



The Alan Turing Institute

Simplicial Models of Social Contagion

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MoN18 Mathematics of Networks, April 2018



Contagion on Networks





Spreading of infectious diseases





Artwork by Mi Jin Lee

Spreading of infectious diseases



M. Barthélemy et al. J. Theor. Biol. (2005)









Social Contagion

Diffusion of information, behaviours, rumours, fads, beliefs, norms...

- Peer pressure
- Social influence
- Complex individual response to repeated exposures





Complex Contagion

Social contagion



Multiple sources of

activation are required for a transmission

D. Centola & M. Macy, Americ. J. Sociol. (2007); N. O. Todas & K. Lerman, Sci. Rep. (2014); D. Guilbeault et al., Springer (2018)

Complex Contagion

Evidence





PLOS ONE

RESEARCH ARTICLE

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

Bjarke Mønsted¹°, Piotr Sapieżyński¹°, Emilio Ferrara^{2,3}°, Sune Lehmann¹° *





⁵Laboratoire de l'Informatique du Parallélisme, INRIA-UMR 5668, IXXI, ENS de Lvon, 69364 Lvon, France





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



Pairwise interactions

INITAL PLOTER BORT

What about group interactions?



Network representation of the social structure

Simplicial complex



A simplicial complex \mathscr{K} on a given set of vertices \mathscr{V} , with $|\mathscr{V}| = N$, is a collection of simples with the extra requirement that if a simplex $\sigma \in \mathscr{K}$, then all the sub-simplices $\nu \subset \sigma$ built from the subset of σ are also contained in \mathscr{K} .



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Notice that



















Not a new idea



Renewed interest among the complex systems community

European Journal of Physics

PAPER

Simplicial complexes and complex systems

Vsevolod Salnikov¹, Daniele Cassese^{1,2} and Renaud Lambiotte³ Published 14 November 2018 • © 2018 European Physical Society <u>European Journal of Physics, Volume 40, Number 1</u> Focus on Complexity



NETWORK NEURO SCIENCE

FOCUS

The importance of the whole: Topological data analysis for the network neuroscientist

Ann E. Sizemore¹, Jennifer E. Phillips-Cremins¹, Robert Ghrist², and Danielle S. Bassett^{1,3,4,5}

¹Department of Bioengineering, School of Engineering and Applied Sciences, University of Pennsylvania, Philadelphia, USA ²Department of Mathematics, College of Arts and Sciences, University of Pennsylvania, Philadelphia, USA ³Department of Physics & Astronomy, College of Arts and Sciences, University of Pennsylvania, Philadelphia, USA ⁴Department of Electrical & Systems Engineering, School of Engineering and Applied Sciences, University of Pennsylvania, Philadelphia, USA

⁵Department of Neurology, Perelman School of Medicine, University of Pennsylvania, Philadelphia, USA

Describing the architecture of complex networks

OPEN OACCESS Freely available online

PLOS ONE

Topological Strata of Weighted Complex Networks

Giovanni Petri^{1*}, Martina Scolamiero^{1,2}, Irene Donato^{1,3}, Francesco Vaccarino^{1,3}

1 ISI Foundation, Torino, Italy, 2 Dipartimento di Ingegneria Gestionale e della Produzione, Politecnico di Torino, Torino, Italy, 3 Dipartimento di Scienze Matematiche, Politecnico di Torino, Torino, Italy





Classification of weighted networks through mesoscale homological features

Ann Sizemore, Chad Giusti, Danielle S. Bassett 🐱

Journal of Complex Networks, Volume 5, Issue 2, June 2017, Pages 245–273,



Describing the architecture of functional and structural brain networks





J Comput Neurosci (2018) 44:115–145 https://doi.org/10.1007/s10827-017-0672-6

Cliques and cavities in the human connectome

Ann E. Sizemore^{1,2} · Chad Giusti¹ · Ari Kahn^{1,3} · Jean M. Vettel^{1,3,4} · Richard F. Betzel¹ · Danielle S. Bassett^{1,5} $^{(5)}$



Describing the architecture of semantic and co-authorship networks







cl-th nucl-ex hep-ph hep-ex gr-qr	0.02	0.11	0.08	0.03	0.04	0.08	0.00
ucl-ex hep-ph hep-ex gr-qr							
hep-ph hep-ex gr-qo	0.00	0.04	0.02	0.06	0.05	0.01	0.03
rep-ex gr-qr	0.02	0.01	0.02	0.01	0.08	0.00	0.06
gr-qe	0.04	0.00	0.00	0.00	0.07	0.00	0.05
~	0.01	0.00	0.00	0.01	0.09	0.00	0.07







The Simplicial Contagion Model

The Model (D=2)



The Model (D=2)



The Model (D=2)



Susceptible

The Model (D=2)



The Model (D=2)



dynamical state variable

 $x_i(t) \in \{0,1\}$

The Model (D=2)



dynamical state variable

$$x_i(t) \in \{0,1\}$$

The Model (D=2)



dynamical state variable

 $x_i(t) \in \{0,1\}$

control parameters

$$\lambda = \beta \langle \mathbf{k} \rangle / \mu$$
$$\lambda_{\Delta} = \beta_{\Delta} \langle \mathbf{k}_{\Delta} \rangle / \mu$$

The Model (D=2)



dynamical state variable

 $x_i(t) \in \{0,1\}$

control parameters

$$\begin{split} \lambda &= \beta \langle k \rangle / \mu \\ \lambda_{\Delta} &= \beta_{\Delta} \langle k_{\Delta} \rangle / \mu \end{split}$$

$$k_{w} : \text{generalised (simplicial) degree} \\ \langle k_{1} \rangle &= \langle k \rangle \\ \langle k_{2} \rangle &= \langle k_{\Delta} \rangle \end{split}$$

The Model (D=2)



dynamical state variable

 $x_i(t) \in \{0,1\}$

control parameters

 $\lambda = \beta \langle \mathbf{k} \rangle / \mu$ $\lambda_{\Delta} = \beta_{\Delta} \langle \mathbf{k}_{\Delta} \rangle / \mu$

macroscopic order parameter

$$\rho(t) = \frac{1}{N} \sum_{i} x_i(t)$$

Empirical Social Structures


The SocioPatterns collaboration



what are the statistical and dynamical properties of the networks of contact and co-presence of people in social interaction?





fine-grained **spatial** (~ m) and **temporal** (<min) resolution

Thanks to D. Paolotti



The SocioPatterns collaboration



Thanks to D. Paolotti



The SocioPatterns collaboration



- •Two power levels => 2 detection ranges
- Face to face situation
- Statistical detection => 20s time resolution
- Small,
- Scalable





The SocioPatterns collaboration



Primary school



Hospital

High-resolution proximity data



0

0

time

High-resolution proximity data



0

0

High-resolution proximity data



0

0

M. Génois and A. Barrat, EPJ Data Science (2018)





SocioPatterns M. Génois and A. Barrat, EPJ Data Science (2018)

High-resolution proximity data

To reduce finite size effects



Duplication of the lists of sizes of the maximal simplifies and simplicial degrees of nodes

High-resolution proximity data

To reduce finite size effects



Duplication of the lists of sizes of the maximal simplifies and simplicial degrees of nodes

PHYSICAL REVIEW E 96, 032312 (2017) **Construction of and efficient sampling from the simplicial configuration model** Jean-Gabriel Young,^{1,*} Giovanni Petri,² Francesco Vaccarino,^{2,3} and Alice Patania^{2,3,†} ¹Département de Physique, de Génie Physique, et d'Optique, Université Laval, GIV 0A6 Québec (Québec), Canada ²ISI Foundation, 10126 Torino, Italy ³Dipartimento di Scienze Matematiche, Politecnico di Torino, 10129 Torino, Italy (Received 29 May 2017; published 22 September 2017) Simplicial complexes are now a popular alternative to networks when it comes to describing the structure of complex systems, primarily because they encode multinode interactions explicitly. With this new description onomes the need for principled null models that allow for easy comparison with empirical data. We propose a natural candidate, the *simplicial configuration model*. The core of our contribution is an efficient and uniform Markov chain Monte Carlo sampler for this model. We demonstrate its usefulness in a short case study by investigating the topology of three real systems and their randomized counterparts (using their Betti numbers). For two out of three systems, the model allows us to reject the hypothesis that there is no organization beyond the local scale.



Simplicial Configuration Model

High-resolution proximity data

To reduce finite size effects



Duplication of the lists of sizes of the maximal simplifies and simplicial degrees of nodes

PHYSICAL REVIEW E 96, 032312 (2017) Construction of and efficient sampling from the simplicial configuration model Jean-Gabriel Young, ^{1,*} Giovanni Petri, ² Francesco Vaccarino, ^{2,3} and Alice Patania^{2,3,†} ¹Département de Physique, de Génie Physique, et d'Optique, Université Laval, GIV 0A6 Québec (Québec), Canada ²ISI Foundation, 10126 Torino, Italy (Received 29 May 2017; published 22 September 2017) Simplicial complexes are now a popular alternative to networks when it comes to describing the structure of complex systems, primarily because they encode multinode interactions explicitly. With this new description comes the need for principled null models that allow for easy comparison with empirical data. We propose a natural candidate, the simplicial configuration model. The core of our contribution is an efficient and uniform

Markov chain Monte Carlo sampler for this model. We demonstrate its usefulness in a short case study by investigating the topology of three real systems and their randomized counterparts (using their Betti numbers). For two out of three systems, the model allows us to reject the hypothesis that there is no organization beyond the local scale.



Simplicial Configuration Model

Processed Simplicial Complex

Same statistical properties of the input complex but of significantly larger size









Empirical simplicial complexes

Generalised degree distributions





Random Model

ER-like Random Simplicial Complexes

- Set of N vertices (0-simplices)
- Set of probabilities $\{p_1, \ldots, p_k, \ldots, p_D\}, p_k \in [0, 1]$

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Case D=2

 (N, p_1, p_2)

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$$(N, p_1, p_2) \longrightarrow \langle k_{\Delta} \rangle \approx (N-1)p_1 + 2\langle k_{\Delta} \rangle (1-p_1)$$

 $\langle k_{\Delta} \rangle = \frac{(N-1)(N-2)p_{\Delta}}{2}$

ER-like Random Simplicial Complexes

- Set of N vertices (0-simplices)
- Set of probabilities $\{p_1, ..., p_k, ..., p_D\}, p_k \in [0, 1]$

Case D=2

 $(N, p_1, p_2) \longrightarrow p_1 = \frac{\langle k \rangle - 2 \langle k_\Delta \rangle}{(N-1) - 2 \langle k_\Delta \rangle}$ $p_\Delta = \frac{2 \langle k_\Delta \rangle}{(N-1)(N-2)} \longrightarrow (N, \langle k \rangle, \langle k_\Delta \rangle)$

Generalised degree distribution











Mean Field Approach

Mean Field approach

Homogeneous mixing hypothesis

- All individuals are the same and behave equally
- Same number of contacts: network of contacts has very small degree fluctuations
- Timescale of infection faster than demographics (closed population)



Mean Field approach

Temporal evolution of the density of infected nodes $\rho(t)$:

D=2

 $d_t \rho(t)$

Mean Field approach

Temporal evolution of the density of infected nodes $\rho(t)$:

D=2 loss of infectiousness

$$d_t \rho(t) = -\mu \rho(t)$$
Temporal evolution of the density of infected nodes $\rho(t)$:

D=2 loss of infectiousness

$$d_t \rho(t) = -\mu \rho(t) + \beta \langle k \rangle \rho(t) \left[1 - \rho(t) \right]$$

new infections from 1-simplices



Temporal evolution of the density of infected nodes $\rho(t)$:

D=2 loss of infectiousness

$$d_t \rho(t) = -\mu \rho(t) + \beta \langle k \rangle \rho(t) \left[1 - \rho(t) \right] + \beta_\Delta \langle k_\Delta \rangle \rho^2(t) \left[1 - \rho(t) \right]$$

new infections from 1-simplices

new infections from 2-simplices





Temporal evolution of the density of infected nodes $\rho(t)$:

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new infections from 1-simplices new infections from 2-simplices

Set of infection probabilities $B \equiv \{\beta_{\omega}, \omega = 1, \cdots, D\}$

(

D

$$d_t \rho(t) = -\mu \rho(t) + \sum_{\omega=1}^{D} \beta_{\omega} \langle k_{\omega} \rangle \rho^{\omega}(t) \left[1 - \rho(t) \right]$$
loss of infectiousness new infections

Results

~0

of infected nodes,

Density





I-simplex Rescaled infectivity, λ infectivity





Temporal evolution of the density of infected nodes ho(t) :

D=2 loss of infectiousness

$$d_t \rho(t) = -\mu \rho(t) + \beta \langle k \rangle \rho(t) \left[1 - \rho(t) \right] + \beta_\Delta \langle k_\Delta \rangle \rho^2(t) \left[1 - \rho(t) \right]$$

new infections from 1-simplices

new infections from 2-simplices

$$d_t \rho(t) = -\rho(t)(\rho(t) - \rho_{2+}^*)(\rho(t) - \rho_{2-}^*)$$

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D=2 loss of infectiousness

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The **steady state** equation $d_t \rho(t) = 0$ has up to three solution in the acceptable range $\rho \in [0,1]$

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$$\rho_{1}^{*} = 0$$

absorbing epidemic-free state

Temporal evolution of the density of infected nodes $\rho(t)$:

D=2 loss of infectiousness

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The **steady state** equation $d_t \rho(t) = 0$ has up to three solution in the acceptable range $\rho \in [0,1]$

$$\label{eq:rho} \begin{split} \rho_1^* = 0 & \qquad \rho_{2\pm}^* = \frac{\lambda_\Delta - \lambda \pm \sqrt{(\lambda - \lambda_\Delta)^2 - 4\lambda_\Delta(1-\lambda)}}{2\lambda_\Delta} \end{split}$$
 absorbing epidemic-free state





region

Dependency on initial conditions



- Considering **high-order** interactions in social contagion processes
 - Social structure modelled as a simplicial complex
 - Contagion occurs in **group interactions** (with different transmission rates)

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 - Discontinuous transition
 - Dependence on the size of the seed (critical mass)

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- Future work:
- Simplagion on more general simplicial complexes HMF
- Inference from structural + dynamical data
- Extension to other dynamical processes Simplicial Kuramoto model

Actually...

 $\dot{\theta}_i = \omega_i + \frac{K}{N^2} \sum_{k=1}^{N} \sum_{k=1}^{N} \sin(\theta_j + \theta_k - 2\theta_i)$ i=1 k=1

Abrupt Desynchronization and Extensive Multistability in Globally Coupled Oscillator Simplices

Per Sebastian Skardal^{1,*} and Alex Arenas²

¹Department of Mathematics, Trinity College, Hartford, CT 06106, USA ²Departament d'Enginyeria Informatica i Matemátiques, Universitat Rovira i Virgili, 43007 Tarragona, Spain

Collective behavior in large ensembles of dynamical units with non-pairwise interactions may play an important role in several systems ranging from brain function to social networks. Despite recent work pointing to simplicial structure, i.e., higher-order interactions between three or more units at a time, their dynamical characteristics remain poorly understood. Here we present an analysis of the collective dynamics of such a simplicial system, namely coupled phase oscillators with three-way interactions. The simplicial structure gives rise to a number of novel phenomena, most notably a continuum of abrupt desynchronization transitions with no abrupt synchronization transition counterpart, as well as, extensive multistability whereby infinitely many stable partially synchronized states exist. Our analysis sheds light on the complexity that can arise in physical systems with simplicial interactions like the human brain and the role that simplicial interactions play in storing information.

• Future work:

- Simplagion on more general simplicial complexes HMF
- Inference from structural + dynamical data
- Extension to other dynamical processes Simplicial Kuramoto model?

Check out the arXiv!

Simplicial models of social contagion

 Iacopo Iacopini,^{1,*} Giovanni Petri,^{2,3} Alain Barrat,^{4,2} and Vito Latora^{1,5,6,7}
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 ³ISI Global Science Foundation,33 W 42nd St10036 New York NY, United States ⁴Aix Marseille Univ, Université de Toulon, CNRS, CPT, Marseille, France ⁵The Alan Turing Institute, The British Library, London NW1 2DB, UK
 ⁶Dipartimento di Fisica ed Astronomia, Università di Catania and INFN, I-95123 Catania, Italy ⁷Complexity Science Hub Vienna (CSHV), Vienna, Austria

Complex networks have been successfully used to describe the spreading of a disease between the individuals of a population. Conversely, pairwise interactions are often not enough to characterize processes of social contagion, such as opinion formation or the adoption of novelties, where a more complex dynamics of peer influence and reinforcement mechanisms is at work. We introduce here a high-order model of social contagion in which a social system is represented by a simplicial complex and the contagion can occur, with different transmission rates, over the links or through interactions in groups of different sizes. Numerical simulations of the model on synthetic simplicial complexes and analytical results highlight the emergence of novel phenomena, such as the appearance of an explosive transition induced by the high-order interactions.

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and thanks to...







Giovanni Petri (ISI Foundation) Alain Barrat (CNRS)

Vito Latora (QMUL)

Backup

Sociopatterns data sets

Dataset	Context	$\langle k angle$	$\langle k_\Delta angle$	$\langle k angle^{ m aug}$	$\langle k_\Delta angle^{ m aug}$
InVS15	Workplace	16.9	7.0	21.0	7.0
SFHH	Conference	15.0	7.6	21.6	7.7
LH10	Hospital	19.1	17.1	25.7	17.5
Thiers13	High school	20.1	10.9	32.0	11.1

Table 1: Average generalized degree of the four real-world simplicial complexes constructed from

the considered data sets (before and after the data augmentation).

SocioPatterns

Simplagion on RSC

Size effects



Simplagion on empirical simplicial complexes

Without data augmentation



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