Christopher John Frederick Cameron, PhD

[1] Department of Molecular Biophysics and Biochemistry, Yale University

With the advent of the Chromosome Conformation Capture (3C) technologies, the ability to quantify long-range interactions of genomic loci at high-resolution has become possible. My PhD dissertation focuses on applying novel implementations of statistical modeling, machine learning, and bioinformatics approaches to 3C data (in particular, 3C Carbon-Copy [5C] and high-throughput [Hi-C]). The resulting analyses provide insight into the regulation of genomes through the organization of chromatin's higher-order structures (e.g., Topologically Associating Domains [TAD]).

Keywords: bioinformatics, 4D regulatory genomics, AI specialist

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Education

2019-Now	**Postdoctoral Researcher**
	Yale University, New Haven, USA
	Advisors: Mark Gerstein and Yong Xiong
2013-2019	**PhD in Computer Science, concentration in Bioinformatics** (Fall 2019)
	McGill University, Montréal, Canada
	Thesis: High-resolution computational analysis of chromatin architecture and function
	Advisors: Mathieu Blanchette and Josée Dostie
2012-2013	**MSc in Bioinformatics** (February 2014)
	University of Guelph, Guelph, Canada
	Thesis: Tissue-to-plasma partition coefficient prediction by a multi-channel restricted boltzmann machine
	Advisors: Andrea Edginton, Ronald Johnson, and Stefan Kremer
2006-2011	**BSc in Biomedical Toxicology, minor in Computer Science** (February 2012)
	University of Guelph, Guelph, Canada
	Thesis: Molecular graph neural networks for toxicology
	Advisor: Stefan Kremer

Positions held

2019-Now	**Postdoctoral Associate**
	Department of Molecular Biophysics and Biochemistry, Yale University
2013-2019	**Research Assistant**
	School of Computer Science, McGill University
2017	**Course Lecturer**
	School of Computer Science, McGill University
2013-2017	**Teaching Assistant**
	School of Computer Science, McGill University
2012-2013	**Graduate Service Assistant**
	School of Computer Science, University of Guelph
2012-2013	**Java Developer**
	School of Environmental Sciences, University of Guelph
2008-2013	**Research Assistant**
	School of Computer Science, University of Guelph

Journal publications

† co-first authors

9. Prost JA, <u>Cameron CJF.</u>, and Blanchette M. **Identifying sequence-based determinants of chromosomal compartments**. *In preparation for submission to Genome Biol.*

8. Bonetti A, Agostini F, Suzuki AM, Hashimoto K, Pascarella G, Gimenez J, Ross L, Nash A, Ghilotti M, Arner E, <u>Cameron CJF</u>, et al. **RADICL-seq identifies general and cell type-specific principles of genome-wide RNA-chromatin interactions**. *In preparation for submission to Nat Genet.*

7. <u>Cameron CJF</u>, Wang XQD, Dostie J, and Blanchette M. **LAMPS: an analysis pipeline for sequence-specific ligation-mediated amplification reads**. *In submission at Bioinformatics.*

6. Wang XQD, <u>Cameron CJF</u>, Segal D, Paquette D, Blanchette M, and Dostie J. **Profiling chromatin landscape at high-throughput and throughput with 2C-ChIP**. *In submission at Methods Mol Biol.*

5. <u>Cameron CJF</u>, Dostie J, and Blanchette M. **Estimating DNA-DNA interaction frequency from Hi-C data at restriction-fragment resolution**. *In review at Genome Biol.* doi:10.1101/377523

4. Wang XQD†, <u>Cameron CJF</u>†, 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, <u>Cameron CJF</u>, 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, <u>Cameron CJF</u>, 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, <u>Cameron CJF</u>, 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. <u>Cameron CJF</u>, Ma EYT, and Kremer SC (2010) **Neural Grammar Networks for Toxicology**. *2010 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology* (Montréal, Canada): 1-8. doi:10.1109/CIBCB.2010.5510322

Conferences with abstract submission

9. <u>Cameron CJF</u>, Dostie J, and Blanchette M (2018) **Prediction of complete Hi-C interaction matrices from sequence-based determinants**. *IRIC 2018 Annual Symposium*, Montréal, Canada

8. <u>Cameron CJF</u>, 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. <u>Cameron CJF</u>, Dostie J, and Blanchette M (2018) **Prediction of complete Hi-C contact maps from genomic sequence alone**. *RECOMB 2018*, Paris, France

6. <u>Cameron CJF</u>, 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. <u>Cameron CJF</u>, Dostie J, and Blanchette M (2016) **Improved Hi-C Contact Maps by Adaptive Density Estimation**. *MRCCT - 1st International Symposium on Immunogenetics of Infectious and Inflammatory Diseases*, Montréal, Canada (Ph.D. poster prize)

4. <u>Cameron CJF</u>, Blanchette M, De Hoon M, and Dostie J (2016) **Identifying ncRNA Drivers of Architectural Change in Chromatin**. *RNA2016*, Kyoto, Japan

3. <u>Cameron CJF</u>, Dostie J, and Blanchette M (2016) **Improved Hi-C Contact Maps by Adaptive Density Estimation**. *GLBIO/CCBC 2016*, Toronto, Canada

2. <u>Cameron CJF</u>, Kaplan M, Drouin A, and Blanchette M (2016) **Linking Transposable Elements to Chromatin Architecture in *Arabidopsis thaliana***. *GLBIO/CCBC 2016*, Toronto, Canada
1. <u>Cameron CJF</u>, 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

2. <u>Cameron CJF</u>, 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, <u>Cameron CJF</u>, 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

2017-2019	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 - Japan Society for the Promotion of Science (JSPS), *Mitacs/JSPS*
2013-2014	Grad Excellence Award in Computer Science, *McGill University*
2013-2014	Walter Hitschfeld Award - Computer Science, *McGill University*

Summary of teaching activities

Fall 2017	COMP 364: Computer Tools for Life Sciences, *McGill University* (with Oliver CG)