



VoltRon: A Spatial Omics Analysis Platform for Multi-Resolution and Multi-omics Integration using Image Registration

Spatial omic technologies necessitate computational tools capable of storing and analyzing spatial omics datasets with multiple modalities and microscopy images. Image analysis is also becoming an integral part of spatial omics, and there is still a need for tools that process and analyze images of microanatomical tissue structures as well as those that incorporate these images to integrate samples and associated spatial omics datasets, e.g. image alignment.

To this end, we have developed VoltRon, a novel platform for end-to-end spatial omics analysis with comprehensive image processing capabilities and a novel spatial data framework that supports a large selection of spatial omics modalities. To connect and integrate spatial multi-omics profiles across tissue slides and sections, VoltRon incorporates scalable image registration workflows for automated synchronization of spatial coordinates and microscopy images. The registration workflow is wrapped in an easy-to-use Shiny application that allows users to manipulate and align images via human-interpretable parameters.

We show that VoltRon's registration workflow outperforms existing alignment algorithms across tasks including both adjacent/serial tissue sections as well as images captured from the same tissue section. VoltRon also offers an end-to-end analysis suite for a large collection of spatial omic datasets; including spots, cells, and molecules as well as regions of interest (ROIs) and even image tiles/pixels that are often ignored in currently available spatial omics analysis platforms.

We demonstrate VoltRon's image registration and data integration capabilities using multiple examples and specifically by aligning annotated histology images of COVID-19 infected lung tissue onto Xenium in situ captured extracellular SARS-CoV-2 viral RNAs to reveal niche specific information on viral activity. VoltRon is implemented in the R programming language (<https://github.com/BIMSBbioinfo/VoltRon>) and more information on VoltRon framework can be found on <https://bioinformatics.mdc-berlin.de/VoltRon>.

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Session Classification: Cross-disciplinary Data Integration