



Malte D. Luecken

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I lead the integrative genomics lab at Helmholtz Munich, between the institute for Computational Biology and the Institute of Lung Health & Immunity. With a background in physics, statistics, and computational biology, I have extensive expertise in single-cell genomics (SCG), machine learning, data integration, and benchmarking. Together with my network of experimental collaborators, I have used this expertise to tackle complex biological and medical challenges in various diseases, with particular focus on the lung. My lab is heavily involved in the Human Cell Atlas (HCA), where I lead the HCA integration team, an international team aiming to build integrated reference atlases for human tissues and organs. I have also co-founded the Open Problems project, a living benchmarking platform that sets standards for computational methods in SCG and has engaged over 3000 machine learning scientists to address challenges in SCG. Overall, my research goal is to build better clinical diagnostic and prognostic models to inform the treatment of disease leveraging large single-cell data resources and methods from machine learning and classical statistics.

Work Experience

Sept 2022 – now

Principal Investigator, Institute for Computational Biology, Institute for Lung Health & Immunity, Helmholtz Munich, Munich, Germany

- Independent group leader of the “Integrative Genomics” group, with 5 PhD students, 2 postdocs, and 4 affiliated group members
- Translating machine learning models on single-cell data to clinical applications in lung research

Sept 2022 – now

Team Lead, Human Cell Atlas Integration Team, Helmholtz Munich, Munich, Germany

- Coordinating data integration activities for the Human Cell Atlas across 6 sites on 3 continents, leading a team of 18 PhD students and Postdocs
- Engaging with stakeholders across 18 tissue biological networks across the Human Cell atlas, which consists of 4000 members

Sept 2024 – now

Consultant, CatalYm GmbH, Munich, Germany

- Technical consulting and supervision of bioinformaticians working on spatial genomics analysis of novel cancer treatments

April 2022 – Jul 2022

Computational biologist, Chan Zuckerberg Initiative Foundation

- Building an automated cell type annotation tool for single-cell desktop visualization platform cellxgene

Mar 2020 – Aug 2022

Team Leader Single-cell Atlasing, Machine Learning Group, Institute for Computational Biology, Helmholtz Munich, Munich, Germany

- Developing and applying methods for data integration of single-cell datasets
- Leading lung and atlas building activities within the lab for 2 large international grants and organising a team of 5-10 PhD students and Postdocs
- Supervision and mentorship of postdocs and PhD students working on data integration and lung research within the Theis lab

Jan 2018 – Aug 2022

Postdoctoral researcher, Machine Learning Group, Institute for Computational Biology, Helmholtz Munich, Munich, Germany

- Developing single-cell RNA-seq analysis tools using Machine Learning methods
- Leading an international effort to standardise benchmarking in single-cell analysis (Open Problems in Single-cell Analysis: <https://openproblems.bio>)
- Spearheading collaborations for single-cell analysis in brain, pancreas and lung
- Supervising Master and PhD students

- Feb 2021 – Oct 2021** **Interim group leader, Machine Learning Group, Institute for Computational Biology, Helmholtz Munich**, Munich, Germany
- Managing a group of 35 PhD students and PostDocs
 - Representing the lab externally in grant meetings and conferences
 - Screening potential PhD and Postdoc candidates
- Nov 2016 – Dec 2017** **Translational bioinformatics consultant, UCB Pharma**, Braine L'Alleud, Belgium
- Developing a software package to detect differentially regulated cellular functions in disease & application to epilepsy and rare genetic variants
 - Piloting the first single cell RNA-seq data analysis project to assess potential of the data generated

Education

- 2012-2017** **DPhil in Systems Approaches to Biomedical Science Industrial Doctorate Center**, at the Department of Statistics, **University of Oxford**
 DPhil Project: Application of Multi-Resolution Partitioning of Interaction Networks to the Study of CompleMx Disease; supervised by Prof. Charlotte M. Deane (Stats), Prof. Gesine Reinert (Stats) and Matthew Page (UCB Pharma)
- Using network approaches to integrate high-throughput biological data sets
 - Developing a methodology to interpret differentially expressed genes in terms of dysregulated cellular functions
- 2007-2012** **BSc MPhys (Master of Physics) with 1st degree, University of Warwick**
 Master's Project: Modelling Sickle Cells with Dr. Ellak Somfai
 4th year: Exchange at the **University of Tokyo**

Courses and Workshops

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| 2024 | Helmholtz Academy "Leading Your Group" workshops (Helmholtz Munich) |
| 2022 | Helmholtz Media training: Interview workshop (Helmholtz Munich) |
| 2020 | Helmholtz Advance career workshops (Helmholtz Munich) |
| 2019 | Supervising doctoral students (Helmholtz Munich) |
| 2018 | Public science communication (Helmholtz Munich) |
| 2017 | Analysis of single cell RNA-seq data (Cambridge) |
| 2015 | Cytoscape 3 App Development (ISMB 2015 AKES workshop) |
| 2013 | Statistical Inference, Statistical Computing (Academy for PhD training in Statistics, APTS), Python Programming Bootcamp |

Invited presentations at peer-reviewed, internationally established conferences, webinars, or advanced schools

2025:

- Invited keynote: Defining and benchmarking open problems in single-cell analysis via community engagement: a living benchmarking platform for single-cell genomics, Ascona benchmarking meeting, Ascona, Switzerland (Mar 2025)
- Invited talk: Single-cell and spatial atlasing in (lung) cancer, Munich Cancer hub, Munich, Germany (Mar 2025)

2024:

- Invited talk: Open problems in single-cell analysis: a living benchmarking platform for single-cell genomics, scverse community meeting, online (Nov 2024)
- Invited talk: Updating the human lung cell atlas, Munich-Chicago lung conference, Munich, Germany (Oct 2024)
- Invited talk: Tailoring the HCA integration team approach, HCA general meeting, Milan, Italy (Sept 2024)

- Invited talk: Building and using single-cell reference atlases, HCA Latin America Symposium, online (Jul 2024)
 - Invited keynote: Optimizing experimental design and data processing for targeted spatial experiments, VIB Spatial omics, Ghent, Belgium (June 2024)
 - Invited talk: Spapros probe-set selection for targeted spatial transcriptomics, DZL annual meeting, Bad Nauheim, Germany (June 2024)
 - Invited talk: Charting the lung: annotations and ontologies, towards a consensus lung cell atlas, ATS C3CLCN workshop, online (April 2024)
 - Invited talk: The Human Lung Cell Atlas, ATS RCMB Webinar, online, (March 2024)
- 2023:**
- Invited talk: An integrative single-cell analysis approach to study COPD endotypes, COPD-iNET symposium, Munich (October 2023)
 - Invited talk: Update on HCA integration pilot projects, HCA General Meeting, Toronto (July 2023)
 - Invited talk: The human cell atlas integration team, HCA Webinar series, online (February 2023)
 - Invited talk: Integrating datasets to build a reference human lung cell atlas, GeneQuant 2023, Freising, Germany (March 2023)
- 2022:**
- Invited keynote: Integrating datasets to build a reference human lung cell atlas, DZG Early Career Scientist Symposium "Single Cell Analysis", online (November 2022)
 - Invited speaker: Benchmarking data integration to build a single-cell reference atlas of the human lung, IBS symposium, online (October 2022)
 - Invited speaker: Using the integrated Human Lung Cell Atlas, ERS General Meeting, European Respiratory Society, Barcelona, Spain (Sept 2022)
 - Invited speaker: The integrated Human Lung Cell Atlas, ERS General Meeting, European Respiratory Society, Barcelona, Spain (Sept 2022)
 - Invited speaker: Creating a usable reference atlas, Human Cell Atlas General Meeting, Vienna, Austria (June 2022)
 - Invited speaker: Benchmarking data integration to build an integrated human lung cell atlas, Single-cell Network Ghent Kickoff, Ghent, Belgium (May 2022)
 - Invited speaker: The integrated Human Lung Cell Atlas, 20th Lung Science Conference, European Respiratory Society, Estoril, Portugal (Mar 2022)
- 2021:**
- Invited speaker: Building and using (multi-modal) single-cell reference atlases, INSERM workshop 265, moved online (Dec 2021)
 - Invited speaker: Building the integrated human lung cell atlas, Single-cell Omics Germany webinar series, online (Oct 2021)
 - Invited panellist: Multimodal single-cell data, open benchmarks & a NeurIPS 2021 competition, Models, Inference & Algorithms (MIA) webinar series, online (Sept 2021)
 - Invited speaker: Leveraging the Lung Cell Atlas to study SARS-CoV-2, Indian Society of Human Genetics Symposium on Host response in COVID, online (Sept 2021)
 - Invited speaker: Integrating diverse single-cell datasets: a consistent view of the healthy human lung, Quantitative Biology Center Tech Talk, online (Sept 2021)
 - Invited speaker: Benchmarking atlas-level data integration in single-cell genomics, EMBL-EBI Industry workshop 2021, online (May 2021)
 - Invited speaker: *Building a high-quality human cell atlas*, Human Cell Atlas Seed Networks Computational Biology Meeting 2021, online (Apr 2021)
 - Invited moderator: *Panel discussion on bottlenecks of single-cell analysis*, Festival of Genomics 2021 (~6000 attendees; Jan 2021)
- 2020:**
- Invited Keynote: *Making optimal use of your single-cell data: from analysis pipelines to integrated atlases*, SinCellMod, Lyon – moved online (Dec 2020)

- Invited speaker: *Draft 1 of the human lung cell atlas: An integrated multicenter dataset*, Chan-Zuckerberg Initiative Human Cell Atlas Seed Networks Conference – moved online (Nov 2020)
- Invited speaker: *Using single-cell atlas datasets: Machine learning for data integration*, Deutsches Zentrum für Lungenforschung Academy Lecture – Machine Learning (Nov 2020)
- Invited speaker: *Single-cell population analysis of SARS-CoV-2 viral entry factors*, American Thoracic Society webinar (June 2020)
- Invited speaker: *Making optimal use of your single-cell transcriptomic data: Building an analysis pipeline*, 10X Genomics Scientific Symposium, Copenhagen – moved online (June 2020)
- Invited Keynote: *Making the most of your data: Building a single-cell RNA-seq pipeline*, Workshop on Computational Models in Biology and Medicine, Bonn (Feb 2020)

2019:

- Invited speaker: M.D. Luecken, *Making optimal use of your single-cell transcriptomic data: Building an analysis pipeline*, Single-cell transcriptomics, Helsinki (September 2019)
- Invited speaker: M.D. Luecken, *Making optimal use of your single-cell transcriptomic data: Building an analysis pipeline*, Next Generation Sequencing Symposium, Heidelberg (September 2019)

Major collaborations and participation in national and international consortia:

- SPACETIME ([EU Horizon Europe Consortium](#), Europe)
- RESPIRE-EXCEL ([Marie Sokolowska-Curie Actions Doctoral Network](#), Europe)
- DiscoVAIR ([EU Horizon 2020 Consortium](#), Europe)
- HCA Lung Seed Network ([Chan-Zuckerberg Initiative Human Cell Atlas consortium](#), global)
- HCA Lung Biological Network ([Chan-Zuckerberg Human Cell Atlas](#)-centered network to perform COVID-19 research)
- Dr. med. Alexander Misharin (Northwestern University, Chicago, USA)
- Dr. Martijn Nawijn (University Medical Center, Groningen, Netherlands)
- Prof. Dr. Aviv Regev (Genentech, San Francisco, USA)
- Dr. Maria Colomé-Tatché (Institute for Computational Biology, Helmholtz Munich, Germany)
- Dr. Sarah Teichmann (University of Cambridge, Cambridge, UK)
- Dr. Kerstin Meyer (GlaxxoSmithKline, UK)
- Dr. Pascal Barbry (University de Côte-d'Azur, CRNS, Nice, France)
- Dr. Herbert Schiller (Institute of Lung Biology and Disease, Comprehensive Pneumology Center, Helmholtz Munich, Germany)
- Prof. Dr. Rui Chen (Baylor College of Medicine, Houston, USA)
- Prof. Francesca Polverino (Baylor College of Medicine, Houston, USA)
- Prof. Dr. Christos Samakovlis (Stockholm University, Sweden)
- Dr. Angela Oliveira Pisco (CZ Biohub, USA)
- Dr. Daniel Burkhardt (NVidia, USA)
- Dr. Robrecht Cannoodt (Data Intuitive, Belgium)
- Prof. Dr. Chloe Villani (Massachusetts General Hospital, Harvard Medicine, Boston, USA)
- Dr. Alen Faiz (University of Technology Sydney, Australia)
- Prof. Dr. Emmanuel Saliba (Helmholtz Center for Infection Research, Germany)
- Prof. Dana Pe'er (Memorial Sloan Kettering Hospital, New York, USA)
- Dr. John Marioni (Genentech, USA)

Industry collaboration projects

- Open problems in Single-cell analysis (Cellarity, Data Intuitive, ImmunAI, Insitro, NVidia)
- NeurIPS 2021 competition for multimodal data integration (Cellarity)
- NeurIPS 2022 Kaggle competition for multimodal cellular time series modeling (Cellarity, ImmunAI)
- NeurIPS 2023 competition for perturbation prediction (Cellarity)
- Open pipelines for single-cell analysis (Data Intuitive, Janssen Pharmaceutica)

Teaching activities

2022 – present

Lecturer at Environmental Health Lung Research School, Helmholtz Munich

Commented [MOU1]: Add workshops for open problems, single-cell genomics

- Lecturing on computational omics analysis, data integration, and single-cell analysis to PhD student in lung research
- 2019 – present** **Lecturer in Bioinformatics, LMU and TU Munich**
- Lecturing on scRNA-seq data processing to Bioinformatics master students
 - Coordinating and organising bioinformatics internships for the Institute
- 2018** **Teaching certificate: “Supporting Learning”, University of Oxford**
- Associate accreditation of the UK higher education association
- 2013 –2015** **Lecturer and Demonstrator in programming, University of Oxford**
- Designing lectures, practical problem sheets and teaching as part of the C and Python module for first year doctoral students
 - Teaching Statistics Masters students R programming

Supervision/Mentoring:

- Since 09.2022: 3 Postdocs, 10 PhD students, 2 master students, 1 intern; Integrative Genomics group, Institute for Computational Biology, Institute for Lung Health & Immunity, Helmholtz Munich
- Until 08.2022: 2 Postdoctoral researchers, 8 PhD students, 2 master students; 7 interns; Machine learning group, Institute for Computational Biology, Helmholtz Munich

Organisational activities:

- Scientific coordinator, Artificial Intelligence & Digital Tools Disease Spanning Working Group, German Center for Lung Research (DZL)
- Chair of the steering board, DZL DataLung school, German Center for Lung Research (DZL; <https://dzl.de/dzl-datalung-school-academy/>)
- Scientific Board member, Environmental Health Lung Research School, Helmholtz Munich
- Scientific team lead, Human Cell Atlas integration team, Human Cell Atlas
- Executive board member and work package 2 leader, SPACETIME Horizon Europe consortium
- Co-organizer, ATS Postgraduate course “Integrative Lung Bioinformatics: From Data to Discovery”, American Thoracic Society Annual Meeting 2025, San Francisco
- Co-organizer, ATS C3CLN Lung Cell Nomenclature workshop, American Thoracic Society Annual Meeting 2024, San Diego
- Technical Advisory board member, Data Coordination Platform, Human Cell Atlas
- Open Problems in Single-cell analysis co-founder and core team (<https://openproblems.bio>)
- Helmholtz Incubator think tank member
- Organizer of the NeurIPS 2023 competition: “Single-Cell Perturbations” (https://openproblems.bio/neurips_2023/)
- Organizer of the NeurIPS 2022 competition: “Multimodal data integration across time and individuals” (https://openproblems.bio/neurips_2022/)
- Organizer of the NeurIPS 2021 competition: “Multimodal data integration” (https://openproblems.bio/neurips_2021/)
- Organising committee for “Single Cell and Spatial Data Analysis“ as a special session for the International Conference on Intelligent Systems in Molecular Biology (ISMB) 2021
- Hackathon organisation: Chan-Zuckerberg Initiative funded single-cell open problems jamboree (Mar 2021), Machine Learning Group hackathon (Oct 2021, Sept 2020, and Sept 2019), Single Cell Omics Germany hackathon (Mar 2019)

Peer review experience:

- Reviewer for: Nature, Nature Methods, Nature Biotechnology, Nature Communications, Nature Protocols, Genome Biology, PLoS one

Selected Awards and Grants

- SCHEMA** Profiling spatial cancer heterogeneity across modalities to benchmark metastasis risk prediction, Helmholtz UNLOCK benchmark project call, coordinator, funding volume €150,000 (total)
- STRIDER** Spatiotemporal investigation of fibrogenesis to identify targets for siRNA therapeutics, Dai-ichi Sankyo grant (2025-2028), co-investigator, funding volume €235,000 (total €720,000)
- RESPIRE-EXCEL** Horizon Marie-Curie Actions Doctoral Network grant (2025-2030), co-investigator, funding volume €260,000 (total €3,280,000)
- SPACETIME** Spatial Analysis of Cancer Evolution in the Tumour Immune Microenvironment Horizon Europe grant (2024-2029), co-investigator & WP2 lead, funding volume €1,387,000 (total €12,104,000)
- Outstanding Reproducibility in Science Award** for "Benchmarking atlas-level data integration in single-cell genomics", Massive Analysis and Quality Control Society (2023)
- Human Cell Atlas Integration team** Chan Zuckerberg Initiative (CZI) grant (2022-2025), co-investigator (not named), funding volume \$4,433,744 (total)
- Open Problems for Single-cell Analysis** CZI grant (2022-2023), funding volume \$500,000 (total)
- Open problems NeurIPS competition** CZI grant for infrastructure building and data generation (start 2021), co-investigator, funding volume \$75,000
- HOPARL** Host-pathogen crosstalk BMBF computational life science grant (2022-2025), contributor and co-author (not named), funding volume €303,181
- DiscovAIR:** Discovering the cellular Landscape of the airways and the lung, EU Horizon 2020 (2019-2022), co-investigator (not named) and co-coordinator of the computational work package, funding volume €242,380
- Helmholtz Information & Data Science Academy (HIDA) Trainee Network grant** to visit the lab of Prof. Joachim Schultze in Bonn for 2 months (2020), est. value €5000
- Helmholtz Advance Career Fellow** to partake in several career workshops joint between Helmholtz Centres in Germany (2019-2020)
- EPSRC Scholarship** covering fees and maintenance costs for the duration of the Doctoral Training Centre Program (2012-2016), est. value £95 000
- JASSO Scholarship** to cover maintenance costs for the 1 year AIKOM exchange to the University of Tokyo (2010-2011), est. value ¥880 000

Publications

Selected Papers, Preprints, and Submitted Manuscripts (*co-first author, ^corresponding author):

Papers:

- M Lotfollahi, C Bright, R Skorobogat, M Dehkordi, X George, S Richter, V Shitov, A Topalova, **MD Luecken**[^], FJ Theis, *Archmap: A web-based platform for reference-based analysis of single-cell datasets*, **Nature Genetics** (accepted); BioRxiv doi: 10.1101/2024.09.19.613883
- C De Donno*, JP Lopez*, **MD Luecken***, A Kos, E Brivio, J Bordes, H Yang, J Deussing, M Schmidt, FJ Theis, A Chen, *Single-cell characterization of the adult male hippocampus suggests a prominent, and cell-type specific, role for Nrgn and Sgk1 in response to a social stressor*, **Molecular Psychiatry** **31**, 1823–1836 (2026)
- J Li, J Wang, IL Ibarra, X Cheng, **MD Luecken**, J Lu, A Monavarfeshani, W Yan, Y Zheng, Z Zuo, SL Zayas Colborn, B Sarahi Cortez, LA Owen, NM Tran, K Shekhar, JR Sanes, JT Stout, S Chen, Y Li,

- MM DeAngelis, FJ Theis, R Chen, *Single-cell atlas of the transcriptome and chromatin accessibility in the human retina*, **Nature Genetics** **58**, 418-433 (2026)
- S Li, **MD Luecken**, JC Marioni, SA Teichmann, P He, *Toward informed batch correction for single-cell transcriptome integration*, **Nature Computational Science** **6**, 123–133 (2026)
 - S Idrees, H Chen, T Sadaf, S F Rehman, MD Johansen, KR Paudel, G Liu, Y Wang, **MD Luecken**, E Hortle, AS Philp, KF Budden, M O'Rourke, GE Kaiko, SEM Lucas, JL Dickinson, PC Allen, JE Powell, L-Y Zhang, DC Chambers, T Corte, G Caramori, M Sauler, PA Wark, J Gote-Schniering, M Lehmann, TM Conlon, TS Kapellos, AÖ Yildirim, R Faner, SC Dharmage, CE Wheelock, M van den Berge, MC Nawijn, F Polverino, GT Belz, SH Chotirmall, LN Segal, A Faiz, PM Hansbro, *Multi-omics to study chronic respiratory diseases and viral infections*, **European Respiratory Review** **35**(179): 240286 (2026)
 - **MD Luecken***, S Gigante, DB Burkhard, R Cannood, DC Strobl, NS Markov, L Zappia, G Palla, W Lewis, D Dimitrov, ME Vineyard, DS Magruder, A Andersson, E Dann, Q Qin, DJ Otto, M Klein, O Borisovna Botvinnik, L Deconinck, L Waldrant, The Open Problems Jamboree Members, JM Bloom, AO Pisco, J Saez-Rodriguez, D Wulsin, L Pinello, Y Saeys, FJ Theis, S Krishnaswamy, *Defining and benchmarking open problems in single-cell analysis*, **Nature Biotechnology** **43**, 1035–1040 (2025)
 - V Shitov, MM Dehkordi, **MD Luecken^**, *Benchmarking Sample Representations from Single-Cell Data: Metrics for Biologically Meaningful Embeddings*, Learning Meaningful Representations of Life (LMRL) Workshop at ICLR 2025 (2025)
 - T Willem, VA Shitov, **MD Luecken**, N Kilbertus, S Bauer, M Piraud, A Buyx, FJ Theis, *Biases in machine-learning models of human single-cell data*. **Nature Cell Biology** **27**, 384–392 (2025)
 - L Zappia, S Richter, C Ramirez-Suastegui, R Kfuri-Rubens, L Vornholz, W Wang, O Dietrich, A Frischberg, **MD Luecken**, FJ Theis, *Feature selection methods affect the performance of scRNA-seq data integration and querying*, **Nature Methods** **22**, 834-844 (2025)
 - SM Salas, P Czarnewski, LB Kummerle, S Helgadottir, C Matsson-Langseth, S Tismeyer, C Avenel, H Rehman, K Tiklova, A Andersson, M Chatzinikolaou, FJ Theis, **MD Luecken**, C Wählby, N Ishaque, M Nilsson, *Optimizing Xenium In Situ data utility by quality assessment and best practice analysis workflows*, **Nature Methods** **22**, 813-823 (2025)
 - AB Firsova, SM Salas, LB Kummerle, XM Abalo, A Sountoulidis, L Larsson, KT Mahubani, J Theelke, Z Andrusivova, L Alonso Galicia, A Lontos, T Balassa, F Kovacs, P Horvath, Y Chen, J Gote-Schniering, M-G Stoleriu, J Behr, KB Meyer, W Timens, HB Schiller, **MD Luecken**, FJ Theis, J Lundeberg, M Nilsson, MC Nawijn, C Samakovlis, *Spatial single cell atlas reveals regional variations in healthy and diseased human lung*, **Nature Communications** **16**, 9745 (2025)
 - M Gerckens, A Richard, P Arnold, T Veit, J Barton, J Götschke, K Milger, T Kauke, C Schneider, S Michel, M Irlbeck, **MD Luecken**, AÖ Yildirim, J Behr, N Kneidinger, C Mümmeler, *Multistate modelling of baseline lung allograft dysfunction in lung transplant recipients*, **ERJ Open Research** **11**(5), 01135-2024 (2025)
 - R Cannoodt, L Deconinck, A Couckuyt, NS Markov, L Zappia, **MD Luecken**, M Interlandi, Y Saeys, W Saelens, *funkyheatmap: Visualizing data frames with mixed data types*, **Journal of Open Source Software** **10.108** (2025): 7698

- A Szalata, A Benz, R Cannoodt, M Cortes, J Fong, S Kuppasani, R Lieberman, T Liu, J Mas-Rosario, R Meinl, J Nourisa, J Tumieli, TM Tunjic, M Wang, N Weber, H Zhao, B Anchang, FJ Theis, **MD Luecken**[^], DB Burkhardt, *A benchmark for prediction of transcriptomic responses to chemical perturbations across cell types*, **Advances in Neural Information Processing Systems** **37**, 20566-20616 (2024)
- M Gerckens, A Richard, P Arnold, T Veit, J Barton, J Götschke, K Milger, T Kauke, C Schneider, S Michel, M Irlbeck, **MD Luecken**, AÖ Yildirim, J Behr, N Kneidinger, C Mümmler, *Multi-state modeling of baseline lung allograft dysfunction in lung transplant recipients*, **ERJ Open Research** **2025** 01135-2024
- Kuemmerle LB, **Luecken MD**^{*}, Firsova AB, Barros de Andrade e Sousa L, Straßer L, Heumos L, Mekki II, Mahbubani KT, Sountoulidis A, Balassa T, Kovacs F, Horvath P, Piraud M, Ertürk A, Samakovlis C, Theis FJ, *Probe set selection for targeted spatial transcriptomics*, **Nature Methods** **21**, 2260-2270 (2024)
- Hrovatin K, Sikkema L, Shitov VA, Heimberg G, Shulman M, Oliver AJ, Mueller MF, Ibarra IL, Wang H, Ramirez-Suastegui C, He P, Schaar AC, Teichmann SA, Theis FJ, **Luecken MD**[^], Considerations for building and using integrated single-cell atlases, **Nature Methods** **22**, 41-57 (2024)
- A Papargyriou, M Najajreh, D Cook, C Maurer, S Bärthel, H Messal, SK Ravichandran, T Richter, M Knolle, T Metzler, A Shastri, R Öllinger, J Jasper, L Schmidleitner, S Wang, C Schneeweis, H Isikawa, T Engleitner, L Mataite, M Semina, H Trabulssi, S Lange, A Ravichandra, M Schuster, S Müller, K Peschke, A Schäfer, S Dobiasch, SE Combs, RM Schmid, AR Bausch, R Braren, I Heid, C Scheel, G Schneider, A Zeigerer, **MD Luecken**, K Steiger, G Kaissis, J van Rheneen, FJ Theis, D Saur, R Rad, M Reichert, *Heterogeneity-driven phenotypic plasticity and treatment response in branched-organoid models of pancreatic ductal adenocarcinoma*, **Nature Biomedical Engineering** (2024)
- L Sikkema, DC Strobl, L Zappia, E Madisson, NS Markov, L-E Zaragosi, M Ansari, M-J Arguel, L Apperloo, C Becavin, M Berg, E Chichelnitskiy, M Chung, A Collin, ACA Gay, BH Kashani, M Jain, T Kapellos, TM Kole, CH Mayr, M von Papen, L Peter, C Ramirez-Suastegui, J Schniering, CJ Taylor, T Walzthoeni, C Xu, LT Bui, C De Donno, L Dony, M Guo, AJ Gutierrez, L Heumos, N Huang, IL Ibarra, ND Jackson, PKL Murthy, M Lotfollahi, T Tabib, C Talavera-Lopez, KJ Travaglini, A Wilbrey-Clark, KB Worlock, M Yoshida, TJ Desai, O Eickelberg, C Falk, N Kaminski, MA Krasnow, R Lafyatis, MZ Nikolic, JE Powell, J Rajagopal, O Rozenblatt-Rosen, MA Seibold, D Sheppard, DP Shepherd, SA Teichmann, AM Tsankov, J Whitsett, Y Xu, NE Banovich, P Barbry, TE Duong, KB Meyer, JA Kropski, D Pe'er, HB Schiller, PR Tata, JL Schultze, AV Misharin, MC Nawijn, **MD Luecken**[^], FJ Theis, *An integrated cell atlas of the human lung in health and disease*, **Nature Medicine** **29**, 1563-1577 (2023)
- AA Almet, H Yuan, K Annusver, R Ramos, Y Liu, J Wiedemann, DH Sorkin, N Xu Landén, E Sonkoly, M Haniffa, Q Nie, BM Lichtenberger, **MD Luecken**, B Andersen, LC Tsoi, FM Watt, JE Gudjonsson, M Kasper, MV Plikus, *A Roadmap for a Consensus Human Skin Cell Atlas and Single-Cell Data Standardization*, **Journal of Investigative Dermatology** **143**(9), 1667-1677 (2023)
- Heumos L, Schaar A, Lance C, Litinetskaya A, Drost F, Zappia L, **Luecken MD**, Strobl D, Sanchez J, Curion F, Best Practice Writing Team, Theis FJ, *Best practices for single-cell analysis across modalities*, **Nature Reviews Genetics** **24**, 550-572 (2023)
- L Vornholz, SE Isay, Z Kurgis, DC Strobl, P Loll, MH Mosa, **MD Luecken**, M Sterr, H Lickert, C Winter, FR Greten, HF Farin, FJ Theis, J Ruland, *Synthetic enforcement of STING signaling in cancer cells appropriates the immune microenvironment for checkpoint inhibitor therapy*, **Science Advances** **9** (11), eadd8564 (2023)

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