Petri nets in epidemiology

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Abstract

This work provides a geometric version of the next-generation method for obtaining the basic reproduction number of an epidemiological model. More precisely, we generalize the concept of the basic reproduction number for the theory of Petri nets. The motivation comes from observing that any epidemiological model has the basic structures found in the SIR model of Kermack-McKendrick. These are three substructures, also given by three Petri nets inside, representing the susceptible population, the infection process, and the infected individuals. The five assumptions of the next-generation matrix given by van den Driessche-Watmough can be described geometrically using Petri nets. Thus, the next-generation matrix results in a matrix of flows between the infection compartments. Besides that, we construct a procedure that associates with a system of ordinary differential equations under certain assumptions, a Petri net that is minimal. In addition, we explain how Petri nets extend compartmental models to include vertical transmission.

1 Introduction

The present work is the geometric completion or counterpart of the next-generation matrix method [DHM90, vdDW02, vdDW08]. Instead of analyzing a specific epidemiological model described by a system of ordinary differential equations (ODEs), we consider an underlying geometric structure that encodes the ODEs by the diagrammatical structure of a Petri net [Rei82]. These structures are called in the literature by stochastic Petri nets in the book of Baez–Biamonte [BB18], providing a rate function that disposes all the parameters of all transitions between all the possible compartments. We encounter Petri nets as efficient structures that have been popular since their inclusion in applied category theory. A Petri net consists of compartments or places (represented by circles), transitions (represented by squares), and arrows between compartments and transitions, together with a rate function that assigns a parameter to each transition. We are interested in Petri nets modeling the course of a pandemic, which can be highly sophisticated. However, we encounter that inside these structures, it is possible to find three substructures that follow the components of the basic SIR model of Kermack–McKendrick [KM27]. We call them the Kermack–McKendrick modules of susceptible, infection-process, and infection (shortly the KM modules). More precisely, we can obtain three sub-Petri nets that encapsulate all the features of the susceptible population (borne, decease, migration, emigration, etc.) into the susceptible module, all the features of the infection process (transitions of infection, and some compartments that connect them) into the infection-process module, and all the features of the infection population (infected, exposed, asymptomatic, carrier, etc.) into the infection module. Van den Driessche–Watmough [vdDW02, vdDW08] present five assumptions in such a way that, for instance, there is no immigration of individuals into the disease compartments and no disappearance of infected individuals, among other particularities.

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The geometric point of view of these five assumptions permits the identification of these assumptions in the KM modules of the underlying Petri net instead of the system of ODEs. We obtain a clearer form of the functions that define the matrices $F$ and $V$ of the next-generation matrix $FV^{-1}$. The basic reproduction number $R_0$ can be defined as the dominant eigenvalue $R_0 = \rho(FV^{-1})$ by the Perron-Frobenius theorem. A geometric interpretation of the coordinates of $FV^{-1}$ was mentioned in [vdDW02, pag. 33] as follows: the $(i, k)$ entry of the product $FV^{-1}$ is the expected number of new infections in compartment $i$ produced by the infected individual originally introduced into compartment $k$. Independently, the author, using Petri nets, found an interpretation of the coordinates matrix $FV^{-1}$ by summing along all the paths of flows in the Petri net, between the infection module traversing the infection-process module and where we have to consider the inclusion of flows from the susceptible module. The basic reproduction number $R_0$ was geometrically interpreted as the expected secondary infection individuals for the longest path that traverses the infection-process module starting and ending in the infection module (an exception is the peculiar model of Malaria where $FV^{-1}$ has zero diagonal). The previous argumentation gives us reasons to call the next-generation matrix the matrix of flows.

The present paper is written for two types of persons: 1) people who want to quickly calculate the basic reproduction number where a geometric diagrammatic performance of the model could be more suitable. Two directions make our approach very attractive. We can start by developing a Petri net modeling of our epidemiological phenomenon, and after the appliance of the rate equation, we can end with the associated system of ODEs. However, we can start with a specific system of ODE, wondering if there is a Petri net that represents it; under some hypotheses, there is a process to realize the Petri net, which we call the inverse problem of Petri nets and ODEs. 2) Experts in mathematical epidemiology search different directions for developing the essence concepts such as the basic reproduction number and herd immunity in terms of other mathematical structures. Petri nets are a promising direction using possible tools of graph theory and stochastic methods, and our work could be the starting point of a new theory where several problems not only in epidemiology can be understood in terms of Petri nets.

This article is organized as follows: in Section 2, we give the prerequisites of the theory of Petri nets, where we introduce the rate equation of a Petri net to obtain the associated system of ODEs. We present several Petri nets for plenty of epidemiological models such as SIR, SIS, SEIR, SEAIR, SCIR, SIWR, SIQR, SEIT, and models for Malaria and vaccinations. Additionally, we will discuss the inverse problem of Petri nets and ODEs. In Section 3, we explain the next-generation matrix method for a system of ODEs representing the model of an epidemiological model. The five assumptions of van den Driessche-Watmough are presented, and we give examples of calculating the basic reproduction number using this analytic method. At the end of the paper, we include the $F$ and $V$ matrices, the next-generation matrix, and the basic reproduction number for all the models studied in Section 2. The Section 4 is the most relevant part of this work. We provide the geometric analogs of these five assumptions, where we previously defined the KM modules of a Petri net to develop the geometric next-generation matrix method for a Petri net. We prove these geometric conditions are enough to define the basic reproduction number as the expected secondary infections in the longest path (except the Malaria model). We provide some examples of applying the geometric procedure for the SEAIR model, the model of Malaria, and the two vaccination models. Finally, in Section 5, we present how to modify the definition of our Petri nets to include another feature, such as the vertical transmission of disease.

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2 Petri nets

Petri nets are promising methods for modeling and simulating biological systems [Rei82, BB18]. Carl Adams Petri designed them [Smi15], a German mathematician dedicated to computer science who lived in the time of general relativity of Einstein. For instance, the locality of time is one of the most essential advantages of Petri nets. The Ph.D. thesis of Petri [Pet62] was forward-thinking and innovative, initiating the theory of Petri nets with fundamental ideas such as sequence, conflict, and concurrency. Indeed the translation to English of this thesis [Pet66] was classified information by the United States Air Force.

A Petri net consists of sets of compartments (species or states), transitions, and arrows with assignment rules. In addition, each compartment has associated ‘tokens’ representing the individuals or quantities that travel around the transitions, passing to other species, efficiently describing a phenomenon or process under study. An important rule in Petri nets is that the firing or execution of a transition is possible precisely when at least a token exists in all the former species or states to the transition. Interesting cases are when arrows have assigned some values indicating the value or proportion this arrow lets pass.

Generalizations of different types of Petri nets exist in the literature depending on the needs of the problem; see [DA10]. To mention a few of them, we have colored Petri nets with tokens taken values in different data types; see [Jen97]. Continuous Petri nets have the feature that the marking of a place is a real (positive) number and no longer an integer representing the number of tokens. Nested Petri nets are an extension of the classic Petri nets where each compartment, transition, and token can be a Petri net. The precise definition of a Petri net is as follows:

**Definition 1.** A Petri net consists of a set of compartments \( S = \{x_1, \ldots, x_k\} \) and a set of transitions \( T = \{z_1, \ldots, z_l\} \), together with a finite set of arrows \( A \) with a matching function \( f : A \rightarrow S \times T \sqcup T \times S \). The arrows are divided into two disjoint subsets \( A = A_1 \sqcup A_2 \) with \( f(A_1) \subset S \times T \) (arrows from species to transitions) and \( f(A_2) \subset T \times S \) (arrows from transitions to species). For \( x_i \in S \) and \( y_j \in T \), we set:

- by \( m_{i,j} = |f^{-1}(x_i, z_j)| \) the number of arrows with source \( x_i \) and target \( z_j \), and
- by \( n_{i,j} = |f^{-1}(z_j, x_i)| \) the number of arrows with source \( z_j \) and target \( x_i \).

An important application of the theory of Petri nets is the connection with ordinary differential equations (ODEs). ODEs are used in many contexts in sciences describing real-life models like physics, medicine, etc., see [Arn84]. The connection of Petri nest with ODE starts with the assumption of a rate function for the transitions

\[
r : \{z_1, \ldots, z_l\} \rightarrow (0, \infty).
\]

These types of Petri nets are called stochastic; see [BB18]. Denote by \( r_j := r(z_j) \); every variable \( x_i \) has associated a rate equation given by the formula

\[
\frac{dx_i}{dt} = \sum_{j=1}^{l} r_j (n_{ij} - m_{ij}) x_1^{m_{1j}} \cdots x_k^{m_{kj}}.
\]

Now, we give plenty of examples of ODEs associated with some Petri nets, mainly focusing on epidemiological models. Our pictures of Petri nets represent the compartments with yellow circles and the transitions with blue squares.

**Example 2.** The formation of water is the basis of life. A water molecule has an oxygen atom with two hydrogen atoms connected by covalent bonds. Take the Petri net with three compartments \( S = \{H, O, W\} \) denoting Hydrogen, Oxygen, and Water. We have only one transition \( T = \{R\} \) denoting the Reaction.
Set by $\alpha = r(R)$ the number of water molecules produced in a unit of time. We represent this process by the Petri net of Figure 1. The following ODE gives the rates equations:

\[
H'(t) = -2\alpha H^2 O,
O'(t) = -\alpha H^2 O,
W'(t) = \alpha H^2 O.
\]

**Example 3.** Kermack-McKendrick [KM27] developed a model that, even at present, is the basic principle used to simulate a pandemic. This structure is known as the SIR model by the compartments Susceptibles $S$, Infected $I$, and Recovered $R$. There are two transitions between the compartments, as shown by the processes of infection and recovery. It is assumed to be a constant population; hence, we have the equation throughout all time $N = S(t) + I(t) + R(t)$. For a historical account of this model and important features, the reader can consult the references [Bra08, Mar15]. In Figure 2, we include the Petri net of the SIR model. The rate equations that conform to the ODE are as follows:

\[
S'(t) = -\beta SI,
I'(t) = \beta SI - \alpha I,
R'(t) = \alpha I.
\]

**Example 4.** A simpler model is provided by relaxing the assumption of permanent immunity in the SIR model, obtaining the SIS model. The infected individuals are recovered and immediately pass to the susceptible compartment. Thus, we have two compartments susceptible $S$ and infected $I$ with an additional transition with parameter $\alpha$ connecting the two compartments from $I$ to $S$. Some infectious diseases are, for example, the common cold or influenza. The SIS model is often used because we can solve analytically the two populations $S(t)$ and $I(t)$ at any point $t$ in time, see [Kuh21, p. 35], where again we assume total population size $N = S(t) + I(t)$ constant in time. We have associated the following ODE:

\[
S'(t) = -\beta SI + \alpha I,
I'(t) = \beta SI - \alpha I.
\]

The associated Petri net to this model is depicted in Figure 3.
Example 5. The SIR model assumes lifelong immunity; however, recovered individuals may lose their immunity and become susceptible again, for instance, to airborne diseases such as seasonal influenza, where immunity may wane over time, for example, the book [VW10]. This is called the SIRS model where again is assumed a constant population throughout all time $N = S(t) + I(t) + R(t)$. Compared to the SIR model, we now have another transition with parameter $\gamma$ connecting the recovered and susceptible compartments. The ODE associated with the SIRS model is as follows:

\[
\begin{align*}
S'(t) &= -\beta SI + \gamma R, \\
I'(t) &= \beta SI - \alpha I, \\
R'(t) &= \alpha I - \gamma R.
\end{align*}
\]

The Petri net of this model is illustrated in Figure 4.

Example 6. Thomas Malthus [Mal98] in the eighteen-century debates about the population increasing contributing to the first census of England, Scotland, and Wales. The Malthusian model assumes that all individuals are identical, the environment is constant in space and time, and, in particular, the resources are unlimited. The population is located in one compartment $N$, and $b$ and $\mu$ denote the birth and death rates, respectively. The Malthusian model becomes $N'(t) = bN - \mu N = rN$ where $r = b - \mu$ is the population growth rate. The population is growing exponentially if $r > 0$, decreasing exponentially if $r < 0$, and constant if $r = 0$. However, we use a simplified logistic model assuming a constant birth rate independent of the population size (we denote the total birth rate by $\Lambda$), with ODE given by the following equation:

\[
N'(t) = \Lambda - \mu N.
\]

The population is asymptotically constant, with $N(t) \to \Lambda/\mu$ as $t \to \infty$. Figure 5 depicts the associated Petri net for this simplified logistic model. It is important to mention that epidemic models without explicit demography are useful on a short time scale, as in the cases of childhood disease and influenza. On the other hand, there are slow diseases, such as HIV, tuberculosis, and hepatitis C, where the demography has to be included in the models.
Example 7. The SEIR model is an immediate generalization of the Kermack-McKendrick SIR model. This model has an additional compartment that comprises infected individuals who are not immediately infectious; hence, there is an incubation phase. The additional compartment is named by $E$, denoting Exposed individuals. There is a transition with a rate $\eta$ from the compartment $I$ to $E$. In addition, a Malthusian model is included in the susceptible compartment, and there are transitions of decrease for all the compartments. This model applies to influenza, measles, mumps, and rubella. There are different variations of the SEIR model in the literature. For instance, the SEIR model has recently been used for the COVID-19 outbreak [SB21]. We take the ODE in [Mar15], associated with the SEIR model:

\[
\begin{align*}
S'(t) &= \Lambda - \beta SI - \mu S, \\
E'(t) &= \beta SI - (\eta + \mu)E, \\
I'(t) &= \eta E - (\alpha + \mu)I, \\
R'(t) &= \alpha I - \mu R.
\end{align*}
\]

The construction of the Petri net associated with this model is found in Figure 6.

Example 8. Some diseases have the characterization that a significant group of individuals remain asymptomatic upon infection and have the possibility to infect other individuals. A recent case is the COVID-19 pandemic [Kuh21], where the SEAIR model is also called the SEIR model. Another example of asymptotic disease is VIH, in which an infected individual can live without symptoms for ten years before progressing to symptoms of AIDS [HAF08]. We have five compartments: the susceptibles $S$, exposed $E$, asymptomatic $A$, infected $I$, and resistant $R$. Now, we distinguish between infection and disease with the compartment $A$, consisting of individuals whose infection does not show symptoms. The symptomatic infected individuals are enclosed in the compartment $I$. Exposed individuals in the compartment $E$ progress to the infectious compartment with probability $p$ and to the asymptomatic compartment $A$ with probability $(1 - p)$. We take the ODE in [Mar15], associated with the SEAIR model:

\[
\begin{align*}
S'(t) &= \Lambda - \beta S(I + qA) - \mu S, \\
E'(t) &= \beta S(I + qA) - (\eta + \mu)E, \\
A'(t) &= (1 - p)\eta E - (\gamma + \mu)A, \\
I'(t) &= p\eta E - (\alpha + \mu)I, \\
R'(t) &= \alpha I + \gamma A - \mu R.
\end{align*}
\]

In Figure 7, we represent the Petri net of the SEAIR model.

Example 9. The SIR model is modified considering an additional compartment of individuals that do not show symptoms or signs of infection, but they transmit the pathogen from their nose, throat, or
feces. Some diseases show a carrier compartment, such as viral hepatitis and poliomyelitis, and bacterial diseases, including diphtheria and meningococcal meningitis, see [Mar15]. This model follows the system of ODES: **SCIR model**

\[
S'(t) = \Lambda - \beta S(I + qC) - \mu S + \rho R, \\
C'(t) = \beta S(I + qC) - (\eta + \gamma + \mu)C, \\
I'(t) = \eta C - (\alpha + \mu)I, \\
R'(t) = \alpha I + \gamma C - (\mu + \rho)R.
\]

Figure 8 illustrates the associated Petri net.

**Example 10.** Waterborne diseases, such as cholera, hepatitis A and E, norovirus, and rotavirus, are a severe problem for public health today. For instance, Cholera is a disease with a long history that came into prominence in the 19th century, killing thousands of people in India. These diseases are studied in [TE10] consider transmission through the water. Infection for each disease is typically through pathogen ingestion (e.g., fecal-oral route). For instance, drinking sewage-contaminated water, eating food prepared by an individual with soiled hands, or acquiring an infection during treatment in a hospital. The ODE is an extension of the classical SIR model by adding a water compartment \( W \) and allowing for both person–person and person–water–person transmission. This is called the SIWR model, with the
Figure 9: The SIWR model.

following ODE:

\[
\begin{align*}
S'(t) &= \mu N - \beta W SW - \beta SI - \mu S, \\
I'(t) &= \beta W SW + \beta SI - (\gamma + \mu)I, \\
W'(t) &= \alpha I - \xi W, \\
R'(t) &= \gamma I - \mu R.
\end{align*}
\]

We can observe in Figure 9 the associated Petri Net where the additional compartment \( W \) is connected to \( I \) by a transition \( \alpha \), and there is an additional transition \( \beta W \) where occurs the person-water-person transmission. The total population is included in the compartment \( N \).

**Example 11.** Malaria is one of the diseases that have their presence constantly in the human population. It is caused by the entry of the malaria parasite called Plasmodium into the bloodstream due to the bite of an infected female Anopheles mosquito. A single bite by a malaria-carrying mosquito can lead to extreme sickness or death. A SIR-type model is studied by Wedajo, Bole, and Koya in [WBK18]. We have two populations (humans/mosquitoes) with a common disease. The species are of two different types. The susceptible, infected, and resistant for humans are denoted by \( \{S_H, I_H, R_H\} \). The susceptible, infected mosquitoes are denoted by \( \{S_M, I_M\} \). Similarly, the transitions are of two different types. We have borne, decease, infection, and recovery for humans, with parameters \( \{\Pi, \mu_H, \beta_{MH}, \sigma\} \). We have borne, decease, and infected mosquitoes, with parameters \( \{\Lambda, \mu_M, \beta_{HM}\} \). Additionally, we have the transitions \( \alpha \), which is given by the decease-death rate for humans, \( \sigma \), the recovery rate for humans, and \( \delta \), the infected-migration rate for humans. This model has the following equations

\[
\begin{align*}
S_H'(t) &= \Pi - \beta_{HM} S_H I_M - \mu_H S_H, \\
I_H'(t) &= \beta_{HM} S_H I_M - (\mu_H + \sigma)I_H - (\alpha - \delta)I_H, \\
R_H'(t) &= \sigma I_H - \mu_H R_H, \\
S_M'(t) &= \Lambda - \beta_{MH} S_M I_H - \mu_M S_M, \\
I_M'(t) &= \beta_{MH} S_M I_H - \mu_M I_M.
\end{align*}
\]

The associated Petri net is depicted in Figure 10.

Now, we study the Petri nets associated with control strategies implemented in epidemiological models of SIR type. We base our systems of ODE on the book [Mar15].

**Example 12.** Vaccination is one of the most outstanding achievements of public health. For instance, vaccination has led to the complete eradication of smallpox worldwide and a near eradication of polio. There are two points in which vaccination models can differ from one another. The first model treats vaccination as equivalent to going through the disease, so the vaccinated individuals are recovered individuals. Here, we are assuming a perfect vaccine where everybody is completely protected. We use a SIR model as in [Mar15, p. 217], where we add a compartment \( N \), meaning the whole population. The individuals pass through a transition with rate \( \mu \), where a fraction \( p \) are vaccinated and \( q = 1 - p \) pass...
Figure 10: A SIR model for Malaria.

Figure 11: First model of vaccination.

to the susceptible class. The associated ODE is given as follows:

\[
\begin{align*}
S'(t) &= q\mu N - \beta SI - \mu S, \\
I'(t) &= \beta SI - (\mu + \alpha)I, \\
R'(t) &= p\mu N + \alpha I - \mu R.
\end{align*}
\]

The associated Petri net is a combination of the usual SIR model in Example 3 with the addition of a compartment \( N \) meaning the whole population, and a transition \( \mu \) with output two arrows to the Susceptible and Recovery compartments, respectively. We have the picture of this Petri net in Figure 11.

**Example 13.** The second model for vaccination is when we consider vaccines rarely perfect. We denote by \( V \) the compartment of vaccinated individuals. The susceptible population is vaccinated with rate \( \psi \), and the vaccinated individuals can pass to the infection compartment with transition rate \( \beta \delta \), where \( 0 \leq \delta \leq 1 \) and \( \epsilon := 1 - \delta \) is the vaccine efficacy. The proportion of individuals who recover to the vaccinated class has a rate of \( \chi \). This is combined with an SIS model as in [Mar15, p. 219], obtaining
the following ODE:

\[
\begin{align*}
S'(t) &= \Lambda - \beta SI/N - (\mu + \psi)S + \chi \gamma I, \\
I'(t) &= \beta SI/N + \beta \delta VI/N - (\mu + \gamma)I, \\
V'(t) &= \psi S - \beta \delta VI/N - (1 - \chi)\gamma I - \mu V.
\end{align*}
\]

This example reveals how mitigation strategies are shown in the Petri nets by modifying the transit of susceptible populations into infection transitions. For instance, in the Petri net associated with the previous ODE in Figure 12, the transit is modified by arrows arriving at the infection transitions associated with \( \beta \) and \( \beta \delta \).

**Example 14.** Quarantine is one of the more antique control strategies to prevent the spread of disease. It is especially important when vaccination or treatment is not possible. We take the system of ODEs in [Mar15, p. 95]. A compartment is added to the SIR model, which comprises the isolated individuals in quarantine, denoted by \( Q \). Now, it is denoted as an active class \( A(t) = S(t) + I(t) + R(t) \) of all the mixing individuals. The system of ODEs is as follows:

\[
\begin{align*}
S'(t) &= \Lambda - \beta SI/A - \mu S, \\
I'(t) &= \beta SI/A - (\alpha + \gamma + \mu)I, \\
Q'(t) &= \gamma I - (\eta + \mu)Q, \\
R'(t) &= \alpha I + \eta Q - \mu R.
\end{align*}
\]

Figure 13 depicts the associated Petri net. A weighted arrow exists between the susceptible compartment \( S \) and the transition associated with the parameter \( \beta \). The weight of this arrow is \( 1/A \), which controls the flow from \( S \) to the transition of \( \beta \).

**Example 15.** The treatment of a disease can be incorporated into the SEIR model, where a compartment of treatment replaces the compartment of recovered individuals. An additional transition considers the case the treatment may not be successful and takes individuals to the compartment of infected individuals. The presence of relapsing individuals leads to ambiguity in the computation of the reproduction number. This happens in the SEIT model in [Mar15, p. 95]. However, we found a SEIT model used as a model for tuberculosis in [FCF00], where the basic reproduction number can be calculated. The model has the following system of ODEs:

\[
\begin{align*}
S'(t) &= \Lambda - \beta c SI/N - \mu S, \\
E'(t) &= \beta c SI/N - p \beta c EI/N - (\mu + \kappa)E + \sigma \beta c TI/N, \\
I'(t) &= p \beta c EI/N + \kappa E - (\mu + r + d)I, \\
T'(t) &= r I - \sigma \beta c TI/N - \mu T.
\end{align*}
\]

We depict in Figure 14 the associated Petri net of this model.
Figure 13: The SIR model with quarantine.

Figure 14: The SEIT model used for tuberculosis.
2.1 Inverse problem of Petri nets and ODEs

For the moment, we have a procedure to uniquely associate a system of ODEs for a Petri net provided with a rate function; see Section 2. It can be of great interest in the opposite direction: is it possible to somehow associate a Petri net with a given system of ODEs? Immediately, we have simple counterexamples as

\[
\begin{align*}
\frac{dx_1}{dt} &= \alpha x_2, \\
\frac{dx_2}{dt} &= \alpha.
\end{align*}
\]  

(5)

It is impossible to assign a Petri net because of the possibilities of arrows between \(x_2\) and \(\alpha\). For instance, start with the first equation \(\frac{dx_1}{dt} = \alpha x_2\), so we have arrows \(x_2 \rightarrow \alpha\) and \(\alpha \rightarrow x_1\), but using the second equation \(\frac{dx_2}{dt} = \alpha\) we must have an arrow \(\alpha \rightarrow x_2\) and no arrow arriving to \(\alpha\)!

The proposal avoids cases of systems of ODEs in which the arrows that end in each transition are ambiguous. More precisely, we consider the set of variables of a system of ODEs \(S := \{x_1, \ldots, x_k\}\) and identify the set of parameters \(T := \{z_1, \ldots, z_l\}\). We verify that all the equations in the ODEs are built of monomials of the form

\[
f(x_i, z_j) \cdot z_j \cdot x_1^{m_{j,1}} \cdots x_1^{m_{j,k}}
\]  

(6)

where the description of these elements is as follows:

- \(z_j\) is an element of the set \(T\);
- \(m(z_j) := x_1^{m_{j,1}} \cdots x_1^{m_{j,k}}\) is monomial inside the set \(m(T)\); and
- \(f(x_i, z_j)\) is an integer function.

Thus, it is possible to construct a well-defined function

\[
m : T \rightarrow M(S),
\]  

(7)

Recollect all the functions of exponents \(m_i : T \rightarrow \mathbb{N} \cup \{0\}\) which assign the exponent of the variable \(x_i\) inside the monomial \(m(y)\) to each transition. Notice that if the monomial \(m(y)\) does not contain the variable \(x_i\), the value \(m_i(y)\) is zero.

We want to emphasize that this procedure does not apply if any previous constructions cannot be accomplished.

To recover the Petri net we consider the values \(n_{i,j} = f(x_i, y_j) + m_i(y_j)\) and \(m_{i,j} = m_i(y_j)\). This Petri net resulting from the present procedure is minimal in the sense that we can take different values \(n'_{i,j} = n_{i,j} + k_{i,j}\) and \(m'_{i,j} = m_{i,j} + k_{i,j}\) with the same function \(f(x_i, y_j) = n'_{i,j} - m'_{i,j}\).

3 The basic reproduction number

The basic reproduction number \(R_0\) is one of the most essential concepts in mathematical epidemiology. Historical references [Hee02, Per18] assert this number \(R_0\) started in demography and ecology, but it gained popularity in epidemiology, where it is a threshold parameter that controls the spread of an infectious or contagious disease.

There are several definitions of \(R_0\) depending on the field of study. In epidemiology, this quantity is defined as the expected number of new cases of an infection caused by a typical infected individual in a population consisting of susceptibles only. In mathematics, there is a method proposed by Diekmann–Heesterbeek–Metz [DHM90] and elaborated by Van Den Driessche–Watmough [vdDW02, vdDW08], which defines \(R_0\) as the dominant eigenvalue of the so-called next-generation matrix.
3.1 The next generation matrix method

We start with an ordinary differential equation (ODE) where the individuals are sorted into compartments \( \{x_1, \ldots, x_m\} \). Assume the first \( n < m \) compartments contain the infected individuals. Denote by \((x, y)\) the pair where \(x\) consists of the first coordinates \(x_1, \ldots, x_n\) and \(y\) consists of \(x_{n+1}, \ldots, x_m\). The rate equation associated with the \(i\)th compartment, \(0 < i < n\), can be written as follows

\[
x_i'(t) = F_i(x, y) - V_i(x, y),
\]

The function \(F_i\) denotes the rate secondary infections increase the \(i\)th disease compartment, and \(V_i\) denotes the rate disease progression, death, and recovery decrease the \(i\)th compartment.

A disease-free equilibrium (DFE) is a state where the epidemiological model remains in the absence of disease. We need some assumptions to ensure the existence of this equilibrium and to ensure that the model is well-posed. In what follows, we enumerate these assumptions established by van Den Driessche–Wartmough [vdDW08], which are equivalent to those in [vdDW02].

(A1) Assume \(F_i(0, y) = 0\) and \(V_i(0, y) = 0\) for all \(y \geq 0\) and \(i = 1, \ldots, n\).

(A2) Assume \(F_i(x, y) \geq 0\) for all nonnegative \(x\) and \(y\) and \(i = 1, \ldots, n\).

(A3) Assume \(V_i(x, y) \leq 0\) whenever \(x_i = 0\), \(i = 1, \ldots, n\).

(A4) Assume \(\sum_{i=1}^{n} V_i(x, y) \geq 0\) for all nonnegative \(x\) and \(y\).

(A5) All solutions with initial condition of the form \((0, y)\) approach a point \((0, y_0)\) as \(t \to \infty\). This point is referred to as the disease-free equilibrium.

As a consequence, we obtain the disease compartments are decoupled from the remaining equations \((x_1'(t), \ldots, x_n'(t))^t = (F - V)(x_1, \ldots, x_n)^t\), where the \(n \times n\) matrices \(F\) and \(V\) are given by

\[
F = \left( \frac{\partial F_i}{\partial x_j}(0, y_0) \right) \quad \text{and} \quad V = \left( \frac{\partial V_i}{\partial x_j}(0, y_0) \right),
\]

for \(i, j = 1, \ldots, n\). The basic reproduction number is defined by the dominant eigenvalue of the nonnegative generation matrix \(FV^{-1}\) as follows

\[
R_0 = \rho(FV^{-1}).
\]

The interpretation of the entries in the next generation matrix \(FV^{-1}\) is explained by van den Driessche–Wartmough [vdDW02]. Assuming the population remains near the DFE and excepting re-infection, the \((j, k)\) entry of \(V^{-1}\) is the average time this individual spends in compartment \(j\) during its lifetime. The \((i, j)\) entry of \(F\) is the rate at which infected individuals in compartment \(j\) produce new infections in compartment \(i\). Hence, the \((i, k)\) entry of the product \(FV^{-1}\) is the expected number of new infections in compartment \(i\) produced by the infected individual originally introduced into compartment \(k\). The previous fact is crucial for the next section, where we define the basic reproduction number of a Petri net.

In what follows, we apply the next-generation matrix method to the SEAIR model, the model of Malaria, and the two vaccination models. The reader can find a list of this type of examples for a variety of models in epidemiology in Table 6 at the end of the paper.

**Example 16.** We consider the SEAIR model from the book [Mar15], which was studied in Example 8. The infection compartments contain exposed \(E\), asymptomatic \(A\), and infected \(I\). The associated function \(F\) and \(V\) are:
\[ F_E = \beta S(I + qA) \quad V_E = \left(\eta + \mu\right)E \]
\[ F_A = 0 \quad V_A = \eta(p - 1)E + (\gamma + \mu)A \]
\[ F_I = 0 \quad V_I = -\eta pE + (\alpha + \mu)I \]

Consequently, the \( F \) and \( V \) matrices are given as follows:

\[
F = \begin{pmatrix}
0 & \beta qS & \beta S \\
0 & 0 & 0 \\
0 & 0 & 0
\end{pmatrix}, \\
V = \begin{pmatrix}
\eta + \mu & 0 & 0 \\
\eta(p - 1) & \gamma + \mu & 0 \\
-\eta p & 0 & \alpha + \mu
\end{pmatrix}
\]

with the next-generation matrix

\[
FV^{-1} = \begin{pmatrix}
\frac{\beta qS}{(\eta + \mu)(\gamma + \mu)} & \frac{\beta pS}{(\eta + \mu)(\alpha + \mu)} & \frac{\beta S}{\gamma + \mu} \\
0 & 0 & 0
\end{pmatrix},
\]

and the basic reproduction number is

\[
R_0 = \frac{\beta q(1 - p)qS}{(\eta + \mu)(\gamma + \mu)} + \frac{\beta pS}{(\eta + \mu)(\alpha + \mu)}.
\]

**Example 17.** The model of Malaria in [WBK18] has the infection compartments \( I_H \) and \( I_M \). The functions \( F \) and \( V \) are as follows:

\[
F_{I_H} = \beta_{HM} S_H I_M, \\
F_{I_M} = \beta_{MH} S_M I_H, \\
V_{I_H} = (\mu_H + \alpha + \sigma)I_H - \delta I_H, \\
V_{I_M} = \mu_M I_M
\]

Consequently, the \( F \) and \( V \) matrices are given as follows:

\[
F = \begin{pmatrix}
0 & \beta_{HM} S_H \\
\beta_{MH} S_M & 0
\end{pmatrix}, \\
V = \begin{pmatrix}
\alpha - \delta + \mu_H + \sigma & 0 \\
0 & \mu_M
\end{pmatrix}
\]

with the next-generation matrix

\[
FV^{-1} = \begin{pmatrix}
0 & \frac{\beta_{HM} S_H}{\alpha - \delta + \mu_H + \sigma} \\
\frac{\beta_{MH} S_M}{\alpha - \delta + \mu_H + \sigma} & 0
\end{pmatrix},
\]

and the basic reproduction number is

\[
R_0 = \sqrt{\frac{\beta_{HM} \beta_{MH} S_H S_M}{(\alpha - \delta + \mu_H + \sigma)\mu_M}}.
\]

This case is special since the basic reproduction number is not realized as an element of the diagonal of \( FV^{-1} \).

**Example 18.** The basic reproduction number for the two models of vaccinations is as follows:

- For the first model in Example 12, the disease-free equilibrium with \( I = 0 \) and \( S'(t) = 0 \) implies that \( S = qN \), which is the flow from the susceptible compartment to the transition of \( \beta \). The \( F \)-matrix and \( V \)-matrix are \( (\beta S) \) and \( (\mu + \alpha) \), which implies that the basic reproduction number is \( R_0 = \beta S/(\mu + \alpha) \). Without vaccination at the disease-free equilibrium \((p = 0)\), we obtain \( R_0 = \beta N/(\mu + \alpha) \). In the presence of vaccination, we obtain the basic reproduction number

\[
qR_0 = \frac{\beta qN}{(\mu + \alpha)}.
\]
For the second model of vaccination in Example 13, the disease-free equilibrium with $I = 0$, $S'(t)$ and $V'(t) = 0$ implies that $S = \Lambda \mu / (\mu + \psi)$ and $V = \Lambda \psi / (\mu + \psi)$. They are the flows from the susceptible and vaccination compartment to the infection transitions associated with $\beta$ and $q\beta$, respectively. Since the equation of the total population is $N'(t) = \Lambda - \mu N$, the equilibrium total population size is $N = \Lambda / \mu$. The $F$-matrix and $V$-matrix are $(\beta S / N + \beta \delta V / N)$ and $(\mu + \gamma)$, which implies that the basic reproduction number is $R_0 = (\beta S / N + \beta \delta V / N) / (\mu + \gamma)$. In the disease-free equilibrium at the equilibrium total population, we obtain
\[ \frac{S}{N} = \frac{\mu}{\mu + \psi}, \quad \text{and} \quad \frac{V}{N} = \frac{\psi}{\mu + \psi}. \] (9)
and the basic reproduction number is
\[ R_0 = \frac{\beta (\mu + \delta \psi)}{(\mu + \gamma)(\mu + \psi)}. \] (10)

4 The basic reproduction number of a Petri net

The basic reproduction number is not only a concept that pertains to epidemiology. For instance, there are applications outside epidemiology in phenomena that are different from a pandemic or the growth of a population: In informatics, we can use a particular type of SEIR model to give a mathematical explanation of computer virus propagation [Cor20, Mur88]; also, the standard SIR model is used in [BLT12] to simulate key properties of real spreading cascades of file sharing. The SIR model is used in social networks to study rumor spreading; see [WW15]. A summary of interesting applications is found in [Rod16].

The next-generation matrix method has assumptions (A1)-(A5) from Section 3, which assures that the basic reproduction number is the dominant eigenvalue of the next-generation matrix. Now, we give a geometric variant of the next-generation matrix method, which provides a geometric version of the assumptions (A1)-(A5).

4.1 Geometric next-generation matrix method

The SIR model of Kermack–McKendrick [KM27] comprises three states or compartments (susceptibles, infected, and resistant) and two transitions given by the infection process and recovery transition. Nevertheless, the basic reproduction number calculation does not depend on the resistant compartment. This property also fulfills a highly sophisticated epidemiological model. A Petri net associated with any epidemiological model can be understood by merging all its components into three substructures or clusters given by the susceptible population, the infected population, and the infection process. They define the following sub-Petri nets:

- **The susceptible module**: consider the Petri net composed of the susceptible compartments and all the transitions that model the behavior of the susceptible population (borne, decease, migration, emigration, etc.).

- **The infection-process module**: consider the Petri net composed of the infection transitions and some compartments that connect them (for example, when it occurs, reinfection of two different diseases, communication between two other infection transitions, etc.).

- **The infection module**: consider the Petri net with all the different disease compartments of the study population (infected, exposed, asymptomatic, carrier, etc.). The transitions included are
Figure 15: Susceptible, infection-process and infection modules for the SEAIR model.

those relating between disease compartments and all the transitions with the input of a disease compartment.

We will call these structures the Kermack–McKendrick modules or, shortly, the KM modules.

Example 19. The SEAIR model has the compartments \{S, E, A, I, R\} denoting Susceptibles, Exposed, Asymptomatic, Infected and Resistant. The KM modules are described as follows: The susceptible module is a Malthusian model (see Example 6) associated with the susceptible population. The Petri net has one specie \(S\) and two transitions given by birth and decease. The infection-process module is the disjoint union of the infection transitions with parameters \(q\beta\) and \(\beta\). The infection module is a Petri net with compartments \{E, A, I\} and transitions with parameters \{\(\eta\), \(\gamma\), \(\alpha\)\} and three transitions of decease denoted by \(\mu\). These modules are illustrated in Figure 15.

Example 20. The malaria model has compartments \(S_H, I_H, R_H, S_M, I_M\) where two different types of populations interact. The KM modules are described as follows: The susceptible module is a disjoint union of two Malthusian models associated with the human and mosquito populations. The infection-process module comprises only the two transitions with parameters \(\beta_{HM}, \beta_{MH}\). The infection module has two disjoint components, each associated with one of the compartments \{\(I_H, I_M\)\} with transitions to those with input from one of these compartments. These modules are illustrated in Figure 16.

The mathematical definition of the KM modules consists of three disjoint Petri nets inside the whole Petri net.

Definition 21. Assume a Petri net with a set of compartments \(S\), a set of transitions \(T\), a set of arrows \(A\), and a matching function \(f\). The \textbf{KM modules} are defined by three disjoint subsets of compartments \(S_S, S_IP, S_I \subset S\), three disjoint subsets of transitions \(T_S, T_IP, T_I \subset T\), three disjoint subsets of arrows \(A_S, A_I, A_IP \subset A\), and three functions \(f_i : A_i \rightarrow S_i \times T_i \cup T_i \times S_i\), for \(i \in \{S, IP, I\}\), such that \(f_i = f|_{A_i}\).

The next-generation matrix method has assumptions (A1)-(A5) to guarantee that the basic reproduction numbers result as the dominant eigenvalue of the next-generation matrix.

Denote the compartments of the whole Petri net by \(S = \{x_1, \ldots, x_k\}\) with the disease compartments by \(S_I = \{x_1, \ldots, x_s\}\). The geometric version of the assumptions (A1)-(A4) are as follows:

(G1) Only three types of arrows between the KM modules are forbidden:
Susceptible module  Infection-process module  Infection module

\[ \begin{array}{ccc}
\mathcal{I}_1 & \mathcal{A} & \mathcal{\beta}_M \\
\mathcal{I}_H & \mathcal{\mu}_M & \mathcal{\theta}_M \\
\mathcal{I}_I & \mathcal{\mu}_I & \mathcal{\sigma} \\
\mathcal{I}_M & \mathcal{\mu}_M & \mathcal{\theta}_M \\
\end{array} \]

Figure 16: Susceptible, infection-process and infection modules for the model of Malaria.

- from a susceptible transition \( z_j \in T_S \) to an infection compartment \( x_i \in T_{IP} \);
- from a susceptible compartment \( x_i \in S_S \) to an infection transition \( z_j \in T_I \); and
- from a infection-process compartment \( x_i \in S_{IP} \) to an infection transition \( z_j \in T_I \).

There are no restrictions for arrows inside a specific module (Susceptible, Infection-Process, Infection).

\( G2 \) Assume an infection transition \( z_j \in T_{IP} \) such that for all disease compartment \( x_i \in S_I \), we have \( m_{ij} = 0 \); therefore, we obtain \( n_{ij} = 0 \) for all disease compartment \( x_i \in S_I \).

This condition means all new infections are secondary infections arising from infected hosts; there is no immigration of individuals into the disease compartments.

\( G3 \) If \( x_i \in S_I \) and \( z_j \in T_{IP} \cup T_I \), then we have the inequality \( n_{ij} \geq m_{ij} \).

This means that there is no disappearance of infected individuals.

\( G4 \) We require a positive outflow of all the disease compartments. Thus, for compartments and transitions inside the infection module, i.e., \( x_i \in S_I \) and \( z_j \in T_I \), we have the inequality

\[ \sum_{i=1}^{s} (m_{ij} - n_{ij}) \geq 0. \]

For the compartments \( S = \{x_1, \ldots, x_k\} \) and the disease compartments \( S_I = \{x_1, \ldots, x_s\} \), with \( s \leq k \), consider \( x_i \in S_I \), which has rate equation given by the sum

\[ x'_i(t) = \sum_{z_j \in T_{IP}} r_j(n_{ij} - m_{ij})x_1^{m_{1j}} \cdots x_k^{m_{kj}} - \sum_{z_j \in T_I} r_j(m_{ij} - n_{ij})x_1^{m_{1j}} \cdots x_s^{m_{sj}}. \]

Notice that there is no sum over susceptible transition \( T_S \) since there are no arrows between \( T_S \) and \( S_I \). Additionally, in the second summand, the variables go up to \( s \) since there are no arrows from \( S_S \cup S_{IP} \) to \( T_I \).

The function \( F_i \) and \( V_i \) from the next-generation matrix method are now given by the following expressions:

\[ F_i(x_1, \ldots, x_k) := \sum_{z_j \in T_{IP}} r_j(n_{ij} - m_{ij})x_1^{m_{1j}} \cdots x_k^{m_{kj}} \quad \text{and} \quad V_i(x_1, \ldots, x_k) := \sum_{z_j \in T_I} r_j(m_{ij} - n_{ij})x_1^{m_{1j}} \cdots x_s^{m_{sj}}. \]  

(11)
Theorem 22. The KM modules of a Petri net with the assumptions (G1)-(G4) satisfy the assumptions (A1)-(A4) of the next-generation matrix method.

Proof. Assume $S = \{x_1, \cdots, x_k\}$ are the whole compartments and $S_I = \{x_1, \cdots, x_s\}$ are the compartments in the infection module, with $s \leq k$. In order to shorten the notation, set $x = \{x_1, \cdots, x_s\}$, $y = \{x_{s+1}, \cdots, x_k\}$, and denote $x^{m_j} := x_1^{m_{j1}} \cdots x_s^{m_{js}}$ and $y^{m_j} := x_{s+1}^{m_{j(s+1)}} \cdots x_k^{m_{jk}}$. The functions $F_i$ and $V_i$ have the following expressions:

$$F_i(x, y) = \sum_{z_j \in T_I} r_j(n_{ij} - m_{ij})x^{m_j}y^{m_j} \quad \text{and} \quad V_i(x, y) = \sum_{z_j \in T_I} r_j(m_{ij} - n_{ij})x^{m_j}.$$

From assumption (G1), it follows that there are no arrows between a susceptible transition $z_j \in T_S$ and a disease compartment $x_i \in S_I$; hence, the rate equation has the form

$$x'_i = F_i(x, y) - V_i(x, y).$$

For (A1), assume $x = 0$, hence $V_i(0, y) = 0$ and $F_i(0, y) = \sum_{z_j \in T_I} r_j n_{ij} y^{m_j}$ which is also zero by the assumption (G2). For (A2), take $x, y \geq 0$ and from assumption (G3) it follows that for $x_i \in S_I$ and $z_j \in T_I$, we obtain $n_{ij} \geq m_{ij}$. For (A3), we can write $V_i(x, y)$ by the sum

$$V_i(x, y) = \sum_{z_j \in T_I, m_{ij} \neq 0} r_j(m_{ij} - n_{ij})x^{m_j} + \sum_{z_j \in T_I, m_{ij} = 0} r_j(m_{ij} - n_{ij})x^{m_j}.$$

Thus in the case $x_i = 0$, $1 \leq i \leq s$, we obtain $V_i(x, y) = \sum_{z_j \in T_I} r_j(-n_{ij})x^{m_j} \leq 0$. Finally, for (A4), we use the assumption (G4) and the sum has the form

$$\sum_{i=1}^{s} V_i(x, y) = \sum_{i=1}^{s} \sum_{z_j \in T_I} r_j(m_{ij} - n_{ij})x^{m_j} = \sum_{z_j \in T_I} r_j \left( \sum_{i=1}^{s} m_{ij} - n_{ij} \right) x^{m_j} \geq 0.$$

For Petri nets, we can also define the $F$ and $V$ matrices used in the next-generation matrix method by

$$F = \left( \frac{\partial F_i}{\partial x_j}(0, y) \right) \quad \text{and} \quad V = \left( \frac{\partial V_i}{\partial x_j}(0, y) \right),$$

for $x_j \in S_I$. For $x_j \in S \setminus S_I$, we obtain $\partial F_i/\partial x_j(0, y) = \partial V_i/\partial x_j(0, y) = 0$. As in [vdDW08] the disease compartments $x$ are decoupled from the remaining equations and can be written as $x' = (F - V)x$.

For $x_j \in S_I$, we differentiate $F_i(x, y)$ and we obtain

$$\frac{\partial F_i}{\partial x_j}(x, y) = \sum_{z_l \in T_I} r_l(n_{il} - m_{il})m_{jl}x_1^{m_{j1}} \cdots x_{j-1}^{m_{j(i-1)}}x_j^{m_{ji}} \cdots x_s^{m_{js}}x_{s+1}^{m_{j(s+1)}} \cdots x_k^{m_{jk}}.$$

From assumption (G3) we have $n_{il} \geq m_{il}$ for $x_i \in S_I$ and $z_l \in T_I$. It follows that each entry of $F$ is nonnegative. This is denoted by $F \geq 0$.

For $x_i \in S_I$, we differentiate $V_i(x, y)$ and we obtain

$$\frac{\partial V_i}{\partial x_j}(x, y) = \sum_{z_l \in T_I, m_{ji} \neq 0} r_l(m_{il} - n_{il})m_{jl}x_1^{m_{j1}} \cdots x_{j-1}^{m_{j(i-1)}}x_j^{m_{ji}-1} \cdots x_s^{m_{js}}x_{s+1}^{m_{j(s+1)}} \cdots x_k^{m_{jk}}.$$
From assumption (G3) we have \( n_{ij} \geq m_{ij} \) for \( x_i \in S_I \) and \( z_l \in T_I \). It follows that the off-diagonal entries of \( V \) are negative or zero.

In short, we obtain a nonnegative matrix \( F \geq 0 \) and a matrix \( V \in \mathbb{R}^{n \times n} := \{ (a_{ij}) \in \mathbb{R}^{n \times n} : a_{ij} \leq 0, i \neq j \} \). An important subset of \( Z^{n \times n} \) are the matrices of the form \( A = sI - B \) with \( s > 0, B \geq 0 \), such that the spectral radius of \( B \) satisfies the inequality \( s \geq \rho(B) \). They are called M-matrices, which have been deeply studied \([BJ70]\). One characterization of a non-singular M-matrix is the existence of a positive diagonal matrix \( D \) such that \( AD \) has all positive row sums. From assumption (G4), we ensure that the row sums of \( V \) are positive or zero. Since \( V \in \mathbb{R}^{n \times n} \), we obtain that \( V \) is a (possibly singular) \( M \)-matrix. Similar to \([vdDW08]\), we assume that \( V \) is non-singular.

An important property of M-matrices is that if \( A \in \mathbb{R}^{n \times n} \), then \( A^{-1} \geq 0 \) if and only if \( A \) is a non-singular M-matrix. Consequently, since \( V \) is a non-singular M-matrix, the inverse is nonnegative \( V^{-1} \) \( \geq 0 \). As a consequence, \( I - VF^{-1} \in \mathbb{R}^{n \times n} \) and by the following calculation \( (V - F)^{-1} = V^{-1}(I - VF^{-1})^{-1} \),

the matrix \( I - VF^{-1} \) is a non-singular M-matrix if and only if \( V - F \) is a non-singular M-matrix. The Perron–Frobenius theorem \([BJ70, \text{thm. 2.1.1}]\) implies that \( (I - VF^{-1})^{-1} \) exists if and only if \( \rho(FV^{-1}) < 1 \).

Now we are in conditions to give the last assumption (G5) given in \([vdDW02, vdDW08]\) as follows:

\[(G5) \quad \text{The matrix } V - F \text{ is a non-singular M-matrix. This is equivalent to the eigenvalues of } V - F, \text{ which all have positive real parts.}\]

The basic reproduction number is defined by the spectral radius \( R_0 = \rho(FV^{-1}) \). Consequently, the disease-free equilibrium is locally asymptotically stable if \( R_0 < 1 \) and unstable if \( R_0 > 1 \). In the next section, we describe a geometric interpretation of the next-generation matrix \( FV^{-1} \) for Petri nets, called the flow matrix.

### 4.2 Geometric interpretation of the next-generation matrix

The present section is motivated by the following assertion of van den Driessche–Watmough \([vdDW02, \text{p. 33}]\) about the next-generation matrix: the \((i, k)\) entry of the product \( FV^{-1} \) is the expected number of new infections in compartment \( i \) produced by the infected individual originally introduced into compartment \( k \).

Consider a Petri net with compartments \( S \) and transitions \( T \) with KM modules satisfying the assumptions (G1)-(G5). A path between two compartment \( x, x' \in S \) consists of a sequence of compartments \( x_{i_1}, \ldots, x_{i_k} \), with \( x_{i_1} = x \) and \( x_{i_k} = x' \), and a sequence of transitions \( z_{i_1}, \ldots, z_{i_{k-1}} \), with arrows \( x_{i_l} \rightarrow z_{i_l} \) and \( z_{i_l} \rightarrow x_{i_{l+1}} \), for \( 1 \leq l \leq k - 1 \). We are interested in paths between compartments with the following properties:

- each path does not have repeating compartments and repeating transitions;
- all the compartments \( x_{i_1}, \ldots, x_{i_k} \) belong to the infection compartments \( S_I \); and
- all the transitions \( z_{i_1}, \ldots, z_{i_{k-1}} \) belong to the infection module except once which belongs to the infection-process module.

For \( x, x' \) disease compartments, we denote by \( \text{Path}(x, x') \) all the paths from \( x \) to \( x' \) that traverse at some point some transition \( \beta \) in the infection-process module. Consider a path in \( \text{Path}(x, x') \) and denote by \( x_{i_l} \) the compartment just before the associated transition \( \beta \); see Figure 17 for an illustration. For each compartment \( x_{i_l} \), with \( 1 \leq l \leq k - 1 \), we have a subset of transitions \( Z_{i_l} \), at length one from the compartment. Thus all the transitions \( z_{i_l,j} \), for \( 1 \leq l \leq k - 1 \) and \( 1 \leq j \leq r_{i_l} \), with only one arrow \( x_{i_l} \rightarrow z_{i_l,j} \) and no return arrow. We assume the compartment \( Z_{i_l} \) does not include the infection transition \( \beta \). We denote these sets by \( Z_l = \{ z_{l,j} : 1 \leq j \leq r_{i_l} \} \).
Figure 17: A path between the compartments $x = x_{i_1}$ and $x' = x_{i_k}$ passing through the transition $\beta$.

**Assumption 23.** Notice that one assumption in our models is that there is only one arrow from each $x_{ij}$ to $z_{ij}$, for $1 \leq j \leq r_i$, and not return arrows. For instance, the Example 10 is a counterexample since there are arrows $I \rightarrow \alpha$ and $\alpha \rightarrow I$. Another assumption is that there are no arrows from a susceptible compartment $x$ to a transition $z_{il}$, for $1 \leq l \leq k - 1$ and $1 \leq j \leq r_i$. For instance, a counterexample is presented by an SIS model in ecoepidemiology [Ven06], where a Lotka-Volterra model is combined with competition and mutualism. Nevertheless, these issues can be implemented in our geometric next-generation matrix model. The proper expectation values of secondary infections can be worked out to generalize our construction to other contexts, which is an interesting project in the future.

**Proposition 24.** Assume a path $\gamma \in \text{Path}(x, x')$ of the form $(x_{i_1}, \cdots, x_{i_k}; z_{i_1}, \cdots, z_{i_{k-1}}; \beta)$ passing through the infection transition $\beta$. Additionally, we assume $z_{il} = z_{ij}$ for $1 \leq l \leq k - 1$ and denote by $\alpha_{ij}$ the parameter associated with $z_{ij} \in Z_{il}$ for $1 \leq j \leq r_i$ and $1 \leq l \leq k - 1$. Therefore, the expected time an individual spends to cross the path $\gamma$ is obtained by the formula

$$E(\gamma) = \left( \prod_{l=1}^{k-1} \alpha_{il} \right) \left( \prod_{l=1}^{k-1} \sum_{t=1}^{r_i} \alpha_{it} \right)^{-1}.$$  

(12)

*Proof.* Whenever we pass through the compartment $x_{ij}$, $1 \leq l \leq k - 1$, we divide by the sum of the parameters corresponding to the transitions in $Z_{il}$. The transition associated with $\beta$ does not contribute to the time we spend to pass the compartment $x_{it}$ because there is, in a certain sense, a return arrow.
canceling the arrow $x_i \rightarrow \beta$. Finally, whenever we pass through the transition $z_i$, we must multiply by $\alpha_i$ where recall we assumed $z_i = z_{i1}$ for $1 \leq l \leq k - 1$.

Each path $\gamma \in \text{Path}(x, x')$ passes to the unique infection transition $\beta$, associated with a flow of susceptible individuals that linearly depends on $\beta$. We denote this flow of susceptible individuals by $S(\gamma)$.

The matrix of flows of a Petri net $(S, T)$ with $S = \{x_1, \ldots, x_k\}$, $T = \{z_1, \ldots, z_l\}$ and disease compartments $S_I = \{x_1, \ldots, x_s\}$, with $s \leq k$, is a $(s \times s)$-matrix which we denoted by $M(S, T, T_I)$ with entries given as follows

$$M(S, T, T_I)_{ij} := \sum_{\gamma \in \text{Path}(x_i, x_j)} S(\gamma) E(\gamma).$$

(13)

We have the following immediate consequence as an application of Theorem 22 and the discussion from the last section.

**Corollary 25.** The next-generation matrix associated with the rate equation of a Petri net $(S, T)$ satisfying the assumptions (G1)-(G5) is equal to the matrix of flows.

**Example 26.** Now, we use this geometric procedure to calculate the basic reproduction of the SEAIR model (see Example 8). We have already found the next-generation matrix in Table 6 at the end of the paper, but now we check that this coincides with the matrix of flows. The KM modules were also described in Figure 15. It is easy to verify that the arrows between the KM modules satisfy the (G1)-(G5) conditions of the geometric next-generation method. The matrix of flows is as follows:

$$E \begin{pmatrix} \frac{\beta \eta (1-p)qS}{(\eta + \mu)(\gamma + \mu)} & E & A \\ 0 & \frac{\beta \eta pS}{(\eta + \mu)(\alpha + \mu)} & 0 \\ 0 & 0 & \frac{\beta S}{(\alpha+\mu)} \end{pmatrix}$$

(14)

The term associated with the $E-E$ coordinate corresponds to the two paths of flows in the following pictures:

![Diagram](image1)

The terms associated with the $E-A$ and $E-I$ correspond to the following paths:

![Diagram](image2)

Notice that the other terms in the matrix (14) are zero because the possible paths do not pass through...
an infection transition. The basic reproduction number is the dominant eigenvalue of the matrix (14) as follows:

\[ R_0 = \frac{\beta \eta (1-p) q S}{(\eta + \mu)(\gamma + \mu)} + \frac{\beta \eta p S}{(\eta + \mu)(\alpha + \mu)}. \]  

(15)

**Example 27.** The KM modules of the model of Malaria are found in Example 20 where we have the condition (G1)-(G5). The next-generation matrix of the model of Malaria was given in Table 6 at the end of the paper. We want to notice the particularity of the form of this matrix, which is as follows:

\[
\begin{pmatrix}
I_H & \frac{I_M}{\beta_M S_M} \\
I_M & \frac{I_H}{\alpha - \delta + \mu_{M} + \sigma}
\end{pmatrix}
\]

(16)

Notice that the diagonal entries are zero, so the eigenvalues are calculated by a square root. This case is special since no path realizes the basic reproduction number. The two nontrivial components of the matrix of flows (16) are realized by the following two paths:

**Example 28.** We have already verified in Example 18 the next-generation matrix for the first model of vaccination is given by the following matrix:

\[
I \left( \frac{\beta S_{I}}{\alpha + \mu} \right)
\]

(17)

The unique term \(I-I\) corresponds to the following path:

Similarly, in Example 18, we found the next generation matrix for the second model of vaccination by the matrix

\[
I \left( \frac{\beta S/N + \beta V/N}{\gamma + \mu} \right)
\]

(18)
The unique term $I - I$ is composed of two summands corresponding to the following two paths:

![Petri net diagram](image)

Notice that vaccination is implemented in these paths of the Petri net as valves that adjust the flow of susceptible individuals in the infection transitions associated with $\beta$ and $\delta \beta$.

## 5 Application to vertical transmission

The present section aims to interpret part of the work of van den Driessche in [vdD08] in terms of Petri nets. Biological features are included in [vdD08] as the vertical transmission of disease, the immigration of infective individuals, and temporary immunity. As we saw in Section 3, the mathematical definition of the basic reproduction number $R_0$ depends on the assumptions (A1)-(A5) satisfied by the compartmental models. Some of these assumptions are broken for example by the immigration of infected individuals, see assumption (G2) from Section 4.1. At the moment, we do not know how to extend the geometric next-generation method for this phenomenon; our procedure behaves well for vertical transmission.

Usually, in compartmental models, the transmission is horizontal between infective and susceptible individuals. However, we can consider vertical transmission, where the disease transfers from an infective parent to an unborn or newly born offspring. Some diseases satisfying this phenomenon are Chagas’ disease, hepatitis B, and HIV/AIDS. In this model, a fraction $q$ of offspring of infected individuals are assumed infected at birth, and a fraction $p = 1 - q$ of such offspring are susceptible.

Van den Driessche [vdD08] implements vertical transmission in the SIRS and SEIR models. For the SIRS model, there are two manners to represent the associated ODE in terms of Petri nets. The disease is assumed not fatal; thus, the total population size $K = S + I + R$ remains constant. The model is a modification of the SIRS model with the form

\[
\begin{align*}
S'(t) &= [-\beta SI + bK - bS + bR] + p\tilde{b}I \\
I'(t) &= [\beta SI - \gamma I] + q\tilde{b}I - \tilde{b}I \\
R'(t) &= [\gamma I - bR]
\end{align*}
\]

(19)

where the usual SIRS model is described inside square brackets, and we add the summands given by the vertical transmission in blue. The associated two Petri nets are described as follows:

- we can use a Petri net where the fraction $p$ is included together with the parameter $\tilde{b}$ inside a transition with input the compartment $I$ and output the compartment $S$, see the Figure 18;

- instead, we can use a Petri net with weighted arrows to add a transition associated with the parameter $\tilde{b}$ with two outputs, one going to the compartment $S$ weighted by $p$. The other goes to the compartment $I$ weighted by $q$, and only one input from the compartment $I$, see Figure 19.

Notice that the basic reproduction number of the first Petri net coincides with that of the SIRS model. The flow from the susceptible module to the infection module is found considering the disease-free equilibrium $(S, I) = (K, 0)$; hence, the total population $K$ gives the flow. The basic reproduction number is given by
Figure 18: The SIRS model with vertical transmission.

Figure 19: The SIRS model with vertical transmission in a Petri net with weighted arrows.
Figure 20: SEIR model with vertical transmission.

the sum

$$R_0 = \frac{\beta K}{\gamma + b} + \frac{q\tilde{b}}{\gamma + b},$$

(20)

where the summand $\frac{\beta K}{\gamma + b}$ correspond to the basic reproduction number of the SIRS model, the summand $\frac{q\tilde{b}}{\gamma + b}$ corresponds to the loop based at the compartment $I$ and passing to the transition associated with $\tilde{b}$.

Now, we consider the vertical transmission implemented by van den Driessche [vdD08] to the SEIR model coming from [LSW01]. For this purpose, we require Petri nets to admit additional types of arrows. Normally, an arrow represents a flow between compartments and transitions, and these flows depend on the input and output of each arrow. We assume the possibility that these flows are independent of the transition occurring as input or output, depending on the situation. This independence means that we do not consider this transition when calculating the rate equation associated with the compartment. These new types of arrows are represented as dashed lines in our pictures of Petri nets.

In [LSW01], the vertical transmission implemented in the SEIR model with the ODE

$$S'(t) = [b - bS - \beta SI] - pbE - qbI$$
$$E'(t) = [\beta SI - (\epsilon + b)E] + pbE + qbI$$
$$I'(t) = [\gamma E - (\gamma + b)I]$$
$$R'(t) = [\gamma I - bR]$$

(21)

Like before, the usual SEIR model is described inside square brackets, and we add the summands given by the vertical transmission in blue. Similar to the SIRS model case, two Petri nets represent the ODE (21) depending on the use of weighted arrows. We describe these Petri nets:

- Two additional transitions are added to the SEIR model with parameters $pb$ and $qb$, with two dashed arrows starting in the susceptible compartment and arriving at each of these two transitions. Additionally, normal arrows are starting in these new transitions and arriving at the exposed and infected compartment, plus other arrows to match the ODE, see Figure 20;

- Two transitions are added to the SEIR model with the same parameter $b$, with two dashed arrows starting in the susceptible compartment weighted with the fractions $p$ and $q$ and arriving at each of these two transitions. Additionally, there are normal arrows weighted with the fractions $p$ and $q$, starting in these new transitions and arriving at the exposed and infected compartment, plus other arrows to match the ODE, see Figure 21.
The basic reproduction number is obtained in [vdD08, p. 151] using the next-generation matrix

\[
\begin{pmatrix}
\frac{\beta \epsilon + q b \epsilon}{(b + \epsilon)(b + \gamma)} & \frac{p b}{b + \epsilon} & \frac{q b + \beta}{b + \gamma} \\
0 & 0 & 0 \\
0 & 0 & 0
\end{pmatrix}
\]  

(22)

All the flows starting and ending in the exposed compartment give the dominant eigenvalue. The sum gives the basic reproduction number

\[
R_0 = \frac{\beta \epsilon + q b \epsilon}{(b + \epsilon)(b + \gamma)} + \frac{p b}{b + \epsilon},
\]

(23)

Where the summand \(\beta \epsilon / ((\epsilon + b)(\gamma + b))\) correspond to the basic reproduction number of the SEIR model, the summand \(q b \epsilon / ((\epsilon + b)(\gamma + b))\) corresponds to the loop based at the compartment \(E\) passing at \(I\) and the transition \(q b\) (in the weighted arcs correspond to the transition \(b\) and the arc weighted with \(q\)). The summand \(p b / (\epsilon + b)\) corresponds to the loop based at the compartment \(E\) passing to the transition \(p b\) (in the weighted arcs correspond to the transition \(b\) and the weighted arc with \(p\)).

6 Conclusions

The analysis of various disease models in epidemiology revealed that even though the model structure can be highly sophisticated, the structural background follows the basic SIR model. This was the objective of introducing the Kermack-McKendrick modules (susceptible/infection-process/infection). Apart from that, we found five conditions (G1)-(G5) about the type of possible arrows between the Kermack-McKendrick modules and geometric conditions for the population flows that assure the basic reproduction number can be defined by the matrix of flows. In conclusion, we ended with a particular case of the next-generation matrix method from a different point of view that provides an accessible manner of understanding the basic reproduction number by summing up all the flows of secondary infections.

Petri nets are efficient structures that can be used in epidemiological problems. By building geometric diagrams composed of substructures Petri nets, such as Malthusian models, SIR type models, mitigation strategies, and vaccination adjustments, among others, they provide a useful form of interaction in the design of models in epidemiology in a geometrical manner that recovers the system of ordinary differential equations using the rate equation. Reciprocally, we can start with a system of ordinary differential equations associated with an epidemiological model. Under certain hypotheses, it is possible to associate a Petri net in which rate equations recover the original ODEs. We found these two interactions between
The diagrammatical model of a Petri net and its associated ODE very useful, where special features like the basic reproduction number have interpretations in geometric and analytic types. We expect this to motivate developments in the area, like geometric interpretations of other important concepts, such as herd immunity.

The basic reproduction number $R_0$ was geometrically interpreted as the expected secondary infection individuals for the longest path that traverses the infection-process module starting and ending in the infection module. Something interesting is how vaccination is revealed in the modification of $R_0$ as valves that adjust the flow of susceptible individuals in the intersection point of the path with the infection-process module.

Finally, we can accomplish the vertical transmission in models of SIR’s type using arrows with flows in only one direction. Consequently, this prevents the generalization of the theory of Petri nets to other biological features, such as the immigration of infective individuals and temporary immunity. For the moment, we do know the scope of the theory of Petri nets to model processes that step outside the assumptions of the present work.

**Conflict of interest** The author declares no conflicts of interest.

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| MODEL  | ODE                                                                 | F-Matrix | V-Matrix | Next Generation Matrix | $R_0$ |
|--------|---------------------------------------------------------------------|----------|----------|------------------------|--------|
| SIR    | $S'(t) = -\beta SI$, $I'(t) = \beta SI - \alpha I$, $R'(t) = \alpha I$ | $(\beta S)$ | $(\alpha)$ | $\begin{pmatrix} 1 & 1 \\ 0 & 0 \end{pmatrix}$ | $\frac{\beta S}{\alpha}$ |
| SIS    | $S'(t) = -\beta SI + \alpha I$, $I'(t) = \beta SI - \alpha I$     | $(\beta S)$ | $(\alpha)$ | $\begin{pmatrix} 1 & 1 \\ 0 & 0 \end{pmatrix}$ | $\frac{\beta S}{\alpha}$ |
| SIRS   | $S'(t) = -\beta SI + \gamma R$, $I'(t) = \beta SI - \alpha I$, $R'(t) = \alpha I - \gamma R$ | $(\beta S)$ | $(\alpha)$ | $\begin{pmatrix} 1 & 1 \\ 0 & 0 \end{pmatrix}$ | $\frac{\beta S}{\alpha}$ |
| SEIR[Mar15] | $S'(t) = \Lambda - \beta SI - \mu S$, $E'(t) = \beta SI - (\eta + \mu)E$, $I'(t) = \eta E - (\alpha + \mu)I$, $R'(t) = \alpha I - \mu R$. | $\begin{pmatrix} 0 & \beta S \\ 0 & 0 \end{pmatrix}$ | $\begin{pmatrix} \eta + \mu & 0 \\ -\eta & \alpha + \mu \end{pmatrix}$ | $\begin{pmatrix} \frac{\beta S}{\eta + \mu} & \frac{\beta S}{\alpha + \mu} \\ \frac{\beta S}{\eta + \mu} & \frac{\beta S}{\alpha + \mu} \end{pmatrix}$ | $\frac{\beta S}{\alpha}$ |
| SEIR[SB21] | $S'(t) = \Lambda - (\beta + \gamma')SI - \mu S$, $E'(t) = \beta SI - (\eta + \mu)E$, $I'(t) = \eta E - (\alpha + \mu)I$, $R'(t) = \alpha I - \mu R$. | $\begin{pmatrix} 0 & \beta S \\ 0 & 0 \end{pmatrix}$ | $\begin{pmatrix} \eta + \mu & 0 \\ -\eta & \alpha + \mu \end{pmatrix}$ | $\begin{pmatrix} \frac{\beta S}{\eta + \gamma' + \mu} & \frac{\beta S}{\alpha + \gamma'} \\ \frac{\beta S}{\eta + \gamma' + \mu} & \frac{\beta S}{\alpha + \gamma'} \end{pmatrix}$ | $\frac{\beta S}{\alpha}$ |
| SEAIR[Mar15] | $S'(t) = \Lambda - \beta(SI + qA) - \mu S$, $E'(t) = \beta SI - (\eta + \mu)E$, $A'(t) = (1-p)qE - (\gamma + \mu)A$, $I'(t) = pqE - (\alpha + \mu)I$, $R'(t) = \alpha I + \gamma A - \mu R$. | $\begin{pmatrix} 0 & \beta qS & \beta S \\ 0 & 0 & 0 \end{pmatrix}$ | $\begin{pmatrix} \eta + \mu & 0 & 0 \\ -\eta(1-p) & \gamma & \mu \\ -\eta p & -\eta p & \alpha + \mu \end{pmatrix}$ | $\begin{pmatrix} \frac{\beta qS}{\eta + \mu} & \frac{\beta qS}{(\eta + \gamma + \mu)} & \frac{\beta qS}{\eta + \gamma + \mu} \\ \frac{\beta qS}{\eta + \mu} & \frac{\beta qS}{(\eta + \gamma + \mu)} & \frac{\beta qS}{\eta + \gamma + \mu} \\ \frac{\beta qS}{\eta + \mu} & \frac{\beta qS}{(\eta + \gamma + \mu)} & \frac{\beta qS}{\eta + \gamma + \mu} \end{pmatrix}$ | $\frac{\beta qS}{\alpha}$ |
| SEAIR[Bas21] | $S'(t) = -\beta_1 SA - \beta_2 SL$, $E'(t) = \beta_1 SA + \beta_2 SL - \gamma E$, $A'(t) = \gamma E - (\sigma + \mu)A$, $I'(t) = \sigma A - \mu I$, $R'(t) = \mu A + \mu I$. | $\begin{pmatrix} 0 & \beta_1 S & \beta_2 S \\ 0 & 0 & 0 \end{pmatrix}$ | $\begin{pmatrix} \gamma & 0 & 0 \\ -\gamma & \mu + \sigma & 0 \\ 0 & -\sigma & \mu \end{pmatrix}$ | $\begin{pmatrix} \frac{\beta_1 S}{\mu + \sigma} & \frac{\beta_2 S}{\mu + \sigma} & \frac{\beta_2 S}{\mu + \sigma} & \frac{\beta_2 S}{\mu + \sigma} \\ \frac{\beta_1 S}{\mu + \sigma} & \frac{\beta_1 S}{\mu + \sigma} & \frac{\beta_1 S}{\mu + \sigma} & \frac{\beta_1 S}{\mu + \sigma} \\ \frac{\beta_2 S}{\mu + \sigma} & \frac{\beta_2 S}{\mu + \sigma} & \frac{\beta_2 S}{\mu + \sigma} & \frac{\beta_2 S}{\mu + \sigma} \end{pmatrix}$ | $\frac{\beta_1 S}{\mu + \sigma} + \frac{\beta_2 S}{\mu + \sigma}$ |
| MODRL | ODE | F-Matrix | V-Matrix | Next Generation Matrix | $r_0$ |
|-------|-----|----------|----------|------------------------|-------|
| SCIRS[Mar15] | $S'(t) = \Lambda - \beta S(I+qC) - \mu S + \rho R,$  
$C'(t) = \beta S(I+qC) - (\eta + \gamma + \mu)C,$  
$I'(t) = \eta C - (\alpha + \mu)I,$  
$R'(t) = \alpha I + \gamma C - (\mu + \rho) R.$ | \[
\begin{pmatrix}
\beta q & \beta S \\
0 & 0
\end{pmatrix}
\begin{pmatrix}
\eta + \gamma + \mu & 0 \\
-\eta & \alpha + \mu
\end{pmatrix}
\begin{pmatrix}
\beta q & \beta S \\
0 & 0
\end{pmatrix}
\begin{pmatrix}
\beta q & \beta S \\
0 & 0
\end{pmatrix}
\] |  |  |
| SIWR[WBK18] | $S'(t) = \mu N - \beta W SW - \beta SI - \mu S,$  
$I'(t) = \beta W SW + \beta SI - (\gamma + \mu)I,$  
$W'(t) = \alpha I - \xi W,$  
$R'(t) = \gamma I - \mu R.$ | \[
\begin{pmatrix}
\beta S & \beta W S \\
0 & 0
\end{pmatrix}
\begin{pmatrix}
\gamma + \mu & 0 \\
-\alpha & \xi
\end{pmatrix}
\begin{pmatrix}
\beta S & \beta W S \\
0 & 0
\end{pmatrix}
\begin{pmatrix}
\beta S & \alpha \beta W S \\
0 & 0
\end{pmatrix}
\] |  |  |
| SIQR[Mar15] | $S'(t) = \Lambda - \beta SI/A - \mu S,$  
$I'(t) = \beta SI/A - (\alpha + \gamma + \mu)I,$  
$Q'(t) = \gamma I - (\eta + \mu)Q,$  
$R'(t) = \alpha I + \eta Q - \mu R.$ | \[
\begin{pmatrix}
\beta S & 0 \\
0 & 0
\end{pmatrix}
\begin{pmatrix}
\alpha + \gamma + \mu & 0 \\
\eta + \gamma & \eta + \mu
\end{pmatrix}
\begin{pmatrix}
\beta S & 0 \\
0 & 0
\end{pmatrix}
\begin{pmatrix}
\beta S & \alpha \beta S \\
0 & 0
\end{pmatrix}
\] |  |  |
| SKIT[FCF00] | $S'(t) = \Lambda - \beta c SI/N - \mu S,$  
$E'(t) = \beta c SI/N - (\mu + \kappa)E + \sigma \beta c T1/N,$  
$I'(t) = \beta d E/NI + \kappa E - (\mu + r + d)I,$  
$T'(t) = r I - \sigma \beta c T1/N - \mu T,$ | \[
\begin{pmatrix}
\frac{T d c \sigma}{N} + \frac{\beta c}{N} & 0 \\
0 & 0
\end{pmatrix}
\begin{pmatrix}
\kappa + \mu & 0 \\
0 & \alpha + \gamma + \mu
\end{pmatrix}
\begin{pmatrix}
\frac{T d c \sigma}{N} + \frac{\beta c}{N} & 0 \\
0 & 0
\end{pmatrix}
\begin{pmatrix}
\frac{T d c \sigma}{N} + \frac{\beta c}{N} & 0 \\
0 & 0
\end{pmatrix}
\] |  |  |
| Malaria[WBK18] | $S'(t) = \Pi - \beta MH SM_{IH} - \mu MH,$  
$I_{H}'(t) = \beta MH SM_{IH} - (\mu H + \alpha + \sigma) I_{H} + \delta I_{H},$  
$R_{H}'(t) = \sigma I_{H} - \mu R_{H},$  
$S_{M}'(t) = \lambda - \beta MH SM_{IH} - \mu MH,$  
$I_{M}'(t) = \beta MH SM_{IH} - \mu M I_{M}.$ | \[
\begin{pmatrix}
0 & \beta MH SM \\
0 & 0
\end{pmatrix}
\begin{pmatrix}
0 & 0 \\
0 & \alpha + \delta + \mu H + \sigma
\end{pmatrix}
\begin{pmatrix}
0 & \beta MH SM \\
0 & 0
\end{pmatrix}
\begin{pmatrix}
0 & \frac{\beta MH SM}{\alpha + \delta + \mu H + \sigma} \\
0 & 0
\end{pmatrix}
\] |  |  |