

## SpatialData: a FAIR framework for spatial omics data in Python

Spatial omics technologies entail a diverse set of techniques to measure molecular variation in tissue. Current infrastructure and analysis frameworks lack support for the large diversity of spatial omics data. Here, we introduce SpatialData, a novel data representation for processing and visualizing large, multi-modal and multi-resolution spatial omics data. SpatialData builds upon established formats such as AnnData[1] and MuData[2], and OME-NGFF[3], a state-of-the-art data format for bioimage analysis, to provide performant storage and analysis of spatial omics data. We also introduce *napari-spatialdata*, a napari plugin[4] for interactive visualization of spatial multi-modal data. SpatialData is tightly embedded in the scverse[5] ecosystem, and aims at building a bridge between the single cell analysis and the imaging community of the python scientific computing ecosystem. SpatialData seamlessly integrates with existing tools yet opens new avenues for data analysis and method development. We showcase how SpatialData can be used to integrate different modalities and measurements in spatial omics data, its scalable capabilities and how existing tools can be used to gain new insights from efficient representation of spatial multi-modal data.

### References

1. [Virshup I et al. bioRxiv. 2021](#)
2. [Bredikhin D et al. Genome Biol. 42, 2022](#)
3. [Moore J et al. Nat Methods. 18, 2021](#)
4. [Sofroniew N napari/napari: 0.4.4rc0. 2021](#)
5. [scverse. https://scverse.org/](https://scverse.org/)