

# 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

2016 ContiBAIT

2013 flowBin

BAIT

2011 flowType

2008 OntoDAS

## Mentorship

2014 Eva Yap (Masters Student, completed 2017)

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

## Work Experience

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

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

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

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