MatriSPACE: Spatial Transcriptomics Toolbox to Explore the Extracellular Matrix in Health and Disease

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INTRODUCTION

The extracellular matrix (ECM) and its associated molecules, collectively known as the matrisome, play a crucial role in tissue organisation across health and disease states, influencing cellular behaviour, signalling pathways, and treatment responses. Traditional bulk sequencing methods fail to capture the spatial heterogeneity of matrisome components within tissues. Spatial transcriptomics has emerged as a powerful technology to address this limitation, enabling the study of gene expression patterns with their spatial context. MatriSPACE is an R package and shiny app that serves as a comprehensive toolbox for the analysis and visualisation of matrisome gene expression patterns in both healthy and diseased tissues using spatial transcriptomics data. This user-friendly toolbox allows researchers to uncover spatial relationships between ECM components and other tissue features, offering new insights into tissue biology and potentially identifying novel targets.

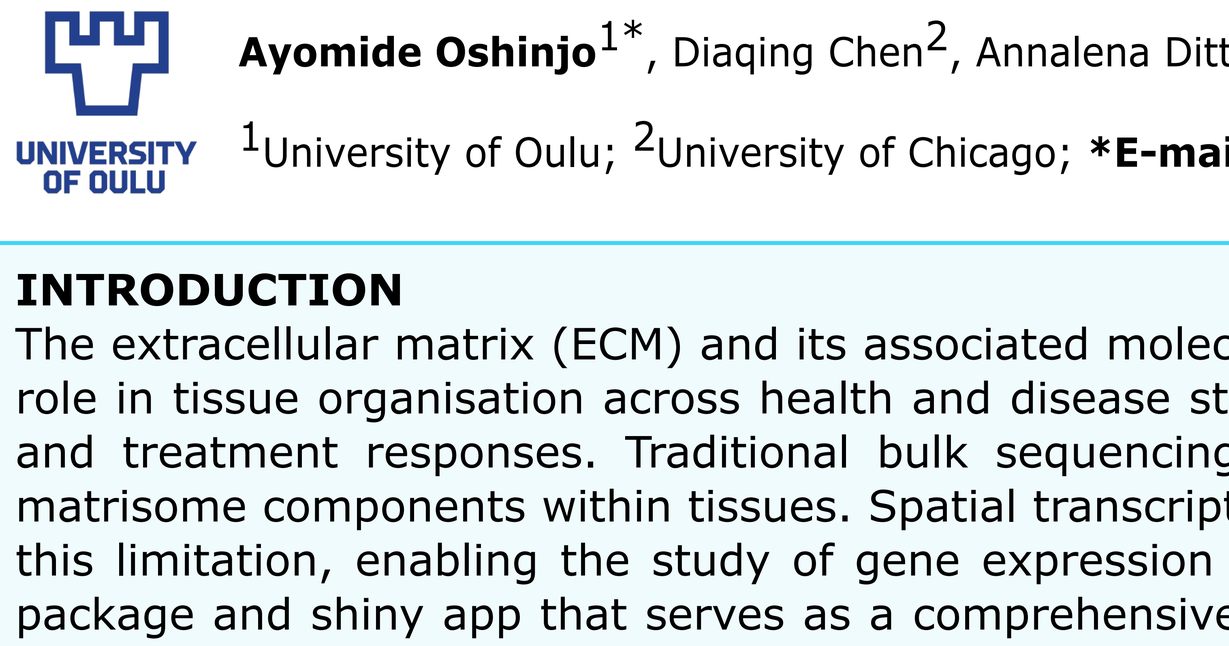

Figure 1. MatriSPACE overview.
(A) Schematic of the MatriSPACE workflow.
(B) Screenshot of different panels of the MatriSPACE beta interface

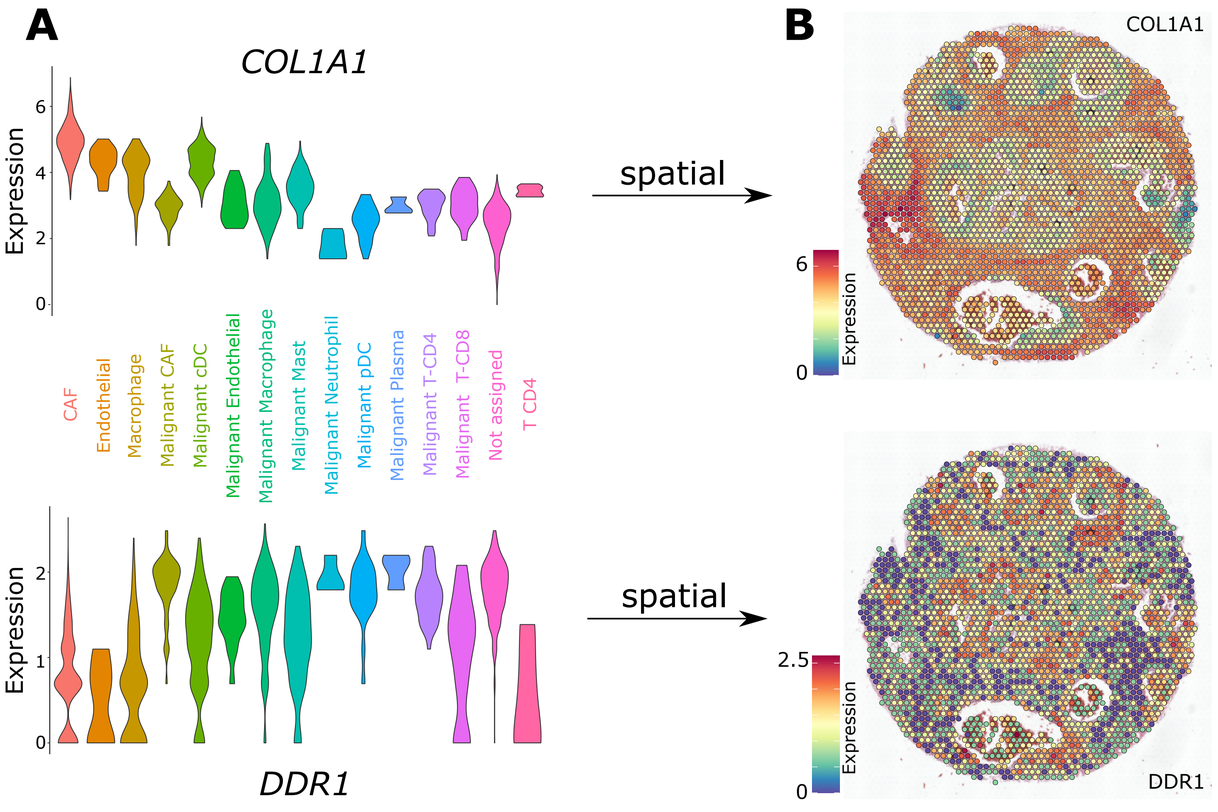

Figure 2. ECM genes *COL1A1* and *DDR1*. (A) Expression across deconvoluted cell types. (B) Spatial expression maps across tissue sections.

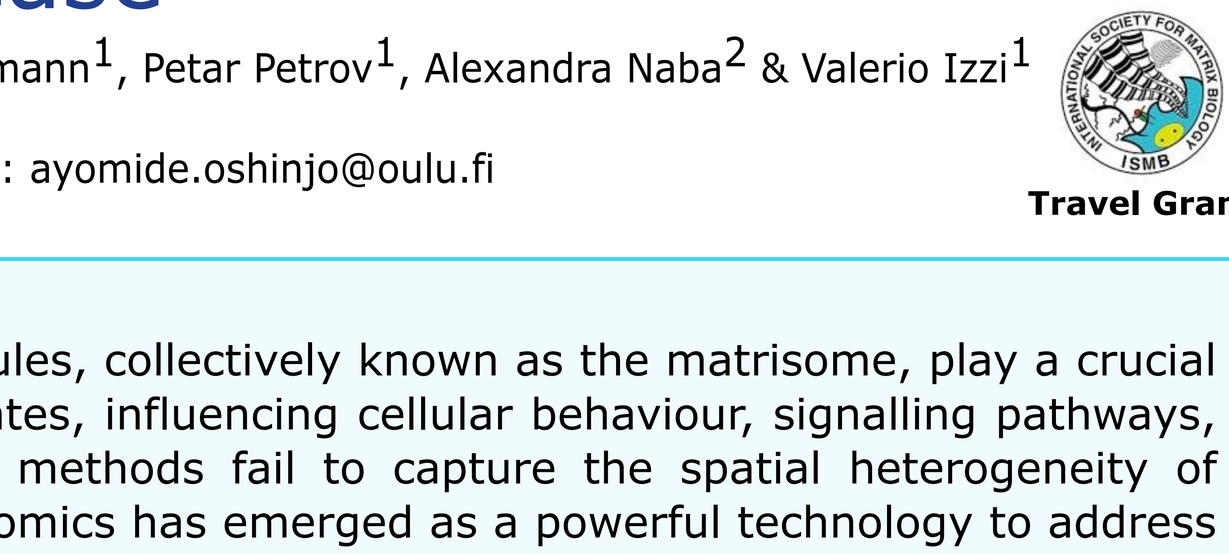

Figure 3. Spatial analysis of ECM genes. (A) Quantized gene similarity map of COL1A1 and DDR1.(B) Spatial autocorrelation plot showing localized expression patterns (H: high, L: low).

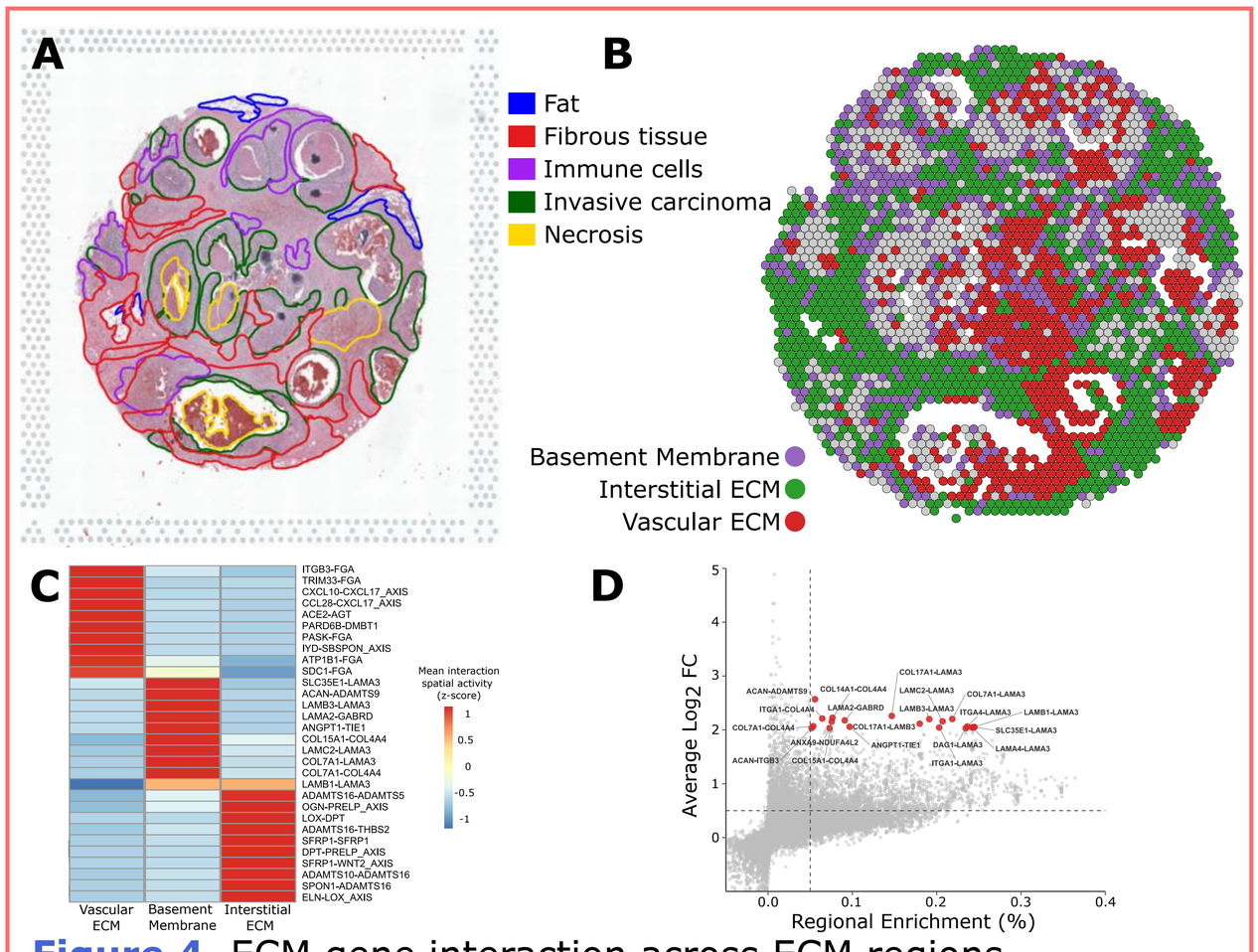

Figure 4. ECM gene interaction across ECM regions
(A) Pathologist annotation (B) Computational definition of ECM regions (C) ECM Domain-specific interaction profiles (D) Basement membrane volcano plot showing fold change vs. percentage difference.

CONCLUSIONS AND FUTURE DIRECTIONS

MatriSPACE is a key tool for exploring matrisome spatial expression and interactions across both healthy and diseased tissues, fundamental to understanding tissue heterogeneity. With internal and user datasets, it enables systematic investigation of ECM spatial patterns in diverse contexts. Future updates will incorporate advanced analysis methods to enhance our understanding of ECM dynamics.

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