

Christopher John Frederick Cameron, PhD

¹ Department of Molecular Biophysics and Biochemistry, 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: AI specialist, bioinformatics, 4D regulatory genomics, structural biology

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Education

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

Positions held

2019–Now	Postdoctoral Associate <i>Department of Molecular Biophysics and Biochemistry, Yale University</i>
2013–19	Graduate Research Assistant <i>School of Computer Science, McGill University</i>
2017	Course Lecturer <i>School of Computer Science, McGill University</i>
2013–17	Teaching Assistant <i>School of Computer Science, McGill University</i>
2012–13	Graduate Service Assistant <i>School of Computer Science, University of Guelph</i>
2012–13	Java Developer <i>School of Environmental Sciences, University of Guelph</i>
2008–13	Research Assistant <i>School of Computer Science, University of Guelph</i>

Journal publications

[†] co-first authors

11. Kirchhof M, [Cameron CJF](#) and Kremer SC. **ABCNet: predicting chromosomal compartments directly from reference genomes**. *In preparation*.
10. 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**. *In submission at PLoS One*. doi:[10.1101/841494](#)
9. Prost JA[†], [Cameron CJF](#)[†] and Blanchette M. **SACSANN: identifying sequence-based determinants of chromosomal compartments**. *In submission at PLoS Comput Biol*. doi:[10.1101/2020.10.06.328039](#)
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

1. [Cameron CJF](#), Ma EYT and Kremer SC (2010) **Neural Grammar Networks for Toxicology**. *2010 IEEE Symp on Computational Intelligence in Bioinformatics and Computational Biology* (Montréal, Canada): 1-8. doi:[10.1109/CIBCB.2010.5510322](#)

Conferences with abstract submission

10. [Cameron CJF](#), Tagare H, Gerstein M 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, Canada
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, France
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, Czech Republic
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, Canada (PhD poster prize)

4. [Cameron CJE](#), Blanchette M, De Hoon M and Dostie J (2016) **Identifying ncRNA Drivers of Architectural Change in Chromatin**. *RNA2016*, Kyoto, Japan
3. [Cameron CJE](#), Dostie J and Blanchette M (2016) **Improved Hi-C Contact Maps by Adaptive Density Estimation**. *GLBIO/CCBC 2016*, Toronto, Canada
2. [Cameron CJE](#), Kaplan M, Drouin A and Blanchette M (2016) **Linking Transposable Elements to Chromatin Architecture in *Arabidopsis thaliana***. *GLBIO/CCBC 2016*, Toronto, Canada
1. [Cameron CJE](#), Fraser J, Dostie J and Blanchette M (2014) **Chromosome conformation capture data improves long-range eQTL prediction**. *2014 CSHL Conference on Epigenetics & Chromatin*, Huntington, USA

Book chapters, reviews and non-refereed publications

3. Wang XQD, [Cameron CJE](#), Segal D, Paquette D, Blanchette M and Dostie J (2021) **Profiling Chromatin Landscape at High Resolution and Throughput with 2C-ChIP**. In: Bodega B., Lanzaolo 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 CJE](#), 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 CJE](#) 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, Czech Republic
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, Barbados
1. (August 2016) **The 3D Genome**. *Beijing Institute of Genomics (BIG) at the Chinese Academy of Sciences*, Beijing, China

Awards and scholarships

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

Summary of teaching activities

2020-Now	CCTP completion & CIRTL associate
Fall 2017	COMP 364: Computer Tools for Life Sciences, <i>McGill University</i> (with Oliver CG)

Peer review

2020	Intelligent Systems for Molecular Biology (ISMB)
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