

Soroor Hediyezh-zadeh

CONTACT INFORMATION

✉ soroor.hediyezhzadeh@helmholtz-munich.de

RESEARCH PROFILES

🌐 LinkedIn

🏠 Website

🔍 Google Scholar profile

🔗 <https://github.com/soroorh>

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RESEARCH INTERESTS

Generative Models, Representation Learning, Multimodal Foundation Models, Agentic and Reasoning models, Autonomous systems, post-training, Adaptive AI for Biology, Experimental Design, Drug Discovery, Target Discovery

EDUCATION

Helmholtz Munich

2021 - 2026 (expected)

Institute of Computational Biology (ICB)

Doctor of Philosophy (PhD)

Project title: *Modeling pharmacological β -cell treatment in diabetes using deep representation learning*

Supervisors: Fabian J. Theis, Heiko Lickert

Awards & Honors:

- 2023: Helmholtz Munich Best Paper Award
- 2024: German Academic Exchange (DAAD)- funded Research Stay at the Broad Institute, Fei Chen Lab & Schmidt Center (September - December 2024)
- 2025: Rising Stars in Data Science (Stanford University/UC San Diego/UChicago)

The University of Melbourne

2020 - 2022

Department of Medical Biology (WEHI)

Master of Philosophy (MPhil)

Thesis: *Statistical and Machine learning models for the analysis of label-free mass spectrometry data*

Supervisors: Melissa J Davis, Andrew I. Webb

Awards: Australian Government Postgraduate Award

The University of Melbourne

2017-2019

School of Mathematics and Statistics

M.S., Statistics and Stochastic Processes

Thesis: *Differential expression analysis of RNA-seq data at the transcript level*

Supervisors: Gordon K Smyth, Melissa J Davis, Yunshun Chen

The University of Melbourne

2012-2015

School of Mathematics and Statistics

B.S., Statistics and Stochastic Processes

Undergraduate Project: *Statistical analysis of RNA-seq data*

Supervisors: Gordon K Smyth, Alexandra Garnham

EMPLOYMENT

Walter and Eliza Hall Institute of Medical Research 2016-2020

Bioinformatics Division

Research Assistant

Advisor: Melissa J Davis

Role: Analysis of high-throughput sequencing data, including RNA-seq, ChIP-seq, ATAC-seq, SLAM-seq, scRNA-seq, and shot-gun proteomics data. Developed methods for data integration, understanding cellular heterogeneity in single-cell RNA-seq data. Also co-supervised a visiting student March 2019 - June 2019.

The University of Melbourne

2014-2016

School of Engineering, Systems Biology Laboratory

UROP Student/Research Technician

Project title: *Identifying the molecular networks disrupted in metastasising carcinoma*

Supervisor: Melissa J Davis

Role: Database development, transcription factor motif analysis

IN THE NEWS

►Helmholtz AI interview about my research [Link]

►I received a shout-out from a young female scientist in a blog post by *Ion Optics* [Link]. It is always a pleasure to mentor emerging young female leaders.

►Human Cell Atlas (HCA) coverage on the release of the HEOCA atlas, one of the first two organoid single-cell atlas [Link]. See also the media coverage by Helmholtz Munich [Link] and Roche [Link]. We applied *scDECAF* in this study to compare tissue to organoid models through the lens of drug target signatures.

►The *STEM-Tisch* initiative was featured in a post by Helmholtz Munich Diversity Office [Link]

►*msImpute* was highlighted in the MCP journal as an outstanding article [Link]

PUBLICATIONS

Note: * indicates co-authorship

Preprints

- [1] Hedyeh-zadeh*, S., Toh*, T. S., Dufva, O., Serra, G., Jakhmola, R., Fourneaux, C., ... Garnett, M. J. (2026). *Perturbation-guided mapping of colorectal cancer cell states to causal mechanisms*. bioRxiv, 2026-03.
- [2] Litinetskaya, A., Shulman, M., Hedyeh-zadeh, S., Moinfar, A. A., Curion, F., Szalata, A., ... Theis, F. J. (2024). *Multimodal weakly supervised learning to identify disease-specific changes in single-cell atlases*. bioRxiv, 2024-07.
- [3] Hedyeh-zadeh*, S., Whitfield*, H. J., Kharbanda, M., Curion, F., Bhuva, D. D., Theis, F. J., Davis, M. J. (2023). *Identification of cell types, states and programs by learning gene set representations*. bioRxiv, 2023-09.
- [4] Aliee, H., Kapl, F., Hedyeh-Zadeh, S., Theis, F. J. (2023). *Conditionally Invariant Representation Learning for Disentangling Cellular Heterogeneity*. arXiv preprint arXiv:2307.00558.
- [5] Hedyeh-zadeh, S., Davis, M. J., Webb, A. I. (2021). *PIPP: Improving peptide identity propagation using neural networks*. bioRxiv.

Peer-Reviewed Journal Articles

- [1] Zheng*, Z., Hediye-Zadeh*, S., Liu, J., Theis, F. J. (2026). *Beyond single-axis designs: multi-objective optimization for complex perturbation atlases*. **ICLR 2026 MLGenX**.
- [2] Pinto, G. R., Cho, S. H., Özleyen, S. Y., Von Schack, D., Apruzzese, W., Hediye-Zadeh*, S., Theis*, F. J. (2026). *Structured and interpretable patient embeddings from Single-Cell Foundation Models*. **ICLR 2026 Gen2**. [Co-last author]
- [3] Schunke, L., Hediye-Zadeh, S., Salas, S. M., Can, A. O., Munich, H., Theis, F. J. (2026). *Generative Modeling of Spatial Transcriptomics via Gaussian Mixture Flow Matching*. **ICLR 2026 Gen2**.
- [4] Xu*, Q., Halle*, L., Hediye-Zadeh, S., Kuijs, M., Riedweg, R., Kilik, U., ... Camp, J. G. (2025). *An integrated transcriptomic cell atlas of human endoderm-derived organoids*. **Nature Genetics**, 1-12.
- [5] Kuemmerle, L. B., Luecken, M. D., Firsova, A. B., Barros de Andrade e Sousa, L., Straßer, L., Mekki, I. I., ... Hediye-zadeh, S. (11/21), ... & Theis, F. J. (2024). *Probe set selection for targeted spatial transcriptomics*. **Nature methods**, 1-11.
- [6] Ali*, M., Kuijs*, M., Hediye-Zadeh, S., Treis, T., Hrovatin, K., Palla, G., ... Theis, F. J. , *GraphCompass: spatial metrics for differential analyses of cell organization across conditions*, **Bioinformatics**, Volume 40, Issue Supplement 1, July 2024, Pages i548–i557, <https://doi.org/10.1093/bioinformatics/btae242>
- [7] Hediye-Zadeh, S., Fischer, T., Theis, F. (2024). *Disentanglement via mechanism sparsity by replaying realizations of the past*. **ICLR 2024 Workshop on Machine Learning for Genomics Explorations**.
- [8] Behrens, K., Brajanovski, N., Xu, Z., Viney, E. M., DiRago, L., Hediye-Zadeh, S., Davis, M. J., Pearson, R. B., Sanij, E., Alexander, W. S., & Ng, A. P. (2024). *ERG and c-MYC regulate a critical gene network in BCR::ABL1-driven B cell acute lymphoblastic leukemia*. **Science advances**, 10(10), eadj8803. <https://doi.org/10.1126/sciadv.adj8803>
- [9] Baldoni, P. L.*, Chen, Y.*, Hediye-Zadeh, S., Liao, Y., Dong, X., Ritchie, M. E., ... & Smyth, G. K. (2024). *Dividing out quantification uncertainty allows efficient assessment of differential transcript expression with edgeR*. **Nucleic Acids Research**, 52(3), e13-e13.
- [10] Goh, W., Sudholz, H., Foroutan, M., Scheer, S., Pfefferle, A., Delconte, R. B., ..., Hediye-Zadeh, S. (14/25) ... & Huntington, N. D. (2024). *IKAROS and AIOLOS directly regulate AP-1 transcriptional complexes and are essential for NK cell development*. **Nature Immunology**, 1-16.
- [11] De Donno, C., Hediye-Zadeh, S., Moinfar, A. A., Wagenstetter, M., Zappia, L., Lotfollahi, M., Theis, F. J. (2023). *Population-level integration of single-cell datasets enables multi-scale analysis across samples*. **Nature Methods**. [Helmholtz Munich Best Paper Award]
- [12] Sharma, S., Chung, C. Y., Uryu, S., Petrovic, J., Cao, J., Rickard, A., ... Hediye-Zadeh, S. (54/73), ... Paul, T. A. (2023). *Discovery of a highly potent, selective, orally bioavailable inhibitor of KAT6A/B histone acetyltransferases with efficacy against KAT6A-high ER+ breast cancer*. **Cell Chemical Biology**.
- [13] Hediye-Zadeh, S., Webb, A. I. , Davis, M. J. (2023). *MsImpute: Estimation of missing peptide intensity data in label-free quantitative mass spectrometry*. **Molecular and Cellular Proteomics**. [Outstanding Technological Innovation article by MCP journal]

- [14] Heumos*, L., Schaar*,A.C., Lance, C., Litinetskaya, A., ..., Hediye-Zadeh, S., ... , Schiller,H., and Theis, F. J. (2023). *Best practices for single-cell analysis across modalities*. **Nat Rev Gen.**
- [15] Lotfollahi, M., Rybakov, S., Hrovatin, K., Hediye-Zadeh, S., Talavera-López, C., Misharin, A. V., Theis, F. J. (2023). *Biologically informed deep learning to query gene programs in single-cell atlases*. **Nature Cell Biology**, 1-14.
- [16] Chi, L. H., Cross, R. S., Redvers, R. P., Davis, M.,Hediye-Zadeh, S., Mathivanan, S., ... Anderson, R. L. (2022). *MicroRNA-21 is immunosuppressive and pro-metastatic via separate mechanisms*. **Oncogenesis**, 11(1), 38.
- [17] Souza-Fonseca-Guimaraes, F., Rossi, G. R., Dagley, L. F., Foroutan, M., McCulloch, T. R., Yousef, J., ..., Hedyah-Zadeh, S. (11/14),... Huntington, N. D. (2022). *Tgf and cis inhibition overcomes NK-cell suppression to restore antitumor immunity*. **Cancer Immunology Research**, 10(9), 1047-1054.
- [18] Hediye-zadeh, S., Lotfollahi, M., Theis, F. J. *Continual single-cell architecture surgery for reference mapping*. **ICML 2022 Workshop on Computational Biology**.
- [19] Juan, B. P. S., Hedyah-Zadeh, S., Rangel, L., Rodriguez, V., Milioli, H. H., Kohane, F., ... Chaffer, C. L. (2022). *The anti-androgen seviteronel sensitizes triple-negative breast cancer to chemotherapy*. **Cancer Research**, 82(12_Supplement), 1029-1029.
- [20] El-Saafin, F., Bergamasco, M. I., Chen, Y., May, R. E., Esakky, P., Hediye-Zadeh, S., ... Voss, A. K. (2022). *Loss of TAF8 causes TFIID dysfunction and p53-mediated apoptotic neuronal cell death*. **Cell Death Differentiation**, 29(5), 1013-1027.
- [21] Brown, L. M., Hediye-Zadeh, S., Sadras, T., Huckstep, H., Sandow, J. J., Bartolo, R. C., ... Ekert, P. G. (2022). *SFPQ-ABL1 and BCR-ABL1 utilize different signalling networks to drive B-cell acute lymphoblastic leukaemia*. **Blood Advances**.
- [22] Wang, M., Zadeh, S., Pizzolla, A., Thia, K., Gyorki, D. E., McArthur, G. A., ... Neeson, P. J. (2022). *Characterization of the treatment-naïve immune microenvironment in melanoma with BRAF mutation*. **Journal for Immunotherapy of Cancer**, 10(4).
- [23] Sharma, S., Chung, J., Uryu, S., Rickard, A., Nady, N., Khan, S., ... Hediye-zadeh, S. (47/51) Paul, T. (2021). *First-in-class KAT6A/KAT6B inhibitor CTx-648 (PF-9363) demonstrates potent anti-tumor activity in ER+ breast cancer with KAT6A dysregulation*. **Cancer Research**, 81(13_Supplement), 1130-1130.
- [24] Grisar, S., Dulberg, S., Beck, L., Zhang C., Itan, M., Hediye-zadeh, S. (6/24), ... & Munitz, A. *Metastasis-entrained eosinophils enhance lymphocyte-mediated anti-tumor immunity*. **Cancer Research**, 81(21), 5555-5571.
- [25] Adolphe , C., Millar, A., Kojic, M., Barkauskas, D., Sundström, A., Swartling, F., Hediye-zadeh, S., Tan,C.W., Davis, M. & Genovesi, L. *SOX9 defines distinct populations of cells in SHH medulloblastoma but is not required for Math1-driven tumour formation*. **Molecular Cancer Research**, 19(11), 1831-1839.
- [26] Jacquelot, N., Seillet, C., Wang, M., Pizzolla, A., Liao, Y., Hediye-Zadeh, S., ... & Belz, G. T. (2021). *Blockade of the co-inhibitory molecule PD-1 unleashes ILC2-dependent antitumor immunity in melanoma*. **Nature Immunology**, 1-14.

- [27] Kojic, M., Gawda, T., Gaik, M., Begg, A., Salerno-Kochan, A., Kurniawan, N. D., ..., Soroor HediyeH-zadeh (11/40), ... & Wainwright, B. J. (2021). *Elp2 mutations perturb the epitranscriptome and lead to a complex neurodevelopmental phenotype*. **Nature communications**, 12(1), 1-18.
- [28] Huang, Q., Jacquelot, N., Preaudet, A., HediyeH-Zadeh, S., Souza-Fonseca-Guimaraes, F., McKenzie, A. N., ... & Belz, G. T. (2021). *Type 2 Innate Lymphoid Cells Protect against Colorectal Cancer Progression and Predict Improved Patient Survival*. **Cancers**, 13(3), 559.
- [29] Moujalled, D. M., Hanna, D. T., HediyeH-Zadeh, S., Pomilio, G., Brown, L., Litalien, V., ... & Maragno, A. L. (2020). *Cotargeting BCL-2 and MCL-1 in high-risk B-ALL*. **Blood advances**, 4(12), 2762-2767.
- [30] Emery-Corbin, S. J., Hamey, J. J., Ansell, B. R., Balan, B., Tichkule, S., Stroehlein, A. J., ..., HediyeH-Zadeh, S. (9/18),... & Jex, A. R. (2020). Eukaryote-conserved methylarginine is absent in diplomonads and functionally compensated in Giardia. **Molecular biology and evolution**, 37(12), 3525-3549.
- [31] Ng, A. P., Coughlan, H. D., HediyeH-Zadeh, S., Behrens, K., Johanson, T. M., Low, M. S. Y., ... & Boudier, T. (2020). *An Erg-driven transcriptional program controls B cell lymphopoiesis*. **Nature Communications**, 11(1), 1-14.
- [32] Wee, K., HediyeH-zadeh, S., Duszyc, K., Verma, S., Nanavati, B., Khare, S., ... & Budnar, S. (2020). *Snail induces epithelial cell extrusion by regulating RhoA contractile signaling and cell-matrix adhesion*. **Journal of Cell Science**.
- [33] Carmichael, C. L., Wang, J., Nguyen, T., Kolawole, O., Benyoucef, A., De Mazière, C., ..., HediyeH-zadeh, S. (10/37), ... & Vo, A. N. Q. (2020). *The EMT modulator SNAI1 contributes to AML pathogenesis via its interaction with LSD1*. **Blood**.
- [34] Louis, C., Guimaraes, F., Yang, Y., D'Silva, D., Kratina, T., Dagley, L., HediyeH-Zadeh, S., ... & Babon, J. J. (2020). *NK cell-derived GM-CSF potentiates inflammatory arthritis and is negatively regulated by CIS*. **Journal of Experimental Medicine**, 217(5).
- [35] Delconte, R. B., Guittard, G., Goh, W., HediyeH-Zadeh, S., Hennessy, R. J., Rautela, J., ... & Huntington, N. D. (2020). *NK Cell Priming From Endogenous Homeostatic Signals Is Modulated by CIS*. **Frontiers in Immunology**, 11, 75.
- [36] Goh, W., Jackson, J. T., HediyeH-zadeh, S., Delconte, R. B., Andoniou, C. E., Rautela, J., ... & Huntington, N. D. (2020). *Hhex Is Essential for NK Cell Persistence by Repressing Bcl2l11-Dependent Apoptosis*. **CELL-REPORTS-D-19-05014**.
- [37] Rautela, J., Dagley, L. F., De Oliveira, C. C., Schuster, I. S., HediyeH-Zadeh, S., Delconte, R. B., ... & Kita, B. (2019). *Therapeutic blockade of activin-A improves NK cell function and antitumor immunity*. **Science signaling**, 12(596), eaat7527.
- [38] Cursons, J., Souza-Fonseca-Guimaraes, F., Foroutan, M., Anderson, A., Holand, F., HediyeH-Zadeh, S., ... & Davis, M. J. (2019). *A gene signature predicting natural killer cell infiltration and improved survival in melanoma patients*. **Cancer immunology research**, 7(7), 1162-1174.
- [39] Mielke, L. A., Liao, Y., Clemens, E. B., Firth, M. A., Duckworth, B., Huang, Q., ..., HediyeH-Zadeh, S. (11/25), ... & Belz, G. T. (2019). *TCF-1 limits the formation of Tc17 cells via repression of the MAF-RORYt axis*. **Journal of Experimental Medicine**, jem-20181778.

- [40] Cursons, J., Pillman, K. A., Scheer, K. G., Gregory, P. A., Foroutan, M., Hediye-Zadeh, S., ... & Davis, M. J. (2018). *Combinatorial targeting by MicroRNAs co-ordinates post-transcriptional control of EMT*. **Cell systems**, 7(1), 77-91.
- [41] Rautela, J., Souza-Fonseca-Guimaraes, F., Hediye-Zadeh, S., Delconte, R. B., Davis, M. J., & Huntington, N. D. (2018). *Molecular insight into targeting the NK cell immune response to cancer*. **Immunology and cell biology**, 96(5), 477-484.
- [42] Foroutan, M., Cursons, J., Hediye-Zadeh, S., Thompson, E. W., & Davis, M. J. (2017). *A transcriptional program for detecting TGFB-induced EMT in Cancer*. **Molecular Cancer Research**, 15(5), 619-631.

Selected Poster Abstracts

- [1] Hediye-Zadeh, S., Fischer, T., Theis, F. (2024). *Mechanism transport between multiple data modalities using causality- inspired neural networks*. **Single Cell Biology 2024**.
- [2] Hediye-Zadeh, S., Fischer, T., Theis, F. (2024). *Disentanglement via mechanism sparsity by replaying realizations of the past*. **ICLR 2024 Workshop on Machine Learning for Genomics Explorations**.
- [3] Soroor Hediye-zadeh, Mohammad Lotfollahi, Fabian Theis. *Continual single-cell architecture surgery for reference mapping*. **ICML 2022 Workshop on Computational Biology**
- [4] Soroor Hediye-Zadeh, Yi Xie, Holly Whitfield and Melissa Davis. *Reference-free cell type annotation and phenotype characterisation in single cell RNA sequencing by learning geneset representations*. **ICML 2021 Workshop on Computational Biology**
- [5] Soroor Hediye-Zadeh and Andrew Webb. *Improving confident peptide identifications across mass spectrometry runs by learning deep representations of TIMS-MS1 features*. **ICML 2021 Workshop on Computational Biology**
- [6] Abstract 1130: *First-in-class KAT6A/KAT6B inhibitor CTx-648 (PF-9363) demonstrates potent anti-tumor activity in ER+ breast cancer with KAT6A dysregulation* Shikhar Sharma, Jay Chung, Sean Uryu, Amanda Rickard, Natalie Nady, Showkhin Khan, Zhenxiong Wang, Yong Zhang, Haikuo Zhang, Pei-Pei Kung, Eric Greenwald, Karen Maegley, Patrick Bingham, Hieu Lam, Ylva E. Bozikis, Hendrik Falk, Elizabeth Allan, Vicky M. Avery, Miriam S. Butler, Michelle A. Camerino, Catalina Carrasco-Pozo, Susan A. Charman, Melissa J. Davis, Mark A. Dawson, Dawson Sarah-Jane, Melanie de Silva, Matthew L. Dennis, Olan Dolezal, Rachel Lagiakos, Geoffrey J. Lindeman, Laura MacPherson, Stewart Nuttall, Thomas S. Peat, Bin Ren, Alexandra E. Stupple, Elliot Surgenor, Chin Wee Tan, Tim Thomas, Jane E. Visvader, Anne K. Voss, Francois Vaillant, Karen L. White, James Whittle, Yuqing Yang, Soroor Hediye-Zadeh, Paul A. Stupple, Ian P. Street, Brendon J. Monahan and Thomas Paul **Cancer Res** July 1 2021 (81) (13 Supplement) 1130; DOI: 10.1158/1538-7445.AM2021-1130

SUPERVISION &
MENTORING

Zihe Zheng, PhD, TUM/Helmholtz Munich, 2025.
Suhan Cho, PhD, TUM/Helmholtz Munich, 2025.
Goncalo Pinto, PhD, TUM/Helmholtz Munich, 2025.
Lisa Schunke, MSc CS Informatics, TUM, 2025.
Layla Zadina, BSc Robotics, TUM, 2025.
Lars Pechowski, BSc Mathematics, TUM, 2025.

Zhiyuhan Song, MSc CS Informatics, TUM, 2025.
Johannes Weindl, MSc CS Informatics, TUM, 2024.
Mikkel Rassmusen, MSc CS, DTU, 2024. *Now PhD graduate student DTU.*
Ismail Benayed, BSc Robotics, TUM, 2024.
Georgiana Barbut, MSc Robotics, TUM, 2024. *Now PhD applicant Vienna*
Rashika Jakhmola, MSc Mathematics, TUM. *Now PhD graduate student DKFZ.*
Lucas Ronchetti, BSc CS, TUM, 2023.
Tom Fischer, MSc Mathematics, TUM, 2023.
Rasmus Moller Larsen, MSc CS, DTU, 2023. *Now PhD graduate student Helmholtz Munich*
Jack Finlay, Visiting HIDA scholar, Duke University, 2023.
Yi Xie, Visiting student, WEHI, 2019. *Now PhD student China.*

SELECTED INVITED TALKS *MsImpute: Estimation of missing peptide intensity values in label-free mass spectrometry.* BioC Asia 2021. Virtual. [Recording]

Mapping phenotypic similarities using single cells manifold, Joint GIW/ABACBS 2019. Sydney, Australia.

Mapping phenotypic similarities using single cells manifold, 10X Genomics User Group, Melbourne, November 2019.

Supervised deconvolution of population heterogeneities in single cell RNA-seq via similarity-based embeddings, Victorian Cancer Bioinformatics Symposium 2019.

Supervised deconvolution of population heterogeneities in single cell RNA-seq via similarity-based embeddings, OZ Single Cells meeting 2019.

Using Docker to make biomedical research outcomes reproducible, Tech Talk: Using Docker-like Containers in Service Deployment (Online Meetup) [Link] (April 2018)

Computational workflows for research students: towards a reproducible research, COMBINE Student Symposium. (November 2016)

OPPAR: Outlier Profile and Pathway Analysis, bioCasia2016. (November 2016)

TALKS AND SEMINARS *Emerging topics in continual learning for computational biology*, ContinualAI Seminars, March 2023. [Abstract] [Recording]

Machine Learning in Biology: Learning meaningful representations of life, WEHI Machine Learning Interest Group, June 2020.

Methods for imputation, differential expression and multi-Omics integration of proteomics data, WEHI Bioinformatics Seminars, April 2019

FUNDS & AWARDS	Stanford Rising Stars in Data Science 2025 [Link] German Academic Exchange (DAAD) scholarship (Awarded Aug 2024) Single Cell Biology 2024 conference Travel Bursary Partial funds from Colonial Foundation towards MPhil degree 2020-2021 Australian Postgraduate Award (Fee Remission) 2020-2022 ICML 2021 Workshop on Computational Biology Fellowship WiML ICLR 2021 Registration Fee Funding, 2021 WiML NeurIPS 2020 Registration Fee Funding, 2020 WEHI Bioinformatics Travel Award, 2020 Kellaway Excellence Education Award, 2019 BiocAsia 2016 meeting Travel Award Winter School in Mathematical and Computational Biology Travel Bursary, 2014 Australian Neurogenetics Conference Travel Award, 2014
PROGRAMMING LANGUAGES	Proficient: R, Python, Bash, L^AT_EX
SOFTWARE	msImpute: Peptide-level imputation in mass spectrometry label-free proteomics by low-rank approximation. DOI: https://doi.org/doi:10.18129/B9.bioc.msImpute scDECAF: Reference-free cell type and phenotype annotation by learning geneset representations. source code: https://github.com/DavisLaboratory/scDECAF oppar - An R/Bioconductor package for outlier profile analysis in cancer samples. DOI: https://doi.org/doi:10.18129/B9.bioc.oppar
PROFESSIONAL SERVICES	<i>Program/Proceedings Reviews</i> ▷ICLR 2026 reviewer (Gen2 Workshop) ▷ICLR 2026 reviewer (LMRL Workshop) (Invited) ▷NeurIPS 2025 reviewer (CauScien Workshop) ▷Nature Communications ▷ICLR 2025 reviewer (LMRL Workshop) ▷AISTATS 2024 reviewer (Machine Learning track) ▷ISMB/ECCB 2023 Proceedings programme external reviewer ▷useR! 2018 conference organising committee; abstract reviewer <i>Committees and Societies</i> ◆Helmholtz Munich STEM-Tisch (2022 - 2024) - Co-founder ◇WEHI Machine Learning Special Interest Group (2020 - 2021) - Co-organiser ◇WEHI Deep Learning in Medical Biology Symposium 2020 - Co-organiser ◇R-Ladies Melbourne co-founder (2017 - Feb 2019) [Link 1] [Link 2] ◇ABACBS 2017 organising committee - COMBINE training coordinator <i>Workshops and Events</i>

- Helmholtz Munich Virtual Cell Workshop. July 2026. *Co-organiser*
- Deep probabilistic and generative modeling. R-Ladies Melbourne, May 2026. *Speaker* [Recording]
- Helmholtz Munich Perturbation Modeling Forum. Jan 2026. *Co-organiser, presenter*
- Package development and publishing in R. R-Ladies Urmia, June 2022. *Speaker*
- Producing publication-ready documents in R Markdown. R-Ladies Melbourne, Feb 2019. *Speaker and co-organiser*
- Semi-parametric and non-parametric models in R. R-Ladies Melbourne, December 2018. *Speaker and co-organiser*
- Parallel Programming in R. R-Ladies Melbourne, March 2018. *Speaker and co-organiser*
- Introduction to R Shiny. R-Ladies Melbourne, November 2017. *Speaker and co-organiser*
- COMBINE R for Bioinformatics. May 2017. *Training instructor and organiser*
- Version Control and Project Management with Git. R-Ladies Melbourne, May 2017. *Speaker and co-organiser*
- COMBINE R software Carpentry workshop. April 2017. *Training instructor and organiser*

ACADEMIC REFERENCES

Prof. Dr. Dr. Fabian Theis. Director of Computational Health Department. Helmholtz Munich.

Prof. Melissa Davis. Director of Computational Biology. Isomorphic Labs.

Dr. Mathew Garnett. Senior Group Leader, Somatic Genomics Programme. Wellcome Sanger Institute.