nf-core/molkart

An end-to-end pipeline for the analysis of Molecular Cartography™ data

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Motivation

Imaging-based spatial transcriptomic methods with subcellular resolution are becoming more popular and more powerful. One of such technologies is Molecular Cartography™ developed by Resolve Biosciences. It uses combinatorial single-molecule fluorescent in-situ hybridization (smFISH) of currently up to 100 different targeted transcripts. Efficient analysis of spatial transcriptomic data, like the one produced by Molecular Cartography, is a complex, multistep process that requires several stages of image processing.

Pipeline input

The Molecular Cartography™ platform provides users with a decoded spot table with the x, y, z position, and gene information for each transcript in the imaged area.

x	y	z	gene
3031	1338	7	Zm00001d044857
3326	1180	7	Zm00001d044857
3425	947	7	Zm00001d044857
3437	939	7	Zm00001d044857
3526	1044	7	Zm00001d044857
...	...	...	...

To help guide cell segmentation, an image of the same area with reconstructed tiles showing nuclear staining is provided. A membrane, or different stain to further help with segmentation can additionally be acquired.

Data from the Maize dataset provided by Resolve Biosciences shown.

Pipeline workflow

Highlights

Choice of state-of-the-art segmentation options and different compartments

Examples:

mesmer (whole-cell)

cellpose (nuclear)

Image preprocessing options to improve segmentation.

Mindagap, **CLAHE**

Image subset creation for segmentation model training with ilastik or Cellpose

Custom segmentation model application with ilastik and Cellpose. custom model

Future plans

Implementation of spot-based segmentation options such as Baysor and BOMS

Support for spatial feature frameworks and downstream processing

Additional QC metrics such as PCA of spots

Scan for links and connect!

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