CURRICULUM VITAE
Lukas M. Weber, PhD

CONTACT DETAILS

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EDUCATION AND TRAINING

Postdoctoral

2019–2023	Postdoctoral Research Fellow
	Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health
	Advisor: *Dr. Stephanie Hicks*

Degrees

Ph.D. (2019)	Biostatistics, University of Zurich, Switzerland
	Advisor: *Dr. Mark D. Robinson*
	Thesis: *Statistical and computational method development and benchmarking for analysis of high-dimensional single-cell cytometry data*
M.Sc. (2014)	Statistics, ETH Zurich, Switzerland
	Advisors: *Dr. Mark D. Robinson, Dr. Peter Bühlmann*
	Thesis: *Model selection techniques for detection of differential gene splicing*
B.Sc. Hons (2010)	Physics, Australian National University, Canberra, Australia
M.Ec. (2005)	Economics, University of Western Australia, Perth, Australia
B.Sc. (2002)	Physics & Mathematics, University of Western Australia, Perth, Australia

PROFESSIONAL EXPERIENCE

Faculty

○ Assistant Professor, Department of Biostatistics, Boston University School of Public Health (2023–current).

Other Professional Experience

○ Teaching Assistant: Institute of Molecular Life Sciences, University of Zurich, Switzerland. (2015–2019).
○ Teaching Assistant: Seminar for Statistics, ETH Zurich, Switzerland. (2013–2014).
○ Scientific Assistant: Swiss Federal Institute of Aquatic Science and Technology (Eawag), Switzerland. (2014–2014).
○ Policy Officer / Senior Policy Officer: Department of Climate Change, Canberra, Australia. (2011–2012).
○ Policy Analyst: Department of the Treasury, Canberra, Australia. (2006–2011).
○ Research Assistant: University of Western Australia, Perth, Australia. (2000–2004).

PROFESSIONAL MEMBERSHIPS

○ New England Statistical Society (NESS). (2024–current).

○ American Statistical Association (ASA) Section on Statistics in Genomics and Genetics (SSGG). (2023–current).

○ American Statistical Association (ASA). (2023–current).

○ Eastern North American Region (ENAR) of the International Biometric Society (IBS). (2022–current).

HONORS AND AWARDS

○ Paper on nnSVG for the identification of spatially variable genes (Weber et al., 2023) featured in **Editors' Highlights for Biotechnology and Methods** by the editors of the peer-reviewed journal *Nature Communications* (2023).

○ Selection as part of **2023 Emerging Leaders in Computational Oncology** symposium at Memorial Sloan Kettering Cancer Center, New York, NY, United States. (2023).

○ **Travel Awardee** for attendance at *American College of Neuropsychopharmacology (ACNP) 2022*, Phoenix, AZ, United States. (2022).

○ Awarded **K99/R00 Pathway to Independence Award** (NIH NHGRI) on the development of unsupervised statistical methodology for analysis of spatially-resolved transcriptomics data. (2022).

○ Awarded **Early Career Research Symbiont Award** in recognition of efforts to create reproducible data and software resources. (2021).

○ **Student Travel Award** for attendance at *ICCABS 2018: IEEE 8th International Conference on Computational Advances in Bio and Medical Sciences; Workshop on Computational Advances for Single-Cell Omics Data Analysis (CASCODA)*, Las Vegas, NV, United States. (2018).

○ **Student Travel Award** for attendance at *CYTO 2018: 33rd Congress of the International Society for Advancement of Cytometry*, Prague, Czechia. (2018).

○ **Student Travel Award** for attendance at *CYTO 2017: 32nd Congress of the International Society for Advancement of Cytometry*, Boston, MA, United States. (2017).

○ Paper on comparison of clustering algorithms in high-dimensional cytometry (Weber and Robinson, 2016) recognized as an **Editor's Choice** article in the peer-reviewed journal *Cytometry Part A*. (2016).

FUNDING

○ **K99/R00 NIH Pathway to Independence Award**.
National Human Genome Research Institute (NHGRI), National Institutes of Health (NIH).
Project title: *Unsupervised statistical methods for data-driven analyses in spatially resolved transcriptomics data*.
K99 mentor: *Dr. Stephanie Hicks*. K99 co-mentors: *Dr. Keri Martinowich, Dr. Roger Peng*.
Award no. K99HG012229 (K99 phase); R00HG012229 (R00 phase).
Funding duration: 02/2022–09/2023 (K99 phase); 01/2024–12/2026 (R00 phase).

○ **Forschungskredit (Candoc) der Universität Zürich**.
Competitive internal grant funding for PhD research projects at the University of Zurich, Switzerland.
Award no. FK-17-100.
Funding duration: 08/2017–06/2018.

TRAINEES AND STUDENT RESEARCH ADVISING

Student Research Advising

Master's degrees research projects:

○ Lauren Rusnak (2024). MS Applied Biostatistics (Research Experience Project), Boston University.

○ Jonathan Huang (2024). MS Applied Biostatistics (Research Experience Project), Boston University. (Joint mentorship with Dr. Huimin Cheng.)

Doctoral Thesis Committees

Committee membership:

○ Yuankai Zhang (2024–current). PhD Biostatistics, Boston University.

OTHER SERVICE AND PROFESSIONAL ACTIVITIES

Conferences

Organizational activities for conferences:

○ Session organizer for invited presentations, *Joint Statistical Meetings (JSM) 2023*. Session topic: *Statistical methods for multiple-sample spatially-resolved transcriptomics data*.

Peer Review (Journals)

Peer review activities for the following journals:

○ Nature Communications (2023 x1, 2022 x2, 2021 x1, 2020 x3, 2019 x1)
○ Bioinformatics (2024 x4, 2023 x3, 2020 x1, 2019 x1)
○ Genome Biology (2024 x1, 2023 x3, 2022 x1, 2019 x2)
○ Cytometry Part A (2024 x1, 2020 x1, 2019 x1, 2018 x4, 2017 x1)
○ Communications Biology (2023 x1)
○ PLOS Computational Biology (2022 x1)
○ GigaScience (2021 x2)
○ Journal of Open Source Software (2020 x2, 2019 x1)
○ Scientific Reports (2018 x2, 2017 x1)

Peer Review (Funding Applications)

○ Boston University School of Public Health, Population Health Data Science Program, Seed Funding Awards. (2023, 3x applications).

Other Service Activities

○ Presentation on research topics for graduate student projects ("Spring Research Blitz"), Department of Biostatistics, Boston University School of Public Health. (2024).
○ Evaluating applications and meeting applicants for PhD program, Department of Biostatistics, Boston University School of Public Health. (2023-24 applications).
○ Reviewing papers for Biostatistics Student Paper Competition, Department of Biostatistics, Boston University School of Public Health. (2024, 3x papers).
○ Presentation on research topics for graduate student projects ("Meet the Mentor"), Department of Biostatistics, Boston University School of Public Health. (2023).

PUBLICATIONS

*A complete list of publications is also available from Google Scholar. The * indicates equal authorship.*

Preprint Articles

1 Hippen A.A., Davidson N.R., Barnard M.E., **Weber L.M.**, Gertz J., Doherty J.A., Hicks S.C., and Greene C.S. (2023). *Deconvolution reveals compositional differences in high-grade serous ovarian cancer subtypes.* bioRxiv (preprint).

Journal Articles (Peer-Reviewed and Published)

1. **Weber L.M.***, Divecha H.R.*, Tran M.N., Kwon S.H., Spangler A., Montgomery K.D., Tippani M., Bharadwaj R., Kleinman J.E., Page S.C., Hyde T.M., Collado-Torres L., Maynard K.R., Martinowich K.*, and Hicks S.C.* (2023). *The gene expression landscape of the human locus coeruleus revealed by single-nucleus and spatially-resolved transcriptomics.* eLife, 12:RP84628.

2. Tippani M., Divecha H.R., Catallini II J.L., Kwon S.H., **Weber L.M.**, Spangler A., Jaffe A.E., Hyde T.M., Kleinman J.E., Hicks S.C., Martinowich K., Collado-Torres L., Page S.C., and Maynard K.R. (2023). *VistoSeg: Processing utilities for high-resolution images for spatially resolved transcriptomics data.* Biological Imaging, 3, e23.

3. Hippen A.A., Omran D.K., **Weber L.M.**, Jung E., Drapkin R., Doherty J.A., Hicks S.C., and Greene C.S. (2023). *Performance of computational algorithms to deconvolve heterogeneous bulk ovarian tumor tissue depends on experimental factors.* Genome Biology, 24, 239.

4. **Weber L.M.**, Saha A., Datta A., Hansen K.D., and Hicks S.C. (2023). *nnSVG for the scalable identification of spatially variable genes using nearest-neighbor Gaussian processes.* Nature Communications, 14, 4059. (Note: Article featured in "Editors' Highlights for Biotechnology and Methods".)

5. Tiberi S., Crowell H.L., Samartsidis P., **Weber L.M.**, and Robinson M.D. (2023). *distinct: a novel approach to differential distribution analyses.* Annals of Applied Statistics, 17, 2, 1681–1700.

6. Krieg C., **Weber L.M.**, Fosso B., Hardiman G., Mileti E., El Aidy S., Marzano M., Robinson M.D., and Guglietta S. (2022). *Complement downregulation promotes an inflammatory signature that renders colorectal cancer susceptible to immunotherapy.* Journal for ImmunoTherapy of Cancer, 10, e004717.

7. Pardo B., Spangler A., **Weber L.M.**, Hicks S.C., Jaffe A.E., Martinowich K., Maynard K.R., and Collado-Torres L. (2022). *spatialLIBD: an R/Bioconductor package to visualize spatially-resolved transcriptomics data.* BMC Genomics, 23, 434.

8. Righell D.*, **Weber L.M.***, Crowell H.L.*, Pardo B., Collado-Torres L., Ghazanfar S., Lun A.T.L., Hicks S.C.*, and Risso D.* (2022). *SpatialExperiment: infrastructure for spatially-resolved transcriptomics data in R using Bioconductor.* Bioinformatics, 38(11), 3128-3131.

9. Petrillo M., Fabbri M., Kagkli D.M. et al. (2022). *A roadmap for the generation of benchmarking resources for antimicrobial resistance detection using next generation sequencing.* F1000Research, v2, 10, 80.

10. **Weber L.M.**, Hippen A.A., Hickey P.F., Berrett K.C., Gertz J., Doherty J.A., Greene C.S., and Hicks S.C. (2021). *Genetic demultiplexing of pooled single-cell RNA-sequencing samples in cancer facilitates effective experimental design.* GigaScience, 10, 9, giab062.

11. Liechti T., **Weber L.M.**, Ashhurst T.M., Stanley N., Prlic M., Van Gassen S., and Mair F. (2021). *An updated guide for the perplexed: cytometry in the high-dimensional era.* Nature Immunology, 22, 1190–1197.

12. Hippen A.A., Falco M.M., **Weber L.M.**, Erkan E.P., Zhang K., Doherty J.A., Vähärautio A., Greene C.S., and Hicks S.C. (2021). *miQC: An adaptive probabilistic framework for quality control of single-cell RNA-sequencing data.* PLOS Computational Biology, 17, 8, e1009290.

13. Maynard K.R.*, Collado-Torres L.*, **Weber L.M.**, Uytingco C., Barry B.K., Williams S.R., Catallini J.L. II, Tran M.N., Besich Z., Tippani M., Chew J., Yin Y., Kleinman J.E., Hyde T.M., Rao N., Hicks S.C., Martinowich K.*, Jaffe A.E.* (2021). *Transcriptome-scale spatial gene expression in the human dorsolateral prefrontal cortex.* Nature Neuroscience, 24, 425–436.

14. Shaul M.E., Eyal O., Guglietta S., Aloni P., Zlotnik A., Forkosh E., Levy L., **Weber L.M.**, Levin Y., Pomerantz A., Nechushtan H., Eruslanov E., Singhal S., Robinson M.D., Krieg C., and Fridlender Z.G. (2020). *Circulating neutrophil subsets in advanced lung cancer patients exhibit unique immune signature and relate to prognosis.* FASEB Journal, 34, 3, 4204–4218.

15. **Weber L.M.**, Saelens W., Cannoodt R., Soneson C., Hapfelmeier A., Gardner P.P., Boulesteix A.-L., Saeys Y., and Robinson M.D. (2019). *Essential guidelines for computational method benchmarking.* Genome Biology, 20, 125.

16. **Weber L.M.** and Soneson C. (2019). *HDCytoData: Collection of high-dimensional cytometry benchmark datasets in Bioconductor object formats.* F1000Research, 8, 1459, v2.

17 **Weber L.M.**, Nowicka N., Soneson C., and Robinson M.D. (2019). *diffcyt: Differential discovery in high-dimensional cytometry via high-resolution clustering.* Communications Biology, 2, 183.

18 Krieg C., Nowicka M., Guglietta S., Schindler S., Hartmann F.J., **Weber L.M.**, Dummer R., Robinson M.D., Levesque M.P.* and Becher B.* (2018). *High-dimensional single-cell analysis predicts response to anti-PD-1 immunotherapy.* Nature Medicine, 24, 2, 144–153.

19 Nowicka N., Krieg C., Crowell H.L., **Weber L.M.**, Hartmann F.J., Guglietta S., Becher B., Levesque M.P., and Robinson M.D. (2019). *CyTOF workflow: differential discovery in high-throughput high-dimensional cytometry datasets.* F1000Research, 6, 748, v4.

20 **Weber L.M.** and Robinson M.D. (2016). *Comparison of clustering methods for high-dimensional single-cell flow and mass cytometry data.* Cytometry Part A, 89A, 1084–1096. (Note: Selected as an "Editor's Choice" article.)

21 Hartmann F.J., Bernard-Valnet R., Quériault C., Mrdjen D., **Weber L.M.**, Galli E., Krieg C., Robinson M.D., Nguyen X.H., Dauvilliers Y., Liblau R.S., and Becher B. (2016). *High-dimensional single-cell analysis reveals the immune signature of narcolepsy.* Journal of Experimental Medicine, 213, 12, 2621–2633.

22 Burger A., Lindsay H., Felker A., Hess C., Anders C., Chiavacci E., Zaugg J., **Weber L.M.**, Catena R., Jinek M., Robinson M.D., and Mosimann C. (2016). *Maximizing mutagenesis with solubilized CRISPR-Cas9 ribonucleoprotein complexes.* Development, 143, 2025–2037.

23 Jackson K., **Weber L.M.**, and Tennant M. (2016). *A retrospective study of the effectiveness of four different treatments of periodontal disease in equine cheek teeth.* Journal of Veterinary Dentistry, 33, 2, 83–89.

24 Robinson M.D., Kahraman A., Law C.W., Lindsay H., Nowicka M., **Weber L.M.**, and Zhou X. (2014). *Statistical methods for detecting differentially methylated loci and regions.* Frontiers in Genetics, 5, 324, 1–7.

PRESENTATIONS

Presentations (Invited)

1 Personalized Health 2024, ETH Zurich, Zurich, Switzerland. (2024). (Keynote presentation). *Methods for scalable R-based analysis workflows for spatial transcriptomics data.*

2 University of Zurich, Zurich Seminars in Bioinformatics, Zurich, Switzerland. (2024). *Spatially variable genes: Methods, benchmarking, and future directions.*

3 NESS 2024: New England Statistics Symposium, Storrs, CT, United States. (2024). *smoothclust: Identification of spatial domains by spatial smoothing in spatial transcriptomics data.*

4 University of Southern California, Division of Biostatistics, Seminar Series, Los Angeles, CA, United States. (2023). *nnSVG for the identification of spatially variable genes and unsupervised analyses of spatial transcriptomics data.*

5 Columbia University, Department of Biostatistics, Statistical Genomics and Genetics Seminar Series. (Virtual). (2023). *nnSVG for the identification of spatially variable genes and unsupervised analyses of spatial transcriptomics data.*

6 Boston University, Chobanian and Avedisian School of Medicine, Section on Computational Biomedicine, Spatial Biology Seminar Series. (Virtual). (2023). *nnSVG for the identification of spatially variable genes and unsupervised analyses of spatial transcriptomics data.*

7 Joint Statistical Meetings (JSM) 2023, Toronto, Canada. (2023). *nnSVG for preprocessing, feature selection, and quality control in multi-sample spot-based spatially-resolved transcriptomics data.*

8 Statistical Methods in Imaging Conference 2023, Annual Meeting of the ASA Statistics in Imaging Section, Minneapolis, MN, United States. (2023). *nnSVG: scalable identification of spatially variable genes using nearest-neighbor Gaussian processes.*

9 Emerging Leaders in Computational Oncology 2023, Memorial Sloan Kettering Cancer Center, New York, NY, United States. (2023). *Unsupervised statistical methods and data-driven analysis workflows for spatially-resolved transcriptomics.*

10 European Conference on Computational Biology (ECCB), Workshop NTB-W04. (Virtual). (2022). *Scalable identification of spatially variable genes with nnSVG and Bioconductor.*

11 R/Medicine. (Virtual). (2022). *Unsupervised analyses of spatially-resolved transcriptomics data with nnSVG and R/Bioconductor.*

12 Sydney Bioinformatics Seminar Series, Sydney Precision Bioinformatics Alliance, University of Sydney. (Virtual). (2022). *nnSVG: scalable identification of spatially variable genes in spatially-resolved transcriptomics data.*

13 ENAR (Eastern North American Region of the International Biometric Society) Spring Meeting, Houston, TX, United States. (2022). *nnSVG: scalable identification of spatially variable genes using nearest-neighbor Gaussian processes.*

14 ICCABS 2018 (IEEE 8th International Conference on Computational Advances in Bio and Medical Sciences): 1st Workshop on Computational Advances for Single-Cell Omics Data Analysis (CASCODA), Las Vegas, NV, United States. (2018). *Methods, tools, and resources for differential discovery in high-dimensional cytometry data.*

15 1st Swiss Cytometry Meeting, Lausanne, Switzerland. (2018). *Statistical methods for differential discovery in high-dimensional cytometry data.*

16 European Bioconductor Meeting 2017, Cambridge, United Kingdom. (2017). *Statistical methods for differential discovery in high-dimensional cytometry data.*

Presentations (Other)

1 BioC2024: Bioconductor Conference, Grand Rapids, MI, United States. (2024). *smoothclust: Identification of spatial domains by smoothing for compositional analyses in spatial transcriptomics data.*

2 STATGEN 2024: Conference on Statistics in Genomics and Genetics, Pittsburgh, PA, United States. (2024). *smoothclust: Identification of spatial domains by spatial smoothing in spatial transcriptomics data.*

3 Boston University, School of Public Health, Department of Biostatistics, Boston, MA, United States. (2023). *Unsupervised statistical methods and data-driven analysis workflows for spatially-resolved transcriptomics.*

4 Ohio State University, College of Medicine, Department of Biomedical Informatics, Columbus, OH, United States. (2023). *Unsupervised statistical methods and data-driven analysis workflows for spatially-resolved transcriptomics.*

5 University of Colorado, School of Medicine, Department of Biomedical Informatics. (Virtual). (2023). *Unsupervised statistical methods and data-driven analysis workflows for spatially-resolved transcriptomics.*

6 Emory University, Rollins School of Public Health, Department of Biostatistics and Bioinformatics, Atlanta, GA, United States. (2023). *Unsupervised statistical methods and data-driven analysis workflows for spatially-resolved transcriptomics.*

7 University of Utah, School of Medicine, Department of Human Genetics, Salt Lake City, UT, United States. (2023). *Unsupervised statistical methods and data-driven analysis workflows for spatially-resolved transcriptomics.*

8 University of Minnesota, School of Public Health, Division of Biostatistics, Minneapolis, MN, United States. (2023). *Unsupervised statistical methods and data-driven analysis workflows for spatially-resolved transcriptomics.*

9 Northwestern University, Feinberg School of Medicine, Department of Cell and Developmental Biology. (Virtual). (2023). *Unsupervised statistical methods and data-driven analysis workflows for spatially-resolved transcriptomics.*

10 Bioc2022 Bioconductor annual conference, Seattle, WA, United States. (2022). *nnSVG: scalable identification of spatially variable genes using nearest-neighbor Gaussian processes.*

11 BLAST Working Group seminar, Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, United States. (2022). *nnSVG: scalable identification of spatially variable genes using nearest-neighbor Gaussian Processes.*

12 Bioc2021 Bioconductor annual conference. (Virtual). (2021). *Workshop on 'Orchestrating Spatially-Resolved Transcriptomics Analysis with Bioconductor (OSTA)'.*

13 Bioc2021 Bioconductor annual conference. (Virtual). (2021). *Workshop on 'SpatialExperiment'.* (Joint presentation with Dario Righelli and Helena L. Crowell.)

14 European Bioconductor Meeting 2020. (Virtual). (2020). *Workshop on 'SpatialExperiment'.* (Joint presentation with Dario Righelli and Helena L. Crowell.)

15 Bioc2020 Bioconductor annual conference. (Virtual). (2020). *Unsupervised analysis of transcriptome-scale spatial gene expression data in the human prefrontal cortex.*

16 Johns Hopkins University 13th Annual Genomics and Bioinformatics Symposium and Poster Session, Baltimore, MD, United States. (2019). *Comparison of dimension reduction algorithms for visualization of single-cell data.*

17 European Bioconductor Meeting 2018, Munich, Germany. (2018). *HDCytoData package: High-dimensional cytometry benchmark datasets in Bioconductor formats.*

18 CYTO 2017: 32nd Congress of the International Society for Advancement of Cytometry, Boston, MA, United States. (2017). *Statistical methods for differential discovery in high-dimensional cytometry data.*

19 IMLS Scientific Retreat 2017 (Institute of Molecular Life Sciences, University of Zurich), Emmetten, Switzerland. (2017). *Comparison of clustering methods for high-dimensional single-cell flow and mass cytometry (CyTOF) data.*

20 European Bioconductor Developers' Meeting 2015, Cambridge, United Kingdom. (2015). *regsplice: Lasso-based model selection for improved detection of differential exon usage.*

21 C1omics 2015: Single-Cell Omics Methods and Applications, Manchester, United Kingdom. (2015). *Comparison of clustering methods for high-dimensional single-cell flow and mass cytometry data.*

Posters

1 American College of Neuropsychopharmacology (ACNP) 2023, Tampa, FL, United States. (2023). *nnSVG for the identification of spatially variable genes and improved computational analyses of spatial transcriptomic data from postmortem brain tissue.*

2 National Human Genome Research Institute (NHGRI) Research Training and Career Development Annual Meeting 2023, Salt Lake City, UT, United States. (2023). *nnSVG: scalable identification of spatially variable genes using nearest-neighbor Gaussian processes.*

3 American College of Neuropsychopharmacology (ACNP) 2022, Phoenix, AZ, United States. (2022). (Travel awardee.) *The gene expression landscape of the human locus coeruleus revealed by single-nucleus and spatially-resolved transcriptomics.*

4 ASHG Institute for Genomic Medicine Symposium on Spatial Omics. (Virtual). (2020). *Unsupervised analysis of transcriptome-scale spatial gene expression in human dorsolateral prefrontal cortex using spatial transcriptomics data.*

5 Genome Informatics. (Poster and lightning talk.) (Virtual). (2020). *Unsupervised analysis of transcriptome-scale spatial gene expression in human dorsolateral prefrontal cortex using spatial transcriptomics data.*

6 CYTO 2018: 33rd Congress of the International Society for Advancement of Cytometry, Prague, Czechia. (2018). *diffcyt: Differential discovery in high-dimensional cytometry via high-resolution clustering.*

7 Ascona Workshop 2017: Statistical Challenges in Single-Cell Biology, Ascona, Switzerland. (2017) *Statistical methods for differential discovery in high-dimensional cytometry data.*

8 ICML 2016 (International Conference on Machine Learning): Workshop on Computational Biology, New York, NY, United States. (2016). *Comparison of clustering methods for high-dimensional single-cell flow and mass cytometry (CyTOF) data.*

9 SIB Days: Swiss Institute of Bioinformatics annual conference, Biel/Bienne, Switzerland. (2016). *Comparison of clustering methods for high-dimensional single-cell flow and mass cytometry (CyTOF) data.*

10 IMLS Scientific Retreat 2015 (Institute of Molecular Life Sciences, University of Zurich), Morschach, Switzerland. (2015). *Improving power to detect differential exon usage by L1-regularization (lasso) model selection.*

TEACHING ACTIVITIES

Workshops

○ *Workshop on Data Visualization Techniques and Tools* (with Dr. Prasad Patil), Population Health Data Science Program, Boston University School of Public Health. (2024).

○ *GitHub for R Projects* (with Dr. Shariq Mohammed), Biostatistics Student Association Seminar Series, Department of Biostatistics, Boston University School of Public Health. (2024).
○ Data Carpentry, University of Zurich, Switzerland. (2017).
○ Mass Cytometry and Data Analysis Workshop, University of Zurich, Switzerland. (2017).
○ Mass Cytometry and Data Analysis Workshop, University of Zurich, Switzerland. (2017).
○ Data Carpentry, University of Zurich, Switzerland. (2016).
○ Data Carpentry, University of Zurich, Switzerland. (2016).
○ Software Carpentry, ResBaz Perth, Murdoch University, Australia. (2016).

Coursework Teaching Assistance

○ *SPH BS 831 Genomics Data Mining and Statistics (guest lecture on single-cell RNA sequencing and spatial transcriptomics analysis workflows), Dr. Seung Hoan Choi*, Boston University School of Public Health. (2024).
○ *Statistical Programming Paradigms and Workflows (guest lectures on version control using git and GitHub), Dr. Stephanie Hicks*, Johns Hopkins Bloomberg School of Public Health. (2022).
○ *Advanced Data Science (guest lecture on resampling techniques), Dr. Stephanie Hicks*, Johns Hopkins Bloomberg School of Public Health. (2019).
○ *Practical Bioinformatics (session on R Markdown and R programming), Dr. Mark Robinson*, University of Zurich. (2019).
○ *Statistical Analysis of High-Throughput Genomic and Transcriptomic Data (session on analysis of high-dimensional cytometry data), Dr. Mark Robinson*, University of Zurich. (2018).
○ *Practical Bioinformatics (session on analysis of single-cell RNA-sequencing data), Dr. Mark Robinson*, University of Zurich. (2018).
○ *Statistical Analysis of High-Throughput Genomic and Transcriptomic Data (session on analysis of high-dimensional cytometry data), Dr. Mark Robinson*, University of Zurich. (2017).
○ *Practical Bioinformatics (teaching assistant), Dr. Mark Robinson*, University of Zurich. (2015).
○ *Statistik II (applied statistics and R programming, teaching assistant for exercise sessions)*, ETH Zurich. (2014).
○ *Wahrscheinlichkeit und Statistik (probability and statistics, teaching assistant for exercise sessions)*, ETH Zurich. (2013).

SOFTWARE PACKAGES AND PROJECTS

Links to additional code and data resources are available from GitHub.

Software Packages

1 **nnSVG**: R/Bioconductor package to identify spatially variable genes in spatial transcriptomics data. Available from Bioconductor.

2 **SpatialExperiment**: R/Bioconductor data structure for storing spatial transcriptomics datasets. (Joint project with Dario Righelli and Helena L. Crowell.) Available from Bioconductor.

3 **ggspavis**: R/Bioconductor package containing visualization functions for spatial transcriptomics data. (Joint project with Helena L. Crowell.) Available from Bioconductor.

4 **diffcyt**: R/Bioconductor package implementing a computational framework for differential discovery analyses in high-dimensional cytometry data. Available from Bioconductor.

5 **regsplice**: R/Bioconductor package implementing statistical methodology for detection of differential splicing (differential exon usage) in RNA-sequencing data. Available from Bioconductor.

Other Software Projects

1 **Best Practices for Spatial Transcriptomics Analysis with Bioconductor**: Online book containing interactive example analysis workflows for spatial transcriptomics data. Link.

2 **CrispantCal**: R/Shiny web application to calculate injection mix volumes for CRISPR-Cas9 experiments (described in: Burger et al. 2016). Link.

Data Packages

1. **WeberDivechaLCdata**: R/Bioconductor package containing datasets from paper on analyses of single-nucleus and spatial transcriptomics data from the human locus coeruleus (Weber and Divecha et al. 2022). Available from Bioconductor.

2. **STexampleData**: R/Bioconductor package containing a collection of spatial transcriptomics datasets in SpatialExperiment Bioconductor format. Available from Bioconductor.

3. **HDCytoData**: R/Bioconductor package containing a collection of publicly available high-dimensional cytometry benchmark datasets in Bioconductor formats. Available from Bioconductor.