

Fatemeh Vafae

Curriculum Vitae

School of Biotechnology and Biomolecular Sciences
University of New South Wales, Sydney NSW 2006

☎ (+614) 0301-2736

☎ (+612) 9385-3281

✉ f.vafae@unsw.edu.au

🌐 www.VafaeLab.com

Research Interests

Artificial intelligence, computational biology and bioinformatics, machine learning, optimization, data visualization, deep learning, biomarker discover, cancer informatics, drug discovery.

Current Appointments

- 2/2021– **Deputy Director**, *Data Science Centre*, University of New South Wales, Sydney, Australia.
- 5/2020– **Health Data Science Lead**, *Data Science Centre*, University of New South Wales, Australia.
- 5/2017– **Senior Lecturer**, *School of Biotechnology and Biomolecular Sciences (BABS)*, University of New South Wales, Sydney, Australia.

Former Academic Positions

- 3/2013– **Research Fellow**, *School of Mathematics and Statistics & Charles Perkins Centre*, University of Sydney, Australia.
5/2017
Research: Computational biomedicine, systems biology, bioinformatics
- 8/2011– **Postdoctoral Associate**, *University Health Network, Ontario Cancer Institute, Department of Computer Science*, University of Toronto, Canada.
9/2012
Research: Computational biology, cancer informatics

Education

- 5/2011 **Ph.D.**, *Computer Science*, University of Illinois at Chicago, USA.
Thesis Topic: Controlling Genetic Operator Rates in Evolutionary Algorithms
- 8/2006 **B.Sc.**, *Computer Engineering*, Sharif University of Technology, Tehran, Iran.
Thesis Topic: Design and implementation of Multi-Media Value Added Service Provider

Awards and Recognition

- 2021 Women in AI Australia and New Zealand Award Finalist
- 2019 UNSW Science Visiting Research Fellowship
- 2009 Grace Hopper Celebration of Women in Computing Award, Anita Borg Inst

Research Income

Last 3 Years Metrics: Net value of **\$5.75M** (unapportioned) in research & industry-based funding schemes.

- 2021 – 2025 Funding body: *Medical Research Future Fund, Australian Government*, Title: An Australian-specific Multicentre Double-Blinded Randomised Controlled Trial of Genotype-guided versus Standard Psychotropic Therapy in Moderately-to-Severely Depressed Patients Initiating Pharmacotherapy. Chief Investigators: Wu K, Fitzgerald, Grieve, Harris, Hood, Rogers, Schofield, Shrestha, Usherwood, **Vafae F** (Lead AI)
\$2.95M
- 2019 – 2021 Funding body: *Cooperative Research Centres Project (CRC-P), Australian Government*, Title: Smart Sensor & Deep Learning Behavioural Engine for Personalised Health Monitoring. Chief Investigators: Mehta H, Varnes P, Liu G, **Vafae F** (AI Lead), Salvado O, Wentworth J, Hoek A, Shaw J, Crowder R, Wiebenga R, McGuinness R.
\$2.15M

- 2020 – 2021 Funding body: *Cellular Genomics Future Institute, UNSW*, Title: Fast and scalable denoising and integration of large-scale single-cell sequencing data. Chief Investigators: **Vafaee F** (CIA), Lovell N, Arcot S.
\$100K
- 2019 – 2021 Funding body: *Mark Hughes Foundation Brain Cancer Innovation Project Grant*, Title: Combining artificial intelligence and genomics to non-invasively monitor glioblastoma patients and predict tumour recurrence. Chief Investigators: **Vafaee F** (CIA), Howell V, Jurisica I.
\$150K
- 2021 – 2022 Funding body: *Digital Grid Future Institute, UNSW*, Title: EV adoption in Smart Cities: with AI-enabled mental map configuration to enhance the individuals, decision-making. Chief Investigators: Waller T, Rashidi T, **Vafaee F**, Najmi A.
\$60K
- 2021 – 2022 Funding body: *Industry Network Seed Funding, UNSW*, Title: Deep learning-based integration of different modalities of data – multi-omics and beyond. Chief Investigator: **Vafaee F**.
\$18K
- 2019 – 2020 Funding body: *CINSW Sydney Vital Translational Cancer Research - Research Seed Funding Award*, Title: Understanding of the involvement of inflammation in cancer progression and the development of resistance to treatments - Bioinformatician Funding Source. Chief Investigators: Howell V, **Vafaee F**
\$64K
- 2020 – 2021 Funding body: *Research Infrastructure Scheme, UNSW*, Title: Nanopore-based long read sequencer and Viaflo sample prep station for the Ramaciotti Centre for Genomics. Chief Investigators: Wilkins M, Cavicchioli R, Edwards R, Janitz M, Hazel M, Lan R, Murray V, Oates E, Tree J, **Vafaee F**, Waters P, White P, Zhang Li (co-CIs alphabetically sorted)
\$50.3K
- 2019 – 2021 Funding body: *Vertex Innovation Funds*, Title: Exosomal Biomarkers for Early Prediction of Cystic Fibrosis Related Diabetes. Chief Investigators: Waters S, Kicic A, Jaffe A, **Vafaee F**, Verge C, Widger J, Yvnone B et al.
€157K
- 2019 – 2020 Funding body: *UNSW Scientia Education Investment Fund*, Title: Micro-credentials in bioinformatics/systems biology, genetics/genomics and protein structural biology. Chief Investigators: Whitaker N, **Vafaee F**, Oates E, Marquis C, Gaela A, et al.
\$100K
- 2019 – 2019 Funding body: *UNSW Research Technology Services*, Title: AI-empowered Brain Genomics (Machine learning and Cloud Computing Schemes) . Chief Investigator: **Vafaee F**
\$30K
- 2019 – 2019 Funding body: *UNSW Faculty Research Grants Program*, Title: Cell-identity mapping from massive single-cell data using deep learning. Chief Investigator: **Vafaee F**
\$9288
- 2015 – 2016 Funding body: *SPARC Implementation Fund*, Title: The Sydney 1000 Cancer Project–Stage 1 Gastrointestinal Cancers Immunophenotyping Study. Chief Investigators: Charles K, Clarke S, Diakos C, Pavlakis N, Engel A, Gill A, Kneebone A, Hart D, Smith A, Byrne S, McGuire H, **Vafaee F**, King M.
\$175K
- 2014 – 2015 Funding body: *Ramsay Research and Teaching Fund*, Title: Routine application of next generation sequencing for identifying Actionable Mutations in patients with non-small cell lung cancer. Chief Investigators: Pavlakis N, Howell V, Colvin E, **Vafaee F**.
\$60K

Research Funding Under-Review

Net requested value of **\$7.1M** (unapportioned) from in Category I research funding schemes.

- 2021 – 2025 Funding body: *Medical Research Future Fund, Genomics Health Future Mission (APP2007587)*, Title: Incorporating novel biomarkers with a breast cancer blood test that transforms screening. Chief Investigators: **Vafaee F** (CIA), Frazer H, Sowmya A, Batarseh A, Petrie D, Bednarz T, Gallego-Ortega D, Millar E.
\$2.6M requested
- 2021 – 2023 Funding body: *Australian Research Council, ARC Linkage (200300748)*, Title: Deep learning-based integration of different modalities of data – multi-omics and beyond. Chief Investigators: **Vafaee F** (CIA), Arcot S, Hayens, P, Bednarz T, Batarseh A.
\$625K requested

- 2021 – 2025 Funding body: *Medical Research Future Fund, EPCDRI - Improving Diagnosis in Cancers with Low Survival Rates (APP2008996)*, Title: Microbial based biomarkers powered by artificial intelligence for early detection of liver cancer in Australia. The Australian Liver Cancer Microbiome Consortium. Chief Investigators: Zekry A, El-Omar E, **Vafae F** (CIC), Sowmya A, McCaughan G, Nicholson J, Holmes E, Roberts S, Fung K, Behary J.
\$3.89M requested
- 2021 – 2023 Funding body: *Australian Research Council, ARC Discovery Project (DP220101938)*, Title: Decoding regulatory RNA function in bacteria. Chief Investigators: Tree J, **Vafae F** (CIB)
\$750K requested
- 2021 – 2023 Funding body: *Australian Research Council, ARC Discovery Project (DP220102550)*, Title: Understanding chromatin interactions with machine learning techniques. Chief Investigators: Tree JRokney H, Hutvagner G, **Vafae F** (CIC).
\$650K requested

Publications

Last 3 Years Metrics: 16 peer-reviewed articles (total career 34), 73% corresponding author, 100% Q1 journals and 87.5% top 10 percentile journals. 696 citations since 2016, i10-index: 21 (Google Scholar), Field-Weighted Citation Impact: 3.08 (CiteScore, 2017 – 2019). Produced 8 software/analysis-pipelines accessible via the VafaeLab GitHub Repository or as cloud-based software.

Journal Papers (Corresponding or senior authorship is marked by *)

- 2020 Azad AKM, Dinarvand M, Nematollahi A, Swift J, Lutze-Mann L, **Vafae F***, A comprehensive integrated drug similarity resource for in-silico drug repositioning and beyond, *Briefings in Bioinformatics*, bbaa126, doi:10.1093/bib/bbaa126.
- 2020 Colvin EK, Howell VM, Mock S, Samimi G, **Vafae F***, Expression of long noncoding RNAs in cancer-associated fibroblasts linked to patient survival in ovarian cancer, *Cancer Science*, doi:10.1111/cas.14350.
- 2020 Walsh K, Voineagu M, **Vafae F*** Voineagu I*, TDAview: an online visualization tool for topological data analysis, *Bioinformatics*, btaa600, doi:10.1093/bioinformatics/btaa600
- 2020 Bayati M, Rabiee H, Mehrbod M, **Vafae F**, Ebrahimi D, Forrrest A, Alinejad-Rokny H. CANCERSIGN: a user-friendly and robust tool for identification and classification of mutational signatures and patterns in cancer genomes, *Scientific Reports*, vol. 10, doi:10.1038/s41598-020-58107-2
- 2020 Dinarvand M, Spain MP, **Vafae F***, Pharmacodynamic Functions of Synthetic Derivatives for Treatment of Methicillin-Resistant Staphylococcus aureus (MRSA) and Mycobacterium tuberculosis, *Frontiers in Microbiology*, bbaa126, doi:10.3389/fmicb.2020.551189.
- 2020 Ebrahimkhani S, Beadnall HN, Barnett MH, Suter CM, Buckland ME, **Vafae F***. Serum exosome microRNAs predict multiple sclerosis disease activity after fingolimod treatment, *Molecular Neurobiology*, doi:10.1007/s12035-019-01792-6
- 2019 Su Z, Burchfield J, Yang P, Humphrey S, Yang G, Francis D, Yasmin S, Shin SY, Norris D, Fisher-Wellman K, Wang QP, Parker B, Neely G, **Vafae F**, Chiu J, Yeo R, Hogg P, Fazakerley D, Nguyen L, Kuyucak S, James D. Global redox proteome and phosphoproteome analysis reveals novel mode of Akt regulation, *Nature Communications*, vol. 10, pp. 5486, doi:10.1038/s41467-019-13114-4.
- 2019 Wong M, Braidly N, Pickford R, **Vafae F**, Crawford J, Muenchhoff J, Schofield P, Attia J, Brodaty H, Sachdev P, Poljak A. Plasma lipidome variation during the second half of the human lifespan is associated with age and sex but minimally with BMI. *PLOS ONE*, vol 14, doi.org/10.1371/journal.pone.0214141
- 2018 Ebrahimkhani S, **Vafae F**, Hallal S, Wei H, Lee M, Young P, Satgunaseelan L, Shivalingam B, Suter C, Buckland M, Kaufman K. Deep sequencing of circulating exosomal microRNA allows non-invasive glioblastoma diagnosis. *NPJ precision oncology, Nature*, 2(28, doi:10.1038/s41698-018-0071-0

- 2018 **Vafaee F**, Diakos C, Kirschner MB, Reid G, Michael MZ, Horvath LG, Alinejad-Rokny H, Cheng ZJ, Kuncic Z, Clarke S . A data-driven, knowledge-based approach to biomarker discovery: application to circulating microRNA markers of colorectal cancer prognosis. *NPJ systems biology and applications, Nature*, 4(1), 20, doi:10.1038/s41540-018-0056-1
- 2018 Chaudhuri R, Krycer JR, Fazakerley DJ, Fisher-Wellman KH, Su Z, Hoehn KL, Yang JYH, Kuncic Z, **Vafaee F*** & James DE. The transcriptional response to oxidative stress is part of, but not sufficient for, insulin resistance in adipocytes *Scientific Reports*, 8, doi:10.1038/s41598-018-20104-x.
- 2018 Contaldi C, **Vafaee F***, Nelson PC. Bayesian network hybrid learning using an elite-guided genetic algorithm. *Artificial Intelligence Review Journal* 1-28, doi:10.1007/s10462-018-9615-5.
- 2018 **Vafaee F***, Dashti H, Alinejad-Rokney H. Transcriptomic Data Normalization. *Encyclopedia Of Bioinformatics and Computational Biology, Reference Module in Life Sciences*, Elsevier, doi: 10.1016/B978-0-12-809633-8.20209-4.
- 2017 **Vafaee F***, Colvin EK, Mok SC, Birrer MJ, Howell VM, & Samimi G. Functional prediction of long non-coding RNAs in ovarian cancer-associated fibroblasts indicate a role in metastasis. *Scientific Reports* 4;7(1):10374. doi: 10.1038/s41598-017-10869-y.
- 2017 Ebrahimkhani S, **Vafaee F**, Young PE, Hur S, Hawke S, Devenney E, Beadnall H, Barnett MH, Suter C, & Buckland M. Exosomal microRNA signatures in multiple sclerosis reflect disease status. *Scientific Reports*, 7. doi:10.1038/s41598-017-14301-3
- 2016 **Vafaee F***, Krycer J, Ma Xiuquan, Burykin T, James D, Kuncic Z. ORTI: an open-access repository of transcriptional interactions for interrogating mammalian gene expression data, *PLOS ONE*. 11(10), 1-21.
- 2016 **Vafaee F***. Using Multi-objective Optimization to Identify Dynamical Network Biomarkers as Early-warning Signals of Complex Diseases, *Nature-Scientific Reports*, 24;6:22023. doi: 10.1038/srep22023.
- 2016 Parker N R, Hudson A L, Khong P, Parkinson J F, Ikin R, Zhu Y, Cheng Z J, **Vafaee F**, Chen J, Wheeler H R, Howell V.) Intratumoral heterogeneity of DNA repair pathways in glioblastoma, *Nature-Scientific Reports*, 4;6:22477. doi: 10.1038/srep22477.
- 2016 Domanova W, Krycer J, Chaudhuri R, Yang P, **Vafaee F**, Fazakerley D, Humphrey S, James D, Kuncic Z. (2016) Identifying kinase substrate relationships using temporal data from large-scale phosphoproteomics studies, *PLOS ONE*. 11(6), 1-14.
- 2015 Rollo J , Banihashemi N, **Vafaee F**, Crawford J, Kuncic Z, Holsinger D. Unravelling the mechanistic complexity of Alzheimer's disease with systems biology, *Alzheimer's & Dementia*, doi:10.1016/j.jalz.2015.10.010.
- 2014 Kotlyar M, Pastrello C, Pivetta, F, Lo Sardo A, Cumbaa, C, Li, H, Naranian, T, Niu Y, Ding Z, **Vafaee F**, Broackes-Carter F, Petschnigg, J, Mills, G.B, Jurisicova, A, Stagljjar, I, Maestro, R, & Jurisica, I. In silico prediction of physical protein interactions and characterization of interactome orphans, *Nature Methods*, 12(1):79-84.
- 2013 **Vafaee F***, Rosu D, Broackes-Carter F, and Jurisica I. Novel semantic similarity measure improves an integrative approach to predicting gene functional associations. *BMC Systems Biology*, 7:22.
[Journal Papers \(under-review/pre-print\)](#)
- 2021 Capraro A *et al.*, **Vafaee F** and Waters S., Ageing impairs the airway epithelium defence response to SARS-CoV-2. Under Editorial Decision by *nature*
- 2021 Koch F, Sutton G, Voinugea I, **Vafaee F***, Supervised Application of Internal Validation Measures to Benchmark Dimensionality Reduction Methods in scRNA-seq Data. Under-review by *Briefings in Bioinformatics* (Impact Factor: **8.99**) bioRxiv doi:2020.10.29.361451
- 2021 Zandavi, SM, Rashidi T, **Vafaee F***, Forecasting the Spread of COVID-19 Under Control Scenarios Using LSTM and Dynamic Behavioral Models. Under review by *IEEE Transactions on Cybernetics* (Impact Factor: **11.47**), arXiv doi:2005.12270

- 2021 AKM Azad, Fatima S, **Vafaee F***, An integrative resource for network-based investigation of COVID-19 combinatorial drug repositioning and mechanism of action. Under review by *Patterns* by Cell Press, chemRxiv, doi: 10.26434/chemrxiv.13271096.v1
- 2021 Safarchi A, Fatima S, Ayati Z, **Vafaee F***, AAn Update on Novel Approaches for Diagnosis and Treatment of SARS-CoV-2 Infection. *Critical reviews in Biotechnology*, Impact Factor: **8.01**), Under Editorial Assessment.
- 2021 Rashidi TH, Shahriari S, Azad AK, **Vafaee F***, Real-time time-series modelling for prediction of COVID-19 spread and intervention assessment. Under review by *Scientific Reports* medRxiv doi: 10.1101/2020.04.24.20078923
- 2021 Batarseh M, **Vafaee F**, Hosseini-Beheshti E, Chen A, Cohen A, Juillard A, Henry Hunt N, Mariani M, Mitchell M, Grau G, Lipidome profiles of plasma microvesicles differ in experimental cerebral malaria, compared to malaria without neurological complications. bioRxiv doi: 10.1101/2020.07.28.224170
- 2021 Gano C, Failes T, Arndt G, Mahns D, Fatema S, Coorsen J, Saedisomeolia A, Bucci J, de Souza P, **Vafaee F** and Scott K, Effect of cellular genotype on pairwise synergy profiles of phytochemicals in prostate cancer cells. bioRxiv, doi: TBA

Refereed Proceedings

- 2017 Contaldi C, **Vafaee F***, Nelson PC. The Role of Crossover Operator in Bayesian Network Structure Learning Performance: a Comprehensive Comparative Study. *ACM, Genetic & Evolutionary Computation*, 769-776.
- 2014 **Vafaee F***. Learning the structure of large-scale Bayesian networks using genetic algorithm, *ACM, Genetic and Evolutionary Computation*, 855-862.
- 2014 **Vafaee F**, Turan G, Nelson PC & Berger-Wolf TY. Balancing the exploration and exploitation in an adaptive diversity guided genetic algorithm, *IEEE, Evolutionary Computation*, 2570-2577.
- 2014 **Vafaee F**, Turan G, & Nelson PC. Among-site rate variation: adaptation of genetic algorithm mutation rates at each site, *ACM, Genetic & Evolutionary Computation*, 863-870.
- 2010 **Vafaee F**, Turan G, & Nelson PC. Optimizing Operator Rates Using a Markov Chain Model of Genetic Algorithms, *ACM, Genetic & Evolutionary Computation*, 721-728.
- 2010 **Vafaee F** & Nelson PC. An explorative and exploitative mutation scheme, *IEEE, Evolutionary Computation*, 1-8.
- 2009 Xu B, **Vafaee F** & Wolfson O. In-network query processing in mobile p2p databases, *ACM, Advances in Geographic Information Systems*, 207-216.
- 2009 **Vafaee F** & Nelson PC. A genetic algorithm that incorporates an adaptive mutation based on an evolutionary model, *IEEE, Machine Learning and Applications*, 101-107.
- 2008 **Vafaee F**, Xiao W, Nelson PC, & Zhou C. Adaptively evolving probabilities of genetic operators, *IEEE, Machine Learning and Applications*, 292-299.

Abstracts peer-reviewed

- 2020 Batarseh A, Beheshti E, **Vafaee F**, Chen A, Cohen A, Juillard A, Mariani M, Grau G, Lipidomics profiles of plasma microvesicles differ in experimental cerebral malaria, compared to malaria without neurological complications, *Australasian Extracellular Vesicles Conference*
- 2019 Koch F and **Vafaee F***, Effect of dimensionality reduction on clustering single cell RNA-sequencing, *ISMB/ECCB 2019, Intelligent Systems for Molecular Biology*, July 2019, Switzerland.
- 2019 Bataresh A, **Vafaee F et al.**, Plasma microvesicles lipidomics of Cerebral malaria in mice model, *World inflammation Conference*, September 2019, Sydney Australia.
- 2017 Ebrahimkhani S, Barnett Michael, **Vafaee F**, Suter C, & Buckland M. An optimized protocol used to extract and profile EV small RNA from limiting amounts of human and mouse serum, *ISEV workshop on Diet, Environment and Extracellular Vesicles*, January 2017, Melbourne, Australia.

- 2016 Ebrahimkhani S, **Vafaee F**, Barnett Michael, Cropley J, Jayasooriah N, Suter C, & Buckland M. Small Non-coding RNAs from Serum Derived Extracellular Vesicles are Potential Biomarkers in Multiple Sclerosis, *ASMR NSW Annual Scientific Meeting*, May 2016, Sydney, Australia.
- 2015 **Vafaee F**, Colvin EK, Mok SC, Birrer MJ, Howell VM, & Samimi G. Analysis of long non-coding RNAs expression profiles in ovarian cancer-associated fibroblasts, *Intl. Conference on Health Informatics and Technology*, July 2015, Valencia, Spain.
- 2015 Parker NR, Hudson AL, Khong P, Parkinson JF, Ikin R, Chen ZJ, **Vafaee F**, Helen R. & Wheeler HR, Howell VM. Intratumoral heterogeneity of DNA repair pathways in glioblastoma, *Advances in Brain Cancer Research, American Association for Cancer Research Annual Meeting*, May 2015, Washington D.C., USA.
- 2015 Colvin EK, **Vafaee F**, Mok SC, Birrer MJ, Howell VM, & Samimi G. Differential expression of long non-coding RNAs in ovarian cancer-associated fibroblasts versus normal ovarian fibroblasts, *Advances in Ovarian Cancer Research, American Association for Cancer Research Annual Meeting*, April 2015, Philadelphia, USA.
- 2015 **Vafaee F**, Krycer J, James D, & Kuncic Z. Unravelling dynamic transcriptional responses to oxidative stress, *Intl. Conf. on Systems Biology (ICSB 15)*, Nov. 2015 Singapore.
- 2015 Cheng ZJ, Krycer J, Su T, Fazakerley D, Kuncic Z, & **Vafaee F**. Elucidating the cellular response to oxidative stress by a holistic and integrative multi-omics analysis, *Intl. Conf. on Systems Biology (ICSB 15)*, Nov. 2015 Singapore.
- 2014 **Vafaee F**, Holsinger D, & Conrad M. Temporal dynamics of oxidative stress-related gene transcription in the human prefrontal cortex during neurodegeneration, *Society of Free Radical Research International (17th SFRRI)*, March 2014 Kyoto, Japan.
- 2014 **Vafaee F** & Holsinger D Modelling the transcription of oxidative stress and neurodegeneration related genes in the mouse hippocampus during aging. *Intl. Conf. on Systems Biology (ICSB 14)*, Sep. 2014 Melbourne, Australia.
- 2014 Wong M, Norris D, Burchfield J, Krycer J, **Vafaee F**, Domanova W, Kuncic Z, & James D. (2014) Dynamic systems model of insulin signalling pathway for identifying causes of insulin resistance, *Intl. Conf. on Systems Biology (ICSB 14)*, Sep. 2014 Melbourne, Australia.
- 2014 Domanova W, Wong M, Parker B, Burchfield J, **Vafaee F**, Kuncic Z, & James D. Dynamic *in silico* reconstruction of the insulin signalling network, *Intl. Conf. on Systems Biology (ICSB 14)*, Sep. 2014 Melbourne, Australia.
- 2014 Domanova W, Krycer J, **Vafaee F**, James D, & Kuncic Z. Modelling the insulin signalling network: unravelling the molecular mechanisms of insulin resistance, *Intl. Conf. on Bioinformatics (InCoB2014)*, Aug. 2014 Sydney, Australia.
- 2013 Wong M, Domanova W, **Vafaee F**, Krycer J, Burchfield J, James D, & Kuncic Z. Network reconstruction and simulation of insulin resistance in adipocytes, *Computational Models for Life Science, (CMLS 13)*, Nov. 2013 Sydney, Australia.

Editorship and Peer Review

- 2017 – Associate Editor of Journal of Artificial Intelligence Review (SNIP 3.623, Percentile: 99%)
- 2018 – Associate Editor of Journal of PLOS ONE (SNIP 1.205, Percentile: 91% Multidisciplinary)
- 2019 – Guest Editor of Journal of Entropy (Genomics Special Issue)
- 2013 – Reviewer of journals of *Briefing in Bioinformatics* (SNIP 2.126, Percentile: 97%), *Bioinformatics* (SNIP 1.813, Percentile: 91%), *Cancers* (SNIP 1.567, Percentile: 92%), *Therapeutic Advances in Medical Oncology* (SNIP 1.783, Percentile: 83%), *Artificial Intelligence Review* (SNIP 3.623, Percentile: 99%), *Scientific Reports* (SNIP 1.365, Percentile: 93%)

Executive Leadership

- 2020 – 2024 Deputy Director of **Data Science Hub**, UNSW Sydney
- 2019 – 2023 Member of **National Computational Merit Allocation Committee**, NCMAC

- 2018 – 2021 Member of **Women in Research Network** Executive Committee, UNSW Sydney
- 2018 – 2020 Member of School's **Executive Team** (UNSW Sydney - School of BABS)
- 2018 – 2021 **Bioinformatics Coordinator** (UNSW Sydney - School of BABS)
- 2014 – 2017 Member of **Ramaciotti Facility Informatics** Advisory Committee, University of Sydney

Professional Community Membership

- 2017 – International Society of Computational Biology, www.iscb.org
- 2018 – Sydney Vital Translational Cancer Research Community, sydneyvital.org.au
- 2019 – WiMLDS: Women in Machine Learning & Data Science, wimlds.org/
- 2020 – CONCERT: Centre for Oncology Education & Research Translation, www.concert.org.au
- 2020 – Melanoma and Skin Cancer Trials - Artificial Intelligence Working Group, www.masc.org.au/

Conference and Seminar Organisation

- 2019 Lead Organiser of **AI in Biomedicine Symposium** (UNSW - Sydney)
- 2018 Lead Organiser of **UNSW Bioinformatics Connect** (UNSW - Sydney)
- 2019 Program Committee Member of 30th **International Conference on Genome Informatics**
- 2019 Program Committee Member of the **Australian Bioinformatics And Computational Biology Society**, ABACBS
- 2015 Local Organising Committee Member of *AMSI BioInfoSummer* hosted by the Australian Mathematical Sciences Institute
- 2014 Organiser of the University of Sydney *Visiting Scholar Seminars* for Prof Tanya Berger-Wolf from University of Illinois at Chicago, USA
- 2013 Organiser of the University of Sydney *Visiting Scholar Seminars* for Prof Tilman Grune from German Institute of Human Nutrition, Germany

Conference Presentations and Invites Talks

International Conferences

- 9/2018* 12th Biennial Ovarian Cancer Research Symposium, Washington, USA
published in Clinical Cancer Research by AACR, doi: 10.1158/1557-3265.OVCASYMP18-TMIM-067.
- 5/2017* International Society for Extracellular Vesicles Annual Meeting, Toronto, Canada
published in Journal of Extracellular Vesicles, doi: 10.1080/20013078.2017.1310414.
- 7/2017* 26th International Genetic and Evolutionary Computation Conference, Berlin, Germany
published by Association for Computing Machinery, doi: 10.1145/3071178.3071240.
- 7/2015 Intl. Conference on Health Informatics and Technology, Valencia, Spain
Topic: Analysis of long non-coding RNAs expression profiles in ovarian cancer-associated fibroblasts.
- 7/2010 Genetic and Evolutionary Computation Conf. (GECCO 2010), Portland, USA
Topic: Optimizing Genetic Operator Rates Using a Markov Chain Model of GAs.
- 10/2009 International Conf. on Machine Learning and Applications (ICMLA 09), Miami, FL USA
Topic: A Genetic Algorithm That Adapt Mutation Based On an Evolutionary Model.
- 12/2008 International Conf. on Machine Learning and Applications (ICMLA 08), San Diego, USA
Topic: Adaptively Evolving Probabilities of Genetic Operators.

* Presented by my student/first-author; could not fly overseas due to maternity leaves and carer responsibilities

National Seminars

- 2/2020 Inaugural Mark Hughes Foundation Brain Cancer Symposium, Hamilton, Australia
- 5/2020 Australian National University Webinar, ANU, Sydney, Australia
- 10/2019 Australasian Leadership Computing Symposium, Canberra Australia
- 7/2019 Research Technology Seminar, University of New South Wales, Sydney, Australia

- 8/2017 Biotechnology & Biomolecular Seminars, University of New South Wales, Sydney, Australia
- 6/2017 Sydney Bioinformatics Research Symposium, University of Sydney, Sydney, Australia
- 9/2016 Statistical Bioinformatics Seminar, University of Sydney, Sydney, Australia
- 10/2014 Kolling Institute of Medical Research, Translational Research Meeting, Sydney, Australia
Topic: Systems Biology: Towards understanding the molecular mechanism of complex diseases.
- 5/2014 Kolling Institute of Medical Research, Bill Walsh Cancer Research, Sydney, Australia
Topic: Systems Biology: To unravel the molecular complexity underpinning pathogenesis.
- 12/2013 University of Sydney, Charles Perkins Centre, Sydney, Australia
Topic: Systems Biology: Towards understanding pathogenesis molecular complexity.
- 10/2013 Royan Institute, Reproductive Biomedicine and Stem Cell, Tehran, Iran
Topic: Modelling of cellular processes–application in stress activated pathways in chronic diseases
- 8/2011 University of Toronto, Toronto, Canada, Topic: Functional Gene Association Prediction.
- 6/2011 Harvard Medical School, Brigham and Women’s Hospital, Boston, USA
Topic: Genetic Algorithms, Introduction, Applications, and Parameter Adaptation.
- 5/2010 University of Illinois at Chicago, Maths, Stats & Computer Science Seminar, Chicago, USA
Topic: Genetic Algorithms: Theory and Practice.

Supervision and Mentorship

- 7/2019–**Postdoctoral Research Associate**, *Miad Zandavi*, School of BABS, UNSW Sydney.
Present Research: Single-cell sequencing data analytics
- 8/2018–**Postdoctoral Research Associate**, *Mojdeh Dinarvand*, School of BABS, UNSW Sydney.
Present Research: Drug discovery
- 2/2020–**Postdoctoral Research Associate**, *Shadma Fatima*, School of BABS, UNSW Sydney.
Present Research: Cancer biomarker discovery
- 9/2020–**Postdoctoral Research Associate**, *Azadeh Safarchi*, School of BABS, UNSW Sydney.
Present Research: Metagenomics and bioinformatics
- 8/2018–**Postdoctoral Research Associate**, *AKM Azad*, School of BABS, UNSW Sydney.
9/2020 Research: Bioinformatics, Deep learning
- 2/2020–**PhD Student**, *Daniel Formoso*, School of Medical Sciences, UNSW Sydney.
Present Research: Lateral Gene Transfer Bioinformatics
- 11/2018–**Research Associate**, *Forrest Koch*, School of BABS, UNSW Sydney.
Present Research: Cell-identity mapping from massive single-cell data
- 9/2019–**Research Associate**, *Mohamed Al-Mouiee*, School of BABS, UNSW Sydney.
Present Research: Machine learning on Cloud (Google Cloud Platform)
- 9/2019–**Research Associate**, *Abhishek Vijayan*, School of BABS, UNSW Sydney.
Present Research: Biomarker discovery, machine learning
- 9/2019–**Honours Student**, *Afia Tanzim*, School of BABS, UNSW Sydney.
9/2020 Research: Bioinformatics of Host-pathogen Interaction
- 2/2020–**Honours Student**, *Paolo Valdz*, School of BABS, UNSW Sydney.
12/2020 Research: Computational Drug Repositioning
- 9/2021–**Honours Student**, *Michael O’Dea*, School of BABS, UNSW Sydney.
9/2022 Research: Multi-omics Data Integration in breast cancer
- 2/2021–**Honours Student**, *Sebastian Porter Zadro*, School of BABS, UNSW Sydney.
12/2022 Research: Combinatorial Drug Repositioning
- 2/2021–**Honours Student**, *James Tawdros*, School of BABS, UNSW Sydney.
12/2022 Research: Microbiome biomarker discovery

Past

- 8/2015– **PhD Student**, *Saideh Ebrahimkhani*, Brain & Mind Research Inst, University of Sydney.
 12/2018 Research: Identification of exosomal microRNA Biomarkers in the progression of Multiple Sclerosis
- 11/2018– **SVRP Student**, *Rohan Dugdale*, School of BABS, UNSW Sydney.
 2/2019 Research: Deep learning for multi-omics integration
- 8/2018– **Research Associate**, *Cameron Stewart*, School of BABS, UNSW Sydney.
 3/2019 Research: Deep learning, autoML, machine learning
- 1/2016– **MSc Student**, *Carlo Contaldi*, Dept. of Computer Science, University of Illinois at Chicago.
 6/2017 Research: Bayesian network hybrid learning using a parent reducing site-specific mutation rate genetic algorithm
- 2/2016– **Talented Student Project**, *James Gatenby*, Biochemistry, University of Sydney.
 7/2016 Research: Genomic analysis of the link between cancer and thrombosis
- 11/2013– **PhD Thesis**, *Westa Domanova*, School of Physics, University of Sydney.
 7/2016 Research: Modelling molecular mechanisms of insulin resistance.
- 10/2014– **Vacation Project**, *Jason Cheng*, Master of Medical Physics, University of Sydney.
 12/2014 Research: Integrative multi-omics analysis of cellular response to oxidative stress.
- 5/2014– **M.Phil Project**, *Joseph Chan*, Sydney Medical School, University of Sydney.
 2/2015 Research: Identifying common inflammatory gene signatures in cancers.
- 6/2014– **Postgraduate Project**, *Jason Cheng*, Master of Medical Physics, University of Sydney.
 9/2014 Research: Biomarker identification and survival analysis in colorectal cancer.
- 5/2011– **MSc Thesis**, *Nirari Barm*, Dep. of Computer Science, University of Illinois at Chicago.
 1/2012 Research: Effects of parameter settings on the performance of multiple population genetic algorithms with different topologies.

Teaching

- Terms 1-3 **BABS3301**, *Biomolecular Science Laboratory Project - Advanced*, School of BABS, UNSW.
 2019 - 2020 Role: Course coordinator
- Term 2 **BINF3010/9010**, *Applied Bioinformatics*, School of Computer Science, UNSW.
 2019 - 2020 Role: Lecturer, non-coding RNAs
- Term 2 **BABS3291**, *Genes, Genomes and Evolution*, School of BABS, UNSW.
 2018 - 2020 Role: Lecturer, Network Genomics module
- Term 2 **BIOC3111**, *Molecular Biology of Proteins*, School of BABS, UNSW.
 2018 - 2020 Role: Lecturer, Systems Biology module
- Term 1 **BABS3151**, *Human Genetics*, School of BABS, UNSW.
 2018 - 2020 Role: Lecturer, Systems Biology module

Community Engagement and Outreach Activities

- 8/2020 Co-organiser of WiRN event [Shadow CVs: A guide to building resilience](#), UNSW Sydney
- 5/2020 Co-organiser of [Gender-based inequality during COVID-19](#), hosted by Centre for Social Impact
- 3/2020 Co-organiser of [WiRN Science Outreach](#), UNSW Sydney
- 9/2019 Co-organiser of WiRN event [International Engagement for Women in Academia](#), UNSW Sydney
- 3/2019 Co-organiser of WiRN Learn&Lunch Series [Preparing for Mid-career](#), UNSW Sydney

Research Collaborators & Industry Partnerships

Industrial Partners

- Nutromics Pty. Ltd, Australia: <http://www.nutromics.com.au>
- BCAL diagnostics, Australia: <https://www.bcaldiagnostics.com>
- SBX Corporation, Japan: <https://www.sbx-corp.com/>

Hospital & Institutional Collaborations

- Kolling Institute of Medical Research

- Garvan Institute for Medical Research
- Ingham Institute for Applied Medical Research
- Centre for Healthy Brain Ageing, University of New South Wales
- Brain & Mind Research Institute, University of Sydney
- Australian National University, Canberra
- Charles Perkins Centre, University of Sydney
- St Vincent's Hospital
- Royal Prince Alfred Hospital
- Royal North Shore Hospital

International Collaborations

- Krembil Research Institute and University Health Network, University of Toronto, Canada
- National Institute of Health, Division of Cancer Prevention, USA
- University of Illinois at Chicago, Artificial Intelligence Laboratory, Chicago, USA