BioSET

Biomarker-based Spatial co-Expression analysis in Tumor environments

Bio+MedVis Challenge 2025

(3D Microscopy Imaging Challenge)

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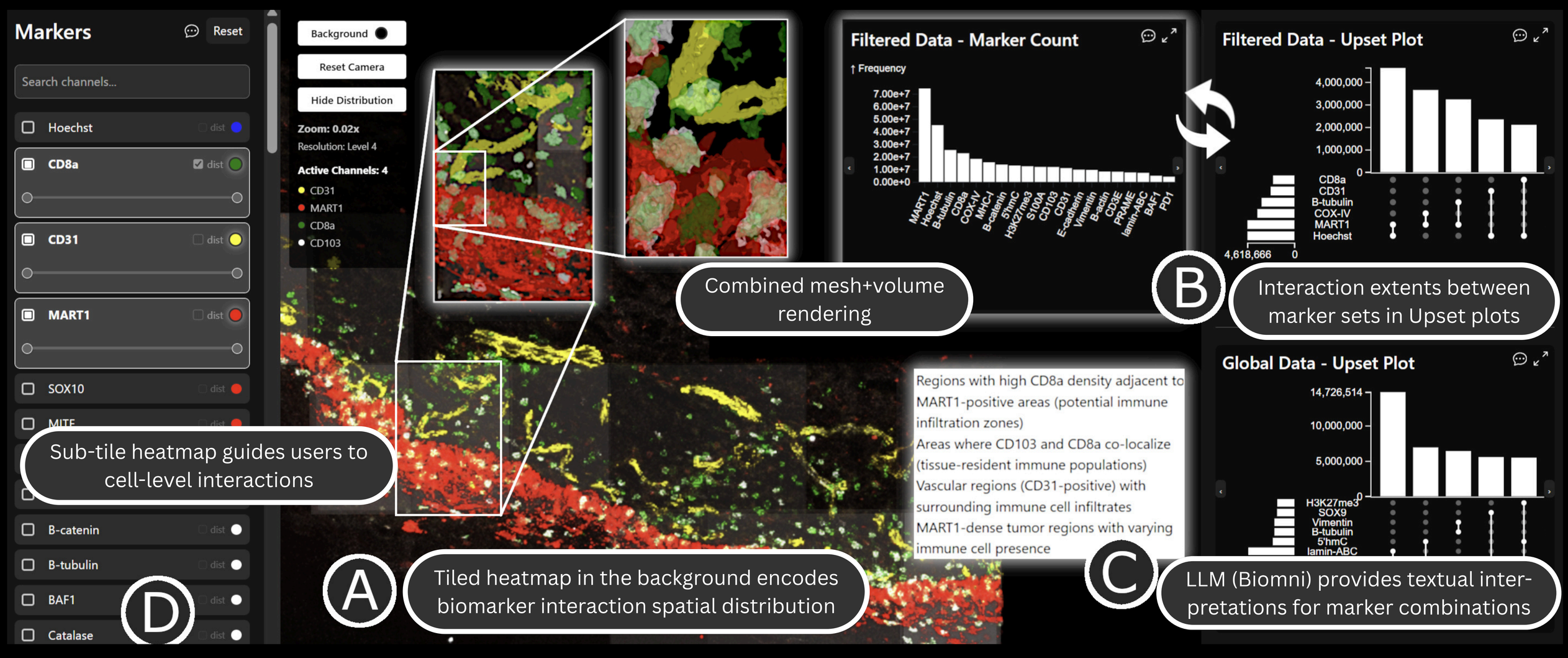
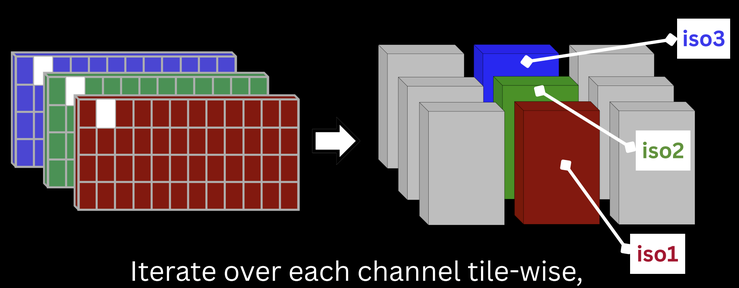
Immunoflorescence (IF) [*Lin16*] imaging has become an established method to study the location of proteins in biological tissue and characterize cellular microenvironments of diseases, most notably cancer. The resulting image data comprises multiple channels, each representing a spatial distribution of a biomarker. A new frontier in this domain is the progression from 2D to 3D imaging technologies, leading to large and complex multi-volumetric data and accompanied analysis challenges. **In this context, a key requirement is to reveal where specific biomarkers are co-expressed and at what scale.**



BioSET analyzes biomarker interactions, and integrates the findings into a web based visual analytics tool. **(A)** A multi-volume viewer renders the selected markers **(D)** in 3D, with a background tile heatmap summarizing interaction extent. Clicking a tile opens a high-res volume+mesh view with a sub-tile heatmap that steers the user to cell-level sites. **(B)** UpSet plots reveal frequent global co-expressions and those conditioned on the current selection. **(C)** Biomni (LLM agent) adds concise biological context for the chosen interactions.

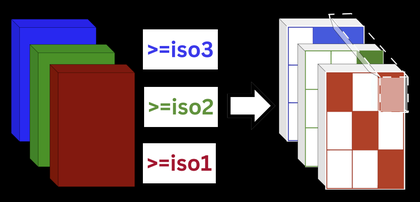
Processing

Isovalue Detection

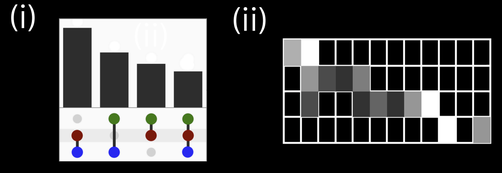


Iterate over each channel tile-wise, using Pekar et al's [*Pekar01*] isovalue detection

Co-expression Analysis

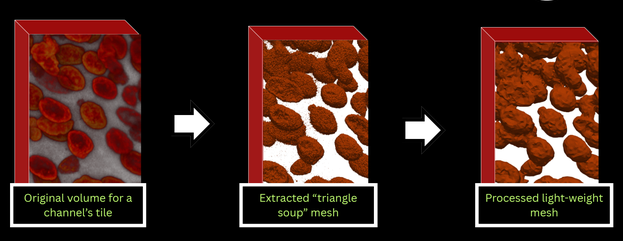


Threshold each channel-tile using detected isovalues



(i) Global co-expression (tile-summed) & (ii) Tile-wise spatial co-expression

Mesh Processing

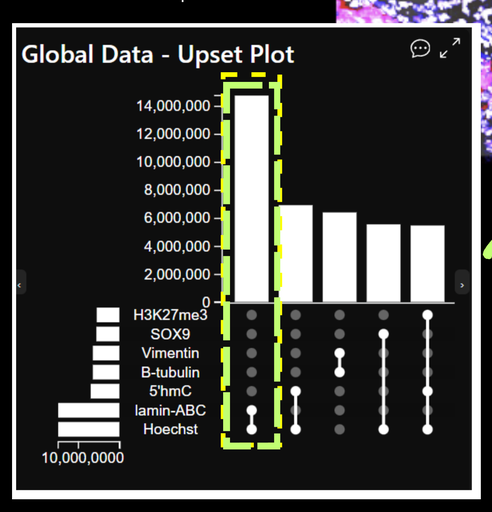


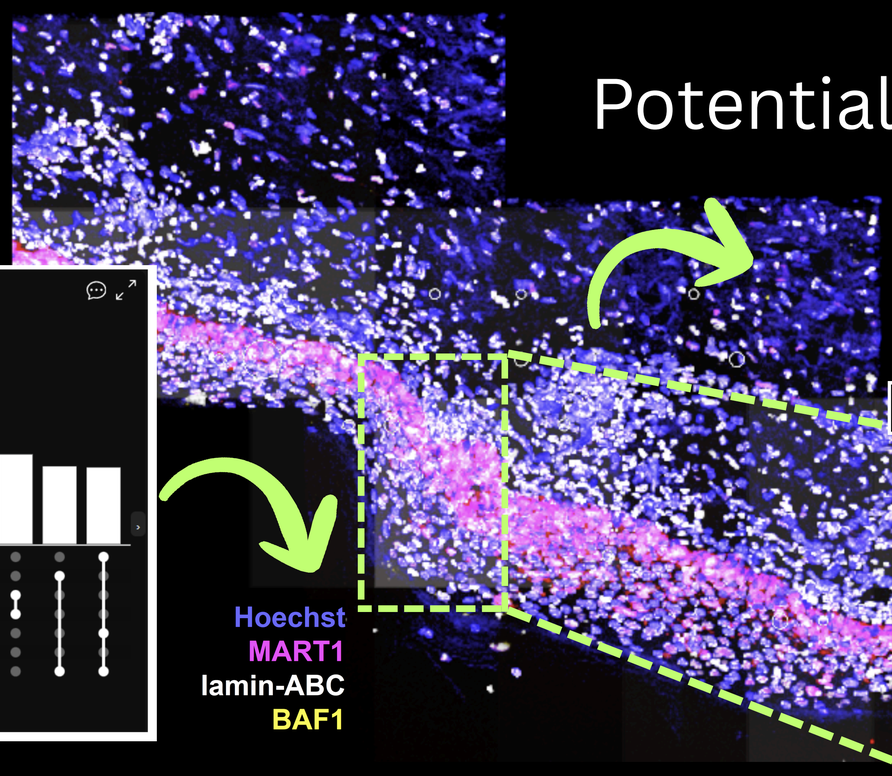
We use FlyingEdges3D [*Schroeder15*] and the detected isovalues to extract surfaces, on which we perform filtering, hole filling and alpha wrapping [*Alliez24*]

Case Study.

Potential Nuclear Envelope Rupture

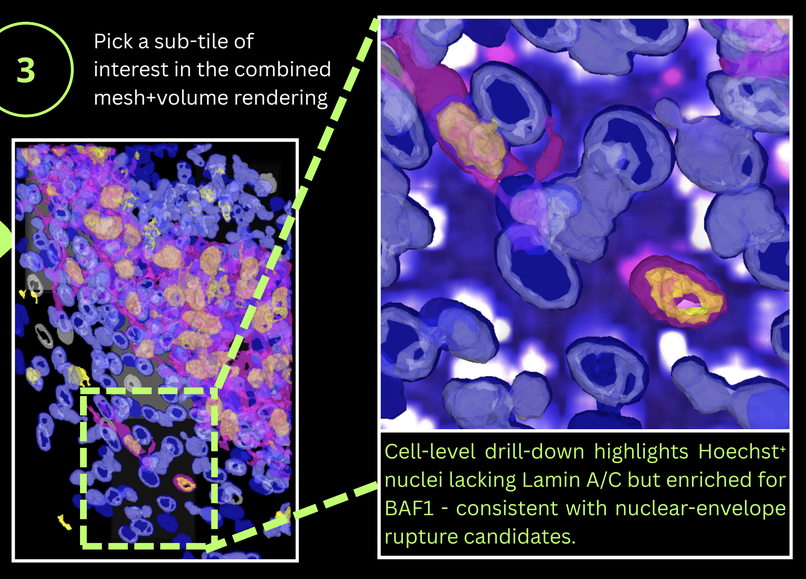
1 We select markers based on most frequent combinations in the plot.





2 Pick a tile showing large co-expression extent in the heatmap.

3 Pick a sub-tile of interest in the combined mesh+volume rendering



Cell-level drill-down highlights Hoechst⁺ nuclei lacking Lamin A/C but enriched for BAF1 - consistent with nuclear-envelope rupture candidates.

[*Lin16*] Lin JR, Fallahi-Sichani M, Chen JY, Sorger PK. Cyclic Immunofluorescence (CycIF), A Highly Multiplexed Method for Single-cell Imaging. Curr Protoc Chem Biol. 2016 Dec 7;8(4):251-264. doi: 10.1002/cpch.14. PMID: 27925668; PMCID: PMC5233430.

[*Pekar01*] V. Pekar, R. Wiemker, and D. Hempel. "Fast detection of meaningful isosurfaces for volume data visualization". In: Proceedings Visualization, 2001. VIS '01. 10/2001, pp. 223–230.

[*Schroeder15*] W. Schroeder, R. Maynard, and B. Geveci. "Flying edges: A high-performance scalable isocontouring algorithm". In: IEEE LDAV. 2015, pp. 33–40.

[*Alliez24*] P. Alliez et al. "3D Alpha Wrapping". In: CGAL User and Reference Manual. 6.0.1. CGAL Editorial Board, 2024.

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