Soroor Hediyeh-zadeh

CONTACT Information

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RESEARCH PROFILES

⋒ Website

3 Google Scholar profile

• https://github.com/soroorh

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EDUCATION

The University of Melbourne

2020-2023

Department of Medical Biology (WEHI)

Doctor of Philosophy

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] Huang, Q., Jacquelot, N., Preaudet, A., <u>Hediyeh-Zadeh, S.</u>, 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.
- [2] Moujalled, D. M., Hanna, D. T., <u>Hediyeh-Zadeh, S.</u>, 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.
- [3] Emery-Corbin, S. J., Hamey, J. J., Ansell, B. R., Balan, B., Tichkule, S., Stroehlein, A. J., ..., Hediyeh-Zadeh, S.,... Jex, A. R. (2020). Eukaryote-conserved methylarginine is absent in diplomonads and functionally compensated in Giardia. Molecular biology and evolution, 37(12), 3525-3549.
- [4] 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.
- [5] Wee, K., <u>Hediyeh-zadeh</u>, 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**.
- [6] Carmichael, C. L., Wang, J., Nguyen, T., Kolawole, O., Benyoucef, A., De Mazière, C., ..., <u>Hediyeh-zadeh</u>, S., ... Vo, A. N. Q. (2020). *The EMT modulator SNAI1 contributes to AML pathogenesis via its interaction with LSD1*. **Blood**.
- [7] 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).
- [8] 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.
- [9] Goh, W., Jackson, J. T., <u>Hediyeh-zadeh, S.</u>, Delconte, R. B., Andoniou, C. E., Rautela, J., ... <u>Huntington, N. D. (2020)</u>. *Hhex Is Essential for NK Cell Persistence by Repressing Bcl2l11-Dependent Apoptosis*. **CELL-REPORTS**-D-19-05014.
- [10] Rautela, J., Dagley, L. F., De Oliveira, C. C., Schuster, I. S., <u>Hediyeh-Zadeh, S.</u>, Delconte, R. B., ... Kita, B. (2019). Therapeutic blockade of activin-A improves NK cell function and antitumor immunity. Science signaling, 12(596), eaat7527.
- [11] Cursons, J., Souza-Fonseca-Guimaraes, F., Foroutan, M., Anderson, A., Hollande, 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.
- [12] Mielke, L. A., Liao, Y., Clemens, E. B., Firth, M. A., Duckworth, B., Huang, Q., ... Hediyeh-Zadeh, S. (2019). TCF-1 limits the formation of Tc17 cells via repression of the MAF-RORYt axis. Journal of Experimental Medicine, jem-20181778.
- [13] Cursons, J., Pillman, K. A., Scheer, K. G., Gregory, P. A., Foroutan, M., <u>Hediyeh-Zadeh, S.</u>, ... Davis, M. J. (2018). Combinatorial targeting by Mi-<u>croRNAs co-ordinates post-transcriptional control of EMT.</u> Cell systems, 7(1), 77-91.
- [14] Rautela, J., Souza-Fonseca-Guimaraes, F., <u>Hediyeh-Zadeh, S.</u>, Delconte, R. B., Davis, M. J., Huntington, N. D. (2018). <u>Molecular insight into targeting the NK cell immune response to cancer. Immunology and cell biology</u>, 96(5), 477-484.

[15] Foroutan, M., Cursons, J., Hediyeh-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.

TALKS

Selected Invited 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 similaritybased embeddings, Victorian Cancer Bioinformatics Symposium 2019.

Supervised deconvolution of population heterogeneities in single cell RNA-seq via similaritybased 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, COM-BINE Student Symposium. (November 2016)

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

Talks and SEMINARS

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

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, LATEX, 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

Workshops

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 coorganiser

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) - 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