

Changes in contact pattern due to measures based on SARS-CoV-2 certificates.

Bachelors thesis covering the changes in contact patterns due to
implementing different SARS-CoV-2 certificates.

Thomas van den Brink

Bachelors thesis commissioned by the University of Utrecht.
Supervised by dr. M.C.J. Bootsma.
Date of completion: **24th June 2022**



**Universiteit
Utrecht**

Faculty of Bèta sciences
The University of Utrecht
The Netherlands

Acknowledgments

I would like to express my deepest gratitude to dr. M.C.J. Bootsma for making the time every week to sit together and discuss the project, questions, and other interesting topics. I felt very reassured after every meeting.

Special thanks goes out to my friend O. Roef for proofreading the thesis and providing helpful feedback.

Finally, I would like to thank my family and friends for helping me keep sane throughout these tumultuous times.

Abstract.

We would like to implement COVID certificates into the model used to predict the spread of the COVID-19 disease. The model uses matrices to give a first order approximation to the spread of a disease in set time intervals. When introducing the COVID-19 certificates, certain assumptions made by the model do not hold anymore. Therefore we will need to adjust the model in a fitting way to retain the assumptions while still being able to implement the certificates. But when changing the model, the natural question arises: How much do we change the model by implementing the COVID certificates?

We will make this question our research question and will throughout the thesis try to answer it. By investigating, building and validating the model, we will build up the structure needed to answer the research question and will prove mathematical properties the model possesses. Not only will we look at the model itself, we will also investigate and build the process to change the model, as described in the article [\[2\]](#).

Because of the multiple ways of changing the model, have we chosen to limit ourselves to researching the changes brought into the model due to changes in contact patterns.

After showing multiple ways to alter the contact patterns, we also relate the changes to the real world. When relating the degree of change in the contact pattern to the reproduction number, we see that a change in contact patterns of a certain degree does not imply that the reproduction number will change at all.

Contents

1	Introduction to SARS-CoV-2.	1
2	Introducing the research question.	2
3	Introducing the model.	3
3.1	The compartments.	4
3.2	Interaction between the compartments.	4
3.3	Infections and narrowing in on the variables.	5
3.4	The next generation matrix (NGM).	5
3.5	The variable R	6
3.6	Modelling different locations.	7
3.7	Introducing SARS-CoV-2 certificates.	7
3.8	The changing contact structure.	9
3.8.1	Altering the contact structure.	9
3.8.2	Further elaboration on the model.	13
4	Mathematically validating the model.	16
4.1	Claims made in the article.	16
4.1.1	Preservation of the symmetric contact structure.	16
4.1.2	Preservation of the total amount of contacts.	18
4.2	The new contact matrix being well-defined.	20
4.3	Continuity of the model.	22
4.4	Uniqueness of the model.	23
5	Degree of change in the contact matrix.	25
5.1	Example 1.	28
5.2	Example 2.	30
5.3	Example 3.	33
5.4	Example 4.	36
6	Conclusion.	37
6.1	Answering the research question.	37
A	The computer model.	39
B	Bibliography	43

Chapter 1

Introduction to SARS-CoV-2.

This report investigates a model to predict the spreading and circulation of a disease among the population and researches possible intervening measures to halt or slow down the spread of the disease. The last couple of years, the world has had to struggle and fight against the COVID-19 disease. To make use of this recent example, we will give a short introduction to the disease.

The SARS-CoV-2 virus (Severe Acute Respiratory Syndrome Coronavirus 2), which is best known for causing the disease that has plagued humanity since 2019. The SARS-CoV-2 virus is the cause of the disease known as COVID-19 or COVID for short. The disease shocked the world with its rapid growth and wide range of unknown symptoms. Where one individual will have a small fever or barely a cough, the other individual could end up in an Intensive Care Unit (ICU) on a assisted breathing apparatus.[3]

Because of the lack of information surrounding the virus and the fear of ICUs overflowing with patients suffering from COVID disease, the government issued primitive COVID measures to try and slow the spread of the virus. Working from home, keeping distance from one another and washing your hands were the most repeated measures, whilst researchers were continuing their research on the virus.

Right now it would look like due to the high degree of vaccinated individuals, the disease has been overcome. However, with uncertainty about the duration of the effect of the COVID vaccine and with different variants of the virus emerging from different parts of the world, it is important to continue research on the disease.

Although this report investigates a mathematical model to predict the spread of diseases, most of the report will be general and will not mention the COVID-19 disease or the SARS-CoV-2 virus. In the developed examples, we will use the disease to show results.

Chapter 2

Introducing the research question.

In this report we will examine the model explained in the article [2], build it ourselves, and mathematically validate the model to try to confirm the choices made in the model.

In the model used, due to the implementation of a COVID certificate, the contact structure has to be changed to keep certain requirements assumed to be true. One part of the model that will change is the contact structure, denoted in the model as a matrix \mathbf{K} . By researching the model and trying to validate certain properties, we will try to answer the main research question and show the consequences to the matrix \mathbf{K} when implementing COVID certificates.

Our main research question that we will try to answer is:

How does the contact structure change due to measures based on a COVID certificate?

By building and explaining the model, the changes made to the model, and certain mathematical properties of the model, we hope to arrive at the answer of our research question in a natural and understandable way.

Chapter 3

Introducing the model.

To model diseases precisely, we would need immense amounts of data, ranging from the transmission processes, to the interaction the disease has with an individual's immune system, to knowing every activity every person does at every point in time that causes a contact. This would be an immense amount of data to track one individual, let alone the entire model population. Even if we hypothetically had all the empirical data we desired, there may not be a reason for every activity a person performs or every contact that is created. By fine tuning models to such high standards as reality, it has been known that the outcome could stray further from reality by implementing more variables than a simple linear model would provide.¹ As we can see, it is very hard to model the precise effects a particular disease would have on the population. Therefore, we will not bother with the most realistic model, but instead we will make use of a simplified model of the disease to try to deduce what happens to the population in general terms.

There are various different types of models to choose from which are used to model diseases, but the model of our choice and which we will be using is the model described in the article: *The impact of different strategies using a corona ticket on the reproduction number* [2], which describes a linearised multi-time SIR model. Instead of looking at every individual, a compartmental model will divide the population into disjoint compartments that will interact with each other. To avoid the requirement for incredible amounts of data, the model generalises the individuals and splits the population into disjoint compartments. For every individual belonging to the same compartment, the model imparts the same generalised variables to them. Every compartment has a model spokesperson, if you will.

¹The European Union's failure to adjust the fishing quantity [7].

3.1 The compartments.

For the model described in the article [2] to work, the population theoretically needs to be build up of an infinite amount of individuals. In reality the population will never reach infinity, but when taking a sufficiently large population, the model can be used to give a relatively precise approximation. We divide the population into $m \in \mathbb{N}$ disjoint compartments.

Because of the population being theoretically infinite but still countable, we assume that all compartments are countable. Furthermore, we define the variable β_j , which denotes the fraction of individuals belonging to compartment j . We note that when adding all compartments, the total sum equals the total population: $\sum_{j=1}^m \beta_j = 1$.

3.2 Interaction between the compartments.

After generalising the population to a set of disjoint compartments, it seems logical to also generalise the interactions between two compartments. We generalise the interactions to fit the first-order approximation of the model.

We will generalise the interactions between individuals of two compartments to just one type and call this type of interaction a “contact”.

The assumption we will mention now is very important and is one of the few assumptions that this model makes about contacts. The assumption is based on the intuition that whenever an individual is in contact with you, you will be in contact with the individual. We call the contacts symmetric and formulate the formal assumption as follows.

The number of contacts between two compartments is symmetric.

We denote with k_{ij} the expected amount of contacts between an individual of compartment j with individuals of compartment i within a set time interval. The time intervals can be adjusted accordingly to give the outcome the model requires to give, but will not be important to us for now. The previously stated assumption can now be written in mathematical notation:

$$N_j k_{ij} = N_i k_{ji}.$$

where N_i and N_j denote the number of individuals belonging to compartment i and j respectively. We remark that when taking the compartments to be countable, we will need to use the variables β_j and β_i to solve this equation. But when looking at real data, we can use the variables N_j and N_i .

If compartment i is relatively small compared to compartment j , the amount of contacts an individual of compartment i needs to make with individuals of compartment j will be relatively higher than an individual of compartment j makes with individuals of compartment i .

3.3 Infections and narrowing in on the variables.

We have now generalised our model to the desired degree. When we model a disease it is very important for the model to make a distinction between *Infected* and *Susceptible* individuals. After all a currently sick person generally does not get twice as sick if put into contact with another person suffering from the same disease. Therefore it is important to model the interactions between the two different types of individuals, in those contacts is where the disease will spread.

As described in the material [1], and [4], the amount of susceptible persons an infected individual infects depends on both the amount of contacts and the probability of transmission per contact. We have already established the amount of contacts between different individuals in the previous section. For the chance of transmission, in the model, we divide the parameters who are involved in calculating the probability of transmission into two categories:

1. The category containing all parameters that relate to one's susceptibility.
2. The category containing all parameters that relate to one's infectiousness.

Since we consider all individuals of a compartment to have the same attributes, all parameters of both categories are therefore also assumed the same. Because of this homogeneity, we can group the parameters together per category and per compartment, gaining the set of variables: r_j^S and r_j^I , a compartment- j -individual's *Susceptibility* and *Infectiousness* respectfully.

3.4 The next generation matrix (NGM).

Now we have defined all required variables, we can create what is called the *next generation matrix*. This $m \times m$ matrix, denoted with \mathbf{A} , has the property that when multiplied by the $m \times 1$ vector I_n , the vector containing the elements $(I_n)_j$ denoting the amount of infected individuals of compartment j at time interval n , will create the new $m \times 1$ vector I_{n+1} , containing the amount of infected individuals per compartment at time interval $n + 1$.

$$I_{n+1} = \mathbf{A}I_n. \quad (3.1)$$

For the model to function, we will need to create the next generation matrix \mathbf{A} . It will be easier to find the elements of \mathbf{A} and define the next generation matrix from all its elements. From [1] the elements of the matrix \mathbf{A} are defined to be the expected number of new infections starting in state i caused by an infected individual in state j . We denote this element by a_{ij} .

The expected number of infections a_{ij} is the probability of transmission per contact multiplied by the amount of expected contacts. The expected amount of contacts is previously defined as k_{ij} .

We will define the variable R , the variable which dictates the transmission probability per contact. Since the variable R will help us answer our research question, the variable is quickly explained in the next section.

In the model, susceptibility and infectiousness are not neglected and are therefore influencing the variable R . We have defined the variables denoting an individual's infectiousness and susceptibility as r_j^I and r_j^S respectively.

The element a_{ij} is given by the multiplication of the following variables:

$$a_{ij} := (R \cdot r_i^S \cdot r_j^I) \cdot k_{ij} = R \cdot r_i^S \cdot k_{ij} \cdot r_j^I. \quad (3.2)$$

For ease of use, and to create the next generation matrix \mathbf{A} , we will rewrite the known variables in matrix notation. From all k_{ij} , we will be creating the contact matrix $\mathbf{K} = (k_{ij})_{1 \leq i, j \leq m}$ and we will be writing the two compartment dependent parameters in two separate diagonal matrices: $\text{diag}(r_1^S, r_2^S, \dots, r_m^S)$ and $\text{diag}(r_1^I, r_2^I, \dots, r_m^I)$. The next generation matrix \mathbf{A} is build up of:

$$\mathbf{A} = R \cdot \text{diag}(r_1^S, r_2^S, \dots, r_m^S) \cdot \mathbf{K} \cdot \text{diag}(r_1^I, r_2^I, \dots, r_m^I). \quad (3.3)$$

We have now constructed the simple next generation matrix \mathbf{A} , to be able to calculate the total amount of infections per time interval n throughout a pandemic.

We want to remark the assumption about contacts being symmetrical, does not mean that the contact-matrix \mathbf{K} itself is a symmetric matrix.

3.5 The variable R .

In [1] it is shown that the basic reproduction number R_0 equals the spectral radius of the next generation matrix \mathbf{A} :

$$R_0 = \rho(\mathbf{A}) = \lim_{k \rightarrow \infty} \|\mathbf{A}^k\|^{\frac{1}{k}} = \max \{|\lambda_1|, \dots, |\lambda_m|\}, \quad (3.4)$$

where λ_i are eigenvalues of the matrix \mathbf{A} . Therefore we see that the basic reproduction number equals the largest eigenvalue of the matrix \mathbf{A} .

The value R_0 should only be used at the start of a pandemic when individuals are not yet aware and counteracting the spread of the disease. Over time the value for R_0 will typically decrease because of change in behaviour, natural immunity or because of the measures taken by the population.

Therefore we define the effective reproduction number: R_e , which denotes the reproduction number in later time intervals n .

$$R_e = R \cdot R_0 = R \cdot \rho(\mathbf{A}),$$

where R is the same variable dictating the transmission probability per contact. We remark that we can adjust the basic reproduction number with the variable R to get a good fit with the model. We remark that the basic reproduction number equals $R_0 = 1 \cdot \rho(\mathbf{A})$ and the variable R equals:

$$R = \frac{R_e}{\rho(\mathbf{A})}, \quad (3.5)$$

when $\rho(\mathbf{A})$ is non-zero. If $\rho(\mathbf{A}) = 0$, then the matrix \mathbf{A} is nilpotent, which means that the model will terminate after the step n for which $\mathbf{A}^n = \mathbf{0}$. This would indicate that the disease is exterminated after time interval n and is highly unlikely in reality.

3.6 Modelling different locations.

Now that we have recreated the backbone of the model, as described in [2], the article mentions making a distinction between different locations which we denote as $\ell \in \mathcal{L}$, where \mathcal{L} denotes the set containing all locations in the model.

When we consider multiple different locations an individual in the population can visit, we can factor in the importance every location has to the total amount of infections. Let R^ℓ be a fraction of the variable R denoting the ease of transmission at location ℓ per contact, relative to the other locations. The next generation matrix associated with location ℓ becomes:

$$\mathbf{A}_\ell = R^\ell \cdot \text{diag}(r_1^S, r_2^S, \dots, r_m^S) \cdot \mathbf{K}_\ell \cdot \text{diag}(r_1^I, r_2^I, \dots, r_m^I). \quad (3.6)$$

where \mathbf{K}_ℓ contains the amount of expected contacts occurring at location ℓ . The next generation matrix \mathbf{A} is given by enumerating over all the location dependent next generation matrices:

$$\mathbf{A} = \sum_{\ell \in \mathcal{L}} \mathbf{A}_\ell = \mathbf{A}_1 + \mathbf{A}_2 + \mathbf{A}_3 + \dots \quad (3.7)$$

By dividing the contacts per location and adjusting the variable R^ℓ , we are able to take different locations into consideration in the model.

3.7 Introducing SARS-CoV-2 certificates.

As we have stated before, the model explained in the previous sections was, for simplicity, worked out in undivided compartments. This means that up until now we have not made the distinction between the certificate-holding individuals and individuals without a certificate.

We introduce the SARS-CoV-2 certificates into the model. As previously explained, we have split the initial population into m disjoint compartments interacting with each other. With the introduction of the SARS-CoV-2 certificates, every compartment is split again. The compartment $1 \leq i \leq m$ is split into the set of individuals with certificates, the compartment V_i , and the set of individuals without certificates, the compartment U_i . Instead of the m compartments, the model will use the $2m$ disjoint compartments to model the interactions between people.

We will now look back at the setup we have done in previous sections to get to the next generation matrix \mathbf{A} . We will adjust the model now that we have double the compartments to work with. We will try to use as much of the established model as possible. Recall equation 3.6:

$$\mathbf{A}_\ell = R^\ell \cdot \text{diag}(r_1^S, r_2^S, \dots, r_m^S) \cdot \mathbf{K}_\ell \cdot \text{diag}(r_1^I, r_2^I, \dots, r_m^I),$$

for the next generation matrix dependent on location $\ell \in \mathcal{L}$. We will adjust the two diagonal matrices: $\text{diag}(r_1^S, r_2^S, \dots, r_m^S)$ and $\text{diag}(r_1^I, r_2^I, \dots, r_m^I)$, to be able to make a distinction in the parameters for the individuals with and without a certificate. To be able to make the distinction, we will have to double the

dimension of both diagonal matrices and designating half of the diagonal to U -individuals and half to V -individuals. The doubled diagonal matrices become:

$$\begin{aligned}\mathbf{S} &:= \text{diag}(r_{u_1}^S, \dots, r_{u_m}^S, r_{v_1}^S, \dots, r_{v_m}^S), \\ \mathbf{I} &:= \text{diag}(r_{u_1}^I, \dots, r_{u_m}^I, r_{v_1}^I, \dots, r_{v_m}^I),\end{aligned}$$

where we have defined a symbol for both diagonal matrices to prevent having to write them out multiple times. Do not confuse the diagonal matrix \mathbf{I} , with the vector I_n whose elements denote the amount of infected individuals for all compartments at time interval n .

To make the matrix multiplication work, we would need a $2m \times 2m$ contact matrix \mathbf{K} . We remark however that when we split all the individuals of each compartment into two categories, that the value for the expected amount of contacts between different compartments did not change. To get the $2m \times 2m$ contact matrix we desire, we simply construct the new contact matrix to be build up from columns and rows containing twice the contact matrix \mathbf{K} .

We have almost adjusted the model for the extra compartments we added. Right now, if we were to calculate the adjusted next generation matrix depending on location $\ell \in \mathcal{L}$ as:

$$\mathbf{A}_\ell = R^\ell \cdot \mathbf{S} \cdot \begin{pmatrix} \mathbf{K}_\ell & \mathbf{K}_\ell \\ \mathbf{K}_\ell & \mathbf{K}_\ell \end{pmatrix} \cdot \mathbf{I}, \quad (3.8)$$

the quantity of contacts between compartments would be doubled, since now both the compartment V_i and U_i are multiplied by the amount of expected contacts. To adjust for this we introduce the variables v_i and u_i . Let u_i and v_i be the fractions of compartment i denoting the fraction of people that belong to U_i and V_i respectively. The only thing we need to do is add the fraction of both populations to the newly constructed contact matrix. However, since we will be adjusting the contact matrix \mathbf{K} in a later chapter, for ease of use, we implement the fractions into one of the diagonal matrices. Our arbitrary choice is the matrix \mathbf{S} . We denote with $\hat{\mathbf{S}}$ the matrix with added fractions u_i and v_i :

$$\hat{\mathbf{S}} := \text{diag}(r_{u_1}^S u_1, \dots, r_{u_m}^S u_m, r_{v_1}^S v_1, \dots, r_{v_m}^S v_m).$$

Now the new next generation matrix dependent on location $\ell \in \mathcal{L}$ is given by:

$$\mathbf{A}_\ell = R^\ell \cdot \hat{\mathbf{S}} \cdot \begin{pmatrix} \mathbf{K}_\ell & \mathbf{K}_\ell \\ \mathbf{K}_\ell & \mathbf{K}_\ell \end{pmatrix} \cdot \mathbf{I}.$$

When enumerating over all the location dependent next generation matrices and keeping in mind the coefficient R^ℓ , we get the total generation matrix:

$$\mathbf{A} = \sum_{\ell \in \mathcal{L}} \mathbf{A}_\ell = \mathbf{A}_1 + \mathbf{A}_2 + \mathbf{A}_3 + \dots$$

We have introduced the SARS-CoV-2 certificates into the model and have sufficiently build up the model to be able to answer the research question.

3.8 The changing contact structure.

When introducing any form of restriction or resistance to participate at an event, it is logical to expect a reduction in attendance. For example, when we restrict people to join by implementing a 2G policy (or a 2G + 1G policy) and thoroughly control the population, denying any individual without proof of vaccination or health, no type U -individual will make it through the screening.

We remark that by implementing restrictions or resistance to participate, there will be not only a reduction in the participation of individuals of type U , a fraction of the type V -individuals is expected to also not participate. This could be due to a precaution or because they normally participate with type U -individuals.

Due to restrictions on participating, the number of attending individuals of a compartment could diminish. When fewer individuals participate at location ℓ , a problem arises. Unless the amount of attending individuals is reduced equally for both compartments, the contact structure will not remain symmetric:

$$N_j k_{ij} \neq N_i k_{ji},$$

which means that our current contact structure can no longer be used.

To make sure we still have a working contact structure that meets our assumption, we will have to alter the contact structure to create symmetry again.

Before explaining the process to change the contact matrix \mathbf{K} , we remark that the article requires an assumption for the process of changing contact matrix:

The total amount of contacts per compartment remains unchanged.

This means that before and after the process, the total amount of contacts for compartment i should equal: $\sum_{j=1}^m k_{ji}$, for every $1 \leq i \leq m$.

3.8.1 Altering the contact structure.

The calculations to change the contact structure to regain contact symmetry, which are explained in this section, are provided in the same article [2] which explains the inner workings of the model.

Before taking one step into the calculations, we would like to remark that the whole process described below is worked out for one location, and the process will have to be worked through for every location dependent next generation matrices \mathbf{A}_ℓ . For simplicity in notation, we will omit the subscript ℓ from all variables, but do remember that every variable used in the next calculations depends on the location $\ell \in \mathcal{L}$.

We will first and foremost define the reduction of compartment j :

$$\rho_j := u_j \rho_{u_j} + v_j \rho_{v_j}, \quad (3.9)$$

where ρ_{u_j} and ρ_{v_j} are the fractions denoting the reduction in attendance for the compartments U_j and V_j respectively. We remark that whenever the total reduction ρ_j equals 1, the participation will not have changed whilst when the total reduction ρ_j equals 0, the entire compartment will not be present.

We create a permutation σ , ordering all reductions from most- to least reduced:

$$\rho_{\sigma(1)} \leq \rho_{\sigma(2)} \leq \dots \leq \rho_{\sigma(m)},$$

The process to alter the contact matrix \mathbf{K} is recursively defined, and so we start by defining the starting condition.

The starting step:

We look at the total amount of contacts of compartment $\sigma(1)$ before we change anything. The total amount of contacts of compartment $\sigma(1)$ is given by: $\sum_{i=1}^m k_{i\sigma(1)}$, and we divide these contacts with every compartment $1 \leq j \leq m$.

We will divide the total amount of contacts based on the relative reduction of the contacted compartment. The process takes the reduction in contacts with the contacted compartment j and relates it to the total reduction of the contacts in compartment $\sigma(1)$.

The reduction in contacts with the contacted compartment j is given by: $\rho_j k_{j\sigma(1)}$, and the total reduction of contacts in compartment $\sigma(1)$ is given by: $\sum_{i=1}^m \rho_i k_{i\sigma(1)}$. The beginning step is therefore build up as:

$$\tilde{k}_{j\sigma(1)} = \frac{\rho_j \cdot k_{j\sigma(1)}}{\sum_{i=1}^m \rho_i k_{i\sigma(1)}} \cdot \sum_{i=1}^m k_{i\sigma(1)}. \quad (3.10)$$

After having calculated the element $\tilde{k}_{j\sigma(1)}$, we calculate the element $\tilde{k}_{\sigma(1)j}$. We do this to ensure symmetry in contacts between the compartments. We define the element $\tilde{k}_{\sigma(1)j}$ with the same train of thought as the element $\tilde{k}_{j\sigma(1)}$:

$$\tilde{k}_{\sigma(1)j} = \frac{\rho_{\sigma(1)} \cdot k_{\sigma(1)j}}{\sum_{i=1}^m \rho_i k_{i\sigma(1)}} \cdot \sum_{i=1}^m k_{i\sigma(1)} = \frac{\tilde{k}_{j\sigma(1)}}{k_{j\sigma(1)}} \cdot \frac{\rho_{\sigma(1)}}{\rho_j} \cdot k_{\sigma(1)j}, \quad (3.11)$$

where the second form of the element $\tilde{k}_{\sigma(1)j}$ is helpful when the value of the element $\tilde{k}_{j\sigma(1)}$ is known. By defining both elements $\tilde{k}_{j\sigma(1)}$ and $\tilde{k}_{\sigma(1)j}$ in this manner, we ensure the conservation of contacts and the symmetry in contacts between compartments.²

²See section 4.1.1 for the proof of symmetry in contacts and section 4.1.2 for the proof of conservation of contacts.

The recursive step:

In this step we assume that we have calculated all elements of $\tilde{\mathbf{K}}$ relating to the most reduced compartment $\sigma(1)$ up until compartment $\sigma(n-1)$. We define the process for the the n th highest reduced compartment alike to the starting step.

When looking at the total total amount of contacts of compartment $\sigma(n)$ there could be elements of the contact structure $\tilde{\mathbf{K}}$ that are already defined by the previously computed compartments. Therefore we look at the amount of left-over contacts still to be divided, and will relate them to the total reduction of the compartments still to be looked at. We remark that whenever we have previously defined a contact to compartment $\sigma(n)$, we have already taken into account the reduction of both compartments. To not count reductions twice, we will therefore only be looking at the reduction of the compartments still to be calculated.

The reduction in contacts with the contacted compartment $\sigma(j)$ is given by: $\rho_{\sigma(j)}k_{j\sigma(n)}$, but by our remark, the total reduction of contacts in compartment $\sigma(n)$ has changed to: $\sum_{i=n}^m \rho_{\sigma(i)}k_{\sigma(i)\sigma(n)}$. The last change to implement is the change of total amount of contacts to total amount of leftover contacts, which equals the total amount with the allotted contacts subtracted from it: $(\sum_{i=1}^m k_{i\sigma(n)} - \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)})$.

When we build up the element $\tilde{k}_{\sigma(j)\sigma(n)}$ with the same train of thought as the starting step, the element $\tilde{k}_{\sigma(j)\sigma(n)}$ equals:

$$\tilde{k}_{\sigma(j)\sigma(n)} = \frac{\rho_{\sigma(j)} \cdot k_{\sigma(j)\sigma(n)}}{\sum_{i=n}^m \rho_{\sigma(i)} k_{\sigma(i)\sigma(n)}} \cdot \left(\sum_{i=1}^m k_{i\sigma(n)} - \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)} \right). \quad (3.12)$$

As with the starting step, after having calculated the element $\tilde{k}_{\sigma(j)\sigma(n)}$, we calculate the element $\tilde{k}_{\sigma(n)\sigma(j)}$. We do this to ensure symmetry in contacts between the compartments. We define the element $\tilde{k}_{\sigma(n)\sigma(j)}$ to follow the same logic as the symmetric element in the starting step:

$$\tilde{k}_{\sigma(n)\sigma(j)} = \frac{\tilde{k}_{\sigma(j)\sigma(n)}}{k_{\sigma(j)\sigma(n)}} \cdot \frac{\rho_{\sigma(n)}}{\rho_{\sigma(j)}} \cdot k_{\sigma(n)\sigma(j)}. \quad (3.13)$$

By defining our recursive process this way, we have successfully retained the symmetrical structure of contacts between compartments and have retained the total amount of contacts per compartments.

We have now defined the process to change the contact matrix \mathbf{K} into the contact matrix $\tilde{\mathbf{K}}$, recursively.

Effects of the process on the next generation matrix.

We close out this section by giving some of the implications the implementation of SARS-CoV-2 certificates, together with the changing contacts structure, has on the next generation matrix. The changes of implementing the certificates are twofold; because of reduction in attendance, the amount of individuals attending at different locations will decrease and cause the infectiousness to decrease, and the fractions u_i and v_i relating to the semi-compartment U_i and V_i of compartments $1 \leq i \leq m$ will change because of the lower attendance.

The reduction in attendance causing a reduction in overall infectiousness can be implemented by introducing the reduction per compartment: ρ_{u_i} and ρ_{v_i} into the model. We will do so by implementing both variables into the matrix \mathbf{I} , altering the diagonal matrix.

The reduction in attendance also alters the fractions u_i and v_i . The fractions have to change to adjust for the changing total attending population. Therefore we scale both u_i and v_i by their respective reduction, and compare it to the total reduced population: $\rho_{u_i}^\ell \cdot u_i + \rho_{v_i}^\ell \cdot v_i$. The fractions take the following form:

$$\tilde{u}_i^\ell = \frac{\rho_{u_i}^\ell \cdot u_i}{\rho_{u_i}^\ell \cdot u_i + \rho_{v_i}^\ell \cdot v_i}, \quad \tilde{v}_i^\ell = \frac{\rho_{v_i}^\ell \cdot v_i}{\rho_{u_i}^\ell \cdot u_i + \rho_{v_i}^\ell \cdot v_i}.$$

We remark that the equation $\tilde{u}_i^\ell + \tilde{v}_i^\ell = 1$ still holds.

After substituting \tilde{u}_i^ℓ and \tilde{v}_i^ℓ into the matrix $\hat{\mathbf{S}}$ and implementing the variables ρ_{u_i} and ρ_{v_i} into the matrix \mathbf{I} , we rename both diagonal matrices to:

$$\begin{aligned} \tilde{\mathbf{S}}_\ell &:= \text{diag}(r_{u_1}^S \tilde{u}_1^\ell, \dots, r_{u_m}^S \tilde{u}_m^\ell, r_{v_1}^S \tilde{v}_1^\ell, \dots, r_{v_m}^S \tilde{v}_m^\ell), \\ \tilde{\mathbf{I}}_\ell &:= \text{diag}(\rho_{u_1}^\ell r_{u_1}^I, \dots, \rho_{u_m}^\ell r_{u_m}^I, \rho_{v_1}^\ell r_{v_1}^I, \dots, \rho_{v_m}^\ell r_{v_m}^I). \end{aligned}$$

As stated before, the variables are dependent on the location ℓ . For clarity, we have included the sub- and superscript for the location into the equations.

The new next generation matrix for location ℓ will take the form of:

$$\tilde{\mathbf{A}}_\ell = R^\ell \cdot \tilde{\mathbf{S}}_\ell \cdot \begin{pmatrix} \tilde{\mathbf{K}}_\ell & \tilde{\mathbf{K}}_\ell \\ \tilde{\mathbf{K}}_\ell & \tilde{\mathbf{K}}_\ell \end{pmatrix} \cdot \tilde{\mathbf{I}}_\ell.$$

where, as we have seen before, the total new generation matrix is comprised of all location dependent next generation matrices:

$$\tilde{\mathbf{A}} = \sum_{\ell \in \mathcal{L}} \tilde{\mathbf{A}}_\ell = \tilde{\mathbf{A}}_1 + \tilde{\mathbf{A}}_2 + \tilde{\mathbf{A}}_3 + \dots$$

3.8.2 Further elaboration on the model.

We have, as of now, defined the change in contact structure relating to our research question. For completeness we will mention the additional methods used in the article. We display them in this section but would like to remark that we will not build further upon these methods. This section is meant to give the finishing information of the model and can be disregarded when only reading the necessary information to answer the research question.

Clustering in the contact matrix.

Human beings have preferences and make conscious or unconscious choices who to spend their time with. This means that certain individuals will group, or cluster, together and skew the amount of contacts into the clustered direction.

We define the relative preference h_{ij} of a type U_j -individual for individuals of type U_i -individuals over type V_i -individuals. The purpose of the variable h_{ij} is to define what fraction of the contacts k_{ij} , or when changed \tilde{k}_{ij} , is with type U_i -individuals or V_i -individuals. In essence, the variable h_{ij} adds another layer to the separation of contacts. We remark that h_{ij} is a non-negative number.

The fraction of the total contacts of type U_j -individuals who are with type U_i -individuals is defined as:

$$\frac{h_{ij} \cdot u_i}{h_{ij}u_i + v_i}$$

Similarly, we can define the fraction of the total contacts of type U_j -individuals belonging to type V_i -individuals as:

$$\frac{h_{ij} \cdot v_i}{u_i + h_{ij}v_i}$$

By symmetry of contacts, one can define the preference of type V -individuals with type U_i -individuals to be $\frac{h_{ij} \cdot u_i}{h_{ij}u_i + v_i}$. The left over contacts are with other type V -individuals and are equal to $1 - \frac{h_{ij} \cdot u_i}{h_{ij}u_i + v_i}$. Once h_{ij} is defined, h_{ji} is set as well. We remark that only one level of clustering can be added per pair of compartments. We would like to remark that the preferences h_{ij}^ℓ can be dependent on location $\ell \in \mathcal{L}$ if the situation calls for it.

Although this method works mathematically, there is not enough information to calculate and therefore implement the preference h_{ij} into the model.

Considering compensating behaviour.

So far we have introduced a reduction in participation into the model due to certificates being implemented. In the model we have, without explicitly stating it, assumed that the people not present are isolated and therefore not susceptible to other individuals. It is however very unrealistic to think a person not at an event spends their time not doing anything.

We introduce a term which takes into account the actions of individuals not being present at location ℓ and call it compensating behaviour. We assume that the attendance at the compensating-behaviour-events is defined by:

$$\rho_{u_1}^{\ell_C} = \rho^\ell(1 - \rho_{u_i}^\ell), \quad \rho_{v_1}^{\ell_C} = \rho^\ell(1 - \rho_{v_i}^\ell)$$

for type U_i -individuals and type V_i -individuals respectively, with $1 \leq i \leq m$. The term ρ^ℓ denotes the fraction of individuals who are not attending the event at location ℓ , but do participate at the compensating event. When constructing a model for these alternative events, we construct the contact matrix $\tilde{\mathbf{K}}^{\ell_C}$ in the same exact way we have explained in previous section, but instead of ordering the reductions $(\rho_i^\ell)_{1 \leq i \leq m}$, we order the compensating reductions $(\rho_i^{\ell_C})_{1 \leq i \leq m}$.

We denote with $\tilde{u}_i^{\ell_C}$ and $\tilde{v}_i^{\ell_C}$ the relative attendance of type U -individuals and type V -individuals respectively who are present at these compensating events at location ℓ . The relative attendances $\tilde{u}_i^{\ell_C}$ and $\tilde{v}_i^{\ell_C}$ are described by:

$$\tilde{u}_i^{\ell_C} = \frac{\rho_{u_i}^{\ell_C} \cdot u_i}{\rho_{u_i}^{\ell_C} \cdot u_i + \rho_{v_i}^{\ell_C} \cdot u_i}, \quad \tilde{v}_i^{\ell_C} = \frac{\rho_{v_i}^{\ell_C} \cdot v_i}{\rho_{u_i}^{\ell_C} \cdot u_i + \rho_{v_i}^{\ell_C} \cdot u_i}$$

After filling in every variable in their respected position, the location dependent next generation matrix is given by:

$$\tilde{\mathbf{A}}_{\ell_C} = R^{\ell_C} \cdot \tilde{\mathbf{S}}_{\ell_C} \cdot \begin{pmatrix} \tilde{\mathbf{K}}_{\ell_C} & \tilde{\mathbf{K}}_{\ell_C} \\ \tilde{\mathbf{K}}_{\ell_C} & \tilde{\mathbf{K}}_{\ell_C} \end{pmatrix} \cdot \tilde{\mathbf{I}}_{\ell_C}.$$

where the altered variables are substituted into the two diagonal matrices as:

$$\begin{aligned} \tilde{\mathbf{S}}_{\ell_C} &= \text{diag}(r_{u_1}^S \tilde{u}_1^{\ell_C}, \dots, r_{u_m}^S \tilde{u}_m^{\ell_C}, r_{v_1}^S \tilde{v}_1^{\ell_C}, \dots, r_{v_m}^S \tilde{v}_m^{\ell_C}), \\ \tilde{\mathbf{I}}_{\ell_C} &= \text{diag}(\rho_{u_1}^{\ell_C} r_{u_1}^I, \dots, \rho_{u_m}^{\ell_C} r_{u_m}^I, \rho_{v_1}^{\ell_C} r_{v_1}^I, \dots, \rho_{v_m}^{\ell_C} r_{v_m}^I). \end{aligned}$$

As we have seen before, the next generation matrix is comprised of all location dependent next generation matrices:

$$\tilde{\mathbf{A}}_C = \sum_{\ell \in \mathcal{L}} \tilde{\mathbf{A}}_{\ell_C} = \tilde{\mathbf{A}}_{1_C} + \tilde{\mathbf{A}}_{2_C} + \tilde{\mathbf{A}}_{3_C} + \dots$$

When we have enough information the model could run over more locations to try and calculate a more precise course of the disease.

Considering interventions involving testing of individuals.

The last topic the article touches involves the infectiousness of individuals. We define the reduction in infectiousness as $f_{u_i}^\ell$ for type U -individuals and $f_{v_i}^\ell$ for type V -individuals, both of compartment i at location $\ell \in \mathcal{L}$. The reduction can be because of multiple different factors; vaccines being introduced, individuals being more careful or any other reason that lowers the infectiousness.

We implement the reduction by simply multiplying every $f_{u_i}^\ell$ and $f_{v_i}^\ell$ with the corresponding element in the diagonal matrix $\tilde{\mathbf{I}}^\ell$. The partial next generation matrix is given by:

$$\tilde{\mathbf{A}}_\ell = R^\ell \cdot \tilde{\mathbf{S}}_\ell \cdot \begin{pmatrix} \tilde{\mathbf{K}}_\ell & \tilde{\mathbf{K}}_\ell \\ \tilde{\mathbf{K}}_\ell & \tilde{\mathbf{K}}_\ell \end{pmatrix} \cdot \hat{\mathbf{I}}_\ell,$$

where the variables $f_{u_i}^\ell$ and $f_{v_i}^\ell$ are put into the diagonal matrix:

$$\hat{\mathbf{I}}_\ell = \text{diag}(\rho_{u_1}^\ell f_{u_1}^\ell r_{u_1}^I, \dots, \rho_{u_m}^\ell f_{u_m}^\ell r_{u_m}^I, \rho_{v_1}^\ell f_{v_1}^\ell r_{v_1}^I, \dots, \rho_{v_m}^\ell f_{v_m}^\ell r_{v_m}^I).$$

The total new generation matrix remains the sum of all partial next generation matrices:

$$\tilde{\mathbf{A}} = \sum_{\ell \in \mathcal{L}} \tilde{\mathbf{A}}_\ell = \tilde{\mathbf{A}}_1 + \tilde{\mathbf{A}}_2 + \tilde{\mathbf{A}}_3 + \dots$$

We would like to remark that the reduction in infectiousness depends on a lot of factors and is therefore difficult to precisely determine. Nonetheless when an estimation is made about the reduction in infectiousness, the model is well prepared to adjust to this reduction.

The calculation of parameters $r_{u_j}^S$ and $r_{v_j}^S$.

When using the model, it is necessary to calculate the parameters $r_{u_j}^S$ and $r_{v_j}^S$. The article gives us the variables making up the parameters, but it makes a clear distinction between naive individuals, individuals who have yet to be infected, and unvaccinated individuals with an undocumented infection.

Let the fractions z_j and $(1 - z_j)$ denote the distribution of compartment j , denoting the fraction of naive individuals and infected without a documented infection individuals respectively. When we assume that every individual with an undocumented infection has the same infectiousness and susceptibility as individuals of compartment V_j , we have:

$$r_{u_j}^S = z_j \cdot r_{u_j}^{S_n} + (1 - z_j) \cdot r_{v_j}^S. \quad (3.14)$$

When calculating $r_{v_j}^S$ we need to take into account the correlation between higher susceptibility and greater likeliness to get infected. Hence we obtain:

$$r_{v_j}^S = \frac{z_j \cdot r_{u_j}^{S_n} \cdot r_{u_j}^{I_n} + (1 - z_j) \cdot r_{v_j}^S \cdot r_{v_j}^I}{z_j \cdot r_{u_j}^{S_n} + (1 - z_j) \cdot r_{v_j}^S}. \quad (3.15)$$

Chapter 4

Mathematically validating the model.

4.1 Claims made in the article.

4.1.1 Preservation of the symmetric contact structure.

The article claims to construct the element $\tilde{k}_{\sigma(n)\sigma(j)}$ to be symmetric in contacts to $\tilde{k}_{\sigma(j)\sigma(n)}$ for every element in the constructed contact matrix $\tilde{\mathbf{K}}$. We show that the element $\tilde{k}_{\sigma(n)\sigma(j)}$ does indeed cause a symmetry in the total number of contacts.

Proof. Let σ be the permutation ordering the set of compartment reductions and let $N_{\sigma(n)}$ and $N_{\sigma(j)}$ be the number of participants of the compartments n and j respectively, under σ . Here n and j are arbitrarily chosen between 1 and m .

Our assumption regarding symmetric contacts must be rewritten in the new situation, namely, the number of participating individuals decreases and the contact structure changes. The amount of reduction in participation is given by $\rho_{\sigma(n)}$ and $\rho_{\sigma(j)}$ for compartments n and j respectively. Therefore the amount of participating individuals after restrictions equals $\rho_{\sigma(n)} \cdot N_{\sigma(n)}$ and $\rho_{\sigma(j)} \cdot N_{\sigma(j)}$ for compartment n and j respectively. With the change in contact structure, our assumption is transcribed into the following equation:

$$\rho_{\sigma(n)} \cdot N_{\sigma(n)} \cdot \tilde{k}_{\sigma(j)\sigma(n)} = \rho_{\sigma(j)} \cdot N_{\sigma(j)} \cdot \tilde{k}_{\sigma(n)\sigma(j)}. \quad (4.1)$$

We use the given form for $\tilde{k}_{\sigma(n)\sigma(j)} = \frac{\tilde{k}_{\sigma(j)\sigma(n)}}{k_{\sigma(j)\sigma(n)}} \cdot \frac{\rho_{\sigma(n)}}{\rho_{\sigma(j)}} \cdot k_{\sigma(n)\sigma(j)}$, to show symmetry:

$$\begin{aligned} \rho_{\sigma(j)} \cdot N_{\sigma(j)} \cdot \tilde{k}_{\sigma(n)\sigma(j)} &= \rho_{\sigma(j)} \cdot N_{\sigma(j)} \cdot \frac{\tilde{k}_{\sigma(j)\sigma(n)}}{k_{\sigma(j)\sigma(n)}} \cdot \frac{\rho_{\sigma(n)}}{\rho_{\sigma(j)}} \cdot k_{\sigma(n)\sigma(j)} \\ &= \rho_{\sigma(n)} \cdot N_{\sigma(j)} \cdot \frac{\tilde{k}_{\sigma(j)\sigma(n)}}{k_{\sigma(j)\sigma(n)}} \cdot k_{\sigma(n)\sigma(j)}. \end{aligned}$$

We remark that under the unaltered contact matrix \mathbf{K} , the old assumption regarding symmetric contacts still holds true:

$$\begin{aligned}
\rho_{\sigma(j)} \cdot N_{\sigma(j)} \cdot \tilde{k}_{\sigma(n)\sigma(j)} &= \rho_{\sigma(n)} \cdot N_{\sigma(j)} \cdot \frac{\tilde{k}_{\sigma(j)\sigma(n)}}{k_{\sigma(j)\sigma(n)}} \cdot k_{\sigma(n)\sigma(j)} \\
&= \rho_{\sigma(n)} \cdot N_{\sigma(j)} \cdot k_{\sigma(n)\sigma(j)} \cdot \frac{\tilde{k}_{\sigma(j)\sigma(n)}}{k_{\sigma(j)\sigma(n)}} \\
&= \rho_{\sigma(n)} \cdot N_{\sigma(n)} \cdot k_{\sigma(j)\sigma(n)} \cdot \frac{\tilde{k}_{\sigma(j)\sigma(n)}}{k_{\sigma(j)\sigma(n)}} \\
&= \rho_{\sigma(n)} \cdot N_{\sigma(n)} \cdot \tilde{k}_{\sigma(j)\sigma(n)}.
\end{aligned}$$

With some simple manipulation and substitution of the equation, we have shown the symmetry in contacts between compartments:

$$\rho_{\sigma(n)} \cdot N_{\sigma(n)} \cdot \tilde{k}_{\sigma(j)\sigma(n)} = \rho_{\sigma(j)} \cdot N_{\sigma(j)} \cdot \tilde{k}_{\sigma(n)\sigma(j)},$$

for every arbitrary pair n and j in between 1 and m . □

4.1.2 Preservation of the total amount of contacts.

In this section we will prove that the new contact matrix $\tilde{\mathbf{K}}$ retains the total amount of contacts per compartment. For every compartment $1 \leq n \leq m$, the total amount of contacts remains the same:

$$\sum_{i=1}^m k_{\sigma(i)\sigma(n)} = \sum_{i=1}^m \tilde{k}_{\sigma(i)\sigma(n)}$$

We remark that when summing over the entire column, every element under the permutation σ is added up. Therefore we can switch between the notation: $\sigma(i)$ and i itself, which is important when looking at the base case $n = 1$.

We prove the preservation of contacts with induction on n .

Proof. The **base case**: Let $n = 1$.

The elements $\tilde{k}_{j\sigma(1)}$ for $1 \leq j \leq m$ are given by:

$$\sum_{j=1}^m \tilde{k}_{j\sigma(1)} = \sum_{j=1}^m \left[\frac{\rho_j \cdot k_{j\sigma(1)}}{\sum_{i=1}^m \rho_i k_{i\sigma(1)}} \cdot \sum_{i=1}^m k_{i\sigma(1)} \right]$$

We remark that the summation over j only influences the numerator of the fraction. Therefore this equation can be rewritten as follows:

$$\begin{aligned} \sum_{j=1}^m \tilde{k}_{j\sigma(1)} &= \sum_{j=1}^m \left[\frac{\rho_j \cdot k_{j\sigma(1)}}{\sum_{i=1}^m \rho_i k_{i\sigma(1)}} \cdot \sum_{i=1}^m k_{i\sigma(1)} \right] \\ &= \frac{\sum_{j=1}^m [\rho_j \cdot k_{j\sigma(1)}]}{\sum_{i=1}^m \rho_i k_{i\sigma(1)}} \cdot \sum_{i=1}^m k_{i\sigma(1)} \\ &= \sum_{i=1}^m k_{i\sigma(1)}. \end{aligned}$$

We have now proven that for $n = 1$ the matrix $\tilde{\mathbf{K}}$ preserves the total amount of contacts.

The **induction step**:

Assume all compartments $\sigma(1), \sigma(2), \dots, \sigma(n-1)$ preserve contacts in the contact matrix $\tilde{\mathbf{K}}$. The total amount of contacts for compartment $\sigma(n)$ is given by:

$$\sum_{j=1}^m \tilde{k}_{\sigma(j)\sigma(n)} = \sum_{j=1}^m \left[\frac{\rho_{\sigma(j)} \cdot k_{\sigma(j)\sigma(n)}}{\sum_{i=n}^m \rho_{\sigma(i)} k_{\sigma(i)\sigma(n)}} \cdot \left(\sum_{i=1}^m k_{i\sigma(n)} - \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)} \right) \right].$$

We make the same remark as in the base case, the summation over j only effects the numerator of the fraction, the other variables do not depend on j :

$$\sum_{j=1}^m \tilde{k}_{\sigma(j)\sigma(n)} = \frac{\sum_{j=1}^m [\rho_{\sigma(j)} \cdot k_{\sigma(j)\sigma(n)}]}{\sum_{i=n}^m \rho_{\sigma(i)} k_{\sigma(i)\sigma(n)}} \cdot \left(\sum_{i=1}^m k_{i\sigma(n)} - \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)} \right).$$

We split the summation over j into two parts, one summation from 1 until $n-1$, and one summation from n up until m :

$$\begin{aligned}
\sum_{j=1}^m \tilde{k}_{\sigma(j)\sigma(n)} &= \sum_{j=1}^m \left[\frac{\rho_{\sigma(j)} \cdot k_{\sigma(j)\sigma(n)}}{\sum_{i=n}^m \rho_{\sigma(i)} k_{\sigma(i)\sigma(n)}} \cdot \left(\sum_{i=1}^m k_{i\sigma(n)} - \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)} \right) \right] \\
&+ \sum_{j=n}^m \left[\frac{\rho_{\sigma(j)} \cdot k_{\sigma(j)\sigma(n)}}{\sum_{i=n}^m \rho_{\sigma(i)} k_{\sigma(i)\sigma(n)}} \cdot \left(\sum_{i=1}^m k_{i\sigma(n)} - \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)} \right) \right] \\
&= \frac{\sum_{j=1}^{n-1} [\rho_{\sigma(j)} \cdot k_{\sigma(j)\sigma(n)}]}{\sum_{i=n}^m \rho_{\sigma(i)} k_{\sigma(i)\sigma(n)}} \cdot \left(\sum_{i=1}^m k_{i\sigma(n)} - \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)} \right) \\
&+ \frac{\sum_{j=n}^m [\rho_{\sigma(j)} \cdot k_{\sigma(j)\sigma(n)}]}{\sum_{i=n}^m \rho_{\sigma(i)} k_{\sigma(i)\sigma(n)}} \cdot \left(\sum_{i=1}^m k_{i\sigma(n)} - \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)} \right)
\end{aligned}$$

We look at both parts separately and will later on bring them together to show the preservation of contacts.

We start with the summation from n up to m . We remark that although the indice is different in the numerator and denominator, the sum is the same. Therefore, as long as the denominator does not equal zero, the sum from n up to m equals the total left-over contacts of compartment $\sigma(n)$:

$$\frac{\sum_{j=n}^m [\rho_{\sigma(j)} \cdot k_{\sigma(j)\sigma(n)}]}{\sum_{i=n}^m \rho_{\sigma(i)} k_{\sigma(i)\sigma(n)}} \cdot \left(\sum_{i=1}^m k_{i\sigma(n)} - \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)} \right) = \sum_{i=1}^m k_{i\sigma(n)} - \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)}.$$

We will now look at the summation from 1 to $n-1$. We remark that the summation from 1 to $n-1$ equals by definition:

$$\begin{aligned}
\sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)} &:= \sum_{j=1}^{n-1} \left[\frac{\rho_{\sigma(j)} \cdot k_{\sigma(j)\sigma(n)}}{\sum_{i=n}^m \rho_{\sigma(i)} k_{\sigma(i)\sigma(n)}} \cdot \left(\sum_{i=1}^m k_{i\sigma(n)} - \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)} \right) \right] \\
&= \frac{\sum_{j=1}^{n-1} [\rho_{\sigma(j)} \cdot k_{\sigma(j)\sigma(n)}]}{\sum_{i=n}^m \rho_{\sigma(i)} k_{\sigma(i)\sigma(n)}} \cdot \left(\sum_{i=1}^m k_{i\sigma(n)} - \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)} \right)
\end{aligned}$$

We now bring both parts together to prove the preservation of contacts:

$$\begin{aligned}
\sum_{j=1}^m \tilde{k}_{\sigma(j)\sigma(n)} &= \frac{\sum_{j=1}^{n-1} [\rho_{\sigma(j)} \cdot k_{\sigma(j)\sigma(n)}]}{\sum_{i=n}^m \rho_{\sigma(i)} k_{\sigma(i)\sigma(n)}} \cdot \left(\sum_{i=1}^m k_{i\sigma(n)} - \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)} \right) \\
&+ \frac{\sum_{j=n}^m [\rho_{\sigma(j)} \cdot k_{\sigma(j)\sigma(n)}]}{\sum_{i=n}^m \rho_{\sigma(i)} k_{\sigma(i)\sigma(n)}} \cdot \left(\sum_{i=1}^m k_{i\sigma(n)} - \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)} \right) \\
&= \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)} + \sum_{i=1}^m k_{i\sigma(n)} - \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)} = \sum_{i=1}^m k_{i\sigma(n)}
\end{aligned}$$

We have now proven by induction that the process preserves contacts for all elements of the contact matrix \mathbf{K} . \square

4.2 The new contact matrix being well-defined.

For the model to be well-defined, we will need to check the requirements imposed by the article [2], and check if the contacts will be strictly non-negative. In the previous sections we checked the requirements and in this section we will proof that the elements of the altered contact matrix $\tilde{\mathbf{K}}$ are strictly non-negative when following the process, altering the matrix \mathbf{K} into the matrix $\tilde{\mathbf{K}}$.

Proof.

We will prove that the elements $\tilde{k}_{\sigma(i)\sigma(j)}$ are strictly non-negative for i and j between 1 and m . We will prove this using induction on the order $\sigma(n)$:

Before initiating the base case and induction step, we will first introduce the necessary objects to finish this proof. Let \mathbf{K} be a well-defined contact matrix, i.e. the elements of the contact matrix \mathbf{K} are strictly non-negative. Let $\rho_{\sigma(j)}$ be the total reduction of compartment j under the permutation σ . We remark that the total reduction of a compartment is bounded: $0 \leq \rho_{\sigma(j)} \leq 1$.

We will first look at the **base case**:

Let $n = 1$, the elements $k_{j\sigma(1)}$ and $k_{\sigma(1)j}$ of compartment $\sigma(1)$ are mapped to their respective counterparts in the matrix $\tilde{\mathbf{K}}$ using the following equations:

$$\tilde{k}_{j\sigma(1)} = \frac{\rho_j \cdot k_{j\sigma(1)}}{\sum_{i=1}^m \rho_i k_{i\sigma(1)}} \cdot \sum_{i=1}^m k_{i\sigma(1)}, \quad \tilde{k}_{\sigma(1)j} = \frac{\tilde{k}_{j\sigma(1)}}{k_{j\sigma(1)}} \cdot \frac{\rho_{\sigma(1)}}{\rho_j} \cdot k_{\sigma(1)j}.$$

We will analyse both equations and prove the elements $\tilde{k}_{j\sigma(1)}$ and $\tilde{k}_{\sigma(1)j}$ remain strictly non-negative. We will start with the first equation:

$$\tilde{k}_{j\sigma(1)} = \frac{\rho_j \cdot k_{j\sigma(1)}}{\sum_{i=1}^m \rho_i k_{i\sigma(1)}} \cdot \sum_{i=1}^m k_{i\sigma(1)}$$

We remark that two strictly non-negative numbers multiplied or added together, will result in a strictly non-negative number. Therefore we can state that both the numerator and the total amount of contacts are strictly non-negative:

$$\rho_j \cdot k_{j\sigma(1)} \geq 0, \quad \text{and} \quad \sum_{i=1}^m k_{i\sigma(1)} \geq 0.$$

When combining both inequalities, we can conclude that the denominator is not only strictly non-negative, for the process to be defined it has to be strictly positive:

$$\sum_{i=1}^m \rho_i k_{i\sigma(1)} > 0.$$

We conclude that the whole equation is build up of strictly non-negative components and therefore has to be strictly non-negative:

$$\tilde{k}_{j\sigma(1)} = \frac{\rho_j \cdot k_{j\sigma(1)}}{\sum_{i=1}^m \rho_i k_{i\sigma(1)}} \cdot \sum_{i=1}^m k_{i\sigma(1)} \geq 0.$$

When looking at the second equation we simply state that we have analysed every variable and every variable in the equation is strictly non-negative. Therefore the second equation also has to be strictly non-negative:

$$\tilde{k}_{\sigma(1)j} = \frac{\tilde{k}_{j\sigma(1)}}{k_{j\sigma(1)}} \cdot \frac{\rho_{\sigma(1)}}{\rho_j} \cdot k_{\sigma(1)j} \geq 0.$$

We will now look at the **induction step**:

Assume all elements $\tilde{k}_{\sigma(i)\sigma(j)}$ belonging to the compartments:

$$\sigma(1), \sigma(2), \dots, \sigma(n-1),$$

are strictly non-negative. Then for the compartment $\sigma(n)$, the elements are denoted by the following two equations:

$$\begin{aligned} \tilde{k}_{\sigma(j)\sigma(n)} &= \frac{\rho_{\sigma(j)} \cdot k_{\sigma(j)\sigma(n)}}{\sum_{i=n}^m \rho_{\sigma(i)} k_{\sigma(i)\sigma(n)}} \cdot \left(\sum_{i=1}^m k_{i\sigma(n)} - \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)} \right), \\ \tilde{k}_{\sigma(n)\sigma(j)} &= \frac{\tilde{k}_{\sigma(j)\sigma(n)}}{k_{\sigma(j)\sigma(n)}} \cdot \frac{\rho_{\sigma(n)}}{\rho_{\sigma(j)}} \cdot k_{\sigma(n)\sigma(j)}. \end{aligned}$$

Following the base case, it is evident from the second equation that whenever $\tilde{k}_{\sigma(j)\sigma(n)}$ is strictly non-negative, then $\tilde{k}_{\sigma(n)\sigma(j)}$ will be non-negative as well. It rests us to prove that the elements $(\tilde{k}_{\sigma(j)\sigma(n)})_{1 \leq j \leq m}$ are strictly non-negative.

From the base case, we remark that both parts of the equation:

$$\rho_{\sigma(j)} \cdot k_{\sigma(j)\sigma(n)} \geq 0 \quad \text{and} \quad \sum_{i=n}^m \rho_{\sigma(i)} k_{\sigma(i)\sigma(n)} > 0,$$

are both strictly non-negative. So it rests us to show that the part

$$\sum_{i=1}^m k_{i\sigma(n)} - \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)},$$

is strictly non-negative.

By the preservation of total amount of contacts, we can state:

$$\sum_{i=1}^m k_{i\sigma(n)} = \sum_{i=1}^m \tilde{k}_{\sigma(i)\sigma(n)} \geq \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)},$$

where the inequality is based on the fact that a partial sum: $\sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)}$ of strictly non-negative elements is less or equal to the full sum of strictly non-negative elements: $\sum_{i=1}^m \tilde{k}_{\sigma(i)\sigma(n)}$. Therefore we can conclude that the left-over total amount of contacts is strictly non-negative:

$$\left(\sum_{i=1}^m k_{i\sigma(n)} - \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(n)} \right) \geq 0.$$

We have now proven that the process of turning a random well-defined contact matrix \mathbf{K} into the altered contact matrix $\tilde{\mathbf{K}}$ results in the contact matrix $\tilde{\mathbf{K}}$ being well-defined. \square

4.3 Continuity of the model.

We will show that the process of obtaining the new contact matrix $\tilde{\mathbf{K}}$ from the contact matrix \mathbf{K} is a continuous in reduction. By doing so, we can argue that with the process, we can alter any well-defined contact matrix \mathbf{K} into the altered contact matrix $\tilde{\mathbf{K}}$ in a continuous manner.

Let \mathbf{K} be a contact matrix and $P = (\rho_{\sigma(1)}, \dots, \rho_{\sigma(m)})$ be the vector containing all reductions, in sorted order, needed for the process to transform the contact matrix \mathbf{K} into the new contact matrix $\tilde{\mathbf{K}}$. We define the family of functions:

$$\tilde{k}_{\sigma(i)\sigma(n)}(P, \mathbf{K}) = \frac{\rho_{\sigma(j)}}{\sum_{i=1}^m \rho_{\sigma(i)} k_{\sigma(i)\sigma(n)}} \cdot \left(\sum_{i=1}^m k_{i\sigma(1)} - \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(1)} \right), \quad (4.2)$$

which sends the element k_{ij} of \mathbf{K} to the element $\tilde{k}_{\sigma(i)\sigma(n)}$ using the values of P . We assume the elements of \mathbf{K} to be known and constant for the process.

The function is build up of elements contained in P , the constant elements from the matrix \mathbf{K} and functions contained within the same family of functions. We remark that functions consisting solely of constants, variables or polynomial combinations of both, are continuous. We also remark that compositions of continuous functions are continuous again. We will proof that the family of functions is continuous by using induction on n .

Proof. Proof by induction:

The **Base case**:

Let $n = 1$. We look at the starting function in the family which is defined as:

$$\tilde{k}_{j\sigma(1)} = \frac{\rho_j \cdot k_{j\sigma(1)}}{\sum_{i=1}^m \rho_i k_{i\sigma(1)}} \cdot \sum_{i=1}^m k_{i\sigma(1)},$$

and see it is a polynomial composition of the constants $k_{\sigma(i)\sigma(j)}$ for i and j between 1 and m , and the variables denoting reductions $\rho_{\sigma(k)}$, for k between 1 and m . Therefore we conclude the function $\tilde{k}_{j\sigma(1)}$ to be continuous.

The **Induction step**:

Assume all functions $\tilde{k}_{\sigma(i)\sigma(1)}(P, \mathbf{K})$ up until $\tilde{k}_{\sigma(i)\sigma(n-1)}(P, \mathbf{K})$ are continuous for $1 \leq i \leq m$. The next function in the family; $\tilde{k}_{\sigma(i)\sigma(n)}(P, \mathbf{K})$ is defined to be:

$$\tilde{k}_{\sigma(i)\sigma(n)}(P, \mathbf{K}) = \frac{\rho_{\sigma(j)}}{\sum_{i=1}^m \rho_{\sigma(i)} k_{\sigma(i)\sigma(n)}} \cdot \left(\sum_{i=1}^m k_{i\sigma(1)} - \sum_{i=1}^{n-1} \tilde{k}_{\sigma(i)\sigma(1)} \right),$$

and when we follow the same train of thought as the base case, we see that this function is build up of polynomial compositions of the constants $k_{\sigma(i)\sigma(j)}$ for i and j between 1 and m , the variables denoting reductions $\rho_{\sigma(k)}$, for k between 1 and m and the functions $\tilde{k}_{\sigma(i)\sigma(p)}$, which are continuous for $1 \leq p \leq n - 1$.

The function $\tilde{k}_{\sigma(i)\sigma(n)}(P, \mathbf{K})$ is therefore a composition of continuous functions, making the function itself continuous. We have now proven that the family of functions altering matrix \mathbf{K} into the matrix $\tilde{\mathbf{K}}$ is continuous in reductions. \square

4.4 Uniqueness of the model.

In this section we show that due to the requirements imposed by the article [1], there is no unique contact matrix that meets the requirements. The way the process transforms contact matrix \mathbf{K} into the altered contact matrix $\tilde{\mathbf{K}}$ is one possibility that meets the requirements, but there exists other possible contact matrices that do meet the requirements.

By constructing the new contact matrix $\hat{\mathbf{K}}$ in a specific way, we will show that the contact matrix meeting the requirements and chosen by the process: $\tilde{\mathbf{K}}$, is not unique.

We construct the matrix $\hat{\mathbf{K}}$ as follows:

We start with a well-defined contact matrix \mathbf{K} and create the matrix $\hat{\mathbf{K}}$ to be the zero matrix corresponding to the dimensions of the matrix \mathbf{K} . Now we choose the sum of the elements k_{ij} for $1 \leq i \leq m-1$ and $1 \leq j \leq i$ to be less than or equal to the total sum of contacts $\sum_{i=1}^m k_{ij}$, to create a lower triangle matrix with the last row filled with zeros.

The matrix $\hat{\mathbf{K}}$ will take the form of a lower triangle matrix without substituting the last row:

$$\hat{\mathbf{K}} = \begin{bmatrix} \hat{k}_{11} & & & & 0 \\ \hat{k}_{21} & \hat{k}_{22} & & & \\ \hat{k}_{31} & \hat{k}_{32} & \ddots & & \\ \vdots & \vdots & \ddots & \ddots & \\ \hat{k}_{(m-1)1} & \hat{k}_{(m-1)2} & \cdots & \hat{k}_{(m-1)(m-1)} & 0 \\ 0 & 0 & \cdots & 0 & 0 \end{bmatrix}$$

We remark that the matrix $\hat{\mathbf{K}}$ has to have the property of symmetric contacts between compartments, therefore the elements above the diagonal of the matrix corresponding to a non-zero element below the diagonal, are determined by their corresponding elements below the diagonal of the matrix.

The matrix $\hat{\mathbf{K}}$ will take the form of a filled in matrix without having values in the last row and last column:

$$\hat{\mathbf{K}} = \begin{bmatrix} \hat{k}_{11} & \hat{k}_{12} & \cdots & \hat{k}_{1(m-1)} & 0 \\ \hat{k}_{21} & \hat{k}_{22} & \cdots & \hat{k}_{2(m-1)} & 0 \\ \hat{k}_{31} & \hat{k}_{32} & \cdots & \hat{k}_{3(m-1)} & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ \hat{k}_{(m-1)1} & \hat{k}_{(m-1)2} & \cdots & \hat{k}_{(m-1)(m-1)} & 0 \\ 0 & 0 & \cdots & 0 & 0 \end{bmatrix}$$

Now we remark that the matrix $\widehat{\mathbf{K}}$ also possesses the property of conservation of contacts. By this property, the elements in the last row, who have a non-zero sub-row above them, are determined and not free of choice. But now we remark that again by the property of symmetry, the last column can now be filled in, apart from the last element \widehat{k}_{mm} .

$$\widehat{\mathbf{K}} = \begin{bmatrix} \widehat{k}_{11} & \widehat{k}_{12} & \cdots & \widehat{k}_{1(m-1)} & \widehat{k}_{1m} \\ \widehat{k}_{21} & \widehat{k}_{22} & \cdots & \widehat{k}_{2(m-1)} & \widehat{k}_{2m} \\ \widehat{k}_{31} & \widehat{k}_{32} & \cdots & \widehat{k}_{3(m-1)} & \widehat{k}_{3m} \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ \widehat{k}_{(m-1)1} & \widehat{k}_{(m-1)2} & \cdots & \widehat{k}_{(m-1)(m-1)} & \widehat{k}_{(m-1)m} \\ \widehat{k}_{m1} & \widehat{k}_{m2} & \cdots & \widehat{k}_{m(m-1)} & 0 \end{bmatrix}$$

Lastly, we use the property of conservation of contacts to conclude that the last element \widehat{k}_{mm} is also determined.

As shown, we can create a new contact matrix $\widehat{\mathbf{K}}$ who fulfils the requirements, by choosing the lower diagonal matrix of dimension $(m-1)$, the other elements are determined by our choice of these elements. This means that there is a free choice in the elements \widehat{k}_{ij} for $1 \leq i \leq m-1$ and $1 \leq j \leq i$, as long as the total column sum does not exceed $\sum_{i=1}^m k_{ij}$. The total amount of free choices equals:

$$1 + 2 + \dots + m - 1 = \sum_{k=1}^{m-1} k = \frac{m(m-1)}{2},$$

where the second equality comes from the proven equality¹: $\sum_{k=1}^n k = \frac{k(k+1)}{2}$.

By carrying out the construction of the contact matrix $\widehat{\mathbf{K}}$, the matrix is well-defined and meets the requirements of the article.

When we are looking at the space of all possible values to choose the $\frac{m(m-1)}{2}$ variables from, we claim that, by the setup of our contact matrix $\widehat{\mathbf{K}}$, the space has a non-zero measure. This means that apart from the empty set, where we would have zero free choices in the $\frac{m(m-1)}{2}$ variables, the space contains at least one other set of possible values to choose from.

The existence of a non-zero measure in the space of possible variable values, implicates the contact matrix chosen by the process to meet the requirements to not be unique. We conclude the contact matrix meeting the requirements of the process, $\widehat{\mathbf{K}}$, is not unique.

¹This summation has been proven in the first year course: *bewijzen in de wiskunde*.

Chapter 5

Degree of change in the contact matrix.

In this chapter we will run through three example scenarios to show the change in the contact matrix due to the varying levels of participation. We show these examples to show the degree of change in the contact matrices.

We will also show the maximum eigenvalue of the matrix \mathbf{K} and of the matrix $\tilde{\mathbf{K}}$ under different reduction orders σ . We do this to show the degree of influence the ordering of the reduction has on the process of changing the matrix \mathbf{K} into $\tilde{\mathbf{K}}$ and ultimately on the results of the model.

In the following examples, an explanation will be given on the setup of the original contact matrix \mathbf{K} , the order of reductions σ and the change in the maximum eigenvalue. After the small block of text, there will be 6 heat maps, 1 corresponding to the original contact matrix \mathbf{K} and 5 corresponding to the contact matrices $\tilde{\mathbf{K}}$, made with different processes.

Throughout the three examples, we use the following contact matrix \mathbf{K} :

$$\mathbf{K} = \begin{bmatrix} 10 & 9 & 8 & 7 & 6 & 5 & 4 & 3 & 2 & 1 \\ 9 & 8 & 7 & 6 & 5 & 4 & 3 & 2 & 1 & 2 \\ 8 & 7 & 6 & 5 & 4 & 3 & 2 & 1 & 2 & 3 \\ 7 & 6 & 5 & 4 & 3 & 2 & 1 & 2 & 3 & 4 \\ 6 & 5 & 4 & 3 & 2 & 1 & 2 & 3 & 4 & 5 \\ 5 & 4 & 3 & 2 & 1 & 2 & 3 & 4 & 5 & 6 \\ 4 & 3 & 2 & 1 & 2 & 3 & 4 & 5 & 6 & 7 \\ 3 & 2 & 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 \\ 2 & 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 \\ 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 & 10 \end{bmatrix}$$

We only use one matrix \mathbf{K} to be able to compare between examples and we made the matrix symmetric for the ease of noticing changes in the heat maps. In the examples we will alter every other variable to show the points we want to make.

The six heat maps in every example will display different processes to change the contact matrix \mathbf{K} . We have numbered the processes for keeping track of the heat maps:

1. The first heat map will show the original contact matrix \mathbf{K} .
2. The second heat map will depict the contact matrix $\tilde{\mathbf{K}}$ made following the methods described in [2].
3. The third heat map will depict the contact matrix $\tilde{\mathbf{K}}$ but with the order of reductions reversed. So we start at the least reduced compartment and work our way to the most reduced compartment.
4. The fourth heat map will depict the contact matrix $\tilde{\mathbf{K}}$ but without ordering the reductions. We simply state that $\sigma(i) = i$ for all compartments.
5. The fifth heat map will depict the contact matrix $\tilde{\mathbf{K}}$ but with a randomly chosen order of reductions. This does not add anything, but is nice to implement.
6. The sixth and last heat map will depict the diagonal contact matrix $\tilde{\mathbf{K}}$, where every compartment now only interacts with itself. This is a very extreme measure and is only meant to be compared with.

The figure 5.1 gives an example heat map of the contact matrix \mathbf{K} .

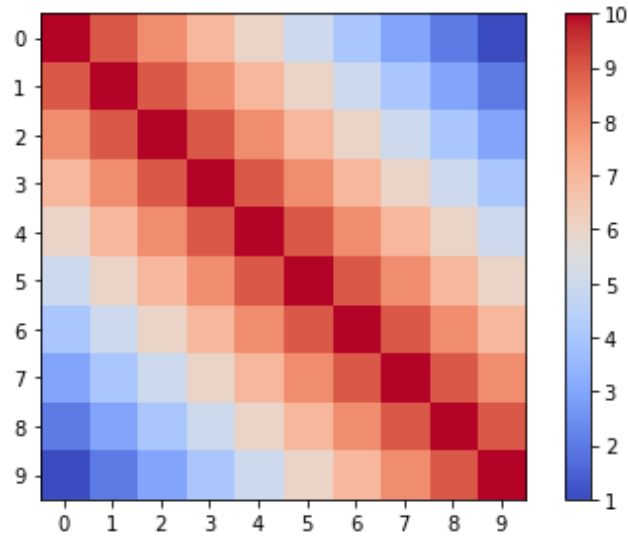


Figure 5.1: The heat map of the unchanged matrix \mathbf{K} .

The influence on the spectral radius.

When altering the contact matrix and reduction, we would like to be able to answer how these alterations influence the outcome of the model, i.e. the growth in the number of infected individuals over a set time interval n .

To do so, we remark that we will look at the spectral radius of the matrix \mathbf{A}_ℓ , since we have previously defined the reproduction number to be equal to:

$$R_e^\ell = R^\ell \cdot \rho(\mathbf{A}_\ell) = R^\ell \cdot \max \{|\lambda_1^\ell|, \dots, |\lambda_m^\ell|\}.$$

Therefore, when we alter the contact matrix \mathbf{K} or the set of reductions for the compartments, we can measure the influence of these changes by looking at the change in the maximum eigenvalue.

Because different contact matrices have different eigenvalues, we will look at the relative change in maximum eigenvalue:

$$d_r(i, j) = \frac{\rho(\mathbf{A}_i) - \rho(\mathbf{A}_j)}{\rho(\mathbf{A}_j)},$$

where the indices i and j denote the number for the method used to calculate the altered contact matrix $\tilde{\mathbf{K}}$.

Because we are looking at the changes in contact structure, do we choose to look at the change in maximum eigenvalue of the contact structure. This means that we will be looking at the relative change:

$$d_r(i, j) = \frac{\rho(\mathbf{S}_i \cdot \mathbf{K}_i \cdot \mathbf{I}_i) - \rho(\mathbf{S}_j \cdot \mathbf{K}_j \cdot \mathbf{I}_j)}{\rho(\mathbf{S}_j \cdot \mathbf{K}_j \cdot \mathbf{I}_j)}, \quad (5.1)$$

where for calculations sake, we have set every diagonal matrix \mathbf{S}_k and \mathbf{I}_k to be equal to the identity matrix.

Although we have set the matrices \mathbf{S}_k and \mathbf{I}_k to be equal to the identity matrix for calculation purposes, we would like to remind you that the variables within these matrices do matter. The individual contacted and the compartment of the individual that initiated the contact, does matter when looking at the chance of transmission.

5.1 Example 1.

In this example, we would like to show that when choosing every compartment reduction $\rho_{\sigma(j)}$ to be close to each other, then the contact matrix $\tilde{\mathbf{K}}$ will not differ much from the original matrix \mathbf{K} . In this example, we have taken the extreme and given every compartment the same reduction. By the continuity in reductions, we can say that when we are getting closer to equality in reduction for every compartment, then the contact matrix will change less and less.

Since the reduction depends on both attendance and relative reduction:

$$\rho_j := u_j \rho_{u_j} + v_j \rho_{v_j},$$

we have put all variable to the same value: $u_j = \frac{1}{2} = v_j$ and $\rho_{u_j} = \frac{1}{2} = \rho_{v_j}$, to obtain a homogeneous reduction across all compartments.

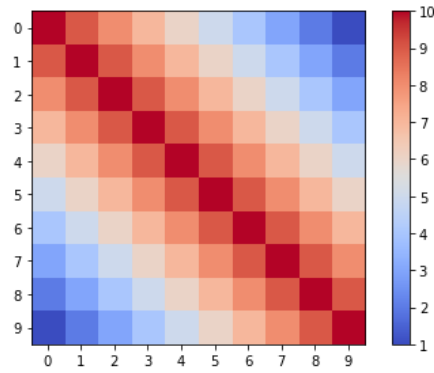


Figure 5.2: The heat map of the unchanged matrix \mathbf{K} .

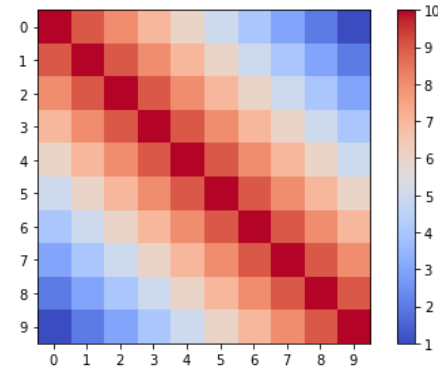


Figure 5.3: The heat map of the contact matrix $\tilde{\mathbf{K}}$ with process (2).

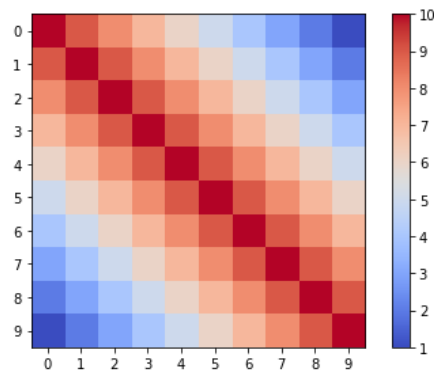


Figure 5.4: The heat map of the contact matrix $\tilde{\mathbf{K}}$ with process (3).

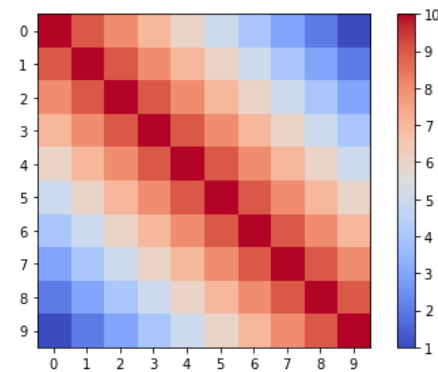


Figure 5.5: The heat map of the contact matrix $\tilde{\mathbf{K}}$ with process (4).

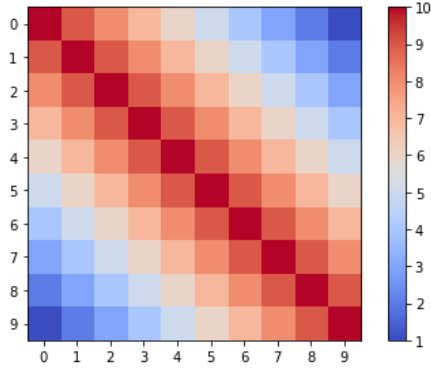


Figure 5.6: The heat map of the contact matrix $\tilde{\mathbf{K}}$ with process (5).

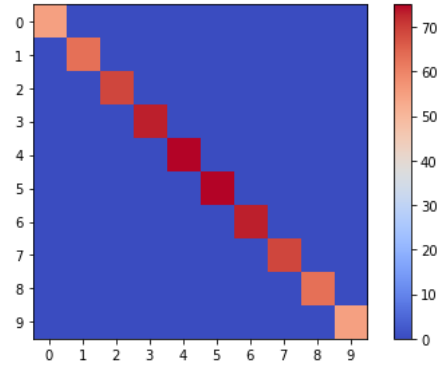


Figure 5.7: The heat map of the diagonal contact matrix $\tilde{\mathbf{K}}$.

Although it is hard to verify using different shades of colours, we have calculated all new contact matrices and have seen that, even with the random ordering, the contact matrix remains unchanged. Only when we forcefully put the total amount of contacts per compartment on the diagonal, will the contact matrix change.

We have put the relative change in maximum eigenvalue per process in the tabel 5.1:

Heat map number i :	$d_r(i, 2)$
1	0.0
2	0.0
3	0.0
4	0.0
5	0.0
6	0.10554

Table 5.1: The relative changes in maximum eigenvalue.

We remark that the relative change in eigenvalue corroborates the findings in the figure ?? up until figure 5.6. Apart from the diagonal matrix, the maximum eigenvalue of the contact matrix has not changed at all.

We conclude that whenever we have a homogeneous reduction across all compartments, that the model does not change much.

5.2 Example 2.

In this example, we want to show what happens when a high attendance compartment is being rejected due to a COVID certificate. As an example we can think of the 2G policy. We would like to remark that the example used is an extreme case.

We have taken the following composition for the compartments:

Let \mathbf{u} be the vector that contains all elements u_i denoting the fraction of individuals belonging to U_i . In this example we have chosen \mathbf{u} to be:

$$\mathbf{u} = \left(\frac{1}{5}, \frac{1}{4}, \frac{1}{3}, \frac{1}{2}, 1, 1, \frac{1}{2}, \frac{1}{3}, \frac{1}{4}, \frac{1}{5} \right)^T.$$

We remark that we can calculate the fraction of individuals belonging to V_i with the equation: $v_i = 1 - u_i$. We have set up the example in such a way that the population in some compartments consists largely of individuals of type U_i . Now, we have chosen the reduction for all compartments of type V_i to be homogeneous. We put $\rho_{v_i} = 0.9$, a small portion of the individuals stayed home as a precaution. The relative reduction for type U_i individuals are given by:

$$\rho_U = \left(1, 0.9, 0.6, 0.4, 0.01, 0.01, 0.4, 0.6, 0.8, 1 \right)^T.$$

Both vectors combined create the total reduction vector to be equal to:

$$P = (0.92, 0.9, 0.8, 0.65, 0.01, 0.01, 0.65, 0.8, 0.875)^T$$

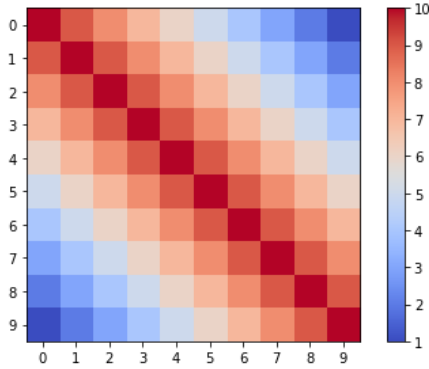


Figure 5.8: The heat map of the unchanged matrix \mathbf{K} .

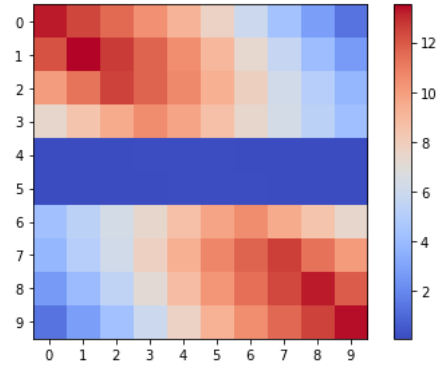


Figure 5.9: The heat map of the contact matrix $\tilde{\mathbf{K}}$ with process (2).

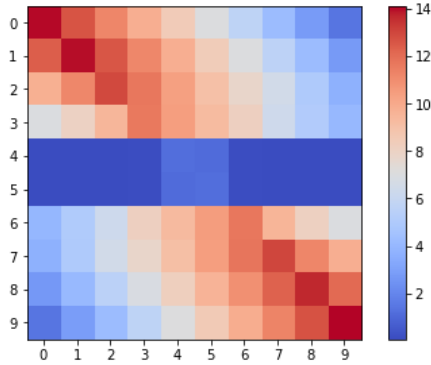


Figure 5.10: The heat map of the contact matrix $\tilde{\mathbf{K}}$ with process (3).

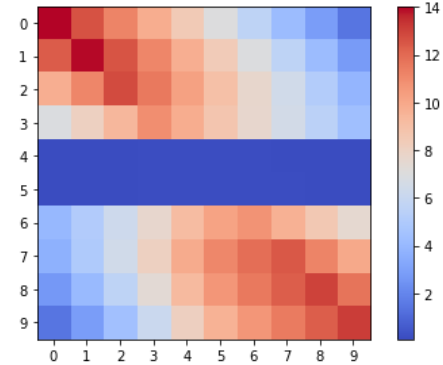


Figure 5.11: The heat map of the contact matrix $\tilde{\mathbf{K}}$ with process (4).

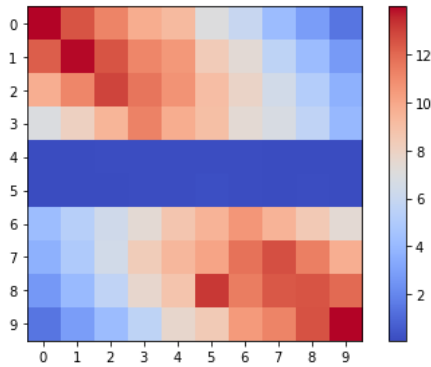


Figure 5.12: The heat map of the contact matrix $\tilde{\mathbf{K}}$ with process (5).

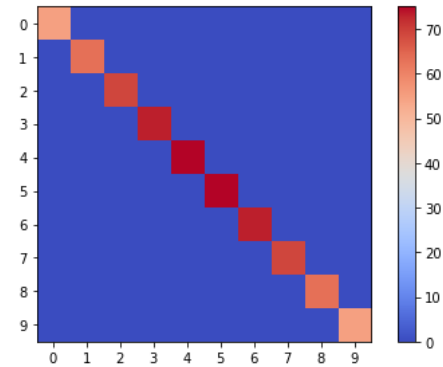


Figure 5.13: The heat map of the diagonal contact matrix $\tilde{\mathbf{K}}$.

Because of the way that we have set up this example, we can see that the contact matrix $\tilde{\mathbf{K}}$ differs quite a bit from the original contact matrix \mathbf{K} . This change is largely due to two previously highly attending compartments now being close to absent.

We see that the other compartments, in the absence of the two compartments, divide the contacts evenly, which means that the diagonal retains the most contacts. This is due to the symmetry in reductions. Apart from the two compartments, the contact matrix $\tilde{\mathbf{K}}$ mimics the same structure as the contact matrix \mathbf{K} .

We see that the process with reversed order of reduction has more contacts in the middle, and the random order of reductions has distributed the contacts off the diagonal. These are distinct differences compared to the other processes.

To be able to look at the change in outcome, we have put the relative change in maximum eigenvalue per process in the table 5.2:

Heat map number i :	$d_r(i, 2)$
1	0.04211
2	0.0
3	0.00042
4	0.00015
5	0.00015
6	0.15414

Table 5.2: The relative changes in maximum eigenvalue.

As we can see in 5.2, the relative change in maximum eigenvalue due to using the process is $d_r(1, 2) = 0.04211$. The reproduction number has gone down by about four percent. This is due to the fact that there are less people to infect other individuals or get infected.

Furthermore, we see that in this case, ordering does not make a big difference in the value for R_e . The biggest change, which we expected, is the extreme case of the diagonal contact matrix $\tilde{\mathbf{K}}$.

Although there is a big difference in the figures 5.7 up until 5.12, the outcome of the model has not changed much and does not seem to be heavily influenced by different orders of reduction.

5.3 Example 3.

In this example we will only look at individuals of type U_i , therefore setting the participation of all V_i individuals to zero. We do this to give an example of how the contacts of the contact matrix can migrate to one side, when the other side is absent. By only looking at the type that will be limited to participate, we exaggerate the effect seen in the heat maps.

Since the type V_i individuals are absent, the reduction is given by: $\rho_{\sigma(i)} = u_i \cdot \rho_{u_i}$. The vectors we have used are the vector with elements u_i for every compartment:

$$\mathbf{u} = \left(\frac{1}{5}, \frac{1}{4}, \frac{1}{3}, \frac{1}{2}, 1, 1, \frac{1}{2}, \frac{1}{3}, \frac{1}{4}, \frac{1}{5} \right)^T,$$

and the vector containing all absolute reductions ρ_{u_i} for all compartments:

$$\rho_U = \left(\frac{1}{15}, \frac{1}{14}, \frac{1}{13}, \frac{1}{12}, \frac{1}{11}, \frac{1}{10}, \frac{1}{9}, \frac{1}{8}, \frac{1}{7}, \frac{1}{6} \right)^T.$$

The vector of total reductions P consists of numbers containing many decimals. Therefore, the vectors \mathbf{u} and ρ_U are given, but we will not take up space on this page by writing the vector P in its entirety .

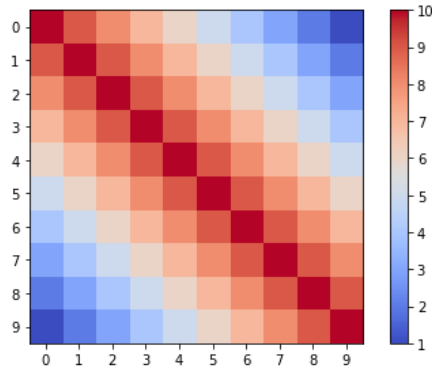


Figure 5.14: The heat map of the unchanged matrix \mathbf{K} .

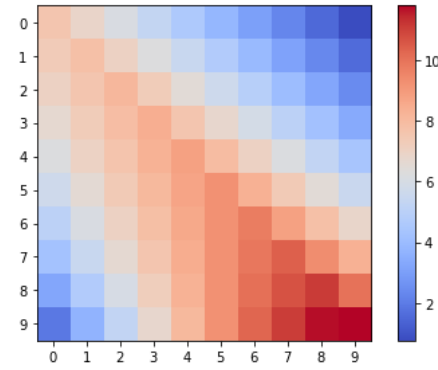


Figure 5.15: The heat map of the contact matrix $\tilde{\mathbf{K}}$ with process (2).

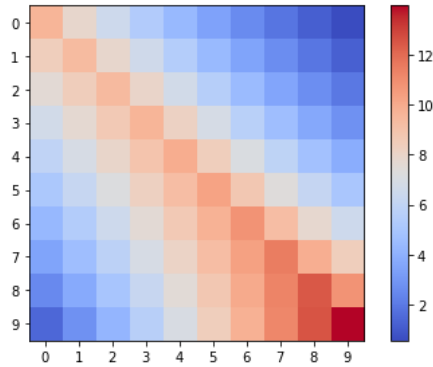


Figure 5.16: The heat map of the contact matrix $\tilde{\mathbf{K}}$ with process (3).

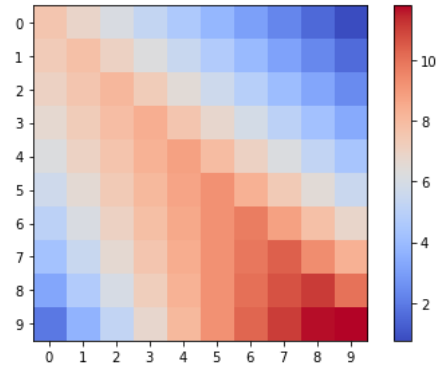


Figure 5.17: The heat map of the contact matrix $\tilde{\mathbf{K}}$ with process (4).

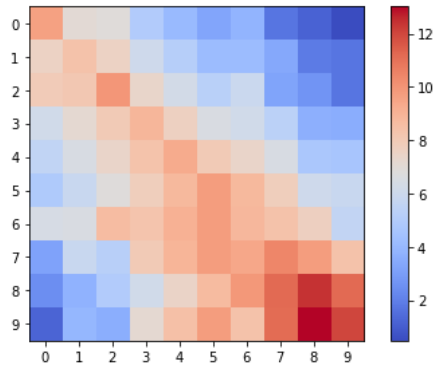


Figure 5.18: The heat map of the contact matrix $\tilde{\mathbf{K}}$ with process (5).

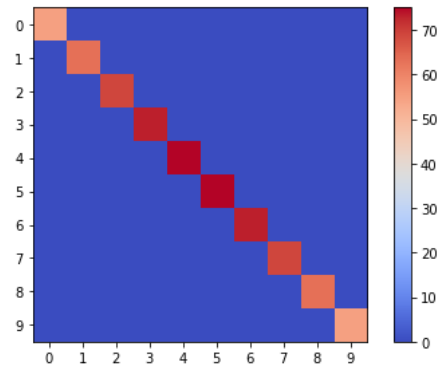


Figure 5.19: The heat map of the diagonal contact matrix $\tilde{\mathbf{K}}$.

As we can see in the figures 5.13 up until 5.18, the contacts have shifted to the bottom right, since the compartments in the top left have a low attendance and low type U representation. We see that these heat maps, and therefore the contact matrices $\tilde{\mathbf{K}}$ differ a lot from the original contact matrix \mathbf{K} .

We see that the random order heat map and the diagonal contact matrix $\tilde{\mathbf{K}}$ differ the most, which was expected from the diagonal contact matrix, but it seems that the random order has hit an order that spreads the form of the contact matrix more than what the other processes have done.

To be able to look at the change in outcome, we have put the relative change in maximum eigenvalue per process in the table 5.3:

Heat map number i :	$d_r(i, 2)$
1	0.00754
2	0.0
3	0.00079
4	0.0
5	0.00034
6	0.11394

Table 5.3: The relative changes in maximum eigenvalue.

As we can see in 5.3, the relative change in maximum eigenvalue due to using the process is $d_r(1, 2) = 0.00754$. The reproduction number has gone down by seven thousandths of a percent. This very small change is due to the fact that there are less people to infect other individuals or get infected.

As with Example 2, we see that ordering does not make a big difference in the value for R_e . The biggest change, which was also the biggest change in Example 1 and Example 2, is the extreme case of the diagonal contact matrix $\tilde{\mathbf{K}}$.

Even though there are quite a few big difference in the figures 5.13 up until 5.18, the outcome of the model changes by a tiny fraction of a percent. This Example does not seem to be heavily influenced by different orders of reduction.

5.4 Example 4.

In this section we would like to give an example where a different ordering of reductions fails to create a well-defined contact matrix $\tilde{\mathbf{K}}$.

We start with the 3×3 contact matrix \mathbf{K} and the reduction vector P :

$$\mathbf{K} = \begin{bmatrix} 0 & 10 & 10 \\ 10 & 0 & 0 \\ 10 & 0 & 0 \end{bmatrix}, \text{ and } P = \begin{bmatrix} 0.5 \\ 0 \\ 1 \end{bmatrix}.$$

Let us start the order of reductions with ρ_3 , so put $\sigma(1) = 3$.

We calculate the element $\tilde{k}_{1\sigma(1)} = \tilde{k}_{13}$:

$$\begin{aligned} \tilde{k}_{13} &= \frac{\rho_1 \cdot k_{13}}{\sum_{i=1}^m \rho_i k_{i3}} \cdot \sum_{i=1}^m k_{i3} \\ &= \frac{\frac{1}{2} \cdot 10}{\frac{1}{2} \cdot 10} \cdot 10 = 10 \end{aligned}$$

Now by symmetry of the altered contact matrix $\tilde{\mathbf{K}}$ we get the following equation:

$$\rho_3 \cdot N_3 \cdot \tilde{k}_{13} = \rho_1 \cdot N_1 \cdot \tilde{k}_{31},$$

which when substituting in all known values, becomes:

$$1 \cdot N_3 \cdot 10 = \frac{1}{2} \cdot N_1 \cdot \tilde{k}_{31}$$

From the unaltered contact matrix \mathbf{K} , we get the following ratio:

$$N_1 \cdot k_{31} = N_3 \cdot k_{13},$$

when filling in all known values, we get:

$$10 \cdot N_1 = 10 \cdot N_3.$$

Therefore, we can conclude that $N_1 = N_3$, and since the variables N_1 and N_3 do not change, when substituting in $N_1 = N_3$ into our first symmetry equation we get:

$$1 \cdot N_3 \cdot 10 = \frac{1}{2} \cdot N_3 \cdot \tilde{k}_{31}$$

This would imply that $\tilde{k}_{13} = 20$, taking all contacts of the compartment and leaving nothing for the element k_{31} .

We know if the matrix $\tilde{\mathbf{K}}$ is well-defined, then the element \tilde{k}_{31} is non-zero. So to get a well defined contact matrix, there will have to be more contacts than the compartments had previously. This is in contradiction with the preservation of contacts, and therefore we conclude that the process does not deliver a well-defined contact matrix which meets the requirements.

Chapter 6

Conclusion.

6.1 Answering the research question.

In this paper we have tried to answer our main research question:

How does the contact structure change due to measures based on a COVID certificate?

and have researched, explained, and built the model.

By investigating, proving, and testing certain properties of the model, we have gotten closer to giving an answer to the research question. The biggest factors that influence the degree of change in the contact matrix are the relative difference in attendance of a compartment in combination with the total reduction of a compartment. We have shown multiple different ways to alter the contact matrix and shift contacts towards a preferred direction.

When the relative difference in attendance differs greatly, we can expect the contact matrix to either migrate its contacts to one side of the matrix, or we get a couple of rows in the matrix where relatively little to no contact is had. When we increase the reduction in the compartments equally, the contact matrix does not change, but if we reduce the attendance unequally to one side of the matrix, it enforces the behaviour of contacts migrating to the opposite side of the matrix.

We have shown that a greatly differing contact matrix due to measures based on COVID certificates, does not implicate that the reproduction number is altered with the same degree of change.

We have furthermore shown that the process of altering the contact matrix \mathbf{K} into the contact matrix $\tilde{\mathbf{K}}$ is a well defined, continuous process which retains symmetry of contacts and conserves the total amount of contacts per compartment.

We have shown that there is not a unique contact matrix meeting the requirements of the process, and therefore although we have faith in the choices that are made in the process, we haven't proven that this method of altering the contact matrix is mathematically the best possible way.

We would like to conclude the thesis with the statement that the process defined is a mathematically sound and sturdy process, but if it is the best method of implementing COVID certificates has yet to be proven.

Appendix A

The computer model.

The computer model used to calculate results.

```
1 import numpy as np
2 import random as r
3 import matplotlib.pyplot as plt
4
5
6 def K_matrix(K: np.array, rho: np.array, case: int = 0) -> np.array
7 :
8     '''The datastructure used to compute the adjusted contact
9     matrix K_l.'''
10    k = np.zeros((len(K),len(K)))
11
12    '''The permutation sigma to order relative reduction in
13    participation.'''
14    if case == -1:
15        p = list(np.argsort(rho))[:, -1]
16    elif case == -2:
17        p = list(np.argsort(rho))
18        r.shuffle(p)
19    elif case == 2:
20        p = list(range(len(rho)))
21    else:
22        p = np.argsort(rho)
23
24    '''A list of column sums of the matrix K'''
25    sum_col_K = np.sum(K, axis = 0)
26
27    '''The calculations used on the rows and columns of the matrix
28    K.'''
29    if case == 1:
30        for idx in range(len(K)):
31            k[p[idx]][p[idx]] = sum_col_K[p[idx]]
32
33        '''Return the calculated matrix K_l.'''
34        return k
35
36    for idx in range(len(rho)):
37
38        sum_col_k = np.sum(k, axis = 0)
39
40        sum_rho = sum([rho[p[kdx]] * K[p[kdx]][p[idx]]
41                      for kdx in range(idx, len(rho))])
```

```

39     for jdx in range(idx - 1, len(K)):
40         if k[p[jdx]][p[idx]] == 0 and k[p[idx]][p[jdx]] == 0:
41             k[p[jdx]][p[idx]] = rho[p[jdx]] * K[p[jdx]][p[idx]]
42     *           \
43     p[idx]]) / \
44                                     (sum_col_K[p[idx]] - sum_col_k[
45                                     sum_rho
46     [idx]] * \
47                                     k[p[idx]][p[jdx]] = k[p[jdx]][p[idx]] / K[p[jdx]][p
48                                     rho[p[idx]] / rho[p[jdx]] *
49                                     \
50                                     K[p[idx]][p[jdx]]
51     elif rho[p[jdx]] == 0:
52         k[p[jdx]][p[idx]] = 0
53         k[p[idx]][p[jdx]] = 0
54
55     '''Return the calculated matrix K_l.'''
56     return k

```

Listing A.1: The code used to adjust contactmatrix \mathbf{K} .

```

1
2 def participation(frac: np.matrix, rho: np.matrix) -> np.matrix:
3     '''Calculates the relative attendance of an age group i at
4     location l.'''
5     return [frac[idx] * rho[idx][0] + (1- frac[idx]) * rho[idx][1]
6             for idx in range(len(frac))]
7
8 def check_sym(K: np.array, N: np.array) -> bool:
9     '''Checks if the contactstructure is symmetric.'''
10    for idx in range(len(K)):
11        for jdx in range(len(K)):
12            if round(N[idx] * K[jdx][idx], 5) != round(N[jdx] * K[
13            idx][jdx], 5):
14                return False
15    return True
16
17 def check_cont(K: np.array, k: np.array) -> bool:
18     '''Checks if the contactstructure is symmetric.'''
19     print(np.sum(K, axis = 0), np.sum(k, axis = 0))
20     if np.array_equal(np.sum(K, axis = 0), np.sum(k, axis = 0)):
21         return True
22     return False

```

Listing A.2: The helper functions used to check and calculate the model.

```

1  '''Workspace'''
2  K = np.array([
3      [10., 9., 8., 7., 6., 5., 4., 3., 2., 1.],
4      [9., 10., 9., 8., 7., 6., 5., 4., 3., 2.],
5      [8., 9., 10., 9., 8., 7., 6., 5., 4., 3.],
6      [7., 8., 9., 10., 9., 8., 7., 6., 5., 4.],
7      [6., 7., 8., 9., 10., 9., 8., 7., 6., 5.],
8      [5., 6., 7., 8., 9., 10., 9., 8., 7., 6.],
9      [4., 5., 6., 7., 8., 9., 10., 9., 8., 7.],
10     [3., 4., 5., 6., 7., 8., 9., 10., 9., 8.],
11     [2., 3., 4., 5., 6., 7., 8., 9., 10., 9.],
12     [1., 2., 3., 4., 5., 6., 7., 8., 9., 10.],
13 ])
14
15 '''Vector with elements - fraction agegroup i is U_i.'''
16 frac_1 = np.array([1/2 for row in range(len(K))])
17 frac_2 = np.array([1/5, 1/4, 1/3, 1/2, 1, 1, 1/2, 1/3, 1/4, 1/5])
18 frac_3 = np.array([1 for row in range(len(K))])
19
20 '''Vector with (u,v)_i; u_i,v_i = participation level of U_i, V_i
21     respectively.'''
22 rho_1 = np.array([(1/2, 1/2) for row in range(len(K))])
23 rho_2 = np.array([(1,.9), (.9,.9), (.6,.9), (.4,.9), (0.01,.9),
24                 (0.01,.9), (.4,.9), (.6,.9), (.8,.9), (1,.9)])
25 rho_3 = np.array([(1/15,0), (1/14,0), (1/13,0), (1/12,0), (1/11,0),
26                 (1/10,0), (1/9,0), (1/8,0), (1/7,0), (1/6,0)])
27
28
29 '''Vector with rho_i for all agegroups i.'''
30 par_1 = participation(frac_1, rho_1)
31 par_2 = participation(frac_2, rho_2)
32 par_3 = participation(frac_3, rho_3)
33
34 Par = [par_1, par_2, par_3]
35
36 '''Vector N with N_i the amount of individuals of agegroup i.'''
37 N = np.array([10000 for indice in range(len(K))])
38 N_1 = N * par_1
39 N_2 = N * par_2
40 N_3 = N * par_3
41
42 '''Calculating K_2, the adjusted contact matrix.'''
43 for par in Par:
44     k_1 = K_matrix(K, par, 0)
45     k_2 = K_matrix(K, par, -1)
46     k_3 = K_matrix(K, par, 1)
47     k_4 = K_matrix(K, par, -2)
48     k_5 = K_matrix(K, par, 2)
49
50     '''The maximum eigenvalue for both the matrix K as matrix k.'''
51     lambda_K = max(np.linalg.eig(K)[0])
52     lambda_k_1 = max(np.linalg.eig(k_1)[0])
53     lambda_k_2 = max(np.linalg.eig(k_2)[0])
54     lambda_k_3 = max(np.linalg.eig(k_3)[0])
55     lambda_k_4 = max(np.linalg.eig(k_4)[0])
56     lambda_k_5 = max(np.linalg.eig(k_5)[0])

```

Listing A.3: The code used to adjust contactmatrix **K**.

```

1  '''Print statements to test output.'''
2  print(f"This is situation: {Par.index(par) + 1}")
3  print("\n")
4  # print(f"The initial matrix K:\n{K}")
5  print(f"Check if symmetric and contacts:\
6      {check_sym(K, N_1)}, {check_cont(K, K)}")
7  print(f"Max eigenvalue matrix K: {lambda_K}")
8  print("\n")
9
10 # print(f"The altered matrix k_1:\n{k_1}")
11 print(f"Check if symmetric and contacts:\
12     {check_sym(k_1, N_2)}, {check_cont(K, k_1)}")
13 print(f"Max eigenvalue matrix k_1: {lambda_k_1}")
14 print(f"Relative change in max eigenvalue:\
15     {abs(lambda_k_1 - lambda_K)/lambda_K}")
16 print("\n")
17
18 # print(f"The altered matrix k_2:\n{k_2}")
19 print(f"Check if symmetric and contacts:\
20     {check_sym(k_2, N_2)}, {check_cont(K, k_2)}")
21 print(f"Max eigenvalue matrix k_2: {lambda_k_2}")
22 print(f"Relative change in max eigenvalue:\
23     {abs(lambda_k_2 - lambda_k_1)/lambda_k_1}")
24 print("\n")
25
26 # print(f"The altered matrix k_3:\n{k_3}")
27 print(f"Check if symmetric and contacts:\
28     {check_sym(k_3, N_2)}, {check_cont(K, k_3)}")
29 print(f"Max eigenvalue matrix k_3: {lambda_k_3}")
30 print(f"Relative change in max eigenvalue:\
31     {abs(lambda_k_3 - lambda_k_1)/lambda_k_1}")
32 print("\n")
33
34 # print(f"The altered matrix k_4:\n{k_4}")
35 print(f"Check if symmetric and contacts:\
36     {check_sym(k_4, N_2)}, {check_cont(K, k_4)}")
37 print(f"Max eigenvalue matrix k_4: {lambda_k_4}")
38 print(f"Relative change in max eigenvalue:\
39     {abs(lambda_k_4 - lambda_k_1)/lambda_k_1}")
40 print("\n")
41
42 # print(f"The altered matrix k_5:\n{k_5}")
43 print(f"Check if symmetric and contacts:\
44     {check_sym(k_5, N_2)}, {check_cont(K, k_5)}")
45 print(f"Max eigenvalue matrix k_5: {lambda_k_5}")
46 print(f"Relative change in max eigenvalue:\
47     {abs(lambda_k_5 - lambda_k_1)/lambda_k_1}")
48 print("\n")

```

Listing A.4: The print statements to get the info out of the model.

```

1  for matrix in [K, k_1, k_2, k_3, k_4, k_5]:
2      fig, ax = plt.subplots()
3      im = ax.imshow(matrix, "coolwarm")
4
5      ax.set_xticks(np.arange(len(K)))
6      ax.set_yticks(np.arange(len(K)))
7
8      plt.colorbar(im)
9      fig.tight_layout()
10     plt.show()

```

Listing A.5: The code to display the heatmaps used in the examples.

Appendix B

Bibliography

- [1] Diekmann, O., Heesterbeek, H., & Britton, T. (2012). *Mathematical tools for understanding infectious disease dynamics*. Princeton University Press.
- [2] Bootsma, M.C.J., et al. (2022). *The impact of different strategies using a corona ticket on the reproduction number*.
- [3] The dedicated COVID-19 government websites used to spread information to the Dutch population. <https://www.rivm.nl/coronavirus-covid-19>, <https://g.co/kgs/FUhkme>
- [4] Brink, T., Brinks, L., van der Have, N., Kanis, M. (2021). *Het modelleren van infectieziekten: De invloed van mondkapjes in collegezalen*.
- [5] Y. A. Kuznetsov, H. Hanßmann (2021). *Basis Differentiaalvergelijkingen*.
- [6] M. A. Holmes (2019). *Introduction to the Foundations of Applied Mathematics*. (2nd edition). Springer
- [7] S. Khalilian, et al. (2010). *Designed for failure: A critique of the Common Fisheries Policy of the European Union*. Elsevier Ltd. https://www.researchgate.net/publication/222162673_Designed_for_Failure_A_Critique_of_the_Common_Fisheries_Policy_of_the_European_Union
- [8] The Matplotlib development team (2012-2022) *The Matplotlib Documentation on creating heatmaps*. https://matplotlib.org/3.4.3/gallery/images_contours_and_fields/image_annotated_heatmap.html#sphx-glr-gallery-images-contours-and-fields-image-annotated-heatmap-py
- [9] Prem K, Cook AR, Jit M (2017) *Projecting social contact matrices in 152 countries using contact surveys and demographic data*. PLOS Computational Biology 13(9): e1005697. <https://doi.org/10.1371/journal.pcbi.1005697>