

Systems and Methods of Single-Cell Segmentation and Spatial Multiomics Analyses

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ABSTRACT

Researchers at the University of California, Davis have developed a novel cell segmentation technology for accurate analysis of non-spherical cells and that offers a comprehensive, high-throughput approach for analyzing the transcriptomic and metabolomic data to study complex biological processes at the single-cell level.

FULL DESCRIPTION

This technology presents a computer-implemented method for single-cell spatial omics analysis, combining advanced imaging and gene expression profiling to accurately analyze cells with complex shapes. It incorporates overlay images created from stained sample images to delineate cell boundaries, facilitating precise segmentation and analysis of individual cells. The cell segmentation method uniquely offers accurate analysis of cells with non-spherical geometry and providing a segmentation framework that recognizes and adapts to unique morphologies of brain cells such the star-shaped astrocytes, as well as the multipolar nature of neurons and glial cells.

Furthermore, this segmentation approach is also tailored for single-cell metabolomics by precisely overlaying cell segmentation map, derived from single-cell transcriptomics data, with a complementary image from imaging mass spectrometry (IMS) data. The fusion of these two sophisticated imaging techniques permits a previously unattainable examination of metabolites across varied cell types in both pathological and healthy tissue samples.

APPLICATIONS

- Drug efficacy evaluation and personalized medicine.
- Revolutionizing disease diagnosis, prognosis, and treatment planning.
- Discovery of new biomarkers for complex diseases.
- Enhanced understanding of cellular diversity within tissues, leading to novel therapeutic targets.

FEATURES/BENEFITS

- Enables comprehensive characterization and quantification of single-cell genomes, transcriptomes, proteomes, epigenomes, and metabolomes.
- Improves scalability, sensitivity, and specificity of single-cell analysis.
- Minimizes sample loss and artifacts, maximizing biological information recovery.
- Capable of analyzing cells with complex shapes and structures, including neuronal cells, fibroblasts, and stem cells.
- Supports a wide range of analysis types, including cell typing, cell-cell communication, protein-protein interaction networks, and more.
- Addresses challenges in analyzing cells with complex and non-standard shapes.
- Addresses limited scalability, sensitivity, and specificity in existing single-cell omics methodologies.
- Overcomes difficulties in integrating multi-omic data for comprehensive single-cell analysis.

PATENT STATUS

Patent Pending

RELATED MATERIALS

- [TransMetaSegmentation \(TMS\): a transcriptome-based segmentation method for spatial metabolomic data](#) - 06/13/2024

CONTACT

Raj Gururajan
rgururajan@ucdavis.edu
tel: 530-754-7637.



INVENTORS

- Lam, Kit S.
- Lin, Siyu
- Wang, Aijun
- Wang, Yongheng
- Zhang, Weidi

OTHER INFORMATION

KEYWORDS

single cell spatial omics,
single cell transcriptomics,
single cell metabolomics,
cell segmentation, gene
expression profiling

CATEGORIZED AS

- **Biotechnology**
 - Bioinformatics
 - Genomics
 - Health
 - Other
 - Proteomics
- **Imaging**
 - Medical
 - Molecular
 - Software
- **Medical**
 - Disease: Central Nervous System
 - Imaging
 - Other
 - Screening
 - Software
- **Research Tools**

- ▶ [Bioinformatics](#)
- ▶ [Other](#)
- ▶ [Screening Assays](#)

RELATED CASES

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University of California, Davis
Technology Transfer Office
1850 Research Park Drive, Suite 100, ,
Davis,CA 95618

Tel: 530.754.8649
techtransfer@ucdavis.edu
<https://research.ucdavis.edu/technology-transfer/>
Fax: 530.754.7620

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