



Epiwork D2.4: Spatially embedded networks: Specific rules for contact in the context of spatial embedding. Properties of the networks subjected to such spatial embedding constraints.

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Contents

- 1 Spatially embedded networks: Specific rules for contact in the context of spatial embedding. Properties of the networks subjected to such spatial embedding constraints. 2**
 - 1.1 Goals 2
 - 1.2 The approach 3
 - 1.3 Metapopulation with social structure 4
 - 1.4 Connectivity 4
 - 1.5 Interaction Probability 6
 - 1.5.1 Additive model 6
 - 1.5.2 Multiplicative model 6
 - 1.6 Spectral properties of network-network systems 7
 - 1.7 Generalization of the Approach, Applications and Perspectives 8

1 Spatially embedded networks: Specific rules for contact in the context of spatial embedding. Properties of the networks subjected to such spatial embedding constraints.

1.1 Goals

This deliverable is a direct product of our activities related to Task 6: Network-Network Duality in Heterogeneous Metapopulation and Contact Patterns II, Theme II of WP2. In a nutshell, we established a mathematical formalism in which social network structures as quantified by an adjacency matrix that reflects connectivity among individuals is mapped onto a metapopulation network between populations of individuals. The concept of metapopulation of communities is general in our approach. It could resemble different geographic locations as well as communities of individuals with different properties, e.g. activity rates, age groups etc. Particular care has been devoted to a rigorous derivation of the correct formulation of a mapping that takes a social contact network of individuals into an effective network of meta-populations needs to be able to fit observational data. The approach is based on and to some extent its direction was chosen based on our results delivered in D2.2. As we have demonstrated in D2.2, the presence of heterogeneous contact rates in a population is insufficient to determine completely a dynamic process and specification regarding the mechanism of interaction among individuals is necessary. In D2.2 we studied two different kinds of mixing dynamics. However, in our previous analysis we were still bound by the mass action rules as individuals were able to interact randomly with one another, albeit not uniformly.

In D2.4 we extend our analysis and study the same kind of mixing dynamics but individuals are adhere to a fixed social network structure. In this manner, individuals will not be able to explore the entire range of possibilities but rather will be constrained by their links.

1.2 The approach

We consider individuals in a metapopulation labeled by their activity and the community m they belong to. The metapopulation consists of M different communities coupled by exchange of individuals. We denote by $N(m, \alpha)$ the density of individuals in m that have an activity potential α . The dynamics is defined by a coupling constant k , that depends on community index as well as activity potentials

$$k = k(m, \alpha; n, \alpha')$$

and will determine the reaction rates among individuals belonging to group m having contact rate α with individuals of group n that have a contact rate α' . The equations that govern disease dynamics in a metapopulation model under the effective coupling approach (see Deliverable D2.2) are given by

$$\partial_t j(m, \alpha) = s(m, \alpha) \sum_n \int d\alpha' k(m, \alpha; n, \alpha') j(n, \alpha') - \beta j(m, \alpha)$$

as part of either an SIS or SIR model for infection dynamics where $j(m, \alpha)$ and $s(m, \alpha)$ are the fraction densities of infecteds and susceptibles, respectively. The total number of individuals with contact rate α and the total number of individuals belonging to group m are given

$$N(\alpha) = \sum_n N(n, \alpha), \quad N_m = \int d\alpha N(m, \alpha).$$

The quantity $c(m, \alpha) = N(m, \alpha) / N$ can be interpreted as the probability of an individual belonging to the category defined by the pair m, α . If in each community m the probability $p(\alpha)$ of having an activity rate α is identical

$$c(m, \alpha) = c_m p(\alpha)$$

the limiting case of statistically decoupled state variables is recovered in which activity rate α and community are independent. The opposite situation is when all the individuals in a group m have a rate α_m . In this case

$$c(m, \alpha) = c_m \delta(\alpha - \alpha_m) \tag{1}$$

and the probability distribution for the contact rates is

$$p(\alpha) = \sum_m c_m \delta(\alpha - \alpha_m).$$

In general, the combined probability $c(m, \alpha)$ does not factorize or can be reduced to a one dimensional process. The relationship of reaction rates $k(m, \alpha; n, \alpha')$ in terms of the activity rates α and community sizes was obtained in Deliverable D2.2.

$$k(m, \alpha; n, \alpha') = \left(\frac{\alpha' P(m, \alpha | n, \alpha')}{c(m, \alpha)} + \frac{\alpha P(m, \alpha' | n, \alpha)}{c(m, \alpha')} \right) \tag{2}$$

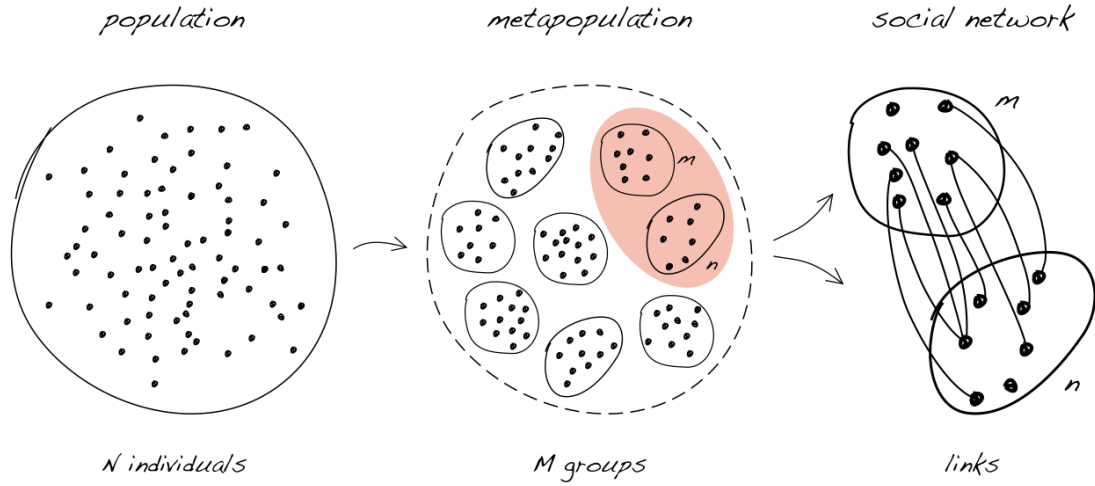


Figure 1: Embedding social contact networks in a metapopulation of communities.

1.3 Metapopulation with social structure

In this Deliverable (D2.4) we make an attempt to answer the following question: how does a social network affect epidemic spreading in heterogeneous metapopulations? We focus on a metapopulation in which all members of each community have the same contact rate α_m . This will make analysis more tractable and will allow us to concentrate on defining the interactions arising through the social network that exist in the metapopulation structure (network network duality). The interactions among the metapopulation groups K_{mn} can be captured by an $M \times M$ matrix

$$K_{mn} = \begin{bmatrix} k_{11} & \cdots & k_{1M} \\ \vdots & \ddots & \vdots \\ k_{M1} & \cdots & k_{MM} \end{bmatrix}$$

In the following we describe the a specific population setting that will help us define the conditional probability $P(m, \alpha | n, \alpha')$. We consider a social structure represented by a static network embedded into the metapopulation structure. We represent the contact network by its adjacency matrix A_{ij} and assume that the network captures the interactions among all individuals present in the metapopulation irrespective of their group status. To ease the analysis in the following sections we impose the following structure to A_{ij} : all individuals from each location are grouped contiguously, such that the indices of the matrix are ordered as follows:

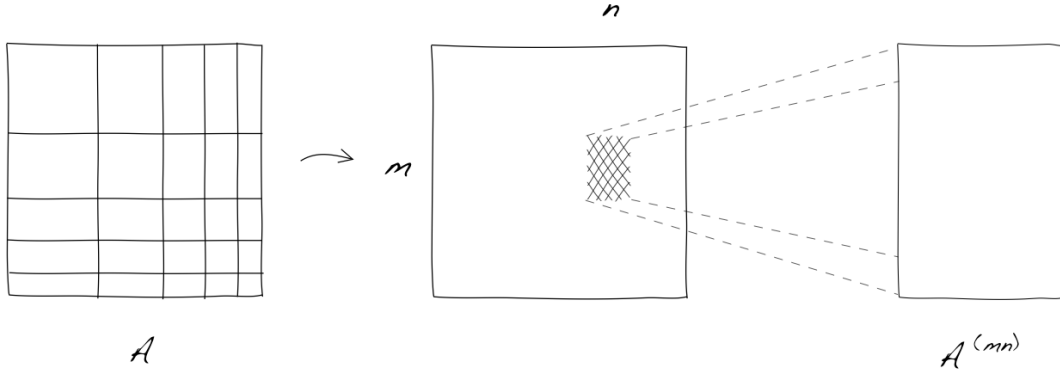


Figure 2: The elements of the adjacency matrix are ordered in such a way that it is formed by block matrices. The block matrix $A^{(nm)}$ represents the links between populations m and n .

$$\underbrace{1, 2, 3, \dots, N_1}_{\text{group 1}}, \underbrace{N_1 + 1, \dots, N_1 + N_2}_{\text{group 2}}, \dots, \underbrace{(N_1 + \dots + N_{m-1}) + 1, \dots, (N_1 + \dots + N_{m-1}) + N_m}_{\text{group } m}, \dots, \underbrace{(N_1 + \dots + N_{M-1}) + 1, \dots, (N_1 + \dots + N_{M-1}) + N_M}_{\text{group } M}$$

The ordering results in the following form of the adjacency matrix \mathbf{A}

$$\mathbf{A} = \begin{bmatrix} A^{(11)} & \dots & A^{(1M)} \\ \vdots & \ddots & \vdots \\ A^{(M1)} & \dots & A^{(MM)} \end{bmatrix}$$

that is now arranged in blocks, see Figure XX.

1.4 Connectivity

Using the block structure of the adjacency matrix, we can compute important quantities to assess the interaction among different groups due to interactions between individuals in the social network. The block matrix $A^{(nm)}$ is given by

$$A^{(nm)} = \begin{bmatrix} A_{11} & \dots & A_{1N_n} \\ \vdots & \ddots & \vdots \\ A_{N_m1} & \dots & A_{N_mN_n} \end{bmatrix}$$

The sum of either the rows or column vectors represent the generalized degree of the individuals of group m to individuals on group n :

$$\hat{k}_{n|m_i} = \sum_{j \in n} A_{j m_i}^{(nm)}$$

and

$$\hat{k}_{n|m} = \begin{bmatrix} \hat{k}_{n|1} & \hat{k}_{n|2} & \cdots & \hat{k}_{n|m_i} & \cdots & \hat{k}_{n|N_m} \end{bmatrix}$$

where the indices run through all individuals in group m , see Figures 1,2. The average degree of the vertices of group m to vertices on group n is given by

$$\hat{k}_{n|m_i} = \sum_{j \in n} A_{j m_i}^{(nm)}$$

$$\hat{k}_{n|m} = \begin{bmatrix} \hat{k}_{n|1} & \hat{k}_{n|2} & \cdots & \hat{k}_{n|m_i} & \cdots & \hat{k}_{n|N_m} \end{bmatrix}$$

We can now define the connectivity between tow different communities as

$$C_{nm} = \frac{\langle \hat{k}_{n|m} \rangle}{N_n}$$

which is also

$$C_{nm} = \frac{1}{N_n} \frac{1}{N_m} \sum_{i \in n, j \in m} A_{ij} = \frac{1}{N_n} \frac{1}{N_m} \sum_{i,j} A_{ij}^{(nm)}$$

i.e., the sum of all connections between groups m and n , normalized by the group sizes. The connectivity among groups will help us specify the interaction strengths between different communities based on knowledge of the underlying social network.

1.5 Interaction Probability

In this section we compute an expression for the conditional probability $P(m, \alpha | n, \alpha')$, Eq.(2). Since we are working with the limiting case defined by Eq. (1) the situation simplifies to determining $P(m|n)$ and k_{nm} . In the case of a social network embedded into a metapopulation with direct coupling, the probability of an individual contacting another individual depends not only on its belonging to a particular population group m but also on the constrains imposed by the social network formed by the individuals.

1.5.1 Additive model

In the case of unilateral interactions, i.e. where the probability is independent of the contact rate, the conditional probability is given by

$$P(n|m) = \frac{N_n}{N} \times \frac{C_{nm}}{\mathcal{N}}$$

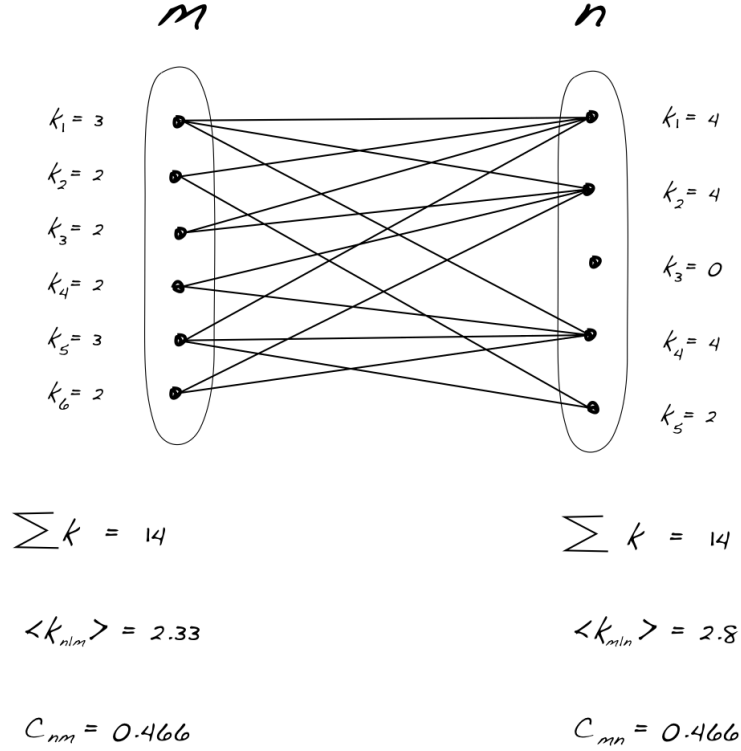


Figure 3: Sketch of a calculation of the connectivity C_{nm} for groups m and n as defined in the text. Notice that while some of the properties, like the average inter-group degree may be different, the connectivity is equal for both groups.

where $\mathcal{N} = \sum_k c_k C_{km}$ is a normalization constant. We obtain for k_{nm} , the coupling term mediating interactions between individuals of group m and n in a metapopulation with a social network:

$$k_{nm} = \left(\frac{\alpha_m}{\sum_k c_k C_{km}} + \frac{\alpha_n}{\sum_k c_k C_{kn}} \right) C_{nm}.$$

1.5.2 Multiplicative model

If we assume that the conditional probability of contacting an individuals in population n increases linearly with the contact rate α_n we obtain

$$P(n|m) = \frac{\alpha_n N_n C_{nm}}{\mathcal{N}} = \frac{c_n \alpha_n C_{nm}}{\sum_k c_k \alpha_k C_{km}}.$$

In this system the interaction rate between communities is given by

$$k_{nm} = \left(\frac{1}{\sum_k c_k \alpha_k C_{km}} + \frac{1}{\sum_k c_k \alpha_k C_{kn}} \right) \alpha_n \alpha_m C_{nm}.$$

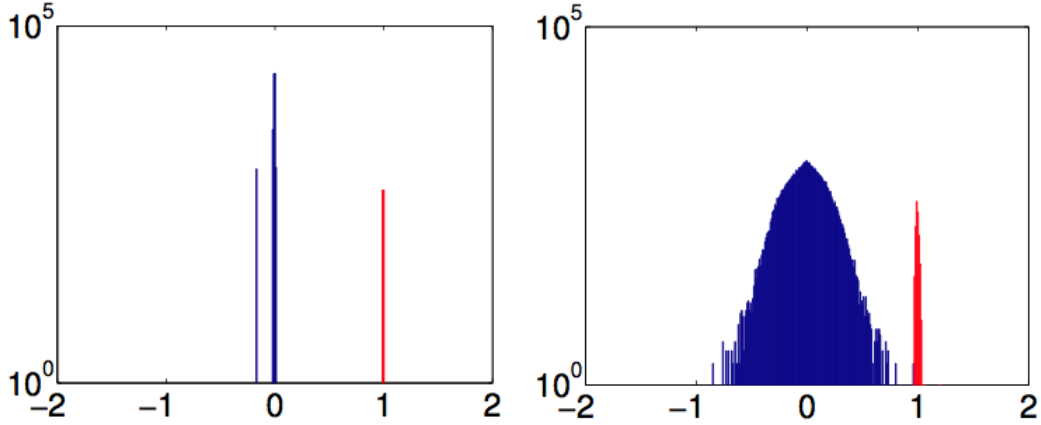


Figure 4: The panels illustrate ER networks with different connectivity left: $p = 0.9$ and right $p = 0.01$. The number of subpopulations is $M = 50$. The largest eigenvalue has been given a red color to distinguish from the bulk of eigenvalues. We notice that for unilateral dynamics, the largest eigenvalue is still distributed near the original value for mean-field dynamics.

which is in general different from the reaction rate in the additive system.

1.6 Spectral properties of network-network systems

In general the key goal of the above approach is to express the interaction rate between populations k_{nm} as a function of the activity rates α_n and the adjacency matrix A_{ij} that quantifies the connectivity of the underlying social network.

$$k_{nm} = \left(\frac{\alpha_m}{\sum_k c_k \alpha_k \frac{1}{N_k} \frac{1}{N_m} \sum_{i,j} A_{ij}} + \frac{\alpha_n}{\sum_k c_k \alpha_k \frac{1}{N_k} \frac{1}{N_n} \sum_{i,j} A_{ij}} \right) \frac{1}{N_n} \frac{1}{N_m} \sum_{i,j} A_{ij}$$

The above equation can be investigated to assess the stability properties of the dynamical system in the equilibrium state $j_m = 0$. The disease free state becomes unstable if at least one eigenvalue $\lambda > \lambda_c = 1$. Figures 4 and 5, show the spectra of a system with $M = 50$ subpopulations and thus 50 different activity rates α_m with fixed mean and variance. Each population has the same size. The embedded social network is chosen to be an Erdos-Renyi graph with link probabilities ranging from 0.1 to 0.9. For both systems, additive and multiplicative coupling, the additional heterogeneity imposed by the social network increases the variability in the spectrum. This effect is more pronounced in the multiplicative coupling scenario. These results imply, that both types of heterogeneity variable activity rates on one hand and connectivity imposed by the social network contributed to the scatter in relaxation. Furthermore,

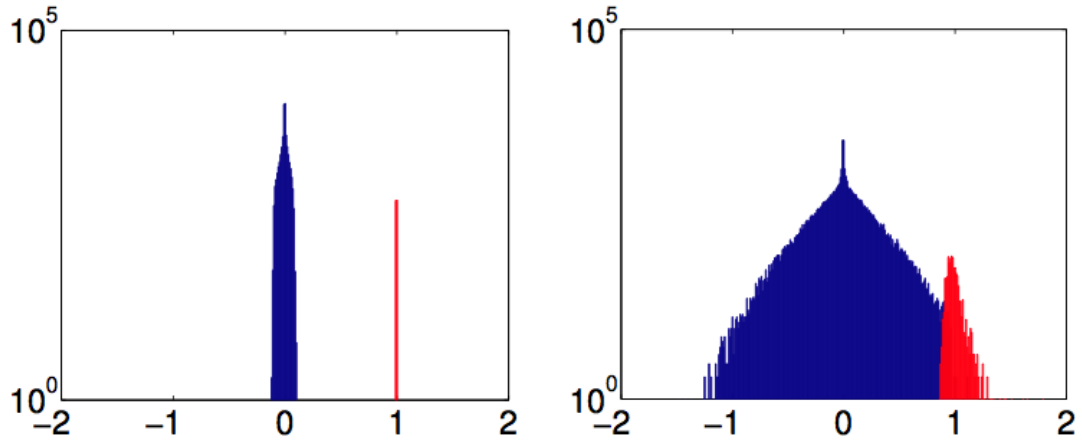


Figure 5: The panels illustrate the spectra of the matrix k_{nm} as in the previous figure for the multiplicative (bilateral) system.

this implies that a system with underlying social structure can possess an unstable disease free state whereas the fully coupled systems does not for all other parameters fixed. Fig. 6 illustrates the variability in the stability determining largest eigenvalue of k_{nm} as a function of connective strength of the underlying network. The sparser the network, the larger the variability in λ_0 .

1.7 Generalization of the Approach, Applications and Perspectives

Given the flexibility of the metapopulation framework, our model can either represent different subpopulations of a single population, in increasing length-scale: 1) different population groups with a highly connected social network; 2) depending whether the adjacency matrix represent mobility fluxes, different neighborhoods of a city; or 3) the relationship among different highly connected geographical communities. In all of the above examples, this formalism would be applicable and its application could help improve health contingency plans in case of a local or regional epidemic outbreak. Several studies have been made in the field of epidemiology addressing the issue of spatial heterogeneity. The metapopulation concept has proven successful both in reproducing as well as predicting epidemiological data. These studies focus on either using the air transportation network together with census data to form a metapopulation structure, or in combination with incidence data fit the coupling between populations. Additional specifications to the population average value of the contact rate and the dispersion of such rates given by the variance $\text{var}()$ are required. This additional information are the rules of interaction that determine the

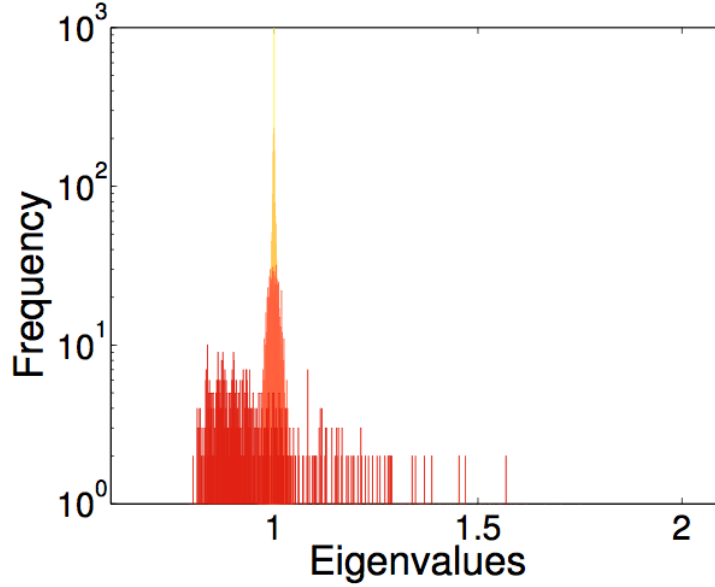


Figure 6: The statistics of the largest eigenvalue as a function of the link probability in the population (yellow: largest, red: smallest). Notice how the values of the eigenvalue disperse as the system deviates from the mean-field regime and enters a regime where the social links are equally important.

mixing pattern among individuals in the population. We have seen that different rules lead to different dynamics of epidemic spreading and in general of other dynamical processes. One of the limitations of this approach, is the fact that although the mixing patterns are not uniform, they still occur randomly among all individuals in the population. For instance, the mixing patterns generated by bilateral transmission dynamics lead to a stark segregation of high-risk individuals as this individuals tend to interact only with other high-risk individuals, and low-risk individuals are excluded of the dynamical process. On the other end of the spectrum, in the regime of unilateral transmission dynamics, individuals are contacted without correlation to the activity of the individuals.

This procedure delivered in D2.4 allows for the translation of other general topologies into an interaction term among different risk groups. We briefly analyze the stability properties of our dynamical system before presenting some preliminary results of agent-based simulations. We have extended the formalism of D2.2 and included a contact network in the population. Such step was taken to investigate the effects of such a structure in the dynamics of spreading processes. As we have shown social structure increases the instability of epidemic processes and therefore could lead to greater epidemics and other interesting epidemic behavior. Translated in the mean-field approach, our framework is an approximation that could shed light regarding the stability of epidemic dynamics in both regimes, unilateral and bilateral transmission dynamics. The less number of links in the equivalent system means that interactions

get concentrated and although repetitive contacts could lead to a slower epidemic outbreak, it also means that in certain circumstances, when low-risk individuals are infected, there is a greater chance of this individuals to transmit the infection and could avoid stochastic extinctions. In the case of multiplicative dynamics, in highly heterogeneous populations, social links function as channels to transmit the disease to other risk groups previously not available in the mean-field regime, thus facilitating the mixing among other risk classes and attenuating the isolation created by the dynamics of segregation. In this way, the resulting dynamics are the interplay between the variance of the distributed contact rates in a population and the topology of the contact network. In the case of additive dynamics, social links could work to transport the infection from low-risk individuals directly to high-risk individuals. Thus, as expected by our formalism, the dynamics in this kind of system resemble that of a metapopulation, where extinction and subsequent reintroduction of a disease leads to longer and bigger epidemic outbreaks. Our mathematical approach is equivalent to that of spatial metapopulations and therefore with minor modifications and considering other questions, this could be applied to investigate the interplay between metapopulation structures and social contact networks. One of the main goals and most important challenge is to combine two apparently contradictory sources of information: aggregated and individual-based data. We have taken a first step in that direction by constructing a formalism that would allow for the marriage of empirical gathered data from different sources such as mobility networks, friendships and social networks.