

# Understanding Immune Response using Statistical and Machine Learning Approaches

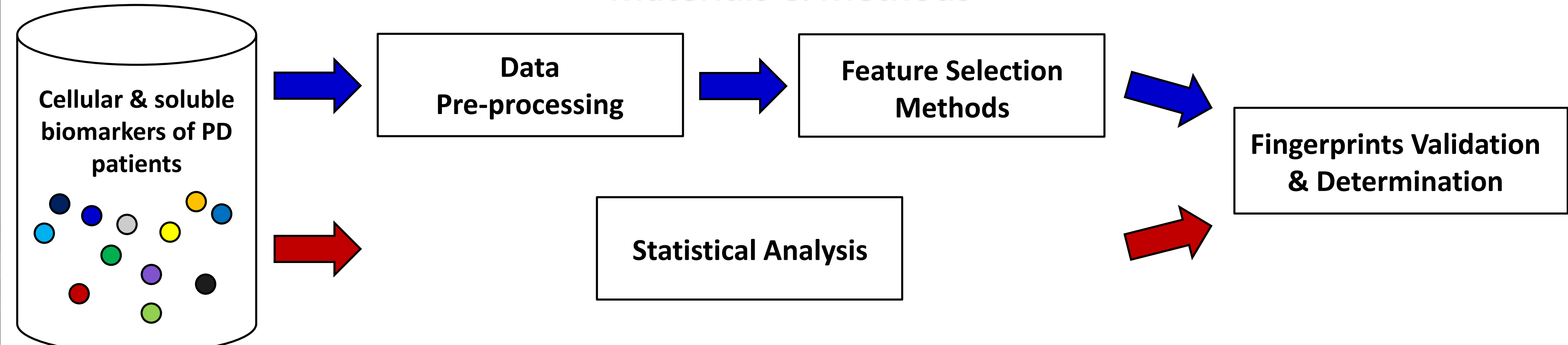
Jingjing Zhang<sup>1</sup>, Simone Cuff<sup>2</sup>, Ann Kift-Morgan<sup>2</sup>, Donald J. Fraser<sup>2,3,4,5</sup>, Nicholas Topley<sup>5</sup>, Matthias Eberl<sup>2,5</sup>

<sup>1</sup>School of Engineering, Newcastle University, Newcastle, UK; <sup>2</sup>Division of Infection and Immunity, School of Medicine, Cardiff University, Cardiff, UK; <sup>3</sup>Wales Kidney Research Unit, Heath Park Campus, Cardiff, UK; <sup>4</sup>Directorate of Nephrology and Transplantation, Cardiff and Vale University Health Board, University Hospital of Wales, Heath Park, Cardiff, UK; <sup>5</sup>Systems Immunity Research Institute, Cardiff University, Cardiff, UK.

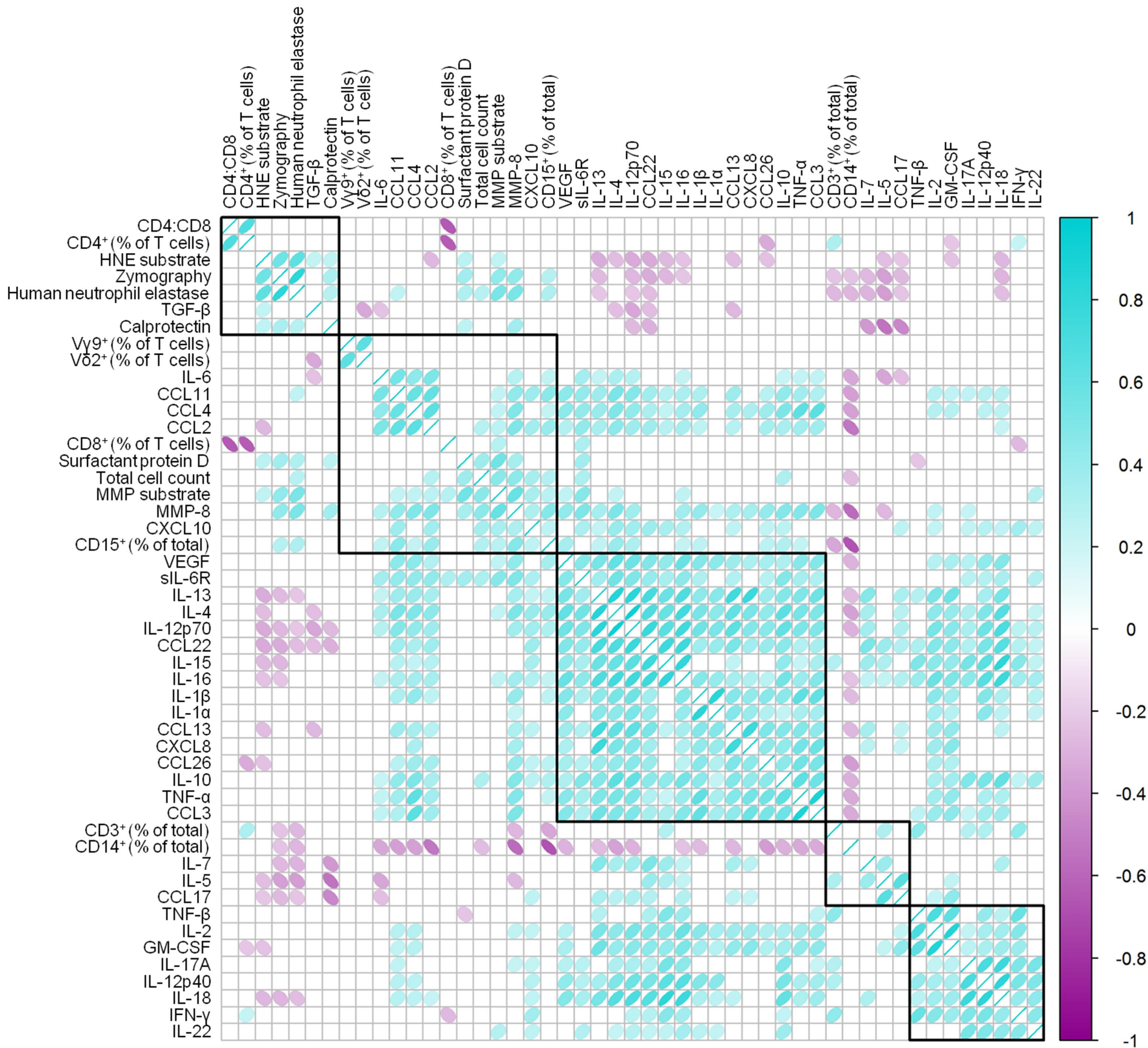
## Introduction

The unequivocal evidence that the immune system distinguishes between different types of organisms and mounts appropriate responses has been missing. This research used a systematic approach applying machine learning algorithms to define pathogen-specific local immune fingerprints and statistical analyses for validation in a total of 83 peritoneal dialysis (PD) patients on the day of presentation with acute peritonitis, based on a broad range of cellular and soluble biomarkers.

## Materials & Methods

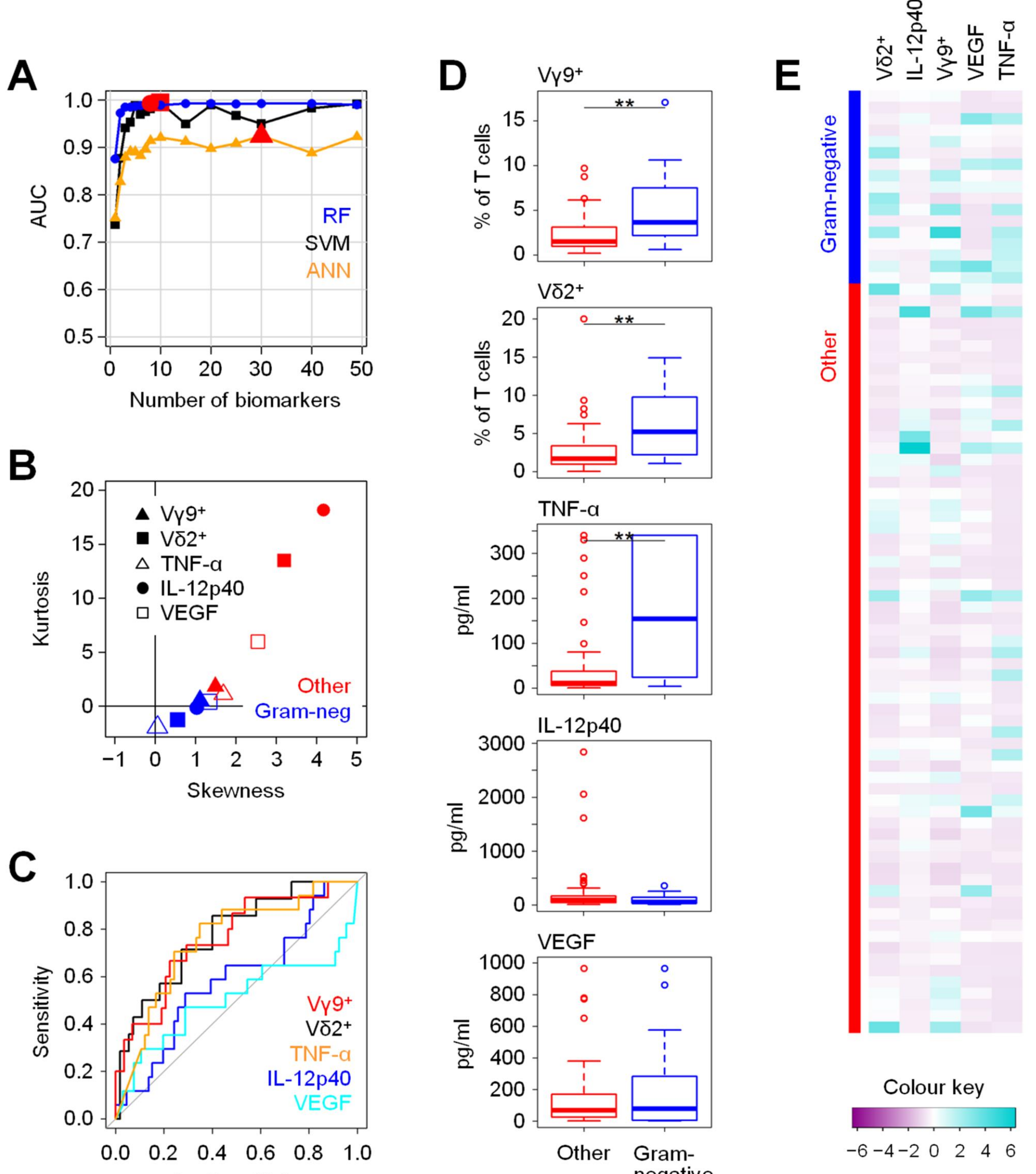


## Correlation analysis of local biomarkers in peritoneal dialysis patients on the day of presentation with acute peritonitis



**Fig.1:** Correlation analysis of local biomarkers in a total of 83 peritoneal dialysis patients on the day of presentation with acute peritonitis. Ellipses depict the correlation coefficients for each pair of biomarkers in the corresponding cell of the matrix, with the direction of the dip and the colour of the shading representing positive and negative correlations, respectively. Only pairs with significant correlations ( $p < 0.05$ ) are shown.

## Feature selection methods define local fingerprints associated with Gram-negative infections and the validation



**Fig.2:** Identification of local immune fingerprints associated with peritonitis caused by Gram-negative bacteria (Gram-negative infections,  $n=17$ ; all other episodes of peritonitis,  $n=66$ ). (A) Performance of RF (Random Forest), SVM (Support Vector Machine) and ANN (Artificial Neural Network) based feature elimination models, shown as AUC depending on the number of biomarkers. Red symbols depict the maximum AUC for each model. (B) Kurtosis and skewness of the top 5 biomarkers selected by RF-based feature elimination. (C) ROC analysis showing specificity and sensitivity of the top 5 biomarkers. (D) Tukey plots of the top 5 biomarkers in patients of the two groups, as assessed by Mann-Whitney tests. (E) Heatmap showing the top 5 biomarkers across all patients presenting with acute peritonitis.

## Summary

