

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

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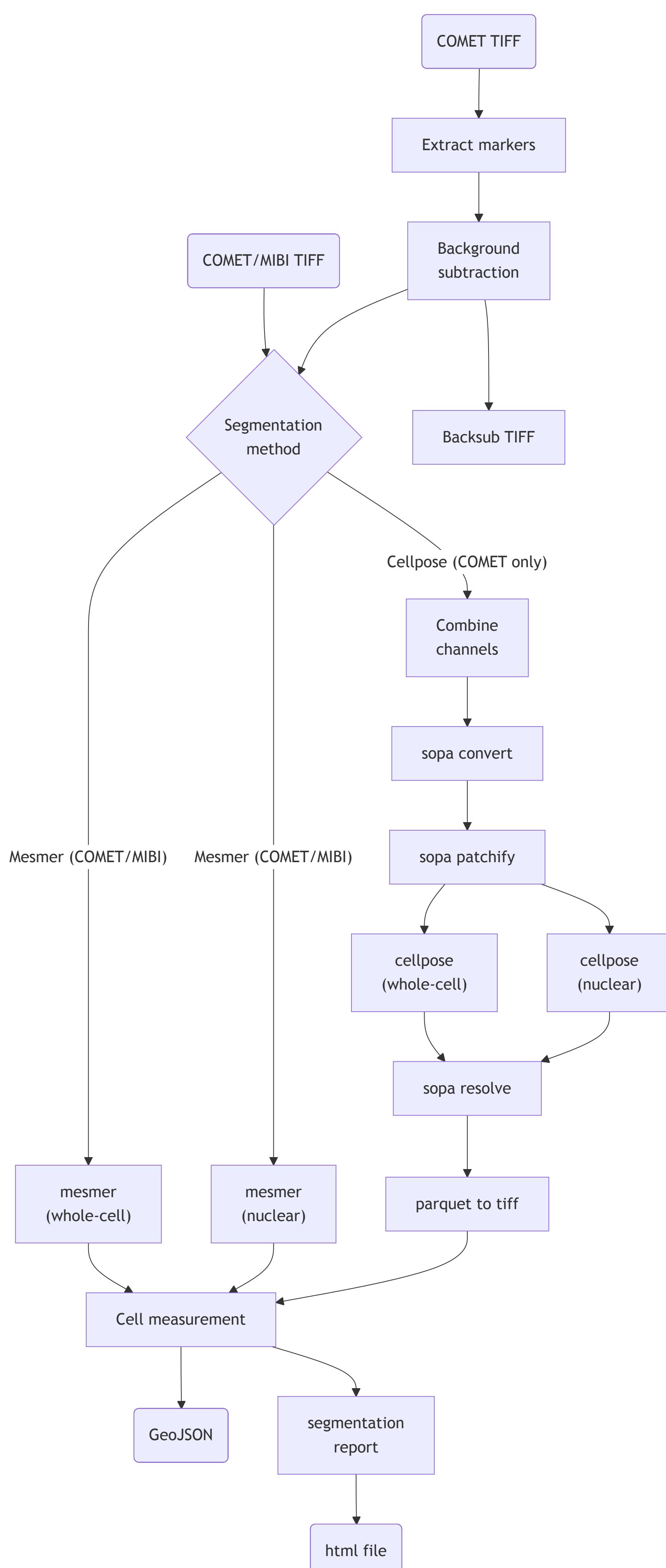
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Background

- 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.

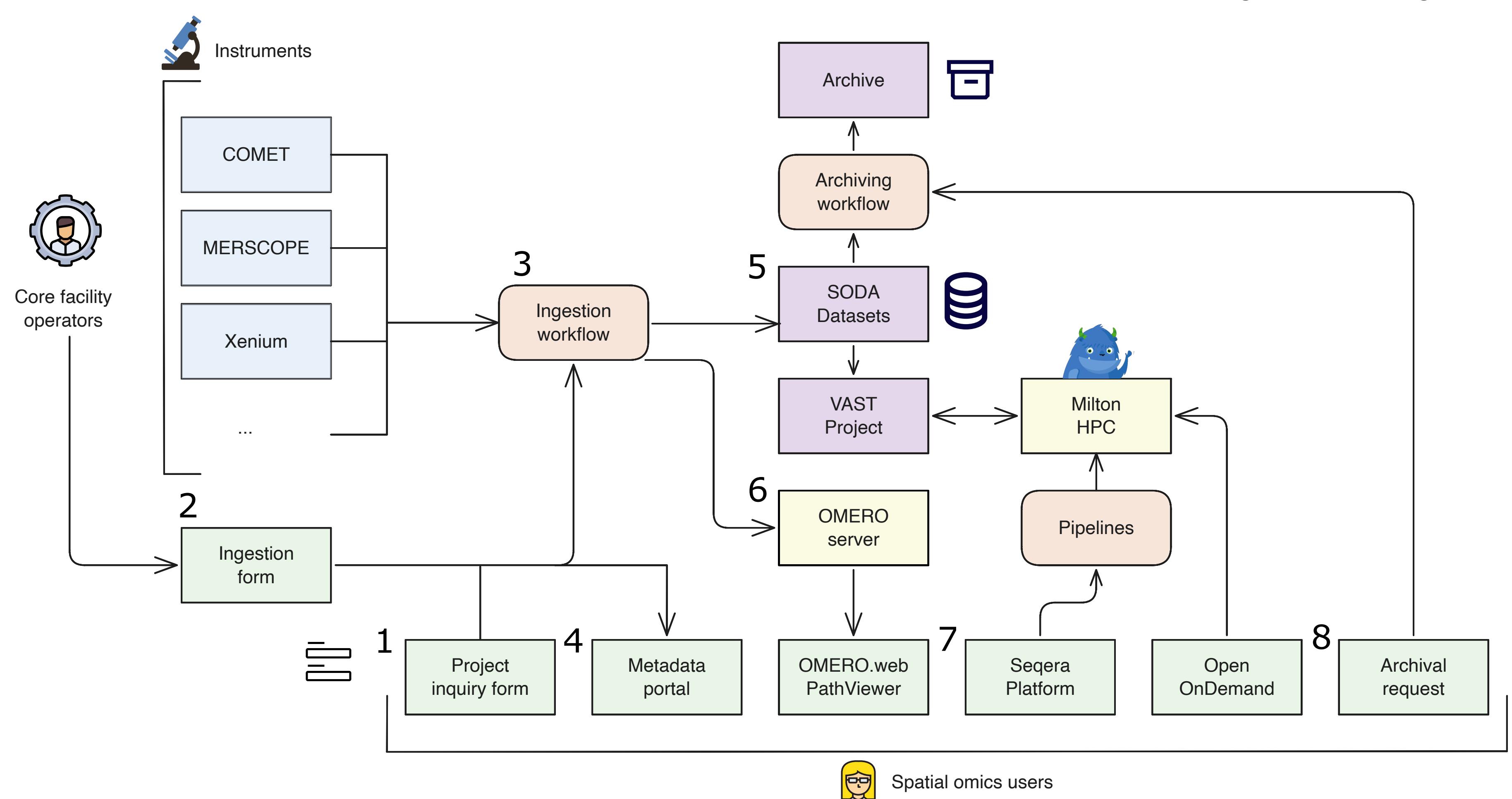
Segmentation pipeline for spatial proteomics

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



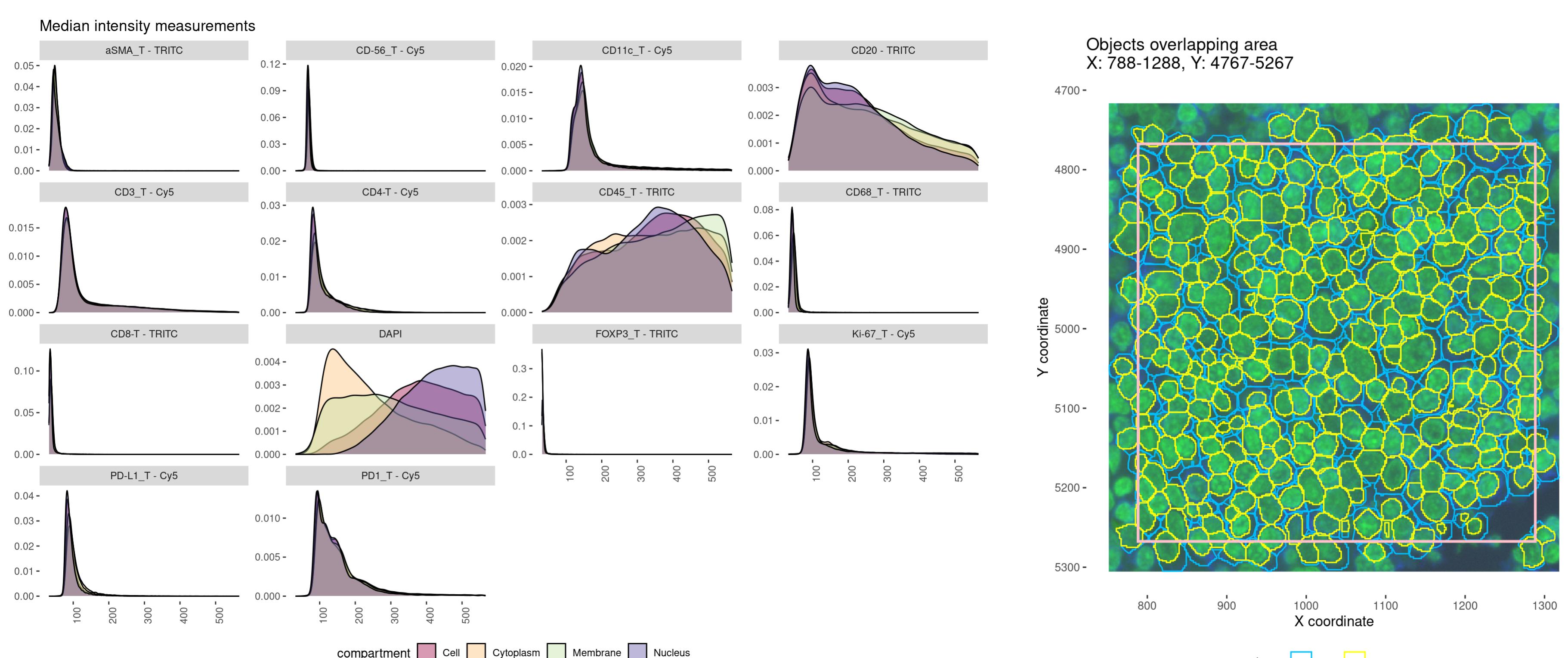
SODA Data Flows

1. Spatial projects are captured in an inquiry form on Monday.com.
2. Core facility operator runs experiment on instrument and submits ingestion form.
3. Ingestion workflow triggers, transferring run to staging area and performing preprocessing.
4. User verifies metadata via metadata portal.
5. Data and metadata are moved into data repository, accessible via VAST projects.
6. Images are imported in-place to OMERO server, accessible via OMERO.web/PathViewer.
7. Pipelines can be run via Seqera Platform on the local HPC. Data can be visualised on VMs using Open OnDemand.
8. 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.

