

Characterisation of host-response heterogeneity in the sepsis transcriptome using two immune axis scores

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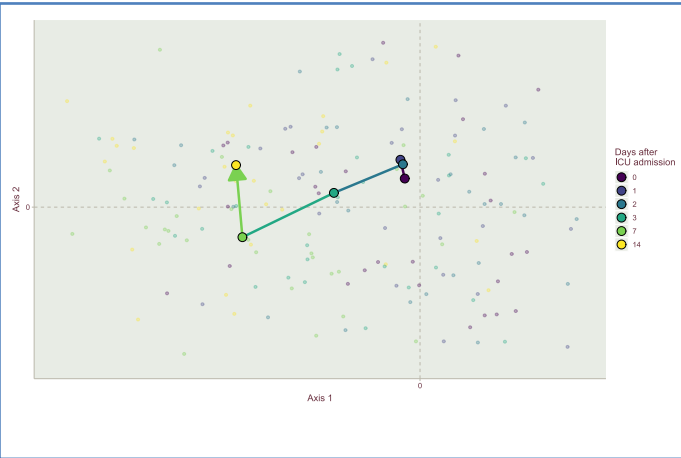
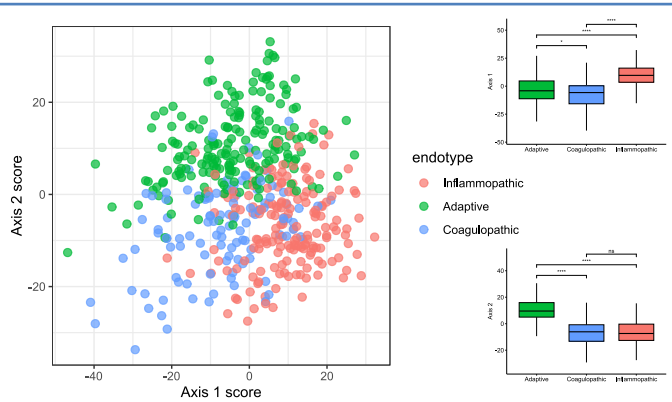
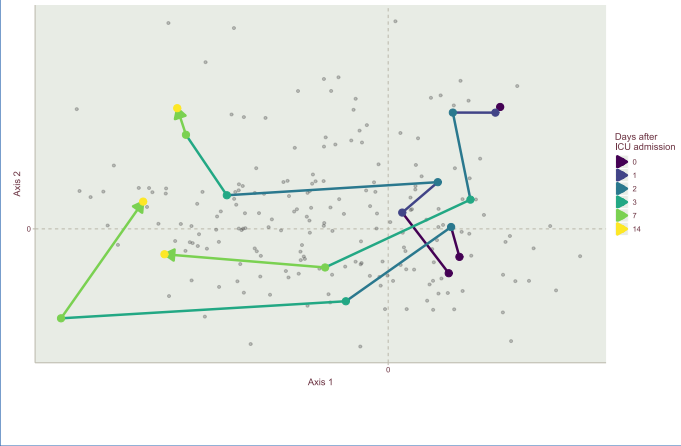
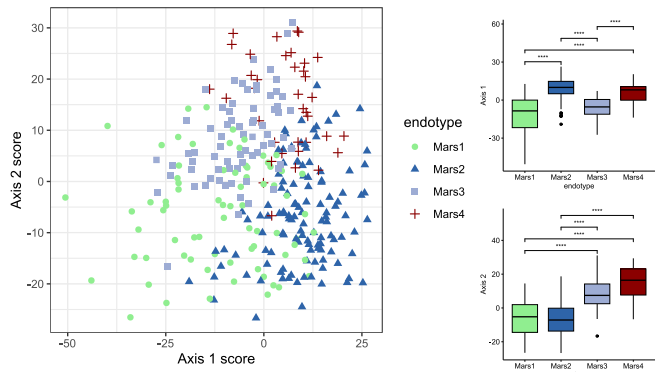
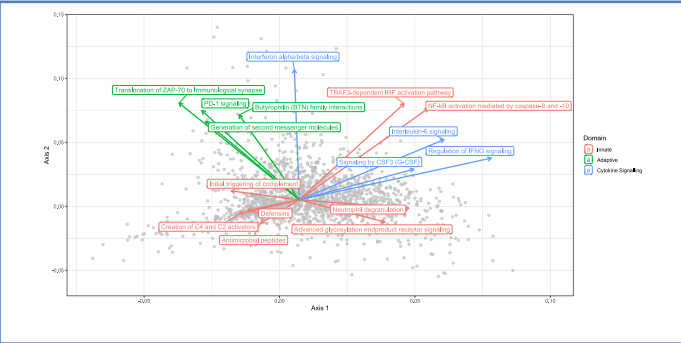
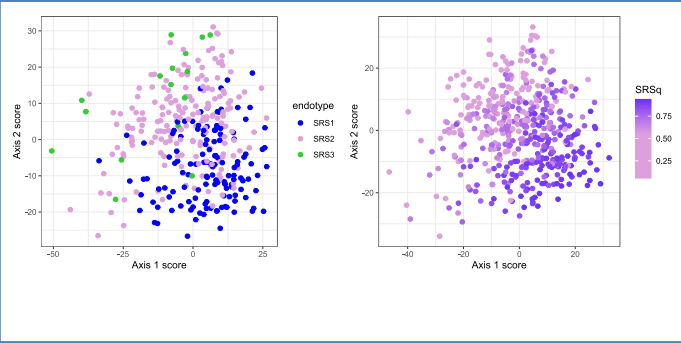
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Background

Host responses during sepsis are highly heterogeneous, complicating the identification of patients at risk of mortality or those potentially benefitting from targeted therapies. Previous studies have identified transcriptomic endotypes to assist with this challenge, to classify patients into categories. Here we introduce a two-dimensional framework for measuring patients’ immune system heterogeneity using two continuous “immune-axis” scores.

Methods

Whole-blood transcriptome was measured in 479 patients with sepsis at ICU admission using microarray (U219). Genes related to the immune system were selected and principal component analysis (PCA) analysis was performed. The first two PC scores are taken as the immune-axes scores. Upon these axes the scatter plot was coloured separately for each of the three existing sepsis endotype systems (Davenport et al., Scicluna et al. and Sweeney et al). Immune system pathway directionality was determined using the centroid of the constituent gene loadings within each Reactome pathway in the “Immune System” domain. A 20-gene signature was developed to enable axis scores to be calculated on different RNA platforms (e.g. RNAseq). Finally the axes scores were calculated for 39 CAP sepsis patients from the placebo arm of an RCT, in which whole-blood transcriptome was measured at multiple time-points (0,1,2,3,7 and 14±2 days after ICU admission) using RNAseq. Individual trajectories were plotted on the two axes and an average trajectory was estimated using linear mixed modelling.



Conclusions

- Two axes explain more than 30% of all immune variation observed in the leukocyte transcriptome of patients with sepsis
- Two axes scores are associated with previous endotype systems (SRS, MARS and Sweeney), and give a new way of visually representing them
- Immune Axis 2 is independently associated with 28-day mortality, after adjusting for age and APACHE IV severity score
- Immune Axis 1 is more related to temporal trajectory (first week after admission)

References

Davenport EE et al. Genomic landscape of the individual host response and outcomes in sepsis: a prospective cohort study. *Lancet Respir Med.* 2016 Apr;4(4)
 Scicluna BP et al. Classification of patients with sepsis according to blood genomic endotype: a prospective cohort study. *Lancet Respir Med.* 2017 Oct;5(10)
 Sweeney TE et al. Unsupervised Analysis of Transcriptomics in Bacterial Sepsis Across Multiple Datasets Reveals Three Robust Clusters. *Crit Care Med.* 2018 Jun;46(6)

