

Krešimir Beštak^{1,2*}, Florian Wünnemann^{1,2*}, Denis Schapiro^{1,2#}, nf-core community

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Motivation

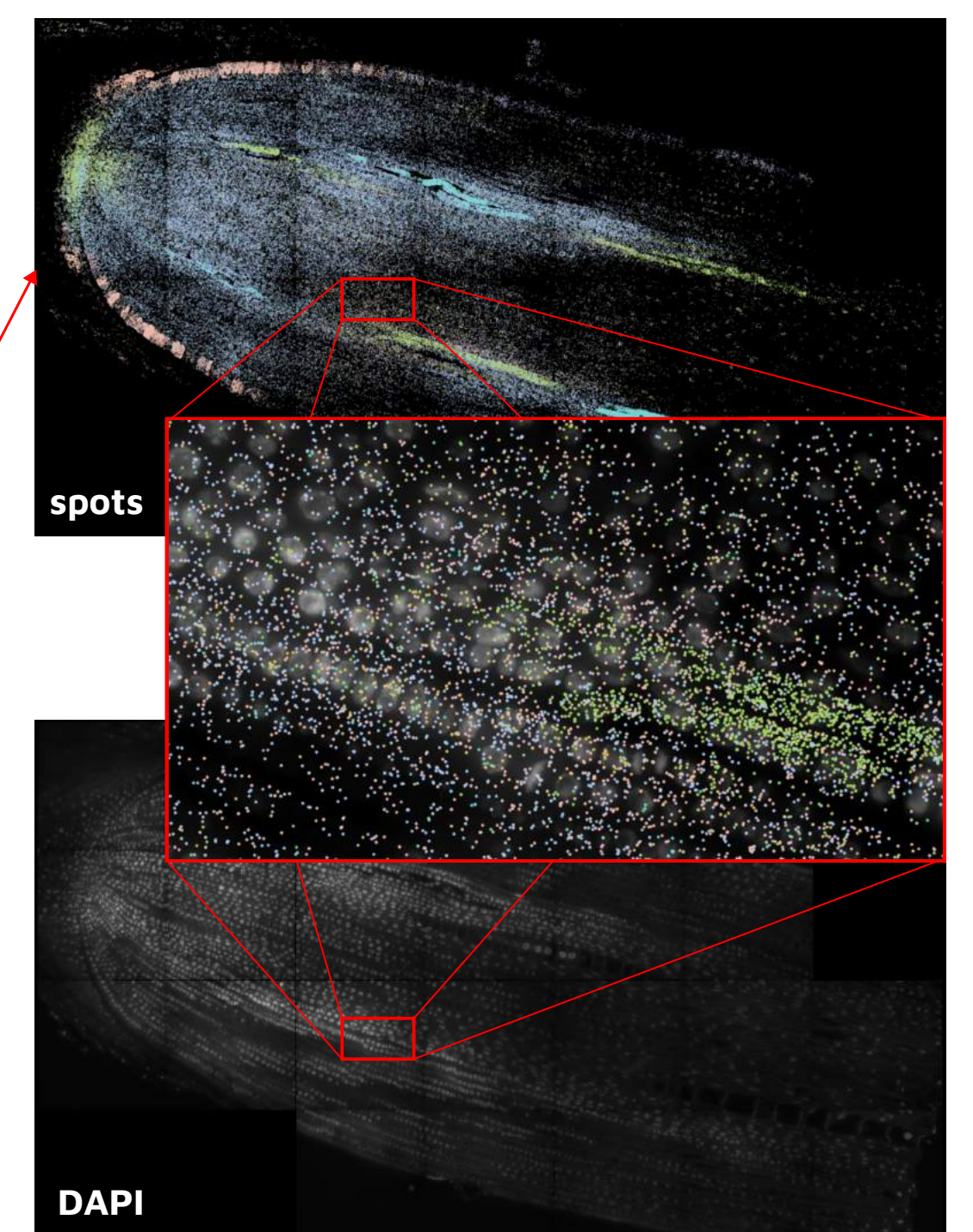
Imaging-based spatial transcriptomic methods with subcellular resolution are becoming more popular and more powerful. One of such technologies is Molecular Cartography™ developed by Resolve Biosciences. It uses combinatorial single-molecule fluorescent in-situ hybridization (smFISH) of currently up to 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.

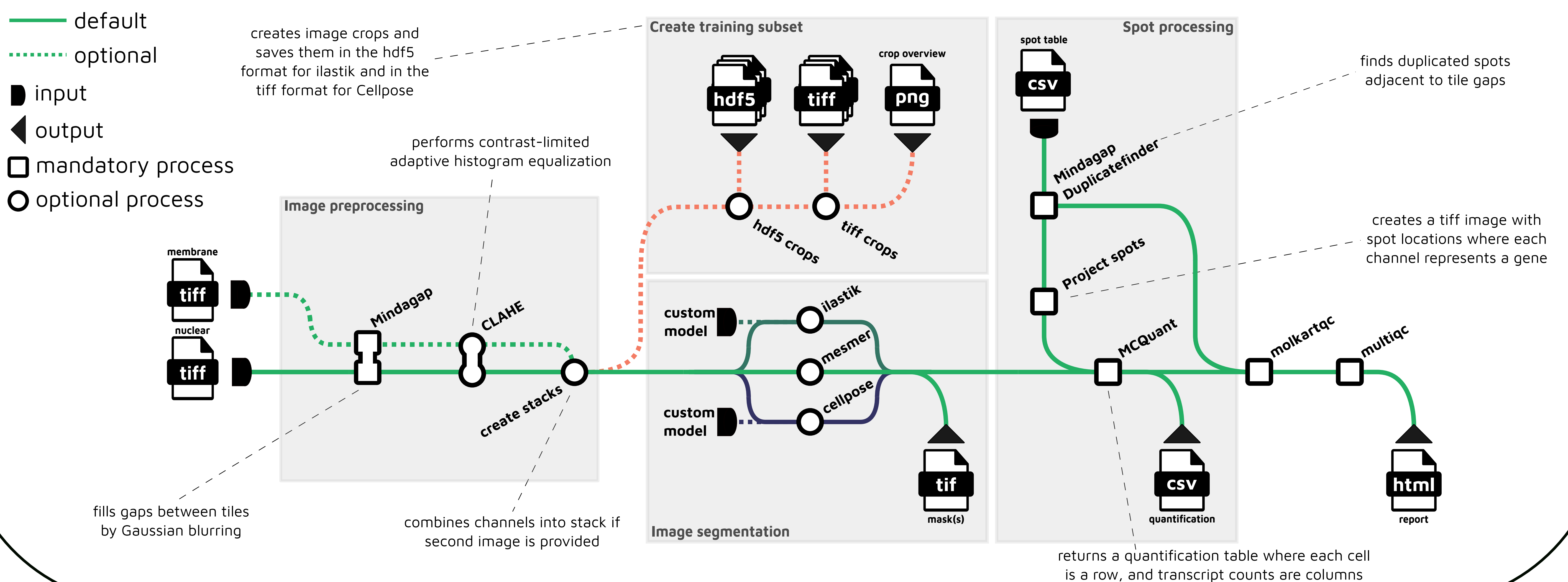
x	y	z	gene
3031	1338	7	Zm00001d044857
3326	1180	7	Zm00001d044857
3425	947	7	Zm00001d044857
3437	939	7	Zm00001d044857
3526	1044	7	Zm00001d044857
...

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.

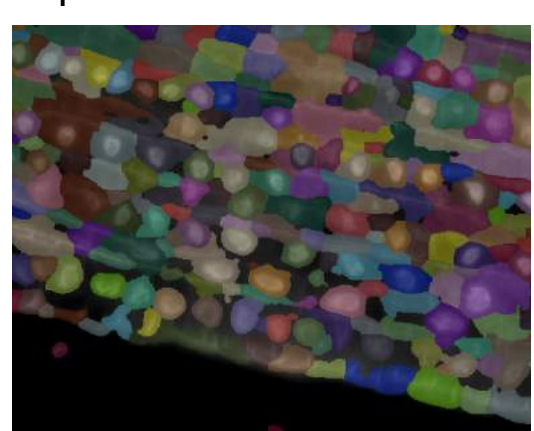
Pipeline workflow



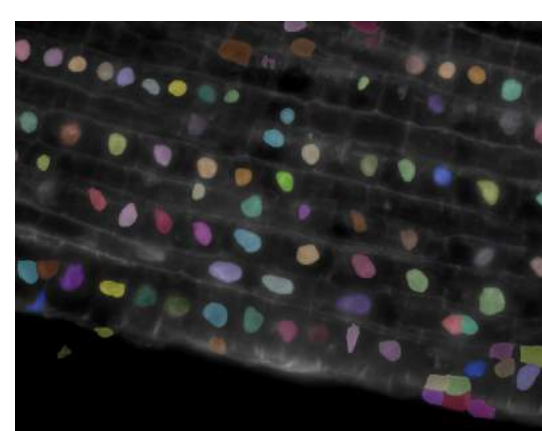
Highlights

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

Examples:



mesmer (whole-cell)



cellpose (nuclear)

Image subset creation for segmentation model training with ilastik or Cellpose

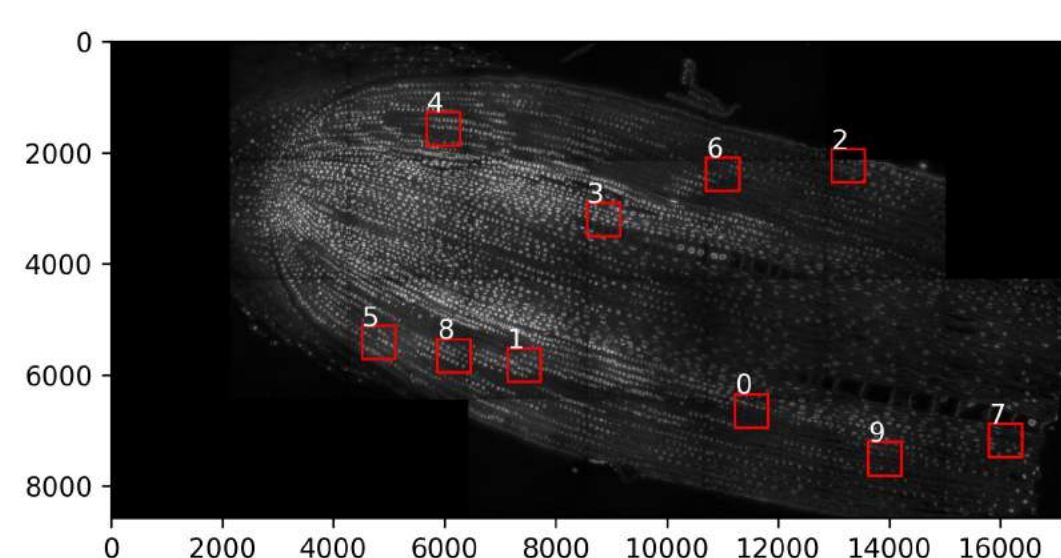


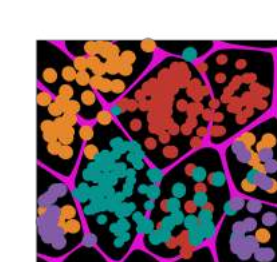
Image preprocessing options to improve segmentation.

Mindagap, CLAHE

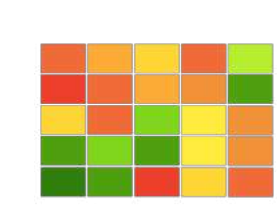
Custom segmentation model application with ilastik and Cellpose.

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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