Christopher John Frederick Cameron, PhD

[1] Department of Molecular Biophysics and Biochemistry, Yale University
[2] Department of Radiology and Biomedical Imaging, Yale University

As a computational biologist, I develop novel statistical, machine learning, and bioinformatics approaches to emerging molecular biology technologies. My postdoctoral research focuses on cryogenic Electron Microscopy (cryo-EM) image processing, specifically addressing the modeling and integration of prior information. During my PhD, I implemented analyses of Chromosome Conformation Capture (3C) and Chromatin ImmunoPrecipitation (ChIP) data that provided insight into the regulation of genomes through the organization of chromatin's higher-order structures.

Keywords: bioinformatics, AI specialist, 4D regulatory genomics, structural biology

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Education

2019–Now	**Postdoctoral Researcher** Yale University, New Haven, USA *Advisors*: Mark B Gerstein, Hemant D Tagare and Yong Xiong
2013–19	**PhD in Computer Science, concentration in Bioinformatics** (October 2019) McGill University, Montréal, CAN *Thesis*: High-resolution computational analysis of chromatin architecture and function *Advisors*: Mathieu Blanchette and Josée Dostie
2012–13	**MSc in Bioinformatics** (February 2014) University of Guelph, Guelph, CAN *Thesis*: Tissue-to-plasma partition coefficient prediction by a multi-channel restricted Boltzmann machine *Advisors*: Andrea Edginton, Ronald Johnson and Stefan Kremer
2006–11	**BSc in Biomedical Toxicology, minor in Computer Science** (February 2012) University of Guelph, Guelph, CAN *Thesis*: Molecular graph neural networks for toxicology *Advisor*: Stefan Kremer

Positions held

2019–Now	**Postdoctoral Associate** *Department of Molecular Biophysics and Biochemistry, Yale University*
2021–Now	**Special Graduate Faculty** *School of Computer Science, University of Guelph*
2013–19	**Graduate Research Assistant** *School of Computer Science, McGill University*
2017	**Course Lecturer** *School of Computer Science, McGill University*
2013–17	**Teaching Assistant** *School of Computer Science, McGill University*
2012–13	**Graduate Service Assistant** *School of Computer Science, University of Guelph*
2008–13	**Research Assistant** *School of Computer Science, University of Guelph*

Journal publications

† co-first or -second authors

13. Leng J, Cameron CJF, Oh S, Khurana E, Noonan JP and Gerstein MB. **LESSeq: local event-based analysis of alternative splicing using RNA-Seq data**. *BioRxiv, in preparation.* DOI:10.1101/841494
12. Prost JA†, Cameron CJF† and Blanchette M. **SACSANN: identifying sequence-based determinants of chromosomal compartments**. *BioRxiv, in preparation.* DOI:10.1101/2020.10.06.328039
11. Tsai P, Cameron CJF, Forni MF, Wasko RR, Naughton B, Horsley V, Gerstein MB and Schlieker C. **Dynamic quality control machinery that operates across compartmental borders mediates the degradation of mammalian nuclear membrane proteins**. *In submission at Mol Cell.*
10. Rozowsky J, Drenkow J, Yang YT, [and 96 others, including Cameron CJF]. **Multi-tissue integrative analysis of personal epigenomes**. *In submission at Science.* DOI:10.1101/2021.04.26.441442
9. Amaya C, Cameron CJF†, Devarkar SC†, Seager SJH, Gerstein MB, Xiong Y and Schlieker C (2021) **Nodal modulator (NOMO) is required to sustain endoplasmic reticulum morphology**. *JBC.* DOI:10.1016/j.jbc.2021.100937
8. Ramilowski J, Yip CW, Agrawal S, [and 115 others, including Cameron CJF] (2020) **Functional Annotation of Human Long Non-Coding RNAs via Molecular Phenotyping**. *Genome Res.* DOI:10.1101/gr.254219.119
7. Cameron CJF, Wang XQD, Dostie J and Blanchette M (2020) **LAMPS: an analysis pipeline for sequence-specific ligation-mediated amplification reads**. *BMC Res Notes*, **13**:273. DOI:10.1186/s13104-020-05106-1
6. Bonetti A, Agostini F, Suzuki AM, [and 26 others, including Cameron CJF] (2020) **RADICL-seq identifies general and cell type-specific principles of genome-wide RNA-chromatin interactions**. *Nat Commun*, **11**:1018. DOI:10.1038/s41467-020-14337-6
5. Cameron CJF, Dostie J and Blanchette M (2020) **HIFI: estimating DNA-DNA interaction frequency from Hi-C data at restriction-fragment resolution**. *Genome Biol*, **21**(1):11. DOI:10.1186/s13059-019-1913-y
4. Wang XQD†, Cameron CJF†, Paquette D, Segal D, Warsaba R, Blanchette M and Dostie J (2019) **2C-ChIP: measuring chromatin immunoprecipitation signal from defined genomic regions with deep sequencing**. *BMC Genomics*, **20**:162. DOI:10.1186/s12864-019-5532-5
3. Roche PJR, Gytz H, Hussain F, Cameron CJF, Paquette D, Blanchette M, Dostie J, Nagar B and Akavia UD (2018) **Double-Stranded Biotinylated Donor Enhances Homology-Directed Repair in Combination with Cas9 Monoavidin in Mammalian Cells**. *CRISPR J*, **1**(6). DOI:10.1089/crispr.2018.0045
2. Malina A, Cameron CJF, Robert F, Blanchette M, Dostie J and Pelletier J (2015) **PAM multiplicity marks genomic target sites as inhibitory to CRISPR/Cas9 editing**. *Nat Commun*, **6**:10124. DOI:10.1038/ncomms10124
1. Ma EYT, Cameron CJF and Kremer SC (2010) **Classifying and scoring of molecules with the NGN: new data sets, significance tests, and generalization**. *BMC Bioinformatics*, **11**(Suppl 8):S4. DOI:10.1186/1471-2105-11-S8-S4

Peer-reviewed conference papers

2. Kirchhof M, Cameron CJF and Kremer SC (2021) **End-to-end chromosomal compartment prediction from reference genomes**. *IEEE BIBM 2021*: 50-57. DOI:10.1109/BIBM52615.2021.9669521
1. Cameron CJF, Ma EYT and Kremer SC (2010) **Neural Grammar Networks for Toxicology**. *IEEE CIBCB 2010* (Montréal, CAN): 1-8. DOI:10.1109/CIBCB.2010.5510322

Conferences with abstract submission

11. Cameron CJF, Sebastian SJH, Tagare HD and Gerstein MB (2022) **Reliably expanding SPA cryo-EM particle sets by machine-learning consensus**. *3DEM GRC/GRS*, Castelldefels, ESP (*GRS*-selected talk)
10. Cameron CJF, Tagare HD, Gerstein MB and Xiong Y (2020) **Improving agreement between structural models and cryo-EM maps in reciprocal space**. *5th NE Cryo-EM Symp*, Boston, USA
9. Cameron CJF, Dostie J and Blanchette M (2018) **Prediction of complete Hi-C interaction matrices from sequence-based determinants**. *IRIC 2018 Annual Symp*, Montréal, CAN
8. Cameron CJF, Dostie J and Blanchette M (2018) **Prediction of complete Hi-C contact maps from genomic sequence**. *SCS and RegSys COSI at ISMB 2018*, Chicago, USA

7. Cameron CJF, Dostie J and Blanchette M (2018) **Prediction of complete Hi-C contact maps from genomic sequence alone**. *RECOMB 2018*, Paris, FRA
6. Cameron CJF, Dostie J and Blanchette M (2017) **High-resolution estimation of true DNA-DNA interaction frequency from Hi-C data**. *SCS and RegGen COSI at ISMB/ECCB 2017*, Prague, CZE
5. Cameron CJF, Dostie J and Blanchette M (2016) **Improved Hi-C Contact Maps by Adaptive Density Estimation**. *MRCCT - 1st International Symp on Immunogenetics of Infectious and Inflammatory Diseases*, Montréal, CAN (PhD poster prize)
4. Cameron CJF, Blanchette M, De Hoon M and Dostie J (2016) **Identifying ncRNA Drivers of Architectural Change in Chromatin**. *RNA2016*, Kyoto, JPN
3. Cameron CJF, Dostie J and Blanchette M (2016) **Improved Hi-C Contact Maps by Adaptive Density Estimation**. *GLBIO/CCBC 2016*, Toronto, CAN
2. Cameron CJF, Kaplan M, Drouin A and Blanchette M (2016) **Linking Transposable Elements to Chromatin Architecture in *Arabidopsis thaliana***. *GLBIO/CCBC 2016*, Toronto, CAN
1. Cameron CJF, Fraser J, Dostie J and Blanchette M (2014) **Chromosome conformation capture data improves long-range eQTL prediction**. *Epigenetics & Chromatin CSHL 2014*, Huntington, USA

Book chapters, reviews and non-refereed publications

3. Wang XQD, Cameron CJF, Segal D, Paquette D, Blanchette M and Dostie J (2021) **Profiling Chromatin Landscape at High Resolution and Throughput with 2C-ChIP. In: Bodega B., Lanzuolo C. (eds) Capturing Chromosome Conformation. Methods in Molecular Biology, vol 2157**. *Humana, New York, NY*. DOI:10.1007/978-1-0716-0664-3_8
2. Cameron CJF, Fraser J, Blanchette M and Dostie J (2016) **Mapping and Visualizing Spatial Genome Organization. In: Bazett-Jones D, Dellaire G (eds) The Functional Nucleus**. *Springer, Cham*. DOI:10.1007/978-3-319-38882-3_16
1. Marhon SA, Cameron CJF and Kremer SC (2013) **Recurrent Neural Networks. In: Bianchini M, Maggini M, Jain L (eds) Handbook on Neural Information Processing**. *Intelligent Systems Reference Library, vol 49. Springer, Berlin, Heidelberg*. DOI:10.1007/978-3-642-36657-4_2

Invited talks

3. (July 2017) **The future of Hi-C**. *Birds of a Feather panel discussion at ISMB/ECCB 2017*, Prague, CZE
2. (April 2017) **High-resolution estimation of DNA-DNA contact frequency from Hi-C data**. *The Physical Basis of Functional Genome Organization: Genome organization as viewed by molecular and visual techniques*, Holetown, BRB
1. (August 2016) **The 3D Genome**. *Beijing Institute of Genomics (BIG) at the Chinese Academy of Sciences*, Beijing, CHN

Awards and scholarships

2017–19	Walter Sumner Fellowship, *Walter Sumner Foundation*
2018	Travel Fellowship Award for ISCB Student Council Symposium, *ISCB SCS*
2017	Graduate Research Enhancement and Travel Award, *McGill University*
2017	Graduate Mobility Award, *McGill University*
2016	Mitacs Globalink Research Award, *Mitacs/Japan Society for the Promotion of Science*
2013–14	Grad Excellence Award in Computer Science, *McGill University*
2013–14	Walter Hitschfeld Award - Computer Science, *McGill University*

Academic service

2021–22	YPA symposium committee member & co-coordinator
2020–Now	CCTP/CIRTL teaching certification: Associate (2020) & Practitioner (2022)
2020–22	Intelligent Systems for Molecular Biology (ISMB) peer reviewer
Fall 2017	COMP 364: Computer Tools for Life Sciences co-instructor (with Oliver CG)

2016–Now Undergraduate and graduate student mentorship ($N = 17$)