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A queuing model with reneging to address disparity between patient bloodtypes

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A queuing model with reneging to address disparity between patient bloodtypes

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1 Introduction

This thesis discusses a comprehensive queuing model tailored specifically for deceased-donor organ transplantation, integrating the dynamics of patient reneging into the analysis. The model will be used to find an optimal way to allow for restricted cross transplantation resulting in more equity concerning the waiting times of different patient groups.

1.1 Organ transplantation [17]

Often, health issues are caused by a damaged or dysfunctional organ. Sometimes, a patient can be helped by an organ transplantation. An organ transplantation occurs when a recipient's (damaged) organ is replaced by the (healthy) organ of someone else, the organ donor. Next to organs, it is also possible to donate certain tissues. In most cases, the organ transplantation will only occur after the donor has (recently) passed away. Living organ donation is however possible for kidney donation and part of the liver. For these types of organs, it is possible for the donor to stay alive without sacrificing quality of life. Living donation yields the opportunity for patients in need of an organ, to look for a suitable donor. Deceased organ transplantation, the kind of organ transplantation that is initiated after the donor has passed away, can be done only under certain conditions. For the quality and success rate of organ transplantation, the organ must receive enough oxygen, even after the donor has passed away. This is possible to achieve when a donor passes away in a hospital. The transplantation also has to be performed rather quickly, since the quality of organs decreases rapidly after death.
A deceased donor has to be declared dead by a medical professional before the transplantation can take place. Most commonly, the doctor identifies a cardiac arrest meaning the blood of the donor has stopped circulating. It can also occur that a donor is declared brain dead before the occurrence of cardiac arrest. This happens when all the brain functions have stopped and will not recover. In this case, the heart of the donor is still beating, providing the organs with oxygen-rich blood until the very last moment. It is not hard to understand that therefore, the success rate of organ transplantation from these types of donors is higher than from donors that passed after cardiac arrest.
A transplantation will not be carried out without some form of consent. Like living donors who can give their consent, deceased donors can also consent to transplantation if they have registered their consent to be a donor during their lifetime. This is documented in a donor register. No organs or tissues will be transplanted if the deceased has objected against organ transplantation in the donor register. If someone has not explicitly stated their wishes before death, consent can be given by close relatives of the deceased. After checking for the donor's consent, the medical professionals will proceed by evaluating if and which organs of the deceased are suitable for transplantation. This information will be shared with an organization that is responsible for matching donor organs with a suitable patient in need of one. In Europe, this is handled by EuroPlant. The donor and the receiving patient have to be compatible to diminish the effects of repulsion. The compatibility's of patient-donor pairs forms an important aspect of this project and will be discussed more deeply now.

1.2 Blood types and their compatibilities [19]

Not all blood is created equal. Key to a successful organ transplantation is the compatibility of the patient-donor pair. A bad match between patient and donor results in adverse symptoms which lead to health complications or death. The most important factor for compatibility is blood type. We start with the basics by explaining different blood types. There are many systems dividing patients into blood-type groups. One of the most well-known divisions is the ABO system. One's ABO blood type is determined by the structure on the outside of your red blood cells which are called antigens. In the ABO system, there are four different options. Patients with blood group A have the A antigen on their red blood cells, patients with blood group B have the B-antigen instead, and blood group AB corresponds to the presence of both A and B antigens. The last possibility, blood group O, stands for the absence of these antigens. Our bodies will reject antigens that are unfamiliar to us. Therefore, in the ABO system patients can always receive blood from the same type as their own. In addition, cross-transplantation (donor and receiver have a different

blood type) is also possible. A patient with blood group AB can receive blood from all other types since blood will not introduce new antigens. However, an AB donor can only donate to other AB patients. With the same reasoning, a blood group O patient can donate to all blood types, but receive only from its own type. The same rules apply to organ and tissue transplantation. The possibilities of cross transplantation are summarized in Figure 1.

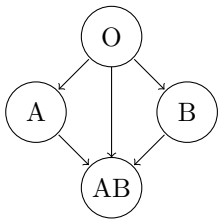

Figure 1: Blood type compatibilities between donor and receiver. The direction of the arrow implies the direction of donation. Identical blood groups are always compatible.

While the ABO blood group system remains the most well-known, several other blood group systems play a role in determining compatibility. The Rh system is the second most important blood group system after ABO. It classifies blood based on the presence or absence of the Rh antigen, also known as Rh factor or D antigen. Blood is categorized as Rh-positive if the antigen is present and Rh-negative if absent. Incompatibility occurs when Rh-negative individuals receive Rh-positive blood, leading to potential immune responses. The Rh system is often combined with the ABO system, which leads to the broadly used appellation A-positive or A-negative for, for example, ABO group A combined with Rh-positivity or Rh-negativity, respectively. Moreover, many more blood-group divisions exist.
Keep in mind that matching a patient with a donor when they have a theoretically compatible blood group is not a guarantee for a successful transplantation. One has to consider that there will always be a risk of adverse reactions in such medical procedures. You can imagine how much more complicated a figure similar to Figure 1 would look if we would consider the Rh factor for all four ABO blood groups and try to display all the blood group compatibilities in such a graph. Let alone, adding other patient divisions or compatibility risks. Therefore, to construct a comprehensible model we will consider the idealized case of ABO-compatibility only.
In the case of organ transplantation, it is important that the patient can receive the blood type of the donor. When considering the ABO blood type system, we speak about an ABO identical transplantation when the blood group of donor and recipient are equal. Moreover, a cross-transplantation occurs when the donor and patient have a different ABO blood type but are still compatible with each other. Lastly, ABO-incompatible transplantation also exists with the help of immunosuppressant medication. This is less common and will not be discussed here.
The occurrence of the different blood types in the Netherlands is summarized in Table 1. Types O and A are both very common and their prevelence is very similar. Blood types B and AB are more rare. Different countries have different distributions. The distribution in the Netherlands is roughly the same as for other Western countries such as Canada and the States. However, blood type B is a lot more common in some other countries such as many Asian countries [10]. In this thesis, we will make use of the Dutch blood type distribution. We expect that the conclusions of this thesis can be applied to countries with a similar blood type distribution. Next to that, the same methods can be used to reach a conclusion for countries that have a blood type distribution that is more distinct from the Dutch distribution.

blood type	prevalence
O	45%
A	43%
B	9%
AB	3%

Table 1: ABO-blood type distribution of the Netherlands, source: Sanquin [19]

1.3 The waiting list

When a patient has a certain condition that could benefit from a donor organ then they can decide together with their doctor if they want to enter a waiting list for organ transplantation. The available organs will be given to the patients on this waiting list. This is not an ordinary waiting list but has some very dynamic properties because it often occurs that people renege from the list due to either a decrease in health status or death or an increase in health to the point that a transplant is no longer needed. The position of a patient on the waiting list is often determined by their medical urgency, blood type, and other health factors. Equity in organ allocation is not easy to achieve and in real life, waiting time disparities are observed frequently. The goal of this thesis is to address equity in waiting times between different blood type groups and to propose a solution for this in the shape of a queuing model with reneging that achieves more equity in terms of expected waiting time and the probability of acquiring a donor organ for the different blood type groups.

1.4 The bloodtype-O problem

Donors of blood type O, especially O-minus, can be seen as universal donors: they can donate to all other ABO blood types. This makes an O-type donor very valuable. However, type-O patients can only receive from type-O donors. If too many type-O organs are donated to patients with blood groups A, B, or AB, then the average waiting time of the type-O patients will rise since they can not be supplemented with organs from other blood types. This leads to an increased waiting time for type O patients and a build-up of O patients on the waiting list. We call this phenomenon the blood type O problem and it is a cause of disparity between the different patient (blood)groups that often occurs in organ transplantation dynamics. This problem is mentioned in multiple scientific papers, such as [20], [13], and [9]. Glander describes the bloodgroup O problem in his 2010 paper in the following way: "The export of blood group O donor kidneys to other blood groups leads to longer waiting times, to a higher death rate and to accumulation of blood group O patients on the waiting list, which will further aggravate the problem in the future.". According to data provided by the Dutch transplantation foundation NTS, we see that on the 31st of December 2021, 55.4% of Dutch patients waiting for a heart transplant are of blood group O, as well as 55.8% of Dutch patients waiting for a lung transplant and 52.8% of patients waiting for a kidney transplant [16]. That is more than half of the patients and quite a bit more than the 45% that we would expect according to the prevalence in the whole population (see Table 1). The blood group O problem is a real-world phenomenon in organ transplantation that is observed in many places worldwide. It is an interesting problem, and in this thesis, we try to solve it in a fair way without penalizing other patient groups.

2 Literature research

We will now discuss a literature overview of organ transplantation modeling, starting with a medical approach and continuing from an applied mathematics/modeling perspective. We will take a closer look at how queuing theory can be used to model the waiting list dynamics and zoom in on the implementation of patient reneging in such models.

2.1 Medical history [4]

The concept of organ transplantation dates back to ancient times, with myths and legends suggesting early attempts to transplant body parts. However, modern organ transplantation began in the 20th century when scientific milestones and medical breakthroughs made organ transplantation actually possible. Not only are surgical skills and knowledge needed to make transplantation a success, but also the right knowledge about immunology. The first successful organ transplantation happened in 1954 when Dr. Joseph Murray performed a kidney transplantation between identical twins, mitigating the risks of adverse reactions. The procedure was a success and paved the way for further advancements in the field [22]. Murray won a Nobel prize in 1990 for his achievement [14] and is still seen as a pioneer in his field. Transplantations have been attempted before, but due to the lack of knowledge and development of immunosuppressant medication, they did not succeed. So while in the mid-20th century surgical advancements had matured enough to allow for organ transplantation to be performed, it was only when more developments were made in the field of

immunology and especially the development of immune represents that organ transplantation became a more used and wider applicable procedure. In the following decades after Murray's success, the medical world succeeded in extending the list of transplantable organs, including the heart, liver, pancreas, and lungs. In 1967, Dr. Christiaan Barnard performed the first successful human heart transplant [6]. Nowadays, organ transplantation is a widely used method to improve and extend the lives of those who suffer from end-stage organ failure. The use of donor organs has been extended to living donors and deceased donors after cardiac arrest.

While the procedure can be a great help to patients in need, the waiting time can be long and demoralizing as organ shortage has been a huge issue ever since the rise of the treatment. A few medical advancements are also made to solve or ease the issue of organ shortage. This can be done by treatments that keep patients as healthy as possible while they wait for a transplant, such as dialysis for patients with kidney failure, and artificial hearts for patients with heart failure. However, in the future, we will maybe even see artificially grown human tissue used for transplantation to solve organ shortage, as this is an active field of research, see [23]. While very promising, 'tissue engineering' as it is called, is still in its infancy. Stem cells can be used to grow human (or animal) tissues. It is currently possible to grow so called 'organoids' from stem cells, which can be seen as smaller and simplified versions of organs: they contain the same cells but lack the complicated structure of a complete organ. It will probably take a long time until organs can be replicated including their complicated structure. However, the potential uses of such simpler organoids look very promising as well. Currently, no organoids have been used on humans but animal tests on mice have shown promising results [8]. As a suggested further reading on this topic, I refer to [8].

Every organ or tissue that is transplanted currently comes from a human body, making it such a scarce and valuable resource. While organ transplantation has saved and improved countless lives since its debut, it also has to deal with long waiting lists and disparity concerns. As we have just listed the role of medical research in tackling these problems, we must agree that the medical world can not solve all of these issues (yet). This is where the importance of operation research and applied mathematics becomes apparent which we will further discuss now.

2.2 Mathematical methods in organ transplantation modeling

Mathematical modeling can be a tool to make the utmost use of the available donor organs. The transplantation process can be seen as a complicated example of a resource allocation problem in operation research, where different allocation methods can be investigated and evaluated in terms of efficiency and equity concerns. Since organ allocation has a lot of factors that add complexity to the challenges in this field, mathematical modeling is a useful tool for evaluating different allocation policies. Especially for healthcare, where real lives are at stake, it is helpful to analyze the best solutions to challenges without first having to test this in real life. The challenges in organ allocation are multifaceted. It is nearly impossible to take into account all facets of the problem, therefore you often see that research papers in the field concentrate on one or a few facets of the problem. Some models try to add as much realism as possible by adding as much detail as possible. A downside of this is that these models will be harder to analyze.

With facing challenges in organ transplantation modeling, one can have multiple approaches such as a deterministic model, or a stochastic model (often a queuing model). It is also possible to use simulation or to analyze real-world data on organ transplantation. The primary goal of all of these models is to enhance the fairness and efficiency of organ distribution systems, ensuring equitable access for patients while optimizing the use of available organs. Equity and efficiency of certain allocation processes can be evaluated by means of certain performance measures. Measures of equity can for example be the patient waiting times or the probability of receiving a transplant in the end. Similarly, measures of efficiency are e.g. the patient survival probability and the quality-adjusted life expectancy, as suggested by Zenios [25]. In this thesis, the focus will be on equity.

Simulation can be a useful tool in stochastic models in which the underlying model is so complicated that theoretical expressions of the values of interest are unheard of. The approach is vastly different from theoretical analysis, which produces a more general expression for the values of interest, either implicit or explicit, where any value of the initial parameters can be filled in to quickly obtain the results. This is not possible for a simulation model, as any change of initial parameters requires you to run the entire simulation again. A simulation always needs numerical values for all the input parameters before it can be performed. These

input variables are often based on real-world data but sometimes a variety of different parameter choices are performed to see how responsive the output is to the initial conditions.
Stochastic models often make use of the Monte Carlo method which is a way to simulate models with uncertainty. Since organ transplantation deals with a lot of uncertainty, this is a suitable method for the topic. Take a look at for example this paper by Zenios [25] which uses Monte Carlo simulation to compare different allocation policies in deceased kidney donation. The paper evaluates four different allocation approaches which are compared by performing a long-term (10-year) simulation to predict the outcome of each allocation method. The performance of the different methods is evaluated according to both equity and efficiency measures. Zenios divides patients not only by blood type but also by race, gender, panel reactivity, body surface area, and tissue type. He lets patients arrive according to a Poisson process. Once a patient is matched with a donor, the patient can exit the system by a successful transplant, but when the transplant does not succeed it can either result in death or in case of survival: relisting or not relisting. These outcomes happen with a certain probability. The Monte Carlo simulation chooses one of these outcomes with a certain probability for each experiment. Then, the experiment is performed many times over, and one can take a long-time average from the simulated data to determine an approximation of the performance measures. Worth noticing is that in the research of Zenios [25], there is no clearly better policy. It seems to be that nearly all improvements in performance measures come at a cost. A paper by Wujciak [24], who also did a computer simulation on cadaveric kidney allocation, confirms this by calling the objective to attain both a high transplant probability *and* a low waiting time, contradictory. Wujciak uses different simulation methods namely dynamic simulation and steady-state simulation, and focuses on mismatch probabilities. A mismatched organ can have great consequences, therefore it is very useful to apply mathematical graph theory and matching to this field. To further illustrate how many mathematical methods can be applied to the topic, here is a paper by Rouhani [18] that uses convex optimization to design an organ transplant network. We will, however, focus on stochastic processes in this thesis and in particular on queuing theory.

Queuing theory

Queuing theory is the mathematical study of queues as a stochastic process. A very basic example of a queuing model that is still very useful for organ transplantation modeling is the single-channel queue, such as the well-studied M/M/1 queue. It is a system with arriving customers and just one server. Applied to organ transplantation this can resemble a waiting list of patients (the queue) where service is attained when a donor organ is received. One step further from the single-channel model is a multi-channel model. This is a queuing system with multiple servers. They can be homogeneous meaning all the servers are identical (e.g. two processors computing tasks at the same speed), or heterogeneous meaning that the servers can have different characteristics (e.g. donor organs of rare blood type AB arrive less frequently than organs of type O). Next to that, it is possible to implement other characteristics into a queuing model, such as impatience.

Queuing theory and reneging

In queuing theory, it is possible to implement aspects of impatience. For example, the impatience of customers. Customers can leave a queue if they have to wait too long for service. However, for healthcare applications, impatience can also be in the form of patients with deteriorating health or patients who pass away. This is very relevant for organ transplant waiting list modeling.
There are multiple ways how impatience can be implemented in queuing models but the two most used ways are the use of reneging or balking. Balking is the phenomenon where a potential customer decides not to enter the queue (for example when the queue is perceived as too long, which can be modeled by a queue exceeding a certain length). Reneging is the phenomenon of customers entering the queue, but leaving it before they receive service. Reneging resembles patient mortality on the transplant waiting list. Therefore we take a closer look at literature that uses reneging in queuing theory models.
We start off with a paper that builds on the basic idea of a single-channel queue. A paper by Robert E. Stanford (1979) [21] extends the single-channel model in such a way that it now includes reneging. It discusses a GI/G/1 queuing system where customers renege after a random time. This paper finds expressions for the probability of reneging, and the waiting time distribution for the waiting time in the queue. It also finds expressions for the steady state probability of the number of customers in the queue, and some other values of interest. It extends to the paper by Ancker and Gafarian called "Queuing with impatient customers

who leave at random" [7], who assume exponentially distributed times. These single-channel examples are quite useful. If we however want to expand the uses of the queuing model, we can not skip the case of multi-channel queues. A good example in literature of a multi-channel queue with reneging is found in another paper by Ancker and Gafarian [2] which discusses queuing with reneging and multiple heterogeneous servers. In this paper, they expand on their previous paper by introducing multiple servers. This paper also includes balking, in the form of modeling the queue in such a way that the queue length is bounded from above. At the end, some special cases are discussed such as an unbounded queue length, which is relevant if you are interested in the case where we have reneging and no balking. It also looks at the case with no reneging, only balking. The paper extends their previous single-channel model with some extra expressions for performance measures. This paper talks about heterogeneous channels, meaning that the parameters of each channel are distinct. In the discussion, they talk about changing the model in such a way that it deals with homogeneous servers. If the average of the parameters of the heterogeneous servers is taken as the parameter of the homogeneous server, then a very similar system is obtained since the waiting time distribution will not change. Their paper further elaborates on the difference between homogeneous and inhomogeneous channels.
Our goal is to design our own queuing model with reneging applied to organ transplantation. We can use the methods from the above-mentioned papers to calculate the performance measures of our own model. Furthermore, it is helpful to look at literature that has already combined queuing theory with organ transplantation.

Queuing theory applied to organ transplantation

This thesis draws inspiration from a paper published in 2014 by David A. Stanford [20]. This publication addresses the blood group O problem (see section 1.4) in an interesting way. It makes use of queuing theory. The author starts by explaining the waiting time disparities between patient (blood) groups in Canada and shows how patients of blood group O are negatively affected by the blood group O problem. It refers to a few other papers that also discuss the blood group O problem. At the time that this paper was released, Canada used an ABO identical allocation policy for allocating deceased donor kidneys and routine liver transplants. Stanley then mentions examples of other countries that use ABO-compatible allocation rules, such as Ireland, leading to the blood group O problem. But he notes that the Canadian model leads to another source of waiting time disparity which has to do with the fact that patients of rare blood types have to wait longer under this allocation rule. Therefore further investigation is needed on these allocation methods and their potential disparities. Stanley does this by first investigating a mathematical model that handles ABO identical transplantations. He then assesses the expected waiting times for the patients of different blood types under this policy and quantifies the disparities between patient groups. He then proposes a second model in which restricted cross-transplantation is allowed. This second model is designed in such a way that he can tweak the amount of allowed cross-transplantations such that the expected waiting times between certain patient groups get equalized. His approach consists of splitting up the blood groups into two groups: O and B patients and donors are grouped together, and A and AB type donors are grouped together. This allows him to restrict the amount of O-type donor organs that get cross-transplantated as much as possible while providing patients of rare blood groups with some extra donors. The mathematical method he uses is queuing theory. He constructs something that he calls the Array of Idealized Transplant Queues (AITQ). This refers to the simplification he made to a real-life transplantation waiting list to enable him to construct his model. What makes the queue idealized is the fact that not all the aspects affecting the transplantation process in real life are considered since he made some simplifying assumptions. He then constructs the model such that patients are placed on the waiting list according to a renewal process. Then, patients are served according to a first-come first-serve basis. For his first model, he uses one server and one queue for each blood type, with no interaction between blood types. This gives him four separate one-channel models. For this, he uses GI/M/1 queuing models. He then finds the result that these four models are time-scaled variants of each other, inversely proportional to the occurrence of each blood group in the population. For example, a patient of blood type AB which is around 15 times scarcer in the (Canadese) population than patients of type O, is expected to wait 15 times longer for a transplant. Then for his second model, where he allows for restricted cross-transplantation, he finds percentages of donor organs that can be cross-transplanted such that comparable waiting times for each blood group can be obtained. In his model,

this percentage can be seen as a probability for each arriving organ to be cross-transplanted. In his paper, he mentioned that his model does not fully take into account abandonment of the queue (which is reneging) and that therefore the waiting times of the patients in his model that remain in the queue are higher than they would be when there are abandonments. He tried to take into account reneging by also looking at an M/M/1 type model as this would resemble the waiting list dynamics with reneging more than a GI/M/1 model. However, in his model reneging is mentioned but not actually implemented. This made me wonder what his research would look like if reneging was implemented into the model. The rest of this thesis will have a similar approach to this paper by Stanford, with additional reneging. This makes the mathematical expressions more involved as we will later see. Implementing reneging into a model that allows for restricted cross-transplantation requires some special conditions to move forward. Moreover, the work that Stanford has done in this field is very useful, and an extension to include reneging will add more realism to the model which can be beneficial as well.

To move forward, it may be helpful to search for papers that combine the three elements of organ transplantation modeling, queuing theory, *and* reneging. The same author, David A. Stanford, has worked on a paper by Drekic et al. (2015) that models deceased-donor transplant queue waiting times with reneging [11]. Their approach is a priority-based model where the patients are divided into priority classes. In real allocation policies, this often happens, such as the MELD score (which stands for "Model for End-stage Liver Disease) for liver transplants. Continuing, Drekic et al. divided the patients into two priority classes (e.g., urgent and non-urgent), and this is implemented by these classes having a different reneging intensity, illustrating the urgency of their transplantation. The non-urgent patients can randomly change to being urgent after spending some time in the system.

Zenios seems to have been the first one to combine queuing theory with organ transplantation modeling. His paper from 1999 [25] models the transplant waiting list in combination with patient reneging. He developed a model that divides the patients and donors into different classes, where "the class definitions are based on the demographic, immunological and physiological characteristics of the patients and donors". Reneging can occur after exponentially distributed times if a patient is not matched with an organ yet. His model closely resembles an $M/M/\infty$ model since he explains that patients can be seen as customers and organs can be seen as "negative customers" decreasing the queue length upon arrival. Given the way that he constructed his model, the model decomposes into multiple independent models (one for each patient class). This prevents the model from becoming too complicated and thus allows him to calculate values of interest. There is a more recent paper by Boxma et al. [5] that models the arriving organs to have their separate queue. He models the transplantation process with a double-matching queue, containing one queue of organs and one queue of patients. The queues can be both empty, but the queue lengths cannot both be higher than zero since this will result in at least one organ-donor match. This helps to implement not only patient reneging but also another type of impatience: the organs can not be preserved for unlimited time. This makes his research very unique. His research will become more and more relevant over time when societal changes (such as an opt-in consent system) decrease the scarcity of organs, compared to nowadays when transplant waiting lists are rarely empty, making organ preservation less of a problem.

3 Objective

The objective of this thesis is to develop, analyze, and propose a mathematical model that provides a better solution to the organ allocation policy in terms of equity in expected waiting times and the probability of receiving a donor, in a way that the negative effects of the blood group O problem are diminished while minimizing the disadvantages for other patient groups.

4 Methodology

The mathematical model will rely on the theory of queuing systems, applied to an idealized transplant queue. We will work with the ABO system that divides the group of patients into four categories: A, B, AB, and O. The +/- adjectives will not be considered since it would make the model a lot more extensive. The waiting list will be modeled in a few different ways by a stochastic queue.

For the arrival process of patients and donors, we assume that these arrive at an exponential rate according

to a Poisson process to make the theoretical analysis of the models possible. According to page 41 of [20], the exponentially distributed times are accurate for modelling the arrival of organs, but for the arrival of patients exponentially distributed times are not accurate since this fails on goodness-of-fit tests. Therefore, to add more realism to the waiting list representation, we combine the Poisson process's exponential arrival rate with the phenomenon of reneging. Reneging occurs when a patient 'leaves' the queue before 'service' is received. This occurs in a real life organ transplantation scenario when either: 1. a patient passes away while on the waiting list, 2. a patient's health deteriorates to such an extent that an organ transplant is not a good option anymore, or less common, 3. a patient's health increases to the point that a transplant is no longer needed.
The paper will highlight two different queuing models. The first model looks at a model that uses only ABO identical transplantation. We discuss this model to show that, although it solves the disparity for blood group O, this way of allocating organs is not in all cases ideal for other blood groups. Then we propose a second model that solves the disparities created in an ABO identical allocation method while keeping the disparity for common blood types, such as blood group O, at a minimum. We show that, in some cases, the last model can increase equity for all blood groups.
Some performance measures will be computed for these theoretical models, preferably explicitly. However, at the end of the paper, some case studies will be done that use real-world data about organ transplantation in the Netherlands, followed by a conclusion, discussion, and recommendation.

Note on programming methods Some numerical results and graphs will be found later in this thesis. These results are generated by using the mathematical expressions for the symbolic performance measures that will be derived in this paper. However, many of these expressions will contain some form of infinite expressions, such as vectors of infinite length, infinite sums, and infinite products. For this reason, the results were first generated in a symbolic programming language that can handle these infinite expressions (Mathematica). This resulted in undesirably long computation times for generating plots. Therefore, the computations are done in MatLab. An upper limit on the state space was used to ensure that the program would not run endlessly. The convergence of these expressions was investigated to ensure that this would not interfere with the final results. A (stochastic) simulation was not used.

5 ABO-identical transplantation

One way to fight the blood group O problem is to disallow all cross-transplantations. While the group of patients having blood group O benefit, this allocation rule could have a negative impact on other patient groups, specifically those with a rare blood type. That is what Stanford found in his paper from 2014 [20]. In his queuing model, he found that an ABO identical allocation rule caused great waiting time disparities for rare blood types. We want to see if using a slightly different queuing model will lead to similar waiting time disparities. This section is to check if ABO-identical transplantation leads to disparity between the groups of patients that have a relatively rare blood type. To do this, we construct a queuing model that consists of four separated queues, one for each blood type.

5.1 Model Description

We will model the waiting list as a stochastic process. Let $t \geq 0, t \in \mathbb{R}$ describe the time. Let $X_i^{(t)}, i \in \{A, B, AB, O\}$ be the amount of patients on the waiting list that have blood type i, at time t, the so called queue length for type i. The patients of bloodgroup $i \in \{A, B, AB, O\}$ will arrive with exponential intensity λ_i and the donor organs of blood group i will arrive with exponential rate $\mu_i, i \in \{A, B, AB, O\}$. Once a patient has entered the waiting list, one of two things can happen. The patient either receives service (an organ will be assigned to this patient), or the patient reneges before an organ is allocated to this patient. After entering the queue, a patient of blood type $i \in \{A, B, AB, O\}$ will renege with exponential rate ν_i.
Each patient has a few random variables attached to them. We define for each patient:

- $t_a \geq 0$ is the time of arrival for this patient.

- $t_s \geq 0$ is the time at which this patient is served, meaning the time that a patient is matched with a donor organ. We define $t_s = \infty$ when no service will be received.
- $t_r \geq 0$ is the time at which the patient reneges from the queue. We define $t_r = \infty$ when the patient will receive service in the end.
- R is the place in queue this patient has, on the moment it reneges, if it reneges at all. We define R=0 when the patient does not renege and hence receives service. So $R \in \mathbb{N}$.
- The probability of receiving service, which is the probability that this patient will be assigned an organ, is, therefore, $\mathbb{P}(t_s < t_r)$, or equivalently $\mathbb{P}(R = 0)$. It is defined on $[0, 1]$.
- $Q_t \in \mathbb{N} \setminus \{0\}$ is the position in the queue this patient has, on time $t \in \mathbb{R}^+$. Q_{t_a} is, therefore, the starting position on the waiting list for this patient.
- $W \in \mathbb{R}^+$ is the total time this patient spends on the waiting list.
- $W_q \in \mathbb{R}^+$ is the remaining time that will be spend on the waiting list, starting on the moment that the patient enters queue position $q \in \mathbb{N} \setminus \{0\}$

In this model, the waiting list will be split into four classes; one class for each blood group. We only allow for ABO-identical transplantation. Therefore, we get four separate queuing models, one for each blood group. This is visually represented in Figure 2. The arrivals of patients on the left side of the figure happen with the corresponding arrival intensity of that blood group, $\lambda_i, i \in \{O, A, B, AB\}$. The patients then enter the queue and get 'served' with the corresponding intensity of organ arrivals $\mu_i, i \in \{O, A, B, AB\}$. Each patient reneges with the intensity $\nu_i, i \in \{O, A, B, AB\}$ corresponding to their blood group. The figure denotes this by an arrow with the subscript $\nu_i, i \in \{O, A, B, AB\}$. I would like to add that the total outflow due to reneging scales with the number of patients in the queue at a given moment. So, for example, for a given time t, the intensity of outflow of patients of blood group $i \in \{O, A, B, AB\}$ is $X_i^{(t)} \cdot \nu_i$.

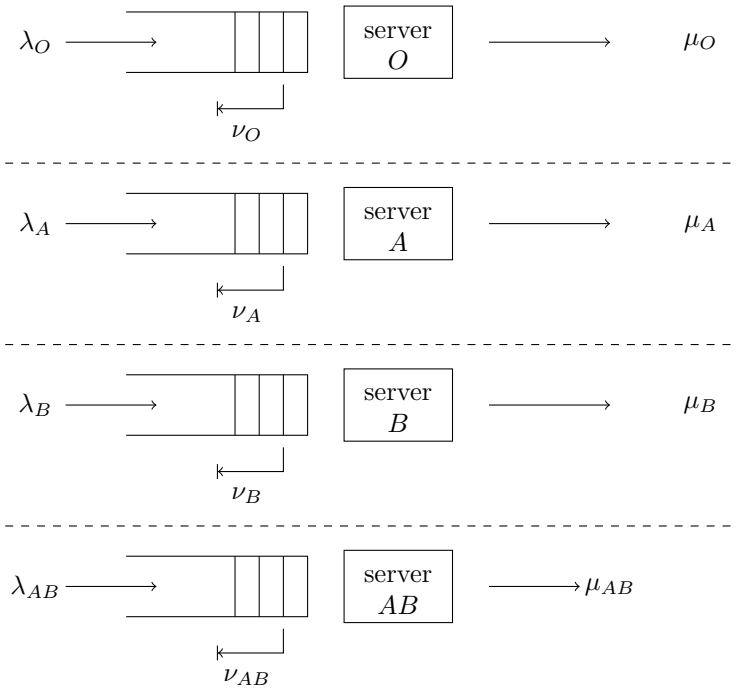

Figure 2: Visual summary of the first model

The only difference between these four models is the set of parameters $\lambda_i, \mu_i, \nu_i, i \in \{O, A, B, AB\}$. We will therefore look at the underlying model for general parameters λ, μ, ν. Later, we will replace this set of

parameters with the blood type-specific parameter sets to make a comparison between the patient classes. We assume that donor organs have to be used immediately. This implies that the queue length cannot be negative. It also implies that a donor organ will be lost when it arrives at a time when the queue is empty. We further assume that there is no upper limit to the number of patients on the waiting list. Our state space is therefore given by $\mathbb{N}$. So $X_{t\geq} \in \mathbb{N}$. If $\nu = 0$, meaning there would be no reneging, then our model equals the well-known M/M/1 model, see Figure 3.

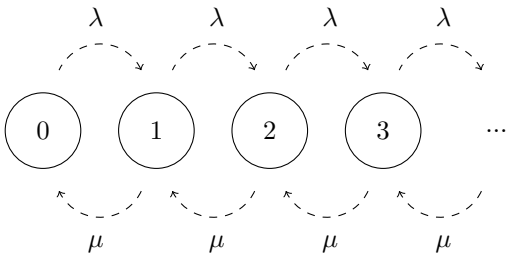

Figure 3: M/M/1 model

The states, depicted by the circles, resemble the number of patients on the waiting list (in the queue). The state of the system increases when a new patient enters the queue (is put on the wait list) and it decreases when a patient is matched to an available organ (which arrive with rate μ_i). The service time is assumed to be instantaneous.

5.1.1 Reneging

Not all patients receive a suitable transplant. Often, the demand for donor organs outweighs the supply [4]. During the waiting period, the health of a patient can improve to the point that a transplant is not needed anymore, or one's health can deteriorate to the point that a transplant is no longer a good option because the patient's health has decreased too much or the patient has passed away. Different health events, such as patient death, cause patients to refrain from the waiting list before they are matched to a suitable donor. In queuing theory, this phenomenon is called reneging, where customers leave the queue before service is acquired. In our model, we assume that once a customer enters the queue, reneging occurs after an exponential amount of time with rate ν (or rate ν_i, for specified blood type $i \in \{O, A, B, AB\}$), for each patient. The queuing model with reneging is illustrated in Figure 4.

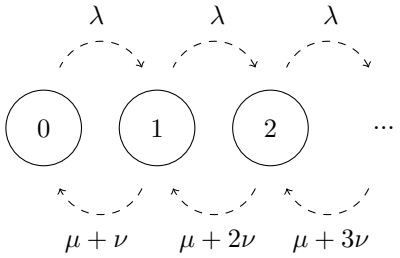

Figure 4: Queuing model with reneging

We want to apply this model to all four blood types and compare it. We will compare some of its performance measures, such as the expected waiting time. For this, we will first need to compute the stationary distribution of this model.

5.2 Stationary distribution

The stationary distribution is a probability vector of the form $\boldsymbol{\pi} = (\pi_0, \pi_1, \pi_2, ...)$ where

$$\pi_k = \lim_{t\to\infty} \mathbb{P}[X_t = k].$$

This denotes the long-term probability of the stochastic process $\{X_t\}_{t\geq 0}$ being in state k. We can compute $\boldsymbol{\pi}$ by first expressing each $\pi_k, k \geq 1$ in terms of π_0 and then use normalization to make sure that the entries of $\boldsymbol{\pi}$ add up to one. This first step is done with the help of the so-called balance equations [1].

$$\begin{aligned}
\pi_0\lambda =& \pi_1(\mu+\nu) \Rightarrow \pi_1 = \frac{\lambda}{\mu+\nu}\pi_0 \\
\pi_1\lambda =& \pi_2(\mu+2\nu) \\
\Rightarrow \pi_2 =& \frac{\lambda}{\mu+2\nu}\pi_1 = \frac{\lambda^2}{(\mu+2\nu)(\mu+nu)}\pi_0 \\
& ... \\
\pi_{n-1}\lambda =& \pi_n(\mu+n\nu) \\
\Rightarrow \pi_n =& \frac{\lambda}{(\mu+n\nu)}\pi_{n-1} \\
\Rightarrow \pi_n =& \frac{\lambda^n}{\prod_{k=1}^{n}(\mu+k\nu)}\pi_0
\end{aligned} \tag{1}$$

Combined with the condition that $\boldsymbol{\pi}$ needs to be a probability vector, so all its entries must sum up to 1, the following stationary distribution is obtained:

$$\begin{cases}
\pi_n = \frac{\lambda^n}{\prod_{k=1}^{n}(\mu+k\nu)}\pi_0 \text{ for } n \geq 0 \\
\sum_{k=0}^{\infty}\pi_k = 1 \Rightarrow \pi_0 = \left(\sum_{n=0}^{\infty}\frac{\lambda^n}{\prod_{k=1}^{n}(\mu+k\nu)}\right)^{-1}
\end{cases} \tag{2}$$

where each of the π_n's can be explicitly calculated when the parameters λ, μ, ν are known.

5.3 Service probabilities

Now that we have calculated the stationary distribution $\boldsymbol{\pi}$, we can start calculating values of interest. The first performance measure that we are interested in is the service probability. We assume that organs will be matched to patients according to the 'first-come, first-serve' allocation rule. When a patient arrives, he will find a number (which can be zero) of patients waiting before him. For this patient to receive service, all patients that have been waiting for a longer time already will either have to receive service or renege, and there needs to be an organ available for the patient itself before it reneges.
Remember that Q_{t_a} is the starting position of a patient in the queue. There are $Q_{t_a} - 1$ other patients waiting in front of this patient at its arrival time t_a. We are first of all interested in the service probabilities, which are the probabilities that a patient will receive service and not renege, given the starting position Q_{t_a} of the patient. We need these conditional service probabilities to calculate the general service probability later. Recall the random variable $R \in \mathbb{N}$. For a patient that reneges, R represents the position in the queue that this patient was in at the moment of reneging. For a patient that receives service, R is defined as 0. The probability of a patient receiving service given that it starts in position $q \in \mathbb{N} \setminus \{0\}$ will be called $\mathbb{P}(R = 0|Q_{t_a} = q)(= \mathbb{P}(t_s < t_r|Q_{t_a} = q))$. The probability of a patient receiving service when nothing is known about the starting position will be called $\mathbb{P}(R = 0)(= \mathbb{P}(t_s < t_r))$.
By the memoryless property of the exponential distribution, we find that there is a recursive relation between the $\mathbb{P}(R = 0|Q_{t_a} = q)$'s, $q \in \{1, 2, ...\}$. This is due to the fact that: if a patient starts in position $q > 1$ and the patient in question shifts one place closer to receiving service (which happens either if a patient in front of it reneges or a patient in front of it receives service), then the patient moves to a situation where the service probability is identical to the service probability for a patient starting in position $q - 1$.
We start by $\mathbb{P}(R = 0|Q_{t_a} = 1)$ (the base case). Then there are no other patients in front of the patient in

question. This patient will either renege or receive service. It reneges with rate ν and receives service with rate μ (which is the arrival rate of the organs). Therefore, the service probability will be:

$$\mathbb{P}(R = 0|Q_{t_a} = 1) = \frac{\mu}{\mu + \nu}$$

For a patient with starting position 2, the journey to receiving service consists of two parts. The first part is moving from position 2 to position 1, and the second part is receiving service from position 1. The probability of receiving service from position one is actually equal to $\mathbb{P}(R = 0|Q_{t_a} = 1)$. To calculate the probability of moving from position 2 to position 1, we see that this happens when the patient that is in position 1 in that moment either receives service (with rate μ) or reneges (with rate ν), before our patient in position 2 reneges (with rate ν). So the probability of moving from position 2 to position 1 will be $\frac{\mu+\nu}{\mu+2\nu}$. And the probability of receiving service starting in $Q_{t_a} = 2$ will therefore be

$$\mathbb{P}(R = 0|Q_{t_a} = 2) = \frac{\mu + \nu}{\mu + 2\nu} \cdot \mathbb{P}(R = 0|Q_{t_a} = 1) = \frac{\mu}{\mu + 2\nu}$$

Similarly for $\mathbb{P}(R = 0|Q_{t_a} = 3)$ we need to calculate the probability of a patient moving from position 3 to position 2, and multiply it by $\mathbb{P}(R = 0|Q_{t_a} = 2)$. A patient moves from position 3 to position 2 if either of the following events happens before the patient on position 3 reneges (with rate ν): The patient on position 1 receives service (with rate μ) or either one of the patients on position 1 or 2 reneges (both with rate ν). Therefore the patient in position 3 will move to position 2 with probability $\frac{\mu+2\nu}{\mu+3\nu}$. And

$$\mathbb{P}(R = 0|Q_{t_a} = 3) = \frac{\mu + 2\nu}{\mu + 3\nu} \cdot \mathbb{P}(R = 0|Q_{t_a} = 2) = \frac{\mu}{\mu + 3\nu}$$

If we continue this process, it is easily verified that the service probability given that the starting position is q, will be given by:

$$\mathbb{P}(R = 0|Q_{t_a} = q) = \frac{\mu}{\mu + q\nu}, q \geq 1 \tag{3}$$

and similarly:

$$\mathbb{P}(R > 0|Q_{t_a} = q) = 1 - \mathbb{P}(R = 0|Q_{t_a} = q) = \frac{q\nu}{\mu + q\nu}, q \geq 1 \tag{4}$$

These are the service probabilities conditioned on the starting position of the patient. We can use this to find the general service probability $\mathbb{P}(R = 0)$ by using the expression we found for the stationary distribution. What we do is we sum over all the possible starting positions, and multiply the probability of starting in this position by the probability of receiving service while starting in this position. Note that the long-term probability of the system being in state k is π_k, the corresponding entry of the stationary distribution. If a patient arrives while the system is in state k, this patient will have a starting position $k + 1$. Therefore, to find $\mathbb{P}(R = 0)$ we use:

$$\begin{aligned}\mathbb{P}(R = 0) &= \sum_{k=0}^{\infty} (\pi_k \cdot \mathbb{P}(R = 0|Q_{t_a} = k + 1)) \\ &= \sum_{k=0}^{\infty} \frac{\mu\pi_k}{\mu + (k + 1)\nu}\end{aligned} \tag{5}$$

We now found the service probability for an unknown starting position, which can be calculated when the parameters λ, μ and ν are known.

5.4 Waiting times

Recall $W \in \mathbb{R}^+$ is the total time a patient spends on the waiting list, the so-called waiting time. When considering waiting times for patients, one can differentiate between:

- Waiting time for an arbitrary patient
- Waiting time for a patient, given that the patient will be matched with a suitable organ

- Waiting time for a patient, given that the patient will leave the queue before a suitable organ becomes available for them.

We are interested in the expectation of all these types of waiting times, namely $\mathbb{E}[W], \mathbb{E}[W|R=0]$, and $\mathbb{E}[W|R>0]$. To do this, we recall the random variable W_q as the remaining waiting time of a patient from position q where $1 \leq q \leq Q_{t_a}, q \in \mathbb{N}$, which does not have to be the starting position.

5.4.1 Waiting time arbitrary patient

Let $\mathbb{E}[W_{Q_{t_a}}]$ be the expected waiting time for an arbitrary patient with position Q_{t_a}. Let $Q_{t_a} = 1$. The patient with starting position 1 will renege after an exponential time distributed with parameter ν or receive service after an exponential time distributed with parameter μ. Just one of these events will occur, and it will be the event that happens after the shortest time. Either of the events will terminate the time in queue for this patient. The expected time in queue for a patient with starting position 1 will therefore be the expectation of the minimum of two exponential distributions with rates μ and ν, which is equal to

$$\mathbb{E}[W_1] = \frac{1}{\mu + \nu}$$

Note that $\mathbb{P}(R = n)$ is the probability of a patient reneging from position n. Note that $\mathbb{P}(R < n)$ is the probability that the patient leaves position n without reneging (the patient moves one position in the queue). We find that

$$\mathbb{P}(R = n) = \frac{\nu}{\mu + n\nu} \tag{6}$$

$$\mathbb{P}(R < n) = 1 - \mathbb{P}(R = n) = \frac{\mu + (n-1)\nu}{\mu + n\nu} \tag{7}$$

and

$$\mathbb{E}[W_n | R = n] = \frac{1}{\mu + n\nu} \tag{8}$$

is the expected waiting time from position n given that the patient reneges in n. The law of total probability allows us to express the total waiting time for an arbitrary patient from position n as follows:

$$\mathbb{E}[W_n] = \mathbb{P}(R = n) \cdot \mathbb{E}[W_n | R = n] + \mathbb{P}(R < n) \cdot \mathbb{E}[W_n | R < n] \tag{9}$$

where the last quantity of this equation embeds a recursive relation since

$$\mathbb{E}[W_n | R < n] = \mathbb{E}[W_{n-1}] + \frac{1}{\mu + n\nu} \text{ for } n > 1. \tag{10}$$

We therefore get the recursive relation

$$\mathbb{E}[W_n] = \mathbb{P}(R = n) \cdot \mathbb{E}[W_n | R = n] + \mathbb{P}(R < n) \cdot \left(\mathbb{E}[W_{n-1}] + \frac{1}{\mu + n\nu} \right). \tag{11}$$

After filling in all the values we know, we are left with

$$\mathrm{E[W}_n] = \tfrac{\nu}{\mu+n\nu} \cdot \tfrac{1}{\mu+n\nu} + \tfrac{\mu+(n-1)\nu}{\mu+n\nu} \cdot \left(\mathbb{E}[W_{n-1}] + \tfrac{1}{\mu+n\nu} \right)$$
$$= \tfrac{\nu}{(\mu+n\nu)^2} + \tfrac{\mu+(n-1)\nu}{\mu+n\nu} \cdot \left(\mathbb{E}[W_{n-1}] + \tfrac{1}{\mu+n\nu} \right)$$

We will proof by induction that this is solved by

$$\mathbb{E}[W_n] = \frac{n}{\mu + n\nu} \tag{12}$$

Proof. The induction hypothesis is satisfied for $n = 1$. Suppose this holds for some $k \geq 1$. Then we have that $\mathbb{E}[W_k] = \frac{k}{\mu+k\nu}$ satisfies the recursive relation. We use this to calculate $\mathbb{E}[W_{k+1}]$.

$$\begin{aligned}
\mathbb{E}[W_{k+1}] =& \frac{\nu}{(\mu+(k+1)\nu)^2} + \frac{\mu+k\nu}{\mu+(k+1)\nu}\left(\frac{k}{\mu+k\nu} + \frac{1}{\mu+(k+1)\nu}\right) \\
=& \frac{\nu}{(\mu+(k+1)\nu)^2} + \frac{\mu+k\nu}{(\mu+(k+1)\nu)^2} + \frac{k(\mu+k\nu)}{(\mu+(k+1)\nu)(\mu+k\nu)} \\
=& \frac{1}{\mu+(k+1)\nu} + \frac{k}{\mu+(k+1)\nu} \\
=& \frac{k+1}{\mu+(k+1)\nu}
\end{aligned}$$

So our hypothesis is also satisfied for $n = k + 1$. By induction we have now shown that the formula holds for all $n \geq 1$. □

Hence we found the expected waiting time for a patient if the starting position is known. We find the general waiting time for an unknown starting position when summing over the stationary distribution as follows.

$$\mathbb{E}[W] = \sum_{n=0}^{\infty} \pi_n \cdot \mathbb{E}[W_{n+1}] \tag{13}$$

5.4.2 Waiting time for patient receiving service

The waiting time for a patient with starting position $Q_{t_a} = q$, given that this patient receives a donor organ is equal to

$$\mathbb{E}[W_q | R = 0] = \sum_{k=1}^{q} \frac{1}{\mu+k\nu} \tag{14}$$

To explain this formula, we introduce the random variable $T_i, i \in \mathbb{N}$ as follows:

$$T_i = \begin{cases} \text{time until patient in position } i \text{ reaches position } i-1 \text{ if this state is ever reached} \\ \infty \text{ if state } i-1 \text{ will not be reached} \end{cases} \tag{15}$$

Since we are now only considering the case where the patient receives service, we find that $T_i < \infty$ for all $i \in \mathbb{N}$. Under this condition, the expectation of the total waiting time W_q given $R = 0$ can now be seen as the sum of expectations of the T_i's, which are the waiting time before each time the patient moves a position ahead in the queue. Note that

$$\mathbb{E}[T_i | T_i < \infty] = \frac{1}{\mu+i\nu} \tag{16}$$

by the property of the expectation of the minimum of exponential distributions. We get

$$\begin{aligned}
\mathbb{E}[W_q | R = 0] =& \sum_{i=1}^{q} \mathbb{E}[T_i | T_i < \infty] \\
=& \sum_{i=1}^{q} \frac{1}{\mu+i\nu}
\end{aligned} \tag{17}$$

To calculate the general expected waiting time for a patient given that it receives service unconditioned of the starting position, we sum over the stationary distribution as follows:

$$\mathbb{E}[W | R = 0] = \sum_{n=0}^{\infty} \pi_n \cdot \mathbb{E}[W_{n+1} | R = 0] \tag{18}$$

5.4.3 Waiting time for patients leaving queue

We will compute the waiting time for patients leaving the queue by again using the law of total probability, which yields the following expression

$$\mathbb{E}[W_n] = \mathbb{P}(R = 0|Q_t = n) \cdot \mathbb{E}[W_n|R = 0] + \mathbb{P}(R > 0|Q_t = n) \cdot \mathbb{E}[W_n|R > 0] \tag{19}$$

In the previous sections, we found an expression for all of the values in this formula except for $\mathbb{E}[W_n|R > 0]$, which we are now interested in. We rewrite this equation as follows:

$$\begin{aligned} \mathbb{E}[W_n] =& \mathbb{P}(R = 0|Q_t = n) \cdot \mathbb{E}[W_n|R = 0] + \mathbb{P}(R > 0|Q_t = n) \cdot \mathbb{E}[W_n|R > 0] \\ & \Rightarrow \\ \mathbb{E}[W_n|R > 0] =& \frac{\mathbb{E}[W_n] - \mathbb{P}(R = 0|Q_t = n) \cdot \mathbb{E}[W_n|R = 0]}{\mathbb{P}(R > 0|Q_t = n)} \end{aligned} \tag{20}$$

Note that we have previously already calculated all the quantities that occur in this formula, see equation (12), (3), (4), and (14). If we fill in all the known quantities, the expression becomes:

$$\begin{aligned} \mathbb{E}[W_n|R > 0] =& \frac{\frac{n}{\mu+n\nu} - \frac{\mu}{\mu+n\nu} \cdot \sum_{k=1}^{n} \frac{1}{\mu+k\nu}}{(\frac{n\nu}{\mu+n\nu})} \\ =& \frac{n - \mu \cdot \sum_{k=1}^{n} \frac{1}{\mu+k\nu}}{n\nu} \\ =& \frac{1}{\nu} - \frac{\mu}{n\nu} \cdot \sum_{k=1}^{n} \frac{1}{\mu + k\nu} \\ =& \frac{1}{\nu} \left(1 - \frac{1}{n} \sum_{k=1}^{n} \frac{\mu}{\mu + k\nu}\right) \end{aligned}$$

Hence, the waiting time for a patient with starting position q, given that this patient does not receive a donor organ (denoted by $R > 0$, symbolizing the event of not receiving service) is equal to

$$\mathbb{E}[W_q|R > 0] = \frac{1}{\nu} - \frac{\mu}{q\nu} \left(\sum_{k=1}^{q} \frac{1}{\mu + k\nu}\right) \tag{21}$$

And the general expectation of the waiting time for patients who renege, with an unknown starting position, is obtained by summing over the stationary distribution.

$$\mathbb{E}[W|R > 0] = \sum_{n=0}^{\infty} \pi_n \cdot \mathbb{E}[W_{n+1}|R > 0] \tag{22}$$

5.5 Analysis

To analyze this model, we will first see how the parameters λ, μ, and ν relate to each other. Afterward, we will compare the performance measures of the model between different blood groups by using real-world data to find typical values for the model parameters for each patient class. The code that generates the graphs can be found in Appendix A, B, and C.

5.5.1 Dependence on parameters of service probabilities

In the middle graph of Figure 5 the service probability $\mathbb{P}(R = 0)$ is plotted for varying values of patient arrival rate λ and fixed $\mu = \nu = 1$. First thing to note is that the service probability is 0.5 when λ is zero which makes sense since in this case there are no new arrivals of patients hence the system behaves like there are never patients waiting in front of you and the arrival of organs and the reneging both happens after an exponential time with rate 1 hence the probability of each of these events is $\frac{1}{2}$. The higher λ, the more

patients arrive per time unit, the higher the demand of organs so the lower the chance for one patient to acquire one. We see that for $\lambda = 10$ the probability of acquiring an organ is approximate $\frac{1}{10}$, which makes sense because, in this case, it is expected that 10 patients arrive per time unit, each patient is expected to renege after one time unit and one organ is becoming available after one time unit. We therefore expect that after one time unit, 10 patients arrive, 9 patients renege and 1 patient acquires service, etcetera. This trend is illustrated in the figure.
Then, we move to the case that $\lambda = \nu = 1$ are fixed, but μ is varying. This is displayed in the left graph of Figure 5. First of all, note what happens to the service probabilities when $\mu = 0$. This implies that no new organs are arriving hence no patient will be served at all, representing a service probability of zero as can be seen in the graph.
Now we look at the service probability for increasing ν. This is displayed in the right graph of Figure 5. Filling in $\nu = 0$ in equation 5 yields that the service probability reduces to the sum of all elements of the stationary distribution, hence 1. This makes sense because in our model reneging is the only way to not receive service, so the service probability indeed starts at 1 when there is no reneging. Note that the numerical step size used makes the service probability appear slightly less than one for $\nu = 0$. The service probability decreases when ν increases, as can be seen in the figure.

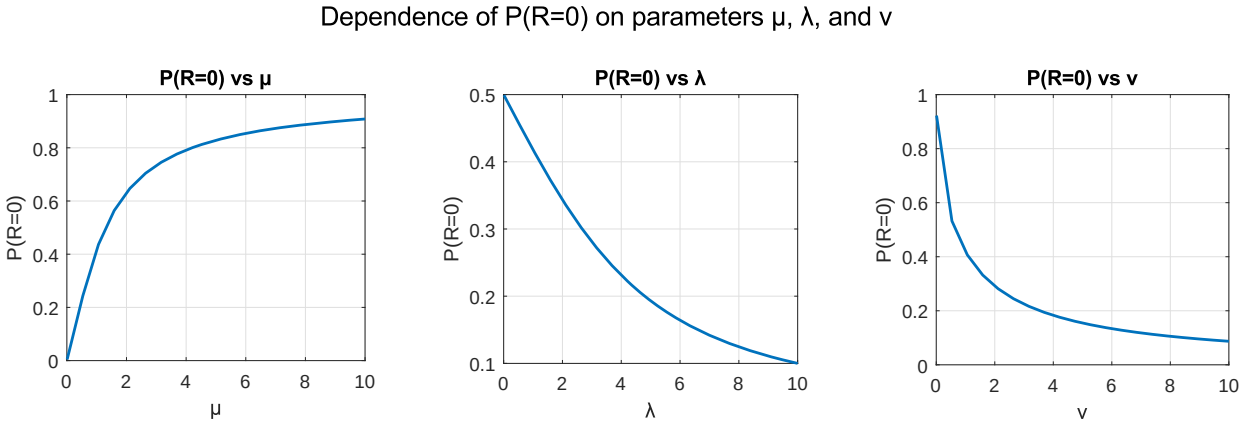

Figure 5: Dependencies of $\mathbb{P}(R = 0)$ on initial parameters

5.5.2 Dependence on parameters of expected waiting times

General waiting time Next, we look at the general waiting time expectation $\mathbb{E}[W]$.
We start by letting λ vary while $\mu = \nu = 1$ are fixed. The results can be seen on the middle graph in Figure 6. As we would expect, a higher λ means more patients arriving, which means a longer waiting time in general. The waiting time starts at $\frac{1}{2}$ for $\lambda = 0$. In the case that λ is close to zero, the queue will be empty most of the time and if a patient arrives in an empty queue this patient will have a 50% chance to either get served or renege based on the fact that $\mu = \nu$ in this experiment. Between $\lambda = 1$ and $\lambda = 10$ the expected waiting time almost doubles.
If we let μ vary instead, we get the graph on the left hand side of Figure 6. $\mu = 0$ signifies the situation where no new organs arrive; therefore $\lim_{\mu \to 0} \mathbb{E}(W) = \infty$. This is not clear from Figure 6 therefore I also added 7 which was generated in Mathematica. A higher μ signifies more availability of organs, until the expected waiting time is nearly instantaneous. So $\lim_{\mu \to \infty} \mathbb{E}(W) = 0$.
Next up, we let ν be the varying parameter. Note that we now look at the waiting time for general patients, which is effectively the time spend on the waiting list. If ν is high, then patients that renege will renege at a quick rate meaning that they will spend a short time on the waiting list. The patients that do acquire service will generally also have a lower waiting time because the amount of patients that are 'in front' of them on the list renege at a high rate. So the overall expectation of waiting time will approach zero for $\nu \to \infty$, see the right graph of Figure 6.

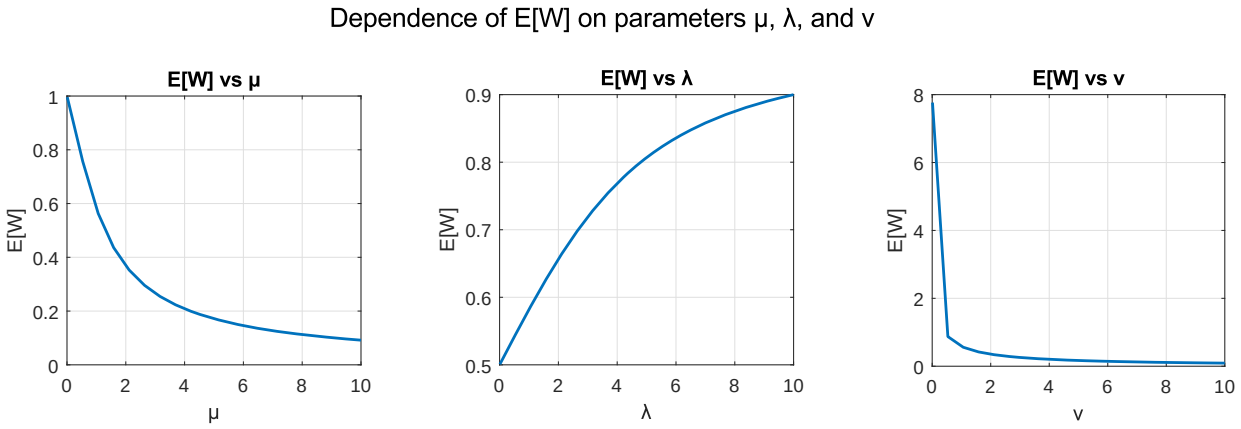

Figure 6: Dependencies of $\mathbb{E}[W]$ on initial parameters

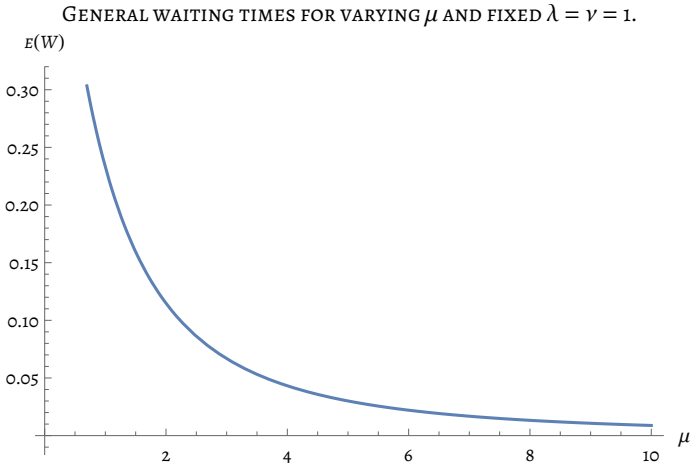

Figure 7: Dependencies of $\mathbb{E}[W]$ on μ

Waiting time for patients receiving service We now look at the case of $\mathbb{E}(W|R=0)$, the expected waiting time given that the patient will be served.
First of, in the middle of Figure 8 we let λ vary. This starts at a waiting time of 0.5 and changing λ from 0 to 10 makes this waiting time quadruple. It is not linear but more straight than the middle graph of Figure 6.
Then, μ is varied. The expected waiting time given that service will be acquired is high for low μ since μ is proportional to the availability of organs. Patients who acquire service will have to wait longer when the time between organs becoming available is higher. Similarly, the waiting time drops and converges to 0 when $\mu \to \infty$. See the left graph of Figure 8.
Then we let ν vary in the right graph of Figure 8. The average waiting time for patients receiving service also drops very quickly for rising ν. If patients renege quickly then the amount of patients that are in front of a patient that receives service in the end, will decrease quickly. So the waiting time for this group will decrease.

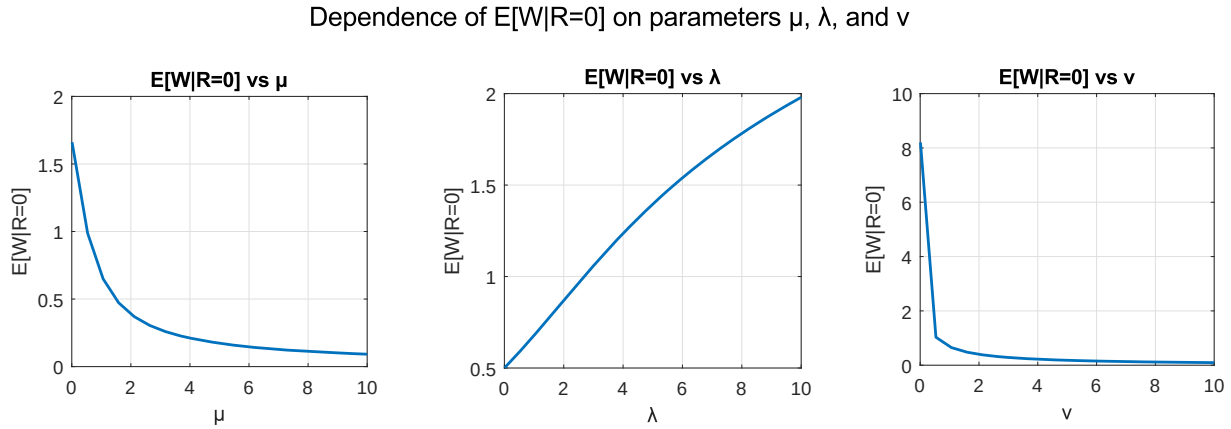

Figure 8: Dependencies of $\mathbb{E}[W|R=0]$ on initial parameters

Waiting time for patients reneging We now look at the dependence on the initial parameters of $\mathbb{E}[W|R>0]$. When λ is varied, see the middle graph on Figure 9, the waiting time increases.
When $\mu = 0$ there is no service. But since we look at the service time of reneging patients, the waiting time does not blow up. Instead, it is equal to the reneging intensity $\nu = 1$. The reneging time decreases when the service intensity is increased. A high μ will make sure most patients get service without reneging, the patients that are about to renege very quickly will have the highest chance of not receiving service. See the left graph in Figure 9.
Then we let ν vary, see Figure 9 on the right side. Clearly, the expected waiting time for reneging patients drops for increased reneging intensity.

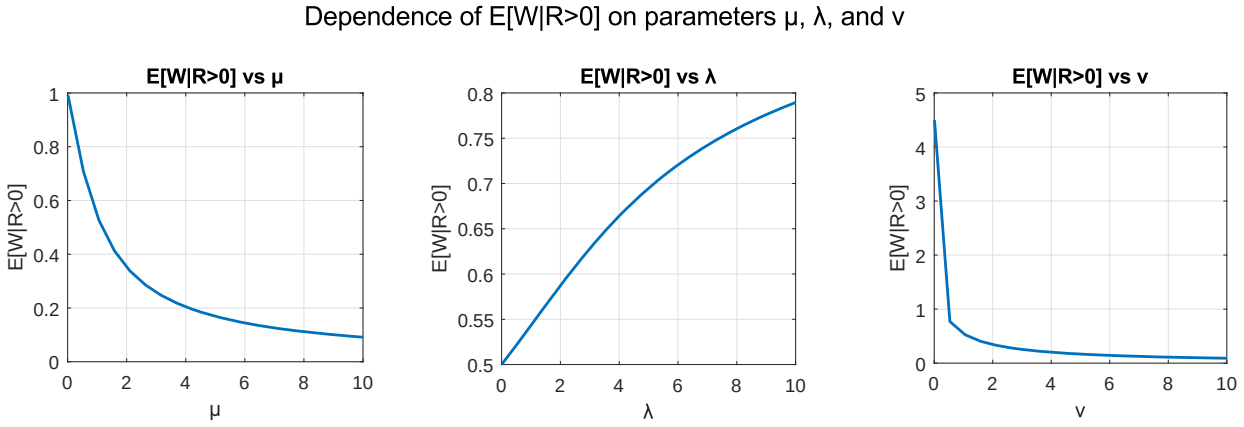

Figure 9: Dependencies of $\mathbb{E}[W|R>0]$ on initial parameters

5.5.3 Conclusion

We see that an increase of the arrival rate λ always results in worse performance measures (longer waiting times, lower service probability). An increasing arrival rate will change the proportions between demand and supply such that there will be more demand compared to supply, which justifies the worse performance measures. An increase of ν is very efficient at lowering the waiting time. However, it is horrible for the service probability. The best way to improve on all performance measures is to increase the service rate μ.

5.6 Case studies

In the next sections, we will do some case studies for the ABO identical model. We look at organ transplantation in the Netherlands and see how the model performs by evaluation performance measures.

5.6.1 Heart donation in the Netherlands

In this section, we will do a case study of heart donation in the Netherlands. Let τ_i be the ratio of blood type $i \in \{O, A, B, AB\}$ in a population. The τ_i's for the Netherlands are given in Table 1. For this case study, the data from the NTS is used (see [15]) to make a realistic guess for the model parameters. This data is summarized in Table 2 and it contains the inflow of the waiting list for a donor heart per year as well as the outflow. The outflow is split into the patients that received a donor heart (service) and the patients that reneged. The reported data is from the period of 2017 until 2021. We use the averages over these years to find realistic estimates of the model parameters.

Year	2017	2018	2019	2020	2021	average
Queue length	107	120	115	132	139	122.6
Inflow	67	57	54	72	73	64.6
Outflow: received donor organ	38	38	38	41	44	39.8
Outflow: reneging	23	20	12	18	22	19

Table 2: Heart transplantation data from Dutch transplantation foundation NTS year report 2021 [15] Tables 2.1, 2.3, and 2.5.

We start by assuming that the blood type distribution of the donor and patient groups is roughly similar to the blood group distribution of the whole population. So $\lambda_i \sim \tau_i$ and $\mu_i \sim \tau_i$ for $i \in \{O, A, B, AB\}$. To find an estimate for $\lambda_i, i \in \{O, A, B, AB\}$, we multiply the average inflow of the total population, which we call $\bar{\lambda}$, by τ_i. Note $\bar{\lambda} = 64.6$ in this case. To find an estimate for μ_i we multiply the average outflow due to service of the total population (which we call $\bar{\mu}$, in this case $\bar{\mu} = 39.8$) by τ_i. We furthermore assume that the intensity of reneging does not depend on the patient's blood type. So $\nu_i \sim \nu_j$ for $i, j \in \{$O,A,B,AB$\}$.
To find an estimation of the $\nu_i's, i \in \{O, A, B, AB\}$ we look at both the average total queue length and the average total outflow due to reneging. We divide the outflow due to reneging by the average number of patients on the list to find an estimation for the rate of reneging. So $\frac{19}{122.6} \approx 0.1549$. To back up this approximation for ν_i, $i \in \{O, A, B, AB\}$ we use a paper about heart transplantation [3] which tells us that around 50% of patients on the heart transplant waiting list are still alive after 3 years (Figure 1c in [3], for patients in the period 2011-2017). This would correspond with a life expectancy on the waiting list of approximately 6 years, corresponding to a ν_i of $\frac{1}{6}$ which is indeed close to our estimate of 0.1549. If we use the estimates for the model parameters given in Table 3, then we can calculate an estimate of the performance measures given in Table 4.

i	O	A	B	AB
λ_i	29.07	27.778	5.814	1.938
μ_i	17.91	17.114	3.582	1.194
ν_i	0.1549	0.1549	0.1549	0.1549

Table 3: Parameter estimates for heart donation based on Table 2.

i	O	A	B	AB
$\mathbb{P}(R = 0)$	0.6161	0.6161	0.6170	0.5872
$\mathbb{E}[W]$	2.4784	2.4784	2.4726	2.6649
$\mathbb{E}[W\|R = 0]$	3.1334	3.1337	3.1517	3.4446
$\mathbb{E}[W\|R > 0]$	1.4593	1.4603	1.8474	1.0877

Table 4: Estimated performance measures for heart donation in the Netherlands

The performance measures in Table 4 are all relatively close for the different blood groups. The rare blood groups even score slightly better on some of the performance measures compared to common blood types. This is different from what we would expect given Stanford's research [20]. We therefore look also at data from other transplantable organs in the Netherlands, to see if we can find a stronger disparity of waiting times under an ABO identical policy.

5.6.2 Lung donation in the Netherlands

We now look at long transplantation data in the Netherlands, see Table 5.

Year	2017	2018	2019	2020	2021	average
Queue length	178	185	171	160	165	171.8
Inflow	114	133	131	117	119	122.8
Outflow: received donor organ	74	89	105	87	91	89.2
Outflow: reneging	42	26	29	37	25	31.8

Table 5: Lung transplantation data from Dutch transplantation foundation NTS year report 2021 [15] Tables 2.1, 2.3, and 2.5.

By using identical methods as in the previous section about heart transplantation, we derive the following parameter estimates for lung transplantation:

i	O	A	B	AB
λ_i	50.76	48.504	10.152	3.384
μ_i	40.14	38.356	8.028	2.676
ν_i	0.1641	0.1641	0.1641	0.1641

Table 6: Parameter estimates for lung donation based on Table 5.

We get the following performance measures when we apply the model to these parameter estimates:

i	O	A	B	AB
$\mathbb{P}(R=0)$	0.7264	0.7264	0.7300	0.7121
$\mathbb{E}[W]$	1.6674	1.6674	1.6452	1.7544
$\mathbb{E}[W\|R=0]$	1.9537	1.9540	1.9491	2.1181
$\mathbb{E}[W\|R>0]$	0.9338	0.9343	0.9675	1.1350

Table 7: Estimated performance measures for lung donation in the Netherlands

First of all, we note that the experiment on lung donation yields a higher service probability and lower waiting times than the experiment on heart transplantation. Next to that, we still do not see big disparities between patient blood groups. The performance measures are relatively close for each blood group. The relatively rare blood group B even scores best on most of the performance measures, which is contrary to what Stanford found [20].

5.6.3 Kidney donation in the Netherlands

The last organ type we will look at is the kidney. The data that we use for this experiment is listed in Table 8. We derive the initial parameters of this experiment in a way analogous to the previous two experiments. This yields the initial parameters listed in Table 9.

Year	2017	2018	2019	2020	2021	average
Queue length	650	719	803	806	877	771
Inflow	1300	1520	1510	1365	1535	1446
Outflow: received donor organ	980	998	952	818	916	932.8
Outflow: reneging	371	368	335	477	374	385

Table 8: Kidney transplantation data from Dutch transplantation foundation NTS year report 2021 [15] Tables 2.1, 2.3, and 2.5.

i	O	A	B	AB
λ_i	650.7	621.78	130.14	43.38
μ_i	419.76	401.104	83.952	27.984
ν_i	0.3141	0.3141	0.3141	0.3141

Table 9: Parameter estimates for kidney donation based on Table 8.

If we apply our model to these initial parameters, we obtain the following performance measures:

i	O	A	B	AB
$\mathbb{P}(R=0)$	0.9254	0.9216	0.6718	0.6451
$\mathbb{E}[W]$	0.2375	0.2497	1.0448	1.1299
$\mathbb{E}[W\|R=0]$	0.2467	0.2599	1.2659	1.4008
$\mathbb{E}[W\|R>0]$	0.1229	0.1294	0.5957	0.6615

Table 10: Estimated performance measures for kidney donation in the Netherlands

The results in Table 10 show a very clear distinction between the two common blood types (A and O), which score good on the performance measures, and the two rare blood types (B and AB) that score worse. The service probability for groups A and B is over 90%, while the service probability of the other blood types is under 70%. AB and B also score a multitude worse than on expected waiting times, patients of these groups are only expected to wait less than a year if they will renege. In the contrary, patients of group O and A are expected to wait around three months (or a little over a month if they renege).
To clarify the differences even more, we adjust Table 10 in such a way that we can see the differences relative to bloodgroup O. In Table 11 the performance measures of bloodgroup O are set to a 100%. Then, the values of the other bloodgroups are filled in relatively to bloodgroup O.

i	O	A	B	AB
$\mathbb{P}(R=0)$	100%	99.6%	72.6%	69.7%
$\mathbb{E}[W]$	100%	105.1%	439.9%	475.7%
$\mathbb{E}[W\|R=0]$	100%	105.4%	513.1%	567.8%
$\mathbb{E}[W\|R>0]$	100%	105.3%	484.7%	538.2%

Table 11: Proportions between the performance measures for kidney donation in the Netherlands, where the performance measures of type O are set to 100%

We see that blood group A performs a tiny bit worse than blood group O. This is roughly in proportion to their difference in prevelance in the population. We expect blood group A to perform slightly worse than group O which is indeed the case. Then, we see that patients of blood group B and AB have to wait roughly 5 times longer than type O patients and patients of these rare blood types score around 30% less on service probability. Next to that, patients of blood group AB score worse than patients of blood group B. The results are ordered in such a way that we can see the following connection: the rarer a blood type is, the worse it performs. However, this is not in proportion to their prevalence in the population such as in Stanford's research [20]. It is roughly in proportion for blood type B which is 5 times more rare than type

O and in this experiment is expected to wait roughly 5 times longer than blood group O. But we do not see this connection for the rare blood group AB since that would mean that patients of type AB would have to wait 15 times longer on average, which is not the case here.

5.7 Conclusion

There are two main things we learned from these experiments. The first one is that the waiting time disparities for ABO identical transplantation are not observed in all organ transplantation scenarios. In the case of lung and heart transplantation in the Netherlands this disparity is not observed. Secondly, when disparity occurs such as in the case of Dutch kidney transplantation, it is not proportional to the prevalence in the population of that blood group such as in Stanford's research [20]. The four models are not time-scaled versions of each other. The introduction of reneging has such an effect on the expected waiting time that the difference between blood group B and AB is much less than what we would expect. The disparity between common (A and O) versus rare (B and AB) blood types is yet still so prominent in some cases such as kidney transplantation in the Netherlands, that this is very undesirable for patients of rare blood groups. Therefore, although an ABO identical policy benefits blood group O patients, we look for another solution that does not penalize patients of rare blood groups if they would otherwise experience disparity.

6 ABO-compatible transplantation

In the previous section, we have seen that allowing only ABO-identical transplantation is not always a good idea due to the possibility of longer waiting times for patients of rare blood types. This was demonstrated in the case of kidney transplantation in the Netherlands. To tackle the blood-group O problem while making sure that rare blood types have similar waiting times, we introduce cross-transplantation for blood types that are ABO-compatible. In short, there are two ways to implement cross-transplantation. First of all, you can allow for all possible cross-transplantations without any restrictions by for example giving an available organ to the longest waiting patient that is compatible with the donor. This can however lead to too little O-organs that are available for O patients (the bloodgroup O problem) since the cross transplantation is unrestricted. Secondly, it is also possible to implement cross-transplantations by introducing certain conditions or restrictions instead of unrestricted cross-transplantation. We want to choose the restrictive conditions in such a way that more equity between patient groups is obtained when this is needed. In the next section, we will look at such a model that makes use of restricted cross-transplantation and analyze it to reach equity between patient groups.

6.1 Restricted ABO-compatible transplantation

Instead of allowing all types of cross transplantation, we look at which cross-transplantations are the most essential and divide the patients into two groups. We proceed as follows. In the blood group distribution of Table 1, we see that there are two common (O and A) and two less common (B and AB) blood types. We want to construct a comprehensible model that can reach equity between patient groups. The policy we will use divides the patient groups into two sub-groups by following the logic proposed by Stanford in 2014, see [20] page 44. The logic is as follows:

1. In the case of ABO-identical transplantation only, the waiting time for blood group B patients can in some cases be disproportionally long since blood group B donors do not arise as quickly as type O donors, see section 5.6.3. To counteract this, some form of cross-transplantation is needed to supplement the B-patients. The group of O-donors is the only group of non-B donors compatible with B patients. Therefore, some amount of O-donor organs need to be transplanted to B-patients.

2. In the case of ABO-identical policy, we also see that in some cases AB patients have to wait unreasonably longer than patients of type O, see section 5.6.3. Therefore, they also need to be supplemented by some form of cross-transplantation. Donors with blood type A, B, or O are compatible with AB-type patients.

3. B-donors donating to AB patients will only lead to an increase of O-donors donating to B-patients since the B-patient group also need to be supplemented. O-donors donating to AB patients will lead to an increased risk of the blood group O problem. Donor group A seems to be suitable for supplementing AB-type patients. Not only is it a large group, but it also shares more commonalities of anti-bodies with the AB patient group which is medically preferable.

In short, we are left with the allocation rule that cross-transplantation is allowed only in the following cases: From O-donors to B patients and from A-donors to AB patients. We revisit Figure 1 with these restrictions. In Figure 10, the directions of ABO-compatible donations that are still allowed are illustrated with a solid arrow, and the compatibilities that are disallowed are illustrated with a dotted arrow. This allocation rule dissects the group of donors and patients into two categories consisting of two blood types each. This dissection allows us to create a model tailored to two blood groups with cross-transplantations, which we can use for both the subgroup of AB and A donors/patients and the subgroup of O and B donors/patients.

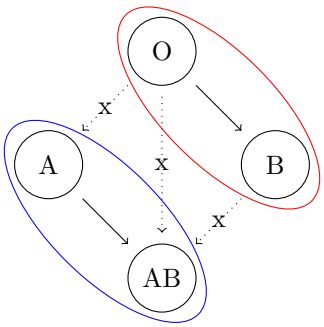

Figure 10: Blood group compatibilities combined with suggested transplantation restrictions part the system in two separate groups.

6.1.1 Possible allocation rules

Let $(u, v) \in \{(\text{AB,A}), (\text{B,O})\}$. We construct a general model for the group of patients and donors that have either bloodtype u or v, where some amount of $v-$donors supplement the $u-$patients. We will do this by making a 2-dimensional queuing model. Let $(U, V) \in \mathbb{N}^2$ be the state of this model, with state space $\mathbb{N}^2$. The variable U represents the amount of u-patients on the waiting list and the variable V represents the amount of $v-$patients on the waiting list. Similar to the model in Section 5, the $u-$ and $v-$patients arrive with (exponential) intensity λ_u, λ_v respectively and renege with intensity ν_u, ν_v respectively. The $u-$ and $v-$type donor organs arrive with intensity μ_u and μ_v respectively. The question that needs to be answered first, is: How many of the $v-$donor organs will be used to supplement the $u-$patient group?
One intuitive solution would be the following. Let $v-$donor organs be transplanted to $v-$patients unless there are no $v-$patients in the queue. Then $v-$donors will be used by $u-$patients. The model we get from this approach is illustrated in Figure 11. In this figure, the blue arrows represent the arrival of patients, the black arrows symbolize the arrival of organs and the red arrows represent the intensity by which patients renege. It can be seen as the two-dimensional version of the model in Figure 4, with the addition of cross-transplantation in the bottom row.

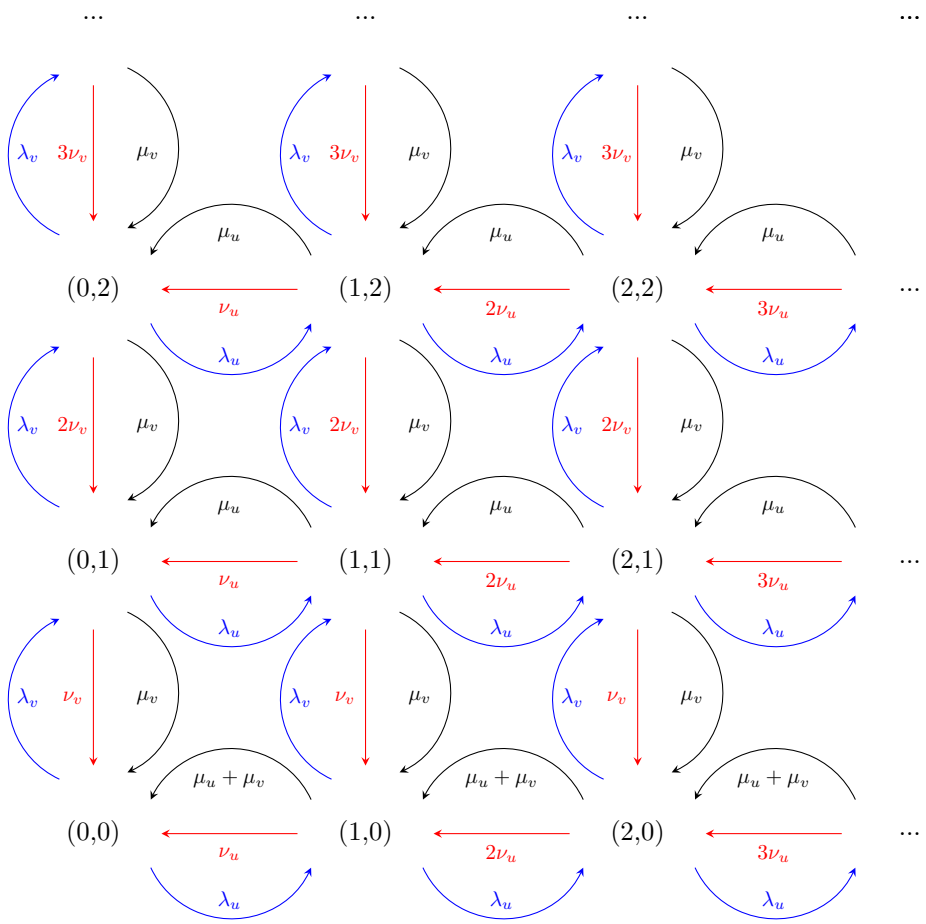

Figure 11: Model where u patients are served with v organs only if there are no v patients.

Now look at the case $\nu_u = \nu_v = 0$, meaning that patients do not renege. In this case, the model coincides with a queuing model that is known in literature as the coupled processor model. Although the idea behind this model is very intuitive and useful, it seems to be the case that the analysis of the coupled processor model is extremely difficult. For a paper about the coupled processor model I refer to Iasnogorodski et al (1979), see [12]. The model in the case when $\nu_u, \nu_v \neq 0$ can be seen as a coupled processor model with reneging, which introduces even more complexity. We therefore refrain from analyzing this model and instead make adjustments.

Suppose that $v-$donors supplement u-patients not only when there are no v-patients, but also in case there are v-patients. When a v-donor arrives when there are both v-patients and $u-$ patients in the system, then the v-donor will be given to a u-patient with probability p, and to a v-patient with probability $1 - p = q$. If there are no v-patients then the v-donor organ will be given to a u-patient unless there aren't any. This makes sure as little organs as possible get lost. A queuing model that uses this allocation rule is illustrated in Figure 12.

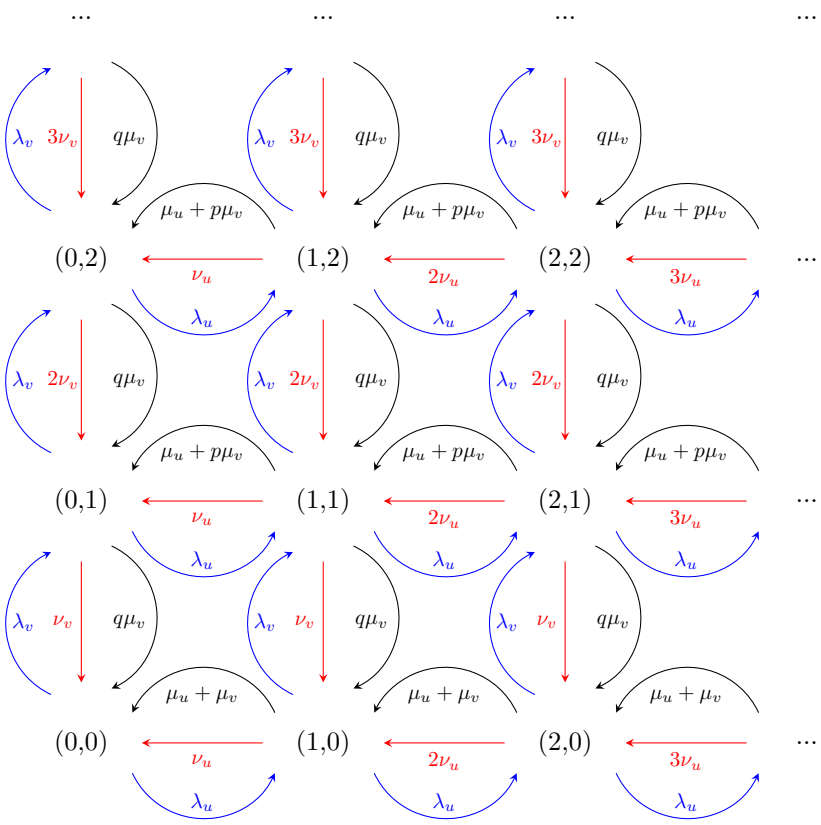

Figure 12: Model where u patients are served with fraction p of v organs if there are $v-$patients waiting

To construct a model that we can analyze, it is important to be able to calculate a stationary distribution. The stationary distribution of this model is hard to calculate due to similar reasons as the previous model. If we look at the rows of the model, then the intensities on these rows are not all equal: the bottom row is distinct.

We make use of the stationary distribution of the ABO-identical model, given in equation 2. Let $\pi_m^{(u)}$ be the stationary distribution of the ABO-identical model applied to blood group u, and $\pi_n^{(v)}$ the stationary distribution of the ABO-identical model applied to blood group v, see 2. Let $\pi_{(i,j)}^{(u,v)}$ be the stationary distribution of the 2D model applied to blood groups (u, v), which we will shorten to $\pi_{(i,j)}$ It would be easiest if the stationary distribution of the 2D model for blood groups u and v could be calculated as the product

$$\pi_{(i,j)}^{(u,v)} = \pi_i^{(u)} \cdot \pi_j^{(v)} \tag{23}$$

We can not prove this because of the exception in the bottom row for this model. The fact that all of the arriving v organs are used on u patients when there are no v-patients ensures that the v-organs will not be wasted unnecessarily. We however think it is reasonable to delete this exception because of the following reasons,

- Real-world organ transplant waiting lists are almost never empty. The demand often outweighs supply, see [4]. It is therefore reasonable to make an exception for when the part of the queue corresponding to $v-$patients on the waiting list is empty.
- Next to that, the v-patient group represents a common blood type (either A or O). This diminishes the chances of an empty v-queue.
- equalizing each row and column will enable us to create a model for which we can calculate the stationary distribution instead of working with a model for which it is very hard to calculate the stationary distribution.

Hence, we now adjust the model by making the assumption that: on average part p of $v-$organs will be used to help $u-$patients, even when there are no $v-$patients. When there are no $v-$patients, then part q of $v-$organs will be lost. The model we obtain is illustrated in Figure 13.

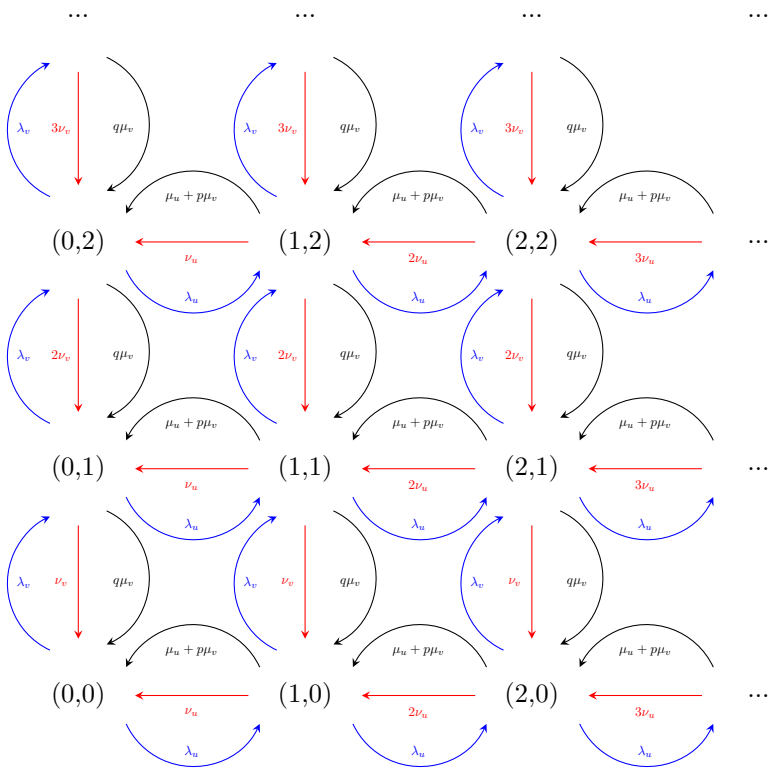

Figure 13: Model where u patients are served with fraction p of v organs.

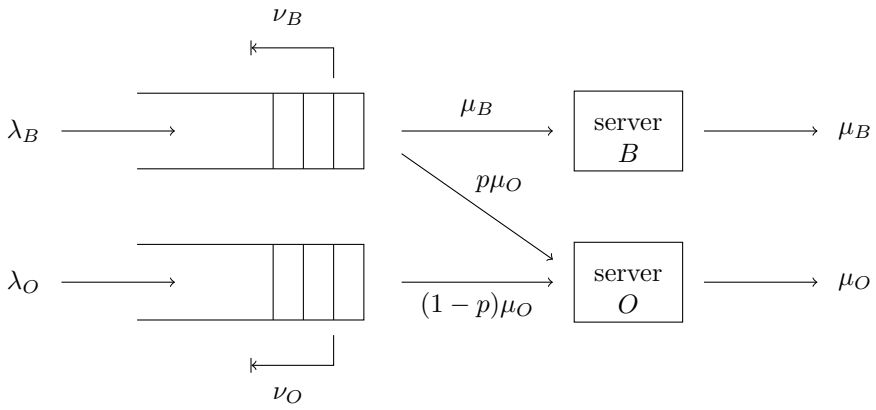

Figure 14: Visual representation of (half of) the proposed model for restricted cross transplantation

Stationary distribution We have now constructed the model in such a way that the intensities on all the rows and the intensities on all the columns are equal. We expect a form of independence between both of the queue lengths U and V. Our guess is, therefore, that the stationary distribution is equal to:

$$\pi_{(i,j)} = C \cdot \frac{\lambda_u^i}{\prod_{k=1}^{i}(\mu_u + p\mu_v + k\nu_u)} \cdot \frac{\lambda_v^j}{\prod_{l=1}^{j}((1-p)\mu_v + l\nu_v)} \text{ where } C = \pi_0^{(u)} \cdot \pi_0^{(v)} \tag{24}$$

or in short

$$\pi_{(i,j)} = C \cdot \pi_i^{(u)} \cdot \pi_j^{(v)} \tag{25}$$

if we define $\pi_i^{(u)}$ and $\pi_j^{(v)}$ such that

$$\begin{cases} \pi_n^{(u)} = \frac{\lambda_u^n}{\prod_{k=1}^n (\mu_u + p\mu_v + k\nu_u)} \pi_0^{(u)} \text{ for } n \geq 0 \\ \pi_0^{(u)} = \left(\sum_{n=0}^{\infty} \frac{\lambda_u^n}{\prod_{k=1}^n (\mu_u + p\mu_v + k\nu_u)} \right)^{-1} \end{cases} \tag{26}$$

$$\begin{cases} \pi_n^{(v)} = \frac{\lambda_v^n}{\prod_{k=1}^n ((1-p)\mu_v + k\nu_v)} \pi_0^{(v)} \text{ for } n \geq 0 \\ \pi_0^{(v)} = \left(\sum_{n=0}^{\infty} \frac{\lambda_v^n}{\prod_{k=1}^n ((1-p)\mu_v + k\nu_v)} \right)^{-1} \end{cases} \tag{27}$$

and $n \in \mathbb{N}$. This is derived from the stationary distribution of the ABO-identical model, see (2), combined with the fact that in this 2D model the service intensities of each group are adjusted.
Note that this distribution is again normalized since

$$\begin{aligned} \sum_{(i,j)\in\mathbb{N}^2} \pi_{(i,j)} &= \sum_{i\in\mathbb{N}} \sum_{j\in\mathbb{N}} \left(\pi_i^{(u)} \cdot \pi_j^{(v)} \right) \\ &= \sum_{i\in\mathbb{N}} \sum_{j\in\mathbb{N}} \left(\pi_i^{(u)} \cdot \pi_j^{(v)} \right) \\ &= \sum_{i\in\mathbb{N}} \pi_i^{(u)} \left(\sum_{j\in\mathbb{N}} \pi_j^{(v)} \right) \\ &= \sum_{i\in\mathbb{N}} \pi_i^{(u)} \cdot 1 = 1 \end{aligned}$$

Hence, the entries of $\pi_{(i,j)}$ sum up to 1, making $\pi_{(i,j)}$ a candidate to be a stationary distribution. This is however not enough, since we also need to show that this is the unique stationary distribution for this model,
which is the case if we are dealing with an irreducible Markov chain [1]. For us this means that every state of the model can be reached by all of the other states. This holds true for the assumption that $\mu_i, \lambda_i > 0, i \in \{O, A, B, AB\}$. Therefore, if (24) satisfies the balance equations, then it is the unique stationary distribution of the model. We will proceed by proving that (24) is a valid stationary distribution of this model by showing that the balance equations are satisfied for all $(i,j) \in \mathbb{N}^2$.

Proof. First, we prove this for the states (i,j) such that $i, j \neq 0$. The global balance equations state

$$\begin{aligned} (\lambda_u + \lambda_v + \mu_u + p\mu_v + (1-p)\mu_v + j\nu_v + i\nu_u)\pi_{(i,j)} =& ((j+1)\nu_v + (1-p)\mu_v)\pi_{(i,j+1)} \\ &+ (\mu_u + p\mu_v + (i+1)\nu_u)\pi_{(i+1,j)} \\ &+ \lambda_v \pi_{(i,j-1)} \\ &+ \lambda_u \pi_{(i-1,j)} \end{aligned} \tag{28}$$

By using our assumption (24), we can express the π's in terms of $\pi_{(i,j)}$ as follows

$$\begin{aligned} \pi_{(i,j+1)} =& \frac{\lambda_v}{(1-p)\mu_v + (j+1)\nu_v} \pi_{(i,j)} \\ \pi_{(i+1,j)} =& \frac{\lambda_u}{\mu_u + p\mu_v + (i+1)\nu_u} \pi_{(i,j)} \\ \pi_{(i,j-1)} =& \frac{(1-p)\mu_v + j\nu_v}{\lambda_v} \pi_{(i,j)} \\ \pi_{(i-1,j)} =& \frac{\mu_u + p\mu_v + i\nu_u}{\lambda_u} \pi_{(i,j)} \end{aligned}$$

We now need to show that the balance equations hold for our assumption. If we make a substitution in (28) and divide by $\pi_{(i,j)}$, we get the following equation

$$\begin{aligned}(\lambda_u + \lambda_v + \mu_u + p\mu_v + (1-p)\mu_v + j\nu_v + i\nu_u) =&((j+1)\nu_v + (1-p)\mu_v)\frac{\lambda_v}{(1-p)\mu_v + (j+1)\nu_v}\\ &+(\mu_u + p\mu_v + (i+1)\nu_u)\frac{\lambda_u}{\mu_u + p\mu_v + (i+1)\nu_u}\\ &+\lambda_v\frac{(1-p)\mu_v + j\nu_v}{\lambda_v}\\ &+\lambda_u\frac{\mu_u + p\mu_v + i\nu_u}{\lambda_u}\\ =&(\lambda_u + \lambda_v + \mu_u + p\mu_v + (1-p)\mu_v + j\nu_v + i\nu_u)\end{aligned}$$

So yes, the balance equations are satisfied, hence our assumption (24) holds for $i, j \neq 0$.
Now let $i = 0, j > 0$. The global balance equations state

$$\begin{aligned}(\lambda_u + \lambda_v + j\nu_v + (1-p)\mu_v)\pi_{(0,j)} =&((j+1)\nu_v + (1-p)\mu_v)\pi_{(0,j+1)}\\ &+(\nu_u + \mu_u + p\mu_v)\pi_{(1,j)} + \lambda_v\pi_{(0,j-1)}\end{aligned} \tag{29}$$

We can express the π's in terms of $\pi_{(0,j)}$ as follows

$$\begin{aligned}\pi_{(0,j+1)} &= \frac{\lambda_v}{(1-p)\mu_v + (j+1)\nu_v}\pi_{(0,j)}\\ \pi_{(1,j)} &= \pi_1^{(u)} \cdot \pi_j^{(v)} = \frac{\lambda_u}{\mu_u + p\mu_v + \nu_u}\pi_0^{(u)} \cdot \pi_j^{(v)} = \frac{\lambda_u}{\mu_u + p\mu_v + \nu_u}\pi_{(0,j)}\\ \pi_{(0,j-1)} &= \frac{(1-p)\mu_v + j\nu_v}{\lambda_v}\pi_{(0,j)}\end{aligned}$$

If we substitute this in (29) and divide out $\pi_{(0,j)}$, we get the following equation

$$\begin{aligned}(\lambda_u + \lambda_v + j\nu_v + (1-p)\mu_v)\pi_{(0,j)} =&((j+1)\nu_v + (1-p)\mu_v)\frac{\lambda_v}{(1-p)\mu_v + (j+1)\nu_v}\\ &+ (\nu_u + \mu_u + p\mu_v)\frac{\lambda_u}{\mu_u + p\mu_v + \nu_u}\\ &+ \lambda_v\frac{(1-p)\mu_v + j\nu_v}{\lambda_v}\\ =&\lambda_v + \lambda_u + (1-p)\mu_v + j\nu_v\end{aligned}$$

So yes, our assumption (24) holds for $i = 0, j > 0$.
Now let $i > 0, j = 0$. The global balance equations state

$$\begin{aligned}(\lambda_u + \lambda_v + i\nu_u + \mu_u + p\mu_v)\pi_{(i,0)} =&(\nu_v + (1-p)\mu_v)\pi_{(i,1)}\\ &+ ((i+1)\nu_u + \mu_u + p\mu_v)\pi_{(i+1,0)}\\ &+ \lambda_u\pi_{(i-1,0)}\end{aligned} \tag{30}$$

We can express the π's in terms of $\pi_{(i,0)}$ as follows

$$\begin{aligned}\pi_{(i,1)} &= \frac{\lambda_v}{(1-p)\mu_v + \nu_v}\pi_{(i,0)}\\ \pi_{(i+1,0)} &= \frac{\lambda_u}{\mu_u + p\mu_v + (i+1)\nu_u}\pi_{(i,0)}\\ \pi_{(i-1,0)} &= \frac{\mu_u + p\mu_v + i\nu_u}{\lambda_u}\pi_{(i,0)}\end{aligned}$$

If we substitute this in (30) and divide out $\pi_{(i,0)}$, we get:

$$\begin{aligned}(\lambda_u + \lambda_v + i\nu_u + \mu_u + p\mu_v) =& (\nu_v + (1-p)\mu_v)\frac{\lambda_v}{(1-p)\mu_v + \nu_v} \\ &+ ((i+1)\nu_u + \mu_u + p\mu_v) \cdot \frac{\lambda_u}{\mu_u + p\mu_v + (i+1)\nu_u} \\ &+ \lambda_u \frac{\mu_u + p\mu_v + i\nu_u}{\lambda_u} \\ =& (\lambda_u + \lambda_v + i\nu_u + \mu_u + p\mu_v)\end{aligned}$$

So yes, our assumption (24) holds for $i > 0, j = 0$.
We are left with the case $i = j = 0$. The balance equations give us

$$(\lambda_u + \lambda_v)\pi_{(0,0)} = (\nu_u + \mu_u + p\mu_v)\pi_{(1,0)} + (\nu_v + (1-p)\mu_v)\pi_{(0,1)} \tag{31}$$

We can rewrite $\pi_{(1,0)}$ and $\pi_{(0,1)}$ in terms of $\pi_{(0,0)}$:

$$\begin{aligned}\pi_{(1,0)} &= \frac{\lambda_u}{\mu_u + p\mu_v + \nu_u} \cdot \pi_{(0,0)} \\ \pi_{(0,1)} &= \frac{\lambda_v}{(1-p)\mu_v + \nu_v} \cdot \pi_{(0,0)}\end{aligned}$$

And these clearly satisfy the balance equations, see (31). We have now shown that our assumption holds for all $(i, j) \in \mathbb{N}^2$, which concludes the proof. □

Service probabilities We distinguish between the service probability for $u-$patients and for $v-$patients. Let R_u be the place in line for a specific $u-$patient to renege, and define $R_u = 0$ if the patient receives service. Let R_v be analogous for $v-$patients. Then the service probabilities for $u-$ and $v-$patients respectively, are given by $\mathbb{P}(R_u = 0)$ and $\mathbb{P}(R_v = 0)$. We proceed by calculating these values.

$$\begin{aligned}\mathbb{P}(R_u = 0) &= \sum_{(i,j)\in\mathbb{N}^2} \frac{\mu_u + p\mu_v}{\mu_u + p\mu_v + (i+1)\nu_u} \cdot \pi^{(u,v)}_{(i,j)} \\ &= \sum_{i\in\mathbb{N}} \frac{\mu_u + p\mu_v}{\mu_u + p\mu_v + (i+1)\nu_u} \sum_{j\in\mathbb{N}} \pi^{(u,v)}_{(i,j)} \\ &= \sum_{i\in\mathbb{N}} \frac{\mu_u + p\mu_v}{\mu_u + p\mu_v + (i+1)\nu_u} \sum_{j\in\mathbb{N}} \pi^{(u)}_i \cdot \pi^{(v)}_j \\ &= \sum_{i\in\mathbb{N}} \pi^{(u)}_i \frac{\mu_u + p\mu_v}{\mu_u + p\mu_v + (i+1)\nu_u} \sum_{j\in\mathbb{N}} \pi^{(v)}_j \\ &= \sum_{i\in\mathbb{N}} \frac{\mu_u + p\mu_v}{\mu_u + p\mu_v + (i+1)\nu_u} \cdot \pi^{(u)}_i\end{aligned} \tag{32}$$

Similarly,

$$\begin{aligned}\mathbb{P}(R_v = 0) &= \sum_{(i,j)\in\mathbb{N}^2} \frac{(1-p)\mu_v}{(1-p)\mu_v + (j+1)\nu_v} \cdot \pi^{(u,v)}_{(i,j)} \\ &= \sum_{j\in\mathbb{N}} \frac{(1-p)\mu_v}{(1-p)\mu_v + (j+1)\nu_v} \cdot \pi^{(v)}_j\end{aligned} \tag{33}$$

General expected waiting time For the expected waiting time for an arbitrary patient (of which the blood group is given) we start by conditioning on the starting position in the queue.
Let $W_u(i, j)$ be the waiting time for a patient of blood type u starting in position (i, j). To determine the

expected waiting time given this starting position, we use the results from Section 5.4.1, equation 12 to obtain

$$\mathbb{E}[W_u(i,j)] = \frac{i}{\mu_u + p\mu_v + i\nu_u} \tag{34}$$

Then, to find the general waiting time for patients of this blood group we sum over all possible starting positions while multiplying with the entries of the stationary distribution.

$$\begin{aligned}
\mathbb{E}[W_u] &= \sum_{(i,j)\in\mathbb{N}^2} \pi_{(i,j)}^{(u,v)} \mathbb{E}[W_u(i+1,j)] \\
&= \sum_{(i,j)\in\mathbb{N}^2} \frac{i+1}{\mu_u + p\mu_v + (i+1)\nu_u} \pi_{(i,j)}^{(u,v)} \\
&= \sum_{i\in\mathbb{N}} \frac{i+1}{\mu_u + p\mu_v + (i+1)\nu_u} \pi_i^{(u)} \sum_{j\in\mathbb{N}} \pi_j^{(v)} \\
&= \sum_{i\in\mathbb{N}} \frac{i+1}{\mu_u + p\mu_v + (i+1)\nu_u} \pi_i^{(u)}
\end{aligned} \tag{35}$$

Similarly, let $W_v(i,j)$ be the waiting time for a patient of blood type v starting in position (i,j). To determine the expected waiting time given this starting position, we use the results from section 5.4.1, equation 12 to obtain

$$\mathbb{E}[W_v(i,j)] = \frac{j}{(1-p)\mu_v + j\nu_v} \tag{36}$$

Then, to find the general waiting time for patients of this blood group we sum over all possible starting positions while multiplying with the entries of the stationary distribution.

$$\begin{aligned}
\mathbb{E}[W_v] &= \sum_{(i,j)\in\mathbb{N}^2} \pi_{(i,j)}^{(u,v)} \mathbb{E}[W_v(i,j+1)] \\
&= \sum_{(i,j)\in\mathbb{N}^2} \frac{j+1}{(1-p)\mu_v + (j+1)\nu_v} \pi_{(i,j)}^{(u,v)} \\
&= \sum_{j\in\mathbb{N}} \frac{j+1}{(1-p)\mu_v + (j+1)\nu_v} \pi_j^{(v)}
\end{aligned} \tag{37}$$

Expected waiting time for patients receiving service By using analogous methods and the equation given in (14), we formulate the expected waiting times for patients receiving service in the 2D model in the following way, starting conditioned on the starting position (i,j).

$$\begin{aligned}
\mathbb{E}[W_u(i,j)|R_u = 0] &= \sum_{(i,j)\in\mathbb{N}^2} \frac{1}{(\mu_u + p\mu_v) + i\nu_u} \\
\mathbb{E}[W_v(i,j)|R_v = 0] &= \sum_{(i,j)\in\mathbb{N}^2} \frac{1}{(1-p)\mu_v + j\nu_v}
\end{aligned} \tag{38}$$

Then, to obtain the waiting time for patients receiving service unconditioned on the starting position, we sum over the stationary distribution as follows.

$$\begin{aligned}
\mathbb{E}[W_u|R_u = 0] &= \sum_{(i,j)\in\mathbb{N}^2} \pi_{(i,j)}^{(u,v)} \mathbb{E}[W_u(i+1,j)|R_u = 0] \\
&= \sum_{(i,j)\in\mathbb{N}^2} \frac{1}{(\mu_u + p\mu_v) + i\nu_u} \pi_{(i,j)}^{(u,v)} \\
&= \sum_{i\in\mathbb{N}} \frac{1}{(\mu_u + p\mu_v) + i\nu_u} \pi_i^{(u)}
\end{aligned} \tag{39}$$

$$\begin{aligned}\mathbb{E}[W_v|R_v=0] &= \sum_{(i,j)\in\mathbb{N}^2} \pi_{(i,j)}^{(u,v)} \mathbb{E}[W_v(i,j+1)|R_v=0] \\ &= \sum_{(i,j)\in\mathbb{N}^2} \frac{1}{(1-p)\mu_v + j\nu_v} \pi_{(i,j)}^{(u,v)} \\ &= \sum_{j\in\mathbb{N}} \frac{1}{(1-p)\mu_v + j\nu_v} \pi_j^{(v)} \end{aligned} \tag{40}$$

Expected waiting time for reneging patients Analogously to the previous computations, we use the equation derived in (21) that represents the expected waiting time for patients reneging in the one-dimensional model, to derive the expected waiting times of the two-dimensional model. We end up with the following formula conditioned on starting position (i,j).

$$\begin{aligned}\mathbb{E}[W_u(i,j)|R_u>0] &= \frac{1}{\nu_u} - \frac{\mu_u + p\mu_v}{i\nu_u} \left(\sum_{(i,j)\in\mathbb{N}^2} \frac{1}{\mu_u + p\mu_v + i\nu_u} \right) \\ \mathbb{E}[W_v(i,j)|R_v>0] &= \frac{1}{\nu_v} - \frac{(1-p)\mu_v}{j\nu_v} \left(\sum_{(i,j)\in\mathbb{N}^2} \frac{1}{(1-p)\mu_v + j\nu_v} \right) \end{aligned} \tag{41}$$

For the general expected waiting times for reneging patients, we sum over the stationary distribution and get the following expressions

$$\begin{aligned}\mathbb{E}[W_u|R_u>0] &= \sum_{(i,j)\in\mathbb{N}^2} \pi_{(i,j)}^{(u,v)} \mathbb{E}[W_u(i+1,j)|R_u>0] \\ &= \sum_{(i,j)\in\mathbb{N}^2} \left(\frac{1}{\nu_u} - \frac{\mu_u + p\mu_v}{(i+1)\nu_u} \left(\sum_{(i,j)\in\mathbb{N}^2} \frac{1}{\mu_u + p\mu_v + (i+1)\nu_u} \right) \right) \cdot \pi_{(i,j)}^{(u,v)} \end{aligned} \tag{42}$$

$$\begin{aligned}\mathbb{E}[W_v|R_v>0] &= \sum_{(i,j)\in\mathbb{N}^2} \pi_{(i,j)}^{(u,v)} \mathbb{E}[W_v(i,j+1)|R_v>0] \\ &= \sum_{(i,j)\in\mathbb{N}^2} \left(\frac{1}{\nu_v} - \frac{(1-p)\mu_v}{(j+1)\nu_v} \left(\sum_{(i,j)\in\mathbb{N}^2} \frac{1}{(1-p)\mu_v + (j+1)\nu_v} \right) \right) \cdot \pi_{(i,j)}^{(u,v)} \end{aligned} \tag{43}$$

6.1.2 Equalizing performance measures

In the next section we will perform some numerical experiments using the expressions that we have calculated in the previous sections. For this we use the same initial data on organ transplantation in the Netherlands of heart, lung and kidney donation. We start by making a distinction between p_A and p_O. Let p_A be the proportion of A-type donor organs used on AB-type patients and p_O is the proportion of O-type donor organs used on B-type patients. Our goal is to apply our two-dimensional queuing model to find a value for p_A such that the performance measures between group A and AB are equalized and to find a value for p_O that equalizes the performance measures of group O and group B.

Case I: Heart transplants in the Netherlands The first case we will discuss is the case of heart transplants in the Netherlands. For this, we use the same data as in the ABO identical model, displayed in Table 2. This yielded the following parameter estimates, displayed in Table 12. We then calculate the performance measures derived in the previous section for different values of p_A and p_O. The results of this case study are displayed in Figure 15.

Blood type	O	A	B	AB
λ	29.07	27.778	5.814	1.938
μ	17.91	17.114	3.582	1.194
ν	0.1549	0.1549	0.1549	0.1549

Table 12: Parameters used in 2D Queuing model applied to heart transplants in NL

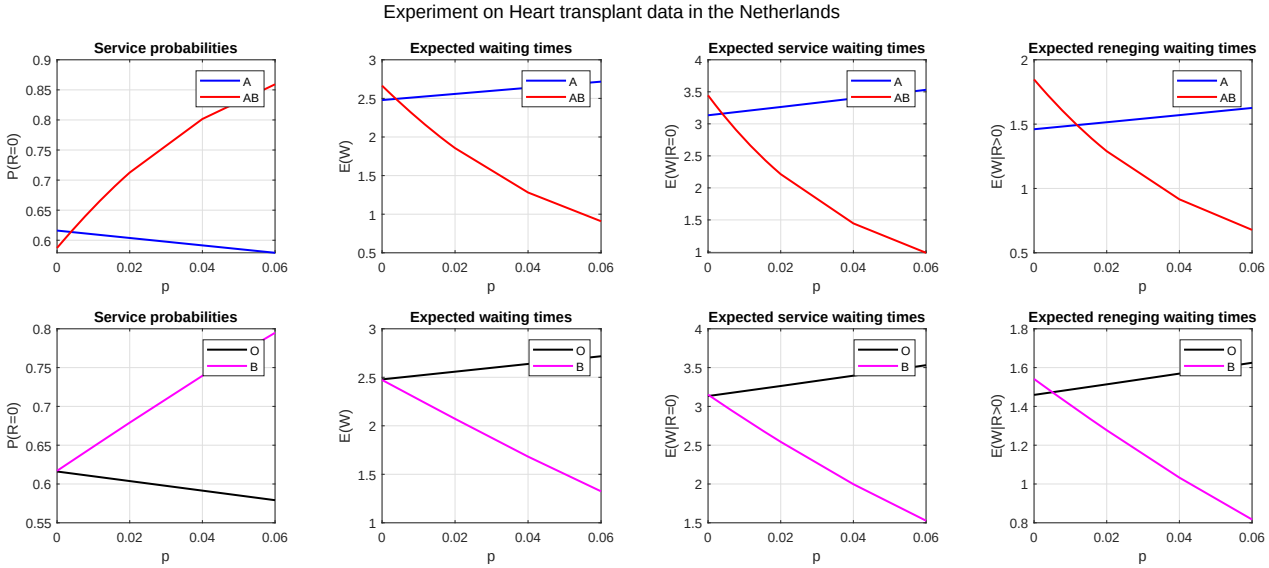

Figure 15: Results of 2D Queuing model applied to heart transplants in NL

In the first row of figures, that are displaying the performance measures for type A and AB patients, we can see that for p_A low enough, the performance measures of the AB patient group are worse than of the A group, resulting in a longer waiting time and lower service probability for group AB. A slight increase in p_A results in better performance measures for group AB, at the cost of worse performance measures for group A. We see that at the point $p_A = 1.5\%$, all the performance measures of group AB (red line) are already performing better than the performance measures of group A (blue line). The first three performance measures ($\mathbb{P}(R = 0), \mathbb{E}[W]$, and $\mathbb{E}[W|R = 0]$) are equalized at approximately the same value for p_A, which ranges between $3.81 \cdot 10^{-3}$ and $3.94 \cdot 10^{-3}$. This is approximately 0.4%. Although the differences between blood groups appear to be very small, the introduction of this p_A is still able to decrease the expected waiting time for AB patients by 2 months. This is at the cost of an increase of expected waiting time for A patients of 1.4 months. Since the disparity between blood groups is not very big to begin with, our method is less effective. If we look at the bottom row of Figure 15, then an increase of the probability p_O displayed on the horizontal axis will only lead to an increase of disparity (When ignoring $\mathbb{E}[W|R > 0]$, since this is less important).

Case II: Lung transplants in the Netherlands We conduct a similar experiment for lung transplantation in the Netherlands, using the parameters in Table 6. The results of this experiment are displayed in Figure 16. While the numbers on the axis are different, the graphs look very similar to the graphs in Figure 15. We will therefore not discuss these results in depth. Instead, we conclude that a very small value of p_A equalizes the performance measures between A and AB but this method is not very effective since the initial differences between these blood groups is small. Next to that, p_O should be zero otherwise disparity between O and B will increase.

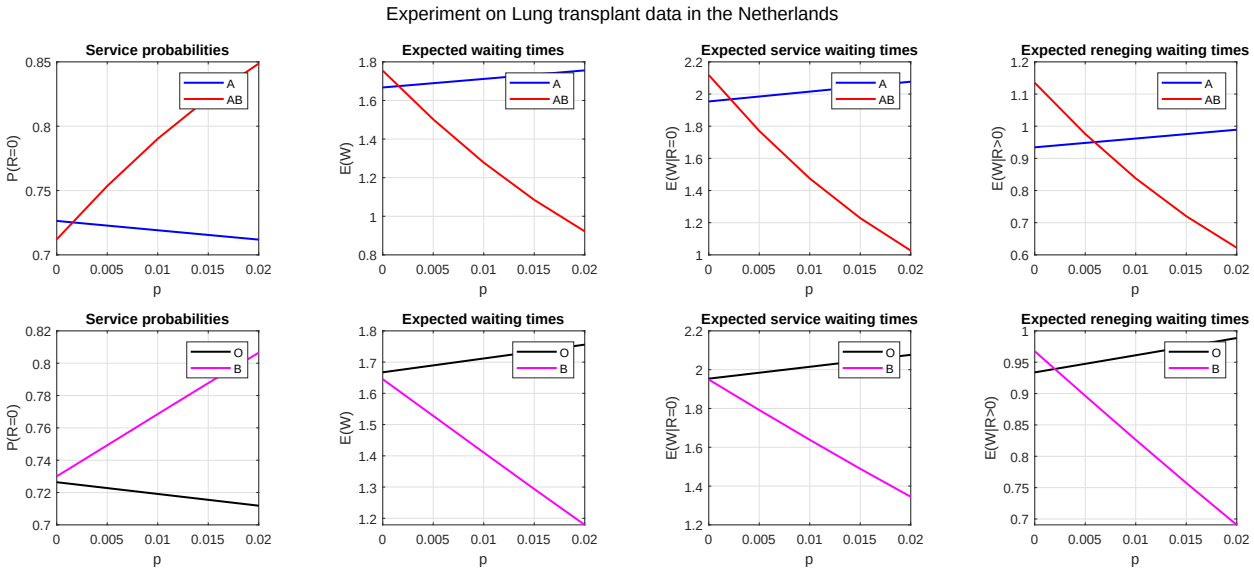

Figure 16: Results of 2D Queuing model applied to Lung transplants in NL

Case III: Kidney transplants in the Netherlands In the previous two cases, we have seen a less strong example of the problem we want to address. For the previous two cases, we used data from the Netherlands for heart and lung donation. The scope on which this occurs is small. The reason for choosing these organs is that these organs are only transplanted from deceased donors, ensuring a more random behavior. Kidney donation happens on a larger scale, but it is less random due to the contribution of living donor donation (which can be planned). Testing our model on kidney donor data is still useful to see how the results change for larger parameters. The parameters used for this experiment are displayed in Table 9. The results of the experiment on kidney data is displayed in Figure 17.

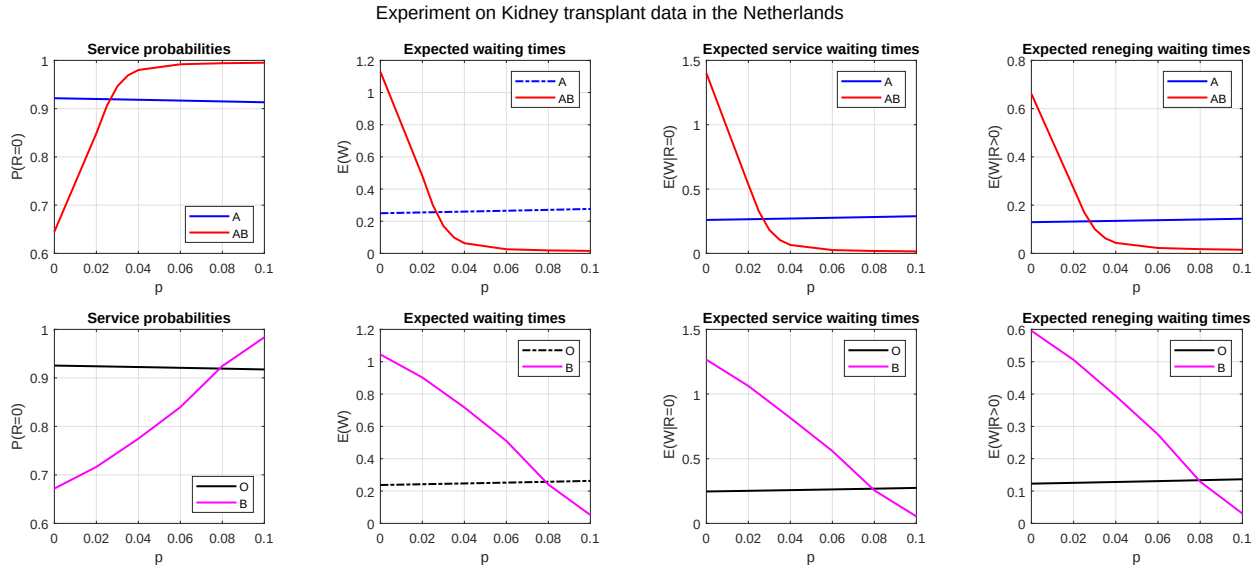

Figure 17: Results of 2D Queuing model applied to Kidney transplants in NL

The results of this experiment are in alignment with our expectations. We can clearly see that for $p = 0$ the rare blood types AB and O are at a big disadvantage. This disadvantage decreases gradually when p_A and

p_O are increased. Until the performance measures for two blood groups are equalized at certain values of p_A and p_O. A good thing to note is that this happens at around the same p-value for both bloodgroups that are in the same subgroup. For the subgroup of A and AB patients, this happens at a value $p_A \approx 0.026$, so around 2.6%. For the subgroup of O and B patients, this happens at a slightly higher value $p_O \approx 0.076$, about 7.6%. As you can see in the figure, the performance measures of the common blood types (displayed by the blue and black lines) almost appear to be a horizontal line. This is, of course, not the case since we know that the performance measures for the common blood types worsen for higher p-value since $p_O = p_A = 1$ leads to a service probability of 0 for patients of group O and A and infinite waiting times for these common blood types. The almost straight blue and black lines are an indication that the performance measures of the common blood groups are very resilient to slight increases in p_A and p_O, while the rare blood types can significantly benefit from this.
If the value of p_A is increased from 0% to 2.6% then the patients of group AB will experience a mean waiting time of around 3 months instead of 13.5 months. This is a decrease of 77%. Meanwhile, the expected waiting time for type-A patients only increases with 2.7%, a difference of a few days. The service probability of type-AB patients increases by 27,4% while the service probability of type-O patients only decreases with 0.22%.
If the value of p_O is increased from 0% to 7.6%, then the patients of group B will experience a mean waiting time of around three months instead of 12.5 months. This is a decrease of 75%. Meanwhile, the expected waiting time for type-O patients increases with 8.3%, from 2.85 months to 3 months(also just a few days). The service probability of type-B patients increases by 24.7% while the service probability of type-O patients only decreases with 0.62%.

7 Conclusion

In this thesis, we developed a way to deal with the blood group O problem that was inspired by the research of Stanford [20]. We used exponentially distributed times and added something that Stanford did not add to his model: patient reneging. This addition makes this research and it's conclusions distinct from the research by Stanford [20]. First of all, including reneging enabled us to not only look at the expected waiting times as performance measures, but also the probability of receiving an organ. Secondly, we see that the intensity of reneging has a big influence on the performance measures. A high reneging intensity decreases expected waiting times at the cost of service probability. Then, we constructed a one-dimensional queuing model that matches patients with donors under an ABO identical policy. The addition of reneging to the research of Stanford proves that it does not always have to be the case that rare blood groups are at a disadvantage under an ABO identical policy since we did not observe this disparity in heart and lung donation in the Netherlands. We did, however, observe this disadvantage for rare blood groups in the experiment on kidney donation in the Netherlands. The disparity found in the ABO identical experiment on kidney donation was undesirable, showing the need for improvement. However, the disparity was not as significant as Stanford's research would suggest. Especially when comparing the performance measures of blood type AB with the other blood types. He significantly overestimated the mean waiting times for rare blood groups by not accounting for reneging.
The two dimensional queuing model dit not suffice to make much improvements to equity in the case of heart and lung transplantation since there were no big disparities to begin with. Adding a nonzero value for p_O even created more disparity. The two dimensional model was however very efficient at creating more equity between patient blood groups in the case of Dutch kidney donation, which had more disparity present in the ABO identical model. In this case, allowing for restricted cross-transplantation has caused impressive improvements in the performance measures of rare blood groups while leaving the common blood groups relatively unaffected.
To conclude, the model for restricted cross-transplantation is very effective at counter-acting the blood group O problem, creating more equity between patient blood groups. Unless the performance of the ABO identical does not show significant disparities between patient groups. Then cross-transplantation is not needed.
The model can be extended to more organ types and transplant population pools to see if it is applicable in different scenarios.

7.1 Discussion

Not all aspects and details of the complicated real-world allocation process could be highlighted in this report. It is therefore important to reflect on the things that could not be implemented and therefore could influence the applicability of the conclusions. We have listed some of these things here

- This report focussed on measurements of equity (waiting times and service probability) and not on efficiency. Life expectation after transplantation, survival chances and other measures of efficiency were not considered.
- We made use of a first-come, first-transplant allocation rule. This is in real life not common since patients are often matched with organs based on medical priority, survival probability, age, geographic location and many other characteristics.
- Complex real-world allocation systems
- The variances or distribution of the waiting times are not taken into account, only the expectation/mean.
- We only took into account the four ABO blood groups, not other blood group divisions (such as Rh factor) or other factors of medical compatibility.
- In the model the assumption was made that reneging can happen for each patient after an exponentially distributed time. Here, the memoryless property of the exponential distribution implies that the amount of time a patient has already waited does not affect the service probability. This does not correspond to real life since spending more time waiting on an organ transplant often comes paired with a deteriorating health affecting the time this patient will survive before getting a transplant.
- In the data on Dutch kidney donation [15], the data on the outflow of the waiting list also contained patients who received service outside of the Eurotransplant zone. Since the contribution of these cases was very small, this was ignored.
- Kidneys can be donated from deceased donors but also from living donors. Transplantation from a living donor can be planned in time and is, therefore, less random. Also, a living donor can be searched for. This also makes it less random. This might influence the applicability of the model to kidney donation.
- The assumption was made that the demand for donor organs would outweigh the supply. But then we zoomed in on a case study of organs in the Netherlands. The numbers involved with lung and heart transplantation in the Netherlands are relatively low. If we look at the ABO identical model and then specifically to the part that deals with only type AB patients, which are just 3% of the population, then the chance of the queue being empty is much more probable. Then there can be periods in which supply outweighs demand.
- The parameters used in the case studies were made with the assumption that the five-year average for years 2017 until 2021 is a good approximation for the years that follow. This disregards a possibility of a decreasing or rising trend in the data, such as if the queue length would get longer every year.
- The data that was used was from 2017 until 2021. During the corona crisis that started in 2020, many non-urgent medical procedures were delayed in the Netherlands. This could disrupt the data, making it less representative for the years that follow.

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A Function definitions in MatLab

```
% Define symbolic variables
syms i l m v n L real
% l = arrival rate
% m = service rate
% v = reneging intensity
% L = upperlimit of queue length

% Custom symbolic product function
function syms_product = syms_product(expr, var, a, b)
syms_product = exp(symsum(log(expr), var, a, b));
end

% Defines rate of service for v patients (vertical) in case of 2D model
function mu_vert = mu_vert_p(mu_u,mu_v,p)
mu_vert = ( 1-p ) * mu_v;
end

% Defines rate of service for u patients (horizontal) in case of 2D model
function mu_hor = mu_hor_p(mu_u,mu_v,p)
mu_hor = mu_u + p*mu_v;
end

% Calculates entries of stationary distribution divided by pi0
function pi_hat = pi_hat(l,m,v,n)
syms k % local variable k used for summation
pi_hat = (l^n)/(symprod(m+k*v,k,0,n));
end

% Calculates the stationary distribution for given parameters
function pi = pi(l,m,v,L)
pi_div = zeros(L,1); % Generate a vector of L zeros
pi_div(1)=1; % The first multiplier must stay a one
for n=(2:L)
    pi_div(n) = pi_hat(l,m,v,n-1); % note the index shift
    if pi_div(n) ==Inf
        pi_div(n)=0;
```

```
        break
    end
end
pi0 = 1/(sum(pi_div)); % Normalise by using pi0
pi = pi_div*pi0; % true pi
end

% Calculates the service probability, conditioned on starting position n
function pser_n = pser_n(l,m,v,n)
pser_n = m/(m+n*v);
end

% Calculates the service probability
function pser = pser(l,m,v,L,pi) %service probabilities pser
pser_n_vec = zeros(L,1);
for n=(1:L) %for each start position
    pser_n_vec(n,1) = pser_n(l,m,v,n);
end
pser = sum( pi .* pser_n_vec ); % sum over the stationary distribution
end

% Calculates General waiting time EW, conditioned on starting position n
function EWn = EWn(l,m,v,n)
EWn = n / (m + n * v);
end

% Calculates General waiting time EW
function EW = EW(l,m,v,L,pi)
EWn_vec = zeros(L,1);
for n=(1:L)
    EWn_vec(n) = EWn(l,m,v,n); % as a vector, conditioned on start
end
EW = sum( pi .* EWn_vec ); % sum over stationary distributon
end

% Service waiting time EWser, conditioned on starting position n:
function EWser_n = EWser_n(l,m,v,n)
syms k % local variable used for summation
EWser_n = symsum(1/(m+k*v),k,1,n);
end

% Service waiting time EWser
function EWser = EWser(l,m,v,L,pi)
EWser_vec = zeros(L,1);
for n=(1:L)
    EWser_vec(n) = EWser_n(l,m,v,n); % as a vector, conditioned on start
end
EWser = sum( pi .* EWser_vec); % sum over stationary distribution
end

%Reneg waiting time EWreg, conditioned on starting position n
function EWreg_n = EWreg_n(l,m,v,n)
syms k % local variable used for summation
EWreg_n = (1/v) - (m/(n*v)) * symsum(1/(m+k*v),k,1,n);
```

```
end

%Reneg waiting time EWreg
function EWreg = EWreg(l,m,v,L,pi)
EWreg_vec = zeros(L,1);
for n=(1:L)
    EWreg_vec(n) = EWreg_n(l,m,v,n); % as a vector, conditioned on start n
end
EWreg = sum(pi .* EWreg_vec); % sum over stationary distribution
end

% Returns parameters of interests in a 4x1 array
function data = data_array(l,m,v,L)
data = zeros(4,1); % create array
pi1 = pi(l,m,v,L); % stationary distribution for given parameters, used
   for all following computations
data(1,1) = pser(l,m,v,L,pi1);  % first row:    Service probability
data(2,1) = EW(l,m,v,L,pi1);    % second row:   General waiting time
data(3,1) = EWser(l,m,v,L,pi1); % third row:    Service waiting time
data(4,1) = EWreg(l,m,v,L,pi1); % fourth row:   Reneging waiting time
end
```

B Experiments in MatLab

```
    %% Experiments 1D model: varying parameters

% Main script for computing and storing data
L = 150;
range = linspace(0.01, 10, 20); % Define the range for the varying
   parameter

% Initialize a 3D array to store the results
% Dimensions: [4 measures, length of range, 3 parameters]
results_1D_vary = zeros(4, length(range), 3);

% Compute and store the data for each parameter
for i = 1:3
    for j = 1:length(range)
        if i == 1
            m = range(j);
            l = 1;
            v = 1;
        elseif i == 2
            m = 1;
            l = range(j);
            v = 1;
        else
            m = 1;
            l = 1;
            v = range(j);
        end
        data = data_array(l, m, v, L);
        results_1D_vary(:, j, i) = data;
```

```
    end
end

%% Experiments 2D model

L = 1000

% Hart:
tic
steps_hart = [0,0.002,0.004,0.006,0.008,0.01,0.012,0.014,0.016,0.018,0.02,
    0.04,0.06];
experiment_hart_OB = p_data(5.814, 29.07,3.582 , 17.91, 0.1549, 0.1549,
   steps_hart, L)
experiment_hart_AAB = p_data(1.938, 27.778, 1.194,17.114, 0.1549, 0.1549,
   steps_hart, L)
toc

% Long:
tic
steps_long = [0,0.005,0.01,0.015,0.02];
experiment_long_OB = p_data(b*l_long,o*l_long,b*m_long,o*m_long,v_long,
   v_long,steps_long, L)
experiment_long_ABB = p_data(ab*l_long,a*l_long,ab*m_long,a*m_long,v_long,
   v_long,steps_long, L)
toc

% Nier:
tic
steps_nier_AAB = [0.026675, 0.0266766, 0.027033, 0.0276892]
steps_nier_OB = [0.078749, 0.07875,0.079148, 0.079392]
experiment_nier_OB = p_data(b*l_nier,o*l_nier,b*m_nier,o*m_nier,v_nier,
   v_nier,[0,0.02,0.04,0.06,0.08,0.1],250)
experiment_nier_ABB = p_data(ab*l_nier,a*l_nier,ab*m_nier,a*m_nier,v_nier,
   v_nier,[0,0.02,0.025,0.03,0.035,0.04,0.06, 0.08,0.1],250)
experiment_nier_ABB = p_data(ab*l_nier,a*l_nier,ab*m_nier,a*m_nier,v_nier,
   v_nier
   ,[0,0.02,0.022,0.024,0.026,0.028,0.03,0.032,0.034,0.036,0.038,0.04,0.06],250)

toc


%%

steps = [0,0.01,0.02,0.03,0.04,0.05,0.06];

data= [29.07,17.91,0.1666666;
    27.778,17.114,0.1666666;
    5.814,3.582,0.1666666;
    1.938,1.194,0.1666666;];%etc
```

C Plotting figures for dependencies on parameters

```
    %% Dependencies
```

```
% Plot the results from the stored data in separate figures
param_names = {'  ', '  ', '  '};
measure_names = {'P(R=0)', 'E[W]', 'E[W|R=0]', 'E[W|R>0]'};

% Iterate over each performance measure
for k = 1:4
    figure;
    % Plot the results for each parameter
    for i = 1:3
        subplot(1, 3, i);
        plot(range, squeeze(results_1D_vary(k, :, i)),'LineWidth',1.5);
        xlabel(param_names{i});
        ylabel(measure_names{k});
        title([measure_names{k} ' vs ' param_names{i}]);
        grid on
    end
    sgtitle(['Dependence of ' measure_names{k} ' on parameters   ,   , and
          ']);
end
```

D Plotting figures for the two-dimensional model

```
%% Kidneys

% Create a new figure
figure(1)

% First subplot
subplot(2, 4, 1) % 2 rows, 3 columns, first subplot
plot(experiment_nier_ABB(:,1), experiment_nier_ABB(:,2), 'b-', 'LineWidth'
    , 1.5)
hold on;
plot(experiment_nier_ABB(:,1), experiment_nier_ABB(:,3), 'r-', 'LineWidth'
    , 1.5)
title('Service probabilities')
xlabel('p')
ylabel('P(R=0)')
legend('A', 'AB')
grid on

% Second subplot
subplot(2, 4, 2) % 2 rows, 4 columns, second subplot
plot(experiment_nier_ABB(:,1), experiment_nier_ABB(:,4), 'b-.', 'LineWidth
    ', 1.5)
hold on;
plot(experiment_nier_ABB(:,1), experiment_nier_ABB(:,5), 'r-', 'LineWidth'
    , 1.5)
title('Expected waiting times')
xlabel('p')
ylabel('E(W)')
legend('A', 'AB')
grid on
```

```
% Third subplot
subplot(2, 4, 3) % 2 rows, 4 columns, third subplot
plot(experiment_nier_ABB(:,1), experiment_nier_ABB(:,6), 'b-', 'LineWidth'
    , 1.5)
hold on;
plot(experiment_nier_ABB(:,1), experiment_nier_ABB(:,7), 'r-', 'LineWidth'
    , 1.5)
title('Expected service waiting times')
xlabel('p')
ylabel('E(W|R=0)')
legend('A', 'AB')
grid on

% Fourth subplot
subplot(2, 4, 4) % 2 rows, 4 columns, fourth subplot
plot(experiment_nier_ABB(:,1), experiment_nier_ABB(:,8), 'b-', 'LineWidth'
    , 1.5)
hold on;
plot(experiment_nier_ABB(:,1), experiment_nier_ABB(:,9), 'r-', 'LineWidth'
    , 1.5)
title('Expected reneging waiting times')
xlabel('p')
ylabel('E(W|R>0)')
legend('A', 'AB')
grid on

% Fifth subplot
subplot(2, 4, 5) % 2 rows, 4 columns, fifth subplot
plot(experiment_nier_OB(:,1), experiment_nier_OB(:,2), 'k-', 'LineWidth',
    1.5)
hold on;
plot(experiment_nier_OB(:,1), experiment_nier_OB(:,3), 'm-', 'LineWidth',
    1.5)
title('Service probabilities')
xlabel('p')
ylabel('P(R=0)')
legend('O', 'B')
grid on

% Sixth subplot
subplot(2, 4, 6) % 2 rows, 4 columns, sixth subplot
plot(experiment_nier_OB(:,1), experiment_nier_OB(:,4), 'k-.', 'LineWidth',
     1.5)
hold on;
plot(experiment_nier_OB(:,1), experiment_nier_OB(:,5), 'm-', 'LineWidth',
    1.5)
title('Expected waiting times')
xlabel('p')
ylabel('E(W)')
legend('O', 'B')
grid on

% Seventh subplot
```

```
subplot(2, 4, 7) % 2 rows, 4 columns, seventh subplot
plot(experiment_nier_OB(:,1), experiment_nier_OB(:,6), 'k-', 'LineWidth',
    1.5)
hold on;
plot(experiment_nier_OB(:,1), experiment_nier_OB(:,7), 'm-', 'LineWidth',
    1.5)
title('Expected service waiting times')
xlabel('p')
ylabel('E(W|R=0)')
legend('O', 'B')
grid on

% Eight subplot
subplot(2, 4, 8) % 2 rows, 4 columns, eight subplot
plot(experiment_nier_OB(:,1), experiment_nier_OB(:,8), 'k-', 'LineWidth',
    1.5)
hold on;
plot(experiment_nier_OB(:,1), experiment_nier_OB(:,9), 'm-', 'LineWidth',
    1.5)
title('Expected reneging waiting times')
xlabel('p')
ylabel('E(W|R>0)')
legend('O', 'B')
grid on

% Add a title for the entire figure
sgtitle('Experiment on Kidney transplant data in the Netherlands')

% Release the hold on the current figure
hold off;


%% Hearts

% Create a new figure
figure(2)

% First subplot
subplot(2, 4, 1) % 2 rows, 3 columns, first subplot
plot(experiment_hart_AAB(:,1), experiment_hart_AAB(:,2), 'b-', 'LineWidth'
    , 1.5)
hold on;
plot(experiment_hart_AAB(:,1), experiment_hart_AAB(:,3), 'r-', 'LineWidth'
    , 1.5)
title('Service probabilities')
xlabel('p')
ylabel('P(R=0)')
legend('A', 'AB')
grid on

% Second subplot
subplot(2, 4, 2) % 2 rows, 4 columns, second subplot
plot(experiment_hart_AAB(:,1), experiment_hart_AAB(:,4), 'b-.', 'LineWidth
    ', 1.5)
```

```
hold on;
plot(experiment_hart_AAB(:,1), experiment_hart_AAB(:,5), 'r-', 'LineWidth'
    , 1.5)
title('Expected waiting times')
xlabel('p')
ylabel('E(W)')
legend('A', 'AB')
grid on

% Third subplot
subplot(2, 4, 3) % 2 rows, 4 columns, third subplot
plot(experiment_hart_AAB(:,1), experiment_hart_AAB(:,6), 'b-', 'LineWidth'
    , 1.5)
hold on;
plot(experiment_hart_AAB(:,1), experiment_hart_AAB(:,7), 'r-', 'LineWidth'
    , 1.5)
title('Expected service waiting times')
xlabel('p')
ylabel('E(W|R=0)')
legend('A', 'AB')
grid on

% Fourth subplot
subplot(2, 4, 4) % 2 rows, 4 columns, fourth subplot
plot(experiment_hart_AAB(:,1), experiment_hart_AAB(:,8), 'b-', 'LineWidth'
    , 1.5)
hold on;
plot(experiment_hart_AAB(:,1), experiment_hart_AAB(:,9), 'r-', 'LineWidth'
    , 1.5)
title('Expected reneging waiting times')
xlabel('p')
ylabel('E(W|R>0)')
legend('A', 'AB')
grid on

% Fifth subplot
subplot(2, 4, 5) % 2 rows, 4 columns, fifth subplot
plot(experiment_hart_OB(:,1), experiment_hart_OB(:,2), 'k-', 'LineWidth',
    1.5)
hold on;
plot(experiment_hart_OB(:,1), experiment_hart_OB(:,3), 'm-', 'LineWidth',
    1.5)
title('Service probabilities')
xlabel('p')
ylabel('P(R=0)')
legend('O', 'B')
grid on

% Sixth subplot
subplot(2, 4, 6) % 2 rows, 4 columns, sixth subplot
plot(experiment_hart_OB(:,1), experiment_hart_OB(:,4), 'k-.', 'LineWidth',
     1.5)
hold on;
plot(experiment_hart_OB(:,1), experiment_hart_OB(:,5), 'm-', 'LineWidth',
```

```
    1.5)
title('Expected waiting times')
xlabel('p')
ylabel('E(W)')
legend('O', 'B')
grid on

% Seventh subplot
subplot(2, 4, 7) % 2 rows, 4 columns, seventh subplot
plot(experiment_hart_OB(:,1), experiment_hart_OB(:,6), 'k-', 'LineWidth',
    1.5)
hold on;
plot(experiment_hart_OB(:,1), experiment_hart_OB(:,7), 'm-', 'LineWidth',
    1.5)
title('Expected service waiting times')
xlabel('p')
ylabel('E(W|R=0)')
legend('O', 'B')
grid on

% Eight subplot
subplot(2, 4, 8) % 2 rows, 4 columns, eight subplot
plot(experiment_hart_OB(:,1), experiment_hart_OB(:,8), 'k-', 'LineWidth',
    1.5)
hold on;
plot(experiment_hart_OB(:,1), experiment_hart_OB(:,9), 'm-', 'LineWidth',
    1.5)
title('Expected reneging waiting times')
xlabel('p')
ylabel('E(W|R>0)')
legend('O', 'B')
grid on

% Add a title for the entire figure
sgtitle('Experiment on Heart transplant data in the Netherlands')

% Release the hold on the current figure
hold off;

%% Lungs

% Create a new figure
figure(3)

% First subplot
subplot(2, 4, 1) % 2 rows, 3 columns, first subplot
plot(experiment_long_ABB(:,1), experiment_long_ABB(:,2), 'b-', 'LineWidth'
    , 1.5)
hold on;
plot(experiment_long_ABB(:,1), experiment_long_ABB(:,3), 'r-', 'LineWidth'
    , 1.5)
title('Service probabilities')
xlabel('p')
ylabel('P(R=0)')
```

```
legend('A', 'AB')
grid on

% Second subplot
subplot(2, 4, 2) % 2 rows, 4 columns, second subplot
plot(experiment_long_ABB(:,1), experiment_long_ABB(:,4), 'b-.', 'LineWidth
    ', 1.5)
hold on;
plot(experiment_long_ABB(:,1), experiment_long_ABB(:,5), 'r-', 'LineWidth'
    , 1.5)
title('Expected waiting times')
xlabel('p')
ylabel('E(W)')
legend('A', 'AB')
grid on

% Third subplot
subplot(2, 4, 3) % 2 rows, 4 columns, third subplot
plot(experiment_long_ABB(:,1), experiment_long_ABB(:,6), 'b-', 'LineWidth'
    , 1.5)
hold on;
plot(experiment_long_ABB(:,1), experiment_long_ABB(:,7), 'r-', 'LineWidth'
    , 1.5)
title('Expected service waiting times')
xlabel('p')
ylabel('E(W|R=0)')
legend('A', 'AB')
grid on

% Fourth subplot
subplot(2, 4, 4) % 2 rows, 4 columns, fourth subplot
plot(experiment_long_ABB(:,1), experiment_long_ABB(:,8), 'b-', 'LineWidth'
    , 1.5)
hold on;
plot(experiment_long_ABB(:,1), experiment_long_ABB(:,9), 'r-', 'LineWidth'
    , 1.5)
title('Expected reneging waiting times')
xlabel('p')
ylabel('E(W|R>0)')
legend('A', 'AB')
grid on

% Fifth subplot
subplot(2, 4, 5) % 2 rows, 4 columns, fifth subplot
plot(experiment_long_OB(:,1), experiment_long_OB(:,2), 'k-', 'LineWidth',
    1.5)
hold on;
plot(experiment_long_OB(:,1), experiment_long_OB(:,3), 'm-', 'LineWidth',
    1.5)
title('Service probabilities')
xlabel('p')
ylabel('P(R=0)')
legend('O', 'B')
grid on
```

```
% Sixth subplot
subplot(2, 4, 6) % 2 rows, 4 columns, sixth subplot
plot(experiment_long_OB(:,1), experiment_long_OB(:,4), 'k-.', 'LineWidth',
    1.5)
hold on;
plot(experiment_long_OB(:,1), experiment_long_OB(:,5), 'm-', 'LineWidth',
   1.5)
title('Expected waiting times')
xlabel('p')
ylabel('E(W)')
legend('O', 'B')
grid on

% Seventh subplot
subplot(2, 4, 7) % 2 rows, 4 columns, seventh subplot
plot(experiment_long_OB(:,1), experiment_long_OB(:,6), 'k-', 'LineWidth',
   1.5)
hold on;
plot(experiment_long_OB(:,1), experiment_long_OB(:,7), 'm-', 'LineWidth',
   1.5)
title('Expected service waiting times')
xlabel('p')
ylabel('E(W|R=0)')
legend('O', 'B')
grid on

% Eight subplot
subplot(2, 4, 8) % 2 rows, 4 columns, eight subplot
plot(experiment_long_OB(:,1), experiment_long_OB(:,8), 'k-', 'LineWidth',
   1.5)
hold on;
plot(experiment_long_OB(:,1), experiment_long_OB(:,9), 'm-', 'LineWidth',
   1.5)
title('Expected reneging waiting times')
xlabel('p')
ylabel('E(W|R>0)')
legend('O', 'B')
grid on

% Add a title for the entire figure
sgtitle('Experiment on Lung transplant data in the Netherlands')

% Release the hold on the current figure
hold off;
```