Transmission matrices used in epidemiologic modelling

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ABSTRACT

Mixing matrices are included in infectious disease models to reflect transmission opportunities between population strata. These matrices were originally constructed on the basis of theoretical considerations and most of the early work in this area originates from research on sexually transferred diseases in the 80s, in response to AIDS. Later work in the 90s populated these matrices on the basis of survey data gathered to capture transmission risks for respiratory diseases. We provide an overview of developments in the construction of matrices for capturing transmission opportunities in populations. Such transmission matrices are useful for epidemiologic modelling to capture within and between stratum transmission and can be informed from theoretical mixing assumptions, informed by empirical evidence gathered through investigation as well as generated on the basis of data. Links to summary measures and threshold conditions are also provided.

1. Introduction

Epidemiologic models capture disease transmission in a population. This disease transmission depends on the interactions between members of the population. Where susceptible hosts interact with infected carriers, the disease can transmit from the latter to the former. These interactions are a key component of modelling approaches. This means epidemiologic modellers are interested in knowing how people move and who encounters who.

The simplest assumption of transmission is homogenous mixing, meaning that all members of the population mix randomly with each other with an equally likely probability. For a stratified population, if the mixing is random within strata it is known as proportional mixing, this is where the mixing between strata is proportional to the size of the population stratum (Jacquez et al., 1988; Sattenspiel and Simon, 1988). One method of capturing and including interactions between population strata (mixing) is transmission matrices. Homophily in transmission matrices occurs when the diagonal elements of the transmission matrix are greater than the off-diagonal elements, which is known as assortative mixing (is also known as like-with-like mixing). When this is not the case, the mixing is considered to be disassortative (like-with-unlike) mixing, which is also sometimes referred to as "negative assortative" mixing (Blower, Hartel, Dowlatabadi, Anderson, & May, 1991). Proportionate mixing falls between the two (Haraldsdottir, Gupta, & Anderson, 1992; Garnett & Anderson, 1993). Separable mixing is when mixing is independent between strata (Diekmann, Heesterbeek, & Metz, 1990; Goeyvaerts et al., 2010).

Understanding human interaction is of interest for multiple scientific disciplines; anthropology, epidemiology, sociology, urban planning, geography, and ecology and so there are many options for populating transmission matrices. Here we would like to provide an overview of transmission matrices, hopefully showing the links between methodological development

arising from various disciplines. We highlight the main papers making up the current state of knowledge on transmission matrices as well as approaches on the topic to provide a foundation for other researchers.

In the following we consider matrices of rates of interaction between strata i and j with entries $0 \leq p_{ij} \leq 1$, but if counts of interactions m are provided, rates can be calculated by normalisation: $p_{ij} = m_{ij}/\sum m_{ij}$.

2. Theoretical transmission matrices

For n population strata, an $n \times n$ transmission matrix is needed. This means n^2 transmission rates could be expected but certain simplifications (such as expectations of symmetry) allow for fewer rates needed to be determined.

2.1. Interaction

Many of the early considerations for mixing hence transmission matrices came from models for sexually transferred infections (STIs) and later developments arose from models for respiratory infections. A matrix used for STI modelling explains "who has sex with whom" (WHSWW) (Aral et al., 1999; Blythe, Castillo-Chavez, Palmer, & Cheng, 1991). In their early gonorrhoea modelling approach, Hethcote, Yorke, and Nold (1982) used a WHSWW matrix with certain heterogeneous mixing assumptions.

Such a matrix can be constructed in myriad ways. One line of thought for the construction of theoretical transmission matrices arose from the force of infection (see *Estimated transmission matrices*). The following options have been considered (Anderson & May 1985; Gay, Hesketh, Morgan-Capner, & Miller, 1995; van Effelterre et al., 2009) but are not exhaustive. Examples are given for $n = 5$.

$$\begin{bmatrix} p_1 & p_1 & p_4 & p_4 & p_5 \\ p_1 & p_2 & p_4 & p_4 & p_5 \\ p_4 & p_4 & p_3 & p_4 & p_5 \\ p_4 & p_4 & p_4 & p_4 & p_5 \\ p_5 & p_5 & p_5 & p_5 & p_5 \end{bmatrix} \tag{1}$$

$$\begin{bmatrix} p_1 & p_1 & p_3 & p_4 & p_5 \\ p_1 & p_2 & p_3 & p_4 & p_5 \\ p_3 & p_3 & p_3 & p_4 & p_5 \\ p_4 & p_4 & p_4 & p_4 & p_5 \\ p_5 & p_5 & p_5 & p_5 & p_5 \end{bmatrix} \tag{2}$$

$$\begin{bmatrix} p_1 & p_1 & p_1 & p_4 & p_5 \\ p_1 & p_2 & p_3 & p_4 & p_5 \\ p_1 & p_3 & p_3 & p_4 & p_5 \\ p_4 & p_4 & p_4 & p_4 & p_5 \\ p_5 & p_5 & p_5 & p_5 & p_5 \end{bmatrix} \tag{3}$$

$$\begin{bmatrix} p_1 & p_1 & p_1 & p_1 & p_1 \\ p_2 & p_2 & p_2 & p_2 & p_2 \\ p_3 & p_3 & p_3 & p_3 & p_3 \\ p_4 & p_4 & p_4 & p_4 & p_4 \\ p_5 & p_5 & p_5 & p_5 & p_5 \end{bmatrix} \tag{4}$$

Including the introduction of a multiplier α which could be used in situations of low case counts (Gay et al., 1995; Klepac et al., 2009) yields additional options

$$\begin{bmatrix} p_1 & p_1 & p_1 & p_1 & p_5 \\ p_1 & p_2 & p_2 & p_2 & p_5 \\ p_1 & p_2 & p_3 & p_4 & p_5 \\ p_1 & p_2 & p_4 & \alpha p_3 & p_5 \\ p_5 & p_5 & p_5 & p_5 & p_5 \end{bmatrix} \tag{5}$$

$$\begin{bmatrix} \alpha p & p & p & p & p \\ p & \alpha p & p & p & p \\ p & p & \alpha p & p & p \\ p & p & p & \alpha p & p \\ p & p & p & p & \alpha p \end{bmatrix} \qquad (6)$$

2.2. Mobility

For theoretic movement of people across space (i.e. migration matrices), options considered include stratifying the population and considering the interactions between those strata. A simplification for when only part of the population mixes is the $2n \times 2n$ matrix of transmission between strata (Sattenspiel, 1988)

$$\begin{bmatrix} 0 & 0 \\ 0 & M_s \end{bmatrix} \qquad (7)$$

where only M_s mixes and can be given by random mixing (a matrix where all rates are equal), purely assortative (a diagonal matrix) or

$$M_s = \begin{bmatrix} p_1 & \dots & p_1 & 0 & \dots & 0 \\ \vdots & \ddots & \vdots & \vdots & \ddots & \vdots \\ p_1 & \dots & p_1 & 0 & \dots & 0 \\ p_2 & \dots & p_2 & p_2 & \dots & p_2 \\ \vdots & \ddots & \vdots & \vdots & \ddots & \vdots \\ p_2 & \dots & p_2 & p_2 & \dots & p_2 \end{bmatrix} \qquad (8)$$

Here the top left denotes a smaller group of size $r \times r(r < n)$ that mixes with one rate ($p_1 = 1/r$) with random mixing ($p_2 = 1/n$) occurring elsewhere in the population.

An alternative starting point for spatial models is the distance matrix (Bapat, 2014) (known as neighbourhood order (Meyer and Held, 2014)).

3. Empirical transmission matrices

The use of the theoretical matrices introduced in the previous section requires an active choice on the part of the modeller and the choice introduces certain assumptions into the modelling. For this reason, data-driven approaches to inform transmission matrices have seen increased use in the literature.

3.1. Interaction

Contact matrices are a form of sociomatrix introduced in Schenzle (1984) and later developments led to pilot studies for populating "who acquires infection from whom" (WAIFW) matrices (Edmunds, O'callaghan, & Nokes, 1997) based in survey data. The landmark social contact survey is POLYMOD (Mossong et al., 2008) which is often considered the catalyst and blueprint for later contact diary surveys for respiratory infections. An overview of later surveys is found in the work by Hoang et al. (2019) and Mousa et al. (2021).

Recent developments include the distinction between symptomatic and asymptomatic infections (Santermans et al., 2017), urban and rural settings (Del Fava et al., 2021; Leung et al., 2023), biological sex (van de Kassteele et al., 2017), the specific contacts of elderly (often defined epidemiologically as those above 65 years of age) (Oh et al., 2021) which introduces elderly facilities as an additional contact setting, contacts of school children (Conlan et al., 2011; Stehlé et al., 2011), contacts of internally-displaced people (van Zandvoort et al., 2022) which introduces the setting of a contact in other houses than ones own, contacts in refugee camps (Walker et al., 2022) which adds contacts in places such as pumps, shelters, and food distribution centres (McCreesh et al., 2022), contacts between healthcare workers (Machens et al., 2013), and by HIV status (Thindwa et al., 2022).

Developments such as considering airborne diseases broadens the earlier focus on respiratory transmission which might not be applicable to all infections as some do not require situations of intimate or immediate contact to spread. The urban-rural divide (Del Fava et al., 2021; Leung et al., 2023) may depend on geographical setting, as other research groups have found little difference in urban and rural contacts (Read et al., 1785). Empirical surveys conducted during synthetic outbreaks have also been evaluated (Klepac et al., 2018). Additionally time-use survey data can be used in place of contact diary surveys to construct contact matrices (van Leeuwen, PHE Joint Modelling Group, & Sandmann, 2022; Zagheni et al., 2008) though the

performance may depend on properties of the pathogen (Hoang et al., 2022). As with WAIFW, the empirical WHSWW can also be populated from survey data (Haraldsdottir et al., 1992; Garnett & Anderson, 1993; Datta, Mercer, & Keeling, 2018; Easterly, Alarid-Escudero, Enns, & Kulasingam, 2018; Granath, Giesecke, Scalia-Tomba, Ramstedt, & Forssman, 1991). Additionally, "who injects with whom" matrices can be useful transmission matrices for blood-borne infections (Smith et al., 2018) as these focus on the population at risk of acquiring this kind of infection (people who inject drugs). Godin et al. (Godin, Kronfli, Cox, Alary, & Maheu-Giroux, 2021) considered a theoretical contact matrix for an incarcerated population and populated it with survey data. WHSWW matrices have been used to examine the impact of condom use (Yamamoto, Ejima, & Nishiura, 2018).

3.2. Mobility

Within urban planning, origin-destination matrices are used to capture and quantify the flow of people from a place of origin to a destination. An example is a matrix with entries (Hufnagel et al., 2004)

$$p_{ij} = \frac{t_{ij}\sum_j t_{ij}}{N_i \sum_i t_{ij}} \tag{9}$$

where t_{ij} denotes the number of passengers with an origin in transport hub i (with N_i people living in its catchment area) and destination transport hub j. The gravity model (Balcan et al., 2009; Xia et al., 2004) considers movement given by

$$m_{ij} \propto \frac{N_i N_j}{f(d_{ij})} \tag{10}$$

where N_i is the population in location i and N_j is the population in location j. Options for the transformation of the distance d_{ij} in the denominator include $f(x) = x$ (identity), $f(x) = \exp(x)$ (exponential), and $f(x) = x^{-\delta}$ (power law). The function f is called an impedance function as it represents the reluctance to make the journey whereby we see that the gravity model makes a trade-off between the amount of mass (hence attraction) in population and the distance required.

The power law function has also been applied to adjacencies (spatial interaction) in spatial distance (Meyer and Held, 2014) as well as empirical commuting volume data (origin-destination) from air-, road-, and sea-based travel (Geilhufe, Held, Skrøvseth, Simonsen, & Godtliebsen, 2014). The gravity model is known as a flux model. Another option of modelling flux is the radiation model (Kraemer et al., 2019; Simini et al., 2012)

$$m_{ij} \propto \frac{N_i N_j}{(N_i + R_{ij})(N_i + N_j + R_{ij})} \tag{11}$$

which includes the population in the radius between i and j denoted R_{ij}. Bjørnstad et al. compared many of these options for pre-vaccination measles surveillance data and found that the gravity and radiation models might not be the best option.

4. Estimated transmission matrices

Balance constraints ensure symmetry in certain empirical or estimated transmission matrices; at population strata level the contacts should be symmetric (Hyman and Li, 1997) also known as requirements of reciprocity. Williams and Anderson (1994) suggest various methods of how to achieve a balanced transmission matrix, including the introduction of an iterative approach adjusting values of the transmission matrix until the balance is below a threshold to ensure balancing is achieved.

4.1. Interaction

For diseases which confer life-long immunity, serological investigation can be used to determine the force of infection. In this setting, the theoretical transmission matrices (see *Theoretical transmission matrices*) as well as later developments (see *Empirical transmission matrices*) have been utilised. Serology is concerned with the quantification of anti-bodies in the blood. If the anti-bodies are present above a pre-specified threshold, the serological test is said to be positive and the person tested is said to be sero-positive, meaning they have had a prior infection. The curve of proportion of results which are seropositive (hence immune) should increase with age and can be determined from a serology survey. For an age-structured approach, the force of infection can be estimated from serology data. The force of infection is the rate at which individuals susceptible to the disease become infected (it is the flow from the S compartment to the I compartment in a traditional SIR compartmental model).

The social contact hypothesis considers disease transmission rates to be proportional to contacts (Wallinga, Teunis, & Kretzschmar, 2006) and so the serological data (force of infection) can be used with either a theoretical or empirical transmission matrix to estimate the underlying transmission of the disease (Goeyvaerts et al., 2010; van Effelterre et al., 2009; Zagheni et al., 2008). These approaches assume time homogeneity and endemic equilibrium. Fumanelli, Ajelli, Manfredi, Vespignani, and Merler (2012) showed how to augment and construct empirical transmission matrices on the basis of demographic data, providing an approach that has been used to construct matrices where an empirical survey has not been

conducted (Arregui, Aleta, Sanz, & Moreno, 2018; Mistry et al., 2021; Prem et al., 2017). The use of online data gathering as an alternative to a contact diary survey has also been considered and evaluated (Koltai, Vásárhelyi, Röst, & Karsai, 2022).

4.2. Mobility

Sattenspiel (Sattenspiel, 1996) suggests a mobility matrix with entries m_{ij} informed by rates of travel. Mobile phone data can be used to determine spatial transmission (Tizzoni et al., 2014).

5. Summary measures for transmission matrices

The Q-statistic compares the diagonal elements of a transmission matrix p_{ii} (Aral et al., 1999) or the eigenvalues w_i (Gupta, Anderson, & May, 1989) with its dimension (here we consider matrices of dimension $n \times n$). It is calculated as (Aral et al., 1999)

$$Q = \frac{\sum_i p_{ii} - 1}{n - 1} \tag{12}$$

or (Gupta et al., 1989)

$$Q = \frac{\sum_i w_i - 1}{n - 1} \tag{13}$$

If $Q > 0$, the transmission matrix exhibits assortative mixing, if $Q = 0$ the transmission matrix exhibits random mixing, and if $Q < 0$ the transmission matrix exhibits disassortative mixing. The trace of the transmission matrix $\sum_i p_{ii}$ itself provides information on the size of the within-stratum (peer) mixing. The lower limit is $Q = \frac{-1}{n-1}$ (Ashby & Gupta, 2013). Some researchers have used the limits of Q ($\frac{-1}{n-1}$ and 1) as a visual aid to plot where their matrix falls on a scale from disassortative to assortative mixing (Garnett et al., 1996).

A similar summary measure was proposed by Newman (2003)

$$r = \frac{\sum_i p_{ii} - \sum_i p_{i+} p_{+i}}{1 - \sum_i p_{i+} p_{+i}} \tag{14}$$

where $p_{i+} = \sum_j p_{ij}$ is the sum of the ith row in the matrix and $p_{+i} = \sum_i p_{ij}$ is the sum of the ith column in the matrix. This measure takes the value $r = 1$ for assortative mixing and $r = 0$ for random mixing.

An alternative measure of assortative mixing is (Keeling and Rohani, 2008)

$$q = \frac{w_1}{w_2} \tag{15}$$

which considers the ratio of the largest and second largest eigenvalues (w_1 and w_2, respectively).

Adjacency matrices induced from networks (Iacobucci, 1994; Kretzschmar and Morris, 1996) may take the same Q for different networks. An example is given in Fig. 1 where Q has a value of $-1/8$ (no assortative mixing) for all three adjacency matrices since their diagonal entries all take values 0, though the mixing between population strata is rather different.

For this reason, the perspective of not-assortative mixing has been considered; while the Q, r, and q statistics consider assortative mixing, the I^2 statistic (Farrington, Whitaker, Wallinga, & Manfredi, 2009; Wallinga et al., 2019) examines instead the disassortative mixing. It is given by

$$I^2 = \frac{\mathbb{E}(i - j)^2}{2\sigma^2} \tag{16}$$

where i and j are the values of the groups, σ^2 is the variance associated with the overall distribution of the groups, and $\mathbb{E}$ denotes the expectation with respect to the density of pairs i and j.

A summary measure such as those outlined above may provide a useful manner of summarising many transmission matrices at once, for instance in approaches where they take on a temporal dimension and vary over time. The summary measure values give an overview of how the transmission matrices may change and may provide a simpler option for a graphical representation of the properties of the transmission matrices. An alternative is to plot the value of specific matrix entries to reflect potential changes to a transmission matrix (Meyer and Held, 2016).

5.1. Interaction

Transmission matrices may be updated to reflect changes in demography (Arregui et al., 2018) or sampled many times during an outbreak setting [examples from the COVID-19 pandemic of the 2020s include: Jarvis et al., 2020; Feehan & Mahmud, 2021; Liu et al., 2021].
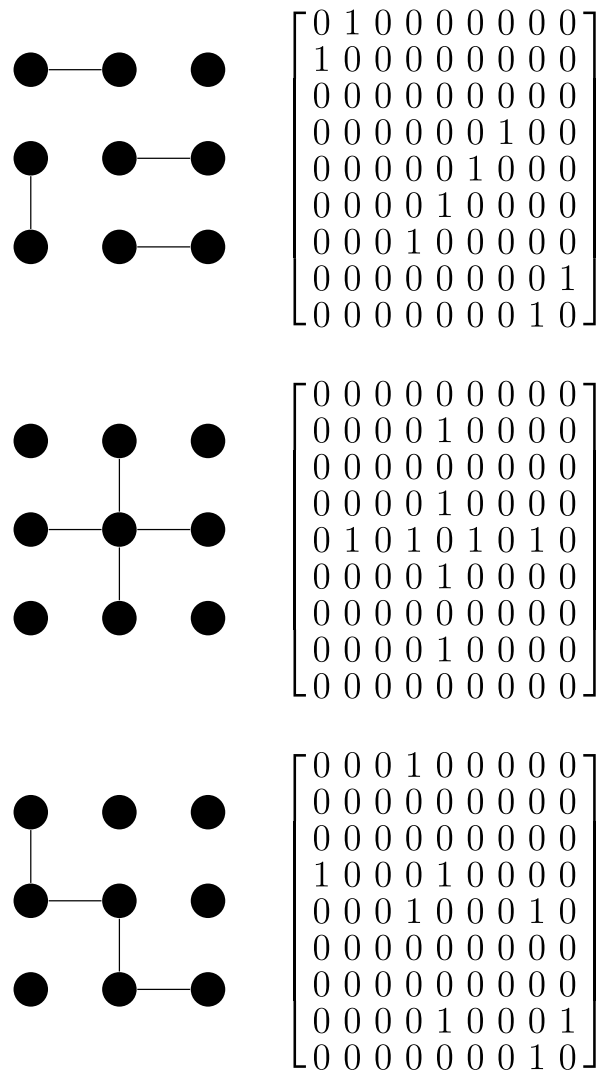
Fig. 1. Examples of networks from Kretzschmar and Morris (1996) (left) and their associated adjacency matrices (right). All take the value of Q at the lower limit.

5.2. Mobility

Transmission matrices be updated by augmenting a transmission weight with an external data source which varies over time such as data tracking changes in mobility [examples from the COVID-19 pandemic of the 2020s include: Alleman et al., 2021; Ensoy-Musoro, Nguyen, Hens, Molenberghs, & Faes, 2023; Grimée, Bekker-Nielsen Dunbar, Hofmann, & Held, 2021].

6. Access

The usefulness of empirical or estimated transmission matrices is greatest when they are made available to other researchers. In order to maximise the usefulness of the empirical matrices, they should be provided as open data. We provide an overview of the openness of options mentioned in this manuscript in Table 1. Programming language-specific initiatives to enable easy access to empirical transmission matrices have been found for R (e.g. the "socialmixr" package (Willem et al., 2020)) but not for other languages used in epidemiologic modelling.

Having harmonised terms and abbreviations (vocabulary) such as the international classifications of diseases (Harrison et al., 2021) provides an advantage to other users of data sets using the same vocabulary. This advantage comes from consistent identifiers and labels across data sets and so allows for the merging of data sets in a simpler manner than when labels and names in data sets are not unified. Similarly, encountering newer data becomes easier as variables are provided in an established and understandable manner. In short, controlled vocabularies improve the interoperability of data sets.

Mossong et al. (2008) established a naming convention for empirical transmission matrices based on social contact data but this convention is not yet *explicitly* described in the scientific literature or included in the FAIRsharing repository (fairsharing.org) allowing users to find it easily. In addition, a definite controlled vocabulary would help provide information in situations where meta data can be shared but the survey itself cannot be shared or cannot be accessed such as when data is provided in a proprietary format.

7. Links to epidemiologic thresholds

If the population being considered is fully susceptible to the disease (immunologically naïve), transmission matrices can be used to determine the basic reproduction number. This threshold is a summary measure of the "baseline" ability of the disease to transmit between an infected carrier and a susceptible host. Nold (1980) defined the spectral radius condition for transmission matrices and Diekmann et al. (1990, 2010) linked the spectral radius to the next generation matrix. Both can be used to obtain an estimate of the basic reproduction number. Caution must be taken of the homogenous mixing fallacy which occurs when an estimate of the basic reproduction number is obtained under an assumption of homogenous mixing when the true mixing is heterogeneous. This incorrect assumption leads to an estimate of the basic reproduction number which is too low which in turn leads to an estimate of the herd immunity threshold (the proportion of the population that needs to be vaccinated to keep the incidence of disease under the epidemic threshold) which is too low (Hethcote, 1996). Farrington, Kanaan, and Gay (2001) examined the effects of including individual heterogeneity and Inaba and Nishiura (2008) extended the concept to obtain the effective next generation which leads to an estimate of the effective reproduction number and removes the requirement of a fully susceptible population. Brooks-Pollock and Danon (2017) linked the next

Table 1
Availability of certain empirical or estimated matrices based on original manuscripts (as of November 2023).

Source	Accessibility (article)	Availability for re-use (matrix)
Haraldsdottir et al. (1992)	free access	partly available; values provided in figure
Del Valle, Hyman, Hethcote, and Eubank (2007)	subscription	partly avaialble; values provided in table
Garnett and Anderson (1993)	free access	partly available; values provided in figure
Schenzle (1984)	subscription	not available
Edmunds et al. (1997)	subscription	not available
Mossong et al. (2008)	open access	not available
Santermans et al. (2017)	subscription	not available
Del Fava et al. (2021)	open access	openly available; article provides link to OSF repository (osf.io/ebwrh)
Leung et al. (2023)	open access	openly available; article provides link to Zenodo repository (zenodo.org/record/7642648)
van de Kassteele et al. (2017)	open access	openly available; provided as supporting information
Oh et al. (2021)	subscription	limited availability; only available upon request
Conlan et al. (2011)	open access	not available; article provides link to website which does not contain data set
Stehlé et al. (2011)	open access	openly available; values provided in table
van Zandvoort et al. (2022)	open access	openly available; article provides link to GitHub repository (github.com/kevinvzandvoort/espicc_somaliland_digaale_contact_survey_2019)
Walker et al., 2022	open access	openly available; article provides link to GitHub repository (github.com/IDAS-Durham/june_mixed_method_CM_results)
McCreesh et al. (2022))	open access	openly available; article provides link to GitHub repository (github.com/NickyMcC/CasualAgeMixing)
Machens et al. (2013)	open access	openly available; values provided in table
Thindwa et al. (2022)	open access	openly available; article provides link to GitHub repository (github.com/deusthindwa/social.contact.rates.estimation.hiv.malawi) which does not contain the matrix but values provided in figure
Klepac et al. (2018)	open access	not available
Zagheni et al. (2008)	free access	not available
van Leeuwen et al. (2022)	subscription	not available
Datta et al. (2018)	open access	partly available; part of data set provided as supporting information
Easterly et al. (2018)	subscription	openly available; article provides link to Zenodo repository (zenodo.org/record/1322780)
Granath et al. (1991)	free access	partly available; values provided in table
Fumanelli et al. (2012)	open access	openly available; provided as supporting information
Prem et al. (2017)	open access	openly available; provided as supporting information
Arregui et al. (2018)	open access	not available
Mistry et al. (2021)	open access	openly available; article provides link to GitHub repository (github.com/mobs-lab/mixing-patterns)
Tizzoni et al. (2014)	open access	openly available; provided as supporting information
Jarvis et al. (2020)	open access	openly available; article provides link to GitHub repository (github.com/jarvisc1/comix_covid-19-first_wave)
Feehan and Mahmud (2021)	open access	openly available; article provides link to Harvard Dataverse repository (dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/M74AJ4)
Smith et al. (2018)	free access	partly available; values provided in figure
Brooks-Pollock and Danon (2017)	free access	partly available; values provided in table

generation matrix to the attributable fraction. Vynnycky and White (2010) examined the relationship between the Q statistic and the basic reproduction number and found it possible to determine the value of Q for which the basic reproduction number is at the epidemic threshold.

8. Discussion

Regarding further reading, earlier reviews provide a nice overview of various aspects not considered in great detail here. We refer the interested reader to Keeling and Eames (2005) for a networks-based perspective on transmission (networks can be represented in matrix form, see Haraldsdottir et al. (1992) and Del Valle et al. (2007) for example). The work by Chowell, Sattenspiel, Bansal, and Viboud (2016) examines the interplay between transmission options considered in this work and early epidemic growth. For more on contact matrices, the systematic reviews by Hoang et al. (2019) and Mousa et al. (2021) may provide fruitful insights. An overview of transmission matrices used with a specific class of surveillance-based regression models known as endemic-epidemic models is found in Bekker-Nielsen Dunbar (2023). For more information on serology and mixing, the book by Hens et al. (2012) is an excellent reference. A data repository with multiple social contact surveys in the format established by Mossong et al. (2008) is found in Willem et al. (2020), all of which are openly available and provided for re-use. An extensive review of mobility models which includes options for populating a transmission matrix is given in Barbosa et al. (2018). More information on the next generation matrix can be found in Heffernan et al. (2005) and Hurford et al. (2010).

CRediT authorship contribution statement

M. Bekker-Nielsen Dunbar: Conceptualization, Writing — original draft, Writing — review & editing.

Declaration of competing interest

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