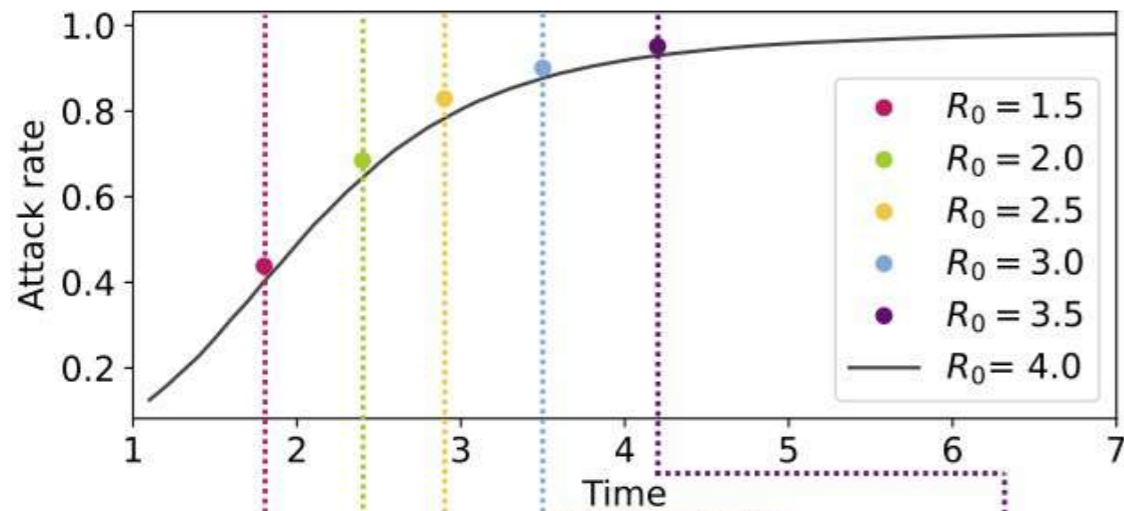
Simulations on an empirical network of contacts in a school population
(SocioPatterns data; similar results with simulations on other data sets)

Propagation patterns

Simple



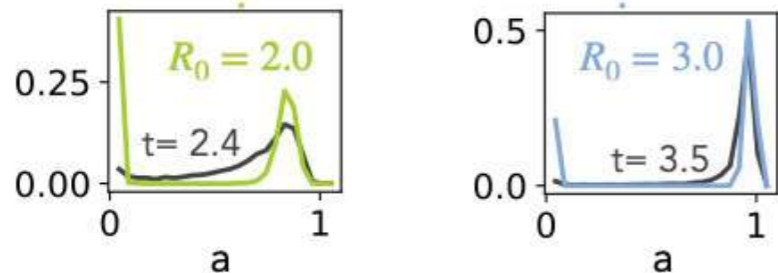
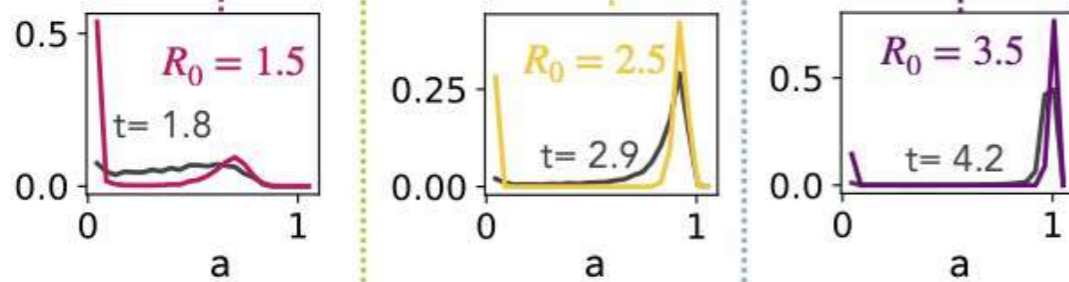
Simulation with a reference $R_0=4$, run until $t \rightarrow C_{ij}(t)$ (here: SIR model)



For t such that
 $\text{attack rate}(R_0=4, t) = \text{final attack rate}(R_0')$,

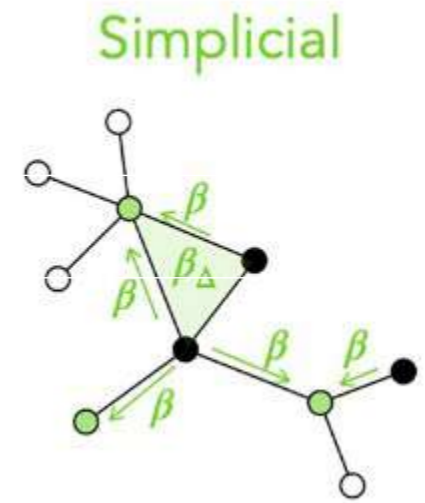
$C_{ij}(t)$ very close to $C_{ij}(R_0')$

→ one set of simulations at large R_0 yields propagation patterns for lower values of R_0



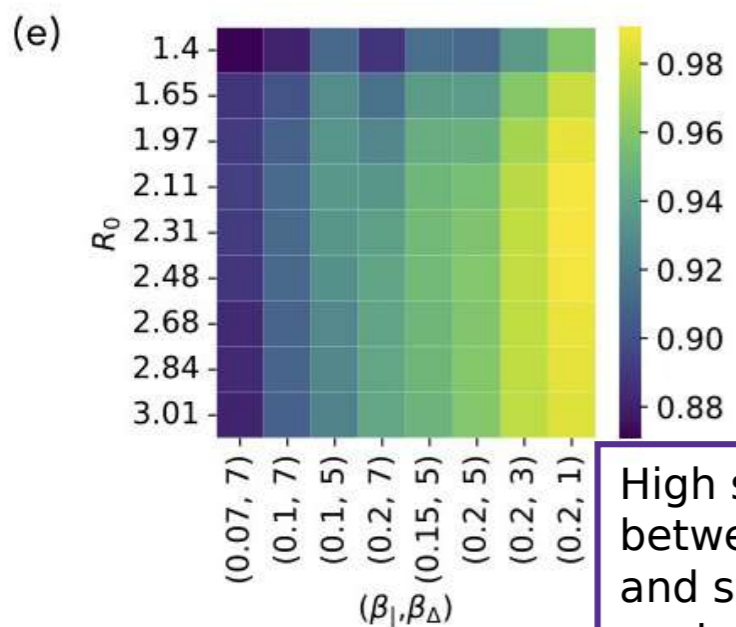
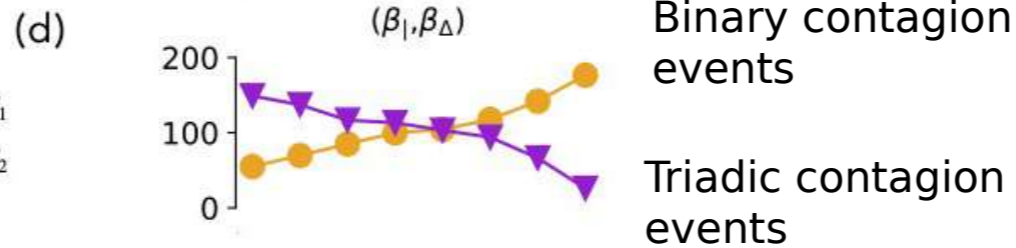
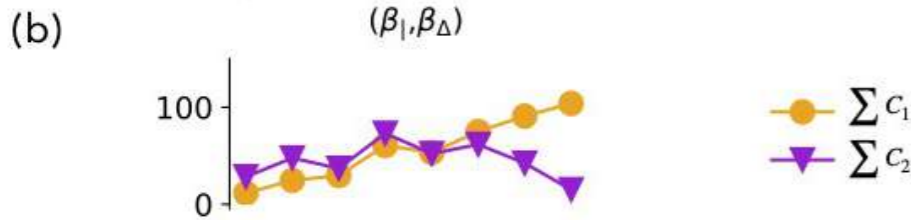
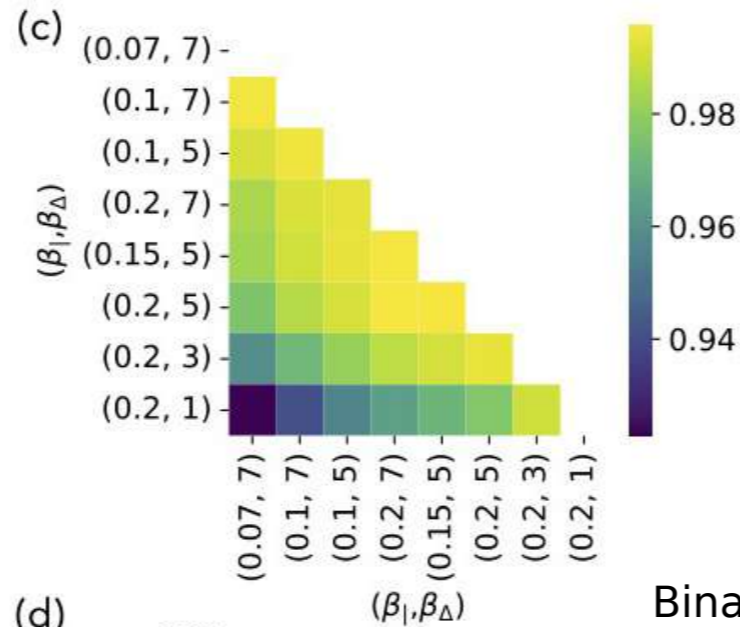
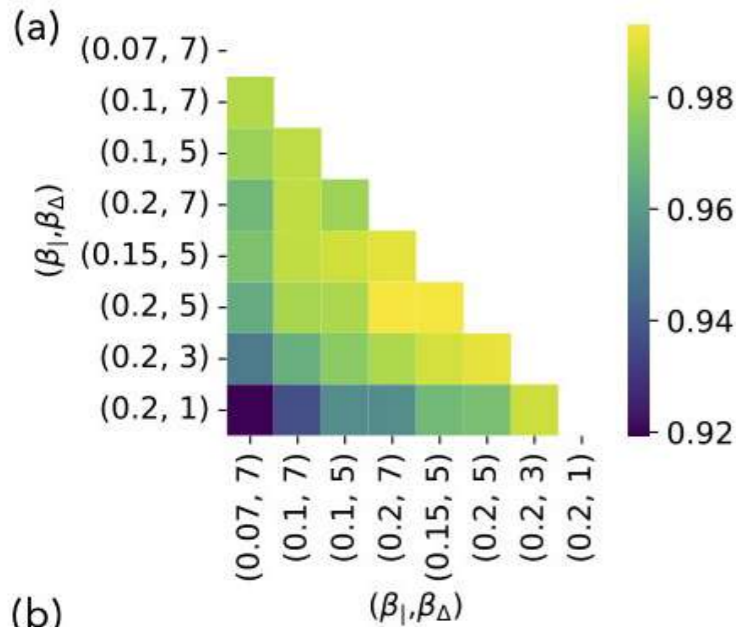
Propagation patterns

Similarity between infection patterns of **complex contagion** models with different parameters



NB: in triadic contagion events $(j,k) \rightarrow i$, both C_{ji} and C_{ki} incremented by $1/2$

$0.6 < a < 0.7$

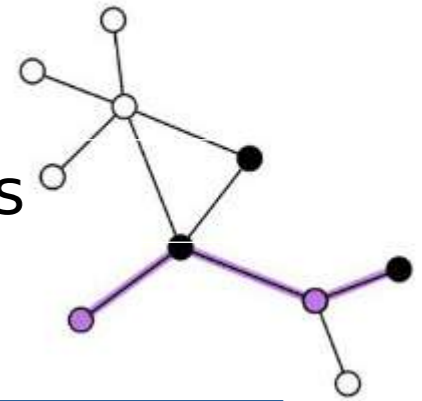


High similarity between simple and simplicial contagion infection patterns

- Similarity remains high
- Dependence on the ratio between contagion events of 2 types (even at fixed attack rate)
- Large similarity with simple: due to correlations between weights of links and of triangles in empirical data

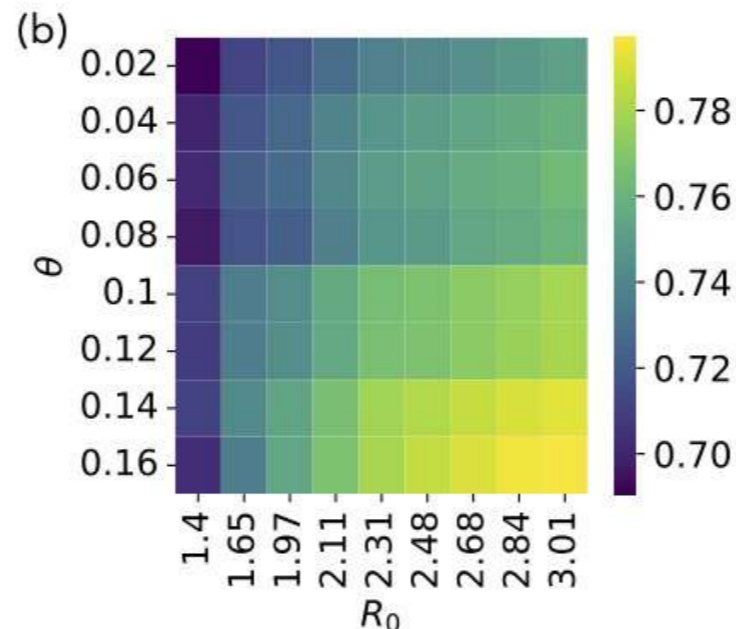
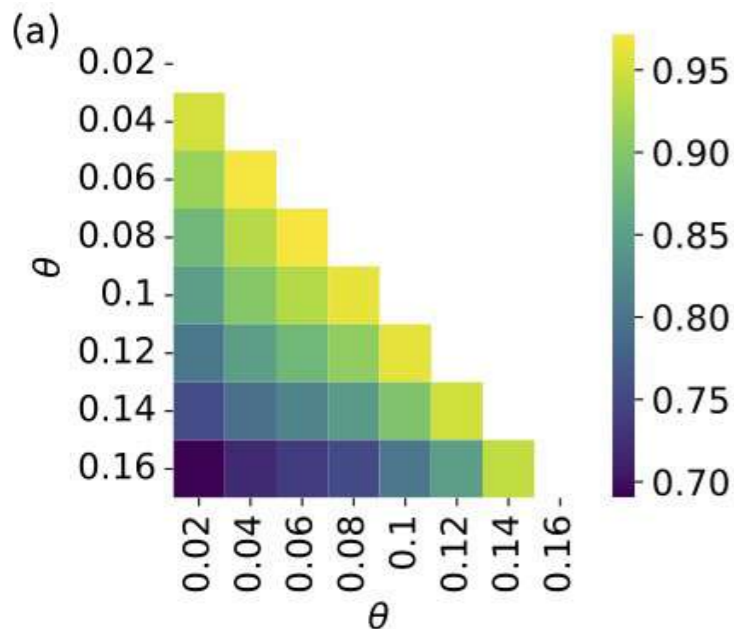
Propagation patterns

Threshold



Similarity between infection patterns of **threshold contagion** models with different parameters

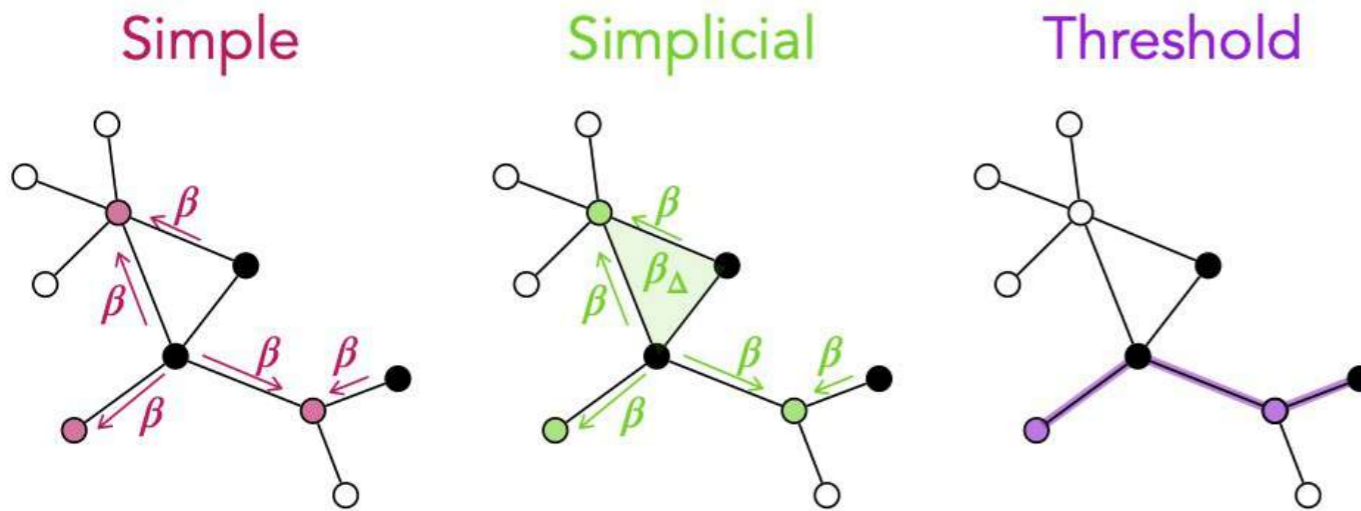
Need to generalize infection patterns definition:
 i contaminated from combined influence of $j=i_1, i_2, \dots, i_k$
 \rightarrow each C_{ji} incremented by the relative contribution of j



Similarity between simple and threshold contagion infection patterns

- Similarities take lower values: stronger parameter dependence
- Larger $\theta \rightarrow$ more similar to simple contagion
- Still rather large values (all infection patterns correlated with link weights)

Propagation patterns



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RESEARCH ARTICLE

Infection patterns in simple and complex contagion processes on networks

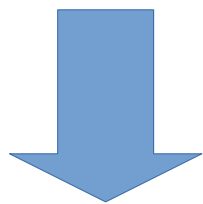
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In summary

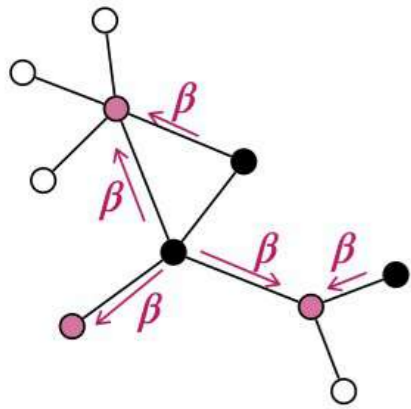
- Very strong robustness of infection patterns in simple contagion models with different dynamics and parameters
- If one defines **spreader/receiver indices**, very strong robustness of **ranking of nodes** across models and parameters



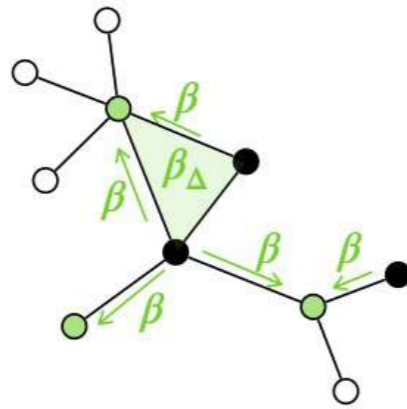
- Possibility to use **simplistic models** to gain insight into propagation patterns of more complex processes, even if parameters unknown
- Possibility to use **purely topological measures** to predict **ranking of nodes** w.r.t. spreading power or sentinel role **for arbitrary diseases**

Propagation patterns

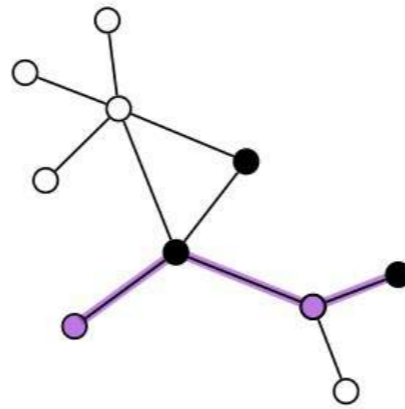
Simple



Simplicial



Threshold



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RESEARCH ARTICLE

Infection patterns in simple and complex contagion processes on networks

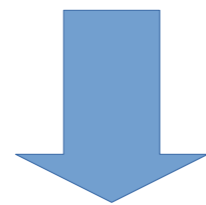
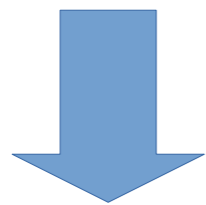
Diego Andrés Contreras , Giulia Cencetti  , Alain Barrat

Version 2

Published: June 10, 2024 • <https://doi.org/10.1371/journal.pcbi.1012206>

In summary

- Patterns less robust for complex contagion processes
 - Depend on ratio between simple vs complex contagion events
 - More sensitive to threshold value in threshold processes
- Similarities remain rather high in all cases



- Information on (social) complex contagion patterns and ranking of influential nodes can still be obtained from simple contagion schematic models
- Can we exploit the remaining differences between patterns to identify the mechanism of an observed propagation process?

- Are the propagation patterns similar or different for different models and types of contagion processes (on a given network)?
- From an observed propagation, can we deduce the type of contagion process (simple, cascade, higher-order)?

Distinguishing processes

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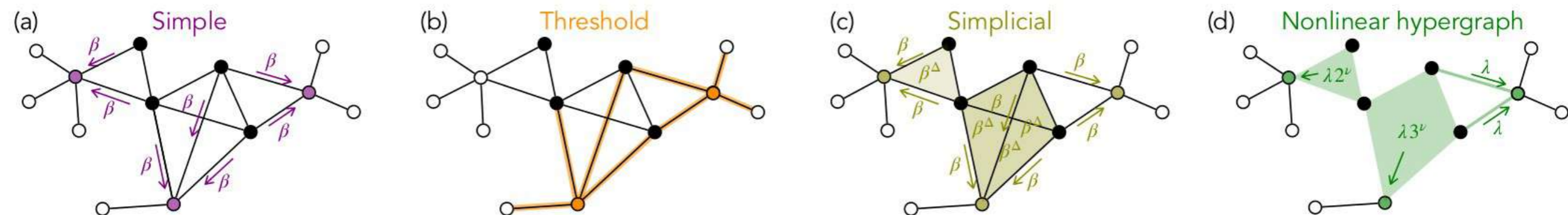
Distinguishing Simple and Complex Contagion Processes on Networks

Giulia Cencetti¹, Diego Andrés Contreras², Marco Mancastrappa², and Alain Barrat²

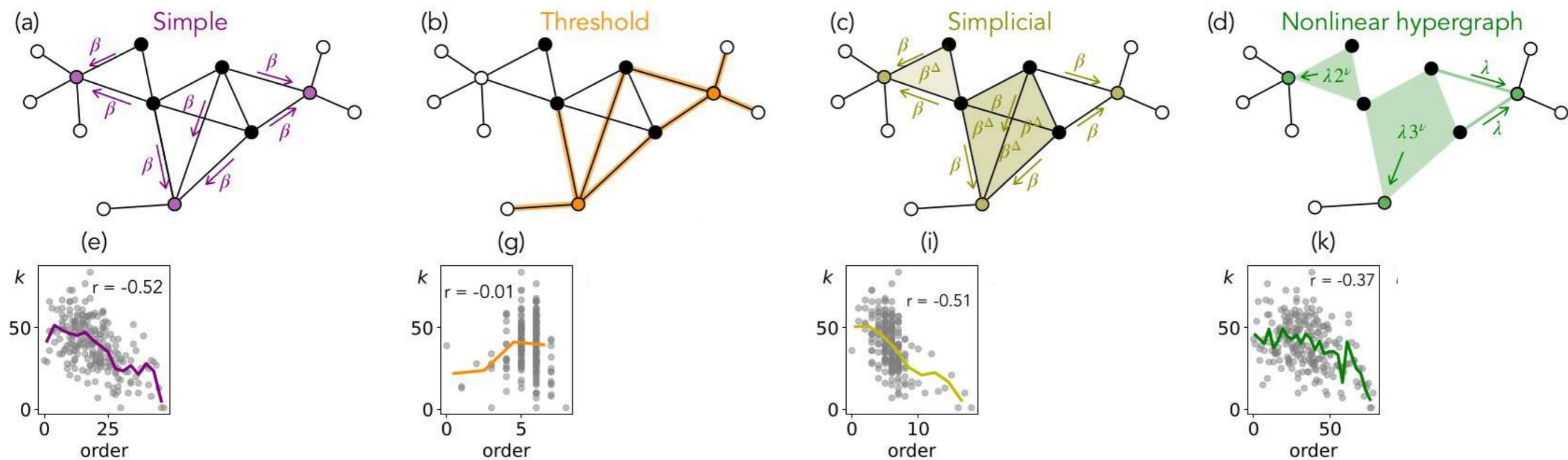
Can we exploit the remaining differences between propagation patterns to identify the mechanism of an observed propagation process?

- Previous results: averaged over realizations of a process
- What about a **single** observed realization of a process?
“**Observed**”: **order** of contagion of nodes + known (hyper)network structure
(no information on contagion events, uses only **local** info)

By observing a single spread, can we identify from which of these 4 processes it was obtained?



Distinguishing processes

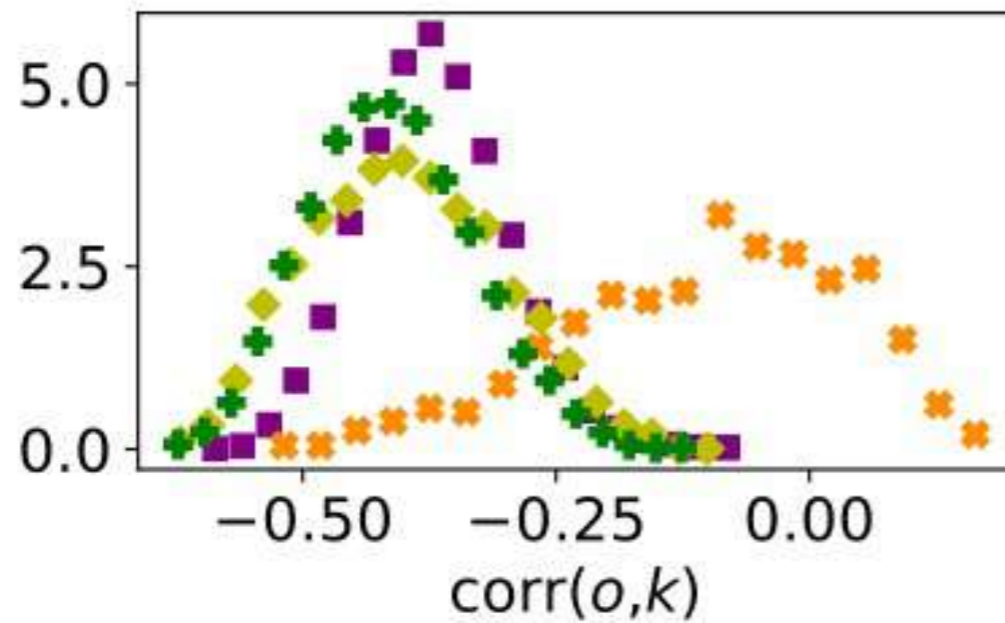


Simple + simplicial + non-lin higher order models: cascading process from hubs to low degree nodes (Barthélemy et al., PRL 2004)

→ **negative correlation** between order of contamination o and degree k

Threshold model: no correlation

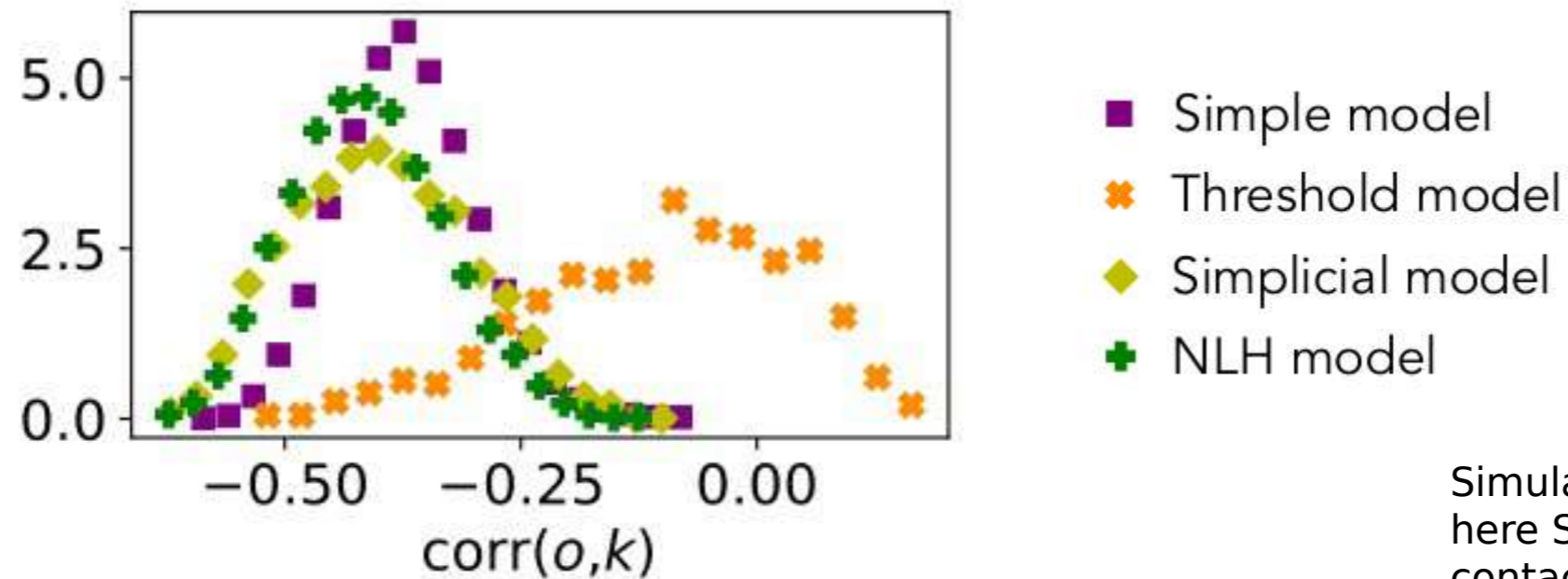
Using $C_1 = \text{corr}(o,k)$ to classify threshold model vs simple/simplicial/Non-linear HO



- Simple model
- * Threshold model
- ◆ Simplicial model
- + NLH model

Simulations on empirical networks, here SocioPatterns data set on contacts in a workplace

Using $C_1 = \text{corr}(o,k)$ to classify threshold model vs simple/simplicial/Non-linear HO



Simulations on empirical networks, here SocioPatterns data set on contacts in a workplace

Procedure: observe run, compute C_1

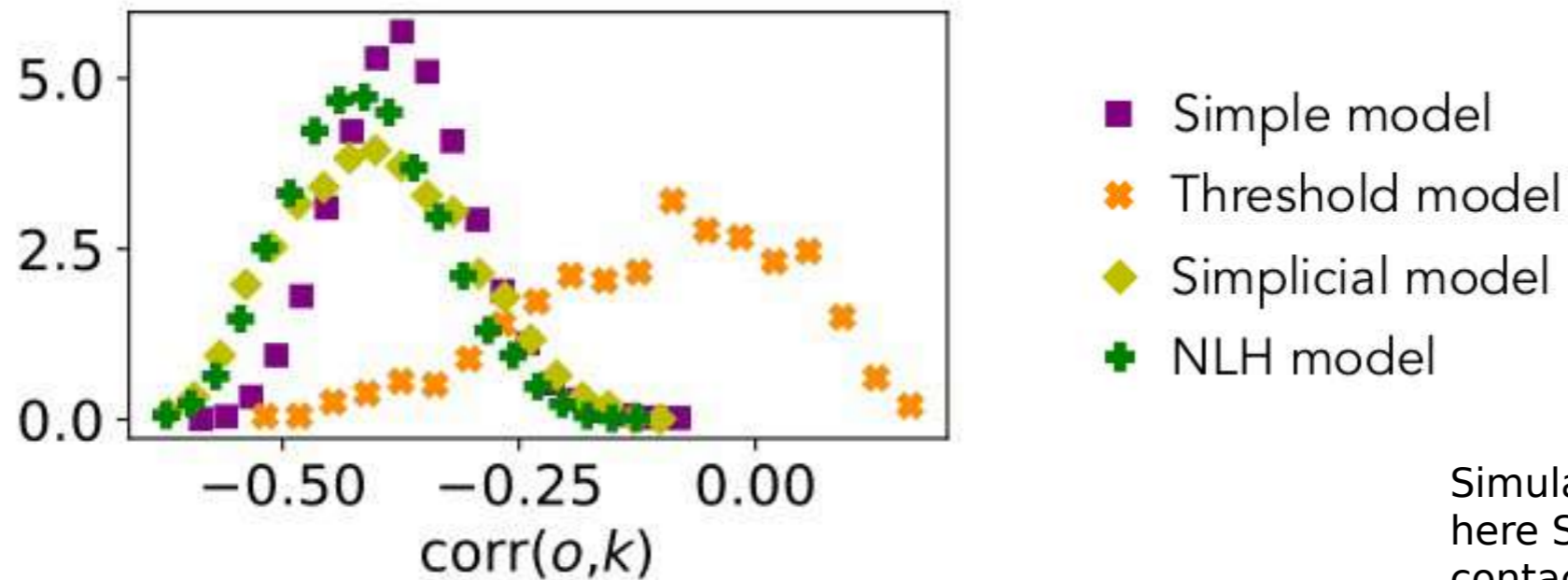
if $C_1 > c$: predict run to be from threshold model

(if the prediction is correct: true positive TP; else false positive FP)

if $C_1 < c$: predict run to be from another model

(if the prediction is correct: true negative TN; else false negative FN)

Using $C_1 = \text{corr}(o,k)$ to classify threshold model vs simple/simplicial/Non-linear HO

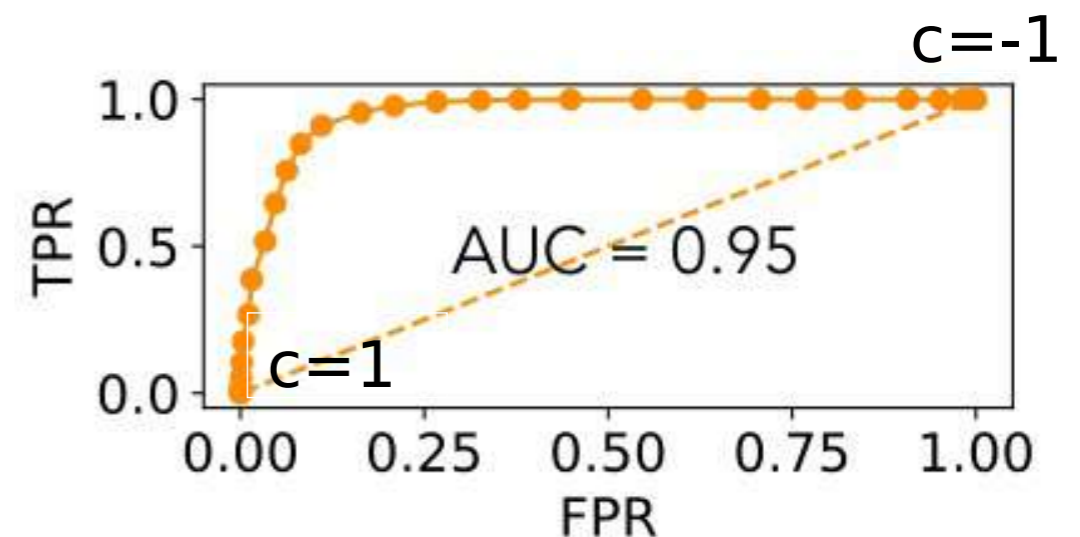


Simulations on empirical networks, here SocioPatterns data set on contacts in a workplace

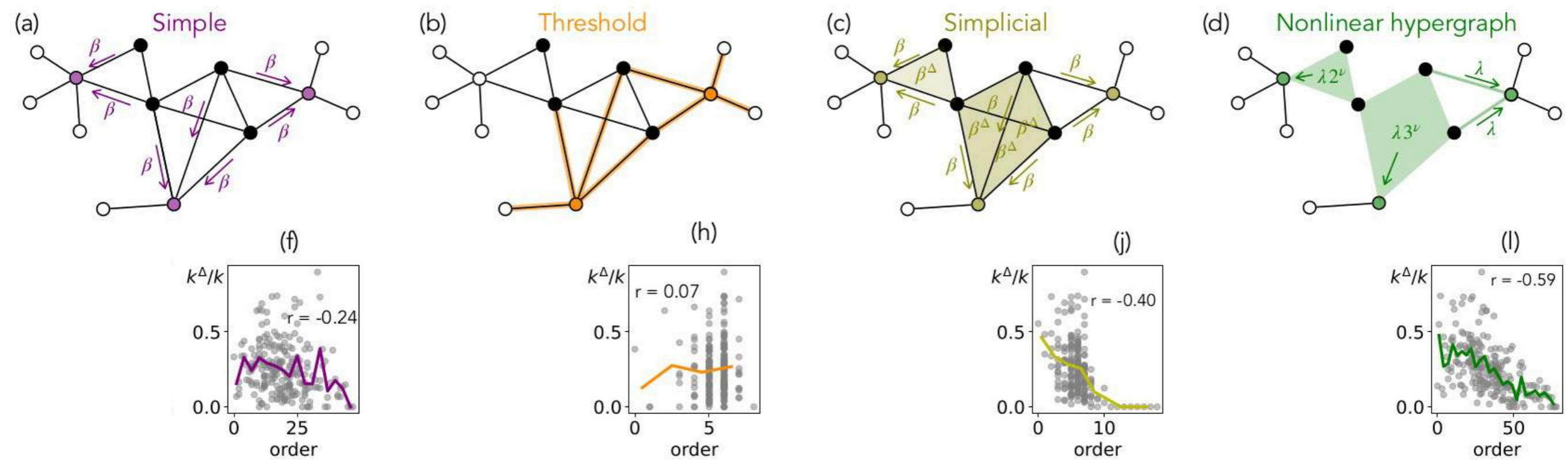
Procedure: observe run, compute C_1
 if $C_1 > c$: predict run to be from threshold model
 (if the prediction is correct: true positive TP; else false positive FP)
 if $C_1 < c$: predict run to be from another model
 (if the prediction is correct: true negative TN; else false negative FN)

To evaluate performance, build ROC curve parametrized by c :
 true positive ratio vs false positive ratio $\text{TPR} = \text{TP}/(\text{TP} + \text{FN})$, $\text{FPR} = \text{FP}/(\text{FP} + \text{TN})$

| | | Predicted condition | |
|------------------|-----------------------------|--|--|
| | | Predicted Positive (PP) | Predicted Negative (PN) |
| Actual condition | Positive (P) ^[a] | True positive (TP), hit ^[b] | False negative (FN), miss, underestimation |
| | Negative (N) ^[d] | False positive (FP), false alarm, overestimation | True negative (TN), correct rejection ^[e] |



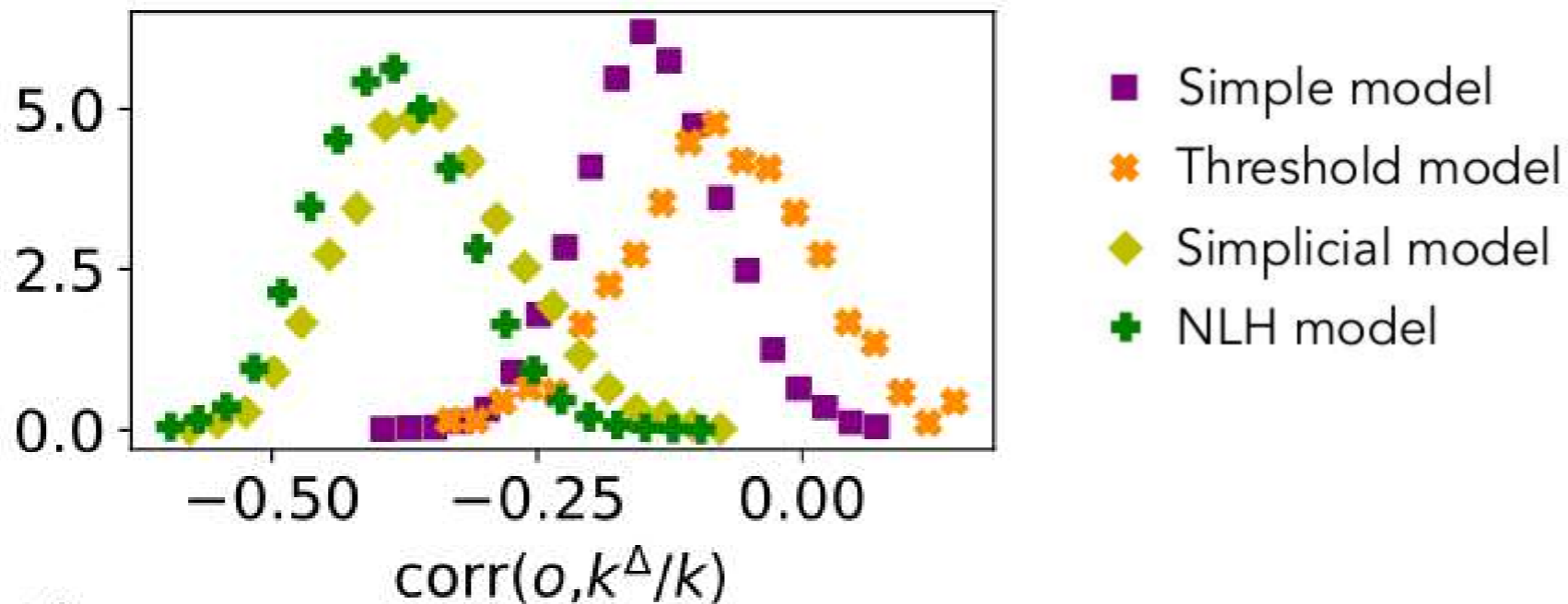
Distinguishing processes



Simplicial + non-lin higher order: nodes belonging to many hyperedges are reached first
→ **negative correlation** between order of contamination and ratio k_Δ/k

Simple + threshold: no correlation

Using $C_2 = \text{corr}(o, k_\Delta/k)$ to classify simplicial or NLH model vs simple/threshold



Procedure: observe run, compute C_2

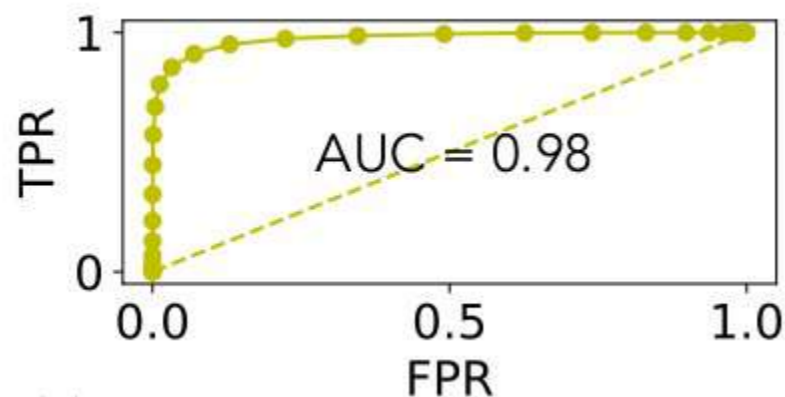
if $C_2 > c$: predict run to be from simple or threshold model

(if the prediction is correct: true positive TP; else false positive FP)

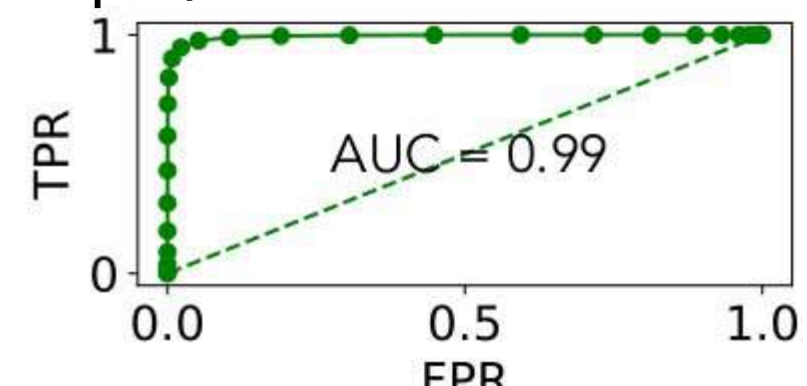
if $C_2 < c$: predict run to be from simplicial or non-linear higher order model

(if the prediction is correct: true negative TN; else false negative FN)

Simplicial vs simple/threshold



Non-linear higher order vs simple/threshold



Building a classifier for the four types of processes

$$C_1 = \text{corr}(o, k)$$

$$C_2 = \text{corr}(o, k_{\Delta}/k)$$

$$C_3 = \text{corr}(o, k_{\Delta})$$

$$C_4 = \text{corr}(o, k_l)$$

Procedure:

perform many runs of each process,
measure correlations,
train a classifier (here: random forest),
evaluate on test runs not used in the training

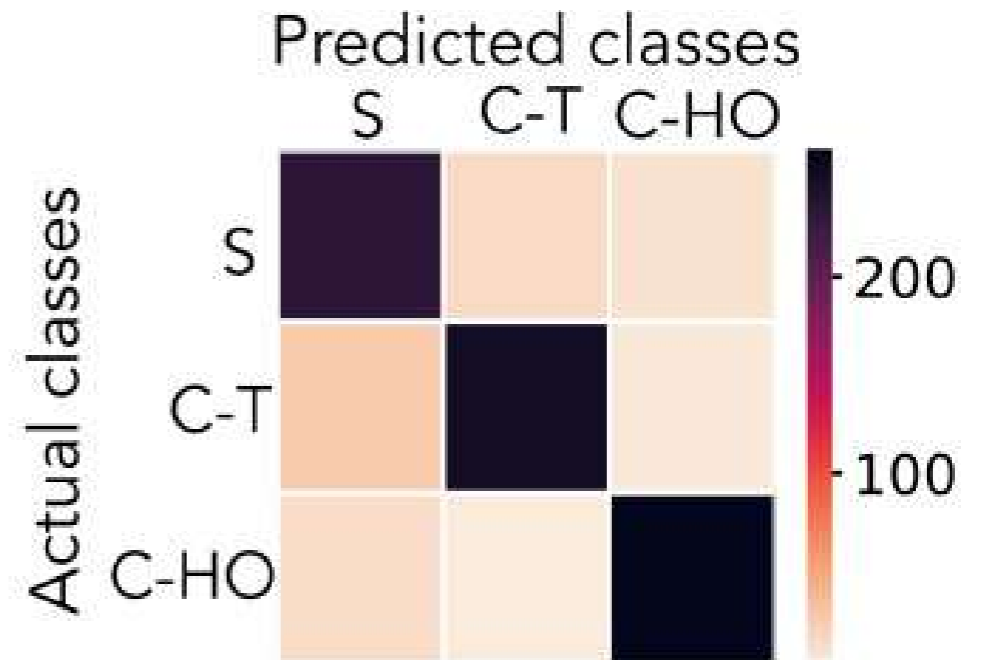
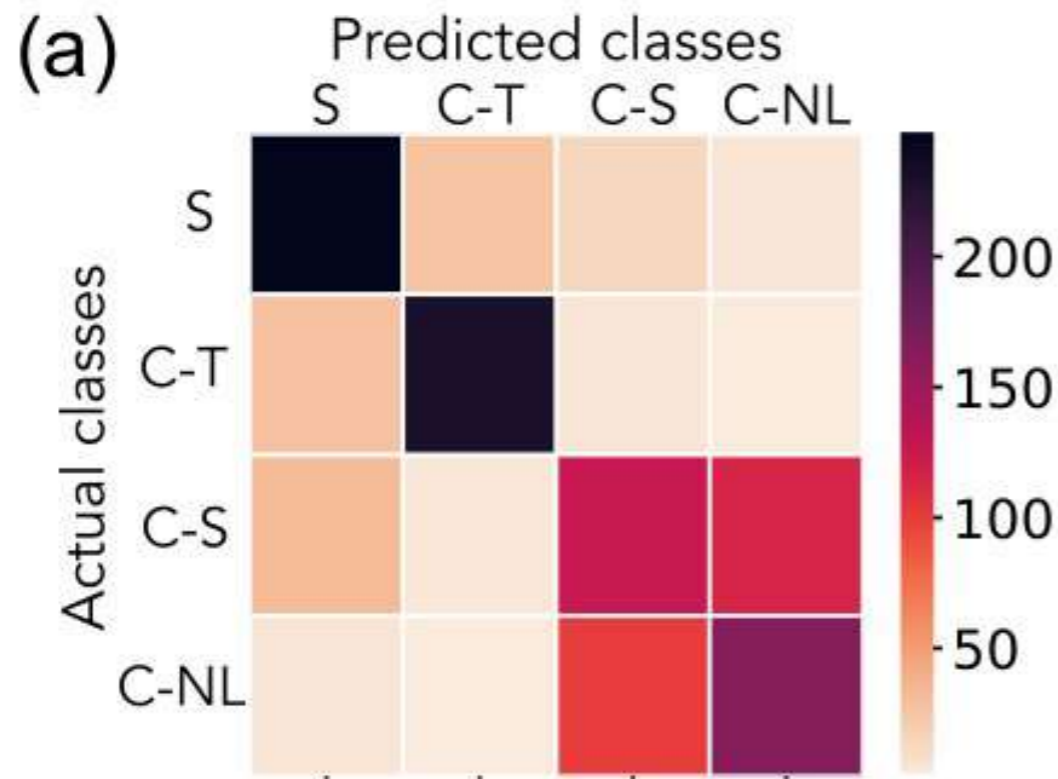
Building a classifier for the four types of processes

$$\begin{aligned} C_1 &= \text{corr}(o, k) \\ C_2 &= \text{corr}(o, k_{\Delta}/k) \\ C_3 &= \text{corr}(o, k_{\Delta}) \\ C_4 &= \text{corr}(o, k_l) \end{aligned}$$

Procedure:
perform many runs of each process,
measure correlations,
train a classifier (here: random forest),
evaluate on test runs not used in the training

Performance:

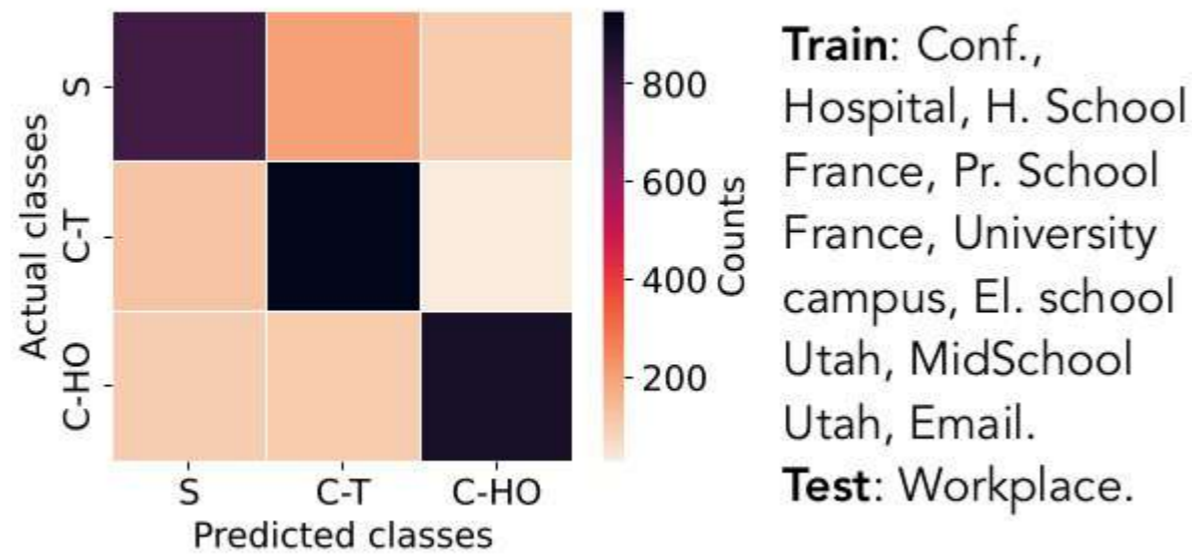
confusion matrix: gives the number of times a run of a model x is classified as from model y
(*diagonal matrix=perfect performance*)



Simulations on empirical networks
(here SocioPatterns data, contacts in a workplace)

What if network unknown?

Train classifier with simulations performed on several known networks, test with simulations on the “unknown” network



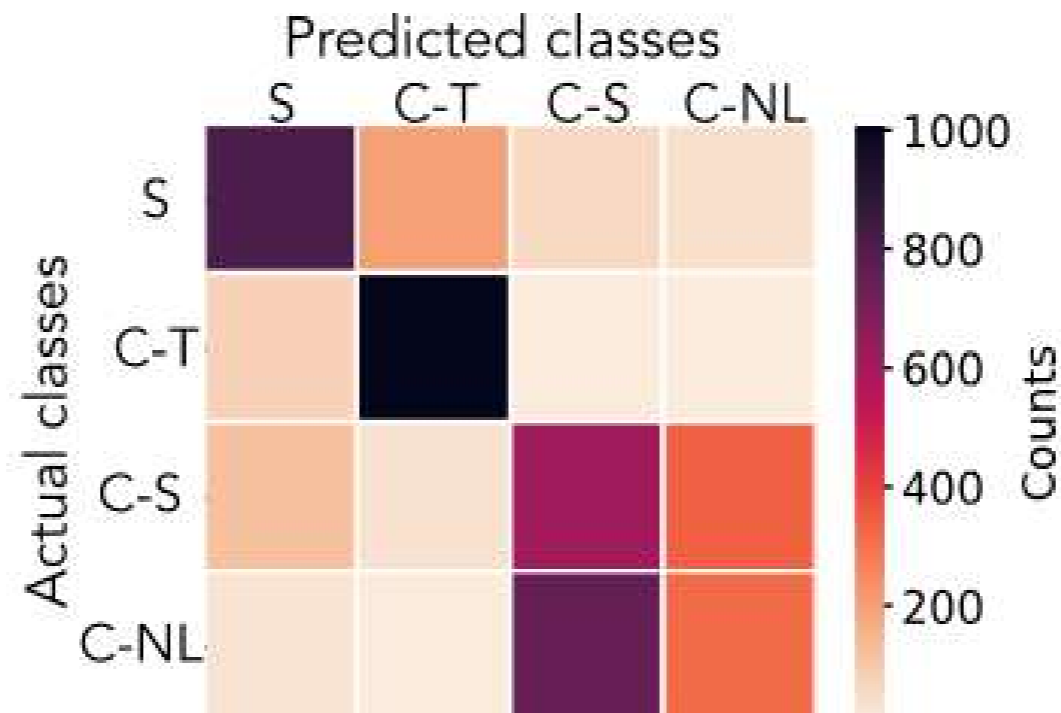
Limitation: strong dependence on individual network properties, hence performance remains limited in many cases

| Test dataset | Workplace | Conf. | Hospital | H. School France | Pr. School France | University campus | El. School Utah | MidSchool Utah | Email |
|--------------|-----------|-------|----------|------------------|-------------------|-------------------|-----------------|----------------|-------|
| Accuracy | 0.81 | 0.80 | 0.63 | 0.63 | 0.52 | 0.56 | 0.63 | 0.70 | 0.51 |

What if network unknown?

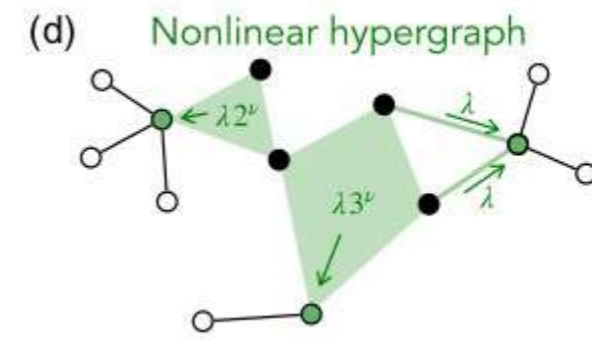
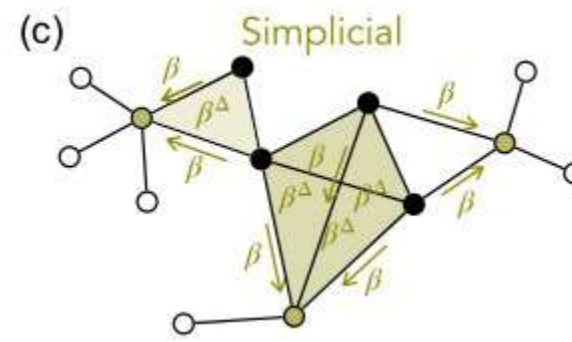
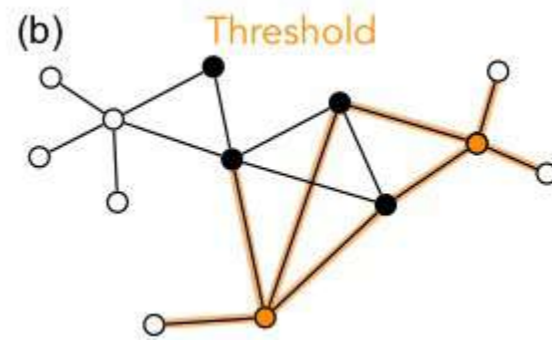
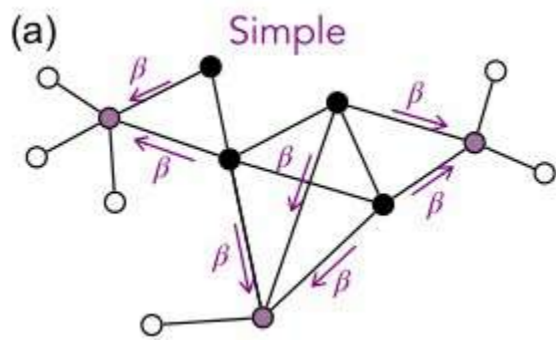
Train classifier with simulations performed on **surrogate (hyper)networks**, which preserve (enough?) statistics of the real one (distributions of total degree, of k_{Δ} , group structure...)

Train: 10 surrogate nets, test: Workplace



Limitation:

best performing surrogate depends on network's properties (modularity),
Need better algorithms to build surrogate hypernetworks



PHYSICAL REVIEW LETTERS 130, 247401 (2023)

Distinguishing Simple and Complex Contagion Processes on Networks

Giulia Cencetti¹, Diego Andrés Contreras², Marco Mancastroppa², and Alain Barrat²

In summary, it is possible to build a classifier that

- Uses only local information
- Does not use information on node's neighbours status
- Does not use information on which edges/hyperedges supported contagion events
- When applied on single instances of an observed process, **can distinguish between a spread driven by simple contagion, a threshold process or a process with higher-order mechanisms**
- Can be trained using processes simulated on surrogate hypernetworks

• What are the most important structures for the propagation?

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Hyper-cores promote localization and efficient seeding in higher-order processes

[Marco Mancastroppa](#), [Iacopo Iacopini](#), [Giovanni Petri](#) & [Alain Barrat](#) 

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• From an observed propagation, can we deduce the type of contagion process (simple, cascade, higher-order)?

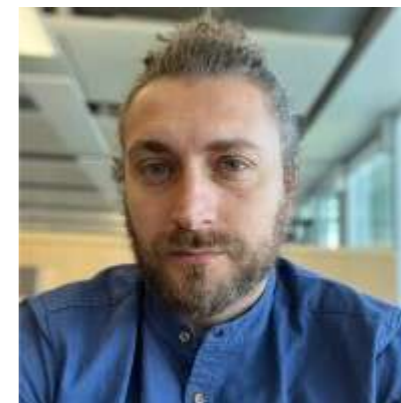
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Iacopo Iacopini



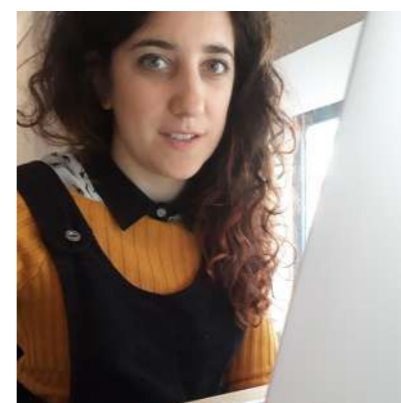
Giovanni Petri



Vito Latora



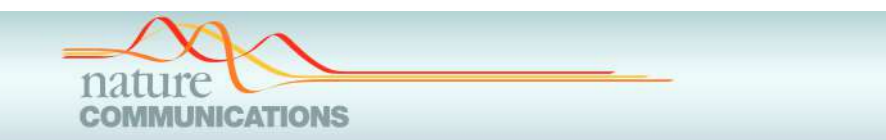
Diego Contreras



Giulia Cencetti



Marco Mancastropa



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Simplicial models of social contagion

Iacopo Iacopini^{1,2}, Giovanni Petri^{3,4}, Alain Barrat^{3,5} & Vito Latora^{1,2,6,7}

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