
Master Thesis

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Combining Machine-Learning and Dynamic Network Models to Improve Sepsis Prediction

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Abstract

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Acronyms Index

ABX:	Antibiotics
AUPRC:	Area Under Precision Recall Curve
AUROC:	Area Under Receiver Operating Curve
BCE:	Binary Cross Entropy
DAMP:	Damage-Associated Molecular Patterns
DL:	Deep Learning
DNM:	Dynamic Network Model
EHR:	Electronic Health Record
FSQ:	Finite Scalar Quantization
GPU:	Graphics Processing Unit
GRU:	Gated Recurrent Unit
ICU:	Intensive Care Unit
JIT:	Just In Time Compilation
LDM:	Latent Dynamics Model
LSTM:	Long Short-Term Memory
MIMIC:	Medical Information Mart for Intensive Care
ML:	Machine Learning
MLP:	Multi Layer Perceptron
MSE:	Mean Squared Error
ODE:	Ordinary Differential Equation
PAMP:	Pathogen-Associated Molecular Patterns
PID:	Proportional-Integral-Derivative
PINN:	Physics Informed Neural Networks
PRR:	Pattern Recognition Receptors
qSOFA:	Quick Sequential Organ Failure Assessment
RAG:	Retrieval Augmented Generation
ReLU:	Rectified Linear Unit
RNN:	Recurrent Neural Networks
SIRS:	Systemic Inflammatory Response Syndrome
SI:	Suspected Infection
SOFA:	Sequential Organ Failure Assessment
SVM:	Support Vector Machine
TUHH:	Hamburg University of Technology
YAIB:	Yet Another ICU Benchmark

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1 Introduction

2 Medical Background (Sepsis)

As the most extreme course of an infectious disease, sepsis poses a very serious health threat, with a high mortality rate and frequent long-term consequences for survivors. In 2017, an estimated 48.9 million people worldwide suffered from sepsis and the same year, 11.0 million deaths were associated with sepsis [2], which makes up 19.7% of yearly deaths, making it the most common cause of in-hospital deaths. Untreated, the disease is always fatal and even with successful treatment, around 40% of those affected suffer long-term consequences, such as cognitive, physical or physiological problems, the so called *post-sepsis syndrome* [3]. Overall, treated and untreated septic diseases in particular represent an enormous burden on the global healthcare system. The observed risk of mortality significantly differs between lower to middle income countries with $> 50\%$ and high income countries with $< 25\%$.

Even though almost half of all sepsis-related deaths occur as a secondary complication of an underlying injury or a non-communicable, also known as chronic disease [4], the underlying triggers but also the individual progressions of sepsis remain highly diverse and heterogeneous. Moreover, a septic condition can not be reduced to a single specific physiological phenomenon, instead it combines multiple complex and interdependent processes across different biological scales.

This complexity has historically made it difficult to define sepsis in a medical precise way compared to other conditions. Multiple definitions have been proposed over time, and the terminology around sepsis and septic-shocks has often been blurry. The most commonly used and accepted sepsis definition characterizes sepsis as a “life-threatening organ dysfunction caused by a dysregulated host response to infection” [5]. The following Section 2.1 provides a detailed overview to this definition, which is referred to as Sepsis-3. Furthermore, Section 2.2 introduces the both the pathology and underlying biology of sepsis in greater detail.

A recent study [6] highlights the importance of early recognition and subsequent treatment of infections in patients, reducing the mortality risk caused from sepsis. Each hour of earlier detection can significantly increase the chance of survival [6], it urges to develop accurate and robust detection and prediction methods, i.e. reducing the time to receive the appropriate medical attention. In Section 2.3 the necessity for reliable and clinically practical sepsis prediction systems is discussed.

2.1. Sepsis-3 Definition

Earlier definitions (Sepsis-1, Sepsis-2 [7]) primarily emphasized Systemic Inflammatory Response Syndrome (SIRS) [7] criteria, focusing on the inflammatory origins of sepsis. These definitions were later criticized for low specificity and under-representation of the multi organ failure due to sepsis. Out of the need for an update of these outdated definitions and partly misleading sepsis models a task force led by the “Society of Critical Care Medicine and the European Society of Intensive Care Medicine”, was formed in 2016. Their resolution, named “Third International Consensus Definitions for Sepsis and Septic Shock” [5], provides until today the most widely used sepsis definition and guidance on sepsis identification.

In general, sepsis does not classify as a specific illness, rather a multifaceted condition of “physiologic, pathologic, and biochemical abnormalities” [5], and septic patients are largely heterogeneous. Also the trigger is explicitly non-specific, since different triggers can cause the same septic condition. Most commonly the underlying cause of sepsis is diarrhoeal disease, road traffic injury the most common underlying injury and maternal disorders the most common non-communicable disease causing sepsis [2].

According to the Sepsis-3 definition, a patient is in a septic condition if the following two criteria are fulfilled:

- a documented or Suspected Infection (SI) and
- the presence of a dysregulated host response

The combination of the two criteria represents an exaggerated immune reaction that results in organ dysfunction, when infection is first suspected, even modest organ dysfunction is linked to a 10% increase of in-hospital mortality. A more medical explanation of what a *dysregulated host response* means is given in the next Section 2.2.

Confirmed or Suspected Infection has no strict medical definition and classification what counts as SI remains a little vague, ultimately it is left for the medical personnel to classify infections or the suspicion of infections. For retrospective data-driven classification it is suggested to characterize any patient prescribed with Antibiotics (ABX) followed by the cultivation of body fluids, or the other way around, with a SI [5]. The timings of prescription and fluid samplings play a crucial role. If the antibiotics were administered first, then the cultivation has to be done in the first 24h after first prescription, if the cultivation happened first, the ABX have to be prescribed in the following 72h [5]. This can be seen in the lower part of figure Figure 1, with the abbreviated ABX. Regardless which happened first, the earlier of the two times is treated as the time of suspected infection onset time.

Dysregulated Host Response is characterized by the worsening of organ functionality over time. Since there is no gold standard for measuring the amount of “dysregulation” the Sepsis-3 consensus relies on the SOFA-score introduced in ([5], [8]). The score is now regularly used to evaluate the functionality of organ systems and helps to predict the risk of mortality, also outside of a sepsis context. The SOFA score is calculated at least every 24 hours and assess six different organ systems by assigning a score from 0 (normal function) to 4 (high degree of dysfunction) to each. The overall score is calculated as sum of each individual system.

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It includes the respiratory system, the coagulation/clotting of blood, i.e. changing from liquid to gel, the liver system, the cardiovascular system, the central nervous system and the renal system/kidney function. A more detailed listing of corresponding markers for each organ assessment can be found in table Table 6 in the Appendix A.1. The magnitude of a patients initial SOFA-score captures preexisting organ dysfunction. An increase in SOFA score ≥ 2 corresponds to an acute worsening of organ functionalities and a drastic worsening in the patients condition, the indicator for a dysregulated response.

2.1.1. Sepsis Classification

The Sepsis-3 definition not only provides the clinical criteria of septic conditions, but also introduces the necessary time windows for sepsis classification. An increase of SOFA ≥ 2 in the 48h before or 24h after the SI time, the so called SI-window, is per Sepsis-3 definition the *sepsis onset time*. A schematic of the timings is shown in figure Figure 1.

With respect to which value the increase in SOFA is measured, i.e. the baseline score, is not clearly stated in the consensus and leaves room for interpretation, commonly used approaches include:

- the minimal value inside the SI-window before the SOFA increase,
- the first value of the SI-window,
- the lowest value of the 24h previous to the increase.

Differences in definitions greatly influence the detection of sepsis, which are used for prevalence estimates for example [9]. Using the lowest SOFA score as baseline, the increase ≥ 2 for patients with inspected infection was associated with an 18% higher mortality rate according to [8] a retrospective Intensive Care Unit (ICU)-data analysis.

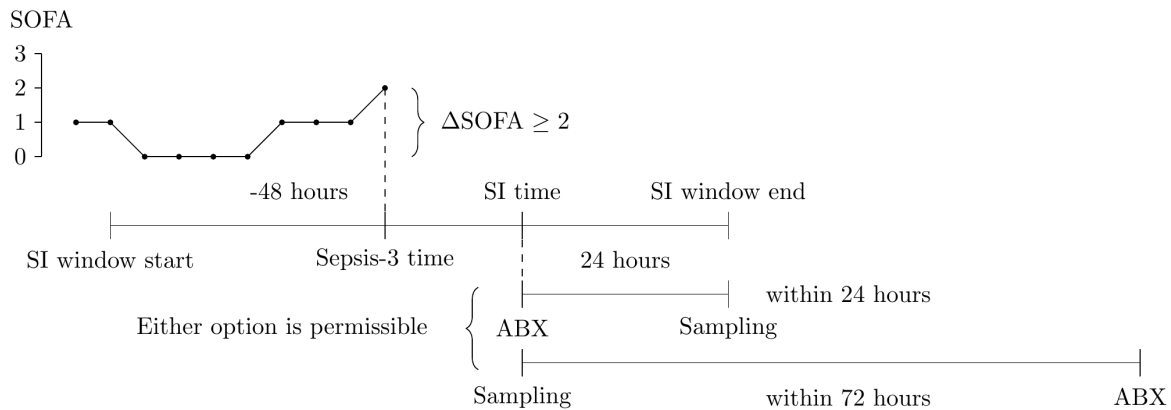


Figure 1: Graphical representation of the timings in the Sepsis-3 definition, taken from [10]

Up until today, even though SOFA was created as a clinical bedside score, some of the markers used in it are not always available to measure or at least not at every 24h [11]. For a faster bedside assessment [8] also introduced a clinical score termed Quick Sequential Organ Failure Assessment (qSOFA), with highly reduced marker number and complexity, it includes:

- Respiratory rate $\geq 22/\text{min}$
- Altered mentation

- Systolic blood pressure ≤ 100 mmHg

Patients fulfilling at least two of these criteria have an increased risk of organ failure. While the qSOFA has a significantly reduced complexity and is faster to assess it is not as accurate as the SOFA score, meaning it has less predictive validity for in-house mortality [8].

There is also the notion of a septic shock, also defined in [5], which an in-hospital mortality above 40%. Patients with a septic shock are can be identified by:

- Sepsis
- Persisting hypotension requiring vasopressors to maintain MAP ≥ 65 mmHg
- Serum lactate level > 2 mmol/L, despite volume resuscitation.

2.2. Biology of Sepsis

This part tries to give an introduction into the biological phenomena that underlie sepsis. Starting with an explanation on how human tissue is reacting to local infections or injuries on a cellular level in Section 2.2.1 and how this can escalate to *cytokine storms* in Section 2.2.2 and ending with systemic organ failure in Section 2.2.3.

Certain details and specificities are left out when not essential for the understanding of this project. More detailed explanations can be found in the primary resources provided throughout this section.

2.2.1. Cellular Origins

Human organ tissue can be differentiated into two broad cell-families called *parenchymal* and *stroma* which are separated by a thin, specialized boundary layer known as the *basal lamina*.

The parenchymal cells perform the primary physiological functions of an organ, with every organ hosting distinct parenchymal cells [12].

Everything not providing organ-specific functionalities forms the stroma, that includes the structural or connective tissue, blood vessels and nerves. The stroma not only contributes to the tissues structure, but it also actively participates in biochemical signaling and immune regulation. This way it helps to maintain a healthy and balanced tissue, the *homeostasis*, and enables coordinated responses to injury or infection [13].

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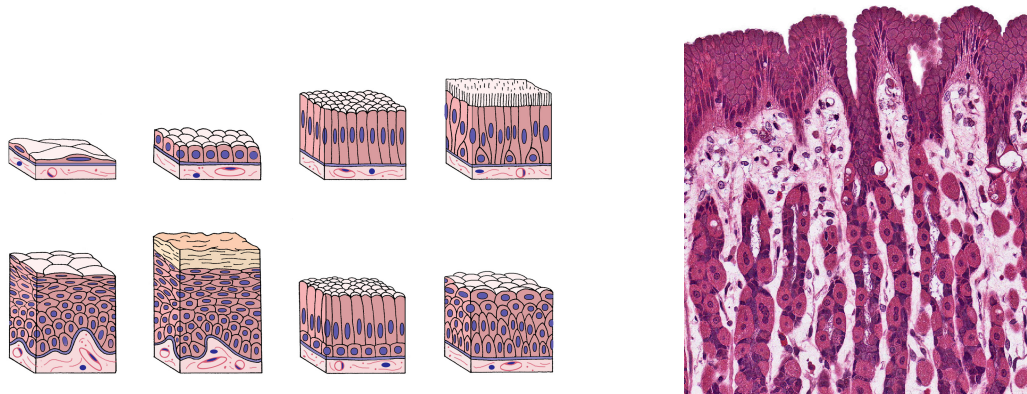


Figure 2: [14], [15]

A pathogen is summarizes all types of organisms that can be harmful to the body, this includes germs, fungi, algae, or parasites. When a pathogen enters the body through the skin, a mucous membrane or an open wound, the first line of non-specific defense, the innate immune system [16], gets activated.

This rapid response does not require the body to have seen the specific pathogen before. Instead, the innate immune system can be triggered by sensing commonly shared features of pathogens, in case of germs known as Pathogen-Associated Molecular Patterns (PAMP), for injury called Damage-Associated Molecular Patterns (DAMP) [17]. The PAMP's and DAMP's can be detected by Pattern Recognition Receptors (PRR), which are found in resident immune cells, as well as stroma cells. Once a pathogen is detected a chain reaction inside the cell leads to the creation and release of signaling proteins called *cytokines* [18].

Cytokines are a diverse group of small signaling proteins which play a special role in the communication between other cells, both neighboring and across larger distances through the bloodstream. They are acting as molecular messengers that coordinate the recruitment of circulating immune cells and will guide them to the location of infection or injury [18].

Besides their role in immune activation where cytokines regulate the production of anti- and pro-inflammatory immune cells which help with the elimination of pathogens and trigger the healing process right after. They are also participating in the growing process of blood cells.

One specialty of these relatively simple proteins is that they can be produced by almost every other cell, with different cells being able to produce the same cytokine. Further, cytokines are redundant, meaning targeted cells can show identical responses to different cytokines [19], these features seems to fulfill some kind of safety mechanism to guarantee vital communication flow. After release cytokines have relatively a short half-life (only a few minutes) but through cascading-effects the cytokines can have substantial impact on their micro-environment.

2.2.2. Cytokine Storms

The hosts dysregulated response to an infection connected to the septic condition is primarily driven by the excessive and uncontrolled release cytokines and other mediators. Under normal circumstances, the release of inflammatory cytokines tightly regulated in time and

magnitude. After the pathogen detection the release is quickly initiated, peaks as immune cells are recruited and automatically fades out once the initial pathogen is controlled and the host returns to a healthy and balanced state, the homeostasis.

In certain scenarios a disturbance to the regulatory mechanisms triggers positive inflammatory feedback loop, followed by a massive release of pro-inflammatory cytokines. These cells further activate additional immune and non-immune cells, which in turn amplify the cytokine production, creating a self-reinforcing cycle of immune activation [20]. This ultimately leads to a continuous and uncontrolled release of cytokines that fails to shut down. With this overreaction, called *cytokine storm*, the immune response and release of inflammatory mediators can damage the body more than the infection itself.

Although the quantity of cytokines roughly correlates with disease severity, concentrations of cytokines vary between patients, time and even different body-parts, making a distinction between an appropriate reaction and a harmful overreaction almost impossible [20]. Out of all cytokines, only a small subset or secondary markers can be measured through blood samples to detect increased cytokine activity. This limited accessibility cytokines difficult to study in general, they prove to be little useful as direct indicators of pathogenesis or diagnostic purposes.

Since the 90s there has been a lot of research focused on cytokines and their role in the innate immune system and overall activation behavior. Multiple therapeutic interventions have been tested in clinical trials, yet none have achieved a significant improvement in survival outcomes [17]. This emphasizes the complexity of sepsis as a systemic syndrome rather than a single-cause disease, and suggests that cytokine storms are an emergent property rather than the result of any one molecular trigger. To this day, the fundamental principles that govern the transition from a regulated immune response to a self-destructive cytokine storm remain not fully understood.

2.2.3. Systemic Consequences and Organ Failure

While more and more cytokines are released, they flood not only infected areas, but also surrounding parts of the tissue and circulation, causing localized inflammatory response to become systemic. The widespread cytokine reaction starts to disrupt the normal metabolism of parenchymal cells in organs due to a deficiency in oxygen and nutrients.

To compensate, cells switch from their usual oxygen-based metabolism to an *anaerobic glycolysis* [21], generating energy less efficiently from glucose. As a result, metabolic by-products such as lactate accumulate making the surrounding environment more acidic, which further harms the cells and leads to more cellular dysfunction.

At the same time, the mitochondria, the “power house” of the cells, start to fail. The walls of blood vessels become leaky, allowing fluids to move into surrounding tissue. This causes swelling and lowers the blood pressure, which in turn reduces the oxygen supply even further [17].

Step by step, the death of cells spreads throughout the body and affects organ functionality. When multiple organs fail simultaneously, the condition becomes irreversible [5]. At this

stage, multi-organ-failure is the final and most lethal form of sepsis, with each additional affected organ the mortality increases drastically.

2.3. The need for sepsis prediction

To this day sepsis, and the more extreme septic shock, remains as an extreme burden to the worldwide healthcare system. It is associated with high rates of incidence, high mortality and significant morbidity. Despite overall advancements in medical care and slowly decreasing prevalence numbers, sepsis continues to be the leading cause of in-hospital death [22].

In germany it was estimated in 2022 that at least 17.9% of intensive care patients develop sepsis, and 41.7% of all hospital treated sepsis patients die during their stay [4]. The economic burden is equally severe, with the annual cost of sepsis treatment in germany estimated to be €7.7 billion based on extrapolated data from 2013.

Globally , the situation is even more concerning, as sepsis remains to be under-diagnosed significantly due to its non-specific symptoms. Environmental and socioeconomic factors such as insufficient sanitation, limited access to clean water and healthcare increases the incidence particularly in low- to middle income countries [2], [22].

A meta-analysis of seven sepsis alert systems found no evidence for improvement in patient outcomes, suggesting insufficient predictive power of analyzed alert systems or inadequate system integration [23]. Nevertheless, positive treatment outcomes depend heavily on timely recognition and intervention [22]. Each hour of delayed treatment increases mortality risk, underscoring the critical importance of early detection [6] while structured screening and early warning systems have demonstrated reductions in time-to-antibiotics and improvements in outcomes [24]. These findings confirm that in principle earlier identification of sepsis improves clinical results, even if existing tools are not yet capable enough, and emphasizes the need for more research in that direction.

A recent study suggests a paradigm shift in sepsis detection—from a symptom-based to a systems-based approach [25]. Instead of waiting for clinical signs, early recognition should integrate multiple physiological and biochemical signals to capture the transition from infection to organ dysfunction. This aligns with the findings of a survey among clinicians regarding AI-Assistance in healthcare [26]. One participant emphasizes that specific vitals signs might be of less importance, rather the change/trend of a patients trajectory should be the prediction target. Another piece of finding of the same study was the preference of trajectories over plain binary event predictions.

However, implementation any data-driven prediction approaches into clinical practice presents challenges. Implementation studies consistently identify barriers such as alert fatigue, workflow disruption, and inconsistent screening uptake. To be effective, predictive systems must integrate seamlessly into and existing workflows provide interpretable output and aid the clinical expertise [26].

Taken together, these insights highlight both the need and the opportunity for improved sepsis prediction. The global burden and clinical urgency justify the development of more

reliable prediction systems. At the same time, the limitations of current alert systems and implementation barriers underline the necessity for models that can integrate dynamic patient data and capture clinical trajectories.

3 Problem definition

This section provides some background on the specific research questions which are investigated in Section 7 using the methods introduced in Section 4 and Section 6 respectively. As discussed in Section 2.3, there is a substantial need for robust methods to identify patients sepsis onset and overall progression. This work provides a proof of concept for such a prediction system.

The increasing availability of high-quality medical data, i.e. multiple physiological markers with high temporal resolution, enables both classical statistical and Machine Learning (ML) (including Deep Learning (DL)) methods (see Section 5). While these purely data-driven approaches often achieve acceptable performance but the explainability of the prediction suffers and limits their adoption in clinical practice.

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In parallel, recent advances in the field of network physiology have introduced new ways to model physiological systems as interacting subsystems rather than isolated organs [27]. The Dynamic Network Model (DNM) introduced in [28] and adapted in [29], allows for a functional description of organ failure in sepsis and shows realistic system behavior in preliminary analysis. An in-depth introduction to the DNM is provided in Section 4. But up until now the dynamic model has not yet been verified on real data. The goal is to investigate how real patients would translate to the model parameters, and how the temporal physiological evolution can be incorporated and if there is a benefit doing so.

To summarize, the specific research questions include:

- **Usability of the DNM:** How and to what extent can the ML-determined trajectories of the DNM be used for detection and prediction, especially of critical infection states and mortality.
- **Comparison with data-based approaches:** How can the model-based predictions be compared with those of purely data-based approaches in terms of predictive power and interpretability.

End this

4 Model Background (Dynamic Network Model)

As outlined in Section 2, the macroscopic multi-organ failure associated with sepsis is driven by a dysregulated cascade of signaling processes on a microscopic level (see Section 2.2). This cascade involves a massive amount of interconnected components, where the connections mechanics and strengths vary over time and space. For example, these interactions differ across tissues and evolve as sepsis progresses, with crossing biochemical thresholds the behavior of cells can be changed [30].

In essence, cell-to-cell and cell-to-organ interaction in septic conditions form a highly dynamic, nonlinear and spatio-temporal network of relationships [31], which cannot be fully understood by a reduction to single time-point analyzes. Even though many individual elements of the inflammatory response are well characterized, we still fail to integrate them into a coherent system-level picture.

To address this complexity, the emerging field of *Network Physiology* provides a promising conceptual framework. Rather than studying components in isolation, network physiology focuses on the coordination and interconnection among the diverse organ systems and subsystems [27]. It enables the study of human physiology as a complex, integrated system, where emergent macroscopic dynamics arise from interacting subsystems that cannot be explained by their individual behavior. This perspective translates to the mesoscopic level, i.e. the in-between of things, where the coupling mechanisms collectively determine the overall physiological function.

In network physiology, the analytical basis of the bodies interacting systems is often graph based. Nodes represent subsystem such as organs or cell populations and links represent functional couplings or communication pathways [27]. Unlike classical graph theory, where dynamics are introduced by changing the graph topology (e.g. adding or removing links or nodes), in *Complex Networks* the links themselves can evolve dynamically in response to other system variables. These adaptive connections allow for information to propagate through the whole network, giving rise to emerging phenomena on global scales for otherwise identical network topologies.

Complex networks are well studied in physics and biology and have been applied to various physiological domains. Early works, such as [32] that have studied the cardiovascular system, while more recent studies have focused on the cardio-respiratory coupling [33] and large-scale brain network dynamics [34]. Network approaches have also provided mechanistic

insights into disease dynamics, for example Parkinson [35] and Epilepsy [36], just to name a few.

Building on these interaction centric principles has opened up new opportunities to study how the inflammatory processes, such as those underlying sepsis, emerge from the complex inter- and intra-organ communication. In particular [28] and [29] have introduced a dynamical system that models the cytokine behavior in patients with sepsis and cancer. This functional model will be referred to as Dynamic Network Model and forms the conceptual foundation for this whole project.

The remainder of this chapter is structured as follows: In Section 4.1 introduces the theoretical backbone of the DNM, the Kuramoto oscillator model, which provides a minimal description of synchronization phenomena in complex systems. Section 4.2 presents the formal mathematical definition of the DNM and its medical interpretation, followed by implementation details in Section 4.3 and a presentation of selected simulation results in Section 4.3.4.

4.1. Theoretical Background: The Kuramoto Oscillator Model

To mathematically describe natural or technological phenomena, *coupled oscillators* have proven to be a useful framework [7], for example, to model the relative timing of neural spiking, reaction rates of chemical systems or dynamics of epidemics [7]. In these cases complex networks of coupled oscillators are often capable of bridging microscopic dynamics and macroscopic synchronization phenomena observed in biological systems.

One of the most influential system of coupled oscillators is the *Kuramoto Phase Oscillator Model* which is often used to study how synchronization emerges from simple coupling rules. In the simplest form it consists of N identical, fully connected and coupled oscillators with phase $\varphi_i \in [0, 2\pi)$, for $i \in 1 \dots N$ and an intrinsic frequency ω_i [7]. The dynamics are given by:

$$\dot{\varphi}_i = \omega_i - \frac{K}{N} \sum_{j=1}^N \sin(\varphi_i - \varphi_j) \quad (4.1)$$

Here the $\dot{\varphi}$ is used as shorthand notation for the time derivative of the phase $\frac{d\varphi}{dt}$, the instantaneous phase velocity. An additional parameter is the global coupling strength K between oscillators i and j .

The model captures the essential mechanism of self-synchronization, and a fundamental collective transition from disorder to order, that underlie many real world processes, which is the reason the model has attracted so much research. When evolving this system with time, oscillator i 's phase velocity depends on each other oscillator j . If $\varphi_j > \varphi_i$ the phase oscillator i accelerates $\dot{\varphi}_i > 0$, if $\varphi_j < \varphi_i$ decelerates. For sufficiently large N the oscillator population can converge towards system-scale states of coherence or incoherence based on the choice of K . Coherent in this case means oscillators synchronize with each other, so they share the same phase and phase velocity, incoherence on the other hand is the absence of synchronization (desynchronized), see Figure 3. Synchronous states can be reached if the coupling is stronger

than a certain threshold $K > K_c$, the critical coupling strength. In between these two regimes there is a transition-phase of partial synchronization, where some oscillators phase- and frequency-lock and others do not.

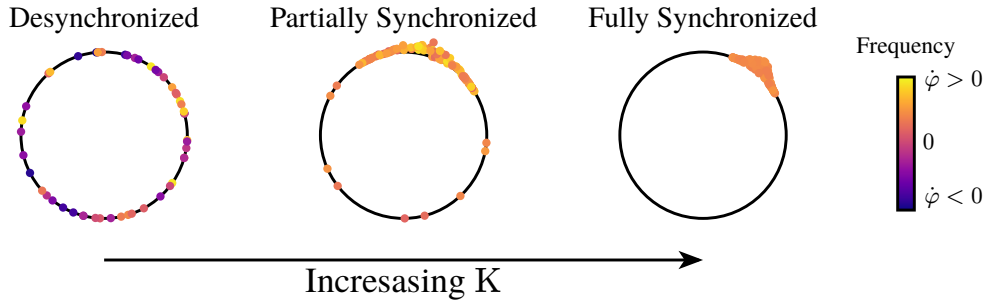


Figure 3: Schematic transition between the two stable regimes for the basic Kuramoto model. From an incoherent system state with desynchronized oscillators (heterogeneous phases and frequencies), to a synchronized system state with phase- and frequency-locked oscillators with increasing coupling strength K).

4.1.1. Extensions to the Kuramoto Model

To more accurately describe real world systems, various extensions of the basic Kuramoto model have been proposed and studied numerically and analytically. Several extensions are directly relevant to the DNM and their definitions and effects on synchronization will be shortly introduced, with additional terms being indicated by the red color:

Phase Lag α introduced in [7] (Kuramoto Sakaguchi 86), brings a frustration into the synchronization process:

$$\dot{\varphi}_i = \omega_i - \frac{K}{N} \sum_{j=1}^N \sin(\varphi_i - \varphi_j + \alpha) \quad (4.2)$$

Positive values of α act as an inhibitor of synchronization by shifting the coupling function, so the coupling does not vanish even when the phases align. As a result the critical coupling strength K_c increases with α .

Adaptive coupling $\mathbf{K} \in \mathbb{R}^{N \times N}$ moves from a global coupling strength K for all oscillator pairs to an adaptive coupling strength for each individual pair κ_{ij} :

$$\dot{\varphi}_i = \omega_i - \frac{1}{N} \sum_{j=1}^N \kappa_{ij} \sin(\varphi_i - \varphi_j) \quad (4.3)$$

$$\dot{\kappa}_{ij} = -\varepsilon(\kappa_{ij} + \sin(\varphi_i - \varphi_j + \beta^\mu)) \quad (4.3)$$

Here adaption rate $0 < \varepsilon \ll 1$ separates the fast moving oscillator dynamics from slower moving coupling adaptivity [37]. Such adaptive couplings have been used to model neural plasticity and learning-like processes in physiological systems [7]. The so called new phase lag parameter β of the adaptation function (also called plasticity rule) plays an essential role. At a value of $\beta^\mu = \frac{\pi}{2}$ the coupling, and therefore the adaptivity, is at a maximum positive feedback, strengthening the link κ_{ij} (Hebbian Rule: fire together, wire together [37])

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and encouraging synchronization between oscillators i and j . For other values $\beta^\mu \neq \frac{\pi}{2}$ the feedback is delayed $\varphi_i^\mu - \varphi_j^\nu = \beta^\mu - \frac{\pi}{2}$ by a phase lag, a value of $\beta^\mu = -\frac{\pi}{2}$ we get an anti-Hebbian rule which inhibits synchronization.

Multiplex Networks represent systems with multiple interacting layers. Multiplexing introduces a way how several Kuramoto networks can be coupled via interlayer links:

$$\dot{\varphi}_i^\mu = \omega_i - \frac{K}{N} \sum_{j=1}^N \sin(\varphi_i - \varphi_j + \alpha^{\mu\mu}) - \sigma^{\mu\nu} \sum_{\nu=1, \nu \neq \mu}^L \sin(\varphi_i^\mu - \varphi_i^\nu + \alpha^{\mu\nu}) \quad (4.4)$$

Here μ and ν represent distinct subsystems, and are connected via interlayer coupling weights $\sigma^{\mu\nu}$, acting one-to-one.

These extensions combined serve as the source of dynamics for the DNM and give rise to more intricate system states than the straightforward synchronization in the base model. Even for single layers, non-multiplexed but phase-lagged and adaptively coupled oscillators, one can observe several distinct system states, neither fully synchronized or desynchronized such as phase and frequency-clusters, chimera- and splay states. The emergence of these states depends on the choice of the coupling strength K and the phase-lag parameters α and β .

In the frequency clustered state, the oscillator phases do not synchronize, but several oscillator groups can form that share a common frequency. For the phase-clustered case, the groups additionally synchronize their phase. Frequency clusters often emerge as intermediate regimes between full synchronization and incoherence [38].

Chimera states, a special type of partial synchronization, occur when only a subset of oscillators synchronizes in phase and frequency, while others remain desynchronized. In contrast to “normal” partial synchronization they occur when the coupling symmetry breaks. In splay states, all oscillators synchronize their frequencies but do not their phases, they instead uniformly distribute around the unit circle [37].

The introduction changes the system behavior once more, for example single layers of a multiplexed system can result in the multi-clustered regime for parameters they would not in the monoplex case. In multiplexed systems it is also possible connected layers end up in different stable state, for example, one in a clustered the other in a splay state.

4.2. Description

Figure bio vs oscillators

The DNM is a **functional** model, that means it **does not try to model things accurately on any cellular, biochemical, or organ level**, it instead tries to model dynamic interactions. At the core, the model does differentiate between two broad classes of cells, introduced in Section 2.2.1, the stroma and the parenchymal cells. It also includes the cell interaction through cytokine proteins and an information flow through the basal membrane. Importantly, the model only handles the case of already infected subjects and tries to grasp if the patients state is prone to a dysregulated host response.

Cells of one type are aggregated into layers, everything associated with parenchymal cells is indicated with an \cdot^1 superscript and is called the *organ layer*, stroma cells are indicated with \cdot^2 and is referred to as non specific *immune layer*. Each layer consists of N phase oscillators $\varphi_i^{1/2} \in [0, 2\pi)$. To emphasize again the function aspect of the model: individual oscillators do not correspond to single cells, rather the layer as a whole is associated with the overall state of all organs or immune system functionality respectively.

The metabolic cell activity is modeled by rotational velocity $\dot{\varphi}$ of the oscillators, the faster the rotation, the faster the metabolism. Each layer is fully coupled via an adaptive possibly asymmetric matrix $\mathbf{K}^{1/2} \in [-1, 1]^{N \times N}$ with elements $\kappa_{ij}^{1/2}$, these couplings represent the activity of cytokine mediation. Small absolute coupling values indicate a low communication via cytokines and grows with larger coupling strength. For the organ layer there is an additional non-adaptive coupling part $\mathbf{A}^1 \in [0, 1]^{N \times N}$ with elements a_{ij}^1 , representing a fixed connectivity within an organ.

The dimensionless system dynamics are described with the following coupled Ordinary Differential Equation (ODE) terms, build on the classical Kuramoto model described in Section 4.1 and its extensions from Section 4.1.1:

$$\dot{\varphi}_i^1 = \omega^1 - \frac{1}{N} \sum_{j=1}^N \{ (a_{ij}^1 + \kappa_{ij}^1) \sin(\varphi_i^1 - \varphi_j^1 + \alpha^{11}) \} - \sigma \sin(\varphi_i^1 - \varphi_i^2 + \alpha^{12}) \quad (4.5)$$

$$\dot{\kappa}_{ij}^1 = -\varepsilon^1 (\kappa_{ij}^1 + \sin(\varphi_i^1 - \varphi_j^1 - \beta)) \quad (4.5)$$

$$\dot{\varphi}_i^2 = \omega^2 - \frac{1}{N} \sum_{j=1}^N \kappa_{ij}^2 \sin(\varphi_i^2 - \varphi_j^2 + \alpha^{22}) - \sigma \sin(\varphi_i^2 - \varphi_i^1 + \alpha^{21}) \quad (4.5)$$

$$\dot{\kappa}_{ij}^2 = -\varepsilon^2 (\kappa_{ij}^2 + \sin(\varphi_i^2 - \varphi_j^2 - \beta)) \quad (4.5)$$

Where the interlayer coupling, i.e. a symmetric information through the basal lamina, is modeled by the parameter $\sigma \in \mathbb{R}_{\geq 0}$. The internal oscillator frequencies are modeled by the parameters $\omega^{1/2}$ and correspond to a natural metabolic activity.

Besides the coupling weights in $\mathbf{K}^{1/2}$ the intralayer interactions also depend on the phase lag parameters α^{11} and α^{22} modeling cellular reaction delay. To separate the fast moving oscillator dynamics from the slower moving coupling weights adaption rates $0 < \varepsilon \ll 1$ are introduced. Since the adaption of parenchymal cytokine communication is assumed to be slower than the immune counterpart [28], it is chosen $\varepsilon^1 \ll \varepsilon^2 \ll 1$, which introduces dynamics on multiple timescales.

Lastly, the most influential parameter is β which controls the adaptivity of the cytokines. Because β has such a big influence on the model dynamics it is called the (*biological*) *age parameter* and summarizes multiple physiological concepts such as age, inflammatory baselines, adiposity, pre-existing illness, physical inactivity, nutritional influences and other common risk factors [29].

All the systems variables and parameters are summarized in together with their medical interpretation.

why no ref?

Table 1: Summarization of notation used in the Dynamic Network Model. Superscripts indicating the layer are left out for readability.

SYMBOL	NAME	PHYSIOLOGICAL MEANING
Variables		
φ_i	Phase	Group of cells
$\dot{\varphi}_i$	Phase Velocity	Metabolic activity
κ_{ij}	Coupling Weight	Cytokine activity
Parameters		
α	Phase lag	Metabolic interaction delay
β	Plasticity rule	Combined of risk factors
ω	Natural frequency	Natural cellular metabolism
ε	Time scale ratios	Temporal scale of cytokine activity
a_{ij}	Connectivity	Fixed intra-organ cell-to-cell interaction
σ	Interlayer coupling	Interaction between parenchymal and immune cells through the basal lamina
Measures		
s	Standard deviation of frequency (see Equation (4.11))	Pathogenicity (Parenchymal Layer)

4.2.1. Pathology in the DNM

A biological organism, such as the human body, can be regarded as a self-regulating system that, under healthy conditions, maintains a homeostatic state [7]. Homeostasis refers to a dynamic but balanced equilibrium in which the physiological subsystems continuously interact to sustain stability despite external perturbations. In the context of the DNM, this equilibrium is represented by a synchronous regime of both layers in the duplex oscillator system. In synchronous states, the organ layer and immune layer exhibit coordinated phase and frequency dynamics, reflecting balanced communication, collective frequency of cellular metabolism and stable systemic function.

Pathology, in contrast, is modeled by the breakdown of the synchronicity and the formation of frequency clusters in the parenchymal layer, i.e. loss of homeostatic balance. In the DNM least one cluster will exhibit increased frequency and one with lower or unchanged frequency. This aligns with medical observation, where unhealthy parenchymal cells change to a less efficient anaerobic glycolysis based metabolism, forcing them to increase their metabolic activity to keep up with the energy demand. Remaining healthy cells are expected to stay frequency synchronized to a lower and “healthy” frequency.

There are two more cases, neither fully healthy nor fully pathologic, representing a vulnerable or resilient patient condition. The healthy but vulnerable case corresponds to a splay state, where phases in the parenchymal layer are not synchronized, but the frequencies are, weakening the overall coherence [29]. A resilient state corresponds to cases where both the phase and frequency of the parenchymal layer are synchronized, but the immune layer exhibits both frequency and phase clustering.

It is important to note, that the ODE dynamics or system variable trajectories **do not** translate to the evolution of a patients pathological state. Instead, the amount of desynchronization of the parenchymal layer when reaching a steady system state can be interpreted as the current state of a patients organ functionality. The “result” or solution of the coupled oscillator system does not provide any temporal insights, but only describe the current condition. Time-steps taken inside the model cannot be compared to any real-world time quantity.

4.3. Implementation

For initial value problems of coupled ODE-systems, such as the DNM, analytical solutions rarely exist [29], and if they exist it is mostly for trivial or other special configurations or by applying aggressive simplifications. To solve these kind of systems one traditionally relies on the numerical integration, approximating the analytical solution.

This subsection describes the implementation for the numerical integration of the DNM defined in Equation (4.5), the choice of initial parameter values and how (de-)synchronicity/disease severity is quantified. One goal of this implementation is to partly reproduce the numerical results presented in [29], since they will be serving as a basis for following chapters.

4.3.1. Technology and Details

The backbone for the present numerical integration is JAX [39], a Python package for high-performance array computation, similar to NumPy or MATLAB but designed for automatic differentiation, vectorization and Just In Time Compilation (JIT). JIT-compilation and vectorization allow high-level numerical code to be translated to highly optimized accelerator-specific machine code, for example Graphics Processing Unit (GPU). This way, performance benefits of massively parallel hardware can be utilized with minimal extra programming cost. For the actual integration a differential equation solver from `diffax` [40] was used, which provides multiple solving schemes fully built on top of JAX.

While [29] uses a fourth-order Runge-Kutta method and a fixed step-size, this implementation¹ uses the Tsitouras 5/4 Runge-Kutta method [41] with adaptive step-sizing controlled by a Proportional-Integral-Derivative (PID) controller. A relative tolerance of 10^{-3} and an absolute tolerance 10^{-6} were chosen, allowing for more efficient integration

¹The code is available at https://github.com/unartig/sepsis_osc/tree/main/src/sepsis_osc/dnm

while keeping an equivalent accuracy. All simulations were carried out in 64-bit floating point precision, necessary for accurate and stable system integration.

Because of the element-wise differences used in the coupling terms $\varphi_i^{1/2} - \varphi_j^{1/2} \in \mathbb{R}^{N \times N}$ the computational cost scales quadratically with the number of oscillators N . These differences are then transformed by the computationally expensive trigonometric sin routine. To accelerate integration, these trigonometric evaluations were optimized following [42]. Terms in the form $\sin(\theta_l - \theta_m)$ were expanded as:

$$\sin(\theta_l - \theta_m) = \sin(\theta_l) \cos(\theta_m) - \cos(\theta_l) \sin(\theta_m) \quad \forall l, m \in \{1, \dots, N\} \quad (4.6)$$

By caching the terms $\sin(\theta_l)$, $\sin(\theta_m)$, $\cos(\theta_l)$, $\cos(\theta_m)$ once per iteration, the number of trigonometric evaluations per iteration is reduced from $2 \cdot [N(N - 1)]$ to $2 \cdot [4N]$, significantly improving performance for mid to large oscillator populations.

Additionally, an alternative implementation based on Lie-algebra formulations was also explored, utilizing their natural representation for rotations in N-D-space. Although theoretically promising in terms of numerical accuracy and integration stability, this approach did not yield practical advantages in performance. Further details on this reformulation are provided in Appendix A.2.

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4.3.2. Parameterization and Initialization

The DNM is dimensionless and not bound to any physical scale, that means there is no medical ground truth of parameter values and their choice is somewhat arbitrary. For the present implementation the parameterization is adopted from the original works [28] and [29] since they have already shown desired properties of (de-)synchronization and valid medical interpretations for these parameter choices.

The majority of their parameter choices heavily simplify the model. First of all, the different natural frequencies are treated as equal and are set to 0 giving $\omega^1 = \omega^2 = \omega = 0$, any other choice of ω just changes the frame of reference (co-rotating frame), the dynamics stay unchanged [29]. The phase lag parameters for the inter layer coupling are both set to $\alpha^{12} = \alpha^{21} = 0$, yielding instantaneous interactions, the intralayer phase lags are set to $\alpha^{11} = \alpha^{22} = -0.28\pi$, which was the prominently used configuration in [29] yielding the desired dynamical properties. The constant intralayer coupling in the parenchymal is chosen as global coupling $a_{ij} = 1$ if $i \neq j$ else 0.

The adaptation rates are chosen as $\varepsilon^1 = 0.03$ and $\varepsilon^2 = 0.3$, creating the two dynamical timescales for slow parenchymal and faster immune cells. The number of oscillators per layer is chosen as $N = 200$ throughout all simulations. To account for the randomly initialized variables, each parameter configuration is integrated for an ensemble of $M = 50$ initializations. This randomization of initial values is used to account for epistemic uncertainties, i.e. systemic errors introduced by modeling simplifications.

In [29] the influence of parameter values for β and σ was investigated and not constant throughout different simulations, with $\beta \in [0.4\pi, 0.7\pi]$ and $\sigma \in [0, 1.5]$, in this work the

interval for β was increased to $[0.0, 1.0\pi]$. An exhaustive summary of all variable initializations and parameter choices can be found in Table 2.

Table 2: Parameterization and initialization of the DNM used for the numerical integration.

SYMBOL	VALUE	SYMBOL	VALUE
Variables			
φ_i^1	$\sim \mathcal{U}(0, 2\pi)$	$\kappa_{i \neq j}^1$	$\sim \mathcal{U}(-1, 1)$
φ_i^2	$\sim \mathcal{U}(0, 2\pi)$	$\kappa_{i \neq j}^2$	clusters of size C and $1 - C$
Parameters			
M	50	N	200
C	20%		
β	$[0.0, 1.0]\pi$	σ	$[0.0, 1.5]$
α^{11}, α^{22}	-0.28π	α^{12}, α^{21}	0.0
ω_1, ω_2	0.0	A^1	$\mathbb{1} - I$
ε^1	0.03	ε^2	0.3

Initial values for the system variables, i.e. the phases and coupling strengths, were not parametrized explicitly, rather sampled from probability distributions. The initial phases $\varphi(0)_i^{1/2}$ are randomly and uniformly distributed around the unit circle for both layers, i.e. $\varphi(0)_i^{1/2} \sim \mathcal{U}[0, 2\pi)$. The intralayer coupling of the parenchymal layer coupling is also chosen randomly and uniformly distributed in the interval $[-1.0, 1.0]$. Since there is no self-coupling, the diagonal is set to 0.

For the immune layer an initial cytokine activation is modeled by clustering the initial intralayer coupling matrix. A smaller cluster of $C \cdot N$ oscillators and a bigger cluster of $(1 - C) \cdot N$ cells. Within the clusters oscillators are connected but not between the clusters. Following [29] the cluster size $C \in [0, 0.5]$ was chosen as 0.2, but as their findings suggest the size of the clusters does not have impact on the systems dynamics. Simulations have shown that even without any clustering, meaning $\mathbf{K}^2 = \mathbb{0}$ or $\mathbf{K}^2 = \mathbb{1}$, the dynamics stay unchanged, making this initialization choice meaning-free, it is stated here just for completeness. An example for initial variable values of a system with $N = 200$ and $C = 0.2$ is shown in Figure 4.

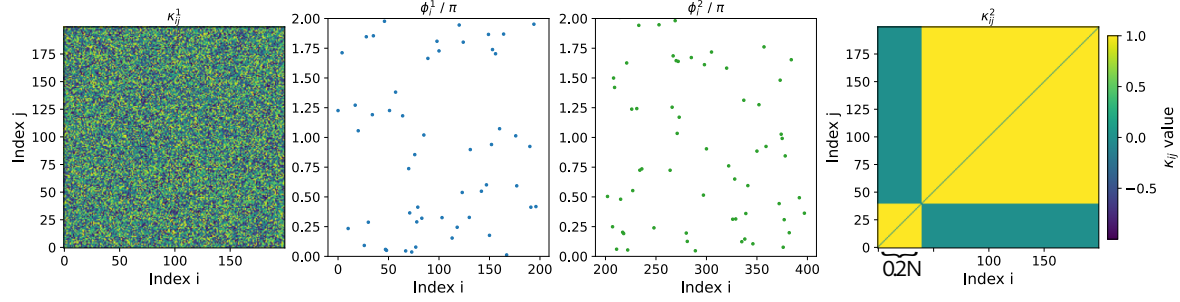


Figure 4: Initializations for the variable values of a DNM with $N = 200$ oscillators per layer. The middle two plots show the phases of the oscillators, with φ_i^1 for parenchymal and φ_i^2 for the immune layer, sampled from a uniform random distribution from 0 to 2π . On the left-hand side is the initialization of the parenchymal intralayer coupling matrix \mathbf{K}^1 from a uniform distribution in the interval from -1 to 1 . On the right-hand side is the two cluster initialization for the coupling matrix \mathbf{K}^2 of the immune layer, with a cluster size of $C = 0.2$, where each cluster is intra-connected, but without connections between the clusters.

To average out the influence of specific random initial values, simulations are performed for ensembles, combining $m \in 1, 2 \dots M$ ensemble members. Throughout this work an ensemble size of $M = 50$ was used.

index for
immune

4.3.3. Synchronicity Metrics

As introduced in Section 4.1, for the complex Kuramoto networks the synchronization behavior is usually the point of interest, in the following two metrics are introduced, relevant to connect the DNM-dynamics to sepsis. There are two relevant states or system configurations that should be identifiable and quantifiable to allow qualified state analyzes: phase and frequency synchronization, for each a distinct measure is required.

Phase synchronization of a layer is commonly measured by the *Kuramoto Order Parameter* [7]:

$$R_2^{1/2} = \frac{1}{N} \left| \sum_j^N e^{i \cdot \varphi_j^{1/2}(t)} \right| \quad \text{with } 0 \leq R_2^{1/2} \leq 1 \quad (4.7)$$

where $R_2^\mu = 0$ corresponds to total desynchronization, the splay-state and $R_2^\mu = 1$ corresponds to fully synchronized state, for convenience from now on the subscript \cdot_2 is omitted, denoting the Kuramoto Order Parameter simply as $R^{1/2}$.

Frequency synchronization measurements are more involved, as a starting point first the notion of a layers *mean phase velocity* has to be introduced, which can be calculated as follows:

$$\bar{\omega}^{1/2} = \frac{1}{N} \sum_j^N \dot{\varphi}_j^{1/2} \quad (4.8)$$

The original definition in [28] and [29] uses an approximated version using the oscillators mean velocity. This is likely because they were not able to recover the actual derivatives $\dot{\varphi}_i^{1/2}$ from their integration scheme and had to work with the phases $\varphi_i^{1/2}$ instead:

$$\langle \dot{\varphi}_j^{1/2} \rangle = \frac{\varphi_j^{1/2}(t+T) - \varphi_j^{1/2}(t)}{T} \quad (4.9)$$

$$\bar{\omega}^{1/2} = \frac{1}{N} \sum_j^N \langle \dot{\varphi}_j^{1/2} \rangle \quad (4.9)$$

for some averaging time window T . But since their choice of T is not documented while having substantial influence on the calculation the direct calculation was preferred.

One can now calculate the standard deviation of the mean phase velocities:

$$\sigma_\chi(\bar{\omega}^{1/2}) = \sqrt{\frac{1}{N} \sum_j^N \left(\langle \dot{\varphi}_j^{1/2} \rangle - \bar{\omega}^{1/2} \right)^2} \quad (4.10)$$

Where $\sigma_\chi = 0$ indicates full frequency synchronization and growing values indicate desynchronization and/or clustering. But non-zero values only reveal that there is some desynchronization of the frequency, but it remains unknown if it is clustered, multi-clustered or fully desynchronized.

Since there are multiple ensemble members m for the same parameterization, and it is expected that different initialization, even though equally parameterized, can exhibit dissimilar behaviors, one can also calculate the *ensemble averaged standard deviation of the mean phase velocity*:

$$s^{1/2} = \frac{1}{M} \sum_m^M \sigma_\chi(\bar{\omega}_m^{1/2}) \quad (4.11)$$

In [29] it was shown numerically that the quantity $s^{1/2}$ is proportional to the fraction of ensemble members that exhibit frequency clusters containing at least one oscillator. This makes s^1 a viable measure for pathology, as increasing values of s^1 or increasing system incoherence then indicate more dysregulated host responses and consequently higher risks of multiple organ failure.

4.3.4. Simulation Results

The original findings of [29] identify β , the combined age parameter, and σ , the interlayer coupling strength which models the cytokine activity, as naturally important parameters in order to understand underlying mechanisms of sepsis progression. In the following subsection multiple simulation results are presented, starting with time-snapshots for different parameterization and initializations. Afterward, the transient and temporal behavior of the metrics $s^{1/2}$ and $R^{1/2}$ is for the same parameterization, as well as the introduction of the β, σ phase space of these metrics.

In Figure 5 snapshots of the system variables are shown for different parameterization, differing only in the choice β and σ , configurations A, B, C and D are listed in Table 3, other parameters are shared between the configurations and are stated in Table 2. Each configuration is expected to represent the current physiological state a single patient.

All following results are for a system with $N = 200$ oscillators, and snapshots taken at time $T_{\text{sim}} = 2000$, the end of the integration time, and show the stationary values at that time point.

Table 3: Specific β - σ combinations to illustrate simulation results.

	A	B	C	D
β	0.5π	0.58π	0.7π	0.5π
σ	1.0	1.0	1.0	0.2

In Figure 5 the left-most columns depicts the coupling matrices for the organ layer \mathbf{K}^1 followed by two columns showing the phase velocities for each oscillator $\dot{\phi}_i^{1/2}$ and two columns showing the oscillator phases each layer $\phi_i^{1/2}$. The right-most column shows the coupling matrix for the immune layer \mathbf{K}^2 . Each layer is sorted first from lowest to highest frequency and secondary by lowest to highest phase for better clarity. Rows C and C' share the same parameterization but are different samples from the same initialization distributions.

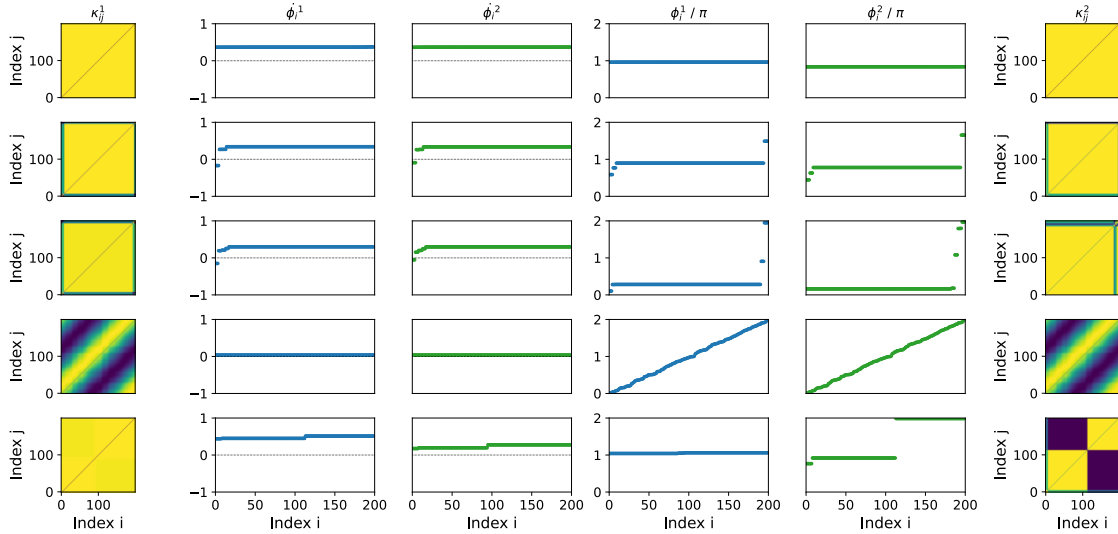


Figure 5: Snapshots of different DNM parametrization and initialization. Configuration A can be regarded as healthy, with phases and frequencies being fully synchronized. In contrast, B and C are pathologic, due to their clustering in $\dot{\phi}^1$. Configuration C' corresponds to a vulnerable state, because of uniformly distributed phases (splay state). Lastly, D is regarded as resilient, since the phases exhibit clustering, but the frequencies $\dot{\phi}^1$ are synchronized.

K colorbar

Row A in Figure 5 is fully synchronized/coherent since it not only has the frequencies synchronized but also the phases and can therefore interpreted as healthy. The coherence can also be seen in the fully homogeneous coupling matrices where both $\mathbf{K}^{1/2}$ show the same coupling strength for every oscillator pair. The rows B and C in contrast show signs of a pathological

state, here both the frequencies three and phases have four distinct clusters respectively. The clusters are also visible in the coupling matrices, where the coupling strength differs based on the cluster. The row for C', even though having the same parameterization as C, can be regarded vulnerable, since the phases uniformly distribute in the $[0, 2\pi)$ interval ($R^{1/2} = 0$), while the frequencies are synchronized. Coupling matrices for C' show traveling waves, which are characteristic for splay states. Observing different results for different initializations justifies the introduction of ensembles. Lastly row D shows a resilient state, where the phases are clustered while the frequencies are synchronized.

For the next result, the ensembles were introduced, every configuration of A, B, C, and D was simulated for $M = 50$ different initializations over an interval of $T_{\text{sim}} = 2000$. The two left-most columns show the standard deviation of the mean phase velocities $s^{1/2}$ for each ensemble member m . The plots show the temporal evolution of metrics for quantifying phase and frequency coherence, with the two right-most columns of Figure 6 show the temporal behavior of the Kuramoto Order Parameter for each individual ensemble member $m \in 1, 2 \dots M$. Where lower values for $R^{1/2}$ indicate decoherence in phases, with its minimum $R^{1/2} = 0$ coincides with a splay state, and for $s^{1/2}$ higher values indicate a larger amount of frequency decoherence and clustering.

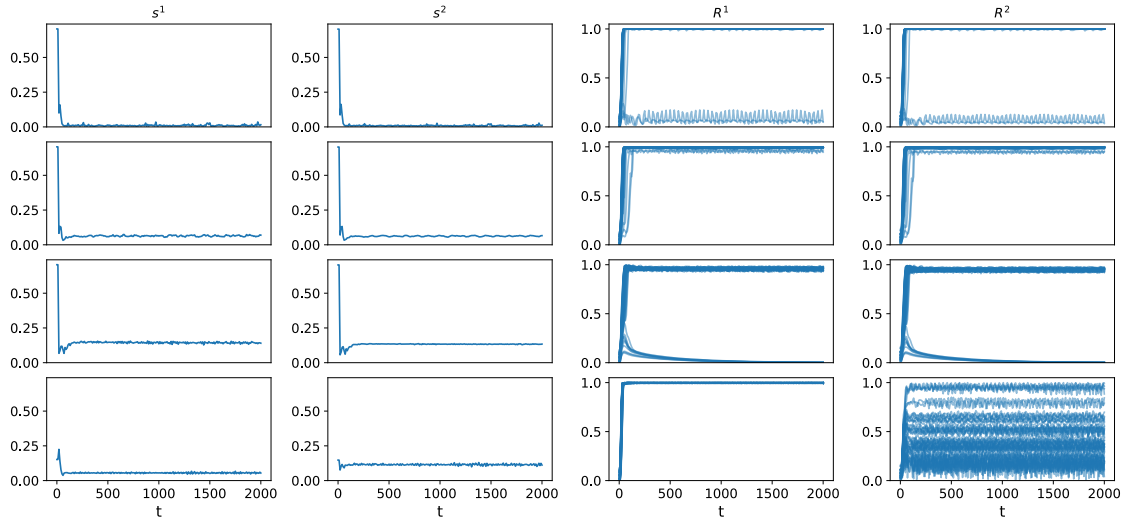


Figure 6: Transient and temporal evolution of the phase- and frequency-synchronization metrics $R^{1/2}$ and $s^{1/2}$, for ensembles of the DNM for the configurations listed in Table 3. Emphasizing the influence of β and σ on the systems synchronization behavior, and presenting different stable emergent system states.

Every ensemble in Figure 6 shows decoherence for early time-points, which is expected for randomly initialized variables, but changes relatively fast through a transient phase $t \in [0.0, 200]$ into systematic stable behavior. The stable states align with the observations made for Figure 5, configuration A has, besides small jitter, mostly synchronized frequencies $s^{1/2} \approx 0$. Also the phases of configuration A are mostly synchronized with $R^{1/2} \approx 1$, only two initializations show decoherence and are oscillating between weak clustering and almost full incoherence. Medically this can be interpreted as a low risk of a dysregulated host response for an otherwise healthy response to the initial cytokine activation. For configuration

B the amount of incoherence inside the ensemble is clearly visible, with $s^{1/2}$ being positive and some more ensemble members exhibiting clustering, indicated by a Kuramoto Order Parameter slightly less than 1. In configuration C the incoherence is even more prominent, larger $s^{1/2}$ and some ensemble members evolving into a splay state, i.e. $R^{1/2} = 0$. For configuration D the overall phase incoherence is again a bit less compared to C, and lower for the organ compared to the immune layer. The phases are coherent for the organ layer but seem almost chaotic for the immune layer, some are synchronized, while others are clustered, in a chimera or almost splay-like state. Over the whole simulation period, the coherency in the immune layer seems not to fully stabilize, rather oscillate around an attractor.

Each of the configurations only differs in the parameter choices for β and σ , yet they evolve into unique and distinct system states. To put these four specific configurations into broader perspective, a grid of β and σ was simulated, in the interval $\beta \in [0, 1]$ with a grid resolution of 0.01 and $\sigma \in [0, 1.5]$ with a resolution of 0.015, creating a grid of 10,000 points. In Figure 7 the metric $s^{1/2}$ is shown in the $\beta - \sigma$ phase space for both layers in the first row, where brighter colors indicate a larger risk of frequency desynchronization, or risk of dysregulated immune response. The second row shows the ensemble mean over $\bar{R}^{1/2}$, i.e. $\bar{R}^{1/2} = \frac{1}{M} \sum_m R_m^{1/2}$, with $M = 50$, where darker colors indicate larger phase desynchronization. The white rectangle indicates the simulated region in [29], $\beta \in [0.4, 0.7]$ and $\sigma \in [0, 1.5]$ for reference. Coordinates of the configurations A, B, C, and D are also labeled.

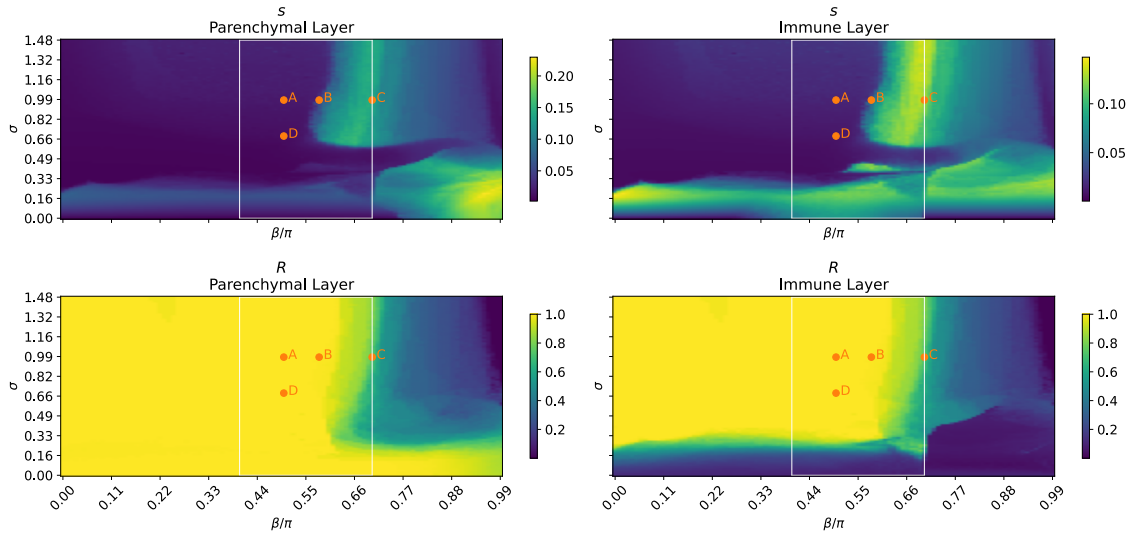


Figure 7: Phase space of the parameters β and σ and illustrating the broader picture their influence on the frequency and phase synchronization of the DNM. White rectangle indicates the grid-limits of the original publication [29].

Generally there is a similarity between phase and frequency desynchronization but no full equality, meaning there are parameter regions where the phase is synchronized and frequency desynchronized and vice versa. Another observation, that smaller values of $\beta < 0.55$ correspond to less desynchronization and stronger coherence, which is in line with the medical interpretation of β where smaller values indicate a younger and more healthy biological age. When crossing a critical value of $\beta_c \approx 0.55$ for the frequency and $\beta_c \approx 0.6$ for the phases,

the synchronization behavior suddenly changes and tends towards incoherence, clustering and pathological interpretations.

For small values of $\sigma < 0.5$ the frequency synchronization and $\sigma < 0.25$ for the phase synchronization, the behavior significantly differs between immune and organ layer. The immune layer tends to fully desynchronize, instead the organ layer only the frequency desynchronizes for larger $\beta > 0.7$. With larger values of $\sigma > 0.5$ the dynamics more or less harmonize between layers and metrics and are mostly depend on β .

4.4. Summary of the DNM

This chapter introduced the Dynamic Network Model as a functional, mesoscopic description of coordinated physiological activity during sepsis, modeling cellular cytokine-based communication. Based on adaptive Kuramoto-type oscillators arranged in a two-layer parenchymal-immune architecture, the model captures a range of emergent regimes like synchronization, clustering, chimera-like patterns, that correspond to interpretable physiological states. Key parameters such as the biological age β and interlayer coupling σ were shown to modulate these regimes. A numerical implementation in JAX enabled efficient simulation and extraction of summary measures such as $R^{1/2}$ and $s^{1/2}$.

Although the DNM model is not mechanistic on a cellular or biochemical level, it provides a structured and interpretable dynamic space. This is valuable for downstream machine learning because it offers:

- i) physiologically meaningful features derived from complex clinical signals,
- ii) a nonlinear dynamical framework that can reflect regime shifts relevant to sepsis progression, and
- iii) a principled way to inject physiological priors into otherwise data-driven models

Together these properties motivate its integration into the subsequent ML pipeline described in the next chapter.

5 State of the Art

This chapter provides a brief overview of the current state of the art in automated sepsis prediction and concludes in Section 5.3 with some fundamental challenges found when assessing sepsis prediction systems. Sepsis prediction models for individual patients can be categorized into two major classes, the model-based and the data-driven approaches.

5.1. Model-Based Approaches

Biological and medical inspired models of sepsis offer high interpretability and explainability, since they explicitly encode causal relationships. However, due to the inherent complexity of sepsis pathophysiology, such mechanistic models remain rare [31]. Most existing works focus on dynamic immune response on a cellular [43], [44], [45], [46], intricate signaling and production mechanisms influenced by varying cell concentration are typically modeled using large systems of coupled differential equations.

To derive risk estimates or disease trajectories, model parameters are fitted to individual patient observations. By simulating physiological trajectories under hypothetical infection scenarios, these models enable to estimate the likelihood of sepsis development [44]. More advanced digital twins which incorporate bidirectional feedback between the mechanistic model and patient data have also been explored in [45].

Validation mechanistic sepsis models is usually done by comparing simulation trajectories to repetitively measured cellular concentrations. Since the required high-resolution immunological measurements are difficult and costly to obtain only small samples of patients have been validated. To date no model-based prediction approaches has yet been evaluated on large-scale clinical datasets, limiting their insight into real-world performance and generalizability.

5.2. Data-Driven Approaches

With the increasing availability of Electronic Health Record and computational resources, ML- and DL-methods have become the dominant paradigm for sepsis prediction systems over the last decade. Data-driven approaches can capture highly nonlinear relationships in heterogeneous clinical data and have demonstrated strong empirical performance in real-world settings. Numerous systems have been proposed and are summarized in surveys

such as [47] and [48]. The technology-landscape is highly diverse and includes classical ML-models (nonlinear regression, random-forests, Support Vector Machine (SVM)s, and gradient-boosted trees such as XGBoost [49]), as well as DL-architectures (standard Multi Layer Perceptron (MLP), recurrent models e.g. Gated Recurrent Unit (GRU)/Long Short-Term Memory (LSTM), attention based e.g. transformers and more specialized models like Gaussian Process Temporal Convolutional Networks [50].

5.3. Challenges in comparing sepsis prediction models

Although many of data-driven models report reasonable performance, direct comparison across studies is fundamentally limited, as highlighted by [48]. The main issues particularly relevant to the Latent Dynamics Model (LDM) methodology are:

- **Prediction Tasks**

Studies differ fundamentally in how they frame the prediction problem. This includes *online training*, where newly arriving medical measurements are incorporated into a continuously updated risk estimate and *offline training*, where only the information available at a fixed observation time is used to predict the risk of sepsis within a prespecified horizon T . Because these setups rely on different information structures and temporal assumptions, their reported performances are not directly comparable. Online prediction is more clinically desirable but also more challenging to implement given the current state of available Electronic Health Record (EHR). Both schemes are shown in Figure 8, notice in offline prediction the horizon T , the specific choice strongly influences the outcome, with smaller horizons the tasks becomes gradually easier. For the online scheme choice of what time range around a sepsis onset qualifies as positive label also significantly changes prediction accuracy and prediction.

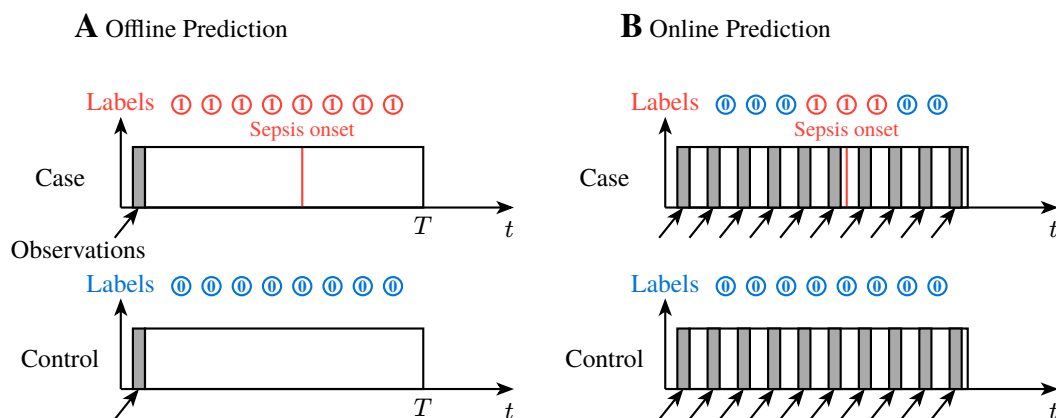


Figure 8: Illustration of the two predictions schemes, *offline* (A) vs. *online* (B) (figure heavily inspired by [48]). The main difference is the provision and utilization and arrival of observation data.

To have a meaningful comparisons between two models, they must be evaluated on the *exact same task*. This includes the scheme (offline or online), the same choice of T for the offline scheme and the labeling window around the measured onset.

- **Sepsis Definition and Implementation**

Sepsis definitions are vary widely across studies but greatly influence the prevalence, cohort composition as well as task difficulty. Intuitively different sepsis definitions are not comparable with each other since they might capture dissimilar medical concepts. Even for the same conceptual definition and same dataset differences in implementation can yield different patient cohorts and therefore different prediction performances [9]. More restrictive definitions typically produce lower prevalence and greater class imbalances making ML-based prediction more difficult but potentially increasing clinical relevance. Less restrictive definitions can artificially inflate prediction performance while reducing practical applicability.

- **Feature selection**

Feature choice also influences both model performance and real-world usability. Using a broader set of features can increase predictive accuracy but risks again the clinical applicability, since extensive measurements may be not routinely available. It also increases the risk of label leakage, where the measurements and medical concepts used to derive the sepsis label are provided to the prediction model as feature input. This way the model would learn the sepsis derivation but not underlying signals which are actually helpful for early sepsis recognition.

5.4. Summary of State of the Art

As of now, neither purely model-based nor purely data-driven approaches were able to fully address the challenges of sepsis prediction. Mechanistic models offer strong interpretability and encode physiological priors, yet their practical usefulness is limited by the scarcity of high-resolution immunological measurements and the lack of large-scale clinical validation. In contrast, data-driven models show strong empirical performance on EHR datasets, but their prediction behavior is often difficult to interpret and show black-box behavior

This work, named the Latent Dynamics Model aims to combine the strengths of both paradigms: mechanistic components of the DNM introduce structured physiological biases that can help stabilize the learning process, and provide more interpretable intermediate quantities. At the same time, the data-driven components allow the model to adapt to real clinical variability and make use of information that is not explicitly captured by the mechanistic structure. In this way, the LDM seeks to make data-driven sepsis prediction models more transparent and more robust to the well-known issues discussed in Section 5.3.

The heterogeneity in prediction tasks, sepsis definitions and feature sets illustrates why each decision of one of these aspects regarding new prediction models should be taken with care. For the sake of reproducibility the choices need to be reported as precisely as possible. Works such as Yet Another ICU Benchmark (YAIB) [1] attempt to address these challenges by providing a common basis for evaluating models by standardizing the dataset, cohort definition,

prediction task, and labeling strategy, thereby enabling fair and reproducible comparison of different approaches.

After introducing the methodology in Section 6, its performance validated on real clinical data in Section 7. The experimental setup makes use of the YAIB framework, and its dataset, cohort definition, prediction task, and labeling implementation are described in detail in Section 7.1, as these settings are adopted for training and evaluating the LDM.

6 Method (Latent Dynamics Model)

This chapter introduces the methodological framework used to address the first research question stated in Section 3:

Usability of the DNM: How and to what extent can the ML-determined trajectories of the DNM be used for detection and prediction, especially of critical infection states and mortality.

format

To investigate this, a deep learning pipeline targeting the online prediction scheme (see Section 5.3) has been developed, in which the DNM is embedded as central part. Instead of predicting sepsis directly, the two components, Suspected Infection and increase in SOFA scores are predicted as proxies creating more nuanced and more interpretable prediction results.

To predict the increase in SOFA, namely the worsening of organ functionality, the main idea is to utilize parameter level synchronization dynamics inside the parenchymal layer of the functional DNM, which is expected to model systemic organ failure. Particularly the parameters β and σ , interpreted as biological age and amount of cellular interaction between immune cells and functional organ cells, are of great interest.

In order to achieve this, the DNM is embedded into a learnable latent dynamical system, where patients are placed into the two-parameter phase space and a recurrent module predicts physiological drift in that space. Pre-computed DNM dynamics give rise to differentiable SOFA and SI estimates. The complete architecture, consisting of the DNM and additional auxiliary modules, which will be referred to as the LDM from now on.

This chapter proceeds in Section 6.1 with the prediction task to be reiterated and the strategy formalized and the introduction of desired prediction properties, together with the justification of modeling choices. Afterwards, in Section 6.2, the individual modules of the LDM will be discussed, focusing on what purpose each serves and how it is integrated into the broader system, especially the DNM.

Notation
table?

6.1. Formalizing the Prediction Strategy

In automated clinical prediction systems, a patient is typically represented through their Electronic Health Record (EHR). The EHR aggregates multiple clinical variables, such as laboratory biomarker, for example from blood or urine tests, or physiological scores and,

further demographic information, like age and gender. Using the information that is available in the EHR until the prediction time-point t , the objective is to estimate the patients risk of developing sepsis at that time t . The following methodology will formalize the online-prediction, where newly arriving observations are continuously integrated into updated risk estimates. To use this prediction system in a clinical setting it is causality is important, this requires that for every prediction at time t only the information available up to that time-point can be used, and no future observations.

6.1.1. Patient Representation

Let t denote an observation time during a patients ICU-stay and the available EHR at that time consisting of D variables. It is assumed that μ does not carry the quantities that directly translate to the sepsis definition. After imputation of missing values, normalization, and encoding of non-numerical quantities, each variable μ_j is mapped to a numerical value:

$$\mu_{t,j} \in \mathbb{R}, \quad j = 1, \dots, D \quad (6.12)$$

These values are collected into a column-vector:

$$\mu_t = (\mu_{t,1}, \dots, \mu_{t,D})^T \in \mathbb{R}^D \quad (6.13)$$

, where the superscript T denoting a transpose operation. The vector μ_t is fully describing the current physiological state of the ICU-patient at observation time point t .

6.1.2. Modeling the Sepsis-3 Target

The goal is derive continuously updated estimates of sepsis risk based on newly arriving observations μ_t over time, with equally spaced and discrete time-steps $t \in \{0, \dots, T\}$. Following the Sepsis-3 definition, the onset of sepsis requires both suspected infection and acute multi-organ failure.

Defining the instantaneous *sepsis onset event* S_t as the occurrence of the Sepsis-3 criteria at time point t within the patients ICU stay as:

$$S_t := A_t \cap I_t \quad (6.14)$$

Here $A_t = \{\Delta O_t \geq 2\}$, indicates an acute worsening in organ function, measured via a change in SOFA-score $\Delta O_t = O_t - O_{\text{base}}$ with respect to some patient specific baseline SOFA-score O_{base} . The choice of O_{base} has to align with the Sepsis-3 definition, for example a 24 h running minimum, the or $O_{\text{base}} = O_{t-1}$. The event I_t is an indicator for a Suspected Infection at time t defined according to the Sepsis-3 definition, spanning the 48 h² before and 24 h after the documented SI-onset-time (see Section 2.1).

Conditioned on the history of observations $\mu_{0:t}$ the target probability is given by:

²Although the label I_t is defined retrospectively using a time window around the infection onset, this does not violate causality. The predictive model only conditions on $\mu_{0:t}$, i.e., information available up to time t . Future observations are used exclusively for label construction during training and available at inference time.

$$\Pr(S_t | \mu_{0:t}) = \Pr(A_t \cap I_t | \mu_{0:t}) \quad (6.15)$$

6.1.3. Heuristic Scoring and Risk Estimation

The direct estimation of the true conditional probability $\Pr(S_t | \mu_{0:t})$ is computationally and statistically challenging due to the temporal dependency between the binary Sepsis-3 criteria. To make the prediction of the target probability more tractable but still connect the statistical estimation to the clinical definition several assumptions and modeling choices are introduced.

Importantly, all assumptions result in differentiable approximations of the real events or probabilities, enabling end-to-end learning of estimators through gradient-based methods.

The central assumption is that infection I_t and multi-organ failure A_t are conditionally independent:

$$\Pr(A_t \cap I_t | \mu_{0:t}) = \Pr(I_t | \mu_{0:t}) \Pr(A_t | \mu_{0:t}) \quad (6.16)$$

Clinically this assumption does not hold, since the majority multi-organ failures stem from an underlying infection, meaning they exhibit strong partial correlations. Yet this assumption is necessary because the DNM, which is an essential building block to the LDM, only captures organ failure risk irrespective of infection states and the independence allows treating both components separately for the prediction. Additionally, this separation improves interpretability, since each component can be analyzed individually.

As a second assumption, although the indication I_t is binary, the target is a temporally smoothed version. The surrogate label $\bar{I}_t \in [0, 1]$ increases linearly in the (48 h) hours preceding the infection onset, it reaches maximum at onset, and it decays exponentially afterwards (24 h). This is mimicking temporal uncertainty of establishment and resolution, for example due to delayed documentation and treatment effects such as antibiotic half-life.

Thus, the overall prediction requires two separate risk estimators:

$$\tilde{A}_t \approx \Pr(A_t | \mu_{0:t}) \quad \text{and} \quad \tilde{I}_t \approx \bar{I}_t \quad (6.17)$$

Both $\tilde{A}_t \in (0, 1)$ and $\tilde{I}_t \in (0, 1)$ are heuristic risk scores serving as approximations for the real event probabilities and the surrogate infection risk score. The original prediction target has been converted from a calibrated probability to a *heuristic risk score* \tilde{S}_t :

$$\Pr(S_t | \mu_{0:t}) \approx \tilde{S}_t := \tilde{A}_t \tilde{I}_t \quad (6.18)$$

Where the infection surrogate infection risk score can be directly derived from the EHR history:

$$\tilde{I}_t := f_\theta(\mu_{0:t}) \quad (6.19)$$

In contrast, \tilde{A}_t is not derived directly from the EHR, instead it relies on estimated SOFA-score dynamics:

$$\hat{O}_t := g_\theta(\mu_{0:t}) \quad (6.20)$$

where \hat{O}_t denotes a latent, differentiable estimation for the true SOFA-score O_t which cannot be derived directly from the available EHR. Given two consecutive estimated SOFA-scores \hat{O}_{t-1} and \hat{O}_t a differentiable increase indicator \tilde{A}_t is calculated to indicate the event of organ failure:

$$\tilde{A}_t = o_{s,d}(\hat{O}_{t-1:t}) = \text{sigmoid}(s(\hat{O}_t - \hat{O}_{t-1} - d)) \quad (6.21)$$

The function $o_{s,d}(\cdot)$ contains two globally learnable parameters, d a threshold and s a sharpness parameter. While the Sepsis-3 definition corresponds to a fixed threshold of $d = 2$, here d is treated as learnable to obtain a smooth, fully differentiable approximation of the discrete SOFA increase criterion and to account for uncertainty in baseline estimation. The choice of the function $\text{sigmoid}(x) = \frac{1}{1+e^{-x}}$ yields a monotonic indicator (larger SOFA increase \rightarrow more likely organ failure) while still being differentiable.

The high-dimensional μ 's have now been condensed into two clinically motivated statistics \tilde{A}_t and \tilde{I}_t . The interaction term $\tilde{A}_t \tilde{I}_t$ mirrors their logical conjunction in the Sepsis-3 definition. It is important to note that \tilde{S} is **not a calibrated probability** but a heuristically derived and empirical risk score based on the Sepsis-3 definition, serving as a differentiable surrogate for the Sepsis-3 sepsis onset criterion $P(S_t | \mu_{0:t})$. Larger values of \tilde{S}_t correspond to higher expected risk of sepsis outbreak.

6.2. Architecture

The previous subsection explained how the sepsis onset target even S_t can be decomposed into the conjunction of suspected infection indication I_t and organ failure event A_t that itself can be calculated from two consecutive SOFA-scores $O_{t-1:t}$. The presented Latent Dynamics Model is designed to estimate the fundamental components \tilde{O}_t and \tilde{I}_t from a history of EHR $\mu_{0:t}$ to derive the heuristic sepsis risk score $\tilde{S}_t \approx S_t$ for individual patients. Each component is estimated by a Recurrent Neural Networks (RNN) module enabling continuous estimation updates based on newly arriving measurements.

The following subsection will introduce the individual modules which are fully differentiable functions with learnable parameters allowing for optimization via first order gradient descent methods. Starting with the estimator module for the suspected infection indication module in Section 6.2.1, followed the organ failure estimation module in Section 6.2.2 which includes the DNM to derive SOFA estimates and lastly an auxiliary regularization module in Section 6.2.3.

Table 4: Summarization of notation used in the Latent Dynamics Model methodology.

SYMBOL	DESCRIPTION
i, N	Patient index and total patients
t, T_i	Time point and trajectory length
$\mu_t \in \mathbb{R}^D$	EHR vector with D variables at time t
$\mu_{0:t}$	EHR history from time 0 to t
$S_t, A_t, I_t \in \{0, 1\}$	Binary sepsis onset, organ failure, and infection events
$O_t, \Delta O_t \in [0, \dots, 24]$	SOFA score and change from baseline
$\bar{I}_t \in [0, 1]$	Continuous surrogate infection indicator
$\hat{O}_t \in \{0, \dots, 24\}$	Estimated SOFA score
$o_{s,d}(\hat{O}_{t-1:t})$	Differentiable increase detection function
$\tilde{S}_t, \tilde{A}_t, \tilde{I}_t \in (0, 1)$	Predicted sepsis, organ failure, and infection risks
$z = (z_\beta, z_\sigma)$	Latent coordinates in DNM parameter space
$\hat{z}_t, \Delta \hat{z}_t$	Predicted latent position and change
$s^1(z)$	Synchronization measure (desynchronicity) in DNM
$h_t \in \mathbb{R}^h$	Hidden state vector
$f_\theta, g_\theta^e, g_\theta^r, d_\theta$	Infection indicator, encoder, recurrent, decoder modules
θ	Learnable parameters
$\mathcal{L}_{\text{sepsis}}, \mathcal{L}_{\text{inf}}, \mathcal{L}_{\text{sofa}}$	Primary sepsis, infection, and SOFA losses
$\mathcal{L}_{\text{focal}}, \mathcal{L}_{\text{diff}}, \mathcal{L}_{\text{dec}}, \mathcal{L}_{\text{spread}}$	Auxiliary focal, directional, decoder, and diversity losses
λ_i	Loss weight for component i
B	Mini-batch size

6.2.1. Infection Indicator Module

The first module of the LDM estimates the presence of a SI, represented by the continuous surrogate indicator \bar{I}_t , the module predicts a continuous surrogate infection risk $\tilde{I}_t \in (0, 1)$. Given N patient trajectories with T_i pairs of EHR vectors and ground truth SI-indicator each:

$$(\mu_{i,t}, \bar{I}_{i,t}), \quad i = 1 \dots N, \quad t = 1 \dots T_i \quad (6.22)$$

a parameterized non-linear recurrent function

$$f_\theta : \mathbb{R}^n \times \mathbb{R}^h \rightarrow (0, 1) \times \mathbb{R}^h \quad (6.23)$$

is trained to map the patients physiological state represented by the EHR to an estimated risk of suspected infection:

$$(\tilde{I}, \mathbf{h}_t)_t = f_\theta(\mu_t, \mathbf{h}_{t-1}) \quad (6.24)$$

The hidden state \mathbf{h}_t propagates temporal information through time. For the first time-step $t = 0$ a learned initial hidden state \mathbf{h}_0 is used.

The model is implemented as a supervised RNN, see Figure 9, optimized with stochastic gradient descent, throughout training minibatches of size B are sampled. To fit the model, Binary Cross Entropy (BCE)-loss which measures the distance between true label \bar{I}_t and the predicted label \tilde{I}_t :

$$\mathcal{L}_{\text{inf}} = -\frac{1}{B} \sum_{i=1}^B \frac{1}{T_i} \sum_{t=0}^{T_i-1} \left[\bar{I}_{i,t} \log(\tilde{I}_{i,t}) + (1 - \bar{I}_{i,t}) \log(1 - \tilde{I}_{i,t}) \right] \quad (6.25)$$

is minimized and thus the estimator provides a differentiable estimate of the surrogate infection activity.

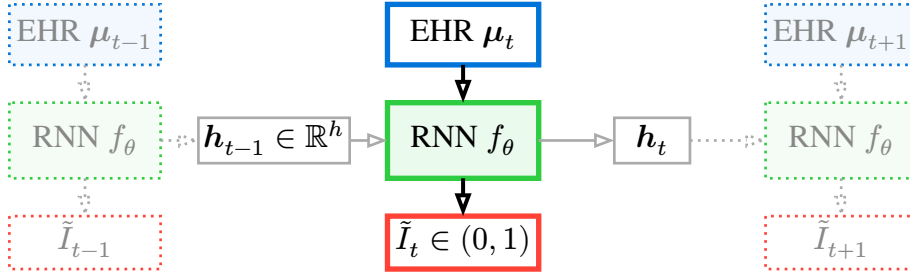


Figure 9: Schematic of the Infection Indicator Module architecture and rollout.

6.2.2. SOFA Predictor Module

The complete SOFA predictor module g_θ is composed two submodules, an initial-encoder g_θ^e and a recurrent latent predictor g_θ^r , each described below. The high level idea is to translate the physiological patient trajectory to a sequence of the DNM parameters β and σ , where the desynchronization of given parameter pairs should match the physiological organ failure. To begin with, Section 6.2.2.1 once more tries to strengthen the connection between organ failure and the DNM, followed by Section 6.2.2.2 presents how the EHR information is embedded evolved inside the DNM parameter space. Lastly in Section 6.2.2.3 is describes how computational cost can be significantly reduced by pre-computing the DNM parameter space.

6.2.2.1. The DNM as SOFA Surrogate

Recalling that the pathological organ conditions within the DNM are characterized by frequency clustering in the parenchymal layer. The amount of frequency clustering is quantified by the ensemble average standard deviation of the mean phase velocity s^1 (see Equation (4.11)). Since s^1 monotonically increases with loss synchrony, it serves as an

interpretable and natural surrogate for the SOFA-score. Increasing values of s^1 indicate a higher SOFA-score and a worse condition of the patients organ system.

Numerical integration of the DNM equations for a given parameter pair $z = (\beta, \sigma)$ yields the corresponding continuous SOFA approximation $\hat{O}(z)$:

$$\hat{O}(z) = \text{round} \left(\frac{24 \cdot s^1(z)}{s_{\max}^1} \right) = \text{round} \left(\frac{24 \cdot s^1(\beta, \sigma)}{s_{\max}^1} \right) \in \{0, 1, \dots, 24\} \quad (6.26)$$

these two parameters were identified as highly influential and interpretable quantities in the original DNM publications [29]. Every other system parameter is assumed constant and chosen as listed in Table 2. The rounding operation is used only for interpretability and evaluation; during training the normalized continuous s^1 -based surrogate is used.

The space spanned by the two parameters is called the *latent space*, coordinate-pairs of that latent space are denoted $z = (z_\beta, z_\sigma)$. In the following $s^1(z)$ and $\hat{O}(z)$ are used synonymously, depending on the context the notation emphasizes the connection to either the DNM or the interpretation as SOFA-score.

The prediction strategy involves the mapping of individual EHR to the latent space, so that the ground truth SOFA-aligns with the desynchronization measure of the latent coordinate. Based off of this initial location (and additional information), the patient will perform a trajectory through the latent space yielding step by step SOFA-score $\hat{O}_{0:T}(z)$ estimates needed to calculate the heuristic organ-condition statistic \tilde{A}_t .

6.2.2.2. Latent Parameter Dynamics

Even though this module is also RNN based, in contrast to the infection indicator module from Section 6.2.1, this module follows a different strategy. Focusing on a single patient, but omitting the i subscript for readability, with its first observation at time $t = 0$, an encoder connects the high-dimensional EHR to the dynamical regime of the DNM, a neural encoder:

$$g_\theta^e : \mathbb{R}^n \rightarrow \mathbb{R}^2 \times \mathbb{R}^h = \mathbb{R}^{2+h} \quad (6.27)$$

where the high dimensional patient state is mapped to a two-dimensional latent vector, and a h dimensional hidden state.

$$(\hat{z}_0, \mathbf{h}_0) = ((\hat{z}_{0,\beta}, \hat{z}_{0,\sigma}), \mathbf{h}_0) = e_\theta(\mu_0) \quad (6.28)$$

This encoding locates the patient within a physiologically meaningful region of the DNM parameter space, which in context of the LDM is called the latent space. The latent coordinate \hat{z}_0 provides the initial condition for short-term dynamical organ condition forecasting. As described in Section 6.2.2.1 the latent coordinates correspond to a DNM synchronization behavior and can therefore be directly interpreted as SOFA-score estimates ($\hat{z} \rightarrow s^1(\hat{z}) \rightarrow \hat{O}(\hat{z})$).

In addition to the estimated parameter pair \hat{z}_0 , the encoder outputs another vector with dimension $h \ll n$ that is a compressed representation of patient physiology relevant for short-term evolution of \hat{z} . This vector $\mathbf{h}_0 \in \mathbb{R}^h$ is the initial hidden space.

Since the heuristic SOFA risk \tilde{A} depends on the evolution of organ function $\hat{O}_{0:t}$, it is necessary to estimate not only the initial state \hat{z}_0 but also its evolution. For this purpose a neural recurrent function:

$$g_\theta^r : \mathbb{R}^{n+2} \times \mathbb{R}^h \rightarrow \mathbb{R}^2 \times \mathbb{R}^h \quad (6.29)$$

is trained to propagate the latent DNM parameters forward in time.

This recurrent mechanism, primed by the hidden state \mathbf{h}_t and previous latent location \mathbf{z}_{t-1} , captures how the underlying physiology influences the drift of the DNM parameters:

$$\Delta \hat{\mathbf{z}}_t, \mathbf{h}_t = r_\theta((\boldsymbol{\mu}_t, \hat{\mathbf{z}}_{t-1}), \mathbf{h}_{t-1}), \quad t = 1, \dots, T \quad (6.30)$$

$$\hat{\mathbf{z}}_t = \hat{\mathbf{z}}_{t-1} + \Delta \hat{\mathbf{z}}_t \quad (6.30)$$

Depending on the movement in the latent space the level of synchrony changes across the prediction horizon, which translates to the pathological evolution of patients. The online-prediction rollout is shown in figure Figure 10.

By predicting the movement in the latent space $\Delta \mathbf{z}_t$ instead of the raw parameters, smooth trajectories can be learned. For the latent sequence this is more desirable compared to the infection indicator, where jumps in predicted values do not matter as much.

To fit the functions, here the placement of latent points \mathbf{z} is guided by a supervision signal:

$$\mathcal{L}_{\text{sofa}} = \frac{1}{B} \sum_{i=1}^B \frac{1}{T_i} \sum_{t=0}^{T_i-1} w_{O_{i,t}} \cdot \left(\frac{O_{i,t}}{24} - s_{i,t}^1 \frac{\hat{\mathbf{z}}}{s_{\max}^1} \right)^2 \quad (6.31)$$

where the class-balancing weight:

$$w_O = \log(1 + (f_O)^{-1}) \quad (6.32)$$

with f_O being the relative frequency of SOFA-score O in the training data. This inverse-frequency weighting up-weights rare high SOFA-scores that are clinically critical but statistically underrepresented. Also notice that both parts, i.e. the continuous approximation (given by the desynchronicity) and ground truth are scaled to the interval $[0, 1]$.

Because gradients can flow backwards through the whole sequence, this loss jointly fits the encoder g_θ^e and recurrent function g_θ^r .

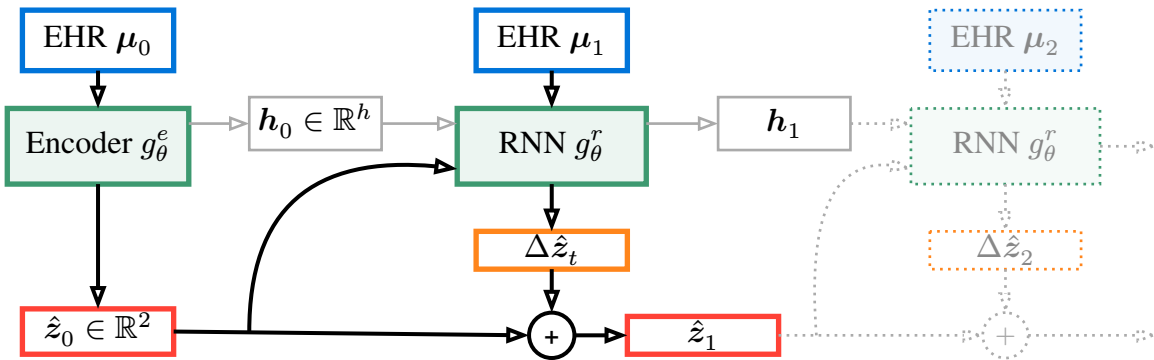


Figure 10: Architecture and online-prediction rollout of the SOFA Predictor Module.

6.2.2.3. Latent Lookup

Intuitively one would numerically integrate the DNM every estimate \hat{z} to receive the $s_{\hat{z}}^1$ -metric for the continuous space in (β, σ) . But to massively reduce the computational burden the space has been quantized to a discrete and regular grid, with the metric pre-computed for each coordinate pair. The space is limited to the intervals $\beta \in [0.4\pi, 0.7\pi]$ and $\sigma \in [0.0, 1.5]$ (the phase space of the original publication [29]). Instead of integrating the DNM over and over, differentiable approximation values are retrieved from the precomputed grid by using localized soft interpolation.

For an estimated coordinate pair $\hat{z} = (\hat{z}_\beta, \hat{z}_\sigma)$ in the continuous (β, σ) -space the quantized metrics are interpolated by smoothing nearby quantization points with a Gaussian-like kernel, which is illustrated in Figure 11.

The smoothing is performed by weighting the amount of desynchronicity $s_{z'}^1$ of quantized nearby latent points z' by the euclidean distance to the estimation \hat{z} . The nearby points are selected by a quadratic slice around the closest quantized point \tilde{z} , with k being the sub-grid size:

$$\tilde{s}^1(\hat{z}) = \sum_{z' \in \mathcal{N}_{k \times k}(\tilde{z})} \text{softmax}\left(-\frac{\|\hat{z} - z'\|^2}{T_d}\right) s^1(z') \quad (6.33)$$

with softmax for $K = k \cdot k$ neighboring points being:

$$\text{softmax}(x)_j = \frac{e^{x_j}}{\sum_{k=1}^K e^{x_k}}, \quad \text{for } j = 1, \dots, K \quad (6.34)$$

and:

$$\mathcal{N}_{k \times k}(\tilde{z}) = \{(\tilde{z}_\beta + i \cdot \beta_{\text{step size}}), (\tilde{z}_\sigma + j \cdot \sigma_{\text{step size}}) \mid i, j \in \{-1, 0, 1\}\} \quad (6.35)$$

With $T_d \in \mathbb{R}_{>0}$ being a learnable temperature parameter which controls the sharpness of the smoothing, with larger values producing stronger smoothing and smaller values converging to the value of the closest point \tilde{z} exclusively.

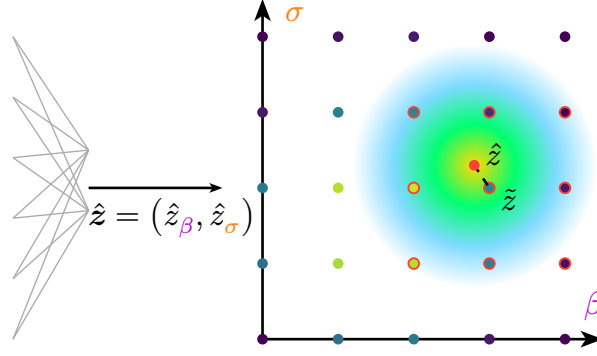


Figure 11: Quantized latent lookup of precomputed synchronization metrics. Point colors represent the amount of desynchronization s^1 in the parenchymal layer. Neighboring points, the $z' \in \mathcal{N}_{3 \times 3}(\tilde{z})$ sub-grid indicated by the red outlines around \tilde{z} , are used smoothed using a Gaussian-like kernel, represented by the color gradient around estimation point \tilde{z} . This allows continuous interpolation the parameter space.

This quantization strategy allows for continuous space approximation from the quantized space, while also making it possible to pre-compute the quantized space and therefore drastically reducing the computational expenses. This quantization strategy, called *latent lookup* is closely related to Finite Scalar Quantization (FSQ) [51], used in Dreamer-V3 [52] for example. Unlike in this approach the values of the latent coordinates in Dreamer-V3 do not have prior semantic meaning associated with them. Both allow for differentiable quantization, with details on the latent lookup implementation, including grid-resolution and kernel size, can be found in Section 7.2.1.

out arrow

In Neural Differential Equations [53] and Physics Informed Neural Networks [54] where the integration of the ODE itself provides gradients directly by backpropagation through the ODE. In contrast, here the gradient information is provided by the nearby quantized points which contribute to estimated synchronicity measure through the smoothing.

6.2.3. Decoder

As shown in the visualization of the DNM phase space in Figure 7 multiple latent coordinates z result in the same amount of desynchronization, which is not surprising, since different physiological states share the same SOFA level. But when different physiological states have a common SOFA-score but from different physiological reasons, their latent representations should be different and unique to that exact physiological state. This should enable to distinguish different triggers of the organ failure inside the latent space, similarly to how it is possible to distinguish the different triggers from the EHR.

In a classical Auto-Encoder [55] setting, to encourage a semantically structured latent space, a decoder module is added as an auxiliary regularization component. A neural decoder network:

$$d_\theta : \mathbb{R}^2 \rightarrow \mathbb{R}^n \quad (6.36)$$

attempts to reconstruct the original EHR features from the latent representation, the resulting desynchronicity of that latent coordinate and the heuristic risk measures:

$$\hat{\mu}_t = d_\theta(\hat{z}_t) \quad (6.37)$$

This way the decoder only learns to disentangle the latent coordinates in \hat{z}_t based on ground future EHRs μ_t , through a supervised loss:

$$\mathcal{L}_{\text{dec}} = \frac{1}{B} \sum_{i=1}^B \frac{1}{T_i} \sum_{t=0}^{T_i-1} (\mu_{i,t} - \hat{\mu}_{i,t})^2 \quad (6.38)$$

The formulation is based on the assumption:

$$\mu_t = \hat{\mu}_t + \varepsilon \quad (6.39)$$

with ε the measurement noise, to hold.

This latent regularization is motivated by *Representation Learning* [55] and ensures that nearby points in the latent (β, σ) -space correspond to physiologically similar patient states. It helps the encoder g_θ^e to learn a meaningful alignment between EHR-derived latent-embeddings and the dynamical DNM landscape.

Using this regularization the latent encoder g_θ^e and the recurrent predictor g_θ^r are encouraged to map temporally consecutive to spatially near latent coordinates, since it is expected that consecutive EHRs do not exhibit drastic changes. Leading smooth patient trajectories through the latent space.

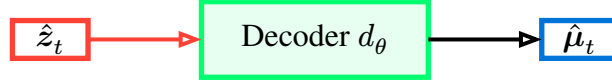


Figure 12: TODO

6.2.4. Training Objective and Auxiliary Losses

The complete LDM is trained end-to-end by combining the previously introduced Infection Indicator Module f_θ and the SOFA prediction module g_θ . The output of these modules yield the components \hat{O}_t , from which \tilde{A}_t can be derived (Equation (6.21)) and \tilde{I}_t , taking these components one can calculate the heuristic sepsis onset risk $\tilde{S}_t = \tilde{A}_t \tilde{I}_t$.

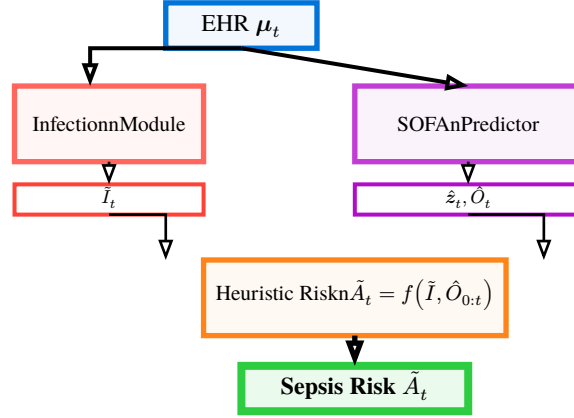


Figure 13: TODO

Besides the losses already presented, to guide the training process multiple auxiliary losses are used and introduced in the following.

Primary Sepsis Prediction Loss

The main training signal aligns the heuristic sepsis score \tilde{S}_t with ground truth sepsis labels:

$$\mathcal{L}_{\text{sepsis}} = -\frac{1}{B} \sum_{i=1}^B \frac{1}{T_i} \sum_{t=0}^{T_i-1} [S_{i,t} \log(\tilde{S}_{i,t}) + (1 - S_{i,t}) \log(1 - \tilde{S}_{i,t})] \quad (6.40)$$

again using the BCE. Because positive labels may be temporally windowed around the true onset of sepsis, the estimated sepsis risk score is computed via causal smoothing:

$$\tilde{S}_t = \text{CS}(\tilde{A}_t) \cdot \tilde{I}_t \quad (6.41)$$

where $\text{CS}(\cdot)$ denotes a causal smoothing operator that maintains elevated predictions in the time-steps preceding sepsis onset. The causal smoothing operation is defined as:

$$\text{CS}(x_t) = \sum_{\tau=0}^r w_{\tau} \cdot x_{t-\tau}, \quad w_{\tau} = \frac{e^{-\alpha\tau}}{\sum_{k=0}^r e^{-\alpha k}} \quad (6.42)$$

with radius r is a hyper-parameter controlling the temporal radius of the smoothing window, and α a learnable decay parameter controlling the length and shape of the smoothing kernel. To handle the sequence boundaries $x_{t-\tau} = 0$ for $t - \tau < 0$.

This smoothing ensures that organ failure predictions remain elevated during the causal window preceding sepsis onset, matching the clinical reality that organ dysfunction typically precedes documented sepsis.

Organ Failure Alignment

To improve the sharpness of organ failure detection, a focal loss [56] penalizes misclassification of the discrete organ failure event:

$$\mathcal{L}_{\text{focal}} = -\frac{1}{B} \sum_{i=1}^B \sum_{t=0}^{T_i-1} \alpha (1 - p_{i,t})^{\gamma} \log(p_{i,t}) \quad (6.43)$$

with $p_{i,t} = A_{i,t} \cdot \tilde{A}_{i,t} + (1 - A_{i,t}) \cdot (1 - \tilde{A}_{i,t})$, γ controlling focus on hard examples and α another weighting to emphasize positive vs. negative samples. The well established focal

loss has been proven to improve performance for high imbalance datasets, which is the case for rare events such as the SOFA increase. With this loss the model is encouraged to align the timing of predicted SOFA increase with the ground truth.

Difference Alignment

To encourage temporally coherent latent dynamics that align with ground truth SOFA progression:

$$\mathcal{L}_{\text{diff}} = \frac{1}{B} \sum_{i=1}^B \sum_{t=0}^{T_i-1} \sum_{t'=t+1}^{T_i-1} w_{t,t'} \cdot \text{ReLU}(-a_{t,t'}) \quad (6.44)$$

where the alignment term measures directional consistency between predicted and true SOFA changes:

$$a_{t,t'} = (\hat{O}_{t'} - \hat{O}_t) \cdot (O_{t'} - O_t) \quad (6.45)$$

and the weight emphasizes larger ground truth changes:

$$w_{t,t'} = |O_{t'} - O_t| + 1 \quad (6.46)$$

The Rectified Linear Unit (ReLU) activation penalizes only misaligned directions (when $a_{t,t'} < 0$), meaning the predicted change points in the opposite direction to the true change. This loss ensures that if a patient's true SOFA-score increases between time t and t' , the predicted score also increases (and vice versa for decreases), without strictly enforcing the magnitude of change.

Latent Space Regularization

To prevent collapse and ensure diverse latent representations:

$$\mathcal{L}_{\text{spread}} = -\log(\text{trace}(\text{Cov}(\hat{\mathbf{Z}}))) \quad (6.47)$$

where $\hat{\mathbf{Z}}$ collects all predicted latent coordinates in a batch and $\text{Cov}(\cdot)$ computes the sample covariance matrix.

The loss is minimized when the total variance of the latent dimensions β and σ increases and it therefore encourages a larger spread inside the latent space.

6.2.5. Combined Objective

The complete LDM is trained end-to-end by jointly optimizing all components with the weighted total loss:

$$\mathcal{L}_{\text{total}} = \lambda_{\text{inf}} \mathcal{L}_{\text{inf}} + \lambda_{\text{sofa}} \mathcal{L}_{\text{sofa}} + \lambda_{\text{dec}} \mathcal{L}_{\text{dec}} + \lambda_{\text{sepsis}} \mathcal{L}_{\text{sepsis}} \quad (6.48)$$

$$+ \lambda_{\text{diff}} \mathcal{L}_{\text{diff}} + \lambda_{\text{focal}} \mathcal{L}_{\text{focal}} + \lambda_{\text{spread}} \mathcal{L}_{\text{spread}} \quad (6.48)$$

The loss weights λ_i balance the contribution of each objective during training. The primary sepsis prediction loss $\mathcal{L}_{\text{sepsis}}$ provides the main learning signal aligned with the clinical task, while component losses \mathcal{L}_{inf} and $\mathcal{L}_{\text{sofa}}$ ensure accurate estimation of the underlying infection

and organ failure indicators. The auxiliary losses ($\mathcal{L}_{\text{focal}}$, $\mathcal{L}_{\text{diff}}$, \mathcal{L}_{dec} , $\mathcal{L}_{\text{spread}}$) regularize the latent space structure and temporal dynamics to improve generalization and interpretability.

All modules f_θ , g_θ^e , g_θ^r , and d_θ are jointly optimized through backpropagation, with gradients flowing through the differentiable DNM lookup mechanism described in Section 6.2.2.3. Specific values for the loss weights λ_i and other hyper-parameters are reported in Section 7.2.

Table 5 provides an overview of all loss components, their purpose, and the modules they supervise.

Table 5: Overview of loss components in the LDM training objective.

LOSS	TYPE	PURPOSE	SUPERVISES
$\mathcal{L}_{\text{sepsis}}$	BCE	Primary sepsis prediction	Full model
\mathcal{L}_{inf}	BCE	Infection indicator	f_θ
$\mathcal{L}_{\text{sofa}}$	Weighted MSE	SOFA estimation	g_θ^e, g_θ^r
$\mathcal{L}_{\text{focal}}$	Focal	Organ failure timing	g_θ^e, g_θ^r
$\mathcal{L}_{\text{diff}}$	Directional	Difference timing	g_θ^r
\mathcal{L}_{dec}	MSE	Latent semantics	$d_\theta, (g_\theta^e, g_\theta^r)$
$\mathcal{L}_{\text{spread}}$	Covariance	Latent diversity	g_θ^e, r_θ

6.3. Summary of Methods

This chapter introduced the proposed model for short-term and interpretable risk prediction of developing sepsis for ICU patients, referred to as Latent Dynamics Model. Starting from the formal task definition, the full processing pipeline and detailed the architecture of the encoder, recurrent latent dynamics module, decoder, and the infection-indicator classifier have been presented. A key component of the approach is the integration of the functional DNM into the latent dynamics, enabling physiologically meaningful and interpretable temporal modeling.

The training losses used for each component and additional auxiliary losses were defined and how they contribute to the overall optimization objective. Finally the chapter also introduced the notation and training setup that will be used throughout the remainder of the thesis.

The next Section 7 presents the Medical Information Mart for Intensive Care (MIMIC)-IV database, a widely used ICU used to benchmark sepsis prediction models, and the exact task and cohort definitions used for baseline comparisons. The relevant evaluation metrics Area Under Receiver Operating Curve (AUROC) and Area Under Precision Recall Curve (AUPRC) used to assess the predictive performance are introduced.

The chapter concludes with implementation details for training the LDM on the MIMIC-IV data and specific architectural choices. Final quantitative and qualitative results are presented and analyzed in Section 8.

7 Experiment

To assess the potential benefits from embedding the Dynamic Network Model into a short-term sepsis prediction system, the Latent Dynamics Model (see Section 6) was trained and evaluated using real-world medical data. This chapter presents the complete experimental setup, including the data basis (data source, cohort selection, preprocessing), the prediction task, and all implementation and training details. Further the chapter will provide details on the implementation and training routine. To begin with, a short overview of the state of the art of model- and data-driven short-term sepsis prediction systems is given.

7.1. Baseline

7.1.1. Data

Figure 14: Sets of [1]

7.1.2. Task

RICU and YAIB use `delta_cummin` function, i.e. the delta SOFA increase is calculated with respect to the lowest observed SOFA to this point.

7.2. Implementation Details

7.2.1. Latent Lookup Implementation

7.3. Metrics (How to validate performance?)

explain
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8 Results

9 Conclusion

Appendix

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A Appendix

A.1 SOFA - Details

Table 6:

CATEGORY	INDICATOR	1	2	3	4
Respiration	PaO ₂ /FiO ₂ [mmHg]	< 400	< 300	< 200	< 100
	Mechanical Ventilation			yes	yes
Coagulation	Platelets [$\times \frac{10^3}{\text{mm}^3}$]	< 150	< 100	< 50	< 20
Liver	Bilirubin [$\frac{\text{mg}}{\text{dl}}$]	1.2-1.9	2.0-5.9	6.0-11.9	> 12.0
Cardiovascular ³	MAP [mmHg]	< 70			
	or Dopamine		≤ 5	> 5	> 15
	or Dobutamine		any dose		
	or Epinephrine			≤ 0.1	> 0.1
	or Noepinephrine			≤ 0.1	> 0.1
Central Ner- vous System	Glasgow Coma Score	13-14	10-12	6-9	< 6
Renal	Creatinine [$\frac{\text{mg}}{\text{dl}}$]	1.2-1.9	2.0-3.4	3.5-4.9	> 5.0
	or Urine Output [$\frac{\text{ml}}{\text{day}}$]			< 500	< 200

³Adrenergica agents administered for at least 1h (doses given are in [$\mu\text{g}/\text{kg} \cdot \text{min}$])

A.2 DNM as Lie Formulation

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