Curriculum Vitae of Dharmesh Dinesh Bhuva

Personal Information

Full name: Dharmesh Dinesh Bhuva
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Brief biography

Dr Dharmesh D Bhuva is a computational systems oncologist in the Davis laboratory at the South Australian Immunogenomics Cancer Institute (SAiGENCI). He submitted his PhD thesis to the department of Mathematics and Statistics at the University of Melbourne in 2020. His research has focused on developing novel systems biology approaches to study cancer systems using data generated from single-cell and spatial molecular technologies. His work has empowered biologist and bioinformaticians with state-of-the-art tools to interrogate and understand molecular data at a systems level.

Dr Bhuva has published in some of the highest-ranking journals in his field, including, *Genome Biology,* and *Nucleic Acids Research*. He has also developed/co-developed 7 open-source R/Bioconductor software packages that have had more than 62,250 downloads. He has tutored computational biology courses at the University of Melbourne and has organised and run various computational biology workshops at the University of Melbourne and across the greater Asia-Pacific region. He has co-supervised 2 MSc Bioinformatics students, mentors four PhD students and currently co-supervises a PhD student.

Qualifications, Prizes and Professional Memberships

Qualifications

- PhD (Mathematics and Statistics)   The University of Melbourne, 2020

- MSc (Bioinformatics)   The University of Melbourne, 2015

- BSc (Computer science)   University of Southampton, 2013

Awards

- Victorian Cancer Bioinformatics Symposium – best written lay summary award, 2021

- The University of Melbourne's Melbourne Research Scholarship, 2016

- The University of Melbourne M.Sc. (Bioinformatics) merit-based bursaries, 2014

Career Profile

2023 – present   Senior research officer, Bioinformatics Division, South Australian Immunogenomics Cancer Institute (SAiGENCI)

- Development of novel spatial statistics methods to analyse sub-cellular spatial molecular data.

- Development of machine learning pipelines to automate analysis of histopathology images.

- Student supervision.

2020 – 2023   Research officer, Bioinformatics Division, The Walter and Eliza Hall Institute of medical research (WEHI)

- Analysis of spatial and single-cell transcriptomics to identify mechanisms of drug-induced phenotypic plasticity in cancer.

- Data analysis for commercial research collaboration between the CRC for Cancer Therapeutics and Pfizer Inc.

- Analysis of generic and drug specific regulatory mechanisms in biological systems using data integration approaches.

- Analysis of multi-omics data associated with drug response across a diverse set of biological models including cell lines and patients.

- Partial supervision of post graduate student

2016 – 2020   PhD student, School of Mathematics and Statistics, The University of Melbourne (Co-supervised by Prof. Edmund Crampin and Assoc. Prof. Melissa J. Davis)

- Analysis of context-specificity in network models, focusing on cancer subtype-specific gene regulatory networks.

- Development of methods to quantify molecular phenotypes across a diverse set of cancer types.

- Analysis of large transcriptomic datasets and experiment specific datasets from patients, cell lines and xenograft data.

- Development of several R packages.

- Partial supervision of post-graduate student.

2019 – 2022   Workshop coordinator (BINF90002 – Elements of bioinformatics), The University of Melbourne

- Prepare and deliver a workshop on the singscore software I developed during my PhD and network analysis in bioinformatics.

2019   Tutor (COMP90016 – Computational genomics), The University of Melbourne

- Supervision of tutorials, preparation and revision of tutorial material, preparation of assignments, preparation of marking sheets and marking, consultations with students, revision of exam, deploying and managing the IT infrastructure for the course.

2018   Tutor (COMP90014 – Algorithms for functional genomics), The University of Melbourne

- Supervision of tutorials, preparation and revision of tutorial material, preparation of assignments, preparation of marking sheets and marking, consultations with students.

All Refereed Publications and Preprints

* co-first author

1. Mohamed A*, **Bhuva DD***, Lee S, Liu N, Tan CW, Davis MJ. vissE.cloud: a webserver to visualise higher order molecular phenotypes from enrichment analysis. *Nucleic Acids Research*. 2023; gkad337.

2. Kulasinghe A, Liu N, Tan CW, Monkman J, Sinclair JE, **Bhuva DD**, Godbolt D, Pan L, Nam A, Sadeghirad H, Sato K, Bassi GL, O'Byrne K, Hartmann C, dos Santos Miggiolaro AFR, Marques GL, Moura LZ, Richard D, Adams M, de Noronha L, Baena CP, Suen JY, Arora R, Belz GT, Short KR, Davis MJ, Souza-Fonseca Guimaraes F, Fraser JF. Transcriptomic profiling of cardiac tissues from SARS-CoV-2 patients identifies DNA damage. *Immunology*. 2023 Mar;168(3):403-19.

3. **Bhuva DD**, Tan CW, Marceaux C, Chen J, Kharbanda M, Jin X, Liu N, Feher K, Putri G, Asselin-Labat ML, Phipson B, Davis MJ. Library size confounds biology in spatial transcriptomics data. *bioRxiv*. 2023:2023-03.

4. Vo T, Balderson B, Jones K, Ni G, Crawford J, Millar A, Tolson E, Singleton M, Kojic M, Robertson T, Walters S, Mulay O, **Bhuva DD**, Davis MJ, Wainwright BJ, Nguyen Q, Genovesi LA. Spatial transcriptomic analysis of Sonic Hedgehog Medulloblastoma identifies that the loss of heterogeneity and promotion of differentiation underlies the response to CDK4/6 inhibition. *Genome Medicine.* 2023 May 1;15(1):29.

5. Kulasinghe A, Tan CW, dos Santos Miggiolaro AF, Monkman J, SadeghiRad H, **Bhuva DD**, Junior JD, de Paula CB, Nagashima S, Baena CP, Souza-Fonseca-Guimaraes P, de Noronha L, McCulloch T, Gustavo RR, Cooper C, Tang B, Short KR, Davis MJ, Souza-Fonseca-Guimaraes F, Belz GT, O'Byrne K. Profiling of lung SARS-CoV-2 and influenza virus infection dissects virus-specific host responses and gene signatures. *European Respiratory Journal*. 2022 Jun 1;59(6).

6. Berthelet J*, Foroutan M*, **Bhuva DD***, Whitfield HJ, El-Saafin F, Cursons J, Serrano A, Merdas M, Lim E, Charafe-Jauffret E, Ginestier C, Ernst M, Hollande F, Anderson RL, Pal B, Yeo B, Davis MJ, Merino D. Computational Screening of Anti-Cancer Drugs Identifies a New BRCA Independent Gene Expression Signature to Predict Breast Cancer Sensitivity to Cisplatin. *Cancers*. 2022 May 13;14(10):2404.

7. **Bhuva DD**, Tan CW, Liu N, Whitfield HJ, Papachristos N, Lee S, Kharbanda M, Mohamed A, Davis MJ. vissE: A versatile tool to identify and visualise higher-order molecular phenotypes from functional enrichment analysis. *bioRxiv*. 2022 Mar 7:2022-03.

8. Perez San Juan B, Hediyeh-Zadeh S, Rangel L, Millioli HH, **Bhuva DD**, Rodriguez V, Bunkum A, Kohane F, Purcell C, Kurumlian A, Castillo L, Lim E, Gill AJ, Ganju V, Dear R, O'Toole S, Vargas C, Hickey TE, Goldstain LD, Lock JG, Davis MJ, Chaffer CL. Targeting phenotypic plasticity prevents metastasis and the development of chemotherapy-resistant disease. *medRxiv*. 2022:2022-03.

9. Genovesi LA, Millar A, Tolson E, Singleton M, Hassall E, Kojic M, Brighi C, Girard E, Andradas C, Kuchibhotla M, **Bhuva DD**, Endersby R, Gottardo NG, Bernard A, Adolphe C, Olson JM, Davis MJ, Wainwright BJ. Systems pharmacogenomics identifies novel targets and clinically actionable therapeutics for medulloblastoma. *Genome Medicine*. 2021 Dec;13(1):1-5.

10. **Bhuva DD**, Cursons J, Davis MJ. Stable gene expression for normalisation and single-sample scoring. *Nucleic acids research*. 2020 Nov 4;48(19):e113-.

11. **Bhuva DD**, Cursons J, Smyth GK, Davis MJ. Differential co-expression based detection of conditional relationships in transcriptional data: comparative analysis and application to breast cancer. *Genome biology*. 2019 Dec;20(1):1-21.

12. **Bhuva DD**, Foroutan M, Xie Y, Lyu R, Cursons J, Davis MJ. Using singscore to predict mutations in acute myeloid leukemia from transcriptomic signatures. *F1000Research*. 2019 Jun 3;8.

13. Foroutan M*, **Bhuva DD***, Lyu R, Horan K, Cursons J, Davis MJ. Single sample scoring of molecular phenotypes. *BMC bioinformatics*. 2018 Dec;19(1):404.

All software packages, and web apps developed (62,252 downloads as of May 2023)

1. [vissE.Cloud](#) (2023)   12,000 accesses (from 22 countries)

2. standR (2022)   956 downloads

3. msigdb (2021)   6,803 downloads

4. vissE (2021)   2,235 downloads

5. emtdata (2021)   841 downloads

6. SingscoreAMLMutations (2019)   1,348 downloads

7. dcanr (2019)   5,427 downloads

8. singscore (2018)   44,642 downloads *(top 10% globally)*

Conference Presentations

1. South Australian Immunogenomics Cancer Institute (SAiGENCI) seminar, Adelaide, Australia, 31st May 2023.
2. **Invited speaker**, Melbourne Mathematical Biology (MMB) seminar, Melbourne, Australia, 25th May 2022.
3. Victorian Cancer Bioinformatics Symposium (VCBS), Melbourne, Australia, 8th October 2021. (Best written lay summary consumer award).
4. Bioinformatics seminar, Walter Eliza Hall Institute, Australia, 27th July 2021.
5. Bioinformatics PhD completion seminar, Walter Eliza Hall Institute, Australia, 19th May 2020.
6. COMBINE/AYRCOB Student symposium, Sydney, Australia, 9th December 2019.
7. Bioinformatics seminar, Walter Eliza Hall Institute, Australia, 12th November 2019.
8. COMBINE Student symposium, Melbourne, Australia, 26th November 2018.
9. Bioinformatics seminar, Walter Eliza Hall Institute, Australia, 15th May 2018.
10. COMBINE Student symposium, Adelaide, Australia, 13th November 2017.

Workshops Delivered

1. **Invited speaker**, Melbourne Bioinformatics, Melbourne, Australia, 29th September 2022
2. **Invited speaker**, Bioinformatics workshop, AMSI Bioinfosummer Online, Australia, 30th November 2021.
3. **Invited speaker**, Lecture and Bioinformatics workshop, WEHI Bioinformatics and Computational Biology Masterclass, Online (targeting south east Asia), 27th August 2021.
4. **Invited speaker**, Bioinformatics workshop, Nanjing University, China, 14th December 2020.

Awards and Funding

Grant	Funding Organisation	Investigators	Status	Amount
Victorian Cancer Bioinformatics Symposium Consumer Award - best written lay summary	-	-	2021	$200
Melbourne Research Scholarship	The University of Melbourne	Dharmesh D. Bhuva	2016-2020	$150,000 fee waiver + $29,000 stipend p.a.
M.Sc. Bioinformatics bursary: Exploring conditional regulatory networks in breast cancer	The University of Melbourne	Dharmesh D. Bhuva	2014-2015	$5,000

Professional Contributions

Current Professional Memberships

- Student member of the Australian Bioinformatics and Computational Biology Society (ABACBS) (2017 - present)

Conference Organisation

- Organising committee, ABACBS National Conference, Melbourne 2022
- Organising committee, WEHI Bioinformatics and Computational Biology Masterclass, Online

Research Collaborations

- Prof. Gabrielle Belz (The University of Queensland, Brisbane, Australia) and a team of clinicians from Hospital Marcelino Champagnat (Brazil); Characterising the molecular traits of an international cohort of ICU patients suffering from severe COVID-19 disease using novel spatial transcriptomic tools.

- Prof. Anne Voss and A/Prof. Tim Thomas (Walter and Eliza Hall Institute of medical research, Melbourne, Australia), Prof. Sarah-Jane Dawson and Prof. Mark Dawson (Walter and Eliza Hall Institute of medical research, Melbourne, Australia), and Pfizer Inc.; Investigating the mechanism of actions for a drug from Pfizer Inc. under a commercial licensing deal.

- Prof. Erik Thompson (Queensland University of Technology and St Vincent's Institute, Brisbane, Australia); Pathways implicated in the epithelial to mesenchymal transition in breast cancer.

- Dr. Laura Genovesi and Dr. Christelle Adolphe (The University of Queensland, Brisbane, Australia); Investigating dormancy induced by Palbociclib treatment in medulloblastoma and the role of hypoxia in medulloblastoma.

- Dr. Delphine Merino (ONJCRI, Melbourne, Australia); Investigating drug response prediction modelling across various cancers.

- Dr. Kate Sutherland (Walter and Eliza Hall Institute of medical research, Melbourne, Australia); Investigating regulatory mechanisms in small cell lung cancer in genomic mouse models.

Supervision and mentoring

- *PhD supervisor:* Malvika D Kharbanda (Co-supervisor, 2023-present)

- *Supervisor for research projects for M.Sc. student:* Malvika D Kharbanda (Co-supervisor, awarded 2022), Ruqian Lyu (Co-supervisor, awarded 2018).

- I mentor PhD students and provide them with advice and support related to their research projects and their PhD administrative tasks.

Teaching

WEHI Bioinformatics and Computational Biology Masterclass

- Delivered an introduction to pathway analysis lecture in computational biology.
- Prepared and delivered a pathway analysis workshop.

University of Melbourne

- Invited Demonstrator for M.Sc. Bioinformatics, BINF90002 (2022): Conducted a biological networks workshop.
- Invited Demonstrator for M.Sc. Bioinformatics, BINF90002 (2021): Conducted a biological networks workshop.

- Invited Demonstrator for M.Sc. Bioinformatics, BINF90002 (2020): Conducted a transcriptomic analysis workflow and discussed biological networks.
- Invited Demonstrator for M.Sc. Bioinformatics, BINF90002 (2019): Demonstrated a transcriptomic analysis workflow in the R programming language.
- Demonstrator for M.Sc. Bioinformatics, COMP90016 (2019, Semester 1): Taught algorithms and scripting, and demonstrated the use of knowledgebases.
- Demonstrator for M.Sc. Bioinformatics, COMP90014 (2018, Semester 2): Taught algorithms, python programming and scripting.

Community presentations and outreach

- Volunteer head tutor to Victorian certificate of education (VCE) high school (grade 10-12) STEM students of the SKLPS Victoria Inc. community, 2015-2017. Conceived the tutoring program in 2015 and managed 5 tutors for various subjects including, mathematics, physics, chemistry, and biology, for the duration of the tutoring program.