

# Statistical and Computational Technologies for Modern Biology



## Challenges

Modern biotechnologies, including single-cell and spatial omics, quantitative imaging, and high-throughput genetic and chemical perturbation assays, generate increasingly complex biological datasets. Extracting robust biological knowledge and clinically actionable insights from these data requires advanced statistical and computational methods.

The Huber Group develops statistical methodologies that power emerging experimental technologies, enable biological discovery, and translate quantitative methods into reusable analytical tools for the life sciences.

## Intellectual Property

- Know-how based statistical methodologies and computational frameworks.
- Copyright associated with open-source software implementations.
- Opportunities for collaborative development and integration of computational methods.

## Technology

The Huber Group develops statistical methods for modern biotechnologies, applies them to biological discovery, and translates them into reusable tools.

- Statistical methods for emerging technologies, including single-cell and spatial omics, quantitative imaging and perturbation assays.
- Statistical inference, machine learning, data exploration and visualisation for complex biological datasets.
- Computational integration of observational molecular profiling with genetic and chemical perturbation experiments to identify causal biological mechanisms and therapeutic intervention points.
- Development of practical computational methods and open-source software through the Bioconductor ecosystem ("Translational Statistics").

**Key features:** statistical inference, machine learning, multimodal data integration, single-cell analysis, spatial omics, quantitative imaging, CRISPR and drug perturbation analysis, reusable computational workflows.

## Internal EMBLEM Reference

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## Key Inventors

Dr. Wolfgang Huber, Group Leader  
"Quantitative Biology and Statistics",  
EMBL Heidelberg, Germany

## EMBLEM TECHNOLOGY TRANSFER GMBH



Boxbergering 107

D-69126 Heidelberg

Germany



Tel.: +49 (0) 6221 363 22 10



[info@embl-em.de](mailto:info@embl-em.de)



[www.embl-em.de](http://www.embl-em.de)

Dr. Laurène Ramos Martins

[martins@embl-em.de](mailto:martins@embl-em.de)

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## Applications

- Single-cell and spatial omics analysis
- Functional precision medicine
- Quantitative imaging
- CRISPR and drug perturbation studies
- Multi-omics integration
- Biomarker discovery
- Drug response analysis

## Software

Representative software implementing the group's methodologies includes DESeq2, LEMUR, HTSeq, glmGamPoi and other Bioconductor packages.

## Resources

- Bioconductor open-source software ecosystem supporting genome-scale data analysis.
- Single-cell, spatial omics, quantitative imaging and perturbation datasets used to develop and validate statistical methods.
- Reusable computational workflows for high-dimensional biological data analysis.

## Benefits

- Statistical methods designed for modern biotechnologies
- Robust analysis of high-dimensional biological data
- Integration of multimodal datasets
- Translation into reusable computational tools
- Open science and reproducible research
- Broad applicability from basic research to precision medicine

## Keywords

# Single-cell omics; # Spatial omics; # Statistical genomics; # Computational biology; # Machine learning; # Precision oncology; # Functional precision medicine; # Bioconductor; # Translational statistics

## Seeking

- Collaborations
- Commercial partners
- Licensing
- Sponsored research

## Commercial Opportunity

Potential applications include pharmaceutical and biotechnology R&D, precision oncology, clinical bioinformatics, AI-enabled life science platforms, drug discovery, biomarker discovery, spatial biology and commercial omics analysis workflows.

## Further Reading

- [1] [10.1038/s41588-024-01996-0](https://doi.org/10.1038/s41588-024-01996-0)
- [2] [10.1038/s41592-024-02212-x](https://doi.org/10.1038/s41592-024-02212-x)
- [3] [10.1038/s41592-025-02772-6](https://doi.org/10.1038/s41592-025-02772-6)
- [4] [10.1038/s41592-023-01814-1](https://doi.org/10.1038/s41592-023-01814-1)

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D-69126 Heidelberg  
Germany



Tel.: +49 (0) 6221 363 22 10



[info@embl-em.de](mailto:info@embl-em.de) Dr. Laurène Ramos Martins



[www.embl-em.de](http://www.embl-em.de) [martins@embl-em.de](mailto:martins@embl-em.de)