James Matthew Ferguson

- **Genomic Systems Analyst**
- **Co-Founder**
- **Senior Software Developer**

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I am a bioinformatician specialising in genomic technologies, real-time nanopore sequencing, signal analysis, machine learning, and associated hardware. I have a background in software development and over 12 years of pathology industry experience.

Skills

Linux/UNIX, **BASH**, **Python**, R statistical programming, **C**, C++, Java, Ruby, Perl, SQL, VB, AHK, High Performance Computing (SGE), Robot Framework, LaTeX. Bioinformatics, data science, system administration, automation, algorithm design, networking, and Laboratory Information Systems (LIS)

Experience

Garvan Institute / Genomic Systems Analyst
June 2017 - PRESENT, Darlinghurst

Cerebro Biosystems / Co-founder and CTO
October 2017 - PRESENT, Darlinghurst

Healius (Primary Healthcare) / Senior Software Developer
December 2017 - PRESENT, St Leonards

Garvan Institute / Research Assistant
Dec 2016 - June 2017, Darlinghurst

Primary Healthcare / Analyst Programmer
June 2015 - June 2017, St Leonards

Douglas Hanly Moir Pathology / Lab Aide
2011 - 2015, Macquarie Park

Davies Campbell De Lambert/Healthscope Pathology / Lab Aide
2009-2011, Ryde

Awards

2020 - Runner-up poster prize - London Calling
2019 - Lighting talk award - ABACBS/GIW
2018 - Palmer Innovation award - Garvan award
2017 - J&J award - Med Tech's Got Talent
2017 - Garvan Award: *For going 'above and beyond' in supporting the bioinformatics culture at Garvan*
2017 - Late breaking poster award - AGTA Conference

Grants

2020 - $90,000. SARS-CoV-2 development grant
2018 - $15,000. Palmer Innovation Award

Patents

M. Singh, G. Al-Eryani, M. Smith, A. Swarbrick, J. **Ferguson** , S. Carswell, K. Jackson. "Phenotypic and molecular characterisation of single cells". PCT/AU2019/050101

M. Smith, **J. Ferguson**, D. Bunadi. "Processing of sequencing data streams". PCT/AU2018/050265

M. Smith, **J. Ferguson**, S. Carswell, D. Bunadi. "Expression profiling". Provisional patent - 2018903657

Professional Experience

2020 - London Calling - Poster/3min talk
2020 - Lorne Genome Conference - Poster
2019 - ABACBS/GIW Conference - Poster/lightning talk
2019 - Lorne Genome Conference - Poster
2018 - Nanopore Community Meeting - San Francisco - Poster
2018 - Lorne Genome Conference - Poster
2018 - CSIRO ON Prime
2018 - Sydney Bioinformatics Research Symposium - Poster
2018 - Monthly "Deep Learning and Beyond" workshop set teaching AI
2018 - Lorne Genome Conference - Poster
2017 - Started Bioinformatic Group Seminar series (BiG Seminars)
2017 - Oz Single-Cell - Poster
2017 - AGTA conference - Poster

Publications

2021 - RJ Edwards, MA Field, **JM Ferguson**, O Dudchenko, J Keilwagen, BD Rosen, GS Johnson, ES Rice, LD Hillier, JM Hammond, SG Towarnicki, AOmer, R Khan, K Skvortsova, O Bogdanovic, RA Zammit, EL Aiden, WC Warren, JWO Ballard. *Chromosome-length genome assembly and structural variations of the primal Basenji dog (Canis lupus familiaris) genome.* BMC genomics, 22, 188 2021. (https://doi.org/10.1186/s12864-021-07493-6)
2020 - H Samarakoon, S Punchihewa,A Senanayake , JM Hammond, I Stevanovski, **JM Ferguson**, R Ragel, H Gamaarachchi, IW Deveson *Genopo: a nanopore sequencing analysis toolkit for portable Android devices.* Communications Biology 3, 538 2020. (https://doi.org/10.1038/s42003-020-01270-z)
2020 - RA Bull, TN Adikari, **JM Ferguson**, JM Hammond, I Stevanovski, AG Beukers, Z Naing, M Yeang, A Verich, H Gamaarachchi, KW Kim, F Luciani, S Stelzer-Braid, JS Eden, WD Rawlinson, SJ van Hal, IW Deveson. *Analytical validity of nanopore sequencing for rapid SARS-CoV-2 genome analysis.* Nature communications, 11, 6272. 2020 (https://doi.org/10.1038/s41467-020-20075-6)
2020 - Smith MA, Ersavas T, **Ferguson JM**, Liu H, Lucas MC, Begik O, Bojarski L, Barton K, and Novoa EM. *Molecular barcoding of native RNAs using nanopore sequencing and deep learning.* Genome research 2020, 30: 1345–1353. (https://doi.org/10.1101/gr.260836.120)
2019 - *JM Ferguson, MA Smith, SquiggleKit: A toolkit for manipulating nanopore signal data*, Bioinformatics, , btz586, (https://doi.org/10.1093/bioinformatics/btz586)

2019 - M Singh, G Al-Eryani, S Carswell, **JM Ferguson**, J Blackburn, K Barton, D Roden, F Luciani, TG Phan, S Junankar, K Jackson, CC Goodnow, MA Smith & A

Swarbrick, *High-throughput targeted long-read single cell sequencing reveals the clonal and transcriptional landscape of lymphocytes*. Nature Communications 10, Article number: 3120 . (https://doi.org/10.1038/s41467-019-11049-4)

Oral Presentations

2020 - AGCT Montreal - "SARS-CoV-2 nanopore sequencing"
2020 - AGTA LIVE - "SARS-CoV-2 nanopore sequencing"
2019 - Nanopore Day Melbourne - "Squiggle Adventures!"
2019 - AGTA conference - "SquiggleKit: A toolkit for manipulating nanopore signal data"
2019 - Singularity University Conference - Tech Demo - live sequencing
2019 - Transhumanist meetup, Sydney - "The Genomics Future"
2019 - Bioinformatics Seminar - Monash University, Melbourne - "SquiggleKit: A toolkit for manipulating nanopore signal data"
2019 - London Calling - London - Tech Demo "SquiggleKit: A toolkit for manipulating nanopore signal data"
2019 - Nanopore HQ global team meeting, Oxford - "A developers perspective"
2018 - Nanopore Community Meeting, San Francisco - Workshop, "The world is your MinION"
2018 - Oz Single-Cell - Workshop, Sydney - "Nanopore Single-Cell Sequencing"
2018 - Sydney Bioinformatics Research Symposium - Fast Forward Talk
2018 - COMBINE seminar, Garvan Institute, Sydney
2018 - UTS biohacking/engineering/medicine society seminar on bioinformatics, University of Technology, Sydney
2018 - Nanopore Day Melbourne (invited speaker), VCCC, Melbourne
2018 - LinuxConf, University of Technology, Sydney
2017 - Biohacking 101: The DIY biology revolution - Kolling Institute, Sydney

Other

Citizenship: Australian

Referees

On Request