



ON NETWORK-BASED EPIDEMIOLOGICAL MODELS: ANALYSIS, SIMULATIONS, AND CONTINUUM LIMIT

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ABSTRACT. This work focuses on network epidemic models that emphasise the role of social contact networks within a given population, coupled with biological processes governing the spread of infectious diseases. In particular, we address the modelling and analysis of disease dynamics on large networks. As a foundational epidemiological framework, we consider the SEIR (Susceptible-Exposed-Infectious-Removed) model, which describes the transmission of infectious diseases among individuals partitioned into subpopulations. We investigate the long-term behaviour of this model while accounting for heterogeneity in infections and social interactions. Applying the theory of graphons, we explore the natural question of the large-population limit and analyze the model's behaviour as the network size approaches infinity. After establishing the existence and uniqueness of solutions to the selected models, we derive analytical results concerning the spectral properties of epidemiological networks. We also present preliminary numerical experiments. The proposed framework can be readily extended to other compartmental models in epidemiology. Given its ability to incorporate heterogeneous interconnections among individuals, it provides a natural approach for studying epidemic phenomena. Moreover, this framework can be further adapted to dynamic networks, including cases where biological parameters vary over time.

1. Introduction. The modelling of infectious disease transmission has a long history in mathematical biology. In recent years, however, it has gained increasing influence on both the theory and practice of disease management and control [4, 20, 27, 42, 44]. The mathematical modelling of infectious disease transmission has progressively evolved toward more powerful and adaptable approaches. Early models primarily focused on understanding the relationships between epidemiological parameters (e.g., transmission rates, infectious periods) and fundamental epidemic measures such as the basic reproduction number or the final epidemic size. Disease control was typically framed in terms of population-wide interventions, such as determining the proportion of individuals requiring vaccination or assessing the effectiveness of a vaccine in reducing transmission. Traditional compartmental models of disease transmission assume that individuals belong to large populations,

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which may be divided into subgroups based on factors such as location, species, or age. Within each group, individuals are considered identical and assumed to mix homogeneously, maintaining equal connectivity beyond their subgroup. While such models have provided valuable insights into disease dynamics, their applicability diminishes as more granular data become available, making them less suitable for addressing specific questions about contact patterns. Frequency-dependent models attempt to represent the number of contacts per individual but struggle to incorporate heterogeneity, effectively assuming an instantaneous redistribution of a fixed number of connections across individuals with uniform probabilities of contact.

In this work, the initial basic model consists of the *Susceptible-Exposed-Infectious-Removed* (SEIR) model, which describes disease transmission and the rate of infected individuals. The SEIR model and its modifications serve as a starting point for describing the spread of various diseases, including tuberculosis [59], measles [5], MERS [29], and more recently, COVID-19 [22]. The basic idea of the SEIR model [42, 44] is to describe the number of infected and recovered individuals based on factors such as the number of contacts, the probability of disease transmission, the incubation period, the recovery rate, and the mortality rate. Since the model focuses on a relatively short period compared to demographic dynamics, it assumes that births and natural (i.e., non-epidemic-related) deaths balance each other. While the behaviour of average quantities over time is generally sufficient to provide useful insights into epidemic spread, the spatial component of many transmission systems has been recognised as pivotal. Consequently, spatially heterogeneous features must be incorporated into the model to represent transmission patterns accurately. A reasonable hypothesis is that the spatial aspects of transmission significantly influence the aggregation characteristics of an epidemic. Thus, we must analyse data using models that incorporate spatial connections. For example, understanding human mobility and developing qualitative and quantitative theories is crucial for modelling and comprehending human infectious disease dynamics across different geographical scales. Similarly, in livestock disease transmission, comprehensive information on livestock movements, cattle interactions, and contact patterns is essential for devising appropriate disease control strategies. Understanding contact risk when herds mix extensively, where different pathogens may be transmitted at various spatial and temporal scales, remains a major challenge [30]. For instance, using data on cattle movements and focusing on their geographical distribution can enhance the analysis of the spread of epizootic diseases [40].

To introduce spatial heterogeneity, we consider metapopulation-based models, where the population is partitioned into large, spatially segregated subpopulations. We note that, in the context considered here, the term spatial does not necessarily mean that different communities or subpopulations reside in geographically separate areas; rather, it indicates that they are identifiable as homogeneous groups with respect to various characteristics (e.g., location, age, occupation, social aspects, etc.). This approach can be generalised beyond its biological interpretation to account for factors and features of groups and small interacting communities [31, 53, 52]. Traditionally, this framework provides an effective means of incorporating more realistic contact structures into epidemic models, often preserving analytical tractability while capturing salient structural inhomogeneities in contact patterns. However, understanding the dynamics of coupled systems on graphs modelling real-life connectivity remains a complex challenge. Conversely, interest often lies in analysing average quantities over large networks [48].

A widely used theoretical approach to epidemic spreading on complex networks involves the mean-field method [65]. In epidemiology, this technique simplifies the diverse and complex interactions among individuals by representing the behaviour of an extensive system with an average or “mean” behaviour, thus making the analysis more tractable. Typically, in a complex network, each node symbolises an individual, while the edges indicate the connections that facilitate disease transmission. The mean-field method operates under the assumption that each interacts with a representative average from the population, rather than with specific individuals. This simplification allows the derivation of differential equations that describe the epidemic’s evolution over time, effectively capturing the overall infection dynamics without simulating every individual interaction. Such an approach enables the investigation of epidemiological parameters, including the basic reproduction number R_0 , the epidemic threshold, and the influence of network structure on disease transmission.

While powerful, the mean-field approach has notable limitations: for example, mean-field models do not capture the variability inherent in real populations, such as differences in susceptibility, contact rates, and social structures. Furthermore, the approximation may not be optimal for all diseases or transmission dynamics; diseases exhibiting strong spatial structures or significant network effects may require more sophisticated models. In this context, two complementary directions have emerged. One is the non-exchangeable mean-field limit, which allows heterogeneity to be retained at the level of node-specific or group-specific properties, and which has generated a substantial body of recent work providing rigorous and flexible frameworks for heterogeneous populations. The other is the continuum (graphon) limit, where one considers a suitable limit of a sequence of networks (graphs), thereby constructing an evolution equation that describes the dynamics on very large graphs within a continuous spatial domain. Many nontrivial undirected graph sequences possess relatively simple limits described by symmetric measurable functions on the unit square, known as graphons [13]. In particular, information about the asymptotic distribution of social contacts can be encoded within the theory of graphons to produce continuum models that approximate the dynamics on large graphs.

Graphons were originally introduced as limits of dense network sequences when the number of nodes tends to infinity [17, 18, 46]. In this framework, the set of nodes converges to the continuum interval $[0, 1]$. Interactions are then modelled via an integrable function $W : [0, 1]^2 \rightarrow \mathbb{R}$, where $W(x, y)$ represents the level of interaction between infinitesimal nodes x and y . For simplicity, we focus mainly on symmetric interactions, i.e., $W(x, y) = W(y, x)$. The limiting dynamical equation becomes an integro-differential equation, with the spatial interactions represented by an integral operator $(T_W f)(x) = \int_0^1 W(x, y)f(y)dy$, $f \in L^2([0, 1])$. For this approach to be effective, in this work, we will consider the following issues:

How can we characterise the limit equation (on the graphon)? Considering a sequence of (simple) graphs $\{G_n\}_{n \in \mathbb{N}}$ with n nodes, as $n \rightarrow \infty$, each G_n can be viewed as a particular piecewise approximation of a graphon. Furthermore, a function $u^n(t)$ defined at the nodes of G_n can be regarded as a piecewise constant function with respect to the space defined on $\mathbb{R}^+ \times [0, 1]$. Then, the discrete dynamical system on G_n can be interpreted as an approximation of the continuum equation derived

from the graphon (cf. Eq. (11)). We can formally deduce the corresponding continuum equation by interpreting the discrete system as a suitable quadrature rule (cf. Eq. (12)).

Do the solutions of the differential systems on the graphs G_n converge, in some suitable sense, to the solution of the continuum equation on the corresponding graphon? In this work, we formulate the continuum system of integro-differential equations and the corresponding discrete system as an operator equation in a Banach space. By defining an appropriate operator that encapsulates both the differential and integral components of the equations, one can utilise powerful fixed-point theorems to establish that iterative sequences converge to a solution within a suitable space. We highlight that in [8] the authors provide a characterisation of the limit and establish the convergence results by employing a different approach based on the weak convergence method and a variational formulation. The method discussed in [8] offers greater flexibility, enabling the tackling of more complex scenarios, particularly in nonlinear contexts or when weak solutions are sought. Although in [8] the authors consider the SIR epidemiological model as a basic case, their approach could be extended to other models, including the SEIR model considered here. Nonetheless, we aim to develop a different approach by providing an alternative proof for the convergence of the discrete solutions to the solution of the continuous system. In the context of epidemic dynamics modelling, the Banach method appears more direct to us, relying heavily on the properties of the space and the operators involved, making it suitable for well-posed problems where control over the solution is more explicit. Our approach is particularly useful for discussing the spectral properties of the integral operator related to a graphon.

Does the continuum model truly approximate some quantity of interest related to the dynamics of the discrete model for large finite n ? In this work, we will study in detail the asymptotic behaviour of the discrete system representing the dynamics of the SEIR model on a graph (network). In doing so, we will seek conditions for the analysis of disease propagation within the network, considering both biological parameters and parameters related to the network's topology. For the discrete operator, i.e., the evolution operator governing the behaviour of the epidemiological model on a graph, spectral properties are highly relevant. Moreover, for very large networks, computing part of the spectrum or performing numerical simulations of the behaviour of individual sub-populations at each node may not be feasible. It is therefore of interest to ascertain whether, in some cases, it is possible to extract information about the spectrum (for example, an estimate of the eigenvalue with the largest modulus) over time by using an operator associated with a reduced graph that involves significantly fewer degrees of freedom. For instance, this can occur if the integral kernel related to the reduced graph has a block-structured form. A similar strategy was proposed in [36, 35] for controlling large-scale linear networks, and in [34] to solve linear quadratic regulator problems for complex networks of dynamical systems.

In addition to their interpretation as the limit of growing networks, graphons can be employed as stochastic or deterministic models for network formation. Specifically, a network with n nodes can be generated by sampling n values x_i , $i = 1, \dots, n$, uniformly at random from the $[0, 1]$ interval, and connecting pairs with an independent probability $W(x_i, x_j)$. Note that this procedure typically produces dense networks. To generate sparse networks, the authors in [15] proposed connecting nodes with probability $\rho_n W(x_i, x_j)$, where $\rho_n \rightarrow 0$ as $n \rightarrow \infty$, but with ρ_n of order

greater than $\ln(n)/n$. In the following, we mainly focus on dense networks; however, most of the results discussed can be extended to the sparser case. We point out that a key task in network analysis is to estimate the underlying network-generating mechanism—namely, how the edges are formed. In practice, however, we usually observe only a tiny fraction of the edges, which makes it difficult to identify the true underlying mechanism. In the case of graphons, the challenging task is to infer the graphon itself from a set of observed networks generated according to it.

The paper is organised as follows. Sec 2 introduces the SEIR model on a graph, focusing on the interplay between disease transmission and contact distribution. While asymptomatic carriers are not explicitly modelled, they could be incorporated through extensions of our framework. Sects 3–4 derive the continuum limit of compartmental models on graphs via an asymptotic procedure based on graphons and examine its relation to discrete SEIR dynamics. Numerical experiments—using a Gamma-distributed number of contacts as in [9]—support the theory.

2. A prototype problem: SEIR model on graphs. We consider the SEIR compartmental model where individuals are classified into different population groups based on the infection status. The model tracks the number of people in each of the following categories: *Susceptibles* (individuals that may become infected), *Exposed* (individuals that have been infected with a pathogen, but due to the pathogen incubation period, are not yet infectious), *Infectious* (individuals that are infected with a pathogen and may transmit it to others), and *Recovered* (individual that is either no longer infectious or has been “removed” from the population). Indeed, we consider diseases with a latent phase during which the individual is infected but not yet infectious: a recent example of the application of this type of model is the description of the transmission of the COVID-19 disease [41].

In the scalar case, the total (initial) population, N , is categorised into four classes, namely, $s(t)$ (susceptible), $e(t)$ (exposed), $i(t)$ (infected-infectious), and $r(t)$ (recovered), where t is the time variable. The basic assumption for the scalar model is the homogeneously mixing population hypothesis, which, roughly speaking, means that a given infectious individual may transmit the disease to any susceptible individual at the same rate. Also, one postulates that all the individuals in the population have the same chances of interacting with each other. People move from S to E based on the number of contacts with I individuals, multiplied by the probability of infection β , where $\beta i(t)/N$ is the average number of contacts with infection per unit time of one susceptible person. The other processes taking place at time t are: the exposed E become infectious I with a rate μ and the infectious recover R with a rate γ . Recovered individuals do not flow back into the S class, as lifelong immunity is postulated. The fractions $1/\mu$ and $1/\gamma$ are the average disease incubation and infectious periods, respectively. We assume that the total population remain constant, i.e., $s(t) + e(t) + i(t) + r(t) = N$. Next, we consider the rescaled variables, which for simplicity we do not relabel, $s(t)/N \rightarrow s(t)$, $e(t)/N \rightarrow e(t)$, $i(t)/N \rightarrow i(t)$, $r(t)/N \rightarrow r(t)$. The ordinary differential equations (ODEs) governing the SEIR model are then

$$\begin{cases} \dot{s}(t) = -\beta s(t)i(t), & \dot{e}(t) = \beta s(t)i(t) - \mu e(t), \\ \dot{i}(t) = \mu e(t) - \gamma i(t), & \dot{r}(t) = \gamma i(t). \end{cases}$$

We consider a meta-population model and a network that is represented by a *simple graph* $\mathcal{G} = (V, E)$ with n vertices (nodes, regions, patches) and m edges (connections). Each edge is described by a couple of nodes (u, v) , $u, v \in V$. We order the nodes and label them with an integer index. We briefly recall that the entries of the adjacency matrix A of the input graph G are $a(i, j) = 1$ for any edge (i, j) of G , and we assume that the adjacency matrix of G is an irreducible matrix, i.e., there are no isolated and unreachable groups. In node j , the corresponding sub-population possesses N_j individuals, while for the global population N : $\sum_{j=1}^n N_j = N$. We assume that individuals can move to a different node, interact with people in that node, and then return to the original one. We denote by $\hat{a}_{jk}$ the total amount of the sub-population j that “goes” to node k and interacts with the people in that node. We call $\hat{A}$ the matrix with entries $\hat{a}_{jk}$, so that $\sum_{k=1}^n \hat{a}_{jk} = N_j$, $j = 1, \dots, n$. Associated to $\hat{A}$, let P^{out} the *probability outgoing matrix* with entries p_{jk}^{out} , where we denote by p_{jk}^{out} the probability (percentage) that the sub-population j “goes” to node k . In addition, we denote by P^{in} the *probability incoming matrix* with entries p_{jk}^{in} , where p_{jk}^{in} is now the probability (percentage) of the sub-population in k that “arrived” from j . Finally, let $M_j = \sum_{k=1}^n \hat{a}_{kj}$ be the total amount of people arrived in node $j = 1, \dots, n$, so that $\sum_{j=1}^n M_j = N$ again. Then, for any $j = 1, \dots, n$, $\sum_{k=1}^n p_{jk}^{out} = \sum_{k=1}^n p_{jk}^{in} = 1$. Moreover, we have $\hat{A} = \text{Diag}(N_1, N_2, \dots, N_n) P^{out} = P^{in} \text{Diag}(M_1, M_2, \dots, M_n)$, where $\text{Diag}(x_1, x_2, \dots, x_n)$ is the diagonal matrix with $(x_1, x_2, \dots, x_n)^T$ on the main diagonal. Following the SEIR model, four different discrete classes are considered for the status of individuals in each: susceptible, exposed, infectious, and recovered. Let $S_j(t)$, $E_j(t)$, $I_j(t)$, $R_j(t)$ the number of individuals in the node j at time t , $S_j(t) + E_j(t) + I_j(t) + R_j(t) = N_j$. We point out that we have assumed, as a hypothesis, a time interval in which we can not consider demography, therefore having constant values of local N_j . Without any interaction with other nodes, within a deterministic approach of the compartmental models, with continuous time t , the epidemic dynamics can be described by the following system of differential equations

$$\begin{cases} \dot{S}_j(t) = -\lambda S_j(t), & \dot{E}_j(t) = \lambda S_j(t) - \mu E_j(t), \\ \dot{I}_j(t) = \mu E_j(t) - \gamma I_j(t), & \dot{R}_j(t) = \gamma I_j(t), \end{cases}$$

where the parameter λ is the force of infection. With respect to the behaviour of an epidemic, λ is the rate at which susceptible individuals become infected or exposed, and it is a function depending on the number of infectious individuals: it contains information about the interactions between individuals that concur with the infection transmission. If we suppose that the population of N_j individuals mix at random, meaning that all pairs of individuals have the same probability of interacting, then the force of infection may be computed as:

$$\begin{aligned} \lambda = & \text{transmission rate} \times \text{effective number of contacts per unit time} \\ & \times \text{proportion of contacts infectious} \sim \beta \frac{I_j}{N_j}, \end{aligned}$$

where β is the infectious rate. We denote by $(s_j(t), e_j(t), i_j(t), r_j(t))$ the rescaled (percentage) quantities of susceptible, infected, removed at time t at the node j normalised to the number N_j of individuals associated with that node. Then, we obtain

$$\begin{cases} \dot{s}_j(t) = -\beta i_j(t) s_j(t), & \dot{e}_j(t) = \beta i_j(t) s_j(t) - \mu e_j(t), \\ \dot{i}_j(t) = \mu e_j(t) - \gamma i_j(t), & \dot{r}_j(t) = \gamma i_j(t), \end{cases}$$

where i_j stands for the derivative of the function ι_j . Now, we take a node j connected with the other nodes as encoded in matrix $\hat{A}$. The variable $S_j(t)$ can change due to the contribution of susceptible people that come from j that reached an adjacent node k and met infectious people in that node. Then, the contribution to $\dot{S}_j$ due to the interactions in node k is given by the $p_{jk}^{out} S_j = \hat{a}_{jk} s_j$ susceptible people that met a population in node k with a proportion of infectious people given by

$$\frac{\#\{\text{infectious people in node } k\}}{\#\{\text{total people in node } k\}} = \frac{\sum_{l=1}^n p_{lk}^{out} I_l}{\sum_{l=1}^n \hat{a}_{lk}} = \sum_{l=1}^n p_{lk}^{in} \iota_l.$$

Let the vectors $\mathbf{X}(t) = (x_1(t), x_2(t), \dots, x_n(t))^T \in \mathbb{R}^n$, with $X = S, E, I, R$, the *SEIR model on the graph G* is

$$\begin{cases} \dot{\mathbf{s}}(t) = -\beta \text{Diag}(\mathbf{s}(t)) A \mathbf{\iota}(t), & \dot{\mathbf{e}}(t) = \beta \text{Diag}(\mathbf{s}(t)) A \mathbf{\iota}(t) - \mu \mathbf{e}(t), \\ \dot{\mathbf{i}}(t) = \mu \mathbf{e}(t) - \gamma \mathbf{\iota}(t), & \dot{\mathbf{r}}(t) = \gamma \mathbf{\iota}(t), \end{cases} \quad (1)$$

where $A = P^{out}(P^{in})^T$ is a weighted adjacency matrix. We have assumed that the parameter β is the same in all nodes. It is possible to easily introduce a different parameter for each node, considering more heterogeneity in the model. Furthermore, both the parameters and the matrix A could be time-dependent: the analysis that we will make is easily adaptable to these cases as well. In particular, the change in the parameters, i.e. for β , may represent a change in the biomedical aspects of the epidemics, while a change in the matrix A is a social activity. Owing to the classical Cauchy Lipschitz Picard Lindelöf Theorem, the Cauchy problem obtained by coupling system (1) with the initial data

$$s_j(0) = s_{j0}, \quad e_j(0) = e_{j0}, \quad i_j(0) = i_{j0}, \quad r_j(0) = r_{j0}, \quad j = 1, \dots, n, \quad (2)$$

has a local in-time solution. Since s_j, e_j, i_j, r_j represent percentages of individuals, the modelling meaningful range is

$$0 \leq s_j(t), e_j(t), i_j(t), r_j(t) \leq 1, \quad s_j(t) + e_j(t) + i_j(t) + r_j(t) = 1, \quad (3)$$

for every $t \geq 0$ and every $j = 1, \dots, n$. The next result states that the solution of (1) does indeed attain values in the above range.

Lemma 2.1. *Assume that $0 \leq s_{j0}, e_{j0}, i_{j0}, r_{j0} \leq 1$ and $s_{j0} + e_{j0} + i_{j0} + r_{j0} = 1$, for every $j = 1, \dots, n$. Then, the solution of the Cauchy problem obtained by coupling (1) with (2) is global in time and satisfies (3).*

Proof. To establish the second condition in (3), it suffices to observe that $\dot{s}_j(t) + \dot{e}_j(t) + \dot{i}_j(t) + \dot{r}_j(t) = 0$ for every $j = 1, \dots, n$. We recall that, if the solution is bounded, then it can also be extended for every $t \geq 0$. Indeed, it suffices to show that $s_j(t), e_j(t), i_j(t), r_j(t) \geq 0$ for every t and every $j = 1, \dots, n$. By the continuous dependence of solutions of ODEs on parameters, it suffices to establish the same property for the family of perturbed systems

$$\begin{cases} \dot{s}_j^\varepsilon(t) = -\beta s_j^\varepsilon(t) \sum_{k=1}^n a_{jk} i_k^\varepsilon(t), & \dot{e}_j^\varepsilon(t) = \beta s_j^\varepsilon(t) \sum_{k=1}^n a_{jk} i_k^\varepsilon(t) - \mu e_j^\varepsilon(t) + \varepsilon, \\ \dot{i}_j^\varepsilon(t) = \mu e_j^\varepsilon(t) - \gamma i_j^\varepsilon(t) + \varepsilon, & \dot{r}_j^\varepsilon(t) = \gamma i_j^\varepsilon(t), \end{cases}$$

where $\varepsilon > 0$ is a parameter converging to 0^+ . First, we observe that, if $s_j^\varepsilon(t) = 0$ for some t , then $\dot{s}_j^\varepsilon(t) = 0$. By the uniqueness part of the Cauchy Lipschitz Picard Lindelöf Theorem, this implies that $s_j^\varepsilon(t) \equiv 0$ if $s_j^\varepsilon(0) = 0$ and hence that $s_j^\varepsilon(t) > 0$ for every t if $s_{j0} > 0$. Next, we set

$$\bar{t}_\varepsilon := \min\{t \geq 0 : e_j^\varepsilon(t) = 0 \text{ or } i_j^\varepsilon(t) = 0 \text{ for some } j = 1, \dots, n\},$$

and we separately consider the following cases. If there is $j = 1, \dots, n$ such that $e_j^\varepsilon(\bar{t}_\varepsilon) = 0$, then, since $s_j^\varepsilon(\bar{t}_\varepsilon), i_j^\varepsilon(\bar{t}_\varepsilon) \geq 0$, we have $\dot{e}_j^\varepsilon(\bar{t}_\varepsilon) \geq \varepsilon$ and hence $\bar{t}_\varepsilon = 0$ and $e_j^\varepsilon > 0$ in a left neighborhood of 0. If there is $j = 1, \dots, n$ such that $i_j^\varepsilon(\bar{t}_\varepsilon) = 0$, then $i_j^\varepsilon(\bar{t}_\varepsilon) \geq \varepsilon$ and hence $\bar{t}_\varepsilon = 0$ and $i_j^\varepsilon > 0$ in a left neighbourhood of 0. This implies that $0 \leq s_j^\varepsilon(t), e_j^\varepsilon(t), i_j^\varepsilon(t)$ for every $t \geq 0$. Since $\dot{r}_j^\varepsilon \geq 0$, then $r_j^\varepsilon(t) \geq 0$ for every $t \geq 0$. By letting $\varepsilon \rightarrow 0^+$, we conclude the proof of the lemma. $\square$

In the following, we adopt the notation $\mathbf{1} = [1, 1, \dots, 1]^\top$, $\mathbf{0} = [0, 0, \dots, 0]^\top$, and, for any vectors $\mathbf{x}, \mathbf{y} \in \mathbb{R}^n$ we write $\mathbf{x} << \mathbf{y} \Leftrightarrow x_i < y_i \ i = 1, 2, \dots, n$, $\mathbf{x} \leq \mathbf{y} \Leftrightarrow x_i \leq y_i \ i = 1, 2, \dots, n$ and $\mathbf{x} < \mathbf{y}$ if $\mathbf{x} \leq \mathbf{y}$ but $\mathbf{x} \neq \mathbf{y}$. The asymptotic behaviour of system (1) is described by the following Lemma.

Lemma 2.2. *Considering the SEIR system (1), the equilibrium points are $\mathbf{P}_\infty = (s_\infty, 0, 0, \mathbf{r}_\infty)$. Also, consider the Cauchy problem obtained by coupling (1) with (2). Under the same assumptions as in Lemma 2.1, every trajectory converges to an equilibrium point $\mathbf{P}_\infty = (s_\infty, 0, 0, \mathbf{r}_\infty)$ with $\mathbf{s}_\infty^\top \mathbf{1} + \mathbf{r}_\infty^\top \mathbf{1} = \mathbf{1}$.*

Proof. Let $(\mathbf{s}, \mathbf{e}, \mathbf{i}, \mathbf{r})$ be an equilibrium point. From the fourth equation in (1), we conclude that $i_j = 0$ for every $j = 1, \dots, n$. By plugging this equality into the third equation of (1), we conclude that $e_j = 0$ for every $j = 1, \dots, n$. This implies that the equilibria are in the form $\mathbf{P}_\infty = (\mathbf{S}_\infty, 0, 0, \mathbf{R}_\infty)$. We are left to prove the second part of the lemma. We recall Lemma 2.1 and, by using the fourth equation in (1) we conclude that, for every $j = 1, \dots, n$, the function r_j is monotone non-decreasing and hence has a limit as $t \rightarrow +\infty$. Also, the limit is confined between 0 and 1. By adding the third and the fourth equation in (1) we get that $i_j + r_j$ is monotone non-decreasing and also has a limit as $t \rightarrow +\infty$. We conclude that i_j has a limit as $t \rightarrow +\infty$. By using the first equation in (1) we infer that for every $j = 1, \dots, n$, s_j is monotone non-increasing and hence has a limit, which is confined between 0 and 1, as $t \rightarrow +\infty$. By adding the first and the second equation in (1) we get that, for every $j = 1, \dots, n$, $s_j + e_j$ is monotone non-increasing and hence has a limit as $t \rightarrow +\infty$. We eventually conclude that e_j has a limit for $t \rightarrow +\infty$. Since the limit point is finite, it must be an equilibrium. The condition $\mathbf{s}_\infty^\top \mathbf{1} + \mathbf{r}_\infty^\top \mathbf{1} = \mathbf{1}$ follows from the equality $s_j(t) + e_j(t) + i_j(t) + r_j(t) = 1$ for every $j = 1, \dots, n$ and $t \geq 0$. $\square$

We now focus on the transient behaviour of system (1). If $\mathbf{s}(t) > \mathbf{0}$, then the matrix $B(t) = \text{Diag}(\mathbf{s}(t))A$ is a non-negative, irreducible matrix. Owing to the Perron-Frobenius Theorem [23], this implies that $B(t)$ has a positive eigenvalue, which we denote by $\lambda_M(t) = \rho(B(t))$, equal to the spectral radius. Also, there is an associated positive eigenvector, which we denote by $\mathbf{V}_M(t) >> \mathbf{0}$. Note that, if $\mathbf{s}(t) \rightarrow \mathbf{0}$, then $\lambda_M(t) \rightarrow 0$. The next result focuses on the transient behaviour of the solutions of (1).

Theorem 2.3. *Consider system (1), let $\lambda_M(t)$ be the dominant eigenvalue of $B(t)$ and $\mathbf{V}_M(t) >> \mathbf{0}$ the corresponding positive left eigenvector.*

- (1) *Assume that for some $\tau \geq 0$ we have $\beta\lambda_M(\tau) \leq \gamma$ then $q_\tau(t) = \mathbf{V}_M(\tau)^\top (\mathbf{e}(t) + \mathbf{i}(t))$ is monotonically decreasing to 0 on $[\tau, +\infty[$.*
- (2) *Assume that $\beta\lambda_M(\tau) > \gamma$ for some $\tau \geq 0$, then there is $t^* > \tau$ such that $q_\tau(t) = \mathbf{V}_M(\tau)^\top (\mathbf{e}(t) + \mathbf{i}(t))$ is monotone non decreasing on $[\tau, t^*[$.*
- (3) *If the limit point of the trajectory under consideration is $(0, 0, 0, 1)$, then there is $\tau > 0$ such that $\beta\lambda_M(\tau) \leq \gamma$ and item (1) applies.*

Proof. We first establish item (1). By multiplying the sum of the second equation and the third equation in (1) by $\mathbf{V}_M(\tau)$, we get

$$\mathbf{V}_M(\tau)^\top [\dot{\mathbf{e}}(t) + \dot{\mathbf{i}}(t)] = \mathbf{V}_M(\tau)^\top (\beta \text{Diag}(\mathbf{s}(t))A\mathbf{z}(t) - \gamma\mathbf{z}(t)).$$

Since $\mathbf{s}(t)$ is monotone non increasing (e.g., proof of Lemma 2.2), then

$$\mathbf{V}_M(\tau)^\top (\beta \text{Diag}(\mathbf{s}(t))) \leq \mathbf{V}_M(\tau)^\top (\beta \text{Diag}(\mathbf{s}(\tau))),$$

for every $\tau \geq t$. This yields

$$\frac{d\mathbf{V}_M(\tau)^\top (\mathbf{e}(t) + \mathbf{z}(t))}{dt} \leq \mathbf{V}_M(\tau)^\top (\beta \text{Diag}(\mathbf{s}(\tau))A\mathbf{z}(t) - \gamma\mathbf{z}(t)), \quad t \geq \tau.$$

Since $\mathbf{V}_M(\tau)^\top (\beta \text{Diag}(\mathbf{s}(\tau))A) = \lambda_M(\tau)\mathbf{V}_M(\tau)^\top$, then

$$\frac{d\mathbf{V}_M(\tau)^\top (\mathbf{e}(t) + \mathbf{z}(t))}{dt} \leq (\beta\lambda_M(\tau) - \gamma) \mathbf{V}_M(\tau)^\top \mathbf{z}(t), \leq 0.$$

To establish the last inequality we have used the inequalities $(\beta\lambda_M(\tau) - \gamma) \leq 0$, $\mathbf{V}_M >> 0$, and $\mathbf{z}(t) \geq 0$. The above inequality implies that $\mathbf{V}_M(\tau)^\top (\mathbf{e}(t) + \mathbf{z}(t))$ is monotone non increasing on $[\tau, +\infty[$, and henceforth converging as $t \rightarrow +\infty$. Owing to Lemma 2.2, the limit is 0. To establish item (2), it suffices to point out that, if $\beta\lambda_M(\tau) > \gamma$, then $\frac{d}{dt} (\mathbf{V}_M(\tau)^\top (\mathbf{e}(t) + \mathbf{z}(t)))_{t=\tau} \geq 0$. To establish item (3), we point out that, if $\mathbf{s}(t)$ converges to 0, then $\lambda_M(t)$ converges to 0 and hence the condition $\beta\lambda_M(\tau) \leq \gamma$ is satisfied for sufficiently large τ . $\square$

Theorem 2.3 implies that, if the parameters β , γ , and the matrix A can change over time, the conditions of the beginning of the epidemic spread or a decrease in quantity $\mathbf{e}(t) + \mathbf{z}(t)$ could occur several times. This property may justify the occurrence of multiple epidemic waves. If the graph G is a complete graph K_n (K_n is a simple undirected graph where every pair of distinct vertices is connected by a unique edge), then we recover the scalar SEIR model by setting $s(t) = \sum_j s_j(t)$, $e(t) = \sum_j e_j(t)$, $i(t) = \sum_j i_j(t)$, $r(t) = \sum_j r_j(t)$. If the proposed model can describe the epidemic phenomenon sufficiently well, then we could consider some problems relating to the forecast of the epidemic itself. Throughout the following, we will denote by $\text{Diag}(v_1, v_2, \dots, v_n)$ a diagonal matrix $n \times n$ with the vector $(v_1, v_2, \dots, v_n)$ on its main diagonal. To study the behaviour under policies aimed at restricting the flow of individuals, such as during a lockdown, we can, for example, introduce the following diagonal matrices $U_{in} = \text{Diag}(u_{loc(i)})_{i=1}^n$ and $V_{out} = \text{Diag}(v_{loc(i)})_{i=1}^n$, where $u_{loc(i)} \in (0, 1]$, $i = 1, \dots, n$ are the control variables for the incoming individuals into the node i , while $v_{loc(i)} \in [0, 1]$, $i = 1, \dots, n$ are the control variables of the outgoing individuals from the node i to other nodes. Then, the routing matrix A and the associated matrices in the model (1), change as $A_{in,out} = UAV$. Before a viral infection starts, the recovery rate γ is usually out of control, then the only way to satisfy the no-epidemic condition is either: control the transmission (which means to reduce β and/or interactions), or immunisation (meaning to increase $r(0)$). Moreover, we aim to limit the economic and social impact as the epidemic occurs. Because the supply of healthcare services is inelastic in the short run, it is important to maintain the maximum number of sick individuals (at least seriously) below the capacity of the actual healthcare system. This result may be achieved by lowering the transmission rate and by controlling the inflow and the outflow of individuals from and into a node.

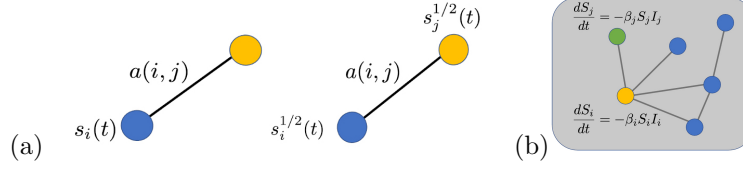


FIGURE 1. (a) Un-symmetric and symmetric weights for the SEIR models on a graph, (b) SEIR model on graphs starting from the governing differential equations of the 1D SEIR model at each node.

Remark 2.4. We emphasise that this type of policy, however, has a social and economic cost and only recent works [1, 11, 45] have started investigating the tradeoff between epidemic and economic costs. To study the “lockdown policies” applied to the various groups (nodes), we have to combine a measure of social cost (i.e. hospitalisation cost), economic loss, and, above all, loss of life. The first objective consists of minimising both total (excess) deaths during the epidemic and/or the public health cost for the hospitalised people. We suppose that it is possible to estimate some index C_H related to the severity of the epidemic in a time interval $[0, T]$, by weighing the total number of infected $C_H = \int_0^T F_s(\mathbf{I}(t))dt$, where the integral is to be understood component by component. Examples for the cost function F_s can be derived by assuming that the number of hospitalised or deceased individuals is proportional to the current number of infected $\mathbf{I}(t)$ as $F_s(\mathbf{I}(t)) = \mathbf{C}^T \mathbf{I}(t)$ (with $\mathbf{C}^T$ constant weight vector).

The reduction of interactions between individuals affects economic activities. A possible model C_E for the economic loss involves the evaluation of the reduction of flow of individuals between nodes with a cost function $C_E = \int_0^T F_E(A - A_{in,out})dt$. A simple choice for the F_E function is the $F_E(A - A_{in,out}) = \hat{\mathbf{C}}^T (A - A_{in,out}) \cdot \mathbf{1}$, with constant weight vector $\hat{\mathbf{C}}^T$. Then, an optimal strategy during the time interval $[0, T]$ is obtained by minimising a global cost function of the following type, $\min_{\mathbf{U}_{in}, \mathbf{V}_{out}} (C_H - C_E)$, with respect to the choice of control variables $\mathbf{U}_{in}, \mathbf{V}_{out}$. The economic damage is supposed to depend mainly on the lost productivity due to illness and also on the forgone productivity due to the blocked sub-populations, which is a function of the quantity $(A - A_{in,out})$ related to the mobility. If the meta-population model represents a non-geographical subdivision but instead is dependent on certain individuals’ features (e.g., age, profession, habits), then we can include information linked to these characteristics.

Spectrum of the SEIR model on graphs. In the following, assume that all the components of $\mathbf{s}(t)$ are strictly positive. Owing to the proof of Lemma 2.1, this amounts to assuming that they are strictly positive at $t = 0$. Let A be the adjacency matrix of the input graph G , i.e., $a(i, j) = 1$ for any edge (i, j) of G . The coefficient matrix $B(t) := \text{Diag}(\mathbf{s}(t))A$ of the SEIR model on a general simple graph, can be interpreted as a weighted adjacency matrix, where the weight associated with the edge (i, j) is $b_{ij}(t) := s_i(t)a_{ij}$; indeed, the weighted adjacency matrix is not symmetric and the weighted graph is directed. To study the spectrum of $B(t)$ and eventually work with a symmetric weighted adjacency matrix, we introduce its “symmetrisation” (Fig., 1) $B_{sym}(t) := \text{Diag}(\mathbf{S}(t))^{1/2} A \text{Diag}(\mathbf{S}(t))^{1/2}$, where the weight associated with the edge (i, j) is $b_{ij}^{sym}(t) := s_i^{1/2}(t)a_{ij}s_j^{1/2}(t)$. Furthermore,

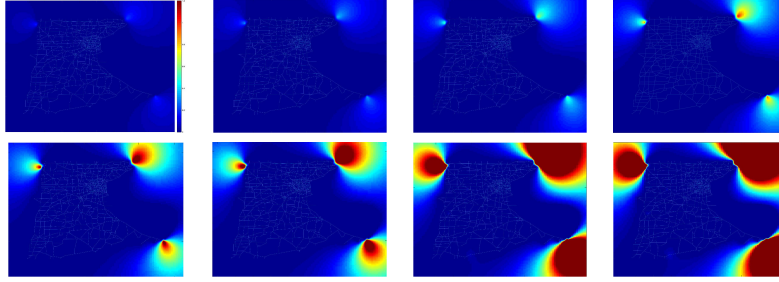


FIGURE 2. Colourmap of the evolution of the variable $I(\cdot)$ (time increases from top to bottom, left to right) on a graph with constant weights, according to the symmetric SEIR model in Eq. (4).

the matrices $B(t)$ and $B_{sym}(t)$ have the same eigenvalues; in fact,

$$\begin{aligned} B(t) - \nu I &= \text{Diag}(S(t))^{1/2} \left(\text{Diag}(\mathbf{s}(t))^{1/2} A \text{Diag}(\mathbf{s}(t))^{1/2} - \nu I \right) \text{Diag}(\mathbf{s}(t))^{-1/2} \\ &= \text{Diag}(\mathbf{s}(t))^{1/2} (B_{sym}(t) - \nu I) \text{Diag}(\mathbf{s}(t))^{-1/2}. \end{aligned}$$

Let $\mathbf{v}$ be an eigenvector of $B(t)$ with eigenvalue ν . Then,

$$\begin{aligned} B(t)\mathbf{v} &= \nu\mathbf{v} \iff \text{Diag}(\mathbf{s}(t))^{-1/2} B\mathbf{v} = \nu \text{Diag}(\mathbf{s}(t))^{-1/2} \mathbf{v} \\ &\iff \mathbf{y} := \text{Diag}(\mathbf{s}(t))^{-1/2} \mathbf{v}, \end{aligned}$$

$$\text{Diag}(\mathbf{s}(t))^{-1/2} B \text{Diag}(\mathbf{s}(t))^{1/2} \mathbf{y} = \nu \mathbf{y} \iff B_{sym}(t) \mathbf{v} = \nu \mathbf{v}.$$

Indeed, $\mathbf{y} := \text{Diag}(\mathbf{s}(t))^{-1/2} \mathbf{v}$ is an eigenvector of $B_{sym}(t)$ with eigenvalue ν , i.e., the spectrum of $B(t)$ is real and it uniquely identifies the spectrum of $B_{sym}(t)$, and vice versa. Note that the eigenvectors $\mathbf{y}_i := \text{Diag}(\mathbf{s}(t))^{-1/2} \mathbf{v}_i$, $i = 1, \dots, n$ are not orthonormal. From these properties, we consider the reduced (the vector $\mathbf{r}$ can be reconstructed from vectors $\mathbf{s}$, $\mathbf{z}$, $\mathbf{e}$) *SEIR* and *symmetric SEIR models on a general simple graph* (Fig., 2)

$$\dot{\mathbf{s}} = -\beta B_{sym}(t) \mathbf{z}, \quad \dot{\mathbf{e}} = \beta B_{sym}(t) \mathbf{z} - \mu \mathbf{e}, \quad \dot{\mathbf{i}} = \mu \mathbf{e} - \gamma \mathbf{z}. \quad (4)$$

Bounds to the spectrum of SEIR on graphs Let d_{max} be the maximum degree of a node in the input graph G , and let d_{avg} be the average degree of a node in G . Let $\nu_1 \geq \nu_2 \geq \dots \geq \nu_n$ be the eigenvalues of the adjacency matrix A of G . Then, the bound $d_{avg} \leq \nu_1 \leq d_{max}$ is applied to estimate the variation of the eigenvalues in linear time. The maximum eigenvalue is computed efficiently through the Arnoldi method [38]. We now derive upper and lower bounds to the eigenvalues of $B(t)$, or equivalently $B_{sym}(t)$ (same eigenvalues):

$$\begin{aligned} \nu_1(B(t)) &= \nu_1(B_{sym}(t)) = \max_{\mathbf{v} \neq \mathbf{0}} \frac{\mathbf{v}^\top \text{Diag}(\mathbf{s}(t))^{1/2} A \text{Diag}(\mathbf{s}(t))^{1/2} \mathbf{v}}{\mathbf{v}^\top \mathbf{v}} \\ &= \max_{\mathbf{y} \neq \mathbf{0}} \frac{\mathbf{y}^\top A \mathbf{y}}{\mathbf{y}^\top \text{Diag}(\mathbf{s}(t))^{-1} \mathbf{y}}, \quad \mathbf{y} := \text{Diag}(\mathbf{s}(t))^{1/2} \mathbf{v}, \\ &\leq \frac{\nu_1(A)}{\min_i \{s_i^{-1}(t)\}} \leq \nu_1(A) \max_i \{\|s_i\|_\infty\} \leq d_{max} \max_i \{\|s_i\|_\infty\}. \end{aligned}$$

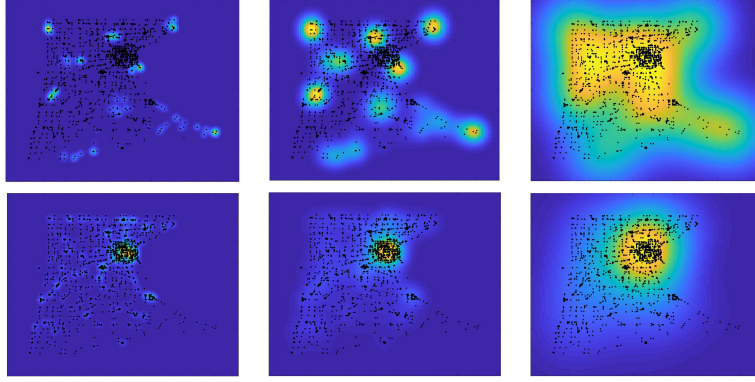


FIGURE 3. Colormap of the evolution of the variable $I(\cdot)$ (time increases from left to right) on a graph with (1st row) constant weights and (2nd row) positive weights (larger weights in the selected seed point), according to the symmetric SEIR model (5).

In an analogous way,

$$\begin{aligned} \nu_1(B_{sym}(t)) &= \max_{\mathbf{v} \neq 0} \frac{\mathbf{v}^\top B_{sym}(t) \mathbf{v}}{\mathbf{v}^\top \mathbf{v}} \geq \frac{\mathbf{1}^\top B_{sym}(t) \mathbf{1}}{\mathbf{1}^\top \mathbf{1}} \geq \frac{1}{n} (\mathbf{1}^\top B_{sym}(t) \mathbf{1}) \\ &\geq \frac{1}{n} \nu_1(A) \sum_i s_i(t) \geq \nu_1(A) \min_i \{s_i(\cdot)\} = d_{avg} \min_i \{s_i(\cdot)\}. \end{aligned}$$

SEIR model and graph Laplacian Let D be the diagonal matrix whose entries are the degrees $d := (d_i)_i$ of the nodes of the input graph and $L := D - A$ the corresponding Laplacian matrix. Then, we rewrite the SEIR model as

$$\begin{aligned} \dot{\mathbf{s}} &= -\beta \text{Diag}(\mathbf{s}(t)) [D - D + A] \mathbf{z}(t) \\ &= -\beta \text{Diag}(\mathbf{s}(t)) [D - L + I_n] \mathbf{z}(t) \\ &= -\beta [\text{Diag}(\mathbf{s}(t))D - \text{Diag}(\mathbf{s}(t))L + \text{Diag}(\mathbf{s}(t))] \mathbf{z}(t) \\ &= -\beta [\text{Diag}((d+1) \circ \mathbf{s}(t)) - \text{Diag}(\mathbf{s}(t))L] \mathbf{z}(t), \end{aligned} \tag{5}$$

where $\text{Diag}(\mathbf{s}(t))L$ is the weighted Laplacian matrix which is related to the diffusion on the graph (Fig. 3). In this case, the models can be regarded as specific non-local epidemiological models represented by integro-differential equations. The kernel of the integral operator now describes diffusion on a graph (see, for example, [56]). The following analysis can also be applied to these non-local models when information about the type of spatial heterogeneity of the population involved is available.

3. Continuum limit of the epidemiological model on graphs. We prove the convergence of the sequence of sub-populations defined on graphs with an increasing number of nodes, where the underlying graphs converge to a graphon. We first introduce graphons and their main properties, along with their implications for the convergence theorem (Sect. 3.1). Then, we address the continuous limit (Sects. 3.2, 3.3) and the convergence of SEIR epidemiological models (Sect. 3.4). Our approach interprets the evolution of populations on a graph as the solution of a differential equation in a suitable Banach space. Related results can be obtained

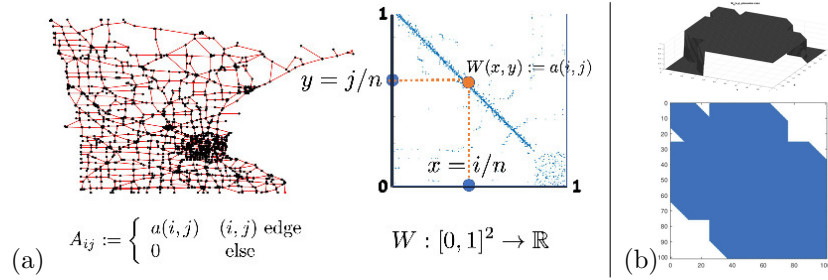


FIGURE 4. (a) Graphon defined by the adjacency matrix of the input graph. (b) Piecewise (or step) graphon for a block model of the epidemic spread.

by extending the framework of [8], which combines a variational formulation with a weak convergence method; however, here we adopt a different functional setting and provide an alternative proof. We also present approximation results relevant for numerically simulating epidemic dynamics on graphs and graphons. Throughout, we restrict attention to the symmetric case—i.e., symmetric adjacency matrices corresponding to simple undirected graphs—which does not preclude applications to control problems or to the study of asymptotic behaviours, as discussed in Sect. 2.

3.1. Basic facts about graphons. Graphon theory was introduced and developed in recent years by Lovász, Szegedy, Borgs, Chayes, Sós, and Vesztegombi among others [14, 15, 16, 18, 46]. A graph $G = (V, E)$ is a set of nodes (vertices) $V(G) = \{1, 2, \dots, n\}$, usually $n = |V(G)|$ where $|\cdot|$ denotes the cardinality of a set, and a set of edges $E(G) \subseteq V \times V$ between the vertices. In what follows, the graphs will be simple, without loops or multiple edges, and finite unless otherwise specified. Weights (real numbers) will be given to the edges of a graph to make it an edge-weighted graph. Moreover, we assume that the graph is undirected, i.e., we identify the edges (i, j) and (j, i) . Let $A = (A_{ij})$ be the adjacency matrix of the graph:

$$A_{ij} = \begin{cases} 1 & \text{if } (i, j) \text{ is an edge,} \\ 0 & \text{otherwise.} \end{cases}$$

Let G and H be graphs, a map ϕ from $V(H)$ to $V(G)$ is a homomorphism if it preserves edge adjacency, that is if for every edge (i, j) in $E(H)$, $(\phi(i), \phi(j))$ is an edge in $E(G)$. Denote by $\text{hom}(H, G)$ the number of homomorphisms from H to G . For example for H with one node and no edge $\text{hom}(H, G) = |V(G)|$, instead when H has two nodes and one edge $\text{hom}(H, G) = |E(G)|$, or when H has three vertices and $E(H) = \{(1, 2), (2, 3), (3, 1)\}$, $\text{hom}(H, G)$ is 6 times the number of triangles in G . Normalising by the total number of possible maps, we get the density of homomorphisms from H to G , $t(H, G) = \frac{\text{hom}(H, G)}{|V(G)|^{|V(H)|}}$. It is defined that a sequence of simple graphs $\{G_n\}_{n \in \mathbb{N}}$ is convergent if G_n becomes more and more similar as n goes to infinity.

Definition 3.1. A sequence of graphs $\{G_n\}_{n \in \mathbb{N}}$ is said to be left convergent if the sequences $t(H, G_n)$ converges for $n \rightarrow \infty$, for every simple graph H .

The breakthrough results of Lovász and Szegedy [46] are that a (left) convergent undirected graph sequence has a limit object, which can be represented as a measurable function.

Definition 3.2. A *graphon* is a bounded measurable functions $W : [0, 1]^2 \rightarrow \mathbb{R}$ that satisfy $W(x, y) = W(y, x)$ for all $x, y \in [0, 1]$.

Let $\mathcal{W}$ denote the space of all the graphons and $\mathcal{W}_0$ is the set of graphons with values in $[0, 1]$. Due to the meaning of the connections between different subpopulations, we consider only graphons in $\mathcal{W}_0$ for our models. We give below the representation Theorem of Lovász and Szegedy [47].

Theorem 3.3. *For every (left) convergent sequence of simple graphs, there is $W \in \mathcal{W}_0$ such that*

$$t(H, G_n) \rightarrow t(H, W) := \int_{I^{|V(H)|}} \prod_{i,j \in E(H)} W(x_i, x_j) dx \quad (6)$$

for every simple graph H , where $I = [0, 1]$. Moreover, for every $W \in \mathcal{W}_0$ there is a sequence of graphs $\{G_n\}_{n \in \mathbb{N}}$ satisfying (6).

It is possible to represent a graph G with a graphon from a suitable family of graphons (Fig. 4a). If $|V(G)| = n$ and choosing any labelling of the nodes, we divide the interval $[0, 1]$ in n sub-intervals I_j^n , $j = 1, 2, \dots, n$ as

$$I_1^n = \left[0, \frac{1}{n}\right]; \quad I_j^n = \left[\frac{j-1}{n}, \frac{j}{n}\right] \quad j = 2, \dots, n, \quad (7)$$

and define the piecewise constant graphon W_G by

$$W_G(x, y) = a_{ij} \text{ if } (x, y) \in I_i^n \times I_j^n. \quad (8)$$

To formalise the convergence of the associated graphons to a graph, we define a metric on the set of labelled graphons. By analogy with the matrix cut norm [33], the cut norm of $W \in \mathcal{W}_0$ is defined as $\|W\|_{\square} := \sup_{S, T \subseteq [0, 1]} \left| \int_{S \times T} W(x, y) dx dy \right|$, where the supremum is taken over all measurable subsets S and T . We point out that the notion of cut-norm for the graphons associated with a sequence of graphs is connected with the notion of the (left) convergence for graph sequences [17, Theorem 3.8]. Loosely speaking, a sequence of graphs is left convergent if the local structure of the graphs is asymptotically stable, in the sense that asymptotically the graphs contain the “same number of copies” of any given subgraph. A drawback of the notion of the cut norm is related to the fact that for two graphs G, G' that are the same but with different node labelling, the corresponding adjacency matrices are not the same. Then, we have $\|W_G - W_{G'}\|_{\square} \neq 0$. This observation leads to the definition of the cut distance.

Definition 3.4. Let $\mathcal{M}$ the set of all measure-preserving bijections $\phi : [0, 1] \rightarrow [0, 1]$, the cut distance between $W, U \in \mathcal{W}$ is defined as $\delta_{\square}(W, U) = \inf_{\phi, \psi \in \mathcal{M}} \|W^{\phi} - U^{\psi}\|_{\square}$, where $W^{\phi}(x, y) = W(\phi(x), \phi(y))$, $U^{\psi}(x, y) = W(\psi(x), \psi(y))$.

Since the cut metric of two different graphons can be zero, strictly speaking, it is not a metric. By identifying graphons U and W for which $\delta_{\square}(W, U) = 0$, we can construct a metric space $(\mathcal{W}_0, \delta_{\square})$ that is compact under this identification [48]. For a sequence of graphons $\{W_n\}_{n \in \mathbb{N}}$ in $\mathcal{W}_0$ it is possible to prove [17] that the convergence of $t(H, W_n)$, as $n \rightarrow \infty$, for any simple graph H is equivalent to requesting that $\{W_n\}_{n \in \mathbb{N}}$ is a Cauchy sequence for $\delta_{\square}$ or that exists $W \in \mathcal{W}_0$ such that $\delta_{\square}(W_n, W) \rightarrow 0$. Using the association between simple graphs and graphons, we have the following result [17].

Theorem 3.5. *Let $\{G_n\}_{n \in \mathbb{N}}$ be any (left) convergence sequence of simple graphs. There exists a graphon $W \in \mathcal{W}_0$ such that $\lim_{n \rightarrow \infty} \delta_{\square}(W_{G_n}, W) = 0$. Conversely, every $W \in \mathcal{W}_0$ is a limit in the cut metric of a convergent sequence of simple graphs.*

The limit in Theorem 3.5 is unique up to the identification of graphons with a cut distance equal to zero. Graphons are then the limit objects of converging graph sequences. As compared to [50, 51], we handle the time-dependent case, the biological characteristics of the epidemics and the contact dynamics can change with respect to time. Moreover, we consider not only a scalar dynamical system on the single node but a vectorial one, and, from the technical hypothesis, we do not require that $W \in L^2([0, 1]^2)$. In recent literature, it is possible to find related works using graphons to study epidemics spread, e.g. [35, 63, 6, 26].

3.2. Convergence of sequence of graphons. We now discuss the continuum limit of compartmental epidemiological models on graph sequences for the case of the SEIR model only, but we are confident our results extend to a large class of compartmental models. Considering the SEIR model defined on a sequence of graphs where the number n of vertices diverges, we want to analyse the limit $n \rightarrow +\infty$. To achieve this, we rely on the graphon theory, which was introduced and discussed in the Introduction. We will assume that:

- g1) the matrix A in the system (1) is a symmetric irreducible matrix, which means that we have the same probability of going from node i to node j and vice versa.
- g2) The graph sequence $\{G_n\}_{n \in \mathbb{N}}$ is a dense sequence, that is, the order of growth of the number of edges of the graphs: $|E(G_n)| = O(|V(G_n)|^2)$ as $n \rightarrow \infty$.
- g3) The parameters β, μ, γ are bounded, integrable, positive functions with respect to the time t .

We point out that, for simplicity, we have considered the matrix of weights A constant and symmetric but that our analysis can easily be extended also to the case of a matrix A variable with time, assuming that it remains irreducible, not negative, and bounded. Finally, our epidemiological models involve the subset $\mathcal{W}_0$ of graphons $W : [0, 1]^2 \rightarrow [0, 1]$, and we will refer to this set as a space of graphons in what follows.

The cut distance in Definition 3.4 reflects well the structural similarities between the two graphs. Moreover, the cut metric is a key tool to study both the convergence and equivalence of graphons. Roughly speaking, the set of simple finite graphs endowed with the cut metric gives rise to a metric space, and the completion of this space is the space of graphons. Graphons, then, are limits of graph sequences in the cut metric. The entries of the matrix of the weights of the model (1) belong to the interval $[0, 1]$, then we will consider the set $\mathcal{W}_0$ as a space of graphons, then $W \in L^1([0, 1]^2)$. It follows that $\|W\|_{\square} = 0$ is equivalent to requiring that $W = 0$ almost everywhere ([43], Lemma 4.7). The cut distance $\delta_{\square}$ is a pseudo-metric; by identifying graphons V and W for which $\delta_{\square}(V, W) = 0$, we can construct the metric space G_0 , which denotes the image of $\mathcal{W}_0$ under this identification. The space G_0 provided with the cut distance is a compact space. With a customary abuse of notation, we refer to both W and its equivalence class as graphons.

For a sequence of simple graphs (and of the corresponding graphons), we have to compute the cut norm of a symmetric matrix. Unfortunately, this problem is unlikely to be tractable, even in an approximate sense. Alon and Naor [3]

relate the cut norm of a symmetric matrix to its Grothendieck norm. It is followed by the results of Grothendieck that the cut norm is between two absolute constant multiples of the Grothendieck norm. The Grothendieck norm is polynomial time computable to arbitrary precision. So we can compute, in polynomial time, an approximation of the cut norm with a multiplicative error less than a constant. Besides the cut norm, it is possible consider the $L^p([0, 1]^2)$ norm for a graphon $W \in \mathcal{W}_0$, $\|W\|_p = \left(\int_{[0, 1]^2} W^p(x, y) dx dy \right)^{1/p}$. On $\mathcal{W}_0$ ([46], Sect. 12.4),

$\|W\|_{\square} \leq \|W\|_{L^1} \leq \|W\|_{L^2} \leq \|W\|_{L^1}^{1/2}$ and convergence with respect to the L^1 norm implies convergence with respect to the cut-norm. Moreover for a 0 – 1 valued graphon W , which is associated to the adjacency matrix, and for a sequence $\{W_n\}$ of graphons such that $\|W_n - W\|_{\square} \rightarrow 0$, then $\|W_n - W\|_{L^1} \rightarrow 0$ ([46], Proposition 8.24). Also, the construction of $\delta_{\square}$ can be extended to any other norm that is invariant under measure-preserving maps, for example $\delta_1(V, W) = \inf_{\phi \in \mathcal{M}} \|V - W^{\phi}\|_1$ and $\delta_2(V, W) = \inf_{\phi \in \mathcal{M}} \|V - W^{\phi}\|_2$.

For any graphons $V, W \in \mathcal{W}_0$, $\delta_{\square}(V, W) \leq \delta_1(V, W) \leq \delta_2(V, W)$ are immediate. Then, the $\delta_{\square}$ distance is dominated by δ_1 and δ_2 , but convergence rates in $\delta_{\square}$ distance could be significantly faster. With additional properties, it is possible to obtain the convergence in the metric δ_1 (or δ_2) from the $\delta_{\square}$ convergence. For example ([62], Lemma 1.8) if the sequence of $\{W_n\}_{n \in \mathbb{N}}$, $W_n \in \mathcal{W}_0$, is a $\delta_{\square}$ convergent sequence with limit W , and if $\lim_{n \rightarrow \infty} \|W_n\|_2 = \|W\|_2$, then the sequence converge to W also in δ_1 . In this work, we focus on the δ_1 metric and in L^1 -based approach to study the convergence of the solutions of a sequence of models (1). Other Authors consider the L^2 framework [36, 35] and the Hilbert–Schmidt kernel operators theory, while in [50] the graphons are assumed to be Lipschitz continuous.

3.3. The continuum limit of epidemiological models. We now discuss our main result concerning the continuum limit of the SEIR model defined on sequences of graphs. Assumption g3) introduces the possibility that the parameters β , γ , μ , are positive time-dependent functions. In this way, it is possible to introduce into the model any changes over time due to external interventions (e.g. lockdown or social distancing) rather than the evolution of the biomedical parameters related to the epidemic. We consider a sequence of simple graph $\{G_n\}_{n \in \mathbb{N}}$, where G_n has n vertices $\{1, \dots, n\}$ and irreducible adjacency matrix. Also, $(a_{jk}^n)_{j,k=1, \dots, n}$ denotes the weighted adjacency matrix of the system (1). We will assume the functions $\beta_j^n(t)$, $\gamma_j^n(t)$, $\mu_j^n(t)$ at the node j of G_n are continuous. More general hypotheses can, however, be considered, considering also discontinuous, but bounded, as for the theory of the Carathéodory differential equations, e.g. [32]: the following results also extend to this case. Then, we consider the following sequence of the SEIR model defined on the set of vertices of the graphs G_n ,

$$\begin{cases} \frac{ds_j^n(t)}{dt} = -s_j^n(t) \frac{1}{n} \sum_{k=1}^n \beta_k^n(t) a_{jk}^n i_k^n(t) \\ \frac{de_j^n(t)}{dt} = s_j^n(t) \frac{1}{n} \sum_{k=1}^n \beta_k^n(t) a_{jk}^n i_k^n(t) - \mu_j^n(t) e_j^n(t) \\ \frac{di_j^n(t)}{dt} = \mu_j^n(t) e_j^n(t) - \gamma_j^n(t) i_j^n(t) \\ \frac{dr_j^n(t)}{dt} = \gamma_j^n(t) i_j^n(t) \\ s_j^n(0) = s_{j,0}^n, e_j^n(0) = e_{j,0}^n, i_j^n(0) = i_{j,0}^n, r_j^n(0) = r_{j,0}^n. \end{cases} \quad j = 1, \dots, n \quad (9)$$

We denote by $\mathbf{s}^n, \mathbf{e}^n, \mathbf{i}^n, \mathbf{r}^n : [0, +\infty) \rightarrow [0, 1]^n$ the solution vectors of (9), with j -th component given by $s_j^n, e_j^n, i_j^n, r_j^n$, $j = 1, \dots, n$, respectively. For each integer value n , using the sub-intervals as defined in (7), we associate a piecewise graphon W_{G_n} in (8). To discuss the limit $n \rightarrow +\infty$ by applying the theory of graphons, we, first of all, have to regard the functions $\mathbf{s}^n, \mathbf{i}^n, \mathbf{r}^n : \mathbb{R}^+ \rightarrow [0, 1]^n$ as functions defined on $\mathbb{R}^+ \times [0, 1]$. To this end, in the following, we always identify any function $\mathbf{u} : \mathbb{R}^+ \rightarrow \mathbb{R}^n$, $\mathbf{u} = (u_j)_{j \in V(G_n)}$, with the piecewise constant function

$$\mathbf{u}_n(t, x) := \sum_{j=1}^n u_j(t) \mathbb{1}_{I_j^n}(x) \quad (10)$$

where $\mathbb{1}_{I_j^n}$ is the characteristic function of the interval $I_j^n = [(j-1)n^{-1}, jn^{-1}[$. Furthermore, for a function $v(t, x)$, $(t, x) \in (\mathbb{R}^+ \times [0, 1])$, we set $v_j^n(t) := \langle v(t, \cdot) \rangle_{I_j^n}$, where we denote with $\langle v \cdot \rangle_{I_j^n}$ the average of the function on the set $I_j^n := [(j-1)n^{-1}, jn^{-1}[$, and $v_n(t, x) = \sum_{j=1}^n v_j^n(t) \mathbb{1}_{I_j^n}(x)$. Whenever we say that a sequence of functions defined on the vertices converges to a limit function defined on $[0, 1]$, we always mean that the corresponding piecewise constant functions are defined as in (10) converge to the given limit. We are now ready to introduce the discrete graphon representation of (9)

$$\begin{cases} \partial_t s_n(t, x) = -s_n(t, x) \int_0^1 \beta_n(t, y) W_{G_n}(x, y) i_n(t, y) dy, \\ \partial_t e_n(t, x) = s_n(t, x) \int_0^1 \beta_n(t, y) W_{G_n}(x, y) i_n(t, y) dy - \mu_n(t, x) e_n(t, x), \quad x \in [0, 1], \\ \partial_t i_n(t, x) = \mu_n(t, x) e(t, x) - \gamma_n(t, x) i(t, x), \\ \partial_t r_n(t, x) = \gamma_n(t, x) i_n(t, x), \\ s_n(0, x) = s_0(x), e_n(0, x) = e_0(x), i_n(0, x) = i_0(x), r_n(0, x) = r_0(x), \end{cases} \quad (11)$$

where $s_0(x), e_0(x), i_0(x), r_0(x)$ are suitable piecewise constant functions. The dynamics of the discrete graphon model can be studied using the original ODE system.

Lemma 3.6. *Let $n > 1$ and $(s_j^n(t), e_j^n(t), i_j^n(t), r_j^n(t))$, $t \geq 0$, $j = 1, \dots, n$ the solution of the Cauchy problem (9), then the corresponding piecewise constant functions $(s_n(t, x), e_n(t, x), i_n(t, x), r_n(t, x))$, is the solution, formulated almost everywhere, of the Cauchy problem (11), $t \geq 0$, $x \in [0, 1]$.*

Proof. First, we observe that the map $t \mapsto (s_n(t), e_n(t), i_n(t), r_n(t))$ is differentiable for almost everywhere $x \in [0, 1]$ and $t > 0$. Then, combining for example the s_j^n components from (9),

$$\begin{aligned} \partial_t s_n(t, x) &= - \sum_{j=1}^n \left(s_j^n(t) \frac{1}{n} \sum_{k=1}^n \beta_k^n(t) a_{jk}^n i_k^n(t) \right) \mathbb{1}_{I_j^n}(x) \\ &= - \sum_{j=1}^n s_j^n(t) \mathbb{1}_{I_j^n}(x) \left(\int_{(j-1)/n}^{j/n} \beta_k^n(t) a_{jk}^n i_k^n(t) \right) \\ &= - \sum_{j=1}^n s_j^n(t) \mathbb{1}_{I_j^n}(x) \left(\int_0^1 \beta_n(t, y) W_{G_n}(x, y) i_n(t, y) dy \right) \\ &= -s_n(t, x) \int_0^1 \beta_n(t, y) W_{G_n}(x, y) i_n(t, y) dy. \end{aligned}$$

The same can be done for the other components of the system (11). Finally, for the initial condition, just use the definition of the functions $s_n(0, x)$, $e_n(0, x)$, $i_n(0, x)$, $r_n(0, x)$. $\square$

If we consider system (9) or, equivalently, the system (11) as a quadrature rule which uses a piecewise constant approximation, we can formally introduce the limit “continuous counterpart” of (9), or (11):

$$\begin{cases} \partial_t s(t, x) = -s(t, x) \int_0^1 \beta(t, y) W(x, y) i(t, y) dy \\ \partial_t e(t, x) = s(t, x) \int_0^1 \beta(t, y) W(x, y) i(t, y) dy - \mu(t, x) e(t, x) \\ \partial_t i(t, x) = \mu(t, x) e(t, x) - \gamma(t, x) i(t, x) \\ \partial_t r(t, x) = \gamma(t, x) i(t, x) \\ s(0, x) = s_0(x), e(0, x) = e_0(x), i(0, x) = i_0(x), r(0, x) = r_0(x) \end{cases} \quad x \in [0, 1] \quad (12)$$

which is the graphon SEIR model (G-SEIR model).

3.4. Well-posedness and properties of the graphon limit. The graphon form Eq.(12) of the SEIR model is an infinite-dimensional bilinear dynamical system, where each point $x \in [0, 1]$ corresponds to a (sub-)community. While the dynamics of (11) describe the evolution of a piecewise constant macroscopic approximation. We now make the following assumptions on the data of the graphon model (12).

Assumption 1. *Assume that the following hypothesis holds for the G-SEIR model (12),*

- i) $W \in L^\infty([0, 1]^2)$ is a non negative graphon $W \geq 0$ a.e. on $[0, 1]^2$, then $W \in L^p([0, 1]^2)$, $p \geq 1$. There is a constant $K_w > 0$ such that $\text{ess sup } |W| \leq K_w$;
- ii) $\beta, \gamma, \mu \in L^\infty(\mathbb{R}_+ \times [0, 1])$, there are constants $c_0 > 0$, $K_0 > 0$ such that $\inf \beta, \inf \gamma, \inf \mu \geq c_0$, and $\text{ess sup } |\beta|, \text{ess sup } |\gamma|, \text{ess sup } |\mu| \leq K_0$;
- iii) $s_0, e_0, i_0, r_0 \in L^\infty([0, 1])$, and $0 \leq s_0, e_0, i_0, r_0 \leq 1$, $s_0(x) + e_0(x) + i_0(x) + r_0(x) = 1$ a.e. on $[0, 1]$.

Let B the Banach space $B_\infty = (L^\infty[0, 1])^4$, with norm $\|\mathbf{u}\|_{B_\infty} = \sum_{i=1}^4 \|u_i\|_{L^\infty}$, where $\mathbf{u} = (u_1, u_2, u_3, u_4) \in B_\infty$ and $\|v\|_{L^\infty} = \|v\|_{L^\infty([0, 1])} = \text{ess sup}_{x \in [0, 1]} |v(x)|$; the positive cone $B_\infty^+ = \{\mathbf{u} = (u_1, u_2, u_3, u_4) \in B_\infty : u_i(x) \geq 0 \text{ a.e. on } [0, 1]\}$ is a proper cone in B_∞ with non-empty interior; finally, $C^0([0, T]; B_\infty)$ is the space of continuous function $v : [0, T] \rightarrow B_\infty$ with norm $\|v\|_{C^0([0, T]; B_\infty)} = \sup_{0 \leq t \leq T} \|v(t)\|_{B_\infty}$. Then, the system (12) can be studied as an ordinary differential equation in Banach space B_∞ . To demonstrate the well-posedness of the problem (12), we first consider some a-priori estimates for the solution and then prove the existence and local uniqueness of the solution, and then extend it to a global solution for every $t > 0$. While it is straightforward to verify an upper bound for the solution, it is necessary to establish the non-negativity of the solution itself. In particular, we will prove the invariance of the cone B_∞^+ with respect to the Cauchy problem (12). Let X a Banach space and $T > 0$, we consider a function $G : [0, T] \times X \rightarrow X$ and we suppose that the solution $u : [0, T] \rightarrow X$ of the following Cauchy problem

$$u'(t) = G(t, u(t)), \quad t \in [0, T], \quad u(0) = u_0 \in X, \quad (13)$$

exists and is unique. We recall that a set $A \subset X$ is said to be forward invariant with respect to G if the solution $u(t)$, $t \in [0, T]$ of (13) takes values in A provided

that $u_0 \in A$ (e.g. [25] Sect. 5.2). Theorems on flow-invariance are well-known in the case $X = \mathbb{R}^n$, for the general case we refer the reader to [54, 55, 21]. In most applications, the set A has a structure which makes the forward invariance easier to show. Suppose that the positive cone X_+ is a non-empty closed subset of X , X_+^* the space of all continuous linear functionals on X_+ , using Theorem 1 and the property (f) of Sect. 4 in [54], we can deduce the following result.

Lemma 3.7. *Let X_+ a proper cone of X with non-empty interior, if for all $(t, y) \in [0, T) \times \partial X_+$, and for all $f \in X_+^*$, such that $f(y) = 0$ we have $f(G(t, y)) \geq 0$, then X_+ is a forward invariant set for the Cauchy problem (13).*

Let $C^1(\mathbb{R}_+; B_\infty)$ the Banach space of differentiable function $v : \mathbb{R}_+ \rightarrow B_\infty$, we state our main result about the Cauchy problem (12).

Theorem 3.8. *Let us assume that hypotheses (1) hold. Then, there exists a unique solution $(s, e, i, r) \in C^1(\mathbb{R}_+; B_\infty)$ of the Cauchy problem (12).*

Proof. Local existence and uniqueness. The system (12) is in the form of (13) where $X = B_\infty$ and for $\mathbf{u} = (s, e, i, r)$

$$G(t, \mathbf{u}) = \begin{bmatrix} G_1(t, \mathbf{u}) \\ G_2(t, \mathbf{u}) \\ G_3(t, \mathbf{u}) \\ G_4(t, \mathbf{u}) \end{bmatrix} = \begin{bmatrix} -s(t, x) \int_0^1 \beta(t, y) W(x, y) i(t, y) dy \\ s(t, x) \int_0^1 \beta(t, y) W(x, y) i(t, y) dy - \mu(t, x) e(t, x) \\ \mu(t, x) e(t, x) - \gamma(t, x) i(t, x) \\ \gamma(t, x) i(t, x) \end{bmatrix}.$$

Let $\mathbf{u} = (s, e, i, r)$, $\hat{\mathbf{u}} = (\hat{s}, \hat{e}, \hat{i}, \hat{r}) \in B_\infty$ such that $\|\mathbf{u}\|_{B_\infty}, \|\hat{\mathbf{u}}\|_{B_\infty} \leq \bar{C}$ for a suitable constant $\bar{C} > 0$. Then,

$$\begin{aligned} & |G_1(t, \mathbf{u}) - G_1(t, \hat{\mathbf{u}})| \\ &= \left| -s(t, x) \int_0^1 \beta(t, y) W(x, y) i(t, y) dy + \hat{s}(t, x) \int_0^1 \beta(t, y) W(x, y) \hat{i}(t, y) dy \right| \\ &\leq \left| -s(t, x) \int_0^1 \beta(t, y) W(x, y) i(t, y) dy + \hat{s}(t, x) \int_0^1 \beta(t, y) W(x, y) i(t, y) dy \right| \\ &\quad + \left| -\hat{s}(t, x) \int_0^1 \beta(t, y) W(x, y) i(t, y) dy + \hat{s}(t, x) \int_0^1 \beta(t, y) W(x, y) \hat{i}(t, y) dy \right| \\ &\leq K_w \bar{C} K_0 (\|s - \hat{s}\|_{L^\infty} + \|i - \hat{i}\|_{L^\infty}). \end{aligned}$$

Similarly, for the other components of G ,

$$|G_2(t, \mathbf{u}) - G_2(t, \hat{\mathbf{u}})| \leq K_w \bar{C} K_0 (\|s - \hat{s}\|_{L^\infty} + \|i - \hat{i}\|_{L^\infty}) + K_0 \|e - \hat{e}\|_{L^\infty},$$

$$|G_3(t, \mathbf{u}) - G_3(t, \hat{\mathbf{u}})| \leq K_0 (\|e - \hat{e}\|_{L^\infty} + \|i - \hat{i}\|_{L^\infty})$$

$$|G_4(t, \mathbf{u}) - G_4(t, \hat{\mathbf{u}})| \leq K_0 \|i - \hat{i}\|_{L^\infty},$$

therefore the following estimate holds uniformly with respect to time,

$$\|G(t, \mathbf{u}) - G(t, \hat{\mathbf{u}})\|_{B_\infty} \leq C^* \|\mathbf{u} - \hat{\mathbf{u}}\|_{B_\infty},$$

where $C^* = \max\{K_w \bar{C} K_0, K_0\}$. Then G is a local Lipschitz function and we have the existence and uniqueness of a local solution $\mathbf{u}(t)$, for $t \in [0, \tau]$, with $\tau > 0$ for the Cauchy problem (12) (e.g., Sect. 1 of [25]). Moreover, estimating the

ratio $(\mathbf{u}(t+h) - \mathbf{u}(t))/h$ for a positive real h , it is possible to deduce that solution $\mathbf{u} \in C^1([0, \tau]; B_\infty)$ (see [49], Sect. 8.3).

Global solution, $t \in \mathbb{R}_+$. Adding the equations of the system (12) we obtain $\partial_t(s(t, x) + e(t, x) + i(t, x) + r(t, x)) = 0$, a.e. on $[0, 1]$. From the assumptions on the initial data, it can be concluded that $s(t, x) + e(t, x) + i(t, x) + r(t, x) = 1$, a.e. on $[0, 1]$. Applying Lemma 3.7 with $X = B_\infty$ and $X^+ = B_\infty^+$, it is possible to show that the components of the solution are almost everywhere non-negative. First of all, a null component s, e, i, r belongs to the boundary ∂B_∞^+ of B_∞^+ , and $G(t, \mathbf{u})$ can be rewritten as a sum of vectors with all but one null component. For a single function $v \in L_+^\infty$, the positive cone of the space L^∞ , and a continuous linear functional f on L_+^∞ such that $f(v) = 0$, then for all $z \in L^\infty$, we have $f(zv) = 0$. Since v is a.e. non-negative, we have

$$-\|z\|_{L^\infty} v \leq zv \leq \|z\|_{L^\infty} v, \quad -\|z\|_{L^\infty} f(v) \leq f(zv) \leq \|z\|_{L^\infty} f(v),$$

but $f(v) = 0$, then $f(zv) = 0$. For example, for the component G_1 , and other equal to zero, if $s \geq 0$ a.e., $-(\int_0^1 \beta(t, y)W(x, y)i(t, y)dy) \in L^\infty[0, 1]$, and the value of the functional is equal to zero. The same happens for all the terms of the decomposition of $G(t, \mathbf{u})$, then the hypotheses of Lemma 3.7 are verified and the positive cone B_∞^+ is a set forward invariant for the Cauchy problem (12). As a consequence $0 \leq s(t, x), e(t, x), i(t, x), r(t, x)$ almost everywhere, so the solution is uniformly bounded and we can define it globally for each $t \in \mathbb{R}_+$. $\square$

We point out that it is not possible to apply techniques based on monotone [58] or quasi-monotone operators [64] because of the sign in the term of the first two components of G . In the case of an SIR model, without the Exposed sub-population, if we do not consider the Removed class, it is possible to rewrite the final system with a quasi-monotone operator. We also observe that Theorem 3.8 can also be applied to the discrete graphon model (11) with minor changes. We now consider the convergence of the solutions of the discrete graphon model (11) (or equivalently of the solutions of the discrete model (9)) to the solutions of the continuous graphon model (12). We consider the L^1 norm, which implies convergence with respect to the cut distance.

Theorem 3.9. *Let $T > 0$, and $(\mathcal{G}_n)_n$ be a sequence of undirected graphs with vertices $\{1, \dots, n\}$ such that the entries a_{jk}^n of the n -th weighted adjacency matrix satisfy the following assumptions: i) $a_{jk}^n = a_{kj}^n$ for every $j, k = 1, \dots, n$; ii) $a_{jk}^n \geq 0$, for every $j, k = 1, \dots, n$; iii) there is $K_G > 0$ such that*

$$\sup_{n \in \mathbb{N}} \sup_{j=1, \dots, n} \frac{1}{n} \sum_{k=1}^n a_{jk}^n \leq K_G. \quad (14)$$

Also, assume that there is a nonnegative graphon $W \in L^\infty([0, 1]^2)$ such that

$$\|W_{\mathcal{G}_n} - W\|_{L^1} \rightarrow 0 \quad \text{as } n \rightarrow +\infty. \quad (15)$$

Assume that $s_{j,0}^n, e_{j,0}^n, i_{j,0}^n, r_{j,0}^n \geq 0$ satisfy $s_{j,0}^n + e_{j,0}^n + i_{j,0}^n + r_{j,0}^n = 1$, that

$$\|\beta_j^n\|_{L^\infty(\mathbb{R}_+)}, \|\mu_j^n\|_{L^\infty(\mathbb{R}_+)}, \|\gamma_j^n\|_{L^\infty(\mathbb{R}_+)} \leq M, \text{ for every } j = 1, \dots, n \text{ and } n \in \mathbb{N}$$

for a suitable constant $M > 0$ and that $\beta^n \rightarrow \beta$, $\beta^n \rightarrow \beta$, $\gamma^n \rightarrow \gamma$, and $\mu^n \rightarrow \mu$ in $L^1(\mathbb{R}_+ \times [0, 1])$, for some $\beta, \gamma, \mu \in L^\infty(\mathbb{R}_+ \times [0, 1])$ such that $\inf \beta, \inf \gamma, \inf \mu > 0$. Let $\mathbf{u}_n = (s_n, e_n, i_n, r_n)$, $n = 1, 2, \dots$, the solution of the discrete graphon Cauchy problem (11) for $t \in [0, T]$, with initial data $s_n(0, x)$, $e_n(0, x)$, $i_n(0, x)$, $r_n(0, x) \in$

$L^\infty([0, 1])$, such that $0 \leq s_n(0, x), e_n(0, x), i_n(0, x), r_n(0, x) \leq 1$, $s_n(0, x) + e_n(0, x) + i_n(0, x) + r_n(0, x) = 1$ a.e. on $[0, 1]$. Suppose that

$$s_n(0, x) \rightarrow s_0(x), e_n(0, x) \rightarrow e_0(x), i_n(0, x) \rightarrow i_0(x), r_n(0, x) \rightarrow r_0(x), \text{ in } L^\infty([0, 1]),$$

with $0 \leq s_0, e_0, i_0, r_0 \leq 1$, $s_0(x) + e_0(x) + i_0(x) + r_0(x) = 1$ a.e. on $[0, 1]$. Then, the sequence $\{\mathbf{u}_n\}$ converges to the solution $\mathbf{u}$ of the continuous graphon Cauchy problem (12), $t \in [0, T]$, in the norm of the space $C^0([0, T]; B_\infty)$.

Proof. The assumptions (1) are verified. The Cauchy problems (11) and (12) can be rewritten equivalently as integral equations (mild solution),

$$\mathbf{u}(t, x) = \mathbf{u}(0, x) + \int_0^t G(\tau, \mathbf{u}(\tau, x)) d\tau, \quad \mathbf{u}_n(t, x) = \mathbf{u}_n(0, x) + \int_0^t G_n(\tau, \mathbf{u}_n(\tau, x)) d\tau,$$

where

$$G_n(t, \mathbf{u}_n) = \begin{bmatrix} G_{n1}(t, \mathbf{u}) \\ G_{n2}(t, \mathbf{u}) \\ G_{n3}(t, \mathbf{u}) \\ G_{n4}(t, \mathbf{u}) \end{bmatrix} = \begin{bmatrix} -s_n(t, x) \int_0^1 \beta_n(t, y) W_{\mathcal{G}_n}(x, y) i_n(t, y) dy \\ s_n(t, x) \int_0^1 \beta_n(t, y) W_{\mathcal{G}_n}(x, y) i_n(t, y) dy - \mu_n(t, x) e_n(t, x) \\ \mu_n(t, x) e_n(t, x) - \gamma_n(t, x) i_n(t, x) \\ \gamma_n(t, x) i_n(t, x) \end{bmatrix}.$$

In the following, we will omit explicitly writing the variables x and y to simplify the notation when the context is clear. Subtracting component by component $\mathbf{u}$ from $\mathbf{u}_n$ as mild solutions we have,

$$s(t) - s_n(t) = (s(0) - s_n(0)) + \int_0^t \left[s_n(\tau) \int_0^1 \beta_n(\tau) W_{\mathcal{G}_n} i_n(\tau) dy - s(\tau) \int_0^1 \beta(\tau) W i(\tau) dy \right] d\tau,$$

$$\begin{aligned} e(t) - e_n(t) &= (e(0) - e_n(0)) + \int_0^t \left[s(\tau) \int_0^1 \beta(\tau) W i(\tau) dy - s_n(\tau) \int_0^1 \beta(\tau) W_{\mathcal{G}_n} i_n(\tau) dy \right] d\tau \\ &\quad + \int_0^t [\mu_n(\tau) e_n(\tau) - \mu(\tau) e(\tau)] d\tau, \end{aligned}$$

$$i(t) - i_n(t) = (i(0) - i_n(0)) + \int_0^t [(\mu(\tau) e(\tau) - \mu_n(\tau) e_n(\tau)) + (\gamma_n(\tau) i_n(\tau) - \gamma(\tau) i(\tau))] d\tau,$$

$$r(t) - r_n(t) = (r(0) - r_n(0)) + \int_0^t [\gamma(\tau) i(\tau) - \gamma_n(\tau) i_n(\tau)] d\tau.$$

For the first component, we have the following estimate,

$$\begin{aligned} &|s(t) - s_n(t)| \\ &\leq |s(0) - s_n(0)| + \int_0^t \left| s_n \int_0^1 \beta_n W_{\mathcal{G}_n} i_n dy - s \int_0^1 \beta W i dy \right| d\tau \\ &= |s(0) - s_n(0)| + \int_0^t \left| -s \int_0^1 \beta W i dy + s_n \int_0^1 (\beta_n W_{\mathcal{G}_n} - \beta W) i dy + s_n \int_0^1 \beta W i_n dy \right| d\tau \\ &= |s(0) - s_n(0)| + \int_0^t |(s_n - s) \int_0^1 \beta W i dy + s_n \int_0^1 (\beta_n W_{\mathcal{G}_n} - \beta W) i_n dy \\ &\quad + s_n \int_0^1 \beta W (i_n - i) dy| d\tau \\ &\leq \|s(0) - s_n(0)\|_{L^\infty} + \int_0^t [K_w K_0 (\|s - s_n\|_{L^\infty} + \|i - i_n\|_{L^\infty}) + \|\beta W - \beta_n W_{\mathcal{G}_n}\|_{L^1}] d\tau. \end{aligned}$$

Similarly, for the other components of $(\mathbf{u} - \mathbf{u}_n)$ we obtain

$$\begin{aligned} |e(t) - e_n(t)| &\leq \|e(0) - e_n(0)\|_{L^\infty} + \int_0^t [K_w K_0 (\|s - s_n\|_{L^\infty} + \|i - i_n\|_{L^\infty}) \\ &\quad + \|\beta W - \beta_n W_{\mathcal{G}_n}\|_{L^1}] d\tau + \int_0^t K_0 \|e - e_n\|_{L^\infty} d\tau, \\ |i(t) - i_n(t)| &\leq \|i(0) - i_n(0)\|_{L^\infty} + \int_0^t K_0 (\|e - e_n\|_{L^\infty} + \|i - i_n\|_{L^\infty}) d\tau, \\ |r(t) - r_n(t)| &\leq \|r(0) - r_n(0)\|_{L^\infty} + \int_0^t K_0 \|i - i_n\|_{L^\infty} d\tau. \end{aligned}$$

Let $D(t) = \|\mathbf{u}(t) - \mathbf{u}_n(t)\|_{B_\infty}$, $\hat{C} = \max\{K_0, K_0 K_w\}$, for $t \in [0, T]$

$$D(t) \leq \|\mathbf{u}(0) - \mathbf{u}_n(0)\|_{B_\infty} + T\|\beta W - \beta_n W_{\mathcal{G}_n}\|_{L^1} + \hat{C} \int_0^t D(\tau) d\tau,$$

then, from Gronwall's Lemma,

$$D(t) \leq [\|\mathbf{u}(0) - \mathbf{u}_n(0)\|_{B_\infty} + T\|\beta W - \beta_n W_{\mathcal{G}_n}\|_{L^1}] (e^{\hat{C}t} - 1).$$

The last term in the previous inequalities is bounded by the quantity $(e^{\hat{C}T} - 1)$, while $\|\mathbf{u}(0) - \mathbf{u}_n(0)\|_{B_\infty} \rightarrow 0$, and $\|\beta W - \beta_n W_{\mathcal{G}_n}\|_{L^1} \rightarrow 0$ as $n \rightarrow +\infty$. Then $D(t) \rightarrow 0$ uniformly with respect to time as $n \rightarrow +\infty$. $\square$

The conditions (14) and (15) are satisfied under fairly reasonable assumptions. More precisely, assume that $\{\mathcal{G}_n\}_{n \in \mathbb{N}}$ is a sequence of graphs such that the corresponding sequence of graphons $\{W_{\mathcal{G}_n}\}_{n \in \mathbb{N}}$ is uniformly bounded in L^∞ and non-negative. Then, there is a graphon W and a re-labelling of the vertices of $\mathcal{G}_n$ such that (15) holds. Note furthermore that any sequence of graphs with uniformly bounded adjacency matrices satisfies also (14). One could also consider the case of time-dependent graphs [8].

Convergence for deterministic samplings. Theorem 3.9 in the previous paragraph describes the continuum limit of (9). In particular, we can conclude that we have the convergence result for any sequence of graphs such that the corresponding sequence of graphons is uniformly bounded. In this sense, the statement of Theorem 3.9 goes “from the sequence of graphs to the limit graphon”. It is possible to investigate the reverse path “from the limit graphon to the approximating sequence of graphs”. More precisely, we fix a limit graphon W and we ask ourselves whether or not one can construct approximating sequences of graphs, initial data and coefficients in such a way that the corresponding solutions of (9) provide a good approximation of the solution of (12).

Remark 3.10. We highlight the importance of estimating a graphon from real data of graphs, or even from segments of graphs, in network science and graph theory for several compelling reasons. A graphon acts as a limit object that embodies the asymptotic behaviour of expansive random graphs, offering a robust framework through which researchers can better comprehend the intricate structure and dynamics of complex networks. By deriving a graphon from empirical data, scientists can reveal hidden patterns and relationships that might elude observation when merely analysing the raw data. This process of estimation not only aids in the identification of community structures within networks but also enhances the modelling of interactions and facilitates the forecasting of prospective connections. Moreover, graphons provide a foundation for developing statistical techniques aimed at hypothesis testing and inference in network analysis, empowering researchers to extract

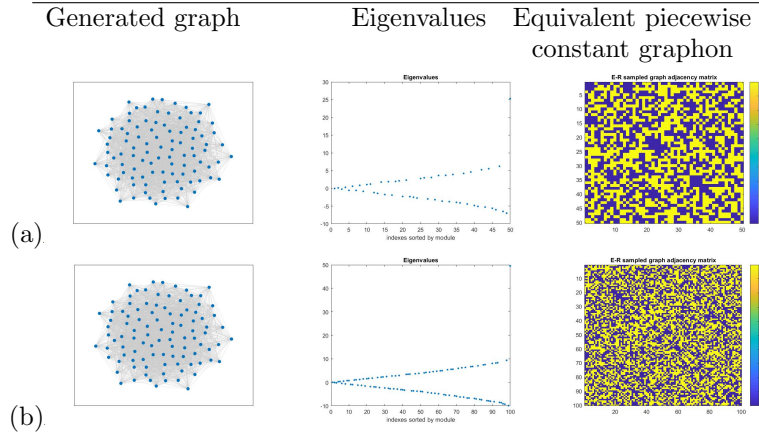


FIGURE 5. Eigenvalue distribution and corresponding piecewise-constant graphon for Erdős-Rényi graphs with (a) 50 and (b) 100 nodes, converging to the graphon limit $W(x, y) = 0.5$. In each line, we report a graphical representation of the graph, of the eigenvalues (ordered by increasing value of their modulus, and the corresponding equivalent piecewise constant graphon. The spectrum shows eigenvalues clustered around 0 and around $0.5 \cdot n$, reflecting the uniform eigenvalue $\lambda = 0.5$ of the limiting graphon. This illustrates how large random graphs can be effectively approximated through low-dimensional spectral representations.

significant insights from their datasets. This is a rapidly developing area of research. In this work, we limit ourselves to studying some relationships between generated graphs and the graphon from which they were generated. This is an essential step for further developments in graphon identification in applications.

We want to construct a sequence of piecewise graphons (or, equivalently, a sequence of graphs), and initial data such that the corresponding solutions of the discrete initial value problem (9) provide a good approximation of the solution of the continuum equation (12). The construction of the sequence of graphs depends on the sampling process of W : there are different approaches, both deterministic and random. We will consider the deterministic approach. Given $n \in \mathbb{N}$, we recall the previously defined average functions $\forall u \in L^1([0, 1])$, $\forall U \in L^1([0, 1]^2)$

$$\langle u \rangle_{I_j^n} = n \int_{I_j^n} u(x) dx, \quad \langle U \rangle_{I_j^n \times I_i^n} = n^2 \int_{I_j^n \times I_i^n} U(x) dx. \quad (16)$$

Using these definitions, given a graphon W we can build a graph G_n with n vertices and weighted adjacency matrix A^n ,

$$A_{i,j}^n = \langle W \rangle_{I_i^n \times I_j^n} \quad (17)$$

We can now show the main property of the deterministic sampling.

Theorem 3.11. *Let's assume that the hypothesis in Assumption 1 holds for the G-SEIR model (12), with $p = 1$ for assumption i). Let W_{G_n} the piecewise graphon associated with the adjacency matrix A^n defined as in (17), and set*

$$\beta_j^n(t) := \langle \beta(t, \cdot) \rangle_{I_j^n}, \quad \mu_j^n(t) := \langle \mu(t, \cdot) \rangle_{I_j^n}, \quad \gamma_j^n(t) := \langle \gamma(t, \cdot) \rangle_{I_j^n}, \quad \text{for every } j = 1, \dots, n,$$

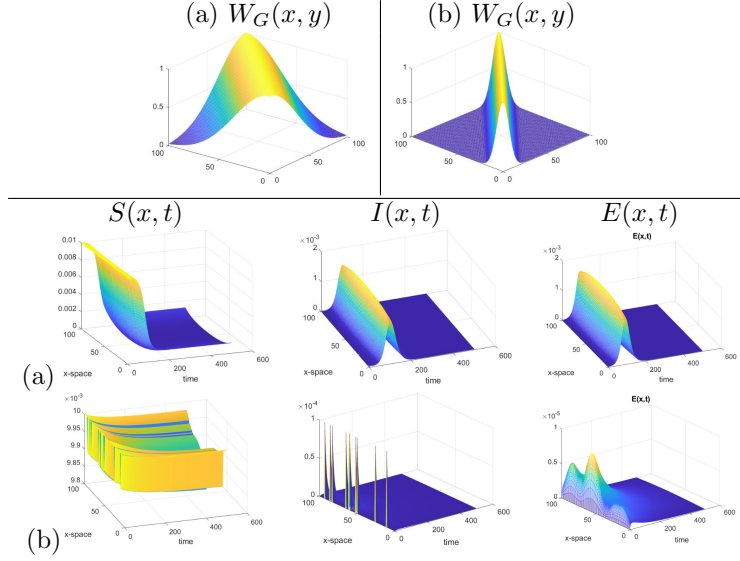


FIGURE 6. Discretization with $n = 100$ points: (a,b) selected Gaussian Kernel $W_G(x, y)$ in Eq. (21), and behaviour of the variables (b) $S(x, t)$, $I(x, t)$, and $E(x, t)$ computed with a forward Euler scheme in time and composite mid-point rule for the integral.

$$s_{0,j}^n := \langle s_0 \rangle_{I_j^n}, \quad e_{0,j}^n := \langle e_0 \rangle_{I_j^n}, \quad i_{0,j}^n := \langle i_0 \rangle_{I_j^n}, \quad r_{0,j}^n := \langle r_0 \rangle_{I_j^n}.$$

Then, for any $T > 0$,

$$\|(s^n, e^n, i^n, r^n) - (s, e, i, r)\|_{C^0([0,T], B_\infty)} \rightarrow 0 \quad \text{as } n \rightarrow +\infty,$$

where $(s^n, e^n, i^n, r^n) : \mathbb{R}^+ \rightarrow [0, 1]^4$ solves (9) and $(s, e, i, r) : \mathbb{R}^+ \rightarrow [0, 1]^4$ satisfies (12), and $B_\infty = (L^\infty[0, 1])^4$.

To prove Theorem 3.11, we can proceed as for Theorem 3.9 using the same estimates coupled with classical results of approximation theory involving a piecewise approximation constructed through the average functions as in (16). In the case of deterministic sampling, we can also handle the time-dependent case, that is W can also depend on the time variable.

Remark 3.12. It is possible to extend the results of Theorem 3.11 by considering a random sampling procedure. A graphon W generates a random graph using a sampling method, e.g. [46]. Let $N \in \mathbb{N}$, the graph G is sampled from W as follows:

1. fixing deterministic latent variables $\{u_i = \frac{i}{n}\}, i = 1, 2, \dots, n$;
2. taking n vertices $\{1, 2, \dots, n\}$ and randomly adding undirected edges between vertices i and j independently with probability $W(u_i, u_j)$ for all $i > j$.

Let W_{Gr_n} the piecewise graphon associated to the random graph Gr_n , the main point is to show that $\|W_{Gr_n} - W\|_{L^1} \rightarrow 0$, as $n \rightarrow +\infty$. To prove this convergence result, it is possible to follow the approach introduced in [19, 14] by introducing a uniform partition $\mathcal{P}$ of the interval $[0, 1]$ with m sub-intervals $I_j, j = 1, \dots, m$, and

the associated graphon $W_{\mathcal{P}, Gr_n}(x, y) := \frac{1}{|I_i| \cdot |I_j|} \int_{I_i \times I_j} W(x, y) dx dy$, $(x, y) \in I_i \times I_j$. To estimate the L^1 distance, we have to consider the inequality

$$\|W_{Gr_n} - W\|_{L^1} \leq \|W - W_{\mathcal{P}}\|_{L^1} + \|W_{\mathcal{P}} - W_{\mathcal{P}, Gr_n}\|_{L^1} + \|W_{\mathcal{P}, Gr_n} - W_{Gr_n}\|_{L^1}.$$

Finally, by using approximation results the terms on the right-hand side of the inequality are infinitesimal for sufficiently large values of n and m .

We observe that it is crucial not only to understand the aspects related to this convergence but also to delve into specific properties and characteristics of the resulting graphs. This study will focus particularly on the spectral properties of both the generated graphs and their corresponding graphons. The importance of spectral properties stems from their essential role in determining the dynamics of epidemic propagation across networks. Indeed, understanding how these properties affect the spread of diseases can yield valuable insights for modelling epidemic scenarios effectively. Moreover, as networks continuously increase in size, it becomes increasingly important to develop tools that enable the estimation of certain characteristics within very large networks, which can be computationally challenging to analyse directly. We consider the graphon operator

$$(T_W f)(x) = \int_0^1 W(x, y) f(y) dy, \quad f \in L^2([0, 1]), \quad (18)$$

which enjoys the following properties.

Lemma 3.13. *Assume $W \in L^2([0, 1]^2)$, then the map T_W defined by (18) is a linear, bounded and compact operator from $L^2([0, 1])$ to $L^2([0, 1])$.*

Proof. We first point out that, owing to the Hölder inequality,

$$\|T_W f\|_{L^2([0, 1])}^2 \leq \int_0^1 \|W(x, \cdot)\|_{L^2([0, 1])}^2 \|f\|_{L^2([0, 1])}^2 dx = \|W\|_{L^2([0, 1]^2)}^2 \|f\|_{L^2([0, 1])}^2,$$

and this shows that the linear map T_W attains values in $L^2([0, 1])$ and that it is a bounded (and henceforth continuous) operator. We are left to show that T_W maps bounded sets in relatively compact sets. Let us fix a bounded set $B \subset L^2([0, 1])$ and a sequence $\{T_W f_n\}_{n \in \mathbb{N}}$ with $\{f_n\}_{n \in \mathbb{N}} \subset B$. Up to subsequences (which we do not relabel), the sequence f_n weakly converges in $L^2([0, 1])$ to some limit function f . To conclude, we show that $T_W f_n$ converges to $T_W f$ in $L^2([0, 1])$. First, we point out that $(T_W f_n)(x)$ pointwise converges to $(T_W f)(x)$ for a.e. $x \in [0, 1]$. Using the Hölder inequality, we get $|(T_W f_n)(x)| = \left| \int_0^1 W(x, y) f_n(y) dy \right| \leq \|W(x, \cdot)\|_{L^2([0, 1])} \|f_n\|_{L^2([0, 1])}$, for a.e. $x \in [0, 1]$. Since the sequence $\{f_n\}_{n \in \mathbb{N}}$ is bounded in $L^2([0, 1])$, then the right hand side of the above inequality belongs to $L^2([0, 1])$. By the Lebesgue Dominated Convergence Theorem, we conclude that $T_W f_n$ converges to $T_W f$ in $L^2([0, 1])$. $\square$

Then, as operators, graphons are Hilbert-Schmidt integral operators. Moreover, the symmetry property of graphons ensures that the Spectral Theorem applies to graphon operators. Notably, the operator T_W has a discrete spectrum, i.e. a countable multiset of nonzero eigenvalues $\{\lambda_1, \lambda_2, \dots\}$ such that $\lambda_n \rightarrow 0$. In particular, every nonzero eigenvalue has a finite multiplicity. Let us define the operator norm $\|T_W\| := \sup_{\|f\|_{L^2([0, 1])}=1} \|T_W f\|_{L^2}$, where T_W the graphon operator related to

a graph sampled from W . We recall that an eigenvalue λ of T_W is a scalar (complex or real) such that $T_W - \lambda \mathbb{I}$ is not invertible, where $\mathbb{I}$ is the identity operator. By

specialising the results concerning Hermitian operators (see e.g. [57]) to the case of graphons, it is straightforward to prove the following result.

Proposition 3.14. *Let T_W be the graphon operator corresponding to a graphon W , then there is a set $\{f_j\}$ of a countable number of orthonormal functions in $L^2([0, 1])$, such that the functions f_j are eigenfunctions to the eigenvalue $\lambda_j \in \mathbb{R}$ ordered as follows: $|||T_W||| = |\lambda_1| \geq |\lambda_2| \geq |\lambda_3| \geq \dots \geq 0$. If the set $\{f_j\}$ is infinite, we have $\lim_{j \rightarrow \infty} \lambda_j = 0$. Furthermore, for any $f \in L^2([0, 1])$, we have the following representations: $T_W f = \sum_{j=1}^{\infty} \lambda_j \langle f, f_j \rangle f_j$, where $\langle \cdot, \cdot \rangle$ is the standard dot product in $L^2([0, 1])$.*

Then, if the eigenvalues and the corresponding eigenfunctions of a graphon are known, one can approximate the graphon by a finite spectral sum. If we consider the case of spreading epidemics in meta-populations, a natural community structure is the stochastic block model, where each block represents a region, a city, a village, or other subsets of the population. The step graphons, related to a suitable partition of $[0, 1]$, with finite rank, encompass the properties of the stochastic block models. Now, the advantage provided by graphons lies in the fact that instead of considering a network with a large number of nodes, we consider a reduced model that maintains the same properties. A suitable graphon for a block models is a step function W such that a partition $P = \{P_1, P_2, \dots, P_n\}$ of measurable sets of $[0, 1]$ exists, and W is constant on every product set $P_i \times P_j$. Here, we will consider the case of a uniform partition with sub-intervals I_j^n defined above. Following [7], it is possible to obtain an asymptotic estimate of the difference between the graphons in the operator norm. In particular, for a fixed value $0 < \nu < 1/e$ with probability $1 - \nu$,

$$|||T_W - T_{W_G}||| = O((\log N/N)^{1/2}) \quad N \rightarrow \infty. \quad (19)$$

For graphons in $\mathcal{W}_0$, the operator norm is equal to the largest, in modulus, eigenvalue, which is real and positive, of the operator $\lambda_1(T_W)$: $|||T_W||| = \lambda_1(T_W)$. Then, using (19), with probability at least $1 - \nu$, $|\lambda_1(T_W) - \lambda_1(T_{W_G})| = O((\log N/N)^{1/2})$, as $N \rightarrow \infty$, and we have an approximation for the condition governing the transmission of the epidemic on the graph G obtained from W . Moreover, in general, for a graphon W , the eigenvalues form two sequences $\mu_1(W) \geq \mu_2(W) \geq \dots \geq 0$, and $\mu'_1(W) \leq \mu'_2(W) \leq \dots \leq 0$ converging to zero. Let $\{W_n\}_{n=1}^{\infty}$ be a sequence of uniformly bounded graphons, converging in the cut norm to a graphon W . Furthermore in [18] the Authors demonstrate that, for every $i \geq 1$, $\lim_{n \rightarrow \infty} \mu_i(W_n) = \mu_i(W)$ and $\lim_{n \rightarrow \infty} \mu'_i(W_n) = \mu'_i(W)$. This implies that if a sequence of graphs converges within the cut metric to a graphon limit, it exhibits a simple spectral characterisation marked by a limited number of non-zero eigenvalues. This finding suggests that such graph sequences can indeed be represented through straightforward low-dimensional spectral approximations. Notably, as the graphs grow in size, the efficacy of these low-dimensional approximations tends to improve, illustrating that the approximations become increasingly reliable with larger networks.

An empirical example in Fig. 5 reinforcing this theory is provided through the analysis of random graphs generated by the Erdős-Rényi model, where $W(x, y) = 0.5$, which serves to demonstrate the discussed concept visually. We can consider the represented graphs as belonging to a sequence of graphs to which correspond piecewise constant graphons that converge to W . For the general Erdős-Rényi model with parameter p , the associated graphon can be defined simply as $W(x, y) = p$

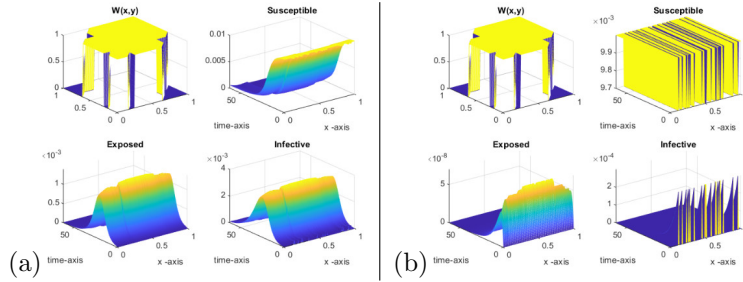


FIGURE 7. A simple block model with a step graphon for which (a) the epidemic spreads and (b) does not spread.

for any $(x, y) \in [0, 1]^2$. This definition highlights the constant probability p that an edge exists between any two vertices, illustrating the uniformity inherent in this random graph formation process. For this constant graphon the function $f(y) \equiv 1$ in an eigenfunction, which corresponds to the eigenvalue p : $\int_0^1 p \cdot 1 \, dy = p = p \cdot 1$. Then, the largest eigenvalue equals p , associated with the constant function. All other eigenvalues are equal to 0, about functions that are orthogonal to the constant function. This simple structure of eigenvalues underscores the inherent uniformity of the Erdős–Rényi model, where connection probabilities remain consistent across all pairs of vertices. Consequently, the spectral properties derived from the graphon yield valuable insights into the dynamics and behaviours of extensive random graphs produced by the Erdős–Rényi process. In Fig. 5, we show that the eigenvalues cluster around zero and a value $p \cdot n$: the presence of the factor n is simply due to the definition of the approximating mean function, see Eq. (16). Furthermore, it is highlighted that there are also viable low-rank approximations for general random graphs produced by dense low-rank models, reinforcing the idea that low-dimensional representations can be broadly applicable in this context. As a consequence, if a step graphon represents sufficiently well the social structure related to the spread of an epidemic, we can consider a low-dimensional model for an approximation of the behaviour of the phenomenon on a large underlying network. In other words, the distribution of the eigenvalues and an approximation of some of them, such as the eigenvalue with the maximum modulus, can be well approximated using a reduced-dimensional step graphon (in this case, the dimensionality can be related to the number of subintervals of the considered partition of the step graphon).

3.5. Epidemic spread on a graphon: a numerical test. We conclude by showing some numerical simulations to illustrate some cases of the behaviour of a SEIR model on a (discrete) graphon. To approximate the SEIR model on a graphon (12), we first consider a discretisation for the space variable x compatible with the result in the Theorem 3.11. Then, starting from the uniform partition of the set $[0, 1]$ with the intervals $\mathbb{1}_{I_j^n}$, where $I_j^n = [(j-1)n^{-1}, jn^{-1}[$, $j = 1, \dots, n$, we approximate the Graphon operator defined by (18) by the composite midpoint rule, $(\tilde{T}_W f)(x_k) = \frac{1}{n} \sum_{j=1}^n W(x_k, x_j) f(x_j)$, where $x_k = (2k-1)/n$, $k = 1, \dots, n$. The

corresponding semi-discrete scheme is the following

$$\begin{cases} \partial_t s(t, x_k) = -s(t, x_k) \frac{1}{n} \sum_{j=1}^n \beta(t, x_j) W(x_k, x_j) i(t, x_j), \\ \partial_t e(t, x_k) = s(t, x_k), \frac{1}{n} \sum_{j=1}^n \beta(t, x_j) W(x_k, x_j) i(t, x_j), \\ \partial_t i(t, x_k) = \mu(t, x_k) e(t, x_k) - \gamma(t, x_k) i(t, x_k), \\ \partial_t r(t, x_k) = \gamma(t, x_k) i(t, x_k), \\ s(0, x_k) = s_0(x_k), e(0, x_k) = e_0(x_k), i(0, x_k) = i_0(x_k), r(0, x_k) = r_0(x_k), \end{cases} \quad (20)$$

$k = 1, \dots, n$. If the probability of disease transmission per contact parameter β is constant, the same results of the Lemma 2.2, and Theorem 2.3 hold for the solution of the semi-discrete system (20). It follows that the dynamics of the transmission of the epidemic are determined in particular by the values of the eigenvalues of the operator $\bar{T}_W$. We point out that $W(x_k, x_j)$ represents a piecewise constant graphon, and then we focus on the spectral properties of the operator T_W corresponding to these last types of graphon. In the following, we assume $W \in \mathcal{W}_0$, where $\mathcal{W}_0$ is the set of all graphons attaining values in $[0, 1]$. The numerical simulations were done using the semidiscrete system (20) coupled with the simple forward Euler scheme with a constant time step τ for integration in time. We point out that more accurate and advanced schemes can be considered with an appropriate stability and convergence analysis. This type of extension and analysis goes beyond the scope of this work, and we refer, for example, to [8] and our forthcoming work for more details. As a first example, we consider a Gaussian kernel like graphon $W(x, y)$,

$$W_G(x, y) = C_W e^{-\frac{1}{2} \left(\frac{(x-x_0)^2}{\sigma_x^2} + \frac{(y-y_0)^2}{\sigma_y^2} \right)}, \quad (21)$$

where C_W is a suitable parameter in order to normalise the values of $W(x, y)$, and (x_0, y_0) are the points on the diagonal of the square $[0, 1] \times [0, 1]$. In all the simulations that we will show, we have used a uniform partition of $[0, 1]$ with $n = 100$ subintervals. The parameters for the SEIR model are the following, from [37] and about the recent epidemic of SARS-CoV-2 in Italy, $\beta = 0.74$, $\mu = 0.5$, $\gamma = 0.14$. In Fig. 6, we represent the numerical results for two cases, controlled by a Gaussian graphon ($\sigma_x = \sigma_y = 0.5$): (a) spread, (b) no spread of the epidemic. In the second numerical example, we consider a simple block model; the corresponding graphon is a piecewise function (Fig. 4(b)). We perform a numerical simulation such that the condition $\beta \lambda_1(T_W) > \gamma$ is satisfied (compare with Theorem 2.3) and the epidemic spreads as in the classical SEIR models (Fig. 7(a)). Finally, in Fig. 7(b), a numerical test with a block model is shown but without the spread of the epidemic.

4. Conclusions and future work. We have introduced and analysed SEIR models on graphs, focusing on their fundamental properties, especially the spectral characteristics of the weighted adjacency matrix. We also examined the continuum limit as graphs grow large, a key step toward understanding disease spread in populations with complex social structures. Future directions include developing inference methods for early epidemic data, refining metapopulation models to capture intricate social and spatial structures, devising efficient computational tools for epidemiological metrics, and integrating within-host and between-host dynamics. Preliminary experiments demonstrate the feasibility of approximating epidemic dynamics in large networks via low-dimensional block models linked to piecewise

constant graphons. We plan to apply this approach to control problems, extending previous linear analyses [36] to nonlinear settings and building on heterogeneous network models [1]. Estimating the underlying graphon remains a critical task; incorporating node attributes (e.g., age, social group, health status) can improve accuracy, as suggested in [61].

Our graph-based framework explicitly captures interaction structures to better understand disease spread and support control strategies aimed at reducing transmission rates or limiting contacts to keep infection peaks manageable. This approach balances epidemic control with minimising social and economic disruption, complementing recent work on epidemic-economic tradeoffs [1]. In many populations, contact patterns are dynamic rather than static, evolving in ways that significantly affect transmission. Dynamic networks better reflect these changes and have crucial implications for targeted surveillance and control, though their analytical treatment remains challenging. Several results here extend naturally to dynamic settings under assumptions like boundedness and stationarity, with spectral estimates adaptable to time-varying parameters. Finally, inspired by recent work on opinion dynamics on graphons [2] using an L^2 framework, we aim to extend these mathematical techniques to epidemiological models, advancing the theoretical understanding of disease dynamics in complex networks. As highlighted by C. Borgs and J.T. Chayes [13], the graphon-based limit could serve as a generative continuous model for networks with statistical properties related to the distribution of connections. We point out that, from the examples considered in this paper, graphon limit could also provide a suitable framework for developing algorithms for the analysis of graph signals.

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