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# Contagion dynamics on higher-order networks

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Abstract	Sections
A paramount research challenge in network and complex systems	
science is to understand the dissemination of diseases, information and behaviour. The COVID-19 pandemic and the proliferation of	Phenomena r higher-order
misinformation are examples that highlight the importance of these dynamic processes. In recent years, it has become clear that studies	Contagion on systems
of higher-order networks may unlock new avenues for investigating	Outlook
such processes. Despite being in its early stages, the examination of social contagion in higher-order networks has witnessed a surge of research and concepts, revealing different functional forms for the spreading dynamics and offering novel insights. This Review presents a focused overview of this body of literature and proposes a unified formalism that covers most of these forms. The goal is to underscore the similarities and distinctions among various models to motivate further research on the general and universal properties of such models. We also highlight that although the path for additional	
theoretical exploration appears clear, the empirical validation of these models through data or experiments remains scant, with an unsettled roadmap as of today. We therefore conclude with some perspectives aimed at providing possible research directions that could contribute to a better understanding of this class of dynamical processes, both from a theoretical and a data-oriented point of view.	

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### **Key points**

• Contagion models in higher-order systems are motivated by problems relating to social interactions and to epidemics. There are various models and their interpretation changes depending on the context, but their mathematical formulation is similar and many models share key features and behaviours.

• Identifying these general and specific properties of models will improve our understanding of higher-order systems as a whole. In this Review, we propose a unified formalism that covers most of the models in the literature.

• Neglecting higher-order effects could completely change the process. For example, a discontinuous transition in a higherorder system could be perceived as continuous in a projected pairwise system.

• Data validation and social experiments on a large scale are still lacking. Although there are structural data for some systems, for many dynamical processes data remain insufficient.

• The study of contagion models in higher-order systems is an inherently interdisciplinary endeavour, in which physics and mathematics can provide new insights and interpretations for social sciences and epidemiology, among others.

### Introduction

Contagion models cover a wide range of processes, including the spread of diseases<sup>1-3</sup>, social contagion<sup>4</sup> and rumour dissemination<sup>5,6</sup>. These diverse processes have been studied across various disciplines and from different perspectives. In the realms of physics and mathematics, contemporary approaches often incorporate heterogeneous interaction patterns<sup>1-3</sup>. However, these models traditionally assume pairwise interactions, encapsulated within graphs, thereby limiting propagation to interactions between two individuals. More recently, this paradigm has been challenged, as new models have been proposed to account for group interactions using hypergraphs<sup>7-12</sup> (Box 1). In other words, the paradigm changes from the one-to-one formalism to the one-to-many or many-to-many interaction types. An illustrative example to gain some intuition is evident in group chats of modern messaging applications, which enable one-to-many interactions, in addition to direct messages between users.

In the literature, the introduction of these models is typically justified by the aim of offering a more accurate depiction of specific social or epidemiological processes. However, most models remain predominantly theoretical, using these real-world phenomena as inspirations for model definitions, yet lacking empirical validation. This shortfall stands in stark contrast to the advancement in the theoretical underpinnings of these processes, which has grown prolifically. Various functional forms have been proposed to describe spreading in higher-order systems, accompanied by a diverse range of analytical techniques. These techniques span from classical approximations in graphs, such as heterogeneous mean-field (HMF) approaches, to innovative methods such as facet approximation (FA)<sup>13</sup>. Thus, this Review emphasizes both the generalities and specificities of these models, aiming to aid future research in generalizing contagion theory within higher-order networks and with the aspiration that it will stimulate further empirical research.

To achieve this goal, we first discuss studies and observations motivating the introduction of higher-order interactions in social and epidemic contagion models. Additionally, we outline a set of open experimental questions that might be addressed with these approaches. We then present a unified formalization that covers the majority of models in the existing literature. Initially, we study this formulation in the limit in which pairwise graphs are recovered, aiming to glean insights into such processes. Subsequently, the section is dedicated to an exploration of diverse approaches proposed for integrating higher-order interactions into these models, highlighting their similarities and distinctions. We conclude by summarizing major challenges and offer theoretical and data-oriented perspectives to pave the way for further research of higher-order contagion models.

### Phenomena motivating higher-order dynamics

In this section, we introduce the phenomena motivating higher-order dynamics in the study of complex systems.

### Sociological motivations

The empirical investigation of coordination, norms and behaviours spreading across networks has garnered considerable attention<sup>14-19</sup>. Social contagion within networks, particularly the emergence of consensus without centralized institutions, stands out as a major area of interest<sup>20-25</sup>. Understanding the dynamics of social contagion and change is a multifaceted challenge owing to the diversity of problems that span across many domains and contexts. Yet, certain commonalities prevail.

Tipping points hold a great deal of interest within this context. Described as a threshold at which a small quantitative change in the system can trigger a nonlinear process that leads to a different state of the system<sup>26</sup>, these points are central to critical mass theory. This theory posits that a minority of committed individuals, upon reaching a critical size, can overturn a social convention<sup>14</sup>. The concept finds ample validation in theoretical models<sup>25,27-29</sup> and empirical studies<sup>30–38</sup>. Intriguingly, observed critical mass thresholds span several orders of magnitude, from 25–40% in some observational studies on social conventions<sup>30</sup> to as low as 0.3% for linguistic norm changes in English<sup>36,38</sup>, or even encompassing just a few individuals relative to the population size in social movements<sup>37,38</sup>.

A pertinent question arises concerning the mechanisms by which small groups evolve into committed minorities. Research spanning sociology, political science<sup>30-32,35,39</sup>, physics and mathematics<sup>4,7,10,25,27-29,40-48</sup> has explored these group interactions, which are now gaining attention in the field of complex systems owing to recent inclusion of higher-order interactions in contagion models. These models offer richer dynamical behaviours, including abrupt transitions, multistability and intermittency. An understanding of social contagion within an increasingly interconnected world is crucial and potentially could guide policy decisions. For instance, these models could facilitate the acceleration of societal changes to address societal challenges such as responding to climate emergencies<sup>24,26,49-53</sup>.

#### **Epidemiological motivations**

Realistic epidemic models often categorize interactions into four main groups: households, schools, workplaces and the broader community. These groupings not only serve as major sources of transmission but also offer a more feasible target for public health interventions than

### Box 1 | Structure of networked systems

A system of interacting individuals can be represented by different mathematical objects according to its type of interaction, namely, pairwise or higher order (see the figure, part **a** for a comparison between the two main higher-order objects), or according to its multilevel organization, which can be single-layer or multilayer (see the figure, part **b**). These objects are described formally as:

- Graph or network: A simple graph is defined as a set of vertices connected by edges that are pairs of vertices (for example, a friendship network). A non-exhaustive set of reviews and books can be found in refs. 1,193,194.
- Multilayer network: A multilayer network is a graph made up of multiple layers, each representing a different context. For example, one might construct a friendship multilayer that separates friends in different social circles or types of interactions (for instance, online and offline). Multilayer systems are particularly suitable for modelling interacting processes, such as epidemics and information spreading. Multilayer networks have many subtypes. We refer to Table 1 in ref. 195 for a comprehensive classification. A non-exhaustive set of reviews and books can be found in refs. 195–199.
- Hypergraph: A graph in which hyperedges (generalized edges) can connect a subset of nodes instead of two nodes. An example

is a collection of WhatsApp groups. Formally, the hypergraph  $\mathcal{H}$  is defined as a set of vertices  $\mathcal{V} = \{v_i\}$  and a set of hyperedges  $\mathcal{E} = \{e_i\}$ , in which  $e_i$  is a subset of  $\mathcal{V}$  with arbitrary cardinality  $|e_i|$ , that is, the hyperedge can contain any number of nodes. The total number of nodes is defined as  $N = |\mathcal{V}|$  and the number of hyperedges as  $M = |\mathcal{E}|$ . Note that it is possible to extend the multilayer concept to hypergraphs.

• Simplicial complex: A simplicial complex is a type of hypergraph whose set of hyperedges is complete, that is, all possible subsets of a hyperedge are also present. In this Review, when we use the term simplicial complex, we are referring to the abstract simplicial complex. Note that there is a distinction between the abstract simplicial complex, which is a hypergraph with downward inclusion, and the geometric simplicial complex, in which objects are continuous. For a full discussion, we refer to ref. 200. Another term for an abstract simplicial complex is an 'independence system' used in combinatorial mathematics.

We also note that in recent years, higher-order systems have been reviewed in refs. 7–9,11,12. Also, some perspective papers focusing on the study of higher-order systems are refs. 10,185,201, and an editorial was published in ref. 202.



do individual-based strategies. Intriguingly, epidemiological studies have revealed widely varied per-contact transmission probabilities within these settings, with households demonstrating the highest rates<sup>54-57</sup>. Larger settings exhibit distinct interaction characteristics compared with smaller groupings, a difference that has a notable impact on disease transmission dynamics<sup>58,59</sup>.

Moreover, the challenges posed by varying per-contact transmission probabilities across different settings are compounded by dose-response dynamics in infection exposure and emerging insights into the mode of transmission for respiratory pathogens such as severe-acute-respiratory-syndrome-related coronavirus (SARS-CoV-2). Indeed, the minimal infective dose required to cause an infection depends on the characteristics of the pathogen, and thus the immune system does not respond equally to all exposures<sup>60</sup>. Similarly, although traditional assumptions on the mode of transmission for SARS-CoV-2 centred around large droplets or fomite-based transmission, surveillance data swiftly indicated airborne transmission as the dominant form of spread<sup>61–65</sup>, even in settings with close-range

interactions<sup>66</sup>. Droplet-based transmission can be easily modelled as a pairwise interaction, but classical models struggle to address airborne transmission<sup>60,67,68</sup>.

Households are particularly suitable for modelling using higherorder networks such as hypergraphs, especially concerning airborne diseases. Despite their apparent simplicity, households exhibit compelling dynamics, notably showcasing higher secondary attack rates compared with other contexts for SARS-CoV-2 and influenza<sup>55,69–74</sup>, and an inverse relationship between secondary attack rate and household size<sup>75,76</sup>.

Airborne transmission also amplifies the probability of superspreading events, which are influenced by various biological, social and environmental factors<sup>59,77,78</sup>. Although nodes with large degrees can simulate such behaviour, it is essential to consider additional heterogeneities because context also shapes these events<sup>54,79</sup>. In fact, during the COVID-19 pandemic, it was observed that up to 70% of cases did not transmit the virus to anyone, and those who did typically infected just one or two others<sup>55,80–82</sup>.

Furthermore, social contagion elements also wield considerable influence on epidemic spread. Mask usage, which can reduce the transmission of respiratory diseases<sup>83–85</sup>, varies greatly around the world owing to cultural and psychological factors, as well as group dynamics<sup>86–90</sup>. Likewise, vaccination uptake is also influenced by social dynamics<sup>91,92</sup>, and some studies even demonstrate that individuals explicitly take into account group dynamics – akin to critical mass processes – to decide when to vaccinate<sup>93</sup>.

### **Other motivations**

The relevance of contagion models is not limited to the epidemiological or social context. Rumour models<sup>5,6</sup> inspired and formed the theoretical basis for the gossip protocol<sup>94</sup>, a powerful paradigm used in the design of reliable and efficient decentralized distributed protocols<sup>95</sup>. The gossip protocol is widely used in peer-to-peer (P2P) networks<sup>95–97</sup>, including the Gnutella P2P network<sup>97</sup>, and cryptocurrency networks such as Bitcoin<sup>98,99</sup> or Ethereum<sup>100</sup> and their derivatives. Moreover, the application of the hypergraph theory has demonstrated its efficacy in modelling wireless and 5G networks, as evident in the existing literature<sup>101–104</sup>. These instances suggest the potential for social contagion models in higher-order networks to inspire novel protocols and methodologies.

### **Contagion on higher-order systems**

There are many approaches to model contagion processes on higherorder structures. In this section, we unify the most common contagion models in hypergraphs using a single equation that can be adapted to capture different behaviours, which can be either social or epidemicinspired. Importantly, we show that this equation can also be reduced to the pairwise case, emphasizing that the higher-order formulation is a generalization of the classical pairwise case.

We focus on the two most paradigmatic contagion models, the susceptible–infected–susceptible (SIS) and the susceptible–infected–recovered (SIR), in hypergraphs. In the thermodynamic limit, the SIS model has a single absorbing state, whereas the SIR has infinitely many absorbing states. Here, we define a hypergraph,  $\mathcal{H}$ , as a set of vertices,  $\mathcal{V} = \{v_i\}$ , and a set of hyperedges,  $\mathcal{E} = \{e_j\}$ , in which  $e_j$  is a subset of  $\mathcal{V}$  with arbitrary cardinality  $|e_j|$ . The number of vertices is  $N = |\mathcal{V}|$ . If max( $|e_j|$ ) = 2, we recover a graph. If for each hyperedge with  $|e_j| > 2$ , its subsets are also contained in  $\mathcal{E}$ , we recover a simplicial complex. In the contagion models, nodes can be in one of the three states: susceptible, infected or recovered (when applicable). Note that it is

common practice to adopt an epidemic-spreading nomenclature even for social contexts. To model these states, we associate each node  $v_i$ with three Bernoulli random variables,  $(X_i, Y_i, Z_i)$ . Accordingly, susceptible individuals are in the state (1, 0, 0), infected individuals are in the state (0, 1, 0) and recovered individuals are in the state (0, 0, 1). We note that the success probability of these Bernoulli random variables is not constant and follows a non-trivial form depending on the hypergraph structure and the state of the system.

The transition between states is defined as a collection of Poisson processes, defining a continuous-time Markovian process and implying that the dynamics have no memory. We associate a healing mechanism to each infected node, modelled as a Poisson process with parameter  $\delta$ . Meanwhile, the propagation mechanism is associated with the hyperedges. So, given the hyperedge  $e_i$ , assuming that we can factorize the spreading rate as a global contribution times a function of the hyperedge size, the spreading is modelled by a Poisson process with parameter  $\lambda \times \lambda^*(|e_i|)$ , in which  $\lambda^*(|e_i|)$  is a function of the cardinality of the hyperedge and can be used to modulate the infection rate. The final component of the model is a function that captures interactions among individuals within a hyperedge. Specifically, the function  $f_i^i(\{Y\})$  models how the hyperedge  $e_i$  affects the state of the node  $v_i$ . Note that the argument of such a function is the (infected) state of all nodes in the hypergraph, here denoted by the set  $\{Y\}$ . In this case, we assume that f depends only on Y's and not on other states or the rates. Under these assumptions, the exact form of an SIS model in hypergraphs is

$$\frac{\mathrm{d}\langle Y_i\rangle}{\mathrm{d}t} = \left\langle -\delta Y_i + \lambda \sum_{j:v_i \in e_j} \lambda^* (|e_j|) X_i f_j^i (\{Y\}) \right\rangle, \tag{1}$$

in which  $\langle \cdot \rangle$  is the expectation operator,  $\lambda$  can be thought of as the control parameter and  $\lambda^*(|e_j|)$  is a local parameter that weights each hyperedge differently depending on its cardinality (that is, the group size). Notably, although  $\lambda^*(|e_j|)$  could be absorbed into  $f_j^i(\{Y\})$ , it has been left out to emphasize the individual contribution of each type of hyperedge to the process. Equation (1) covers the most commonly used models. However, not every higher-order contagion process is easily modelled using equation (1) (see also the section on other contagion models). Here, for organizational purposes, we have focused on an approach in which we can factorize the hyperedge-dependent rates,  $\lambda^*(|e_j|)$ , and in which the functional form depends only on the state of the nodes inside the hyperedges,  $f_j^i(\{Y\})$ , but other approaches can also be considered.

To describe the SIR model, we need an additional equation:

$$\frac{\mathrm{d}\langle Z_i \rangle}{\mathrm{d}t} = \langle \delta Y_i \rangle. \tag{2}$$

To solve equation (1) in its exact form for an arbitrary hypergraph, we need to solve a system of  $2^N$  ordinary differential equations, which is not feasible in most cases. Note that to solve the exact Markov chain, we must describe all possible transitions between microstates. Because we have  $2^N$  possible microstates, we also need  $2^N$  equations in the exact model. However, in some cases, one can use structural symmetries to reduce the system size to N equations. For the simplicial contagion model, such an approach was formulated in a complete simplicial complex<sup>105</sup>, and for the social contagion model based on critical masses, such an approach was formulated

A few papers have presented some results for contagion models using general interaction functions. The SIS model on hypergraphs was

considered using a general formalism and studied in terms of both the exact equations and a mean-field (MF) approach<sup>107</sup>. When the functions *f* are concave, a spectral bound for the expected time to extinction and spectral conditions for the local and global stability of the zero-activity state can be derived<sup>45</sup>. Some of these results have also been extended to non-concave functions. In addition, temporal hypergraphs have been considered<sup>47</sup>, and a spectral threshold for the spreading rate below which the activity dies out has been obtained in terms of a static expectation matrix, which is an expected clique expansion of the hypergraph. Here, zero activity refers to an absorbing state in which there are no infected or active individuals. Conversely, we refer to active states as states in which we have a non-zero number of infected or active nodes.

In the next sections, we review some of the most popular spreading models in hypergraphs and simplicial complexes and show how they can be obtained from equation (1). We also present some generalizations, results and perspectives. Figure 1 is a graphical representation of the different types of interactions in higher-order networks. The one-to-one setting describes the pairwise model and the power-law contagion kernel presented in later sections. The many-to-one setting is used in the simplicial contagion model, whereas the many-to-many is used by the critical mass threshold model. The many-to-one interaction type can be modelled as a special case of the critical mass threshold model and has also been studied in ref. 108. We note that the one-to-one does not necessarily imply a lower-order interaction.

#### The pairwise SIS and SIR

These models have been reviewed elsewhere<sup>2,3</sup> and are outside the scope of this Review. However, for the sake of comparison, it is instructive to recall a few results of phase transitions in graphs, such as localization properties (Box 2), which are of particular interest for higher-order systems<sup>109,110</sup>. Furthermore, the standard SIS pairwise model can be recovered from equation (1) by setting the maximum cardinality of  $\mathcal{H}$  to 2 and considering

$$f_j^i(\{Y\}) = Y_k,\tag{3}$$

in which  $e_j = \{v_i, v_k\}$ . With equation (2), we would also recover the SIR pairwise model, but for the rest of the section, we will focus on the SIS.

Behaviour observed. In a homogeneous network, the transition is continuous, and the critical point is finite and non-zero. But one of the most important results of epidemic spreading in networks is that under an MF approximation, the critical point vanishes for networks in which the second moment of the degree distribution diverges<sup>111</sup>. For this reason, power-law networks, which have degree distribution  $P(k) \sim k^{-\gamma}$ , attracted particular interest, because the second moment diverges for 2 < y < 3. More generally, depending on the network characteristics, the transition can be driven by different activation mechanisms, namely, collective, k-core or hub<sup>112-114</sup>. From a physics perspective, in the collective case, the whole network is active after the critical point. In the *k*-core case, the process is localized in the core of the network. Finally, in the hub activation mechanism, the process is localized around the hubs (Box 2). For multilayer networks, a similar argument has been made about the localization properties of the phase transition. However, in this case, there are additional scenarios: the transition can be delocalized or layer-localized<sup>115</sup>. When layer-localized, these scenarios for simple graphs may also apply.

Note that discontinuous phase transitions can also be found in epidemic processes in graphs but only in very specific cases. One example



**Fig. 1** | **Different types of interactions in higher-order networks.** Functions are separated by how many individuals are required to make the hyperedge active and how many individuals are affected by that function. Here, red nodes represent infected or active individuals and blue nodes represent healthy or inactive individuals. For example, the pairwise interactions are of the form one-to-one. Note, however, that we can also have higher-order one-to-one interactions when the spreading rate depends on a nonlinear function of infected neighbours of a node. The other schemes are higher-order, and their main difference is the number of individuals needed to trigger the spread. This simple classification allows us to easily distinguish between different models.

is a disease spreading in adaptive networks, in which agents change their connections depending on their state<sup>116,117</sup>. For a review of this topic, see ref. 118. One motivation<sup>117</sup> to study the problem is to model how teachers should behave; if they are infected, they can be replaced. However, this seemingly rational behaviour backfires if the spreading rate is sufficient to infect the students before the teacher leaves. In this case, the movement of teachers leads to a higher proportion of infected individuals, as more and more teachers become infected and carry the disease home with them. This outcome implies a discontinuous transition and hysteresis. Another example would be cooperative diseases<sup>119</sup>.

**Analytical approaches.** Most of the analytical approaches have been reviewed elsewhere<sup>2,3</sup>. In our context, the most relevant are:

- MF assumes that the system is completely homogeneous<sup>1-3,111</sup>.
- HMF, also called degree-based mean field, assumes statistical equivalence among nodes with the same degree, neglecting dynamical correlations and partially structural correlations<sup>1–3,111</sup>.
- Quenched mean field (QMF), also called individual-based meanfield or *N*-intertwined mean-field approach, considers structural correlations but neglects correlations between individual states<sup>2,3,120,121</sup>.
- Pair-quenched mean field (PQMF) considers both structure and dynamical second-order correlations<sup>122,123</sup>.
- Approximate master equations (AMEs), which consider the state of nodes and their immediate neighbours, generate large systems of differential equations<sup>124–128</sup>.
- Discrete-time Markov chain approaches are also called microscopic Markov chains (MMCs)<sup>129</sup>. In this approximation, structural correlations are considered, dynamical correlations are neglected and time evolves in discrete steps. This can be regarded as a discrete-time version of the QMF.
- Epidemic link equation (ELE) can be interpreted as the discrete-time version of the PQMF<sup>130</sup>.

An important result not covered in refs. 2,3 is the use of cumulative merging percolation to study the critical properties of the SIS process,

### Box 2 | Dynamical behaviour

Following the nomenclature of statistical mechanics, we characterize a dynamical process using two quantities:

- Order parameter: The order parameter  $\rho$  in the context of contagion is defined as the first moment of the distribution of the fraction  $n_a$ of active or infected individuals,  $P(n_a)$ , or the average. Formally,  $\rho = \langle n_a \rangle$ , in which  $\langle \cdot \rangle$  denotes an expectation value.
- Susceptibility: The susceptibility  $\chi$  measures the variance of  $P(n_a)$  and can be interpreted as the derivative of the order parameter with respect to the control parameter. Formally,  $\chi = \frac{\langle n_a^2 \rangle \langle n_a \rangle^2}{\langle n_a \rangle}$ , following the suggestion in ref. 203.

We also define our process using the following terminology:

 Control parameter: The control parameter in the context of contagion is the spreading parameter λ.

- Critical point: The critical point is the point in the control parameter at which a phase transition is observed (see the definition described subsequently).
- Subcritical and supercritical regimes: If the control parameter is below the critical point, that is,  $\lambda < \lambda_c$ , the process is in the subcritical regime. Conversely, if the control parameter is above the critical point, that is,  $\lambda > \lambda_c$ , the process is in the supercritical regime. Note that this is a simplified definition in which we exclude the Griffiths phase, as it has not been observed in contagion models on hypergraphs.

When a system changes from one macrostate to another, one says that it undergoes a phase transition. Note that, strictly speaking, a phase transition is defined only in the thermodynamic limit. However,



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it is common to use the analogue of this concept in finite systems. This transition can occur in many different ways (for a graphical example, see the figure, part **a**). The ones seen more often in contagion models are as follows:

- First order: Both the order parameter and the susceptibility are discontinuous at the transition.
- Second order: The order parameter is continuous, and the susceptibility diverges at the critical point.
- Hybrid phase transitions: The order parameter is discontinuous and shows scaling. Thus, the susceptibility has a one-sided divergence<sup>204</sup>.

Besides phase transitions, other phenomena are relevant to contagion processes (for a graphical example, see the figure, part **b**):

- Hysteresis: Hysteresis refers to the dependence of the state of a system on its past. That is, for the same value of the control parameter, the state of the system will be different depending on the path followed to reach it.
- Localization: At the critical point, the transition may affect all nodes equally, or it may be restricted to some groups of nodes.

which provides an explanation of the mechanisms behind the phase transition<sup>131</sup>. The behaviour predicted by each theory is summarized in Fig. 2.

### The SIS on hypergraphs

Early work on the SIS model on hypergraphs<sup>107</sup> was motivated by the spread of epidemics in household structures, workplaces and schools. In that model, the infection pressure on susceptible individuals is not proportional to the number of infected individuals, so that

$$f_j^i(\{Y\}) = \begin{cases} m & \text{if } m < c \\ c & \text{otherwise'} \end{cases}$$
(4)

in which  $m = \sum_{k:v_k \in e_j: v_k \neq v_i} Y_k$ . In addition to the exact formulation using the Kolmogorov equations, an MF analysis can be carried out; this approximation performs well for regular random hypergraphs. Moreover, when considering a structure that includes households and workplaces, the MF solution grows faster than the solution to the Kolmogorov formulation, but their steady-state solutions are close. (Note that in ref. 107  $x_i(t)$  is referred to as the state of node *i*, in which  $x_i(t) = 1$  denotes an infected individual.)

To model non-pharmaceutical interventions in realistic scenarios, a temporal hypergraph approach<sup>132</sup> extends the model proposed in ref. 107 by considering both direct (person-to-person, that is, pairwise interaction) and indirect contacts (infection through an intermediary, a contaminated environment). The approach is mainly computational, based on agent-based simulations in which different interventions are evaluated. The results emphasize the role of personal protection and hygiene measures in slowing down the spread of the disease.

#### The simplicial contagion model

An approach<sup>40</sup> to model social contagion processes such as opinion formation or adoption of novelties, in which complex influence mechanisms and reinforcement are present, is to use simplicial complexes One way to measure the localization of a system is to use the inverse participation ratio,  $IPR(\mathbf{v})=(\sum_i |v_i|^4)$ , in which  $\mathbf{v}$  has norm one. In this case, we are most interested in how this measure scales with system size, that is,  $IPR(\mathbf{v}) - N^{-\alpha}$ . More details are given in refs. 109,110,115,191. We note that although this concept is defined at the critical point, it is often used in the supercritical regime. In such a case, the same ideas apply, but they have to be measured differently.

- Multistability: More than two macrostate solutions are possible for a given set of parameters, depending on the initial condition.
- Intermittency: The system presents high and low levels of macroactivity and alternates between them. This implies a bimodal distribution of states *P*(*n<sub>a</sub>*) (ref. 106). In the figure, part **b**, the bimodal state distributions are shown in the side panels. We note that spreading processes in networks often have an unimodal bell-shaped distribution, and bimodal distributions have been observed in the critical mass model in hypergraphs. In this case, they were a consequence of the temporal intermittency (alternating periods of high and low activity) shown in the temporal evolution next to the distributions in the side panels.

(a particular type of hypergraphs) and a multiplicative interaction function. From equation (1), the simplicial contagion model can be obtained using

$$f_{j}^{i}(\{Y\}) = \prod_{k:v_{k} \in e_{j}; v_{k} \neq v_{i}} Y_{k},$$
(5)

and replacing the hypergraph  $\mathcal{H}$  by a simplicial complex. Note that the model still holds for an arbitrary hypergraph, as discussed in ref. 43. Therefore, in this section, we summarize the results for both structures. (Regarding the notation, in ref. 40, the recovery and infection rates are denoted by  $\mu$  and  $\beta_{\omega}$ , respectively, in which the spreading rates are indexed by the cardinality of the hyperedge, that is, the order of the interaction.)

**Behaviour observed.** In ref. 40, an MF approach is proposed for an arbitrary-order simplicial complex, with a focus on analysis of the simplicial complex with dimension 2, that is, triangles and pairwise edges. Analytical and numerical results indicate a discontinuous phase transition with a hysteresis loop. The MF approximation yields a third-order polynomial equation on the order parameter, with two feasible and stable solutions separated by an unstable one. In practice, this means the system reaches one of the feasible and stable solutions, depending on the initial condition, resulting in a bistable regime.

Regarding the phase transition from the disease-free (inactive) state to an endemic (active) state, the interaction function in equation (5) has also been studied<sup>41</sup> in uniform hypergraphs with a power-law degree distribution. In a HMF approach, continuous transitions occur when the hub effect is dominant and hybrid transitions occur when the hub effect is weak<sup>41</sup>. In addition, critical exponents have been calculated analytically and validated numerically. Interestingly, in a QMF approach, a continuous phase transition can necessarily only exist if there are enough pairwise interactions<sup>42</sup>. This result is in agreement with analytical results from a QMF approach, which formalize the critical and tri-critical points<sup>133</sup>. This result regarding the necessity of pairwise interactions may seem to contradict the continuous



Fig. 2| Susceptible–infected–susceptible prevalence  $\rho$  in the pairwise case according to the most common approaches. We present a summary of the predictions of some of the most common approaches, the heterogeneous mean field (HMF), the quenched mean field (QMF), the QMF theory as reinterpreted in refs. 191,192 (QMF\*) and the cumulative merging percolation (CMP). In addition,  $\lambda_c^{\rm LMF}$ ,  $\lambda_c^{\rm CMP}$  and  $\lambda_c^{\rm QMF}$  denote the critical points for the QMF, CMP and HMF theories, respectively. We emphasize that, depending on the network structure, different analytical approaches may have the same critical point prediction. For example, for a power-law degree (k) distribution,  $P(k) - k^{-\gamma}$ , with  $2 < \gamma < 2.5$ , both the QMF and HMF theories predict the same critical point. Figure is adapted from ref. 131, CC BY 4.0.

phase transitions observed in ref. 41. However, it should be noted that analytically, in ref. 41, a HMF approach was used. In such an approach, the network is annealed, which is different from the QMF assumptions in ref. 42. Also, numerically, the simulations in ref. 41 start from a fully infected population that is not sufficiently close to the disease-free state and thus does not satisfy the assumptions of the linear stability analysis used in ref. 42, in which near the disease-free state the probability of having (|e| - 1) infected nodes is negligible.

Higher-order structures have less influence in the initial phase of spreading beyond the transition point<sup>134</sup>, where it is difficult or almost impossible for the process to gain prevalence if only higher-order interactions are present. This result implies that pairwise interactions are necessary to activate higher-order structures. Then, after this period, the higher-order structures accelerate the spreading, making it converge faster to the stable (or metastable in the case of finite structures) state<sup>134</sup>.

Finally, multistability was found in the context of social contagion in higher-order structures in the critical mass threshold model<sup>106</sup> (discussed subsequently). In this case, the ingredient that produced this behaviour was structural heterogeneity in the form of community structure. However, this is not the only feature that generates multistability. In fact, heterogeneity in the propagation parameters in different orders of interactions may be sufficient to have multistability in a complete simplicial complex<sup>105</sup>.

**Analytical approaches.** The MF approach of ref. 40 disregards any structural and dynamical correlations. Alternatively, one can use the pair-based approximation, which explicitly describes the average correlations by taking into account the product between two random variables. This approximation is more accurate than the standard MF model on the random simplicial complex model<sup>135</sup>. Moreover, the pairbased approximation predicts a slightly smaller bistable region when compared with the standard MF model.

The HMF approach has been applied to social contagion in hypergraphs<sup>108</sup> and predicts that the critical point for the disease-free state (inactive or absorbing) only depends on the pairwise interactions. Similar results were also obtained using a dimensionality reduction technique<sup>136</sup>. Interestingly, the same theory also predicts that increasing the heterogeneity in the pairwise interactions postpones the onset of bistable behaviour<sup>108</sup>.

The QMF technique was used<sup>4</sup> in the critical mass social contagion model (which is discussed subsequently). Note that this approach can be derived from equation (7) (discussed subsequently) by setting  $\Theta_j = |e_j| - 1$  to recover the simplicial contagion model and neglecting correlations in  $f_{j'}^i$  which is a QMF requirement. We leave the discussion of this approach to the section on the critical mass threshold model.

Concerning discrete-time approaches, in higher-order systems, the MMC and the ELE show better agreement<sup>137</sup> than the MF approaches when compared with Monte Carlo simulations in random simplicial complexes. The main disadvantage of the ELE is its analytical difficulties<sup>137</sup>. Another discrete-time approach is the network clique cover approximation, called the microscopic epidemic clique equation, which uses a particular edge clique cover to account for dynamical correlations<sup>138</sup>. The microscopic epidemic clique equation usually performs better than the ELE and the MMC<sup>138</sup>. The disadvantage of this approach is its computational complexity, because it describes the system by  $N + \sum_{n=2}^{m} (2^n - n - 1)C^{(n)}$  equations, in which  $C^{(n)}$  is the number of projected cliques with *n* nodes<sup>138</sup>.

The AME approximation has been generalized<sup>109,110,139</sup> to describe hypergraph contagion. The main advantage of this formulation is its analytical tractability, which allows for closed-form implicit expressions for the critical and tri-critical points. This formulation assumes an arbitrary infection rate function and allows for an arbitrary group distribution. The results obtained with AME focus on a power-law infection kernel slightly different from equation (5) and thus are discussed in the section on the power-law infection kernel.

The methods described here are generalizations of network approaches and, with the exception of QMF and PQMF, they neglect structural correlations. However, in higher-order systems, it is expected to find nested structures<sup>13</sup>. Note that a simplicial complex is, by definition, a perfectly nested structure. To explicitly account for this feature, the FA has been proposed. In the FA, this correlation is accounted for by explicitly considering a local MF approximation on nested structures. This is the hypergraph generalization of the clique approximation<sup>124</sup>. Interestingly, by neglecting nestedness in the FA formalism, one can obtain the same set of equations as in the HMF<sup>108</sup>. The accuracy of the FA has been evaluated in a random model that interpolates between a completely nested hypergraph, that is, a simplicial complex, and a random hypergraph<sup>13</sup>. In a completely nested hypergraph, the FA predicted the transition points better than the ELE, HMF and MF approaches. Moreover, the FA on fully nested hypergraphs with only pairwise and triadic interactions predicts that infectious diseases can spread with lower pairwise infectivity, that is, an increase in hyperedge nestedness lowers the invasion threshold by promoting triangular infections. It also predicts the bistable regime when the triadic spread rate is large enough.

**Model variations.** Several modifications of the functional form  $f_j^i(\{Y\})$  in equation (1) and even modifications of equation (1) have been proposed to incorporate more realistic scenarios. Here, we mention some variations and approaches. The SIR model has been proposed<sup>140</sup> in a simplicial complex; the process can be described and an expression for the critical point obtained using an MF approach. Another model studied in simplicial complexes is the susceptible-infected-recovered-susceptible (SIRS) process, which is a combination of the SIS and SIR

models. In this scenario, in addition to the discontinuous transitions and the bistability, the SIRS model also presents a stable limit cycle<sup>141</sup>. Similar effects have also been observed when births and deaths are included in the model; in this case, a steady periodic outbreak emerges under certain conditions<sup>142</sup>. Moreover, based on the model in ref. 141, a fractional SIRS model on simplicial complexes has been proposed<sup>143</sup>, which accounts for time delays caused by the latent and healing periods. In this case, a Hopf bifurcation occurs when the delay is larger than a critical value. A less common model that has also been put forward in this context is the susceptible-infected-water-susceptible (SIWS)<sup>144</sup>. In this case, a 'water' (W) compartment is an infection reservoir modelled as a hyperedge accounting for indirect transmission<sup>144</sup>.

The MF approaches presented in the previous sections aim to describe the process using a deterministic description of the mean. An alternative approach would be to use stochastic differential equations to model unpredictable or random interactions. The simplicial complex SIS has been studied under these assumptions<sup>145,146</sup>. The stability of the origin has been characterized, and the parameter space has been partitioned into unstable, bistable and globally asymptotically stable regions<sup>146</sup>.

Temporality is another key element that has been incorporated into this class of models. This feature has been incorporated into simplicial complexes using the MMC approach by considering only the neighbours and triangles that are active at a given time<sup>147</sup>. Focusing on homogeneous random temporal hypergraphs constrained to pairs and triangles, under the assumption that there are no correlations in the temporal structures, the effect of the higher-order contagion parameter was found to be much weaker compared with the static case<sup>147</sup>. This model has also been used in the analysis of a simplicial temporal network obtained from Wi-Fi data on a university campus<sup>148</sup>.

It is also possible to incorporate distrust dynamics in these models by adding directionality to simplicial complexes. In a model of group interactions, the sign of edges indicates trust (positive) and distrust (negative). When edge signs are randomly assigned and maintained during a group interaction, if distrust is increased, the transition changes from discontinuous to continuous as the bistability region associated with the first-order transition vanishes<sup>149</sup>. Conversely, it is possible to account for social balance theory by biasing the distribution of signs in groups of three individuals. In this case, contagion is determined by the relative proportions of balanced and unbalanced triangles and by which configuration within these two classes is more common.

Rather than adding more realism in the interactions, another line of research focuses on studying the problem of interacting processes. An example is the co-evolution of information and disease spread. Such a process can be modelled using a multiplex approach, in which the information spread is modelled by simplicial complexes and the disease is modelled by pairwise or higher-order interactions<sup>150–158</sup>. Still considering interacting processes but outside the multiplex framework, how a simplicial contagion could drive a simple contagion has been studied<sup>159</sup>. Above a critical driving force, the simple contagion could exhibit both discontinuous transitions and bistability. In addition, unidirectional coupling processes between a higher-order contagion and a simple contagion can impose a discontinuous transition and hysteresis in the simple contagion.

Although the works discussed earlier mostly focus on the interaction between information and an epidemic process, there is also much interest in studying competing pathogens<sup>160</sup>. For two competing simplicial SIS epidemics, a phase diagram with nine regions is obtained<sup>161</sup>. An MMC describing this process has been developed<sup>162</sup>, for which more accurate results are expected. In addition, a relevant feature of this type of process is homophily, which can be broadly defined as the tendency to associate and bond with similar individuals<sup>163,164</sup>. An MMC has been extended<sup>163</sup> to study simplicial competitive spreading dynamics between two states in the context of heterogeneous populations and homophily effects. Such an MMC approach was also used for the SIS model<sup>165</sup> and the SIR<sup>166</sup>. Finally, competitive spreading has also been dealt with<sup>167</sup>.

As a side note, it is also possible to model deactivation as a groupbased process by incorporating higher-order terms in the healing mechanism. This mechanism has been called the 'hipster effect'<sup>108</sup>, motivated by the fact that if a trend is popular, then individuals may be less likely to adopt it. With this modification to the model, the phase diagram exhibits a small band of bistability separating the regions of no infection and a single infected state.

#### The power-law infection kernel

The assumption that there is a linear relationship between the number of infectious contacts and the risk of infection has been challenged using COVID-19 data<sup>60</sup>. The data support proposing a power-law infection kernel defined as:

$$f_{j}^{i}(\{Y\}) = \left(\sum_{k:v_{k} \in e_{j}; v_{k} \neq v_{i}} Y_{k}\right)^{\nu},$$
(6)

in which *v* can modulate the nonlinearity of the process. In particular, when *v* = 1, we recover the linear case (pairwise), whereas social reinforcement and inhibition can be modelled by *v* > 1 and *v* < 1, respectively. Furthermore, if *v* = 1, and  $\lambda^*(|e_j|) = |e_j|^{-\eta}$ , in which  $\eta \in [0, 1]$ , we recover the model analysed in refs. 109,110, in which the same authors used a bipartite representation to develop their analytical description of the model. (Regarding the original notation, in refs. 109,110,139, the number of infected nodes within a hyperedge is denoted as *i*(*t*). Another peculiarity of the notation in refs. 109,110 is that the number of nodes is denoted *m*. We also note that, in ref. 109, *v* is defined with a negative sign, and in the interval [0, 1], whereas in ref. 139, both the sign and the constraint are removed. Finally, these works also use  $\mu$  to denote the recovery rate.)

**Behaviour observed.** In terms of sub-extensive localization (also called mesoscale localization in refs. 109,110,139), the behaviour is driven by the most influential groups (see Box 2 for a definition of localization). Localization also affects the phase diagram, with the effects being amplified by superlinear infection (v > 1). In this case, the critical point scales as  $\lambda_c \sim k_{max}^{-v}$  and for  $\lambda$  near  $\lambda_c$ , the infected nodes are concentrated in the largest groups. This localization pattern inhibits bistability by forcing an endemic state with a very small global fraction of infected nodes<sup>139</sup>.

For the active state, the problem of maximizing influence has been considered<sup>60</sup>. Focusing on the early stages of the spreading, two strategies were proposed for allocating initial seeds to influential spreaders or to influential groups. The group-based strategy tends to perform better for sufficiently nonlinear processes.

In a similar spirit, a relationship between core decomposition and SIS-like and SIR-like contagion processes has been studied<sup>168</sup>. Based on the concept of (k, m)-bipartite core decomposition<sup>169–171</sup>, a family of hypercore centralities was defined, and two versions were proposed: the size-independent hypercore and the frequency-based hypercore. Nodes inside cores with either higher degree, k, or cardinality, m, often

tend to be more infectious during the SIS process, implying that the process is expected to be more localized in this region of the hypergraph. Interestingly, in the Supplementary material of ref. 168, it is shown that the results are also valid for the critical mass threshold model (discussed subsequently). Moreover, considering the naming game in higher-order structures<sup>38</sup>, nodes inside the inner cores may be particularly efficient at overturning a majority convention if they belong to a committed minority.

Crucially, the core decomposition studied in refs. 168,172 is different from the percolation process with a similar name in ref. 173. The main difference is that in the bipartite core decomposition, the hyperedges that may be in an inner core may not be in the original hypergraph. This does not happen in the hypergraph core decomposition<sup>173</sup>.

**Analytical approaches.** A HMF of systems with a power-law infection kernel predicts a discontinuous phase transition, super-exponential spreading and hysteresis<sup>60</sup>. Alternatively, a group-based AME has been proposed to study this type of process<sup>109,110,139</sup>. The main advantage of this approach is its analytical tractability, allowing closed expressions for the critical and tri-critical points. The AME approach was developed for an arbitrary spreading function. Focusing on the power-law kernel, equation (6), AME reveals that a large third moment of the cardinality distribution suppresses the discontinuous phase transitions with a bistable regime<sup>139</sup>.

#### The critical mass threshold model

The critical mass processes studied in the social and political sciences motivate the propagation function<sup>4,106</sup>:

$$f_{j}^{i}(\lbrace Y \rbrace) = H\left(\sum_{k:v_{k} \in e_{j}; v_{k} \neq v_{i}} Y_{k} - \Theta_{j}\right), \tag{7}$$

in which  $H(\cdot)$  is the Heaviside function and  $\Theta_j$  is a positive integer. Note that the simplicial contagion model discussed earlier can be obtained by setting  $\Theta_j = |e_j| - 1$  and using the appropriate hypergraph. Similarly, with  $\Theta_j = 1$ , one would recover the so-called individual contagion, in which nodes within a hypergraph are activated if at least one node is active<sup>108</sup>. (Regarding notation, in refs. 4,106, the critical mass was defined in terms of the indicator operator, whereas here we use the Heaviside function.)

**Behaviour observed.** A hybrid phase transition has been observed in this class of models. In a random regular graph with a single hyperedge covering each vertex (hyperblob), this transition has been characterized using an exact formulation and finite-size analysis<sup>106</sup>. This structure is probably not representative of real systems, but it provides an argument in favour of hybrid phase transitions in this model. Furthermore, this argument is consistent with the susceptibility curves observed in real and artificial hypergraphs<sup>4,106</sup>. These results also agree with results for uniform hypergraphs with a power-law degree distribution<sup>41</sup>, for which continuous transitions occur when the hub effect is dominant and hybrid transitions occur when it is weak (see also the section on simplicial contagion).

In spite of the critical behaviour, the critical mass threshold model also presents multistability and intermittency<sup>106</sup>. Both are related to the presence of a community structure. In the case of multistability, there can be multiple states for the same set of dynamical parameters, and a different state is reached depending on the initial condition. Multistability was also predicted in a complete simplicial complex with a specific rate distribution<sup>40</sup>. Interestingly, an important implication for the way norms evolve may be the presence of multiple equilibria<sup>23</sup>.

Regarding intermittency, the results in ref. 106 suggest that when bridges (hyperedges connecting two different communities) are scarce, the communities are dynamically disconnected. In that case, there may be multiple stable solutions for the same value of  $\lambda$ . Incorporating bridges allows the process to move across communities. However, adding bridges can destroy the multiple stable solutions by merging them into a bimodal distribution of states and creating intermittency. We note that a similar effect was also observed by increasing or decreasing the hyperedge cardinalities of bridges and by changing the critical mass threshold  $\Theta^*$ .

Moreover, the same results for the relationship in core decomposition mentioned in the section on simplicial contagion models are also valid for the critical mass threshold model. In particular, the time to reach the metastable state for the SIS-like process is shorter when the initial seeds are in the inner cores<sup>168</sup>. Also, the final fraction of recovered individuals for the SIR-like process tends to be higher when the seed nodes are placed in the inner core.

**Analytical approaches.** A QMF approach has been proposed, and a closed expression for the critical point presented for the hyperstar (a star graph with a single hyperedge covering each vertex) and the hyperblob<sup>4</sup>. These results have been extended to a general hyper-graph<sup>46</sup>, for which the stability of the disease-free (inactive state) was studied, and both global and local stability conditions were derived. Finally, the QMF approach could also capture multistability<sup>106</sup>. However, the intermittent behaviour is not captured by this approximation. The QMF captures the peaks of the state distribution as if they were metastable states<sup>106</sup>. This is indeed expected as the QMF neglects correlations and stochastic fluctuations.

The composite effective degree Markov chain approach (CEDMA)<sup>174</sup> is an alternative framework to analyse the critical mass model in hypergraphs. The CEDMA classifies nodes according to the number of neighbours and hyperedges in different states. Numerical experiments suggest that the CEDMA presents a higher accuracy than the MMC<sup>174</sup>. The main disadvantage of this approach is the increasing computational cost when considering hypergraphs with higher cardinalities<sup>174</sup>.

#### Other contagion models

Despite the generality of the framework proposed in the section on the contagion on higher-order systems, there are other processes that also fit in the class of contagion models but whose formulation is not straightforward using equation (1).

A variation of the SIR model has been put forward<sup>48</sup> to analyse higher-order connected components of mesoscale-connected structures. The *m*th connected component is a sub-hypergraph in which hyperedges are assumed to be connected if they share at least *m* nodes. This model could still fit in the form of equation (1), but the analysis would be somewhat more complicated.

A multistage model has been proposed to describe the spread of information driven by the spatiotemporal evolution of a public health emergency<sup>175</sup>. This model is a variation of the SIR model in which nodes can be susceptible or infected in areas affected or not by a public health emergency. An MF approach and the critical value have also been studied<sup>175</sup>. The contagion takes place on a simplicial complex with the functional form of equation (5). Moreover, a delay-differential approach has been studied<sup>136</sup>; in this approach, the interaction depends

on the delayed state of the active nodes. This model follows a function of the form of equation (5) but uses delayed states, that is,  $Y_i(t - \tau)$ . Despite the model differences, the obtained critical point agrees with the results observed in other works<sup>176</sup>.

Digital contact tracing on hypergraphs has also been considered<sup>161</sup>. In this model, hyperedges can be in one of two states: traced or untraced. If the individuals in the hyperedge carry the contact tracing application, then spreading in that hyperedge is suppressed. A link percolation process is used to mimic SIR propagation, which is outside the models covered by equation (1). In artificial cases, digital contact tracing reduces the epidemic to a larger cardinality of hyperedges. However, in real hypergraphs, the impact of digital contact tracing is observed to be large for low spreading rates<sup>177</sup>. A different approach to contact tracing has also been proposed<sup>178</sup>, in which the group is traced as a whole, increasing efficiency.

Regarding immunization, strategies discussed in ref. 179 are: immunization of hyperedges with high simultaneous infection probability (defined as the product of the infection probabilities of the nodes in a hyperedge); a generalized version of the edge epidemic importance-based immunization strategy (previously proposed for graphs<sup>130</sup>) and immunization of hyperedges with high H-eigenscore in uniform hypergraphs (for its definition, we refer to refs. 180–182). The herd immunity of the population is achieved sooner with the strategy based on the simultaneous infection probability compared with the epidemic importance-based strategy and it has a lower computational cost<sup>179</sup>. A voluntary vaccination scheme has also been studied<sup>183</sup>, by modelling the spread of disease in an SIR scheme and capturing voluntary vaccination using a game theory approach.

### Outlook

As discussed earlier, there is no unique generalization of the SIS model to higher-order contexts. However, the common feature of the higherorder models is the presence of a nonlinear function  $f_j^i$  ({Y}). The functional form in the pairwise SIS and SIR models, the SIS model on hypergraphs and the power-law infection kernel model is inspired by epidemic processes, whereas the simplicial contagion model and the critical mass threshold model are motivated by social contexts. But if one chooses  $f_j^i$  ({Y}) to be linear, then one can reinterpret the hypergraph as a graph with cliques and recover a weighted version of the classical SIS on networks. This argument is part of the debate about what is a higher-order system<sup>11,184,185</sup>.

#### **Theoretical perspectives**

Social contagion models on higher-order structures exhibit a wider range of behaviours than do pairwise graphs. For example, we have described discontinuous transitions, bistability or multistability and intermittency. However, new phenomena may yet be found. Higher interaction orders create a unique complexity horizon, the implications of which are still largely unknown. Similarly, a systematic characterization of the phase diagram for the aforementioned functions still needs to be improved. Although some efforts have started to tackle this matter, outcomes remain predominantly confined to homogeneous structures. Studies exploring heterogeneous structures, particularly in general cases, are yet to be extensively explored.

A fundamental question is how general each behaviour is. In this Review, we have highlighted the similarities, as many models are dynamically described by equation (1), and the particularities, as each model has a different interacting function  $f_j^i$ . A linear stability analysis suggests that, at least locally, they may share many properties. An exception should be made for the function in equation (7), which is not differentiable in the whole domain. Consider, for example, multistability, which has been found in the critical mass model<sup>106</sup> and in the complete simplicial complex<sup>105</sup>. However, the generality of these results is unknown. In other words, is multistability present in any of the higher-order models?

Each newly identified behaviour also raises the question of its generating mechanisms. Still considering the multistability, in the critical mass model, it is associated with the presence of a community structure<sup>106</sup>. At the same time, it is associated with parameter heterogeneity in the full simplex case<sup>105</sup>. These are two different mechanisms that produce the same behaviour. So the natural question would be, what are the other mechanisms? Moreover, this structure has been shown to produce multiple transitions and even intermittent behaviour in the critical mass model. Would the same be true for the full simplex case? And under what circumstances?

These observations lead to a more fundamental question: what are the sufficient and necessary conditions for these behaviours? As briefly discussed in the section on the pairwise SIS and SIR models, we have a reasonable understanding of the mechanisms behind SIS and SIR behaviour on graphs, something that cannot be said for the higher-order cases. However, given that the graph is a special case of the hypergraph, a general theory should naturally extend these results. There are a number of analyses moving in this direction. One of them is studying the impact of localization in spreading processes, widely discussed in graphs<sup>115</sup>, and also discussed in higher-order cases<sup>110,139</sup>. However, a full understanding of localization, including its connection to graph cases, its generality and the transition mechanisms it might describe, is still lacking.

We emphasize that the functions proposed in the literature probably do not cover specific cases. Thus, studying and proposing new functions is also a direction for future work. However, the functions that model the interactions may turn out to be highly context-dependent, making model validation much more difficult. The same is true for multistage models. Because this field of study is relatively new, most of the literature focuses on the simplest models, namely, SIS and SIR, but as the field progresses, more realistic and specific models should be proposed. Other direct features that can be incorporated are datarich structures via edge-dependent vertex-weighted hypergraphs<sup>186</sup> and different temporal patterns, for example<sup>33,187</sup>.

Notably, most of the mathematical approaches presented here are based on extensions of graph-based MF techniques. These methods have proven to be very useful and have advanced the body of knowledge of higher-order systems. Despite this progress, higher-order systems seem to exhibit different types of correlations<sup>164</sup>, which may affect their accuracy. We note that a systematic analysis of the accuracy of each of the MF approaches presented here is yet to be done. Another perspective is that new higher-order specific techniques can be developed either to correct the MF approaches or to provide new ideas. An example of this would be the FA proposed in ref. 13 (see also the section on simplicial contagion).

### **Data-oriented perspectives**

Models based on mechanistic principles enable the generation of testable hypotheses that can help understand an observed phenomenon. However, most studies to date have used observational data only as a motivation for their modelling choices, without testing any predictions on real data.

In the context of epidemic spreading, the COVID-19 pandemic presents a unique opportunity for model validation as extensive

surveillance data have been collected globally with unprecedented precision, despite its many limitations. However, very few works have used these data for model construction<sup>60,109,110</sup>, and examples of model validation are scarce<sup>188</sup>. We believe that a good starting point for such endeavours is the question discussed in the section on epidemiological motivations, such as the nonlinear relationship among population density, exposure and infection risk<sup>55,60,66,72</sup>, the fact that larger settings exhibit distinct interaction characteristics compared with smaller groups<sup>58,67,69,70</sup> and how group-mediated social contagion impacts mask wearing and vaccine uptake<sup>86,87,93</sup>.

Social contagion has been classically studied in laboratory experiments with important constraints imposed by the desired observable. In higher-order contexts, the challenges are even greater as, for instance, observing a discontinuous jump requires a large number of participants so that the transition can be unambiguously labelled as discontinuous. However, there are some features that may be easier to observe, such as localization or intermittency. Thus, there are still many questions to be addressed on how to design and implement such experiments.

In a broader perspective, even though there are a few ready-to-use real hypergraphs, there are many relational data sets out there that may implicitly include higher-order interactions. Think of co-authorship graphs in which two authors are linked together if they collaborated on a paper. It is straightforward to generalize the data to a hypergraph if information on who collaborated on each paper is available. However, in other contexts, this may not be that easy. For instance, a graph containing social relationships may not include the context in which they were formed or where they usually meet. Along these lines, there are proposals to reinterpret existing data sets using Bayesian methods to infer higher-order data from already collected data<sup>189</sup> or missing higher-order interactions<sup>190</sup>. But to properly validate these approaches, it would be important to take into account higher-order structures in the data collection process.

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#### Author contributions

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#### Competing interests

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