

Kieran O'Neill

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Current Position

Bioinformatics Process Development Coordinator (Jones Lab, Michael Smith Genome Sciences Centre, Vancouver, Canada)

Education

2014 Ph.D. (Bioinformatics) University of British Columbia, Vancouver, Canada

- Thesis: Automated analysis of single cell leukemia data
- Supervisor: Dr Ryan Brinkman
- Research undertaken at the BC Cancer Agency

2008 M.Sc. (Computer Science) University of KwaZulu-Natal, Pietermaritzburg, South Africa

- Dissertation: Relieving the Cognitive Load of Constructing Molecular Biological Ontology Based Queries by means of Visual Aids
- Research undertaken at National Bioinformatics Institute, Cape Town
- Internship at European Bioinformatics Institute, Hinxton, UK

2004 B.Sc.(Hons), University of KwaZulu-Natal, Pietermaritzburg, South Africa

- Dissertation: Creation of an Extensible Environment for the Investigation of Genetic Algorithmic Solutions to 3D Cubic Lattice Protein Folding
- *Cum Laude*
- Dean's commendations for 7/10 semesters attended.
- Certificates of Merit (top in class) 14/43 modules completed.

Awards

2017 Postdoctoral Fellowship, Canadian Institutes of Health Research

2015 Postdoctoral Fellowship, Michael Smith Foundation for Health Research

Poster Prize, *ISMB 2015*

2012 Student Travel Award, *CYTO 2012*

2005 Prestigious Masters Award, *National Research Foundation* (South Africa)

2004 Special Honours Award, *National Research Foundation* (South Africa)

First Author Publications

Research Publications

2020 **K O'Neill**, M Thibodeau, K Dixon, C Reisle, K Mungall, M Krzywinski, Y Shen, H Lim, D Cheng, K Tse, T Wong, E Chuah, A Fok, S Sun, D Renouf, D Schaeffer, C Cremin, S Chia, S Young, P Pandoh, S Pleasance, E Pleasance, A Mungall, R Moore, S Yip, A Karsan, J Laskin, M Marra, K Schrader, S Jones, *Improved structural variant interpretation for hereditary cancer susceptibility using long-read sequencing.*, Genetics in Medicine

2017 K O'Neill, M Hills, M Gottlieb, M Borkowski, A Karsan and P Lansdorp: *Assembling draft genomes using contiBAIT*, Bioinformatics

2015 **K O'Neill**, N Aghaeepour, J Parker, D Hogge, A Karsan, B Dalal R Brinkman: *Deep profiling of multitube flow cytometry data*, Bioinformatics

2014 **K O'Neill**, A Jalali, N Aghaeepour, H Hoos, R Brinkman: *Enhanced flow-Type/RchyOptimyx: a Bioconductor pipeline for discovery in high-dimensional cytometry data*, Bioinformatics

2008 **K O'Neill**, A Garcia, A Schwegmann, R Jimenez, D Jacobson and H Hermjakob: *OntoDas - a tool for facilitating the construction of complex queries to the Gene Ontology*, BMC Bioinformatics

Commentary/Reviews

2017 **K O'Neill**, V Rai and A Kilpatrick: *The International Society for Computational Biology and WikiProject Computational Biology: celebrating 10 years of collaboration towards open access*, Bioinformatics

2016 **K O'Neill** and R Brinkman: *Publishing code is essential for reproducible flow cytometry bioinformatics*, Cytometry A

2013 **K O'Neill**, N Aghaeepour, J Špidlen, R Brinkman: *Flow Cytometry Bioinformatics*, PLoS Computational Biology

Co-authored Publications

2021 H Chin, **K O'Neill**, K Louie, L Brown, K Schlade-Bartusiak, P Eydoux, R Rupps, A Farahani, C Boerkoel, S Jones, *An approach to rapid characterization of DMD copy number variants for prenatal risk assessment.*

- M Hills, E Falconer, **K O'Neill**, A Sanders, K Howe, V Guryev, P Lansdorp, *Construction of Whole Genomes from Scaffolds Using Single Cell Strand-Seq Data.*, International journal of molecular sciences
- V Akbari, J Garant, **K O'Neill**, P Pandoh, R Moore, M Marra, M Hirst, S Jones, *Megabase-scale methylation phasing using nanopore long reads and NanoMethPhase.*, Genome biology
- 2020 H Lin, K Rothe, M Chen, A Wu, A Babaian, R Yen, J Zeng, J Ruschmann, OI Petriv, **K O'Neill**, T Maetzig, D Knapp, N Nakamichi, R Brinkman, I Birol, X Jiang, *The miR-185/PAK6 axis predicts therapy response and regulates survival of drug-resistant leukemic stem cells in CML.*, Blood
- J Grants, J Wegrzyn, T Hui, **K O'Neill**, M Shadbolt, D Knapp, J Parker, Y Deng, A Gopal, R Docking, M Fuller, J Li, M Boldin, C Eaves, M Hirst, A Karsan, *Altered microRNA expression links IL6 and TNF-induced inflamming with myeloid malignancy in humans and mice.*, Blood
- 2018 T Hui, Q Cao, J Wegrzyn-Woltosz, **K O'Neill**, C Hammond, D Knapp, E Laks, M Moksa, S Aparicio, C Eaves, A Karsan, M Hirst: *High-Resolution Single-Cell DNA Methylation Measurements Reveal Epigenetically Distinct Hematopoietic Stem Cell Subpopulations*, Stem Cell Reports
- 2016 K Krowiorz, J Ruschmann, C Lai, M Ngom, T Maetzig, V Martins, A Scheffold, E Schneider, N Pochert, C Miller, L Palmqvist, A Staffas, M Mulaw, S R Bohl, C Buske, M Heuser, J Kraus, **K O'Neill**, C L Hansen, O I Petriv, H Kestler, H Döhner, L Bullinger, K Döhner, R K Humphries, A Rouhi and F Kuchenbauer: *MiR-139-5p is a potent tumor suppressor in adult acute myeloid leukemia*, Blood Cancer Journal
- 2013 N Aghaeepour, G Finak, **The FlowCAP Consortium**, The DREAM Consortium, H Hoos, T Mosmann, R Brinkman, R Gottardo and R Scheuermann: *Critical assessment of automated flow cytometry data analysis techniques*, Nature Methods
- M Hills, **K O'Neill**, E Falconer, R Brinkman and P Lansdorp: *BAIT: Organizing genomes and mapping rearrangements in single cells*, Genome Medicine
- 2012 N Aghaeepour, A Jalali, **K O'Neill**, P Chattopadhyay, M Roederer, H Hoos, R Brinkman *RchyOptimyx: Cellular hierarchy optimization for flow cytometry*, Cytometry A
- N Aghaeepour, P Chattopadhyay, A Ganesan, **K O'Neill**, H Zare, A Jalali, H Hoos, M Roederer, R Brinkman: *Early immunologic correlates of HIV protection can be identified from computational analysis of complex multivariate T-cell flow cytometry assays*, Bioinformatics
- 2010 A Garcia, **K O'Neill**, L Garcia, P Lord, R Stevens, O Corcho, F Gibson *Developing Ontologies within Decentralised Settings*, Semantic e-Science

2008 R Jimenez, A Quinn, A Garcia, A Labarga, **K O'Neill**, F Martinez, G Salazar, H Hermjakob: *Dasty2, an Ajax protein DAS client*, Bioinformatics

Scientific Software

2020 NanoMethPhase

2016 ContiBAIT

2013 flowBin

BAIT

2011 flowType

2008 OntoDAS

Mentorship

2020 Jeremy Fan (Masters Student, ongoing), Sarah Dada (PhD Student, ongoing)

2019 Vahid Akbari (PhD Student, ongoing)

2014 Eva Yap (Masters Student, completed 2017)

2009 Six undergraduate/co-op students during PhD and post-doc

Work Experience

2018 - present **Bioinformatics Process Development Coordinator**, *Jones Lab, Michael Smith Genome Sciences Centre*, Vancouver, Canada

- Coordinate between directors, laboratory, production bioinformatics and students to implement production-scale analysis workflows for use on new sequencing technologies, with a range of applications in health research and beyond.

2014 - 2018 **Postdoctoral Fellow**, *Karsan Lab, Michael Smith Genome Sciences Centre*, Vancouver, Canada

- Mentored masters students, collaborated with biologists and other labs, co-led a small bioinformatics team.

2010 **Scientific Technical Advisor**, *Twentieth Century Fox*, Vancouver, Canada

- Advised on the set of Rise of the Planet of the Apes

2009, 2010 **Teaching Assistant (Biology 200)**, *University of British Columbia*, Vancouver, Canada

2008 **Python Web Developer**, *ReportLab*, London, UK

2001 **Gap Year**, *Various Positions*, London, UK

Volunteer Experience

2016 - 2018 **Member/Founder**, *Equity, Diversity and Inclusion Task Force*, International Society for Computational Biology

2009 - **Present Board Member, Sometime President**, *AMS Bike Co-op and Bike Kitchen*, University of British Columbia, Vancouver, BC, Canada

2000 **Editor**, *NUX Student Newspaper*, University of Natal, Pietermaritzburg, KZN, South Africa