

Predicting Septic Patient Outcomes Based on Serum Cytokines

Rúben Araújo^{1,2,3}, Luís Ramalheira^{1,4,5}, Cristiana Von Rekowski^{1,2,3}, Tiago Fonseca^{1,2,3}, Luís Bento^{1,2,6,7}, Cecília R.C. Calado^{3,8}

¹ NMS – NOVA Medical School, Campo dos Mártires da Pátria 130, 1169-056, Lisboa, Portugal

² CHRC – Comprehensive Health Research Centre, Rua Câmara Pestana 6, 1150-199, Lisboa, Portugal

³ ISEL-Instituto Superior de Engenharia de Lisboa, Instituto Politécnico de Lisboa, Rua Conselheiro Emídio Navarro 1, 1959-007 Lisboa, Portugal

⁴ IPST – Instituto Português do Sangue e da Transplantação, Alameda das Linhas de Torres – nr.117, 1769-001 Lisboa, Portugal

⁵ iNOVA4Health - Advancing Precision Medicine, RG11: Reno-Vascular Diseases Group, NOVA Medical School, Faculdade de Ciências Médicas, Universidade NOVA de Lisboa, 1169-056 Lisbon, Portugal

⁶ Intensive Care Department, ULSSJ—Unidade Local de Saúde São José, Rua José António Serrano, 1150-199 Lisbon, Portugal

⁷ Integrated Pathophysiological Mechanisms, CHRC, NOVA Medical School, Faculdade de Ciências Médicas, NMS, FCM, Universidade NOVA de Lisboa; Campo Mártires da Pátria, 130, 1169-056 Lisboa, Portugal

⁸ Institute for Bioengineering and Biosciences (iBB), The Associate Laboratory Institute for Health and Bioeconomy—i4HB, Instituto Superior Técnico (IST), Universidade de Lisboa (UL), Av. Rovisco Pais, 1049-001 Lisboa, Portugal

Abstract

Background: Cytokine storms significantly influence systemic inflammatory responses and septic patient outcome, highlighting the critical role of cytokine profiling in understanding and predicting patient's outcome [1], which holds significant potential for future clinical and therapeutic applications. The present work aims to evaluate how serum cytokines can predict the outcome of septic patients at intensive care units (ICU). **Methods:** Serum samples from 16 septic patients (7 discharged, 9 deceased) were analyzed using a Milliplex 384-Well High Sensitivity Human T Cell Magnetic Bead Panel to profile a comprehensive set of 21 cytokines: ITAC, GM-CSF, Fractalkine, IFN- γ , IL-10, MIP-3a, IL-12p70, IL-13, IL-17a, IL-1b, IL-2, IL-21, IL-4, IL-23, IL-5, IL-6, IL-7, IL-8, MIP-1a, MIP-1b, and TNF- α . Machine learning tools coupled to a Gini decrease ranking method were employed to identify cytokines critical for discriminating between deceased and discharged patients. **Results:** Preliminary findings indicate that IL-6, MIP-3a, IL-8, IL-12p70, and IL-10 are notably linked to sepsis outcomes. The relevance of these cytokines aligns with existing literature on their roles in inflammation and immune responses [2]. Predictive models constructed using the Naive Bayes models showed promising results, with sensitivity and specificity exceeding 86%. **Conclusion:** This study underscores the importance of cytokine profiling in sepsis, highlighting key biomarkers for predicting patient outcomes.

Keywords: sepsis, serum cytokines, biomarkers, ICU mortality.

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