AI-Driven Human-Machine Interface for Early Detection and Differentiation of Sepsis, SIRS, and Septic Shock with Severity Assessment on Hematology Analyzers

Sukesh C Nair[1], Francoise Durrieu[2], Shubham Rastogi[3].
[1]Christian Medical College, Vellore, India. [2]Bergonie Institute, Bordeaux, France. [3]HORIBA ABX SAS, Montpellier, France

HORIBA ISLH 2025 HALIFAX, NOVA SCOTIA

INTRODUCTION

Sepsis remains a major challenge internationally for healthcare systems with rising incidence due to poor public awareness, delay in early detection and subsequent management. In sepsis, mortality increases with every hour left untreated. The complexities of the definition of sepsis, as well as the lack of a reliable biomarker, hamper early detection of sepsis healthcare setup such as emergency department (ED). The modern HORIBA Yumizen H series (Yumizen H2500/ Yumizen H1500) augmented by AI from multi center data have the potential to provide early predictive Flagging/ Scoring system, that can be cost-efficient to quickly support the diagnosis of SEPSIS evolution and further management right from primary health centers.

METHODS

To demonstrate the capabilities of AI-ML driven sepsis severity to identify patients with sepsis and measure performance of 'Sepsis suspicion Flag / Scoring' to reflect sepsis risk and/or severity on HORIBA Yumizen H Range hematology analyzers. Preprocessing the data and preparation of the model in identifying patients with sepsis in the cohort and measure performance. Attribute a 'SEPSIS suspicion Flag / Scoring' to reflect sepsis risk and/or severity. Retrospective data obtained from the hematology analyzers (n=687), patients with either sepsis, SIRS, or septic shock (Table 1) and controls from the participating centers, Christian Medical College, Vellore. Tamil Nadu. India and Bergonie Institute, Bordeaux, France between 2018 to 2023 subjected to AI-ML modeling.

ALGORITHM OVERVIEW by *GeodAIsics : Generative Manifold Learning (GML)

GeodAIsics	PHASES	
	Training	**Testing**
STEPS	**1.Healthy Digital Twin Estimation**	**1.Healthy Digital Twin Estimation**
	Generate digital twins representing the healthy physiological state for each subject in the reference group (both SEPSIS and non-SEPSIS).	Construct the healthy digital twin for the new (test) subject.
	2.Z-Score Computation	**2.Z-Score Computation**
	Calculate z-scores by comparing real subject data to their corresponding digital twins, capturing individual deviations from the healthy baseline.	Compute the z-score for the test subject to quantify deviations from healthy dynamics.
	3.Dimensionality Reduction	**3.Projection and Inference**
	Learn reduced latent spaces from z-scores to highlight discriminative patterns between SEPSIS and non-SEPSIS groups.	Project the z-score into the learned reduced space to infer the likelihood of SEPSIS vs. non-SEPSIS.

RESULTS

The severity and risk of sepsis are determined using a density-based probability approach. Each test data point is assigned a severity score, with scores above a user-defined threshold classified as septic (Fig.1&2). Notably, lower thresholds result in higher sensitivity but lower specificity. Our model has demonstrated the ability to predict and classify patients with Sepsis, SIRS, and Septic shock with an impressive sensitivity of 91% and specificity of 86% (AUC = 0.89) as presented in Table 2.
The current model performance is created exclusively on CBC hematology parameters which also outperforms the established benchmark FDA authorized AL/ML- Sepsis Immunoscore system(Table 3).
Furthermore, the model's capability to differentiate between sepsis, SIRS, and septic shock will be discussed in detail.

Normal	243
Sepsis	154
Leukocytosis	95
SIRS	59
Anemia	32
Sickle cell	18
Acute lymphocytic leukemia	14
Septic Shock	10
Thrombocytopenia	9
Eritropenia	7
Chronic lymphocytic leukemia	7
Lymphoma	6
Thalassemia	6
Acute myeloid leukemia	4
Multiple myeloma	4
Hemoglobin SC disease	3
Hemolytic anemia	3
Leukopenia	3
Chronic myeloid leukemia	2
Myelofibrosis	2
Thrombocytosis	2
Myelodysplastic syndrome	2
Myeloproliferative syndrome	1
Polycythemia	1

Table 1:Sample data set for sepsis & other pathologies

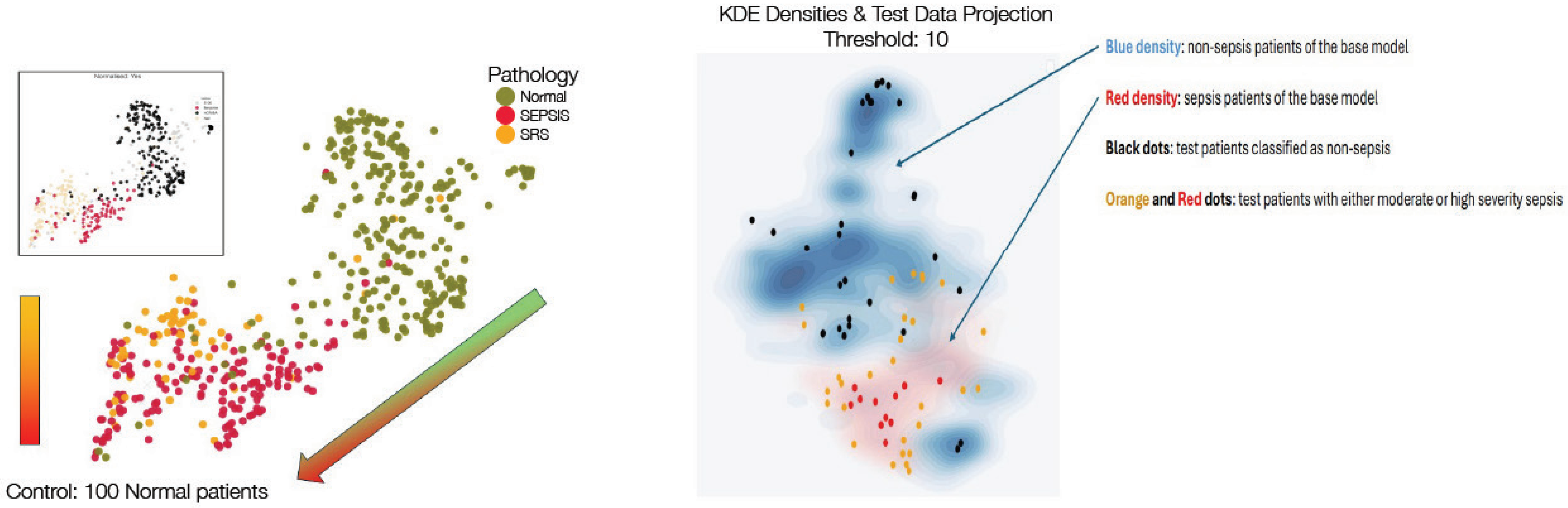

Figure 1& 2:Severity Scoring of Sepsis determined by density-based probability

Sepsis vs. Normal & Sepsis vs. Pathologies

Sepsis/SIRS/Shock versus Normal		Sepsis/SIRS/Shock versus Pathologies	
Sensitivity	Specificity	Sensitivity	Specificity
0.94	0.94	0.92	0.89

Sepsis versus Normal		Sepsis versus Pathologies	
Sensitivity	Specificity	Sensitivity	Specificity
0.86	0.94	0.9	0.84

SIRS versus Normal		SIRS versus Pathologies	
Sensitivity	Specificity	Sensitivity	Specificity
0.82	0.98	0.86	0.94

Table 2:Model Performance of AI-ML from CBC sample data performed on HORIBA Hematology analyzer Yumizen H2500,Yumizen H1500 for Sepsis differentiations v/s normal & non-sepsis samples.

Sepsis vs. both Normal & pathological patients

Sepsis/SIRS/Shock versus non-sepsis		AUC
Sensitivity	Specificity	
0.91	0.86	0.89

Sepsis versus non-sepsis		
Sensitivity	Specificity	
0.90	0.86	0.88

SIRS versus non-sepsis		
Sensitivity	Specificity	
0.84	0.90	0.87

Table 3:Current model performance v/s FDA authorized AI/ML -Sepsis Immunoscore

CONCLUSION

AI-ML driven modeling analysis using only Complete Blood Count data, have shown potentially to revolutionize sepsis detection, diagnosis, and treatment in critical care settings at very early stages. AI algorithms on Hematology analyzers can help identify patients at high risk of developing sepsis, right from primary healthcare centers and doctor's clinics to intervene earlier and prevent conditions progression.