MASTER

Defining a financial forecasting model for healthcare insurance companies
a collaborative Markov chain approach incorporating institutional care pathway traversal

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Master's Thesis

Where innovation starts

Technische Universiteit **Eindhoven** University of Technology

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Abstract

This document concerns an exploratory research towards the application of collaborative Markov chains as a forecasting model within the field of healthcare insurance. The model proposed is based on both predicting care demand and associated institutional pathway traversal.

A system of collaborative Markov chains allows the user to jointly model several probabilistic elements that share dependencies. It describes a collection of Markov chains in which the state of a certain chain within the collection influences transition probabilities in other chains within the collection. It allows the use of different types of techniques to estimate forecasting parameters as an input within one model. It entails a modular structure which allows the user to perform case-based analyses.

Simulation of simplified proof-of-concept cases has shown accurate predictive behaviour. Due to the fact that Markov chains and consequently systems of collaborative Markov chains are probabilistic in nature, simulation of a sufficient number of sampling replication yields results that tend to follow a Normal distribution. The statistical nature of the simulation results lends itself perfectly for consecutive statistical post-processing.

Systems of collaborative Markov chains provide in modelling complex probabilistic systems in which several dependencies might exist. Current challenges within the application of systems of collaborative Markov chains involve the complexity in terms of the number of parameters to estimate and associated running times. Additionally the existence of potential "inactive elements" with respect to the field of healthcare insurance introduces additional challenges in parameter estimation of the model.

Declaration of Authorship

I, Sebastiaan J. van Zelst, declare that this thesis titled,

"Defining a financial forecasting model for healthcare insurance companies"

and the work presented in it are my own.

I confirm that:

- This work was done wholly or mainly while in candidature for a Master of Science degree in the field of Business Information Systems.
- Where I have consulted the published work of others, this is always clearly attributed.
- Where I have quoted from the work of others, the source is always given. With the exception of such quotations, this thesis is entirely my own work.
- I have acknowledged all main sources of help.
- Where the thesis is based on work done by myself jointly with others, I have made clear exactly what was done by others and what I have contributed myself.

Signed: _____

Date: _____

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Writing a master's thesis has shown to be a very challenging endeavour. It takes time to familiarize with the problem at hand, potential solutions and related research. Often when a feeling of optimism occurs with respect to a potential solution found, a simple question like "Did you actually take this parameter into account" can open doorways to new challenges, problems and solutions. The real challenge in that sense is to identify what is relevant and what is not, avoid tunnel vision and make some fun (if possible).

I would not have been able to perform the work in front of you if I wasn't supported by several people on several levels. I would therefore like to acknowledge the support of the following people:

First off, I would like to thank prof. dr. ir. Uzay Kaymak (TU/e) who has guided me throughout the entire project. Whenever I consulted him with some problems he metaphorically "opened the door" to new potential solutions by identifying topics that might be of interest given the problem at hand. The way Uzay guided me greatly influenced the work in front of you, in terms of concepts, structure and content.

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Abbreviations

AR	**A**uto **R**egressive
ARIMA	**A**uto-**R**egressive **I**ntegrated **M**oving **A**verage
DTC	**D**iagnosis **T**reatment **C**ombination
ED	**E**mergency **D**epartment
EPA	**E**uropean **P**athway **A**ssociation
GDP	**G**ross **D**omestic **P**roduct
HIA	**H**ealth **I**nsurance **A**ct
KPI	**K**ey **P**erformance **I**ndicator
MC	**M**onte **Carlo**
MH	**M**etropolis-**H**astings
NZA	**N**ederlandse **Z**org **A**uthoriteit (EN: Dutch Healthcare Authority)
VAR	**V**ector **A**uto **R**egressive

"*Computer Science is no more about computers than astronomy is about telescopes.*"

Edsger W. Dijkstra (1930 - 2002)

Chapter 1

Introduction

1.1 Motivation

During the past decades healthcare costs have been growing rapidly [5, 6, 7, 8]. The growth is identifiable both on a national (i.e. the Netherlands) as an international scale. Literature suggests different causes and possible solutions to the rise in healthcare costs. The Dutch government however, has not yet been able to effectively reduce healthcare costs one way or another.

In a strive to control and potentially reduce the costs within the healthcare system, the Dutch Government recently proposed several regulatory modifications. Up to 70% of the total amount of care products has been assigned a negotiable price between healthcare providers and healthcare insurance companies [9]. As such, the healthcare market is being structured towards managed competition [10] [11].

Within the newly created market, healthcare insurance companies have been assigned to take a leading role in generating a competitive market environment. They are ought to do so by negotiating prices of care products which in turn should lead to competition amongst healthcare providers. The competition should focus on a quality versus costs dimension in which the aim is to "acquire the best care for the best price".

Healthcare insurance companies have not yet been able to succeed in their supposed role of competitive catalyst. Contract negotiations are primarily based on individual institutional performance. A patient however usually visits more than one care provider when being cured for a certain disease. One might for example first visit a general practitioner, secondly a hospital and finally a physiotherapist. Within contracting, the performance of such *institutional* care pathways is currently being neglected.

In [12] the applicability of KPI-based quantification, measurement and comparison of *integrated* care pathways is researched. In essence integrated care pathways and institutional care pathways are very related though differ in general aim of use. We will elaborate on this specific difference in a later stage of the research. In this research we strive to define a financial forecasting model for healthcare insurance companies building on top of the concept of institutional care pathways.

1.2 Background

1.2.1 Healthcare system reform in the Netherlands

In this section we present the most recent healthcare system reform incentives as proposed by the Dutch government, some of which to reduce the costs of healthcare. For a more detailed and elaborate description of the healthcare system in the Netherlands we refer to appendix A.

DTC's and the HIA

The most recent fundamentals of the desired form of the healthcare system have been shaped in 2005 and 2006 with the introduction of the diagnose treatment combination (DTC, DBC in Dutch) and the healthcare insurance act (HIA). A DTC represents a "treatment product". Rather than posting declarations for single treatments, hospitals should post DTC-based declarations to healthcare insurance companies. The HIA states that every natural person living in the Netherlands should have a basic healthcare insurance.

Managed competition

The strategical core of the restructuring incentives is called "managed competition" [13]. Though already recommended by the Dekker Committee in 1986, the restructuring towards such system is currently taking place at full pace. In theory, managed competition is defined as a purchasing strategy to obtain maximum value for both employers and customers. Rules for competition are used which are derived from microeconomic principles in which the goal is to reward those health plans that do the best job of performance on several dimensions (such as quality, costs etc.).

A fundamental difference between regular competition in contrast to managed competition is the existence of "sponsors". In managed competition a sponsor is defined as an entity which represents a group of customers which form the actual demand side. Within the fundamentals of "managed competition" - which is largely based on the healthcare system in the USA - sponsors are intended to overcome the attempts of insurers to avoid price competition [13].

Managed competition in the Netherlands

The system introduced in the Netherlands consists of the basic principles of managed competition [11, 14, 9]. The system is highly regulated by the government which is represented by the "Nederlandse zorg authoriteit' (NZA). In future years the governmental influence should be reduced. In the Netherlands the functioning of the insurance companies could be described as "sponsors" within the market. This sounds contradictory as the main concept of sponsors was introduced against the main functioning of insurers within the U.S. healthcare market. Dutch and U.S.-based healthcare providers however differ significantly and have very different interests. U.S.-based healthcare insurers are often involved in funding medical and pharmaceutical activities, which conflicts with bringing the total costs for care down. In the Netherlands this is not the case.

The overall goal of all actors is to contribute to a system in which high quality care is key and costs are limited to a manageable level. The specific role in this structuring for healthcare insurance companies is defined as [9]: "To try to pursue efficient and appropriate care for their insured, which are translatable to manageable cost development as much as possible." Though this role is discussed upon and criticized [10], healthcare insurance companies are ought to buy adequate and cost manageable by means of contracting among healthcare providers.

1.2.2 The changed role of healthcare insurance companies

The changing healthcare system poses new behavioural requirements to healthcare insurance companies. They should contract healthcare providers to cover expenses made by their insured. As a consequence a patient's treatment will only be covered if he or she visits a healthcare provider which is contracted by their corresponding healthcare insurer.

Within contracting, healthcare providers need some means of performance measurement to take into account when negotiating contracts. Although DTC's provide basic guidance towards suitable pricing, the associated costs are not fixed for a large amount of treatments. Additionally, DTC's are only defined for hospital-based care. Healthcare insurance companies however also cover costs declared by other healthcare providers such as general practitioners, physiotherapists and others.

In general, individual institutional performance measurements are taken into account within contracting negotiations between healthcare insurance companies on the one hand and healthcare providers on the other hand. These performance measures can be any measure the healthcare insurance company deems appropriate such as quality, throughput time etcetera.

Healthcare insurance companies have net been able to actively instigate competition among healthcare providers. The goal of this research is to provide a new type of financial forecasting model that might enable healthcare providers within their contracting endeavours by explicitly taking institutional care pathway performance into account.

1.3 Problem description

The rising costs in healthcare have caused new regulations within the healthcare system in order to bring the overall costs down. These regulations pose new challenges to several actors within the system.

Within the newly created managed competition based system, healthcare insurance companies are assigned to the role of "sponsors". They are ought to contract healthcare providers and strive to purchase the best quality for the best price. A new type of performance analysis within healthcare is performance quantification based upon chains of institutes associated with treatments instead of individual institute performance.

The problem at hand is the need for a financial forecast model which:

- *Incorporates care demand*
- *Allows to incorporate associated institutional care pathway traversal and corresponding costs*
- *Is modular in design such that it allows for multiple case-based forecast computations*

Within this definition we identify a financial forecast[1] model as a model that enables us to compute future costs, in this case based on the combination of care demand prediction and associated institutional care pathway traversal. The set of basic requirements allows healthcare insurance companies to compute future costs in several situations. Additionally, the outcomes of these computations might be used in contract negotiations with healthcare providers. This could lead to a better fulfilment of healthcare insurance companies in their role of competitive catalyst in the healthcare market.

[1]Within this research we identify the concept of forecast and prediction to be equal. Throughout this document the two concepts can be regarded as interchangeable.

1.4 Research questions

According to the main problem definition we have categorized and defined the following research questions:

1. *How do we define and forecast care demand from a healthcare insurance company perspective?*
   A first step towards a prediction concerning future pathway traversal is knowledge of the amount of patients to expect. As traversal of an institutional care pathway is a consequence of being ill, we first need to define how to predict future need for care, which is also called *care demand*.
2. *How do we define and incorporate institutional pathways within the care demand prediction model?*
   If we have defined a model which is able to produce an estimate of care demand, the next step is to integrate the associated pathway traversal. In this way we can determine, given the expected care demand what the expected future institutional care pathway traversal will be.
3. *How do we combine financial pathway performance as a price component with the care demand prediction model?*
   If we have found some means to provide an estimation of future institutional care pathway traversal, a final aspect to look at is how to combine the financial performance of these pathways with the predicted traversal-amount.

1.5 Methodology

To solve the problem and research questions defined we have applied the following methodology:

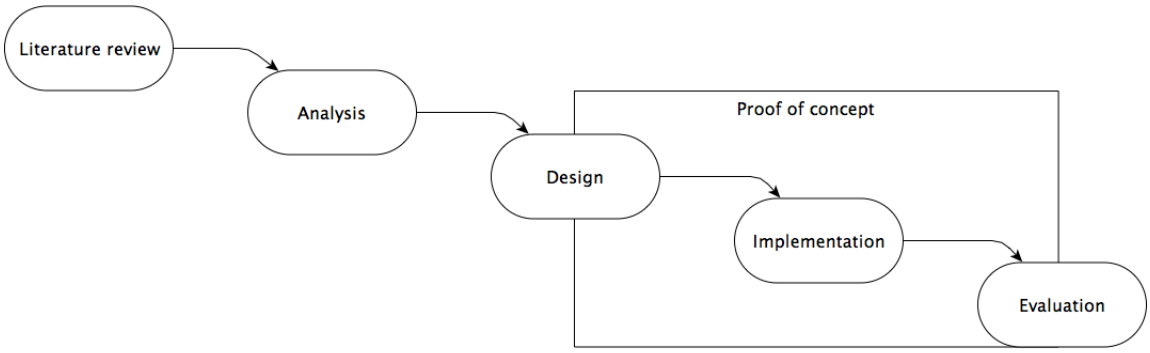


Figure 1.1: Graphical representation of the global methodology used in the research.

Literature review

In this phase we have tried to position the problem in a research-based context. We have investigated what research has been done either on specific topics or related topics with respect to the research questions. The literature is used to provide an overview of what techniques are currently applied and as a basis for model design and development.

Analysis

In this phase we will analyse the problem in an abstract manner by presenting preliminaries with respect to the model design which will be conducted in the next phase. We have defined an abstract mathematical model which helped in structuring the problem as a whole and reduced overall problem complexity.

Design

In the design phase we have tailored the intended model building upon the preliminaries and definitions as presented in the analysis phase. We have presented both the model terminology in general as a problem-specific design using the model terminology.

Implementation

Within this phase we have assessed possible implementation of the proposed model. We have specifically analysed challenges in model implementation which are either solved or yet to be solved.

Evaluation

Within the evaluation we have assessed whether the model proposed is able to accommodate its main goal; a financial forecasting model for healthcare insurance companies. Additionally we have collected lessons learned throughout the research and mapped these onto several dimensions such as managerial implications, future research etcetera.

Proof of concept

During the course of the design, implementation and evaluation phase we have executed a "proof of concept". The proof of concept is two-fold as it consists of a data-analysis part and a simulation part. The data-analysis is mainly intended to assess whether assumptions made in model definition actually hold given real-healthcare data. The simulation part focusses more on the usability, nature of results and so on with respect to the model defined.

1.6 Outline

The remainder of this thesis is structured using the methodology as described in the previous section.

Chapter 2 describes the literature review. Within this part we assess the current state of care demand prediction on several dimensions and we take a look at the terminology of integrated care pathways within healthcare.

Chapter 3 describes the analysis phase. We will present mathematical preliminaries which will be used in the consecutive chapters on terminology of care demand and institutional care pathways.

Chapter 4 describes of the design phase. The definitions and terminology as presented in chapter 3 will be materialized and a suitable basic model will be presented which conforms to the research problem.

Chapter 5 describes the implementation phase. In this chapter we discuss how we should actually implement the model proposed and what the associated challenges will be.

Chapter 6 briefly explains the set-up of the two-fold proof of concept.

Chapter 7 describes the results of the proof of concept. Additionally it will discuss managerial implications and will discuss the general application of the model.

Chapter 8 summarizes the research as a whole and discusses some limitations with respect to the proposed solution and future research possibilities.

Chapter 2

Related research

In this chapter we have assessed related topics with respect to the research. We first consider related research with respect to *care demand prediction* after which we will assess related research with respect to *integrated care pathways*.

The specific reason why we assess *integrated* care pathways in literature and not *institutional* care pathways will briefly be mentioned in section 2.2. A more elaborate motivation can be found in chapter 3, section 3.3, subsection 3.3.4 as section 3.3 provides a definition of institutional care pathways within the context of this research.

2.1 The field of care demand prediction

Within literature several models have been proposed on the topic of care demand prediction.
The general aim of these models is to assess the effect of environmental changes, which are usually a result of various triggers. As an example consider the assessment of several technological developments on public health [15].

Care demand prediction in general is just any statement concerning the future and can thus be seen as a *forecasting method*. Before we specifically delve into care demand prediction we first consider the bare basic fundamentals of forecasting in general [16]:

1. The goal of forecasting is to generate "on the average" good forecasts and minimize forecast errors.
2. In general it is easier to obtain forecasts with high accuracy on groups of items rather than individual items. Group data can produce stable characteristics although it contains individual items consisting of a high degree of randomness.
3. In general, short-term forecast have a better accuracy when compared to long-term forecasts.

As with forecasting in general, care demand prediction models vary on several dimensions (i.e. forecasting length, goal,...). To provide structure we identify three hierarchical categories within analysing the current state of care demand prediction, being:

- *Care demand prediction frameworks*
  Assessing usable steps to follow in order to construct a suitable care demand prediction method or healthcare forecast.

- *Care demand prediction classification*
  Assessing how to classify several interrelated care demand prediction models or healthcare forecast.
- *Care demand prediction models and techniques*
  Assessing what types of models are most often used for what type of care demand prediction or healthcare forecast.

2.1.1 Care demand prediction frameworks

Within literature, little research is done towards care demand prediction frameworks or healthcare forecasting frameworks in general. Often articles present a model producing a forecast and discuss steps such as *data collection*, *model design*, *validation* and *forecast results*. These steps largely correspond to the phases roughly defined in [16]:

1. Model building
2. Forecasting Stage
3. Measuring Forecast Accuracy (continuous assessment)

Though the lack of a standardized methodology might be somewhat trivial as we could apply any general forecasting methodology, the absence of domain specific methodology is specifically pointed out in [1]. The authors give an overview of the current state of healthcare forecasting, consisting of a set of principles, a schematic approach for healthcare forecasting and some additional common data patterns and methodologies.

The principles presented are very similar to the general forecasting principles:

1. Uncertainty and error of health forecasting
2. The focus of health forecasting
3. Data aggregation and accuracy of health forecasting

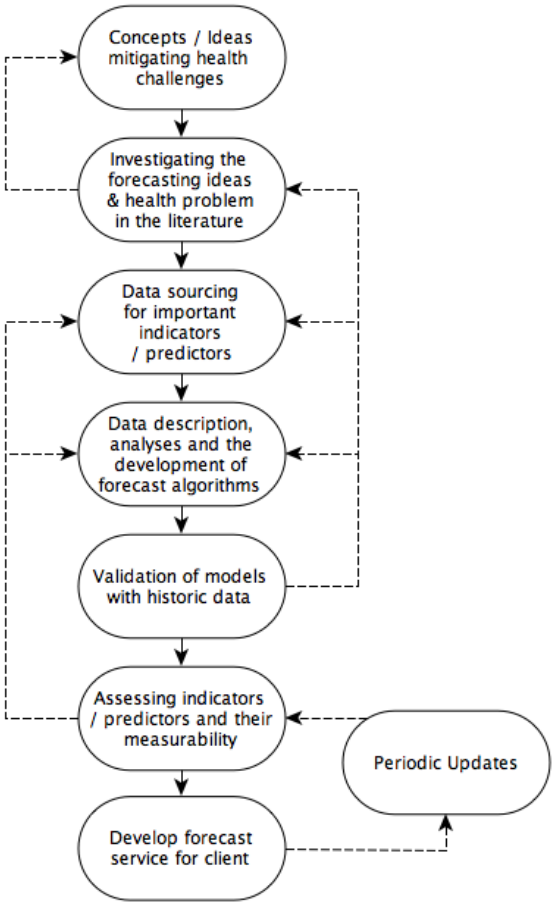


Figure 2.1: A schematic approach to healthcare forecasting as proposed in Soyiri et al. 2013, [1]

The schematic approach to health forecasting as proposed is presented in figure 2.1. We can again identify similarities between the proposed framework and the steps defined within general forecasting theory (i.e. Model building, Forecasting Stage, Accuracy). We can also identify a vast overlap with the general methodology used in this research. Occasionally, authors define a domain specific healthcare forecasting framework. In [17] a framework is proposed for "Assessing and Forecasting Population Health". The authors propose a threefold framework consisting of:

1. Core population model
2. Risk factor/disease modules

3. Forecasting

When inspecting the the steps in the framework provided, we are able to place all three steps in the model building/forecasting algorithm development phase. The framework in this case describes a micro-simulation type model. We will discuss the work proposed by Meijgaard et al. ([17]) in more detail in section 2.1.3.

2.1.2 Care demand prediction classification

Likewise to care demand prediction frameworks, classification terminology for healthcare forecasting is rather scarce. For classification terminologies, the same rationale goes as for frameworks as the terminologies are rather context independent [18]. In [19] a so called "methodology tree" is proposed, which is used to discuss several forecasting methods and can be used as a guide in forecast model selection. The most recent version of the methodology tree provided by Armstrong ([2]) dates to 2010 and is depicted in 2.2.

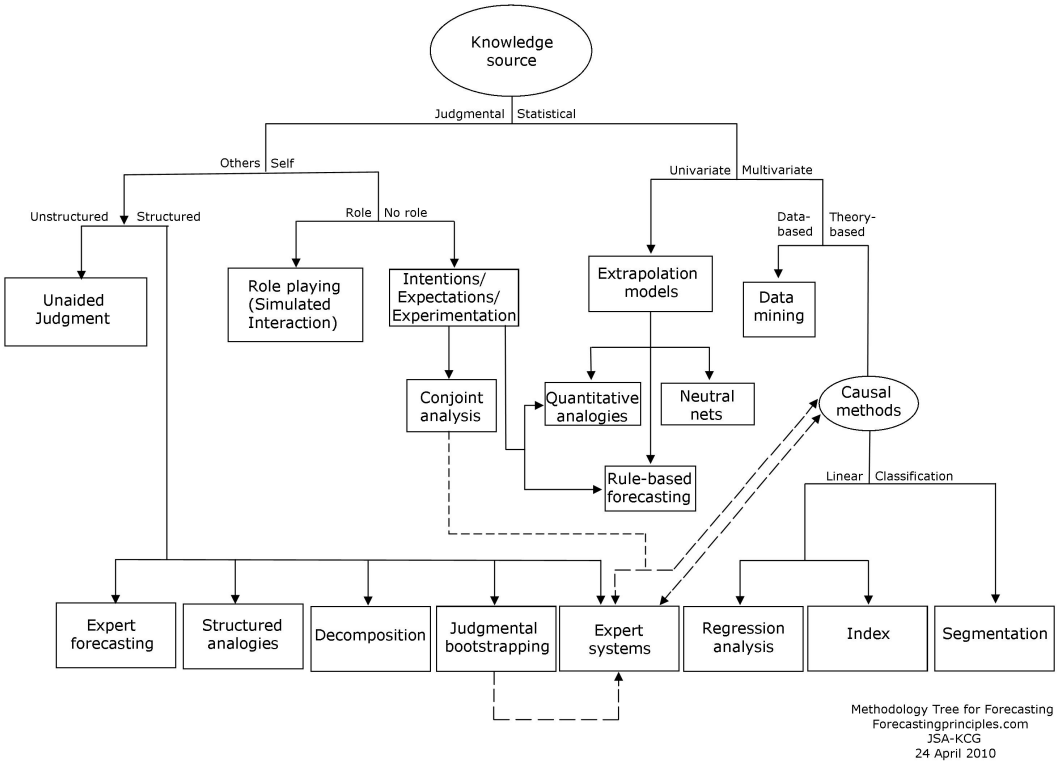


Figure 2.2: Armstrong's methodology tree for forecasting method selection, 2010 [2]

The methodology three (in two older forms (1986 & 2001)) has been analysed, criticized and used by [3]. Apart from those two interrelated methodology tree definitions, three more forecasting classifications (Cetron and Ralph; 1971, Martino; 1972, Bright; 1978) were analysed on three properties:

- Conciseness

- Exclusiveness
- Exhaustiveness

The authors conclude that none of the models possess all three properties. The authors combine the lessons learned from the five models analyzed into their "Forecasting Classification Grid", depicted in figure 2.3.

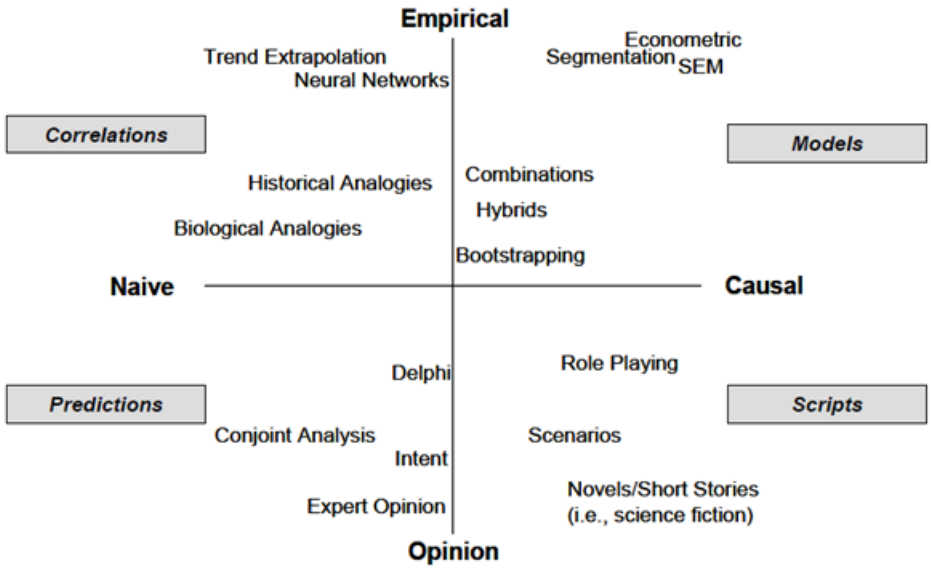


Figure 2.3: The Forecasting Classification Grid as proposed by Gentry et al., 2006 [3]

Although, the authors state that the model supports all three properties stated earlier, the model contains some gray area's itself as pointed out in [18]. One could question whether the existence of such "grey area's" is fully avoidable. Logically we identify some basal similarities between the decision points in the decision tree and the quartiles in the classification grid.

In [16] a brief passage of forecasting classification is presented which has the following structure:

- *Quantiative forecasting methods*
  - Time series models
  - Causal models
- *Qualitative forecasting methods*
  - Exploratory
  - Normative

In this case we even see more direct overlap between the classification models proposed. The classification especially shares great commonality with [3].

2.1.3 Care demand prediction models & techniques

Within health forecasting literature several different types of models are used, which heavily depend on a combination of the data structure and the purposes of the forecast. We will assess

several models which either have been used or developed in the context of healthcare forecasting. We will first present the basic rationale and definitions behind a specific type of model and then assess its use and usability in healthcare forecasting.

Time series models

A commonly used model or approach in forecasting is the use of time series models (a mathematical definition can be found in appendix B, section B.1.). In particular ARIMA models are used very often, initially introduced by Box and Jenkins in 1970. As a basis, such models assume autocorrelation within the data. With respect to the forecasting classification theory discussed in the previous section we can easily place these type of models in the "Quantitative - Time series models" class or the corresponding "Correlations" quadrant of the classification grid.

Several authors have proposed time-series based models with varying forecast goals. In [20], the authors describe a time-series model used to predict ED patient crowding, a goal which is used more often in healthcare forecasting literature. A multivariate VAR method is used with seasonal Holt-Winters exponential smoothing as a benchmark method. The paper does not present the model in detail as the paper's focus leans more towards the crowding problem, though the results indicate the potential usefulness of such model. The authors do state however that "forecasts of the demands for diagnostic resources were not sufficiently reliable to be useful in the clinical setting". Additionally we note that in this particular case, absolute figures are used for model verification without reference domains for verifying these figures.

In [21] a total of three models are compared in terms of accuracy. Again the focus of this study concerned ED patient crowding, though the authors specifically assess multiple models. The authors compare hourly historical average to a seasonal ARIMA model and a sinusoidal model with an AR-structured error term. The authors conclude, similarly to [20] that the time series based prediction models function reasonably well for the short term emergency department crowding problem. Additionally the authors show that the two time-series based models, (i.e. seasonal ARIMA and sinusoidal model) outperform the historical average model.

In [22] clinic visits of the King Faisal University are predicted over a period of two years. Additionally the authors compare the performance of an ARIMA model with simple trend extrapolation. In the particular case the simple trend extrapolation even outperforms the ARIMA model in terms of accuracy. This gives additional raise to the fact that one should assess whether autocorrelation is sufficiently present in the data before using time series models, based on autocorrelation.
The data source used by the authors contains a clear trend though in a specific year, the number of visits drops extremely after which the trend returns in the data the next year. The authors explain the sudden drop due to the second gulf war. The authors choose to replace the irregularity by averaging of the previous and consecutive year.

In [23] a similar problem is stumbled upon when a prediction is made of rate of births for women in the cohorts 20-24 and 25-29 as part of a case study. The second world war seems to negatively impact the upward trend of the pre-war years. The authors propose additional measures to cope with such problems. Either by starting the analysis after world war II (which is chosen due to the fact that it was proven that the trend after WOII was significantly different when compared to the pre-war years) or introduce regression terms in the model involving indicator variables for the affected years.

In [24] traffic accidents are predicted over a forecasting range of two years. The main goals of the paper are two-fold. On the one hand policy regulations regarding the limitation of traffic

accidents are assessed. On the other hand the authors assess whether aggregated or disaggregated data performs best as a basis for prediction. The authors state that the use of disaggregated data is beneficial for overall forecast accuracy. This conclusion partly conflicts with the second basic fundamental property of general forecasting as introduced in the introductory part of this chapter.

Micro-simulation models

Micro-simulation in general Different types of simulation models have been used within healthcare forecasting. The structures of these are not as fixed as the basic ARIMA-models. An simulation technique which is often used within healthcare forecasting is "micro-simulation". Based on [25] we present an informal description of micro-simulation:

Often, micro-simulation models are used to predict several policy effects. The structure of a micro-simulation model mainly determined by relations expressed in mathematically logical relations. Micro-simulation models differ from aggregated macro models on the level of aggregation. Where macro models concern the relationships between national economic sectors and aggregated variables, micro-simulation concern individuals directly, so called "micro-units" (such as persons, households etc.).

As stated the models are most often used to test policy effects and therefore often a basic (forecast) simulation concerning the as-is situation is performed. Such simulation is called a "baseline" simulation. As within micro-simulation, micro-units are simulated over time a micro-simulation usually consists of some "ageing procedure" which simulates ageing of the units throughout time. Within micro-simulation we identify two types of ageing procedures: ***static*** and ***dynamic***. In static ageing, the relations among the variables of each micro-unit are to be generally maintained. Whenever an overall structure change appears, this is expressed by changing the weight of each micro-unit. In dynamic ageing on the other hand each micro-unit is aged individually by an empirically based survivor probability.

Micro-simulation in healthcare forecasting literature In [15] micro-simulation is used to assess the impact of health trends and medical innovation for the future elderly. The authors develop a demographic and economic model which helps to predict the costs and health status for the elderly. The model defined is called the "Fututre Elderly Model" (FEM) in short and is of a micro-simulation type. The model tracks elderly throughout the future and each persons' probability of dying, getting a new disease or entering a new functional state is computed using Monte Carlo techniques. After constructing the basic model, several health trends and medical key technologies were assessed and the effects of these phenomena on the "baseline" were simulated. Interesting to note is that for identification and estimation of key medical technologies, literature studies and qualitative research has been conducted. Thus, although the actual methodology used is micro-simulation, the computational basis is found in conduction of qualitative analysis.

In [17], van Meijgaard et al. propose a micro-simulation framework specifically assigned for population health prediction. As a basis the model uses an extended form of the FEM, as proposed by [15]. The model is extended on three aspects:

1. Extended age range, modelling persons from birth which provides a full life-course model.
2. Incorporation of additional aspects of the dynamics of population demographics (explicit account for changes due to migration)
3. Incorporation of time-varying health risk factors such as obesity.

Apart from extending the FEM model, the authors propose to split up the forecast into three "building blocks":

1. Core population module
2. Risk factor/disease module
3. Forecasting module

In fact this is a more explicit formalization of the usage of FEM in [15]. An important aspect to note here is the difference between using the first two modules or using all three modules. The difference in between these modules is to be found in the projected time frame and effects on specific risk factors and such and not in the forecasting methodology used. When the "forecasting module" is used, the authors basically perform several micro-simulations and project these into the future. Thus the only function of the forecasting module is quantifying the impacts of certain risk factors onto the simulation model in the future.

In [26] a multistate life table model is proposed as well as an associated theoretical framework for building such model. In its basics a multistate life table is defined by a multidimensional matrix which consists of transition probability records. Such probability record is defined as $m_{x,t}^{(i)}$, being the specific type $i \in \{tr, g\} \in I$ transition rate for an x-year-old individual at time $t \in \{1, 2, .., T\}$ with gender $g \in \{male, female\}$ and $tr \in \{nd, d, inc\}$. $m_{x,t}^{(i)}$ can either represent the mortality rate of the nondisabled (nd), the mortality rate of the disabled (d), and the incidence rate (inc). Thus a person can be in three states, either nondisabled, disabled or dead. Accordingly the three state transitions are *nondisabled* $\rightarrow$ *disabled*, *nondisabled* $\rightarrow$ *dead* and *disabled* $\rightarrow$ *dead*. The authors use the Lee-Carter model for computing the transition rates, which is of the following form:

$$ln\ m_{x,t}^{(i)} = \alpha_x^{(i)} + \beta_x^{(i)}\kappa_t^{(i)} + \epsilon_{x,t}^{(i)}$$

In this model, α represents an age-specific constant parameter. κ indicates the time-dependent latent process that quantifies the transition rates over time. β incorporates the effect of age in terms of κ. ϵ functions as a disturbance factor. It is interesting to note that Lee and Carter proposed a random walk ARIMA model to actually compute κ.

Discrete event simulation in healthcare forecasting literature

In a discrete event simulation one tries to simulate a system which consists of discrete events. In the end, a sequence of such events over time is constructed. Each step in time poses a change to the overall system state. With discrete event simulation we assume that between two consecutive events no event can occur, which essentially marks the difference between discrete and continuous simulation.

In [27] a discrete event simulation model is defined consisting of six random processes. The random processes define different elements within patient flow through ED's. For example, patient arrival is modeled as a Poisson process and decisions of patients to leave the ED as a bernoulli trial. Based on patient flows estimated using historical data, the process is simulated for 2, 4, 6 and 8 hours in advance. The overall performance of the simulations shows that the use of a discrete event is suitable for this type of prediction.

2.2 The field of integrated care pathways

Within this research we will base the model defined on chains of institutional visits, indicated by the noun "institutional care pathways". These chains share a great deal of conceptual overlap with

so called "integrated care pathways" a topic subject to a vast amount of research.

In this section we give an overview of research that has been conducted on the topic of "integrated care pathways". Within chapter 3 we will build a specific definition of "institutional care pathways" building on top of the terminology as presented in this chapter and present similarities and differences of the two concepts.

2.2.1 General overview

A vast amount of research has been conducted towards the concept of "integrated care pathways". In general, different definitions of the concept exist which do share some overlap. To provide insight in the main concept we first present an overview of different terminologies used throughout literature and conclude with a more generalized definition proposed to standardize the concept. As the definition of integrated care pathways has developed over time we will present the overview of the concept-development in a chronological fashion.

Clinical-practice based plans

In [28], Kitchiner and Bundred propose a medical action-based definition of integrated care pathways. The authors state about integrated care pathways:

"*They use multidisciplinary guidelines to develop and implement clinical plans which represents current, local best practice for specific conditions*"

Kitchiner and Bundred, 1996 [28]

The authors suggest that by analysing clinical best-practices and incorporating these practices into pathways generates benefits to both patients and healthcare professionals. The authors state that the usage of integrated care pathways poses benefits for patient-centric care in the form of reducing errors and improving clinical outcomes.

Completion and comprehensiveness of care delivery

In [29] Kodner and Spreeuwenberg identify some ambiguity in general concerning the exact definition of integrated care pathways. They identify the usage of it mostly related to "managed care" in the US, "shared care" in the UK and transmural care in the Netherlands. By performing an extended literature review and discussion the authors pose the following interpretation:

"*Integration may be seen as a step in the process of health systems and health care delivery becoming more complete and comprehensive*"

Kodner and Spreeuwenberg, 2002 [29]

As one can see the authors abstract from the medical point of view used in [28] which places emphasis on clinical best practices. The authors account for any type of development that enhances complete and comprehensive care. Note that in [28] these broader forces are acknowledged as well though not explicitly focused upon. More formally, Kodner and Spreeuwenberg define:

"*Integration is a coherent set of methods and models on the funding, administrative, organizational, service delivery and clinical levels designed to create connectivity, alignment and collaboration within and between the cure and care sectors*"

Kodner and Spreewuenberg, 2002 [29]

Influence on inter-professional collaboration

A more substantive analysis towards the effects of integrated care pathways is presented in [30]. The authors state that integrated care pathways have several synonyms which are used throughout general practice and literature.

These are:

- Critical paths
- Care maps
- Collaborative plan of care
- Multidisciplinary action plans
- Care paths
- Anticipated recovery paths

The authors use the following definition for integrated care pathways:

"*Care pathways have been widely promoted as a managed care paradigm. The aim of managed care is to standardize the delivery of health care, the length of stay in the hospital and the clinical management of the patient*"

Atwal and Caldwell, 2002 [30]

Formalizing known patterns of care processes

In [31], Zander investigates eleven international trends within integrated care pathways. The trends analysed are of a clinical fashion though the main aim of the trends discussed concerns potential benefits for healthcare when using integrated care pathways. Zander positions integrated care pathways under an umbrella of a larger set of tools which is known as "structured care methodologies". Zander therefore identifies integrated care pathways, like all other structured management care methodologies as follows:

"*known patterns of care processes, thus adding predictability and providing the transfer of knowledge*".

Zander, 2002 [31]

Again we can identify terms related to standardization of processes that might potentially increase the value of healthcare provision.

2.2.2 A standardized definition

In order to standardize the definition of integrated care pathways, Vanhaecht conducted a PhD research in the related field [32]. The resulting definition is also adopted by the EPA and is defined as follows:

A care pathway is a complex intervention for the mutual decision making and organisation of care processes for a well-defined group of patients during a well-defined period. Defining characteristics of care pathways include:

1. *An explicit statement of the goals and key elements of care based on evidence, best practice, and patients expectations and their characteristics;*

2. *the facilitation of the communication among the team members and with patients and families;*
3. *the coordination of the care process by coordinating the roles and sequencing the activities of the multidisciplinary care team, patients and their relatives;*
4. *the documentation, monitoring, and evaluation of variances and outcomes; and*
5. *the identification of the appropriate resources. The aim of a care pathway is to enhance the quality of care across the continuum by improving risk-adjusted patient outcomes, promoting patient safety, increasing patient satisfaction, and optimizing the use of resources.*

Vanhaeacht, 2007 [32]

We can clearly identify the definition embodying the several definitions proposed in the previous section. Additionally it is defined in such way that it allows for multiple types of methodologies that help to reach the main goal (i.e. by means of the use of "complex interventions").

In [4] the concept of integrated care pathways in conceptualized in a graphical fashion depicted in figure 2.4.

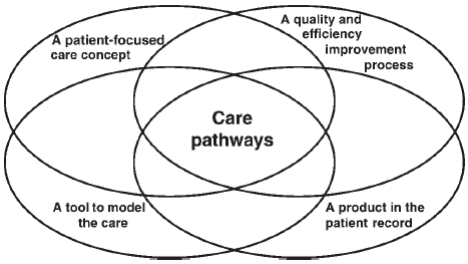


Figure 2.4: Care pathways as a concept, model, process and product as proposed by Panella and Vanhaecht, 2010 [4].

Chapter 3

Analysis

3.1 Preliminaries

Before we strive towards a full fledged model definition we define basic preliminary concepts which form a basis for construction of a financial forecasting model based on institutional care pathways. The mathematical notation used throughout the remainder of the report can be found in appendix B, section B.2.

Insurance companies

We define the set of all possible insurance companies on the *Dutch market* as $\mathbf{Z}$:

$$\mathbf{Z} = \{z|\ z \text{ is a Dutch insurance company}\}$$

We specifically define $\mathbf{Z}$ as being time-independent. Thus, $\mathbf{Z}$ describes any possible insurance company z, in which z is either currently active, not active yet or not active any more.

The timed insurance company function is defined as π_z:

$$\pi_z : \mathbb{Z} \to \mathcal{P}(\mathbf{Z})$$

$$\pi_z(t) \triangleq \mathbf{Z}_t$$

Thus $\mathbf{Z}$ denotes all possible healthcare insurance companies whereas $\mathbf{Z}_t$ denotes all active healthcare insurance companies at time t.

We will introduce definitions for the healthcare market population, diseases, healthcare providers and institutional pathways in the same fashion.

Healthcare market population

We define the set of all possible insurable persons on the *Dutch market* as $\mathbf{P}$:

$$\mathbf{P} = \{p|\ p \text{ is an insurable person on the Dutch market}\}$$

The timed healthcare market population function is defined as π_p:

$$\pi_p : \mathbb{Z} \to \mathcal{P}(\mathbf{P})$$

$$\pi_p(t) \triangleq \mathbf{P}_t$$

In addition to π_p, we define a function $\pi_p^\dagger$:

$$\pi_p^\dagger : \mathbb{Z} \to \mathcal{P}(\mathbf{P})$$

$$\pi_p^\dagger(t) \triangleq \mathbf{P}_t^\dagger$$

The set $\mathbf{P}_t^\dagger$ represents all people which decease at time t and thus:

$$\forall_t (t \in \mathbb{Z} : \mathbf{P}_t^\dagger \cap \mathbf{P}_t = \emptyset)$$

$$p \in \mathbf{P}_t^\dagger \implies p \notin \bigcup_{i=t}^{\infty} \mathbf{P}_i$$

Diseases

We define the set of all possible diseases as $\mathbf{D}$:

$$\mathbf{D} = \{d|\ d \text{ is any disease}\}$$

The timed diseases function is defined as π_d:

$$\pi_d : \mathbb{Z} \to \mathcal{P}(\mathbf{D})$$

$$\pi_d(t) \triangleq \mathbf{D}_t$$

Healthcare providers

We define the set of all possible healthcare providers as $\mathbf{H}$:

$$\mathbf{H} = \{h|\ \text{h is any healhtcare provider}\}$$

The timed healthcare provider function is defined as π_h:

$$\pi_h : \mathbb{Z} \to \mathcal{P}(\mathbf{H})$$

$$\pi_h(t) \triangleq \mathbf{H}_t$$

Institutional pathways

We define the set of all possible institutional pathways as $\mathbf{I}$

$$\mathbf{I} = \{p_i|\ p_i \text{ is any institutional pathway}\}$$

The timed institutional care pathway function is defined as π_i

$$\pi_i : \mathbb{Z} \to \mathcal{P}(\mathbf{I})$$

$$\pi_i(t) = \mathbf{I}_t$$

Within this context a $p_i \in \mathbf{I}_t$ is any path that is likely to be traversed by a patient at time t.

Insurance company membership-set

The previous definitions materialize different elements of the healthcare system in a mathematical fashion. The elements are defined on a global scale. On construction of a financial forecast model for a specific healthcare insurance company we are merely interested in "insurer-specific" elements. Let us construct the relation between the insurer's assets and the global population.

We define a function π_m representing the timed insurer's membership-set:

$$\pi_m : \mathbf{Z} \times \mathbb{Z} \to \mathcal{P}(\mathbf{P})$$

$$\pi_m(z,t) \triangleq M_{(z,t)}$$

Thus $M_{(z,t)}$ depicts the set of persons which are insured by insurance company z at time t. Note that as a result of the mandatory "basic healthcare insurance", in the Netherlands the following constraint holds:

$$\bigcup_z M_{(z,t)} = \mathbf{P}_t \tag{3.1}$$

It is possible that one person p has two different healthcare insurance companies covering different healthcare costs, therefore $\bigcap_z M_{(z,t)}$ is therefore not necessarily empty.

Within the research, we abstract from insurance types. We are only interested in the fact whether a person is insured or not.

3.2 Care demand

We have analysed the healthcare system as a whole and its impact on care demand, *given the viewpoint of a healthcare insurance company.* We have presented the general findings and definitions in this section.

If we decompose (future) care demand, this decomposition leads to knowledge of two basic parameters:

1. Knowledge of what (type of) persons will be a member $M_{(z,t)}$ for (future) values of t.
2. Knowledge of the subset of persons in the (future) $M_{(z,t)}$ groups that will incur a certain disease.

3.2.1 Mutation of $M_{(z,t)}$

When observing a group of natural persons over time, the group will be subject to "mutation". As a group of natural persons is likely to mutate over time this is likely to impact the occurrence of several types diseases and thus care demand as a whole. In this studies, we will divide mutation of the membership-set of a healthcare insurance company into two types: *internal mutation* and *external mutation.*

Internal mutation of $M_{(z,t)}$

We define internal mutation as a mutation force that is taking place caused by population internal factors. If $M_{(z,t)}$ would be to stay the same in terms of its members it will still "change" over time with respect to care demand. We identify the following mutation factors that are likely to influence care demand over time:

- *Ageing*
  Ageing is of specific interest as we already pointed out that age acts as a determining factor in terms of probability of illness. The latter implies that age might be a determining factor in terms of care demand. Note that the impact caused by ageing is likely to be more visible if the forecasting window is rather large, i.e. in the order of years.

- *Socio-economic status*
  Socio-economic status is defined as a measure to express an individual's economic and social position relative to others. To express status we can use several indicators, for example financial or educational status. Roughly two different mechanisms are identified [33]:

  1. *Selection mechanism*
     People residing in poor health are unable to grow in terms of their socioeconomic status.
  2. *Causa selection mechanism*
     People residing with low socioeconomic status will have poor health, (indirectly) caused by their socioeconomic status.

  Particularly the second mechanism, i.e. the causa selection mechanism is of influence and potential interest with respect to internal mutation. A mutation of socio-economic status might potentially influence a change in the demand for care.

External mutation of $M_{(z,t)}$

Opposed to internal mutation we define external mutation as a mutation force that is taking place caused by external factors. Typically these factors concern immigration- and emigration-typed interactions with respect to $M_{(z,t)}$ over time. Before we present definitions concerning external mutation we will first introduce some basic regulatory elements of the Dutch healthcare system that influence external mutation.

Basic insurance Every person living in the Netherlands is required to have a "basic insurance". The minimal healthcare coverage of such insurance is fixed and determined by the Dutch government. Within the Netherlands, a healthcare insurance company is required to accept any person applying for a basic insurance.

Supplementary insurance Apart from basic insurance, healthcare providers can offer supplementary insurance constructs. A supplementary insurance logically supports costs which are not covered by the basic insurance. A healthcare insurance company is allowed to reject persons applying for a supplementary insurance. A person may have a different healthcare insurance company providing his/her supplementary insurance with respect to his/her basic insurance.

Switching We can find the relation between the insurance types in the Netherlands and external population mutation in the "switching point" of clients. As the healthcare market is a (regulated) market environment, people are allowed to switch between different healthcare insurance companies. In general the following rules hold:

- *Basic healthcare insurance & switching*
  In terms of basic healthcare insurance there is one switching point per year, being January 1^{st}. There are however some exceptions possible in which mutation of $M_{(z,t)}$ can occur at any point in time throughout the year:

  – *Birth*

  – *Adulthood*

  - *Starting/quitting a (new) job*
  - *Immigration*
  - *End of military employment*
  - *Divorce*
  - *Intermediate permutation of healthcare insurance policy conditions*

- *Supplementary healthcare insurance & switching*
  For supplementary switching there is no fixed point in time defined.

The relevance of the insurance types with respect to the research is two-fold. On the one hand the type of insurance largely determines the switching point in time of customers and thus the volumes of external mutation. The types however also influence pathway specific costs. Care provided by a physiotherapist is typically not included in a basic insurance, but might be part of several institutional care pathways. As mentioned, a person is not required to have a basic and supplementary insurance at the same insurance company. Therefore it is possible for a healthcare insurance company to only partly fund an institutional care pathway.

As stated in the previous section we abstract from the concept of insurance types within this research. We identify a person either to be a member or not. We did however present some terminology concerning the topic as it has some interesting impacts with respect to care demand and specifically membership mutation.

Membership inflow The set of people entering the insurance company's membership-set at a certain point in time is defined as the healthcare insurance membership-set inflow. We define membership inflow as:

$$\pi_m^{\leftarrow} : (\mathbf{Z} \times \mathbb{Z}) \to \mathcal{P}(\mathbf{P})$$
$$\pi_m^{\leftarrow}(z,t) \triangleq M_{(z,t)}^{\leftarrow}$$

$M_{(z,t)}^{\leftarrow}$ represents the set of natural persons that become a member of healthcare insurance company z at time t. Additionally we define two constraints on the inflow, relating it to $M_{(z,t)}$:

$$\forall_{z,t}(z \in \mathbf{Z}, t \in \mathbb{Z} : M_{(z,t)}^{\leftarrow} \subseteq M_{(z,t)}), \tag{3.2a}$$
$$\forall_{z,t}(z \in \mathbf{Z}, t \in \mathbb{Z}^+ : M_{(z,t)}^{\leftarrow} \cap M_{(z,t-1)} = \emptyset) \tag{3.2b}$$

Membership outflow The set of people leaving the insurance company's membership-set at a certain point in time is defined as the healthcare insurance membership-set outflow.
We define membership outflow as:

$$\pi_m^{\rightarrow} : (\mathbf{Z} \times \mathbb{Z}) \to \mathcal{P}(\mathbf{P})$$
$$\pi_m^{\rightarrow}(z,t) \triangleq M_{(z,t)}^{\rightarrow}$$

Additionally we define two constraint on the outflow, relating it to $M_{(z,t)}$:

$$\forall_{z,t}(z \in \mathbf{Z}, t \in \mathbb{Z} : M_{(z,t)}^{\rightarrow} \cap M_{(z,t)} = \emptyset), \tag{3.3a}$$
$$\forall_{z,t}(z \in \mathbf{Z}, t \in \mathbb{Z}^+ : M_{(z,t)}^{\rightarrow} \subseteq M_{(z,t-1)}) \tag{3.3b}$$

3.2.2 Diseases

Prevalence

The next step in the care demand model is to define the volume of disease occurrence in terms of $M_{(z,t)}$. We define the π_{d_z} function, relating a healthcare insurance company's membership set to a certain disease:

$$\pi_{d_z} : (\mathbf{Z} \times \mathbf{D} \times \mathbb{Z}) \to \mathcal{P}(\mathbf{P})$$
$$\pi_{d_z}(z, d, t) \triangleq D_{(z,d,t)}$$

$D_{(z,d,t)}$ represents the demand for care of a certain insurance company $z \in \mathbf{Z}$ given a certain point t in time and a certain disease d. Therefore the following constraint should hold:

$$\forall_{z,d,t}(z \in \mathbf{Z}, d \in \mathbf{D}, t \in \mathbb{Z} : D_{(z,d,t)} \subseteq M_{(z,t)}) \tag{3.4}$$

$D_{(z,d,t)}$ expresses a group of people being ill at a specific point in time. Prevalence is defined as "the number of people per unit measure (i.e. thousand people / ten thousand ...) being ill at a specific point in time". We will therefore refer to $D_{(z,d,t)}$ as the *absolute prevalence set.*

Incidence

We define a function $\pi^{\leftarrow}_{d_z}$ representing the incidence at a certain point in time:

$$\pi^{\leftarrow}_{d_z} : (\mathbf{Z} \times \mathbf{D} \times \mathbb{Z}) \to \mathcal{P}(\mathbf{P})$$
$$\pi^{\leftarrow}_{d_z} \triangleq D^{\leftarrow}_{(z,d,t)}$$

We pose the following constraints on the incidence set:

$$\forall_{z,d,t}(z \in \mathbf{Z}, d \in \mathbf{D}, t \in \mathbb{Z} : D^{\leftarrow}_{(z,d,t)} \subseteq D_{(z,d,t)}), \tag{3.5a}$$
$$\forall_{z,d,t}(z \in \mathbf{Z}, d \in \mathbf{D}, t \in \mathbb{Z}^+ : D^{\leftarrow}_{(z,d,t)} \cap D_{(z,d,t-1)} = \emptyset) \tag{3.5b}$$

There are two possible causes for a person p to be in $D^{\leftarrow}_{(z,d,t)}$:

1. The person was already member of healthcare insurance company z and got ill, i.e. $p \in M_{(z,t-1)}$
2. The person was not yet a member of healthcare insurance company z but was already ill i.e. $p \in M^{\leftarrow}_{(z,t)}$.

Disease resignation set

We define a function $\pi^{\rightarrow}_{d_z}$ representing the number of people leaving $D_{(z,d,t)}$ at a certain point in time:

$$\pi^{\rightarrow}_{d_z} : (\mathbf{Z} \times \mathbf{D} \times \mathbb{Z}) \to \mathcal{P}(\mathbf{P})$$
$$\pi^{\rightarrow}_{d_z} \triangleq D^{\rightarrow}_{(z,d,t)}$$

We pose the following constraints on the recovery set:

$$\forall_{z,d,t}(z \in \mathbf{Z}, d \in \mathbf{D}, t \in \mathbb{Z} : D^{\rightarrow}_{(z,d,t)} \cap D_{(z,d,t)} = \emptyset), \tag{3.6a}$$
$$\forall_{z,d,t}(z \in \mathbf{Z}, d \in \mathbf{D}, t \in \mathbb{Z}^+ : D^{\rightarrow}_{(z,d,t)} \subseteq D_{(z,d,t-1)}) \tag{3.6b}$$

There are three possible causes for a person p to be in $D^{\rightarrow}_{(z,d,t)}$.

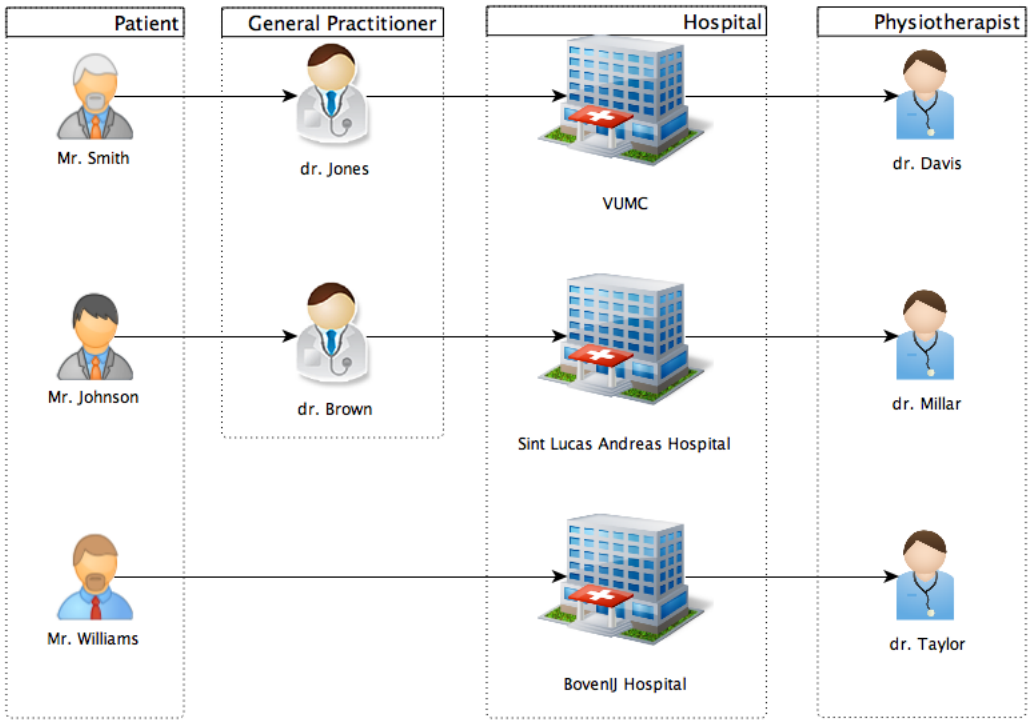
1. The person recovered from disease d, i.e. $p \in M_{(z,t)}$
2. The person deceased (possibly from disease d), i.e. $p \in \mathbf{P}_t^{\dagger}$
3. The person left the healthcare insurance company whilst being in $D_{(z,d,t)}$, i.e. $p \in M^{\rightarrow}_{(z,t)} \wedge p \in \mathbf{P}_t$

3.3 Institutional care pathways

We have defined the concept of institutional care pathways in both a natural language and a more mathematical-typed fashion. We present both definitions here as well as a discussion concerning the level of aggregation when defining institutional care pathways and the relation to integrated care pathways.

3.3.1 A natural language definition

For convenience we present a graphical overview of the idea of institutional care pathways in figure 3.3.1.



Definition

"An institutional care pathway is the sequence of healthcare providers a person p visits for treatment of a certain disease d. The first visit will be based upon incidence of d ($p \in D^{\leftarrow}_{(z,d,t)}$). The last element of the sequence will be based upon leaving the absolute prevalence set ($p \in D^{\rightarrow}_{(z,d,t')}$). A visit in this context is a declared treatment submitted by a healthcare provider to the healthcare company."

3.3.2 Mathematical definition

Institutional care pathways

We define an institutional pathway as an sequence σ^{icp} over $\mathbf{H}$:

$$\sigma^{icp} : \mathbb{Z} \to \mathbf{H}$$

Thus if we would - in natural language - state that person p first visited general practitioner a, then got a treatment at hospital b and finally for a recovery analysis went to physiotherapist c the institutional pathway in mathematical form would look like:

$$\sigma_1^{icp} = a, \sigma_2^{icp} = b, \sigma_3^{icp} = c$$

Care provider visits

We define a person's visits as a function υ_h:

$$\upsilon_h : \mathbf{P} \times \mathbf{D} \times \mathbf{Z} \to \mathcal{P}(\mathbf{H} \times \mathbb{Z})$$

$$\upsilon_h(p, d, z) \triangleq V_{(p,d,z)}$$

As an example for a certain person p', insured at healthcare insurance company z', which has some declarations for disease d' we have the following visit function co-domain:

$$V_{(p',d',z')} = \{(h_1, t_1), (h_2, t_2), (h_3, t_3)\}$$

In this case, we know that for person p' concerning his/her disease d', there have been three declarations at z', which in this case are of healthcare providers h_1, h_2 and h_3 at times t_1, t_2 and t_3 respectively (these are treatment-times). The healthcare providers should be active at the treatment-time declared, in other words:

$$(h_i, t_i) \in V_{(p,d,z)} \implies h_i \in \mathbf{H}_{t_i}$$

We at least assume that there is a partial order on the $\mathbb{Z}$ component of the co-domain.

Note that using υ_h does not allow us to make a distinction between being inflicted by a certain disease d multiple times with times of recovery in between. As this is an exploratory study we assume that a person will only get inflicted once with a certain disease.

Using care provider visits as a basis for pathway reconstruction

The function definition of an institutional care pathway is not yet defined for persons. We assumed the co-domain of υ_h to be partially ordered on its $\mathbb{Z}$ component. It is straightforward to build a corresponding institutional care pathway given a patient's visit-set. Assume again for person p' with disease d' and healthcare insurance company z' the following visit set:

$$V_{(p',d',z')} = \{(h_1, t_1), (h_2, t_2), (h_3, t_3)\}$$

Additionally we assume the following partial order:

$$t_1 \leq t_2 \leq t_3$$

We can now deduce person p''s specific institutional care path for disease d' at healthcare insurance company z':

$$\sigma_1^{icp} = h_1,\ \sigma_2^{icp} = h_2,\ \sigma_3^{icp} = h_3$$

Mapping pathways to membership

We define a function π_{i_z} depicting the set of people insured at company z, suffering from disease d and as a consequence traversing pathway p_i at time t as:

$$\pi_{i_z} : (\mathbf{Z} \times \mathbf{D} \times \mathbf{I} \times \mathbb{Z}) \rightarrow \mathcal{P}(\mathbf{P})$$

$$\pi_{i_z}(z, d, p_i, t) \triangleq I_{(z,d,p_i,t)}$$

We pose the following constraint on $I_{(z,d,p_i,t)}$:

$$\forall_{z,d,p_i,t}(z \in \mathbf{Z}, d \in \mathbf{D}, p_i \in \mathbf{I}, t \in \mathbb{Z} : I_{z,d,p_i,t} \subseteq D_{(z,d,t)})$$

$$\bigcap_{p_i \in \mathbf{I}} I_{(z,d,p_i,t)} = \emptyset$$

3.3.3 Levels of aggregation

There is one more conceptual element that needs motivation with respect to the definition of institutional care pathways, being the level of aggregation. We identify two types:

- *Class-based institutional care pathways*
  In a class-based institutional care pathway setting, pathways are actually defined in terms of an institution's class. We do not differ between the actual institution that has performed the medical action. In case of figure 3.3.1 there would be two pathways identifiable:
  path 1: $\sigma_1^{icp} =$ General Practitioner, $\sigma_2^{icp} =$ Hospital, $\sigma_3^{icp} =$ Psychotherapist
  path 2: $\sigma_1^{icp} =$ Hospital, $\sigma_2^{icp} =$ Psychotherapist
- *Institution-based institutional care pathways*
  Institution-based institutional care pathways are of a lower level of aggregation compared to the class-based typed pathways. We do differ between the actual institution that has performed the medical action. In case of figure 3.3.1 there would be three pathways identifiable:
  path1: $\sigma_1^{icp} =$ dr. Jones, $\sigma_2^{icp} =$ VUMC, $\sigma_3^{icp} =$ dr. Davis
  path2: $\sigma_1^{icp} =$ dr. Brown, $\sigma_2^{icp} =$ St. Lucas, $\sigma_3^{icp} =$ dr. Millar
  path 3: $\sigma_1^{icp} =$ BovenIJ, $\sigma_2^{icp} =$ dr. Taylor

What aggregation level and corresponding type of pathway to use greatly depends on data availability. Note that a hybrid form might be an option as well. If data is sparse, class-based institutional care pathways might be used to "mine" institutional-based pathways out of the given data.

3.3.4 Identifying the difference between "integrated"- and "institutional care pathways"

In this section we will briefly focus on the major difference in terms of terminology concerning "integrated" and "institutional" pathways. We do so by investigating the overall aim of integrated care pathways.

As one should have noted, the definitions of integrated care pathways in literature tend to vary. The common divisor of all these definitions is to provide means which should lead to *optimal care performance*. The actual dimension of the optimality strive is not uniformly defined as there is strictly no need for this. Whether inter-organizational care process optimization or quality of care

is the dimension of optimization, both dimensions contribute to an overall rise in quality of care. The definitions differ however on terms of the actual means used to reach the potential optimization though they are all based on a form of pathway based methodology.

The difference between conventional integrated care pathways and the institutional care pathways as we will use in this research can be found in their general aim. The main use of an institutional pathways is merely of an analytical form. It is ought to act as a basis for *performance specification*. In this research financial performance is assessed though any performance dimension can be used in general.

In integrated care pathway methodology the focus is largely on the integration aspect, which involves cross organizational/care-department cooperation. The given institutional care pathway definitions do not involve any form of cooperation. Whenever two organizations work together within an optimal performing institutional care pathway this might be a strong motivational purpose for other organizations to do so as well.

Institutional care pathways are purely a specification of how patients traversed or will traverse through the healthcare system. They can be used as a basis for care process optimization which is on itself more aligned with integrated care pathways.

Chapter 4

Design

We have assessed the applicability of probabilistic models to act as a model for membership-set mutation as presented in section 4.1. We have specifically assessed the applicability of Markov chains (section 4.2) as a representation for both membership-set mutation and other care-demand associated personal attributes (sections 4.3 and 4.4).

The collection of Markov chains tend to share some dependencies, which lead to the assessment of collaborative Markov chains as a financial forecasting prediction model for healthcare insurance companies. The topic of collaborative Markov chains is presented in section 4.5. We concluded the design phase with an assessment of the incorporation of age into the proposed system of collaborative Markov chains, which we have documented in section 4.6.

4.1 Healthcare insurance membership as a probabilistic model

4.1.1 Customer base classification

A first step is to identify what the membership-set means to an insurance company. In essence we can regard $M_{(z,t)}$ as being an healthcare insurance company's *customer-base*. In [34], Fader and Hardie assess different types of probability models for customer-base analysis. Though this field of research mainly concerns prediction of churn-rates and customer lifetime values, the paper provides some clear and useful terminology on customer-base classification, as presented in figure 4.1.

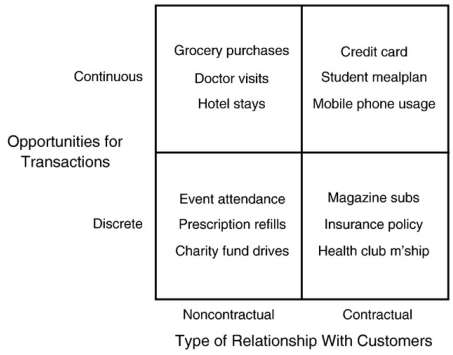


Figure 4.1: The customer-base classification quadrant as proposed by Fader and Hardie.

As we can see in the quadrant, insurance-typed customer-bases are of a "Discrete Contractual" fashion. This is in line with the annual switching-point defined for individuals in terms of healthcare insurance. As we have noted there are several cases in which customer-base transactions are of a continuous fashion within the healthcare insurance market. Therefore Dutch healthcare insurance companies form a special type of company as they belong to the discrete as the continuous relationship group.

As indicated in [34] probabilistic models are often used in the field of customer-base analysis within marketing. Fader and Hardy pose the following motivational description:

"A probability modeler approaches the modeling problem with the mindset that observed behavior is the outcome of an underlying stochastic process. That is, we only have a "foggy window" as we attempt to see our customers' true tendencies, and therefore the past is not a perfect mirror for the future. For instance, if a customer made two purchases last year, is he necessarily a "two per year" buyer, or is there some chance that he might make three or four or perhaps even zero purchases next year? With this kind of uncertainty in mind, we wish to focus more on the latent process that drives these observable numbers, rather than the observables themselves."

Fader and Hardy, 2009 [34]

In addition to the motivation provided by Fader and Hardy, probabilistic models often entail mathematical benefits. Often the result of a probabilistic model or stochastic process is based on some probability distribution. The existence of underlying probability distributions introduces several statistical properties and analytical possibilities with respect to the results produced by the model.

4.1.2 The predictive components of $M_{(z,t)}$ for future values of t

In terms of care demand, a first goal is to determine $M_{(z,t)}$ as accurate as possible for future values of t. Assume we have knowledge of the actual membership-set up to a certain point in time t_{max} and we want to estimate $\hat{M}_{(z,t_e)}$ for some $t_e > t_{max}$ (as t_e is a future value we use $\hat{\theta}$-notation). If we are able to estimate $\hat{M}^{\rightarrow}_{(z,t')}$ and $\hat{M}^{\leftarrow}_{(z,t')}$ for all $t_{max} < t' \leq t_e$, we ware able to express $\hat{M}_{(z,t_e)}$ as:

$$\hat{M}_{(z,t_e)} = (M_{(z,t_{max})} \cup \bigcup_{i=t+1}^{t_e} \hat{M}^{\leftarrow}_{(z,i)}) \setminus \bigcup_{j=t+1}^{t_e} \hat{M}^{\rightarrow}_{(z,j)} \tag{4.1}$$

What equation 4.1 actually expresses is the fact that future membership sets are completely expressible in terms of its mutational components, being the in- and outflow of members. If we actually are able to accurately estimate the mutational components of the membership base we can implicitly compute the future membership base.

In June 2012, an analysis of the healthcare market was reported by the NZA [35]. It contains various interesting topics of which one is the activity of people in terms of changing their healthcare insurance company. The corresponding data is shown in figure 4.2.

What we can learn from figure 4.2 is the growing presence of "switchers" on the market. Both individual as collective-typed switches are present and have been rising up to the year 2012. This fact does not only show that mutation of membership-bases is at least influenced by "switchers" but it is also a strongly growing component. Therefore, in designing the model we will explicitly take "switching" into account.

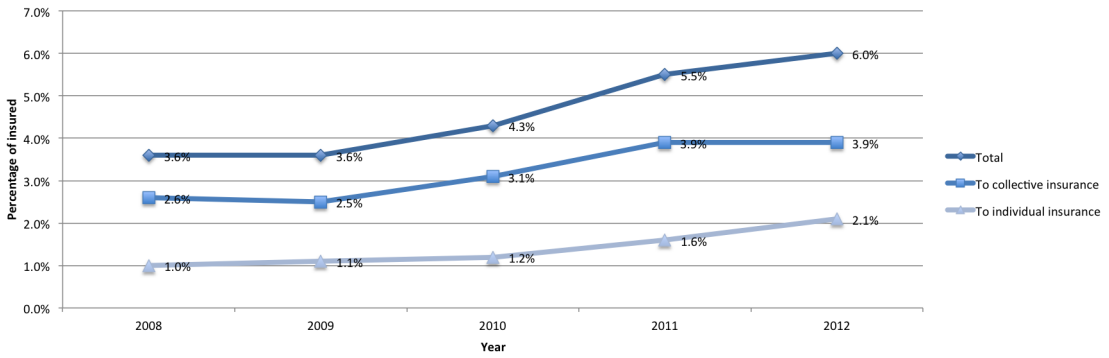


Figure 4.2: An overview of the relative "insurance changing behaviour" within the healthcare system

4.1.3 Membership dynamics probability rules

As we have seen in section 4.1.1 the membership-set falls into a customer-base transaction typed customer relationship. It specifically covers the contractual setting both on a discrete and a continuous transaction-rate. In [34], Fader and Hardy note that Markov chains have been used in customer-base probabilistic modelling, however this has only been done in the non-contractual case. If we now look to a person p's membership to a certain healthcare insurance company z, we can express the following probabilities:

1. The probability that p "still" is a member of z at time $t+1$:
   $P(p \in M_{(z,t+1)} | p \in M_{(z,t)})$
2. The probability that p is "still" not a member of z at time $t+1$:
   $P(p \notin M_{(z,t+1)} | p \notin M_{(z,t)})$
3. The probability that p leaves z at time $t+1$:
   $P(p \notin M_{(z,t+1)} | p \in M_{(z,t)})$ (by definition equivalent to $P(p \in M^{\rightarrow}_{(z,t+1)})$)
4. The probability that p enters z at time $t+1$:
   $P(p \in M_{(z,t+1)} | p \notin M_{(z,t)})$ (by definition equivalent to $P(p \in M^{\leftarrow}_{(z,t+1)})$)

In the given enumeration, the first and the the third probability share a special relation as do the second and the fourth. If a person is "still" a member at time $t+1$, he/she was also a member at time t. If a person leaves at time $t+1$, he/she was by definition a member at time t. As a result, in case one and three at time t the person is in the same state. At time $t+1$ they enter a different state. Logically the same rationale holds for two and four, though the other way around. In terms of probability we can express these relations as follows:

$$P(p \in M_{(z,t+1)} | p \in M_{(z,t)}) + P(p \notin M_{(z,t+1)} | p \in M_{(z,t)}) = 1 \tag{4.2}$$

$$P(p \notin M_{(z,t+1)} | p \notin M_{(z,t)}) + P(p \in M_{(z,t+1)} | p \notin M_{(z,t)}) = 1 \tag{4.3}$$

4.2 Markov chains

It is interesting to note that if we consider the problem at hand as a probabilistic model, we come up with statements of the form:

"*The probability of person p being in state s' at time $t+1$ given that person p is at state s at time t*"

This kind of formulation is very similar to the definition of Markov models.

4.2.1 Markov processes

We let S denote the state space of a system. Let (Ω, F, P) be the probability space. We define a random variable X which represents the system's state at the n^{th} transition:

$$X : \Omega \to S$$

A timed process described by X is a Markov process if the following proposition holds:

$$P(X_{t+1} = x_{t+1} | X_t = x_t, X_{t-1} = x_{t-1}, ..., X_1 = x_1) = P(X_{t+1} = x_{t+1} | X_t = x_t) \tag{4.4}$$

Equation 4.4 states that the probability of entering the next state only depends on the current state. If S is a discrete state space, the Makrov process is also called a *Markov chain.*

A Markov chain basically has two probability types, the initial probabilities p^i and transition probabilities p. We define the initial probability as a function:

$$p^i : S \to \mathbb{R}_{[0,1]}$$

Note that the following equality should always hold:

$$\Sigma_{s \in S}\ p^i(s) = 1$$

The transition probability of state i to state j at time t is defined as a function p:

$$p : S \times S \times \mathbb{Z} \to \mathbb{R}_{[0,1]}$$

$$p(i, j, t) \triangleq p_{i,j}(t) \triangleq P(X_{t+1} = j | X_t = i)$$

Note that equation 4.5 should always hold:

$$0 \leq p_{i,j}(t) \leq 1 \quad \sum_i p_{i,j}(t) = 1,\ \forall_i \tag{4.5}$$

In a "homogeneous" setting, the chain's transition probabilities are time-independent and one can omit the t argument of the probability function.

4.2.2 Initial state vectors and transition matrices

We can represent the given initial state- and transition probability values as an initial state vector and transition matrix respectively. Given $S = \{s_1, s_2, ..., s_N\}$, we can define the initial state vector V_i:

$$V_i = \begin{pmatrix} p^i(s_1) \\ p^i(s_2) \\ \vdots \\ p^i(s_N) \end{pmatrix}$$

For transition the transition matrix we define M_t, in the homogeneous case:

$$M_t = \begin{pmatrix} p_{s_1,s_1} & p_{s_1,s_2} & \cdots & p_{s_1,s_N} \\ p_{s_2,s_1} & p_{s_2,s_2} & \cdots & p_{s_2,s_N} \\ \vdots & \vdots & \vdots & \vdots \\ p_{s_N,s_1} & p_{s_N,s_2} & \cdots & p_{s_N,s_N} \end{pmatrix}$$

In the non-homogeneous form, we need a matrix for each point in time as the probabilities are time dependent:

$$M_t(t) = \begin{pmatrix} p_{s_1,s_1}(t) & p_{s_1,s_2}(t) & \cdots & p_{s_1,s_N}(t) \\ p_{s_2,s_1}(t) & p_{s_2,s_2}(t) & \cdots & p_{s_2,s_N}(t) \\ \vdots & \vdots & \vdots & \vdots \\ p_{s_N,s_1}(t) & p_{s_N,s_2}(t) & \cdots & p_{s_N,s_N}(t) \end{pmatrix}$$

Transition matrices are particularly useful as in fact the probability of reaching a state s_j, given a state s_i in n steps can be easily found by using $M_t^n(s_i, s_j)$. This type of calculations are particularly useful for determining a steady-state distribution of the given system.

4.2.3 Example; Flipping a coin

The most basic example using Markov chains is the stochastic process of flipping a coin multiple times. The corresponding state-space consists of two states, heads and tails, represented by H and T:

$$S = \{H, T\}$$
$$V_i = \begin{pmatrix} \frac{1}{2} \\ \frac{1}{2} \end{pmatrix}$$
$$M_t = \begin{pmatrix} \frac{1}{2} & \frac{1}{2} \\ \frac{1}{2} & \frac{1}{2} \end{pmatrix}$$

We have depicted a graphical representation of the Markov chain in figure 4.3.

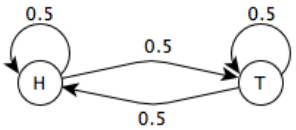


Figure 4.3: Graphical representation of a Markov model for flipping a coin

4.2.4 Semi-Markov chains

We will now consider discrete time semi-Markov chains building on the previous definitions presented concerning Markov chains. Additionally to X, we define a random variable T representing the time of entering the state represented by X_n:

$$T : \Omega \to \mathbb{Z}$$

We define the inter-arrival time τ_n as:

$$\tau_n = T_n - T_{n-1}$$

A sequence described by (X_n, T_n) is called a Markov-renewal process if equation 4.6 holds:

$$P(\tau_{t+1} \leq t, X_{n+1} = x_{n+1} | X_t = n_t, X_{n-1} = x_{n-1}, ..., X_1 = x_1; T_n = t_n, T_{t-1} = t_{n-1}, ..., T_1 = t_1) = P(\tau_{t+1} \leq t, X_{n+1} = x_{n+1} | X_n = x_n; T_n = t_n) \tag{4.6}$$

Equation 4.6 states that the probability that the system will enter state x_{n+1} within t units of time. A semi-Markov model is defined by a new stochastic process (random variable) Y:

$$Y_t := X_n \text{ for } t \in [T_n, T_{n+1})$$

We can immediately identify the various new possibilities provided by the introduction of Y_t. In general if we define ϖ^n as the corresponding holding time distribution for Y_t we can express the relation with the basic Markov process (or chain) as follows:

$$P(\tau_{t+1} \leq t, X_{n+1} = x_{n+1} | X_t = n_t, X_{n-1} = x_{n-1}, ..., X_1 = x_1; T_n = t_n, T_{t-1} = t_{n-1}, ..., T_1 = t_1) = P(\tau_{t+1} \leq t, X_{n+1} = x_{n+1} | X_n = x_n; T_n = t_n) = P(X_{n+1} = x_{n+1} | X_n = x_n) \varpi^n(t) \tag{4.7}$$

If we let each ϖ^n to be exponentially distributed this equation becomes:

$$P(X_{n+1} = x_{n+1} | X_n = x_n)(1 - e^{-\lambda_{x_n} t})$$

The latter describes a continuous Markov process as the holding time distribution is a continuous probability function.

4.3 Modelling healthcare insurance membership as a Markov chain

One should be able to identify the similarities between the proposed membership dynamics probability rules in subsection 4.1.3 and the basic property in Markov theory as presented in section 4.2. In this section have defined three Markov models that can be used to represent membership dynamics.

4.3.1 Two state model

The first model only represents membership and non-membership of a certain person p, in which we define the state-space S_{M_1} as follows:

$$S_{M_1} = \{M_z, \neg M_z\}$$

We can clearly identify the relationship between the Markov model and the membership dynamics probability rules, i.e.:

$$P(X_{t+1} = M_z | X_t = M_z) \equiv P(p \in M_{(z,t+1)} | p \in M_{(z,t)})$$

$$P(X_{t+1} = \neg M_z | X_t = \neg M_z) \equiv P(p \notin M_{(z,t+1)} | p \notin M_{(z,t)})$$

$$P(X_{t+1} = \neg M_z | X_t = M_z) \equiv P(p \notin M_{(z,t+1)} | p \in M_{(z,t)})$$

$$P(X_{t+1} = M_z | X_t = \neg M_z) \equiv P(p \in M_{(z,t+1)} | p \notin M_{(z,t)})$$

Figure 4.4: A basic two state Markov chain model for a person p's healthcare insurance membership behaviour

4.3.2 Three state model

If we look at a person within the healthcare system, we notice that in the two-state model we allow people who are part of $M^{\rightarrow}_{(z,t)}$ because of death to re-enter the membership set. If we want to model decease as well, we can extend the two state model with an additional "sink" state (†) depicting that a person deceased.

$$S_{M_2} = \{M_z, \neg M_z, \dagger\}$$

The corresponding graphical representation of the Markov chain is presented in figure 4.5.

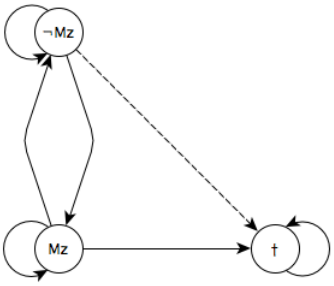


Figure 4.5: A basic three state Markov chain model for a person p's healthcare insurance membership behaviour

In this case we have three additional transitions:

$$P(X_{t+1} = \dagger | X_t = M_z) \equiv P(p \notin M_{(z,t+1)} | p \in M_{(z,t)})$$

$$P(X_{t+1} = \dagger | X_t = \neg M_z) \equiv P(p \notin M_{(z,t+1)} | p \notin M_{(z,t)})$$

$$P(X_{t+1} = \dagger | X_t = \neg M^{\dagger}_z) \equiv P(p \notin M_{(z,t+1)} | p \notin M_{(z,t)})$$

Note that if one of the three newly added transitions occurs, the random variable will no longer be able to be either of value $\neg M_z$ or M_z. The transition $\neg M_z \rightarrow \dagger$ is indicated as a dashed arrow in the graphical representation. We have used a dashed-line visualization here to indicate that the corresponding statistical parameter cannot be estimated by solely using a healthcare insurance company's data-base. In order to estimate this type of mutation, other sources should be used.

Four state model

As a third and final possible model we introduce a four-state based model which also distinguishes between regular or irregular timed membership mutations. We define the state space S as follows:

$$S_{M_3} = \{M_z, \neg M_z^R, \neg M_z^I, \dagger\}$$

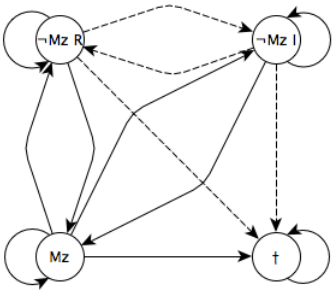


Figure 4.6: A basic four state Markov chain model for a person p's healthcare insurance membership behaviour

The graphical representation of the four-state model is presented in figure 4.6. Again we have indicated interactions within the model that we can not estimate by solely using a healthcare insurance company's data. When using a distinction between regular and irregular mutation, one does not necessarily need to implement time-dependent probabilities. The potential difference in volumes with respect to regular and irregular mutation can in this case be modelled using semi-Markov processes.

4.3.3 Markov chains as a representation for membership dynamics in conclusion

The "memoryless" property

Let us recall the basic assumption of a Markov process:

$$P(X_{t+1} = x_{t+1} | X_t = x_t, X_{t-1} = x_{t-1}, ..., X_1 = x_1) = P(X_{t+1} = x_{t+1} | X_t = x_t)$$

If we translate this property into natural language it reads as follows:
"The probability of reaching the next state x_{t+1} is only depending on the current state x_t. Thus, the path leading to x_t does not influence the probability of reaching x_{t+1}."

One can question whether this assumption does hold with regard to leaving or entering a healthcare insurance company, i.e.:
"Is a person likely to re-enter a healthcare insurance company when he/she has just left?"
"Is a person likely to leave a healthcare insurance company when he/she just became a member?"

For now we assume that the history of a patient does not influence its current decision. We do note that in reality this assumption might likely be incorrect. The problem with the memoryless property can however be solved by using n^{th}-order Markov chains. In a n^{th}-order Markov chain the memory property becomes (for $t > n$):

$$P(X_{t+1} = x_{t+1} | X_t = x_t, X_{t-1} = x_{t-1}, ..., X_1 = x_1) =$$

$$P(X_{t+1} = x_{t+1} | X_t = x_t, X_{t-1} = x_{t-1}, ..., X_{t-n} = x_{t-n+1})$$

Using the terminology presented for n^{th}-order Markov chains we can additionally deduct that regular chains are of 1^{st} order.

What model to choose from?

So far we have introduced three types of Markov chains that represent a client's behaviour through the system, given the viewpoint of a healthcare insurance company. Each model adds a layer of complexity and/or removes a limitation. We will briefly discuss semantic aspects of the models presented which might have an influence with respect to choosing a specific model design.

- *Two state model (figure 4.4)*
  The two state model does not consist of a sink-state that can act as a representation for a person that will never enter the membership set in the future (most likely because of decease cases). If one would like to implement this behaviour in the two state model, one should apply an additional administration of the fact whether or not the person is deceased. Additionally the model does not distinguish between any switching point in time. There are several ways to incorporate this behaviour. Like the decease case we could add administration of what type a person's switching behaviour is, we could again update the probabilities accordingly. We could also neglect the type of a person though still update probabilities of switching at the turn of a year, compared to in-year time steps. Additionally we could use constant probabilities though implicitly tune the parameters to incorporate regular and irregular switching as well.

- *Three state model (figure 4.5)*
  The three state model does provide a representation for decease cases by means of a sink-state. Though this resolves a form of limitation it adds a form of complexity. As noted one has to estimate the probability of the transition $\neg M_z \rightarrow \dagger$, which can not be performed solely using a healthcare insurance company's data. The three state model, like the two state model does not distinguish between the regular and irregular switching points.

- *Four state model (figure 4.6)*
  The four state model adds a distinction with respect to regular and irregular switching. In the case of the four state model, one can apply semi-Markov theory to model the desired behaviour. Note that the model though eliminating some more limitations, it actually introduces additional complexity. When applying the model one has to be able to distinguish between regular and irregular switchers. It is very questionable whether this is actually possible. In this case decease rates for both $\neg M_z^R \rightarrow \dagger$ and $\neg M_z^I \rightarrow \dagger$ have to be determined.

Adding additional healthcare insurance companies

A final remark concerns the states that represent "not being insured at company z", being $\neg M_z$, $\neg M_z^R$ and $\neg M_z^I$. We could choose to extend the models with states that represent membership to a different firm. If we know that apart from our own company z, there are n other insurance companies, $Z_1, Z_2, ..., Z_n$, the state spaces of the models would become:

$$S_{M_1} = \{M_z, M_{Z_1}, M_{Z_2}, ..., M_{Z_n}\}$$

$$S_{M_2} = \{M_z, M_{Z_1}, M_{Z_2}, ..., M_{Z_n}, \dagger\}$$

$$S_{M_3} = \{M_z, M_{Z_1}^R, M_{Z_2}^R, ..., M_{Z_2}^R, M_{Z_1}^I, M_{Z_2}^I, ..., M_{Z_2}^I, \dagger\}$$

4.4 Diseases and institutional care pathways as Markov chains

So far we have looked at modelling future membership of a person to a healthcare insurance as a probabilistic model. Specifically we have chosen to use Markov models to act as our probabilistic model of choice. A Markov model representing personal membership behaviour can produce a statistic concerning values of $\hat{M}_{(z,t)}$. In terms of care demand, this is only half the goal as we still need to produce a statistic that indicates the share of people getting ill. In this section we will inspect whether we can express probability rules for "having a disease" and "traversing an institutional pathway"

4.4.1 Disease

Probability rules

Like membership, for being ill we have defined some terminology in the analysis part which we will use as a basis to construct a probabilistic model. Let us start by investigating some possible interactions of a person with $D_{(z,d,t)}$:

1. Probability of "still" not being inflicted with disease d at time $t+1$:
   $P(p \notin D_{(z,d,t+1)} | p \notin D_{(z,d,t)})$
2. Probability of incidence given disease d at time $t+1$:
   $P(p \in D_{(z,d,t+1)} | p \notin D_{(z,d,t)})$ (by definition equivalent to $P(p \in D^{\leftarrow}_{(z,d,t+1)})$)
3. Probability of prevalence given disease d at time $t+1$:
   $P(p \in D_{(z,d,t+1)} | p \in D_{(z,d,t)})$
4. Probability of resignation from disease d at time $t+1$:
   $P(p \notin D_{(z,d,t+1)} | p \in D_{(z,d,t)})$ (by definition equivalent to $P(p \in D^{\rightarrow}_{(z,d,t+1)})$)

Now let us define a Markov chain, that expresses whether a person is subject to a given disease d:

$$S_d = \{D_d, \neg D_d, \dagger\}$$

Within S_d, D_d indicates a person suffering from disease d, $\neg D_d$ means a person is not suffering from disease d and † again acts as the model's sink. A graphical representation is presented in figure 4.7.

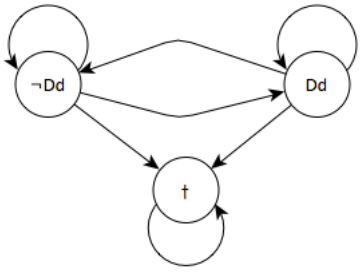


Figure 4.7: Graphical representation of parametrized equivalent of the disease Markov chain

By definition the given probability rules entail some hidden complexity that is not expressible by solely using the Markov model defined. This is mainly due to the relations defined between $M_{(z,t)}$ and $D_{(z,d,t)}$. Strictly speaking the first probability rule can also indicate that a person was

never a member of the firm at time t and $t+1$. To be able to infer the relations between the Markov model proposed and the probability rules we additionally need to assume that there is an additional random variable Y_t that indicates a person's membership with respect to a healthcare insurance company z. $Y_t = M_z$ indicates that p is a member of z at time t, $Y_t = \neg M_z$ indicates that a person is not a member at time t. Additionally assume that $X_t = *$ is used if any $s \in S_d \setminus \{\dagger\}$ is deemed appropriate.

$$P(X_{t+1} = *|X_t = *, Y_t = \neg M_z, Y_{t+1} = \neg M_z) \equiv P(p \notin D_{(z,d,t+1)}|p \notin D_{(z,d,t)})^1$$

$$P(X_{t+1} = \neg D_d|X_t = *, Y_t = \neg M_z, Y_{t+1} = M_z) \equiv P(p \notin D_{(z,d,t+1)}|p \notin D_{(z,d,t)})$$
$$P(X_{t+1} = \neg D_d|X_t = \neg D_d, Y_t = M_z, Y_{t+1} = M_z) \equiv P(p \notin D_{(z,d,t+1)}|p \notin D_{(z,d,t)})$$
$$P(X_{t+1} = D_d|X_t = *, Y_t = \neg M_z, Y_{t+1} = M_z) \equiv P(p \in D_{(z,d,t+1)}|p \notin D_{(z,d,t)})$$
$$P(X_{t+1} = D_d|X_t = \neg D_d, Y_t = M_z, Y_{t+1} = M_z) \equiv P(p \in D_{(z,d,t+1)}|p \notin D_{(z,d,t)})$$
$$P(X_{t+1} = D_d|X_t = D_d, Y_t = M_z, Y_{t+1} = M_z) \equiv P(p \in D_{(z,d,t+1)}|p \in D_{(z,d,t)})$$
$$P(X_{t+1} = \neg D_d|X_t = D_d, Y_t = M_z, Y_{t+1} = M_z) \equiv P(p \notin D_{z,d,t+1}|p \in D_{(z,d,t)})$$
$$P(X_{t+1} = D_d|X_t = D_d, Y_t = M_z, Y_{t+1} = \neg M_z) \equiv P(p \notin D_{z,d,t+1}|p \in D_{(z,d,t)})$$
$$P(X_{t+1} = \dagger|X_t = D_d, Y_t = M_z, Y_{t+1} = \neg M_z) \equiv P(p \notin D_{z,d,t+1}|p \in D_{(z,d,t)})$$

Within the model defined there is also a transition from being healthy to the sink, i.e.:

$$P(X_{t+1} = \dagger|X_t = \neg D_d)$$

The given interaction states that a person can also decease without actually being ill (for disease d). This is a valid situation though not expressible in terms of $D_{(z,d,t)}$ interaction. Note that the given Markov chain represents one specific disease d. If we would assume there are T types of disease d_1, d_2,..., d_T we could reformulate the state space to:

$$S_d = \{\neg D_d, D_{d_1}, D_{d_2}, ..., D_{d_T}, \dagger\}$$

4.4.2 Institutional care pathways

As the focus of this research is not concerning pathway recognition we assume that for a certain disease a set of pathways exists. Modelling institutional pathway traversal comes in two flavours equivalent to the levels of aggregation presented in chapter 3, pathway based and institution based.

Pathway-based traversal

In pathway-based traversal, we assume a person will traverse a "point-to-point" pathway in which the elements are fixed.

Probability rules In the pathway-based traversal case we can define the following probability rules, again given that a person is member of the healthcare insurance company, $p \in M_{(z,t)}$ for t, $t+1$, $t+2$, ...:

1. Probability of person p "still" not traversing *any path* at time $t+1$:
   $P(p \notin I^P_{(z,d,t+1)}|p \notin I^P_{(z,d,t)})$
2. Probability of person p "starting" to traverse path $p_i \in \mathbf{I}_{t+1}$ at time $t+1$:
   $P(p \in I_{(z,d,p_i,t+1)}|p \notin I^P_{(z,d,t)})$

[1] In this case $X_t = \dagger$ and $X_{t+1} = \dagger$ is deemded acceptible as well

3. Probability of person p "keeps" traversing path $p_i \in \mathbf{I}_t \cup \mathbf{I}_{t+1}$ at time $t+1$: $P(p \in I_{(p_i,t+1)} | p \in I_{(z,d,p_i,t)})$
4. Probability of person p to "stop" traversing a path $p_i \in \mathbf{I}_t$ at time $t+1$: $P(p \notin I^P_{z,d,t+1} | p \in I_{(z,d,p_i,t)})$

In pathway-based traversal, each element in the Markov chain state-space is a pathway itself:

$$S_{p_p} = \{\neg p, p_1, p_2, ..., p_n\}$$

A graphical representation is presented in figure 4.8.

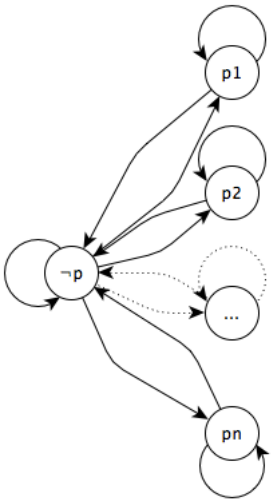


Figure 4.8: Graphical representation of the pathway-based pathway Markov chain

We can infer relationships between the probability rules and the Markov chain as defined, again using an additional random variable Y_t denoting membership. Additionally we use random variable Z_t to denote the fact that a person is ill i.e. $Z_t = D_d$ and $Z_t = \neg D_d$. Note that in this case there is again a vast amount of hidden complexity caused by the definitions of $I_{(z,d,p_i,t)}$, $D_{(z,d,t)}$ and $M_{(z,t)}$. In this case we only show three equivalence relations (of the many) to again show the general idea:

$$P(X_{t+1} = \neg p | X_t = \neg p, Y_t = M_z, Y_{t+1} = M_z) \equiv P(p \notin I^P_{(z,d,t+1)} | p \notin I^P_{(z,d,t)})$$

$$P(X_{t+1} = p_i | X_t = \neg p, Y_t = M_z, Y_{t+1} = M_z, Z_{t+1} = D_d) \equiv P(p \in I_{(z,d,p_i,t+1)} | p \notin I^P_{(z,d,t)})$$

$$P(X_{t+1} = p_i | X_t = p_i, Y_t = M_z, Y_{t+1} = M_z, Z_t = D_d, Z_{t+1} = D_d) \equiv P(p \in I_{(p_i,t+1)} | p \in I_{(z,d,p_i,t)})$$

Institution-based traversal

In institution-based traversal each healthcare provider acts as a state in the state-space. In this case we define the state-space of the corresponding Markov chain as S_{p_i}

$$S_{p_i} = \{\neg p, h_1, h_2, ..., h_n\}$$

Because this strategy has a less fixed structure compared to the models presented so far, we present it by means of an example.

Consider the following example in which we have found the following sequences of institutions, given some disease d:

$$p_1 =< h_1, h_2 >$$
$$p_2 =< h_1, h_2, h_4 >$$
$$p_3 =< h_1, h_3, h_4 >$$
$$p_4 =< h_5, h_2 >$$
$$p_5 =< h_5, h_2, h_4 >$$
$$p_6 =< h_5, h_3, h_4 >$$

Thus we have found six pathways in total, which would lead to a pathway-based state space S_{p_p}:

$$S_{p_p} = \{\neg p, p_1, p_2, p_3, p_4, p_5, p_6\}$$

The corresponding institution-based pathway Markov chain state-space would become:

$$S_{p_i} = \{\neg p, h_1, h_2, h_3, h_4, h_5\}$$

A graphical representation of the corresponding Markov chain is depicted in figure 4.9.

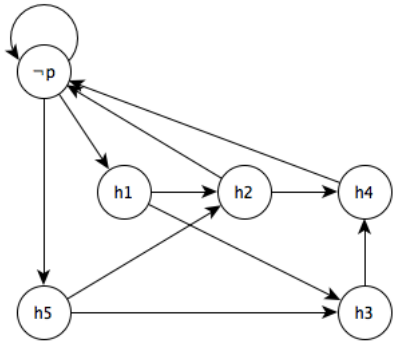


Figure 4.9: Graphical representation of the institution-based pathway Markov chain

There are two important notes with respect to the model in figure 4.9. First, we assume that there are no cycles possible, though logically in real cases this could in fact be possible. Secondly each node representing a healthcare provider has no self-loop. The self loops are omitted as in no trace $< ...h_i, h_i, ... >$ occurs. We advocate modelling self-loops only when these self-loops are indeed part of the pathways identified within the data.

If we would just use conventional Markov chains, a pathway would either take 2 or 3 time-steps (equal to the number of elements in the chain). If we would like to extend the duration of a specific visit we should incorporate additional functionality. For example the use of a *Markov renewal process* would be a solution.

When comparing the institution based approach to the pathway approach, parameter estimation is harder as one has to assess each combination that can occur. On the other hand one can assess the traversal in a more detailed fashion and also investigate single-point optimization within pathways.

4.5 Collaborative Markov chains

4.5.1 Relations amongst the models presented

In the previous sections we have defined three models which present different interesting properties of a person with respect to care demand and institutional care pathway traversal, i.e.:

1. A model representing whether a person is member to a healthcare insurance company
2. A model representing whether a person is ill or not
3. A model representing what *corresponding* institutional care pathway the person is traversing

As we have indicated in the third note traversing a care pathway is defined for a corresponding disease. If a person is not ill, the probability that he or she will traverse an institutional pathway is zero. However if a person becomes ill the probability that he or she will not enter a pathway is likely to be zero or very small. Thus, the probability of a person traversing a pathway strictly *depends* on the fact whether a person is ill.

We need to be able to express both the probability rules as defined earlier as well as the general system's behaviour. We need a system $\mathcal{M}$ of three Markov chains representing the behaviour of persons with respect to healthcare insurance membership, disease and institutional pathway traversal.

$$\mathcal{M} = \{C_M, C_D, C_P\}$$

Within $\mathcal{M}$, C_M represents the membership Markov chain, C_D represents the disease Markov chain and C_P represents the institutional pathway traversal Markov chain. Additionally the probabilities in C_P strictly depend on the state of system C_D.

This type of systems are also known as "collaborative Markov chains".

4.5.2 Defining collaborative Markov chains

Before we introduce basic terminology we present an analogy based on mutual exclusion in a resource sharing setting as the idea of collaborative Markov chains originates from the field of (system) networking theory.

Let us consider a set of processes, that share a set of resources. Whenever a certain process P_1 is in state $s_{P_{1,r_1}}$ it needs to use resource r_1. In this case (i.e. $P_1 = s_{P_{1,r_1}}$) any other process P_X can not enter state $s_{P_{X,r_1}}$ if r_1 is needed by P_X in order to be in state $s_{P_{X,r_1}}$. In other words, the current state of P_1 influences the transition probability of P_X in terms of entering state $s_{P_{X,r_1}}$.

In [36] these types of problems are described and generalized in terms of Markov theory. A definition is given for Markov chain competition and collaboration:

"*The competition and the collaboration between chains simply assumes that when a resource is owned by a component (or when a component is in a specific subset of states) it affects the transition probabilities of the other components of the chain.*"

Fourneau, 2010 [36]

Though the goal of [36] is merely to provide theoretical proof and mathematical properties concerning the tensor and product form of the composite multi-dimensional transition Matrix of

collaborative Markov chains, the main idea behind the models is very applicable in terms of this research. We have used the definitions provided by Forneau as a basis to further specify our model.

Let $\mathcal{M}$ be a set of N (discrete time) Markov chains:

$$\mathcal{M} = \{C_1, C_2, ..., C_N\}$$

We define a function d which represents a *dependency* from a chain to some other chains:

$$d : \mathcal{M} \to \mathcal{P}(\mathcal{M})$$
$$d(C_x) = \{C_y, C_z\} \triangleq C_x \to \{C_y, C_z\}$$

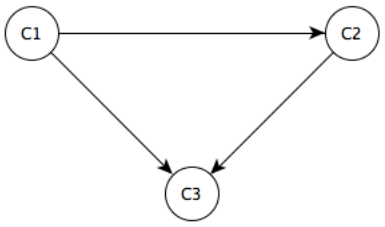
$C_x \to \{C_y, C_z\}$ in this case means that C_x is depending on both $C_y$and C_z. If C_x has no dependencies at all we will just denote this as $C_x \to \emptyset$.

We let $\mathcal{D}_\mathcal{M}$ be the set of all dependencies within $\mathcal{M}$. We can now define a dependency graph $G(\mathcal{D}_\mathcal{M})$ as a graphical representation of $\mathcal{D}_\mathcal{M}$.

Note that $G(\mathcal{D}_\mathcal{M})$ can come in two flavors:

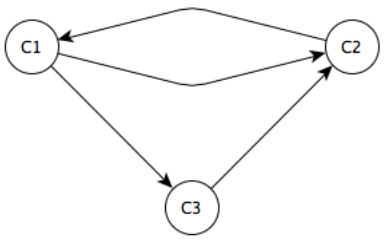
- $G(\mathcal{D}_\mathcal{M})$ *is a directed a-cyclic graph (DAG)*

  Example:
  $\mathcal{M} = \{C_1, C_2, C_3\}$
  $\mathcal{D}_\mathcal{M} = \{C_1 \to \{C_2, C_3\}, C_2 \to \{C_3\}, C_3 \to \emptyset\}$
  $G(\mathcal{D}_\mathcal{M}) =$



- $G(\mathcal{D}_\mathcal{M})$ is a directed cyclic graph (DCG)

  Example:
  $\mathcal{M} = \{C_1, C_2, C_3\}$
  $\mathcal{D}_\mathcal{M} = \{C_1 \to \{C_2, C_3\}, C_2 \to \{C_1\}, C_3 \to \{C_2\}\}$
  $G(\mathcal{D}_\mathcal{M}) =$



Whether or not $G(\mathcal{D}_{\mathcal{M}})$ is cyclic or not has impact on both mathematical as implementational challenges. In [36] several mathematical (in particular linear algebraic) properties are defined for collaborative discrete-time Markov chains with dependencies. More specifically it is shown that for collaborative discrete-time Markov chains with an a-cyclic dependency graph a steady-state distribution in product-form exists. Consequently it is shown that for Markov chains with cyclic dependency graphs, steady-state distributions in product-form do not exist.

4.6 Incorporating age within the proposed system

4.6.1 The impact of age on in- and outflow

Let us explore $M^{\leftarrow}_{(z,t)}$ and $M^{\rightarrow}_{(z,t)}$ in more detail, that is let us explore an influential factor in terms of quantifying these components. Within [35] the results of a study performed by BS Health consultancy are presented, which we have depicted in figure 4.10.

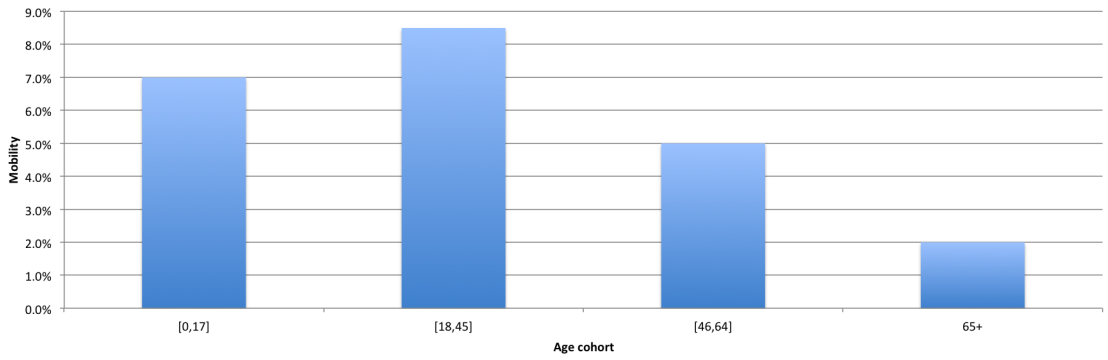


Figure 4.10: Relative mobility within the healthcare system by age cohort.

The study as performed by BS Health consultancy shows us that age is an influential factor in terms of switching activity. As we can see, it states that the [18,45] cohort is the most active cohort. Specifically the elderly seem to be less active.

The reason why switching behaviour is actually depending on age is deemed to be specifically depending on a person's healthcare insurance requirements. Younger persons tend to be more price-oriented whereas elderly people seem to be more quality-oriented. Additionally the existence of "internet-based" healthcare plans seems to be substantially picked up by younger people.

4.6.2 Incorporating age within the proposed collaborative Markov chain system

So far we have posed a system of collaborative Markov chains, in which a Markov chain depicts a personal attribute some of which might influence each-other's transition probabilities. Additionally we have identified that age acts as a determining factor with respect to the probability of "switching behaviour".

We can choose to let age be an input parameter for determining probabilities within the system as a whole, likewise the way we would treat time in case of use of non-homogeneous Markov chains.

However we pose to exploit the concept behind collaborative Markov chains and model age parameters within a new Markov chain, which we will call the age/vitality model.

Age itself is of course very deterministic as it is just an administrative agreement, i.e. every time a year goes by we update a counter. For convenience we present a special case Markov chain (a τ-step Markov chain) which depicts age-development over time. Given that we use a minimum age A_1 and a maximum age A_n:

$$S_a = \{\Omega, A_1, A_2, ..., A_n, \dagger\}$$

A graphical representation is presented in figure 4.11.

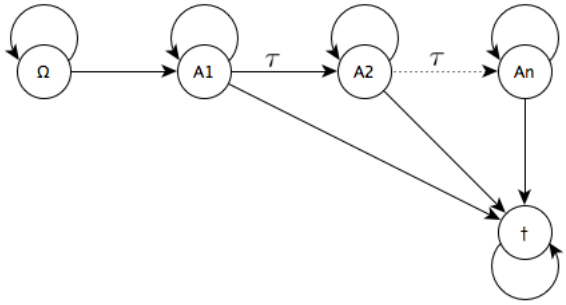


Figure 4.11: Graphical representation of the age/vitality Markov chain

In the given model Ω represents the "source", the state for an unborn person. Given a certain probability a person can get born. He/She will then be in the first age-state (which technically might also represent an age-group). The † state represents the "sink", i.e. the state that indicates that the given person has deceased.

Within the model a person can reach a new age-state by means of a "τ-step". Now what does a τ-step mean in the given context?

A τ-step represents a deterministic state-transition within the state-space that "does not take any time". Additionally the τ-step can happen at any point in time, corresponding to the global time within the model. In fact the model represents a person's vitality where a corresponding age parameter is modelled as a sate within the model itself.

Assume we have a "vitality" Markov chain which looks like this:

$$S' = \{\Omega, \Delta, \dagger\}$$

In S', Ω represents the "source", Δ represents a person being "vital" and † represents the "sink". A graphical representation of S' is depicted in figure 4.12.

Additionally assume that for the S'-model we have some time dependent parameter that indicates a person's age at time t, $d'_A(t)$. Whenever a person is unborn, we assume $d'_A(t) = -\infty$ whenever a person deceased we assume $d'_A(t) = \infty$. We define the relationship amongst the τ-step based model (S) and the vitality model (S') as follows (Where X_t represents the random variable corresponding to S and X'_t to S'):

$$P(X_{t+1} = \Omega | X_t = \Omega) \equiv P(X'_{t+1} = \Omega,\ d'_A(t+1) = -\infty | X'_t = \Omega,\ d'_A(t) = -\infty)$$

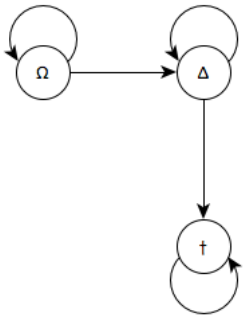


Figure 4.12: Graphical of parametrized equivalent of the age Markov chain

$$P(X_{t+1} = A_1 | X_t = \Omega) \equiv P(X'_{t+1} = \Delta, d'_A(t+1) = A1 | X'_t = \Omega, d'_A(t) = -\infty)$$
$$P(X_{t+1} = A_i | X_t = A_i) \equiv P(X'_{t+1} = \Delta, d'_A(t+1) = A_i | X'_t = \Delta, d'_A(t) = A_i)$$
$$P(X_{t+1} = A_{i+1} | X_t = A_i) \equiv P(X'_{t+1} = \Delta, d'_A(t+1) = A_{i+1} | X'_t = \Delta, d'_A(t) = A_i)$$
$$P(X_{t+1} = \dagger | X_t = A_i) \equiv P(X'_{t+1} = \dagger, d'_A(t+1) = \infty | X'_t = \Delta, d'_A(t) = A_i)$$
$$P(X_{t+1} = \dagger | X_t = \dagger) \equiv P(X'_{t+1} = \dagger, d'_A(t+1) = \infty | X'_t = \dagger, d'_A(t) = \infty)$$

4.7 Final model proposition

Combining the terminology presented in the previous section we come up with the following final model proposition with respect to the problem at hand.

To predict the expected care demand for some disease d and some insurance company z, we pose the usage of a system of collaborative Markov chains $\mathcal{M}$:

$$\mathcal{M} = \{C_M, C_A, C_D, C_P\}$$

Within $\mathcal{M}$, the Markov chains are defined as follows:

- C_M *represents a Markov chain describing personal membership*
  We have assessed and motivated three different basic types of models applicable here, partly depending on data-availability and preference with respect to the use of a Markov renewal process. Additionally we have indicated the potential use of a model consisting of rival insurance companies as states as well.
- C_A *represents a Markov chain describing age development*
  We have posed the use of a τ-step Markov chain to model age as a Markov chain. In terms of age, one can either chose to use individual age or age-groups.
- C_D *represents a Markov chain describing incidence and prevalence*
  We have posed one type of model concerning incidence and prevalence. Additionally we noted the potential addition of disease types to the general disease model design. The value of the state of this chain directly influences the fact whether a person traverses a pathway or not.
- C_P *represents a Markov chain describing institutional care pathway traversal*
  We have posed two types of models concerning institutional care pathway traversal. The types identified are pathway-based and institution-based traversal.

We additionally pose the following dependency-set $\mathcal{D}_{\mathcal{M}}$:

$$\mathcal{D}_{\mathcal{M}} = \{C_M \to \{C_A\}, C_A \to \{C_D\}, C_D \to \{C_A\}, C_P \to \{C_D\}\}$$

Note that within the given definition of $\mathcal{D}_{\mathcal{M}}$ we have incorporated the following dependencies:

- $C_M \to \{C_A\}$
  The probability of a person leaving or entering the membership set is depending on age.
- $C_A \to \{C_D\}$
  Vitality and thus the age development of a person depends on the fact whether a person is healthy or not.
- $C_D \to \{C_A\}$
  The probability of getting a certain disease *might* be depending on age.
- $C_P \to \{C_D\}$
  The probability of a person traversing a pathway is depending on the fact whether a person is ill or not.

Note that additional dependencies might exist as well. Typically healthcare insurance compnaies assume that people who are ill, i.e. $p \in D_{(z,d,t)}$, will not switch any more. If this where to be the case, C_M would depend on C_D as well. This specific example is one of the many additional dependencies which can exist in the system.

We have chosen to present a final model which has a loose structure and provides a range of design decisions still to be made. The reason for this is that it is hard to come up with a unified model in the given context. The current system proposed might be suitable for a prediction of prostate-cancer related pathway traversal. If we would on the other hand want to predict care pathway traversal associated with lung-cancer we might add a chain depicting whether a person is a smoker or not. In that case the combination of this fact and age might influence the incidence probability of a given person within the system. If we would look at breast cancer, gender has great influence on incidence. In such case we could for example add a chain depicting the gender of a person.

Chapter 5

Implementation

5.1 Monte Carlo techniques

As we have seen, a system is proposed that:

- Consists of several Markov chains.
- Consists of dependencies amongst those Markov chains.
- Might, in the context of the problem, consist cyclic dependencies.

As stated, the potential cyclic form of the dependency graph for the system at hand does not allow us to compute a product-form steady state distribution. We could however use Monte Carlo techniques to compute future care demand and associated pathway traversal.

In general MC techniques entail a broad range of computational algorithms in which random sampling is used in order to gain results. Often sampling is used as the given distribution is not easy to capture in some closed-form expression, which is actually the case within this research model proposition. In general these "results" can be classified in two categories [37]:

1. Generate samples $\{x^{(r)}\}_{r=1}^{R}$, given a probability distribution $P(x)$
2. Estimate expectations of functions under a given distribution

As mentioned in [37]:

"The probability distribution $P(x)$, which we will call the target density, might be a distribution from statistical physics or a conditional distribution arising in data modelling."

Mackay, 1998 [**?**]

This statement is very interesting with respect to the research as it is in line with the system of conditional probabilities represented by the use of collaborative Markov chains.

When taking a look at MC methods, a lot of techniques are concerned with finding a sample which respects the target density. Specifically techniques like importance sampling and rejection sampling are based on using a non-normalized distribution $P^*(x)$ (with $P(x) = P^*(x)/Z_p$ where Z_p is some normalizing constant) with the possible addition of a sample density $Q^*(x)$ (with $Q(x) = Q^*(x)/Z_Q$). Usually there is some additional scoring-function that rate a sampled data value. Summarizing these types of methods use approximate distributions (i.e. sample distributions) out of which data values are generated which then are evaluated using some scoring

methodology with respect to the original distribution $P(x)$.

Another class of MC methods are related to the Metropolis Hastings algorithm. The basic difference with respect to importance and rejection sampling is the fact that within MH the sampling distribution $Q(x)$ is actually depending on the current state of the system, which is is denoted as $x^{(t)}$. Again some measure will be used in order to determine whether the newly created value is actually feasible.

The Gibbs sampler is a special case of the MH algorithm for multivariate systems. In the case of a system of K variables sampling is performed in the following manner [37]:

$$x_1^{(t+1)} \sim P(x_1|x_2^{(t)}, x_3^{(t)}, ..., x_K^{(t)})$$

$$x_2^{(t+1)} \sim P(x_2|x_1^{(t+1)}, x_3^{(t)}, ..., x_K^{(t)})$$

$$\vdots$$

$$x_K^{(t+1)} \sim P(x_K|x_1^{(t+1)}, x_2^{(t+1)}, x_{K-1}^{(t+1)})$$

Thus, each next value of a variable is computed using a probability distribution which conditional values are the most up-to-date value of each other variable in the system.

5.2 Using simulation for collaborative Markov chain-based sampling

5.2.1 Sampling within this research

Within this research, the goal is to produce a statement concerning future institutional care pathway traversal. If we revise the basic overview of MC, producing some statement of future institutional care pathway traversal using collaborative Markov chains falls into the first MC classification, i.e.:

Generate samples $\{x^{(r)}\}_{r=1}^{R}$*, given a probability distribution* $P(x)$

In our case $P(x)$ is defined by the system of collaborative Markov chains. The actual structure of the samples to be generated mainly depends on the forecasting window and aim, though in general would be some statistic indicating an amount associated with pathway traversal.

In order to compute $\{x^{(r)}\}_{r=1}^{R}$ we will need some means of computational algorithm in order to sample values which originate from the given system of Collaborative Markov chains. We do not need to accept nor reject any outcome. Within this research we can just perform simulation in a "random walk fashion". We have two basic operations which we should repeat throughout the sampling process:

1. For each Markov Chain compute the next state.
2. Using some dependency update strategy, infer new probabilities within the Markov chains in the system.

Thus using the state of the overall system, for each chain we determine the next state. Depending on what type of dependency propagation used throughout the system, this type of random walk

(as we are randomly selecting a new state that also acts as a new data point) is very similar to Gibbs sampling as we will discuss in more detail in the next section.

With respect to timing within the intend simulation we choose to use a discrete time-base. As "becoming ill" and "recovery of a disease" are typically of a continuous fashion, the actual knowledge of such events are of a discrete fashion with respect to a healthcare insurance company. Typically the level of aggregation of declarations is in days as well. Membership mutation is also an aspect which is administered on a daily basis. Therefore the lowest discrete-time event level should be in the order of days. Note that depending on the length of the simulation we can also choose to scale up this level of aggregation towards months or even years.

5.2.2 Sampling of collaborative Markov chains and forecasting terminology

Within the literature review we have assessed three main topics concerning care demand prediction and forecasting in general being frameworks, classification and techniques. In this subsection we will briefly assess where to position the current proposition of simulation/sampling of collaborative Markov chains within classification and techniques.

Classification

Although we have seen several classification schemes, the common divisor was the difference between *qualitative* and *quantitative* methods (also called opinion versus empirical and judgemental versus statistical). Without further ado we can easily classify the proposed sampling model to be of quantitative class.

A unified sub-classification within quantitative forecasting models is somewhat harder to draw up though in essence we can make a distinction between *naive* and *causal* methods (or univariate versus multivariate). In this specific case we identify the model to exploit several potential causal relations and thus falling within the causal class.

In terms of Gentry's classifcation grid [3], we define our proposed sampling-based model to fall in the category of *models*, i.e. a quantitative causal method. In terms of Armstrong's classification tree [2] the proposed sampling-based model falls in the branch of quantitative multivariate methods.

Techniques

As we will be performing simulation to implement sampling on a personal level we will actually be applying micro simulation. As indicated in the literature review, this is more frequently performed within care demand prediction.

The model proposed shares some similarity to the "future elderly model" used in both [15] and [17]. Within the given model Monte Carlo techniques where also used in order to compute new functional states. Also note that the age/vitality based Markov chain proposed shares some similarities with the multi-state life table model as proposed in [26].

In general we define the technique used within this research as being a discrete-event based micro-simulation technique.

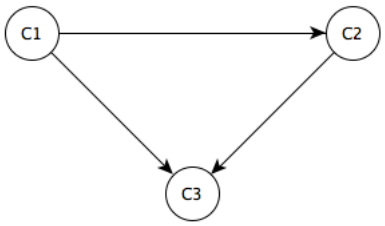
5.3 Dependency propagation

Let us turn our focus towards the possible cyclic dependency graph of the system proposed and its implications. We do so by investigating possible execution order strategies given the nature of the dependency graph. We will reuse the examples introduced in chapter 4, section 4.5.

5.3.1 $G(\mathcal{D}_\mathcal{M})$ is a directed a-cyclic graph (DAG)

$$\mathcal{M} = \{C_1, C_2, C_3\}$$
$$\mathcal{D}_\mathcal{M} = \{C_1 \to \{C_2, C_3\}, C_2 \to \{C_3\}, C_3 \to \emptyset\}$$

$G(\mathcal{D}_\mathcal{M}) =$



If we look at the given dependency graph and we want to propagate each chain's state as fast as possible, we can easily come up with a suitable order of execution. In this case we can just "follow the dependencies": C_2 and C_3 must precede C_1, C_3 must precede C_2, there is no chain that must precede C_3, resulting in:

$$C_3 \to C_2 \to C_1$$

In terms of conditional probability rules this results in:

$$P(C_1^{(t+1)} = c_1 | C_2^{(t+1)} = c_2, C_3^{(t+1)} = c_3)$$
$$P(C_2^{(t+1)} = c_2 | C_1^{(t)} = c_1, C_3^{(t+1)} = c_3)$$
$$P(C_3^{(t+1)} = c_3 | C_1^{(t)} = c_1, C_2^{(t)} = c_2)$$

We can clearly identify the similarities between the given probability rules and the general structure of Gibbs sampling. In fact using such update strategy yields a form of Gibbs sampling.

Thus, for direct a-cyclic graphs apart from any product-form solution we can also explicitly infer an execution order. Of course this is not always trivial and there is not always one unique solution. For example, if we would propose:

$$\mathcal{D}_\mathcal{M} = \{C_1 \to \{C_3\}, C_2 \to \{C_3\}, C_3 \to \emptyset\}$$

We have two possible execution strategies:

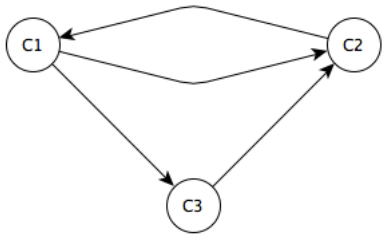
$$C_3 \to C_2 \to C_1$$
$$C_3 \to C_1 \to C_2$$

Note that for more complex or different systems different strategies exist and should already be present within literature, though we do not go into this much detail here as it is not within our research focus.

5.3.2 $G(\mathcal{D}_\mathcal{M})$ is a directed cyclic graph (DCG)

$$\mathcal{M} = \{C_1, C_2, C_3\}$$
$$\mathcal{D}_\mathcal{M} = \{C_1 \to \{C_2, C_3\}, C_2 \to \{C_1\}, C_3 \to \{C_2\}\}$$

$G(\mathcal{D}_\mathcal{M}) =$



If we would in this case "follow the dependencies", we would end up with an unsatisfactory result: C_2 and C_3 must precede C_1, C_1 must precede C_2, C_2 must precede C_3. Clearly there are several options here as well, which we deem as interesting topics for further research, i.e. what is the impact of random selection ordering versus prioritized ordering etcetera.

As solving this problem is currently out of scope we relax the "most up-to-date" property that is both usable in the DAG-case and used by Gibbs:

$$P(C_1^{(t+1)} = c_1 | C_2^{(t)} = c_2, C_3^{(t)} = c_3)$$
$$P(C_2^{(t+1)} = c_2 | C_1^{(t)} = c_1, C_3^{(t)} = c_3)$$
$$P(C_3^{(t+1)} = c_3 | C_1^{(t)} = c_1, C_2^{(t)} = c_2)$$

5.4 Simulation framework

Within the research we have implemented a simulation framework which allows us to generate samples from any arbitrary system of collaborative Markov chains. The framework is based on the procedures as described in the previous sections. A more detailed description of the framework can be found in appendix D. In this section we will briefly describe the simulation framework's basic properties and assess its potential impacts on the resulting samples.

5.4.1 Basic description

The simulation framework is developed in the `Matlab` environment.[1]. It allows the user to define *systems* that consist of *Markov chains*. A Markov chain consists of *states* and *transitions* between those states. Each transition has an associated *probability* which is (re)settable. Each chain additionally consists of an initial state vector.

Apart from conventional Markov chain elements as described above, the system allows the user to specify dependencies and τ-functionality. The user simply specifies a chain's dependencies and associated probability values. The system entity will make sure that corresponding probabilities

[1] Each *italic* element in the basic description has an associated class in the simulation framework. See appendix D for a more detailed description of these classes.

will be updated accordingly. To implement a Markov chain that has τ functionality, the system must be made aware of the fact that the given chain may consist of τ-transitions. Additionally the system administers a data-element for the given chain, an auxiliary data-element initialization function and an auxiliary reference function (which determines whether a τ transition should actually happen). A chain itself is not "aware" of the fact that it consists of possible τ steps. The system entity will update the "current state" of a chain according to τ-functionality.

We have applied hierarchical context-unawareness throughout the entire simulation framework. A probability is not aware of its surrounding transition, which in turn is not aware of its surrounding chain. This logically also holds for the states contained by a chain. A transition does however administer some reference to its from- and to-state.

Additionally the system entity is able to execute a "MC random walk" given a number of time-steps. The MC functionality just repeatedly determines a new state for each chain in the system. Dependency analysis is performed as described in the previous section (i.e. the update strategy posed for cyclic dependency graphs is always used, also in case of acyclic dependency graphs).

As a simulation is intended to be executed multiple times an additional *simulator* entity is part of the simulation framework. In the simulator entity we specify the simulation length, number of elements in one run and the number of replications.

The simulator entity additionally allows us to keep track of the system's statistics, as we are specifically interested in the number of people that are a member, become ill and traverse some institutional pathway. This kind of functionality is implemented by means of "monitors" which allow us to perform transient analysis on the simulation results.

5.4.2 Monitors

As stated the simulator entity allows us to specify monitors which allow us to perform transient analysis of the given system. Monitors come in two flavours:

- *Single monitors*
  A single monitor is defined for one single chain. If we are interested in the amount of people that are a member to our firm, we can define a single monitor for the corresponding state in the corresponding chain. After simulation, the monitor will output the number of elements that where in the given state for each simulation time-point.
- *Combined monitors*
  Combined monitors are defined for two or more chains. They allow us to analyse more specific cases compared to single monitors. We might be interested in monitoring all people that are a member to our firm *and* that are ill at the same time. Consequently we might also be interested in what pathway these people traverse. In such case we will define a monitor on those people that are a member to our firm, that are ill *and* what pathway they traverse as a consequence of their illness. A combined monitor will output the number of people that are in all monitored states at a certain point in time.

By defining monitors we are actually able to post-process the results that are generated by the simulation framework.

5.4.3 Dependency propagation lag within the current simulation implementation

The notion of dependency propagation lag

The relaxation of the "most up-to-date" property poses the potential existence of a phenomenon that we will define as "dependency propagation lag". We will illustrate propagation lag using an example. Assume the case where a person will get ill at time t an will get healthy at time $t + 3$. Thus we normally we expect the person to be in a pathway at time t, $t + 1$ and $t + 2$.

What will actually happen within simulation? At time t, the disease model will reach some state depicting the fact that person p is ill. The institutional care pathway model however will look back one time-step (i.e. $t - 1$), in which the person was still healthy. At time $t + 1$, the institutional care pathway model identifies that the person was ill at time t and will assign some pathway to the person. Repeating this process, the institutional care pathway model will identify the person being healthy again at time $t + 4$. Thus the disease model tells us that a person is ill at time t, $t + 1$ and $t + 2$ whereas the institutional care pathway model will actually tell us this same person was traversing a pathway at time $t + 1$, $t + 2$ and $t + 3$. The actual length of pathway traversal is in accordance with the length of illness with respect to time. The exact points in time do however suffer from propagation lag.

Dependency propagation lag and cyclic dependency graphs

Now let us assess propagation lag with respect to cyclic dependency graphs. Assume that the person's institutional pathway will influence the probability of reviving. Logically traversing a pathway depends on the fact that a person is ill or not, so we end up with a cyclic dependency.

Let D denote the random variable depicting whether a person is ill or not ($\neg d$ = healthy, d = ill). Let random variable P denote what pathway the person traverses ($\neg p$ = no pathway, p_x = traversing pathway x). Additionally assume that for the combination of being ill and traversing no pathway we cannot quantify the probability of reviving thus we assume a person to stay ill in such case.

Consider (hypothetically) that a disease d is very easily treated when in path x and it only takes 1 time step. Normally we would have the following situation:
$\boldsymbol{t}$, $<$**D, P**$>$
1. $< \neg d, \neg p >$
2. $< d, p_x >$
3. $< \neg d, \neg p >$

If we would have *no cyclic dependency*, so D does not depend on P, we would have the following simulation result:
$\boldsymbol{t}$, $<$**D, P**$>$
1. $< \neg d, \neg p >$
2. $< d, \neg p >$
3. $< \neg d, p_x >$
4. $< \neg d, \neg p >$

The following trace would be the result of dependency propagation lag in simulation, given that the cyclic dependency does exist:
$\boldsymbol{t}$, $<$**D, P**$>$

1. $< \neg d, \neg p >$
2. $< d, \neg p >$
3. $< d, p_x >$
4. $< \neg d, p_x >$
5. $< \neg d, \neg p >$

The implications of dependency lag actually differ given the nature of the dependency graph. In the *acyclic* case (the second trace), the number of *individual* occurrences of p_x is correct. The time points at which they occur however is not correct. This means that if we would put a single monitor on P, we would actually get correct results in terms of amounts of pathway traversal. We could additionally need some post-processing to fix the time-lag. Note that this also holds if the time of disease would take longer (i.e. an arbitrary number of $< d, p_x >$ instances in-between $< d, \neg p >$ and $< \neg d, p_x >$).

In the *cyclic* case, the number of individual occurrences of both p_x and d is incorrect, though the number of *combined* occurrences is correct. Again the occurrence is lagged and the system as a whole suffers from an additional time-step of lag.

Note that if a given disease has a typical long time span and associated pathway traversal, the impact of propagation lag is neglect-able. It does however pose more serious issues for more dynamic systems.

5.4.4 The simulation framework in conclusion

Within this research we have build a simulation framework that:

- Allows a user to define systems of collaborative Markov chains, using tables to input both chain and dependency definitions.
- Allows to simulate the system multiple times given some number of elements, simulation time span and number of replications.
- Always implements the dependency updating strategy as defined for cyclic dependency graphs, i.e.:

$$P(C_1^{(t+1)} = c_1 | C_2^{(t)} = c_2, C_3^{(t)} = c_3, \dots C_N^{(t)} = c_n)$$
$$P(C_2^{(t+1)} = c_2 | C_1^{(t)} = c_1, C_3^{(t)} = c_3, \dots C_N^{(t)} = c_n)$$
$$\vdots$$
$$P(C_3^{(t+1)} = c_3 | C_1^{(t)} = c_1, C_2^{(t)} = c_2, \dots C_{N-1}^{(t)} = c_{n-1})$$

- ***Does not include any form of dependency based initialization.***

Chapter 6

Experimental design

6.1 Overview

Within this experimentation is two-fold:

- *Real healthcare data analysis*
  We have analysed real healthcare data to assess feasibility of the model proposed. We specifically assessed data properties with respect to the mathematical models presented throughout the previous chapters.
- *Simplified case-based simulation*
  We have constructed some simplified cases, related to the actual problem at hand to assess the model proposed in general. The cases are defined on top of each other and are designed in an incremental fashion. The systems of collaborative Markov chains used within case-based simulation are very similar to the final model proposition.

Within experimentation we tried to assess whether the assumptions made and definitions proposed are viable. We have also assess viability of the model in terms of simulation and associated results. Lessons learned from data analysis and performing simulation will eventually be combined into a set of managerial implications and recommendations as well as a vivid discussion.

6.2 Data Analysis

W have been able to use data supporting the research made available by Dutch healthcare insurance company X[1] Two datasets were made available of which we specifically the first one has been analysed intensively:

- *Population data*
  A membership-subscription based data-set which can potentially be used as a basic real-life for $M_{(z,t)}$ in which $z =$ "X" and $01-01-2006 \leq t \leq 31-12-2010$[2]
- *Declaration data*
  A declaration based data-set which can potentially be used as a basis for $V_{(p,d,z)}$ (and thus potentially σ^{icp}) in which $z =$ "X", p is variable though at least $p \in M_{z,t}$ and d is variable

[1] The identity of the healthcare provider has been excluded from this report

[2] Note that with respect to the observed increase in "switching behaviour" on the Dutch healthcare insurance market, the data is somewhat outdated.

A more detailed description of the datasets can be found in appendix C, section C.1.

We have assessed the data on the following dimensions:

- Membership volume
- In- and outflow quantification
- Gender distribution
- Impact of age on "switching activity"
- Expected reconstruct-ability of care institutional pathways

To be able to effectively analyse the data it has been manipulated using a manipulation script written in `python`. A description of the data manipulation script can be found in Appendix C, sectionC.2.

6.3 Cases

In this section we present the description of the proof-of-concept cases. We will present input data and discuss potential limitations with respect to simulation results. For example the lack of dependency based initialization within the simulation framework might lead to expected values that differ from the corresponding case result specification.

The tables used as an input for simulation of the cases within the simulation framework as well as the associated simulation framework input code can be found in appendix E.

6.3.1 Case I - Single Markov chain representing membership dynamics

The first case is just a ***single*** Markov chain representing membership dynamics. The case implements a modified version of the four-state model as we have omitted the sink. Additionally we omit any form of irregular membership mutation. The mathematical model used in this case is:

$$S_M = \{M_z, \neg M_z^I, \neg M_z^R\}$$

$$\mathcal{M} = \{S_M\}$$

$$\mathcal{D}(\mathcal{M}) = \{S_M \rightarrow \emptyset\}$$

The data depicted in table 6.1 is used as an input.

Year:	2006	2007	2008	2009
Month:	$1 \rightarrow 12$	$1 \rightarrow 12$	$1 \rightarrow 12$	$1 \rightarrow 12$
State:				
M_z	100	96	92	88
$\neg M_z^I$	100	100	100	100
$\neg M_z^R$	150	154	158	162

Table 6.1: Case I - Input data

The goal is to use the data of 2006 and 2007 to predict membership values for 2008 and 2009. In this case this is just a yearly regular outflow of four people.

6.3.2 Case II - Adding irregular membership mutation

Compared to case I, case II only adds irregular mutation with respect to the membership-set. The case builds on top of case I, thus the regular outflow rates remain equal. As the model is equal to case I we have omitted the mathematical model definition here. The input data is presented in table 6.2.

Year:	2006	2006	2006	2006	2006	2006	2006	2006	2006	2006	2006	2006
Month:	1	2	3	4	5	6	7	8	9	10	11	12
State:												
M_z	100	101	101	101	102	102	102	103	103	103	104	104
$\neg M_z^I$	100	99	99	99	98	98	98	97	97	97	96	96
$\neg M_z^R$	150	150	150	150	150	150	150	150	150	150	150	150

Year:	2007	2007	2007	2007	2007	2007	2007	2007	2007	2007	2007	2007
Month:	1	2	3	4	5	6	7	8	9	10	11	12
State:												
M_z	100	101	101	101	102	102	102	103	103	103	104	104
$\neg M_z^I$	96	95	95	95	94	94	94	93	93	93	92	92
$\neg M_z^R$	154	154	154	154	154	154	154	154	154	154	154	154

Year:	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008
Month:	1	2	3	4	5	6	7	8	9	10	11	12
State:												
M_z	100	101	101	101	102	102	102	103	103	103	104	104
$\neg M_z^I$	92	91	91	91	90	90	90	89	89	89	88	88
$\neg M_z^R$	158	158	158	158	158	158	158	158	158	158	158	158

Year:	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009
Month:	1	2	3	4	5	6	7	8	9	10	11	12
State:												
M_z	100	101	101	101	102	102	102	103	103	103	104	104
$\neg M_z^I$	88	87	87	87	86	86	86	85	85	85	84	84
$\neg M_z^R$	162	162	162	162	162	162	162	162	162	162	162	162

Table 6.2: Case II - Input data

As we can see, we have defined the irregular mutation to be somewhat 'regular' as exactly one person flows from $\neg M_z^I$ to $\neg M_z^R$ every 2^{nd}, 5^th, 8^{th} and 11^{th} month of a year.

6.3.3 Case III - Adding age-based membership mutation

Case III builds on top of case II and is the first case that incorporates the main idea of "collaborative Markov chains". The idea within this case is to introduce an abstract version of an age/vitality model. It consists of three age groups, A_1, A_2 and A_3. In terms of membership mutation we keep the same rates as we used in case II. The only difference is the fact that we have made membership mutation age dependent.

We let members of age group A_2 be responsible for the irregular mutation and we let members of age group A_3 be responsible for the regular mutation. For convenience, the input data for case

III is shown in tables 6.3, 6.4, 6.5 and 6.6 Note that the sum of each age-based membership-group sums up to the equivalent membership-set in case II. Thus $|A1, M_z| + |A_2, M_z| + |A_3, M_z| = 100$ for year 2006, month 1, which equals M_z in case II for that point in time. Additionally note that we do not define any form of ageing within the proof of concept case and thus there is no need for τ-step Markov chains in the actual model.

Within this case we use the following mathematical model:

$$C_M = \{M_z, \neg M_z^I, \neg M_z^R\}$$

$$C_A = \{A_1, A_2, A_3\}$$

$$\mathcal{M} = \{C_M, C_A\}$$

$$\mathcal{D}(\mathcal{M}) = \{C_M \rightarrow \{C_A\}, C_A \rightarrow \emptyset\}$$

Note that due to the lack of dependency based initialization, the expected results of case III will differ from the values for 2008 and 2009 as presented here. This will remain a problem for the remainder of the cases. This is the case as we either need age-based membership initialization or membership-based age initialization which is not possible within the simulation framework. We therefore used the basic age division as presented for January 2006, which is always $\frac{1}{4}$ of a membership group is in A_1, $\frac{1}{2}$ in A_2 and $\frac{1}{4}$ in A_3.

Thus from case III and on it makes less sense to compare the model output to the presented output. In the result chapter we will specifically indicate the *expected values* according to the simulation framework shortcomings.

Year:	2006	2006	2006	2006	2006	2006	2006	2006	2006	2006	2006	2006
Month:	1	2	3	4	5	6	7	8	9	10	11	12
State space:												
A_1, M_z	25	25	25	25	25	25	25	25	25	25	25	25
A_2, M_z	50	51	51	51	52	52	52	53	53	53	54	54
A_3, M_z	25	25	25	25	25	25	25	25	25	25	25	25
$A_1, \neg M_z^I$	25	25	25	25	25	25	25	25	25	25	25	25
$A_2, \neg M_z^I$	50	49	49	49	48	48	48	47	47	47	46	46
$A_3, \neg M_z^I$	25	25	25	25	25	25	25	25	25	25	25	25
$A_1, \neg M_z^R$	38	38	38	38	38	38	38	38	38	38	38	38
$A_2, \neg M_z^R$	75	75	75	75	75	75	75	75	75	75	75	75
$A_3, \neg M_z^R$	37	37	37	37	37	37	37	37	37	37	37	37

Table 6.3: Case III - Input data 2006

Year:	2007	2007	2007	2007	2007	2007	2007	2007	2007	2007	2007	2007
Month:	1	2	3	4	5	6	7	8	9	10	11	12
State space:												
A_1, M_z	25	25	25	25	25	25	25	25	25	25	25	25
A_2, M_z	54	55	55	55	56	56	56	57	57	57	58	58
A_3, M_z	21	21	21	21	21	21	21	21	21	21	21	21
$A_1, \neg M_z^I$	25	25	25	25	25	25	25	25	25	25	25	25
$A_2, \neg M_z^I$	46	45	45	45	44	44	44	43	43	43	42	42
$A_3, \neg M_z^I$	25	25	25	25	25	25	25	25	25	25	25	25
$A_1, \neg M_z^R$	38	38	38	38	38	38	38	38	38	38	38	38
$A_2, \neg M_z^R$	75	75	75	75	75	75	75	75	75	75	75	75
$A_3, \neg M_z^R$	41	41	41	41	41	41	41	41	41	41	41	41

Table 6.4: Case III - Input data 2007

Year:	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008
Month:	1	2	3	4	5	6	7	8	9	10	11	12
State space:												
A_1, M_z	25	25	25	25	25	25	25	25	25	25	25	25
A_2, M_z	58	59	59	59	60	60	60	61	61	61	62	62
A_3, M_z	17	17	17	17	17	17	17	17	17	17	17	17
$A_1, \neg M_z^I$	25	25	25	25	25	25	25	25	25	25	25	25
$A_2, \neg M_z^I$	42	41	41	41	40	40	40	39	39	39	38	38
$A_3, \neg M_z^I$	25	25	25	25	25	25	25	25	25	25	25	25
$A_1, \neg M_z^R$	38	38	38	38	38	38	38	38	38	38	38	38
$A_2, \neg M_z^R$	75	75	75	75	75	75	75	75	75	75	75	75
$A_3, \neg M_z^R$	45	45	45	45	45	45	45	45	45	45	45	45

Table 6.5: Case III - Input data 2008

Year:	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009
Month:	1	2	3	4	5	6	7	8	9	10	11	12
State space:												
A_1, M_z	25	25	25	25	25	25	25	25	25	25	25	25
A_2, M_z	62	63	63	63	64	64	64	65	65	65	66	66
A_3, M_z	13	13	13	13	13	13	13	13	13	13	13	13
$A_1, \neg M_z^I$	25	25	25	25	25	25	25	25	25	25	25	25
$A_2, \neg M_z^I$	38	37	37	37	36	36	36	35	35	35	34	34
$A_3, \neg M_z^I$	25	25	25	25	25	25	25	25	25	25	25	25
$A_1, \neg M_z^R$	38	38	38	38	38	38	38	38	38	38	38	38
$A_2, \neg M_z^R$	75	75	75	75	75	75	75	75	75	75	75	75
$A_3, \neg M_z^R$	49	49	49	49	49	49	49	49	49	49	49	49

Table 6.6: Case III - Input data 2009

6.3.4 Case IV - Adding a disease module

The fourth case is building right on top of the third case. It incorporates an additional chain that indicates whether a person is healthy or not. The basic input with respect to population mutation and age division is again equal to the previous case.

In case IV we have only defined incidence parameters for persons both residing in age bin $A1$ *and* in M_z. Consequently we will only show the additional input for people who reside in both states as depicted in table 6.7 (again note that due to the lack of dependency based initialization the actual expected values will differ from the result specification as depicted here).

In this case we have used the following mathematical model:

$$C_M = \{M_z, \neg M_z^I, \neg M_z^R\}$$
$$C_A = \{A_1, A_2, A_3\}$$
$$C_D = \{\neg D_d, D_d\}$$
$$\mathcal{M} = \{C_M, C_A, C_D\}$$
$$\mathcal{D}(\mathcal{M}) = \{C_M \rightarrow \{C_A\}, C_A \rightarrow \emptyset, C_D \rightarrow \{C_A\}\}$$

Year:	2006	2006	2006	2006	2006	2006	2006	2006	2006	2006	2006	2006
Month:	1	2	3	4	5	6	7	8	9	10	11	12
State space:												
M_z, A_1, $\neg D_d$	23	23	23	23	24	24	24	24	24	23	23	23
M_z, A_1, D_d	2	2	2	2	1	1	1	1	1	2	2	2
Year:	2007	2007	2007	2007	2007	2007	2007	2007	2007	2007	2007	2007
Month:	1	2	3	4	5	6	7	8	9	10	11	12
State space:												
M_z, A_1, $\neg D_d$	23	23	23	22	22	22	22	22	23	23	23	23
M_z, A_1, D_d	2	2	2	3	3	3	3	3	2	2	2	2
Year:	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008
Month:	1	2	3	4	5	6	7	8	9	10	11	12
State space:												
M_z, A_1, $\neg D_d$	23	22	22	22	22	22	22	21	21	21	21	21
M_z, A_1, D_d	2	3	3	3	3	3	3	4	4	4	4	4
Year:	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009
Month:	1	2	3	4	5	6	7	8	9	10	11	12
State space:												
M_z, A_1, $\neg D_d$	21	21	21	21	22	22	22	22	22	22	22	22
M_z, A_1, D_d	4	4	4	4	3	3	3	3	3	3	3	3

Table 6.7: Case IV - Input Data

6.3.5 Case V - Adding integrated care pathways

In case V we again build on top of the previous cases. In this case we have added an additional model which represents two point-to-point institutional pathways, P_A and P_B. Whenever a person of age A_1 gets sick, he/she will traverse one of both pathways with a probability of $\frac{1}{2}$. We will therefore not present the input data as it is just the input of case IV where the sick people are divided over the two pathways as "equal" as possible.

Due to the lack of dependency-based initialization we have initialized pathway traversal with a probability of 0. At the first time point we expect no one to be traversing any pathway. Due to propagation lag predicted pathway traversal will always have a lag of one time-step in this case.

The mathematical model used in this case is:

$$C_M = \{M_z, \neg M_z^I, \neg M_z^R\}$$
$$C_A = \{A_1, A_2, A_3\}$$
$$C_D = \{\neg D_d, D_d\}$$
$$D_P = \{\neg P, P_A, P_B\}$$
$$\mathcal{M} = \{C_M, C_A, C_D, C_P\}$$
$$\mathcal{D}(\mathcal{M}) = \{C_M \rightarrow \{C_A\}, C_A \rightarrow \emptyset, C_D \rightarrow \{C_A\}, C_P \rightarrow \{C_D\}\}$$

6.3.6 Case VI - Adding a circular dependency between disease and institutional pathways

In the final sixth proof of concept case we have introduced a circular dependency. Additionally we have changed the probability of a person getting ill with respect to case IV and V.

A person of age A_1 and member of M_z has a probability of $\frac{1}{2}$ of becoming ill, *the initialization has not changed however*. The probability of remaining in an ill state will be $\frac{4}{5}$ if a person is in path A whereas it is $\frac{1}{5}$ if a person is in path B. Thus people that get in pathway B are more likely revive quicker.

With respect to the mathematical model used in case V, case VI adds an additional dependency resulting in:

$$C_M = \{M_z, \neg M_z^I, \neg M_z^R\}$$
$$C_A = \{A_1, A_2, A_3\}$$
$$C_D = \{\neg D_d, D_d\}$$
$$D_P = \{\neg P, P_A, P_B\}$$
$$\mathcal{M} = \{C_M, C_A, C_D, C_P\}$$
$$\mathcal{D}(\mathcal{M}) = \{C_M \to \{C_A\}, C_A \to \emptyset, C_D \to \{C_A, C_P\}, C_P \to \{C_D\}\}$$

6.3.7 General overlap in terms of case simulation

Though the case differ in terms of input, some elements have been equal throughout the course of simulation:

- Each simulation concerns 350 elements.
- Each simulation will concern the years 2008 and 2009, given a step-size of months.
- The number of replications is 50.

Chapter 7

Results

7.1 Data analysis

7.1.1 Membership volume

We have visualized the development of the membership volume in the data which can be found in figure 7.1. The total number of people in the data-set is 125,675. An overall impression of the graph shows that the overall level of membership volume seems to be showing some minor fluctuations throughout the year. At the turning of the year the membership volume seems to fluctuate somewhat more intensively. To investigate these fluctuations, some basic statistics concerning yearly membership volume development are depicted in table 7.1.

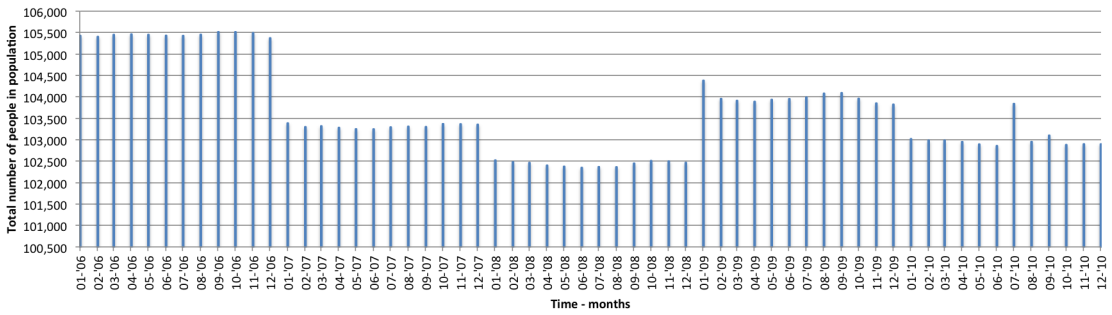


Figure 7.1: Total membership volume development visualized using the full time window (i.e. 01-'06...12-'10)

Year	*2006*	*2007*	*2008*	*2009*	*2010*
Minimum	105,372	103,247	102,348	103,823	102,857
Maximum	105,515	103,386	102,521	104,381	103,839
Mean	105,449.5	103,314	102,436.25	103,984,92	103,021.25
Standard deviation	42.52	45.88	62.5	148.07	266.44
Median	105,450.5	103,304	102,455.5	103,954.5	102,951.5

Table 7.1: Basic statistic properties of membership volume over the period 2006-2010.

We observe the following six interesting points in the data series:

1. In the transition 2006 → 2007 we observe a drop in membership volume. The absolute drop is 1,986 people, which is a drop of 1.88% (Jan 2007 vs. Dec 2006).

2. In the transition 2007 → 2008 we again observe a drop in membership volume. Compared to irregular fluctuations the drop is still fairly large i.e. 833 people, which is a drop of just 0.81% (Jan 2008 versus Dec 2007).

3. Opposed to the previous year transitions, the transition 2008 → 2009 shows an increase of the membership volume. We observe an increase of 1,916 people, which is an increase of 1.87%. (January 2009 versus December 2008)
This phenomenon has been discussed with company X. The rise in insured membership volume is caused by the acquisition of another healthcare insurance company Y.

4. From January 2008 to February 2008 the membership volume seems to reduce with a relative large amount compared to other irregular fluctuations. The drop towards February 2009 concerns 0.41% of the membership volume of January 2009.

5. The transition of 2009 → 2010 is relatively equal to the drop of 2007 → 2008. We observe a drop of 805 persons which is a drop of 0.78% (January 2010 versus December 2009).

6. The last interesting point in the data is a peek in July 2010 in the membership volume. Compared to June 2010 we identify an increase of 982 persons, which is an increase of 0.95%. The increase is followed by an immediate drop of 887 people which is a percentage of 0.85%.

7.1.2 In- and Outflow quantification

As we have seen the membership volume fluctuates over time, we will now present the corresponding in- and outflow figures. A graphical representation is depicted in figure 7.2 which depicts quantities relative to the membership-set volume at the given point in time (i.e. the inflow at June 2006 is relative to the total membership-volume at June 2006).

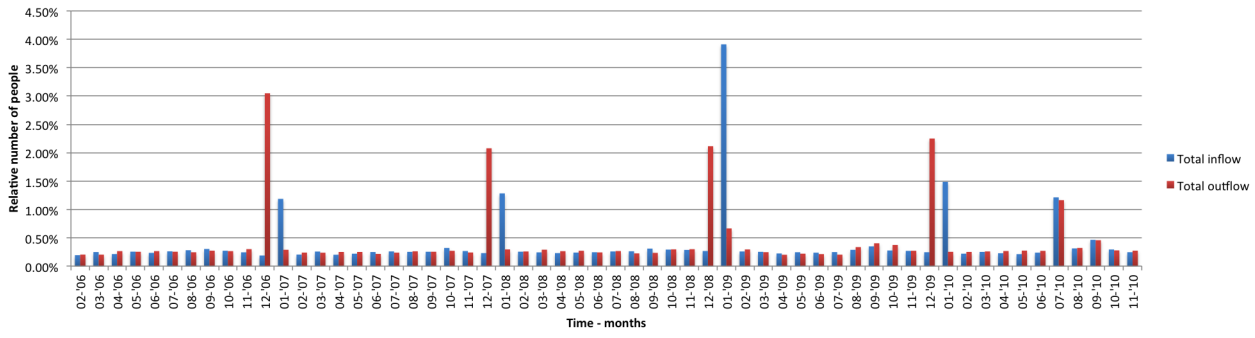


Figure 7.2: In and outflow quantification, relative to the total membership volume in the given month.

The yearly in- and outflow peaks explain the shifts in membership volume at the year turnings. We also identify the outflow being "higher" than normal in January 2009, which explains the additional decline in February 2009. We also observe both the in- and outflow to be extremely high in July 2010. This explains the peak in the corresponding volume as the outflow of July will be propagated to the membership volume in August 2010.
Overall we observe that irregular in- and outflow does not influence the membership volume in a

significant manner.

In table 7.2, the mean and standard deviation of the relative indirect in and outflow are presented. We omitted the yearly in- and outflow and the extraordinary in- and outflow of July 2010. We can verify that over the years, the indirect in- and outflow has rather been constant for the total membership.

Type	*Inflow*	*Outflow*
Mean	0.002572 (0.2572%)	0.002654 (0.2654%)
Standard deviation	0.0004245 (0.04245%)	0.000468 (0.0468%)

Table 7.2: Basic statistic properties of relative indirect in/outflow volumes over the period 2006-2010.

7.1.3 Gender distribution

Now we have looked at membership volume as a whole, it makes sense to look at the impact of in- and outflow on the gender-distribution. The membership volumes of both women and men is depicted in figure 7.3.

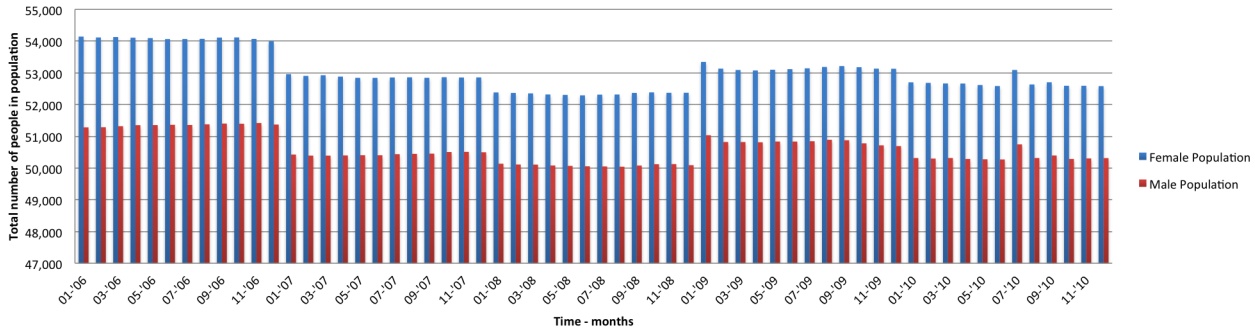


Figure 7.3: Total membership volume development visualized using the full time window, men and women distinct.

We observe that both the male and female volume develop almost equally. The male and female membership are roughly equal and we observe the division to stay rather constant. If we compare the number of female and male persons each month, it turns out to be roughly the same division throughout the given four years as is presented in table 7.3.

Type	*Male share*	*Female share*
Mean	0.488346333	0.511653667
Standard deviation	0.000755843	0.000755843

Table 7.3: Male and female share average and associated standard deviation

7.1.4 Age based healthcare insurance market activity

Let us consider whether the division as proposed by BS Health consultancy also holds for the data provided. It is important to note that we are actually looking to see similar behavioural properties

in the data.

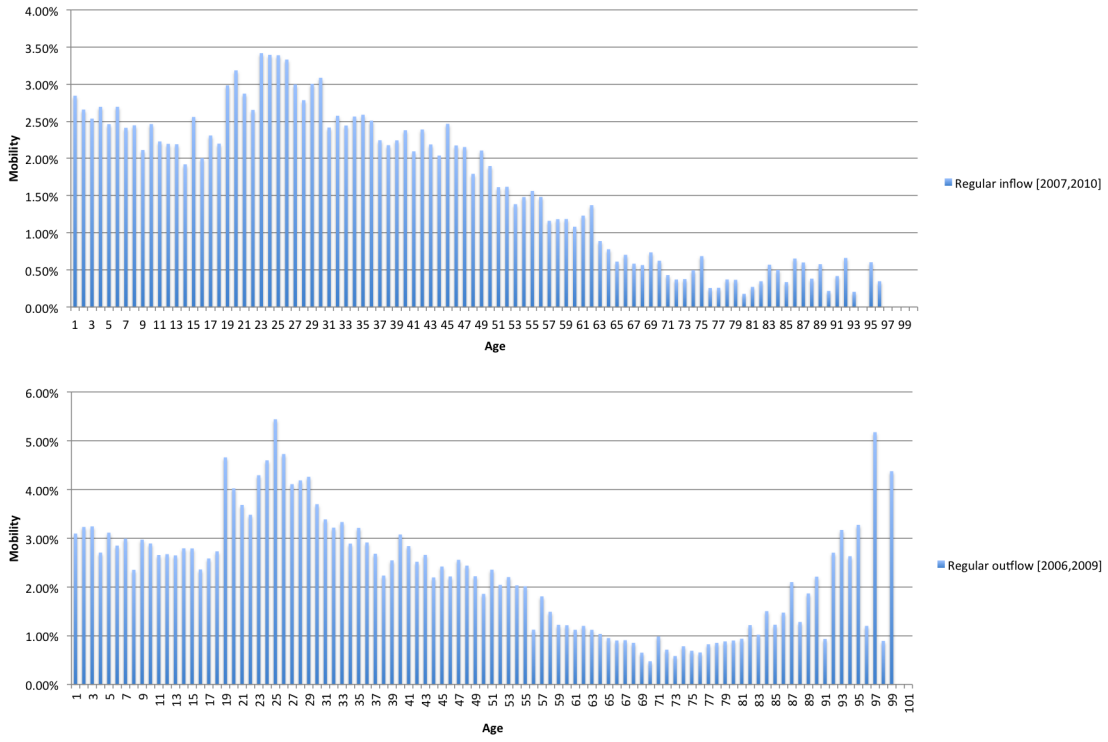


Figure 7.4: Average regular inflow [2007,2010] and regular outflow [2006,2009] of the healthcare data.

We have presented two graphical representations of the regular in- and outflow in figure 7.4. There are however some important aspects of these visualisations which should be taken into account:

- The first graph represents the average regular inflow mobility. That is, the averages of the data points January 2007, January 2008, January 2009 and January 2010. Note that for the inflow, the 0-year old are omitted as these concern birth-rates. Also note that the data is based upon all membership-entrances in January. Thus, depending on the administration of company X there might be some irregular inflow part of the data as well.
- The second graph represents the average regular outflow mobility. That is, the averages of the data points December 2006, December 2007, December 2008 and December 2009. Note that we do not possess the knowledge of reason for leaving. Thus we can not distinguish between outflow caused by switching or caused by death.

When taking a look at the graphs in figure 7.4 we notice a structure which is somewhat similar to the proposed mobility by BS Health consultancy. We notice however that the share in mobility is somewhat lower though this could be the case because the data is possibly from an earlier time frame (this seems to be the case as the BS Healthcare Consultancy research is also conducted in 2012).

For the outflow graph, we see the shares rising as from about 75 years and older. As indicated, we could not filter out outflow caused by death. It is very likely that the high amount of outflow in the older regions is caused by decease cases.

7.1.5 Assessing the reconstruct-ability of pathways

As indicated the focus of the research is not on pathway reconstruct-ability. We do however provide a brief overview of the current data to assess whether the assumption that pathways are constructable actually holds given the data. We will present our assessment in an informal fashion.

- The data does not contain any referral information. Whether this information is partly available within a healthcare insurance company database is not specifically known. The absence of any referral information might be a bottleneck in the quality of potential pathways constructed using the given data.
- 312,556 (100%) out of the total of 312,556 declaration data-rules consist of a *patient identifier*.
- 312,556 (100%) out of the total of 312,556 declaration data-rules consist of a *treatment date*.
- 312,556 (100%) out of the total of 312,556 declaration data-rules consist of a *declaration date*.
- 48,720 (15.6%) out of the total of 312,556 declaration data-rule are *missing an identification parameter* of the corresponding healthcare provider.
- 312,556 (100%) out of the total of 312,556 declaration data-rules consist of a *treatment category*.
- 304,720 (97.5%) out of the total of 312,556 declaration rules are *missing a treatment description*.
- 200,594 (64.2%) out of the total of 312,556 declaration rules are *missing a treatment category*.

Given the fact that each entry has a 100% score on both treatment and declaration date we should technically be able to construct sequences of institute visits. The real problem is however in showing that visits within a sequence are actually related. The lack of knowledge of any form of referral does however pose the problem that we have no guarantee that the visits within the sequences found are actually related. The 100% availability of treatment categories is sadly not particularly helpful as several types of declarations belong to the same category (i.e. as an example category 9 has both very unrelated dentist and hospital declarations). This is probably due to the fact that there are only 13 categories defined. The vast amount of missing values with respect to treatment descriptions and categories are not helpful either.

It remains questionable whether the data concerning declaration rules is representative for the actual data that is available for a healthcare insurance company. Given the dataset reconstruction of institutional pathways would be a very error prone task.

7.1.6 Data analysis in conclusion

We have briefly summarized the general lessons learned throughout the data analysis phase with respect to the problem at hand:

- The data is rather dated with respect to some of the assumptions made in model definition. Because of this fact we can not measure the impact of the increased switching behaviour (i.e. in 2011, 2012) with respect to membership volume.
- The volume seems to remain roughly constant throughout a year. This might lead to a potential simplified version of the proposed membership model as we would be able to neglect irregular mutation.

- The gender distribution seems to remain roughly equal throughout the course of the data. Even the regular switching points seem not to influence the distribution. It seems that activity on the healthcare insurance switching market does not depend on gender.
- The data lacks information on the actual reason of a person leaving the data set (i.e. decease cases versus actual switching). It also lacks the reason of entering, birth is however a more easily inferable element. We therefore have omitted age distribution development (as we actually did look in to this) as we can not pinpoint the different causes of the changing distributions in age, which might lead to false conclusions. We do note that in general the share of "younger" people increases throughout the course of a year whereas the share of "elderly" decreases.
- The age-dependent switching behaviour as proposed within literature seems to be present in the data as well.
- The declaration data seems to lend itself for reconstruction of sequences of treatments. It does seem however to be missing accurate information to determine the interrelatedness of the elements within a sequence constructed.

7.2 Case evaluation

Within this section we have documented the results of simulation of the proof of concept cases. For each of the cases we have performed Normal-distribution fitting, all corresponding visualisations can be found in appendix F. For some cases, the distributions are of equal quality in which we will only show one figurative visualization or no visualisation at all. In cases where the quality of the fits seems to vary we will present more examples with corresponding motivation.

For each case we have provided expected values ($E(\theta)$) the actual computations of these values are omitted. Often these computations concern simple trend extrapolation though in case VI this is a more complex calculation.

On average the simulation averages show good approximate behaviour with respect to the expected values. Because they are a result of a probabilistic model there will be some error. Generally though fluctuation with respect to this error is rather small, which indicates that the system actually follows the predicted *behaviour*. Whenever we present error measures these are always of the form $\varepsilon_{|E(\theta)-\bar{x}_\theta|}$. Thus if $E(\theta) = 1.0$ and $\bar{x}_\theta = 1.5$, then $\varepsilon = 0.5$ and if $E(\theta) = 1.0$ and $\bar{x}_\theta = 0.5$, then $\varepsilon = 0.5$.

We have not assessed any measures with respect to prediction errors made by the system. We just identify the absolute error values and are merely interested in the behaviour of the system and the nature of the results. The prediction errors do not seem to be extremely off with respect to the expected values.

Due to the large amount of variables predicted we have randomly tested some of the proposed normal distributions using a χ^2-test by means of the `chi2gof` function of `MATLAB`. All proposed distribution averages and standard deviations passed these χ^2-tests. As we have not tested all data points we have decided not to report these facts within case result descriptions.

7.2.1 Case I

The results of the simulation are depicted in table 7.4. The simulation has respected the "regular"

Year:	2008	2009
Month:	$1 \rightarrow 12$	$1 \rightarrow 12$
Statistic:		
$E(\lvert M_z \rvert)$	92	88.32
$\bar{x}_{\lvert M_z \rvert}$	92.54	88.14
$s_{\lvert M_z \rvert}$	8.35247	8.32751
ε	0.54	0.18
$E(\lvert \neg M_z^R \rvert)$	158	161.68
$\bar{x}_{\neg M_z^R}$	158.2	162.6
$s_{\neg M_z^R}$	8.41524	8.5117
ε	0.2	0.92
$E(\lvert \neg M_z^I \rvert)$	100	100
$\bar{x}_{\neg M_z^I}$	99.26	99.26
$s_{\neg M_z^I}$	7.96884	7.96884
ε	0.74	0.74

Table 7.4: Results of 2-year simulation of case I

mutation property. i.e. the membership numbers did not change throughout a projected year. Thus for January, February,..., December 2009, $\bar{x}_{\lvert M_z \rvert}$ equals 92.54.

The predicted values for each data point show a good fit with respect to a normal distribution. As an example we have visualised the normal distribution for $\bar{x}_{\neg M_z^R}$ of both 2008 and 2009 combined in figure 7.5. The additional distribution fits are presented in appendix F.

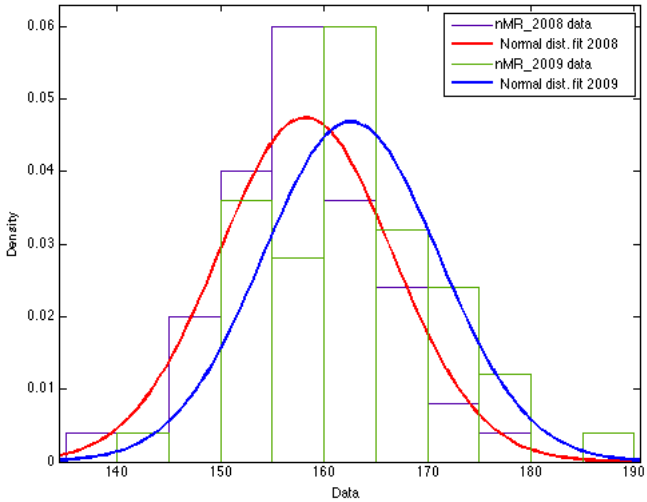


Figure 7.5: Normal distribution fit to $\bar{x}_{\neg M_z^R}$ for both 2008 and 2009; Case I

The results are even very close to the actual results in the generated data. This should come as no surprise. As we have actually defined $P(X_{t+1} = \neg M_z^R | X_t = M_z) = \frac{4}{100}$ (for t **mod** $12 = 0$),

we expect the value of $\neg M_z^R$ being $92 - (92 * \frac{4}{100}) = 88.32$.

7.2.2 Case II

Case II has returned more differing data-points compared to the first case as we have introduced irregular mutation of the membership set in this case. The average results and standard deviations are shown in tables 7.5, 7.6 and 7.7[1].

As we have introduced the notion of "irregular" switching behaviour, we expect every predicted average value for both $|M_z|$ and $|M_z^I|$ to have slightly different values.
We expect $|M_z|$ to increase to 103.32 in the first year of simulation after which we will expect it to decline to 99.48 again on January 2009.

As we can identify in the output, the simulation initially predicts too many people to be a member of M_z (exactly one person). It predicts 1.7 people too less in $\neg M_z^I$ and as a consequence it predicted 0.7 person more than expected in $\neg M_z^R$, not shown in table.

We additionally identify that the simulation shows behaviour as we expect. The prediction error fluctuates though the fluctuation stays within some acceptable boundaries:

$$0.70 \leq \varepsilon_{E(|M_z|)-\bar{x}_{|M_z|}} \leq 1.12$$

$$1.37 \leq \varepsilon_{E(|\neg M_z^I|)-\bar{x}_{|\neg M_z^I|}} \leq 1.82$$

$$0.67 \leq \varepsilon_{E(|\neg M_z^I|)-\bar{x}_{|\neg M_z^I|}} \leq 0.7$$

The simulation of case II shows us that the number of replications might need to be increased in order to get more accurate results. It does however also show that the simulation results in the same behaviour as expected.

Year:	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008
Month:	1	2	3	4	5	6	7	8	9	10	11	12
Statistic:												
$\|M_z\|$	100	101	101	101	102	102	102	103	103	103	104	104
$E(\|M_z\|)$	100	100.31	100.61	100.92	101.22	101.52	101.82	102.13	102.42	102.72	103.02	103.32
$\bar{x}_{\|M_z\|}$	101	101.3	101.66	102.04	102.26	102.54	102.76	102.98	103.34	103.64	103.82	104.1
$s_{\|M_z\|}$	8.26	8.24	8.32	8.49	8.54	8.50	8.46	8.34	8.45	8.50	8.56	8.46
ε	1.00	0.99	1.05	1.12	1.04	1.02	0.94	0.85	0.92	0.92	-0.80	-0.78
$\|\neg M_z^I\|$	92	91	91	91	90	90	90	89	89	89	88	88
$E(\|\neg M_z^I\|)$	92	91.69	91.39	91.08	90.78	90.48	90.18	89.87	89.58	89.28	88.98	88.68
$\bar{x}_{\|\neg M_z^I\|}$	90.3	90	89.64	89.26	89.04	88.76	88.54	88.32	87.96	87.66	87.48	87.2
$s_{\|\neg M_z^I\|}$	7.58	7.58	7.67	7.69	7.77	7.63	7.54	7.53	7.65	7.67	7.69	7.67
ε	1.70	1.69	1.75	1.82	1.74	1.72	1.64	1.55	1.62	1.62	1.50	1.48

Table 7.5: Results of 2-year simulation for M_z,$|\neg M_z^I|$ in 2008; Case II

In terms of Normal-distribution fitting in case II we again observe acceptable results. An interesting normal distribution fit is a fit fitting $\neg M_z^I$ at January, June and December of 2009, depicted in figure 7.6. It is interesting to note the decrease in average volume and the decrease in terms of standard deviation.

[1]Note that there is a minor differences between standard deviations calculated in `python` versus `MATLAB`. Both languages have been used in result analysis.

Year:	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009
Month:	1	2	3	4	5	6	7	8	9	10	11	12
Statistic:												
$\|M_z\|$	100	101	101	101	102	102	102	103	103	103	104	104
$E(\|M_z\|)$	99.48	99.78	100.07	100.36	100.65	100.94	101.23	101.52	101.81	102.10	102.38	102.67
$\bar{x}_{\|M_z\|}$	100.26	100.48	100.94	101.2	101.56	101.8	102.08	102.4	102.7	102.9	103.3	103.56
$s_{\|M_z\|}$	7.88	7.91	8.01	7.96	7.94	8.07	8.10	8.03	8.07	8.13	8.21	8.16
$\varepsilon_{E(\|M_z\|)-\bar{x}_{\|M_z\|}}$	-0.78	-0.70	-0.87	-0.84	-0.91	-0.86	-0.85	-0.88	-0.89	-0.80	-0.92	-0.89
$\|\neg M_z^I\|$	88	87	87	87	86	86	86	85	85	85	84	84
$E(\|\neg M_z^I\|)$	88.39	88.09	87.80	87.51	87.21	86.92	86.63	86.34	86.06	85.77	85.48	85.20
$\bar{x}_{\|\neg M_z^I\|}$	86.94	86.72	86.26	86	85.64	85.4	85.12	84.8	84.5	84.3	83.9	83.64
$s_{\|\neg M_z^I\|}$	7.67	7.71	7.69	7.56	7.54	7.54	7.61	7.61	7.55	7.57	7.50	7.49
ε	1.45	1.37	1.54	1.51	1.57	1.527	1.51	1.54	1.56	1.47	1.58	1.56

Table 7.6: Results of 2-year simulation for M_z,$|\neg M_z^I|$ in 2009; Case II

Year:	2008	2009
Month:	1→12	1→12
Statistic:		
$\|\neg M_z^R\|$	158	162
$E(\|\neg M_z^R\|)$	158	162.13
$\bar{x}_{\|\neg M_z^R\|}$	158.7	162.8
$s_{\|\neg M_z^R\|}$	8.61	8.13
ε	-0.7	-0.67

Table 7.7: Results of 2-year simulation for $|\neg M_z^R|$; case II

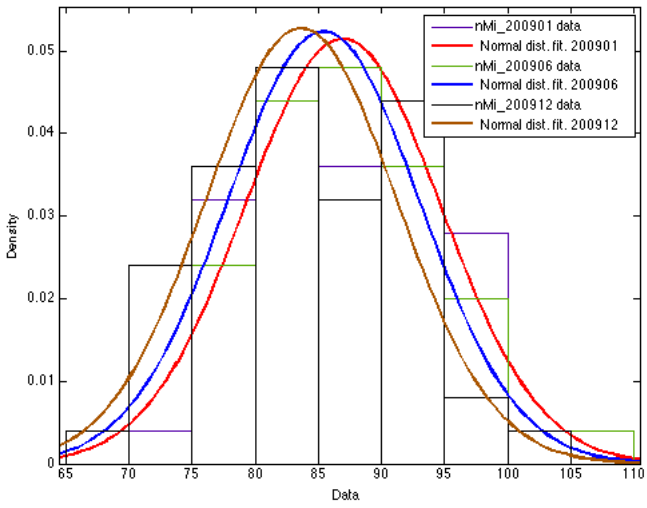


Figure 7.6: Normal distribution fit to $\bar{x}_{\neg M_z^I}$ in 2009; Case II

7.2.3 Case III

The focus of our analysis within case III is with respect to the system's behaviour as we have shown in case I and II that the individual Markov chains simulate according to expectation. As such we do not present ε-measures here.

Only members of age-groups A_2 and A_3 are active on the healthcare insurance switching market. Thus A_1 and any membership group should be constant throughout simulation, which is the case as can be seen in table 7.8.

A_3 on the other hand does show some mutational activity, on a regular basis. It should show a decline with respect to A_3, M_z wheras the decline in members should be added to $A_3, \neg M_z^R$. As the contents of A_3 and any membership set should only change at *January* 2009, we have also depicted the results in table 7.8.

As A_2 shows irregular behaviour, any combination with either M_z and $\neg M_z^I$ should be different throughout the course of simulation. As we can see in tables 7.9 and 7.10, the simulation respects the expected behaviour and shows little prediction errors with respect to the expected values.

Year:	*2008*	*2009*
Months:	*1→12*	*1→12*
$E(\lvert A_1, M_z\rvert)$	25	25
$\bar{x}_{\lvert A_1, M_z\rvert}$	24.46	24.46
$s_{\lvert A_1, M_z\rvert}$	4.47	4.47
$E(\lvert A_1, \neg M_z^I\rvert)$	23	23
$\bar{x}_{\lvert A_1, \neg M_z^I\rvert}$	23.52	23.52
$s_{\lvert A_1, \neg M_z^I\rvert}$	4.27	4.27
$E(\lvert A_1, \neg M_z^R\rvert)$	39.5	39.5
$\bar{x}_{\lvert A_1, \neg M_z^R\rvert}$	38.84	38.84
$s_{\lvert A_1, \neg M_z^R\rvert}$	5.56	5.56
$E(\lvert A_3, M_z\rvert)$	25	21
$\bar{x}_{\lvert A_3, M_z\rvert}$	24.94	20.74
$s_{\lvert A_3, M_z\rvert}$	4.34	4.18
$E(\lvert A_3, \neg M_z^I\rvert)$	23	23
$\bar{x}_{\lvert A_3, \neg M_z^I\rvert}$	23.06	23.06
$s_{\lvert A_3, \neg M_z^I\rvert}$	5.05	5.05
$E(\lvert A_1, \neg M_z^R\rvert)$	39.5	43.5
$\bar{x}_{\lvert A_3, \neg M_z^R\rvert}$	39.88	44.08
$s_{\lvert A_3, \neg M_z^R\rvert}$	5.35	5.48

Table 7.8: Results of A_1 and A_3 and any membership-group; Case III

We identify that case III respects the expected behaviour. We additionally note that the monitors placed on combinations of membership and age states result in good quality normal distributions as well. As an example we have depicted the combination M_z, A_3 for both 2008 and 2009 in figure 7.7.

7.2.4 Case IV

With respect to estimation errors (though omitted in result table 7.11) and behaviour.

The case differs however with respect to the previous cases if we take a look at normal distribution fitting quality. This specifically occurs in case of illness as one can identify in figure 7.8. The reason

Year:	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008
Month:	1	2	3	4	5	6	7	8	9	10	11	12
Statistic:												
$E(\|A_2, M_z\|)$	50.00	50.31	50.61	50.91	51.21	51.51	51.81	52.10	52.40	52.69	52.98	53.26
$\bar{x}_{\|A_2,M_z\|}$	50.48	50.82	51.02	51.44	51.76	52.08	52.36	52.62	52.94	53.3	53.58	53.82
$s_{E\|A_2,M_z\|}$	5.87	5.79	5.72	5.65	5.42	5.64	5.73	5.81	5.68	5.73	5.70	5.71
$E(\|A_2, \neg M_z^I\|)$	46.00	45.69	45.39	45.09	44.79	44.49	44.19	43.90	43.60	43.31	43.02	42.74
$\bar{x}_{\|A_2,\neg M_z^I\|}$	45.68	45.34	45.14	44.72	44.4	44.08	43.8	43.54	43.22	42.86	42.58	42.34
$s_{\|A_2,\neg M_z^I\|}$	5.91	5.87	5.84	5.77	5.73	5.73	5.58	5.54	5.33	5.44	5.47	5.54
$E(\|A_2, \neg M_z^R\|)$	79	79	79	79	79	79	79	79	79	79	79	79
$\bar{x}_{\|A_2,\neg M_z^R\|}$	79.14	79.14	79.14	79.14	79.14	79.14	79.14	79.14	79.14	79.14	79.14	79.14
$s_{\|A_2,\neg M_z^R\|}$	7.41	7.41	7.41	7.41	7.41	7.41	7.41	7.41	7.41	7.41	7.41	7.41

Table 7.9: Result of A_2 and any membership group in 2008; Case III

Year:	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009
Month:	1	2	3	4	5	6	7	8	9	10	11	12
Statistic:												
$E(\|A_2, M_z\|)$	53.55	53.83	54.11	54.39	54.67	54.94	55.22	55.49	55.76	56.03	56.29	56.56
$\bar{x}_{\|A_2,M_z\|}$	53.98	54.36	54.7	54.96	55.3	55.58	55.92	56.24	56.52	56.76	57.04	57.26
$s_{E\|A_2,M_z\|}$	5.74	5.80	5.99	6.07	5.92	5.83	5.71	5.76	5.85	5.91	5.95	5.96
$E(\|A_2, \neg M_z^I\|)$	42.45	42.17	41.89	41.61	41.33	41.06	40.78	40.51	40.24	39.97	39.71	39.44
$\bar{x}_{\|A_2,\neg M_z^I\|}$	42.18	41.8	41.46	41.2	40.86	40.58	40.24	39.92	39.64	39.4	39.12	38.9
$s_{\|A_2,\neg M_z^I\|}$	5.57	5.67	5.76	5.92	5.95	5.90	5.87	5.83	6.05	6.00	6.04	6.16
$E(\|A_2, \neg M_z^R\|)$	79	79	79	79	79	79	79	79	79	79	79	79
$\bar{x}_{\|A_2,\neg M_z^R\|}$	79.14	79.14	79.14	79.14	79.14	79.14	79.14	79.14	79.14	79.14	79.14	79.14
$s_{\|A_2,\neg M_z^R\|}$	7.41	7.41	7.41	7.41	7.41	7.41	7.41	7.41	7.41	7.41	7.41	7.41

Table 7.10: Result of A_2 and any membership group in 2009; Case III

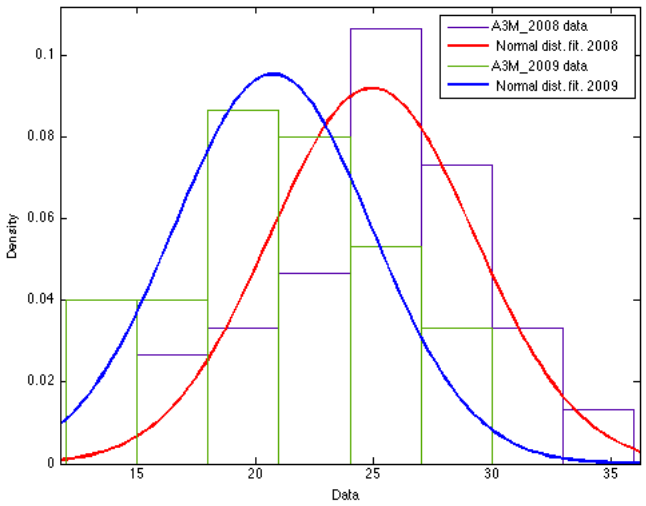


Figure 7.7: Normal distribution fit to $\bar{x}_{|M_z,A_3|}$for both case 2008 and 2009; Case III

for this is the fact that given $\bar{x}$ and s, we would expect a Normal distribution that for a sufficient share consists of values smaller than 0. Logically 0 forms a bare minimum with respect to the number of ill people. Note that the Normal distributions for $M_z, A_1, \neg D_d$ show better results.

Year:	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008
Month:	1	2	3	4	5	6	7	8	9	10	11	12
Statistic:												
$E(\|M_z, A_1, \neg D_d\|)$	23.00	22.93	22.86	22.79	22.72	22.65	22.59	22.52	22.45	22.39	22.32	22.26
$\bar{x}_{\|M_z,A_1,\neg D_d\|}$	23.72	23.7	23.64	23.52	23.44	23.36	23.34	23.28	23.28	23.16	23.14	23.08
$s_{\|M_z,A_1,\neg D_d\|}$	4.33	4.28	4.26	4.26	4.32	4.27	4.38	4.48	4.48	4.43	4.45	4.49
$E(\|M_z, A_1, D_d\|)$	2.00	2.07	2.14	2.21	2.28	2.35	2.41	2.48	2.55	2.61	2.68	2.74
$\bar{x}_{\|M_z,A_1,D_d\|}$	1.74	1.76	1.82	1.94	2.02	2.1	2.12	2.18	2.18	2.3	2.32	2.38
$s_{\|M_z,A_1,D_d\|}$	1.34	1.36	1.42	1.50	1.56	1.59	1.52	1.55	1.55	1.55	1.53	1.60
Year:	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009
Month:	1	2	3	4	5	6	7	8	9	10	11	12
Statistic:												
$E(\|M_z, A_1, \neg D_d\|)$	22.19	22.13	22.06	22.00	21.93	21.87	21.81	21.75	21.69	21.62	21.56	21.50
$\bar{x}_{M_z,A_1,\neg D_d}$	22.96	22.86	22.86	22.78	22.72	22.64	22.62	22.54	22.48	22.4	22.34	22.32
$s_{M_z,A_1,\neg D_d}$	4.51	4.61	4.55	4.59	4.48	4.38	4.39	4.41	4.43	4.41	4.39	4.39
$E(\|M_z, A_1, D_d\|)$	2.81	2.87	2.94	3.00	3.07	3.13	3.19	3.25	3.31	3.38	3.44	3.50
$\bar{x}_{M_z,A_1,D_d}$	2.5	2.6	2.6	2.68	2.74	2.82	2.84	2.92	2.98	3.06	3.12	3.14
s_{M_z,A_1,D_d}	1.63	1.60	1.56	1.59	1.59	1.62	1.65	1.71	1.62	1.75	1.73	1.72

Table 7.11: Case IV - Results

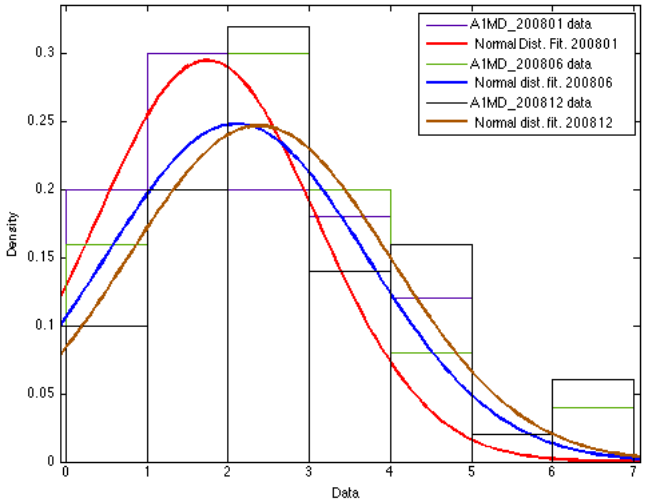


Figure 7.8: Normal distribution fit to $\bar{x}_{|M_z,A_1,D_d|}$ for January, June and December of 2008

7.2.5 Case V

Case V does not differ much with respect to case IV as can be seen in figure 7.12. Practically the only difference is the fact that the number of people being ill are either traversing pathway A or pathway B. Though the predicted behaviour and values are again very acceptable the normal distribution fits are all of bad quality. This is again due to the expected little amount of people in either pathway. The corresponding distribution fits can be found in appendix F.

7.2.6 Case VI

Interesting in case VI is the behaviour of both the expected and predicted values. Like in all other cases the predicted and expected values are very close and roughly show similar behaviour. We

Year:	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008
Month:	1	2	3	4	5	6	7	8	9	10	11	12
Statistic:												
$E(\lvert M_z, A_1, D_d, P_A \rvert)$	0.00	1.00	1.03	1.07	1.10	1.14	1.17	1.21	1.24	1.27	1.31	1.34
$\bar{x}_{\lvert M_z, A_1, D_d, P_A \rvert}$	0	0.92	0.94	1.04	1.1	1.1	1.22	1.24	1.28	1.3	1.34	1.4
$s_{\lvert M_z, A_1, D_d, P_A \rvert}$	0.00	0.96	0.95	0.96	0.92	0.92	0.86	0.86	0.87	0.88	0.95	0.98
$E(\lvert M_z, A_1, D_d, P_B \rvert)$	0.00	1.00	1.03	1.07	1.10	1.14	1.17	1.21	1.24	1.27	1.31	1.34
$\bar{x}_{\lvert M_z, A_1, D_d, P_B \rvert}$	0	1.06	1.08	1.14	1.18	1.24	1.24	1.24	1.3	1.38	1.4	1.42
$s_{\lvert M_z, A_1, D_d, P_B \rvert}$	0.00	0.90	0.89	1.00	1.03	1.05	1.01	0.99	1.00	1.02	1.02	1.00
Year:	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009
Month:	1	2	3	4	5	6	7	8	9	10	11	12
Statistic:												
$E(\lvert M_z, A_1, D_d, P_A \rvert)$	1.37	1.40	1.44	1.47	1.50	1.53	1.56	1.60	1.63	1.66	1.69	1.72
$\bar{x}_{\lvert M_z, A_1, D_d, P_A \rvert}$	1.5	1.56	1.6	1.6	1.62	1.64	1.64	1.7	1.76	1.76	1.8	1.82
$s_{\lvert M_z, A_1, D_d, P_A \rvert}$	1.06	1.06	1.08	1.08	1.09	1.07	1.07	1.08	1.11	1.11	1.10	1.11
$E(\lvert M_z, A_1, D_d, P_B \rvert)$	1.37	1.40	1.44	1.47	1.50	1.53	1.56	1.60	1.63	1.66	1.69	1.72
$\bar{x}_{\lvert M_z, A_1, D_d, P_B \rvert}$	1.42	1.52	1.56	1.58	1.58	1.58	1.62	1.68	1.72	1.78	1.82	1.86
$s_{\lvert M_z, A_1, D_d, P_B \rvert}$	1.00	0.96	1.00	1.06	1.06	1.06	1.06	1.09	1.13	1.17	1.16	1.17

Table 7.12: Case V - Results

expect a steady state solution that is not predicted by the simulation. We do note the predicted values to be very close to a steady state distribution.
The results are presented in table 7.13. A visualization of the results of case VI can be found in figure 7.9.

Year:	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008	2008
Month:	1	2	3	4	5	6	7	8	9	10	11	12
Statistic:												
$E(\lvert M_z, A_1, D_d, P_A \rvert)$	0.00	1.00	6.55	8.12	7.93	7.31	7.85	8.50	8.76	8.63	8.57	8.65
$\bar{x}_{\lvert M_z, A_1, D_d, P_A \rvert}$	0	0.96	6.66	8.36	8.3	7.66	8.02	9.04	9.22	9.18	9.06	8.7
$s_{\lvert M_z, A_1, D_d, P_A \rvert}$	0.00	0.96	2.46	3.06	3.12	2.49	2.63	2.68	2.93	3.12	3.22	3.01
$E(\lvert M_z, A_1, D_d, P_B \rvert)$	0.00	1.00	5.95	4.07	2.25	1.42	2.29	2.68	2.49	2.13	2.09	2.21
$\bar{x}_{\lvert M_z, A_1, D_d, P_B \rvert}$	0	1.12	6.16	4.14	2.46	1.22	2.38	2.66	2.22	2.2	2.14	2.62
$s_{\lvert M_z, A_1, D_d, P_B \rvert}$	0.00	0.99	2.20	1.71	1.73	1.01	1.47	1.57	1.51	1.54	1.46	1.60
Year:	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009	2009
Month:	1	2	3	4	5	6	7	8	9	10	11	12
Statistic:												
$E(\lvert M_z, A_1, D_d, P_A \rvert)$	8.75	8.77	8.75	8.74	8.76	8.77	8.77	8.77	8.77	8.77	8.77	8.77
$\bar{x}_{\lvert M_z, A_1, D_d, P_A \rvert}$	8.72	9.02	8.78	9.02	9.28	9.68	9.64	9.4	9.54	9.7	9.26	9.32
$s_{\lvert M_z, A_1, D_d, P_A \rvert}$	3.19	2.98	2.91	2.69	2.88	2.87	2.76	2.81	2.87	2.93	3.02	3.55
$E(\lvert M_z, A_1, D_d, P_B \rvert)$	2.27	2.23	2.18	2.18	2.20	2.21	2.20	2.19	2.19	2.19	2.19	2.19
$\bar{x}_{\lvert M_z, A_1, D_d, P_B \rvert}$	2.12	2.16	2.24	2.36	2.18	2.36	2.5	2.14	2.1	2.44	2.8	2.34
$s_{\lvert M_z, A_1, D_d, P_B \rvert}$	1.64	1.65	1.32	1.40	1.85	1.53	1.65	1.23	1.24	1.50	1.98	1.57

Table 7.13: Case VI - Results

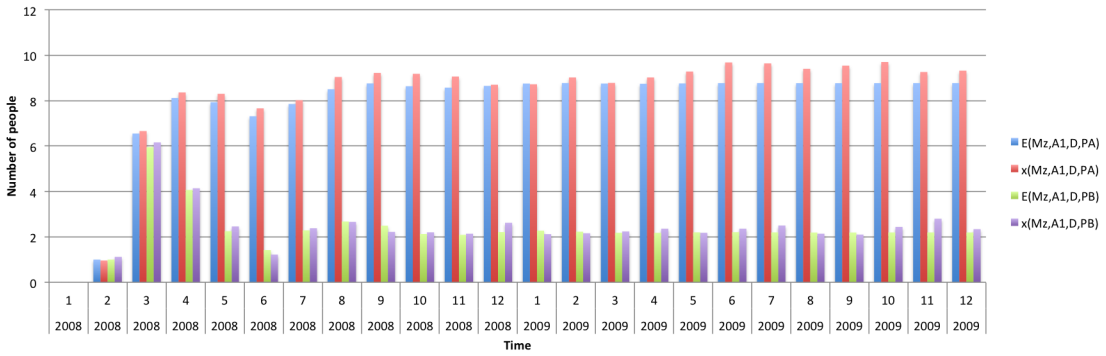


Figure 7.9: Visualization of $E(|M_z, A_1, D_d, P_A|)$, $E(|M_z, A_1, D_d, P_B|)$, $\bar{x}_{|M_z,A_1,D_d,P_A|}$ and $\bar{x}_{|M_z,A_1,D_d,P_B|}$ in case VI.

7.2.7 Case evaluation in conclusion

The proof of concept cases have brought the following insights with respect to collaborative Markov chain simulation:

- Prediction accuracy seems to be rather good with respect to the expected values. We expect errors to go down when the number of replications will be increased.
- According to the central limit theorem (i.e. 50 replications of simulation per case) the simulation results should follow a normal distribution, which is the case.
- In case of a low expected value of a certain state combination, combined with a minimum value normal distribution fitting quality is rather low.

7.3 Managerial implications and recommendations

7.3.1 Implementing the model proposed

Implementation strategy

Using the lessons learned during data analysis and proof of concept case execution we have constructed an implementation strategy that should support healthcare insurance companies in implementing the proposed system. In general the proposed scheme shows similarities with the general methodology used within this research though it is specifically tailored keeping the proposed model in mind. A graphical representation of the proposed implementation strategy is depicted in figure 7.10

1. *Requirement elicitation phase*
   In the requirement elicitation phase one has to determine what the forecasting-requirements are. Questions one might ask within this phase are:
   - What amount of diseases will be simulated? Are we assessing only one disease or are we implementing multiple diseases which potentially influence each other's impact on an individual?
   - What is the typical time-span of prevalence? Is a person typically ill for a couple of days? months? years?

- What is a suitable time step-size given the typical time-span of prevalence?
- What kind of institutional pathway model to use? i.e. pathway-based versus institution based?
- What is a suitable amount of simulation elements?
- What is a suitable time-span in terms of simulation?
- ...

The end goal of this phase is to have an idea of what one wants to predict, what is a suitable time-frame, what type of institutional pathway modelling is associated etcetera.

2. *Model design phase*
In the model design phase, one materializes the requirements set earlier into a concept model. One should design basic models for all elements identified and design a conceptual version of the system of collaborative Markov chains which should be used for simulation.

3. *Parameter identification phase*
In this phase we analyse the concept model designed in the previous phase with respect to the "transition parameters" needed by the model. Within this case we again need to answer several questions. Questions one might ask within this phase are:

   - What parameters do we need to estimate in general?
   - What parameters can we estimating using company data?
   - What parameters have to be estimated using axillary sources?
   - What parameters might be dependent?
   - How to solve dependent parameters? i.e. Use one model parameter to model a certain phenomenon or use combinations of parameters?
   - What are "bottleneck" parameters? i.e. What parameters are complex in terms of estimation, data quality etcetera.
   - ...

4. *Model refinement phase*
Within this phase one might refine the model defined earlier. The refinement should be based on the parameter identification phase. If some parameter for some reason turns out not to be predictable we might refine the model accordingly. Note that modification of the model might lead to new parameters as well. The new parameters should again be identified after which we should potentially refine the model again. The parameter identification and model refinement phase are of an iterative fashion and might be executed multiple time.

5. *Parameter estimation phase*
If the modeller is certain that the model is correct, sound etcetera and all associated parameters can be estimated, the modeller should start estimation. For each parameter, the modeller is able to use a different prediction technique. If within the parameter estimation phase, parameters do turn out to be hard to predict or even unpredictable, the model refinement and parameter identification phase should again be executed.

6. *Model implementation phase*
If the modeller is certain that all parameters within the proposed model are correctly estimated the modeller can start implementing the model. We advise to use a simulation framework which roughly follows the same structure as the one implemented for this specific research.

7. *Simulation phase*
If the model is implemented within the simulation framework of choice, simulation of the system of collaborative chains needs to be performed. Note that in the case of a non cyclic dependency graph one can also compute the steady state distribution in product form.

8. *Evaluation phase*
   The final phase is the evaluation phase in which the simulation output needs to be evaluated. If possible the simulation output should also be assessed in terms of correctness. After the first simulation and evaluation a base-case is constructed. The model is now ready for reuse and can be used to test several changed parameter settings.

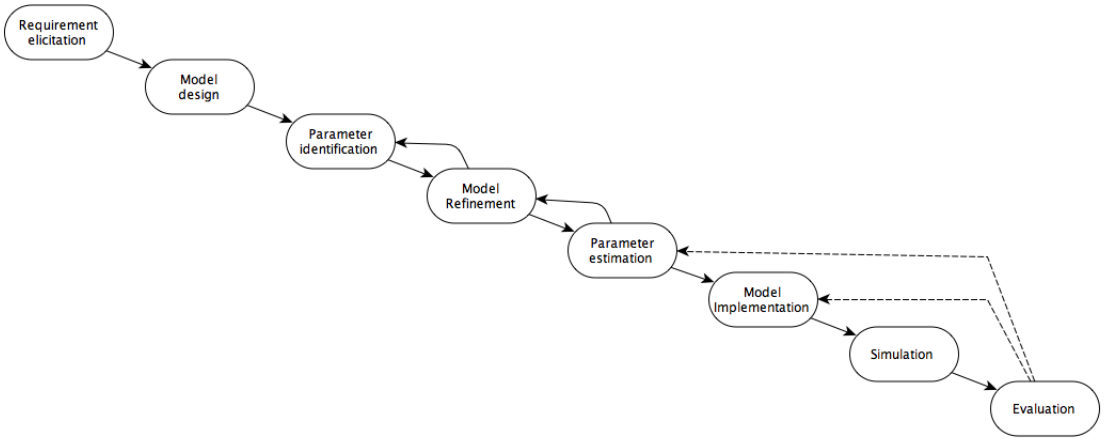


Figure 7.10: Graphical representation of proposed model implementation strategy

Running time

The performance of the simulations are depicted in table 7.14 (The simulation machine specification can be found in appendix G.

Case:	***Average runtime (sec.)***	***Std. on runtime (sec.)***
Case I	283	0.4
Case II	238.52	0.71
Case III	516.42	0.61
Case IV	885	1
Case V	968.34	1.57
Case VI	987	4

Table 7.14: Run-time performance of the proof of concept cases

The nature of the simulation framework implementation and associated running time results does not provide in giving accurate estimations of potential running times for more complex and realistic scenario's. We do hover provide a rough basic analysis and some recommendations with respect to simulation framework implementation.

Basic analysis We identify the performance in terms of running time to be rather bad. We identify the addition of additional chains to the system as a whole to increase running time. If we compare case I and II with case III we identify the running time to be roughly doubled, it is in fact in-between two times the running times of case I and II (case II performs slightly better with respect to case I). In fact the number of chains as well as the total number of has doubled. The running time of case IV is actually higher than expect if we calculate the increase in terms of chains and states. With respect to case V and VI the running time seems to increase less than expected.

Simulation environment We have implemented the simulation environment in `MATLAB`. Though it is a convenient programming language for defining mathematical solutions it is not very suitable compared to the class-based approach as used in the research. If a mathematical programming environment is chosen, such as `MATLAB`, we advise to utilize the programming environment characteristics. In the case of `MATLAB`, it is actually optimized for matrix and vector operations. We therefore advise to utilize this in future implementations. In general it is advisable to implement the simulation framework in a programming environment that is more suitable for computational intensive problems.

Monitor implementation Currently updating of the `simulator`-class monitors is performed *during* execution. During simulation we have noted that this negatively affects the running time. We therefore advise to keep track of each chain's states throughout simulation and post process the associated monitors.

Distributed computing As the simulation of collaborative Markov chains is somewhat a repetitive endeavour it lends itself perfectly for distributed computing. We strongly advise to use distributed computation technology such as `MapReduce` as it positively impacts on the overall running time.

7.3.2 The need for solid Information infrastructures and -provision

Referral administration

As one should have noted, although we assumed that institutional pathways are actually reconstructible given declaration data, the dataset provided for this research tends to show the opposite. What we cannot assess here is the fact whether the query used to generate the dataset was erroneous which results in missing values or whether this data is actually unavailable. To gain insight in this type of data availability an additional assessment concerning healthcare insurance company data should be made.

A data-element that in any case would help in pathway reconstruction is "referral" information. Typically one can not go to a polyclinic (for example the group of urologists) without a general practitioner's referral. If healthcare providers would provide detailed information regarding referral behaviour this would greatly help in institutional pathway reconstruction using declaration data.

Medical history

Within discussions with company X it was indicated that people that are "seriously ill", which often means that several declarations will be made concerning the person, are assumed not to switch in terms of healthcare insurance company. Interestingly though company X also indicated that the medical track-record of a person is not incorporated when a person becomes a member. Thus new members start with a "clean sheet".

Investigating this phenomenon in the public domain yields an NZA report in which the switching-behaviour of chronically disabled [38] is researched. It concludes that it does not differ significantly from "healthy" people. We cannot pinpoint whether the claim made concerning switching behaviour of ill people is correct or not. If it where incorrect it could impact the results of institutional care pathway based forecasts.

If an ill person does switch it might be the case that we identify his/her future treatment trajectory as a valid institutional care pathway for the specific disease at hand. As the eventual goal of

the forecast was to be able to assess an increased throughput of "optimal" institutional pathways given some dimension, we might run into problems here. If we falsely assume a shorter pathway to be valid, caused by the fact that a part of the real institutional care pathway was backed by a different healthcare insurance company, we might underestimate potential costs.

Given the fact that healthcare insurance companies (i.e. healthcare company X) claim that ill people do not switch though they in fact do not collect any medical track record of new patients, they can not justify their claim. Given the potential introduction of erroneous analyses it might be wise to agree on recording past medical declarations/data.

7.4 Discussion

7.4.1 Level of detail of the model proposed

As we have seen healthcare insurance membership dynamics lend itself to be modelled as a system of collaborative Markov chains. The model presented within this research as such concerns the conceptual idea, definitions, analysis and implementation of collaborative Markov chains within the given context.

Let us discuss the level of detail provided by the model proposition by using the example of polynomial functions. Let us consider the general formula of polynomials:

$$f(x) = a_n x^n + a_{n-1} x^{n-1} + ... + a_2 x^2 + a_1 x + a_0$$

A 2^{nd} order polynomial or quadratic function is a specific instantiation of the general formula of polynomials, in which n=2 yielding:

$$f(x) = a_2 x^2 + a_1 x + a_0$$

Still this second order polynomial quadratic function on itself is not able to produce function values. This can only be done if we instantiate a_2, a_1 and a_0. Thus consider:

$$a_2 := a_1 := a_0 := 1$$

yields:

$$f(x) = x^2 + x + 1$$

The terminology on polynomials basically addresses the concept of hierarchy within modelling. The question remains how the models defined within this research hold with respect to the analogy of polynomials as presented just yet.

The basic definition of collaborative Markov chains can roughly be found at the same hierarchical level as the general formula of polynomials. Within the proof of concept cases we have assessed some predictive behaviour of systems that follow this generalized structure.

The final model proposition however is an instantiation of the general idea of collaborative Markov chains. The instantiation has been tested with respect to viability of assumptions in the data analysis part. We have also roughly tested the behaviour of the instantiation during the proof-of-concept cases.

Note that the actual predictive quality of the result generated by a collaborative Markov chain based simulation is strictly depending on the quality of the parameters used as an input. For

example, if we identify some parameter value increase of 5%, though model a decrease of 5%, the model will logically output figures that on average depict an outflow of 5%.

In the light of this perspective the results of this exploratory research do not provide a full fledged prediction, rather a model usable to generate a prediction/forecast equivalent to the first upper hierarchical model levels in the polynomial based analogy. Finding accurate and usable parameters with respect to performing real-data based predictions is left as a challenge for the potential user of the model.

7.4.2 The actual impact of membership dynamics on $M_{(z,t)}$

As we have seen in the evaluation of the "real healthcare data", the impact of membership dynamics with respect to membership volume and structure does not seem to be as large as expected. This might partly be the case because the NZA research actually shows that the switching rates are actually growing in 2011 and 2012, whereas the data covers 2006 to 2010. Whether the age-dependence of switching actually impacts on the membership structure remains to be seen in future analyses of healthcare insurance company data.

7.4.3 Lack of dependency-based initialization within the research

As indicated we did not implement any dependency-based initialization. This basically results in the fact that simulation outcome of some of the proof of concept cases would always result in a certain prediction error with respect to the actual input. Therefore within quantification of the results we have additionally shown *expected values* for certain results as we implicitly where able to incorporate an expected result in the output. An open challenge remains on how to incorporate dependency based initialization.

Chapter 8

Conclusion

8.1 Summary

Within this research we have posed the use of a system of collaborative Markov chains as a financial prediction model for healthcare insurance companies. After evaluation of related research we started with an analysis phase in which we have assessed several topics related to financial forecasting with integration of institutional care pathways. We have provided definitions for the basic membership-structures of a healthcare insurance company, associated incidence and prevalence rates and institutional pathways.

The concepts identified and defined within the analysis phase have been further developed within the design phase. In this phase we have assessed the applicability of Markov chains as a representation for membership dynamics. Consequently we have assessed the applicability of using Markov chains to represent incidence and prevalence and associated institutional care pathway traversal. The conditionality of "associated pathway traversal" within this system of three Markov chains led to the concept of collaborative Markov chains.

The concept of collaborative Markov chains has consequently been introduced. In essence it is a collection of Markov chains of which some of the transition probabilities in chains within the collection are influenced by the state of other chains within the collection.

Research within the healthcare market (which was later been backed in the data analysis phase) showed that age is an influential factor with respect to switching behaviour. In the context of the proposed system this means that probability parameters in the Markov chain depicting membership might differ according to the age of the corresponding person. Age could be incorporated within the system as a data-based parameter. However we have motivated the preference to exploit the general idea of collaborative Markov chains and to incorporate age within a τ-based Markov chain which we defined as being the "age/vitality" chain. Additionally we have provided some equivalence rules between the τ-based age/vitality model and a parametrized vitality-based Markov chain.

In our final design proposition we posed a system of collaborative Markov chains that at least consists of the following chains:

- Membership model; representing membership dynamics
- Age model; representing age/vitality development over time

- Disease model; representing incidence and prevalence
- Pathway traversal model; representing associated institutional care pathway traversal

Within the final design proposition we do not specifically enforce any fixed structure. Additionally we identified that depending on the type of disease(s) assessed the model proposed might even be modified in terms of its structure. We additionally posed the requirement of the following dependencies for any basic model:

1. Membership depends on age.
2. Age depends to some extend on disease.
3. Disease depends to some extend on age.
4. Pathway traversal depends on disease.

The cyclic fashion of the dependency graph led to the assessment of sampling techniques for collaborative Markov chains in general. We have expressed the relation between a random-walk fashioned simulation strategy and the concept of Gibbs sampling.

Within the research we have additionally written a simulation framework to support the proof-of-concept cases. We have provided a basic description of the framework, introduced the concept of monitors and discussed the problem of "propagation lag" within the current simulation framework implementation.

Several properties of a real healthcare dataset have been assessed within the proof of concept phase of the research. The analysis of the data provides a more solid understanding of the actual behaviour of membership groups throughout time. Some of the assumptions made during model definition could be confirmed by means of data analysis (for example the impact of age on switching behaviour). Other assumptions could not always be backed up accordingly. Specifically the actual impact of (irregular) membership-set mutation remains somewhat questionable. Note however that due to both the data being somewhat dated and missing information within the data we could neither acknowledge nor prove some assumptions.

A set of six proof of concept cases was drawn up which found their basis within the final design proposition. All cases show that simulation using a system of collaborative Markov chains results in accurate predictive behaviour. Additionally the results produced by simulation tend to follow a normal distribution which lends itself for possible further statistical analysis of the simulation results.

8.2 Conclusions

Within this section we will conclude in what way we have been able to solve the main problem definition and subsequent research questions as defined within this research. Finally we will relate the model presented to its intended purpose as defined within the motivational section of chapter 1.

8.2.1 Assessing the main problem definition

Let us revisit our main problem definition:
The problem at hand is the need for a financial forecast model which:

- *Incorporates care demand*
- *Allows to incorporate associated institutional care pathway traversal and corresponding costs*
- *Is modular in design such that it allows for multiple case-based forecast computations*

Within this research, we defined a system of collaborative Markov chains that can act as a financial forecasting model. The incorporation of care demand has been accounted for by means of a membership dynamics Markov model and an associated disease model. A part of the care demand component is supported by the addition of the age model within the system.

The system of collaborative Markov chains also consists of a institutional care pathway module which is directly depending on the disease model. Integration of the financial performance of the associated institutional care pathways has however not been studied in depth as the incorporation of associated pathway traversal has been studied in depth.

A system of collaborative Markov chains always needs a set of input parameters. Within the current simulation framework, case-based forecast computations are executed easily by modification of a subset of the input parameters.

8.2.2 Answering the research questions

Within this section we try to answer our initial research questions as presented in the introduction and answer them using the lessons learned throughout execution of the project:

1. *How do we define and forecast care demand from a healthcare insurance company perspective?*
   We have defined care demand as the proportion of members of a healthcare insurance company that is or will get ill. We pose to predict future care demand by implementing a membership model, an age model and a disease model within a system of collaborative Markov chains.
2. *How do we define and incorporate institutional pathways within the care demand prediction model?*
   We have defined institutional pathways as the sequence of healthcare providers that a patient visit during treatment for some disease. We pose to integrate institutional care pathways by adding an additional model into the system of collaborative models as presented earlier by a model representing institutional pathway traversal.
3. *How do we combine financial pathway performance as a price component with the care demand prediction model?*
   We have not specifically assessed the combination of financial pathway performance as a price component with the care demand prediction model. We do note however that combining financial pathway performance is straightforward as the model proposed will output a set of people that are predicted to traverse a certain path. Thus given a certain financial performance for a certain pathway, we can easily calculate the associated financial performance for the predicted group of people traversing the path.

8.2.3 Relating the model to its intended usage

Recall the need for a the model to support a healthcare insurance company in contracting amongst healthcare providers. The model allows its user to compute future care demands and associated pathway traversal. Additionally one should be able to compute the associated costs. Though not

explicitly researched, we could compute these costs by multiplying the predicted traversal with the average costs of an institutional care pathway.

If the healthcare insurance company has performed a simulation given the current situation in terms of financial pathway performance a base-line is constructed. The insurer can now assess what impacts different traversal amounts would have on the predicted associated costs by modifying parameters within the input model.

As an example if a healthcare insurance company has identified that one of three institutional pathways associated with a disease is optimal, the insurer can assess what the impact of an increased throughput of this (type of) path will be. This knowledge is a valuable asset within contracting. The healthcare insurance company can confront healthcare providers that are not in an optimal path that a group of peers is able to perform better. Consequently the insurer could provide contracts similar to the ones provided within an optimal path.

Note that there are several other strategies here, both in terms of contracting as in general with respect to increasing throughput. If a certain optimal institutional care pathway differs from less performing peers on a pathway level (that is different typed providers on the path), the insurer might try to motivate clients to traverse such path. In such case the insurer might however interfere with the role of the medical specialist. These type of strategical constructs are not subject of study here.

Thus the model presented can act as a tool to produce base-line simulations and consequently produce modified cases using parameter modification. The results of these modified cases might act as a basis for contract negotiations.

8.3 Limitations

8.3.1 Complexity

Comparing the proof of concept cases to real life cases

The proof of concept cases used within research are of a very simplistic nature compared to the real healthcare system and to real healthcare insurance company data. As one should have noted however, the input files of the given cases were already of a very complex nature. Apart from the given complexity when simulating simplistic cases, let us look at the additional layers of complexity which come into play when choosing simulation of more realistic cases (some of which we will discuss in more detail in consequent sections):

- *Distinction between regular versus irregular membership mutation*
  Within the proof of concept cases, we have chosen to distinguish between a group of regular and irregular in/out-flowers. Making this distinction allows us to omit the usage of time-dependent probabilities. It poses the requirement to be able to estimate what portion of people would be a "regular" in/out-flower and what portion would be a "irregular" in/out-flower. It is not very likely that we are actually able to pose such division on all non-member elements in the system.
- *Time dependent probabilities*
  Within the proof of concept cases and also in the simulation framework itself, we only implemented time independent probabilities. Even if we would distinguish between regular and irregular in- and outflow, it is still very unlikely that we would not use any form of time

dependency. As we have seen in the Vectis research the activity of people as being switchers is actually rising, thus we expect a larger amount of in- and out-flowers for future years.

- *Age groups*
  In the current proof of concept we only use three age bins. In real life however we would either use individual ages or age bins of a limited size (for example age-bin size 5) which increases complexity of both the age/vitality chain as the associated dependencies.

- *Ageing*
  In the proof of concept, members of a certain age group can not get into a new age group. In real life, people will get older and thus we should allow for such behaviour as well. Within the simulation framework we have implemented means for defining τ steps as we have proposed for the age/vitality chain. We have omitted this in the "proof of concept" cases.

- *Birth Rates*
  In the proof of concept we have omitted any form of "person generation". Thus, in the proof of concept a person is a member of age-group A_1, A_2 or A_3 and he/she will stay in this group infinitely. Determining birth rates are a complex problem in general with respect to systems of collaborative Markov chains.

- *Death rates*
  As with birth rates, we have omitted the death rates in the proof of concept cases. In essence implementing death rates is not a complicated task, however as it forms a sort of "synchronized sink" throughout the system it would cause a "drain" effect. Thus when implementing some sort of death rates one should also implement birth rates (and vice versa). Note that, as mentioned, in the real healthcare data we do not know the cause of leaving and thus these rates are hard to estimate.

- *One disease versus multiple diseases*
  In the proof of concept case we have only looked at one fictional disease with some probability of occurring. In real life cases it might be convenient to model several disease types or even a collection of (related) diseases.

- *Associated pathways*
  Logically, the number of associated pathways will grow according to the number of diseases in the system. Additionally note that the number of pathways in our example case, (only 2) is somewhat low. Especially when using institutional integrated care pathways we expect the number of pathways to be significantly higher.

Providing means for complexity calculation

As we have seen in the previous subsection there are a number of elements within the proof of concept cases that would be more complex in reality. In this section we will construct a definition of the complexity of the system provided.

Let us first analyse the common divisor of all previously mentioned elements which add complexity to the proposed solution in real life cases, i.e.:

"The number of parameters increases"

We therefore deem the number of parameters to be estimated as a valid indicator for the model complexity. We will assess complexity for both time independent an time dependent probabilities.

Time independent probabilities Let us look at a chain C_i within a collaborative Markov environment that has no dependencies at all. Assume the statespace of S_{C_i} consists of n states:

$$S_{C_i} = \{s_1^i, s_2^i, ..., s_n^i\}$$

Logically, the initial state vector is a $1 \times |S_{C_i}|$ vector depicting for each state the initial probability. The transition Matrix is trivially an $|S_{C_i}| \times |S_{C_i}|$ matrix. The total number of parameters to be estimated in this case is those parameters for the initial state vectors together with those of the transition matrix, or $|S_{C_i}| + |S_{C_i}|^2$.

Now, let us take a certain chain C_j, which has some corresponding set of dependencies $d(C_j)$. In this case we need to multiply the complexity as defined in the non-dependent case with the product of all chains in $d(C_j)$.This results in a complexity of:

$$\Pi_{C_k \in d(C_j)} |S_{C_k}|(|S_{C_j}| + |S_{C_j}|^2)$$

As we now know how to compute the complexity of a single chain, we are also able to compute the complexity of a whole system as it is just the sum of the complexity of all the chains in the system.

Time dependent probabilities If time dependent probabilities are implemented this adds an additional multiplicative factor in terms of the number of time-frames used. First let us explore how this impacts in terms of a single chain.

Let us assume we perform a simulation starting at time t_0 and ending at time t_{max}. We assume a time step size of 1, thus the simulation time line would be $t_0, t_0 + 1, ..., t_{max}$. Now let us additionally assume that we have a sequence T that indicates time intervals of time dependent probabilities. For example if $T =< t_0, t_i, t_{max} >$, we have two time-intervals which may consist of different probabilities, i.e. $[t_0, t_i)$ and $[t_i, t_{max})$.If $T =< t_0, t_i, t_j, t_{max} >$ (in which $j > i$) then we would have time intervals $[t_0, t_i)$, $[t_i, t_j)$ and $[t_j, t_{max}]$.

Now the question remains, how does the number of time intervals in which we would like to implement different probabilities affect our complexity measure. Actually this is rather straightforward. First let us inspect the initial state vector/matrix. Clearly the time frames do not influence the number of parameters we need to estimate in terms of initialization, so that part is equal to the time independent case.

Now let us consider the transition matrix. First take the case that we have time independent probabilities again, in that case we can draw up T as $T =< t_0, t_{max} >$. In this case, we need to estimate only one transition matrix (i.e. $|T| - 1$). Now let us take a look at the two-interval case, $T =< t_0, t_i, t_{max} >$. Now we need to estimate two transition matrices, i.e. $\Pi_{C_k \in d(C_j)}(|S_{C_k}|) * |S_{C_j}|^2 * 2$. If we repeat this for the three-interval case we would need a multiplication factor of three.

Note that for every $n-$interval based time sequence T, we have $|T| = n + 1$. Thus an $n-$interval based time dependent probability system needs a multiplication of n with respect to the number of transition matrices, where $|T| = n + 1$.
Thus we can reformulate the number of parameter estimations needed for transition matrix estimation as:

$$\Pi_{C_k \in d(C_j)}(|S_{C_k}|) * |S_{C_j}|^2 * |T - 1|$$

Thus the total complexity of a single chain C_j with time interval sequence T can be formulated as:

$$\Pi_{C_k \in d(C_j)} |S_{C_k}|(|S_{C_j}| + |S_{C_j}|^2 * (|T| - 1))$$

8.3.2 Inactive elements

As indicated, to maintain a realistic simulation we need "sink states". If we do not want our system to "drain", we implicitly need "source states" as well. The problem with Markov-based models in general with a sink state is the fact that the sink will form the steady-state solution of the model as there is a probability to get into the sink and no probability to get out of the sink.

Within the proposed collection of Markov chains we do present a source state depicting people that will be born in the future. Thus, there exist elements that are "inactive" at start and will become active in a later stage of simulation. The existence of inactive elements, a source and sink state does not limit the model of generating viable results though it poses some additional challenges for the modeller:

- *Amount quantification*
  A first challenge is to be able to ***quantify*** the amount of inactive persons at start of simulation. In context of the problem at hand this means quantifying the amount of people expected to be born during the course of simulation.
- *Activity-generation strategy*
  Apart from quantifying the amount of people one has to decide on some "activation strategy". Roughly we can define two strategies:
  - *Probabilistic*
    In a probabilistic activation strategy, we treat the transition from an inactive state to an active state as being probabilistic. For example:
    $P(X_{t+1} = x_{active} | X_t = x_{inactive})$
    There is one problem involved with the probabilistic strategy, i.e. as it is a probabilistic process chance exists that not all inactive elements will be activated throughout simulation.
  - *Deterministic*
    If one decides to implement activation deterministically (i.e. by τ-step technique), one defines a fixed point in time within the simulation at which an inactive element will become active.
    Determination of the actual point in time can of course be of a probabilistic fashion.

  To summarize, in the probabilistic strategy we have no guarantee that an inactive element will actually be active throughout the course of simulation, whereas we do have this guarantee in the deterministic strategy. The deterministic strategy however needs some more administration capacity with respect to the probabilistic strategy.
- *Conditional probability quantification*
  The fact that we incorporate inactive elements might pose some additional challenges to estimation of related parameters. What this basically means is that in the model proposed, we would incorporate activation in the age/vitality model and then synchronize throughout the system using the dependencies within the system. We incorporate it in the age/vitality chains as in the model proposed being inactive basically means being unborn (or death, using sink states). The most logical thing to do is to initialize the age/vitality model first and use a determined initial age/vitality chain to initialize other chains. This means that we need to take the probability of being inactive into account and scale the probabilities of membership to active age states.

Concluding on inactive elements, though a limitation factor, the challenging factors can definitely be handled and if performed correctly it should not affect the quality of the simulation outcome.

8.4 Future research

We identify the following topics as being of potential interest with respect to future research:

- ***Recognition and reconstruction of institutional pathways***
  In this research we assumed that pathways are reconstructible. The question however is whether this is actually the case. There are several dimensions where one could look at with respect to recognition and reconstruction of institutional pathways:
  - What types of diseases lend themselves for pathway-based quantification and analysis and how to classify them?
  - Is the current data quality of "an average healthcare insurance company" a sufficient level for pathway reconstruction?
  - What algorithms are suitable for reconstruction?
  - Can we directly generate Markov chains, pathway based or institutional based, out of insurance company data?
- ***Dependency graph analysis for Collaborative Markov chain simulation***
  As noted we did not implement dependency graph analysis for determination of execution order within simulation. An interesting topic of study is to assess the effects of different dependency graph analysis algorithms on the simulation output. Additionally one could assess how to implement dependency prioritization within the simulation framework.
- ***Solutions in equivalence with combined state-space based single Markov chains***
  We can reconstruct the existence of a Kronecker product-based solution to collaborative Markov chains if it does not have an cyclic dependency graph. Is it however possible to define a mathematical model that supports cyclic graphs as well? Can we build a combined state-space based single Markov chain that represents the collaborative Markov chain system? How do we express the dependencies in the model, given that they are cyclic? i.e. is fuzzy membership to an execution order a viable solution?
- ***Investigating strategical steering mechanisms towards optimized institutional pathways***
  The model proposed allows for assessing different scenario's by inputting different parameters. Assume a healthcare insurance company wants to benefit from an institutional pathway that is rated as "optimal". How should a healthcare insurance company do this? Should the company increase the throughput on a given institutional path? Or should the company use the optimal performance of a given path within contract negotiations?
- ***Defining a meta-model for collaborative Markov chains***
  Currently the simulation framework does not allow any form of visualization. Mainly input tables are used to define chains and dependency relations and such. Can we define a meta-model for collaborative Markov chain models and consequently instantiate a graphical model editor?

Bibliography

[1] I.N. Soyiri and D.D. Reidpath. An overview of health forecasting. *Environmental health and preventive Medicine*, 18:1–9, 2013.

[2] J.S. Armstrong. Methodology tree. `http://www.forecastingprinciples.com/index.php/methodology-tree`, 2010.

[3] L. Gentry, R.J. Calantone, and S.A. Cui. The forecasting classification grid: a typology for method selection. *Journal of Global Business Management*, 2(1):48–60, 2006.

[4] M. Panella and K. Vanhaecht. Is there still need for confusion about pathways? *International Journal of Care Pathways*, 14(1), 2010.

[5] Centraal Plan Bureau. Centraal economisch plan 2012. `http://www.cpb.nl/sites/default/files/publicaties/download/centraal-economisch-plan-2012.pdf`, 2012.

[6] I. Joumard, C. André, and C. Nicq. Health care systems: Efficiency and institutions. `http://search.oecd.org/officialdocuments/displaydocumentpdf/?cote=eco/wkp(2010)25&doclanguage=en`, 2010.

[7] T. Bodenheimer. High and rising health care costs. part 1: Seeking an explanation. *Annals of Internal Medicine*, 142(10):847–854, 2005.

[8] T. Bodenheimer. High and rising health care costs. part 2: Technologic innovation. *Annals of Internal Medicine*, 142(11):932–937, 2005.

[9] Ministerie van Volksgezondheid Welzijn en Sport. Bestuurlijk hoofdlijnenakkoord 2012-2015 tussen de nederlandse vereniging van ziekenhuizen, de nederlandse federatie van universitair medische centra, zelfstandige klinieken nederland, zorgverzekeraars nederland en het ministerie van volksgezondheid, welzijn en sport. `http://www.rijksoverheid.nl/documenten-en-publicaties/besluiten/2011/07/05/bestuurlijk-hoofdlijnenakkoord-2012-2015.html`, 2011.

[10] T. Custers, O.A. Arah, and N.S. Klazinga. Is there a business case for quality in the netherlands? a critical analysis of the recent reforms of the health care system. *Health Policy*, 82(2):226–239, 2007.

[11] S. Heinemann, S. Leiber, and S. Gress. Managed competition in the netherlands - a qualitative study. *Health Policy*, 109(2):113–121, 2013.

[12] M. Boon. Examining the performance of integrated care pathways; on designing a method for healthcare performance quantification. Diploma thesis, Delft University of Technology, 8 2012.

[13] A.C. Enthoven. The history and principles of managed competition. *Health Affairs*, 12(1):24–48, 1993.

[14] A.C. Enthoven and W.P.M.M van de Ven. Going dutch - managed-competition health insurance in the netherlands. *The New England Journal of Medicine*, 357:2421–2423, 2007.

[15] D.P. Goldman, B. Shang, Jayanta Bhattacharya, A.M. Garber, M. Hurd, G.F. Joyce, D.N. Lakdawalla, C. Panis, and P.G. Shekelle. Consequences of health trends and medical innovation for the future elderly. *Health Affairs*, 2005.

[16] N.R. Sanders. Forecasting theory. In J. Webster, editor, *Wiley Encyclopedia of Electrical and Electronics Engineering*, pages 664–675. John Wiley and Sons, 1999.

[17] J. van Meijgaard, J.E. Fielding, and G.F. Kominski. Assessing and forecasting population health: Integrating knowledge and beliefs in a comprehensive framework. *Public health Reports*, 124(6):778–789, 2009.

[18] I.N. Soyiri and D.D. Reidpath. Evolving forecasting classifcations and applications in health forecasting. *International Journal of General Medicine*, 5:381–389, 2012.

[19] J.S. Armstrong. *Principles of Forecasting - A Handbook for Researchers and Practitioners*. International series in operations research & management science 30. Springer, 1 edition, 2001.

[20] S.S. Jones, R.S. Evans, T.L. Allen, A. Thomas, P.J. Haug, S.J. Welch, and G.L. Snow. A multivariate time series approach to modeling and forecasting demand in the emergency department. *Journal of Biomedical Informatics*, 42(1):123 – 139, 2009.

[21] L.M. Schweigler, J.S. Desmond, M.L. McCarthy, K.J. Bukowski, E.L. Ionides, and J.G. Younger. Forecasting models of emergency department crowding. *Academic Emergency Medicine*, 16(4):301–308, 2009.

[22] R.E. Abdel-Aal and A.M. Mangoud. Modeling and forecasting monthly patient volume at a primary health care clinic using univariate time-series analysis. *Computer Methods and Programs in Biomedicine*, 56(3):235–247, 1998.

[23] W.R. Bell. An introduction to forecasting with time series models. *Insurance: Mathematics and Economics*, 3(4):241–255, October 1984.

[24] A. Garcia-Ferrer, A. de Juan, and P. Poncela. Forecasting traffic accidents using disaggregated data. *International Journal of Forecasting*, 22(2):203 – 222, 2006.

[25] J. Merz. Microsimulation – a survey of principles, developments and applications. *International Journal of Forecasting*, 7(1):77–104, May 1991.

[26] I.M. Majer, R. Stevens, W.J. Nusselder, J.P. Mackenbach, and P.H.M. Baal. Modeling and forecasting health expectancy: Theoretical framework and application. *Demography*, 50(2):673–697, 2013.

[27] N.R. Hoot, L.J. LeBlanc, I. Jones, S.R. Levin, C. Zhou, C.S. Gadd, and D. Aronsky. Forecasting emergency department crowding: A discrete event simulation. *Annals of Emergency Medicine*, 52(2):116–125, 2008.

[28] D. Kitchiner and P. Bundred. Integrated care pathways. *Archives of Disease in Childhood*, 75:166–168, 1996.

[29] D.L. Kodner and C. Spreeuwenberg. Integrated care: meaning, logic, applications, and implications - a discussion paper. *International Journal of Integrated Care*, 2, 2002.

[30] A. Atwal and K. Caldwell. Do multidisciplinary integrated care pathways improve interprofessional collaboration? *Scandinavian journal of caring sciences*, 16(4):360–7, 2002.

[31] K. Zander. Integrated care pathways: eleven international trends. *Journal of integrated care pathwyas*, 6:101–107, 2002.

[32] K. Vanhaecht. *The impact of Clinical Pathways on the organisation of care processes.* PhD thesis, Katholieke Universiteit Leuven, 2007.

[33] Wat zijn sociaaleconomische gezondheidsverschillen? `http://www.nationaalkompas.nl/bevolking/segv/wat-zijn-sociaaleconomische-gezondheidsverschillen/`, 2010.

[34] P.S. Fader and B.G.S. Hardie. Probability models for customer-base analysis. *Journal of Interactive Marketing*, 23(1):61 – 69, 2009.

[35] Marktscan zorgverzekeringsmarkt; weergave van de markt 2008-2012. Technical report, Nederlandse Zorgauthoriteit, 6 2012.

[36] J. M. Fourneau. Collaboration of discrete-time markov chains: Tensor and product form. *Perform. Eval.*, 67(9):779–796, September 2010.

[37] D.J.C. Mackay. Introduction to monte carlo methods. In MichaelI. Jordan, editor, *Learning in Graphical Models*, volume 89 of *NATO ASI Series*, pages 175–204. Springer Netherlands, 1998.

[38] Monitor zorgverzekeringsmarkt deelrapportage; het overstapgedrag van chronisch zieken. Technical report, Nederlandse Zorgauthoriteit, 12 2006.

[39] M. van der Burgt, E. van Mechelen-Gevers, and M. te Lintel Hekkert. De gezondheidszorg in een notendop. In *Introductie in de gezondheidszorg*, chapter 1, pages 13–19. Bohn Stafleu van Loghum, 1 edition, 2006.

[40] NZA. Visiedocument theoretisch kader liberalisering vrije beroepen in de zorg. `http://www.nza.nl/104107/10057/Visiedoc_Theoretisch_kader_1.pdf`, 2007.

[41] W. Sauter. The role of competition rules in the context of healthcare reform in the netherlands. `http://www.nza.nl/104107/230942/Research_paper_'The_role_of_competition_rules_in_the_context_of_healthcare_reform_in_the_Netherlands'.pdf`, 2010.

Appendices

Appendix A

The Dutch healthcare system

A.1 Healthcare service levels

Within the healthcare system we define four levels of care [39]:

- *Baseline care*
  Within baseline care (Dutch: "Nulde lijn zorg") healthcare providers are active which provide care in terms of a "consulting" or "educational" basis. A characteristic feature of baseline care is the provision of care to patients before actual health problems occur.
- *Primary care*
  Within primary care (Dutch: "Eerste lijn zorg") health care providers are active which provide generalized care. Medical professionals like general practitioners and obstetricians are active within primary care. A characteristic feature of primary care (as is for baseline care) is the direct accessibility of patients. There is no need for a medical referral to access primary health care services.
- *Secondary care*
  Secondary care (Dutch: "Tweede lijn zorg") mostly acts as a successor of healthcare providers in primary care. Medical professionals within secondary care are most often referred to as specialists and operate in hospitals or private medical clinics.
- *Tertiary care*
  The upper level of care, tertiary care (Dutch: "Derde lijn zorg") concerns academic centers which provide high-end clinical care. Additionally, academic research is conducted within these centers. Mental health care is also a part of the healthcare system. Typically the care provided to mental health patients is concentrated within the primary care level. A patient can however be referred to the secondary care level in case of more serious mental issues.

In general patients first visit a healthcare provider at the primary care level in case they endure any mental or physical problems. If the healthcare provider at the primary care level is not able to cure the patient, he or she will be referred to a healthcare provider at secondary or third level.

A.2 Key actor definition

Though there is no unified model of what actors play a role we define the following key actors within the Dutch healthcare, apart from actual (governmental) system definitions as follows [40, 41]

- *Health consumers*
  In general health consumers are represented by all patients. Every natural person either living or working in the Netherlands is a potential patient within the Dutch healthcare system. The health consumers (i.e. patients) form the demand side of the Dutch healthcare system.

- *Healthcare Providers*
  Healthcare providers are all institutes which provide medical care to the healthcare consumers. An institute could for example be a hospital, a general practitioner, a dentist etc. Healthcare providers act on all four different healthcares service levels defined in section "Healthcare service levels". All together they form the demand side of the Dutch healthcare system.

- *Healthcare Insurance Companies*
  Healthcare insurance companies act as basic as a link between health consumers and healthcare providers. A health consumer pays a premium to the healthcare insurance company. The healthcare insurance company covers costs of her clients if they are in need of medical care by a healthcare provider. Depending on the actual healthcare system definition, they might perform additional activities such as contracting within the healthcare market.

- *Government*
  The government shapes the rules within the healthcare system. Though the intentions are present to reduce the governmental influence within the market, the governmental role will always be present within the system. The NZA embodies the government within the systems and acts as a market manager, making sure the key actors (specifically healthcare providers and health care insurance companies) behave according to rules set by the government. Although the NZA does not have any governmental regulative power, it can set rates, performance measures and budgets when needed[1].

A.3 Actor Interaction

The relations among the different actors defined within the healthcare market are schematically depicted in figure A.1.

Apart from the four key actors defined earlier we identify a fifth entity in the market scheme, the NZA. As stated, the NZA represents the government within the system and acts as a market manager and thus regulates the market. The government itself shapes the market and defines the rules in which actors may behave. Within the market we identify three interrelated submarkets [40, 41] being:

- *Healthcare insurance market*
  In this market, healthcare insurance companies compete in order to cover prospective patients. Patients form the demand side whereas heatlchare insurance companies form the supply side.

- *Healthcare provision market*
  In this market, healthcare providers compete in order to provide care to patients. Though historically this market was not vitally present, the new governmental regulations make this market more vital. Patients form the demand side whereas healthcare providers form the supply side.

[1] `http://www.nza.nl/organisatie/`

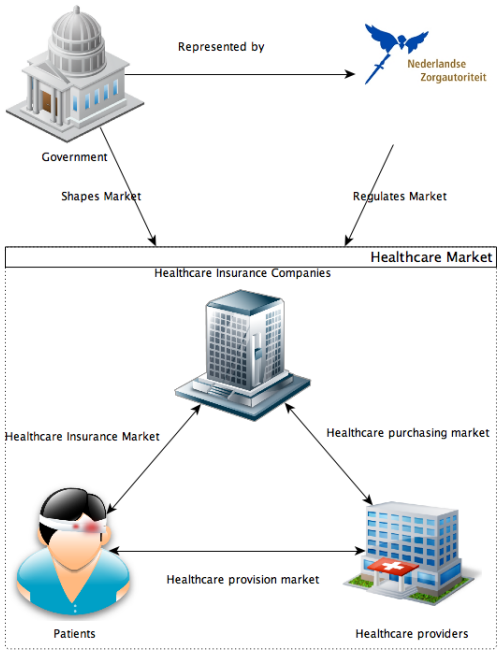


Figure A.1: Schematic representation of the relations among key actors in heatlhcare

- *Healthcare purchasing market*
  In this market, healtcare providers compete in order to get contracts from different healthcare insurance companies. Healthcare insurance companies form the demand side whereas healthcare providers form the supply side.

Appendix B

Mathematical definitions

B.1 Time series models

ARIMA-models use two separate models and combine these [16, 23].
First there is the auto-regressive model:

$$X_t = \phi_1 X_{t-1} + ... + \phi_p X_{t-p} + e_t \tag{B.1}$$

As one can see the AR(p)-model stated in equation B.1 is a weighted sum of the previous encountered value combined with a certain error measure e_t at time t. For now we specifically assume $E(X_t) = 0$ and that X_t is stationary. All e_t's follow an identical $\mathbf{N}(0, \sigma_e^2)$. The AR($p$)-model depicted is of order p.

Secondly there is the moving-average model:

$$X_t = e_t - \theta_1 e_{t-1} - ... - \theta_q e_{t-q} \tag{B.2}$$

The MA model describes a weighted negative sum over the past errors to generate a forecast. In this case the MA(q)-model depicted in equation B.2 is of order q.
Combining the two models into an ARMA(p,q) yields:

$$X_t = \phi_1 X_{t-1} + ... + \phi_p X_{t-p} + e_t - \theta_1 e_{t-1} + ... + \theta_q e_{t-q} \tag{B.3}$$

Additionally, the lag operator L is deifined as:

$$LX_t = X_{t-1},\ L^2 X_t = X_{t-2},\ ...,\ L^i X_t = X_{t-i} \tag{B.4}$$

We can now rewrite B.3 as:

$$(1 - \phi_1 L - ... - \phi_p L^p) X_t = (1 - \theta_1 L - ... - \theta_q L^q) e_t \tag{B.5}$$

If X_t is not stationary, its first, second, ... d^{th} difference might be:

$$X_t - X_{t-1} = (1 - L) X_t$$

$$X_t - 2X_{t-1} + X_{t-2} = (1 - L)[(1 - L) X_t] = (1 - L)^2 X_t$$

Adding the difference equation to make the series stationary leads to an ARIMA(p,d,q) model:

$$(1 - \phi_1 L - ... - \phi_p L^p)(1 - L)^d X_t = (1 - \theta_1 L - ... - \theta_q L^q) e_t \tag{B.6}$$

Note that equation B.6 represents a univariate time-series model (i.e. based on one statistical variable). The multivariate representation is usually presented in vector form, called VARIMA.

B.2 Notation

We denote S as being a set.
The powerset of S is denoted by $\mathcal{P}(S) = \{S' | S' \subseteq S\}$.
A *sequence* of length n over elements in S is defined as a function σ:

$$\sigma : \{1, 2, ..., n\} \to S$$

Notation wise we define:

$$\sigma =< s_1, s_2, ..., s_n > \text{ in which } \sigma(1) = s_1,\ \sigma(2) = s_2,\ ...,\ \sigma(n) = s_n$$

Additionally we will write σ_i as a notation for $\sigma(i)$, representing the i^{th} element in the sequence σ.
The set of all finite sequences over S is denoted as S^*.

The set of positive integers is denoted as $\mathbb{Z}$ and includes 0, as defined in equation B.7.

$$\mathbb{Z} = \{0, 1, 2, ..., \infty\} \tag{B.7}$$

The set of positive integers excluding 0 is denoted as $\mathbb{Z}^+$, as defined in equation B.8.

$$\mathbb{Z}^+ = \mathbb{Z} \backslash \{0\} \tag{B.8}$$

Appendix C

Data

C.1 Detailed description

C.1.1 Population data

Raw data

The data-set that can be used to quantify $M_{(z,t)}$ is provided in a membership-subscription form, an example of this is shown in figure C.1. As stated, the data concerns actual healthcare insurance company membership data ranging from January 1^{st}, 2006 to December 31^{st}, 2010.

The data-rows can be read as:
"Person p with birth year y and gender g was member of the insurance company from date d_s to date d_t".

A person p is identified by a unique person identifier. The exact source of this person's identifier is unknown and this knowledge is not needed in order to perform the analysis desired (thus anonymity of the data does not impact the analysis). As one can see in figure C.1, a person can have multiple membership entries. For example take person $p_{0010818901}$ (i.e. Identified by ID 0010818901, first column). In this case we see two membership entries for person $p_{0010818901}$:
$1-1-2009 \rightarrow 31-12-2009$ and $1-1-2010 \rightarrow 31-12-2010$.

Properties

The population data consists of the following properties:

- *File type*
  Comma separated value (.csv, cross-platform, ';' as column denominator)
- *Number of rows (including headers)*
  $647,224$
- *Number of columns*
  7
  - **column 1**: Person ID1 (unique for each person p); `String` of `Digits`; example: $'0010818901'$

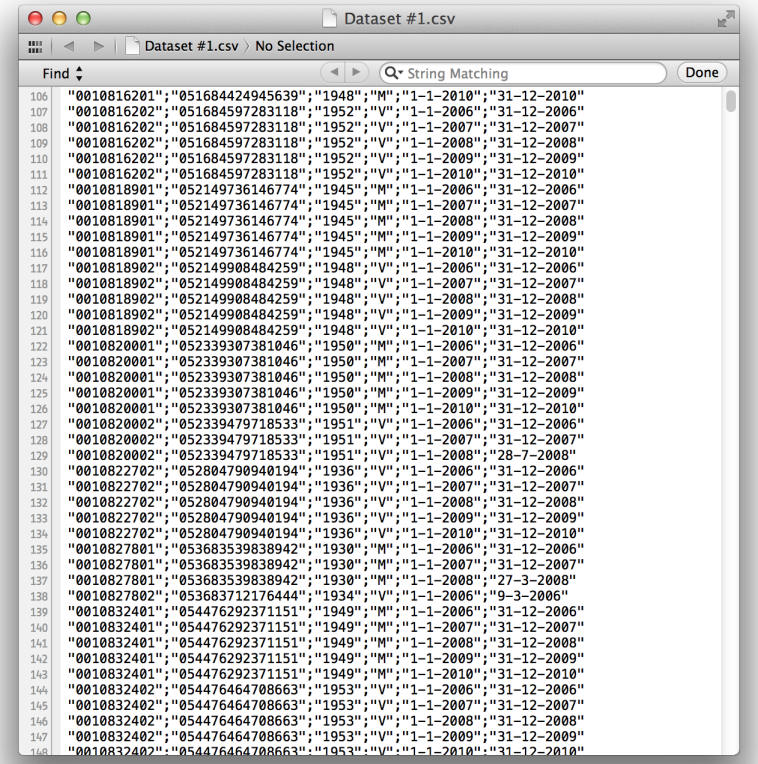


Figure C.1: A screen-shot of the population data provided

- **column 2**: Person ID2 (unique for each person p); `String` of `Digits`; example: $'052149736146774'$
- **column 3**: Birth year; four `Digits`; example: 1945
- **column 4**: Gender; 1-character `String`; either 'M' or 'V'
- **column 5**: Date from; `Date`; example: $1-1-2009$
- **column 6**: Date to; `Date`; example: $31-12-2009$

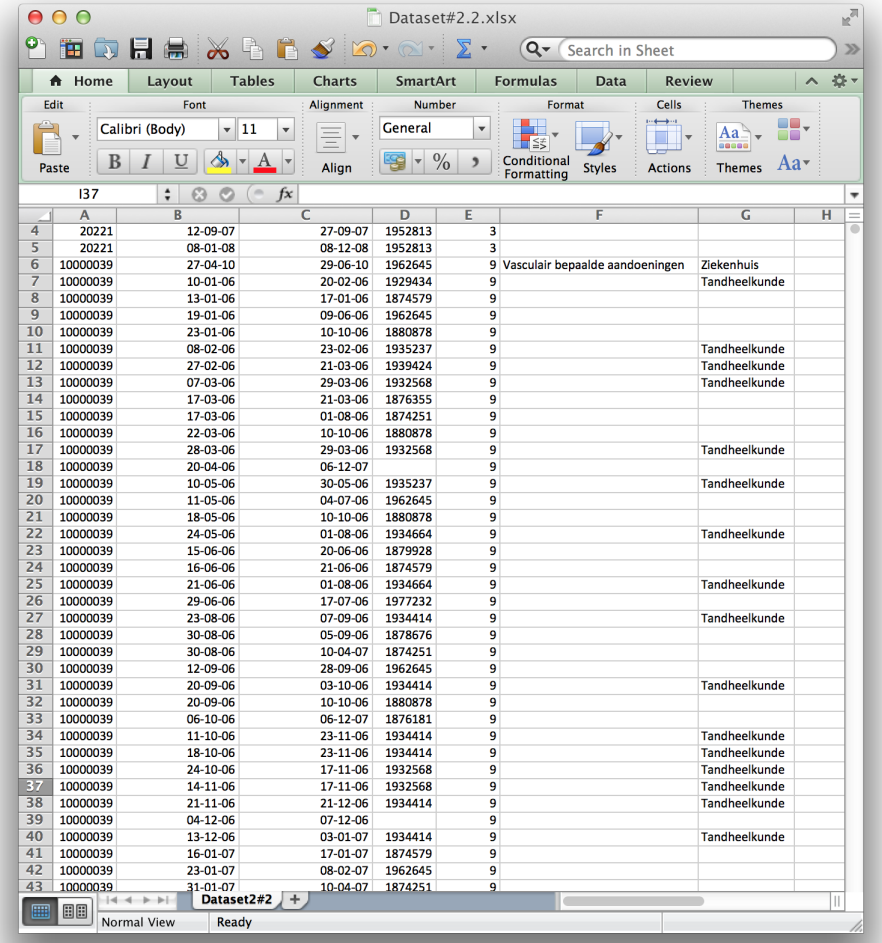
Taking a quick look into the data screen-shot gives us already some interesting observations:

- For each year of membership, a person seems to have a new entry in the data. The "year" of the from and to date seems to equal for each data row.
- People seem to be able to "leave" (cause unknown) the population described by the data at arbitrary times (look for $p_{0010827801}$ and $p_{0010827802}$, lines 137 & 138, in the example screen-shot).

C.1.2 Declaration data

Raw data

The data-set consisting of associated declarations concerning the persons which are present in dataset 1 is depicted in figure C.2. In this data-set we can read the data-row as follows:



	A	B	C	D	E	F	G
4	20221	12-09-07	27-09-07	1952813	3		
5	20221	08-01-08	08-12-08	1952813	3		
6	10000039	27-04-10	29-06-10	1962645	9	Vasculair bepaalde aandoeningen	Ziekenhuis
7	10000039	10-01-06	20-02-06	1929434	9		Tandheelkunde
8	10000039	13-01-06	17-01-06	1874579	9		
9	10000039	19-01-06	09-06-06	1962645	9		
10	10000039	23-01-06	10-10-06	1880878	9		
11	10000039	08-02-06	23-02-06	1935237	9		Tandheelkunde
12	10000039	27-02-06	21-03-06	1939424	9		Tandheelkunde
13	10000039	07-03-06	29-03-06	1932568	9		Tandheelkunde
14	10000039	17-03-06	21-03-06	1876355	9		
15	10000039	17-03-06	01-08-06	1874251	9		
16	10000039	22-03-06	10-10-06	1880878	9		
17	10000039	28-03-06	29-03-06	1932568	9		Tandheelkunde
18	10000039	20-04-06	06-12-07		9		
19	10000039	10-05-06	30-05-06	1935237	9		Tandheelkunde
20	10000039	11-05-06	04-07-06	1962645	9		
21	10000039	18-05-06	10-10-06	1880878	9		
22	10000039	24-05-06	01-08-06	1934664	9		Tandheelkunde
23	10000039	15-06-06	20-06-06	1879928	9		
24	10000039	16-06-06	21-06-06	1874579	9		
25	10000039	21-06-06	01-08-06	1934664	9		Tandheelkunde
26	10000039	29-06-06	17-07-06	1977232	9		
27	10000039	23-08-06	07-09-06	1934414	9		Tandheelkunde
28	10000039	30-08-06	05-09-06	1878676	9		
29	10000039	30-08-06	10-04-07	1874251	9		
30	10000039	12-09-06	28-09-06	1962645	9		
31	10000039	20-09-06	03-10-06	1934414	9		Tandheelkunde
32	10000039	20-09-06	10-10-06	1880878	9		
33	10000039	06-10-06	06-12-07	1876181	9		
34	10000039	11-10-06	23-11-06	1934414	9		Tandheelkunde
35	10000039	18-10-06	23-11-06	1934414	9		Tandheelkunde
36	10000039	24-10-06	17-11-06	1932568	9		Tandheelkunde
37	10000039	14-11-06	17-11-06	1932568	9		Tandheelkunde
38	10000039	21-11-06	21-12-06	1934414	9		Tandheelkunde
39	10000039	04-12-06	07-12-06		9		
40	10000039	13-12-06	03-01-07	1934414	9		Tandheelkunde
41	10000039	16-01-07	17-01-07	1874579	9		
42	10000039	23-01-07	08-02-07	1962645	9		
43	10000039	31-01-07	10-04-07	1874251	9		

Figure C.2: A screen-shot of the declaration data-set version 2 as provided

"Person p has a declaration record for treatment date d_t, which was posted as a declaration on date d_d by healthcare provider h. Additionally the declaration consists of a DKG-group indicator, an optional treatment description and an optional treating institute type."

Properties

The population data (second version) consists of the following properties:

- *File type*

Microsoft excel file (.xlsx extension)

- *Number of rows (including headers)*
  $312,556$
- *Number of columns*
  7
  - **column 1**: Person ID (unique for each person p); `String` of `Digits`; example: $'10000039'$
  - **column 2**: Treatment date; `Date`; example: $1-1-2009$
  - **column 3**: Declaration date; `Date`; example: $1-1-2009$
  - **column 4**: Declaring institute ID; `String` of `Digits`; example $'1952813'$
  - **column 5**: DKG group; `Integer`; example: 3
  - **column 6**: Treatment description; `String` (Dutch); example: *'Vasculair bepaalde aandoeningen'*
  - **column 7**; Type of declaring institute; `String` (Dutch); example: *'Ziekenhuis'*

The screen-shot already shows some problems concerning the data:

- Not all declarations consist of an associated declaring institute. The exact cause of this is unclear, it could either be missing data or an erroneous query.
- The presence of the treatment description seems to be rather sparse.
- The presence of declaring institute seems to be rather sparse.

C.2 Manipulation

The programming language used for the manipulation is `python` as it is lightweight and very low-level in terms of basic set-up. The script has a very linear type of execution order and roughly performs three main activities:

- Generate a person-based membership transaction set
- Calculate for each relevant point in time the number of persons belonging to a population set (i.e. population-member, inflow, outflow).
- Assess whether the calculated population volumes are correct.

We will present these main steps and supporting steps in more detail, each in a separate paragraph.

Calling the script

One can call the script in the command prompt by typing (given that one is visiting the directory where the script `population_data_maniuplator.py` is in):
`python population_data_maniuplator.py <input_data>.csv [bin size]`
The first argument logically starts the `python` script. The second argument concerns the input data file which should have the same structure as the data presented in the previous appendix section. The third parameter is optional and allows the user to specify a bin size which should be used to group the population members in terms of age groups. If no bin size argument is supplied, the default bin size equals 1.

Initialization

The script consists of a `class` called `PopulationDataManipulator`. The class basically comprises some functions which allow us to manipulate the data-set in such way that it provides in the needed information concerning population knowledge. Upon class initiation, the population data and bin size are stored as class objects.

Membership transaction set

In the first phase, the script generates a person-based membership transaction set. For each person, we store the birth date and person ID. Additionally we store each associated membership interval. The generated data structure is stored as a `class variable` called `self.membershipTransactions`.

Calculation of population memberships

If the membership transaction set is set-up properly, we can use it to generate the membership volumes (and corresponding in and out-flow). The time-steps used are in terms of *months*. In membership generation we respect the following rules:

- If a person has been member for at least one day in a certain month m, this person is considered member of the population during that month m, i.e $P_{(z,m)}$.
- If a person was not a member in month m, but was a member during month $m+1$, the person is a member of the inflow of month $m+1$, i.e. $M^{\leftarrow}_{(z,m+1)}$
- If a person was member of the population in month m, but is not a member during month $m+1$, the person is a member of the outflow of month m, i.e. $M^{\rightarrow}_{(z,m)}$. We have chosen this structure as usually a person leaves somewhere within December. We want all these people to be par of the outflow set. Note that this might conflict with the basic definition of $M_{(z,t)}$.

The script however does not literally store each person's individual membership though it counts the number of memberships of each person per month, resulting in $|M_{(z,t)}|$, $|M^{\leftarrow}_{(z,t)}|$ and $|M^{\rightarrow}_{(z,t)}|$.

Additional assumptions and associated correctness

The script assumes and proves two additional assumptions regarding the transnational input data:

- A transaction in the input data always consists of a from and to date falling in the same year.
- A person's transactions can never overlap.

Both assumptions are proven programmatic within the script. This means that each proposition is tested by means of an `assertion`.

Result Verification

For each computed month membership volume the script checks whether it is expressible in terms of its input and output components. Again to prove the correctness property an programmatic proof is provided. Again we make use of the `assert` construct which will `raise` an `exception` if the equation is violated.

Manipulation output

For the given input data the manipulation script passes all tests. The script outputs its generated population volume data to a `.csv` file.

Appendix D

Simulation framework

The simulation framework has been designed in an object-oriented fashion. In this appendix we have described the main properties and functioning of each class. We have also pointed out some interesting functions which might need some additional clarification.

D.1 `State` Class

The state class represents a state object and only consists of one single property:

- `id` of type `char`

Thus we just create a `handle` object called `State` with an additional id property. The class is a handle such that when copying a state variable, we actually create a ***reference***. In other words the following code:

```
a = State('a');
b = a;
```

Will not create a copy of `a` but rather a reference to the object created and stored in `a`. Thus if we would be able to change some parameter of a State (which is not the case in the current implementation), this change will be both visible in `a` and `b`. A state object thus is not aware knowledge of its environment.

D.2 Probability Class

The probability class has one mentionable property:

- `currentProbability` of type `Decimal` in domain $[0, 1]$.

A Probability class instance has a certain numeric value between or equal to 0 and 1. This value is (re)settable. As well as the State class, the probability class is not aware of its environment and is inheriting from the `handle` class.

Note that the Probability class also has a property `timedFunction`. The property is intended for time-based probability values (i.e. non-homogeneous Markov chain) though this is currently not implemented.

D.3 `Transition` Class

The `Transition` class logically represents a transition in a Markov chain. It connects two `State` objects. Additionally it keeps track of a `Probability` object. As indicated, both the `State` class and the`Probability` class are inheritances of the `handle` class and thus the `Transition` class maintains references.
The transition class consists of the following notable properties:

- `fromState` of type `State`
- `toState` of type `State`
- `probability` of type `Probability`
- `markovRenewal` of type `function_handle`

The `markovRenewal` is of type `function_handle`. This means that the user of the framework can specify a function which executes a user-defined Makrov renewal function. Currently, the Markov renewal function needs a time-stamp as an input (i.e. the simulation framework makes sure the "current time" is given as an input).
The `Transition` class provides means for executing the Markov renewal function by means of a `public function` called `executeMarkovFunciton`.

D.4 `Chain` Class

The `Chain` class provides means for the user to define a Markov chain. A chain consists of some states (`State` class) and provides means for making transitions in between those states (using the `Transition` class).
A chain does not have any knowledge of the time its surrounding system is in. It does however determine its next state by itself.
The `Chain` class consists of the following notable properties:

- `states`, a set of `State`-typed objects.
- `transitions`, as set of `Transition`-typed objects.
- `initialStateVec`, the initial state vector of the chain, an `array` of `decimals` all between 0 and 1 with a total sum of 1.
- `currentState`, a `State`-typed object depicting the current state.

A chain can determine its next state in two ways. Either by using the initial state vector (which is only used initially) or just by using the "current state" and its associated transitions. For determining the initial state the chain class just randomly selects a starting point, using the initial state vector (see function `determineInitialState()`).

To determine the next state, the chain additionally needs the time of the system that it is containing it. The chain will first determine what the next state will be according to its current state and the values of the associated transition probabilities. It will afterwards assess whether the chain should actually update its current state to the new sate. To determine this, the chain passes the given system time to the Markov renewal function reference maintained by the chain's `Transition`-objects.

Thus, the chain determines every time-step what the new state will be (by determining what transition is next) and afterwards determines by means of the Markov renewal function reference whether this transition will actually happen. For further reference see the `determineNextState`-function.

There is one additional notable procedure present within the `Chain` class. As we proposed a system which contains of multiple Markov chains which share dependencies, the `Chain` class needs to provide means for updating its transition probabilities throughout simulations. The `Chain` class consists of a procedure which provides means for updating transition probability values in a chain called `updateTransitions()`. It expects a set of tuples as an input which may contain the following arguments:

- `transition` of type `string` or `Transition`.
- `probability` of type `decimal` in between 0 and 1.
- `markovRenewal` (optional) of type `handle`, used for referencing a Markov renewal function.

For performance optimization, the update function only updates transitions in the chain which actually have the current state as a source state. Currently, the `Chain` class does not reset the probabilities, these will just maintain their last updated value.

D.5 `System` class

As mentioned, the `Chain` class has no information concerning its surrounding system. This functionality is accounted for by the `System` class. The system maintains the collection of cooperative chains. It additionally allows for adding dependencies among two or more chains within the system. Additionally it allows for the addition of multiple data elements which might trigger deterministic actions within a chain (an example of this is maintaining a birth year for updating the age module).
The `System` class consists of the following notable properties:

- `chains`, `array` of type `Chain`
- `currentYear` of type `int` (used for age calculation)
- `currentMonth` of type `int` (used for age calculation)
- `dependencyMatrix`
- `detDataElements` of type `containers.Map()`
- `stateSpace` of type `char`
- `time` of type `int`
- `traces`, `array` of type `char`

The `System` class provides means for the user to simulate itself. The corresponding `public procedure` is called `monteCarloRandomWalk`, which takes the number of time-steps to be simulated as an input. If the system detects it needs to be initialized first, it will take care of this by itself.

During simulation of a time step (taken car of by a `private procedure` called `simulateSystemTimeStep`) the system first check whether the state space has changed compared to the previous time step. If

so, it updates the system's state space and checks whether some dependencies will imply changing transition probabilities in some of the contained chains.

After potentially updating transition probabilities, the system will determine the next state and additionally (if applicable for the chain at hand) check for any τ transitions. The `System` class will record for each chain its state over time. It will record these state spaces in the `trace` property.

D.5.1 `Simulator` class

The final class which is part of the simulation framework is the `Simulator` class. It allows the user to run simulations with the predefined system. Upon creation, the user specifies what system should be simulated, for what number of elements and how long a single simulation should run. The `Simulator` class consists of the following notable properties:

- `combinedMonitors`
- `monitors`
- `nbElements` of type `int`
- `simulationLength` of type `int`
- `system` of type `System`

Additionally to providing means for simulation, the simulator allows the user to track the simulation results. The user is able to define two types of "monitors" in order to capture results of simulating:

- Single monitors - based on a ***single*** chain's state.
- Combined monitors - based on a specified combination of ***multiple*** states.

The simulator will output the specified monitors in a `.csv` file in which it outputs per monitor the number of elements which was in the specified state at the given time.

Appendix E

Proof of concept - Case inputs

E.1 Case I

E.1.1 Simulation - Code

```
for i = 1 : 50
    clear

    %-- Population Module --%
    population = Chain('population', 'population_chain_input_table')

    %-- System --%
    system = System('system', 2008)
    system.addChains([population])

    %-- Simulator --%
    simulator = Simulator('simulator', system, 350,  24)
    simulator.addMonitor('population', '*')
    simulator.simulate()
    simulator.outputMonitors('path_to_output_folder')
end
```

E.1.2 Simulation - Input data

Initial state vector

The contents of the initial state vector is depicted in table E.1.

M_z	$\neg M_z^R$	$\neg M_z^I$
$\frac{92}{350}$	$\frac{158}{350}$	$\frac{100}{350}$

Table E.1: The initial-state vector of C_M; case I

Transition- & Markov renewal matrices

The contents of the simulation transition and Markov renewal matrices are depicted in tables E.2 and E.3.

	M_z	$\neg M_z^R$	$\neg M_z^I$
M_z	$\frac{96}{100}$	$\frac{4}{100}$	0
$\neg M_z^R$	0	1	0
$\neg M_z^I$	0	0	1

Table E.2: The transition matrix of C_M; case I

	M_z	$\neg M_z^R$	$\neg M_z^I$
M_z	`null`	`@yearlyTransition`	`null`
$\neg M_z^R$	`null`	`null`	`null`
$\neg M_z^I$	`@yearlyTransition`	`null`	`null`

Table E.3: The Markov renewal matrix of C_M; case I

E.2 Case II

E.2.1 Simulation - code

The input code of case II is equal to case I.

E.2.2 Simulation - Input data

Initial state vector

The initial state vector of case II is depicted in table E.4.

M_z	$\neg M_z^R$	$\neg M_z^I$
$\frac{100}{350}$	$\frac{158}{350}$	$\frac{92}{350}$

Table E.4: The initial-state matrix of C_M; case II

Transition- & Markov renewal matrices

The transition- and Markov renewal matrices are depicted in table E.5 the Markov renewal matrix is equal to case I (i.e. table E.3).

	M_z	$\neg M_z^R$	$\neg M_z^I$
M_z	$\frac{96}{100}$	$\frac{4}{100}$	0
$\neg M_z^R$	0	1	0
$\neg M_z^I$	$\frac{8}{2400}$	0	$1 - \frac{8}{2400}$

Table E.5: The transition-matrix of C_M; case II

E.3 Case III

E.3.1 Simulation - Code

```
for i = 1 : 50

    clear

    population = Chain('population', 'population_chain_input_table')

    age = Chain('age', 'age_chain_input_table')


    %-- System --%
    system = System('system', 2008)
    system.addChains([population, age])
    system.addDependency('population', 'population_dependency_definition_table')

    %-- Simulator --%
    simulator = Simulator('simulator', system, 350,  24)
    simulator.addMonitor('population', '*')
    simulator.addMonitor('age', '*')
    simulator.addCombinedMonitor({'age', 'population'}, {'*', '*'})
    simulator.simulate()
    simulator.outputMonitors('path_to_output_folder')

end
```

E.3.2 Simulation - Input data

Initial state vectors

The initial state vector of C_M (membership chain) is equal to the initial state vector of case II (table E.4). The initial state vector of C_A (age/vitality chain) is depicted in table E.6.

A_1	A_2	A_3
$\frac{1}{4}$	$\frac{1}{2}$	$\frac{1}{4}$

Table E.6: The initial-state vector of C_A; case III

Transition- & Markov renewal processes

The input transition matrix for C_M is depicted in table E.7. As changing age groups is not implemented, the transition matrix of C_A is just the identity matrix I of size 3. Again the Markov renewal matrix remains unchanged.

	M_z	$\neg M_z^R$	$\neg M_z^I$
$A1, M_z$	1	0	0
$A1, \neg M_z^R$	0	1	0
$A1, \neg M_z^I$	0	0	1
$A2, M_z$	1	0	0
$A2, \neg M_z^R$	0	1	0
$A2, \neg M_z^I$	$\frac{1}{150}$	0	$1 - \frac{1}{150}$
$A3, M_z$	$\frac{21}{25}$	$\frac{4}{25}$	0
$A3, \neg M_z^R$	0	1	0
$A3, \neg M_z^I$	0	0	1

Table E.7: The dependency transition-matrix of C_M; case III

E.4 Case IV

E.4.1 Simulation - Code

```
for i = 1 : 50

    clear

    population = Chain('population', 'population_chain_input_table')

    age = Chain('age', 'age_chain_input_table')

    disease = Chain('disease', 'disease_chain_input_table')


    %--- System ---%
    system = System('system', 2008)
    system.addChains([population, age, disease])
    system.addDependency('population', 'population_dependency_definition_table')
    system.addDependency('disease', 'disease_dependency_definition_table')

    %--- Simulator ---%
    simulator = Simulator('simulator', system, 350, 24)
    simulator.addMonitor('population', '*')
    simulator.addMonitor('age', '*')
    simulator.addMonitor('disease', '*')
    simulator.addCombinedMonitor({'age', 'population', 'disease'}, {'*', '*', '*'})
    simulator.simulate()
    simulator.outputMonitors('path_to_output_folder')

end
```

E.4.2 Simulation - Input data

Initial state vectors

The initial state vectors of C_M and C_A are equal to these of case III, and are as a consequence omitted here.
We do present an initial state vector for C_D. Note that we have not implemented dependency-

based initialization and use the input data of the combination M_z, A_1, D_d as an input for the initial state vector of C_D. The corresponding initial state vector is presented in table E.8.

$\neg D_d$	D_d
$\frac{23}{25}$	$\frac{1}{25}$

Table E.8: The initial-state vector of C_A; case III

Transition- & Markov renewal matrices

Like with initialization, the transition- and Markov renewal matrices have not changed with respect to the previous case and are therefore omitted here. The transition matrix for C_D is depicted in table

	$\neg D_d$	D_d
$A1, M_z, \neg D_d$	$\frac{299}{300}$	$\frac{1}{300}$
$A1, M_z, D_d$	$\frac{1}{300}$	$\frac{299}{300}$
$A1, \neg M_z^R, \neg D_d$	1	0
$A1, \neg M_z^R, D_d$	0	1
$\vdots$	$\vdots$	$\vdots$
$A3, \neg M_z^I, D_d$	0	1

Table E.9: The dependency transition-matrix of C_D; case IV

E.5 Case V

E.5.1 Simulation - Code

```
for i = 1 : 1

    clear

    population = Chain('population', 'population_chain_input_table')

    age = Chain('age', 'age_chain_input_table')

    disease = Chain('disease', 'disease_chain_input_table')

    pathway = Chain('pathway', 'pathway_chain_input_table')


    %-- System --%
    system = System('system', 2008)
    system.addChains([population, age, disease, pathway])
    system.addDependency('population', 'population_dependency_definition_table')
    system.addDependency('disease', 'disease_dependency_definition_table')
    system.addDependency('pathway', 'pathway_dependency_definition_table')

    %-- Simulator --%
    simulator = Simulator('simulator', system, 350, 24)
    simulator.addMonitor('population', '*')
    simulator.addMonitor('age', '*')
    simulator.addMonitor('disease', '*')
    simulator.addMonitor('pathway', '*')
    simulator.addCombinedMonitor({'age', 'population', 'disease'},...
        {'A1', 'P', '*'})
    simulator.addCombinedMonitor({'age', 'population', 'disease', 'pathway'},...
        {'A1', 'P', 'Sick', '*'})
    simulator.simulate()
    simulator.outputMonitors('path_to_output_folder')

end
```

E.5.2 Simulation - Input data

Initial state vectors

In case V, we inherit all initial state vectors from case IV. Additionally as there is no dependency based initialization we initialize the pathway chain with a probability 1 in state $\neg P$. We omit the corresponding vector here.

Transition- & Markov renewal matrices

in case V, the transition and Markov renewal matrices of C_M, C_A and C_D have not changed. Note that, we do not take any age-group in consideration here as this is accounted for by the disease transition matrix.

	$\neg P$	P_A	P_B
$\neg D_d, \neg P$	1	0	0
$\neg D_d, P_A$	1	0	0
$\neg D_d, P_B$	1	0	0
$D_d, \neg P$	0	$\frac{1}{2}$	$\frac{1}{2}$
D_d, P_A	0	1	0
D_d, P_B	0	0	1

Table E.10: The dependency transition-matrix of C_D; case IV

E.6 Case VI

Case VI is equal to case V with respect to the model used and the simulation code, thus we omit these here. We have only changed the transition matrix of C_D. Due to the size of the corresponding input matrix, we *only* show the data rows that do not consist of a "self-loops".

	$\neg D_d$	D_d
$M_z, A_1, \neg P, \neg D_d$	$\frac{1}{2}$	$\frac{1}{2}$
M_z, A_1, P_A, D_d	$\frac{1}{5}$	$\frac{4}{5}$
M_z, A_1, P_B, D_d	$\frac{4}{5}$	$\frac{1}{5}$

Appendix F

Proof of concept - Distribution fitting

F.1 Case I

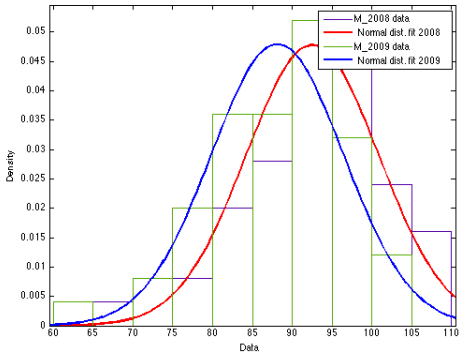


Figure F.1: Normal distribution fit to $\bar{x}_{M_z}$ for both 2008 and 2009; Case I

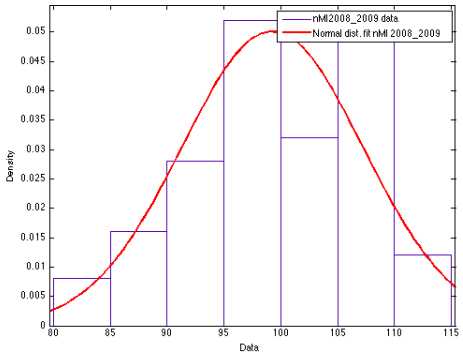


Figure F.2: Normal distribution fit to $\bar{x}_{\neg M_z^I}$ for both 2008 and 2009; Case I

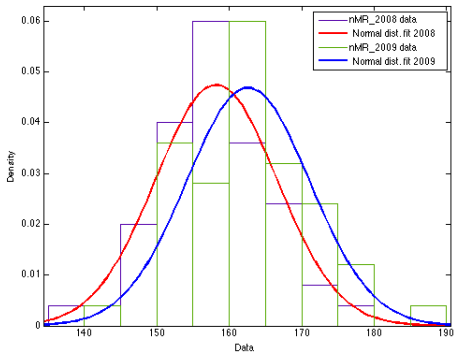


Figure F.3: Normal distribution fit to $\bar{x}_{\neg M_z^R}$ for both 2008 and 2009; Case I

F.2 Case II

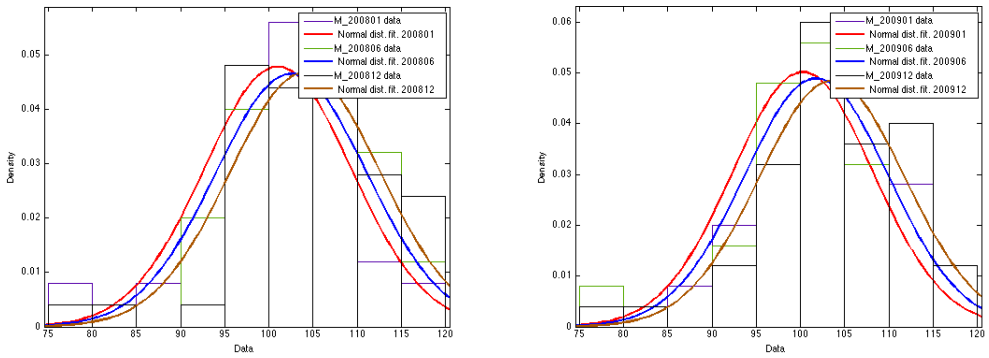


Figure F.4: Normal distribution fit to $\bar{x}_{M_z}$ for both 2008 and 2009; Case II

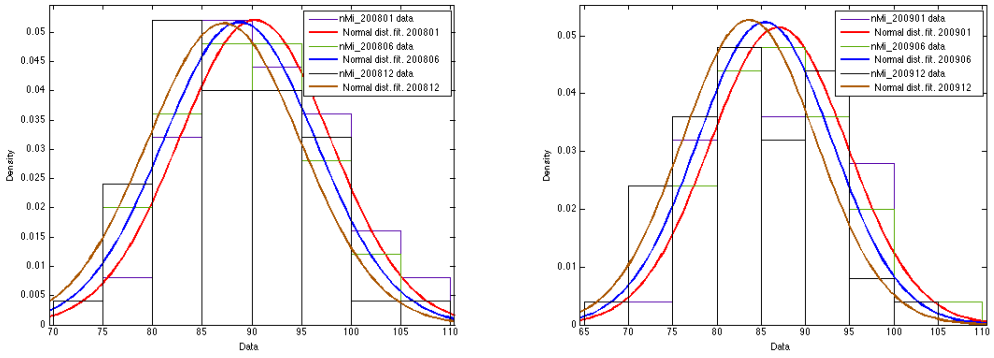


Figure F.5: Normal distribution fit to $\bar{x}_{\neg M_z^I}$ for both 2008 and 2009; Case II

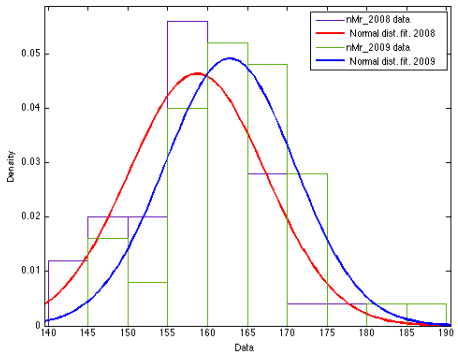


Figure F.6: Normal distribution fit to $\bar{x}_{\neg M_z^R}$ for both 2008 and 2009; Case II

F.3 Case III

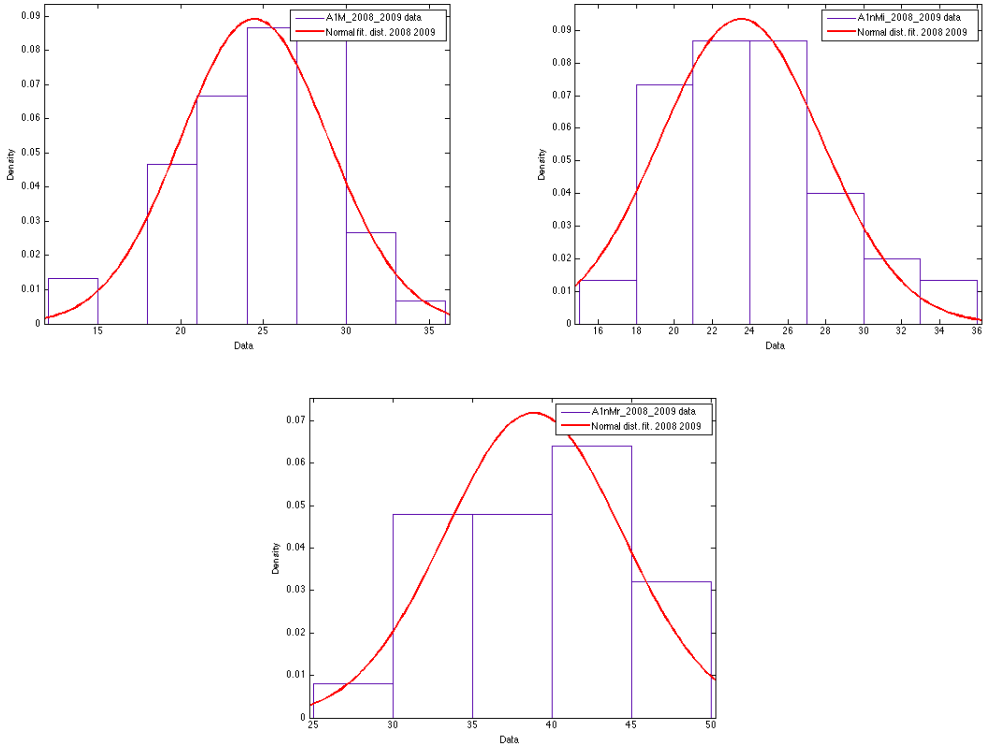


Figure F.7: Normal distribution fit of $\bar{x}_{|M_z,A_1|}$, $\bar{x}_{|\neg M_z^I,A_1|}$ and $\bar{x}_{|\neg M_z^R,A_1|}$ for both 2008 and 2009; Case III

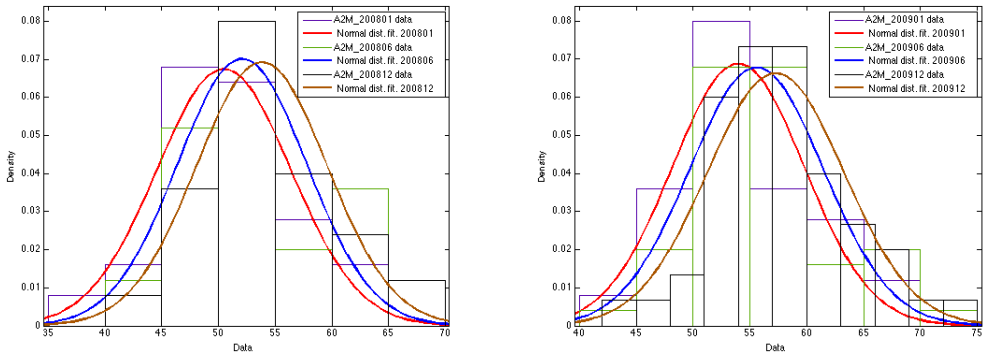


Figure F.8: Normal distribution fit of $\bar{x}_{|M_z,A_2|}$ for both 2008 and 2009; Case III

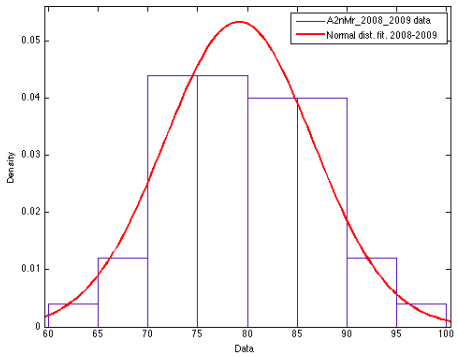


Figure F.9: Normal distribution fit of $\bar{x}_{|\neg M_z^R,A_2|}$ for both 2008 and 2009; Case III

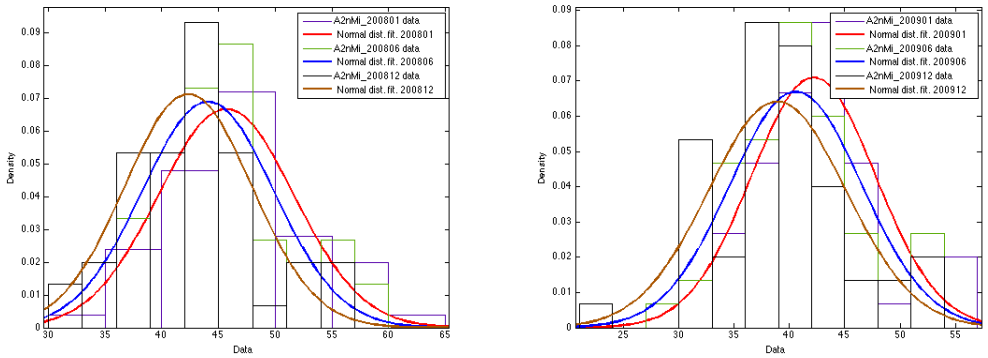


Figure F.10: Normal distribution fit of $\bar{x}_{|\neg M_z^I,A_2|}$ for both 2008 and 2009; Case III

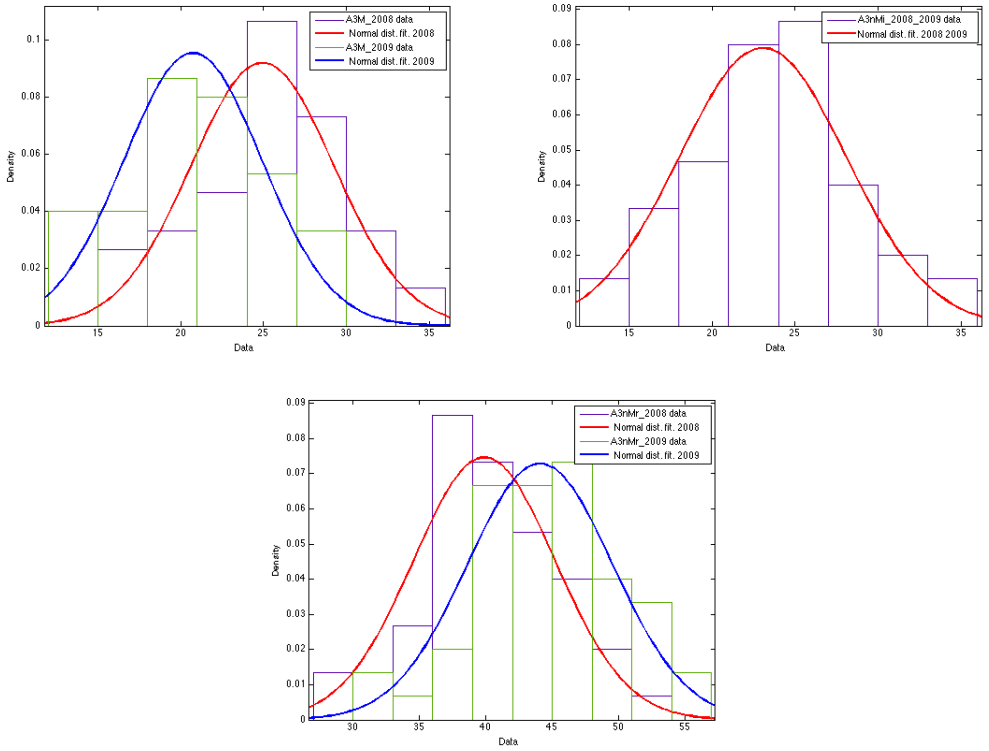


Figure F.11: Normal distribution fit to $\bar{x}_{|M_z,A_3|}$, $\bar{x}_{|\neg M_z^I,A_3|}$ and $\bar{x}_{|\neg M_z^R,A_3|}$ for both 2008 and 2009; Case III

F.4 Case IV

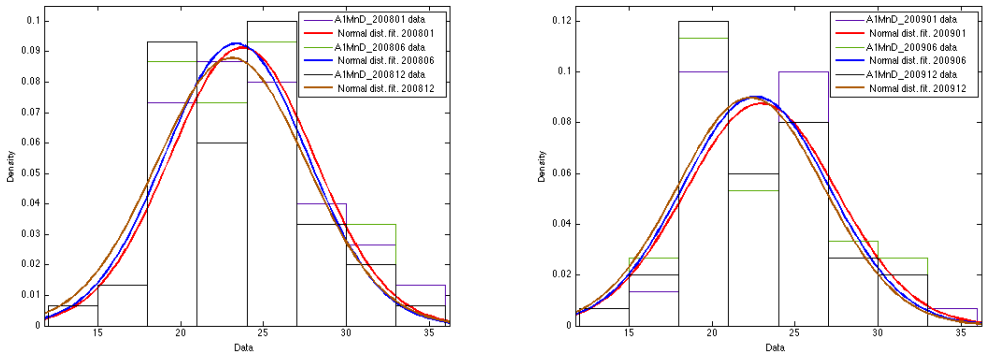


Figure F.12: Normal distribution fit to $\bar{x}_{M_z,A_1,\neg D}$ for January, June and December in both 2008 and 2009; Case IV

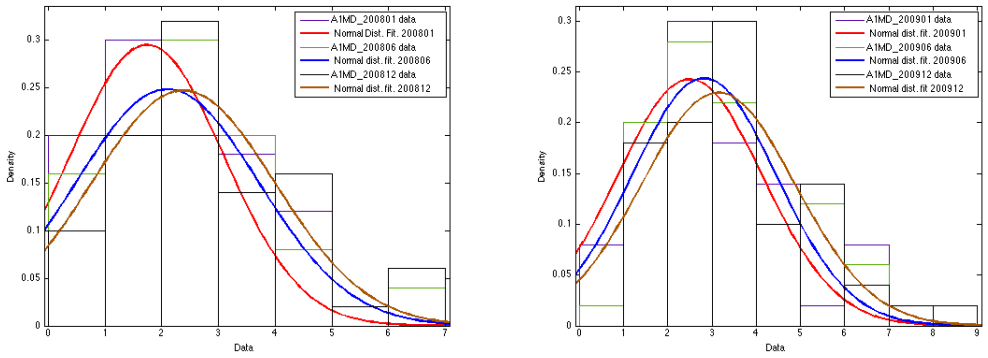


Figure F.13: Normal distribution fit to $\bar{x}_{M_z,A_1,D}$ for January, June and December in both 2008 and 2009; Case IV

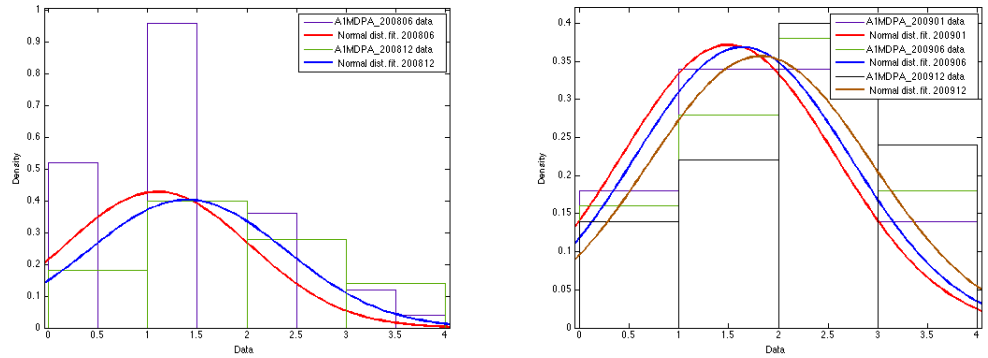


Figure F.14: Normal distribution fit to $\bar{x}_{M_z,A_1,D,P_A}$ for January, June and December in both 2008 and 2009; Case V

Figure F.15: V

F.5 Case V

F.6 Case VI

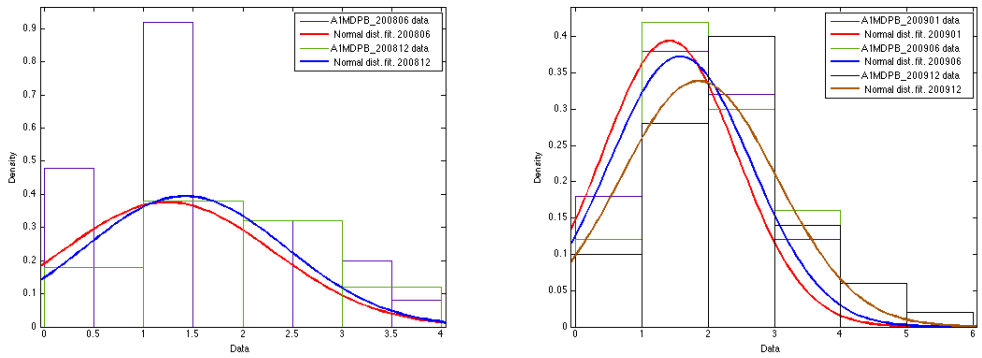


Figure F.16: Normal distribution fit to $\bar{x}_{M_z,A_1,D,P_B}$ for January, June and December in both 2008 and 2009; Case V

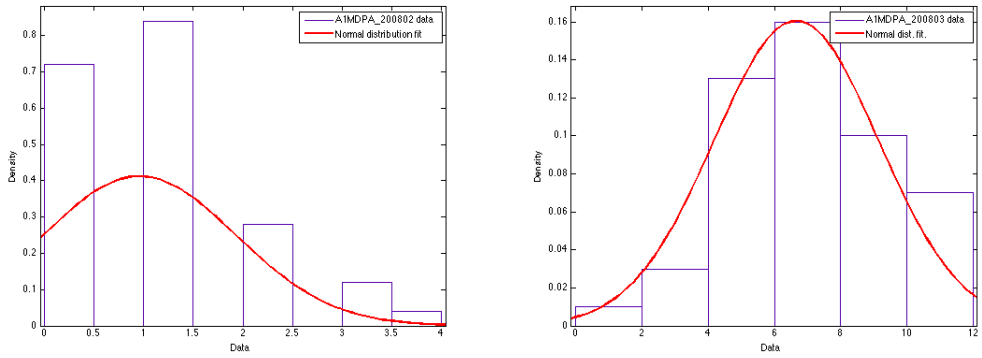


Figure F.17: Normal distribution fit to $\bar{x}_{M_z,A_1,D,P_A}$ for February, March 2008; Case VI

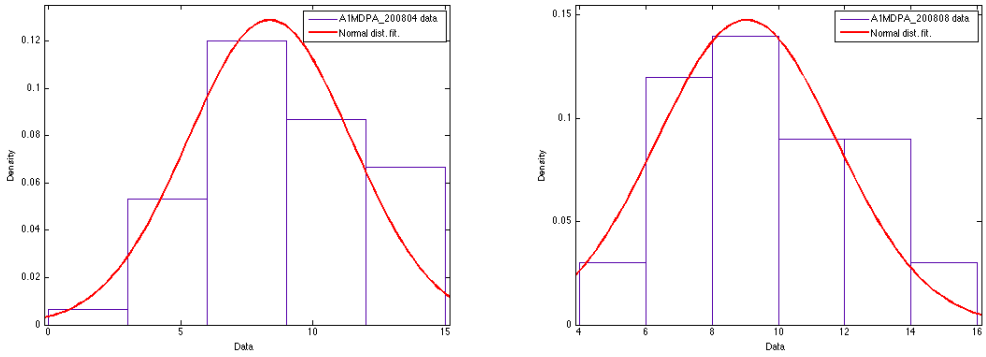


Figure F.18: Normal distribution fit to $\bar{x}_{M_z,A_1,D,P_A}$ for April, August 2008; Case VI

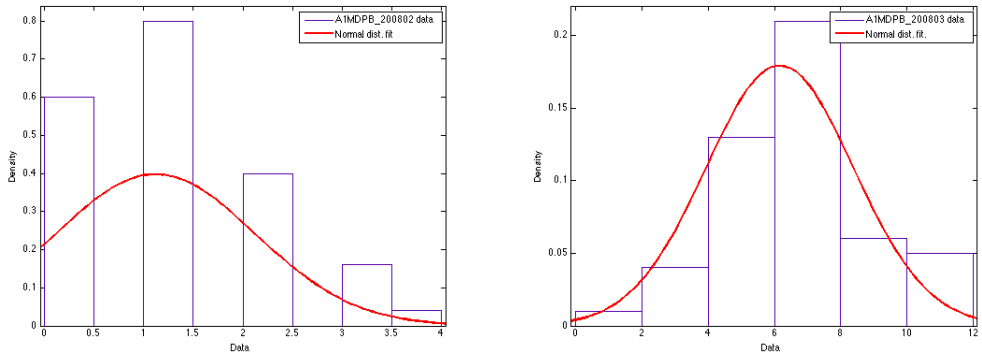


Figure F.19: Normal distribution fit to $\bar{x}_{M_z,A_1,D,P_B}$ for February, March 2008; Case VI

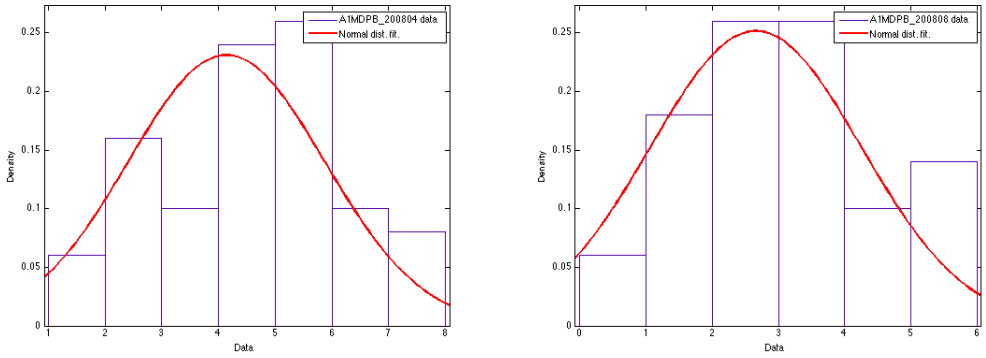


Figure F.20: Normal distribution fit to $\bar{x}_{M_z,A_1,D,P_B}$ for April, August 2008; Case VI

Appendix G

Proof of concept - Simulation machine specifications

The system configuration of the machine used for execution is depicted in table G.1.

Architecture	x86_64
CPU op-mode(s)	32-bit, 64-bit
CPU(s)	16
Thread(s) per core	2
Core(s) per socket	4
CPU socket(s)	2
NUMA node(s)	2
Vendor ID	GenuineIntel
CPU family	6
Model	26
Stepping	5
CPU MHz	2260.973
Virtualization	VT-x
L1d cache	32K
L1i cache	32K
L2 cache	256K
L3 cache	8192K
NUMA node0 CPU(s)	0,2,4,6,8,10,12,14
NUMA node1 CPU(s)	1,3,5,7,9,11,13,15
OS Version	Linux version 2.6.35.14-106.fc14.x86_64 (mockbuild@x86-09.phx2.fedoraproject.org) (gcc version 4.5.1 20100924 (Red Hat 4.5.1-4) (GCC)) #1 SMP Wed Nov 23 13:07:52 UTC 2011
Release	Fedora release 14 (Laughlin)

Table G.1: System configuration of machine used for proof of concept case execution