

Bringing highly multiplexed imaging pipelines to nf-core



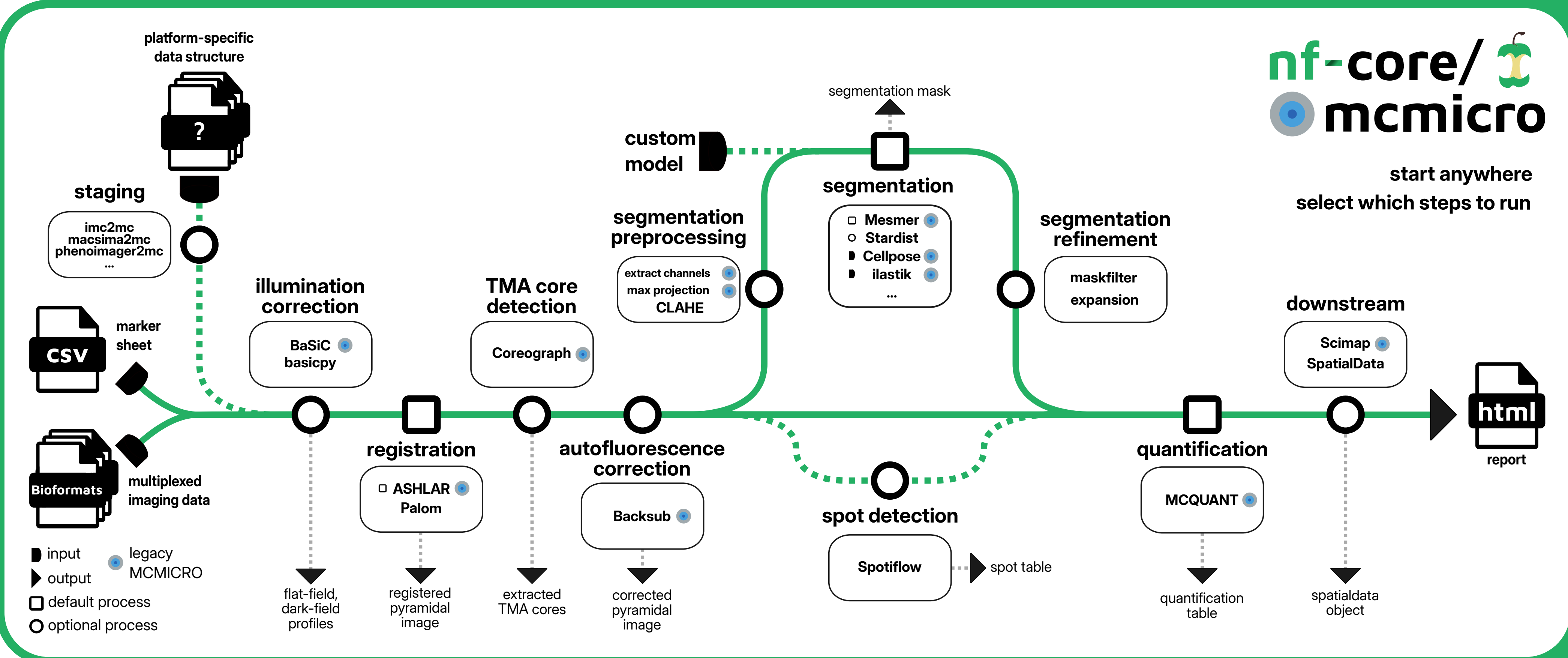
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Background

Unlocking the full potential of emerging imaging-based spatial omics technologies requires high-throughput, scalable, adaptable, and reproducible data processing. As the spatial omics field continues to grow, the need for workflow standardization that ensures long-term sustainability is becoming increasingly important. The nf-core community, tools and guidelines provide a strong foundation to accelerate spatial omics workflow development.

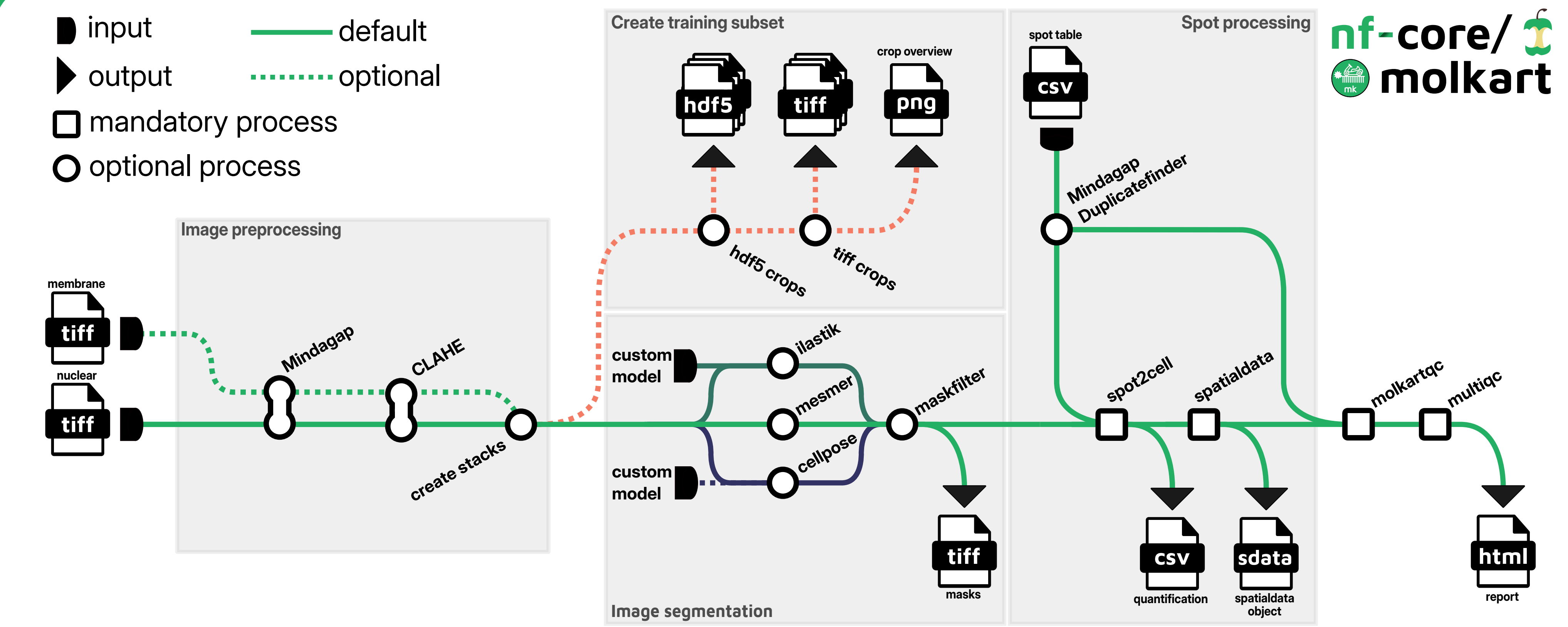
nf-core/mcmicro: adapting and expanding the MCMICRO pipeline within nf-core



MCMICRO was originally developed and conceived as a multiple-choice microscopy Nextflow pipeline utilizing many state-of-the-art tools for high-throughput processing of large Bioformats-compatible antibody-based highly multiplexed imaging data (Schapiro et al., 2022). To ease community maintenance, we have been adding pipeline modules to nf-core and expanding its functionality.

nf-core/molkart: pipeline for processing targeted spatial transcriptomic data

Initially developed for Molecular Cartography data, nf-core/molkart is able to process any dataset of images for segmentation with a matched transcript position table. The pipeline includes a built-in option to create crops that can be used for training custom segmentation models that can be reused in segmentation steps, providing flexibility and enhanced customization.



Future plans

- Full SpatialData support
- GPU support
- Performance optimization
- Implementations of new state-of-the-art tools

Connect and contribute

- nf-core #mcmicro, #molkart
- nf-core/mcmicro, nf-core/molkart
- nf-co.re/join

Scan for visual guides!

