

Kieran R Campbell

CONTACT INFORMATION E-mail: kieranrcampbell@gmail.com
Website: kieranrcampbell.github.io

PROFILE I am a postdoctoral fellow at the Department of Statistics, University of British Columbia and Department of Molecular Oncology, BC Cancer Agency working on methods for Bayesian modelling and inference in single-cell cancer biology.

EXPERIENCE **University of British Columbia** Vancouver, Canada **November 2017 - present**
Banting Postdoctoral Fellow

Postdoctoral research in the Department of Statistics at UBC and the Department of Molecular Oncology at the BC Cancer Agency, working on methods for Bayesian modelling and inference in single-cell cancer genomics. This position is funded by a Banting Postdoctoral Fellowship from the Canadian Institute of Health Research and a fellowship from the Canadian Statistical Sciences Institute (CANSSI).

European Bioinformatics Institute Hinxton, UK **June 2014 - August 2014**
Research Intern (statistical genomics)

CERN Geneva, Switzerland **June 2013 - August 2013**
Summer Intern (computational physics)

Institut Laue-Langevin Grenoble, France **June 2012 - September 2012**
Summer Intern (computational physics)

Agilent Technologies Edinburgh, UK **June 2010, 11 - September 2010, 11**
Summer Intern (computer science)

EDUCATION **University of Oxford**

D.Phil Computational & Statistical Genomics, 2014 - 2017

- Dissertation Topic: “Probabilistic modelling of genomic trajectories”
- Mixture of projects concerning the statistical analysis of high-dimensional genomics data. Focus on using Bayesian hierarchical latent variable models for the inference of single-cell trajectories and propagation of uncertainty to downstream analysis.
- Supervisors: Chris Yau (WTCHG / Department of Statistics) & Caleb Webber (DPAG)
- Examiners: Chris Holmes (Oxford) & Magnus Rattray (Manchester)

University of Cambridge

M.Phil Computational Biology, 2013 - 2014

- Distinction - 82% average
- Dissertation Topic: “Statistical models of tumour cell signalling from spatially resolved proteomics data”

University of Edinburgh

BSc. (Hons) Mathematical Physics, 2009 - 2013

- First class honours - 86% average

HONORS, AWARDS,
AND FUNDING

Banting Postdoctoral Fellowship (C\$140k), 2018-2020
Postdoctoral Fellowship of the UBC Data Science Institute (C\$40k), 2018-2019
Postdoctoral Fellowship of the Canadian Statistical Sciences Institute (C\$22.5k), 2017-2018
Postdoctoral Fellowship of the Alan Turing Institute, 2017-2020 (*Declined*)
St John's College Oxford Special Grant (£900), July 2017
HITSeq Travel Award (\$1000), July 2016
Medical Research Council Studentship, University of Oxford, 2014-2017
Medical Research Council Studentship, University of Cambridge, 2013-2014
Graduate tutors' prize, Fitzwilliam College Cambridge, 2014
Mary Stuart Memorial Prize for graduating with the highest grade in the School of Physics & Astronomy, University of Edinburgh, 2013
Class Medal for Mathematical Physics, University of Edinburgh, 2012
Nicol Foundation Scholarship, University of Edinburgh, 2011
Marion AS Ross Prize, University of Edinburgh, 2011
Margaret Campbell-Scott Scholarship, University of Edinburgh, 2009, 2010

PEER-REVIEWED
PUBLICATIONS

Kieran R Campbell and Christopher Yau, *Uncovering genomic trajectories with heterogeneous genetic and environmental backgrounds across single-cells and populations* Nature Communications 2018

Kieran R Campbell and Christopher Yau, *A descriptive marker gene approach to single-cell pseudotime inference* Bioinformatics 2018

Kieran R Campbell and Christopher Yau, *Probabilistic modeling of bifurcations in single-cell gene expression data using a Bayesian mixture of factor analyzers* [version 1; referees: 2 approved]. Wellcome Open Research 2017, 2:19

Davis McCarthy, **Kieran R Campbell**, Aaron TL Lun, Quin F Wills, *scater: pre-processing, quality control, normalisation and visualisation of single-cell RNA-seq data in R* Bioinformatics 2017

Kieran R Campbell & Christopher Yau, *switchde: Inference of switch-like differential expression along single-cell trajectories* Bioinformatics 2016

Kieran R Campbell & Christopher Yau, *Order Under Uncertainty: Robust Differential Expression Analysis Using Probabilistic Models for Pseudotime Inference* PLOS Computational Biology 2016

PRESENTATIONS

Talk (invited) Bayesian latent variable models for understanding (pseudo-) time-series single-cell gene expression data **Mathematical Biology Seminar Series, Pacific Institute for Mathematical Sciences**, Vancouver, Canada, November 2017

Talk (invited) Bayesian latent variable models for understanding (pseudo-) time-series single-cell gene expression data **Department of Statistics Seminar, UBC**, Vancouver, Canada, November 2017

Talk Pseudotemporal disease trajectories from cross-sectional data **TransMed COSI at ISMB**, Prague, Czech Republic, July 2017

Talk (invited) Single-cell trajectories: theory and applications. **Norwich Single-Cell Symposium**, Earlham Institute, Norwich UK, May 2017

Talk Stratification of patient trajectories using covariate latent variable models. **Statistical Methods for Post-genomic Data**, London UK, January 2017

Poster Stratification of patient trajectories using covariate latent variable models. **NIPS Machine**

Learning in Healthcare, Barcelona Spain, December 2016

Talk Bayesian latent variable models for single-cell trajectory learning. **Probabilistic Modelling in Genomics**, Oxford UK, September 2016

Talk Bayesian latent variable models for single-cell trajectory learning. **Young Statisticians' Meeting**, London UK, August 2016

Talk Bayesian latent variable models for single-cell trajectory learning. **Hitseq High Throughput Sequencing Algorithms and Applications**, Orlando USA, July 2016

Talk Incorporating prior information in single-cell trajectory inference, **Quantitative genomics**, London UK, June 2016

Talk Bayesian Gaussian Process latent variable models for pseudotime inference in single-cell RNA-seq data, **NIPS Machine Learning in Computational Biology Workshop**, Montreal Canada, December 2015

Talk Bayesian Gaussian Process latent variable models for pseudotime inference in single-cell RNA-seq data, **C1omics Methods & Applications**, Manchester UK, November 2015

Poster Laplacian Eigenmaps & Principal Curves for high-resolution pseudotemporal ordering of single-cell gene expression data, **Single Cell Genomics**, Utrecht Netherlands, September 2015