




starfish: scalable pipelines for image-based transcriptomics

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Summary

The exploding field of single cell transcriptomics has begun to enable deep analysis of gene expression and cell types, but spatial context is lost in the preparation of tissue for these assays. Recent developments in biochemistry, microfluidics, and microscopy have come together to bring about an “alphabet soup” of technologies that enable sampling gene expression *in situ*, with varying levels of spatial resolution, sensitivity, and genetic depth. These technologies promise to permit biologists to ask new questions about the spatial relationships between cell type and interactions between gene expression and cell morphology. However, these assays generate very large microscopy datasets which are challenging to process using general microscopy analysis tools. Furthermore, many of these assays require specialized analysis to decode gene expression from multiplexed experimental designs.

starfish is a Python library for processing images generated by microscopy-based spatial transcriptomics assays. It lets biologists build scalable pipelines that localize and quantify RNA transcripts in image data generated by any hybridization- or sequencing-based *in situ* transcriptomics method, from classic RNA single-molecule FISH to combinatorial barcoded assays. Image processing of an experiment is divided into fields of view (FOV) that correspond to the data produced by a microscope at a single location on a microscope slide. *starfish* lets users register and pre-process images in each FOV, localize spots representing tagged RNA molecules in 3D, decode the identity of those molecules according to the experimental design, segment cells, assign the spots to cells, then aggregate spots into a cell x gene expression matrix. This spatially-annotated gene expression matrix can then be analyzed and visualized in downstream tools for single-cell biology, such as Seurat (Stuart et al. (2019)), Bioconductor (Huber et al. (2015)), ScanPy (Wolf, Angerer, & Theis (2018)), and cellxgene (Megill et al. (2020)).

To enable large scale processing of these data, *starfish* leverages a 5-dimensional imaging data model (x, y, z, round, channel) backed by the cloud-friendly `spacetx-format` file format, and [slicedimage](#), an interface for lazy, distributed loading of `spacetx-format` datasets. Furthermore, *starfish* implements comprehensive logging of all data processing steps for provenance tracking, reproducibility, and transparency. *starfish* is built on top of popular Python tools like `xarray` (Hoyer, Fitzgerald, Hamman, & others (2016)) and `scikit-image` (Walt et al. (2014)).

To help new users get started and support the broader single cell biology community in learning how to work with these data, *starfish* maintains example datasets and reference implementations ported from published assays, including MERFISH (Moffitt et al. (2016)), In Situ Sequencing (Ke et al. (2013)), osmFISH (Codeluppi et al. (2018)), BaristaSeq (Chen, Sun, Church, Lee, & Zador (2017)), smFISH (Long et al. (2018)), DARTFISH (Cai & Zhang (2019)), STARmap (Wang et al. (2018)), and seqFISH (Shah et al. (2018)).

starfish was developed alongside the [SpaceTx project](#), a CZI-funded effort to compare spatial transcriptomics methods in the context of determining cell types in the brain (Lein et al. (2018)). *starfish* is currently in use by multiple research groups, including the [Allen Institute for Brain Science](#), the [Chan Zuckerberg Biohub](#), and the [Zhang Lab at UC San Diego](#). These groups support multiple large-scale projects profiling *in situ* gene expression, including the SpaceTx consortium, the [Human Cell Atlas](#), the [BRAIN Initiative Cell Census Network](#), and the [HuBMAP Consortium](#).

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