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MONTAGE: Unlocking Spatial Biology to Analyze Tumour Microenvironment

Stanford researchers have developed MONTAGE, a powerful computational framework designed to identify groups of cells, called spatial communities, and map how these groups change across biological functions linked to cancer progression. Unlike conventional methods that simply catalog cell types, MONTAGE reveals how cells are organized, interact, and evolve within tumors, providing a dynamic view of the tumor environment.

By working with detailed single-cell imaging and sequencing data as well as with larger bulk gene expression datasets from many patients. MONTAGE identifies distinct "spatial communities" of cells and maps how they shift across biological functions such as metabolism, immune activation, or invasion. This ability to connect cellular architecture with biological functions and patient outcomes positions MONTAGE as a powerful tool for biomarker discovery, patient stratification, and the development of spatially targeted therapies.

Stage of Development
Proof of concept

Applications

- Map tumor microenvironment and functional cell dynamics
- Identify spatial biomarkers linked to cancer progression and outcomes
- Enable spatially informed therapeutic discovery across cancers

Advantages

- Reveals dynamic cell interactions tied to clinical outcomes, not just cell counts
- Scales from single-cell to large patient datasets

- Adaptable to new spatial-omics platforms
- User-friendly R package for MONTAGE developed by the inventors

Publications

- Weiruo Zhang, Zinaida Good, Marc A. Baertsch, Guolan Lu, John W. Hickey, Rachel Hildebrand, Serena Chang, Andrew J. Gentles, John B. Sunwoo, Quynh-Thu Le, Christina S. Kong, Garry P. Nolan, Sylvia K. Plevritis (2025). "MONTAGE: A Computation Framework to Identify Spatially Resolved Functional Enrichment Gradients in the Tissue Microenvironment via Spatial Communities." *bioRxiv*.

Innovators

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