

WEHI's SODA-Hub provides an end-to-end analysis environment for spatial omics from data ingestion to cell segmentation

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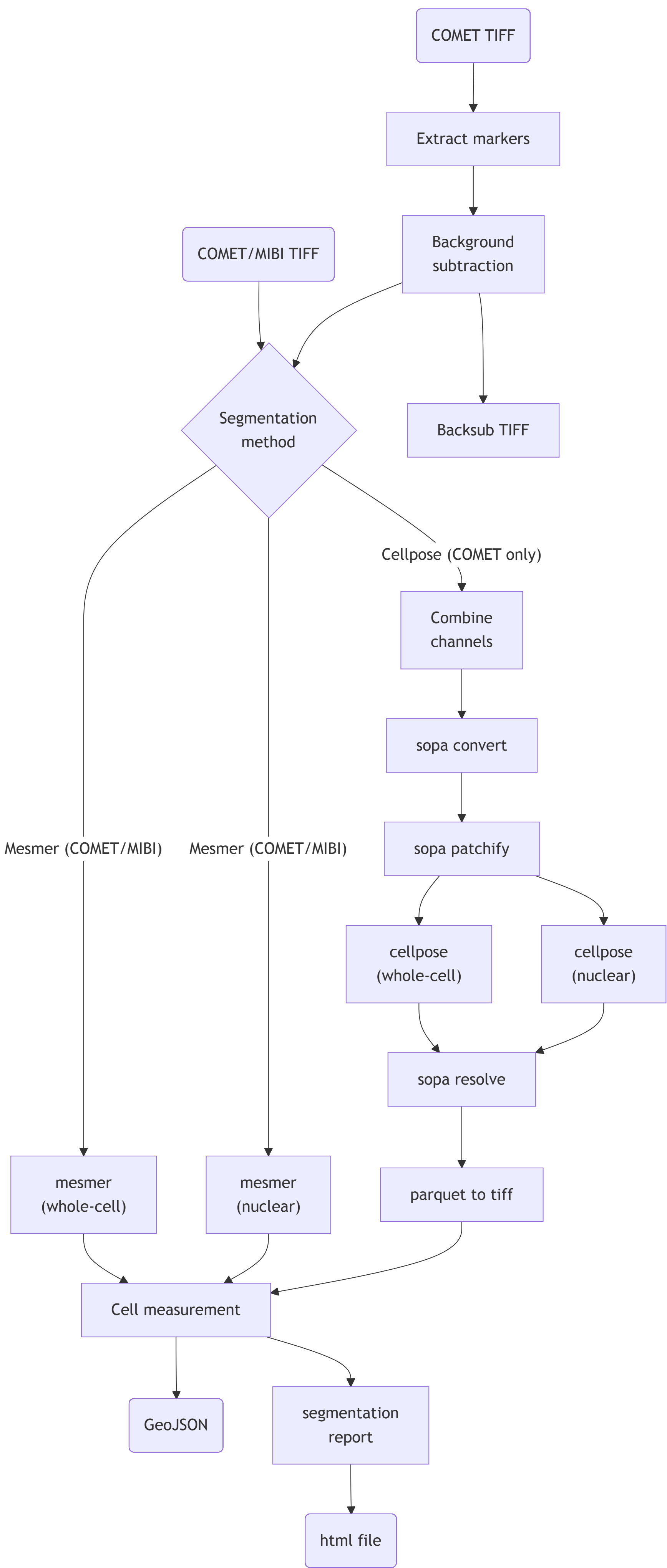
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Background

- Spatial omics technologies hold great promise for unravelling disease mechanisms and have the potential to lead to novel precision diagnostics.
- Large data volumes and multimodal nature of spatial technologies present challenges in data management and processing.
- To address this, WEHI has established the Spatial Omics Data Analytics (SODA) Hub to provide a streamlined environment for spatial analysis, from data ingestion to analysis pipelines.
- The SODA-Hub is a collaborative effort between WEHI's Bioinformatics Division, Research Computing Platform, Bioimage Analysis Core and WEHI's spatial researchers.

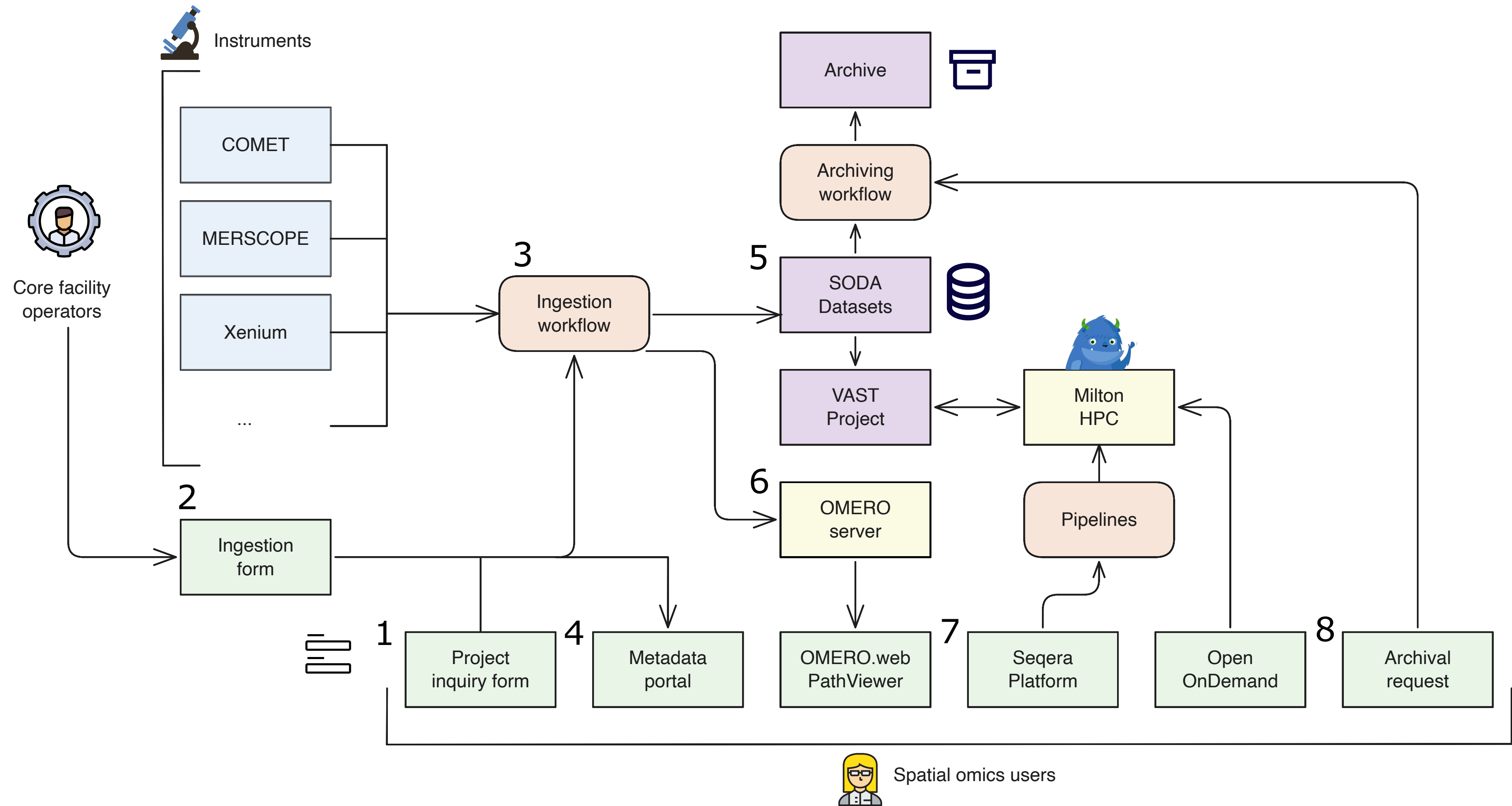
Segmentation pipeline for spatial proteomics

- WEHI-SODA-Hub/sp_segment is a cell segmentation pipeline for COMET and MIBI.
- User friendly: easy to run via Sequera Platform.
- Portable: dependencies handled.
- Scalable: patch large images and parallelise.
- Data provenance: detailed run & QC reports.
- Comprehensive: includes cell measurements output ready for phenotyping.



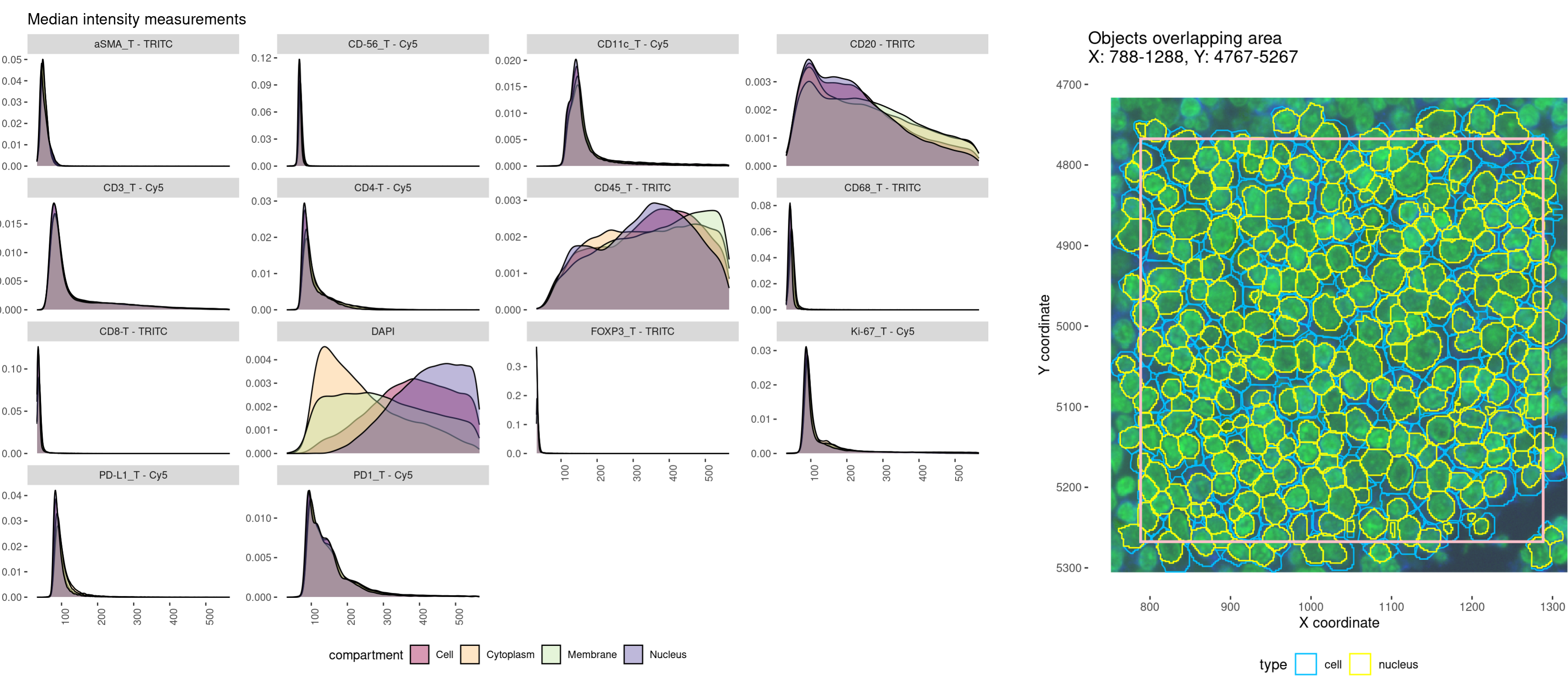
SODA Data Flows

- Spatial projects are captured in an inquiry form on Monday.com.
- Core facility operator runs experiment on instrument and submits ingestion form.
- Ingestion workflow triggers, transferring run to staging area and performing preprocessing.
- User verifies metadata via metadata portal.
- Data and metadata are moved into data repository, accessible via VAST projects.
- Images are imported in-place to OMERO server, accessible via OMERO.web/PathViewer.
- Pipelines can be run via Sequera Platform on the local HPC. Data can be visualised on VMs using Open OnDemand.
- User can archive data for long-term storage.



Report Generation

- The WEHI-SODA-Hub/sp_segment pipeline generates a segmentation report to aid in quality control and data provenance.
- Capture parameters for the given run, view cell measurement and intensity distributions, and preview cell geometry.



Visualising results

- SODA's preprocessing workflow will generate baseline segmentations ready for visualisation.
- Image data can be managed via OMERO.web.
- PathViewer can be used for viewing images and annotations.
- Segmentations can be overlaid, compared and filtered based on cell measurements.
- QuPath can also be used to access OMERO images via the OMERO extension.

