

Ph.D in Bioinformatics (Medcine)

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RESEARCH EXPERTISE KEYWORDS

Shell (Bash) • Python • R • Pipeline • NGS data • Hi-C • SNPs • Epigenetics • Data integration

RESEARCH EXPERIENCE

DAVIS LAB, WEHI May. 2021 - Present | Melbourne, Australia

Collaboration: Arutha Kulasinghe's lab in Queensland University of Technology

Spatial Profiling of Lung and Heart SARS-CoV-2 and Influenza Virus Infection. Main responsibilities:

- Analysing spatial transcriptomics data.
- Differential analysis.

DAVIS LAB, WEHI May. 2021 - Present | Melbourne, Australia

Developing computation protocol to analyse spatial transcriptomics data from the NanoString GeoMX Human Whole Transcriptome Atlas platform. Main responsibilities:

- Analysing spatial transcriptomics data.
- Normalisation method benchmarking and development.
- Journal article writing.

JIMMY BREEN'S LAB, SAHMRI Feb. 2019 - Jun. 2020 | Adelaide, Australia

Collaboration: Simon Barry's lab in Women's and Children's Hospital

Developing computation pipeline to filter T1D risk variants and investigating the potential mechanisms of the identified SNPs. Main responsibilities:

- Analysing Hi-C, ATAC-seq, ChIP-seq and SNPs data.
- Building the filtering computational pipeline.
- Investigating SNPs by integrating with regulatory T cell-specific epigenome data.
- Journal article writing.

JIMMY BREEN'S LAB, SAHMRI Jan. 2020 - present | Adelaide, Australia

Collaboration: Hamid Alinejad-Rokny's lab in UNSW

Identifying candidate enhancers of human cell lines and tissues from statistically signficant Hi-C interactions of public Hi-C data. Main responsibilities:

- Public Hi-C & capture Hi-C data mining.
- Building a computational pipeline to analyse Hi-C data based on the instruction of 4DN project.
- Data integration and downstream analysis.
- Journal article writing.

JIMMY BREEN'S LAB, SAHMRI Jul. 2020 - Present | Adelaide, Australia

Collaboration: Sam Buckberry's lab in the University of Western Australia

Analysing Hi-C data to identify A/B comparts and compared the genome compartmentalisation among different conditions Main responsibilities:

• Analysing Hi-C data and identifying and comparing A/B compartments under different experimental conditions.

BIOINFORMATICS HUB, UNIVERSITY OF ADELAIDE Oct. 2018 - Jan. 2019 | Adelaide, Australia

Collaboration: John Williams' lab in the Davies Research Centre, University of Adelaide

Identifying and comparing toplogically-associated domains (TADs) between cattle Angus breed and Brahman breed. Main responsibilities:

• Analysing cattle Hi-C data and identifying TADs from Hi-C interactions.

PUBLICATIONS & AWARDS

PUBLICATIONS

Journal articles

Liu, N., Sadlon, T., Wong, Y.Y., Pederson, S.M., Breen, J. and Barry, S.C., 2020. **3DFAACTS-SNP:** Using regulatory T cell-specific epigenomics data to uncover candidate mechanisms of Type-1 Diabetes (T1D) risk. bioRxiv. (peer review in progress)

Liu, N., Low, W.Y., Alinejad-Rokny, H., Pederson, S., Sadlon, T., Barry, S. and Breen, J., 2020. **Seeing the forest through the trees:**Identifying functional interactions from Hi-C. bioRxiv. (peer review in progress)

Brown, C.Y., Sadlon, T., Hope, C.M., Wong, Y.Y., Wong, S., Liu, N., Withers, H., Brown, K., Bandara, V., Gundsambuu, B. and Pederson, S., 2020. Molecular Insights Into Regulatory T-Cell Adaptation to Self, Environment, and Host Tissues: Plasticity or Loss of Function in Autoimmune Disease. Frontiers in Immunology, 11, p.1269.

Wan, Q., Leemaqz, S.Y.L., Pederson, S.M., McCullough, D., McAninch, D.C., Jankovic-Karasoulos, T., Smith, M.D., Bogias, K.J., Liu, N., Breen, J. and Roberts, C.T., 2019. Quality control measures for placental sample purity in DNA methylation array analyses. Placenta, 88, pp.8-11.

Conference Poster

Ning Liu, Timothy Sadlon, Stephen Pederson, Simon Barry & James Breen; Investigating computational analysis pipelines and genomic proximity interactions in T lymphocytes; ABACBS 2017 Conference and Lorne Genome 2018 Conference; November, 2017 and February, 2018

Ning Liu, Hamid Alinejad-Rokny, Timothy Sadlon, Stephen Pederson, Simon Barry & James Breen; Identifying statistically significant Hi-C interactions from regulatory T cells and development of HiC-QC; ABACBS 2018 Conference; November, 2018 Ning Liu, Timothy Sadlon, Stephen Pederson, Simon Barry & James Breen; Using regulatory T cell-specific epigenomics data to uncover candidate mechanisms of Type-1 Diabetes (T1D); ABACBS 2019 Conference; November, 2019

AWARDS

Best Poster Talk of COMBINE Symposium 2019 from ABACBS.

Travel Grant of ABACBS Conference 2019 from ABACBS.

Travel Grant of ABACBS Conference 2018 from ABACBS.

Travel Grant of EMBL Australia PhD Course 2018 from EMBL Australia.

Outstanding Academic Achievement Award 2015-2016 from Faculty of Sciences, University of Adelaide. Outstanding Academic Achievement Award 2016-2017 from Faculty of Sciences, University of Adelaide.

EDUCATION

SAHMRI & ROBINSON RESEARCH INSTITUTE, UNIVERSITY OF ADELAIDE, AUSTRALIA | PHD OF BIOINFORMATICS (MEDICINE)

School of Paediatrics and Reproductive Medicine, Expected October 2020 | Adelaide, SA

UNIVERSITY OF ADELAIDE, AUSTRALIA | MASTER OF BIOTECHNOLOGY (BIOMEDICAL)

School of Molecular and Microbiology Science, Completed Jul 2017 | Adelaide, SA · GPA: 6.6/7.0

XIA'MEN UNIVERSITY, CHINA | BACHELOR OF SCIENCE

Major in Immunology, Biotechnology and Genetics, and minor in C programing and biostatistics, School of Life Science | Completed Jun 2015 | Xia'men, ChinaMajor • GPA: 3.3/4.0

OHTER ACTIVITIES

Workshop tutor of bioinforamtics workshops: Fall into bioinformatics in 2019, Spring into bioinformatics in 2019, and RAdelaide workshop 2017 & 2018. Workshop instructor of postgraduate course Genomics Applications (BIOINF 7150) in 2020.

Workshop tutor of postgraduate course Bioinformatics and Systems Modelling (BIOTECH 7005) in 2018.

Acitve member of ABACAS since 2016.

Executive committee of COMBINE in 2018 & 2019.

Executive committee of COMBINE SYMPOSIUM 2017 & 2018..

Membership in Golden Key International Honour Society from 2015.