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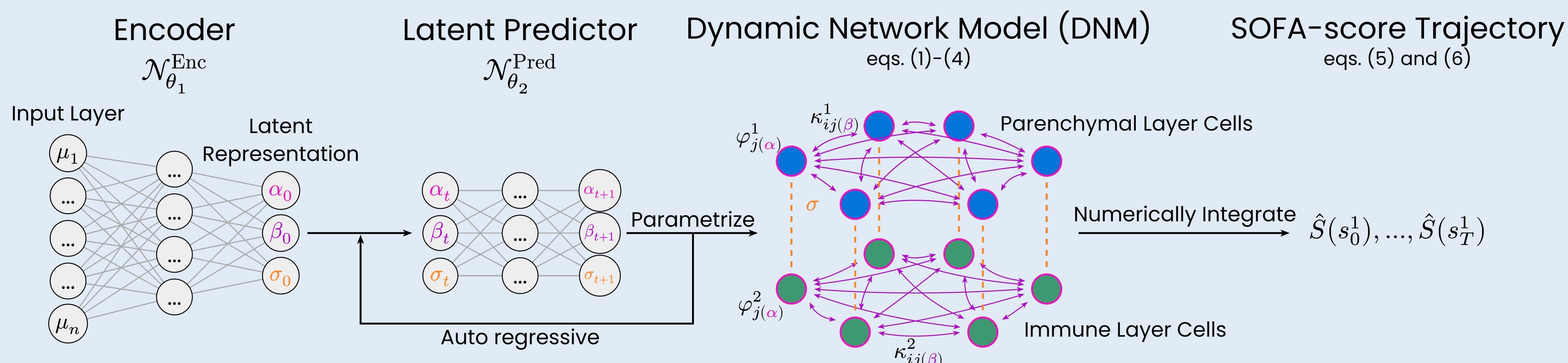
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Architecture of the End-to-End pipeline



SOFA-score

Sequential Organ Failure Assessment [3]

- Assesses 6 organ systems to measure their failure.
- Higher score (0–24) means greater risk of death.
- Used in hospitals to track patients status, especially in sepsis.

The Dynamic Network Model

The “Dynamic Network Model” (DNM), introduced in [1] and mathematically defined in Eqs. 1-4, represents the interaction between parenchymal cells (functional organ cells) denoted φ_i^1 , and immune cells, denoted φ_i^2 , using a two layer partly adaptive oscillator network, with $i = 1, \dots, N$, where $\kappa_{ij}^{1/2}$ are adaptive coupling weights.

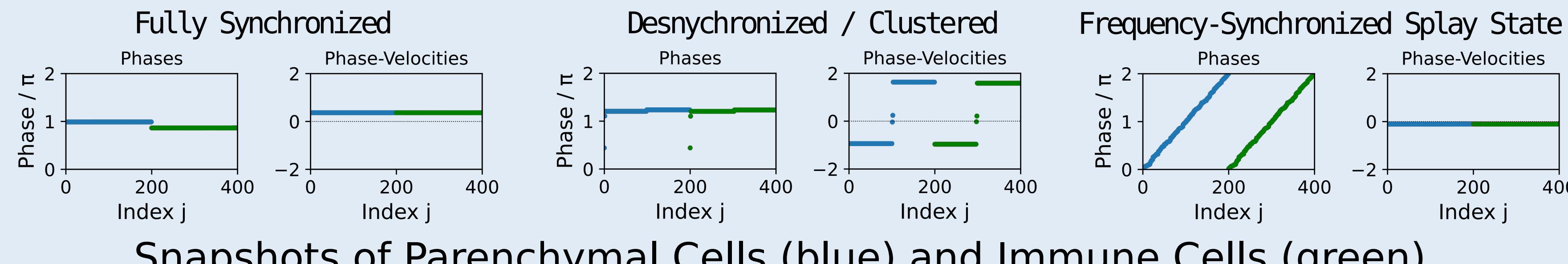
$$\dot{\varphi}_i^1 = \omega^1 - \frac{1}{N} \sum_{j=1}^N ((a_{ij}^1 + \kappa_{ij}^1) \sin(\varphi_i^1 - \varphi_j^1 + \alpha^{11})) - \sigma \sin(\varphi_i^1 - \varphi_i^2 + \alpha^{12}) \quad (1)$$

$$\kappa_{ij}^1 = -\varepsilon^1 (\kappa_{ij}^1 + \sin(\varphi_i^1 - \varphi_j^1 - \beta)) \quad (2)$$

$$\dot{\varphi}_i^2 = \omega^2 - \frac{1}{N} \sum_{j=1}^N (\kappa_{ij}^2 \sin(\varphi_i^2 - \varphi_j^2 + \alpha^{22})) - \sigma \sin(\varphi_i^2 - \varphi_i^1 + \alpha^{21}) \quad (3)$$

$$\kappa_{ij}^2 = -\varepsilon^2 (\kappa_{ij}^2 + \sin(\varphi_i^2 - \varphi_j^2 - \beta)) \quad (4)$$

Different stable synchronization patterns can occur based on the parameterization:



It is hypothesized that synchronized states in the parenchymal layer represent a healthy patient, whereas desynchronized states most likely capture pathological conditions [2]. The amount of desynchronization is expressed by the ensemble average of the standard deviation of the mean phase velocities, defined by:

$$s^\mu = \frac{1}{M} \sum_{i=1}^M \sqrt{\frac{1}{N} \sum_{j=1}^N (\langle \dot{\varphi}_j^\mu \rangle - \bar{\omega}^\mu)^2} \quad (5)$$

Method

Using the MIMIC-III database [4], for each patient's state snapshot with features (μ_1, \dots, μ_n) at time t , we want to predict the SOFA-score S step-wise $T = 6$ hours into the future. Our approach includes the encoding of patient states into the latent DNM parameter space and track their evolution auto-regressively.

The DNM-System size is $N = 200$ oscillators per layer. To account for sensitivity to initial conditions, we simulate ensembles of size $M = 50$ with stochastic initializations of κ 's and φ 's.

To guide learning, we use a loss function with three additive components:

1. Classification $BCE(p(l_k), t_k)$: Binary cross-entropy over $k = 1 \dots 24$ SOFA levels, with the ground truth SOFA score t_k and logits $l_k = \frac{s^1 - \tau_k}{T}$ where the thresholds τ_k and temperature T are learnable.

2. Reconstruction $MSE(\hat{\mu} - \mu) = \sum_i^n \frac{(\mu_i - \hat{\mu}_i)^2}{n}$: between the original observations and their reconstruction by a neural decoder ($\hat{\mu} = \mathcal{N}_{\theta_3}^{\text{Dec}}(\alpha, \beta, \gamma)$), encouraging semantic structure in the latent space.

3. Correlation Penalty $CP(\alpha, \beta, \sigma) = \frac{1}{3}(\rho_{\alpha\beta}^2 + \rho_{\beta\sigma}^2 + \rho_{\alpha\sigma}^2)$: Where ρ_{XY} is the correlation between X and Y , helping to disentangle the latent representation.

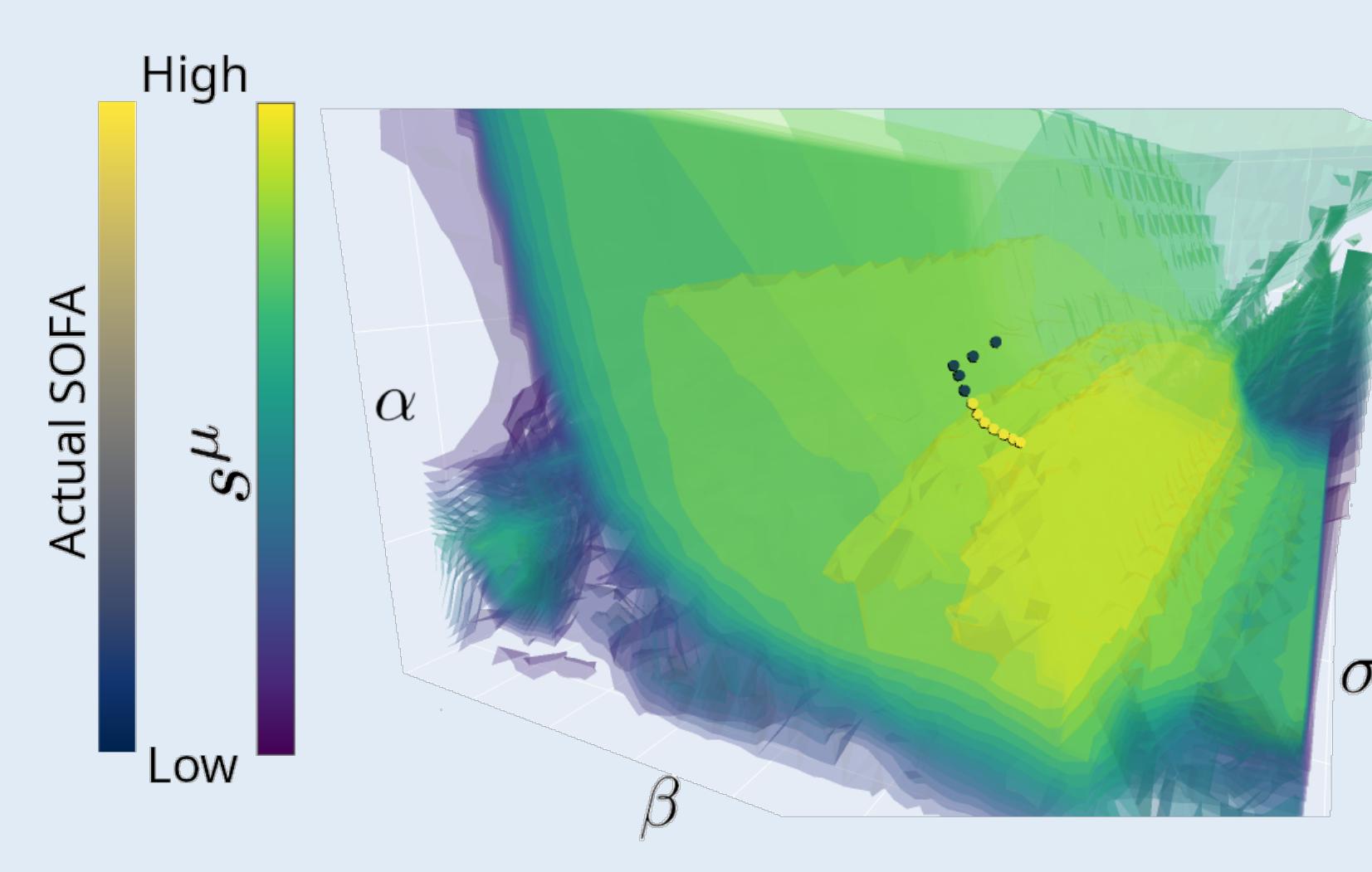
Final SOFA-score prediction:

$$\hat{S}(s_\mu^1) = \max(k | s_\mu^1 > t_k) \quad (6)$$

Results & Discussion



Prediction on a held-out test dataset



Latent space trajectory of a single patient

- We successfully project real patient data to the latent space of the DNM.
- We are able to capture patient trajectories within the model and make predictions about their development.

Future Work:

- Include predictions about patient infections.
 - ▷ The DNM naturally provides this via its second layer.
 - ▷ This would capture the whole Sepsis-3 definition.
- Analyze the semantic latent space structure.
- Rigorous quantitative analysis and comparison with SOTA.

¹ J. Sawicki, R. Berner, T. Löser and E. Schöll “Modeling tumor disease and sepsis by networks of adaptively coupled phase oscillators”, *Frontiers in Network Physiology*, 2674-0109, 2022.

² R. Berner, J. Sawicki, M. Thiele, T. Löser and E. Schöll “Critical Parameters in Dynamic Network Modeling of Sepsis”, *Frontiers in Network Physiology*, 2674-0109, 2022.

³ M. Singer et al. “The Third International Consensus Definitions for Sepsis and Septic Shock (Sepsis-3)”, *JAMA*, 2315:801-810, 2016.

⁴ A. Johnson et al. “MIMIC-III Clinical Database (version 1.4)”, *PhysioNet*, RRID:SCR_007345, 2016.



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