

Soroor Hediyezh-zadeh

CONTACT INFORMATION

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RESEARCH PROFILES

🌐 LinkedIn
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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 and Causal 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 causal 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	<p>Walter and Eliza Hall Institute of Medical Research 2016-2020 <i>Bioinformatics Division</i> 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.</p> <p>The University of Melbourne 2014-2016 <i>School of Engineering, Systems Biology Laboratory</i> UROF Student/Research Technician Project title: <i>Identifying the molecular networks disrupted in metastasising carcinoma</i> Supervisor: Melissa J Davis Role: Database development, transcription factor motif analysis</p>
SELECTED INVITED TALKS	<p><i>Emerging topics in continual learning for computational biology</i>, ContinualAI Seminars, March 2023. [Abstract] [Recording]</p> <p><i>MsImpute: Estimation of missing peptide intensity values in label-free mass spectrometry</i>. BioC Asia 2021. Virtual. [Recording]</p> <p><i>Mapping phenotypic similarities using single cells manifold</i>, Joint GIW/ABACBS 2019. Sydney, Australia.</p>
FUNDS & AWARDS	<p>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</p>
PROGRAMMING LANGUAGES	Proficient: R, Python, Bash, L ^A T _E X
SOFTWARE	<p>msImpute: Peptide-level imputation in mass spectrometry label-free proteomics by low-rank approximation. DOI: https://doi.org/doi:10.18129/B9.bioc.msImpute</p> <p>scDECAF: Reference-free cell type and phenotype annotation by learning geneset representations. source code: https://github.com/DavisLaboratory/scDECAF</p>

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*

SUPERVISION & MENTORING

Lucas Ronchetti, BSc student, Technical University of Munich (TUM), 2023
Thesis Title: An uncertainty-aware deep learning framework for match-between-runs in TIMS-MS/MS proteomics data

Tom Fischer, MSc student, Technical University of Munich (TUM), 2023
Thesis Title: Continual learning of causal mechanisms: applications in bulk and single cell transcriptomics

Rasmus Moller Larsen, MSc student, Technical University of Denmark (DTU), 2023

Thesis Title: Deep generative modelling for single cell mass spectrometry

Jack Finlay, Visiting HIDA scholar, Duke University (visiting Helmholtz Munich), 2023

Research project: Linking healthy cell atlases to disease cell atlases: applications to an integrated Colorectal Cancer Atlas

Yi Xie, Visiting student, WEHI, 2019

Research project: Identification of cell types, states and programs by learning gene set representations