BITS :: Call for Abstracts 2021 - Oral communication

Type	Oral communication
Session	Gene regulation, transcriptomics and epigenomics
Title	SpatialExperiment: infrastructure for spatially resolved transcriptomics data in R using Bioconductor
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Motivation

Spatially resolved transcriptomics is a new set of technologies allowing to joint measure gene expression with gene spatial location for up to thousands of genes at near-single-cell, single-cell, or sub-cellular resolution. The combined analysis of molecular and spatial information helps to discover new insights about biological processes that manifest in a spatial manner within tissues. However, to efficiently analyze these data, specialized data infrastructure is required, which facilitates storage, retrieval, subsetting, and interfacing with downstream tools.

Methods

Here, we describe SpatialExperiment, a new data infrastructure for storing and accessing spatially resolved transcriptomics data, implemented within the Bioconductor framework in the R programming language. SpatialExperiment extends the existing SingleCellExperiment for single-cell data from the Bioconductor framework, which brings with it advantages of modularity, interoperability, standardized operations, and comprehensive documentation.

Results

We'll demonstrate the structure and user interface with examples from the 10x Genomics Visium and seqFISH platforms. We retain that SpatialExperiment can be used to handle alternative spatial technological platforms which measure multiple modalities, such as spatial immunofluorescence or proteomics.
We also provide access to example datasets and visualization tools in the STexampleData, TENxVisiumData, and ggspavis packages. SpatialExperiment is freely available from Bioconductor at https://bioconductor.org/packages/SpatialExperiment. The STexampleData, TENxVisiumData, and ggspavis packages are available from GitHub and will be submitted to Bioconductor.

Info

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Figure

Availability	https://bioconductor.org/packages/SpatialExperiment/

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