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Learning in a Causal Probabilistic Network

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Dissertation submitted 2016

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Personal Information

Logan Morgan Ward
Born December 20, 1988, Lower Hutt, New Zealand.

Academic Profile and Research Experience

Logan received his BE (1st Class Honours) in Mechanical Engineering from University of Canterbury, New Zealand in 2010. Following a brief tenure as a research engineer at Industrial Research Limited (a New Zealand Crown Research Institute), he moved to Denmark to pursue his M.Sc. in Biomedical Engineering and Informatics, with the degree awarded by Aalborg University in 2012. He began his PhD studies at Aalborg University's Department of Health Science and Technology in September 2012. During the PhD study, Logan had contributions accepted at five international conferences, with the results of his research producing four papers (two published, one invited and under review, one submitted) and a patent application.

ENGLISH SUMMARY

Sepsis is a severe response to infection, characterised by systemic inflammation leading to tissue damage and organ dysfunction. In septic patients, early, appropriate antibiotic treatment is vital, more so in patients with severe sepsis.

The aim of this PhD project was to further develop an existing causal probabilistic network (CPN) model of sepsis through learning: both manually through evidence-based adjustments to the model and automatically through machine learning from patient databases. The model forms part of a larger CPN used by the decision support system Treat, which provides advice for optimal antibiotic treatment.

The results of the project were described in four papers. Paper I described the manual learning process where continuous distributions were introduced for infection variables. Paper I showed that manual learning is an effective, albeit limited, method of constructing a CPN. On a small validation dataset, the manually learned CPN presented a non-significant improvement in prediction of patients with bacteraemia compared to the previous model. Papers II and III described the automatic learning process wherein the model was tuned to function as a standalone predictor of 30-day mortality. The tuned model was significantly better than both the previous model and other scoring systems described in the literature. Paper IV presented an application of the standalone model tuned to predict bacteraemia. It showed that risk-based stratification of patients suspected of sepsis could be used to improve the cost-effectiveness of rapid diagnostics, e.g. polymerase chain reaction, which would otherwise be too expensive to use for all patients.

The resulting models for the prediction of bacteraemia and 30-day mortality can be used as standalone systems or reintegrated with the Treat decision support system. As a standalone model, the output can be considered as an intelligent biomarker for sepsis, tuned from real patient data. Future work involves the development of a more complete picture of the inflammatory response, including the time-course, which could enable earlier detection of infection or treatment revision in patients for whom infections are not microbiologically documented.

DANSK RESUME

Sepsis er kroppens respons til alvorlig infektion, kendetegnet ved systemiske inflammation som fører til vævsbeskadigelse og organ dysfunktion. I septiske patienter er tidlig, dækkende antibiotika behandling afgørende, desto mere i patienter med svær sepsis.

Formålet af dette PhD projekt var at videreudvikle en existerende kausalt probabilistisk netværk (engelsk: Causal Probabilistic Network, eller CPN) model for sepsis igennem læring: både manual læring igennem evidens-baserede justeringer af modellen og automatisk læring igennem maskin-læring fra patientdatabaser. Modellen er en del af et større CPN inkluderet i beslutningsstøttesystemet Treat, som giver råd om optimal antibiotika behandling.

Projektets resultater blev beskrevet i fire artikler. Artikel I beskrev den manuelle læringsproces, hvor kontinuerte fordelinger blev introduceret for infektionsvariabler. For et mindre valideringsdatasæt, viste CPN'et baseret på manuel læring ikke signifikant forbedring i forudsigelse af patienter med bakteræmi sammenlignet med den tidligere model. Artikel II og III beskrev den automatiske læringsproces, hvori modellen blev tunet til at fungere som en enestående prædiktor af 30-dages mortalitet. Den tunede model var signifikant bedre end både den forrige model og andre scoringsystemer beskrevet i literaturen. Artikel IV viste en anvendelse af den selvstændige model tunet til at forudsige bakteræmi. Den viste at risiko-baseret stratificering af patienter mistænkt for sepsis kunne bruges til at øge cost-effectiveness af hurtig diagnostiske metoder, f.eks polymerase chain reaction, som ville ellers være for dyr til at bruge på alle patienter.

De resulterende modeller for forudsigelse af bakteræmi og 30-dages mortalitet kan bruges som selvstændige systemer eller kan integreres med beslutningsstøttesystemet Treat. Anvendt som selvstændigt system, kan outputtet betragtes som en intelligent biomarkør for sepsis, tunet fra rigtige patientdata. Fremtidigt arbejde involverer udvikling af et mere komplet billede af den inflammatorikse respons, inklusiv tidsforløbet, som kunne give mulighed for tidligere detektion af infektion eller revidering af behandling af patienter, hvis infektioner ikke er mikrobiologisk dokumenteret.

ACKNOWLEDGEMENTS

I have learned a lot during my time as a PhD student at Aalborg University, and the experience has certainly helped me grow both professionally and personally. A new language, a new culture and limitless opportunity to travel was all part and parcel. The academic- and life-lessons learned stand me in good stead for whatever comes next.

First, I would like to thank my PhD supervisor, Steen Andreassen, for his ongoing support and optimism, and continuing belief that a breakthrough was just around the corner.

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Thank you to everyone at Treat Systems for their help with accessing data and the models provided.

I would like to express my gratitude to my colleagues at AAU, in particular those at MMDS. Thank you for all the support, good cheer and company.

Thank you to all those who "forced" me to speak Danish – through making my life difficult you have made it so much easier.

Thank you to all my friends and family for their support and always believing in me.

Last but certainly not least I would like to thank Vladina, for keeping me on track and focused on the end goal, and more importantly, keeping me sane.

TABLE OF CONTENTS

LIST OF PAPERS

This thesis is based on a collection of papers, which will be referred to in the text by their corresponding roman numerals:

- **Paper I:** Ward, L., Mogensen, M.L., Paul, M., Leibovici, L and Andreassen, S. (2014), A Bayesian Approach to Model-Development: Design of Continuous Distributions for Infection Variables. *19th World Congress of the International Federation of Automatic Control (IFAC) 24-29 August, 2014, Cape Town, South Africa*
- **Paper II:** Ward, L., and Andreassen, S. (2015), A Bayesian Approach to Model-Development: Automatic Learning for Tuning Predictive Performance. *9th IFAC Symposium on Biological and Medical Systems, 31 August – 2 September, 2015, Berlin, Germany.*
- **Paper III:** Ward, L., Paul, M., Andreassen, S. Automatic Learning of Mortality in a CPN model of the Systemic Inflammatory Response Syndrome. *(invited, under review: Mathematical Biosciences (Special Issue))*
- **Paper IV:** Ward, L., Leibovici, L., Paul, M., and Andreassen, S. Risk-assessment can improve cost-effectiveness of PCR testing of bacteremia (Submitted)

CHAPTER 1. INTRODUCTION

Sepsis is a severe manifestation of a systemic infection and is associated with high mortality rates: ranging from 15-60% (Angus et al. 2001, Martin et al. 2003, Vincent et al. 2006). Early treatment with appropriate antimicrobials is vital: failure to initiate early appropriate antimicrobial therapy increases mortality with an odds ratio of approximately 2 (Paul et al. 2010). The decision support system Treat provides advice on empirical antimicrobial therapy (before a pathogen is identified) and can significantly increase the fraction of patients receiving appropriate antimicrobial therapy (Kristensen et al. 1999, Paul et al. 2006b, Leibovici, Paul & Andreassen 2010, Kofoed et al. 2009), however there are additional clinical decisions during the course of an infection that are not addressed by Treat. In chronological order from the view of an infectious episode, these are: 1) early detection of the onset of infection; 2) risk assessment to determine the diagnostic and treatment strategy; and 3) revision of therapy a few days after the initiation of therapy. This project focuses on the risk assessment of patients suspected of infection.

Risk assessment of patients suspected of infection serves two purposes: to determine the diagnostic strategy and to determine the aggressiveness of empirical therapy. In each case, severity of illness is a driving factor. The current standard for sepsis diagnosis is blood culture, which typically takes 2-4 days. In comparison, new rapid molecular methods such as polymerase chain reaction (PCR) direct from blood are much faster, identifying a pathogen in 6-12 hours (Liesenfeld et al. 2014, Mwaigwisya, Assiri & O'Grady 2015). Molecular methods are however much more expensive, and it is not currently feasible to order these tests for all patients suspected of infection. A similar prioritisation exists when considering antimicrobial treatment: although broad-spectrum antimicrobials may be able to eradicate most pathogens, they have more undesirable side effects, have led to an increase in C. difficile infections and widespread increase in resistance to antimicrobials (Vernaz et al. 2009, Bartlett 2006, Laxminarayan et al. 2013). In each case, a mathematical risk assessment allows for the balancing of costs and benefits.

Diagnosis and assessment of sepsis severity: SIRS

Traditionally, the relationship between infection and sepsis is understood to be as depicted in Figure 1.1, where SIRS is the Systemic Inflammatory Response Syndrome and bacteraemia refers to an infection in the blood-stream. SIRS is a non-specific state of inflammation, defined at a 1992 consensus conference of the Society of Critical Care Medicine and American College of Chest Physicians (Bone et al. 1992).

A patient has SIRS if they meet two or more of the following criteria:

- Temperature >38°C or <36°C
- White blood cell (WBC/leukocyte) count <4000 or >12000 cells/cm³
- Heart rate > 90 bpm (tachycardia)
- Respiratory rate > 20 breaths per minute

Sepsis is SIRS caused by an infection and non-infectious SIRS (NSIRS) refers to any other aetiology such as trauma/surgery, burns or pancreatitis. Within SIRS and sepsis, patients are also graded by severity, for example: severe sepsis is sepsis complicated by organ dysfunction, and septic shock is severe sepsis with systolic blood pressure less than 90 mmHg, refractory to fluid resuscitation.
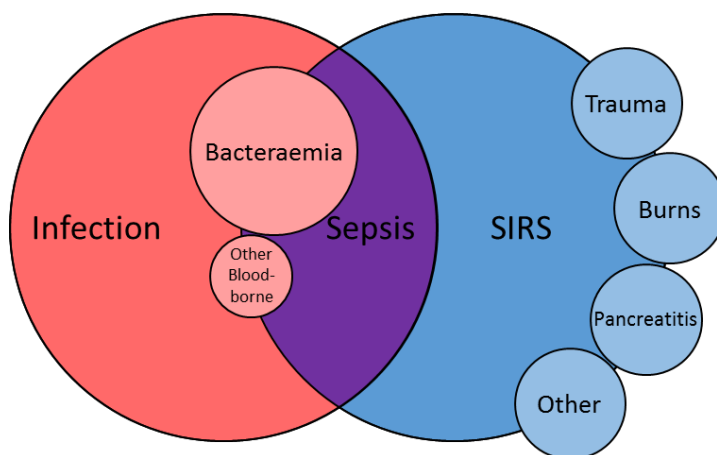
Figure 1.1: The relationship between infection, sepsis and SIRS. Other blood-borne infections refer to all of those not caused by bacteria. Diagram adapted from (Bone et al. 1992)

The idea of SIRS is still part of the most commonly used definition of sepsis, however it has been criticised by leading sepsis researchers – it is unspecific and overall not very useful (Vincent 1997). In reality, almost all patients with an infection have some degree of sepsis: they all have some degree of systemic involvement from the immune system. Figure 1.2 proposes an alternate view where patients with an infection instead fall into strata based the severity of their sepsis. The state of "no sepsis" refers to those with minor infection, for example an infected cut on a finger. The proposed states of sepsis severity are somewhat analogous to sepsis, severe sepsis and septic shock; the new names allow some departure from the literature definitions.

The continuous severity spectrum described in Figure 1.2 is that used in the Treat decision support system. At its core, Treat is a stochastic model of the interaction of
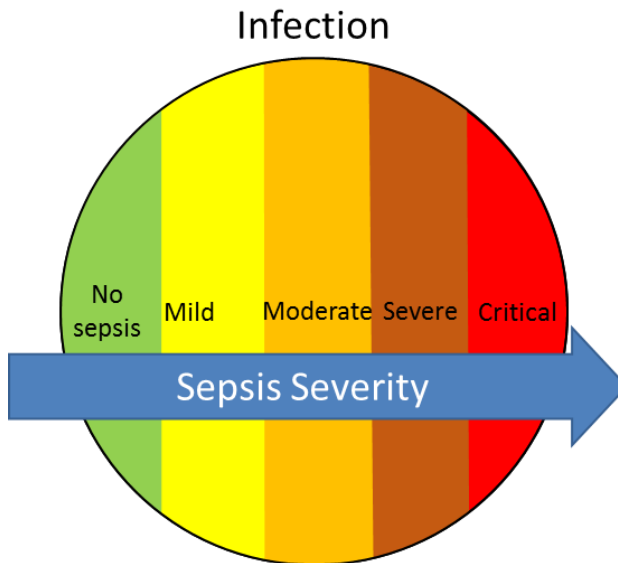
Infection

Figure 1.2: An alternative view: almost all patients with an infection have some degree of sepsis and can be stratified by severity

bacteria, antimicrobials and the patient's inflammatory response. This interaction is modelled in a Causal Probabilistic Network (CPN). The part of the model which deals with the inflammatory response is known as the Sepsis CPN. The Sepsis CPN is the main contributor in evaluating the severity of illness. The Sepsis CPN's performance as a diagnostic or prognostic indicator can be evaluated by assessing its ability to predict clinical outcomes such as positive blood culture (bacteraemia) and 30-day mortality.

Several other methods for scoring sepsis or (general) illness severity are described in the literature. The majority of clinical scores are based on logistic regression models. These clinical scores tend to focus on information available at the bedside. Scores used for sepsis patients include the modified rapid emergency medicine score (mREMS) (Olsson, Terént & Lind 2004, Howell et al. 2007), the mortality in the emergency department sepsis (MEDS) score (Shapiro et al. 2003), and the sequential organ-failure assessment (SOFA) (Vincent et al. 1996).

Aim of the PhD study

The PhD study centres on the development of a family of models for the gradation of the severity of sepsis. The starting point for the project is Treat's Sepsis CPN, with the goal of updating the Sepsis CPN and improving its performance in predicting bacteraemia and 30-day mortality. The approach taken to solve the problem follows

a Bayesian philosophy: a stepwise updating of *a priori* understanding based on the knowledge available. In this case domain knowledge is acquired from the literature, opinions of clinical experts and from patient databases.

Figure 1.3 presents an overview of the PhD project in three stages. Chapter 2 presents the background, including CPN technology and an overview of sepsis and its manifestations, Chapters 3 and 4 present the manual and automatic learning stages of model development, respectively, and Chapter 5 presents an application of the learned SepsisFinder model: selection of high-risk patients for rapid diagnostic testing. Chapter 6 then contains a discussion of key points and main findings of the thesis, and suggestions for future work.
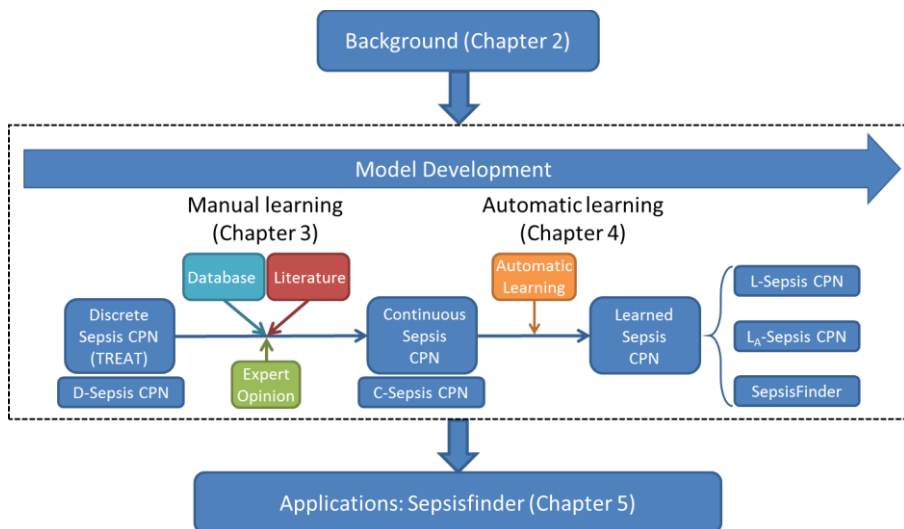
Figure 1.3: PhD Project Framework

The initial phase of the PhD project focused on building knowledge and understanding of how sepsis develops and the typical markers, signs and symptoms seen in patients. Literature concerned with the construction and performance of the Treat CPN was also investigated. The Treat CPN serves as an example of a CPN model that was constructed largely manually, that is, without applying machine learning techniques. A search was also conducted into learning from data in medicine and the machine learning methods available, notably expectation maximisation (EM) learning. This research was important in building the domain knowledge required to successfully construct a CPN and forms the background material presented in Chapter 2.

The next phase of the project focused on model development, shown in the dashed box in Figure 1.3. Stepwise improvement of the model via learning was conducted in

two stages: first by manual learning (Chapter 3) and then subsequently by automatic learning (Chapter 4).

Chapter 3 summarises the work carried out in the manual learning stage: a set of continuous distributions for infection variables that improve Treat's prediction of bacteraemia. The result of the manual learning was the Continuous (C-) Sepsis CPN. This method of constructing CPNs was proven to be robust, and was the method used in constructing the Treat CPN. This Chapter is based on Paper I.

Chapter 4 describes the automatic learning process and the results of tuning two CPNs: one to predict 30-day mortality and one to predict bacteraemia in patients suspected of sepsis. Applying machine learning gives the potential to use the knowledge contained in patient databases, something that has not formally been done in the Treat model. The result represents a significant improvement over the model described in Paper I. This Chapter is based on Papers II and III which described two Learned Sepsis CPNs, the L-Sepsis CPN (Paper II) and the L_A-Sepsis CPN (Paper III) that were tuned to predict 30-day mortality. Chapter 4 also describes the SepsisFinder model, which was tuned to predict bacteraemia using a similar learning strategy.

The third and final phase of the project is concerned with the application of the tuned SepsisFinder model, and is described in Chapter 5. The SepsisFinder model is used for risk-assessment, where the predicted probability of bacteraemia can be used to define a group of high-risk patients for whom rapid diagnostic testing may be cost-effective. Paper IV describes the use of SepsisFinder in assessing the cost-effectiveness of one rapid diagnostic technique, PCR, in the emergency department. This application was also described as part of a patent application (Application number: PA 2015 00514) which centred on the idea that one parameter (sepsis severity) can be used for many purposes, including but not limited to the prediction of bacteraemia and 30-day mortality.

The main findings and scientific contribution of the thesis are discussed in Chapter 6. Suggestions for future work are also addressed, including the re-integration of the Sepsis CPN within Treat, and the use of Sepsisfinder to describe the time-course of infection. A full description of the time-course of infection would provide an opportunity to address two of the remaining clinical problems not addressed by Treat: early detection of the onset of infection and revision of therapy.

CHAPTER 2. BACKGROUND

This chapter provides the medical and technical background for the PhD project. The type of mathematical model used in Sepsisfinder, a Causal Probabilistic Network (CPN) is introduced. The basic principles of CPNs including how they are constructed and used are explained. The medical problem-area, sepsis, is also discussed from the modeller's perspective, using the Treat CPN as an example. This chapter represents the knowledge input to the modelling stage of the PhD project, seen as the highlighted portion of Figure 2.1.
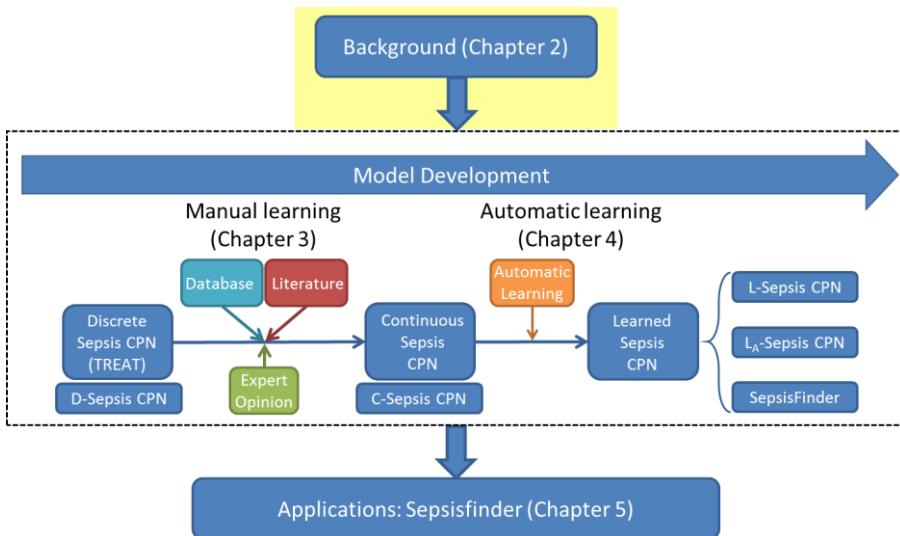
Figure 2.1 PhD project framework. This chapter describes the background (highlighted)

2.1. CPN MODELLING

CPNs, also referred to as Bayesian networks are a type of stochastic model. A CPN can be represented graphically by a set of nodes, linked together by arrows as shown in Figure 2.2. The arrows represent causal relationships between variables. Numerically these arrows can be thought of as conditional probability tables. The task of constructing a CPN consists of specifying the graphical structure and filling out the associated conditional probability tables. Once constructed, the CPN updates the probability distributions according to the axioms of probability theory based on the entered evidence. CPNs are ideal for creating diagnostic models: inferences can be made about unobservable variables based on available evidence, and when accompanied by decision theory and utility functions they can also provide advice on treatment selection.

Flu	
Yes	P(Flu=yes) = 0.05
No	P(Flu=no) = 0.95

	Flu	
Fever	Yes	No
Yes	P(Fever=yes|Flu=yes) = 0.90	P(Fever=yes|Flu=no) = 0.02
No	P(Fever=no|Flu=yes) = 0.10	P(Fever=no|Flu=no) = 0.98

$P(Flu_i)$

$P(Fever_j|Flu_i)$

Figure 2.2: Simple CPN model with one cause (Flu) and one effect (Fever). Two tables are shown: the top table specifies the a priori likelihood of Flu, and the bottom table is the conditional probability table for fever given flu. Adapted from (Andreassen 2000).

Figure 2.2 contains all the information required for probabilistic reasoning. For example, it is possible to calculate the probability for Fever, P(Fever), as the sum of the joint probabilities of Fever given Flu as in Equation 2.1:
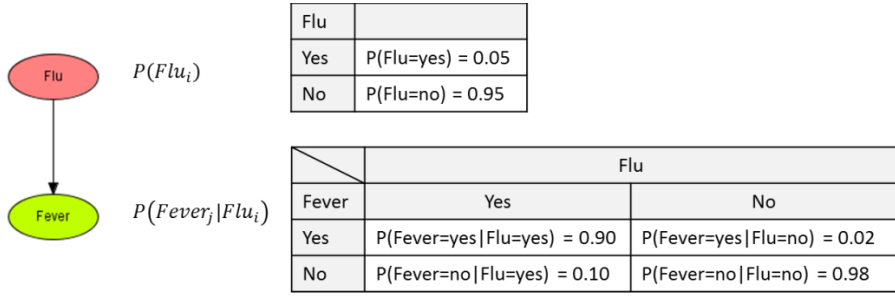
$$P(Fever)=P(Fever|Flu=yes)P(Flu=yes)+P(Fever|Flu=no)P(Flu=no) \qquad (2.1)$$

Using Equation 2.1 we can calculate that P(Fever=yes) = 0.90*0.05 + 0.02*0.95 = 0.064 and P(Fever=no) = 0.10*0.05 + 0.98*0.95 = 0.936. Causal reasoning is simple in this case as these probabilities are specified and can be read directly from the conditional probability table. The ability to provide diagnostic reasoning, inferring the likelihood of a cause based on the observation of an effect is perhaps less apparent. Bayes' Theorem provides the foundation for this type of reasoning; it relates the conditional probability of event A given another event B to the conditional probability of B given A. In this case A and B are Flu (the cause) and Fever (the effect), as in Figure 2.2, and Bayes' Theorem can be written as:

$$P(Flu|Fever)=\frac{P(Flu)P(Fever|Flu)}{P(Fever)} \qquad (2.2)$$

Equation 2.2 is vital to understanding how inference works in CPNs. In this simple two variable case, we know the conditional probability P(Fever|Flu) and the *a priori* probability of flu, P(Flu), and then observing Fever=yes, we can solve Bayes' equation to infer the probability of Flu=yes, as in Equation 2.3. The factor P(Fever|Flu)/P(Fever) in Equation 2.2 can be seen as the effect of the evidence: the factor which the prior probability of Flu (P(Flu)) is multiplied by to give the posterior probability.

$$P(Flu=yes|Fever=yes)=\frac{P(Flu=yes)P(Fever=yes|Flu=yes)}{P(Fever=yes)} = \frac{0.05*0.90}{0.064}=0.703 \qquad (2.3)$$

The example shown in Figure 2.3 is another simple CPN, this time with two causes: flu and throat infection, and two symptoms: fever and sore throat. Fever and sore throat can each be caused by flu and/or throat infection, as indicated by the arrows. The conditional probability tables are filled out when constructing the CPN, specifying the joint probabilities for sore throat and fever respectively, given flu and throat infection: P(Fever| Flu, Throat infection) and P(Sore throat | Flu, Throat infection) (Figure 2.3, panel A). In this case, observing Fever=no and Sore throat=yes allows us to infer that a throat infection is much more likely than the flu (Figure 2.3, panel B).

Flu	
Yes	0.11
No	0.89

Throat Infection	
Yes	0.11
No	0.89

	Fever			
Flu	Yes		No	
Throat Infection	Yes	No	Yes	No
Yes	0.99	0.9	0.9	0.02
No	0.01	0.1	0.1	0.98

	Sore_throat			
Flu	Yes		No	
Throat Infection	Yes	No	Yes	No
Yes	0.91	0.1	0.9	0.01
No	0.09	0.9	0.1	0.99
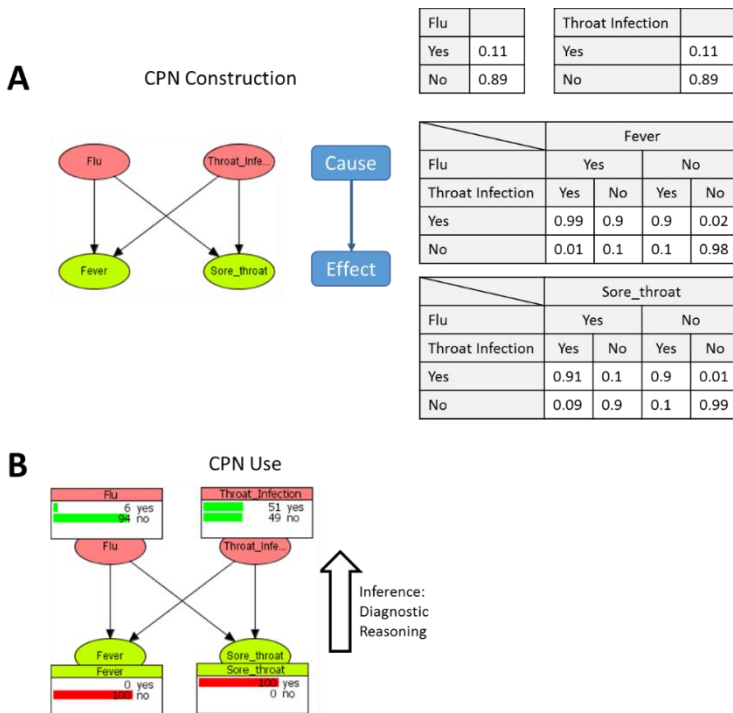
Figure 2.3: Construction and use of a simple CPN. During construction (panel A), the structure and probability tables are specified using a top-down approach, following the flow of causality. During use (panel B), when the effects are observed, diagnostic reasoning can be applied, using the evidence to make inferences about the likely cause. Adapted from (Andreassen 2000).

The example in Figure 2.3 is simple enough that the inferred probabilities could be calculated by hand. However, inference quickly becomes complicated as more nodes and dependencies are added. For more complex CPNs, software solutions become necessary. All CPNs used in this thesis were constructed using the commercial software package Hugin (Hugin Expert A/S, Aalborg, Denmark), which was also used to perform inference.

2.2. LEARNING IN CPNS

The construction of a CPN provides a unique opportunity for the fusion of data and knowledge. Importantly, this knowledge may come from any one (or more) of a number of sources: in the medical domain these could be patient databases, expert opinion and reports in the scientific literature. Before beginning construction of a model, it is important to understand the problem area: for the infectious process this would include the pathogenesis and pathophysiology and what can be observed in a patients, for example blood gases, haematology, vital signs etc. The model variables and structure are then identified based on the knowledge acquired: this can be done manually or automatically, the latter referring to the use of machine learning techniques. During the construction of the CPN, the conditional probabilities may themselves be considered stochastic variables; *a priori* distributions may be assigned, and the result of learning is the set of *a posteriori* distributions.

2.2.1. MANUAL LEARNING

In the context of this thesis, manual learning refers to the specification of CPN structure and conditional probability tables without applying machine learning techniques. Manual learning therefore refers to all other forms of knowledge acquisition; review and meta-analysis of the scientific literature, uni- or multivariate analysis of patient data, or the transformation of expert opinion into explicit conditional probabilities. Manual learning can be an effective method for constructing CPNs: the Treat CPN, described in section 2.3 was constructed in this way. Manual learning was also applied in the construction of the models described in this thesis. The specific learning strategy used in described in Chapter 3 which is based on Paper I.

2.2.2. MACHINE LEARNING

Machine learning from patient data can be used instead of or as a supplement to the manual learning process used to construct a CPN. Traditionally, machine learning is used to form classification models where cases must be assigned to one of two or more groups based on a set of parameters (measurements/observations) which may be continuous or categorical variables or regression models (prediction). If the classification of each case is used as an input at the learning stage, the process is termed "supervised" learning, whereas if the classification is not used as an input, learning is "unsupervised".

A range of machine learning algorithms exist, each with certain advantages and disadvantages dependent on the type of problem. For this thesis, the discussion will be limited to Expectation Maximisation (EM) learning (Lauritzen 1995), a maximum likelihood method. An algorithm for EM learning is available in the Hugin software.

The learning process proceeds as follows. The CPN constructor specifies which conditional probability tables should be learned: this may be any or all tables and/or parts thereof. It is also possible to enforce zeros in conditional probability tables to define impossibilities. Following the specification of what is to be learned, the EM algorithm begins to iterate. The algorithm maximises the likelihood of all cases, calculated as the product of the joint probability of the data for each case. In Hugin, the algorithm terminates either when the specified maximum number of iterations is reached or the tolerance for the difference in log-likelihood between two successive iterations is reached.

If all of the nodes in a CPN are observed, and these observations are recorded in the case data for learning, the learning process degenerates to counting and becomes trivial. However, this is not the case for the sepsis model. The sepsis CPN contains several latent (unobservable) variables which is an added difficulty where learning is concerned. This is coupled with the fact that medical/clinical databases are typically plagued by missing data; not every patient receives the same tests.

2.3. THE TREAT MODEL OF INFECTION

The Treat CPN was constructed via a semi-formal approach, using the literature, expert opinion and patient data to specify the conditional probability tables. The success of this technique has been demonstrated empirically through the success of Treat (Kristensen et al. 1999, Paul et al. 2006b, Leibovici, Paul & Andreassen 2010, Kofoed et al. 2009). The Treat CPN, shown in Figure 2.5, is very large, containing approximately 6000 nodes. Within the CPN, eleven sites of infection are modelled, each with local symptoms and findings and a set of relevant pathogens. One small section of Treat describes the inflammatory response: the Sepsis CPN, highlighted in Figure 2.5. Treat is specifically designed to account for geographical, demographical and other hospital-specific differences in pathogen prevalence and resistance to antimicrobials; it is calibrated to each specific hospital as part of the installation process.

Treat's advantage over clinicians is due to the ability of the CPN to hold knowledge in the form of large arrays of conditional probability tables and to handle complex probability calculus. The prescription of empirical antibiotic treatment involves a set of decision points which the clinician must go through. First, the clinician must decide whether the patient has an infection, and if so, where the infection is focused. Based on the likely focus of infection, the clinician must then decide what the most likely causative pathogen is. Given the most probable pathogen, which treatment offers the best balance of coverage (dependent on local resistance patterns), potential side-effects and cost? Empirical antimicrobial prescribing is not a trivial task, it involves complex decision-making, and computerised decision support tools may be able to improve the practice (Leibovici et al. 1999). The set of decisions made when

prescribing antimicrobials can be equated to the multiplication of large conditional probability matrices, which is not a task that humans excel at.
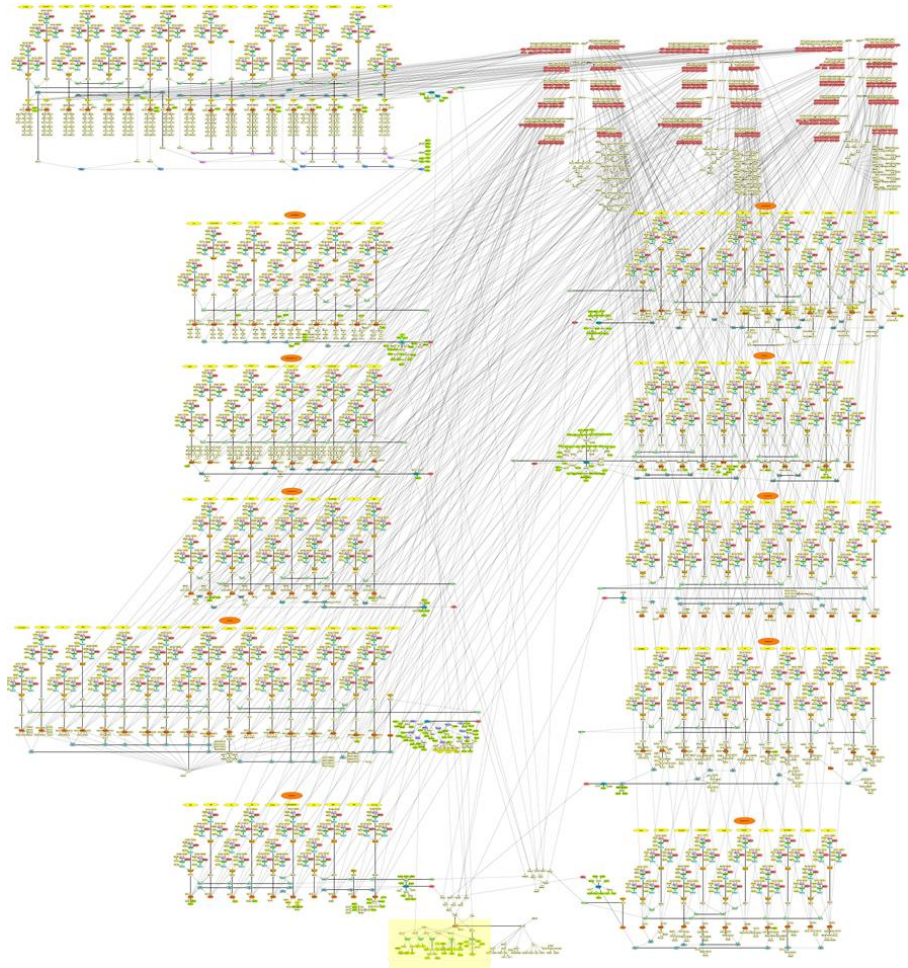
Figure 2.5: The Treat CPN. The structure of the CPN is divided into 11 sites of infection, where the base units are pathogens. One small part of the network, the Sepsis CPN (highlighted), deals with the inflammatory response.

Treat has been described extensively in the literature, from the original concept (Andreassen et al. 1999, Leibovici et al. 2000), through its development into a tool suitable for research (Andreassen et al. 2005) to the results achieved through clinical trials of the system (Paul et al. 2006b, Paul et al. 2006a, Paul et al. 2007, Leibovici et al. 2007, Leibovici, Paul & Andreassen 2010). Treat was developed collaboratively by researchers at Aalborg University (AAU) and Rabin Medical Centre, Israel as part

of an EU funded project (EU 5th framework, Information Society Technologies, contract no.: IST-9999-11459) The stochastic model of infection shown in Figure 2.5 is combined with decision theory to provide advice that seeks to maximize the probability of effective treatment while minimizing both the direct cost of the treatment as well as the ecological cost of furthering antimicrobial resistance and any side effects that may occur.

In an observational trial run in three major European hospitals, Treat showed great improvements versus clinician-only regimes, improving covering antibiotic treatment from 57% to 70% (Paul et al. 2006b). Treat also showed improvements when used in a cluster-randomized interventional trial with appropriate empirical antibiotic treatment in 73% of cases in interventional wards compared with 64% in control wards (Paul et al. 2006b). Long-term (6 month) survival was also higher in interventional wards, and even higher in cases where Treat's recommendations were followed (Leibovici, Kariv & Paul 2013).

2.4. SEPSIS: THE MODELLER'S PERSPECTIVE

This section uses Treat's Sepsis CPN to explain sepsis from a modelling point of view, describing its construction. To build a causal model, it is necessary to understand the pathogenesis and pathophysiology of sepsis, and how this can be recognised in terms of measureable variables such as clinical chemistry, blood gases, haematology, etc. Section 2.4.1 describes what happens to a patient during sepsis in terms of the physiological changes typically seen in sepsis patients. The variables used by the Sepsis CPN and their links to sepsis pathophysiology are also described. Section 2.4.2 describes how CPN models can be used to describe a patient's condition, defining the conditional probability tables linking the model parameters and patient condition. This step can also be thought of as the development of a composite biomarker.

2.4.1. WHAT HAPPENS TO A PATIENT DURING SEPSIS

The response to an infection depends on the severity of the disease, as well as other host-specific factors: comorbidities and immune-status modifiers (immunosuppressant drugs etc.). The SIRS criteria are present in most patients as they are part of the general response to infection. Increasing severity of sepsis is generally associated with a greater degree of organ dysfunction and/or failure. Figure 2.7 describes some of physiological alterations seen in sepsis: all major organ systems are involved. Inflammatory variables shown in the white box are common manifestations of sepsis that are not linked to any organ damage specifically.

General variables
Altered mental status
Fever or Hypothermia
Tachycardia
Tachypnea
Significant edema/positive fluid balance
Hyperglycaemia

Inflammatory variables
C-Reactive Protein
Procalcitonin
Leukocytosis or leukopenia
Increase in immature leukocytes

Organ dysfunction variables
Arterial hypoxemia
Coagulation abnormalities
Ileus
Thrombocytopenia (platelets)
Hyperbilirubinemia
Acute oliguria
Creatinine increase

Haemodynamic variables
Arterial hypotension
Venous oxygen saturation
Cardiac index

Tissue perfusion variables
Hyperlactatemia
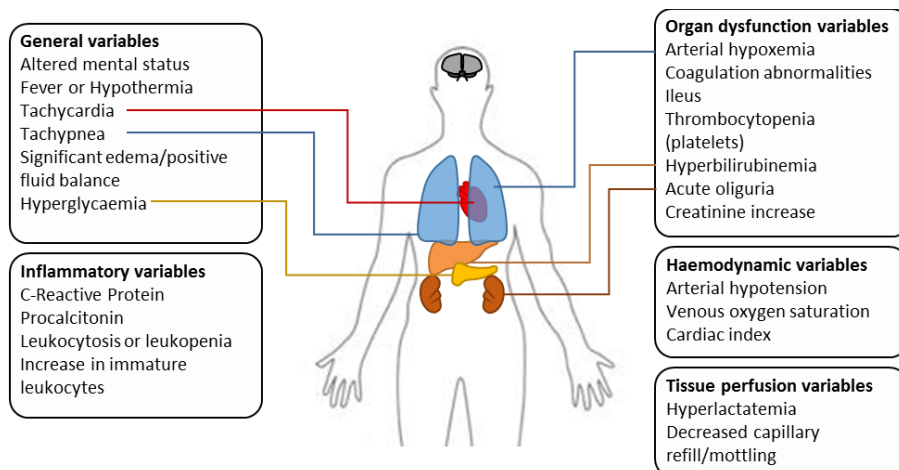Decreased capillary refill/mottling

Figure 2.7: Physiological changes seen during sepsis according to the 2001 International Sepsis Definitions Conference (Levy et al. 2003). Sepsis patients may present with some or all of these.

Table 2.1: Treat infection variables and their relation to sepsis pathophysiology and sepsis severity. + designates higher values and - designates lower values of the variables.* designates significant predictor (p<0.05)

Infection Variable (units)	Change in the variable for given severity				Predictive Ability (AUC)	
	Mild	Moderate	Severe	Critical	Bacteraemia	30-day Mortality
Temperature (°C)	-/+	++	++	++ or --	0.62*	0.48
Heart rate(beats/min)	++	++	++	++	0.59*	0.54*
Respiratory rate (breaths/min)	+	++	++	+++	0.52	0.63*
Leukocytes (cells/mm^3)	+	++	++	++ or --	0.53	0.56*
Creatinine (mg/dl)	+	+	++	+++	0.61*	0.59*
Albumin (g/l)	-	--	---	----	0.63*	0.72*
CRP (mg/l)	+	+++	+++	++++	0.63*	0.45
Lactate (mmol/l)	-/+	-/+	+	++	0.67*	0.54
Mental-status	-/+	-	-	--		
Blood pressure (mmHg)	-/+	-/+	-	---	0.57*	0.57*

Table 2.1 takes a detailed look at a selection of the variables noted in Figure 2.7: those used in the Sepsis CPN, and their association with sepsis. The choice of variables was based on availability of measurements/recorded data in available patient databases as well as expert opinion regarding the variables involved in the systemic response to infection. For each variable, + and − indicate that higher- or lower values, respectively, are associated with given sepsis severities. The changes in each variable given sepsis severity are based on those in the Treat Sepsis CPN. The predictive ability is measured by the area under the ROC curve (AUC). An AUC = 0.5 is indicative of no discrimination and AUC = 1 is perfect discrimination. To compute the AUC, it was assumed that a higher value of the variable would predict bacteraemia and 30-day mortality, with the exception of albumin and systolic blood pressure, where the opposite was assumed. The dataset used consists of 3589 patient cases collected during trials of Treat at Beilinson Hospital, Petah Tiqva, Israel, between 2004 and 2011. The dataset is described further in Chapter 4.

After identifying candidate model variables, it is necessary to specify the model structure. The simplest version of a CPN is the so-called "naive Bayes" model, where all of the effects are directly linked to one cause, as shown in Figure 2.8. However, "naive Bayes" requires that all of the variables are independent, which is not the case for many of the sepsis variables. The original constructors of the Sepsis CPN got around this problem by performing a factor analysis − a dimensional reduction technique − to group the observable parameters beneath a set of statistically constructed independent factors (Leibovici et al. 2000). The result was four intermediate factors that described 80% of the variation in the data. The model
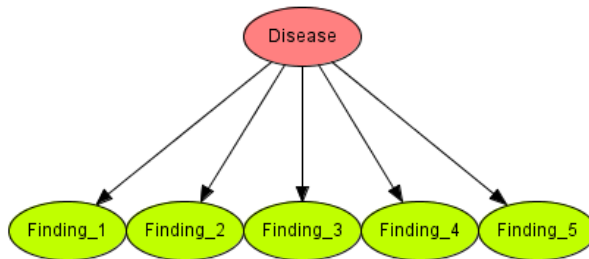

Figure 2.8 "Naive Bayes" model of a disease

structure is shown in Figure 2.9.It was speculated that these factors may have physical analogues − when the same method was used on a set of data including inflammatory mediators, it was found that interleukin 6 (IL-6) had a loading of 0.91 on 'fever factor' − fever factor could be renamed IL-6 and given real units, and tumour necrosis factor alpha (TNF-α) had a loading of 0.50 on 'shock factor' − i.e. it is a major cause of shock factor (Leibovici et al. 2000). The correlation with real physical parameters provides further validation of the technique.
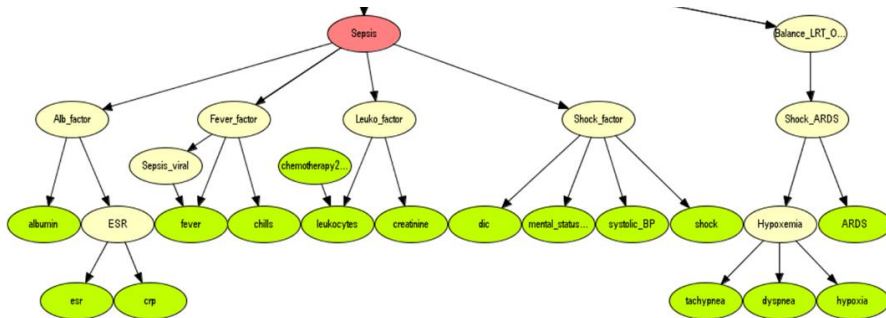
Figure 2.9: Structure of Treat's sepsis CPN. Sepsis (red) causes changes in the set of observable parameters (green nodes) through four intermediate factors: 'Fever_factor', 'Alb_factor', 'Leuko_factor' and 'Shock_factor' (yellow nodes).

2.4.2. DESCRIBING THE PATIENT'S CONDITION

We want to express the severity of a patient's sepsis on a scale from no sepsis to critical sepsis. To do this, we need to make a mathematical description of how each of the infection variables in the Sepsis CPN behave according to the severity of sepsis. The construction of the CPN model takes therefore a top-down approach, asking, for example: given that a patient has moderate sepsis, what is their temperature? The temperature of the 'patient' is then expressed as a probability distribution. This probability distribution may be continuous Gaussian distributions or discrete distributions, the latter was used in the original Sepsis CPN.

Table 2.1 is constructed from a combination of literature knowledge and expert opinion. Finding the numbers to complete the construction of the CPN can then be seen as the conversion of Table 2.1 to a set of conditional probability tables. For patients with no sepsis, it is assumed that they will fall within the normal range.

The construction of the sepsis CPN is completed by translating the knowledge contained in Table 2.1 into conditional probability tables. In the original Treat sepsis network, the factor nodes had three states: no, moderate and severe. Figure 2.10 uses temperature as an example to show how these distributions look for each state of sepsis. In addition to the no sepsis group, the former Treat sepsis CPN recognised four severity groups for bacterial sepsis: mild, moderate, severe and critical. The green bars and the numbers next to them reflect the probability of a patient having a temperature in the specified range, given that they have the degree of sepsis highlighted by the red bar. As expected from Table 2.1, there is little distinction between the temperature distributions for moderate, severe and critical sepsis, but they are all significantly different to the no sepsis group.
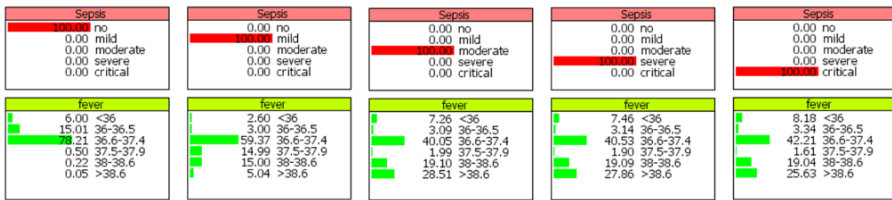
Figure 2.10: Distribution of temperature (fever) for patients with, from left to right, no; moderate; severe; and critical sepsis. The red bars highlight the given severity of sepsis and the green bars represent the respective probability distributions across the temperature groups.

Once the specification of the conditional probability tables is complete, the CPN can be compiled and used. An example of the CPN in use is shown in Figure 2.11. The evidence entered into the model is given by the black text below the nodes. The monitor windows show the inferred probabilities. It is possible to see that each of the "factor nodes" can be activated differently; in this case "Leuko_factor" has more severe evidence entered into its children, showing almost 50% probability of the state "severe", much higher than that observed for "Alb_factor" and "Fever_factor". The children of "Shock" are all set to no or normal, resulting in the probability of "Shock" less than 0.001%. The combined evidence is used to infer that the patient most likely has "moderate" sepsis.
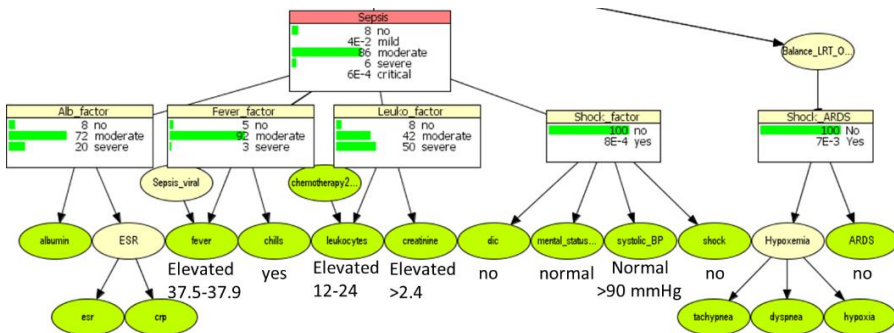

Figure 2.11: The Treat sepsis CPN in use. Evidence entered is shown by the text beneath the nodes, and monitor windows are opened to show the inferred probabilities. Figure adapted from (Andreassen et al. 2005).

CHAPTER 3. MANUAL LEARNING: DEVELOPMENT OF CONTINUOUS DISTRIBUTIONS

This chapter is based on Paper I, entitled "A Bayesian Approach to Model Development: Design of Continuous Distributions for Infection Variables". This paper described the process of updating the Treat Sepsis CPN, subsequently referred to as the discrete sepsis or D-Sepsis CPN, to the continuous sepsis or C-Sepsis CPN. This "manual learning" process represents the first stage of the PhD project's model development stage, highlighted in Figure 3.1.
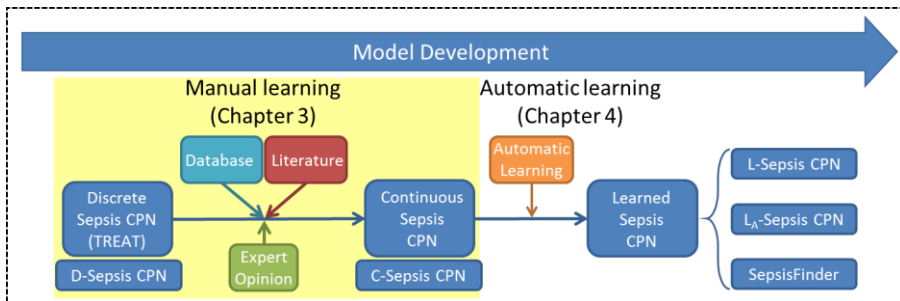
Figure 3.1 Sepsis CPN development framework. Dark blue boxes represent the stages of model development for the Sepsis CPN, other boxes represent the inputs to each construction or learning phase. This chapter describes the highlighted section: the development of the C-Sepsis CPN from the D-Sepsis CPN.

The aim of constructing the C-Sepsis CPN was to improve the performance of Treat and remove some of the undesirable behaviour associated with discrete nodes. "Jumping" in the assessment of the patient state was one such behaviour: the discretization of temperature meant that an increase from 38.6 °C to 38.7 °C could result in a large jump in the assessed illness severity, while an increase from 38.5 °C to 38.6 °C led to no change.

The distributions for each infection variable were learned manually via a semi-formal process where the discrete variables in the D-Sepsis CPN were converted to continuous variables and revised based mainly on expert opinions and the literature. In the C-Sepsis CPN, each infection variable is described as a normal- or log-normal distribution for five illness severities termed no, mild, moderate, severe and critical. A literature search was conducted for each infection variable; some variables were well reported in the literature as they have been researched as sepsis biomarkers while others had little literature available. To describe the process of defining continuous

variables we looked at two examples, one for which much literature is available, CRP, and one for which little is available, albumin.

For CRP, the literature search returned 1654 studies, of which 20 were relevant and of sufficient quality to conduct a meta-analysis. The meta-analysis involved grouping patients according to the severity of their illness, and the aetiology (infectious/non-infectious). In all, nine classifications were used: 4 infectious; viral infection, sepsis, severe sepsis and septic shock, and 5 non-infectious; healthy, no SIRS (patients who may be ill but do not meet the SIRS criteria), SIRS, severe SIRS and non-septic shock. A pooled, log-normal distribution was calculated for each of the nine classifications, the result of which was the 9 distributions shown in Figure 3.2.
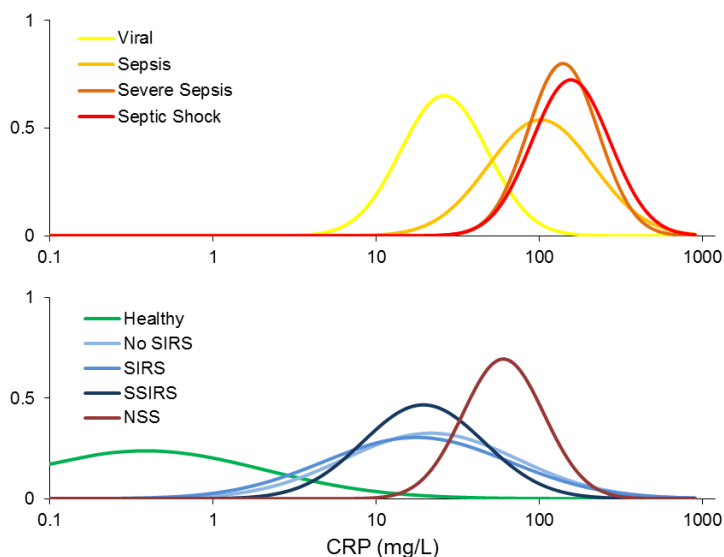

Figure 3.2 Log-normal distributions for 4 infectious (top panel) and 5 non-infectious (bottom panel) patient groups. Individual distributions are the result of meta-analysis of literature studies. Figure from Paper I (Ward et al. 2014).

The distributions described in Figure 3.2 were formed based on literature definitions of sepsis and SIRS patients, and must therefore be mapped to the five illness severities used in the C-Sepsis CPN. The C-Sepsis CPN distributions shown in Figure 3.3 were defined after input from experts, the details of how this was done are described in Paper I.

A similar literature search was conducted for albumin, however none of the 244 resulting papers were suitable for defining explicit distributions for albumin stratified by sepsis severity and/or aetiology. The impossibility of a meta-analysis meant that sepsis/SIRS severity-based distributions for albumin must be designed in a different
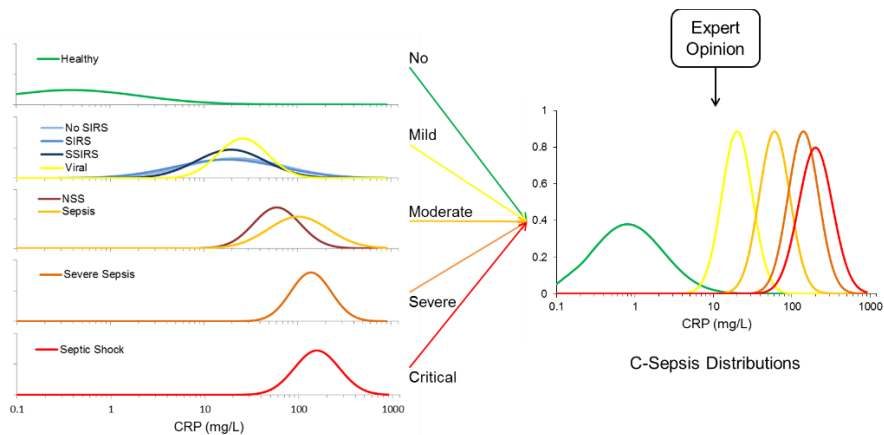
Figure 3.3 Transformation of the normal distributions from the meta-analysis (left) to the C-Sepsis distributions (right). Figure from Paper I (Ward et al. 2014).

way. The discrete distributions used in the D-Sepsis CPN were used along with data from the Treat study (Paul et al. 2006b) to set the range to be covered by the set of distributions. Literature was available to define a distribution for the "no" severity; the distribution was taken from a large study of albumin as a predictor of mortality (Corti et al. 1994). Albumin is also a concentration-dependent predictor of poor outcome (Vincent et al. 2003), with low albumin being correlated with high severity. The distributions implemented in the C-Sepsis CPN are shown in Figure 3.4.
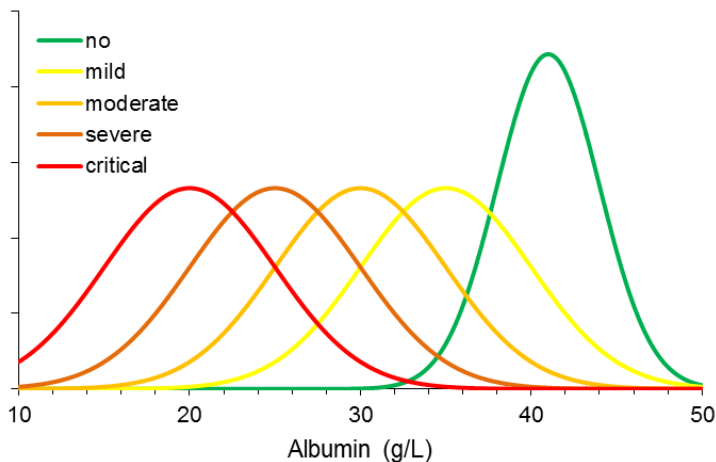

Figure 3.4 C-Sepsis distributions for Albumin. Figure from Paper I (Ward et al. 2014).

As a validation step, the predictive abilities of the D-Sepsis and C-Sepsis CPNs were compared. The Treat CPN, in addition to providing treatment advice, can be used to make a prediction of the probability of bacteraemia. The data used was collected from 263 patients suspected of infection in the acute ward at Hvidovre Hospital, Copenhagen University Hospital, Denmark from November 2011 to May 2012. Of the included patients, 19 (7.2%) had bacteraemia.

The predictive ability of each model (Treat with the D-Sepsis CPN, Treat with the C-Sepsis CPN) was assessed using the area under the ROC curve (AUC): greater area under the curve means better predictive ability. The AUC for the C-Sepsis CPN model was 0.80 (95% Confidence interval (CI) 0.70-0.90) while the AUC for the D-Sepsis CPN model was 0.73 (95% CI 0.62-0.85). The two curves are shown overlaid in Figure 3.5. The difference between the two curves was not statistically significant (p=0.3), however it suggests that the manual construction of continuous nodes in the Treat sepsis CPN can improve the prediction of bacteraemia. This result provided motivation for further testing using a larger database, and further development of the model through the application of automatic learning methods to adjust the prior probability distributions. In subsequent use of the C-Sepsis model, other issues were noted such as extremely large odds ratios when approaching the upper- and/or lower limits of the physiological range for some of the infection variables, notably CRP.
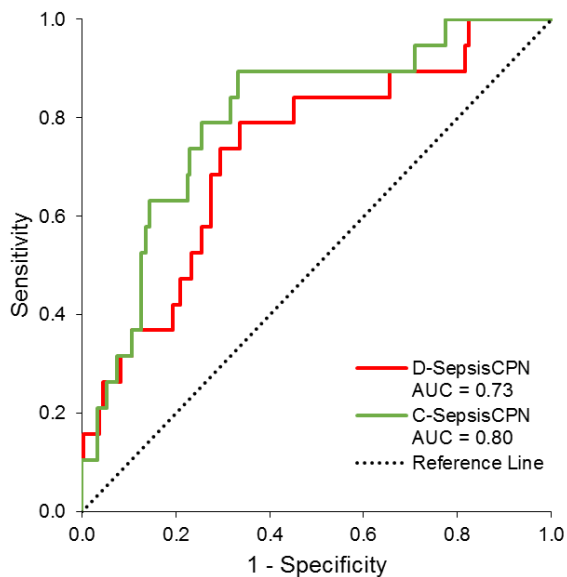

Figure 3.5 ROC curves for bacteraemia prediction for Treat with the D-Sepsis and C-Sepsis CPNs. Figure from Paper I (Ward et al. 2014).

CHAPTER 4. AUTOMATIC LEARNING: MODEL TUNING TO IMPROVE PREDICTIVE PERFORMANCE

Following the manual learning described in Chapter 3, the C-Sepsis CPN was transformed into a Learned Sepsis CPN as described by the highlighted section of the model-development framework in Figure 4.1. This chapter is based on Papers II and III, which describe the steps taken to tune the C-Sepsis CPN to predict 30-day mortality, with the results being the L-Sepsis CPN (Paper II) and the LA-Sepsis CPN (Paper III). Using a similar learning strategy, the C-Sepsis CPN was also tuned to predict bacteraemia, forming a standalone "SepsisFinder" model.
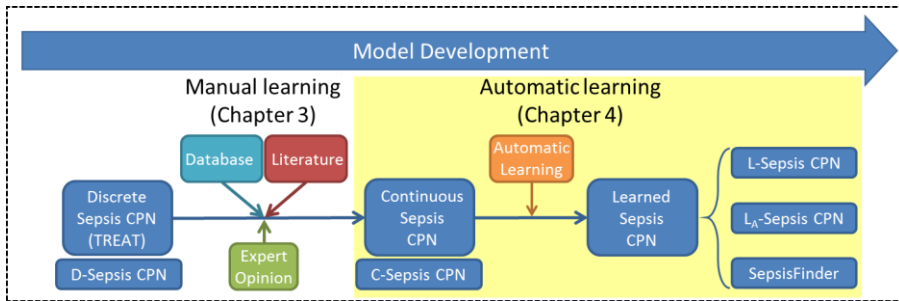

Figure 4.1 Sepsis CPN development framework. Dark blue boxes represent iterations of the Sepsis CPN, the other boxes represent the inputs to each construction or learning phase. This chapter describes the highlighted section: the development of the L-Sepsis CPN from the C-Sepsis CPN.

The C-Sepsis CPN removed the undesirable behaviours of the D-Sepsis CPN, such as jumps in the assessment of the patient state in response to small changes in the input variables. Validation using a small dataset (263 patients) showed a non-significant improvement over the D-Sepsis CPN for the prediction of bacteraemia. However, other undesirable behaviours were noticed, such as excessively large odds-ratios in patients who presented with values of infection variables in ranges that weren't suitably covered by the continuous distributions. The aim of automatic learning was to improve the predictive performance of the network.

The data material used for learning was taken from a set of patient data collected during trials and/or studies of the Treat system (Andreassen et al. 2005, Paul et al. 2006b) at Beilinson Hospital, Rabin Medical Centre in the period from 2004-2011. Patients were included in the studies based on suspicion of infection which included those for whom blood was drawn for culture, those receiving antimicrobials not for

prophylaxis, those with SIRS and those with a clinically identified focus of infection (Paul et al. 2006b). The data included information on infection variables such as the patients' vital parameters, clinical chemistry and blood gases, empirically prescribed treatments, the results of blood and other cultures including *in vitro* susceptibility testing, 30-day mortality, and a final clinical diagnosis. The diagnosis allowed patients to be divided into infectious- and non-infectious groups: data were available for 3589 patients, of whom 2855 had a confirmed infectious or non-infectious diagnosis. The infectious diagnoses also allowed sub-groups to be defined for different sites of infection, for example lower respiratory tract or urinary tract infections. The remaining 734 patients had an unknown or uncertain final diagnosis.

The EM learning algorithm offered by Hugin was used to learn the L_A-Sepsis CPN (Section 2.2.2). The previous semi-formal "manual" learning process connected continuous distributions to literature defined sepsis severities: sepsis, severe sepsis and septic shock, which were then related to our own severity states: no, mild, moderate, severe and critical. Automatic learning from data allows us to move a step further away from the literature distributions and relate our sepsis severity states directly to patient mortality. This represents an important step in the development of the L_A-Sepsis CPN.
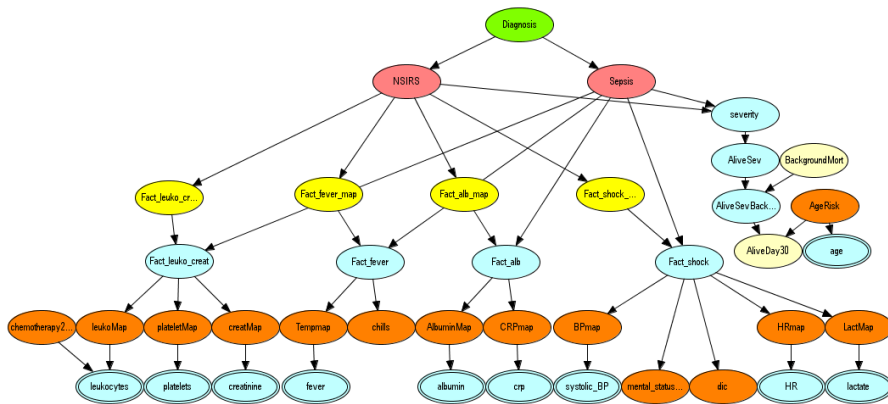

Figure 4.2 The L_A-Sepsis CPN structure, figure from Paper III. Nodes are represented by ovals, causal links by arrows. Causality is expressed through conditional probability tables. The nodes with double rings represent stochastic variables with continuous probability distributions. The remaining nodes have discrete probability distributions. NSIRS is the non-infectious systemic inflammatory response syndrome. Nodes not learned are shown in blue.

The structure of the L_A-Sepsis CPN is shown in Figure 4.2 Three potential causes for death are given: NSIRS, sepsis and background, where background represents all other causes. NSIRS and sepsis are assumed to have the same mortality rates for a given illness severity (Vincent et al. 2006, Dulhunty et al. 2008). Mortality rates are loosely based on the pneumonia severity index (PSI) (Fine et al. 1997) in combination with the sepsis literature, where the latter is used to define the mortality rates for

severe and critical sepsis. The mortality rates used are 0%, 1%, 8%, 45% and 75% for no, mild, moderate, severe and critical, respectively.
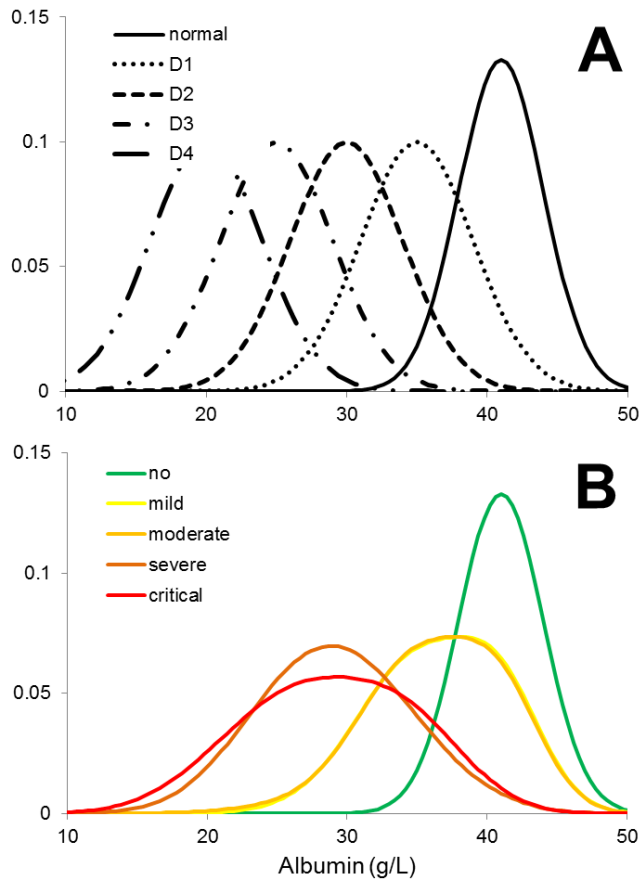

Figure 4.3 An example of initial specified distributions (A) and learned composite distributions (B) for one of the variables in the sepsis CPN: albumin. Each of the distributions in Panel B is a linear combination of the distributions in Panel A. Figure from Paper II (Ward, Andreassen 2015).

Figure 4.3 shows the result of automatic learning for one of the infection variables: albumin. A set of normal distributions, covering the physiological range observed in the patient data, was generated for each variable. Panel A shows these distributions for albumin. Through the EM learning process composite curves are learned for each severity state by learning the tables for the "factor-mapping" nodes (yellow in Figure 4.2). The resulting curves, shown in Panel B, are linear combinations of the curves in Panel A. As noted in Chapter 3, albumin is a concentration-dependent predictor of outcome, which is confirmed here: the more severe states are associated with lower

albumin, although the differences between the mild/moderate and severe/critical distributions are minimal.

Another feature introduced in the C-Sepsis CPN was the possibility to differentiate between NSIRS and sepsis. During automatic learning, the links between the NSIRS severities and the four sepsis factors are learned (Figure 4.2: yellow nodes). Each factor can be considered a branch of the immune system, as suggested by the factors' correlation with inflammatory mediators (Section 2.4.1). Each branch may be activated differently according the aetiology of inflammation, i.e. infectious or non-infectious. Panel A of Figure 4.4 shows the difference in temperature for sepsis = moderate and NSIRS = moderate. Patients with the infectious aetiology (sepsis) present with a higher fever than those without infection (NSIRS) for a given severity of illness. For variables that do not differentiate between infection and no infection, such as systolic blood pressure (Figure 4.4 Panel B), no such difference is seen.
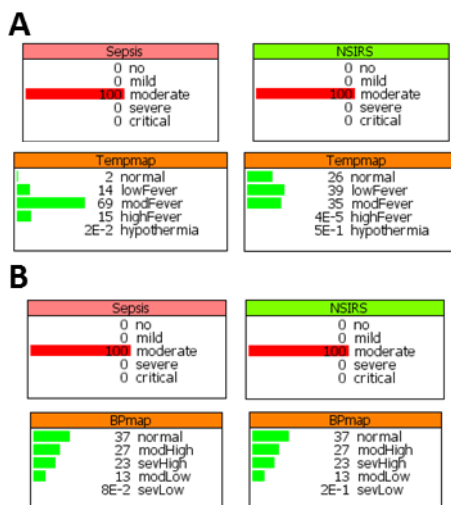
Figure 4.4 Conditional probability distribution for temperature (panel A) and systolic blood pressure (panel B) for Sepsis and NISIRS patients with severity = moderate. Figure from Paper III.

The area under the ROC curve is used to assess the ability of each model to predict 30-day mortality. Figure 4.5 shows ROC curves for the C-Sepsis, L-Sepsis and L_A-Sepsis CPNs. The AUCs for the C-, L- and L_A-Sepsis CPNs were 0.65, 0.74, and 0.79 respectively. Each improvement (C- to L-, L- to L_A-) was also statistically significant ($p=10^{-8}$, $p=0.0004$ respectively). To guard against overfitting, cross-validation was also carried out as part of the development of the L- and L_A-Sepsis CPNs, this is described in further detail in Papers II and III.

Figure 4.5 ROC curves for the prediction of 30-day mortality for the C-Sepsis, L-Sepsis and L_A-Sepsis CPNs. Figure from Paper III.

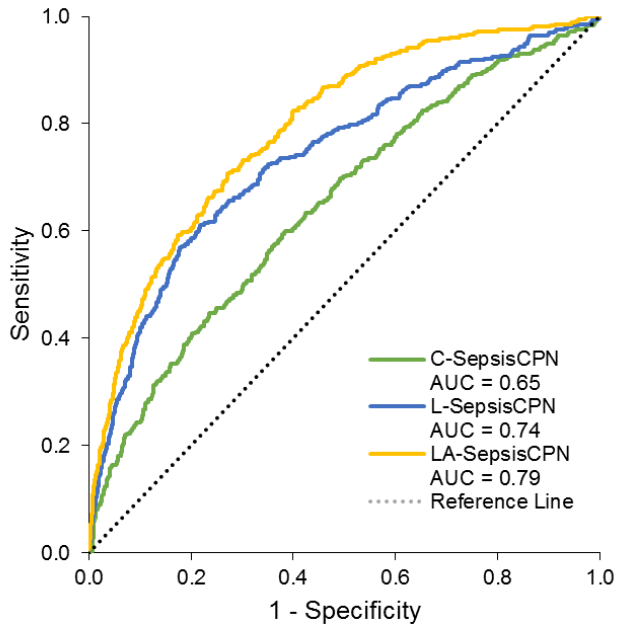In a clinical setting, patients may be graded by a clinical score such as SIRS or mREMS (modified Rapid Emergency Medicine Score) (Olsson, Terént & Lind 2004, Howell et al. 2007). Both SIRS and mREMS could be calculated for only 708 patients (25% of all patients). The 30-day mortality for these patients was 9.9%. Another score, the MEDS (Mortality in Emergency Department Sepsis) score (Shapiro et al. 2003), could not be calculated given the available patient data. Figure 4.6 shows ROC curves for the prediction of 30-day mortality for the LA-Sepsis CPN, mREMS and SIRS scores. The LA-Sepsis CPNs prediction of 30-day mortality outperforms the SIRS and mREMS scores. The AUC of the LA-Sepsis CPN also compares well with the reported performance of MEDS, where the AUC ranged from 0.75-0.88 (Carpenter et al. 2009). The low number of patients for whom the clinical scores could be calculated underlines the advantage offered by CPNs with their ability to handle missing data.

In addition to the discriminative ability assessed by the ROC curve, calibration is assessed by the Hosmer-Lemeshow statistic. Figure 4.7 shows the calibration curve for the L_A-Sepsis CPN. Perfect calibration is seen on the curve as a straight y=x line, i.e. predictions match the observations. A non-significant Hosmer-Lemeshow test result (p>0.05) signifies that the model is well calibrated. The L_A-Sepsis CPN is therefore a well-calibrated model.
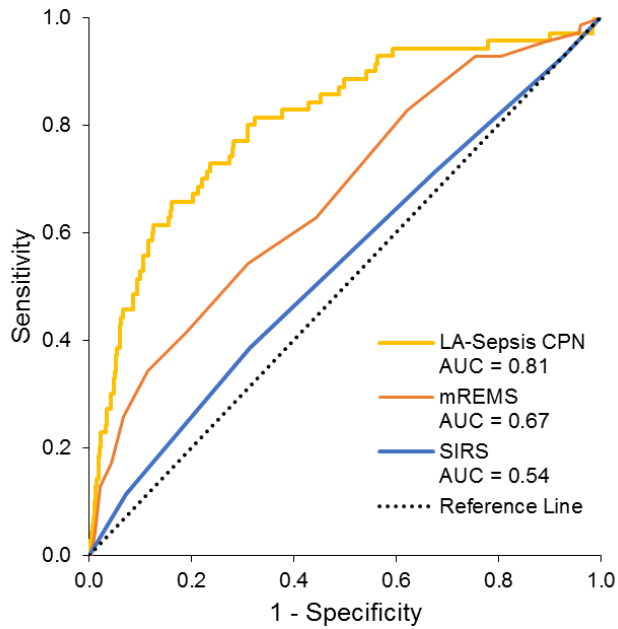
Figure 4.6 ROC curves for the prediction of 30-day mortality for the L$_A$-Sepsis CPN, and the SIRS and mREMS scores.
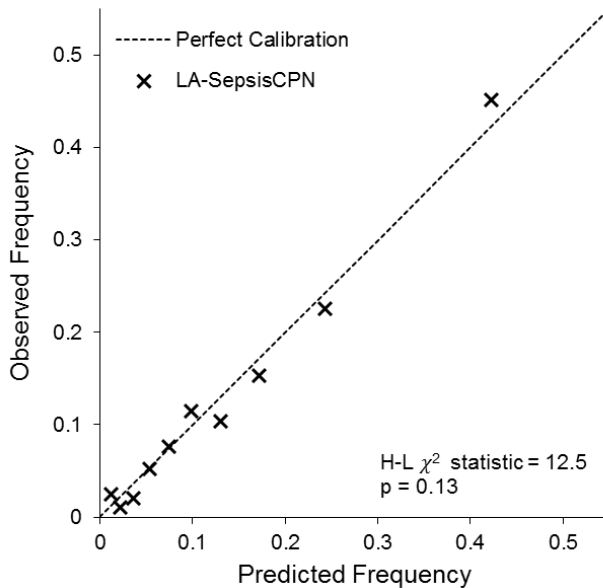

Figure 4.7 Hosmer-Lemeshow calibration curve for the prediction of 30-day mortality using the L$_A$-Sepsis CPN. Figure from Paper III.

Despite the model being well-calibrated overall, we noted some differences in calibration when conducting a sub-group analysis. Figure 4.8 shows regression lines for patients in the two most prevalent infection sites: lower respiratory tract (LRT) infections and urinary tract infections (UTI). There were 697 LRT infections with 128 deaths and 486 UTIs with 41 deaths. The gradients of the regression lines in Figure 4.8 show that for a given severity of the immune response, an LRT infection is more likely to lead to death. This trend was visible for both the L-Sepsis and L_A-Sepsis CPNs.

Prior to the L_A-Sepsis CPN, the Sepsis CPNs were limited to describing the manifestations of sepsis and NSIRS. Risk factors are commonly included in clinical scores such as MEDS. The inclusion of age as a risk-factor in the L_A-Sepsis CPN resulted in a significant improvement in the prediction of 30-day mortality compared to the L-Sepsis CPN. Reintegration within Treat means including a range of other risk factors, including but not limited to comorbidities and the site of infection. The difference between UTI and LRT infections shown in Figure 4.8 suggest that knowledge of the site of infection has the potential to further improve the predictive performance.
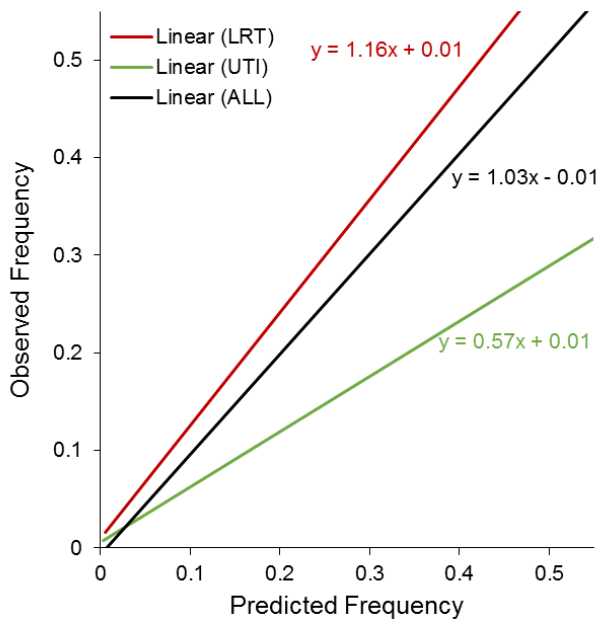

Figure 4.8 Regression lines for the observed 30-day mortality vs. the L_A-Sepsis CPN's predicted 30-day mortality for all 2855 patients (black), 697 patients with a lower respiratory tract infection (red) and 486 patients with a urinary tract infection (green). Figure from Paper III.

Using a similar learning strategy, the C-Sepsis CPN was also tuned to predict bacteraemia, with the result being the "SepsisFinder" model (unpublished). The same 2855 patient cohort was used for the validation of both the L_A-Sepsis CPN and Sepsisfinder. There were 309 patients (10.8%) with bacteraemia. Using SepsisFinder as a standalone model (not integrated within Treat), the AUC for the prediction of bacteraemia was 0.74 (95% CI 0.71-0.76). Figure 4.9 shows ROC curves for the 2885 patients from Beilinson Hospital, along with curves for the prediction of bacteraemia in two cohorts of Danish patients: 263 patients including 19 (7.2%) with bacteraemia from Hvidovre Hospital (HvH) and 199 patients including 11 (5.5%) with bacteraemia from Sygehus Lillebælt (SLB). The AUC for SepsisFinder's prediction of bacteraemia was 0.74 (95% CI 0.63-0.85) for the HvH patients and 0.79 (95% CI 0.67-0.92) for the SLB patients. SepsisFinder's stable performance across the three cohorts suggests that it may not require calibration for local conditions; the response to sepsis is demographically and geographically invariant.

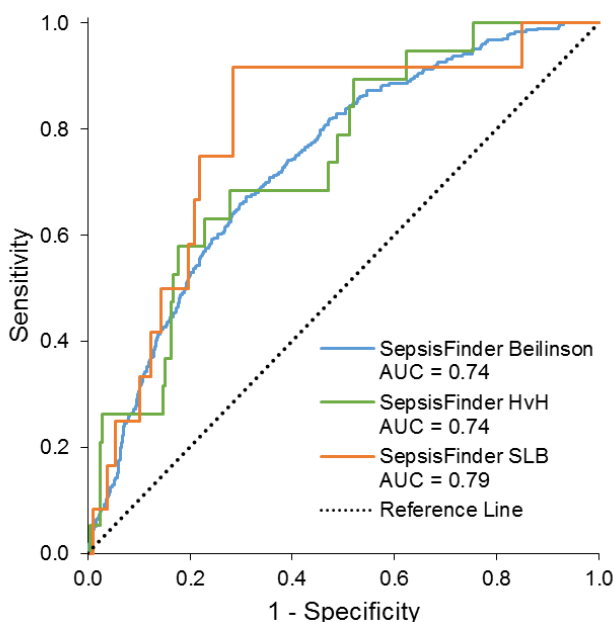*Figure 4.9 ROC curves for the prediction of bacteraemia using the SepsisFinder model on three cohorts of patients: n=2885 patients from Beilinson Hospital, n=263 patients from Hvidovre Hospital (HvH) and n=199 patients from Sygehus Lillebælt (SLB).*

CHAPTER 5. APPLICATIONS OF SEPSISFINDER

This chapter is in part based on Paper IV, which describes one application of the SepsisFinder model described in Chapter 4: identifying candidates for rapid-diagnostic testing through risk-based stratification of patients suspected of infection. This application represents the final stage of the PhD project, an overview of which is shown in Figure 5.1.
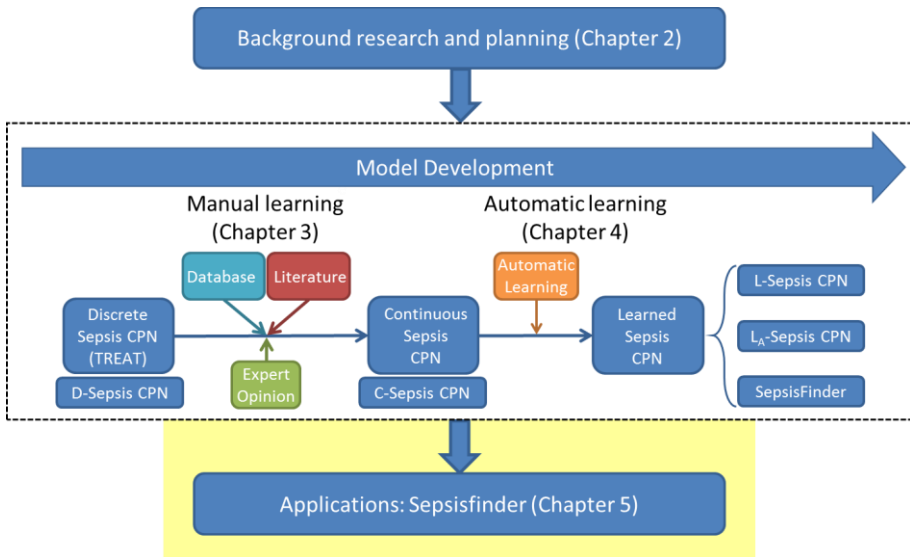
Figure 5.1 PhD project framework. This chapter is associated with the highlighted section: Applications.

Chapter 3 and Chapter 4 described the construction of the C-Sepsis CPN and the L- and L_A-Sepsis CPNs and SepsisFinder, through the manual construction to automatic learning to tune the CPN. Chapter 4 described tuning the model to predict 30-day mortality, and the use of the same technique to tune the SepsisFinder model to predict bacteraemia. The prediction of bacteraemia has significant commercial potential: rapid diagnostic methods can identify the causative pathogen in sepsis patients much faster than blood culture, however they are also much more expensive. Identifying a group of "high-risk" patients where the probability of a positive test is higher has the potential to increase the cost-effectiveness of these tests. In paper IV, PCR testing was used as an example to illustrate this principle.

We assumed that the added value of a PCR test is defined for the incremental increase in the number of patients receiving appropriate treatment, due to the identification of pathogens via PCR. This value is realized as a reduction in mortality: the odds ratio for 30-day mortality for patients receiving inappropriate empiric treatment against those receiving appropriate treatment is approximately 1.60 (Paul et al. 2010). We measure cost-effectiveness relative to standard clinical practice (blood culture alone), with the costs being the total healthcare costs and the effect being the incremental reduction in mortality. The cost-effectiveness is assessed by the incremental cost-effectiveness ratio (ICER) in terms of euros (€) per life-year saved. The ICER is defined in Equation 5.1. The difference in total healthcare costs, $\Delta cost$, is approximated by the two largest contributors: PCR testing, where n_{PCR} is the number of tests conducted and $cost_{PCR} = €300$ (Lehmann et al. 2010, Alvarez et al. 2012) is the cost per test, and the cost of hospitalisation, where $n_{A,add}$ is the additional number of patients receiving appropriate treatment, ΔLOS is the difference in length of stay (in days) for patients receiving appropriate and inappropriate treatment and $cost_{bed}$ is the cost of a bed-day. The incremental effectiveness is measured in terms of the number of life-years saved, where n_{surv} is the incremental number of survivors and $LY_{surv} = 5.43$ years (Lehmann et al. 2010) is the number of life-years saved per survivor.

$$\text{ICER} = \frac{\Delta cost}{\Delta \text{LY}} = \frac{n_{PCR}cost_{PCR} - n_{A,add}\Delta LOS cost_{bed}}{n_{surv}LY_{surv}} \tag{5.1}$$

The data material for the assessment was the 3589 patients described in Chapter 4. Of these patients, 377 had true-positive bacteraemia. True-positive bacteraemia is defined by positive blood culture of a pathogen determined to be clinically significant. The significance of the pathogens found by blood culture was assessed by Treat, Coagulase negative staphylococci, bacillus sp., corynebacteria sp., bacteroides sp. and anaerobic gram-positive rods were all considered non-significant isolates.

The cost-effectiveness analysis used a combination of findings from the dataset along with figures from the literature, with the two being compared where possible. In Figure 5.2 the high-risk group was selected as those patients with model predicted probability of bacteraemia, p_{BC+}, greater than a given threshold $P_{BC+} > 20\%$. The high-risk group consisted of $n = 700$ patients and the fraction of these patients with positive blood culture, f_{BC+}, was 23.9%. The ICER for the high-risk group was €6,934 (95% CI €3,669 - €12,484) per life-year and €24,056 (95% CI €15,936 – €38,959) per life-year for the complementary low-risk group. Confidence intervals were calculated for a 10,000 trial Monte-Carlo sensitivity analysis wherein all parameters in the cost-effectiveness model were varied independently according to their underlying statistical distributions.
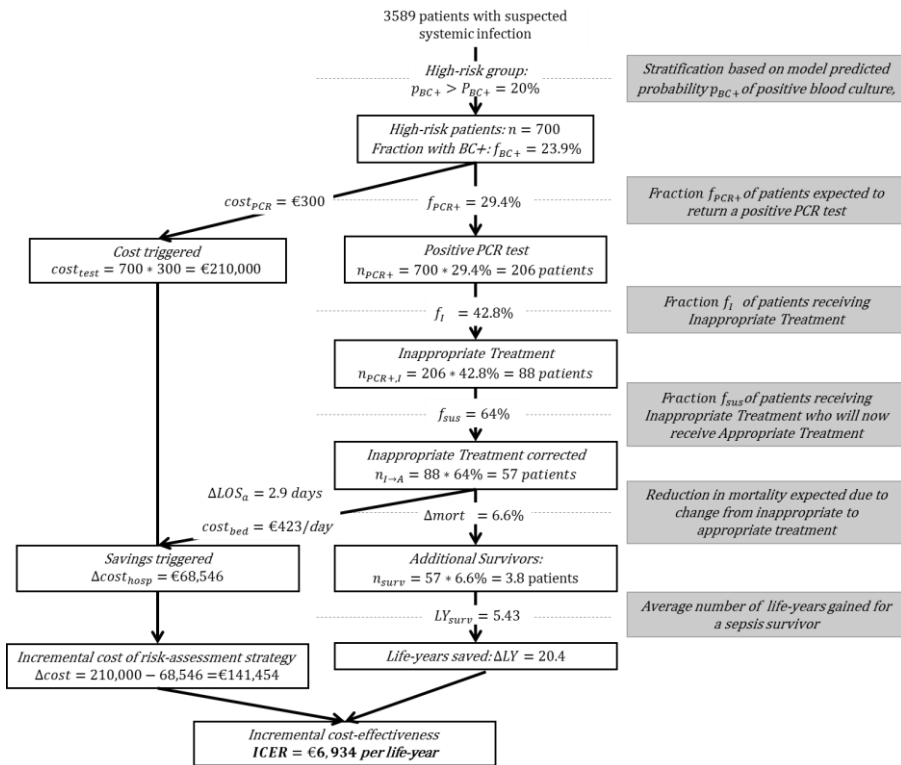
Figure 5.2 Figure from Paper IV. Calculation of the ICER - value is added for the incremental increase in the number of patients receiving appropriate treatment due to the pathogen being identified by PCR

The sensitivity to the model's selection of a high-risk group was assessed by repeating the cost-effectiveness analysis for a range of thresholds, P_{BC+}, from 0% to 35% in steps of 2.5%. Table 5.1 presents the median ICER for the low- and high-risk group for each threshold, P_{BC+}. When the threshold was removed, the ICER was €16,774 per life-year. The ICER in the high-risk group ranged down to €1,353 per life-year for P_{BC+} = 32.5%, while the ICER in the low-risk group reached a maximum of €534,355 per life-year when P_{BC+} = 2.5%.

Table 5.1: ICERs for complementary low- and high-risk groups for thresholds, P_{BC+}, ranging from 0% to 35% in steps of 2.5%

Threshold, P_{BC+} (%)	$n_{low-risk}$ (%)	$ICER_{low-risk}$ (€/life-year)	$n_{high-risk}$ (%)	$ICER_{high-risk}$ (€/life-year)
0	0 (0.0)	-	3589 (100.0)	16774
2.5	736 (20.5)	534355	2853 (79.5)	12606
5.0	1237 (34.5)	158789	2352 (65.5)	10423
7.5	1734 (48.3)	71570	1855 (51.7)	8906
10.0	2081 (58.0)	42017	1508 (42.0)	8553
12.5	2349 (65.5)	32920	1239 (34.5)	7177
15.0	2546 (70.9)	29870	1043 (29.1)	7735
17.5	2723 (75.9)	27768	866 (24.1)	6775
20.0	2889 (80.5)	24056	700 (19.5)	6934
22.5	3074 (85.7)	21367	515 (14.3)	7090
25.0	3309 (92.2)	20845	280 (7.8)	4281
27.5	3471 (96.7)	18815	118 (3.3)	2653
30.0	3541 (98.7)	17528	48 (1.3)	2353
32.5	3582 (99.8)	16924	7 (0.2)	1353
35.0	3589 (100.0)	16774	0 (0.0)	-

Figure 5.3 presents the results of the Monte-Carlo analyses for the full range of P_{BC+}. Panel A shows the results for the high-risk group, and Panel B the results for the complementary low-risk group. A threshold of $P_{BC+} = 0\%$ meant that all patients were assigned to the high-risk group and a threshold of $P_{BC+} = 35\%$ meant that all patients were assigned to the low-risk group. The threshold for cost-effectiveness defined by the National Institute for Clinical Excellence (NICE) (Appleby, Devlin & Parkin 2007) is £20,000 to £30,000 (about €35,000, shown as a dashed line in both panels).

When looking at the high-risk group alone, cost-effectiveness is demonstrated (according to NICE) even when the threshold is removed: the ICER for all patients is €16,774 per life-year which is significantly lower than the cost-effectiveness threshold of €35,000 per life year. However, this result does not tell the full story. By removing the threshold we are including a large number of low-risk patients for testing. We may instead choose our high-risk group by removing those patients for whom PCR testing is not cost-effective. At a threshold of $P_{BC+} = 10.0\%$, the patients (58.0% of all patients) below this threshold have an ICER = €42,017 per life-year saved. For these patients, PCR testing is not cost-effective. If the high-risk group is taken as all patients above this threshold, the ICER is €8,553 per life-year.

In addition to the ICER, hospitals must also consider other practical factors when choosing to run a test. The absolute cost is important along with the throughput of the laboratories running the test: it may be simply impractical to run PCR tests on

every patient suspected of infection. So although we have found that it is not cost-effective to run PCR for patients below a threshold of $P_{BC+} = 10.0\%$, this threshold does not necessarily define the choice of "high-risk" patients for whom testing should be done. If the number of patients being tested is limited by laboratory throughput, the threshold for "high-risk" will be set higher. Raising the threshold further will have the dual effect of reducing the number of tests and increasing the incremental benefit of each test, seen as the ICER falling with increasing threshold.
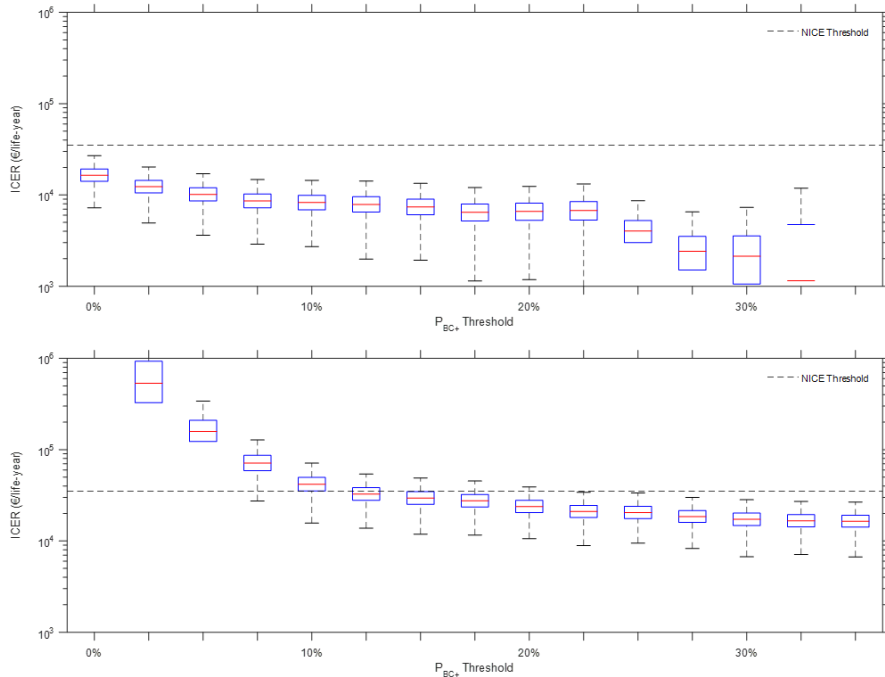
Figure 5.3 Figure from Paper IV. Boxplot for the Monte-Carlo analysis repeated at cut-offs of $P_{BC+} = 0\%$ to 35% in steps of 2.5%. Panel A shows the results for the high-risk group and Panel B for the low-risk group.

Risk-based stratification can be used to improve the cost-effectiveness of PCR by removing patients for whom PCR testing is not cost-effective. PCR in an inpatient population also provides an opportunity to increase appropriate treatment rates in the highest-risk patients before they are transferred to the ICU, perhaps even preventing ICU admissions.

CHAPTER 6. DISCUSSION

This chapter discusses the significance of the work completed during the PhD project and offers suggestions for the direction of future work.

6.1. MAIN FINDINGS

Manual learning: Design of continuous distributions for infection variables

Starting with the D-Sepsis CPN that was part of Treat, the first goal of the PhD project was to introduce continuous distributions for infection variables, forming the C-Sepsis CPN. This was done manually, combining expert opinion with knowledge gleaned from the literature, a method that has been proven successful several times in CPN construction. The C-Sepsis CPN was validated by comparing the predictive ability of the C-Sepsis and D-Sepsis CPNs with the remainder of the Treat model being identical. The C-Sepsis CPN had an AUC of 0.80 for the prediction of bacteraemia and the AUC for the D-Sepsis CPN was 0.73. The C-Sepsis CPN represented a sizable improvement in predictive performance, although the small data material meant that the result was not statistically significant. In addition to the improvement in predictive performance, the introduction of continuous variables solved the problem of "jumping" seen in the D-Sepsis CPN, where the discretization of variables meant that, for example, a change in temperature of 0.1°C could result in a large jump in the assessed illness severity.

Automatic learning: Tuning via automatic learning to improve predictive performance

Despite its success, manual learning is limited in what can reasonably be achieved. The availability of data in the literature was sub-optimal for the majority of parameters. Additionally, the manual construction involved what was effectively single-variable analysis. Automatic learning provided a structured way to further improve the model, tuning it to predict clinical outcomes; either diagnostic (presence of bacteraemia) or prognostic (30-day mortality).

To facilitate machine learning, the C-Sepsis CPN was clipped out of the Treat model, and tuned as a standalone entity. The C-Sepsis CPN also allows for discrimination between infectious and non-infectious inflammation: sepsis and NSIRS. The learning strategy allowed the model to learn the different effects of sepsis and NSIRS on individual branches of the inflammatory response.

The L-/L$_A$-Sepsis CPNs resulting from automatic learning were validated by testing their predictive ability for 30-day mortality. The learned CPNs substantially

outperformed both SIRS and the mREMS score: the AUC for 30-day mortality was 0.81, 0.67 and 0.54 for the L_A-Sepsis CPN, the mREMS score and SIRS, respectively. The comparison with clinical scores also highlighted one of the advantages of CPN models – their ability to handle missing data. For the patient group studied, SIRS and mREMS scores could be calculated for approximately 50% and 25% of the patients, respectively. Other scores such as SOFA or MEDS could not be calculated for these patients.

The performance of the L_A-Sepsis CPN as a standalone model for mortality prediction also motivated the tuning of another version of the Sepsis CPN to predict bacteraemia – SepsisFinder. SepsisFinder's performance in the prediction of bacteraemia was stable across patients from both Denmark and Israel, suggesting that the Sepsis CPNs may not require calibration for local conditions, that is, the sepsis response is temporally, demographically and geographically invariant. This is empirical evidence for one of the tenets used in the construction of Treat: that some parts of the model require calibration, while other parts, including the Sepsis CPN, do not.

The SepsisFinder and L_A-Sepsis CPNs represent a significant step forward from Treat's original D-Sepsis CPN. Both models (considered as standalone entities) have greater predictive performance than the Treat model for bacteraemia- and 30-day mortality prediction, while using significantly fewer variables. Another advantage of the SepsisFinder and L_A-Sepsis CPNs is the ability to continually adjust and improve the models as more data becomes available.

Applications: Risk-based stratification of patients to improve cost-effectiveness of rapid diagnostics

It was assumed that SepsisFinder, a "lightweight" model tuned to predict bacteraemia, could be used to stratify patients into risk-groups, as has previously been done using Treat (Paul et al. 2006a). The SepsisFinder model uses up to 12 routinely collected variables as opposed to over 100 used by Treat. The AUC for the prediction of bacteraemia using the SepsisFinder model was 0.75, an improvement on the AUC of 0.70 reported for Treat on a similar cohort (Paul et al. 2006a).

One of the opportunities for utilising such risk assessment is in tailoring the diagnostic workup of patients suspected of sepsis. Expensive diagnostics can be made cost-effective by limiting them to patients where 1) they will most likely be able to influence treatment and 2) the influence on the treatment will give most benefit. SepsisFinder can improve the cost-effectiveness of expensive rapid diagnostics by identifying patients for whom testing would not be cost-effective. In a cohort of 3589 patients, SepsisFinder was able to select 58% of patients for whom PCR testing would not be cost-effective (ICER = €42000 per life-year).

If the predictive ability could be further improved, such a risk-assessment could even be able to guide treatment vs. no treatment without performing the expensive test. Biomarkers such as procalcitonin and CRP have been suggested as useful candidates for guiding treatment (van der Does et al. 2016). The SepsisFinder model as a whole outperforms any individual variable, including CRP, allowing us to think of SepsisFinder as an intelligent biomarker. The addition of procalcitonin or other biomarkers to SepsisFinder could potentially further improve the cost-effectiveness of PCR testing.

6.2. FUTURE WORK

The work described in this thesis will be continued as part of an Industrial PostDoc project; a collaboration between Treat Systems ApS and Aalborg University, partially funded by Innovationsfonden Danmark. Over a two year period it is expected that the risk-assessment model of SepsisFinder will be refined and tested clinically, while development begins on modules aimed at the early recognition of infection and revision of treatment in patients for whom infections are not microbiologically documented. In addition to work on the SepsisFinder model, the L_A-Sepsis CPN will be reintegrated within the Treat model.

SepsisFinder: Standalone risk-assessment

The SepsisFinder model, which had greater predictive power than that seen in published versions of the Treat model, has value as a standalone system. The future of SepsisFinder is in its use as an "intelligent biomarker".

The future strategy for the development of SepsisFinder is fundamentally different to that used in the development of existing clinical scores. Typically, clinical scores focus on information and measurements that are easily obtained at the bedside. However, the integration of hospital wide electronic health records and other IT systems present an opportunity for easy access to a greater amount of information. Furthermore, it allows the departure from the subjective evaluations often required at the bedside, moving towards the use of objective, measured data. Throughout the PostDoc project, Sepsisfinder will be refined and tested clinically, and a laboratory-variable-only version, SepsisFinderLite will be created.

Risk-assessment software such as SepsisFinder or SepsisFinderLite also has immediate commercial potential. Reliable, model-based stratification of patients into risk-groups provides an opportunity to identify target populations to improve cost-effectiveness. For example, a group of high-risk patients may be eligible for expensive rapid diagnostic testing in addition to routine blood cultures.

Early-Warning and Treatment revision

The models described in this dissertation may also be extended to create a more complete picture of the response to sepsis by adding a temporal dimension.

The entire time-course of the infection should be considered: until now, point estimates of the risk of bacteraemia/30-day mortality have been made at the time when a patients is clinically recognised as having an infection. This use is valuable in and of itself as an initial triage tool/risk-stratification and impacts decisions on patient workup/treatment. However, this **intelligent biomarker** may also be useful at other time points.

One such use could be as an in-hospital monitoring tool for the early detection of hospital-acquired infections. The impact of such technology would be significant, since time is critical in sepsis patients. Early identification of infection has the potential to reduce the time to diagnosis and appropriate, live-saving treatment.

An intelligent tool for assessing the clinical success or failure of antibiotic treatment is also needed; the causative pathogen (and hence the susceptibility to antibiotics) is found in less than half of all patients with an infection. For these patients, there is no objective measure of whether the treatment is appropriate and it is difficult to justify treatment escalation or de-escalation. It is hoped that a SepsisFinder module can provide support for the decision to revise treatment.

Re-integration within Treat

The original goal of tuning the Sepsis CPN was to improve the overall performance of Treat's decision support. The improvements seen in the predictive performance of the standalone versions of the Sepsis CPN provide reason to believe that re-integration will give an improvement in performance. Additionally, Treat includes information on the site of infection, which is related to mortality (Chapter 4). Therefore, it is expected this can further improve performance. However, the re-integration is not a trivial cut and paste task. Re-integration will involve some degree of automatic learning in the full Treat CPN. To our knowledge, there is no existing descriptions of learning in such large CPNs, and computational problems are bound to arise.

Treat Steward, the software package which includes the Treat CPN, is a fully integrated system that combines antimicrobial stewardship with advanced decision support. The purpose of antimicrobial stewardship is to promote the rational use of antimicrobials, preserving their effectiveness as the prevalence of resistant microbes increases. It is hoped that the improvements made to Treat Steward's decision support through the re-integration of the L_A-Sepsis CPN will help in the fight against antimicrobial resistance.

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