

Soroor Hediyezh-zadeh

CONTACT INFORMATION

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RESEARCH PROFILES

🏠 Website

🔍 Google Scholar profile

🔗 <https://github.com/soroorh>

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EDUCATION

The University of Melbourne

2020 - 2021 (Expected)

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 shotgun 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

Peer-Reviewed Journal Articles

- [1] Adolphe, C., Millar, A., Kojic, M., Barkauskas, D., Sundström, A., Swartling, F., Hediyezh-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. Accepted in **Molecular Cancer Research**

- [2] 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.
- [3] Kojic, M., Gawda, T., Gaik, M., Begg, A., Salerno-Kochan, A., Kurniawan, N. D., ..., Soroor Hediye-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.
- [4] Huang, Q., Jacquelot, 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.
- [5] 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.
- [6] 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 methylarginine is absent in diplomonads and functionally compensated in Giardia. **Molecular biology and evolution**, 37(12), 3525-3549.
- [7] 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.
- [8] 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**.
- [9] 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 SNAI1 contributes to AML pathogenesis via its interaction with LSD1.* **Blood**.
- [10] 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).
- [11] 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.
- [12] 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**.
- [13] 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.
- [14] 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.

- [15] 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.
- [16] 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.
- [17] 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.
- [18] 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.

Prominent Poster Abstracts

- [1] 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*. **Computational Biology Workshop - ICML 2021**
- [2] Soroor Hediye-Zadeh and Andrew Webb. *Improving confident peptide identifications across mass spectrometry runs by learning deep representations of TIMS-MS1 features*. **Computational Biology Workshop - ICML 2021**
- [3] 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

SELECTED INVITED TALKS *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.

	<i>Supervised deconvolution of population heterogeneities in single cell RNA-seq via similarity-based embeddings</i> , OZ Single Cells meeting 2019.
	<i>Using Docker to make biomedical research outcomes reproducible</i> , Tech Talk: Using Docker-like Containers in Service Deployment (Online Meetup). (April 2018)
	<i>Computational workflows for research students: towards a reproducible research</i> , COMBINE Student Symposium. (November 2016)
	<i>OPPAR: Outlier Profile and Pathway Analysis</i> , bioCasia2016. (November 2016)
TALKS AND SEMINARS	<i>Machine Learning in Biology: Learning meaningful representations of life</i> , WEHI Machine Learning Interest Group, June 2020.
	<i>Methods for imputation, differential expression and multi-Omics integration of proteomics data</i> , WEHI Bioinformatics Seminars, April 2019
AWARDS	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, Bash, L ^A T _E X, Python
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>Workshops</i> Producing publication-ready documents in R Markdown. R-Ladies Melbourne, Feb 2019. <i>Speaker and co-organiser</i> Semi-parametric and non-parametric models in R. R-Ladies Melbourne, December 2018. <i>Speaker and co-organiser</i> Parallel Programming in R. R-Ladies Melbourne, March 2018. <i>Speaker and co-organiser</i>

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*

Committees and Societies

WEHI Machine Learning Special Interest Group (2020 - present) - Co-organiser

WEHI Deep Learning in Medical Biology Symposium 2020 - Co-organiser

R-Ladies Melbourne co-organiser (2017 - Feb 2019)

useR! 2018 conference organising committee

ABACBS 2017 organising committee - COMBINE training coordinator