

(SD2024-269) Bento: An open-sourced toolkit for subcellular analysis of spatial transcriptomics data

Tech ID: 33847 / UC Case 2021-Z08-1

ABSTRACT

Bento is an open-source software toolkit that uses single-molecule information to enable spatial analysis at the subcellular scale. Bento ingests molecular coordinates and segmentation boundaries to perform three analyses: defining subcellular domains, annotating localization patterns, and quantifying gene-gene colocalization. The toolkit is compatible with datasets produced by commercial and academic platforms. Bento is integrated with the open-source single-cell analysis software ecosystem.

TECHNOLOGY DESCRIPTION

The spatial organization of molecules in a cell is essential for their functions. While current methods focus on discerning tissue architecture, cell-cell interactions, and spatial expression patterns, they are limited to the multicellular scale.

Researchers from UC San Diego present Bento, a Python toolkit that takes advantage of single-molecule information to enable spatial analysis at the subcellular scale. Bento ingests molecular coordinates and segmentation boundaries to perform three analyses: defining subcellular domains, annotating localization patterns, and quantifying gene-gene colocalization. We demonstrate MERFISH, seqFISH + , Molecular Cartography, and Xenium datasets. Bento is part of the open-source Scverse ecosystem, enabling integration with other single-cell analysis tools.

APPLICATIONS

The audience includes scientists and companies analyzing spatial transcriptomics imaging data. This is especially valuable to scientific cores (e.g. bioinformatics, microscope imaging, DNA sequencing) that produce data and analysis for partnering labs.

ADVANTAGES

STATE OF DEVELOPMENT

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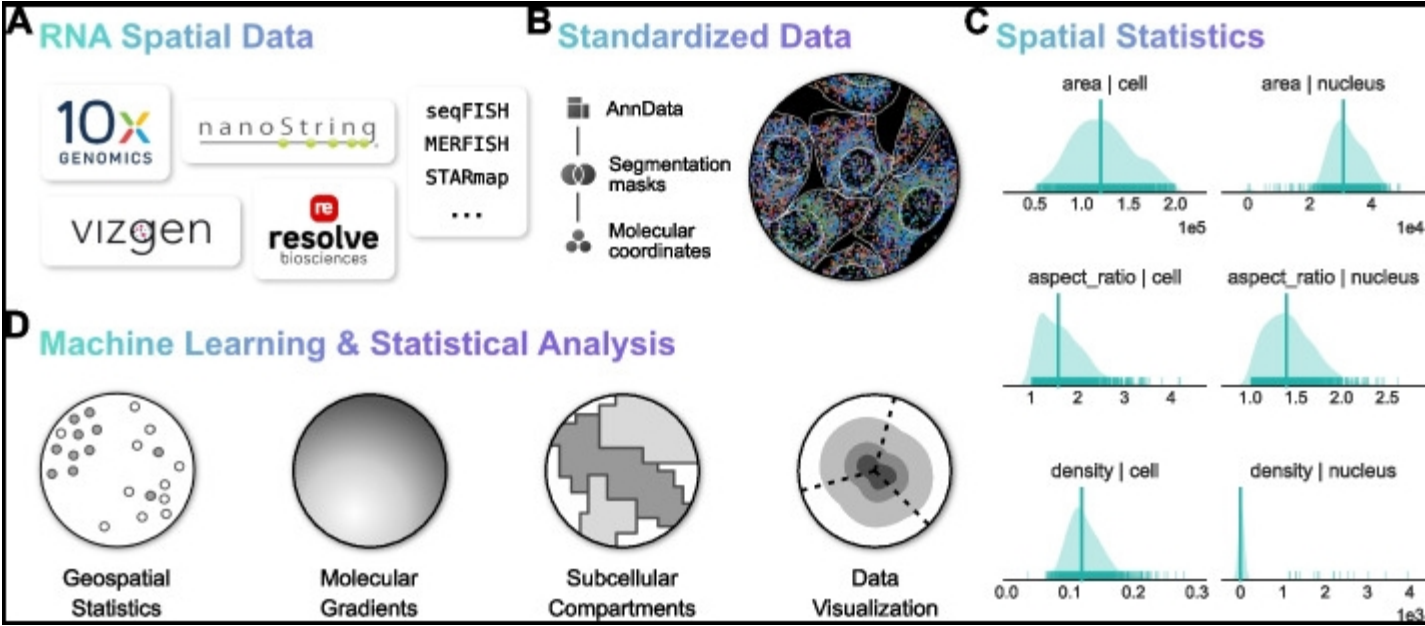
OTHER INFORMATION

CATEGORIZED AS

- ▶ **Biotechnology**
 - ▶ Genomics
 - ▶ Other
- ▶ **Medical**
 - ▶ Imaging

RELATED CASES

2021-Z08-1



Workflow and functionality of the Bento toolkit. A Single-molecule resolved spatial transcriptomics data from commercial or custom platforms are ingested into Bento where it is converted to the AnnData format (B), where it can be manipulated with Bento as well as a wide ecosystem of single-cell omics tools. C Geometric statistics are illustrated for the seqFISH + dataset, including metrics describing cell and nuclear geometries and cell density to assess overall data quality. D Bento has a standard interface to perform a wide variety of subcellular analyses.

INTELLECTUAL PROPERTY INFO

RELATED MATERIALS

► Mah CK, Ahmed N, Lopez NA, Lam DC, Pong A, Monell A, Kern C, Han Y, Prasad G, Cesnik AJ, Lundberg E, Zhu Q, Carter H, Yeo GW.

Bento: a toolkit for subcellular analysis of spatial transcriptomics data. *Genome Biol.* 2024 Apr 2;25(1):82. - 04/02/2024

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