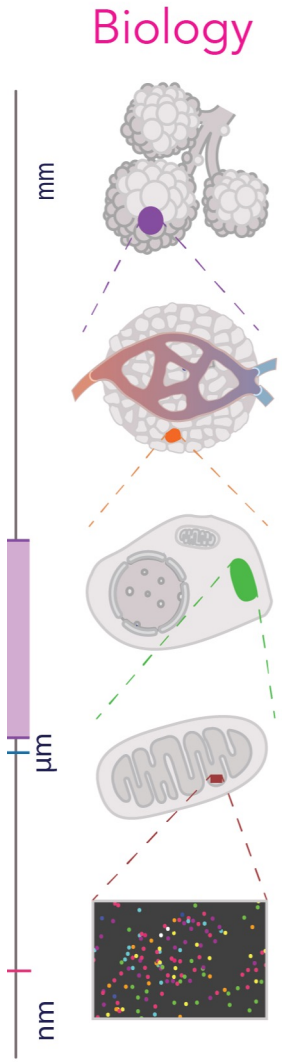
Giotto Suite: a multi-scale and technology-agnostic spatial multi-omics analysis ecosystem

Jiaji George Chen, Joselyn Cristina Chávez-Fuentes, Matthew O'Brien, Junxiang Xu, Edward Ruiz, Wen Wang, Iqra Amin, Irzam Sarfraz, Pratishtha 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



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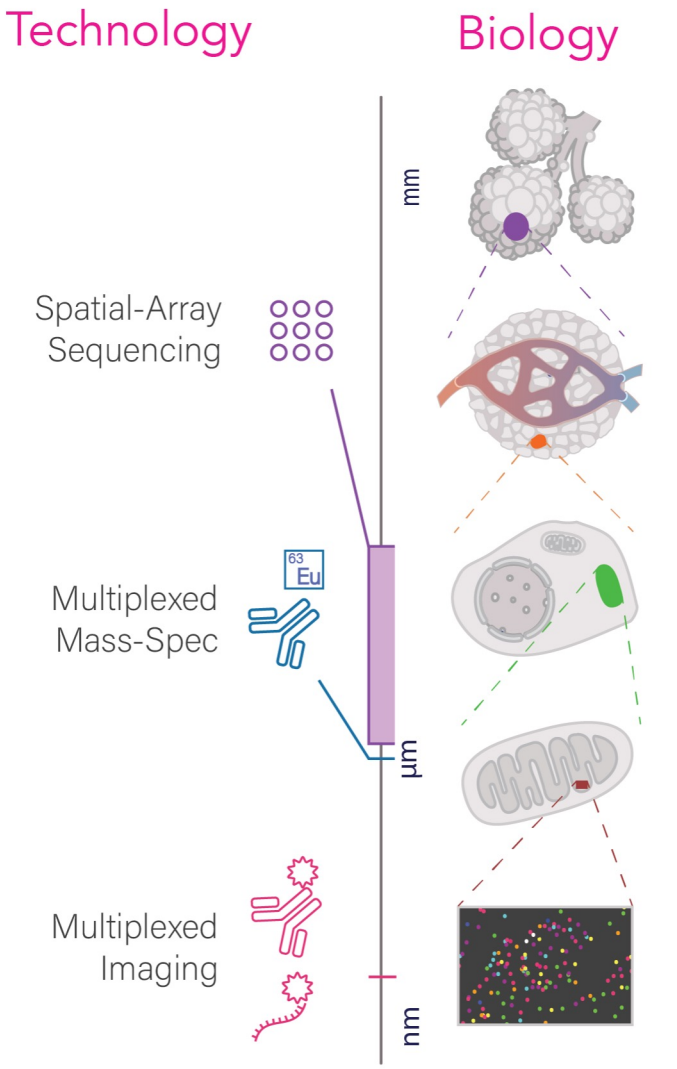

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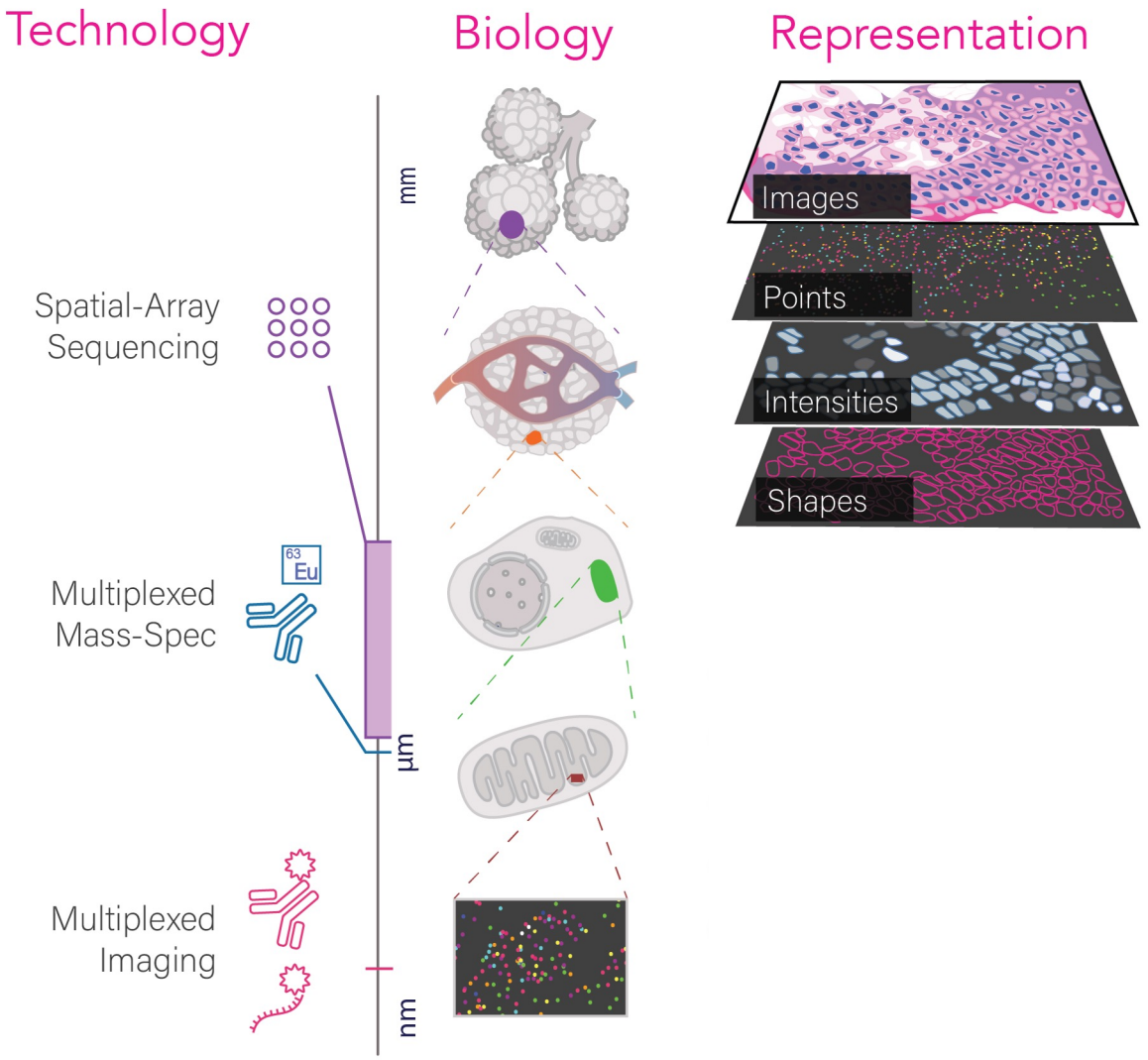

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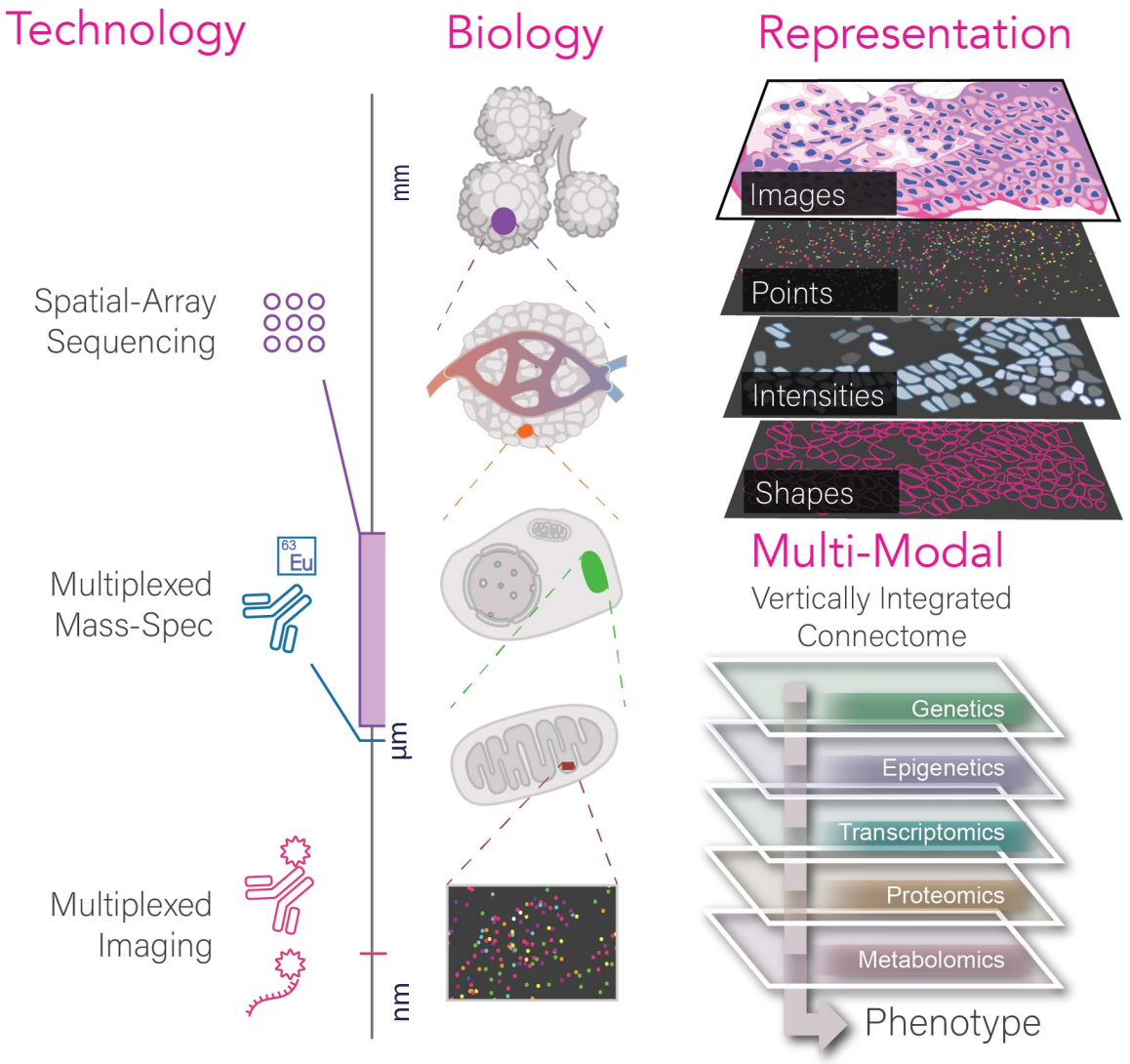
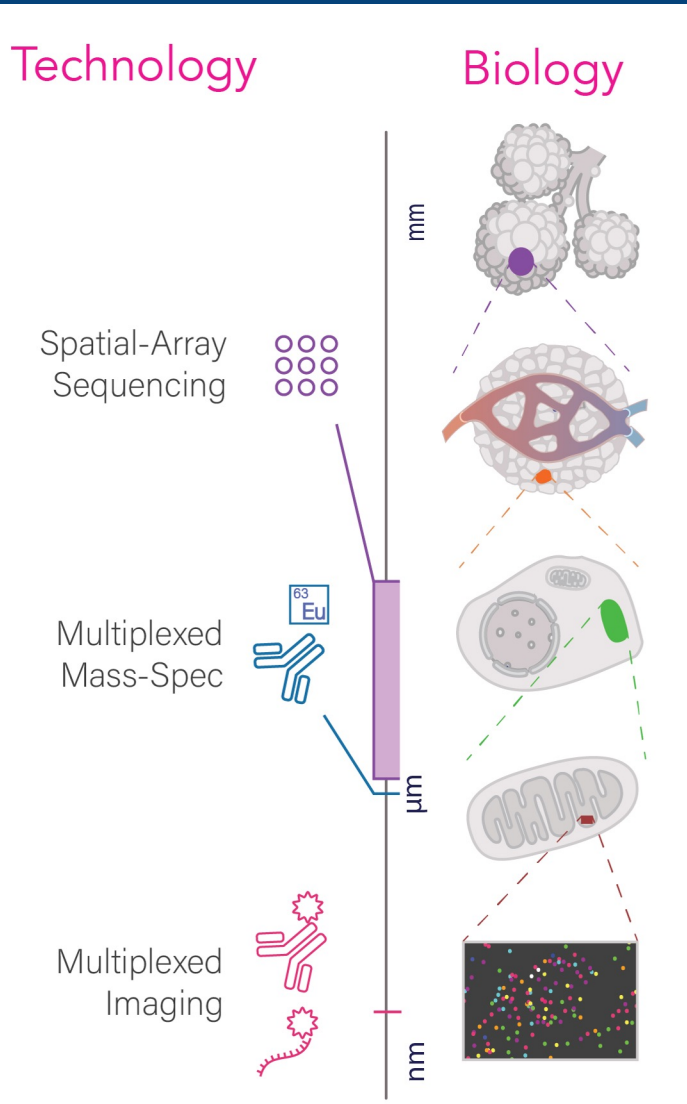
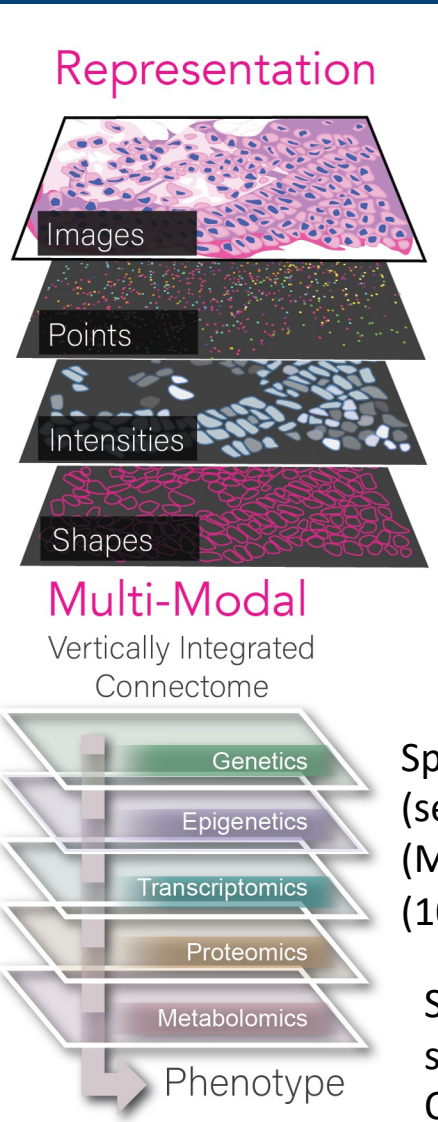


Spatial omics biology can be measured in many ways





Nanostring CosMx

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

How can we make complex spatial data analysis easy?

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

Bringing computation to biology by bridging the last mile

Anne E. Carpenter & Shantanu Singh

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Bringing computation to biology by bridging the last mile

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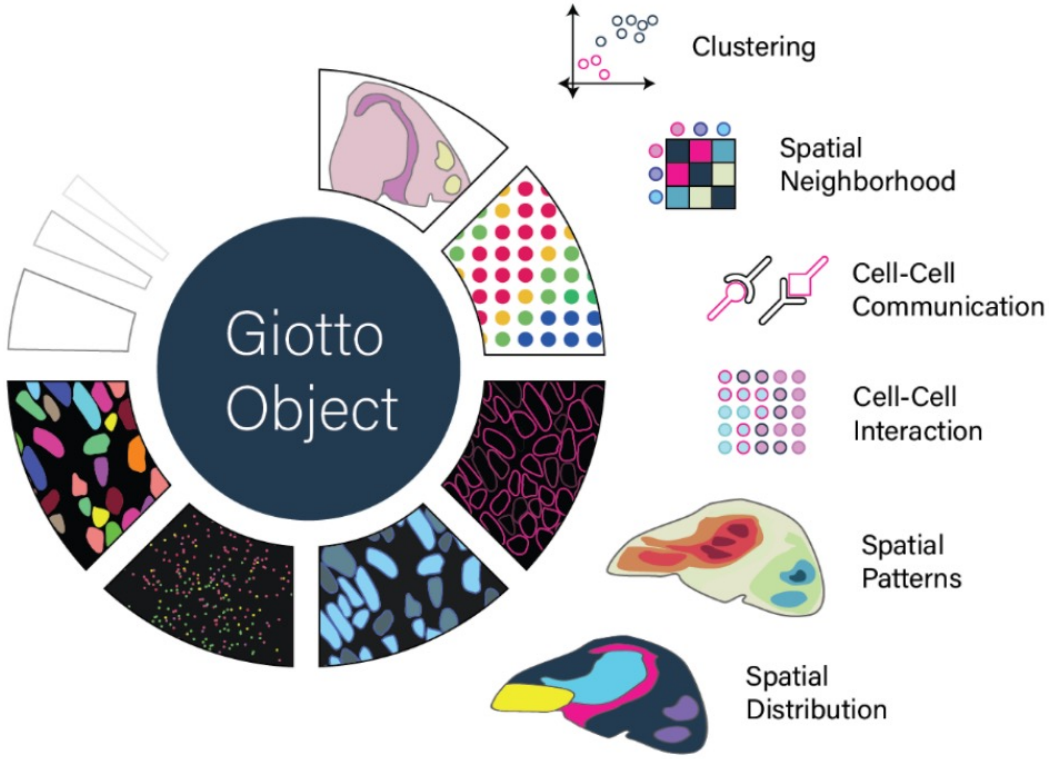
"Usable tools are the 'last mile' bridge between what computer science makes possible and what biologists are able to put to widespread use in their research."

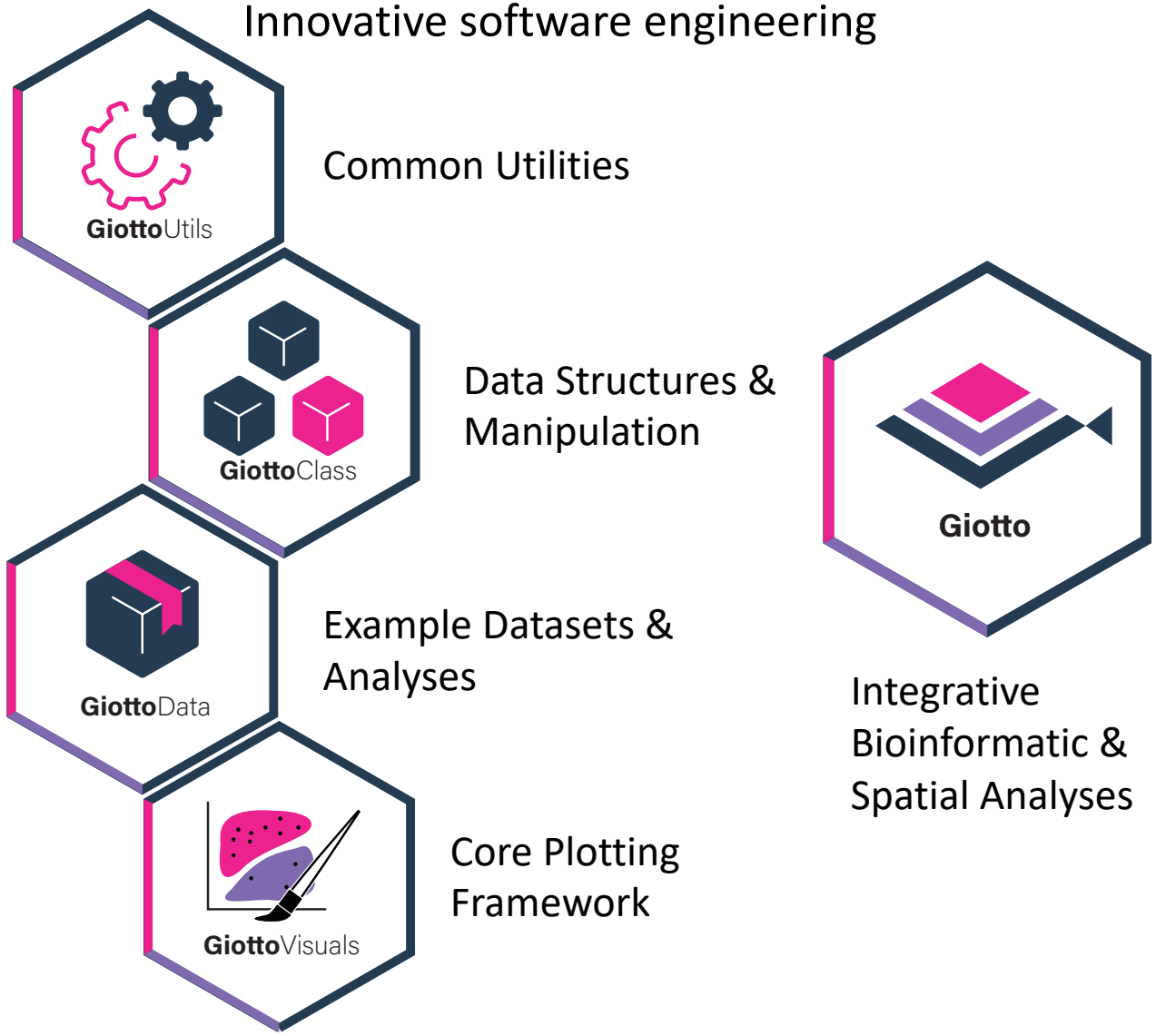
Software engineering to support next generation spatial data analysis

Flexible and scalable spatial data analysis



Software engineering to support next generation spatial data analysis

Innovative software engineering



Common Utilities

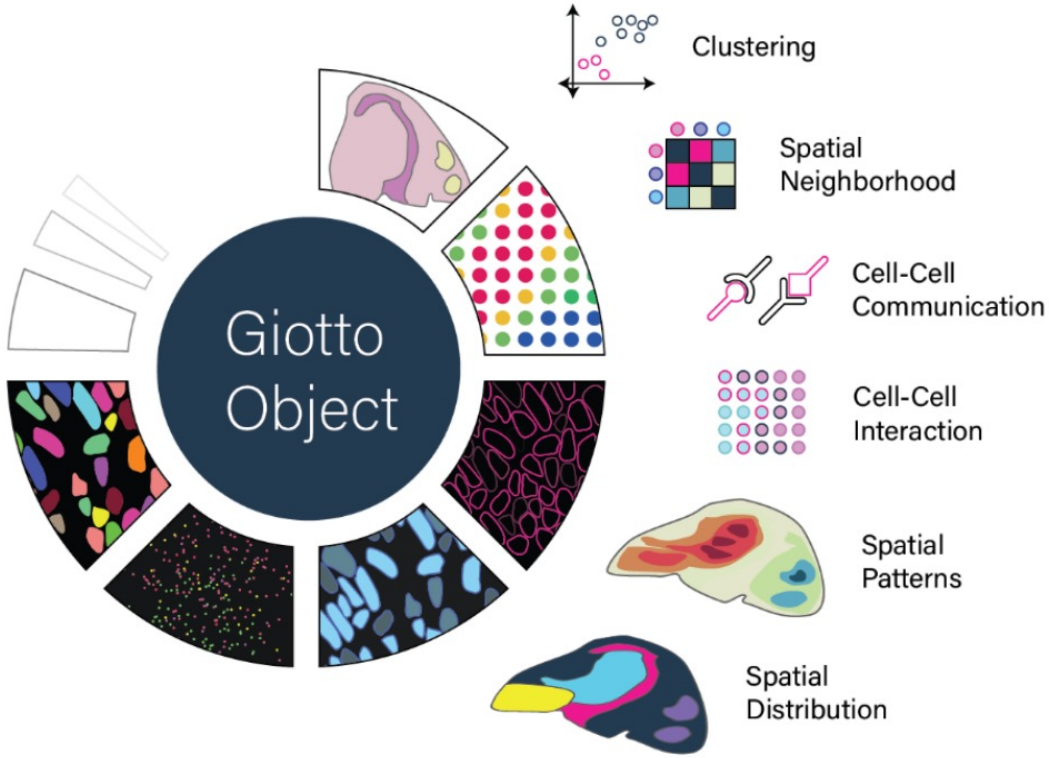
Data Structures & Manipulation

Example Datasets & Analyses

Core Plotting Framework

Integrative Bioinformatic & Spatial Analyses

Flexible and scalable spatial data analysis



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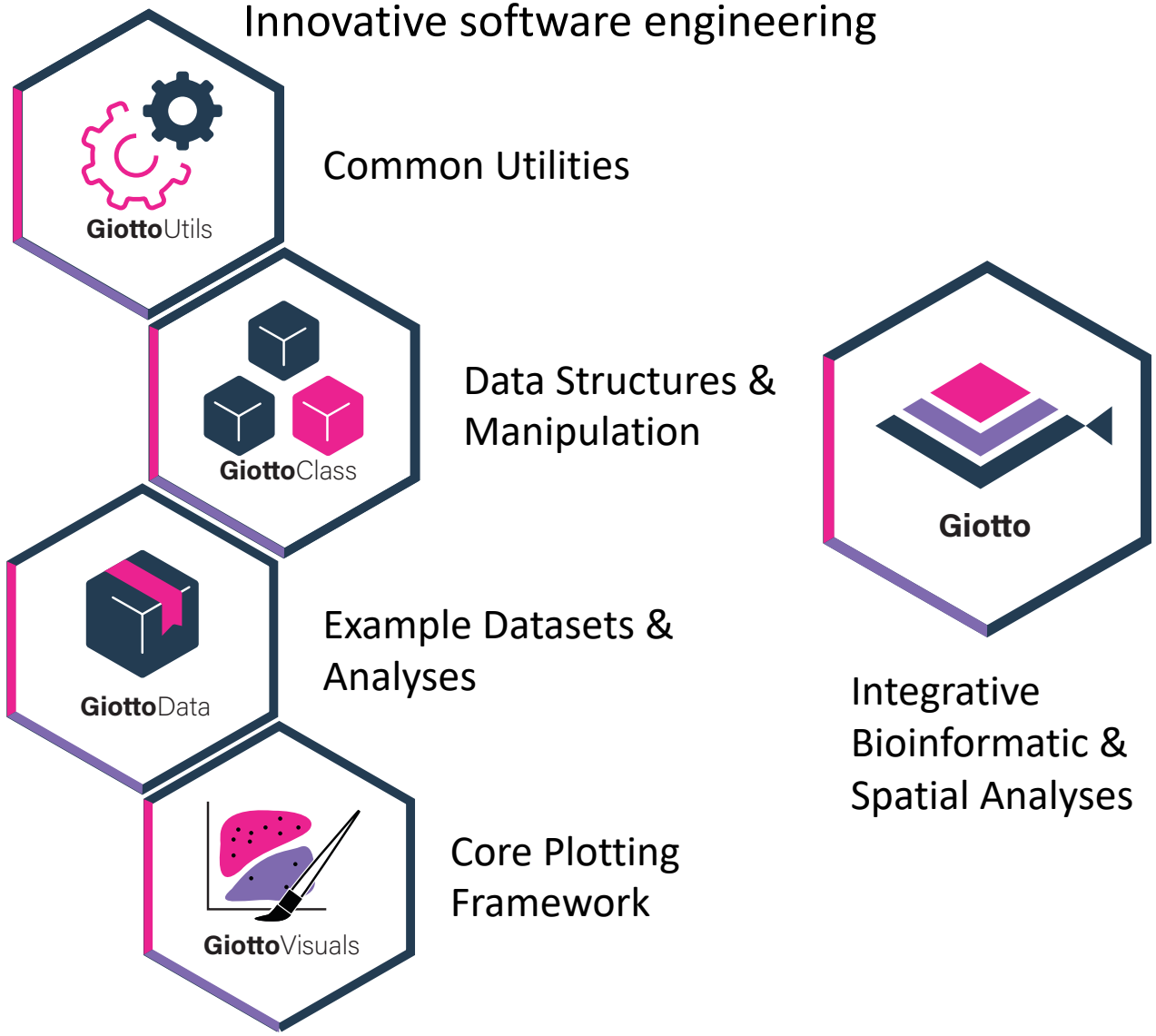

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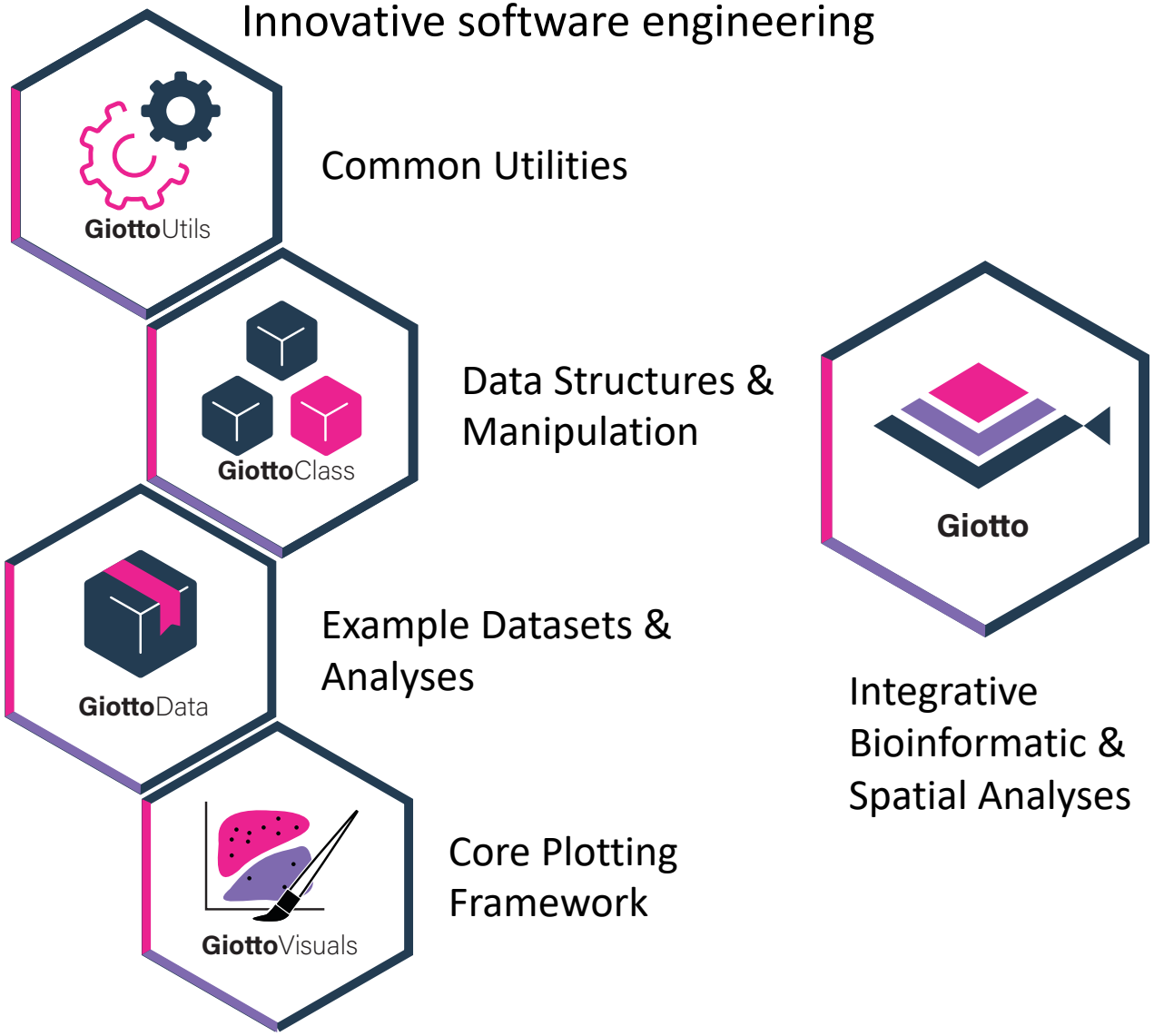
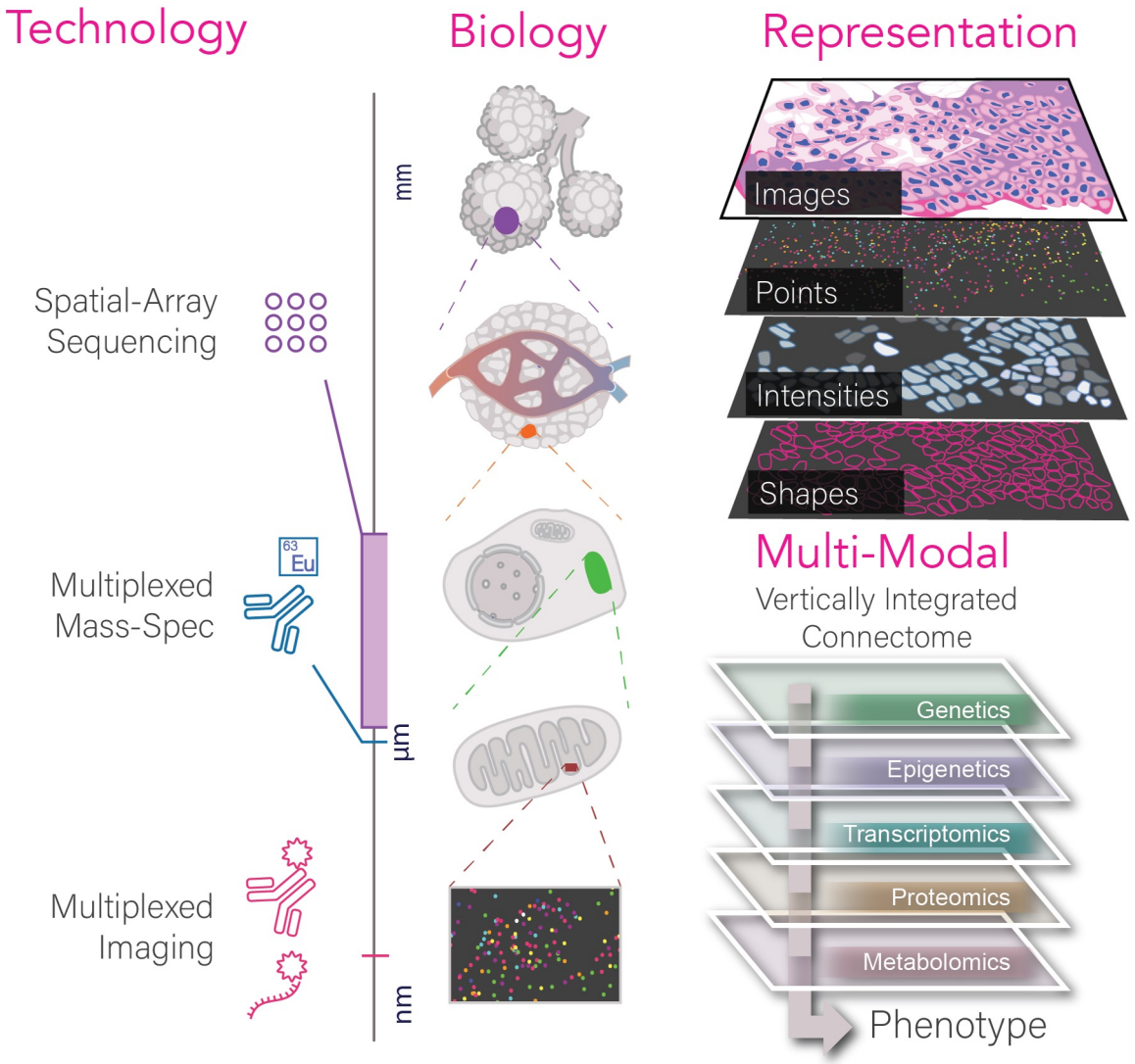
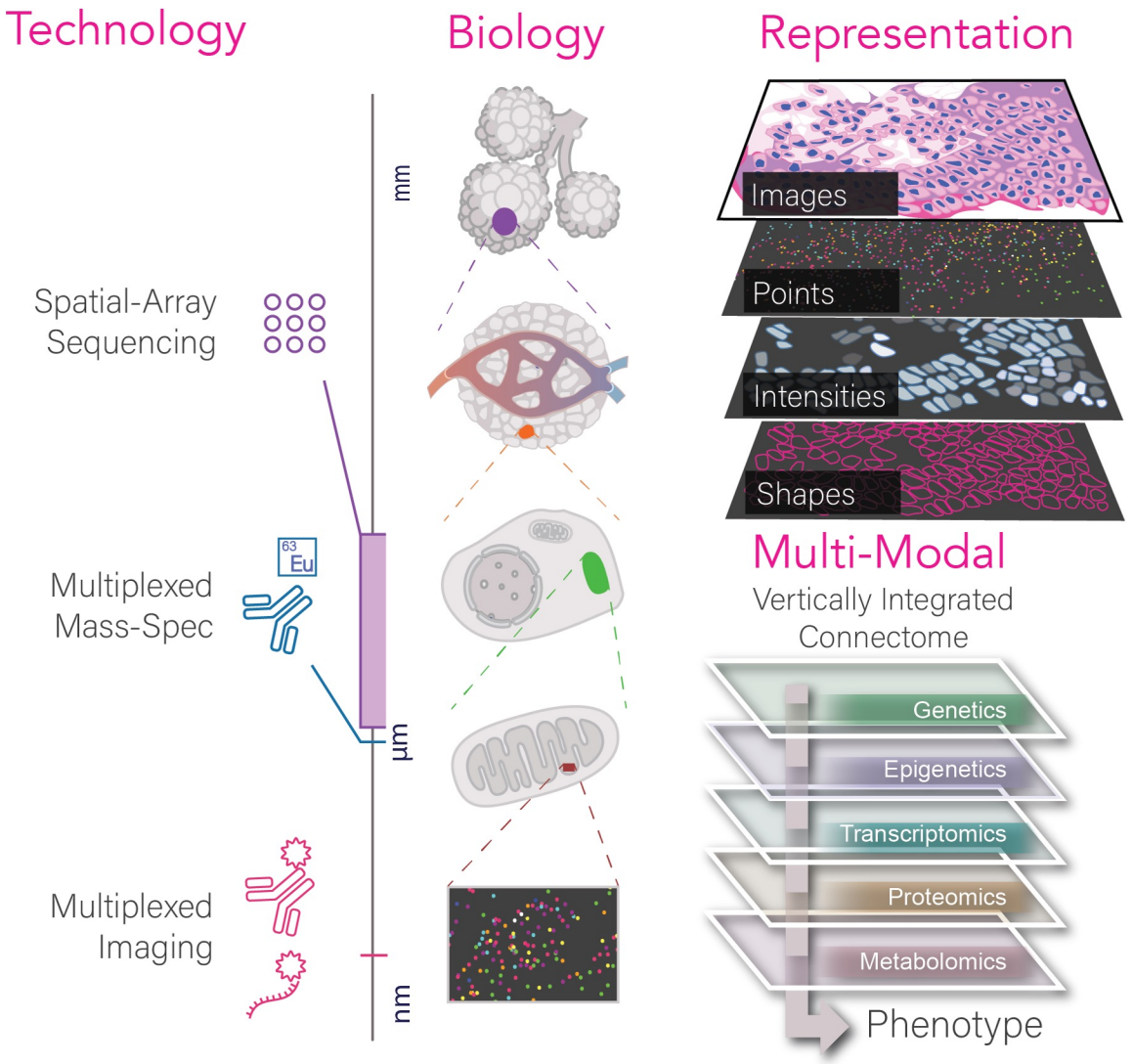




Representations for all type of data at multiple scales



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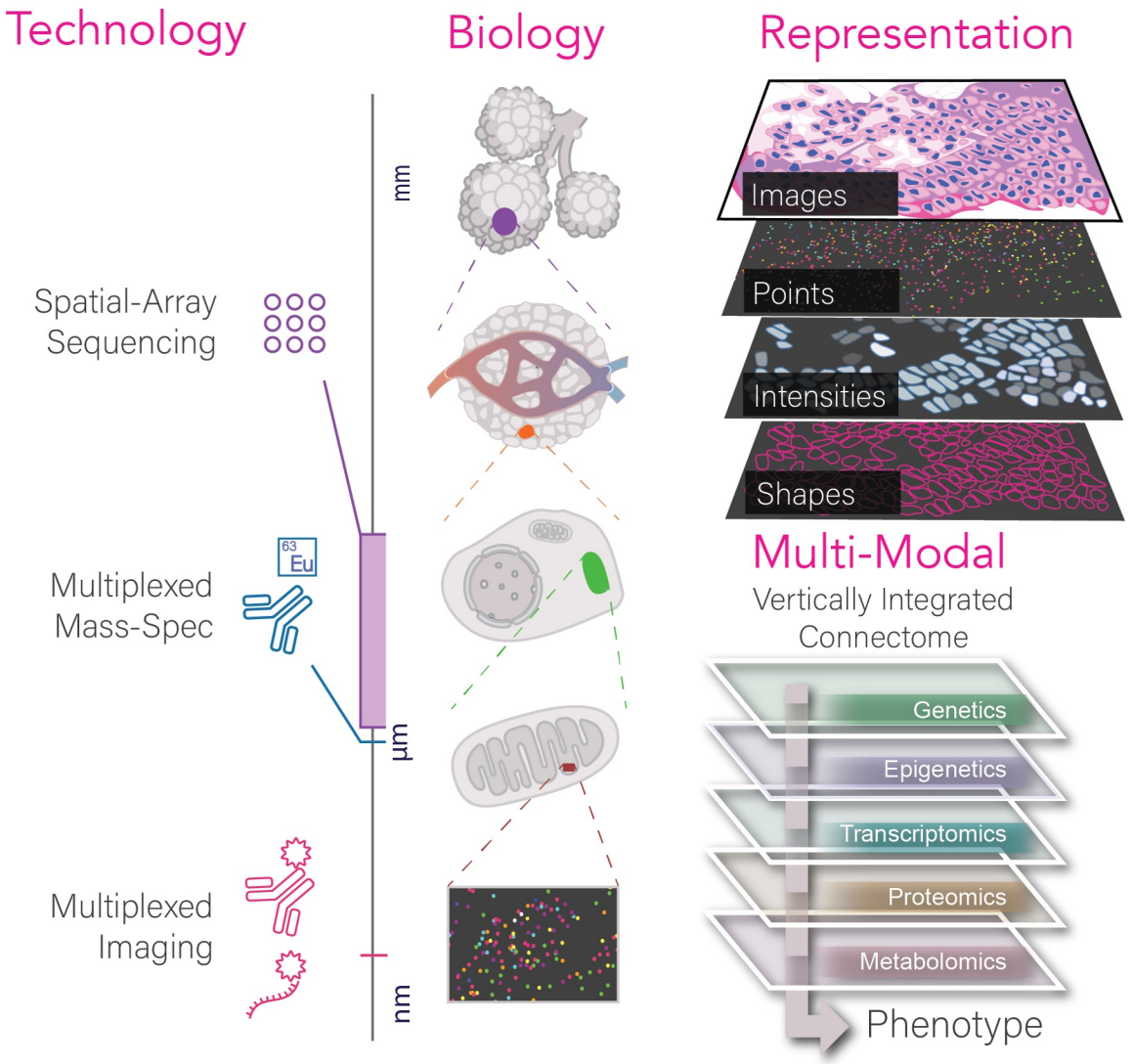

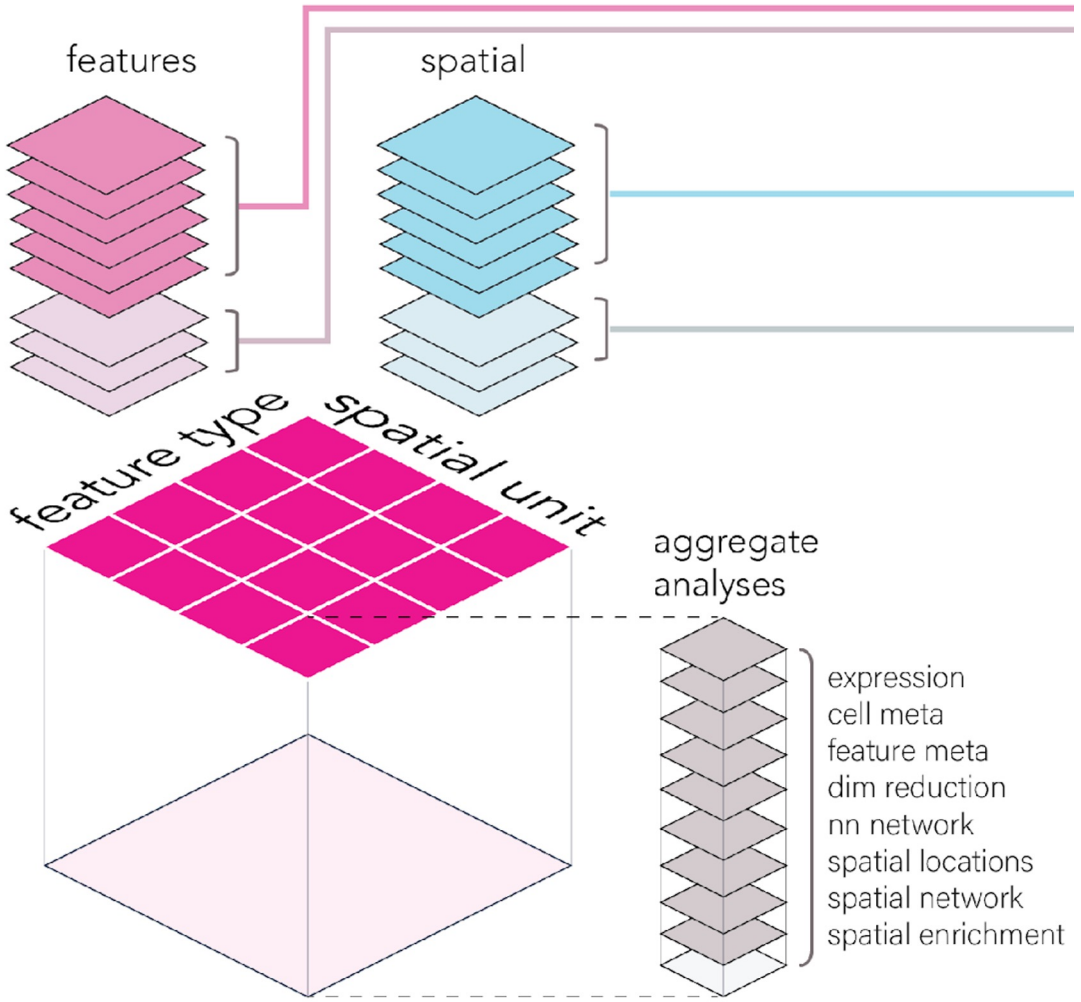

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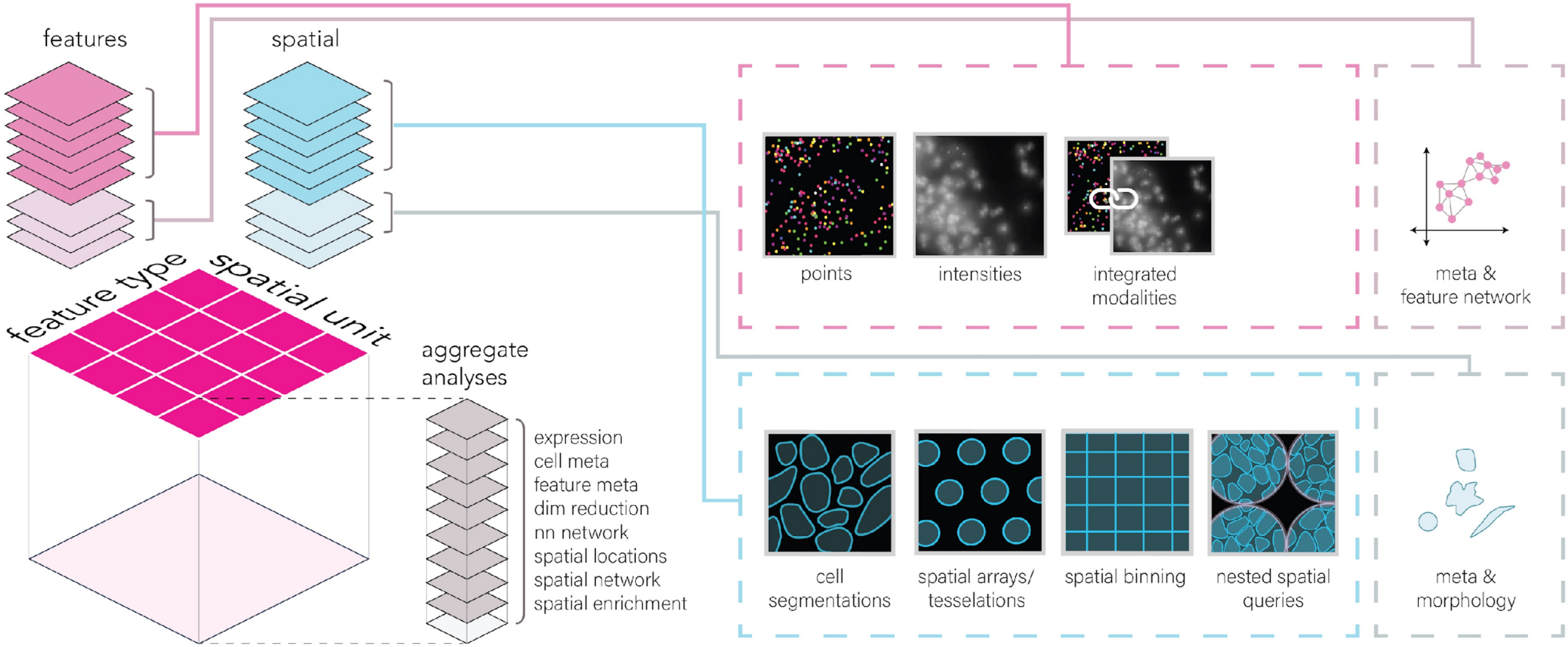
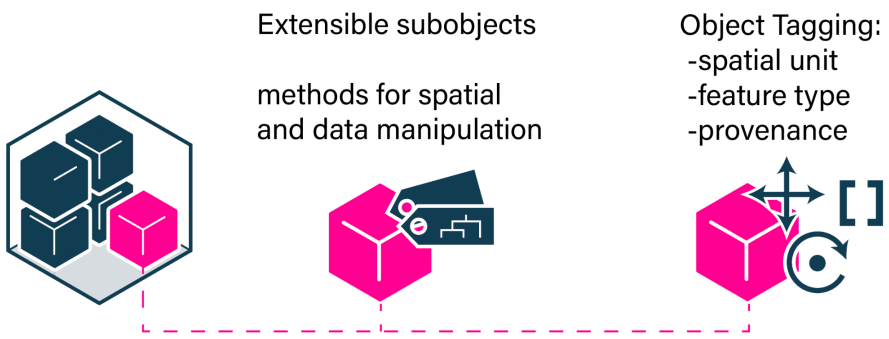


Flexible data structures and operations

Dedicated Subobject Classes



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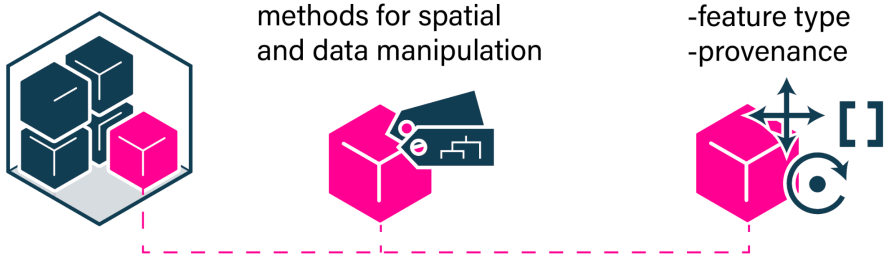

Extensible subobjects

methods for spatial
and data manipulation

Object Tagging:
-spatial unit
-feature type
-provenance

Spatial data wrangling

ext()

spatShift()

spin()

rescale()

shear()

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

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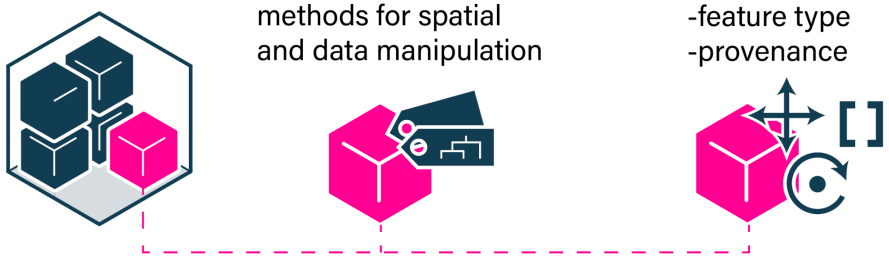

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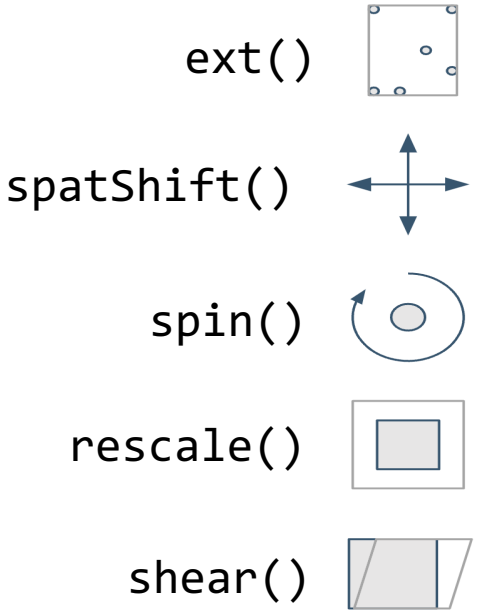

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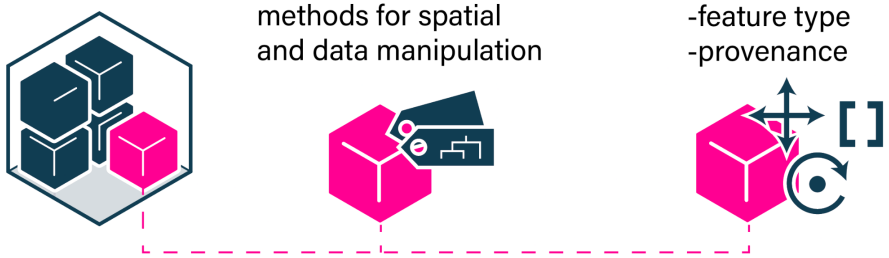
Joining spatial objects

shift z_stack no_change

Flexible data structures and operations

Dedicated Subobject Classes



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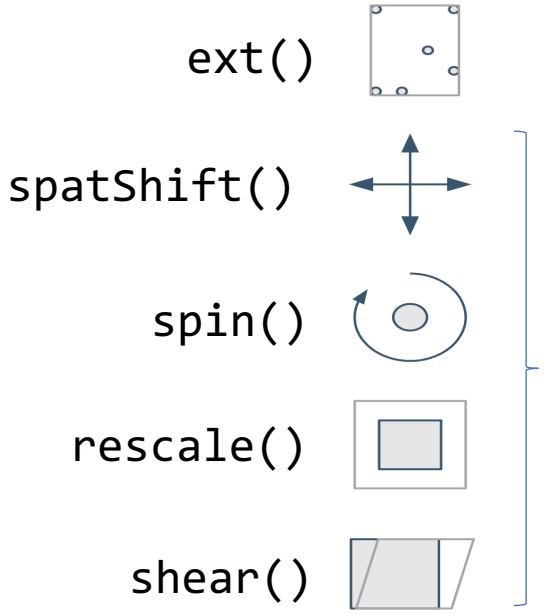

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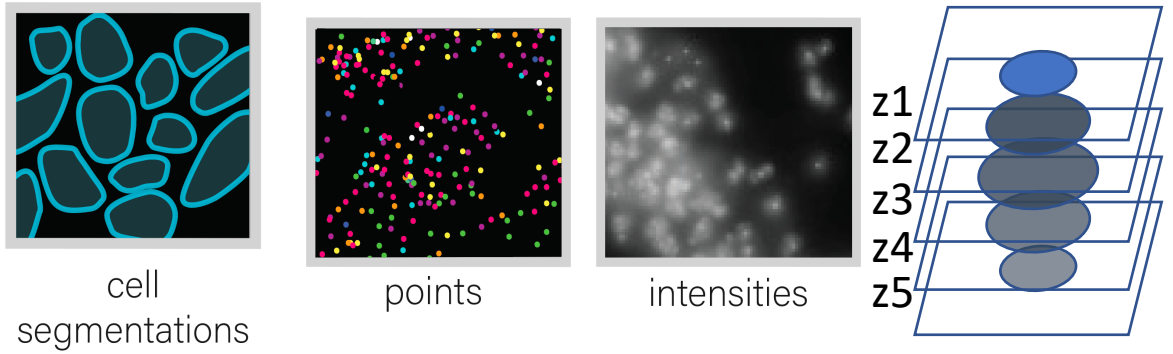
shear     : c("0.016260162601626", "0")
scale     : c("2.02210754385589", "3.04138126514911")
translate : c("1000", "20")
```

affine()

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

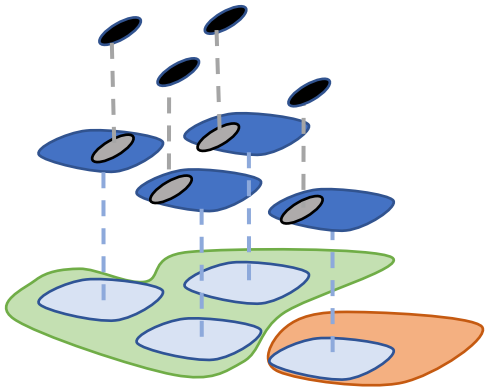
Joining spatial objects

Spatial data aggregation

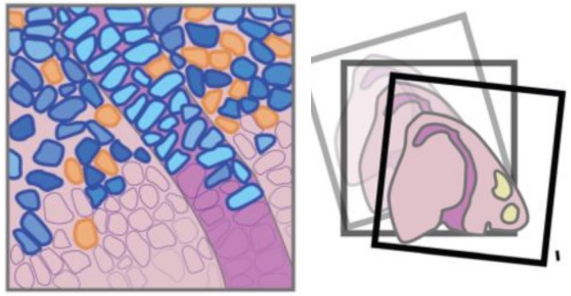


Tutorials & examples:

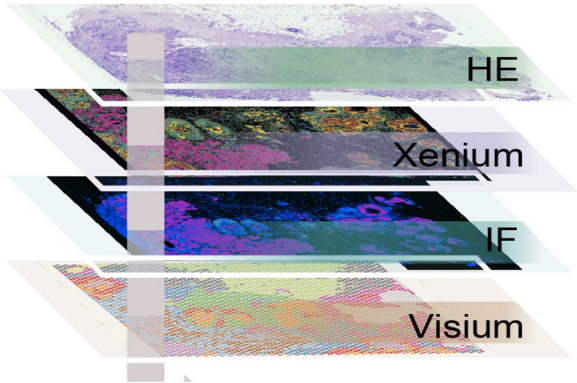
Multi-scale



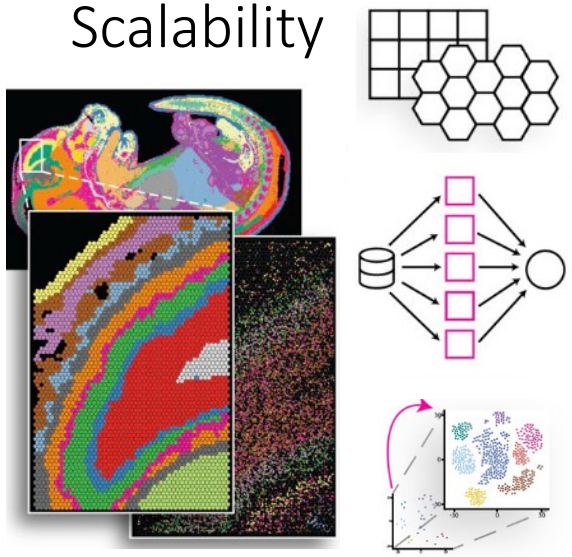
Registration & segmentation



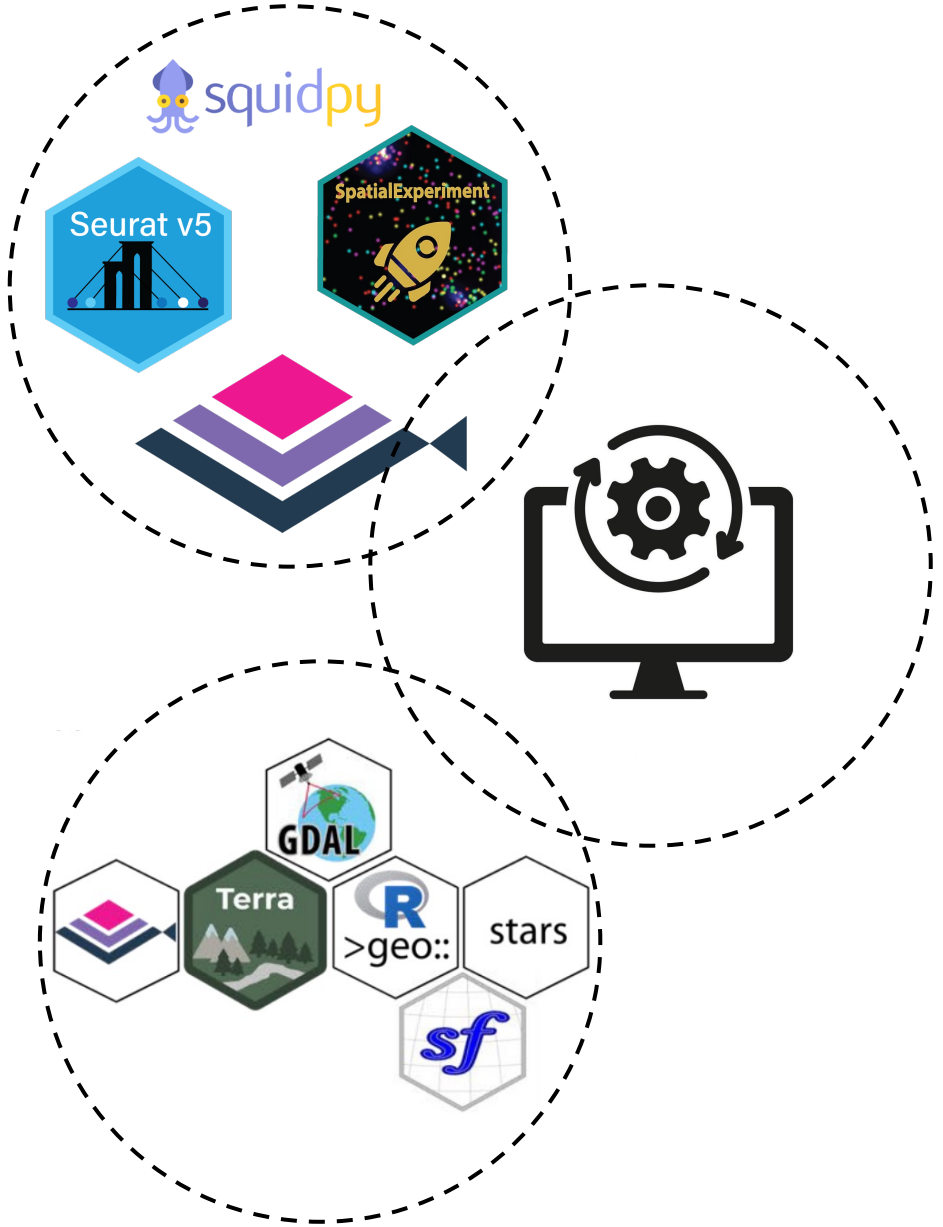
Multi-modal



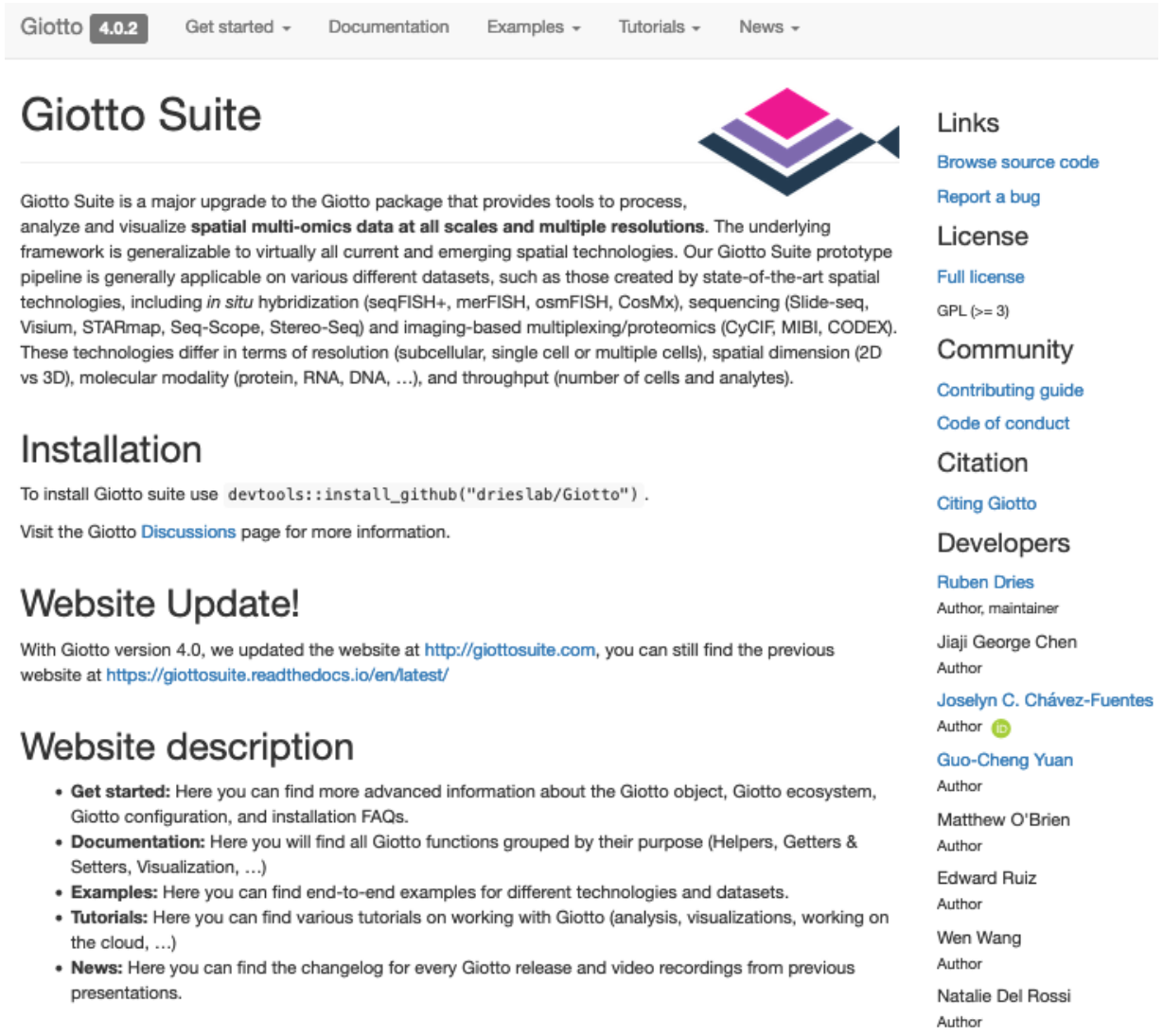
Scalability



Community & tool building:



Website: www.giottosuite.com



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**

Website: www.giottosuite.com

Giotto 4.0.2 | Get started | Documentation | Examples | Tutorials | News

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

BY DEVELOPER

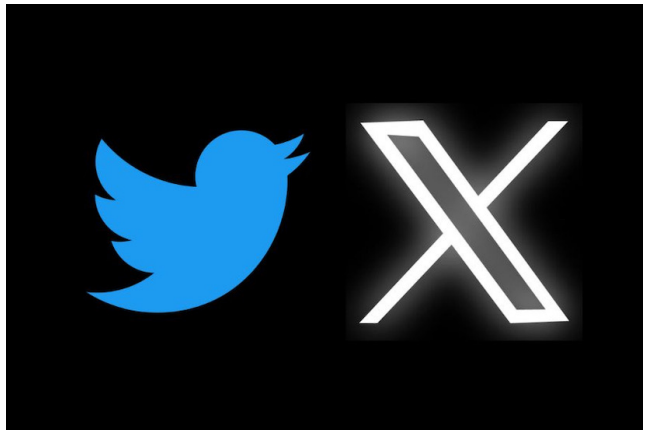
BY TESTER

Website: www.drieslab.com

Interested to:

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

Reach out to rdries@bu.edu



@GiottoSpatial

@RnDries

Acknowledgements: Giotto Suite work

Dries Laboratory
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Wen Wang
Weiping Ma
Crystal Shin
Azra Krek
Xuan Cao
Adriana Sistig
Pratishtha Guckhool
Natalie Del Rossi

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Chan Zuckerberg Initiative

Alex's Lemonade Stand Foundation for Childhood Cancer

Boston University

Boston Medical Center — Exceptional care. Without exception.

Neuroendocrine Tumor Research Foundation

Department of Defense — United States of America

NIH

American Cancer Society