



DISSERTATION

A Comparative Analysis of System Dynamics and Agent-Based Modelling for Health Care Reimbursement Systems

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Abstract

System dynamics and agent-based modelling are two methods for modelling dynamical systems. While both emphasize that complex dynamics can evolve from simple rules and relationships, they have also important differences. Agent-based models are considered to be more flexible, but normally have a higher computational demand than system dynamics models.

The central goal of this study is therefore to compare both approaches and investigate their similarities and differences. Moreover, it tries to answer the question of under which conditions one of the two methods is preferable or how they could complement each other. The motivation for these research questions comes from the author's modelling work on the study of reimbursement systems for physicians in extramural health care. A further goal is therefore to investigate how agent-based modelling and system dynamics could be applied to this field of research.

The thesis puts both methods on a common system-theoretic basis as it introduces the concept of a stochastic dynamical system, which is able to cover approaches that include randomness, such as agent-based modelling, but also contains deterministic dynamical systems (in particular system dynamics models) as a special case. It is then shown that system dynamics defines a dynamical system via its equivalence to differential equation systems. For agent-based modelling, a formal definition based on the Stochastic Discrete Event System Specification (STDEVS) is given. The thesis then presents a comparative analysis of the two methods regarding several aspects such as their suitability for modelling heterogeneity, the consequences of aggregation, and the representation of feedback. It is shown that the concept of a *rate* is used to describe change equivalently both in system dynamics and agent-based modelling.

The thesis argues that the two methods can complement each other beneficially

if the most important dynamical relationships of a problem are first analysed with a system dynamics model, which does not have to incorporate aspects such as heterogeneity that are hard to capture in the method. On the contrary, a transformation can later lead to an equivalent agent-based model for further development. The approach is demonstrated for a physician reimbursement model, which allows for a comparison of the dynamic impact of different reimbursement systems both on physicians' treatment style and on the population's health and which is presented in both a system dynamics and an agent-based version. Future research in this application area can build upon the model structure developed here, and the proposed modelling process has the ability to combine the strengths of the two methods with little additional effort.

Kurzfassung

System Dynamics und agentenbasierte Modellbildung sind zwei Methoden zur Modellierung dynamischer Systeme. Beide basieren auf dem Konzept, dass einfache Regeln und Zusammenhänge komplexes dynamisches Verhalten hervorbringen können. Trotzdem gibt es wesentliche Unterschiede: Agentenbasierte Modelle werden beispielsweise als flexibler angesehen, haben aber im Normalfall einen höheren Rechenaufwand.

Ein zentrales Ziel der vorliegenden Studie ist daher, die beiden Modellierungsansätze hinsichtlich ihrer Gemeinsamkeiten und Unterschiede zu vergleichen. Darüber hinaus soll eine Antwort darauf gegeben werden, unter welchen Bedingungen eine der Methoden zu bevorzugen ist oder wie sich die beiden Methoden gegenseitig ergänzen können. Diese Fragestellungen wurden dabei von Modellierungsprojekten des Autors zum Vergleich von Bezahlungssystemen für Ärztinnen und Ärzte im niedergelassenen Bereich des Gesundheitssystems motiviert. Ein weiteres Ziel dieser Arbeit ist daher herauszuarbeiten, wie agentenbasierte Modellierung und System Dynamics in diesem Forschungsfeld angewandt werden können.

Als gemeinsame systemtheoretische Basis für beide Methoden wird das Konzept eines stochastischen dynamischen Systems eingeführt. Es deckt Ansätze mit stochastischen Elementen, wie etwa agentenbasierte Modellierung, ab, enthält aber auch deterministische dynamische Systeme als Spezialfall. Tatsächlich definiert ein System-Dynamics-Modell über die Äquivalenz zu Differentialgleichungssystemen ein dynamisches System. Für agentenbasierte Modelle wird eine formale Definition auf der Basis der Stochastic Discrete Event System Specification (DEVS) gegeben. Anschließend werden beide Methoden anhand verschiedener Aspekte wie ihrer Eignung für die Modellierung von Heterogenität, der Konsequenzen von Aggregation und der Abbildung von Feedback vergleichend analysiert. Es wird gezeigt, wie

das Konzept einer *Rate* in einem gewissen Sinn äquivalent sowohl in System Dynamics als auch in der agentenbasierten Modellbildung für die Beschreibung von Veränderung verwendet wird.

Die vergleichenden Analysen lassen darauf schließen, dass sich beide Methoden gut ergänzen, wenn im Modellierungsprozess zuerst die wichtigsten dynamischen Zusammenhänge mit einem System-Dynamics-Modell untersucht werden. Dieses muss dabei Aspekte, die mit System Dynamics schwer abzubilden sind, vorerst nicht berücksichtigen, kann aber später über eine Transformation in ein äquivalentes agentenbasiertes Modell übergeführt werden. Der Ansatz wird in der Arbeit anhand eines Modells der Bezahlung von Ärztinnen und Ärzten demonstriert, mit dem der Einfluss unterschiedlicher Bezahlungssysteme sowohl auf den Behandlungsstil der Ärztinnen und Ärzte als auch auf die Gesundheit der Bevölkerung untersucht werden kann und das jeweils in einer Version für beide Methoden vorgestellt wird. Die hier vorgestellten Modellstrukturen können als Grundlage für zukünftige Forschung in diesem Anwendungsfeld dienen, und der vorgeschlagene Modellbildungsprozess bietet die Möglichkeit, die Stärken von System Dynamics und agentenbasierter Modellbildung mit geringem Zusatzaufwand zu vereinen.

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Chapter 1

Introduction

System dynamics and agent-based modelling represent two distinct modelling approaches: The former takes a top-down perspective and tries to model the system under study according to its major components and their interactions, whereas the latter is a bottom-up approach because it investigates a potentially large number of microscopic elements that, together with their interactions, constitute the whole system and its behaviour (Macal, 2010).

Both methodologies have been applied to the field of health care. It is often argued that agent-based modelling is more flexible and that it is easier to represent a system in great detail with agent-based modelling than with system dynamics. The main disadvantage that agent-based simulations had in the past, namely longer computing time, does not seem to be a big problem with the hardware of today.

However, the process of agent-based modelling and simulation (ABMS), from problem definition through conceptual modelling, implementation, verification and validation up to the analysis and presentation of results, is far less standardized than the process of system dynamics (SD). This might come from the fact that one person created most of the methodology of SD (for a history, see Forrester, 1995), whereas in the ABMS community there is not even a common definition of an agent. Moreover, agent-based models are not built up from a limited few defined elements as are SD models, which are mainly built from stock and flow variables, augmented by parameters, auxiliaries, and table functions.

As a further example, consider the available diagramming techniques for con-

ceptual modelling: It is standard for SD modellers to use causal loop diagrams and stock and flow diagrams. The latter are even used directly in the implementation. Agent-based models do not have such a standard representation in diagram form, although, for example, Heath (2010) as well as Onggo and Karpal (2011) propose types of diagrams to serve this function.

Despite such differences, Scholl (2001) recognizes that both fields do overlap significantly in their fields of application and that they might complement each other. Therefore, he calls for a cross study of the literature and suggests that valuable insights might be gained from applying the two methods to the same areas.

One field of study where no standard modelling approach has been established yet is the analysis of different reimbursement systems for providers of health care. Models in this area of application should answer the question of which schemes of payment for doctors are optimal and what possible consequences of each scheme could be. They must be able to incorporate, for example, the influence of reimbursement on treatment decisions and health consequences for patients. All diseases that lead to the consumption of health services play a role in this problem (not just one as in typical decision-analytic modelling of isolated health care interventions), which makes it even harder to deal with.

This thesis compares SD and ABMS both in general and with a special focus on the application to health care reimbursement systems. On the one hand, it will thus be important for future simulation studies in this particular field, where the selection of the best modelling method is a key question. In particular, it is not clear when and why the simulation of individuals should be more advantageous than an aggregated representation with global quantities. On the other hand, the results of the thesis will also be applicable to other areas of application where there is potential for SD and ABMS.

1.1 Goals and Research Questions

Independently from the application field of health care reimbursement systems, the thesis has two main goals:

- To compare ABMS and SD and investigate their similarities and differences
- To analyse the conditions under which one of these two methods is preferable and how they can complement each other

These goals should lead to general insights that are applicable to other areas of health care as well as to modelling and simulation with SD and ABMS in general. However, a narrower focus is also necessary in order to test the developed concepts and to propose concrete model structures. The third goal is thus:

- To investigate how ABMS and SD are applicable to the study of health care reimbursement systems

Several research questions follow from the goals stated above:

1. What constitutes a system dynamics or an agent-based model?
2. Do both methods share a common basis in systems theory?
3. What creates the dynamic behaviour in an agent-based model and in an SD model?
4. Is there a common description of changes in individuals' states in ABMS and SD?
5. Under which circumstances is aggregation permissible in simulation models?
6. Is it possible to transform an SD model into an equivalent AB model and vice versa, and if so, under which conditions?
7. How can SD and ABMS complement each other?
8. What are the core dynamic structures in SD and agent-based models for comparing reimbursement systems?

System dynamics is a methodology with fixed building blocks (stocks, flows) and strict semantics. In contrast, there is no universally accepted definition of what an agent-based model is exactly. Tolk et al. even state that interest in such a definition

has decreased in recent years. However, a comparison of the two methodologies needs at least a working definition of SD as well as ABMS (Question 1) and, preferably, a common system-theoretic basis, which is the task of Question 2.

Dynamic models are tools for the analysis of dynamic behaviour. Both methodologies generate this behaviour on the basis of the models' structure and rules for their execution (i.e., simulation). Questions 3 and 4 ask what drives behaviour in SD and ABMS models and if these mechanisms are similar.

An oft-mentioned difference between the two methodologies is that SD uses aggregated quantities to describe system behaviour, whereas ABMS maps individuals separately. This leads to Question 5, because it is not clear when aggregation can occur without severely distorting results.

Modelling methods have their advantages and disadvantages. If a researcher starts building a model using one method because certain advantages of that model seem to be important, is the choice then fixed, or is it possible to attain the same perspective on the system or problem under study without much difficulty using another method? Question 6 deals with the transformation of a given model in either SD or ABMS into one based on the other methodology.

This problem is particularly important if one method, although most convenient for describing the system, has severe disadvantages in one or more stages of the modelling cycle. Agent-based models, for example, can easily be computationally expensive, which might prevent extensive sensitivity analyses with many simulation runs. On the other hand, system dynamics might not be able to cope with certain system structures (e.g., networks) and complex interventions. Maybe both methods could complement each other, either through hybrid models or different use scenarios (Question 7).

Lastly, Question 8 calls for the development of simple model structures, both in SD and ABMS, that capture the most important dynamic relationships of the problem of comparing health care reimbursement systems without too much distracting detail complexity. Every epidemic model, for example, uses the positive feedback loop caused by more infectious people infecting even more additional individuals who in turn become infectious, even though implementation can differ depending on the modelling method. It would be beneficial if such core dynamic structures could be also identified for health care reimbursement systems.

1.2 Structure of the Thesis

Both SD and ABMS are modelling methods that make it possible to describe dynamical systems. Chapter 2 develops the system theoretic foundations of such systems, in particular of those with stochastic behaviour, as agent-based models often include discrete events where the time between events follows a probability distribution.

On the basis of this, Chapter 3 and Chapter 4 describe the two modelling methods in detail, both in terms of informal basic characteristics and in terms of possible formal descriptions according to the definition of a dynamical system given in Chapter 2. Each of the two chapters includes one real-world example where SD and ABMS, respectively, are used to develop a model for the analysis of different reimbursement systems in extramural health care.

The theoretical comparison follows in Chapter 5, where topics such as aggregation, heterogeneity, feedback, and rates as a tool for describing change in both SD and ABMS are covered. This chapter concludes with the recommendation that SD and ABMS could complement each other in the modelling process if first SD is used to develop a model that captures the important dynamic structure of a problem without paying attention to detail complexity and this SD version is later transformed into an equivalent agent-based model if necessary. Finally, Chapter 6 demonstrates this approach for a physician reimbursement model, where implementations using both modelling methods lead to practically identical results, which shows that the transformation from SD into an equivalent ABMS model is possible.

Chapter 2

System Theoretic Foundations

2.1 Introduction

Models can be created with just an intuitive understanding of the underlying modelling method, but this comes with the disadvantage that rigorous mathematical statements about the methods are then impossible. These statements require that models and systems are defined as mathematical objects, rooted ultimately in an axiomatic system such as set theory.

Neither system dynamics nor agent-based models have universally accepted mathematical definitions¹. As the enterprise of this thesis is to compare SD and ABMS and statements should be as rigorous and valid as possible, it is necessary to give at least working definitions of both model types. We will also show how they can be seen as special cases of a class of more general mathematical objects: *stochastic dynamical systems*. Note that while SD models are deterministic in the sense that under the same initial conditions and input they always produce the same state trajectories and output, deterministic systems can be seen as a special class of stochastic systems where one possible system behaviour is always reproduced with probability 1, that is, the probability measure of the behaviour is a Dirac measure.

The main purpose of this chapter is to give a useful definition of a stochastic dynamical system. It is structured in the following way:

¹SD models are often identified with differential equation systems, but this is not the original definition. An equivalence between the two will be established in Section 3.4.2.

- First, Section 2.2 clarifies what the terms *model* and *system* mean in this context.
- Section 2.3.1 introduces the concept of a *general stochastic system*, which is described as a probability space according to the theory of Willems (2013). We show that this definition is also applicable for *input-output systems*.
- Section 2.3.2 defines *stochastic dynamical systems*, which are systems with time-dependent behaviour and an internal state. It also contains a proof that this definition is compatible with general stochastic systems (every stochastic dynamical system describes a general stochastic input-output system).
- Finally, Section 2.4 provides a survey of other definitions of systems.

2.2 Models and Systems

An intuitive idea of modelling and simulation is that a model is a tool for solving problems and answering questions that are related to a certain system. The method consists of creating an (often formal and simplified) representation – the model – and performing experiments, so-called simulations, with it. These simulations can show the behaviour of the system under different circumstances, which may be formalized as input and initial states.

We want to treat certain objects in the physical world as systems, for example a hospital, the population of a country, or its health care system, but physical objects are not mathematical objects and cannot satisfy a formal mathematical definition. Therefore, we will give a general but informal definition of systems, and then a formal definition of the special class of a *mathematical system*. What constitutes a model will only be formal if all involved systems are mathematical systems.

Definition 2.1 (System). A collection of interacting or interdependent objects is called a *system*. These objects are the *components* of the system.

Most systems interact with the outside world rather than exist in isolation. Their *system boundaries* separate them from the environment. A system can still interact with its surroundings by the *input* that it receives and the *output* that it

generates. We call such a system an *open system*, as opposed to a *closed system*, which exists in isolation (von Bertalanffy, 1950, p. 155).

There are two important aspects of a system: its *structure* and its *behaviour*. Structure describes the components and how they are interconnected. What follows from this structure, the outcomes that the system generates under various circumstances, constitute its behaviour, which can be measured in the form of data. Zeigler, Praehofer, and Kim (2000, p. 25) emphasize this role of a system as “a source of observable data”.

We call the system that is the actual object of an analysis the *object system* (or *source system*) and denote it by Σ_O . However, the structure and the full behaviour of Σ_O can be complicated, hard to understand, or hard to use in experiments, in particular because usually it is a system from the real world and includes physical objects or even humans. A *model system* Σ_M that is in certain key ways similar to Σ_O , but simplified and easily accessible, might be preferable to work with.

Obviously, Σ_M should be related to Σ_O in some way. Let us denote with C_O and C_M the sets of components of the two systems. Then, Ferstl and Sinz (2013, p. 22) require the specification of a *model mapping* $f: C_O \rightarrow C_M$. One can also specify that f is a homomorphism if both C_O and C_M have an algebraic structure, which is the *algebraic modelling approach*, in contrast to the *general approach* without the requirement of a homomorphism (Mesarovich & Takahara, 1975, pp. 218–220).

Even without that, there is a problem with this approach of mapping the structures of two systems. Suppose the system of interest is a specific country or, more specifically, its human population. A single differential equation for the number of humans in the country might be our model system. The components of this model system might be the number of humans (a state variable), the change of humans per time unit, the number of births per year as a constant, and possibly others. What constitutes a good model mapping? Every human can be seen as a component of the object system, so f has to map him or her to a component of Σ_M , and naturally this will be the number of humans. However, there might be components for which we do not want to have a counterpart in the model system (e.g., the animals, trees, and buildings of the country). No component of it is a reasonable stand-in for an animal. In the model, they are unnecessary.

A better approach is to map behaviour instead of structure. Suppose we observe a particular behaviour b in Σ_O , then for Σ_M there should be a counterpart b' . In the example above, b might describe the development of the country over time, including its population, animals, trees, buildings, and all other components. The corresponding b' of the model system only describes the number of humans at every modelled time point. Two different possible behaviours b_1 and b_2 of Σ_O will be mapped to the same b' as long as they give always the same number of humans. The mapping ignores behaviour related to components that are of no interest. In the following definition, we assume that every system has a set of all its possible behaviours, the universal set of behaviour \mathbb{U} .

Definition 2.2 (Model). A triple (Σ_O, Σ_M, f) , where Σ_O and Σ_M are systems and $f: \mathbb{U}_O \rightarrow \mathbb{U}_M$ is a surjective mapping, is a *model*. We call Σ_O the object system, Σ_M the model system, and f the *model mapping*.

A model consists of three parts, two systems and the model mapping, but less strictly one can also speak of a system Σ_M as the model of the system Σ_O . The model mapping is then only implicit. This is the usual way in which the term model is used, in particular because a model mapping can only be formally defined for formal systems. For real systems (and in modelling studies the original object system will most often be a real system) an “appropriate interpretation” (Ferstl & Sinz, 2013, p. 22) must substitute for this formal mapping.

The focus on behaviour instead of structure is influenced by the behavioural approach to systems theory (Willems, 1991). Section 2.4 gives more information on this.

2.3 Stochastic Systems

2.3.1 General Stochastic Systems

The object or source system is usually a predetermined real system. Modellers try to construct and experiment with an alternative model system to learn about this object system. These alternative systems might be physical systems, but in our context, they are only mathematical systems, that is, mathematical objects on the

basis of axiomatic set theory that consist of interrelated components. Typically, these components enter the definitions in the form of sets, and a mathematical relation between these sets describes the interaction.

An example of such a definition is the concept of a general *input-output system* (see Ferstl & Sinz, 2013, p. 16; Mesarovich & Takahara, 1975, p. 11; Pichler, 1975, p. 22). Such a system has two components, an input and an output, and describes which possible input elements are related to which possible output elements. More formally, an input-output system is a triple (U, Y, B) , where U is the set of possible inputs, Y is the set of possible outputs, and B is a non-empty relation between U and Y , which means that $B \subseteq U \times Y$. This representation views the system as a processor that receives an input and produces an output. An element y of Y can either be a possible output for an element u of U , in which case $(u, y) \in B$ (which can be written as uBy), or not. Several different outputs can be possible for an input. We call the relation B the behaviour of the system, which follows the practice of Willems (1991).

This definition of a system defines a crisp subset of behaviour. A single element of the universal set of all possible behaviour ($U \times Y$ in the case of an input-output system) has just two possibilities: It either is in the subset of the behaviour or is not. Such a deterministic definition of a mathematical system includes systems formulated in a deterministic modelling method such as system dynamics, but it makes it impossible to describe how likely a behaviour is.

Agent-based models often have stochastic elements, for example the time until an agent takes a certain action might follow a probability distribution. A great variety of different behaviours are possible, but some are far more likely than others. Many phenomena in health care are not exactly predictable, no matter how much information on the present and past state of the system is known. Examples for this are the progression of a disease and mortality: Many attributes of a patient might alter the risk for a specific event, but whether it will happen in a certain time span is in most situations uncertain. What can be known is which future course of events is more likely than another. From this it is clear that a useful definition of a mathematical system should allow for the incorporation of probability, or formally, a probability space. Indeed, Willems (2013) defines a stochastic system as a probability space:

Definition 2.3 (Stochastic System). A *stochastic system* is a probability space, that is, a triple (Ω, \mathcal{F}, P) where Ω is a non-empty set (the *outcome space*), \mathcal{F} is a σ -algebra on Ω , and $P: \mathcal{F} \rightarrow [0, 1]$ is a probability measure on \mathcal{F} . The elements of \mathcal{F} are the *events*.

How does this definition correspond to deterministic mathematical models? According to Willems, a deterministic model differentiates between two subsets of the universal set of behaviour: Elements that are possible behaviour (the behaviour B) and elements that are impossible (all other elements, i.e., the complement of B). Therefore, the equivalent of a deterministic model is a stochastic system with $\mathcal{F} = \{\emptyset, B, B^c, \Omega\}$, where $P(B) = 1$ and $P(B^c) = 0$.

It is more difficult to find a suitable probability space for the representation of a stochastic input-output model than it is in the deterministic case, where the behaviour of the system, B , would simply consist of all input-output pairs that the deterministic system might produce. Willems (2013) proposes a solution for simple examples, the symmetric and asymmetric binary channels, which we also want to use for the motivation of the problem. A construction analogue to the concept of a stochastic process will then allow us to generalize the solution to arbitrary stochastic input-output systems.

Example 2.4 (Deterministic Binary Channel). A binary channel has two input elements, $U = \{u_0, u_1\}$, and two output elements, $Y = \{y_0, y_1\}$. Assume that the channels always maps u_0 to y_0 and u_1 to y_1 . The behaviour of the channel is then the set $B = \{(u_0, y_0), (u_1, y_1)\}$, and it is clear how to construct the equivalent stochastic system (see the discussion above).

Example 2.5 (Stochastic Binary Channel). In the stochastic case, the binary channel has the same input and output sets. However, it maps u_0 only with a certain probability p_0 to y_0 and to y_1 otherwise (i.e., with probability $1 - p_0$). Similarly, it maps u_1 to y_1 with probability p_1 and to y_0 with probability $1 - p_1$.

Which probability space would represent this system? It is normally senseless to assign a probability to the event that one of the input elements occurs, because this lies outside the model boundary and should therefore not be part of the system description. But if we set $\Omega = U \times Y = \{(u_0, y_0), (u_0, y_1), (u_1, y_0), (u_1, y_1)\}$ and assume that $\mathcal{F} = 2^\Omega$, as would seem reasonable, then we must assign probabilities

to the events $\{(u_0, y_0), (u_0, y_1)\}$ and $\{(u_1, y_0), (u_1, y_1)\}$. We could try to incorporate that we are totally uninformed about the probability of the input elements by specifying $P(\{(u_0, y_0), (u_0, y_1)\}) = P(\{(u_1, y_0), (u_1, y_1)\}) = \frac{1}{2}$.

This is similar to specifying a non-informative prior in Bayesian probability theory, which is, however, a non-trivial task (see the discussion in Irony and Singpurwalla (1997)). Signal spaces are normally infinite and infinite-dimensional function spaces. It is not clear how to specify a non-informative marginal probability measure on the space of input signals.

The example of the stochastic binary channel demonstrates the problems with the construction of the probability space that constitutes the stochastic system. Willems solves this for the binary channel in the following way: He sets $\Omega = U \times Y \times E$, where $E = \{e_1, e_2, e_3, e_4\}$ is an auxiliary set, and assumes for \mathcal{F} the coarse σ -algebra that is generated by the events

$$\begin{aligned} E_1 &= \{(u_0, y_0, e_1), (u_1, y_0, e_1)\} \\ E_2 &= \{(u_0, y_0, e_2), (u_1, y_1, e_2)\} \\ E_3 &= \{(u_0, y_1, e_3), (u_1, y_0, e_3)\} \\ E_4 &= \{(u_0, y_1, e_4), (u_1, y_1, e_4)\}. \end{aligned}$$

Furthermore, he sets the probabilities for these events to

$$\begin{aligned} P(E_1) &= p_0(1 - p_1) \\ P(E_2) &= p_0p_1 \\ P(E_3) &= (1 - p_0)(1 - p_1) \\ P(E_4) &= (1 - p_0)p_1. \end{aligned} \tag{2.1}$$

The probabilities of the outputs, given a particular input, are then brought back by the concept of a *constrained probability* and subsequent marginalization to eliminate the e 's. We do not give the details here (refer to Willems [2013]), but proceed to the generalization of this mechanism and take a different point of view, which might be more intuitive.

Assume that a stochastic input-output system consists of an input set U and an

output set Y . Under a given $u \in U$, the system produces an output element that is not fixed, but can be described as a probability variable η_u . It would be possible to make Y into a probability space (with a certain σ -algebra \mathcal{E} , for example the Borel sets if Y is a topological space), separately for every $u \in U$, as in the following definition.

Definition 2.6 (Input-Output System). A *stochastic input-output system* is a structure $(U, Y, (\mathcal{E}_u)_{u \in U}, (P_u)_{u \in U})$, where U and Y are non-empty sets (the *input set* and the *output set*), $(\mathcal{E}_u)_{u \in U}$ is a family of σ -algebras on Y , and $(P_u)_{u \in U}$ is a family of probability measures on these σ -algebras such that for all $u \in U$, (Y, \mathcal{E}_u, P_u) is a probability space.

For a deterministic system, the σ -algebras on the output set would again be the coarse σ -algebras $\{\emptyset, B_u, (B_u)^c, Y\}$. We can then construct a stochastic system according to Definition 2.3 as $(U \times Y, \{\emptyset, B, B^c, U \times Y\}, P)$, where $B = \{(u, y) : u \in U, y \in B_u\}$ and $P(B) = 1$.

Indeed, it is always possible to find a suitable probability space (and thus, a stochastic system) that corresponds to a given input-output system. The main idea is that for every input $u \in U$ the output is a (Y, \mathcal{E}_u) -valued random variable $\eta_u: \Omega \rightarrow Y$ from one and the same probability space (Ω, \mathcal{F}, P) to the measurable space (Y, \mathcal{E}) . The family $(\eta_u)_{u \in U}$ can be seen as a *random mapping*. Intuitively, we imagine that first, a particular element $\omega \in \Omega$ of the probability space is sampled. The output is then predetermined for every possible input element, but we have to select one specific $u' \in U$ and can only observe the output $\eta_{u'}(\omega)$, while the realizations of all other random variables $(\eta_u)_{u \in U \setminus \{u'\}}$ are discarded.

As ω should determine the output for every $u \in U$, it seems natural to identify it with a mapping $\omega: U \rightarrow Y$ from the input into the output space. Therefore, we define $\Omega := Y^U$, that is, the sample space is the set of mappings from U to Y . Additionally, for any subset $J \subset U$, we write $\Omega_J := Y^J$.

Definition 2.7 (Canonical Projection). Let U and Y be non-empty sets. Then for two non-empty subsets $J \subset K \subset U$ the *canonical projection* from Ω_K onto Ω_J is

defined by

$$\begin{aligned}\pi_J^K : \Omega_K &\rightarrow \Omega_J \\ \omega &\mapsto \omega|_J\end{aligned}$$

and we write $\pi_J := \pi_J^U$ and $\pi_j := \pi_{\{j\}}$. The latter is the j -th *coordinate mapping*.

On the sample space Ω , the product σ -algebra $\mathcal{F} := \bigotimes_{u \in U} \mathcal{E}_u$ is defined as the smallest σ -algebra such that all coordinate mappings are measurable. There exists a unique probability measure $\bigotimes_{u \in U} P_u$ on (Ω, \mathcal{F}) such that for all finite subsets $J \subset U$, the push-forward measure $\pi_J(P)$ equals the finite product measure $\bigotimes_{u \in J} P_u$ (see Bogachev [2007]). We call $P := \bigotimes_{u \in U} P_u$ the *product measure* of the family $(P_u)_{u \in U}$. Note that for a finite number of sets $E_1 \in \mathcal{E}_{j_1}, \dots, E_n \in \mathcal{E}_{j_n}$, the probability of the Cartesian product is

$$P(E_1 \times \dots \times E_n) = P_{j_1} \otimes \dots \otimes P_{j_n}(E_1 \times \dots \times E_n) = P_{j_1}(E_1) \cdot \dots \cdot P_{j_n}(E_n).$$

It turns out that the probability space (Ω, \mathcal{F}, P) is the natural stochastic system that represents the input-output system.

Theorem 2.8. *Let $\Sigma_{IO} = (U, Y, (\mathcal{E}_u)_{u \in U}, (P_u)_{u \in U})$ be a stochastic input-output system. There then exists a stochastic system Σ and a family $(\eta_u)_{u \in U}$ of (Y, \mathcal{E}_u) -valued independent random variables such that*

$$P_{\eta_u} = \eta_u(P) = P_u,$$

that is, the distributions P_{η_u} of the random variables equal the corresponding probability measures P_u of Σ_{IO} .

Proof. Choose

$$\Sigma = (\Omega, \mathcal{F}, P) = (Y^U, \bigotimes_{u \in U} \mathcal{E}_u, \bigotimes_{u \in U} P_u)$$

as a stochastic system and for $(\eta_u)_{u \in U}$ the coordinate mappings $(\pi_u)_{u \in U}$. From the definition of the product σ -algebra \mathcal{F} , the coordinate mappings are measurable and, therefore, random variables. As a product measure, P fulfills $\eta_u(P) = \pi_u(P) = P_u$.

The family of random variables $(\eta_u)_{u \in U}$ is independent if for all finite subsets $J \subset U$ and all $E_j \in \mathcal{E}_j$, $j \in J$ the relationship

$$P(\{\omega \in \Omega : (\forall j \in J : \eta_j \in E_j)\}) = \prod_{j \in J} P(\{\omega \in \Omega : (\eta_j \in E_j)\}) \quad (2.2)$$

holds. Because the random variables are also the coordinate mappings, we get

$$\{\omega \in \Omega : (\forall j \in J : \eta_j(\omega) \in E_j)\} = \left\{ \omega \in \Omega : \pi_J(\omega) \in \prod_{j \in J} E_j \right\}.$$

Thus,

$$P(\{\omega \in \Omega : (\forall j \in J : \eta_j \in E_j)\}) = (\pi_J(P)) \left(\prod_{j \in J} E_j \right),$$

and because the push-forward measure $\pi_J(P)$ equals, according to the definition of P , the finite product measure $\bigotimes_{j \in J} P_j$, we see that

$$(\pi_J(P)) \left(\prod_{j \in J} E_j \right) = \prod_{j \in J} P_j(E_j).$$

Again, by the definition of the product measure, P_j is nothing else than the push-forward measure under the coordinate mapping π_j (which is η_j), so that

$$\prod_{j \in J} P_j(E_j) = \prod_{j \in J} (\eta_j(P))(E_j) = \prod_{j \in J} P(\{\omega \in \Omega : (\eta_j \in E_j)\}),$$

which proves (2.2). □

Example 2.9 (Stochastic Binary Channel, continued). The stochastic binary channel describes a stochastic input-output system with input set $U = \{u_0, u_1\}$ and output set $Y = \{y_1, y_2\}$. For every $u \in U$, the σ -algebra \mathcal{E}_u is the discrete σ -algebra $\mathfrak{P}(Y) = \{\emptyset, \{y_0\}, \{y_1\}, \{y_0, y_1\}\}$. The probability measures are given by

$$\begin{aligned} P_{u_0}(\{y_0\}) &= p_0 & P_{u_0}(\{y_1\}) &= 1 - p_0 \\ P_{u_1}(\{y_0\}) &= 1 - p_1 & P_{u_1}(\{y_1\}) &= p_1 \end{aligned}$$

For the corresponding stochastic system, we can choose (Ω, \mathcal{F}, P) as in the proof of Theorem 2.8:

$$\Omega = \{\omega_1, \omega_2, \omega_3, \omega_4\},$$

where the ω_k are mappings from U to Y and given (in set notation) by

$$\omega_1 = \{(u_0, y_0), (u_1, y_0)\}$$

$$\omega_2 = \{(u_0, y_0), (u_1, y_1)\}$$

$$\omega_3 = \{(u_0, y_1), (u_1, y_0)\}$$

$$\omega_4 = \{(u_0, y_1), (u_1, y_1)\}.$$

With the product σ -algebra \mathcal{F} , all coordinate mappings have to be measurable, that is, $\pi_0^{-1}(\mathcal{E}_0) \subset \mathcal{F}$ and $\pi_1^{-1}(\mathcal{E}_1) \subset \mathcal{F}$. But the preimages of the singeltons,

$$\begin{aligned} \pi_0^{-1}(y_0) &= \{\omega_1, \omega_2\} & \pi_0^{-1}(y_1) &= \{\omega_3, \omega_4\} \\ \pi_1^{-1}(y_0) &= \{\omega_1, \omega_3\} & \pi_1^{-1}(y_1) &= \{\omega_2, \omega_4\}, \end{aligned}$$

already generate the discrete σ -algebra, so that $\mathcal{F} = \mathfrak{P}(\Omega) = \mathfrak{P}(Y^U)$. Finally, we have to construct the product measure P on this σ -algebra, which is finite in this case. It follows that

$$\begin{aligned} P(\omega_1) &= P_{u_0}(\{y_0\})P_{u_1}(\{y_0\}) &= p_0(1 - p_1) \\ P(\omega_2) &= P_{u_0}(\{y_0\})P_{u_1}(\{y_1\}) &= p_0p_1 \\ P(\omega_3) &= P_{u_0}(\{y_1\})P_{u_1}(\{y_0\}) &= (1 - p_0)(1 - p_1) \\ P(\omega_4) &= P_{u_0}(\{y_1\})P_{u_1}(\{y_1\}) &= (1 - p_0)p_1, \end{aligned} \tag{2.3}$$

which is equivalent to the formulas in (2.1) that Willems gave. (This specifies the whole probability measure because of its additivity.)

If we want to restrict the input to, for example, u_0 , we can use the random variable $\eta_0 = \pi_0$ and get back its distribution:

$$\begin{aligned} P_{\eta_0}(y_0) &= P(\omega_1) + P(\omega_2) &= p_0 = P_{u_0}(\{y_0\}) \\ P_{\eta_0}(y_1) &= P(\omega_3) + P(\omega_4) &= 1 - p_0 = P_{u_0}(\{y_1\}) \end{aligned} \tag{2.4}$$

2.3.2 Stochastic Dynamical Systems

In the previous definitions, the input and output sets were simply assumed to be non-empty. Nothing was said about the nature of their elements.

Time systems, in contrast, are systems whose components are *time signals*, that is, their behaviour can change at every time point. This class of systems is important because many problems that arise in the health care system involve timing. One example is the course of a disease over time.

Which mathematical structure can represent time? It should be at least a totally ordered additive group. In this work, we will be more restrictive:

Definition 2.10 (Time Set). A *time set* \mathbb{T} is a subset of \mathbb{R} that is either discrete (*discrete time*) or an interval with finite or infinite endpoints (*continuous time*).

Typical examples of time sets are \mathbb{Z} and $\mathbb{Z}_{\geq 0}$ for discrete time as well as \mathbb{R} and $\mathbb{R}_{\geq 0}$ for continuous time. The definition excludes mixed time sets such as $[0, 1] \cup \mathbb{Z}_{\geq 0}$. We can now also formulate the definition of a time signal.

Definition 2.11 (Time Signal). A *time signal* f is a mapping from a time set \mathbb{T} to a non-empty set W , which is called the *signal space*.

A further concept is the *state* of a system. In the deterministic case, the state at any time point determines the future (input-output) behaviour unambiguously. The equivalent for a stochastic system is that the probability distribution of future behaviours depends only on the present state.

We will require in the definition of a stochastic dynamical system that it has input and output, such that two important components are the input-value set U and the output-value set Y . Both input and output should be time signals and have values in U and Y , respectively. The output space will therefore be $Y^{\mathbb{T}}$, but for the input space a restriction $\mathcal{U} \subset U^{\mathbb{T}}$ might be better.

Consider, for example, a system described by differential equations, such as the first order system

$$\begin{aligned} \frac{dy}{dt} &= u - y \\ y(0) &= 0 \end{aligned} \tag{2.5}$$

where u is the input function and y is the output function. If u is continuous, then the right-hand side of (2.5) is continuous and therefore the initial value problem has a solution according to the Peano existence theorem. (It is even unique because the right-hand side is Lipschitz continuous in y .) But if u is not continuous, a solution might not exist, such as in the case where the input u is the Heaviside step function

$$H: \mathbb{R} \rightarrow \{0, 1\}$$

$$t \mapsto H(t) := \begin{cases} 1 & \text{for } t \geq 0 \\ 0 & \text{for } t < 0. \end{cases}$$

Proposition 2.12. *The initial value problem (2.5) with input $u = H$, where H is the Heaviside step function, has no solution.*

Proof. A solution y would have to fulfill

$$\frac{dy}{dt}(t) = \begin{cases} -y(t) & \text{for } t < 0 \\ 1 & \text{for } t = 0, \end{cases}$$

and as a differentiable function it must be continuous. Since $y(0) = 0$, for $\epsilon > 0$ there exists a $\delta > 0$ such that $|y(t)| < \epsilon$ for all t with $|t| < \delta$. In particular, for $\delta < t < 0$ we have $|\frac{dy}{dt}(t)| = |-y(t)| < \epsilon$. If we choose, for example, $\epsilon = \frac{1}{2}$, we can therefore fix a point $t_1 < 0$ such that $y(t) < \frac{1}{2}$ for all t with $t_1 \leq t < 0$. But as a derivative, $\frac{dy}{dt}$ must have the intermediate value property according to Darboux's theorem and, therefore, take all values between $\frac{dy}{dt}(t_1)$ and $\frac{dy}{dt}(0) = 1$ on the interval $[t_1, 0]$, which leads to a contradiction. \square

In the example above, it might therefore be a natural choice to take the set of all continuous functions $C(\mathbb{T})$ as input space \mathcal{U} , because this secures that a solution of (2.5) (i.e., a corresponding output) exists for each input. In Chapter 3, we will see how to allow larger input spaces using the concept of weak solutions.

Additionally, a stochastic dynamical system should have a state space X . At every time point $t \in \mathbb{T}$, it will be in a state $x(t)$, and the state together with the

input should determine the output and the future states. This can be expressed by two mappings:

1. the *state transition map* ϕ , which describes the future states
2. the *output map* η , which describes the output given the present state and the input.

A suitable state transition map should fulfil a few important properties such as consistency with the present state and causality. We will require the same properties as Hinrichsen and Pritchard (2010), but extend the definition to the stochastic case.

Definition 2.13 (Stochastic State Transition Map). Let \mathbb{T} be a time set, (X, \mathcal{E}_X) be a measurable space (the state space), U be a non-empty set (the input value set), $\mathcal{U} \subset U^{\mathbb{T}}$ be a non-empty set of time signals (the input space). Furthermore, let (Ω, \mathcal{F}, P) be a probability space. A map

$$\phi: D_\phi \rightarrow X$$

with domain $D_\phi \subset \mathbb{T}^2 \times X \times \mathcal{U} \times \Omega$ is a *stochastic state transition map* if it satisfies the following properties:

1. **Measurability:** Let $t, t_0 \in \mathbb{T}$, $x_0 \in X$, $u \in \mathcal{U}$, and $\omega \in \Omega$ such that $(t, t_0, x_0, u, \omega) \in D_\phi$. Then the function $\phi_{t,t_0,x_0,u}: \Omega \rightarrow X$, $\omega \mapsto \phi(t; t_0, x_0, u, \omega)$ is $(\Omega, \mathcal{F}) - (X, \mathcal{E}_X)$ measurable.
2. **Interval property:** For every $t_0 \in \mathbb{T}$, $x_0 \in X$, $u \in \mathcal{U}$, and $\omega \in \Omega$ the set $T_{t_0,x_0,u,\omega} := \{t \in \mathbb{T} : (t; t_0, x_0, u, \omega) \in D_\phi\}$ is an interval containing t_0 .
3. **Consistency:** For every $t_0 \in \mathbb{T}$, $x_0 \in X$, $u \in \mathcal{U}$, and $\omega \in \Omega$ the mapping ϕ has the value $\phi(t_0; t_0, x_0, u, \omega) = x_0$ at the initial time t_0 .
4. **Causality:** Let $u, v \in \mathcal{U}$ be two different inputs. Then for any time point $t_1 \in T_{t_0,x_0,u,\omega} \cap T_{t_0,x_0,v,\omega}$ where $u(t) = v(t)$ for all $t \in [t_0, t_1[$ it holds that $\phi(t_1; t_0, x_0, u, \omega) = \phi(t_1; t_0, x_0, v, \omega)$.

5. Cocycle property: If for a time point $t_1 \in T_{t_0, x_0, u, \omega}$ the state transition map has the value $x_1 = \phi(t_1; t_0, x_0, u, \omega)$, then $T_{t_1, x_1, u, \omega} \subset T_{t_0, x_0, u, \omega}$ and it holds that $\phi(t; t_0, x_0, u, \omega) = \phi(t; t_1, x_1, u, \omega)$ for all time points $t \in T_{t_1, x_1, u, \omega}$.

It is quite cumbersome to always write all five arguments of ϕ . If it is clear from the context that four of the five arguments are fixed, then we simply set

$$\begin{aligned} \phi_{\mathbb{T}}: \mathbb{T} &\rightarrow X, & t &\mapsto \phi_{\mathbb{T}}(t) := \phi(t; t_0, x_0, u, \omega) \\ \phi_{\mathcal{U}}: \mathcal{U} &\rightarrow X, & u &\mapsto \phi_{\mathcal{U}}(u) := \phi(t; t_0, x_0, u, \omega) \\ \phi_{\Omega}: \Omega &\rightarrow X, & \omega &\mapsto \phi_{\Omega}(\omega) := \phi(t; t_0, x_0, u, \omega), \end{aligned}$$

and call $\phi_{\mathbb{T}}$ a *state trajectory*.

The interval property guarantees that the state trajectory is defined on an interval containing t_0 . Obviously, $\phi_{\mathbb{T}}(t_0)$ should equal x_0 , which holds because the state transition map is consistent. That a trajectory should not depend on the future of the input is the definition of causality. Finally, without the cocycle property we could get different values depending on whether we use the state transition map directly from t_0 to t or indirectly via the intermediate time point t_1 . Randomness adds the further necessary property that each ϕ_{Ω} is a random variable (i.e., a measurable function). Altogether, we are now able to define a stochastic dynamical system.

Definition 2.14 (Stochastic Dynamical System). A structure

$$\Sigma = (\mathbb{T}, U, \mathcal{U}, X, Y, (\Omega, \mathcal{F}, P), \phi, \eta)$$

is a *stochastic dynamical system* with time set \mathbb{T} , input value set U , input function space \mathcal{U} , state space X , output space Y , probability space (Ω, \mathcal{F}, P) , state transition map ϕ , and output map η if

- \mathbb{T} is a time set,
- $\mathcal{U} \subset U^{\mathbb{T}}$ is a non-empty space of time signals,
- X , and Y are non-empty sets,

- (Ω, \mathcal{F}, P) is a probability space,
- $\phi: D_\phi \rightarrow X$ and $\eta: \mathbb{T} \times X \times U \rightarrow Y$ are mappings such that ϕ is a state transition map with domain $D_\phi \subset \mathbb{T}^2 \times X \times \mathcal{U} \times \Omega$ according to Definition 2.13.

Again, this definition should correspond to the more general definitions in the last section. More precisely, does every stochastic dynamical system describe a general stochastic input-output system (and, with Theorem 2.8, a general stochastic system)?

First, we have to construct suitable input and output spaces U_{IO} and Y_{IO} . For every input element, the probability measure on the output space should be fixed. Therefore, it must include the input functions u of the dynamical system, the initial time t_0 , and the initial value x_0 , such that $U_{IO} = X \times \mathbb{T} \times \mathcal{U}$.

The output space is problematic, because the dynamical system produces output trajectories with different domains. Thus, Y_{IO} is not a subset of $Y^{\mathbb{T}}$. Let $\mathcal{S} \subset \mathfrak{P}(\mathbb{T})$ be the set of all intervals in \mathbb{T} . Then we define

$$Y_{IO} := \bigcup_{T \in \mathcal{S}} Y^T,$$

such that the output space is the set of all functions from an interval in \mathbb{T} to the output value space Y .

For any element (t_0, x_0, u) of the input space U_{IO} , we define a mapping

$$\begin{aligned} \Psi(\cdot, t_0, x_0, u): \Omega &\rightarrow Y_{IO} \\ \omega &\mapsto \Psi(\omega, t_0, x_0, u), \end{aligned} \tag{2.6}$$

where $\Psi(\omega, t_0, x_0, u)$ is the function on the domain $T_{t_0, x_0, u, \omega}$ such that

$$\Psi(\omega, t_0, x_0, u)(t) = \eta(t, \phi(t; t_0, x_0, u, \omega), u(t)) \tag{2.7}$$

for all $t \in T_{t_0, x_0, u, \omega}$.

Now we can define the σ -algebra $\mathcal{E}_{(t_0, x_0, u)}$ to be the largest σ -algebra on Y such that $\Psi(\cdot, t_0, x_0, u)$ is measurable (that is, the intersection of all σ -algebras on Y such that the mapping is measurable), and the natural probability measure $P_{(t_0, x_0, u)}$

on this σ -algebra is given by

$$P_{(t_0, x_0, u)}(E) = P(\{\omega \in \Omega : \Psi(\omega, t_0, x_0, u) \in E\}) \quad (2.8)$$

for all $E \in \mathcal{E}_{(t_0, x_0, u)}$. In this sense, there exists a corresponding general stochastic input-output system for every stochastic dynamical system.

The advantage of this formulation as a stochastic dynamical system over the more general system descriptions is that it more closely resembles how dynamic computer models and simulations work. On the other hand, via the intermediate step of constructing a corresponding input-output system and Theorem 2.8 it is possible to represent it as a general stochastic system, that is, as one probability space. Any question about the system is then nothing else than a question about random variables on this probability space. For example, a cost-effectiveness model generates output trajectories and calculates costs and effectiveness (e.g., in quality-adjusted life years) from it. The corresponding probability space has elements that are functions from the input space (whose elements are combinations of initial time, initial state, and input signal) to the output space (whose elements are output trajectories). Costs and effectiveness for a given input element are real-valued random variables on this probability space.

Once again, deterministic dynamical systems should be a special case of stochastic dynamical systems. They can be formulated by using a probability space with only one element: $\Omega = \{\omega_0\}$. Thus, the concept can cover SD as well as ABMS models.

2.4 Related Work

This section gives an overview on other definitions that can be found in the literature to show how they relate to the definitions we gave in this chapter. There are differences between what authors understand by, for example, a dynamical system, because some use the term for all systems that have time-dependent behaviour, while others require them to have a state space. Some authors consider only input-output systems. However, we regard these differences as minor and not fundamental.

2.4.1 Informal Definitions of Systems

As already stated, informal definitions have the advantage of being applicable to all possible objects. When it comes to the general concept of a system, such a definition includes mathematical systems, but also mental and physical systems.

Von Bertalanffy (1950, p. 143) for example defines it as “a complex of interacting elements”. Interaction means that there exists a relation R between the elements² and that it influences their behaviour (i.e., the elements would behave differently if they were in no relation or in a different one). The system is therefore more than the sum of its parts, and moreover, understanding the behaviour of each element in isolation is insufficient for deducing the behaviour of the system as a whole.

Pugachev and Sinitsyn (2001, p. 1) give a similar definition: “A set of interacting subjects of any nature is called *a system*.”

In contrast, Zeigler et al. (2000, p. 25) use in their framework the term system in the form of *source system* and view it as “the real or virtual environment that we are interested in modeling”. For them a simulation model “is a *set of instructions, rules, equations, or constraints for generating I/O behavior*”³.

Pichler (1975, p. 12) proposes a different perspective for models as simply scientific descriptions of real phenomena, and here systems are always formal scientific constructions that either serve to simulate the behaviour of the model or are proposed as a basis for model construction (these two tasks are the endeavour of systems theory). Therefore, from this point of view systems can serve as representations of models and not the other way around. They are always formal constructions and Pichler does not speak of the real phenomenon as a system. In our terminology, the equivalent of these formal constructions are mathematical systems.

All the definitions above that are applicable for real systems are quite consistent. In summary, a system is a set of interacting components and may be the “prototype” for a model that is supposed to represent the system and to be able to replicate its behaviour.

² R in this context is not a relation in the mathematical sense, i.e., a subset of the Cartesian product of two sets

³I/O means input-output. An input is given and the model generates the corresponding output through simulation

2.4.2 Formal Definitions of Systems

Most system theoretic formalizations in the literature are limited to the deterministic case. As with the definitions in this work, they also rely on mathematical constructs and thus ultimately on set theory.

Some authors restrict their work to input-output systems. In contrast, Mesarovich and Takahara (1975) construct their systems theory on a more fundamental level. They start from a general notion of a system that formalizes the concept of a set of interacting components, where interaction means essentially a restriction on possible behaviour. Their *general system* is a relation $S^G \subseteq \prod_{i \in I} V_i$, where $V = \{V_i | i \in I\}$ is a family of non-empty sets with index set $I \neq \emptyset$. Ferstl and Sinz (2013, p. 14) include additionally a set $R^G \subseteq \{(V_i, V_j) | i, j \in I \wedge i \neq j\}$ – the *structure* – and call S^G the *behavior* of the system. The V_i are called *system components*. This definition is clearly a formalization of the concept described by von Bertalanffy.

The structure R^G formally describes which system components interact. The elements of a component can be seen as its possible individual behavior, and the system behaviour R^G is a restriction on all feasible combinations of individual behaviour. However, one cannot necessarily derive the behaviour of a component from the given behaviour of all others, because there might be more than one corresponding tuple in S^G , e.g., for the trivial case

$$S^G = \prod_{i \in I} V_i.$$

Other types of system descriptions, such as the input-output system, are specialized forms of the general definition. The input-output system, for example, consists only of the two components U and Y , and in the case of a time system, the elements of the components are time signals.

Different requirements for dynamical systems can be found in the literature. Willems (1991), for example, calls every system whose behaviour consists of time signals a dynamical system. A state space is not a necessary requirement. Others, such as Hinrichsen and Pritchard (2010), restrict dynamical systems to systems with a state space. This richer concept is suitable for comparing SD and ABMS

models, because both methods naturally facilitate state-space descriptions.

Dynamical systems with stochastic behaviour are a less developed area than their deterministic equivalents. There is the theory of *random dynamical systems* developed by L. Arnold (2003), which analyses dynamical systems that are perturbed by noise. Stochastic differential equations are a typical example. While the theory fits well to this case, it is less convenient to describe the actions of stochastic agents as basically deterministic actions that are disturbed by some stochastic process.

Alternatively, we will treat the actions of agents to be stochastic themselves, and Definition 2.14 formalizes the idea that the state transition and output maps of a stochastic dynamical system depend directly on the chosen element ω of the underlying probability space. One may think of ω as the seed of the pseudo-random number generator that is used in a typical simulation model. It uniquely determines the resulting stream of pseudo-random numbers and, therefore, the value of the state transition map for a given initial time point, initial state, and input element at every future time point.

2.5 Conclusions

The system theoretic foundations in this chapter provide a common basis for the description of both deterministic and stochastic dynamical systems. It is thus precisely clear what is meant by a dynamical system in general as well as in the stochastic case. We will see that SD and ABMS are both methods that can be used to describe such dynamical systems, although they have different properties.

Mathematical systems are studied because they can be used as models for real systems. Definition 2.2 specified what a model is. There are always two systems with a certain relation involved. The model system can then represent the object system, which is normally the real system from the physical world. However, it could also be a mathematical model itself. We can thus study if, for example, a dynamical system formulated with one modelling method (e.g., SD) is interchangeable with one formulated using another method (e.g., ABMS).

Chapter 3

System Dynamics

3.1 Introduction

System Dynamics (SD) is the first modelling methodology that is described in this work. Historically, SD is older than agent-based modelling. It is also a very cohesive theory. The fact that a single person, Jay W. Forrester, created most of the methodology might be one of the key reasons for this. The central elements of SD (e.g., stocks and flows) are fixed and clearly defined. Additionally, recommendations on the modelling process, especially diagramming techniques such as causal diagrams and stock-and-flow diagrams, are part of the literature on the methodology. This can be seen as a standard for the modelling process not only in SD, but also in other methods.

The next chapter builds upon the SD description and makes it clear that ABMS, on the contrary, is much less cohesive and well-defined than SD. Nevertheless, both methodologies have a clear concept of what is responsible for the dynamics of a system.

3.2 The History of System Dynamics

The roots of SD lie in control theory and equation-based modelling. Jay W. Forrester was an engineer by training and transferred the ideas of control theory from technical systems to industrial and socio-economic systems while he was working at the MIT

Sloan School of Management in the 1950s (Forrester, 1995).

His first fields of application for the new methodology were industrial systems and the dynamics of urban planning (Forrester, 1961, 1969). The focus on industrial systems is responsible for the original name of the methodology: *industrial dynamics*. Forrester's influential textbook also bore this name.

Forrester's early work on industrial systems illustrates two concepts important to SD: *feedback* and *delays*. Together they are responsible for the dynamic behaviour of the system. An example is a supply chain, where products are delivered from a factory to a retailer over several intermediate stations (North & Macal, 2007, pp. 63–65). Every station can place orders, which depend on the state of the local inventory and on the expected future demand.

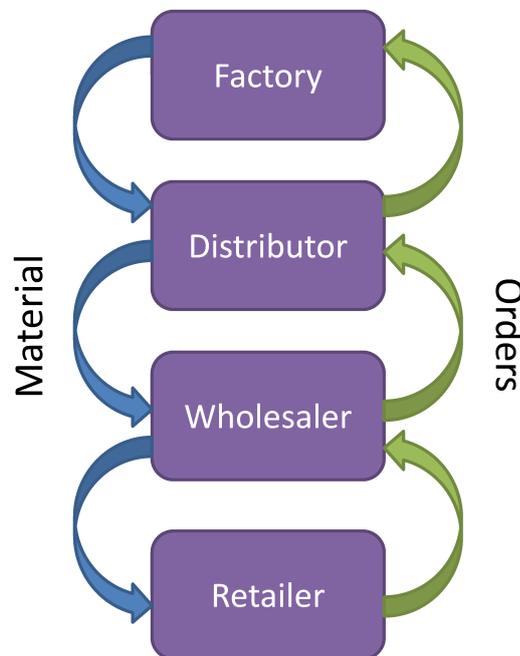


Figure 3.1: Supply chain with four levels: factory, distributor, wholesaler, and retailer. Orders are sent to the next highest level up in the chain (e.g., from retailer to wholesaler), while the material flow goes in the other direction (e.g., from factory to distributor).

The inventory levels influence their own values: A low inventory level induces more orders, which in turn increases the inventory level. This is an example of a

feedback structure, that is, a case in which one variable of the system influences its own change over time. In the supply chain example, feedback alone would stabilize the system. However, the inventory level does not rise instantaneously on account of the new orders; it takes some time for the new products to be delivered. This is a delay, and together with the feedback structure it causes overshoot of the inventory level, which decreases orders, but again there is a delay and it takes some time for deliveries to be reduced. Altogether, the structure of the system inevitably leads to oscillations with increasing amplitude, a phenomenon that is called the bull whip effect.

Urban dynamics revealed another aspect of social systems: *policy resistance*, which means that reasonable policies for solving a problem often just make things worse because of the structure of the system. For example, Forrester (1969) showed that the strategy of building more low-cost housing to revive depressed areas in cities cannot work. Available low-cost housing attracts more people, but this also raises unemployment in the depressed area. The standard of living declines and the income in the area is too low to maintain the buildings. They are abandoned and become excess housing. Housing then becomes even cheaper and attracts even more people, but the excess housing also occupies land that would be needed for job-creating buildings.

The success of SD in these first applications resulted in studies of a broad range of problems, with “Limits to Growth”, a study for the Club of Rome, probably being the most famous one. It built upon previous work from Forrester (1973) on the future development of the earth, its population and resources as a whole. Both studies predicted that the excessive growth of the world’s population, its economy and pollution would lead to certain collapse. Newer studies have come to the conclusion that the world is still on a path leading to disaster.

Both the work on urban dynamics and world dynamics demonstrate policy resistance. Often the goal of system dynamics studies is not only to find an optimal solution or to predict the further course of a system, but to explain why past policies did not work. This leads to a better understanding of the system and points to possible improvements.

In the past, system dynamics has found many areas of application. Health care is one example. Homer and Hirsch (2006) list various health care topics where

system dynamics has been applied, from disease epidemiology and drug addiction to patient flows in emergency departments and health care capacity planning. They also suggest that system dynamics could be helpful in creating more complete models of population health, which might incorporate multiple interacting diseases.

3.3 The Building Blocks of System Dynamics Models

3.3.1 Stocks and Flows

One major advantage of SD is that only a few basic elements are necessary to build a model. Every SD model consists of *stocks* and *flows* (equivalently, they are often called *levels* and *rates*). Stocks are variables that accumulate a certain quantity. Through this accumulation, stocks represent the memory and state of the system.

Flows are the other important variable type. They have no memory, because at every time point, their value depends only on the current values of the stocks. But they represent stock changes, because flows are the sole quantities that the stocks directly accumulate. More specifically, a flow F may be an inflow of a certain stock S , in which case S is increased by F , or it may be an outflow of S , in which case S is decreased by F .

These two elements are enough to describe the entire dynamics of a system. Actually, if the dependence of the flows on the stocks is specified through equations, the system is equivalent to a system of ordinary differential equations (see Section 3.4.2), where the stocks are the state variables and the flows are the right-hand sides of the differential equations. Together with initial values for the stocks, an initial value problem is given, which has a unique solution under the condition well-known from the theory of differential equations that the right-hand side is continuous in time and Lipschitz continuous in the state variable. In this regard, SD is just another way of describing differential equations.

However, the systematic way of deriving the equations is the real benefit of the method. The stock and flow structure is important on its own, even without the equations, because even it alone gives qualitative insight into the possible and

probable dynamic behaviour of a system. Moreover, it has a standardized graphical notation, the *stock and flow diagram*. Figure 3.2 shows a simple stock and flow diagram.

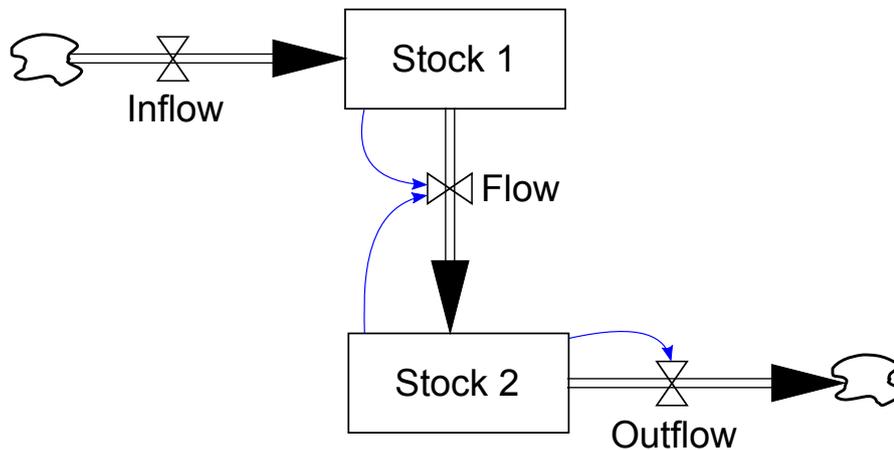


Figure 3.2: A stock and flow diagram that consists only of stocks (depicted as boxes) and flows (depicted as pipes with valves in the middle). If the source or sink of a flow is not important because it lies outside the system boundary, a small cloud symbol is drawn instead. Blue arrows show causal dependencies.

In the diagram, boxes depict stocks and pipes with valves in their middle depict flows. Every flow that ends in a stock is an inflow for this stock, whereas every flow that begins in a stock is an outflow. Stock 1 has one inflow that begins in a source outside the model boundary, depicted by a cloud symbol. Similarly, an outflow goes from Stock 2 into a sink. The flow in the middle is both an outflow for Stock 1 and an inflow for Stock 2.

There is an additional causal structure in the diagram. The blue arrows show on which stocks the flows depend. For example, the flow between Stock 1 and Stock 2 depends on both of them. On the other hand, it would be an error to use Stock 1 in the equation of the outflow from Stock 2, because there is no blue arrow from Stock 1 to Flow, which means that it is independent of Stock 1. Fortunately, SD simulation software is capable of automatically detecting such inconsistencies between diagram and equations.

3.3.2 Auxiliaries and Constants

Stock and flow diagrams with only stocks, flows, and their causal dependencies along with equations could describe every possible SD model, but often different concepts and effects are involved in a flow equation. In this case, it is beneficial to include intermediary variables to state these relationships directly in the stock and flow diagram. They are called *auxiliaries* because of their not necessary but often helpful nature. Like flows, these variables can depend on stocks and other auxiliaries. It must always be possible to calculate their value from all values of the stocks.

Additionally, stock and flow diagrams can include constant values as separate quantities. Of course, it would be possible to just write these values in the equations of auxiliaries or flows, but as in computer programming the use of such “magic numbers” is considered to be bad practice. The SD methodology tries to encourage modellers to make concepts graphically explicit and to give them meaningful names.

3.4 Describing Dynamical Systems Using System Dynamics

3.4.1 What Is a Modelling Method?

Besides SD and ABMS, many additional modelling methods exist, such as discrete event process models, Petri nets, bond graphs, and systems of differential or difference equations. Each of them describes a way of formulating a model that can be executed on a computer or for whom a solution can be calculated. But how does this relate to the concept of a dynamical system given in Definition 2.14?

Clearly, most modelling methods do not simply state two potentially complicated mappings such as in this definition. On the other hand, for every formulated model there should exist a corresponding dynamical system in the sense of Definition 2.14.

Definition 3.1 (Modelling Method). Let \mathcal{D} be the set of all stochastic dynamical systems. A *modelling method* is a pair (\mathcal{M}, τ) , where \mathcal{M} is a non-empty set, the *model space*, and τ is a mapping from \mathcal{M} to \mathcal{D} .

According to this definition, a modelling method must describe a set of possible models and map each of these models to a (stochastic) dynamical system. It is not necessary for τ to be injective, because a modelling method might allow for the formulation of different models that describe the same dynamic behaviour (i.e., map to the same dynamical system). However, every model should have a corresponding dynamical system.

3.4.2 Formal Description of System Dynamics

Definition 3.2 (System Dynamics Model). A *system dynamics model* with m stocks (levels), n flows (rates), k_a auxiliaries, and k_p parameters consists of n flow or rate equations $f_i: D_{f_i} \rightarrow \mathbb{R}$, $i \in \{1, \dots, n\}$, where $D_{f_i} \subset \mathbb{R}^m \times \mathbb{R}^{k_a} \times \mathbb{R}^{k_p}$, k_a auxiliary equations $g_j: D_{g_j} \rightarrow \mathbb{R}$, $j \in \{1, \dots, k_a\}$, where $D_{g_j} \subset \mathbb{R}^m \times \mathbb{R}^{k_a} \times \mathbb{R}^{k_p}$, and the flow coupling $FC \in (\{0, \dots, m\}^2 \setminus \{(i, i) : i \in \{0, \dots, m\}\})^n$.

The flow coupling FC denotes which stocks a flow connects. Here, the index 0 represents a source or sink. The pair $(i, 0)$ in the flow coupling stands, for example, for a flow from the i -th stock into a sink. A flow from the i -th stock into the stock with index j would be represented by the pair (i, j) .

All variables of a system dynamics model have values in \mathbb{R} . We write $\mathbf{x}(t) \in \mathbb{R}^m$ for the state vector of stocks at time t , $\mathbf{r}(t) \in \mathbb{R}^n$ for the vector of flows, $\mathbf{a}(t) \in \mathbb{R}^{k_a}$ for the vector of auxiliaries, and $\mathbf{p} \in \mathbb{R}^{k_p}$ for the parameter vector.

In the following, we want to find a corresponding differential or integral equation system for an SD model and define the state transition mapping and the output mapping via the solution of this equation system. This is impossible if the equations for the auxiliary variables form *algebraic loops*: Suppose that there are three auxiliary variables a_1 , a_2 , and a_3 in the model, and that the equations are $a_1 = g_1(\mathbf{x}, \mathbf{a}, \mathbf{p}) = a_2$, $a_2 = g_2(\mathbf{x}, \mathbf{a}, \mathbf{p}) = a_3$, and $a_3 = g_3(\mathbf{x}, \mathbf{a}, \mathbf{p}) = a_1$. Obviously, the equations are redundant and reduce to $a_1 = a_2 = a_3$, which has infinitely many possible solutions.

The question is which preconditions secure that there are no algebraic loops involving auxiliaries. This involves the concept of causal links.

Definition 3.3 (Causal Link). In a system dynamics model, a variable v_1 , where v_1 is a stock, an auxiliary, or a parameter, is a *direct cause* of an auxiliary or flow

v_2 if the corresponding auxiliary equation g_j (or f_j) depends on v_1 , that is, if the value of g_j (or f_j) is not the same for all values of v_1 , where all other variables are fixed. Likewise, a flow v_1 is a direct cause of a stock v_2 if it is an outflow or inflow of v_2 . In both cases, the model has a *causal link* from v_1 to v_2 .

Beginning from a variable, it is possible to follow causal links.

Definition 3.4 (Causal Chain). A sequence v_1, \dots, v_k of variables with $k \in \mathbb{N}$ is called a *finite causal chain* of length k beginning at v_1 if for every $i \in \mathbb{N}$ with $1 \leq i < k$ there is a causal link from v_i to v_{i+1} . Likewise, a sequence $(v_i)_{i \in \mathbb{N}}$ is called an *infinite causal chain* beginning at v_1 if it has the same property as in the finite case.

Definition 3.5 (Causal Loop). A *causal loop* of length k is a finite causal chain v_1, \dots, v_k where $v_1 = v_k$ and $v_i \neq v_j$ if $1 < i < k$ or $1 < j < k$.

If and only if there is a causal loop that involves just auxiliary variables the equations form an algebraic loop. We will now define a matrix that stores all causal links between auxiliaries. It is possible to see if an SD model includes a causal loop with only auxiliary variables from the structure of this matrix.

Definition 3.6 (Link Matrix). The *link matrix* L of an SD model with auxiliary variables a_1, \dots, a_{k_a} is the matrix where $L_{i,j}$ is 1 if there is a causal link from a_i to a_j and 0 otherwise.

Obviously, auxiliaries that have only causal links to flows do not pose any problem. But also other auxiliaries with causal links only to these first kind of auxiliaries cannot be part of an algebraic loop. We can pursue this strategy further and thus classify them:

Definition 3.7 (Causal Order). An auxiliary is of *causal order* 0 if it has no causal link to any other auxiliary. It is of order 1 if it has only causal links to auxiliaries of order 0. Generally, an auxiliary has causal order n if it has links to auxiliaries of order $n - 1$, but not causal links to auxiliaries of higher order. All other auxiliaries have infinite causal order.

Lemma 3.8. *An auxiliary a_0 has infinite causal order if and only if it is part of a causal loop involving only auxiliaries or if there is a causal chain beginning at a_0 that ends in such a causal loop.*

Proof. No auxiliary in a causal loop has causal order 0, because every auxiliary in the loop has a causal link to the next auxiliary in the loop. It follows that also no auxiliary can be of order 1, because an auxiliary of order 1 only has links to order-0 auxiliaries. The same holds for every finite order. Finally, if a causal chain ends in an auxiliary that is part of a causal loop, all auxiliaries of the causal chain have infinite order, which can be seen recursively.

On the other hand, suppose that a_0 is not part of a causal loop with only auxiliaries and there is also no causal chain beginning at a_0 that ends in a loop. As there are only k_a auxiliaries and no auxiliary can be part of a causal chain twice if the chain contains no loop, every causal chain that starts at a_0 is finite. If a_0 has infinite order, at least one of the auxiliaries to whom it has a causal link, denoted by a'_0 , has to have infinite order too. Again, one of the auxiliaries to whom a'_0 has a causal link has to have infinite order. In this way, it would be possible to construct an infinite causal chain where every auxiliary has infinite order, which is in contradiction of the fact that every causal chain starting from a_0 is finite. \square

Figure 3.3 shows an example of a causal diagram with only auxiliary variables. All auxiliaries in the loop have infinite causal order. Additionally, a_0 has infinite causal order because it has a link to another auxiliary of infinite order. The other auxiliaries (a_5 , a_6 , and a_7) have finite order.

Proposition 3.9. *An SD model contains a causal loop involving only auxiliaries if and only if it is not possible to renumber the auxiliaries such that the link matrix is a lower triangle matrix.*

Proof. First, suppose that the model has a causal loop involving only auxiliaries. For the link matrix to be a lower triangle matrix, a variable a_i can only have a causal link to a_j if $j < i$. One variable a' of the causal loop has to be the variable with the lowest number of all variables in the loop. As a variable in the loop, it has a causal link to the next variable in the loop. This variable must then have a

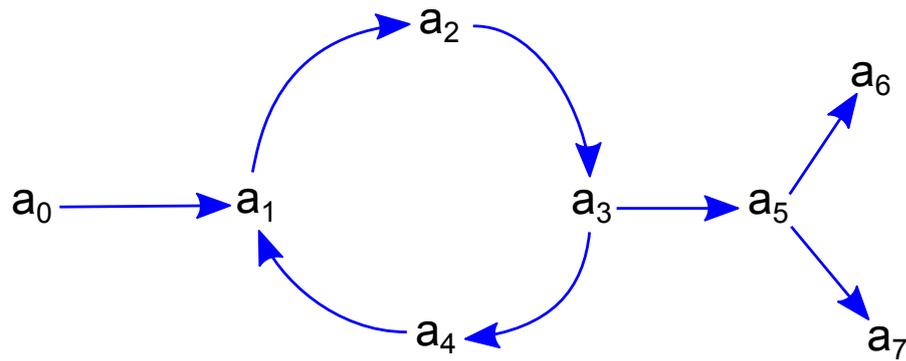


Figure 3.3: In this causal diagram, a_6 and a_7 have causal order 0 (they have no link to any other auxiliary). The only other variable with finite causal order is a_5 , which has causal order 1 because it has only links to variables of order 0. All other auxiliaries in the diagram have infinite causal order.

lower number than a' , which leads to a contradiction. Therefore, the link matrix cannot be of lower triangular form.

Now suppose that no causal loop involves only auxiliaries. Lemma 3.8 shows that then all auxiliaries must have finite causal order. We can therefore numerate the auxiliaries according to their order: First, we take all order-0 auxiliaries, then all order-1 auxiliaries, and so on. Each auxiliary can have only links to auxiliaries with lower order, which shows that the link matrix is of lower triangular form. \square

The last proposition gives a characterisation of the system dynamics models whose equations do not form algebraic loops. These models allow for the formation of a differential equation system which depends only on the values of stocks and parameters.

Proposition 3.10. *If a system dynamics model contains no causal loops of only auxiliaries, the flow equations can be written just in terms of stocks and parameters.*

Proof. In a system dynamics model, the flow equations might be given as functions that depend not only on stocks and parameters, but also on the values of auxiliaries. However, according to Proposition 3.9, the auxiliaries of a system dynamics model without algebraic loops can be enumerated such that the link matrix is of lower triangular form. The value of the first auxiliary a_1 depends only on stocks and parameters, that is, there is a function $g'_1: D'_{g_1} \rightarrow \mathbb{R}$ such that

$g'_1(\mathbf{x}(t), \mathbf{p}) = g_1(\mathbf{x}(t), \mathbf{a}(t), \mathbf{p})$ for all $(\mathbf{x}(t), \mathbf{a}(t), \mathbf{p}) \in D_{g_1}$, where the domain D'_{g_1} is the restriction of D_{g_1} to the set $\mathbb{R}^m \times \mathbb{R}^{k_p}$. The second auxiliary a_2 may depend on a_1 as well, but as the value of a_1 is a function of only stocks and parameters, so is a_2 . In general, as a_i for $1 \leq i < k_a$ depends only on stocks and parameters, so does a_{i+1} .

Finally, as all auxiliaries can be written as functions of stocks and parameters, all flow equations are also only functions of stocks and parameters. \square

This result guarantees that it is possible to find a differential equation system that is equivalent to the system dynamics model. Two problems could arise:

1. The differential equation system might not have a solution.
2. The differential equation might have more than one solution.

In both cases, it is not clear how to define the state transition mapping of the corresponding dynamical system. We should thus require the differential equation system to have a unique solution.

Chapter 2 provided a proof that the initial value problem (2.5) has no classical solution if the input is the Heaviside step function. This is unsatisfactory, as the Euler method that is typically used for the simulation of SD models does not have any problems with this system. Only the first step, which can be made arbitrarily small, is affected by the discontinuity. For all further steps, the input function equals 1.

It is possible to solve the differential equation for $t \geq 0$ with variation of constants and ignore the discontinuity at $t = 0$, which leads to the solution $y(t) = 1 - e^{-t}$. For $t < 0$, we can set $y(t) = 0$. The “solution” has the following properties:

1. It is Lipschitz continuous.
2. It fulfils the differential equation for $t \neq 0$.

It seems natural to accept this function as a solution. This leads to one kind of a generalized or weak solution concept: a solution in the sense of Carathéodory.

Definition 3.11 (Carathéodory Solution). A function is a *Carathéodory solution* of an ordinary differential equation system on an interval $I \subset \mathbb{R}$ if it is absolutely continuous and satisfies the differential equations almost everywhere on I .

The function y in the example above is absolutely continuous, because it is even Lipschitz continuous, and it satisfies the differential equation everywhere apart from $t = 0$, that is, almost everywhere, thus it is a Carathéodory solution. Note that an absolutely continuous function is differentiable almost everywhere. For comparisons with other generalized solution concepts, see al Shammari (2006).

Definition 3.12 (State Trajectory of a System Dynamics Model). Let \mathcal{M}_{SD} be a system dynamics model with no algebraic loop. The differential equation system

$$\frac{d\mathbf{x}}{dt}(t) = \mathbf{f}(\mathbf{x}(t), \mathbf{p}), \quad (3.1)$$

where $\mathbf{x}(t)$ is the state vector containing the values of the stocks, \mathbf{p} is the parameter vector, and \mathbf{f} is the vector of flow equations that depends only on the stocks and the parameters as in Proposition 3.10, is called the *equivalent differential equations system* of \mathcal{M}_{SD} . For an initial state x_0 at time t_0 , a Carathéodory solution of this system is called a *state trajectory* of the system dynamics model.

Through this definition, it is possible to specify a state transition map that corresponds to the SD model. For every fixed values of t_0 and x_0 , we can set it to the value of the state trajectory on the maximum interval where a unique Carathéodory solution exists. It is permissible that this interval contains only t_0 . Obviously, the state transition map obeys the other necessary properties such as consistency. Note that a system dynamics model has no separate input variables. Therefore, the input space of the corresponding dynamical system consists only of one element.

There is no single correct choice for an output map. An SD model usually has no dedicated output variables. However, the values of all stocks and auxiliaries can be seen as output. The output space is then $\mathbb{R}^m \times \mathbb{R}^{k_a}$.

Overall, it is clear that we can find a dynamical system that accurately represents the SD model. This system is deterministic (i.e., the probability space in the definition of the stochastic dynamical system has only one element). What we have also seen in this section is that for analytical purposes, it is correct to substitute the actual SD model, which is a collection of stocks, flows, auxiliaries, and parameters coupled by flow equations and auxiliary equations, with a differential equation system.

3.5 Case Example: Modelling the Influence of Group Practices with System Dynamics

3.5.1 Introduction

This section illustrates how a research question about the influence of different reimbursement systems in health care can be addressed with system dynamics. The focus will lie on methodological considerations, not on the specific results, which are published elsewhere, for example in Einzinger, Jung, Popper, and Pfeffer (2014).

Reimbursement systems describe how physicians are paid for the medical services they provide to patients. In the extramural sector in Austria (outside hospitals), physicians are mostly self-employed. Therefore, we can exclude reimbursement systems with a salary.

Remaining major types of reimbursement systems are:

1. *Fee-for-service systems*: Physicians receive payment for each medical service (e.g., injections).
2. *Per case flat rates*: Physicians receive a fixed payment for a case or an episode of care.
3. *Per capita flat rates*: Physicians receive a fixed payment per patient and time period.

Mixed types are also possible, as it is for example possible to pay per case flat rates, but reimburse some special medical services separately. This is the current reimbursement system in Austria.

Research question

Many physicians in Austria practice alone or with colleagues of the same specialty. However, the law now allows for the establishment of group practices with physicians of different specialties, such that for instance an internist and a pulmonologist could work together.

The plan is for these group practices to be reimbursed with different reimbursement systems than single practices. Specifically, schemes with flat rates are an option.

The research question of the study was how the organizational change (the merger to a group practice) and the change in reimbursement system would influence 1) the reimbursement of physicians (i.e., the costs for the payers) and 2) the numbers of served cases and provided medical services. The unit of analysis was a region of care, where several physicians of each of the two specialties reside. It is assumed that only one group practice is formed, while the other physicians continue practicing alone as shown in Figure 3.4.

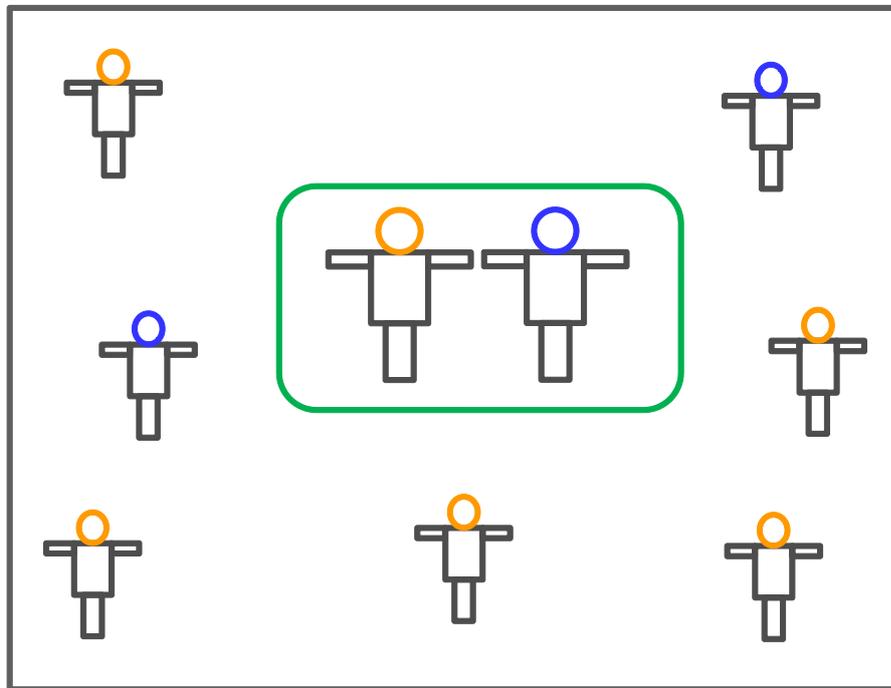


Figure 3.4: From all physicians of two specialties (symbolized by two different colours) in a region of care, two form a group practice.

Additionally to the base scenario (status quo without a group practice), four group practice scenarios were defined, each with a different reimbursement system:

- *Scenario 1*: No change in reimbursement system
- *Scenario 2*: Cap of case value

- *Scenario 3*: Per case flat rates
- *Scenario 4*: Mixed system with per case flat rates for cases inside group practice and cap of case values for other cases

The Cause of Dynamics

The key question for modelling the situation above as a dynamical system or, more specifically, as a system dynamics model is what drives the dynamics. In system dynamics terms, one or more dynamic hypotheses are necessary. Additionally, the scenarios should lead to different behaviour of the system, because otherwise the model would not be helpful in gaining insights on their influences.

There are two interventions that differ between the scenarios: Firstly, while all physicians work alone in the base scenario, two physicians form a group practice in Scenarios 1–4. Secondly, the group practice physicians get paid differently.

It was assumed that the group practice would have a direct effect on referrals. Suppose that an internist has to refer a patient to a pulmonologist. Usually, patients would get a referral and then seek any physician of the corresponding specialty themselves. However, if the internist works in a group practice with a pulmonologist it is very likely that the patient will stay in the group practice for the referral. This would lead to a rise in cases that are referred to the group practice pulmonologist, provided the referrals from other internists stay the same.

It is then assumed that the surplus in cases in relation to the situation before the group practice can change the physicians' treatment style. They might, for example, provide fewer medical services on average, which would again reduce their workload. Additionally, a physician with many referred cases might attract fewer new cases, for example due to long waiting lists. A model of this will thus include feedback loops.

Different reimbursement systems affect two unique factors. On the one hand, doctors might get paid more or less for the same work and would eventually adapt their treatment style (e.g., provide more services to compensate for a payment loss). On the other hand, a different reimbursement system can change which treatment style earns the most money. It does not make sense for a physician to provide more unique services than necessary in order to receive greater payment in a pure per

case flat rate system. Therefore, physicians' income is also part of feedback loops, whose polarity can change according to the scenario.

3.5.2 Formulation as a System Dynamics Model

Aggregation of Physicians: Four Modules

System dynamics requires the formulation of a model in terms of global variables as stocks, flows, auxiliaries, and parameters. In the problem of the group practice study, several physicians play a role, not only the two group practice physicians. The structure of how cases, consultations, medical services, and reimbursement are modelled is similar for all physicians (as if they were one type of “agent”). There is of course some difference between specialties and between the physicians in the group practice and other physicians, but it did not seem to be necessary to distinguish between different physicians of the same specialty who are not in the group practice, so they were aggregated. Overall, practically every variable in the model exists fourfold, one per specialty and practice style (group practice versus single practice), like in four different *modules*, see Figure 3.5.

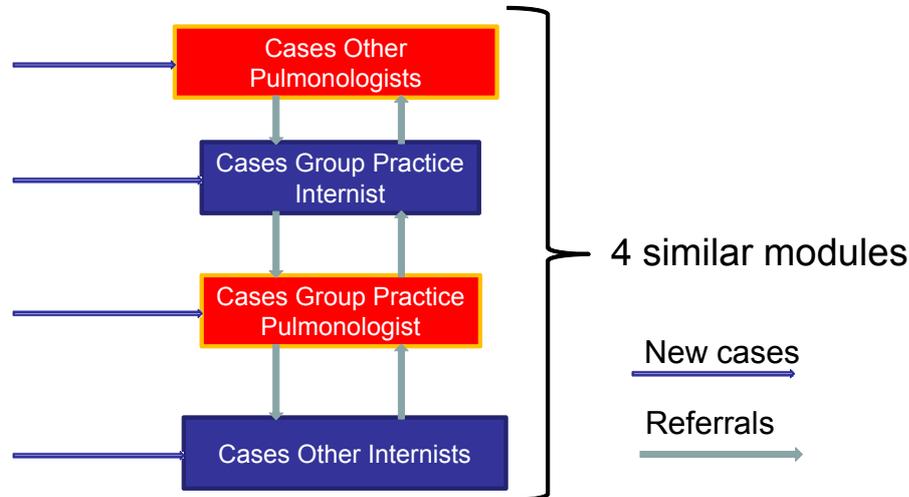


Figure 3.5: The group practice model consists of four modules, because nearly every variable exists fourfold, per specialty and practice style. They are connected through their referred cases. It is assumed that there are no referrals between physicians of the same specialty.

Technically, these modules were realised in the form of *array variables*, which are a standard feature of many SD simulators. Array variables allow for the combination of similar variables that differ only along one or more *dimensions*. For example, when modelling a population, age might be such a dimension. It is possible to count the number of individuals in the population at every age separately. One could store these numbers in single variables $p_0, p_1, \dots, p_{99}, p_{100+}$, but to create such a large number of variables in a graphical SD simulator would be cumbersome and the diagrams would become cluttered. Alternatively, the modeller creates only one array variable p that is indexed by age to get single numerical values. Townshend and Turner (2000), for example, used array variables to model population heterogeneity for different age and risk groups in a system dynamics study on the effectiveness of Chlamydia screening. Arrays are a convenient feature, but they do not change the mathematical structure of the model.

The model assumes only one connection among the four different modules: through referrals. Physicians refer a certain proportion of their patients to their colleagues of the other specialty (specialties other than the two in the group practice are omitted), whose cases increase through these referrals. It is assumed that there are no referrals to other physicians of the same specialty. The proportion of referrals to the partner in the group practice is supposed to be higher in the group practice scenarios than before the merger, so the referral part is an important feature of the model.

Integrating Reimbursement at Discrete Intervals in a Continuous Model

System dynamics is a continuous time method, that is, the time set is always an interval in \mathbb{R} . Moreover, according to the last section, while the flows as functions of time might have discontinuities, the stocks must be at least absolutely continuous.

Reimbursement, on the contrary, has a strong time discrete nature. In Austria, the reimbursement period is a quarter of a year for most health insurance providers. At the end of every quarter, reimbursement takes place for all claims accrued during that period.

The quantity that an SD stock represents might, in reality, change at discrete times in discrete steps. Often it is justified, however, to model it continuously

because if many discrete items are aggregated in a stock, the increase or decrease by one item is relatively small and the continuous flow can be a good approximation to the quantized flow (Sterman, 2000).

Reimbursement is different. After a comparatively large time interval (a quarter of a year), all accumulated claims get cleared. The cases, consultations, and medical services that are counted during a reimbursement period are thus reset to zero.

In principle, the flows, measured in units per quarter of year, could serve as approximations, because if these flows do not change much they nearly equal the state of the stocks after one quarter. However, there are two things that speak against this approach:

1. New cases, consultations, and medical services are not stocks. They do not accumulate a quantity.
2. Domain experts from health insurance providers would be uncomfortable with a model that does not resemble the discrete reimbursement interval.

Therefore, the model handles reimbursement as a discrete event after every time unit, that is, after every quarter of year. At this event, it reimburses accumulated cases, consultations, and medical services, which are set to zero. Figure 3.6 shows that during each quarter of year, the cases of a physician rise nearly linearly before they are reset. The model is thus not purely time-continuous in the strict sense, but it can be seen as an SD model that is restarted after every time unit, with different initial values. This is different from real hybrid models that have both continuously changing variables and discrete state events.

Cases, Consultations, and Medical Services

During each reimbursement period, the model has to simulate the quantities that are important for reimbursement. Physicians can get paid for each individual *medical service*, which are normally listed in a catalogue of accountable services. They may also receive lump sums, either for every patient they saw in a reimbursement period (which constitutes a *case*), or for each time a patient visited them (each visit constitutes a *consultation*).

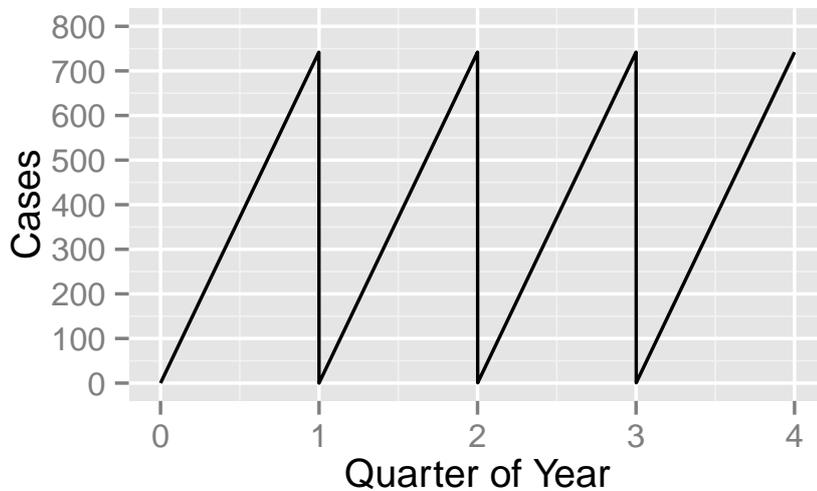


Figure 3.6: The accumulated cases of one physician during one year. At the end of every reimbursement period of one quarter of year, the cases are reimbursed and set to zero.

It is difficult for physicians to induce new cases, because patients decide to make first contact. On the other hand, doctors can decide for each new case how many consultations the patient should make and how many services they provide. In the model, the flow of new cases is multiplied by an average number of consultations per case to get the flow of new consultations. Similarly, these are multiplied by an average number of medical services per consultation to get the flow of new medical services. Figure 3.7 shows how the three different quantities are related to reimbursement.

Every module has three stocks for accumulating cases and consultations, respectively, and six stocks for medical services. First, there are three types of cases:

1. *Lone cases*: The patient does not visit a physician of the other specialty in the same quarter of year.
2. *Cases with group practice physician*: The patient visits the group practice physician of the other specialty in the same quarter of year.
3. *Cases with the rest*: The patient visits not the group practice physician, but

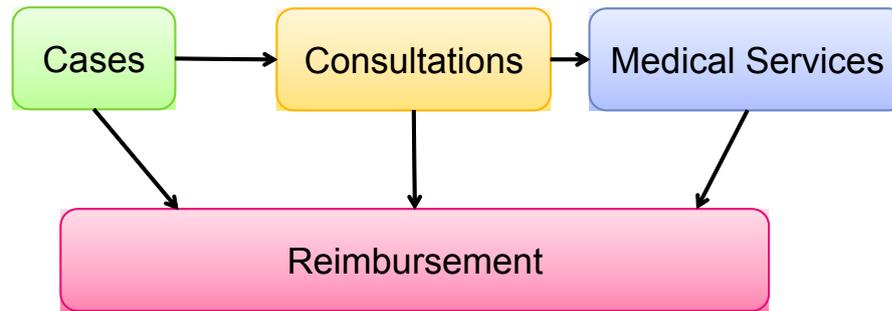


Figure 3.7: The flow of new consultations equals the flow of new cases multiplied by the average consultations per case. Similarly, new medical services depend on new consultations. All three quantities determine the reimbursement at the end of the quarter.

one of the other physicians of the other specialty in the same quarter of year.

It was necessary to separate these because some reimbursement systems pay differently, for example, in cases where both group practice physicians are involved. Additionally, average consultations per case and medical services per consultation differ between cases that are treated alone and cases involving both specialties.

Second, only a subset of medical services are billable by both specialties. These services are of special interest, in particular examinations, because they could unnecessarily be provided twice, once by each of the two treating physicians. Therefore, the model separates such services (*avoidable double examinations*) from medical services that only one specialty can provide (*special services*).

Each of the stocks for the three quantities has just one inflow (new cases, consultations, medical services) and no outflow, because they are reset by the discrete event. However, a new case adds only one consultation (and its accompanying medical services), whereas the other consultations are added with a third order delay. Thus, there is an additional implicit stock and flow structure, because a third order delay is realized with three stocks.

Feedback in the Model

An SD model without feedback is not feasible, as in this case only time-dependent variables drive the model behaviour, which would be determined exogenously and

not endogenously. If the real system behaved like this an SD model would be unnecessary for understanding it.

However, it is unlikely that a real system can exist without a feedback loop. An extreme value argument illustrates this: Suppose one million patients try to get an appointment with one physician. The physician could not serve all these patients, thus, there must be some feedback that dampens new cases if the physician already has too much work. He or she can either refuse new cases or reduce the time spent per case.

The group practice model concentrates mainly on feedback loops that involve either the workload of physicians or their income (from reimbursement). Figure 3.8 shows the loops for workload. A physician's workload is calculated as a certain fixed amount for every consultation and an additional time for every medical service. Feedback effects are given in terms of workload relative to normal workload. Therefore, it was possible to normalize workload such that a value of 1 represents a normal workload. The parameter values (how long is the fixed time of a consultation relative to normal workload, how long is an average medical service) were then calibrated, that is, an amount of cases, consultations, and services as found in the data leads to a workload value of 1.

Physicians' perceived workload does not change immediately, but only after a delay. It influences the average number of consultations per case and the average number of medical services per consultation because it is assumed that physicians are able to decrease these under higher workload. They can also refuse certain new patients, such that new cases decrease. Fewer new cases, consultations, and medical services in turn decrease workload, which closes balancing (i.e., dampening) feedback loops.

Figure 3.9 shows feedback loops involving physicians' income. They are similar to the feedback loops with workload, except for the fact that the number of new cases is not influenced and that the loops can also be reinforcing, depending on the scenario: In a fee-for-service system, physicians can increase their income by providing more services and consultations, but with per case flat rates, income does not change in this way. It might even be beneficial to invest less time per case and try to attract more cases instead. Additionally, it was assumed that physicians are more willing to work more per case without extra payment if they feel adequately

reimbursed.

Income is only changed once per quarter of a year through reimbursement. During a period of reimbursement, it is constant. Perceived income, however, changes continuously by exponential smoothing:

$$\begin{aligned} & \text{Perceived Relative Income}(t) \\ &= 1 + \int_0^t \frac{\text{Relative Income}(s) - \text{Perceived Relative Income}(s)}{\text{Income Adjustment Time}} ds \end{aligned} \quad (3.2)$$

At the beginning, doctors perceive income to be normal (i.e., perceived income equals 1).

The feedback loops involving income are balancing for a reimbursement system in which medical services and consultations are reimbursed separately. For a per case flat rate system, they are reinforcing.

A cap on the average case value puts additional pressure on physicians' behaviour. If the average case value is beyond the cap, the physician works for free. The model assumes that this pressure increases gradually as the case value approaches the cap. Figure 3.10 shows the corresponding feedback loops, which are only active in scenarios with a reimbursement cap (Scenario 2 and Scenario 4).

All feedback effects were discussed with an expert group from the health insurance providers. They all involve nonlinear table functions. It is unreasonable that doctors would be able or even willing to change their treatment style (e.g., average number of medical services) too far from the norm. Therefore, in general the change of effect (for example, of income on number of medical services) decreases farther away from the norm values. The resulting table function is s-shaped, not linear. It is difficult to parametrize these relationships from data, so the assumptions involved the opinion of the experts.

3.5.3 The Group Practice Model in Use

Most parameters, such as the normal number of services per consultation, the normal income for each specialty, and normal case numbers, could be derived from the average values in data taken from health insurance providers. The simulation in the base scenario (present situation with no merger to a group practice) should reproduce these values. Therefore, the few parameters that could not be parametrized

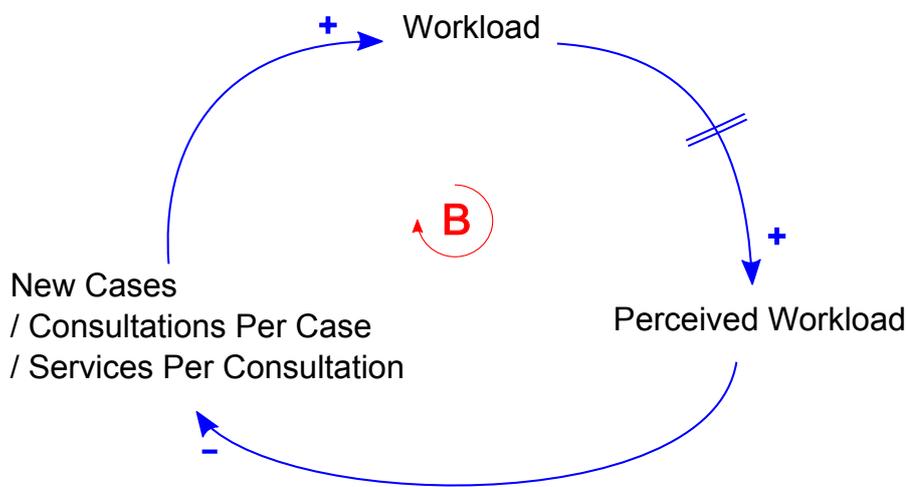


Figure 3.8: A higher workload increases (with a delay) physicians’ perceived workload, which causes them to reduce the average consultations per case and medical services per consultation. Additionally, they can refuse new patients, which reduces new cases. All three effects decrease their workload, which closes balancing feedback loops.

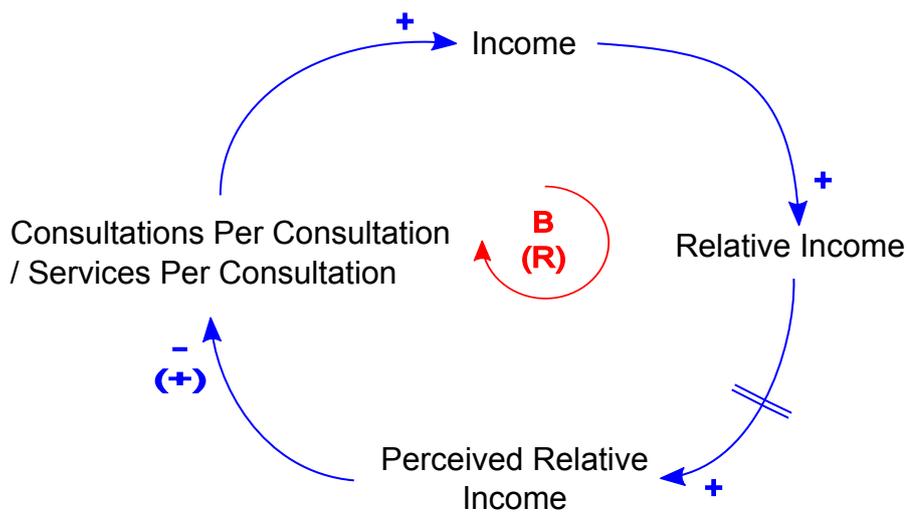


Figure 3.9: A higher income increases (with a delay) the income relative to the target income of physicians. This in turn increases their perceived relative income, which causes them to reduce the average consultations per case and medical services per consultation. (In a reimbursement system with per case flat rates, the polarity of this link changes.) Fewer consultations per case and medical services per consultation decrease income, which closes balancing (reinforcing) feedback loops.

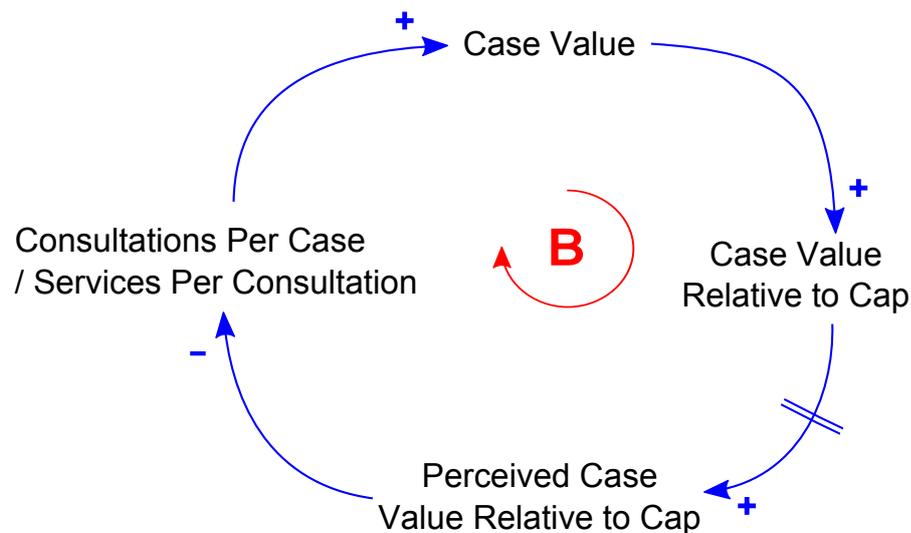


Figure 3.10: With a cap on the average case value (reimbursement per case), the higher the actual case value is in comparison to the cap the less desirable it is for the physician to work more. This in turn decreases the case value, which closes dampening feedback loops.

with the available data (the fixed value of workload for a consultation and the workload per medical service, which was assumed to differ between specialties) were calibrated to match this condition.

The other scenarios simulate the forming of a group practice. As the system is in equilibrium before the merger, it is possible to start the model with the corresponding initial values and the parameters set to the values after the merger (i.e., the two group practice physicians work together right from the start of the simulation).

Many feedback loops of the model are dampening. This makes the simulation runs very stable: The model quickly approaches an equilibrium. In general, the values of the variables (e.g., cases, income, case value) after 12 quarters are compared.

Overall, two different specialty combinations (internist and pulmonologist) and parametrizations from two different health insurance providers (regional health insurance of Vienna and of Upper Austria) were analysed. All scenarios were simulated with standard assumptions as well as with the assumptions that either

the group practice physicians could acquire more new cases (e.g., because of longer opening hours) or that they would double their referral rates. For the results, see Einzinger et al. (2014).

The implementation as an SD model had an important benefit: Simulations take only a few seconds. It was thus possible to create a decision support tool with which clients can analyse the results for a large set of different parameter values without needing to work with the original model. The decision support tool is implemented in a standard desktop spreadsheet software and contains the results of about 1.4 million pre-calculated simulation runs (Jung, Einzinger, Pfeffer, & Popper, 2014).

3.6 Conclusions

This chapter introduced SD as a method to specify a dynamical system. While differential equations are not specified directly, each feasible SD model has an equivalent differential equation system. It is reasonable to allow a generalized solution concept in the sense of Carathéodory because in applications the right-hand sides can have discontinuities.

The group practice model is one example of how SD was applied to a real world problem involving different health care reimbursement systems. It was only possible to use SD because the physicians outside of the emerging group practice could be aggregated. On the other hand, the method allows for concentration on the feedback loops that create the dynamics of the system, and the simulations are fast, which is a precondition for analysing a large number of different parameter settings. These features are important for comparisons with other modelling methods.

Chapter 4

Agent-Based Modelling and Simulation

4.1 Introduction

ABMS is the second modelling technique of this thesis. There are several important differences to SD:

- It typically models a large number of individuals who constitute the system (bottom-up view).
- There are different definitions of what constitutes an agent and, therefore, an agent-based model.
- Agents are not restricted to consist of only a few different elements, in contrast to SD models.
- There are no standard diagrams for conceptual modelling.

The present chapter gives an overview on the roots of ABMS and different definitions of the concept. We also propose a working definition that is adapted to our purpose but does not claim to be universal. Finally, an example of an agent-based model for the comparison of reimbursement systems is presented.

4.2 The Roots of Agent Based Modelling and Simulation

ABMS is, compared to SD, a rather new modelling method. It has its root in the study of complex adaptive systems (CAS), which consist of a potentially large number of interacting individual components and can adapt, for example to a changing environment. Many biological systems (e.g., an ant colony) have these characteristics and thus served as a motivation for the emergence of CAS (Macal & North, 2010; North & Macal, 2007, p. 45).

Schelling (1971) proposed one of the first models of a social system that can be called agent-based. In his model, two types of people (agents) are placed on a rectangular area partitioned into rows and columns (Figure 4.1). Each individual is discontent if the proportion of people of the same kind in his or her neighbourhood (the nearby cells) is under a threshold. The discontent individuals move to another free place where they are content. Surprisingly, even if people demand only half of their neighbours to be of their own kind, strong segregation emerges.

Schelling's model is a good example of agents with only one simple rule and a global behaviour (segregation) that is not obvious from the behaviour of the individuals. It can be simulated without the use of a computer, for example with two different kinds of coins on paper or on a chessboard. The discrete space of the model is one possibility of an environment for agents, which shows the relationship with cellular automata. Other fields that influence ABMS are artificial intelligence, network science, and the study of complex systems.

4.3 The Building Blocks of Agent-Based Models

According to Macal and North (2010), an agent-based model or system typically consists of three parts:

- The agents of the system with all their properties and their behaviour.
- Interactions and relationships (e.g., through a connection network) between the agents.

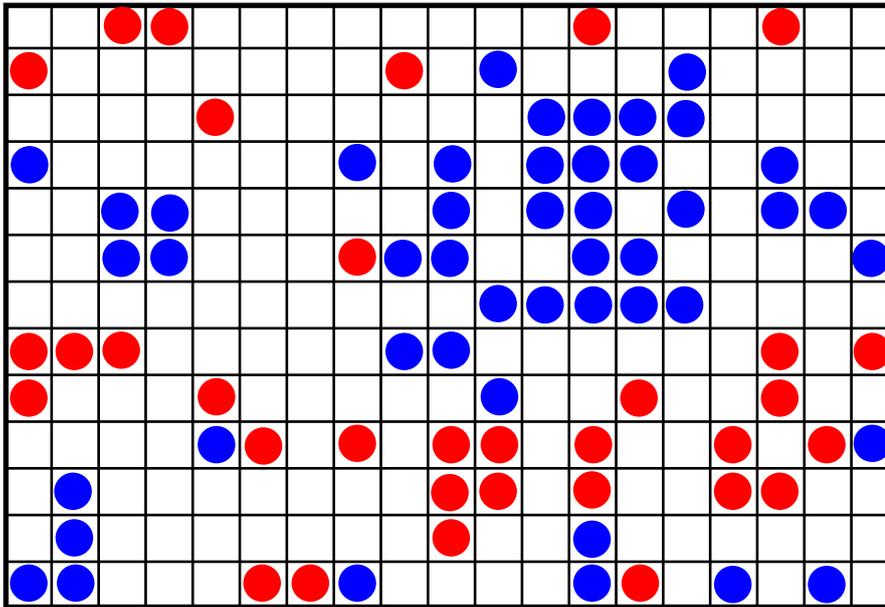


Figure 4.1: In this example of the Schelling segregation model, two types of individuals (red and blue) live in an environment that consists of cells arranged in 19 columns and 13 rows.

- An environment where the agents live and with whom they interact.

The agents are of course a necessary component of every agent-based model. Additionally, an agent-based model without some kind of interaction between the agents would not have any advantage over simulating each agent individually, such as in a microsimulation model. Agents without an environment (e.g., an underlying space) are, on the other hand, imaginable.

In the Schelling model of the last section, the people who live on the rectangular grid are the agents. The space with its cells is the environment. Individuals are only influenced by other people in their neighbourhood, that is, in the surrounding cells, which clarifies the relationships of the agents.

A key problem is that there is no single definition or set of requirements for what constitutes an agent. Before proposing a working definition of an agent-based model, we therefore give an overview of typical properties of agents in the literature.

4.3.1 What Constitutes an Agent

There is not yet any standard definition of an agent. This does not have to be a general problem:

Over the years, this interest in finding a formal consensus decreased and emphasis was placed on application domains of the agent paradigm. Fortunately, as other scientific areas show as well, a commonly agreed-upon definition is not a prerequisite for the success of a concept in practice. (Tolk & Uhrmacher, 2010, p. 76)

On the other hand, many agent definitions overlap substantially. They can serve as a starting point for a working definition.

On the most basic level, an agent is at least an object, because it has both *attributes* and *behaviour* (North & Macal, 2007, p. 24). This shows the strong relationship with objects in object-oriented programming, where the attributes of an object are its fields (variables) and its behaviour are its methods (functions). Therefore, it is natural that most implementations of agent-based models use object-oriented programming.

D’Inverno and Luck (2004, pp. 15–17) propose the framework SMART for agency, which consists of a hierarchy of the terms

1. Entity
2. Object
3. Agent
4. Autonomous Agent

Each term has one additional definition compared to the preceding term. Entities are just a collection of attributes. Objects, as stated above, also have behaviour, agents have *goals*, and autonomous agents have *motivations*; they “pursue their own *agendas* as opposed to functioning under the control of another agent” (d’Inverno & Luck, 2004, p. 17). All objects are entities, all agents are objects, and all autonomous agents are of course agents.

The key to what agents add to pure objects in SMART are the goals. For d’Inverno and Luck, a goal is a state of the world that should be achieved. The problem is that it is open to subjective interpretation if an object of a simulation has such a goal. Does a ball bouncing on a surface have the goal of obeying the laws of physics? Do individuals in an agent-based epidemic model, who have contacts and potentially infect each other, have any goals? If not, is such a model not agent-based, but rather consists just of objects? (Maybe individual-based would then be a better term for these models.)

It seems that goals play a bigger role in the modelling process as guidelines for the modeller on how agents should behave in specific circumstances. For example, an agent who controls orders to a producer further upstream in a supply chain models an individual in the real world. If he wants to incorporate realistic behaviour the modeller can ask which goals that individual might have. The agent in the model should select a behaviour that can at least be believed to be able to fulfil these goals.

The selection mechanisms of behaviour are a further characteristic of agents. They have *rules* for how to choose an action based on their goals, their state, and the state of the environment (or rather, their knowledge of the environment). North and Macal (2007, pp. 27–28) add that agents are also *adaptive* because they have selection rules (“rules to change rules”). This allows agents to adapt their behaviour and to learn. In the view of North and Macal, objects that lack one or more of the necessary features of agents, such as adaptivity, are *proto-agents*.

There are several other characteristics of agents in the literature. Wooldridge (1997), for example, requires the following four properties:

- **Autonomy:** Agents have their own encapsulated state that is not directly accessible to other agents, and they can decide on their own actions.
- **Reactivity:** Agents live in an environment, which they can perceive and where they can take actions in reaction to changes in this environment.
- **Pro-activeness:** Agents can also take actions on their own initiative in order to pursue their goals.

- **Social ability:** Agents communicate with each other and can use their communication to achieve their goals.

Epstein (1999) adds further characteristic features of agent-based models:

- **Heterogeneity:** Typically, agents differ in their characteristics. For example, they may have different parameter values (e.g., age or body weight of a patient agent).
- **Explicit Space / Local Interactions:** Agents are often situated in a spatial environment, such as a three-dimensional euclidean space or a network. Interactions are often restricted to the local surroundings (e.g., neighbours).
- **Bounded Rationality:** Agents typically do not have knowledge of everything in their environment, and their computing power is limited, for example to the use of heuristics to find an optimal decision.

An important problem is that, as Drogoul, Vanbergue, and Meurisse (2003) note, these terms are weak and metaphorical. There is no direct translation into computational properties. The same is true for formal mathematical modelling. However, a formal description of agents should be guided by the concepts listed above.

4.3.2 Agent-Based Models as Dynamical Systems

We restrict our formal description to discrete event agent-based systems, such that only a finite number of changes can happen in a finite time interval. The global time set should be a continuous subset of \mathbb{R} . Most often, it will be the finite interval $[0, t_{end}]$ for $t_{end} \in \mathbb{R}_+$. A good starting point are the discrete event system specification (DEVS) formalisms, which were originally developed by Zeigler et al. (2000).

A DEVS has an input and an output set. It can send an output from its output port to the input port of a DEVS to which it is coupled. The message passing of agents does the same, with the exception that agents do not have to obey a strict coupling. A network among agents might exist that restricts the messages that can be passed, but it could change.

There are extensions of the DEVS formalism that incorporate such a change in structure (Barros, 1997). Based on these dynamic structure DEVS approaches, several authors have tried to create formalisms for agent-based systems, such as Duboz, Versmisse, Quesnel, Muzy, and Ramat (2006) and Steiniger, Krüger, and Uhrmacher (2012). However, we try to keep it as simple and abstract as possible. The network description, for example, should not be an explicit element of the definition.

Another problem with most existing DEVS approaches is that they are deterministic, while many applications only allow stochastic descriptions of agents, in particular in health care. It is usually not possible to model for example disease onset as a deterministic event. Instead, stochastic rates are used. A formal description for agent-based modelling should thus allow stochastic elements.

Actually, deterministic DEVS formalisms can be used for stochastic modelling. A DEVS consists of sets and functions. One such function, for example, is the internal transition function δ_{int} . In an internal transition, it maps the old state x_1 to a new state x_2 . If we add a random number as an argument of the function the result becomes stochastic.

For a more rigorous and general incorporation of randomness in DEVS, the concept of probability spaces is necessary. Castro, Kofman, and Wainer (2010) propose a formalism, STDEVS, that substitutes the internal and external transition function of classic DEVS with new functions G_{int} , G_{ext} , P_{int} , and P_{ext} . These functions generate a probability space that depends on the present state of the DEVS. Thus, a new state is not deterministically chosen, but stochastically from the probability space on the state space.

Could STDEVS serve as a formal definition of agent-based models? To answer this question, we have to think about what should be part of an agent and what an agent should be able to do. First, agents should have a state. Only an agent itself should be able to change its state directly because of autonomy. On the other hand, agents must have the ability to communicate with each other (social ability). In order to achieve this, they pass messages out of some message space to other agents. Agents should be able to both react to messages and act pro-actively on their own. Note that for finding out about the state of another agent, an agent should have to send a message and wait for the reply. Every agent is fully autonomous and should

not have to reveal its state if it does not want to.

Indeed, a DEVS produces output values from an output set Y , which can be seen as messages to other DEVS. It has a state (which is an element of the state space X), and only its own transition functions can change this state directly (autonomy). The external transition functions represent the reactive component of the DEVS, while the internal transition functions allow it to act on its own.

However, agents should not be restricted to only send messages to connected agents. They should be able to choose a certain receiver or even to randomly select one. A problem is that a DEVS does not “know” other DEVS in its environment. In order to select one receiver randomly, each agent would thus have to store a list of all other agents, which is undesirable.

We propose another mechanism: When an agent produces an output (i.e., sends a message), it attaches a parameter called a *mode* m . This parameter could represent, for example, the intention to send the message to a random receiver. The environment of the agent then forwards the message according to the mode the sender specified. We can thus define agents similar to the STDEVS:

Definition 4.1 (Agent). An agent is a tuple

$$A = (U, X, Y, M, G_{\text{int}}, G_{\text{ext}}, P_{\text{int}}, P_{\text{ext}}, \lambda, ta),$$

where

- U is the input set,
- X is the state space,
- Y is the output or message set,
- M is the set of modes,
- $G_{\text{int}}: X \rightarrow 2^X$ is a function that assigns a subset of X to every state x ,
- $P_{\text{int}}: X \times 2^X \rightarrow [0, 1]$ maps a subset of X to a probability dependent on the present state,
- $G_{\text{ext}}: X \times \mathbb{R}_0^+ \times U \rightarrow 2^X$ is a function that assigns a subset of X to every state x , elapsed time e since the last event, and input message u ,

- $P_{\text{ext}}: X \times \mathbb{R}_0^+ \times U \times 2^X \rightarrow [0, 1]$ maps a subset of X to a probability dependent on the present state, the elapsed time, and the input message,
- $\lambda: X \rightarrow Y \times M$ is the output function, and
- $ta: X \rightarrow \mathbb{R}_0^+$ is the time advance function.

For a given state x , the probability space for an internal transition is given by $(X, \sigma(G_{\text{int}}(x)), P_{\text{int}}(x, \cdot))$. Similarly, the probability space for an external transition is $(X, \sigma(G_{\text{int}}(x, e, u)), P_{\text{ext}}(x, e, u, \cdot))$.

The agents are together situated in an environment. This is the analogue to a coupled DEVS model. In this case, however, it must also be able to distribute a message to a random receiver, based on the mode of the message.

Definition 4.2 (Agent-Based Model). An agent-based model consists of agents in an environment, which is given by the tuple

$$N = (U_N, Y_N, M_N, D, \{A_d\}, G_\rho, P_\rho, \{R_d\}, \{Z_{i,d}\}, \text{Select}),$$

where

- U_N, Y_N , and M_N are the input, output, and set of modes analogue to the agent definition,
- D is the set of agent references, such that for each $d \in D$, A_d is the corresponding agent,
- $G_\rho: M_N \rightarrow 2^{D \cup \{N\}}$ is a function that assigns a subset of all agents including the environment to every mode m ,
- $P_\rho: M_N \times 2^{D \cup \{N\}} \rightarrow [0, 1]$ maps a subset of all agents including the environment to a probability dependent on the mode,
- $R_d: M_d \rightarrow M_N$ is the mode translation function for $d \in D$,
- $Z_{i,d}$ is the message translation function from i to d , where $Z_{N,d}: X_N \rightarrow X_d$ for $i = N$, $Z_{i,N}: Y_i \rightarrow Y_N$ for $d = N$, $Z_{i,d}: Y_i \rightarrow X_d$ otherwise, and

- *Select*: $2^D \rightarrow D$ is the selection function that controls the priority of simultaneous events. For every subset of agents, it chooses one agent out of this subset.

The agent-based model is thus similar to a coupled DEVS model, but the output of an agent A_d is not simply passed to connected agents. Instead, the output message has a mode m with it, which is translated by the mode translation function R_d to a mode $m' \in M_N$ of the environment. According to this mode, the functions G_ρ and P_ρ construct a probability space on the set of all agents including the environment itself. This models that the message can go to any other agent or to the output of the environment.

The definition is already rather complex, but still it applies only to a restricted subset of all commonly used agent-based models, because it does not allow for agents to be created or destroyed. However, the formalism is powerful enough to represent, for example, the agent-based version of the physician reimbursement model that will be presented in Chapter 6, because there the agent populations will be fixed.

Unfortunately, it is not clear how to construct the probability space that is needed in Definition 2.13 for a stochastic state transition map in order to derive a corresponding stochastic dynamical system. On the other hand, implementation of an agent-based model has to rely on random numbers and in particular, on a stream of uniformly distributed random numbers $r \sim U(0, 1)$. A fixed countably infinite sequence of such random numbers leads to a unique system trajectory. Thus, for agent-based models with probability spaces that can be represented by random numbers there is a corresponding stochastic dynamical system whose underlying probability space consists of countably infinite sequences of random numbers.

4.4 Case Example: The GAP-DRG Model for Comparing Reimbursement Systems in Extramural Health Care

4.4.1 Introduction

Apart from group practices, the choice of reimbursement system is also generally important. According to Czypionka, Riedel, Obradovits, Sigl, and Leutgeb (2011), it provides strong incentives that influence the provision of medical services, both in the negative and positive sense. They summarize in their work the economic theory of optimal reimbursement, which analyses theoretical economic models to ascertain the effects of reimbursement systems. For example, Ellis (1998) states that cost-based (fee-for-service) payment leads to over-provision of services, while prospective payment, where only a lump sum is paid, results in under-provision of services to high-severity patients.

The GAP-DRG (General Approach for Patient-oriented Ambulant DRGs) project of the Main Association of Austrian Social Insurance Institutions was a research project on per case flat rates in the extramural health care sector. It was based on a comprehensive database of reimbursement data from practically all Austrian health insurance providers and data on all hospital cases. The reimbursement data were originally linked to the unique social security numbers of the patients, but to assure privacy, all these numbers were converted to pseudonyms. The database originally encompassed a time frame of two years, 2006 and 2007.

One goal of the GAP-DRG project was to develop medically and economically homogeneous diagnosis related groups, based on the available reimbursement data, and to assign flat rates to these groups. The second goal was to develop a model to analyse the influence of different reimbursement systems, especially of flat rates, on costs compared to the reimbursement system currently in use.

To achieve this last goal, the problem was depicted as in Figure 4.2. It shows what has to be modelled to explain reimbursement. Medical problems (i.e., diseases and other conditions) are probably the primary cause of patients consulting a medical provider, who provides medical services based on his or her treatment

decisions. Reimbursement, in turn, depends on these provided services and on the reimbursement system. Of course, medical services might also be paid for with lump sums if a flat rate system is in use.

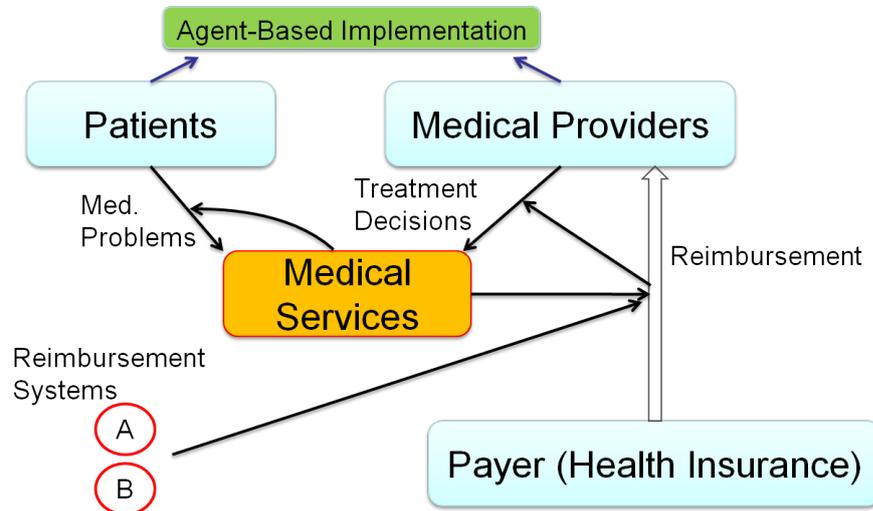


Figure 4.2: Patients and medical providers are the two main types of individuals. Patients have medical problems and consult providers, whose treatment decisions lead to the provision of medical services. Based on these medical services and depending on the reimbursement system, the payer reimburses the providers.

The model had to allow for the analysis of reimbursement of every specialty (e.g., internists, general practitioners, ophthalmologists) and preferably also of the distribution of this reimbursement. All physicians with a given specialty do not necessarily have the same treatment style and provide the same services, so differences in the payments that individual physicians receive are to be expected and should be possible in the model. Finally, patients might consult different providers if something in the system changes. For example, there might be a scenario where patients always must go to their family physician first and cannot consult a more specialized physician directly. To which physicians the patients then go will be dependent on what these physicians offer.

For these reasons, an agent-based approach seemed to be the most suitable method for building the model. Patients and medical providers were obvious candidates for agents. Agent-based models have also the flexibility to map the process

from the onset of patients' medical problems to the provision of medical services and on to reimbursement in a level of detail where even single services can be simulated. The next section describes the structure of the GAP-DRG model (Einzinger et al., 2013), which was designed to fulfill these requirements.

4.4.2 Formulation as an Agent-Based Model

Basic Structure

Figure 4.3 shows the structure of the model in terms of its objects. It contains two agent types, the patients (`Patient`¹) and medical providers (`MedicalProvider`). Both are embedded in a common environment (`Main`).

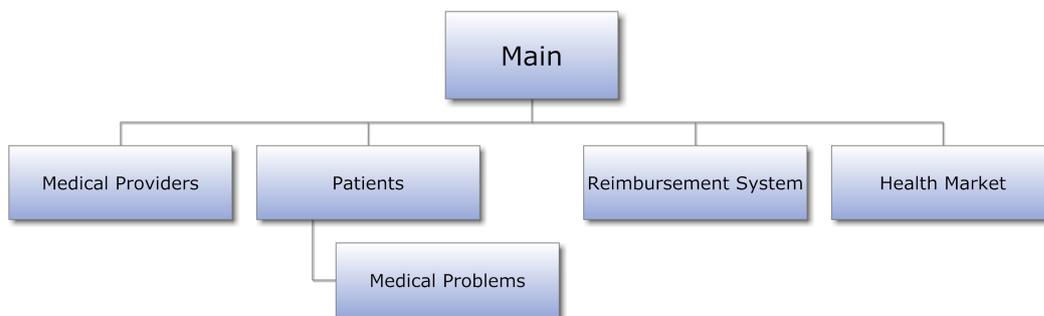


Figure 4.3: The structure of objects in the model. The object `Main` is the environment; all other agents and objects are embedded in it. Medical providers (`MedicalProvider`) and patients (`Patient`) are the two types of agents. Patients can develop medical problems (`MedicalProblem`), which they store internally (i.e., they are part of the patients' state). Additionally, there is a health market object (`HealthMarket`) in the environment that handles the requests of patients for providers. An exchangeable reimbursement system object `ReimbursementSystem` handles reimbursement.

Patient agents have the rules that they consult providers depending on their medical need, which is ultimately determined by their medical problems. They might also consult a physician for medical check-ups without any disease, but this probably counts only for a minority of cases, and grouping mechanisms of per case

¹Class names and variable names are written in typewriter font.

flat rates are usually based on diagnoses, so the change in reimbursement system would mainly concern cases with a medical problem. In the model, patients can get one or more medical problem objects, which they store internally.

A central health market object (`HealthMarket`) handles the search of patients for providers. It stores the position of each provider. If a patient sends a request to the health market, it only returns providers within an acceptable distance of the patient. This is one example of locality and limited knowledge that is typical of many agent-based models.

The reimbursement system (`ReimbursementSystem`) is also an object in the agents' environment. Medical providers communicate with it similarly to in real life. For each visit, they send information on the visit (patient number, date, provided services, diagnoses) to the reimbursement system, which performs reimbursement at the end of each reimbursement period (a quarter of a year).

One important strength of the models' design is that `ReimbursementSystem` is an abstract class. Therefore, concrete implementations of this type are easily exchangeable. All reimbursement systems have to obey the same interface. The providers always send all the information that any reimbursement system could use. A reimbursement system with per case flat rates would therefore get information on the provided medical services and the diagnoses, even though it only uses the diagnoses to calculate the reimbursement. A fee-for-service system, on the other hand, ignores the diagnoses and pays for each single service.

The simulation period is usually the years 2006 and 2007 because the available data for parametrization are also from this period. A simulation with the present reimbursement system should therefore closely reproduce the data, whereas an alternative scenario with another reimbursement system shows what would have happened in those years with this other system.

Model Assumptions

As the model maps the whole process of service provision in great detail, simplifying assumptions are necessary. There are typically thousands of different diagnosis codes in classification schemes such as the International Statistical Classification of Diseases and Related Health Problems (ICD), and the number of treatment

decisions is similarly complex. Typical health care models focus on one specific disease, its co-morbidities and its treatments. But the reimbursement system in extramural health care concerns all medical problems that are treated there. This also makes parametrization of the model more difficult. Therefore, the approach presented here treats medical problems in a generic way, such that for every disease, the same statistical analyses can be used to derive which medical services patients typically get.

Since, for example, the prevalence of medical problems depends on demographic attributes, the patient agents also have age and sex as parameters. The demography of the agent population corresponds to the Austrian population according to official statistics. However, Austria has more than eight million inhabitants, which causes memory problems in simulations with the same number of patient agents, so simulations were typically performed with a scaling factor of 0.1, such that one agent in the model represents ten individuals of the real population.

Patient agents have an exact age, which increases during the simulation. However, for the parametrization with statistical analyses it was useful to work with a classification into age groups of five years, with the exception of the first and last age group, which contain newborns in their first year of life and people over the age 90, respectively.

The model incorporates births and deaths of the patients, which all happen in one single event in the middle of each year to avoid the scheduling of a large number of additional events. The number of newborn patient agents is fixed according to the birth numbers from official statistics of the two years 2006 and 2007. It does not depend, for example, on the number of women of fertile age in the simulation.

Mortality, on the other hand, depends on the individual patient. In the middle of every year, the simulation tests each patient against a death probability to determine whether he or she survives. This probability changes with age, and morbidity can have a strong influence.

It would be problematic to not consider the effect of medical problems on the mortality of patients in the model because in this case, individuals without any diseases would die at the same rate as highly multi-morbid individuals. As a consequence, the proportion of multi-morbid individuals, especially in old age, would be too high. Information on the numbers related to causes of death are

available from official statistics, so a methodology was developed that allowed us to incorporate the knowledge of how many death cases a certain medical problem causes directly (Einzinger, Jung, & Pfeffer, 2012).

Theoretically, all diseases that are treated in the extramural health care sector have to be incorporated into the model, but they were reduced to a manageable number of selected chronic diseases on the basis of their prevalence and economic importance. Specifically, these selected diseases are:

1. Diabetes
2. Hypertension
3. Coronary Heart Disease
4. Asthma and COPD
5. Degenerative Joint Disease
6. Chronic Back Pain
7. Incontinence

Obesity and the acute conditions intestinal infectious diseases, acute respiratory infections, pneumonia, and influenza were also considered for inclusion as medical problems. However, it was impossible to identify obese patients in the reimbursement data, and the identification of acute episodes also poses serious problems. These medical problems were therefore excluded.

Patients can either already have a medical problem at the beginning of the simulation or get it during the simulation. The first case is determined by the prevalence of the disease, which is treated as a probability in the model. It is tested for every patient and every disease if the patient has the disease at simulation start. Assume, for example, that the prevalence of a certain disease is 0.1 in a particular age class of female patients, then such a patient has a probability of 0.1 of having the medical problem at simulation start.

On the other hand, patients who do not have a certain medical problem can get it depending on the incidence rates of the disease. It is assumed that the time until a patient develops a particular disease is exponentially distributed (however,

the incidence rate changes if the patient arrives at a higher age class). If a patient can develop k different diseases with the incidence rates $\lambda_1, \dots, \lambda_k$ the time to the development of the first additional disease is also exponentially distributed and has the sum of the individual incidence rates as its overall rate. Therefore, the model always draws the time of the next incidence of a disease for a patient, and then the patient agent determines the particular disease (the probability for each disease is the proportion of its corresponding incidence rate to the overall rate).

An important additional assumption is that the different diseases are independent of each other, that is, patients have the same probability of developing, for example, a coronary heart disease regardless of whether they already have hypertension and diabetes or not. This simplifies model calculations and the parametrization from data, but is clearly only a crude approximation for some disease combinations such as in the example above. Future research will need to analyse and probably include correlations between related medical problems.

The next question is which health care need patients with a specific combination of medical problems have and where they receive medical services. Service need in the model is expressed as services listed in the Meta-tariff catalogue from Austrian health insurance providers, which includes medical services such as intravenous injections and electrocardiograms. Overall, the catalogue comprises over a thousand different services.

The information on which medical services a patient with a diseases such as diabetes typically consumes during one reimbursement period (i.e., a quarter of a year) was derived statistically from the available reimbursement data. Patient diagnoses are not registered in the data, so it was necessary to use drug prescription data as an indicator for the diagnoses. Weisser, Endel, Endel, and Filzmoser (2010) developed a method that allows probabilities for diagnoses to be derived from the drugs that a patient receives. For example, a patient with a prescription for insulin has diabetes with a 100% probability, because only diabetes patients get insulin.

Based on these relationships between drug data and diagnoses, the statistical experts in the project team evaluated which services patients with each of the included medical problems typically get and with what frequency. These services are the ones that often occur in a fixed time period around a diagnosis, that is, around a drug prescription that indicates the diagnosis. Figure 4.4 shows how

the frequencies of the services were counted. The most frequent services build the service bundle for the medical problem. A cut-off point was determined to decide how many of the most frequent services would be included.

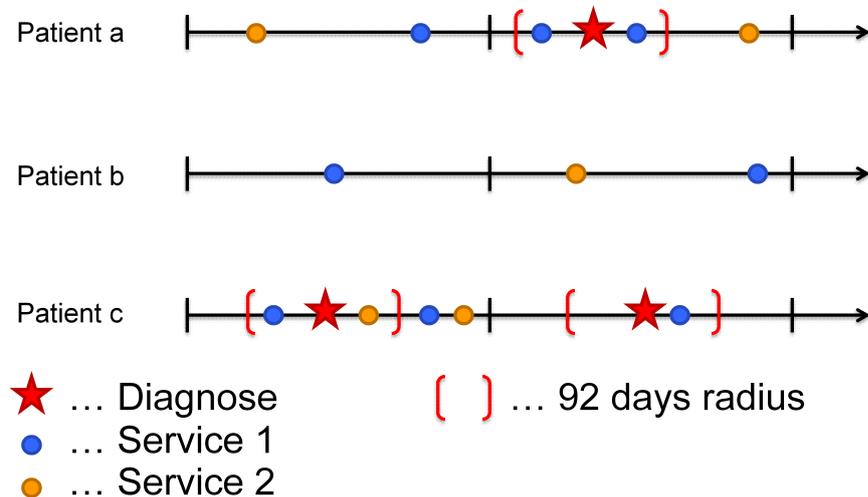


Figure 4.4: Example for the derivation of service bundles from reimbursement data. It shows two-year timelines (2006 and 2007) for three patients. The stars represent a diagnosis of a particular disease or, more exactly, that the patient has a drug prescription that is linked statistically to that disease. Medical services that the patients got within 92 days of a diagnosis are counted. In this case, Service 1 would be counted four times and Service 2 would be counted once. The services of Patient b do not count for this medical problem because he or she did not have the corresponding diagnosis.

Each service in a service bundle for a specific medical problem has a corresponding frequency distribution, which states how many times patients with that diagnosis got the service in a quarter of a year where they had the diagnosis. In the simulation, once per quarter every one of a patient's medical problems samples from these frequency distributions. Thus, each medical problem generates its service need.

A crucial assumption is how the various diseases of a multi-morbid patient contribute to the patient's overall medical need. In the GAP-DRG model, a patient's need is the maximum need of any of his or her medical problems in the same quarter of a year. Suppose, for example, that a patient has diabetes and hypertension, and

that his diabetes samples two intravenous injections, while his hypertension samples one intravenous injection and one electrocardiogram. The overall service need of the patient is then two intravenous injections and one electrocardiogram.

While the medical services that correspond to a diagnosis are an input to the model, the specialties where the patients get these services are endogenously determined. The idea is that the specialties differ in terms of their *service portfolios*, which comprise all medical services that a physician may provide. For every specialty and service, the percentage of physicians who got the service reimbursed at least once in the two year period captured by the reimbursement database was evaluated and serves as the probability that a medical provider in the model is initialized with the service in his or her portfolio.

Every quarter of year, all of a patient's medical problems generate their service need. The patient then sends a request to the health market with his position and his overall service need. First, the health market checks for two conditions:

1. Only physicians inside a search distance of the patient are eligible. The search distance can differ. General practitioners have a lower search distance, while there is no such limitation for laboratories.
2. All medical providers have only a limited capacity per day for treating patients. This was assumed because single physicians with favourable service portfolios should not attract an unreasonable number of patients. Patients register in a first-in, first-out queue. If the queue is too long, new patients will not receive this physician from the health market.

Figure 4.5 shows an example of how these conditions are applied.

After the health market has found a list of eligible providers, it has to determine which of these providers the patient should consult. On the one hand, they should cover the patient's service need. On the other hand, the patient should not consult unnecessary providers. The selected physicians should cover the services in an optimal way, which means that a minimal number of physicians should cover as many services as possible. A selection of physicians is better than another selection if it meets more of the service need. If two selections cover the same amount of services, then the selection with fewer medical providers is better.

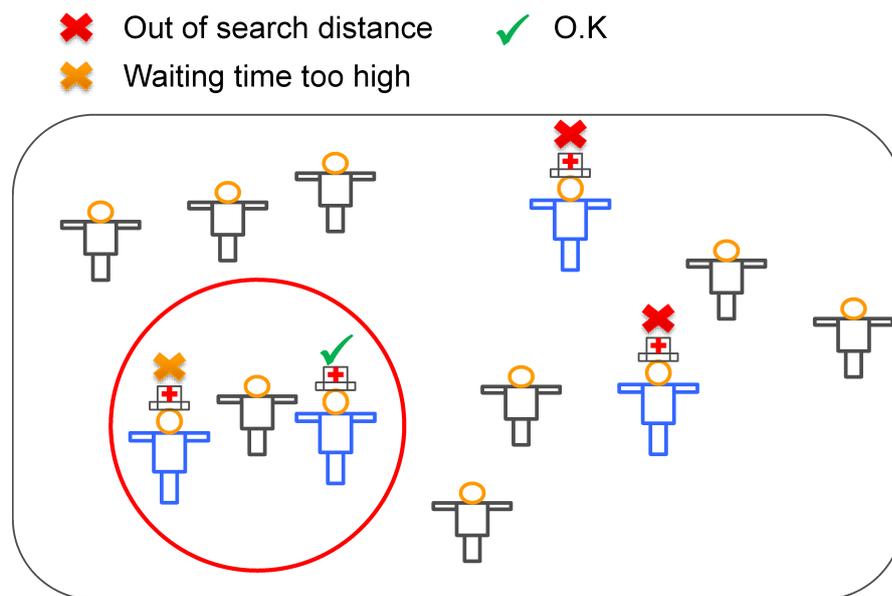
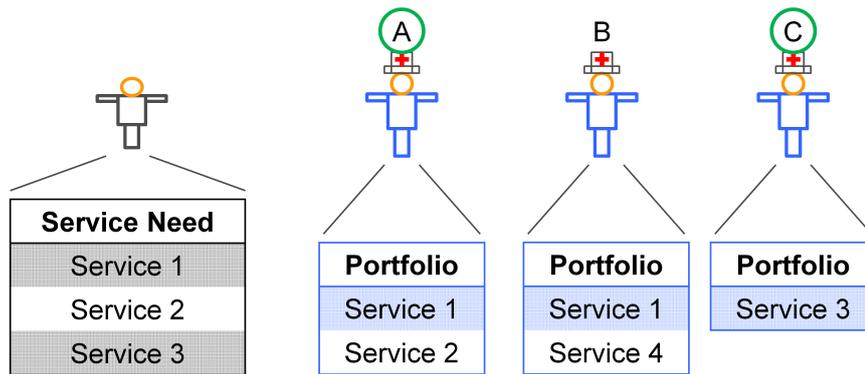


Figure 4.5: Patients and medical providers are distributed on a two-dimensional rectangular space. If the patient in the lower left corner needs physicians to provide medical services, she can choose only among the two physicians who are inside her search distance (red circle). One of these two providers already has too many patients in his or her queue, so only one provider is left in this example.



Cover with as few providers as possible: Choose A and C

Figure 4.6: In this example, a patient needs three different medical services. Three physicians are available for the patient. He tries to cover the services with as few providers as possible. One physician alone does not provide all three services, but the patient can cover his service need with only Physician A and Physician C.

Mathematically, this optimization describes a variant of the minimum set cover problem: For a universe \mathbb{U} and a collection $S = \{S_1, \dots, S_k\}$ of subsets of the universe, what is the minimum subset of S that covers the maximum possible amount of elements of \mathbb{U} ? In the case of the provider search, the service need is the universe \mathbb{U} and the service portfolios of the physicians (more exactly, the services in the portfolios that are also part of the service need) are the collection S .

The minimum set cover problem is an NP-hard problem. However, the greedy algorithm, which consists of choosing in each step the element of S that covers the largest number of still uncovered elements of \mathbb{U} , is an efficient approximation algorithm (Vazirani, 2003, pp. 16–17). The health market uses the greedy algorithm, with a few alterations: Some specialties cannot be consulted by all patients. Only children and adolescents can go to paediatricians, and only women may visit a gynaecologist. Furthermore, it is not possible to consult a laboratory without a referral, so the algorithm can only pick laboratories after another specialty. Finally, patients can go only to one medical provider with a given specialty per reimbursement period.

A further question is how many visits to the returned providers a patient makes.

Physicians can provide each different service once in one visit. If a patient consults a physician and needs two intravenous injections, then she will get only one on the first visit. Earlier versions of the model included the rule that patients always visit a physician with the average frequency of visits in a quarter of a year that patients had in the database, restricted to quarters of year where they visited the corresponding specialty at least once. However, the validation process showed that this leads to undesirable effects: If the service need includes only medical services that the patient should get once, more than one visit is unnecessary. Conversely, if the patient needs a medical service several times, she might not get the right amount.

Therefore, the assumption was changed. Patients make visits to providers as long as there are no services left that the patient needs and the physician can provide. Thus, the service need and the portfolios of the providers determine the number of visits.

Every time that medical providers treat a patient in their queue, they send a message with a visit object to the reimbursement system. Visit objects include the ID of the provider and the patient, the date of the visit, and information for reimbursement such as provided services and the diagnoses that were treated.

The reimbursement system stores the information it needs. A per case flat rate system, for example, can ignore the individual medical services, but it needs to know which of a patient's medical problems were treated and which physicians he consulted. At the end of a reimbursement period, several reimbursement statistics are updated. For example, the reimbursement system stores how much payment each specialty received in a quarter of year. The model saves these statistics to text files for later analysis.

4.4.3 Validation of the GAP-DRG Model

The model maps the health care process, from the occurrence of diseases to the reimbursement of medical services, in great detail. Many assumptions were necessary, and a big part of the process arises endogenously in the simulation; it is not directly specified as input. It is thus not clear from the outset that the model produces patterns similar to reality. Therefore, external validations that are only

partly dependent on the source data are possible (Eddy et al., 2012). Various measures from the simulation can be compared with analyses of the data, such as how many different specialties patients consult during a quarter of a year and how many times a medical service is provided (of a particular specialty, for a certain medical problem type).

One example of the importance of the validation process concerns the number of different specialties consulted in one reimbursement period. While the average numbers from the model and the database were similar (1.66 in the model versus 1.48 in the data), the differences in the distributions, which are shown in Figure 4.7, are more pronounced. Fewer patients in the model than in the database have contact with only one specialty, but more with two different specialties.

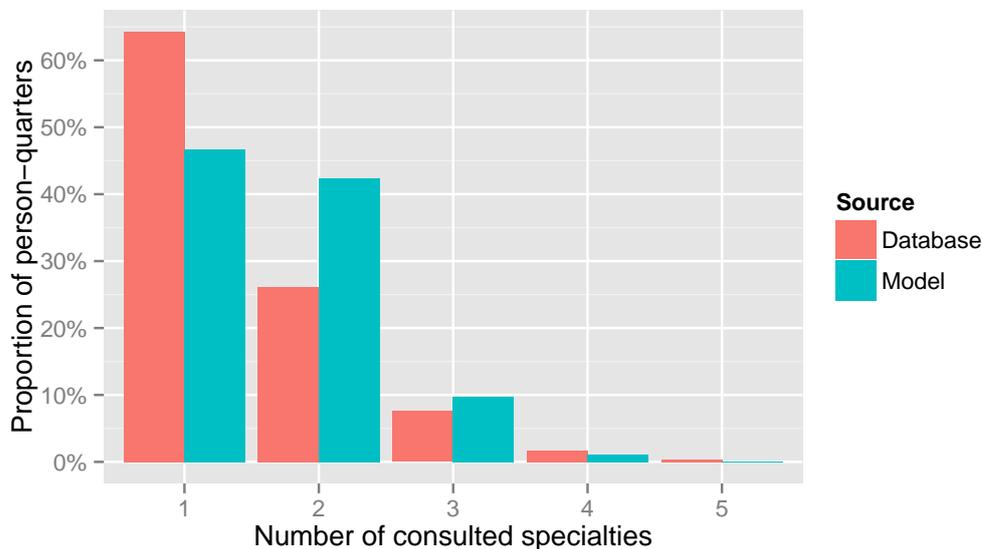


Figure 4.7: The distribution of the person-quarters of year in which a patient consulted a given number of different specialties under normal parameter values of search distance and provider capacity, from evaluations of the database and from the model.

In the model, there are two types of parameters with high uncertainty: the patients' search distances and the providers' capacities. The assumed standard values were probably rather low. For example, the search distance for a general practitioner was 5 kilometres in the model, and physicians had a capacity of 20

cases per day during a week.

Sensitivity analyses showed that while qualitative results on the relative differences between reimbursement systems did not change with higher values for these parameters, there was a significant influence on the number of specialties that patients must consult. As Figure 4.8 shows, the proportion of quarters of year where patients consulted only one specialty nearly matched the value from the database at higher parameter values. The proportion consulting two specialties is still higher, but also closer to the data. A further increase in the search distance and the capacity of the providers would improve this, but the proportion of person-quarters with three or more consulted specialties is already a bit too high and would become worse. Other (and probably more complex) adaptations are necessary to obtain an even better fit.

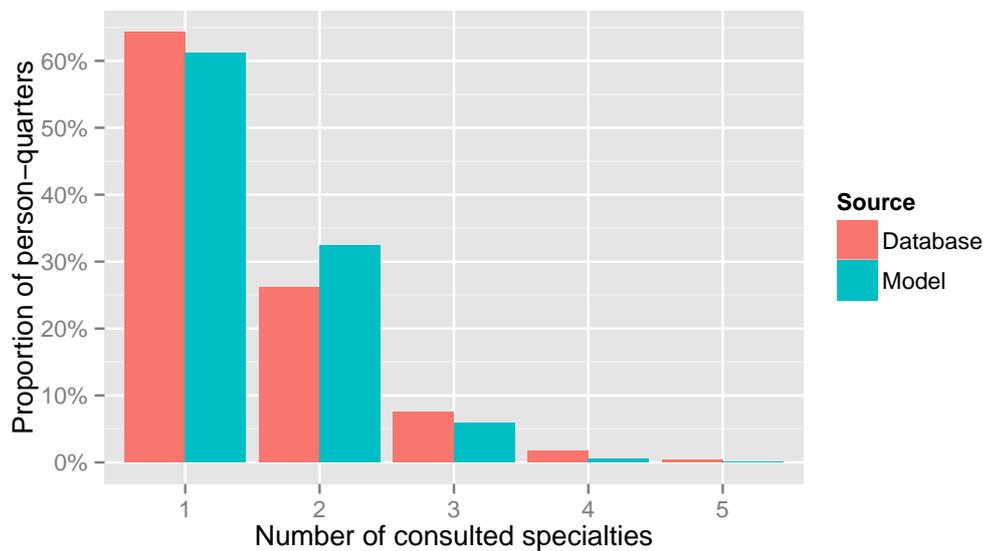


Figure 4.8: The distribution of the person-quarters of year in which a patient consulted a given number of different specialties under higher parameter values of search distance and provider capacity, from evaluations of the database and from the model.

This example shows that a model of such detail also needs quite detailed validation tests, as many different aspects of the model have to correspond with the data. On the other hand, this testing of assumptions and theories provides an

opportunity to gain knowledge on processes related to health care.

4.4.4 The GAP-DRG Model in Use

Several scenarios with different reimbursement systems were implemented using the GAP-DRG model. In addition to the overall costs for extramural health care, deferrals of costs between the specialties are of great importance.

Working with the model showed that the fair design of per-case flat rates as reimbursement systems is not an easy task. Simple sharing mechanisms for the flat rates, such as the equal distribution to all involved medical providers, can lead to less income for physicians who normally provide a large portion of medical services, while doctors who only provide a few services to a case might be better off.

Results have to be taken with caution as issues like the one shown in the last section appear and are currently being used to improve the model. On the other hand, work with the model generates new insights that are often plausible and at least thought-provoking impulses.

Simulations of the GAP-DRG model take much longer than simulations of the group practice model. It is thus not possible to analyse a huge number of combinations of parameter values. Additionally, simulation runs have statistical variation, though it is small compared to the differences brought about by different reimbursement systems.

4.5 Conclusions

This chapter presented agent-based modelling and simulation with both its differing but largely overlapping characteristics in the literature and discussed attempts at creating a formal definition. Most notably, the method is based on the simulation of often a large number of individuals in a bottom-up approach and is very flexible. As we defined it, ABMS describes stochastic systems and uses discrete events where agents can change their own state and interact with other agents as well as the environment in which they live.

The case example of this chapter was the GAP-DRG model. It is far more detailed than it would be possible with an SD model. This greater level of detail

provides additional opportunities for assumption testing, but comes at the price of more sources of error and the need to conduct more validation tests.

Chapter 5

Comparison of SD and ABMS

5.1 Introduction

Many different modelling methods allow for the formulation of models as dynamical systems. Examples besides SD and ABMS are traditional process-oriented discrete event simulation, Markov cohort models, and microsimulation models.

It is possible to represent a problem with practically any modelling method (Roberts et al., 2012). While ordinary differential equations, for example, usually describe individuals in a population in an aggregated way, they could be used to describe each member of the population individually. (Though we have restricted agent-based models to a discrete event timing, in a wider sense agent-based models can allow each agent to be described with differential equations.) This would of course yield a large number of equations and forfeit the advantages of an aggregated description. Depending on the problem, one modelling method can therefore lead to a more natural and compact model formulation than other methods. It is thus useful to analyse the attributes of the modelling methods under investigation, SD and ABMS, and to describe which characteristics of problems favour their utilization.

Different modelling methods focus on different aspects of a problem. Examples are feedback in SD models and emergent behaviour, that is, global behaviour that arises from the actions of individuals, in ABMS. On the other hand, some aspects have equivalent descriptions in various modelling methods. For instance, both SD and ABMS model change, because they are methods of describing dynamical

systems. SD does this with its flows, while in a discrete event ABMS model, events change the state and are often scheduled after stochastically determined time spans. As we will show, both mechanisms can be seen as variants of the unifying concept of a *rate*.

5.2 Classifications of Modelling Methods

A classification is an equivalence relation, where objects that are related to each other are in the same class (Pawlik, Popper, & Breitenecker, 2007). At best, it should be able to classify each conceivable method. Often methods are classified along various different dimensions. The following taxonomy is an example of such a classification.

5.2.1 Taxonomy According to Brennan et al.

Brennan et al. (2006) propose a taxonomy of modelling methods for economic evaluations of health technologies, which is arranged along a horizontal and a vertical axis. It assumes that a population is modelled.

On the horizontal axis, the primary distinguishing characteristic is if the method represents the population at the individual or aggregated level. In the latter case, similar individuals are aggregated by counting.

Aggregated models are further divided into deterministic and stochastic approaches. Methods at the individual level are supposed to be always stochastic, but the taxonomy distinguishes between Markovian and non-Markovian ones. The latter allow for distributions other than the exponential distribution (continuous time models) and geometric distributions (discrete time models) for modelling the time until the next event.

On the horizontal axis, the primary distinguishing characteristic is whether or not the method allows interaction between individuals. In modelling methods that do not allow interaction the change of one individual's state only depends on his or her own state. This is typical for Markov cohort models and microsimulation models. A microsimulation, for example, can calculate the time trajectory of every individual independently because the probability of a state transition depends only

on the current state of the individual.

The taxonomy further divides the vertical axis according to how time is used in the model. In methods without interaction, the only distinction made is between untimed models (e.g., decision trees), which are not dynamical systems, and models with time. Methods with interaction, on the contrary, are divided into discrete time and continuous time methods.

Overall, modelling methods in the taxonomy of Brennan et al. are divided along the following dimensions:

1. Aggregate level vs. individual level
2. Interaction vs. no interaction
3. Stochastic vs. deterministic (used only for aggregated level)
4. Markovian vs. non-Markovian (used only for individual level)
5. Untimed vs. timed (used only for methods without interactions)
6. Discrete time vs. continuous time (used only for methods with interactions)

In the taxonomy, SD is a deterministic aggregated method, which determines its place on the horizontal axis. In terms of the vertical axis, it allows for interactions and uses continuous time.

While the authors do not explicitly mention ABMS in their taxonomy, they do include discrete event simulation, which has the same features in the taxonomy. Like SD, ABMS allows for interactions and uses continuous time (events may happen at an arbitrary time point on the continuous axis). However, it models the population at the individual level and allows for non-Markovian distributions. Note that in order to comply with the definition of a dynamical system, for each agent every time till a future event has to be included in its state.

Overall, both methods allow for interaction and continuous timing, which is why they occupy the same vertical position in the taxonomy. They differ in that SD is deterministic and aggregates the population, whereas ABMS is stochastic and models a population at the individual level. Therefore, they are on opposite sides of the horizontal axis.

5.2.2 Classification According to Borshchev and Filippov

Borshchev and Filippov (2004) classify the four methods SD, ABMS, (process-based) discrete event models, and dynamic systems (here the term is restricted to physical modelling). They use the distinction between discrete and continuous timing differently than Brennan et al., because for them, models that change state in discrete events are discrete and only models where state changes continuously are continuous.

The other dimension that the authors use is the level of abstraction. Models that are highly aggregated, have little detail, and analyse the object system at a strategic level possess high abstraction. On the other end of the spectrum, models that map individual objects without much aggregation, have high detail, and analyse the object system at a operational level possess low abstraction.

In the classification of Borshchev and Filippov, SD is a continuous method, while ABMS is predominantly discrete. Additionally, SD is placed at a high level of abstraction, while the authors state that ABMS cover the whole range of abstraction, from low to high. Agent-based models can map a system in high detail, when the agents represent people or even smaller units, but they can also use a higher level of abstraction, such as when the agents represent groups of people or companies.

5.2.3 Comparison of Further Attributes Used for Classification

The previous classification schemes use only a few characteristics to classify modelling methods. However, SD and ABMS differ in many more attributes. Schieritz and Milling (2003), for example, present various differences between the two approaches. Table 5.1 shows an extended list that compares SD and ABMS in twelve different attributes.

The modelling perspective of ABMS is a bottom-up one, where the modelling process starts with individuals and small parts of a system to get an understanding of the system's global behaviour. SD, on the contrary, looks primarily at the global state of a system and breaks it down into its major components (Macal, 2010). This corresponds to the different levels of aggregation that are typical. In SD, individuals

Table 5.1: A comparison of SD and ABMS in several different dimensions.

Attribute	SD	ABMS
Perspective	Top-down	Bottom-up
Level of aggregation	Aggregated variables	Individuals
Randomness	Deterministic	Possibly stochastic
Timing	Continuous	Discrete events
State space	Continuous	Arbitrary
Elements with state	Stocks	Agents, Environment
Origin of change	Flows	Events
Structural elements	Feedback loops	Agent connections
Structural changes	Change of loop dominance	Change of structure
Detailed formulation	Equations	Agent rules
Exogenous influence	Exogenous variables	Environment
Space	Through compartments	Explicit space

are not modelled separately, but counted in stocks of people with similar states (e.g., infected individuals, susceptible individuals). These stocks are only further disaggregated if it seems necessary.

As already discussed, time and state changes in SD are continuous, and it describes deterministic systems. With the same initial conditions, an SD model describes just one time trajectory. ABMS typically uses discrete events instead of a continuous change, and the time spans between events often follow probability distributions. Thus, agent-based models describe a probability space of time trajectories, where every trajectory is piecewise constant (the overall state of the system does not change between events, and there are only a finite number of events in a finite time span).

SD uses only real variables, but ABMS allows arbitrary sets to make up the state space. On the other hand, most often agents also have real variables or at least a finite set of states.

The state of an SD model consists of the values of its stocks (explicitly or in the form of delays, which are internally implemented with one or more stocks). In an agent-based model, the overall state consists of the individual states of all agents and the environment. State can only change through flows in the case of SD and through events in the case of a discrete event ABMS.

Structural properties of a model play an important role in creating dynamic

behaviour. In an SD model, causal links connect the variables, such as stocks and auxiliaries, and form balancing or reinforcing feedback loops that are essential for determining which dynamic modes of behaviour are possible (Sterman, 2000, pp. 108–127). Connections between agents, on the contrary, state which agents are able to interact (i.e., send messages to each other). These connections or links can have the form of a network or they can be implicitly given by spatial relationships. One important difference to the causal links of SD models is that connections between agents can dynamically change during simulation.

After a modeller has formulated the general structure of a model (stocks and flows, agent types and their underlying environment), further specifications are necessary to create an executable model. These specifications take the form of equations in the case of SD. Agents, on the contrary, need rules (of execution). Typically, they are formulated in a logical if-then form. Additionally, besides endogenous relationships in an SD model and the behaviour of agents, influences from the outside world are often included via exogenous variables (sometimes with the help of table functions), which influence other SD quantities, or via an environment for the agents.

Finally, an oft-mentioned difference between SD and ABMS is the capability of agent-based models to explicitly express spatial relationships. Agents can have coordinates in a spatial environment, move in this space and communicate with nearby agents. SD can incorporate space if it models only a limited number of individuals and has stocks for place, velocity, and other necessary spatial variables. However, in the typical case of an aggregated population, the representation of space is problematic.

A possible approach is to discretise the spatial environment into compartments and to split the stocks of the SD model according to these compartments. For example, Nguyen, Taillandier, Drogoul, and Auger (2012) infer a differential equation model from an agent-based model of two species that compete for a common food resource. The food in the agent-based version is randomly arranged in patches on a two-dimensional environment. Since each patch is inhabited by only one species after a certain initial period, the authors simplified the environment to consist of two distinct food patches or compartments. Thus, the population divides into members of Species *A* living in Patch 1, members of Species *A* living in Patch 2,

members of Species B living in Patch 1, and members of Species B living in Patch 2. The differential equation model gave similar results to the agent-based model (in particular, it reaches the same equilibrium).

5.3 Aggregation and Heterogeneity

The level of aggregation was one of the major differences between SD and ABMS in the classifications discussed in the last section. It is thus appropriate to analyse the nature and the legitimacy of aggregation for health care models, especially regarding the application to reimbursement systems, in detail. In this section, we assume for simplicity that the systems are autonomous and have no input. It is then possible to treat the output map η as a mapping from the state space X to the output space Y .

5.3.1 What to Aggregate: Patients, Diseases, Cases, Consultations

Usually, decision-analytic models in health care explicitly represent patients, either individually or as an aggregated population. The group practice model of Section 3.5, however, only includes cases (and derived from it, consultations) on the patient side, because it is focused on the providers and their behaviour after the merger to a group practice. Cases are an external factor in these models. There is no feedback of the providers' treatment decisions on the patient population. Their workload, however, influences the amount of new cases they get.

This example shows that not all problems need an explicit incorporation of patients. If only one disease is considered, modelling diseases can also be equivalent. However, as the GAP-DRG model shows, the explicit incorporation of multiple diseases makes it necessary to link all attributes to patients.

5.3.2 How to Aggregate

Suppose that of n agents, every individual's state is an element of the state space X_{ind} . An example is an agent-based SI model, where $X_{ind} = \{Susceptible, Infected\}$.

The state space of the overall model is therefore n -dimensional.

An SD equivalent of this model has only a 2-dimensional state space, which consists of the numbers of susceptible and infected individuals (it is even sufficient to have only one of these numbers as the sum always has to be n). This aggregation is only feasible because it reduces the dimension of the state space. An SD model with an n -dimensional state space would not be more efficient or mathematically tractable than an agent-based model with n agents.

Aggregation can therefore be described by a mapping $\zeta: X \rightarrow X'$ from a state space X to a state space X' , where X is high-dimensional and X' usually has a low dimension. In the case of an aggregated SD model, this aggregated state space is an \mathbb{R}^k with a small k .

5.3.3 When Is Aggregation Admissible?

What we want from an aggregation is the following: It should map the state of a complex high-dimensional model, in particular an agent-based model with a large number of agents, to a state space with low dimension.

Not all such mappings are acceptable. If too much information gets lost the resulting model is useless or it is not possible to calculate the change of state. On the other hand, a certain amount of information loss is admissible. This depends on what we are interested in.

Example 5.1 (Aggregation of the SI model). Important outcomes of an infectious disease model are typically how many individuals are infected at a certain time point under a particular policy (e.g., a vaccination) and how much an epidemic costs. While it is possible in an agent-based model to record the state of particular agents that is usually of interest only for purposes of verification and validation, that is, to look for errors in the model.

Suppose that there is a fixed amount of n agents in an SI model. The state of the whole model at a particular time point is then an element of $X_{ind}^n = \{Susceptible, Infected\}^n$. However, we are only interested in the value of the output mapping $\eta: X_{ind}^n \rightarrow Y$, where the output in $Y = \{0, \dots, n\}$ represents the number of infected individuals.

If the state space of the aggregated model, X' , equals this output space, then some of the information is lost. It is impossible to infer from a state $x'(t) = 3$ which three agents are infected. However, it suffices for the requested output information. The other question is if we can calculate the future state trajectory from it. This works only if the future number of infected individuals depends only on the present number and not on which agents are infected in particular. With a homogeneous mixing assumption (where each agent can transmit the disease to all other agents with equal likelihood), this is usually true, but in general the further spread of the disease will depend on the places occupied by the infected agents in a contact network.

The situation presented in this example leads to a generalized definition.

Definition 5.2 (Admissible Aggregation). Let Σ be a stochastic dynamical system with state space X , state transition map ϕ , and output map $\eta: X \rightarrow Y$. An aggregation mapping $\zeta: X \rightarrow X'$ to another state space is *admissible* if there exists a state transition map ϕ' for the aggregated state space and an output map η' such that the diagram in Figure 5.1 commutes. If the aggregated model is deterministic, then we require this in the sense that the future state of the aggregated model is the expected value of the aggregation of the future state of the original model.

This definition makes clear what requirements an aggregation must fulfil. Interestingly, the conditions do not only depend on the inner workings of the original (agent-based) model, but also on the output quantity of interest. They illustrate why the question or problem that a modelling project addresses is so important and strongly influences the modelling method and the structure of a model.

5.3.4 Heterogeneity

Aggregation, especially aggregation by counting similar individuals, is strongly related to the heterogeneity of the individuals in a system and whether this influences the evolution of the output quantity of interest. In Example 5.1, aggregation to the number of infected individuals only works if these individuals are homogeneous. If they differ from each other, either because some agents have more social contacts than others and are therefore more likely to transmit the disease quickly, or

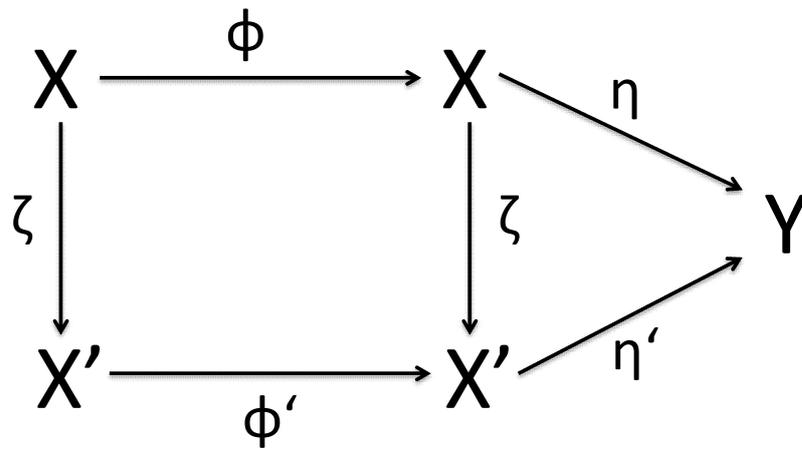


Figure 5.1: For the aggregation mapping ζ to be admissible, this diagram must commute: On the one hand, going from a state in X to another state at a future time point by ϕ and then aggregate with ζ must give the same result (i.e., with the same probability) as aggregation first and then going to the aggregated state at the future time point with the state transition map ϕ' . On the other hand, two states x and x' that correspond through aggregation must also map to the same output y through the output maps η and η' .

because they have different attributes (e.g., infection probabilities due to good or bad immune system), then it is important to know which individuals are infected in order to predict the future course of the disease.

While one single real number might not be enough to represent the state of the system in an aggregated yet sufficiently informative way there can still exist aggregation mappings of a low dimension that are admissible. For example, if patients were similar except for a difference between men and women, then instead of counting the overall number of individuals with the interesting property (e.g., infection with a disease) the state of the system could be represented by the number of men and the number of women with this property. There are, however, a few problems with this approach:

1. Not all attributes have values in a finite set. For continuous attributes, such as the weight of patients, aggregation by counting individuals is only possible with discrete classes, which can introduce error into the model. It is possible to reduce this error with a finer classification, at the cost of increasing the number of classes.
2. Each additional attribute multiplies the number of classes that have to be counted, and thus the dimension of the aggregated state space (see Figure 5.2). This can quickly eliminate the advantage of aggregation. Brennan et al. (2006) suggest the use of individual-based models if dimensionality gets too large.

Models for the analysis of reimbursement systems, such as the GAP-DRG model, can have to incorporate not only attributes such as age, weight, sex, or insurance status, but also a large number of medical problems. This makes the representation of heterogeneity in the form of co-morbidities a major problem in these models. There are not only patients who have diabetes or coronary heart problems, but also patients with multiple chronic conditions, and they all can have different service needs.

Osgood (2009) calls the approach of splitting a population in an aggregated model into all combinations of the discriminating attributes “attribute-based disaggregation”. He compares it with several other aggregated and individual-based approaches. An important one is based on ageing chains and co-flows.

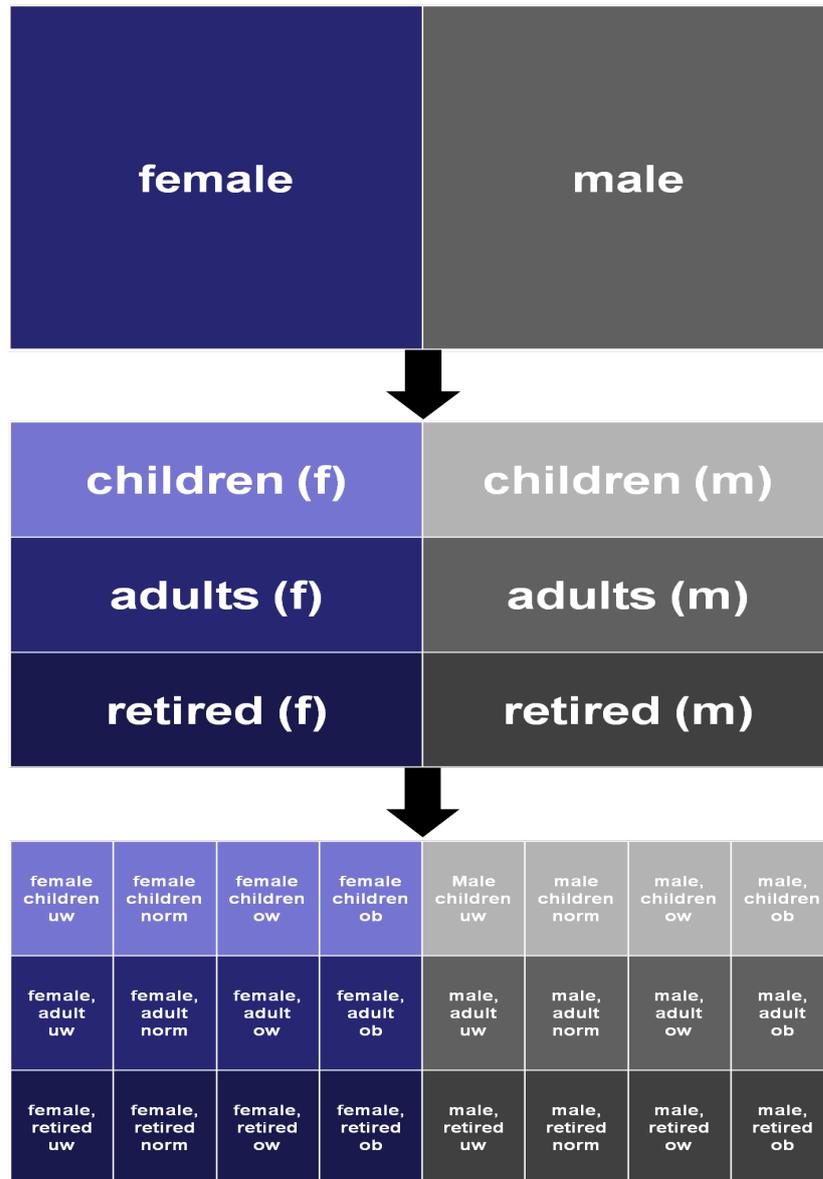


Figure 5.2: If heterogeneous individuals are counted, for each additional attribute where they can differ the number of classes is multiplied (curse of dimensionality). In this example, first only the distinction between males and females is taken into account. As broad age classes and the body mass index classes uw = underweight, norm = normal, ow = overweight, and ob = obese are added, the number of classes quickly rises to 24.

The name of ageing chains comes from a model structure that represents each age class of a population as a stock. Ageing flows connect consecutive stocks. This structure is also well suited to model patients' progression through various stages of a disease. For co-morbidities, it is possible to have several parallel ageing chains. While this approach allows for a reduced number of different stocks, it has some other drawbacks: it is not possible to track the number of individuals with a certain combination of co-morbidities. One can know the number of patients with diabetes and of patients with coronary heart disease, but not patients who have both conditions. This approach would thus not be feasible for the level of detail in the GAP-DRG model.

A large number of heterogeneous classes can be very cumbersome in an SD model. The biggest problem is that the inclusion of a great deal of heterogeneity makes it hard to incorporate a detailed feedback structure. If there are already many stocks and the feedback structure that emanates from each stock has a few parameters and auxiliaries then the overall number of variables will be even larger. Furthermore, the graphical nature of SD models is then stretched to its limits.

For these reasons, if modellers incorporate such detailed heterogeneity into a model at one place, they often have to aggregate it again at another place. One example is an SD model of the prevalence of obesity in Austria, which incorporates a fine-grained population model with 96 age classes, each for men and women (Glock, Einzinger, & Breitenecker, 2012). For modelling the disease prevalence, where a distinction between people with underweight, normal weight, overweight, and obesity becomes necessary, it aggregates these age classes to broader ones. In an agent-based model, this would not be necessary.

5.3.5 The Dangers of Ignoring Heterogeneity

As heterogeneity typically makes aggregation less feasible, it is interesting to analyse what the consequences of ignoring it are. We will use a very simple, analytically tractable, yet representative example.

Example 5.3 (Model of One Chronic Disease). Suppose we have a fixed population of 1000 individuals who are all healthy in the beginning. They can develop a disease that is not curable, that is, an individual who has the disease will stay chronically

ill. All the men have the same incidence rate, as well as all the women.

Let x_1 be the number of healthy men, y_1 the number of men with the disease, x_2 the number of healthy women, and y_2 the number of women with the disease. Furthermore, let r_1 and r_2 be the incidence rates of men and women, respectively. The situation is then described by the differential equation system

$$\begin{aligned}\frac{dx_1}{dt} &= -r_1x_1 \\ \frac{dy_1}{dt} &= r_1x_1 \\ \frac{dx_2}{dt} &= -r_2x_2 \\ \frac{dy_2}{dt} &= r_2x_2.\end{aligned}\tag{5.1}$$

On the other hand, if we do not distinguish between men and women, then the differential equation system would be

$$\begin{aligned}\frac{dx}{dt} &= -rx \\ \frac{dy}{dt} &= rx.\end{aligned}\tag{5.2}$$

Can this system give the same result as (5.1)? In this case, we have the equality

$$rx = \frac{dy}{dt} = \frac{dy_1}{dt} + \frac{dy_2}{dt} = r_1x_1 + r_2x_2,$$

which leads to

$$r = \frac{r_1x_1 + r_2x_2}{x_1 + x_2}.$$

Differentiation of both sides and plugging in the equations for x_1 and x_2 in (5.1) further shows that

$$\frac{dr}{dt} = -(r_1 - r_2)^2 \frac{x_1x_2}{(x_1 + x_2)^2}.$$

The rate r is thus only a constant if $r_1 = r_2$ unless x_1 or x_2 is zero.

In other words, if there are men and women in the population, the average incidence rate of the disease, r , changes over time. The reason for this is that if, for example, men have a higher incidence rate, the proportion of men in the healthy

population decreases over time, and thus the average incidence rate in the healthy population that is still left also decreases.

The analysis of this example shows that it is only possible to ignore heterogeneity in a model if another assumption, namely that the incidence rate of the disease is constant, is dropped. But calculating the change in the rate requires one to keep track of the heterogeneous composition of the population, so that is not an option.

On the other hand, it can be acceptable to treat the heterogeneous groups in an aggregated way if the parameters do not differ too much. Figure 5.3 shows the time trajectories of the number of people with the disease, compared for the model with heterogeneity and for the aggregated model. It was assumed that the population consists of an equal proportion of men and women. The incidence rate r_1 for the men was fixed to 0.1 per time unit, while the incidence rate r_2 for women takes the values of 0.1, 0.2, 0.3, and 0.5. Of course, the two models give the same results for a value of 0.1 for r_2 . Even if the incidence rate of women is doubled, the two trajectories only differ minimally. Finally, there is a big difference at the value of 0.5, which is largest at Time 8 (909 individuals in the aggregated model versus 766 individuals in the heterogeneous model).

Again, the research question driving the model is important for deciding if the mistake of not ignoring heterogeneity is acceptable. If the goal is a quantitative prediction of the process a substantial error is problematic. (However, the error may still be small compared to other modelling errors and uncertainties.) If the model serves to analyse and explain dynamic modes of behaviour, quantitative accuracy is not necessary. In the example above, the qualitative behaviour is the same in both the heterogeneous and the aggregated model. Incorporation of the right feedback structure is more important than going into detail with heterogeneity.

5.4 Feedback in SD and ABMS

Feedback is one of the central concepts of the SD methodology. It is present if a quantity influences itself indirectly over its causal effects on other quantities in the system. In a causal diagram, this is always represented as a feedback loop through the quantity. Note that feedback affects only future values of a variable, because

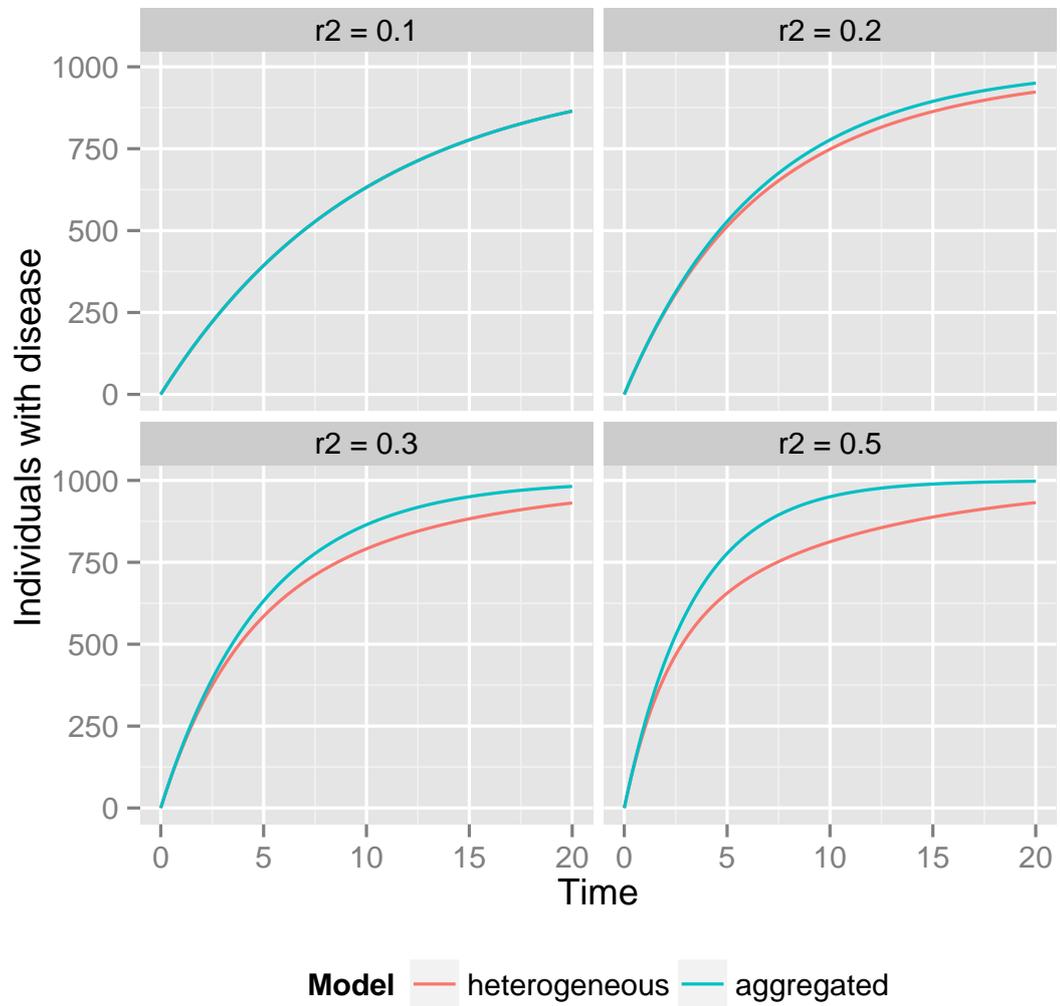


Figure 5.3: The number of individuals with the disease in a population with 500 men and 500 women, compared for the models in (5.1) (heterogeneous) and in (5.2), for a female incidence rate of 0.1, 0.2, 0.3, and 0.5, respectively. The male incidence rate is fixed at 0.1.

there must always be a stock and a flow involved in a feedback loop and the stock accumulates the change in the flow over time, not instantly.

Feedback is the only way for an SD model to endogenously generate dynamic behaviour. A model without feedback loops is driven by its exogenous variables and is therefore useless for an explanation of dynamics.

Is the dynamic behaviour of an agent-based model also driven by feedback? The states of agents are the equivalent of the stocks in an SD model, whereas events are the equivalent of flows (see Table 5.1). Therefore, feedback is present if there is some quantity derived from the state of agents that influences events that in return can change the quantity.

Feedback can exist even if the agents are independent of each other (i.e., if they do not interact or communicate). In the previous example, where individuals can change their state by acquiring a disease, the greater the number of agents who are still healthy, the greater the number who can develop the disease, which decreases the number of healthy agents in return. Of course, this is analogue to the feedback loop in the differential equation (SD) model.

Feedback of higher complexity of course also involves the interaction of agents. Martinez-Moyano and Macal (2013) present an SD and an agent-based version of an SIR model, where individuals can have one of the three states susceptible, infected, and recovered. The flow of agents from the state susceptible to the state infected depends on the interactions of these agents with agents who are already infected. In our terminology, the greater the number of agents who are susceptible and infected, the more frequently events where an infected agent has contact with a susceptible agents and transmits the disease will happen.

The authors also propose a new diagram type for depicting the feedback structure of agent-based models: the *agent feedback diagram*. These diagrams are similar to the stock and flow diagrams of SD, but, in line with the correspondence between SD stocks and the state of agents, they show agents in a certain state as boxes and agents' possible state changes as flows. Additionally, it is possible to depict the interactions of agents that determine these state changes in an agent feedback diagram. For an example, see (Martinez-Moyano & Macal, 2013) or the diagram in the next chapter.

In conclusion, feedback is present in agent-based models just as in SD models.

The modelling process of ABMS does not, however, focus explicitly on feedback as a source of the dynamics of a system. Rather, it results implicitly as a consequence of the (interaction) rules of the agents.

5.5 Rates as a Universal Tool for Describing Change in SD and ABMS

5.5.1 Introduction

Apparently, the flows between levels that count individuals in an SD model and the events that change the state of agents in ABMS have a strong similarity. The larger a flow is and the more events happen in a certain amount of time, the more individuals change their state.

In the context of how often events happen and how fast the state of a system changes there are a few terms that are used inconsistently and often lead to confusion, namely *fraction*, *risk*, *rate*, *fractional rate*, *ratio*, *probability*, and *proportion*. Especially the difference between risk and rate has a long tradition of error and was ignored for a long time in the context of epidemiology. Vandembroucke (2003) describes the history of this problem.

The concept of a rate is particularly important for studying equivalent descriptions in SD and ABMS. In SD, the term “rate” is even used as a synonym for flow. On the other hand, in survival analysis, which deals with the times until certain events (e.g., death, machine failure) happen, (hazard) rates also play an important role. In this case, however, they are related to the probability distributions that describe survival times.

It is not immediately obvious how these different types of rates (continuous rates of change versus stochastic rates) are equivalent. The purpose of this section is thus to clarify their relationship, but first, the concept of “risk” is analysed, because it is often confused with rates.

5.5.2 Risk

Risk is commonly expressed as a probability. One definition of risk is “the possibility that something unpleasant or unwelcome will happen” (Oxford Dictionaries, 2013). Probability measures the degree of possibility. Therefore, the terms risk and probability can be used synonymously for unpleasant or unwelcome future events. In health care, the onset of a disease (*incidence*), disease progression, and death (*mortality*) are typical examples of such events.

As a synonym for probability in the cases mentioned above, risk shares its attributes: It is described as a dimensionless number between 0 and 1, which represents (in a frequentist sense) the limit of the relative frequency of the corresponding outcome (the event of interest, e.g., the onset of disease in a certain time span) in a series of independent trials when the number of trials approaches infinity.

While probability or risk itself is a dimensionless number without a time unit, time does often play a role because the event of interest may be that something happens *within a certain period of time*. For example, a person’s risk of dying in the time span of one year could be 0.1. The probability as a number is dimensionless, but it relates to an event in the period of one year.

The terms risk and rate both appear as a central concept in several modelling methodologies. Before rates are introduced, the following subsection presents Markov models as an example of a model that relies on risks.

A Modelling Methodology That Uses Risks: Markov Models

Markov models consist of a set of states and probabilities for the transitions between them (Briggs & Sculpher, 1998). They represent a special type of *stochastic processes*. Parzen (1962/1999, p. 22) defines a stochastic process as “a family of random variables $\{X(t), t \in T\}$ indexed by a parameter t varying in an index set T ”. Normally the parameter t represents time. If for any n and time points t_1, t_2, \dots, t_n the conditional distribution of the random variable X_n depends only on the value of $X(t_{n-1})$ for known values of $X(t_1), X(t_2), \dots, X(t_n)$, then the stochastic process fulfills the so-called *Markov property* and is called a *Markov process* (Parzen, 1962/1999, p. 188). Formally, the Markov property states that

$\forall x_1, x_2, \dots, x_n \in \mathbb{R}$:

$$\begin{aligned} \mathbf{P}[X(t_n) \leq x_n \mid X(t_1) = x_1, \dots, X(t_{n-1}) = x_{n-1}] \\ = \mathbf{P}[X(t_n) \leq x_n \mid X(t_{n-1}) = x_{n-1}] \end{aligned} \quad (5.3)$$

If both the index set and the state space of a Markov process are discrete sets, then it is called a *discrete parameter Markov chain*. For each $t \in T$ and states j and k from the state space we define the *transition probability* $p_{j,k}(t)$ as $\mathbf{P}[X(t+1) = k \mid X(t) = j]$. The transition probabilities from one time point t form a *transition matrix*. All transition matrices together with the *unconditional probability vector*

$$\mathbf{p}(0) = \begin{pmatrix} p_0(0) \\ p_1(0) \\ \vdots \\ p_j(0) \\ \vdots \end{pmatrix} = \begin{pmatrix} \mathbf{P}[X_0 = 0] \\ \mathbf{P}[X_0 = 1] \\ \vdots \\ \mathbf{P}[X_0 = j] \\ \vdots \end{pmatrix}, \quad (5.4)$$

completely determine the Markov process (Parzen, 1962/1999, p. 196).

In medical decision making, a typical Markov model would assume that each patient runs through a Markov process, where the health states of the patient correspond to the states of the process (Sonnenberg & Beck, 1993). The initial unconditional probability vector describes the initial distribution of patients. For example, all patients could start the process in the state "healthy". The transition probability $p_{j,k}(t)$ is the probability that a patient who is in state j at time t will be in state k at time $t+1$. For discrete Markov models the index t is often called *cycle* instead of time.

5.5.3 Rates

Confusion with Risk

A simple example shows the problem with rates. Suppose that $x(t)$ is the number of healthy individuals at time t . Additionally, let p be the risk (or probability) of developing a certain disease within one year. It follows that, on average, $p \cdot x(0)$

individuals should develop the disease during the first year.

Someone who is unaware of the difference between risks and rates might model the number of healthy individuals with the following differential equation:

$$\begin{aligned}\frac{dx}{dt}(t) &= -px(t) \\ x(0) &= x_0\end{aligned}$$

This might seem correct, because the derivative of x at time 0 equals $p \cdot x_0$. However, as x decreases the derivative increases, and thus it is on average less than $p \cdot x_0$.

The exact solution of the differential equation is $x(t) = x_0 \exp(-pt)$. Thus, after one year $x(0) - x(1) = (1 - \exp(-p)) x_0$ individuals have got the disease. From the inequality $1 - \exp(-p) < p$, which holds for $p > -1$ (this is always true when p describes a probability), it follows that these are indeed less individuals than expected.

Taylor series expansion at $p = 0$ leads to an additional insight. The n -th derivative of $1 - \exp(-p)$, for $n \geq 1$, is $(-1)^{n+1} \exp(-p)$. This leads to the Taylor series

$$(1 - \exp(-p)) x_0 = \sum_{n=1}^{\infty} (-1)^{n+1} \frac{p^n}{n!} x_0 = px_0 + \mathcal{O}(p^2),$$

which shows that $p \cdot x_0$ is the linear approximation of the number of individuals that have got the disease after one year in the differential equation. This approximation gets worse for larger values of p , that is, for diseases that occur frequently.

What would be the correct form of the differential equation? Suppose that at every instant of time the derivative of x should equal a constant fraction r of the number of healthy individuals, that is

$$\frac{dx}{dt}(t) = -rx(t). \tag{5.5}$$

Additionally, we know the fraction of healthy individuals after one year. The solution of Equation 5.5 for the initial value $x(0) = x_0$ is $x_0 \exp(-rt)$. For $t = 1$ this leads to the equation

$$px_0 = (1 - \exp(-r)) x_0,$$

which can be solved for r :

$$r = -\ln(1 - p) \quad (5.6)$$

Equation 5.6 is the classic conversion formula for a probability p into a *rate* r , which is the parameter of Differential Equation 5.5. With the correct conversion, the solution of the differential equation has the desired property: It is equivalent to the formulation with probabilities or risks. However, why is the parameter r called a rate?

Definition of a Rate

According to Miller and Homan (1994, p. 52), a rate is conceptually the “*instantaneous potential* for change in one variable per unit change in another variable”. Mathematically, it is nothing else than a derivative (Elandt-Johnson, 1975; Miller & Homan, 1994): A quantity Y changes with every unit change in the quantity X according to the *instantaneous rate* R , which calculates to

$$R = -\frac{dY}{dX}.$$

In dynamic models, the quantity X will be in most cases nothing else than time. Furthermore, change is often described relative to the size of Y , which leads to the relative rate r , where

$$r = \frac{-\frac{dY}{dt}}{Y(t)}. \quad (5.7)$$

These definitions work well when there is just one reason for change. For example, let m be the (relative) death rate in the population N , and assume that individuals leave the population only through death and cannot join the population during the time horizon of interest:

$$\frac{dN}{dt} = -mN(t). \quad (5.8)$$

It follows that

$$m = -\frac{\frac{dN}{dt}}{N(t)},$$

and thus m actually is a relative rate.

However, if new individuals join the population with the relative birth rate b ,

the equation changes to

$$\frac{dN}{dt} = (b - m)N(t). \quad (5.9)$$

In this case, $b - m$ can be expressed in the form of a relative rate as in Equation 5.7, but not b or m themselves. As both variables are usually called rates, a good definition should include them. Furthermore, Equation 5.7 has a minus sign on the right hand side. This works for the death rate but not for the birth rate. We propose a better definition, which uses a decomposition of the derivative and solves the problems mentioned above. It is restricted to rates of change where time is the unit on the denominator.

Definition 5.4 (Rate Decomposition). Let $Y, G_1, G_2, \dots, G_m, L_1, L_2, \dots, L_n$ be elements of $\mathbb{R}^{\mathbb{T}}$, where \mathbb{T} is a time set. If Y is differentiable and $\frac{dY}{dt} = \sum_{i=1}^m G_i - \sum_{j=1}^n L_j$, then the sets $G = \{G_1, G_2, \dots, G_m\}$ and $L = \{L_1, L_2, \dots, L_n\}$ are a *rate decomposition* of $\frac{dY}{dt}$ or, equivalently, of the change of Y . The elements of G are called *growth rates* and the elements of L are called *loss rates*. Generally, all elements of G and L are rates.

An infinite number of rate decompositions are possible. For example, the derivative of the number of individuals in the population, N , in the above example could be expressed by one growth rate, as $rN(t)$, or as the sum of one growth rate $bN(t)$ and one loss rate $mN(t)$. Furthermore, an infinite number of other decompositions are mathematically equivalent (e.g., the sum of $(b - 1)N(t)$ and $(m + 1)N(t)$), but the decomposition into births and deaths has also contextual meaning and is therefore preferable.

The definition of a relative rate follows in a natural way:

Definition 5.5 (Relative Rate). If R is a rate (as in Definition 5.4) and if there exists an $r \in \mathbb{R}^{\mathbb{T}}$ such that $R(t) = r(t)Y(t), \forall t \in \mathbb{T}$, then r is a *relative rate*.

Note that a relative rate for a given rate of a rate decomposition always exists if the rate equals 0 for all time points where the quantity Y equals 0.

Example 5.6 (Rates of a Population Model). A population model describes the dynamic changes in the number of people in a population (or in subgroups of a

population). Equation 5.9 is a simple example of such a model. The rate decomposition with $G = \{bN\}$ and $L = \{mN\}$ shows that bN and mN can be seen as rates and b and m as relative rates. However, it is also possible to use the *relative net birth rate* $n = b - m$. Then, the net birth rate nN is the difference of births and deaths and thus the total change in the population:

$$\frac{dN}{dt} = nN$$

It builds a trivial rate decomposition.

Rates of Stochastic Events

The quantities of interest in Section 5.5.3 changed continuously in time, and this change was deterministic. However, there are two other modelling approaches for the progress of time: discrete time and discrete events (Cellier, 1991, pp. 11–15). Definition 5.4 is not directly applicable to either of the two.

Time is continuous in discrete event modelling, but the state of the system changes only at a finite number of time points in each finite time interval. The time points of future events may be sampled from probability distributions. In this case, discrete event models are stochastic.

Suppose, for example, that a population consists of 100 individuals with a certain highly lethal disease, and that the time until death of an individual is a random variable T that follows an exponential distribution:

$$T \sim \text{Exp}(\lambda).$$

The parameter λ is called the *rate parameter* of the exponential distribution. Figure 5.4 shows an example of a survival curve for this setting. What connection exists between this parameter and the definitions of rates (Definition 5.4 and 5.5)?

In the deterministic case, the rate (in the case of a trivial rate decomposition) represented the change of a certain quantity, which is the number of individuals

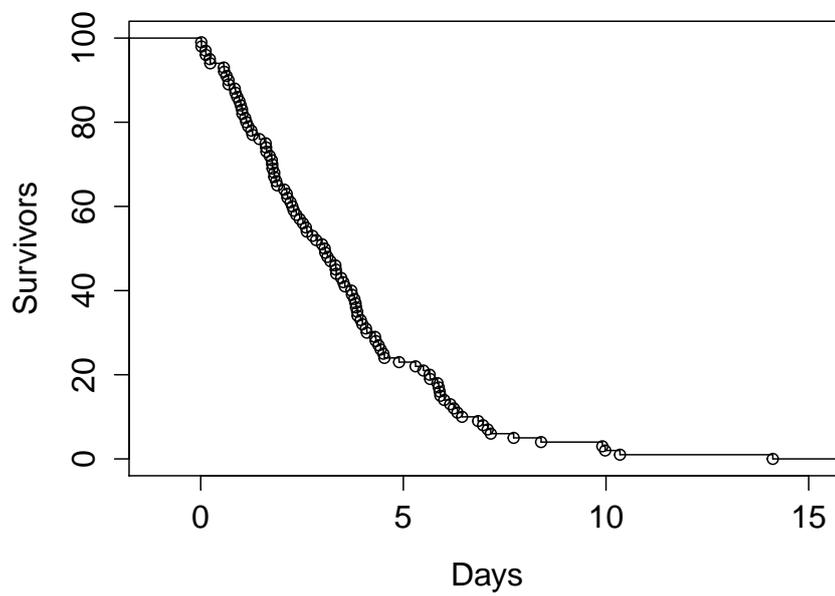


Figure 5.4: An empirical survival curve of 100 people who die after an exponentially distributed time with rate $\lambda = 0.3$.

alive, N , in the example above. The relative rate r should then calculate to

$$r = \frac{\frac{dN}{dt}}{N(t)}.$$

However, there will not be more than 100 different time points at which somebody from the population actually dies. At these time points, the derivative of N does not exist. At every other time point, the change equals zero. Even worse, in every trial with 100 individuals with the disease, these time points would be different just from random variation.

An alternative is the expected value of individuals alive at time point t . This value is fixed:

$$\mathbb{E}(N(t)) = N(0)\mathbf{P}[T > t]$$

Note that $\mathbf{P}[T > t]$ is exactly how the survival function of a distribution, $S(t)$, is defined. In this sense, the expression $N(0)S(t)$ is equivalent to the solution of Equation 5.8. In the case of the exponential distribution, the cumulative distribution function is $F(t) = 1 - \exp(-\lambda t)$, and from $S(t) = 1 - F(t)$ it follows that

$$\mathbb{E}(N(t)) = N(0)S(t) = N(0)\exp(-\lambda t).$$

The deterministic model should explain the expected value of the number of individuals alive without the random variation. That is, the solution of Equation 5.8, which is $N(t) = N(0)\exp(-mt)$, should be equal to $\mathbb{E}(N(t))$. This is the case if the rate parameter λ is equal to the relative death rate m . Furthermore, the rate parameter of the distribution fulfills the definition of a relative rate (Definition 5.5) if the survival function is exchanged for the quantity Y that changes with the rate. This leads to the *hazard function* of the distribution, which is defined as

$$h(t) = \frac{f(t)}{S(t)} = \frac{-\frac{dS}{dt}}{S(t)}. \quad (5.10)$$

The term *hazard rate* is therefore justified.

Variance that Results from Stochastic Rates

The survival function describes the expected number of individuals in the original state for each time point. It can be equal to the solution of a deterministic differential equation. How can the actual quantity, which changes through stochastic events, differ from the expected value?

Note: In the following, death of the individual will be the event of interest. However, the same applies to every type of event that may happen only once.

For each of the $n = N(0)$ individuals, the value of the survival function $S(t)$ describes the probability of surviving longer than t . Whether or not an individual is alive at time t can thus be seen as an experiment with two alternative outcomes (yes and no). Thus, $N(t)$ follows a binomial distribution:

$$N(t) \sim \text{Bin}(n, S(t))$$

Its variance $\text{var}(N(t))$ equals $nS(t)(1 - S(t))$. Thus, it is highest when $S(t) = 0.5$, that is, at the time point t where the probability of surviving at least until t is exactly 0.5, which can be seen from setting the derivative of the variance to zero.

A further question is more complicated to answer: For a certain proportion q of the n individuals, what is the distribution of the time point t_q at which the i -th individual dies, where $i = \lfloor nq \rfloor + 1$?

This problem translates into a problem of distribution of order statistics. The time of death of each of the n individuals is a random variable, denoted by X_1, X_2, \dots, X_n . The i -th order statistic, $X_{i:n}$, is the i -th random variable that results from arranging X_1, X_2, \dots, X_n into non-decreasing order, such that $X_{1:n} \leq X_{2:n} \leq \dots \leq X_{n:n}$. Note that while the original random variables may be independent, the order statistics are not.

It follows that the distribution of the i -th individual's time of death is the distribution of the i -th order statistic. For the case where X_1, X_2, \dots, X_n are independent and identically distributed (i.i.d.) with a common absolutely continuous cumulative distribution function (cdf) F (that is, they come from a continuous distribution and the probability density function f exists), B. C. Arnold, Balakrishnan, and Nagaraja (1992/2008, pp. 9–13) derive formulas for the pdf of the i -th

order statistic, denoted by $f_{i:n}$, and its cdf $F_{i:n}$:

$$f_{i:n}(x) = \frac{n!}{(i-1)!(n-i)!} (F(x))^{i-1} (1-F(x))^{n-i} f(x) \quad (5.11)$$

$$F_{i:n}(x) = \sum_{k=i}^n \binom{n}{k} (F(x))^k (1-F(x))^{n-k}. \quad (5.12)$$

Closed-form expressions of the expected value and the variance of order statistics exist for particular distributions. The most important example is the case of the exponential distribution, i.e., the case where the hazard rate for all individuals is constant.

Theorem 5.7. *If the survival times of n individuals are i.i.d. random variables from a common exponential distribution, i.e., the hazard rate of each individual equals a common constant λ , then the survival time of the i -th individual that dies, $X_{i:n}$, is a random variable with expected value*

$$\mathbb{E}(X_{i:n}) = \sum_{k=1}^i \frac{1}{\lambda(n-k+1)}$$

and variance

$$\text{var}(X_{i:n}) = \sum_{k=1}^i \frac{1}{\lambda^2(n-k+1)^2}.$$

*Proof.*¹ The joint density function of the order statistics $X_{1:n} \leq X_{2:n} \leq \dots \leq X_{n:n}$ is given by

$$f_{1,2,\dots,n:n}(x_1, x_2, \dots, x_n) = n! \prod_{i=1}^n f(x_i), \quad -\infty < x_1 \leq x_2 \leq \dots \leq x_n < \infty.$$

For the exponential distribution with pdf $f(x) = \lambda e^{-\lambda x} \mathbf{I}_x(0, \infty)$, where $\lambda > 0$, this leads to

$$f_{1,2,\dots,n:n}(x_1, x_2, \dots, x_n) = n! \lambda^n e^{-\lambda \sum_{i=1}^n x_i}, \quad 0 \leq x_1 \leq x_2 \leq \dots \leq x_n < \infty.$$

¹The proof follows the proof for the special case of a standard exponential distribution given in (B. C. Arnold et al., 1992/2008, pp. 72–73).

Consider the transformation

$$\mathbf{h}: \mathbb{R}^n \rightarrow \mathbb{R}^n, \quad \mathbf{x} \mapsto \mathbf{z},$$

where $z_i = (n - i + 1)(x_i - x_{i-1})$, and define the multivariate random variable $\mathbf{Z} = (Z_1, \dots, Z_n)^T$ as $\mathbf{Z} := \mathbf{h}(\mathbf{X})$, where $\mathbf{X} = (X_{1:n}, \dots, X_{n:n})^T$. The determinant of the Jacobian matrix of the transformation is $n!$ and, therefore, $1/n!$ for the inverse of the transformation. Furthermore, the sum of the random variables is invariant under the transformation, because

$$\sum_{i=1}^n z_i = \sum_{i=1}^n (n - i + 1)(x_i - x_{i-1}) = \sum_{i=1}^n x_i.$$

It follows that the transformed random variables have joint density function

$$f_{Z_1, Z_2, \dots, Z_n:n}(z_1, z_2, \dots, z_n) = \lambda^n e^{-\lambda \sum_{i=1}^n z_i}, \quad 0 \leq z_1, z_2, \dots, z_n < \infty,$$

which shows that they are i.i.d. random variables from the exponential distribution with rate parameter λ (i.e., its expected value is $1/\lambda$).

It is then easy to see that

$$\mathbb{E}(X_{i:n}) = \mathbb{E}\left(\sum_{k=1}^i \frac{Z_k}{n - k + 1}\right) = \sum_{k=1}^i \frac{1}{\lambda(n - k + 1)}$$

and

$$\text{var}(X_{i:n}) = \text{var}\left(\sum_{k=1}^i \frac{Z_k}{n - k + 1}\right) = \sum_{k=1}^i \frac{1}{\lambda^2(n - k + 1)^2}.$$

□

A desirable property of the i -th survival time, where $i = \lfloor nq \rfloor + 1$, is that the mean value of $X_{i:n}$ should equal the value of the inverse cumulative distribution function F^{-1} at q , where $F^{-1}(q) = \sup \{x : F(x) \leq q\}$ for $q \in [0; 1)$ and $F^{-1}(1) = \sup \{F^{-1}(q) : q < 1\}$ (for $q < 1$ this is the biggest possible q -quantile), because then the i -th survival time of the n individuals would be an unbiased estimate of the (biggest) time point at which the probability for having died equals q . This is true

asymptotically, and for an absolutely continuous F with a pdf f that is continuous and positive at $F^{-1}(q)$ the i -th order statistic is asymptotically normal, or, more precisely, for $n \rightarrow \infty$,

$$\sqrt{n}f(F^{-1}(q)) \frac{X_{i:n} - F^{-1}(q)}{\sqrt{q(1-q)}}$$

converges in distribution against a standard normal distribution (B. C. Arnold et al., 1992/2008, pp. 223–224).

Summary of the Results on Rates

Overall, a rate describes how a quantity changes over time. For any quantity Y , the relative (or fractional) rate is given by (5.7).

In stochastic individual-based models, hazard functions of the probability distributions that model the time to events are relative rates, because they describe the relative change in the corresponding survival functions. SD cannot incorporate stochastic variability of a stock of individuals, but it can model the expected value of the number of individuals that are left in the stock, which equals the initial number of individuals times the survival function. From (5.10) it follows that the equation for the flow R must be

$$R = -h(t)N(t),$$

where h is the hazard function and N is the expected number of individuals left in the stock. Note that $N(t) = N(0)S(t)$.

In the special case where the probability distribution is an exponential distribution, the hazard function is equal to a constant relative rate r . This is thus equivalent to one of the most common rate equations in SD, which multiplies the current value of a stock with a constant relative rate.

The last section studied the variance of a stochastic individual-based model, which makes it possible to predict how much such a model might differ from the expected values. At a particular point in time, the variance grows linearly with the number of individuals, n . This shows that the standard deviation relative to n decreases.

Furthermore, the time at which the i -th of n individuals has changed his or her

state in an individual-based model is an asymptotically normal estimator of the q -quantile of the distribution function if $i = \lfloor nq \rfloor + 1$. The bigger the population is, the better the time at which a certain fraction of the population has changed its state will estimate the expected value.

5.6 Transformations Between Models

5.6.1 Transformation of SD Models into Agent-Based Models

Stocks that Count Agents

The last chapter introduced rates and showed the equivalence of rates in SD and ABMS models, as they can describe the deterministic change of level variables (the cause for dynamics in SD) and the stochastic occurrence of events (the cause for dynamics in stochastic ABMS models in discrete-event time). This allows for the formulation of equivalent models in both methodologies, where the levels in the SD model count the number of agents that are in a certain state (Borshchev & Filippov, 2004).

The scheme works in the direction from SD to ABMS in the following way:

1. Identify the kinds of individuals who are counted in the levels of the SD model. Normally, this can be seen from the units of the levels. For example, there could be levels accumulating patients. Each of these kinds of individuals leads to one type of agent.
2. Add attributes to the agents so that distinct values of the attributes correspond to the different levels in the SD model which accumulate individuals of this type.
3. For every inflow or outflow of individuals in the levels, add one type of event to the model that changes the state of agents. These events might:
 - (a) Change the state of an agent, which is equivalent to flows between levels
 - (b) Create a new agent, which is equivalent to flows starting at a source.

- (c) Destroy an agent, which is equivalent to flows leading to a sink.
4. Include the rest of the SD structure in the environment of the agents. For some levels, it might also be possible to model it inside the agents, for example in the case of a coflow structure.
 5. Make the events dependent on the agents that are in the respective states and on the rest of the SD structure included inside the agents and in the environment. The rates at which events happen are given by the equations of the flows in the SD model (see Section 5.5).

5.6.2 Stocks that Average an Agent Attribute

Stocks in SD models do not always represent the number of individuals in a particular state. They can also track the average value of an attribute that each individual in a population has, for example if the attribute is continuous and if it is not feasible to split the population into a finite number of classes according to the attribute.

Such an aggregation can be problematic. Suppose, for example, that the attribute of interest is the weekly workload of doctors. If its average value is 40 hours per week, it is unclear whether all doctors work 40 hours or if some doctors work less and some work considerably more. But this could lead to different average decision-making. If all doctors have a normal workload, they might treat every patient optimally, while treatment errors might occur if some doctors are overworked. Thus, assumptions on the distribution of the attribute have to be implicitly incorporated into the formulation of the decision if only the average value is an input into the decision function.

When a quantity in an SD model represents an average attribute value, an obvious approach is to assume that each agent in an equivalent agent-based model has the same attribute value. This works, for example, for parameters.

Often in an SD model, however, a quantity is the average perceived value of a certain input. A standard approach to model this is exponential smoothing, that is, if $u(t)$ is the input, $x(t)$ is the perceived value of the input, and τ is the delay time then

$$\frac{dx}{dt} = \frac{u(t) - x(t)}{\tau}.$$

What is an equivalent rule for the state of agents where they perceive the input at discrete events? For example, every patient that arrives at a doctor and is treated adds a certain amount to the weekly workload of the doctor. How does the perceived workload change for the doctor agent?

Suppose that the doctor has a perceived workload of 40 hours per week and that a new patient whose treatment takes 0.5 hours arrives 0.1 weeks (16.8 hours) after the last patient. The doctor can treat the workload since the last patient as a constant quantity, that is, as 5 hours per week. To derive a formula for the update of his perceived workload, we assume that it is based on exponential smoothing of the constant input $u = 5$ hours/week with a delay time of $\tau = 2$ weeks.

If t_0 is the time of the last patient, t_1 the time of the present patient, and x_0 the perceived value at t_0 , then the doctor updates his perceived workload according to the solution of the initial value problem

$$\begin{aligned}\frac{dx}{dt}(t) &= \frac{u - x(t)}{\tau} \\ x(0) &= x_0.\end{aligned}\tag{5.13}$$

This differential equation can be solved with variation of constants, which leads to

$$x(t_1) = u + (x_0 - u) \exp\left(-\frac{t_1 - t_0}{\tau}\right).\tag{5.14}$$

In the example above, the doctor would update his perceived workload to

$$x(t_1) = 5 + (40 - 5) \exp\left(-\frac{0.1}{2}\right) \approx 38.29 \text{ hours/week.}$$

The longer the time since the last event is in comparison with the delay time, the more the agent adapts his or her perceived value in favour of the new input, which it approaches exponentially. Overall, (5.14) is a good equivalent to the SD formula of exponential smoothing.

5.6.3 Approaches for Transforming Agent-Based Models into SD Models

In principle, any output trajectory from an agent-based model could be approximated with a differential equation system, as any differentiable function is trivially the solution to such a system. The key problem is how to find such a system without needing to simulate the agent-based model. Furthermore, it is only of value if it has a comparably low dimension. One could also try to perform system identification for a differential equation system by collecting data from the agent-based model, but with limited excitation possibilities (no input signal) this is problematic.

The biggest problem is that agent-based models can have very complex interaction structures and considerable heterogeneity. Agent-based SIR epidemic models are a good example. Bicher and Popper (2013) analyse one such model with a technique called *diffusion approximation*, which uses interpolation arguments and Taylor series expansion to infer a partial differential equation that describes the density of the global state of the system and an ordinary differential equation system that describes the mean value. The latter system turns out to be the classic SIR differential equation system. Homogeneous mixing is a prerequisite for this result, because the transition rates of the system must only rely on the counts of agents in each state. If a heterogeneous network connects the agents, these counts are not an admissible aggregation in the sense of Definition 5.2, because in this case the spread of the disease does not only depend on the total number of infected agents, but also on the connections that the infected agents have.

Rahmandad and Sterman (2008) compare several types of contact networks in agent-based models and their influence on disease spread. They show that the results can quantitatively differ from the results of a differential equation model that is equivalent to homogeneous mixing. As expected, an epidemic spreads more slowly in less connected networks and its peak is lower. On the other hand, all simulations produced qualitatively similar behaviour.

Keeling (1999) proposes an approach that does not only take into account the numbers of individuals in each of the three states susceptible, infected, and recovered, but extends the state to incorporate figures for the nine possible types of pairs (e.g., susceptible-infected, infected-infected). Due to symmetries, this only

requires five additional dimensions.

While these approaches are of analytical value, they seem to be restricted to rather simple agent-based models where agents can only have a few different states. Agent-based models of far greater detail complexity, such as the GAP-DRG model, do not facilitate such techniques. However, the great strength of simulation models is that they can cope with dynamic complexity. The model with the most detail complexity is not necessarily the best one, and thus there might be a better approach than constructing a complex agent-based model, where there is no hope of finding a compact corresponding equation system, in the first place.

5.7 Conclusions and Proposed Integration of SD and ABMS into the Modelling Process

SD and ABMS differ in several dimensions. While SD models are deterministic, continuous-timed, and highly aggregated, agent-based models allow for stochastic variation, are typically timed with discrete events, and can cope with large heterogeneity in agents, agent interactions, and the (spatial) environment. But these advantages come at a price: Obviously, ABMS is often computationally far more expensive, which might render it impossible to conduct extensive simulation experiments (especially for sensitivity and uncertainty analysis with many parameters) in modelling projects under time constraint.

There is, however, a more serious danger for modellers that relates to the power of agent-based modelling. Senge (1990, pp. 71–72) emphasizes that often the dynamic complexity (when it is not obvious which dynamic behaviour a system produces through its cause and effect structure) is more important and provides more leverage to change the behaviour of a system than the detail complexity (when the system has many variables). But with agent-based models, it is tempting to incorporate a large amount of detail complexity right from the start. This increases the possibility of modelling errors because many aspects of the system will be unknown, it would be very time-consuming to research them all, and a rich agent-based model can be a highly complex piece of software. Additionally, the incorporation of dynamic complexity can suffer.

The two presented case examples in Chapter 3 and Chapter 4 illustrate that both modelling methods, on their own, can have serious drawbacks. In the group practice model, dynamic feedback is incorporated via the workload and reimbursement of the physicians. Thus, it captures at least a part of the dynamic complexity of the real system. On the other hand, SD is not well suited to explicitly model the discrete reimbursement period, where all previous cases are reimbursed at the end of quarter of a year.

The GAP-DRG model, in contrast, has great detail complexity. This makes several aspects of modelling, such as parametrisation, verification, and model communication harder and tends to shift the focus away from the dynamic complexity and the driving feedback structure of the system.

It seems that choosing one modelling method, even only for this particular problem (the analysis of reimbursement systems in extramural health care), is only the second best option. A better way is to combine the strengths of both SD and ABMS.

The modelling process in the SD methodology is well structured and uses many techniques, such as causal loop diagrams and stock and flow diagrams, for capturing the dynamic complexity and the most important feedback loops of the system. These steps lead very quickly to an executable SD model. As shown in the last section, the transformation of an SD model into an agent-based model is far easier than a transformation in the other direction. Therefore, it makes sense to first develop an SD model and restrict it to the incorporation of aspects for which this method is well suited, and then to transform it into an equivalent agent-based model only if this is necessary.

This approach has several advantages:

- The SD modelling process can lead to a better focus on the dynamic complexity and feedback structure right from the start, from which the agent-based model will also benefit.
- It is not necessary to incorporate every aspect into the SD model, even if it is difficult to model, because there is always the option of saving it for the agent-based model.
- The SD model can stay fairly aggregated, which makes it more manageable.

- Transforming the SD model into an equivalent agent-based model should be possible with relatively little overhead. It is conceivable that it might be possible to even automatize this in the future.
- It is a good verification test to have two separately implemented models that should render approximately the same behaviour.
- When the separate further development of the agent-based model starts iteratively, it becomes clear what the greater detail complexity can add.
- Even in later stages when the agent-based model is not equivalent to the SD model any more, it can be desirable to use the SD model for certain tasks, such as extensive sensitivity analysis. The results can also lead to insight on the agent-based model to a certain extent.

Historically, the field of epidemic models seems to have followed this path. The classic differential equations of the SIR model were long established before the first agent-based epidemic models. Thus, the most important driving dynamics were always clear and available for orientation. Many different modelling techniques could then produce equivalent behaviour and even incorporate additional aspects, such as spatial effects (Schneckenreither, Popper, Zauner, & Breiteneker, 2008), but they always had to measure up against the classic model, which arguably captures the most essential feedback structure in a compact form. Even today, textbooks on infectious disease modelling often use differential equation models to illustrate concepts for maximal insight (see, for example, Vynnycky & White, 2010).

There are of course problems where properties that are directly suited to agent-based modelling play a central role. For example, a model of robots playing a soccer game should clearly incorporate the spatial aspect and the goal-driven behaviour of the participants. In health care and epidemiology, however, the decision rules of people are often not well-known and usually approximated by simple relationships, predominantly of a stochastic nature. These areas should therefore be better suited to a modelling process that starts with SD models to understand the dynamics before elaborating it into an agent-based model.

The following chapter follows the proposed approach and first develops an SD model that captures the important dynamics and the feedback structure that involve the reimbursement of physicians. It shows that it is indeed feasible to transform this model into an equivalent agent-based model, which can then be further elaborated.

Chapter 6

Modelling Physician Reimbursement in Both Methods

6.1 Introduction

The proposed modelling process from the last chapter uses SD to create a first model that should capture the most important feedback structures of a problem. Detail complexity and things that are hard to deal with in SD (e.g., heterogeneity, spatial relationships, network structures) can be spared at this stage because the option to transform the model into an agent-based one is available.

In the present chapter, we demonstrate this process with a simplified model of physician reimbursement that includes the interaction between patients, their disease state, and the pressures on physician behaviour from reimbursement and their workload. The focus lies on the dynamic structure. Parameters are set to plausible values, but not parametrized from data like the real world case examples in Chapter 3 and Chapter 4.

6.2 Problem and Textual Model Description

A good modelling study starts with a description of the problem or research question that should be answered. In the case of reimbursement systems in extramural health care, one of the central questions is how different reimbursement systems

influence the amount of provided health services, the quality of service, and the costs for the payer as well as how an optimal reimbursement system should be designed. According to Czypionka et al. (2011), most of the theory of optimal service reimbursement is based upon the work of Ellis and McGuire (1986), who develop an analytical model and derive conclusions from solving for an optimum of the physicians' utility function, which includes their profit (more specifically, the profit of the hospitals where they are employed) and the benefit to the patients.

Such models do not study dynamic behaviour and how physicians react over time to potentially changing pressures in the system. Physicians' treatment decisions can produce feedback by changing the future need of the patients, which in turn influences their decisions (e.g., if their workload changes). Therefore, dynamic simulation models might add additional insight to the already available theory. The central research question is thus which dynamic behaviour physician's choice of service extent shows under different reimbursement systems and how it influences patient health (i.e., which quality is achieved).

It follows that a model must include at minimum the health state of the population, its influence on the physicians and their treatment decisions (which amount of services they provide), and the feedback of the treatment to the health of the population. There are many different factors influencing medical decision making (Eisenberg, 2002), but we focus on two of them, physician income and workload. The group practice model followed the same approach.

6.2.1 The Health of the Population

Consider a fixed population of n individuals. People with good health are part of the *healthy population* (*HP*). They may become symptomatically ill with an average *incidence rate* (*IR*), which depends on a *fractional incidence rate* (*fir*) after which they belong to the *sick population seeking treatment* (*SPST*). In this state, individuals are in need of medical treatment and will consult physicians.

Patients who get *successful treatments* (*ST*) become healthy again. However, there are also *unsuccessful treatments* (*UT*) that do not fully cure them. Such individuals are then part of the *latently sick population* (*LSP*). As such, they do not immediately need medical treatment, but after *relapses* (*R*), which take

on average the *time to relapse* (ttr), they become again *sick population seeking treatment*.

Like the GAP-DRG model (and unlike the group practice model), this structure keeps track of diseased individuals. It also allows that they stay ill without immediately seeking treatment. However, the kind of disease or the occurrence of multiple parallel diseases are not considered. Furthermore, the model does not explicitly keep track of chronic diseases that may never heal. These simplifications are due to the focus on dynamics instead of detail, which could be added in later modelling steps but would complicate the models in a first step and thus hinder insight.

What is new in this model structure, compared to the GAP-DRG and the group practice model, is the possibility of taking quality into account. Higher quality manifests in a higher *fraction of success* (FOS) of treatments. In the GAP-DRG model, medical services have no influence on patients' state of health, and the group practice model does not consider the health of the patients explicitly.

6.2.2 Cases and Services per Doctor

Persons in the *sick population seeking treatment* generate a certain amount of *cases* (C) for physicians per day at a *case rate per person* ($crpp$). For every case, an individual changes his or her state to either healthy or latently sick.

The number of *cases per doctor* (CPD) and day depends on the *cases* and on the *number of doctors* (nod). Every case has a *service need per case* ($snpc$), which leads to the *service need per doctor* ($SNPD$). This represents the amount of medical services that would be the optimal treatment. The resulting *services per doctor* (SPD) that an average physician performs per day depend on the true need, but also on the *service extent* (SE), which controls if the physicians provides on average too many or too few services per case.

6.2.3 Workload and Reimbursement

It is assumed that the more services per day a physician has to perform the higher his *workload* (W), which is measured relative to a *standard service volume* (ssv), is. However, doctors do not instantaneously adapt their *perceived workload* (PW),

upon which their reactions are based, but only after a certain *time to perceive workload* (*ttpw*).

In general, reimbursement is some mixture of per case flat rates and fee-for-service payment. The *reimbursement per doctor* (*RPD*) thus consists of the *case reimbursement* (*CR*), which is calculated from the *cases per doctor* and the *per case flat rate* (*pcfr*), and the *service reimbursement* (*SR*), which equals the *services per doctor* times the *average service tariff* (*ast*).

Again, doctors adapt their *perceived reimbursement* (*PR*) after a certain *time to perceive reimbursement* (*ttpr*). The *normalized reimbursement* (*NR*) is then the reimbursement relative to some *standard reimbursement* (*sr*).

6.2.4 Service Extent and Its Influence on the Success of Treatment

The *service extent* measures how many services doctors provide relative to the true *service need per doctor*. Thus, values under 1 correspond to under-provision and value above 1 to over-provision of services.

Both the perceived reimbursement and workload of a doctor influence his or her service extent. If both assume their standard values they exercise the *standard effect of reimbursement on service extent* (*serse*) and the *standard effect of workload on service extent* (*seuse*). In this case, the *effect of reimbursement on service extent* (*ERSE*) and the *effect of workload on service extent* (*EWSE*) both assume the value 1. If reimbursement increases, its effect on *service extent* decreases, because doctors do not have to work as much to reach their target income. Furthermore, if workload increases, its effect on *service extent* also decreases, because doctors try to spend less time on each patient to reduce their workload.

The model assumes that there is both a *positive effect of service extent* (*PESE*) and a *harmful effect of service extent* (*HESE*). If the service extent equals 1 the *fraction of success* equals the *optimal fraction of success* (*ofos*). A lower service extent decreases the *positive effect of service extent*, because doctors do not provide all necessary services. Conversely, a higher service extent leads to a *harmful effect of service extent*. In both cases, the resulting *fraction of success* will be sub-optimal.

6.3 Feedback in the Model

The described structure includes several feedback loops. Figure 6.1 shows a simplified causal loop diagram of the model.

The most obvious feedback loops B1 (Target Income) and B2 (Desired Workload) are balancing loops through service extent and reimbursement or workload:

Balancing Loop B1 (Target Income): The more services per case doctors provide, the higher the reimbursement. When they perceive an increase in reimbursement they in turn reduce their service extent.

Balancing Loop B2 (Desired Workload): In the same manner as with reimbursement, doctors who perceive an increased workload decrease their service extent.

There is also a reinforcing loop R1 (Prevention), which involves the health of the population and the positive effect of service extent on the fraction of success. On the other hand, B3 (Bad Treatment) is another balancing loop and involves the harmful effects of over-treatment.

Reinforcing Loop R1 (Prevention): If service extent increases and more individuals become healthy through the positive effects of service extent, physicians' workload and reimbursement decrease, because future cases are prevented. Thus, they have more time and motivation to increase their service extent. Note that this feedback loop is only active if the service extent is below the optimal level.

Reinforcing Loop R2 (Bad Treatment): This feedback loop, on the contrary, becomes active if the service extent is above the optimal level. The harmful effects of services increase and thus more people become latently sick. In the long term, this leads to more relapses and more cases. Workload and reimbursement increase, which provokes a decrease in service extent.

6.4 Implementation as a System Dynamics Model

After the creation of a causal diagram, it is necessary to determine which variables are stocks or flows. The model mainly includes the stocks of healthy individuals, sick individuals seeking treatment, and latently sick individuals. It follows that flows are the variables that influence these stocks.

Physicians perceive their workload and reimbursement only with a delay (they average the input over time). If these delays are, for example, first order exponential delays, then their implementation also involves a stock. Thus, the model includes three explicit and two implicit stocks. Table 6.1 shows a detailed description of the model equations and parameters. Plausible values based on educated guesses were chosen for the parameters. In contrast to the presented case examples, no real data was involved. This is unproblematic for demonstration purposes and avoids the disclosure of potentially sensitive health insurance data.

Table 6.1: Model documentation of the SD physician reimbursement model.

Formulations and comments	Units
$HP(t) = HP(0) + \int_0^t ST(s) - IR(s)ds$ <p>The healthy population, HP, declines because of incident cases (i.e., new diseases) through the incidence rate, IR. On the other hand, people become healthy again through successful treatments, ST.</p>	Person
$SPST(t) = SPST(0) + \int_0^t IR(s) + R(s) - ST(s) - UT(s)ds$ <p>The sick population seeking treatment, $SPST$, accumulates individuals who become initially sick through the incidence rate, IR, or have relapses, R. People leave this stock through either successful or unsuccessful treatments, ST or UT.</p>	Person
$LSP(t) = LSP(0) + \int_0^t UT(s) - R(s)ds$ <p>Individuals enter the latently sick population, LSP, after unsuccessful treatments, UT, and seek treatment again after relapses, R.</p>	Person

Continued on next page

Table 6.1 – continued from previous page

Formulations and comments	Units
$IR(t) = fir \cdot HP(t)$ <p>The incidence rate, IR, of newly ill people depends on the fractional incidence rate, fir, and the number of people in the healthy population, HP.</p>	Person/Day
$R(t) = \frac{LSP(t)}{ttr}$ <p>Relapses, R, take on average the time to relapse, ttr, and can occur for individuals in the latently sick population, LSP.</p>	Person/Day
$ST(t) = FOS(t) \cdot C(t)$ <p>Cases, C, become successful treatments, ST, according to the fraction of success, FOS.</p>	Person/Day
$UT(t) = (1 - FOS(t)) \cdot C(t)$ <p>Unsuccessful treatments, UT, are cases, C, that are not successful treatments according to the fraction of success, FOS.</p>	Person/Day
$C(t) = crpp \cdot SPST(t)$ <p>Persons who seek treatment ($SPST$) become cases, R, with an average case rate per person, $crpp$.</p>	Case/Day
$CPD(t) = \frac{C(t)}{nod}$ <p>Cases, C, divided by the number of doctors, nod, gives the average number of cases per doctor, CPD.</p>	Case/(Doctor*Day)
$SNPD(t) = snpc \cdot CPD(t)$ <p>The service need per doctor, $SNPD$, equals the cases per doctor, CPD, multiplied by the service need per case, $snpc$.</p>	Service/(Doctor*Day)
$SPD(t) = SE(t) \cdot SNPD(t)$ <p>The services per doctor, SPD, is the fraction of service need per doctor, $SNPD$, that is given by service extent, SE.</p>	Service/(Doctor*Day)
Continued on next page	

Table 6.1 – continued from previous page

Formulations and comments	Units
$CR(t) = pcfr \cdot CPD(t)$ <p>The case reimbursement, CR, per doctor is the per case flat rate, $pcfr$, multiplied by the number of cases per doctor, CPD.</p>	Euro/(Doctor*Day)
$SR(t) = ast \cdot SPD(t)$ <p>The service reimbursement, SR, per doctor is the average service tariff, ast, multiplied by the services per doctor, SPD.</p>	Euro/(Doctor*Day)
$RPD(t) = CR(t) + SR(t)$ <p>The total reimbursement per doctor, RPD, consists of the case reimbursement, CR, and the service reimbursement, SR.</p>	Euro/(Doctor*Day)
$PR(t) = \text{smooth}(RPD(t), tpr, R0)$ <p>The perceived reimbursement, PR, is the first order exponential smooth of the reimbursement per doctor, RPD, where time to perceive reimbursement, tpr, is the average delay time. Its initial value is the standard reimbursement, $R0$.</p>	Euro/(Doctor*Day)
$NR(t) = \frac{PR(t)}{R0}$ <p>Normalized reimbursement, NR, is the perceived reimbursement, PR, relative to the standard reimbursement, $R0$.</p>	Dimensionless
$ERSE(t) = \text{TableForERSE}(NR)$ <p>The table function $\text{TableForERSE}()$ applied to the normalized reimbursement, NR, gives the effect of reimbursement on service extent, $ERSE$.</p>	Dimensionless
$W(t) = \frac{SPD(t)}{ssv}$ <p>Workload, W, is measured by the services per doctor, SPD, relative to a standard service volume, ssv.</p>	Dimensionless

Continued on next page

Table 6.1 – continued from previous page

Formulations and comments	Units
$PW(t) = \text{smooth}(W(t), ttpw, 1)$ The perceived workload, PW , is the first order exponential smooth of the workload, W , where time to perceive workload, $ttpw$, is the average delay time. Its initial value equals 1, which represents the case where services per doctor equals the standard service volume.	Dimensionless
$EWSE(t) = \text{TableForEWSE}(PW)$ The table function $\text{TableForEWSE}()$ applied to the perceived workload, PW , gives the effect of workload on service extent, $EWSE$.	Dimensionless
$SE(t) = ERSE \cdot serse \cdot EWSE \cdot sewse$ Service extent, SE , is the product of the effect of reimbursement on service extent, $ERSE$, the standard effect of reimbursement on service extent, $serse$, the effect of workload on service extent, $EWSE$, and the standard effect of workload on service extent, $sewse$. It describes how many service per case doctors provide in relation to the true service need per case.	Dimensionless
$PESE(t) = \text{TableForPESE}(SE)$ The table function $\text{TableForPESE}()$ applied to service extent, SE , gives the positive effect of service extent, $PESE$. This describes the positive effect of necessary services on health.	Dimensionless
$HESE(t) = \text{TableForHESE}(SE)$ The table function $\text{TableForHESE}()$ applied to service extent, SE , gives the harmful effect of service extent, $HESE$. This describes the harmful effect of unnecessary services (i.e., additional services that are not part of the service need) on health.	Dimensionless

Continued on next page

Table 6.1 – continued from previous page

Formulations and comments	Units
$FOS(t) = \frac{PESE}{HESE} \cdot ofos$ The positive effect of service extent, $PESE$, divided by the harmful effect of service extent, $HESE$, gives the proportion of the optimal fraction of success, $ofos$, that is the actual fraction of success, FOS . It represents the proportion of cases where a person gets cured.	Person/Case
$n = 100\,000$ There are one hundred thousand individuals in the population.	Person
$fir = 0.01$ We assume that the fractional incidence rate, fir , for becoming ill is 0.01 per day, that is, people develop a disease every 100 days on average.	1/Day
$ttr = 30$ The average time to relapse, ttr , is assumed to be 30 days for a latently sick person.	Day
$crpp = 0.1$ The case rate per person, $crpp$, is assumed to be 0.1 cases per day and person, that is, a sick person seeking treatment becomes a case at a doctor's office after 10 days on average.	Case/(Person*Day)
$snp_c = 5$ It is assumed that patients have a service need per case, snp_c , of 5.	Service/Case
$nod = 100$ There are 100 doctors in the model (i.e., one doctor per 1000 patients).	Doctor
$pcfr = 20$ The per case flat rate, $pcfr$, is 20 euros per case.	Euro/Case
$ast = 6$ According to the average service tariff, ast , a service costs 6 euros.	Euro/Service

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Table 6.1 – continued from previous page

Formulations and comments	Units
$tpr = 45$ It is assumed that the average time to perceive reimbursement, tpr , is half of a quarter of a year, or 45 days.	Day
$tpw = 10$ It is assumed that the average time to perceive workload, tpw , is 10 days.	Day
$ofos = 0.9$ The optimal fraction of success, $ofos$, is assumed to be 0.9, which means that under optimal treatment the person is healed in 90 % of cases.	Person/Case
$serse = 1.5$ It is assumed that the standard effect of reimbursement on service extent, $serse$, is 1.5. Thus, even the standard reimbursement leads to an extension of services (doctors would like to get more reimbursement then they do at present).	Dimensionless
$seuse = 0.8$ It is assumed that the standard effect of workload on service extent, $seuse$, is 0.8. Thus, the standard service volume has a reducing influence on service extent (doctors would like to work less then they do at present).	Dimensionless

See Appendix A for the definition of the table functions that are used in the equations.

Initial values for the stocks in the model are also necessary. For a theoretical analysis, a useful assumption is that the system should be in equilibrium, where the in- and outflows to each stock cancel each other out. This leads to the following equation system:

$$\begin{aligned}
IR &\equiv ST \\
R &\equiv UT \\
R0 &\equiv RPD \\
W &\equiv 1
\end{aligned} \tag{6.1}$$

From the last two equations of 6.1, it follows that in equilibrium, the effects of reimbursement and of workload on the fraction of success FOS are both equal to 1: Only the standard effects remain. Thus, we can set

$$FOS = \frac{ofos}{\text{TableForHESE}(se\text{se} \cdot se\text{wse})}.$$

Note that with the parameter values of the standard effects of reimbursement ($se\text{se}$) and of workload ($se\text{wse}$), the positive effect of service extent equals 1.

With this value for FOS , we can substitute the expressions for the rates into the first two equations of (6.1) and solve for the initial values of the sick population seeking treatment, $SPST$, as well as the latently sick population, LSP . The initial value for the healthy population, HP , follows from the fact that the total population equals n :

$$\begin{aligned}
SPST(0) &= \frac{n}{ttr \cdot (1 - FOS) \cdot crpp + 1 + FOS \cdot crpp / fir} \\
LSP(0) &= n - \left(1 + \frac{FOS \cdot crpp}{fir}\right) \cdot SPST \\
HP(0) &= n - SPST - LSP
\end{aligned} \tag{6.2}$$

In equilibrium, the service extent equals $se\text{se} \cdot se\text{wse}$. As the sick population seeking treatment is known from (6.2), we can express the standard reimbursement, $R0$, and the standard service volume, ssv , as

$$\begin{aligned}
R0 &= \frac{pcf\text{r} + ast \cdot se\text{wse} \cdot se\text{se} \cdot snpc}{nod} (crpp \cdot SPST) \\
ssv &= \frac{se\text{wse} \cdot se\text{se} \cdot snpc}{nod} (crpp \cdot SPST).
\end{aligned} \tag{6.3}$$

Thus, all values for initializing the model in equilibrium are known.

6.5 Transformation Into an Agent-Based Model

6.5.1 Introduction

The developed SD model is easily transformable into an equivalent agent-based model with the same global parameters.

Implicitly, there are two types of agents. It is clear that the three stocks healthy population, sick population seeking treatment, and latently sick population count persons. Therefore, the agent-based model must also contain n person-agents.

The second agent type is the doctors. While there are no stocks that count the numbers of physicians in particular states, the variables service extent, perceived reimbursement, perceived workload, and others represent average values of a population of individuals (doctors). Therefore, agents of this second type, according to the number of doctors, have to be part of the model.

It is important to note that the modeller must provide information on whether a stock or variable represents an agent count, an average value of a property that each agent of a population has, or a real global quantity because this depends on implicit knowledge of the system. An automatic algorithm for the transformation of an SD model into an agent-based one could not infer this on its own.

6.5.2 Agent Type *Person*

The stocks that count individuals transfer directly to the states of the agents. State charts are a convenient way to express agent behaviour (Borshchev & Filippov, 2004). They include the states and the possible transitions between states. In the transformed agent-based model, these transitions are equivalent to the flows of the SD model. The structure of the stock and flow diagram and of the state chart is therefore essentially the same. Figure 6.2 shows the state chart of persons in the agent-based physician reimbursement model.

The transitions from the states *healthy* or *latently sick* to the state *sick seeking treatment* are triggered by rates (the *fractional incidence rate* and the inverse of the *time to relapse* as in the SD model). This means that the time until the person makes the transition is exponentially distributed, which follows the equivalence shown in Section 5.5.

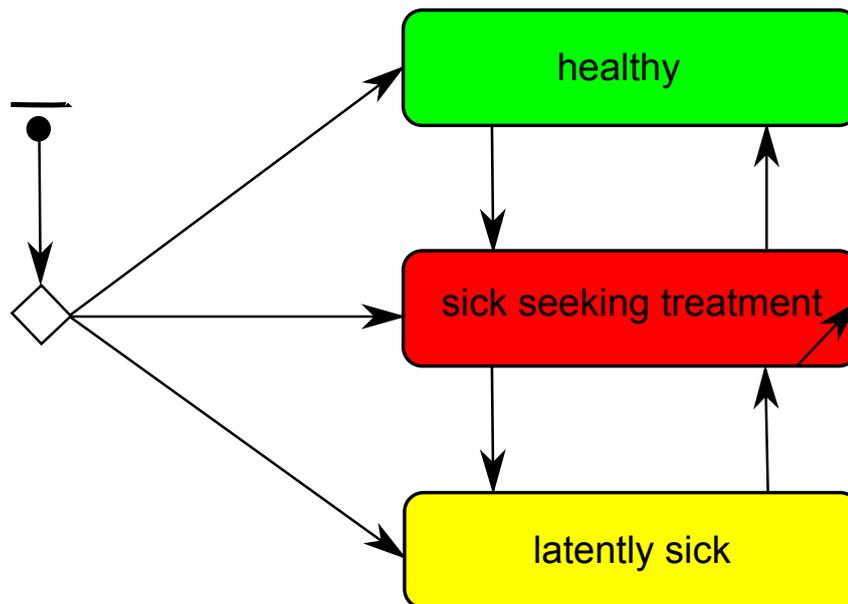


Figure 6.2: The behaviour of the agent type person as a state chart, which maps the stock and flow structure of the SD model. A person can be in one of the three states *healthy*, *sick seeking treatment*, and *latently sick*. Transitions represent people getting ill, successful and unsuccessful treatments (leading back to *healthy* or to *latently sick*), as well as relapses. Additionally, the arrow inside *sick seeking treatment* symbolizes the event when a sick person consults a doctor.

Transitions in the other direction, which represent successful and unsuccessful treatments, are not directly triggered. Instead, in the state *sick seeking treatment*, the person will send a message after an exponentially distributed time (according to the *case rate* of sick persons) to a random doctor. The message contains the *service need per case* as a value. The doctor will then return a message with the *amount of services* he or she provides to the patient (see the next section).

Upon receiving the message, the person calculates the *service extent* as the fraction of the *amount of services* from the provider and the *service need per case*. The probability of success is then calculated in the same way as in the SD model with the table functions for positive and harmful effect of service extent and the *optimal fraction of success*. This probability is used for a binary random experiment, which determines whether the treatment was successful (the person transitions to state *healthy*) or unsuccessful (the person transitions to state *latently sick*).

Just as the stocks in the SD model need initial values, each person-agent must be in one of the three health states at the start of a simulation. This initial state is also determined by a random experiment, where the probability of being in a certain state equals the initial value of the corresponding stock in the SD model divided by the total number of persons, n . Thus, the initial value is nothing else but the expected value of the number of agents in the stock.

6.5.3 Agent Type *Doctor*

Doctors do not have a discrete state. Instead, their state consists of four different variables: *perceived workload*, *perceived reimbursement*, *service extent*, and *time of last case*.

Each time a doctor gets a message from a patient seeking treatment, he or she takes the following steps:

1. Calculate the amount of services that the patient gets. It equals the service need of the patient multiplied by *service extent*.
2. Send a message with the amount of services to the patient.
3. Update the *perceived workload* with the amount of services as input.

4. Update the *perceived reimbursement* with the reimbursement, which is a function of the amount of services, as input.
5. Update the *service extent*.
6. Set the *time of last case* to the present time.

The update of the *perceived workload* and the *perceived reimbursement* uses (5.14) from Section 5.6.2. *Time to perceive workload* and *time to perceive reimbursement* are the corresponding delay times. The new input value for the perceived workload is the amount of services divided by the time span since the last case of the doctor and the *standard service volume*. The reimbursement of the present case equals the *per case flat rate* plus the *average service tariff* multiplied by the amount of services, and the new input value for the perceived reimbursement is the reimbursement of the present case divided by the time span since the doctor's last case.

The *service extent*, on the other hand, is a direct function of *perceived workload* and *perceived reimbursement*. It is calculated in the same way as in the SD model. Note that the state space of the doctors could thus be reduced, because *service extent* follows directly from the perceived values of workload and reimbursement.

6.6 Comparison of Simulation Results

The last two sections presented two models of physician reimbursement. While we constructed the ABMS version using the relationship between stochastic and deterministic rates from Section 5.5 and the discrete event formulation of exponential smoothing (see Section 5.6.2), it is not clear that both models show the same behaviour. A certain variability in the agent-based version is expected, because it describes a stochastic dynamical system, but with 100 000 agents this should be small, and the expected value should not differ from the SD results.

Both versions of the model were implemented in the simulation software AnyLogic 6.9.0 because it supports both SD and ABMS. Simulations of the SD model used the RK4 integration method with a time step of 0.001 days. All necessary system dynamics elements were directly available in the software. State charts,

Table 6.2: Equilibrium values for the SD physician reimbursement model.

Variable/Parameter	Equilibrium Value	Unit
Healthy Population	85 628.44	Person
Sick Population S. Treatm.	10 015.02	Person
Latently Sick Population	4 356.53	Person
Standard Reimbursement	560.84	Euro/(Doctor*Day)
Standard Service Volume	60.09	Service/(Doctor*Day)

transition rates, and messages between agents were also supported by AnyLogic, but some functionality had to be coded in functions, such as the discrete event formulation of exponential smoothing. This confirms that agent-based modelling and simulation needs more advanced programming skills.

Therefore, this section compares the behaviour of both models in various scenarios. It will also make clear how the models can implement a per case flat rate reimbursement system.

6.6.1 Base Run: The Models in Equilibrium

As stated in Section 6.4, it makes sense to assume that the system is in equilibrium at the moment. The SD model produces a constant behaviour if it is initialized with the equations (6.2) and (6.3). Table 6.2 shows the corresponding values. (Normalized reimbursement and perceived workload are constantly 1 in the SD model in equilibrium, which leads to a value of 1.2 for service extent.)

The agent-based model, on the contrary, does not show exactly constant behaviour because of the stochastic variation. However, as Figure 6.3 and Figure 6.3 show, the fluctuations are very small around the SD equilibrium values.

6.6.2 Scenario: Per Case Flat Rates

Per case flat rates do not reimburse single services, but only cases. The average service tariff, *ast*, is therefore zero in this scenario. On the other hand, the per case flat rate, *pcfr*, must be higher to compensate for the missing service reimbursement. We set it to 56 euros, because this equals the per case flat rate in the base run (20 euros) plus the average service tariff (6 euros) multiplied by the service extent in

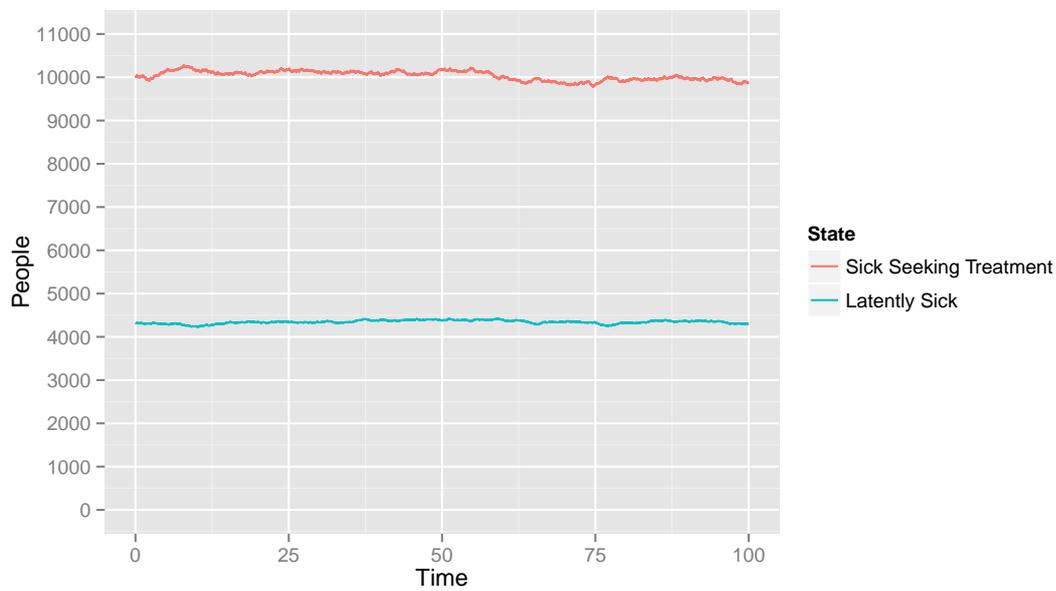


Figure 6.3: The number of persons who are sick seeking treatment or latently sick in the base run of the agent-based physician reimbursement model.

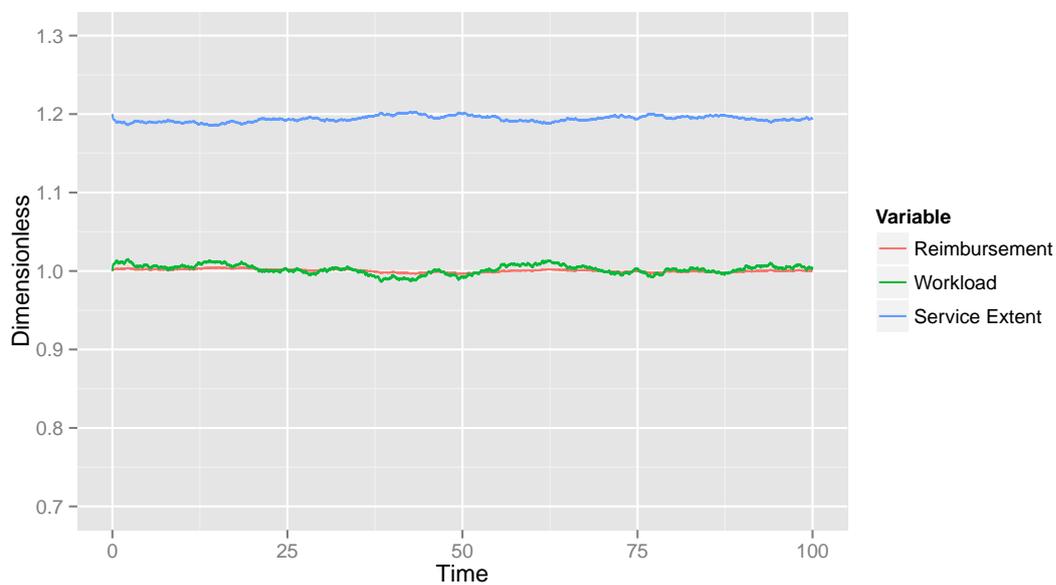


Figure 6.4: Normalized Reimbursement, perceived workload, and service extent in the base run of the agent-based physician reimbursement model.

equilibrium (1.2) and the service need per case (5).

The second effect is that now the service extent does not have a direct influence on reimbursement. Therefore, it does not make sense for a physician to increase it in order to receive more payment (or decrease it if he or she has more than enough). This cuts the causal loop B1 (Target Income), such that the effect of reimbursement on service extent is always 1, which lowers the service extent in comparison to the base run (where standard service extent is 1.2).

In contrast, the group practice model assumes that there is also an effect of reimbursement on the average number of services per case in a per case flat rate system, but that it works in the other direction: A physician increases the service extent if he or she feels that reimbursement is more adequate (i.e., higher). This is also a possible assumption, but empirical data or expert opinion would be necessary to decide if it is true and how large its effect is.

Figure 6.5 and Figure 6.6 show the results from both the SD and ABMS versions of the model. Only the perceived workload influences the service extent, so it is below the optimal value instead of too high as in the base run. Thus, the doctors provide less services to the patients, and their perceived workload decreases. In turn, they increase the service extent slightly. Additionally, the new level of the service extent is more beneficial to the patients than it is in the base run, which causes the number of latently sick patients to drop.

Again, there are only minimal differences between the results of the SD and the AB model. The output trajectories for service extent are even nearly indistinguishable. Other curves, for example the sick population seeking treatment, show some minor differences, but only over a very limited time span due to small stochastic variations.

6.6.3 Scenario: Increase of Incidence Rate

An important test of system behaviour is the reaction to a certain change of an input or a parameter. In this scenario, we assume that the fractional incidence rate doubles from 0.01 to 0.02 after 10 days, which leads to far more individuals getting sick (e.g., during a pandemic).

In principle, it is only necessary to change the parameter in both versions of the

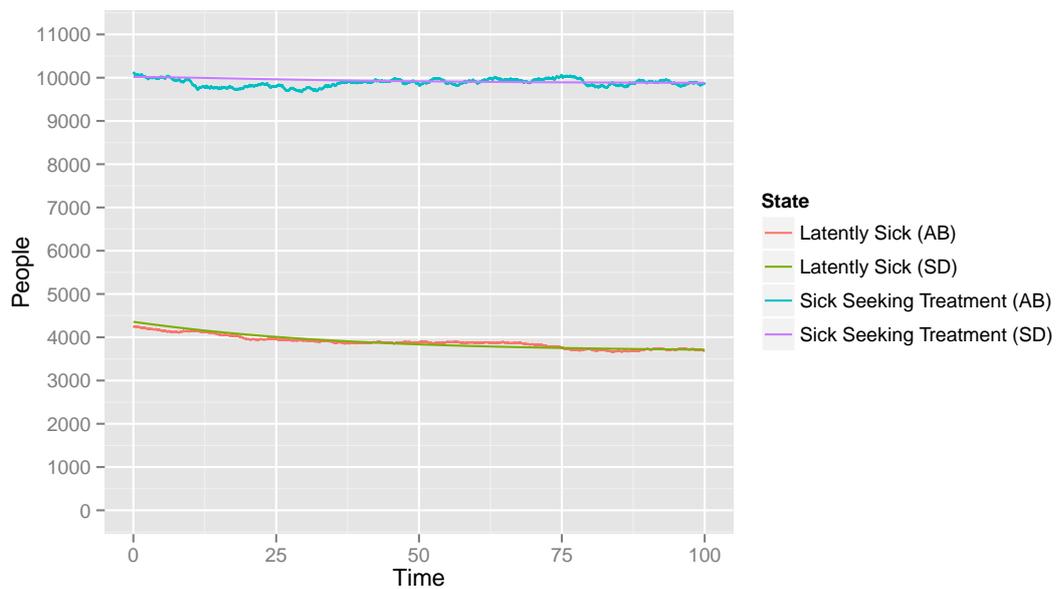


Figure 6.5: The number of persons who are sick seeking treatment or latently sick in the scenario with per case flat rates as the reimbursement system, for the AB and SD physician reimbursement models.

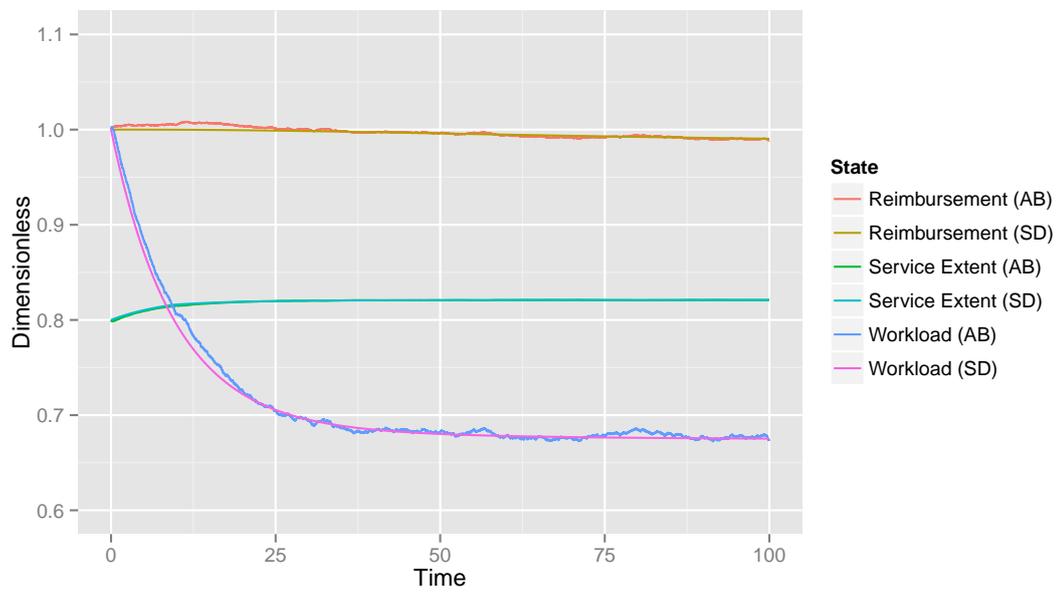


Figure 6.6: Normalized Reimbursement, perceived workload, and service extent in the scenario with per case flat rates as the reimbursement system, for the AB and SD physician reimbursement models.

model. However, the modeller must make sure that the new rate instantaneously takes effect in the agent-based model for all agents. The time to the transition from healthy to sick seeking treatment must be re-sampled for each agent in order to achieve this. Otherwise, the increase in sick population would be delayed in the agent-based model in comparison to the SD version.

Figure 6.7 and Figure 6.8 show the results for both models. As expected, the number of sick individuals seeking treatment increases sharply after the change in the fractional incidence rate. It saturates at a bit more than 17 thousand. The latently sick population increases nearly linearly.

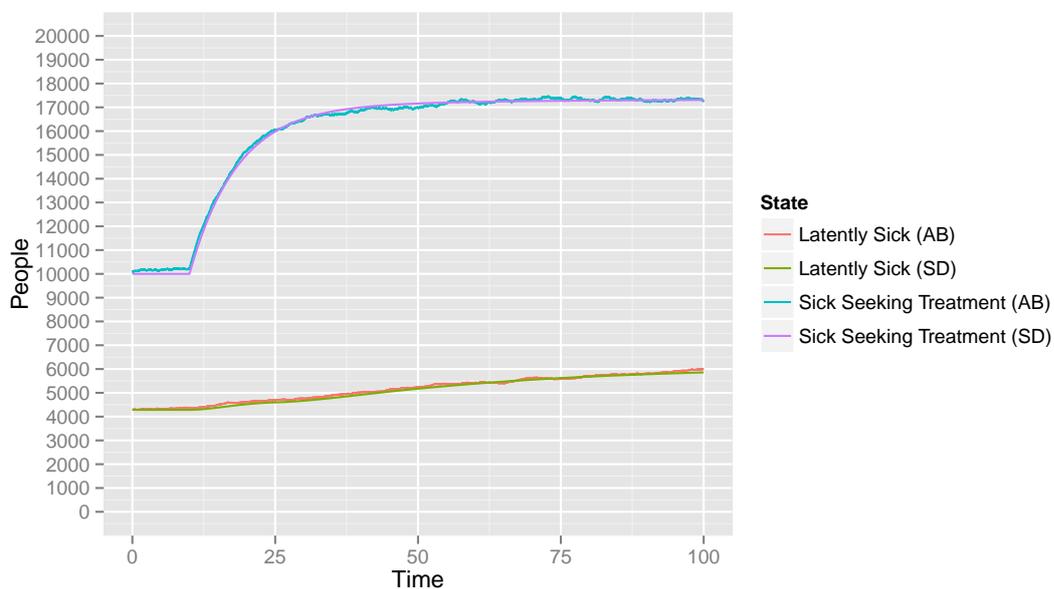


Figure 6.7: The number of persons who are sick seeking treatment or latently sick in the scenario where the fractional incidence rate changes from 0.01 to 0.02 after 10 days, for the AB and SD physician reimbursement models.

As a result, the perceived workload and reimbursement of the doctors also increase sharply. This causes them to lower the service extent. At about time 50, the perceived workload starts to decrease again. Again, the results of the SD and ABMS model versions are nearly identical.

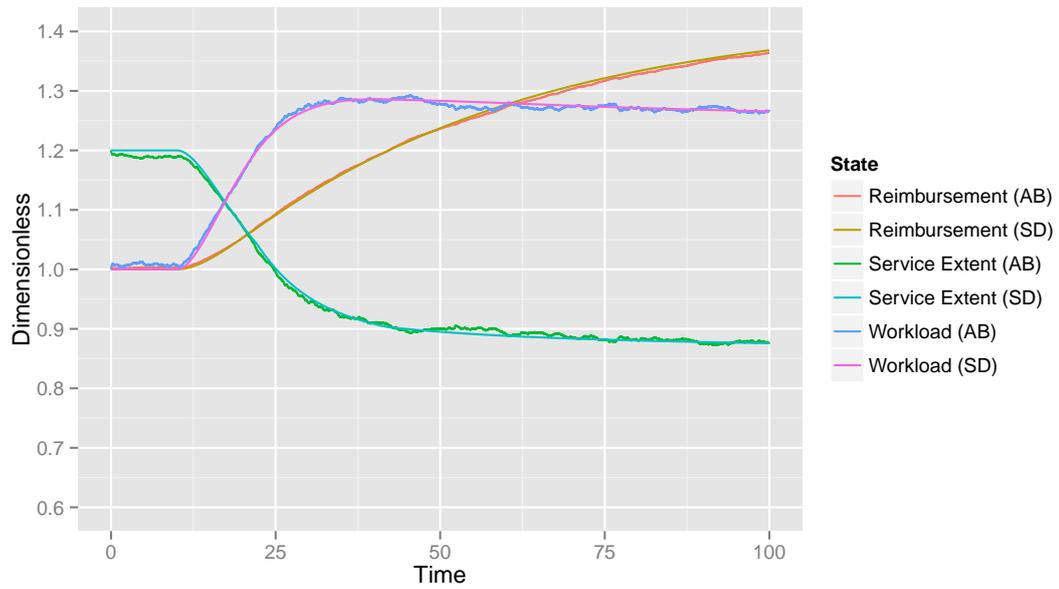


Figure 6.8: Normalized Reimbursement, perceived workload, and service extent in the scenario where the fractional incidence rate changes from 0.01 to 0.02 after 10 days, for the AB and SD physician reimbursement models.

6.6.4 Scenario: Increase of Incidence With Per Case Flat Rates

Reimbursement with per case flat rates can potentially change the reaction of the system to a higher incidence rate in the population. Thus, this section studies a scenario with both a higher incidence rate and per case flat rates for reimbursement.

Figure 6.9 and Figure 6.10 show the corresponding results. The perceived workload of the doctors drops initially because of the lower service extent, which is provoked by the different reimbursement system. However, the perceived workload (and the reimbursement) increases sharply after the change in incidence.

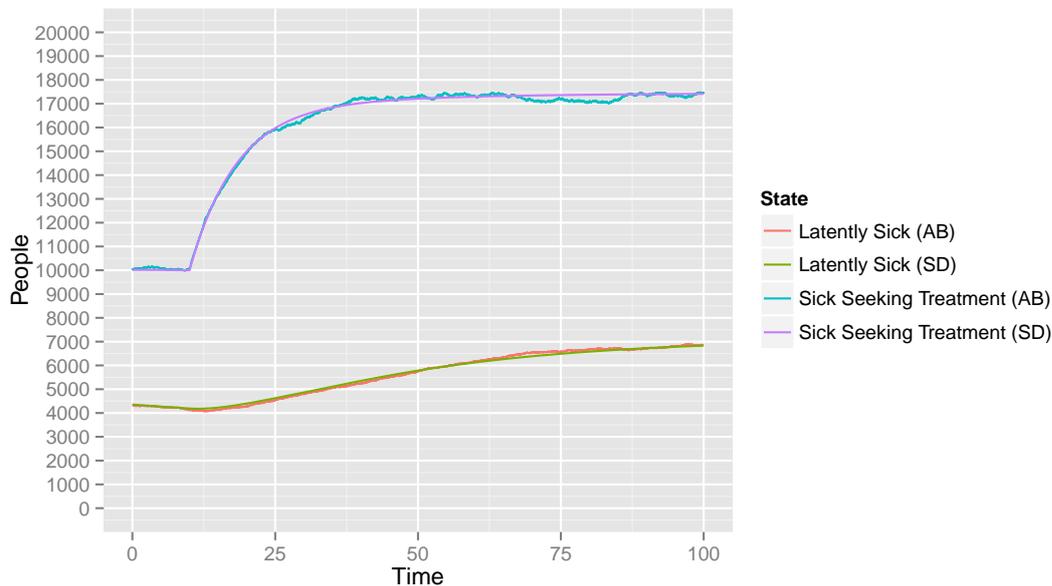


Figure 6.9: The number of persons who are sick seeking treatment or latently sick in the scenario with an increase in the fractional incidence rate and a per case flat rate reimbursement system, for the AB and SD physician reimbursement models.

This causes service extent to decrease even more. Thus, the treatment is worse than it was in the last section. As a consequence, there are about a thousand more latently sick individuals at the end of simulation than without the per case flat rate reimbursement system. This shows that under the assumptions of the models, the system reacts better under the mixed system of per case flat rates and single

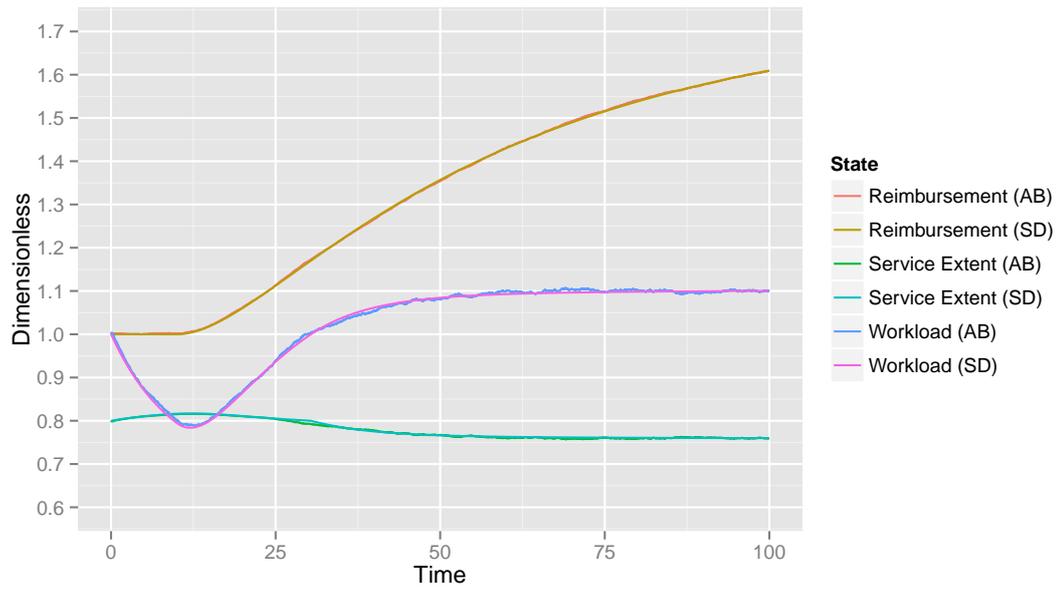


Figure 6.10: Normalized Reimbursement, perceived workload, and service extent in the scenario with an increase in the fractional incidence rate and a per case flat rate reimbursement system, for the AB and SD physician reimbursement models.

service reimbursement. Again, both model versions lead to nearly identical results.

6.7 Conclusions

The physician reimbursement model depicts the most important properties of both the GAP-DRG and the group practice model. It incorporates epidemiology (people who develop diseases) as well as physician behaviour based on their workload and their reimbursement, which depends on the applied reimbursement system. However, the model was built to be as simplified and abstract as possible in order to favour dynamic complexity over detail complexity. This facilitates the utilization of the SD modelling process, although it is possible to transform the result into an equivalent agent-based model. Both model versions show the same behaviour in many different scenarios, apart from stochastic variation in the agent-based case, which is very small, however, when the number of individuals is large.

Chapter 7

Summary and Conclusions

This study set out to compare system dynamics and agent based models, with a special focus on the modelling of health care reimbursement systems as a field of application. The importance of the right choice of a modelling method for a certain problem is often emphasized, and there are some recommendations in the literature (see, for example, the taxonomy and recommendations of Brennan et al., 2006). In practice, however, there might not always be simply one optimal decision, but rather each method has advantages and disadvantages. No matter if a problem is tackled with SD or ABMS, traps and difficulties can arise that would not have occurred with the other methodology.

System dynamics is, for example, not well suited for modelling a heterogeneous population that is partitioned in many different dimensions (e.g., age, sex, disease state). Such models can quickly get unmanageable, partly because of the obligatory graphical notation. In contrast, agent-based models are very flexible, but this can beguile the modeller into the incorporation of a lot of detail complexity at the cost of dynamic complexity. Such a model has little value to study dynamics and is also prone to error.

On the other hand, there are features of SD that have a direct equivalent in ABMS and vice versa. In particular, change in a system dynamics model is represented by the flows or rates, whereas agents change their state in events, which can be triggered by stochastic rates. Moreover, while feedback is a special focus of SD, it is also present in ABMS through the interactions of agents. These

similarities, but also the differences in advantages and disadvantages that modellers face when using the two methods, suggested that a more extensive comparison would be valuable.

7.1 Summary of Findings

The first research question of Chapter 1 asked what constitutes a system dynamics or an agent-based model, respectively. This was answered in the two method-specific chapters, Chapter 3 and Chapter 4. We can see an SD model as a collection of stocks, flows, auxiliaries, and parameters together with rate equations and auxiliary equations. Additionally, it must be specified which stocks are coupled by flows (flow coupling).

SD models are not allowed to have algebraic loops, where only auxiliary variables depend on each other without any accumulating stock in between. This work proposes formal definitions of causal links, causal chains, and causal loops, which make it possible to show that if there are no algebraic loops, (i.e., no causal loops of only auxiliaries) the flow equations of the SD model can be written just in terms of stocks and parameters (see Proposition 3.10). Thus, the model has an equivalent formulation as a differential equation system. Moreover, the links between auxiliaries form a link matrix, and the model has no algebraic loops if and only if it is not possible to transform this matrix into a lower triangle form by renumbering the auxiliaries.

Agent-based models consist of agents and an environment. Agents have their own state and can perform actions. It is possible to ensure autonomy of the agents by demanding that only an agent itself can change its state directly. Communication with others is only conducted via messages. Possible formalizations of ABMS are usually based on the DEVS formalism. We presented a new approach that is based on STDEVS (Castro et al., 2010) but where agents have no fixed coupling. Instead, they have more flexibility to send messages to different, even randomly chosen receivers.

Systems theory can serve as a rigorous mathematical foundation for modelling and simulation. Most approaches describe only deterministic systems, but many agent-based models are stochastic. Therefore, the concept of a stochastic dynamical

system is necessary. General stochastic systems can be described with a probability space (Willems, 2013). We based our definition of a stochastic dynamical system on deterministic dynamical systems, as defined by Hinrichsen and Pritchard (2010), but added a probability space on which the state transition map also depends. Deterministic dynamical systems (e.g., SD models) are a special case where the probability space has only one element. It is thus possible to see both agent-based and SD models as descriptions of stochastic dynamical systems.

Another question that this thesis tried to answer is: What creates the dynamic behaviour in both model types? Feedback can be seen as the central mechanism that determines which modes of behaviour a system might show. In SD, causal loop diagrams and stock and flow diagrams always laid emphasis on feedback relationships. ABMS, on the contrary, has no such focus, but feedback is nevertheless present in agent-based models if the states of agents influence future events that in turn may change these same states. An especially important case is when agents, depending on their state, influence the states of other agents through interaction. Agent feedback diagrams (Martinez-Moyano & Macal, 2013) make these feedback processes explicit.

SD models describe change through flows, while agents change their state through stochastically distributed events. The concept of *rates* covers both. In general, a rate describes how some quantity changes over time. Flows in SD are also called rates because they represent the change of the stocks. Hazard functions for survival times (or the time to any other type of event than death) describe the change of the survival function and, thus, the expected value of individuals who have not had the corresponding event yet. Therefore, they are often called hazard rates.

A stochastic agent-based model and an SD model can be equivalent in the sense that a stock in the SD model represents the expected value of the number of agents in the respective state. This is the case if the outflow of the stock, relative to the value of the stock (the relative rate), equals the hazard function of the event that represents the corresponding change of the agents' state. An important special case of the equivalence is when the relative rate is constant, as in

$$\frac{dN}{dt} = rN,$$

where N is the value of the stock and r is the constant relative rate. This describes the situation where the agents change their corresponding state after an exponentially distributed time, where r is the rate parameter of the exponential distribution.

It is even possible to derive formulas that describe the variance that results from stochastic rates. The number of individuals that are still in their original state at time t if they change it after a stochastically distributed time span is binomially distributed with the corresponding value of the survival function, $S(t)$, as its mean. Its variance grows linearly with the total number of individuals, n , and thus the standard deviation grows only with the square root. Relative to n , the deviation becomes smaller if more agents are simulated, a result which is well-documented empirically. Furthermore, with the theory of order statistics it is also possible to derive formulas for the distribution of the time when the i -th individual changes the state. Indeed, if q is a probability and $i = \lfloor nq \rfloor + 1$ then the survival time of the i -th individual is an asymptotically unbiased estimate of the time point where the probability of having changed state is q .

While there is a strong equivalence between the rates in SD and ABMS models, individual-based models are typically better at coping with heterogeneity and need less aggregation. Aggregated models, on the contrary, usually have a state space with a lower dimension. One important question is when such an aggregation is admissible. This work showed that the answer depends on the output quantity of interest. An aggregation is admissible if it is possible to calculate the future value of the output from only the knowledge of the present aggregated state. However, even if it is not possible to aggregate correctly, for example because of heterogeneity, the resulting error may be small (compare the example in Section 5.3.5).

How to transform an SD model into an agent-based version depends on the nature of its stocks. On the one hand, there can be stocks that count individuals in certain states. The types of individuals (e.g., patients, doctors) must be identified and lead to corresponding agent types, which have variables and parameters for representing the states that are counted in the stocks. Additionally, the modeller has to include events that change the states of agents as specified by the flows in the SD model. On the other hand, global variables might also represent average values of an attribute of the individuals. For parameters, it is feasible to assume

that each agent has the same parameter value unless heterogeneity is important. If, on the contrary, the quantity is the average perceived value of a certain input, discrete exponential smoothing as derived in Section 5.6.2 is a feasible approach to implement inside the agents.

There are approaches in the literature that try to deduce aggregated equations from individual-based models. One such method is diffusion approximation (Bicher & Popper, 2013). However, it needs the condition that the counts of agents in each state are an admissible aggregation, which is violated, for example, by complex network structures. While there are also approaches that try to circumvent this (e.g., Keeling, 1999), it does not seem feasible to transform large models that use the flexibility of the agent-based approach into fully equivalent differential equations.

Instead, we propose a different approach that starts with the construction of an SD model for new problems where the important dynamics and the feedback structure are not already identified. The structured approach of SD with its focus on feedback and dynamics instead of detail complexity is ideal for the first steps in a modelling study. A later transformation into an equivalent agent-based model is easier than the other way round, and it will prevent the modeller from including too much detail complexity into the model right from the beginning.

This approach was tested in Chapter 6. The constructed physician reimbursement model was developed in SD and then transformed into an agent-based model. It includes the health state of persons in the population and the decision structure of doctors, who react to their reimbursement and their workload by adapting the service extent. Most notably, apart from very small stochastic variation, both model versions lead to identical results.

7.2 Conclusions

The choice between modelling methods is not simply a technical question of which one is superior. Both differential equations (i.e., SD) and agent-based models are, in principle, capable of approximating any desired behaviour. However, the key question is how likely it is with a certain modelling method that a modeller will manage to produce a reasonably good model (good enough for the problem at hand)

with an acceptable amount of effort and time. A method will perform well if it allows one to focus on the really important aspects of a problem without including too much unnecessary detail.

Traditionally, the literature focuses on certain properties of a problem that favour a certain modelling method. For example, if a modeller wants to include many heterogeneous classes of individuals, an agent-based approach is called for, because dividing global quantities in an SD model into many different dimensions can very quickly make it unmanageable. But the idea of “if your problem has this property, then that is the right approach” over-simplifies the modelling process. Modelling and simulation should lead to insight and enhanced understanding of a problem. This is seen in one final model, but it is perhaps even better achieved with a chain of models that build iteratively on each other.

Therefore, answers to the question above might differ depending on the stage of the modelling process or on previous attempts to tackle a problem. The final version of a model might be an agent-based one, but this might only have been developed after several SD models that were already able to explain much of the dynamic behaviour of a system. Infectious disease models have followed this path, because practically every modeller knows of the classic SIR differential equation approach before any attempt to construct a sophisticated agent-based model. It is clear that any such model must include the positive feedback effect of more infectious individuals having a larger capacity of infecting susceptible individuals. While the results of models with different contact networks may differ significantly (Rahmandad & Sterman, 2008), they show qualitatively similar behaviour because the basic feedback structure is the same.

As system dynamics is a methodology with a strong focus on feedback, it is pedagogically well suited for the first attempts to model a problem. The goal should be to gain as much insight as possible while keeping detail complexity low. If important aspects of the problem that are easily tractable with SD are exhausted, a transformation into an equivalent agent-based version could allow for the incorporation of things like heterogeneity. The agent-based physician reimbursement model of the last chapter, for example, could be further enhanced, but the SD model is always there as a reference. Additionally, tests could be conducted to see if new features in the agent-based version are also easy to implement in SD.

One limitation of this work is that there is no way to prove that modellers could not directly create a good agent-based model without exploring the feedback structure first in SD. This is certainly possible, but probably unlikely. Only empirical studies could show if there is a pedagogical advantage to first concentrating on the general feedback structure among global quantities without using an individual-based approach from the start. However, the similarities between the two methods that were shown in this work suggest that they can complement each other in this way.

Future research might develop methods to automatically transform a model constructed in SD into an agent-based one. This would require the modeller to indicate which stocks count agents and which stocks represent average values of an agent attribute, but it could speed up the transformation process. Ideally, it would take just one click to derive an equivalent agent-based version of an SD model. This could also stimulate research on which properties of a system are hard to model in system dynamics and how much results differ when they are not included.

Feedback plays a strong role in both modelling methods, be it between global quantities or through the interaction of agents. The identification and quantification of the causal effects that are part of a feedback structure from observational data will thus be a further important area for future research. Robins and Hernán (2009) present causal inference methods that allow for the analysis of the causal effect of a time-varying exposure on an outcome, where the exposure is allowed to depend on the former values of measured covariates and vice versa, that is, exposure and confounders form feedback loops. Such methods might therefore also prove valuable for the parametrization of both system dynamics and agent-based simulation models.

Appendix A

Table Functions of the Physician Reimbursement Model

A.1 Effect of Reimbursement on Service Extent

It is assumed that the service extent decreases with increasing reimbursement (s-shaped form). The influence is between 1.5 (if the physician gets no reimbursement) and 0.8.

Table A.1: The values of the table function TableForERSE.

Argument	Value
0.0	1.50
0.2	1.47
0.4	1.42
0.6	1.35
0.8	1.20
1.0	1.00
1.2	0.90
1.4	0.85
1.6	0.81
1.8	0.80

A.2 Effect of Workload on Service Extent

Just as for reimbursement, the effect of workload on service extent is decreasing (s-shaped form). It is assumed that even with a very small workload, the service extent is not increased much. On the other hand, it is reasonable that for high values of workload, it tends to zero.

Table A.2: The values of the table function TableForEWSE.

Argument	Value
0.0	1.050
0.2	1.045
0.4	1.038
0.6	1.030
0.8	1.020
1.0	1.000
1.2	0.900
1.4	0.750
1.6	0.500
1.8	0.200
2.0	0.100
2.2	0.050
2.4	0.000

A.3 Positive Effect of Service Extent

Service extent has an increasing positive effect on treatment success if it is below the true service need (i.e., below 1). For higher values, the table function is constant.

Table A.3: The values of the table function TableForPESE.

Argument	Value
0.0	0.50
0.2	0.70
0.4	0.85
0.6	0.92
0.8	0.97
1.0	1.00
2.0	1.00

A.4 Harmful Effect of Service Extent

Service extent has no harmful effect if it is below the true service need (i.e., below 1). For higher values, the harmful effect is increasing.

Table A.4: The values of the table function TableForHESE.

Argument	Value
0.0	1.000
1.0	1.000
1.1	1.025
1.2	1.050
1.4	1.110
1.6	1.250
1.8	1.660
2.0	2.500

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List of Symbols

$(\mathcal{E}_u)_{u \in U}$	Family of σ -algebras, indexed by input elements u
(\mathcal{M}, τ)	Modelling method with model space \mathcal{M}
(Ω, \mathcal{F}, P)	Probability space with outcome space Ω , σ -algebra \mathcal{F} , and probability measure $P: \mathcal{F} \rightarrow [0, 1]$
$(P_u)_{u \in U}$	Family of probability measures, indexed by input elements u
$\bigotimes_{u \in U} \mathcal{E}_u$	Product σ -algebra of a family of σ -algebras $(\mathcal{E}_u)_{u \in U}$
$\bigotimes_{u \in U} P_u$	Product measure of a family of probability measures $(P_u)_{u \in U}$
$\text{Bin}(n, p)$	Binomial distribution with n trials and success probability p
$\eta: \mathbb{T} \times X \times U \rightarrow Y$	Output map of a stochastic dynamical system
η_u	Probability variable for the output of a stochastic input-output system given an input u
$\text{Exp}(\lambda)$	Exponential distribution with rate parameter λ
$\mathbb{E}(N(t))$	Expected value of the random variable $N(t)$
$\lambda: X \rightarrow Y \times M$	Output function of an agent
\mathbb{R}	Set of real numbers

\mathbb{R}_+	Set of positive real numbers
\mathbb{Z}	Set of integers
$\mathbb{Z}_{\geq 0}$	Set of non-negative integers
\mathcal{D}	Set of all stochastic dynamical systems
\mathcal{E}	σ -algebra on an output space Y
\mathcal{M}	Model space
\mathcal{M}_{SD}	System dynamics model
$\mathcal{S} \subset \mathfrak{P}(\mathbb{T})$	Set of all intervals in \mathbb{T}
$\mathcal{U} \subset U^{\mathbb{T}}$	Input function space
$\mathfrak{P}(Y)$	Power set of Y
FC	Flow coupling of system dynamics model
$Select: 2^D \rightarrow D$	Select function of an environment
$ta: X \rightarrow \mathbb{R}_0^+$	Time advance function of an agent
$\omega \in \Omega$	Random outcome
Ω_J	Cartesian product of the output set Y over a subset J of an index set
$\phi: D_\phi \rightarrow X$	State transition map of a stochastic dynamical system
$\phi_{\mathbb{T}}: \mathbb{T} \rightarrow X$	State trajectory
π_J	Canonical projection from Ω_U onto Ω_J , where $J \subset U$
π_j	Coordinate mapping for the j -th coordinate
π_J^K	Canonical projection from Ω_K onto Ω_J , where $J \subset K$
$\mathbf{P}[E]$	Probability of the event E

Σ_{IO}	Input-output system
Σ_M	Model system
Σ_O	Object system
W	Signal space
τ	Delay time
\mathbb{T}	Time set
\mathbb{U}	Universal set of behaviour
$U(0, 1)$	Standard uniform distribution
$\mathbf{a}(t)$	Vector of auxiliaries at time t
\mathbf{p}	Vector of parameters
$\mathbf{r}(t)$	Vector of flows at time t
$\mathbf{x}(t)$	State vector of stocks at time t
$\text{var}(N(t))$	Variance of the random variable $N(t)$
$\zeta: X \rightarrow X'$	Aggregation mapping from state space X to state space X'
A	Agent
$B \subseteq U \times Y$	Behaviour of an input-output system
$C(\mathbb{T})$	Set of continuous time functions
C_M	Components of model system
C_O	Components of object system
D	Set of agent references
$F: \mathbb{T} \rightarrow [0, 1]$	Cumulative distribution function

$f: \mathbb{T} \rightarrow W$	Time signal from time set \mathbb{T} to signal space W
$f: C_O \rightarrow C_M$	Model mapping between object system and model system
$F_{i:n}$	Cumulative distribution function of the i -th order statistic of a sample of size n
$f_{i:n}$	Probability density function of the i -th order statistic of a sample of size n
$G_\rho: M_N \rightarrow 2^{D \cup \{N\}}$	Function that assigns a subset of all agents including the environment to every mode $m \in M_N$
$G_{\text{int}}, G_{\text{ext}}$	Functions that assign subsets of the state space X of an agent
$H: \mathbb{R} \rightarrow \{0, 1\}$	Heaviside step function
$h: \mathbb{T} \rightarrow [0, \infty[$	Hazard function of a distribution
L	Link matrix of an SD model
M	Set of modes of an agent
N	Environment
p	Risk or probability
$P_\rho: M_N \times 2^{D \cup \{N\}} \rightarrow [0, 1]$	Probability function that maps a subset of all agents including the environment to a probability dependent on the mode
$P_{\text{int}}, P_{\text{ext}}$	Probability functions of an agent
R	Rate
r	Relative rate
$R_d: M_d \rightarrow M_N$	Mode translation function of an environment

$S: \mathbb{T} \rightarrow [0, 1]$	Survival function of a distribution
U	Set of inputs
u	Input element
$U_N, Y_N, \text{ and } M_N$	Input set, output set, and set of modes of an environment
uBy	The pair (u, y) is an element of the behaviour B
X	State space of a dynamical system
$x(t)$	State at time point t
$X_{i:n}$	i -th order statistic for a sample of size n
Y	Set of outputs
y	Output element
$Z_{i,d}$	Message translation function from i to d



Curriculum Vitae

Personal information

Name Patrick Einzinger
Date of birth 1984-03-19
Place of birth Tulln
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Professional experience

- 09.2010 – 02.2012, **Lecturer**, *Vienna University of Technology*, Vienna.
since 09.2013 Courses “Modellbildung und Simulation im Health Technology Assessment” and “AKMOD: Computerunterstützte Modellierung kontinuierlicher Systeme”
since 03.2010 **Employee**, *dwh GmbH*, Vienna.
Project management and work in various modelling and simulation projects
- 05.2009 – 02.2010 **Employee**, *Landsiedl, Popper OEG*, Vienna.
Work in the project “GAP-DRG” and other modelling and simulation projects
- 10.2008 – 02.2010 **Tutor**, *Vienna University of Technology*, Vienna.
Assistance for the courses “AKANW: Projektpraktikum aus Techn. Mathematik”, “AKMOD: Computerunterstützte Modellierung kontinuierlicher Systeme”, “Mathematik 1 f. ET” and “Mathematik 2 f. ET”
- 1999 – 2007 **Internships during summer holidays**, *Austrian ministry of the interior, Wiener Städtische, Siemens AG Österreich (7x)*, Vienna.

Education

- since 10.2009 **Doctoral program in technical sciences**, *Vienna University of Technology*, Vienna.
- 2003 – 2009 **Studies of technical mathematics**, *Vienna University of Technology*, Vienna.
- 1994 – 2002 **Secondary education**, *BG und BRG Krems Piaristengasse 2*, Krems an der Donau.

Language skills

German native speaker
English fluent
French good command
Italian basic communication skills

Programming skills

very good Java, R, SQL
good C, Matlab, L^AT_EX
basic knowledge HTML, Maple, Python

Other academic activities

- 09.2013 Session chair at the Winter Simulation Conference, Washington, DC, USA
- 2013 Reviewer for the International Journal of Privacy and Health Information Management (IJPHIM)
- 12.2011 Reviewer for the MATHMOD 2012 conference, Vienna, Austria