



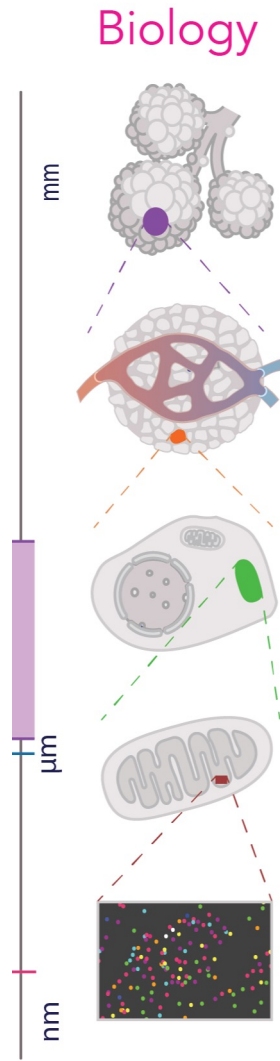
CELEBRATING 10 YEARS OF  
THE PREPRINT SERVER FOR BIOLOGY

## **Giotto Suite: a multi-scale and technology-agnostic spatial multi-omics analysis ecosystem**

Jiaji George Chen, Joselyn Cristina Chávez-Fuentes, Matthew O'Brien, Junxiang Xu, Edward Ruiz, Wen Wang, Iqra Amin, Irzam Sarfraz, Pratishta Guckhool, Adriana Sistig, Guo-Cheng Yuan,  Ruben Dries

**doi:** <https://doi.org/10.1101/2023.11.26.568752>

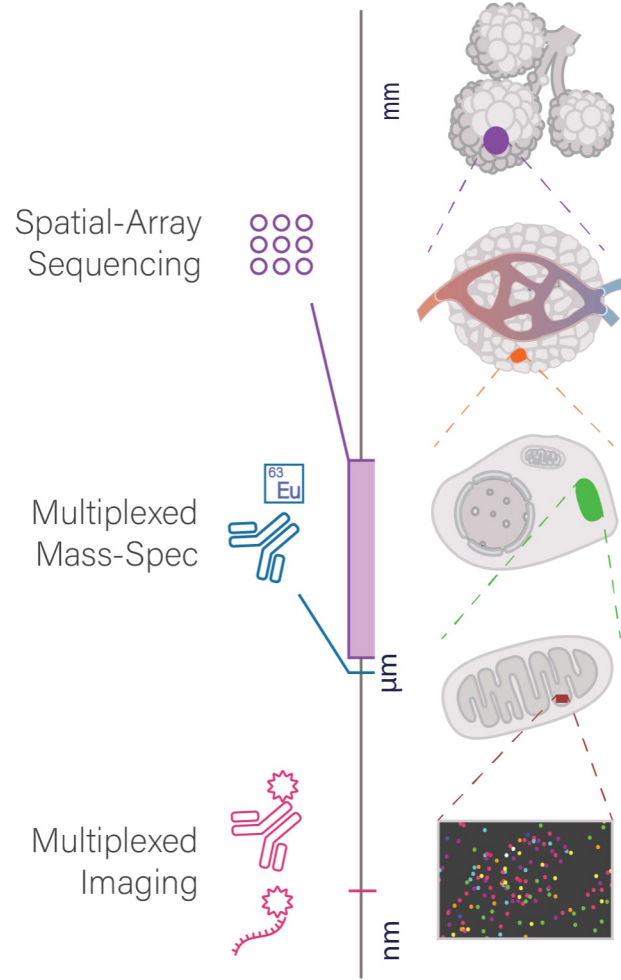
# Spatial omics biology happens at multiple scales



# Spatial omics biology happens at multiple scales

Technology

Biology



# Spatial omics biology happens at multiple scales

## Technology

Spatial-Array Sequencing



Multiplexed Mass-Spec

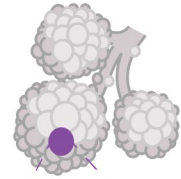


Multiplexed Imaging

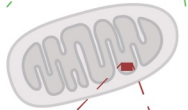
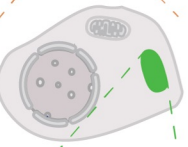
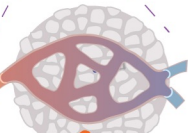


## Biology

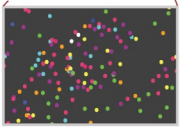
mm



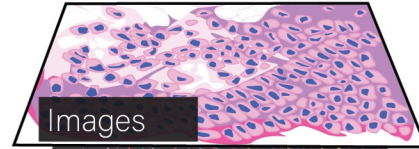
$\mu\text{m}$



nm



## Representation



# Spatial omics biology happens at multiple scales

## Technology

Spatial-Array Sequencing



Multiplexed Mass-Spec

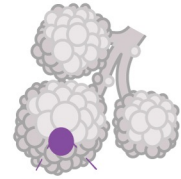


Multiplexed Imaging

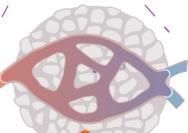


## Biology

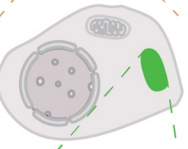
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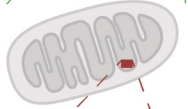
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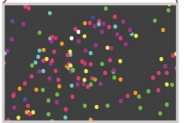
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μm

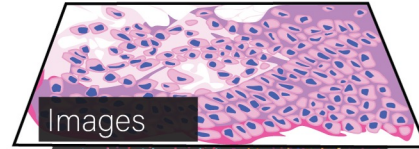


nm

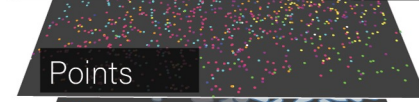


## Representation

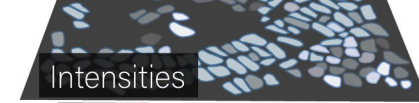
Images



Points



Intensities



Shapes



## Multi-Modal

Vertically Integrated  
Connectome

Genetics

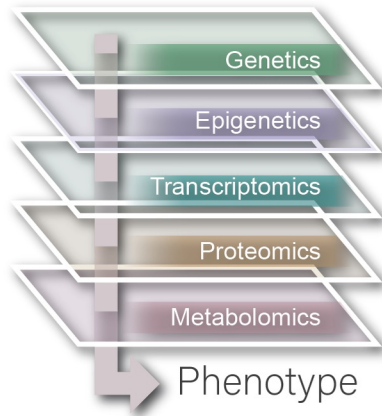
Epigenetics

Transcriptomics

Proteomics

Metabolomics

Phenotype



# Spatial omics biology can be measured in many ways

## Technology

Spatial-Array Sequencing



Multiplexed Mass-Spec



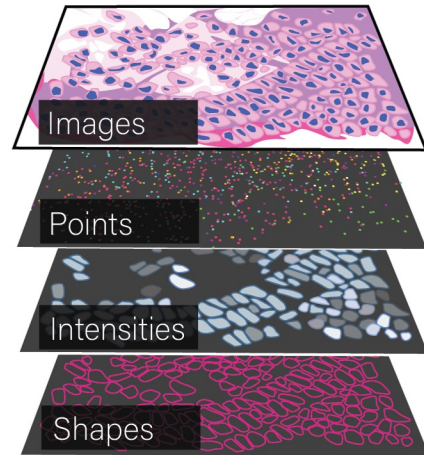
Multiplexed Imaging



## Biology

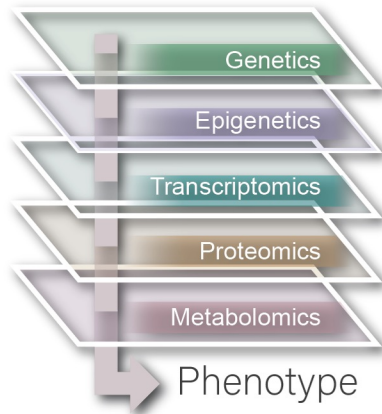


## Representation



## Multi-Modal

Vertically Integrated Connectome



DBiT-seq (AtlasXomics),  
Visium (10X Genomics),  
Slide-seq (Curio Bioscience)

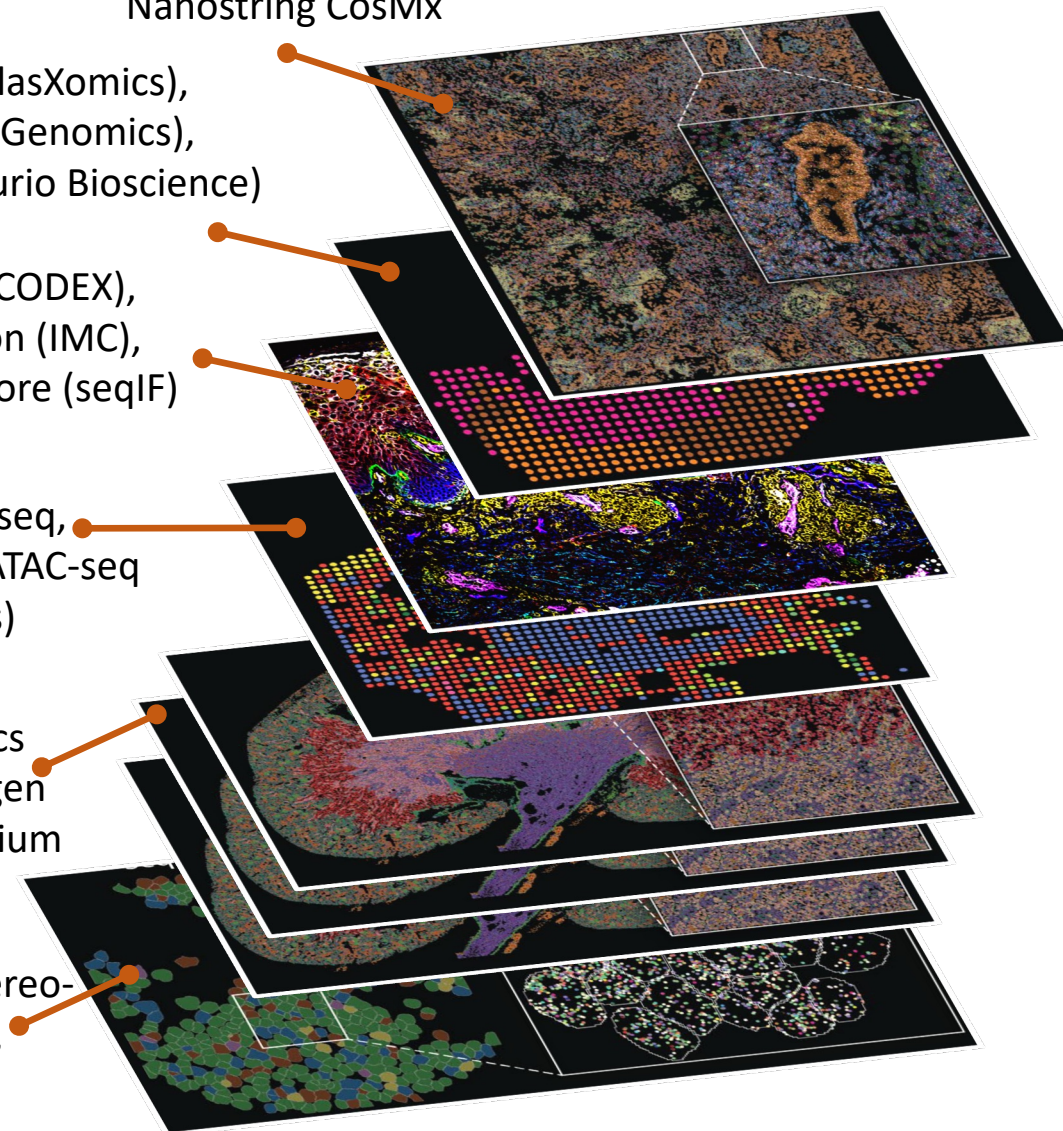
Akoya (CODEX),  
Hyperion (IMC),  
Lunaphore (seqIF)

Spatial CITE-seq,  
CUT&RUN, ATAC-seq  
(AtlasXomics)

Spatial Genomics  
(seqFISH+), Vizgen  
(MERFISH), Xenium  
(10X Genomics)

Seq-Scope, stereo-  
seq (STOmics),  
Open-ST

## Nanostring CosMx



# How can we make complex spatial data analysis easy?

<https://doi.org/10.1038/s41556-023-01286-7>

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## Bringing computation to biology by bridging the last mile

Anne E. Carpenter & Shantanu Singh

 Check for updates

# How can we make complex spatial data analysis easy?

<https://doi.org/10.1038/s41556-023-01286-7>

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## Bringing computation to biology by bridging the last mile

Anne E. Carpenter & Shantanu Singh

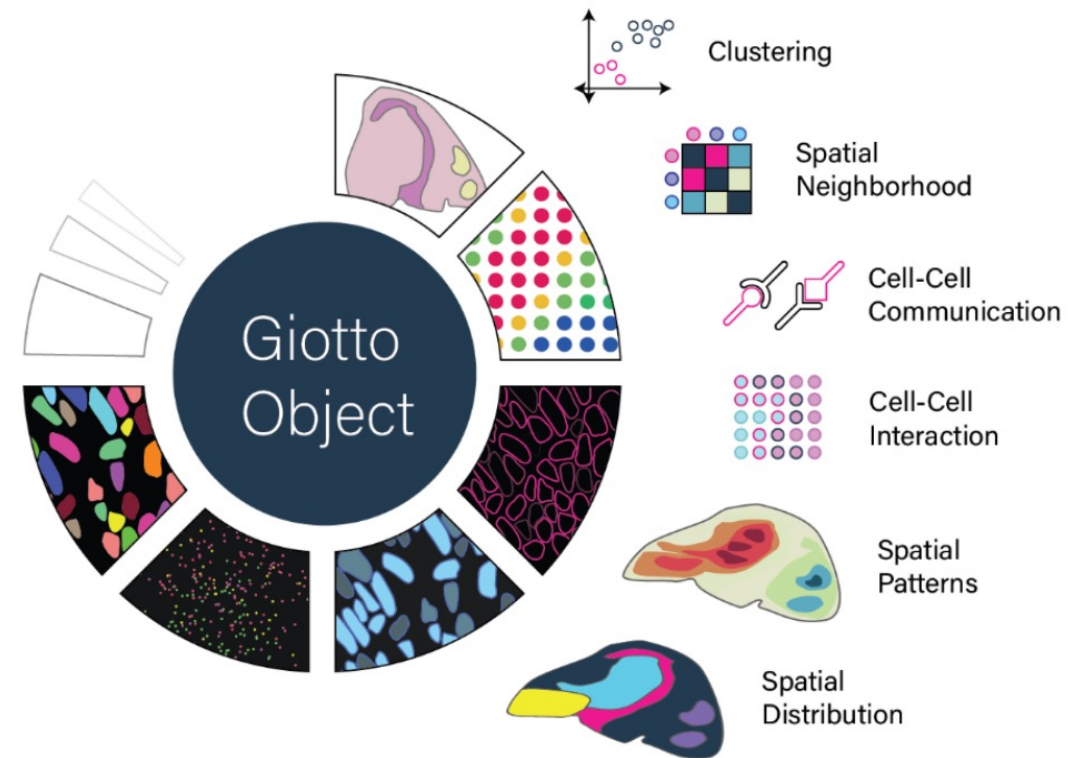
 Check for updates

*“Usable tools are the ‘last mile’ bridge between what computer science makes possible and what biologists are able to put to widespread use in their research.”*



# Software engineering to support next generation spatial data analysis

Flexible and scalable spatial data analysis



# Software engineering to support next generation spatial data analysis

## Innovative software engineering

Common Utilities



GiottoUtils

Data Structures & Manipulation



GiottoClass

Example Datasets & Analyses



GiottoData

Core Plotting Framework



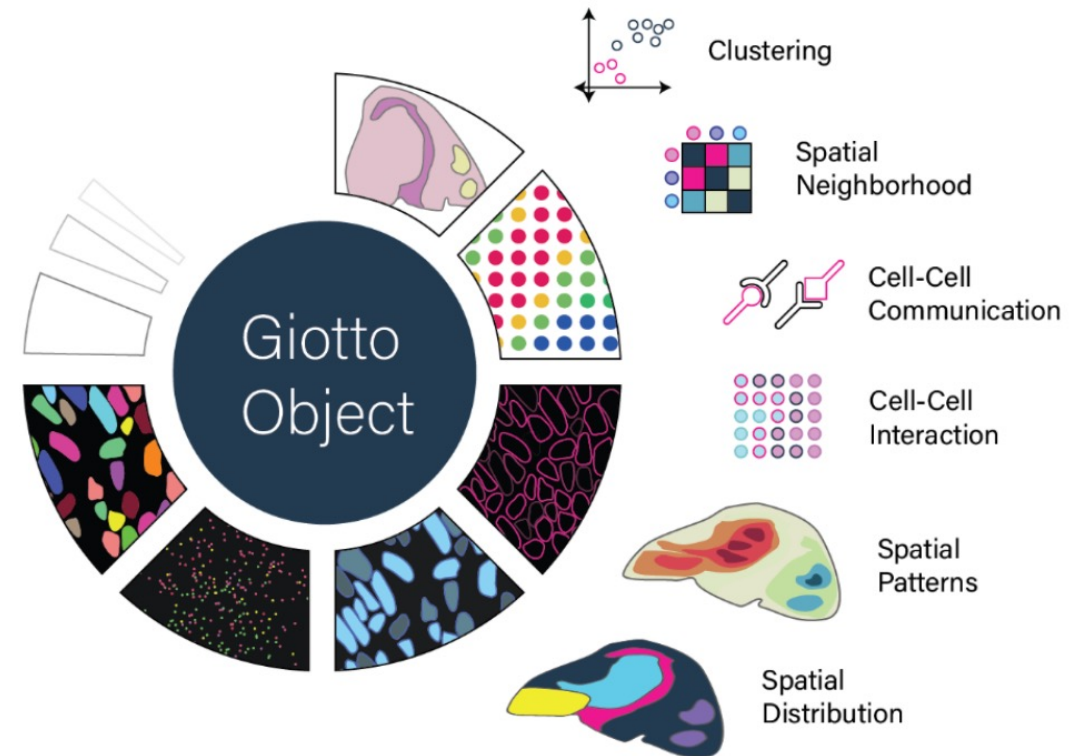
GiottoVisuals



Giotto

Integrative  
Bioinformatic &  
Spatial Analyses

## Flexible and scalable spatial data analysis



# Software engineering to support next generation spatial data analysis

## Innovative software engineering

Common Utilities



GiottoUtils

Data Structures & Manipulation



GiottoClass

Example Datasets & Analyses



GiottoData

Core Plotting Framework



GiottoVisuals

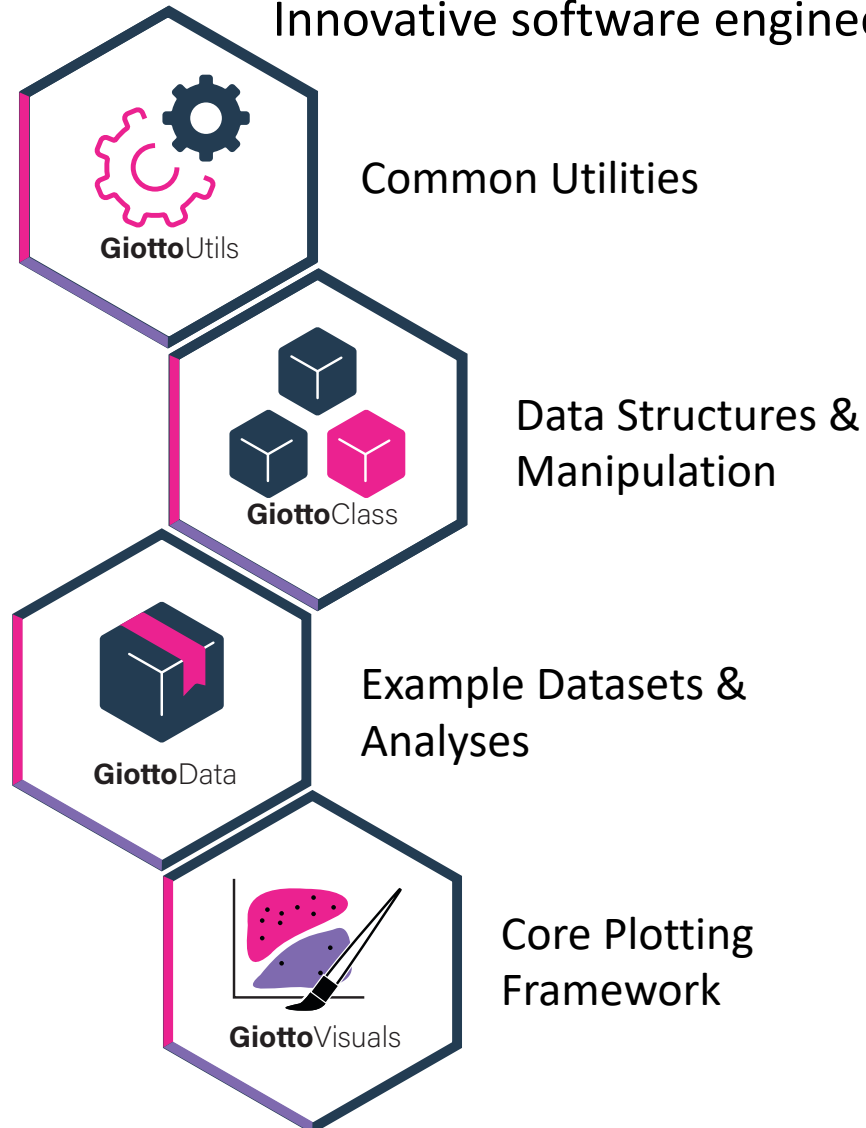


Giotto

Integrative  
Bioinformatic &  
Spatial Analyses

# Software engineering to support next generation spatial data analysis

## Innovative software engineering



**Giotto**  
Integrative  
Bioinformatic &  
Spatial Analyses

## Technology

Spatial-Array  
Sequencing



Multiplexed  
Mass-Spec

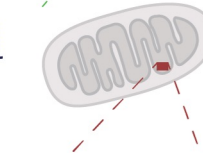
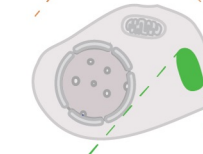
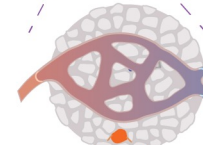
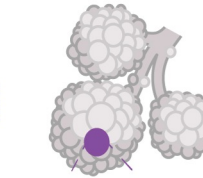


Multiplexed  
Imaging



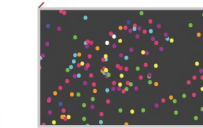
## Biology

mm

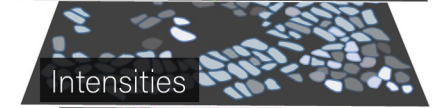
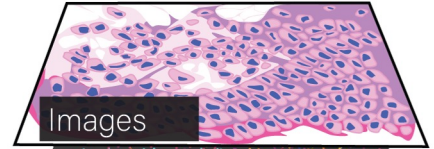


µm

nm

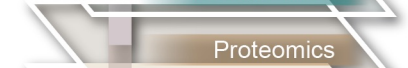
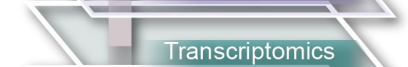
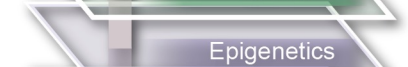


## Representation



## Multi-Modal

Vertically Integrated  
Connectome



Phenotype

# Representations for all type of data at multiple scales

## Technology

Spatial-Array Sequencing



Multiplexed Mass-Spec

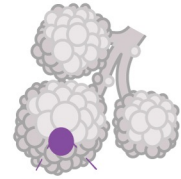


Multiplexed Imaging

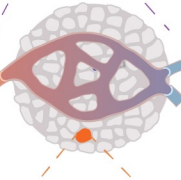


## Biology

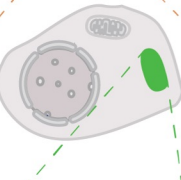
mm



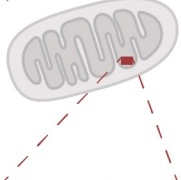
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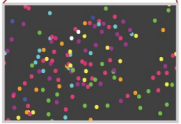
μm



μm

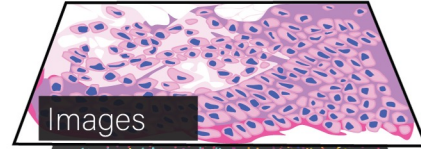


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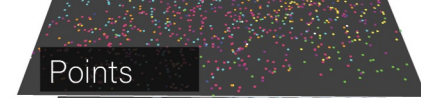


## Representation

Images



Points



Intensities



Shapes



## Multi-Modal

Vertically Integrated  
Connectome

Genetics

Epigenetics

Transcriptomics

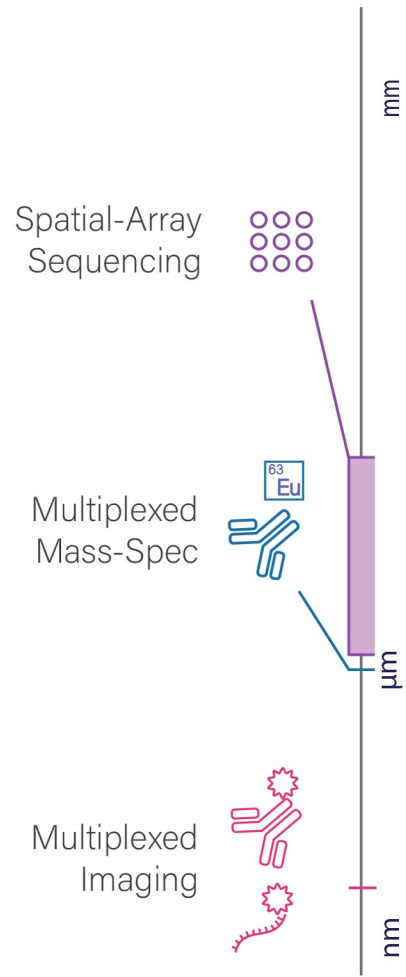
Proteomics

Metabolomics

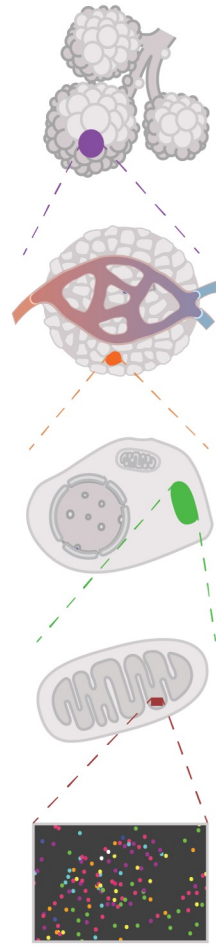
Phenotype

# Representations for all type of data at multiple scales

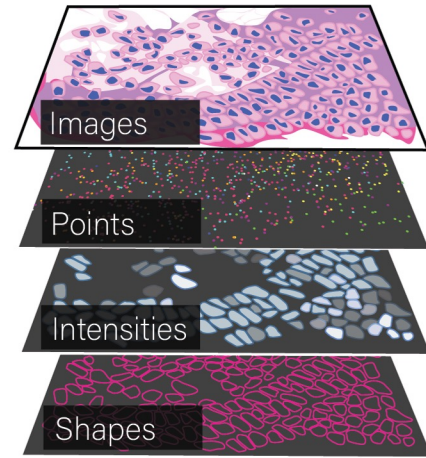
## Technology



## Biology

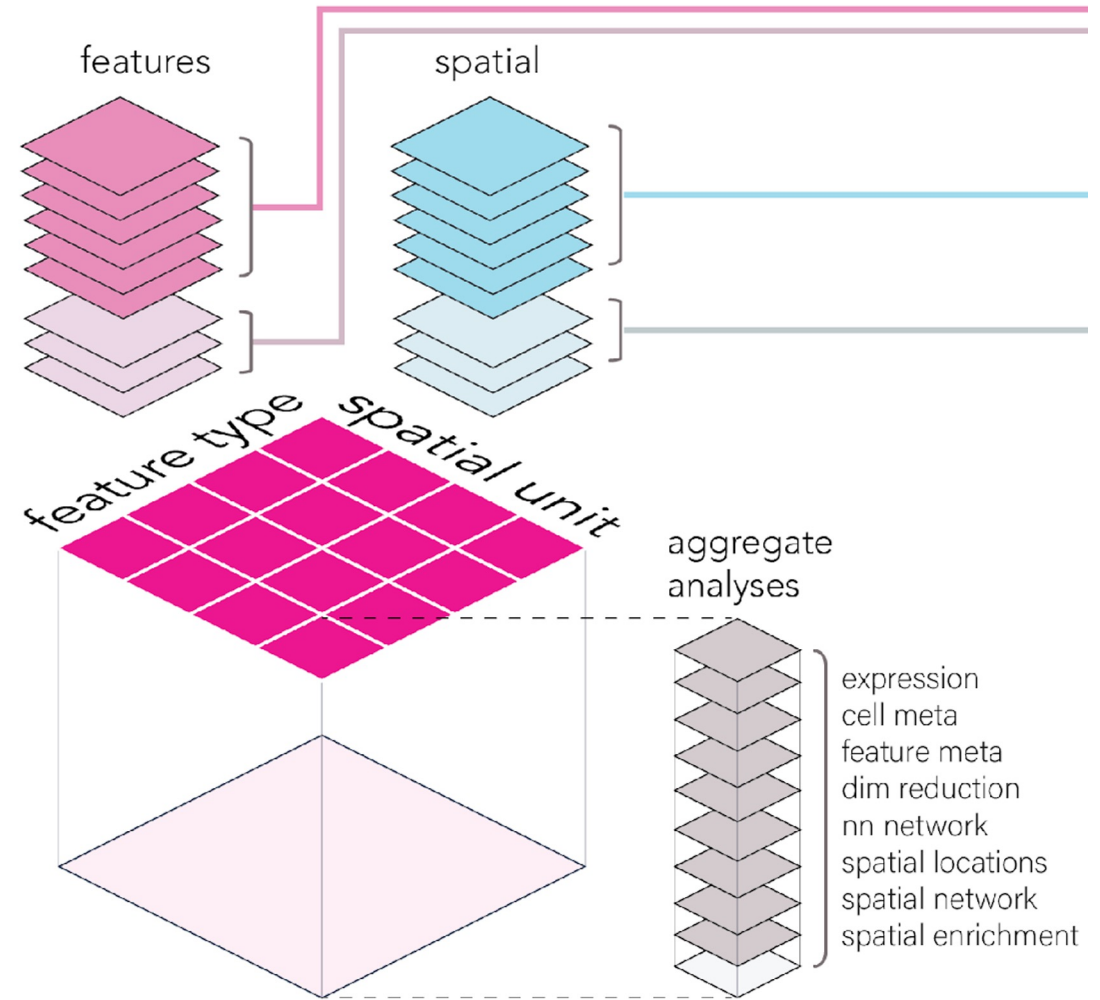
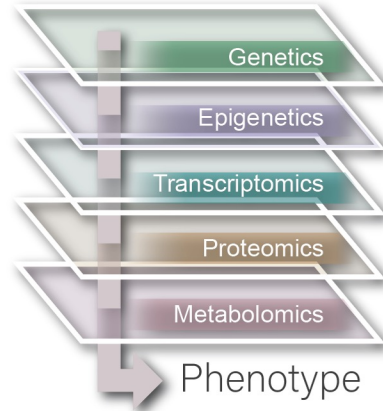


## Representation

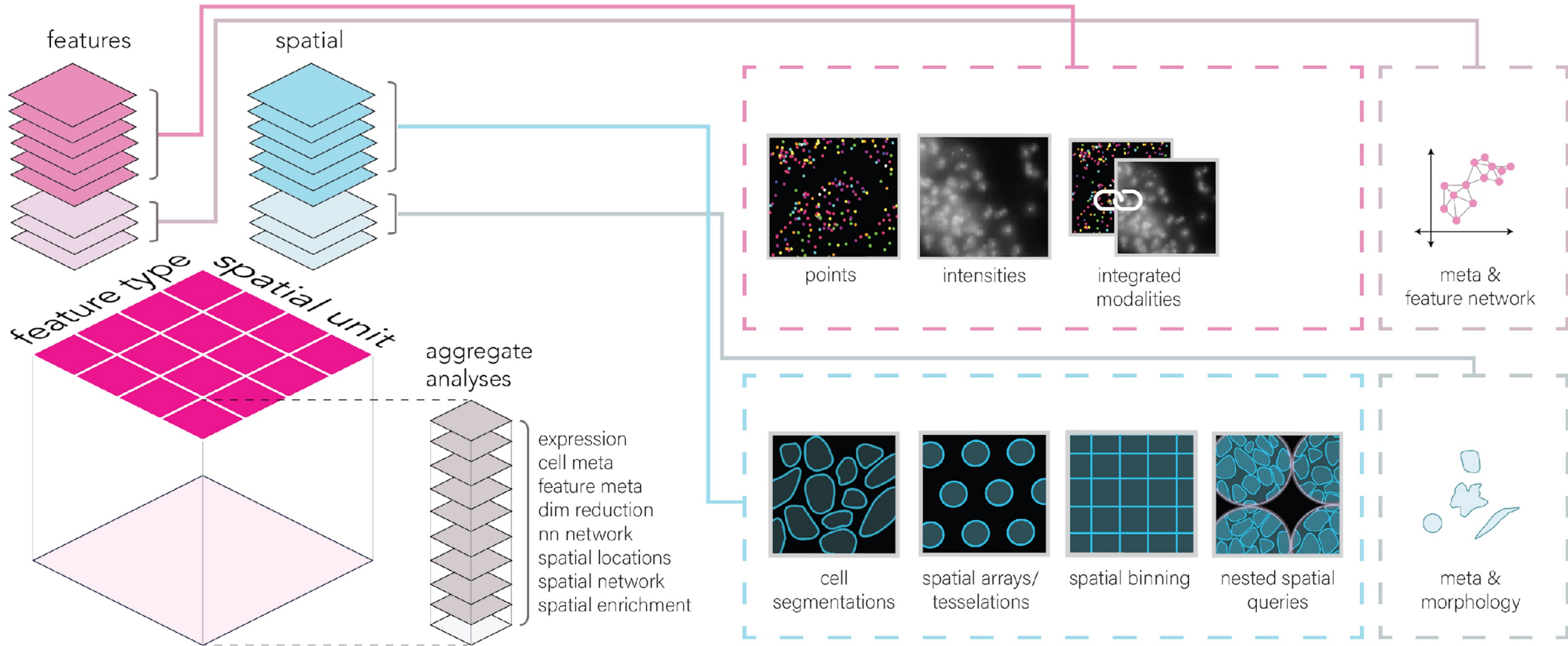


## Multi-Modal

Vertically Integrated Connectome

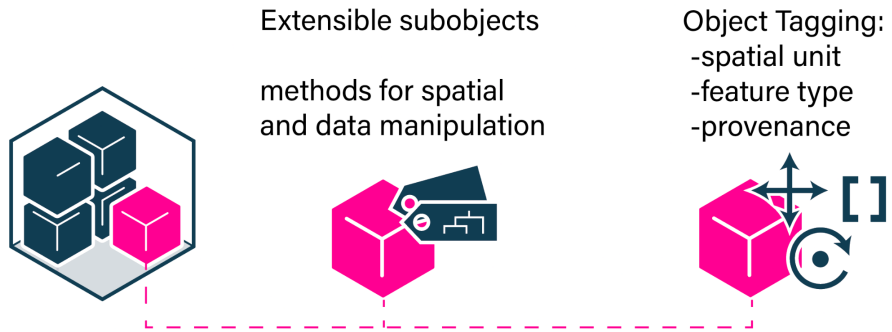


# Representations for all type of data at multiple scales



# Flexible data structures and operations

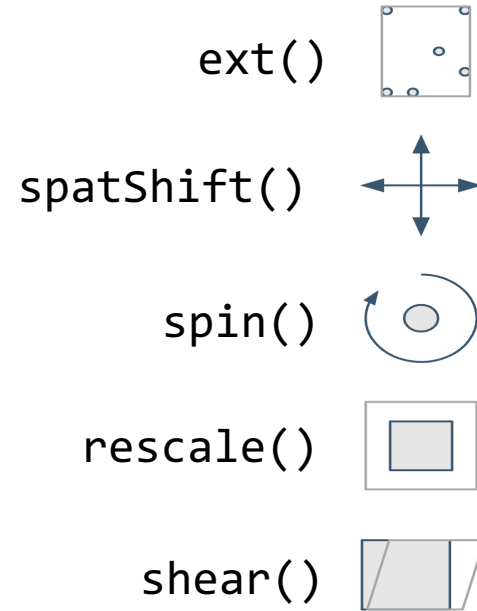
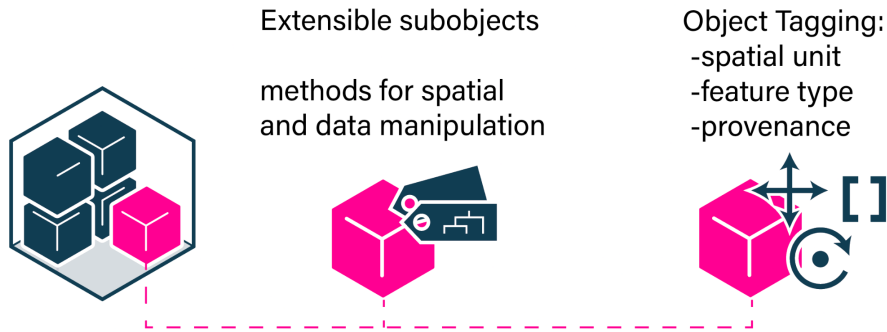
## Dedicated Subobject Classes





# Flexible data structures and operations

## Dedicated Subobject Classes



## Spatial data wrangling

### decomp\_affine()

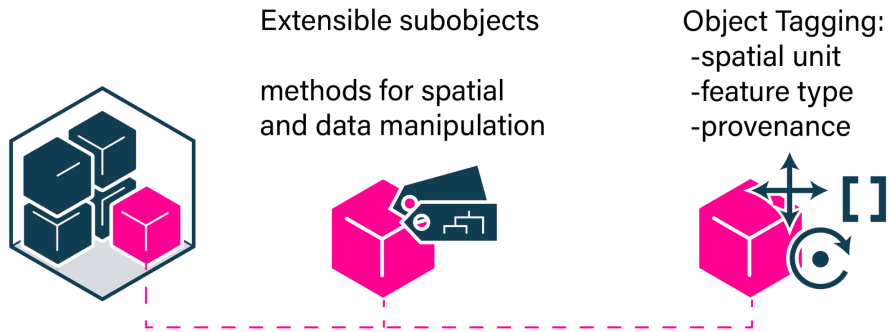
```
<affine_decomp>  
rotate : -0.165148677414627  
shear : c("0.016260162601626", "0")  
scale : c("2.02210754385589", "3.04138126514911")  
translate : c("1000", "20")
```

### affine()

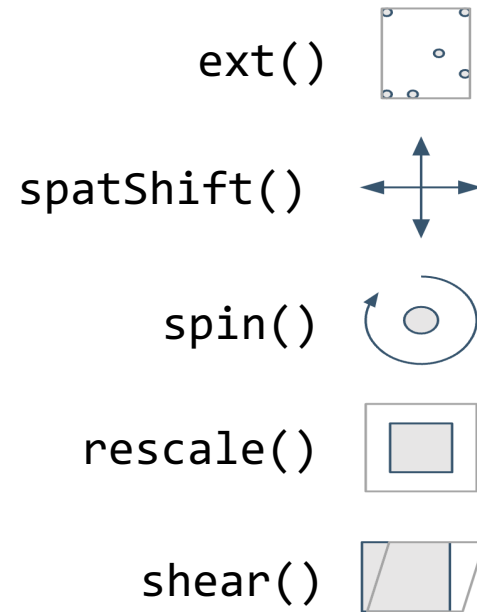
```
[,1] [,2] [,3]  
[1,] 2.0 0.5 1000  
[2,] -0.3 3.0 20  
[3,] 100.0 29.0 1
```

# Flexible data structures and operations

## Dedicated Subobject Classes



## Spatial data wrangling



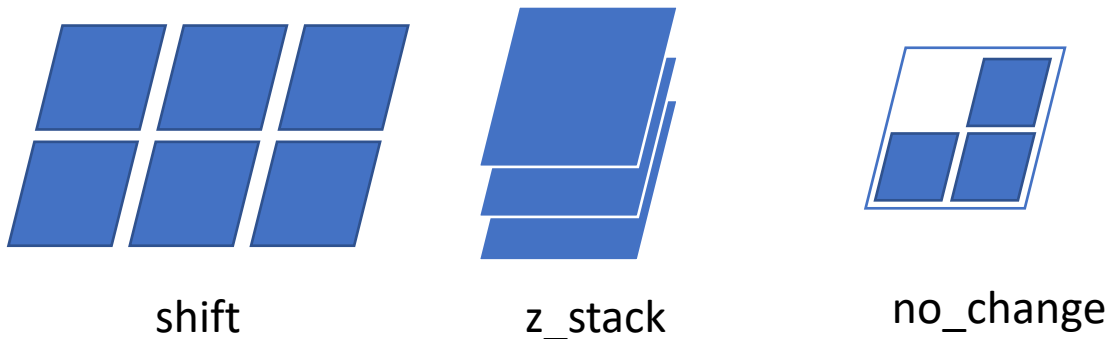
## decomp\_affine()

```
<affine_decomp>
rotate   : -0.165148677414627
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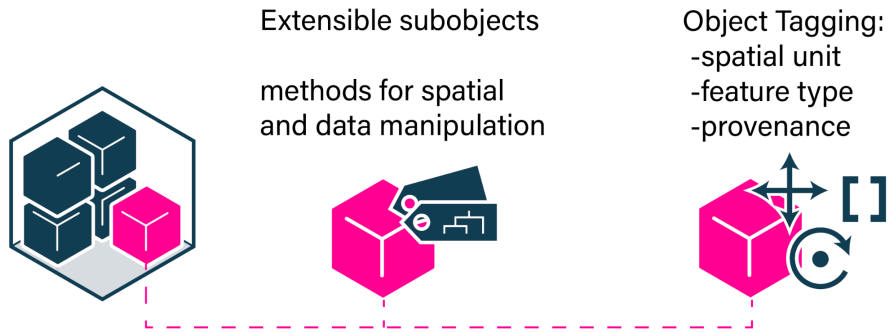
```
 [,1] [,2] [,3]
[1,]  2.0  0.5 1000
[2,] -0.3  3.0  20
[3,] 100.0 29.0  1
```

## Joining spatial objects

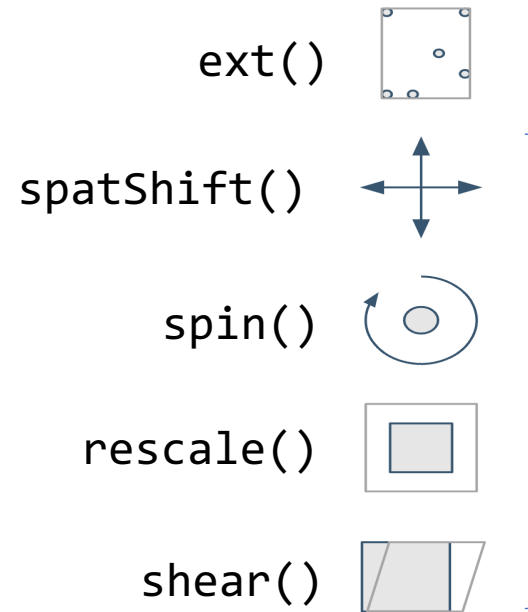


# Flexible data structures and operations

## Dedicated Subobject Classes



## Spatial data wrangling



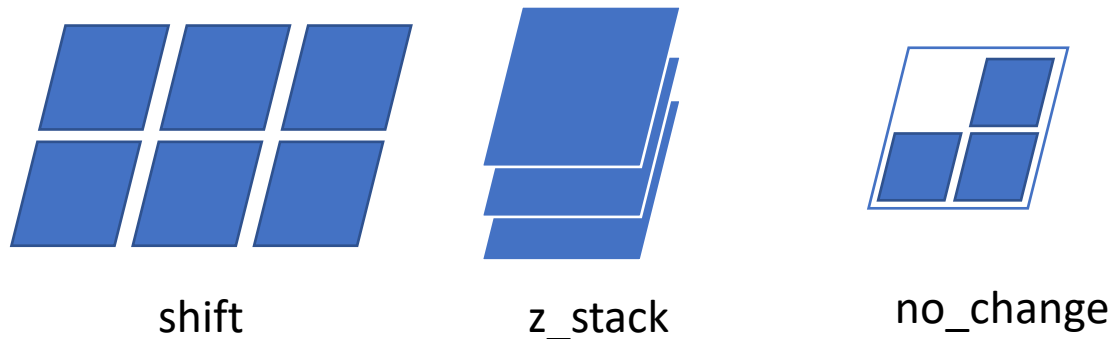
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```
<affine_decomp>
rotate   : -0.165148677414627
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scale    : c("2.02210754385589", "3.04138126514911")
translate: c("1000", "20")
```

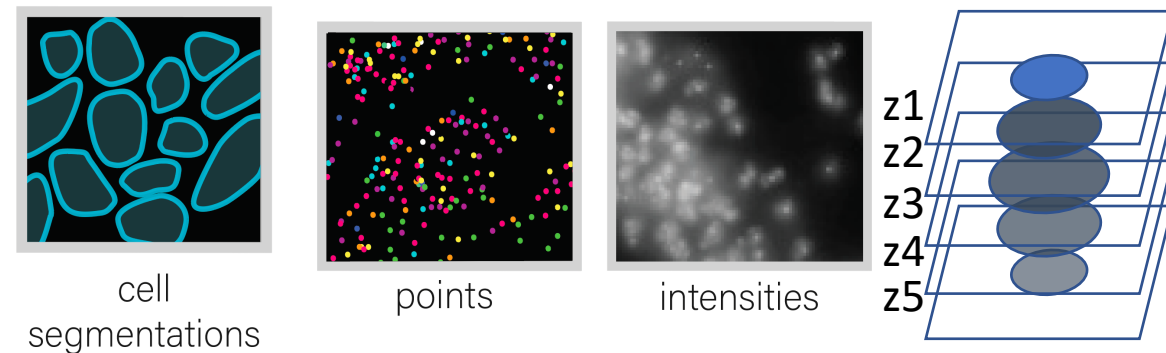
## affine()

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

## Joining spatial objects

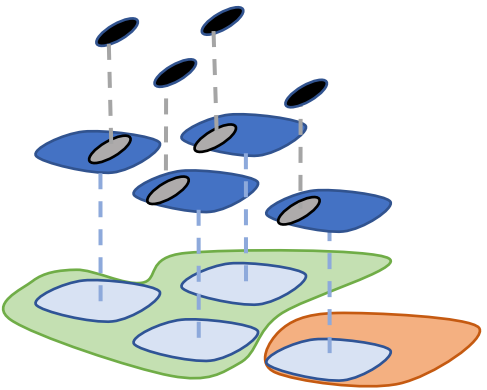


## Spatial data aggregation



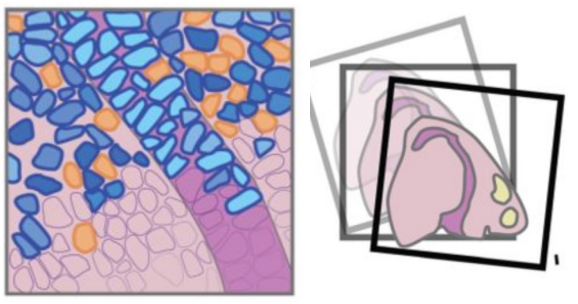
# Tutorials & examples:

### Multi-scale



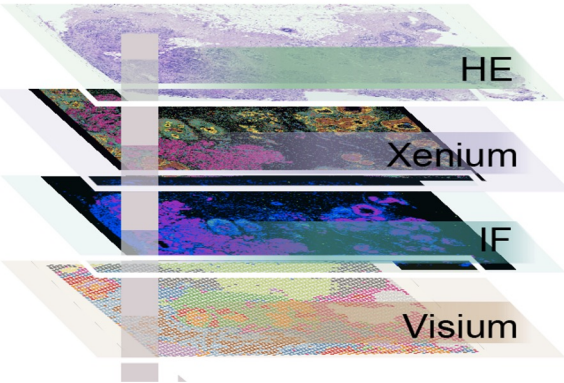
A diagram illustrating multi-scale analysis. At the bottom, a large green cell contains several smaller blue cells. Above it, several individual blue cells are shown at a higher magnification, with dashed lines indicating their correspondence to the cells in the larger cell below.

### Registration & segmentation



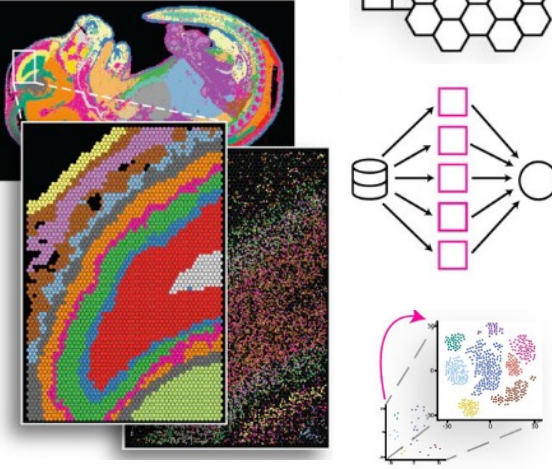
A diagram illustrating registration and segmentation. On the left, a histological image of tissue is shown with blue and orange regions. On the right, a corresponding anatomical map of a brain slice is shown, with a black box indicating a region of interest that is aligned with the histological image.

### Multi-modal



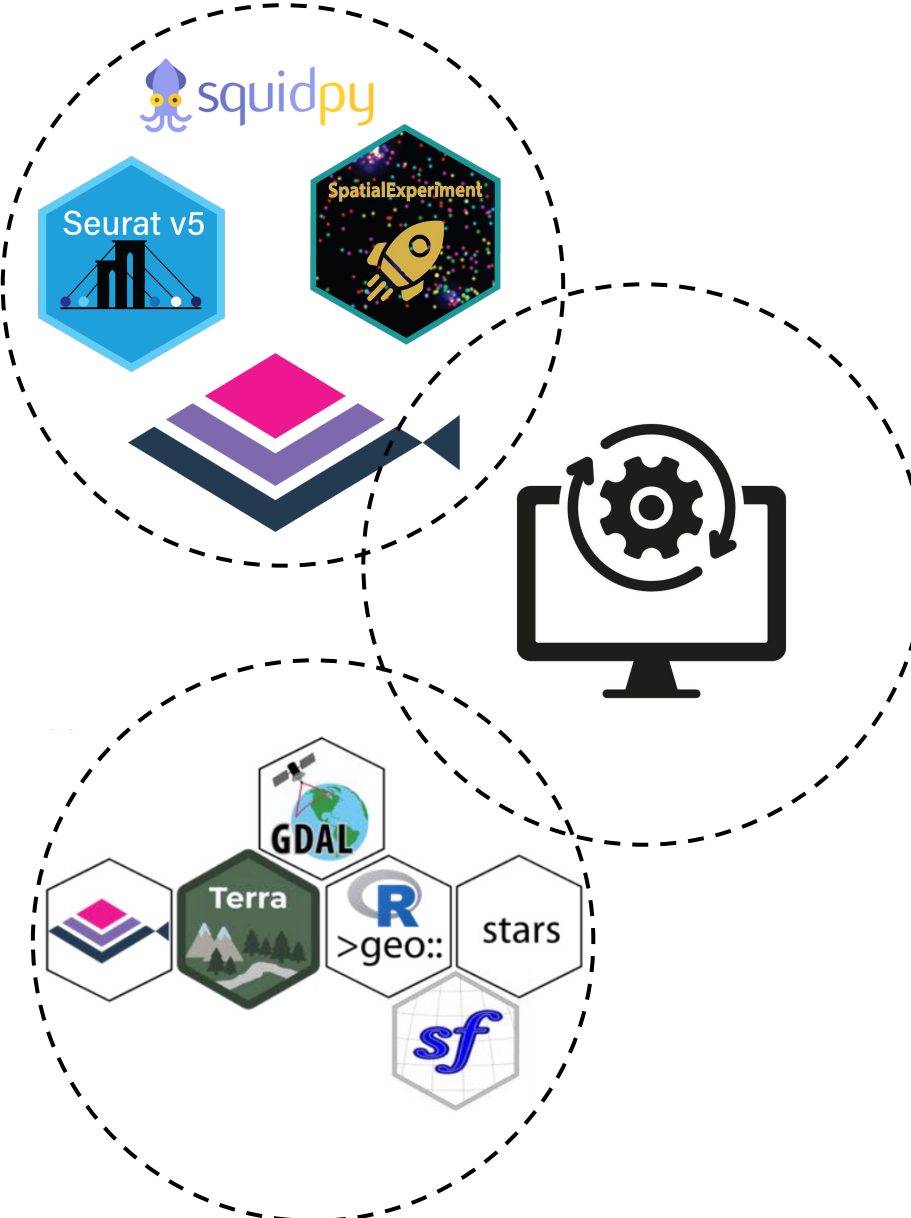
A diagram illustrating multi-modal data integration. It shows four stacked layers of data: HE (Histology), Xenium (Spatial Transcriptomics), IF (Immunofluorescence), and Visium (Spatial Transcriptomics). A vertical grey bar indicates a region of interest that is analyzed across all four modalities.

### Scalability



A diagram illustrating scalability. It shows a large, colorful spatial transcriptomics map on the left. To the right, a grid of cells is shown, followed by a diagram of a neural network or processing pipeline with a database icon, and a smaller map showing a zoomed-in view of a region.

# Community & tool building:



A diagram illustrating community and tool building. It features a central computer monitor icon with a gear and a circular arrow, representing a workflow or tool. Surrounding this are two large dashed circles containing various logos and icons. The top circle includes logos for squidpy, Seurat v5, and SpatialExperiment. The bottom circle includes logos for GDAL, Terra, >geo::, stars, and sf. A central stack of colored squares (pink, purple, blue) is also present.

## 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 (seqFISH+, merFISH, osmFISH, CosMx), sequencing (Slide-seq, Visium, STARmap, Seq-Scope, Stereo-Seq) and imaging-based multiplexing/proteomics (CyCIF, MIBI, CODEX). 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

To install Giotto suite use `devtools::install_github("drieslab/Giotto")`.

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

## Website Update!

With Giotto version 4.0, we updated the website at <http://giottosuite.com>, you can still find the previous website at <https://giottosuite.readthedocs.io/en/latest/>

## Website description

- **Get started:** Here you can find more advanced information about the Giotto object, Giotto ecosystem, Giotto configuration, and installation FAQs.
- **Documentation:** Here you will find all Giotto functions grouped by their purpose (Helpers, Getters & Setters, Visualization, ...)
- **Examples:** Here you can find end-to-end examples for different technologies and datasets.
- **Tutorials:** Here you can find various tutorials on working with Giotto (analysis, visualizations, working on the cloud, ...)
- **News:** Here you can find the changelog for every Giotto release and video recordings from previous presentations.

### Links

[Browse source code](#)

[Report a bug](#)

### License

[Full license](#)

GPL (>= 3)

### Community

[Contributing guide](#)

[Code of conduct](#)

### Citation

[Citing Giotto](#)

### Developers

[Ruben Dries](#)

Author, maintainer

[Jiaji George Chen](#)

Author

[Joselyn C. Chávez-Fuentes](#)

Author

[Guo-Cheng Yuan](#)

Author

[Matthew O'Brien](#)

Author

[Edward Ruiz](#)

Author

[Wen Wang](#)

Author

[Natalie Del Rossi](#)

Author

### For users:

- **Examples:** vignettes for different datasets and technologies
- **Tutorials:** what can you do in or with Giotto?
- **News page** for regular updates

### For developers:

- **Giotto Ecosystem** and sub-websites
- **Giotto Class Structure** to understand data structures
- **Contribution page**

## 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 (seqFISH+, merFISH, osmFISH, CosMx), sequencing (Slide-seq, Visium, STARmap, Seq-Scope, Stereo-Seq) and imaging-based multiplexing/proteomics (CyCIF, MIBI, CODEX). 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

To install Giotto suite use `devtools::install_github("drieslab/Giotto")`.

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

## Website Update!

With Giotto version 4.0, we updated the website at <http://giottosuite.com>, you can still find the previous website at <https://giottosuite.readthedocs.io/en/latest/>

## Website description

- **Get started:** Here you can find more advanced information about the Giotto object, Giotto ecosystem, Giotto configuration, and installation FAQs.
- **Documentation:** Here you will find all Giotto functions grouped by their purpose (Helpers, Getters & Setters, Visualization, ...)
- **Examples:** Here you can find end-to-end examples for different technologies and datasets.
- **Tutorials:** Here you can find various tutorials on working with Giotto (analysis, visualizations, working on the cloud, ...)
- **News:** Here you can find the changelog for every Giotto release and video recordings from previous presentations.

### Links

[Browse source code](#)

[Report a bug](#)

### License

[Full license](#)

GPL (>= 3)

### Community

[Contributing guide](#)

[Code of conduct](#)

### Citation

[Citing Giotto](#)

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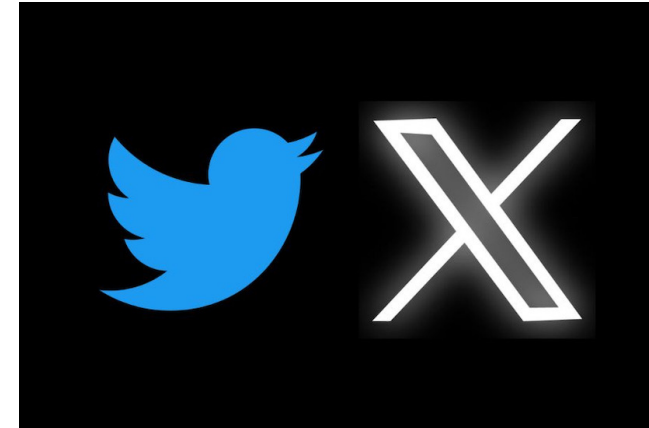


BY  
TESTER

Interested to:

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

Reach out to [rdries@bu.edu](mailto:rdries@bu.edu)



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# Acknowledgements: Giotto Suite work

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