

Soroor Hediyezh-zadeh

CONTACT INFORMATION

✉ soroor.hediyezhzadeh@helmholtz-munich.de

RESEARCH PROFILES

🏠 Website
🔗 Google Scholar profile
🌐 <https://github.com/soroorh>
🆔 0000-0001-7513-6779

RESEARCH INTERESTS

Deep generative models, Continual Learning, Causal representation learning, Continual Causality

EDUCATION

Helmholtz Munich

2021 - 2024

Institute of Computational Biology (ICB)

Doctor of Philosophy (PhD)

Thesis title: *Continual representation learning for the study of molecular aberrations and perturbations in single cell gene expression data*

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

Supervisors: Fabian J. Theis, Heiko Lickert

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

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

PUBLICATIONS

Pre-prints

- [1] Baldoni, P. L., Chen, Y., Hediye-zadeh, S., Liao, Y., Dong, X., Ritchie, M. E., ... Smyth, G. K. (2023). *Dividing out quantification uncertainty allows efficient assessment of differential transcript expression*. bioRxiv, 2023-04.
- [2] Huntington, N., Goh, W., Foroutan, M., Scheer, S., Pfefferle, A., Sudholz, H., ..., Hediye-Zadeh, S. (14/22), ..., Nutt, S. (2022). *IKAROS and AIOLOS activate AP-1 transcriptional complexes and are essential for natural killer cell development*.
- [3] De Donno, C., Hediye-Zadeh, S., Wagenstetter, M., Moinfar, A. A., Zappia, L., Lotfollahi, M., Theis, F. J. (2022). *Population-level integration of single-cell datasets enables multi-scale analysis across samples*. bioRxiv, 2022-11.
- [4] Hediye-zadeh, S., Martin, J., Davis, M. J., Webb, A. I. (2021). *PIPP: Improving peptide identity propagation using neural networks*. bioRxiv.

Peer-Reviewed Journal Articles

- [1] Hediye-Zadeh, S., Webb, A. I., Davis, M. J. *MsImpute: Estimation of missing peptide intensity data in label-free quantitative mass spectrometry*. **Molecular and Cellular Proteomics** (Accepted).
- [2] Heumos*, L., Schaar*, A.C., Lance, C., Litinetskaya, A., ..., Hediye-Zadeh, S., ... , Schiller, H., and Theis, F. J. *Best practices for single-cell analysis across modalities*. **Nat Rev Gen.**
- [3] 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.
- [4] 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.
- [5] Souza-Fonseca-Guimaraes, F., Rossi, G. R., Dagley, L. F., Foroutan, M., McCulloch, T. R., Yousef, J., ..., Hediye-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.
- [6] Hediye-zadeh, S., Lotfollahi, M., Theis, F. J. *Continual single-cell architecture surgery for reference mapping*. **ICML 2022 Workshop on Computational Biology**.
- [7] Juan, B. P. S., Hediye-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.
- [8] 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.
- [9] 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**.
- [10] Wang, M., Zadeh, S., Pizzolla, A., Thia, K., Gyorki, D. E., McArthur, G. A., ... Neeson, P. J. (2022). *Characterization of the treatment-naive immune microenvironment in melanoma with BRAF mutation*. **Journal for Immunotherapy of Cancer**, 10(4).
- [11] 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.
- [12] 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.
- [13] 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.
- [14] Jacquilot, 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.
- [15] Kojic, M., Gawda, T., Gaik, M., Begg, A., Salerno-Kochan, A., Kurniawan, N. D., ..., Soroor Hediye-zadeh (11/40), ... & Wainwright, B. J. (2021). *Etp2 mutations perturb the epitranscriptome and lead to a complex neurodevelopmental phenotype*. **Nature communications**, 12(1), 1-18.
- [16] Huang, Q., Jacquilot, N., Preaudet, A., Hediye-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.
- [17] Moujalled, D. M., Hanna, D. T., Hediye-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.
- [18] Emery-Corbin, S. J., Hamey, J. J., Ansell, B. R., Balan, B., Tichkule, S., Stroehlein, A. J., ..., Hediye-Zadeh, S. (9/18), ... & Jex, A. R. (2020). *Eukaryote-conserved*

- methyldarginine is absent in diplomonads and functionally compensated in *Giardia*. **Molecular biology and evolution**, 37(12), 3525-3549.
- [19] Ng, A. P., Coughlan, H. D., Hediye-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.
 - [20] Wee, K., Hediye-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**.
 - [21] Carmichael, C. L., Wang, J., Nguyen, T., Kolawole, O., Benyoucef, A., De Mazière, C., ..., Hediye-zadeh, S. (10/37), ... & Vo, A. N. Q. (2020). *The EMT modulator SNAIL1 contributes to AML pathogenesis via its interaction with LSD1*. **Blood**.
 - [22] Louis, C., Guimaraes, F., Yang, Y., D'Silva, D., Kratina, T., Dagley, L., Hediye-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).
 - [23] Delconte, R. B., Guittard, G., Goh, W., Hediye-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.
 - [24] Goh, W., Jackson, J. T., Hediye-zadeh, S., Delconte, R. B., Andoniou, C. E., Rautela, J., ... & Huntington, N. D. (2020). *Hhex Is Essential for NK Cell Persistence by Repressing Bcl2l1-Dependent Apoptosis*. **CELL-REPORTS-D-19-05014**.
 - [25] Rautela, J., Dagley, L. F., De Oliveira, C. C., Schuster, I. S., Hediye-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.
 - [26] Cursons, J., Souza-Fonseca-Guimaraes, F., Foroutan, M., Anderson, A., Hol-lande, F., Hediye-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.
 - [27] Mielke, L. A., Liao, Y., Clemens, E. B., Firth, M. A., Duckworth, B., Huang, Q., ..., Hediye-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.
 - [28] 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.
 - [29] 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.
 - [30] 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] Soroor HediyeH-zadeh, Mohammad Lotfollahi, Fabian Theis. *Continual single-cell architecture surgery for reference mapping*. **ICML 2022 Workshop on Computational Biology**
- [2] Soroor HediyeH-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**
- [3] Soroor HediyeH-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**
- [4] 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. Stuppel, Elliot Surgenor, Chin Wee Tan, Tim Thomas, Jane E. Visvader, Anne K. Voss, Francois Vaillant, Karen L. White, James Whittle, Yuqing Yang, Soroor HediyeH-Zadeh, Paul A. Stuppel, 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

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). (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

AWARDS

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

Program/Proceedings Reviews

▷ISMB/ECCB 2023 Proceedings programme external reviewer

▷useR! 2018 conference organising committee; abstract reviewer

Committees and Societies

◆Helmholtz Munich STEM-Tisch (2022 - present) - 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)

◇ABACBS 2017 organising committee - COMBINE training coordinator

Workshops

- ▶ 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*