

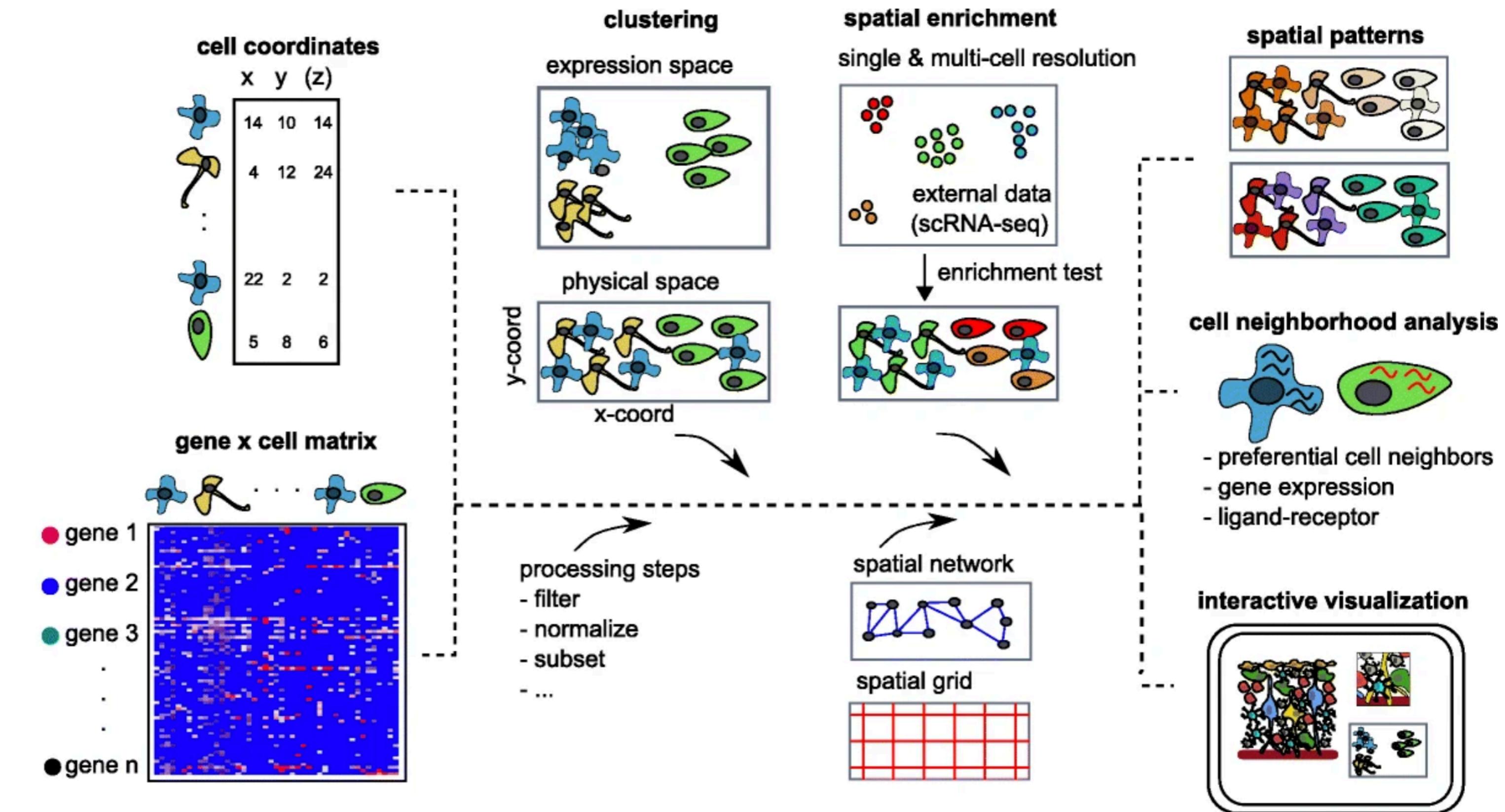
Giotto Suite

Spatial Omics Workshop

Introduction to the Giotto Framework



The Giotto package

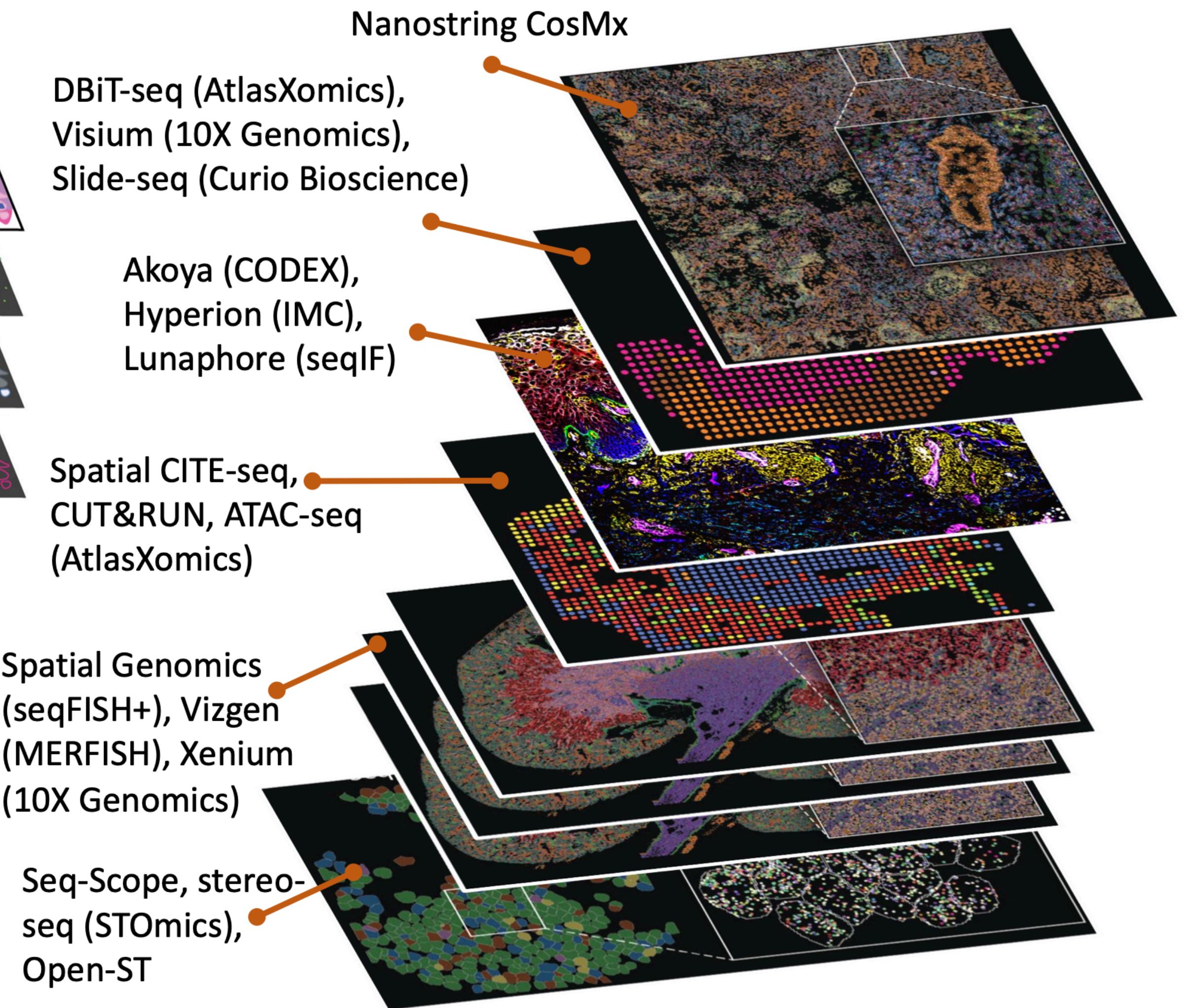
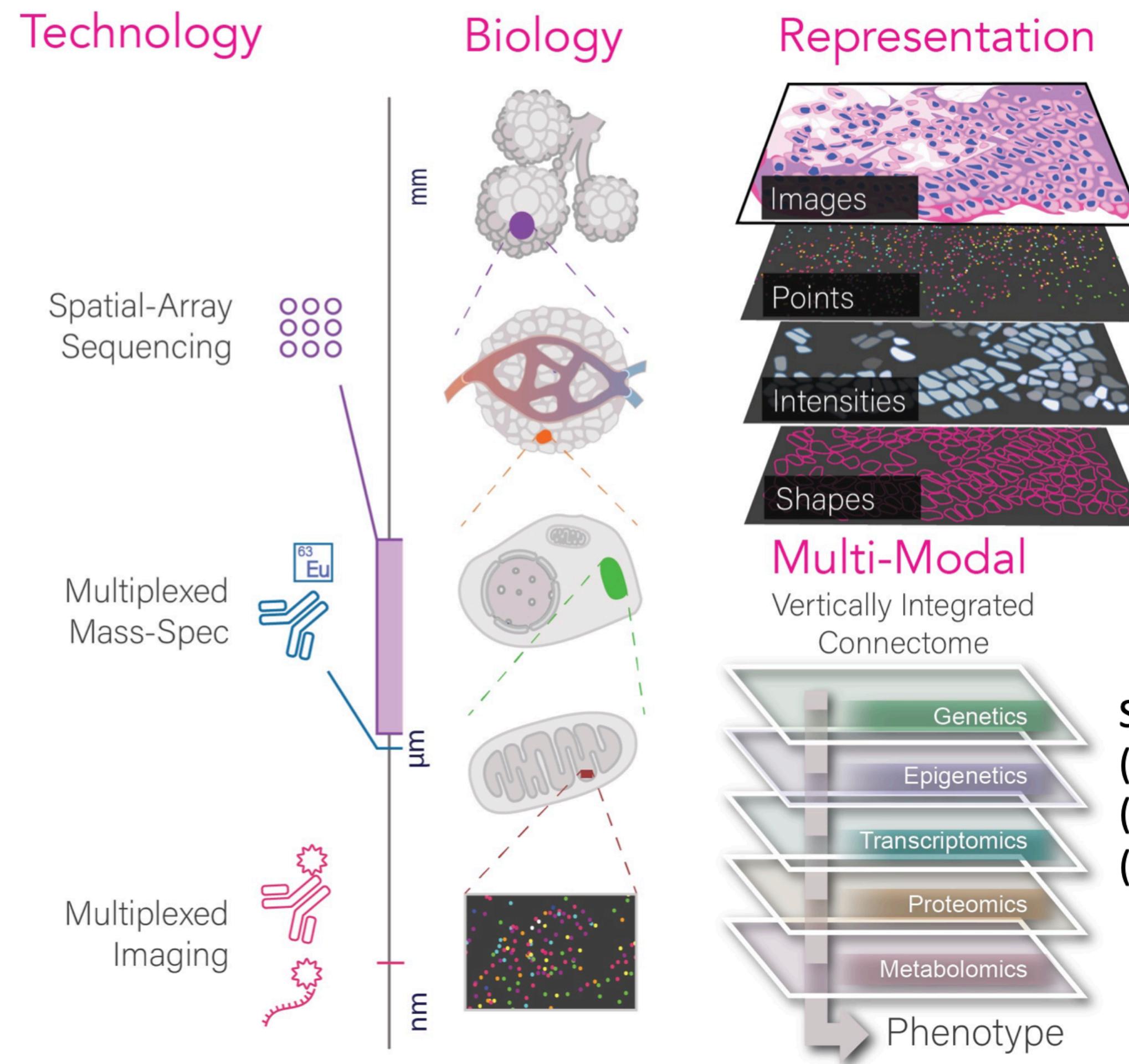


<https://github.com/drieslab/Giotto>

<https://spatialgiotto.com>

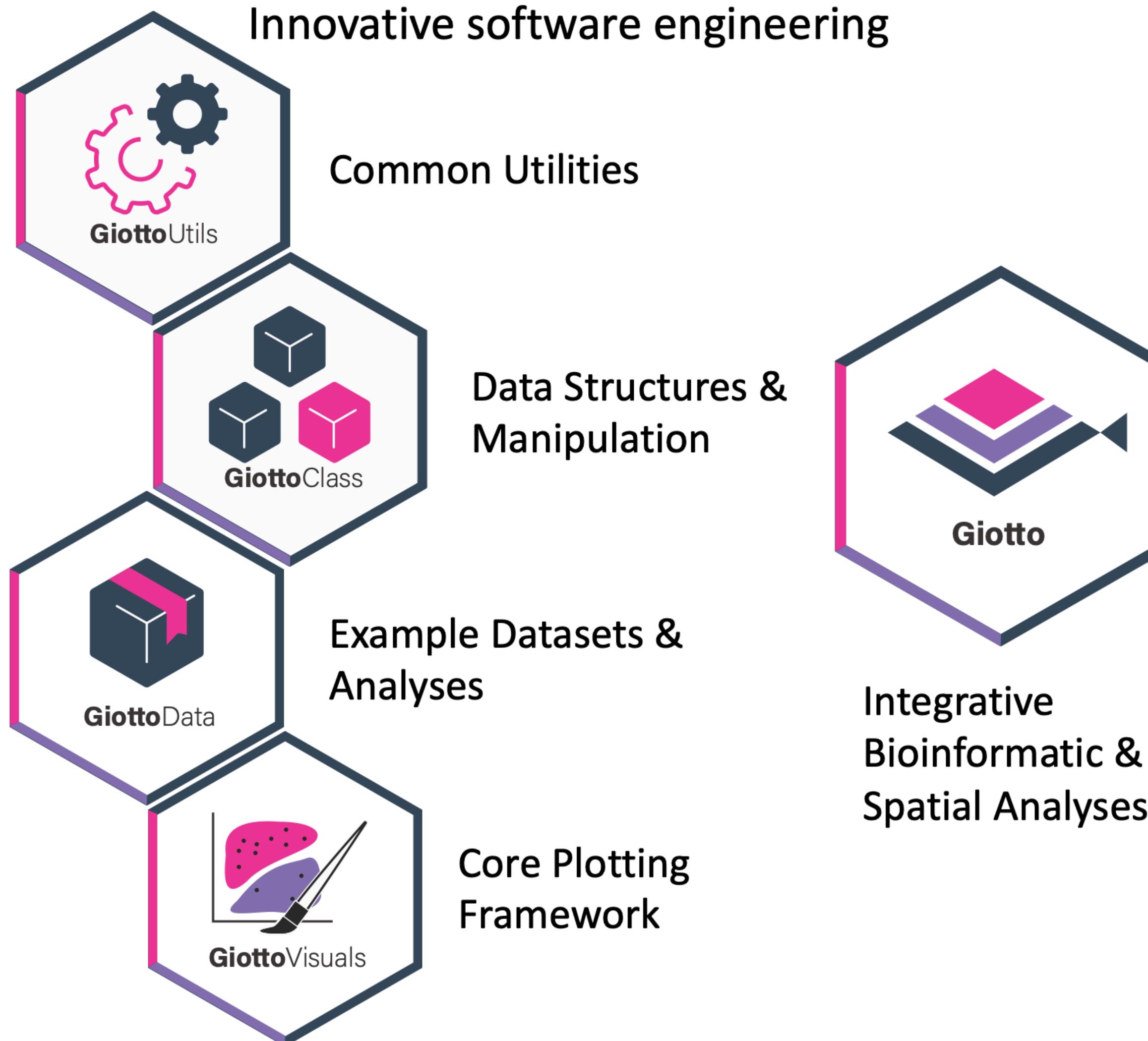
Dries, et al. 2021; Del Rossi, et al. 2022

Spatial omics biology can be measured in many ways

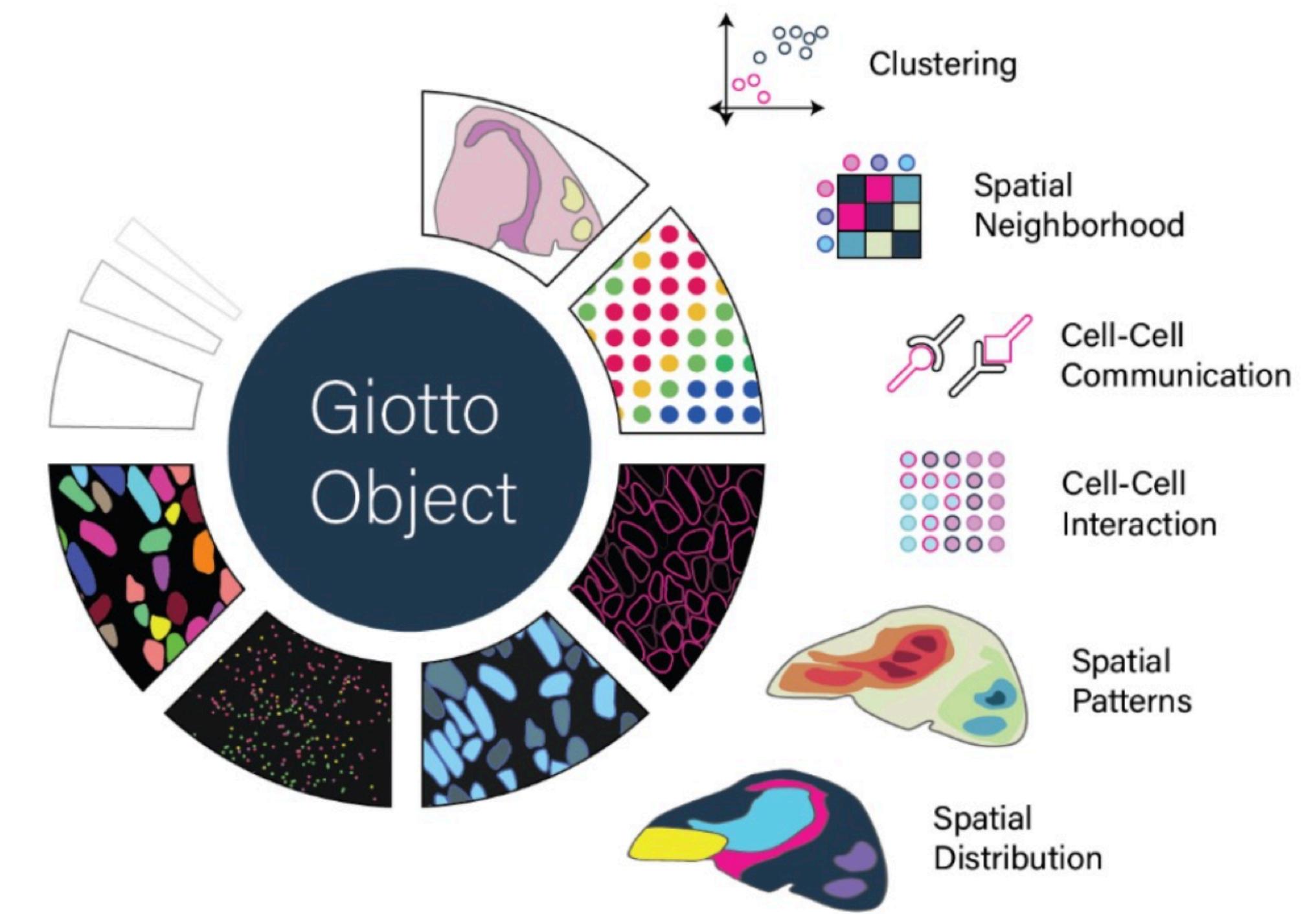


**How can we make complex spatial data analysis
easy?**

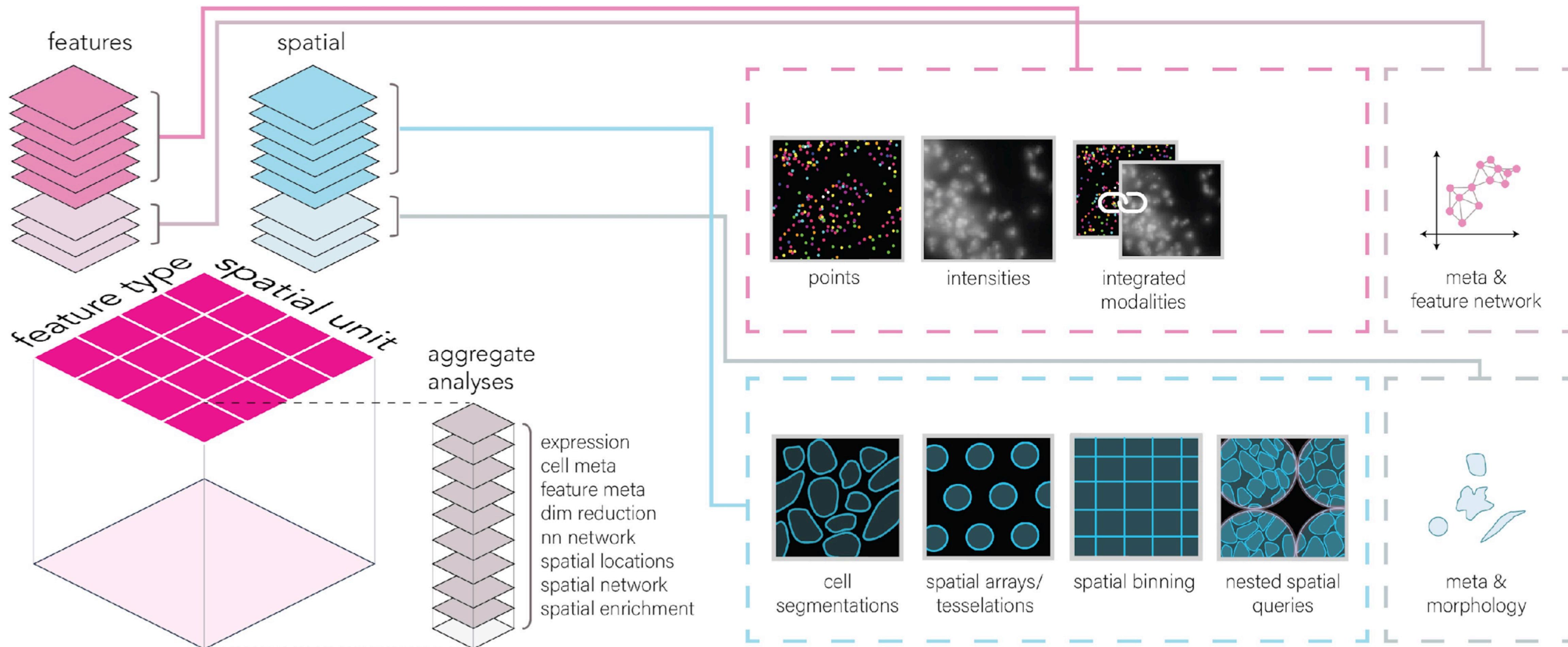
Giotto Suite



Flexible and scalable spatial data analysis

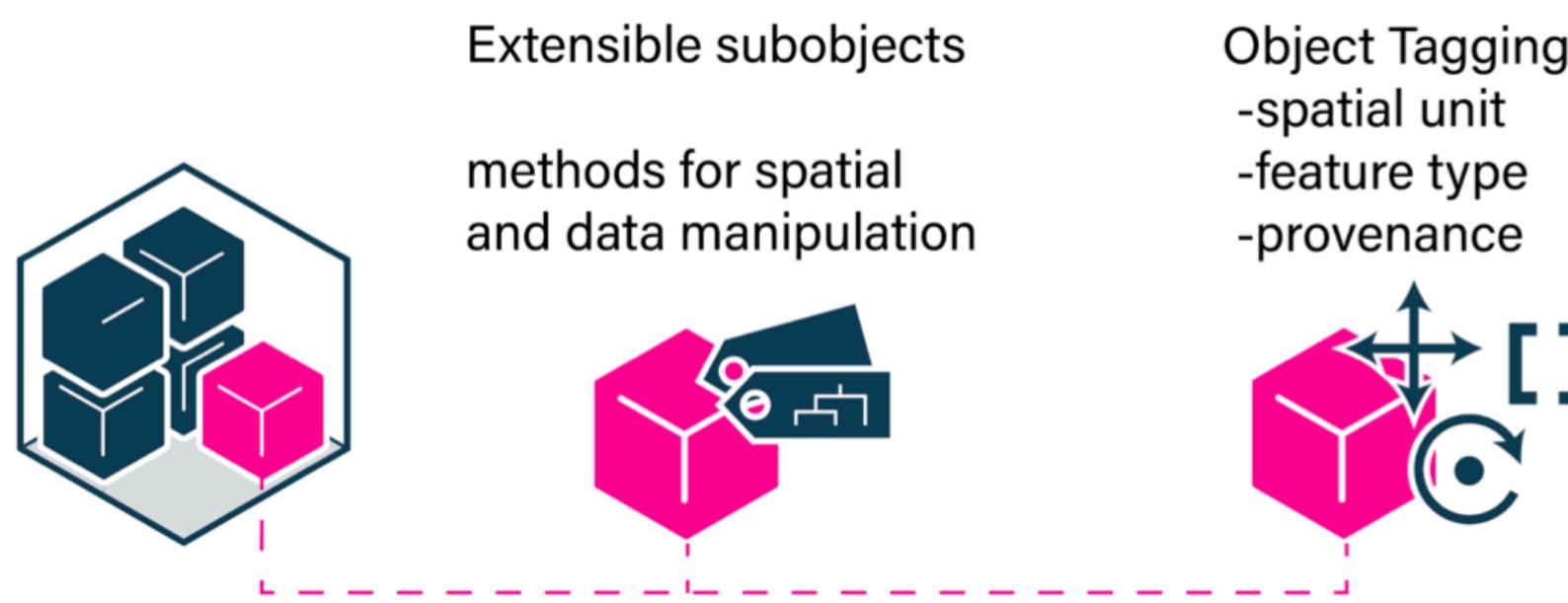


Representation of data at multiple scales

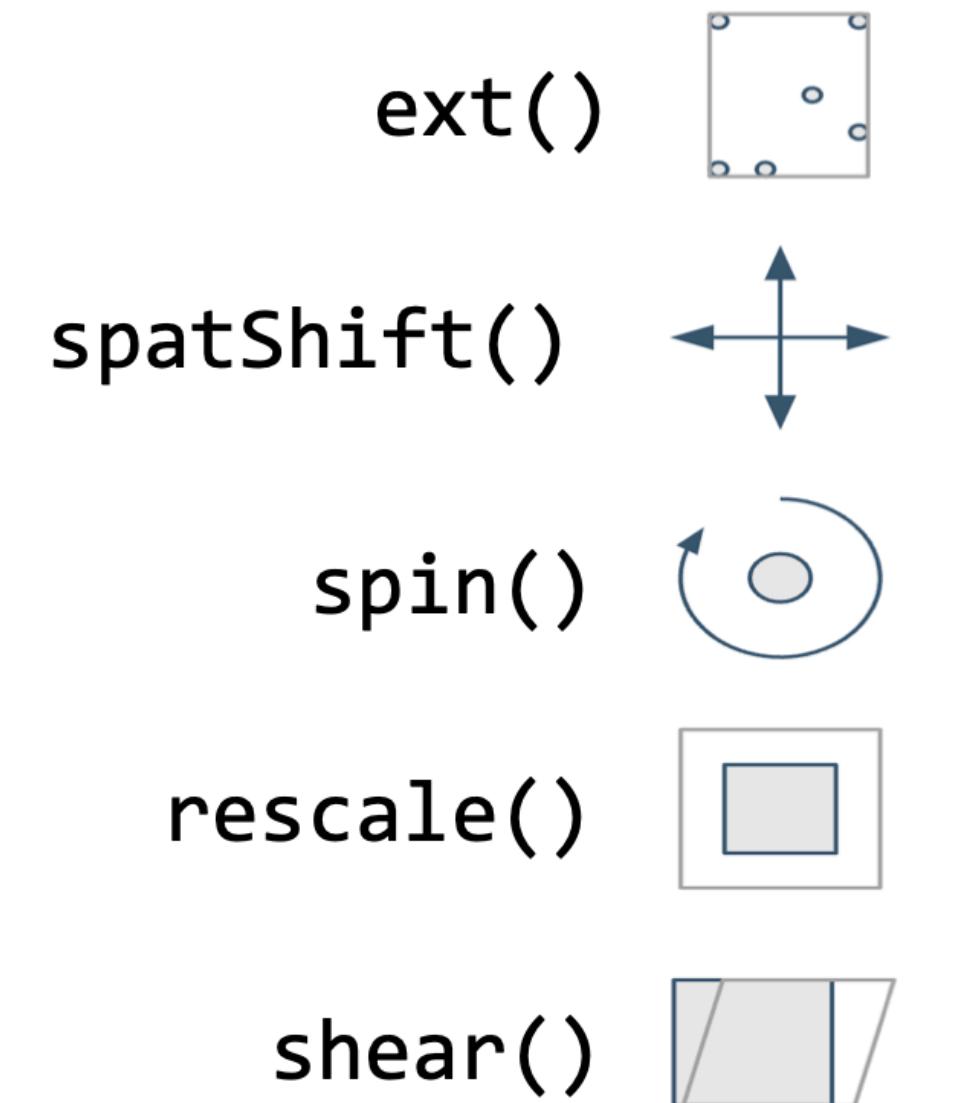
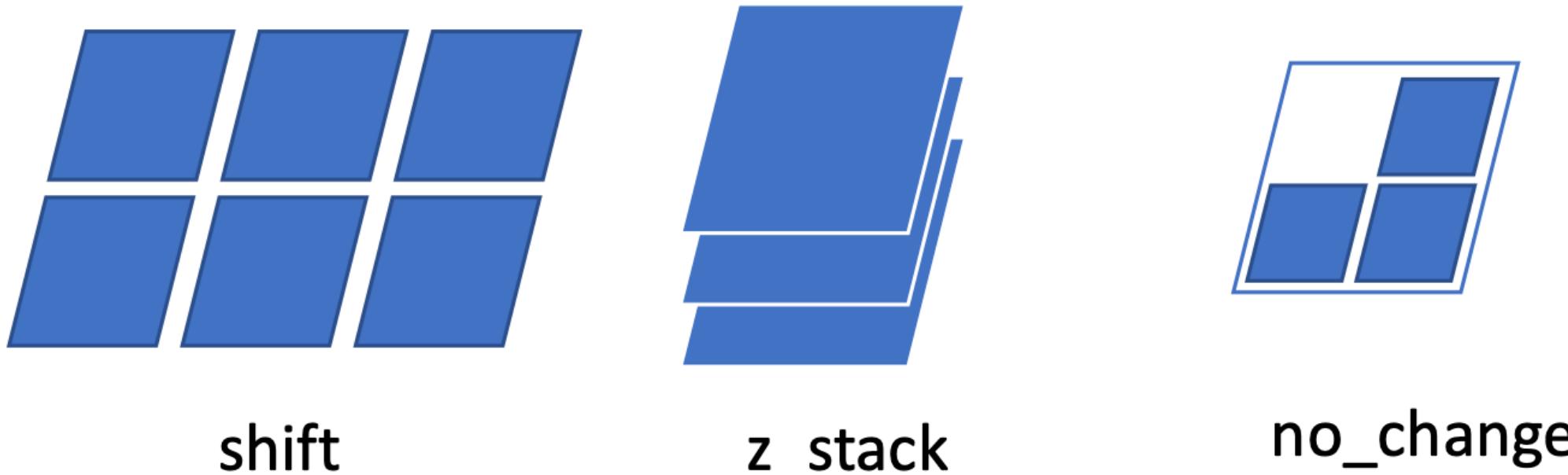


Flexible data structures and spatial operations

Dedicated Subobject Classes



Joining spatial objects



Spatial data wrangling

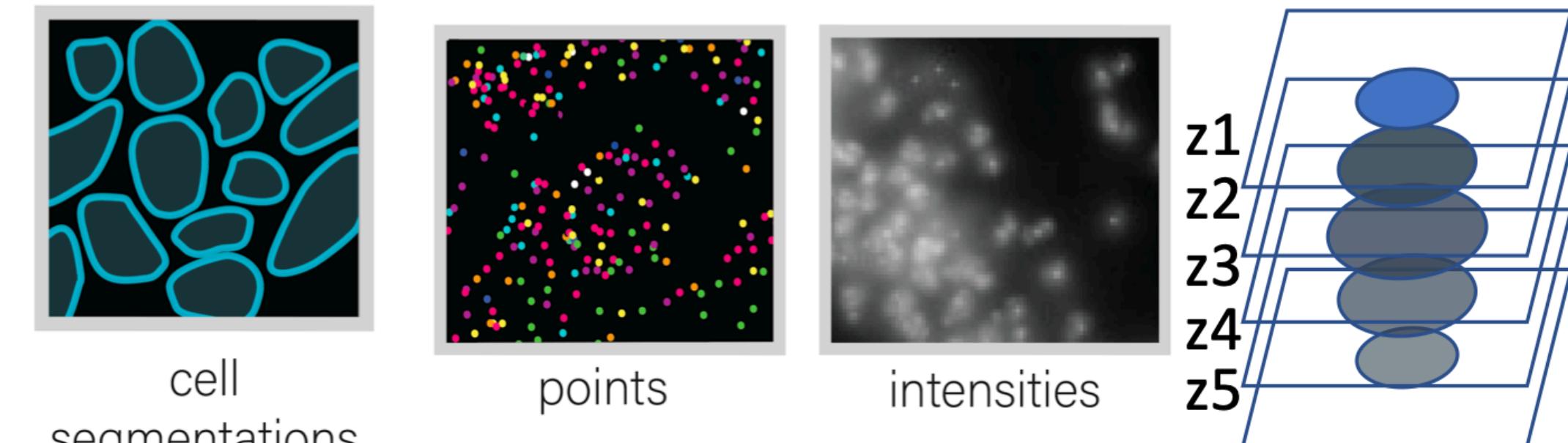
decomp_affine()

```
<affine_decomp>
rotate   : -0.165148677414627
shear    : c("0.016260162601626", "0")
scale    : c("2.02210754385589", "3.04138126514911")
translate: c("1000", "20")
```

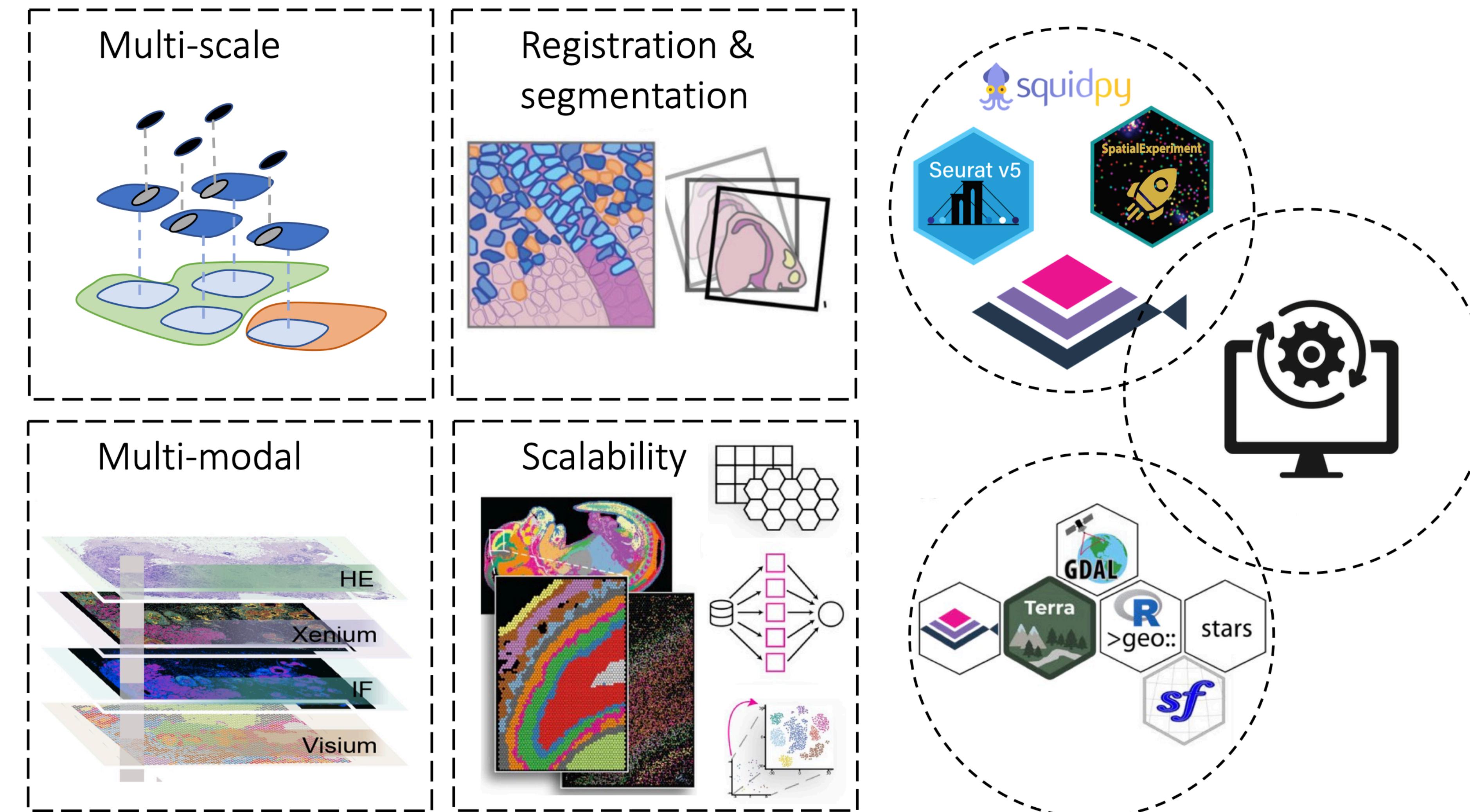
affine()

[,1]	[,2]	[,3]
[1,]	2.0	0.5 1000
[2,]	-0.3	3.0 20
[3,]	100.0	29.0 1

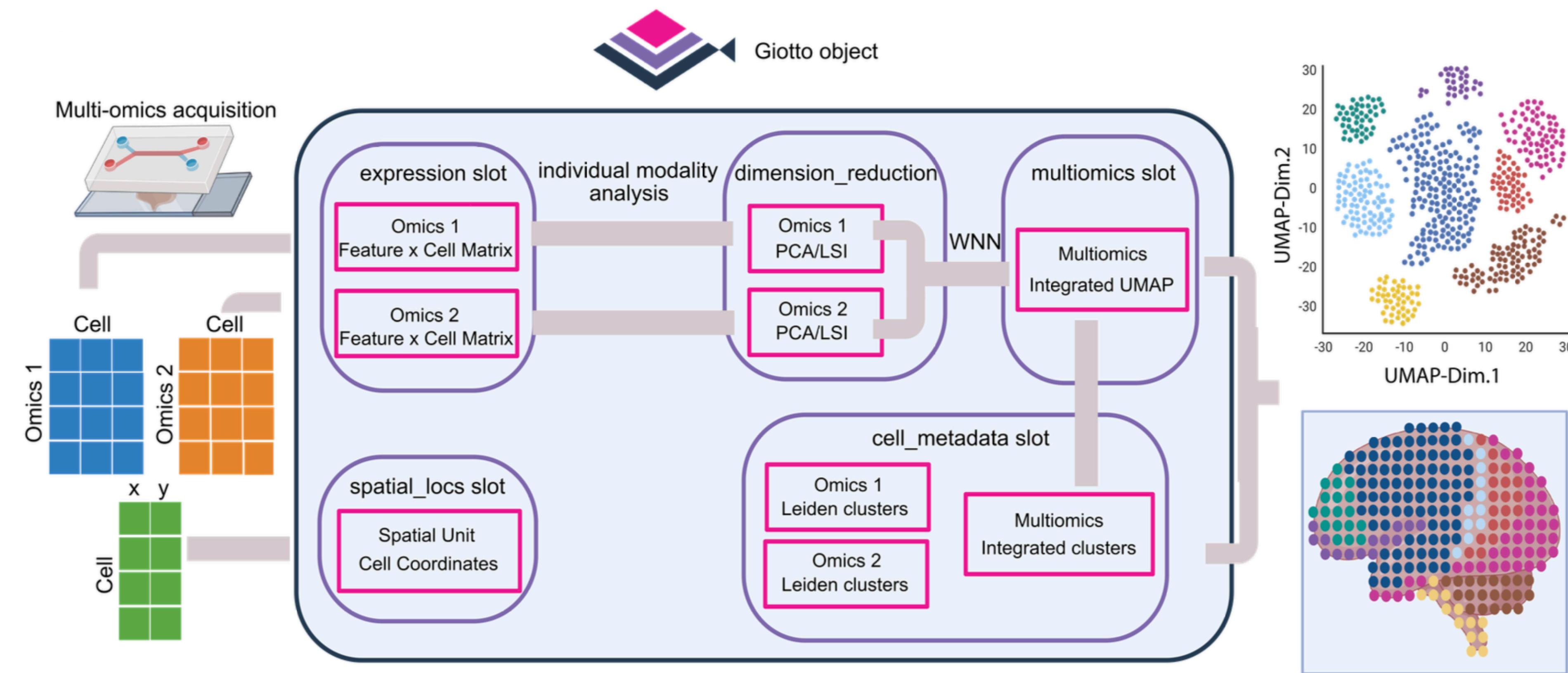
Spatial data aggregation



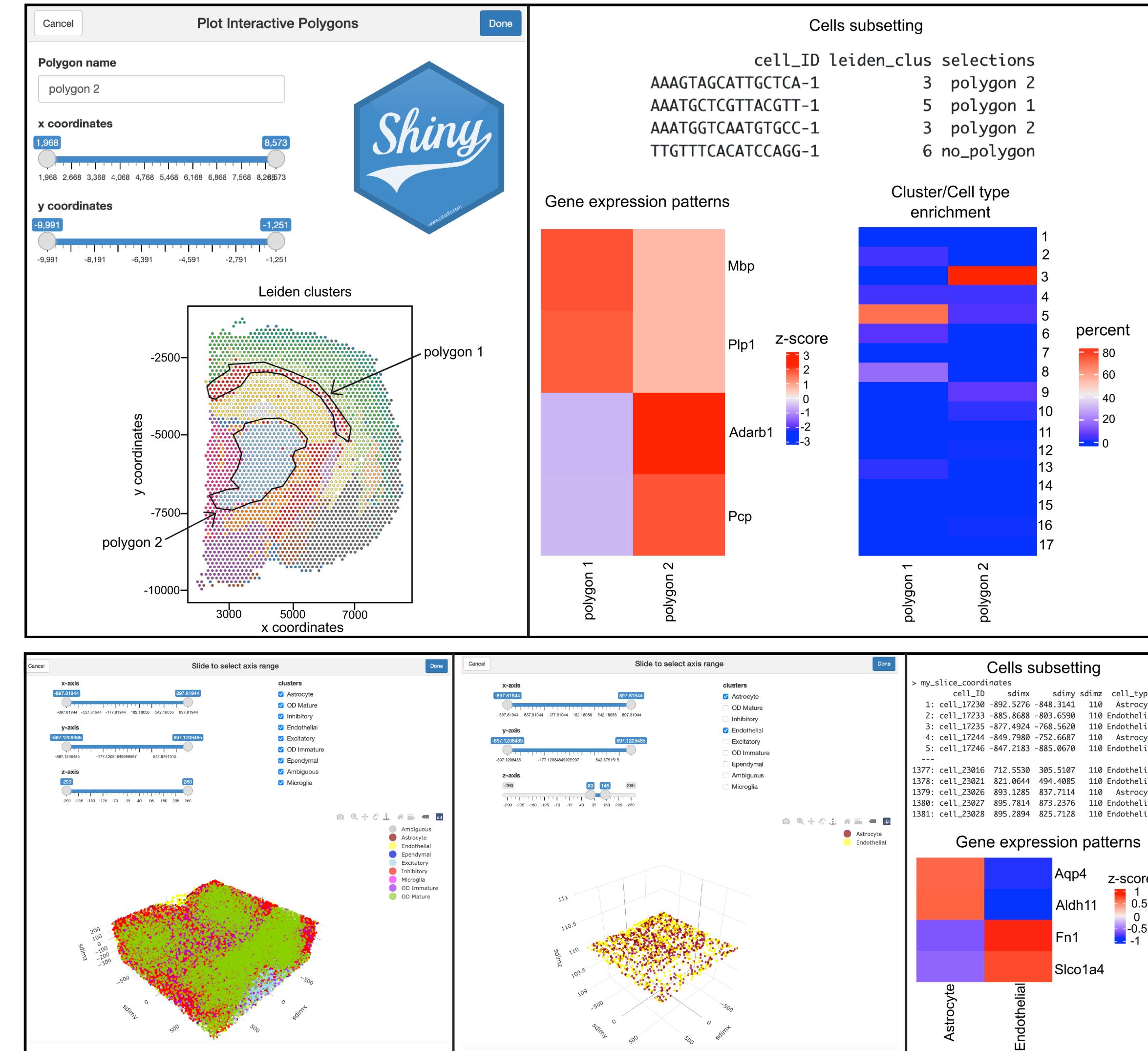
Main features of Giotto Suite



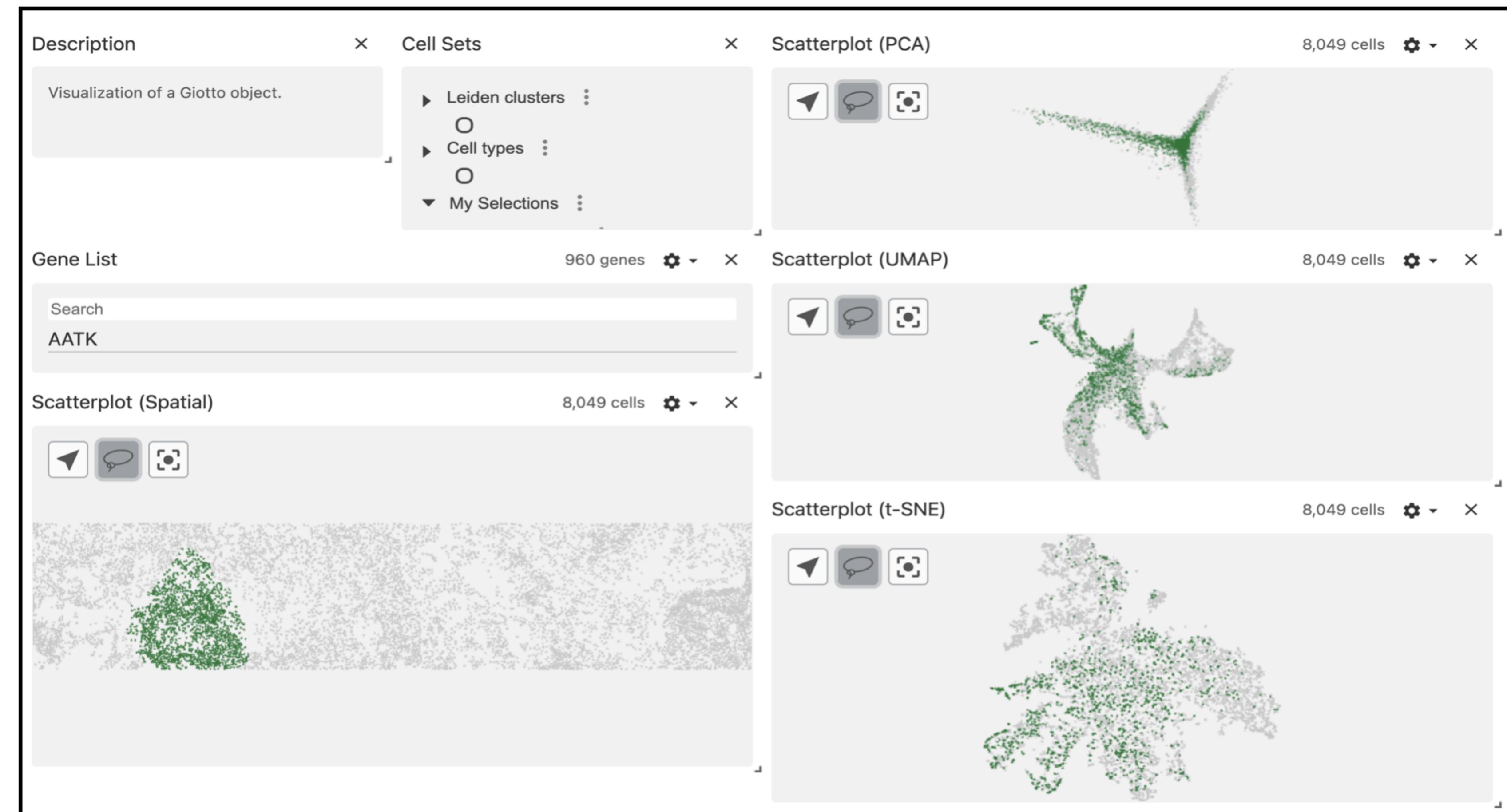
Multi-omics integration



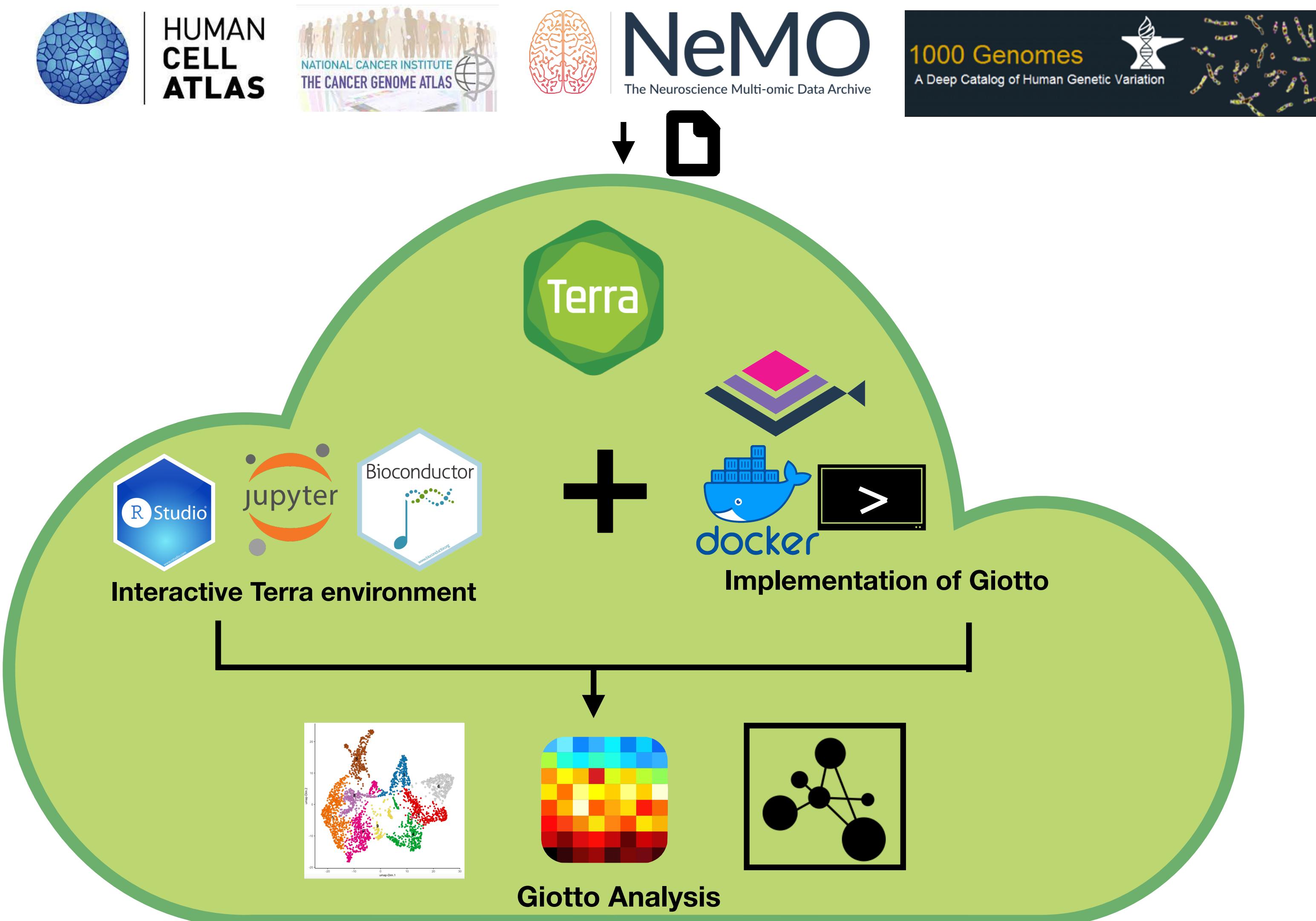
Interactive selection



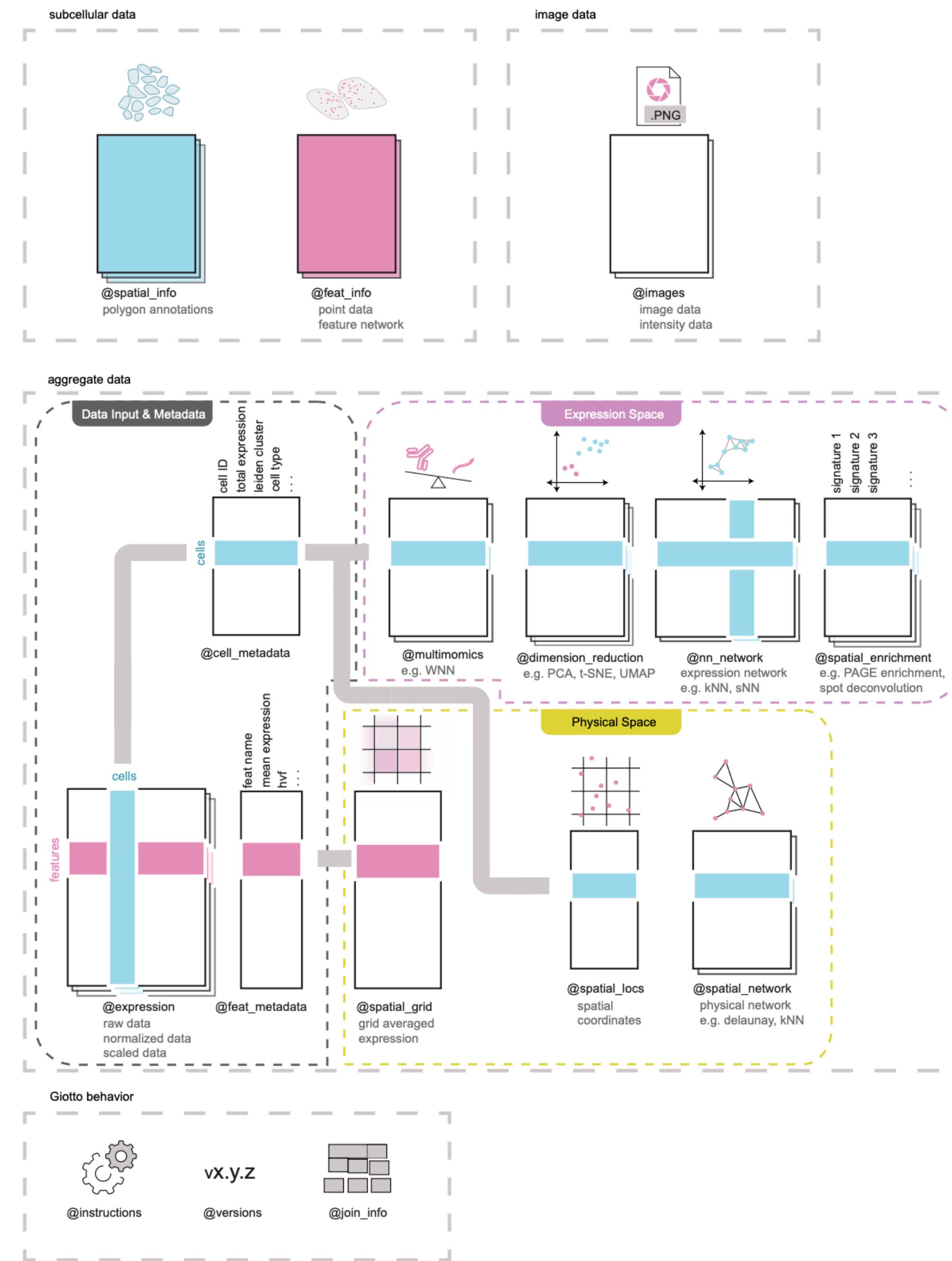
Integration with vitessceR for large datasets



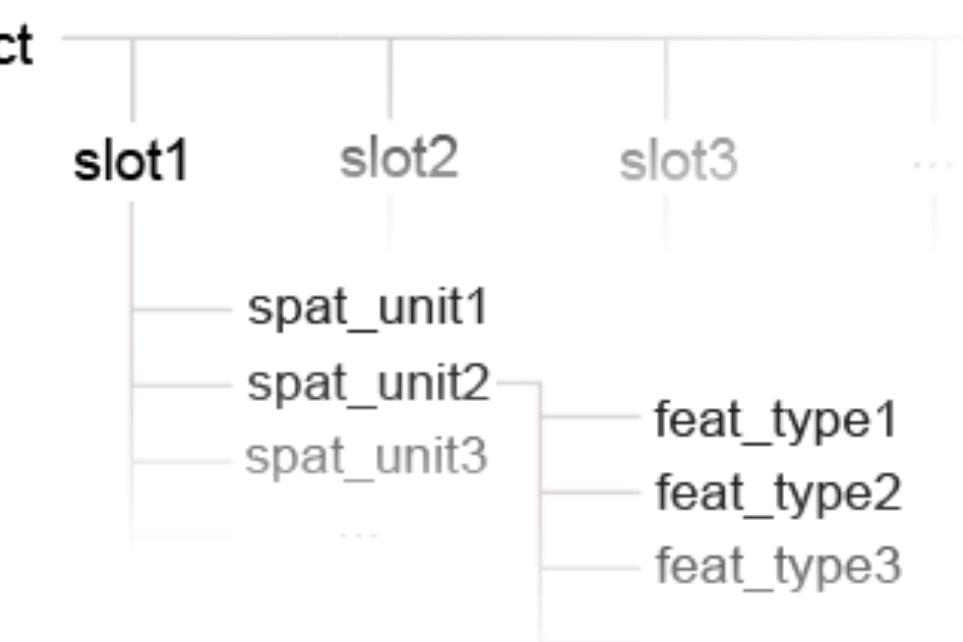
Running Giotto in the Cloud



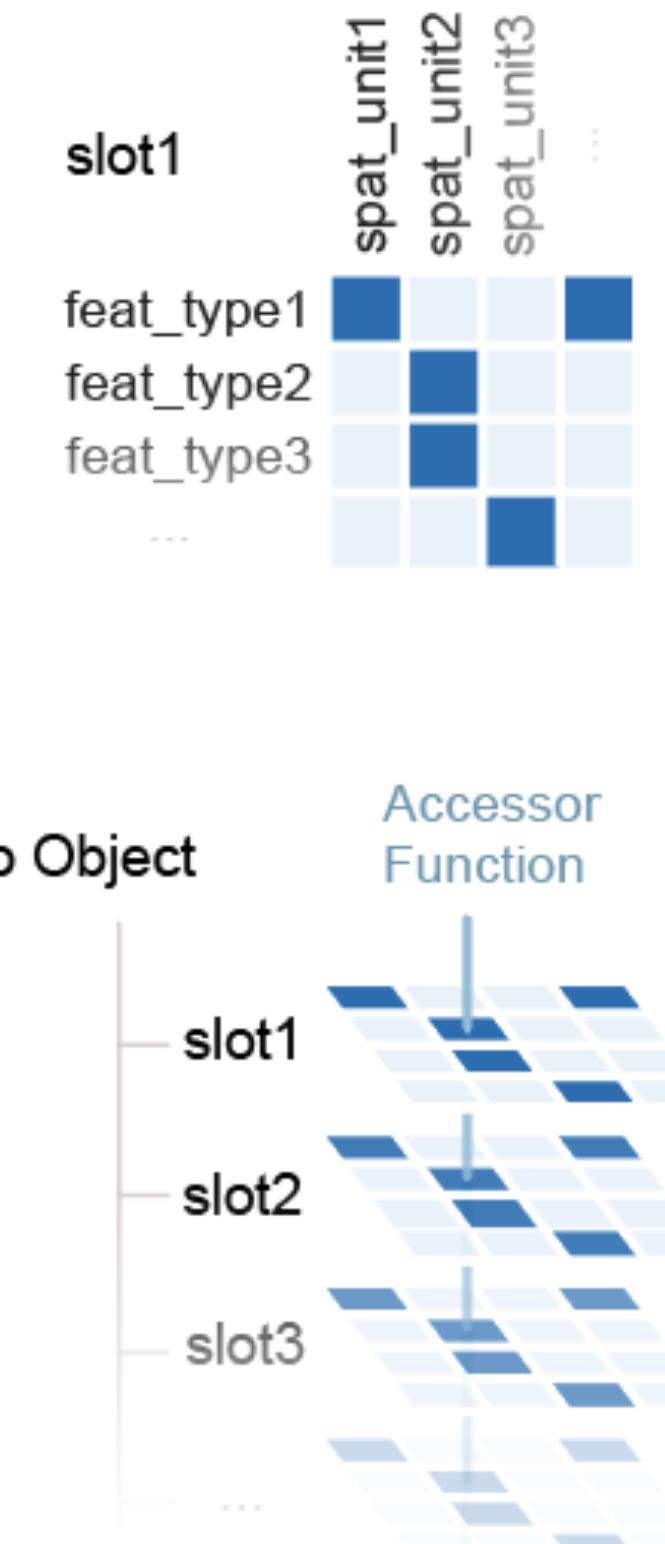
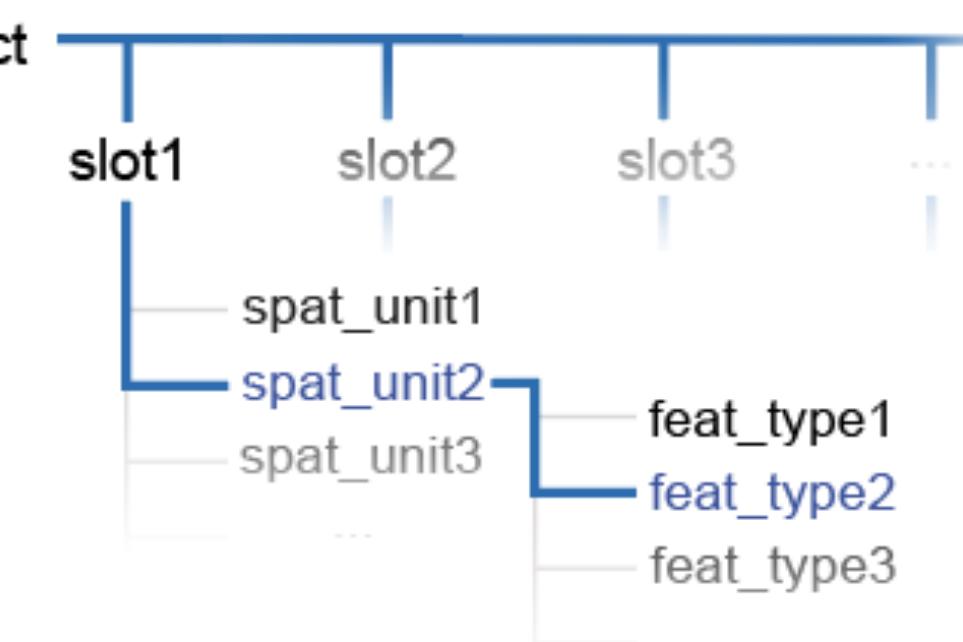
The Giotto object



Giotto Object



Giotto Object



Accessing the Giotto object information

Slot	Nested	Example	Internal Accessors
@expression	spat_unit - feat_type - name	cell - rna - raw	getExpression() setExpression()
-----	-----	-----	-----
@cell_metadata	spat_unit - feat_type	cell - rna	getCellMetadata() setCellMetadata()
-----	-----	-----	-----
@feat_metadata	spat_unit - feat_type	cell - rna	getFeatMetadata() setFeatMetadata()
-----	-----	-----	-----

Slot	Nested	Example	Internal Accessors
@spatial_grid	spat_unit - name	grid- grid	getSpatialGrid() setSpatialGrid()
	-----	-----	-----
@dimension_reduction	approach - spat_unit - feat_type - method - name	cells - cell - rna - pca - pca	getDimReduction() setDimReduction()
	-----	-----	-----
@multiomics	spat_unit - feat_type - method - name	cell - rna-protein - WNN - theta_weighted_matrix	getMultiomics() setMultiomics()
	-----	-----	-----

Slot	Nested	Example	Internal Accessors
@nn_network	spat_unit -		getNearestNetwork()
	method -	cell - sNN - sNN_results1	setNearestNetwork()
	name		
-----	-----	-----	-----
@spatial_enrichment	spat_unit -		getSpatialEnrichment()
	feat_type -	cell - rna - results1	setSpatialEnrichment()
	name		
-----	-----	-----	-----
@spatial_info	spat_unit	cell	getPolygonInfo()
			setPolygonInfo()
-----	-----	-----	-----
@spatial_locs	spat_unit -	cell - raw	getSpatialLocations()
	name		setSpatialLocations()
-----	-----	-----	-----

Slot	Nested	Example	Internal Accessors
@spatial_network	spat_unit -	cell - Delaunay_network1	getSpatialNetwork()
	name		setSpatialNetwork()
<hr/>			
@feat_info	feat_type	rna	getFeatureInfo()
			setFeatureInfo()
<hr/>			
@images	name	image	getGiottolImage()
			setGiottolImage()
<hr/>			
@largeImages	name	image	getGiottolImage()
			setGiottolImage()
<hr/>			
@instructions			instructions()

Giotto Suite website

Giotto 4.2.1

Get started ▾

Documentation

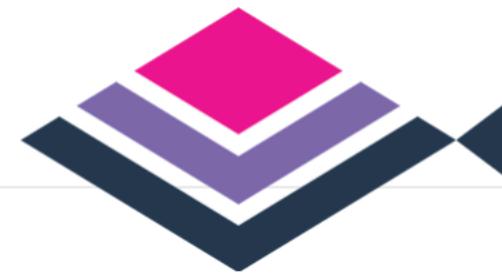
Examples ▾

Tutorials ▾

News ▾

Contributing ▾

Giotto Suite



Giotto Suite is a major upgrade to the Giotto package that provides tools to process, analyze and visualize **spatial multi-omics data at all scales and multiple resolutions**. The underlying framework is generalizable to virtually all current and emerging spatial technologies. Our Giotto Suite prototype pipeline is generally applicable on various different datasets, such as those created by state-of-the-art spatial technologies, including *in situ* hybridization, sequencing, and imaging-based multiplexing/proteomics. These technologies differ in terms of resolution (subcellular, single cell or multiple cells), spatial dimension (2D vs 3D), molecular modality (protein, RNA, DNA, ...), and throughput (number of cells and analytes).

Installation

Local installation

To install Giotto suite, please see our [installation page](#)

Visit the Giotto [Discussions](#) page for more information.

Containers

If you prefer to skip the installation process, check the tutorials for using Giotto Suite with our [Docker](#) and [Singularity](#) containers.

Website Updates

Location change

This website (<http://giottosuite.com>) is for Giotto Suite v4.0 and greater. You can still find the previous website at <https://giottosuite.readthedocs.io/en/latest/> (defunct)

<http://giottosuite.com>

Links

[Browse source code](#)

[Report a bug](#)

License

[Full license](#)

[MIT + file LICENSE](#)

Community

[Contributing guide](#)

[Code of conduct](#)

Citation

[Citing Giotto](#)

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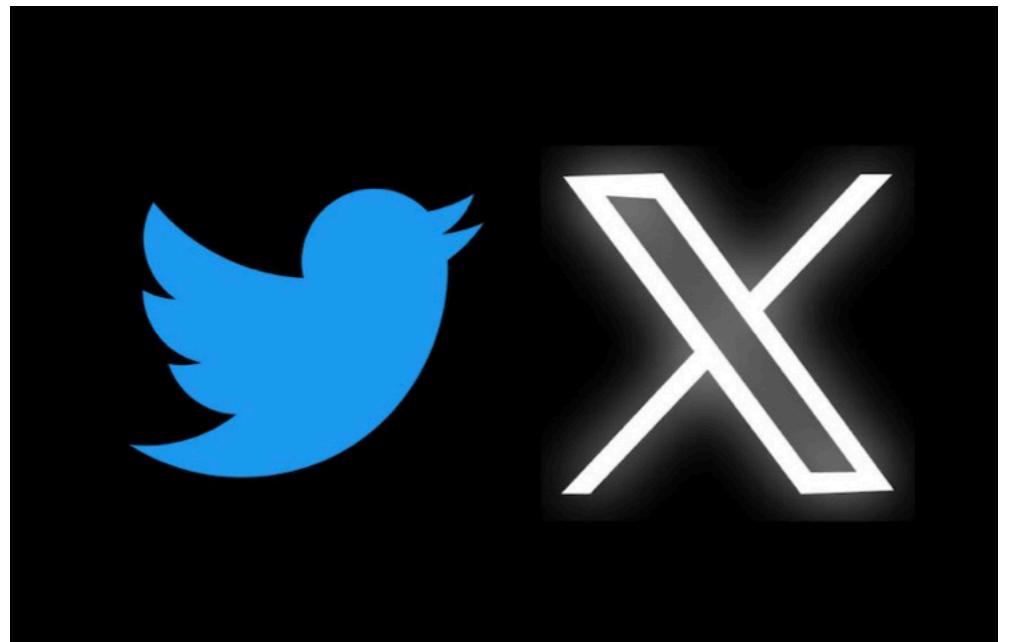
Author

Contributions

Interested to:

- Contribute to Giotto?
- Add your tool to Giotto?
- Collaborate?

Reach out to rdries@bu.edu



@GiottoSpatial

@RnDries

Acknowledgments



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EXCEPTIONAL CARE. WITHOUT EXCEPTION.

