

## Christopher John Frederick Cameron

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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 Ph.D. dissertation focuses on this biochemical technology (in particular, 3C Carbon-Copy [5C] and high-throughput [Hi-C]) by using novel implementations of statistical modeling, machine learning, and bioinformatics approaches to understand how cells regulate themselves through the organization of chromatin's higher-order structures.

Keywords: bioinformatics, 4D regulatory genomics, AI specialist

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### Positions held

<b>2019-Present</b>	<b>Postdoctoral Researcher</b> <i>Department of Molecular Biophysics and Biochemistry, Yale University</i>
<b>2013-2019</b>	<b>Research Assistant</b> <i>School of Computer Science, McGill University</i>
<b>2017</b>	<b>Course Lecturer</b> <i>School of Computer Science, McGill University</i>
<b>2013-2017</b>	<b>Teaching Assistant</b> <i>School of Computer Science, McGill University</i>
<b>2012-2013</b>	<b>Graduate Service Assistant</b> <i>School of Computer Science, University of Guelph</i>

### Education

<b>2019-Present</b>	<b>Postdoctoral Researcher</b> Yale University, New Haven, USA <i>Advisors:</i> Mark Gerstein and Yong Xiong
<b>2013-2019</b>	<b>Ph.D. in Computer Science (conc. in Bioinformatics)</b> McGill University, Montréal, Canada <i>Thesis:</i> High-resolution computational analysis of chromatin architecture and function <i>Advisors:</i> Mathieu Blanchette and Josée Dostie
<b>2012-2014</b>	<b>M.Sc. in Bioinformatics</b> (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
<b>2006-2012</b>	<b>B.Sc. in Biomedical Toxicology</b> (February 2012) University of Guelph, Guelph, Canada <i>Thesis:</i> Molecular Graph Neural Networks for Toxicology <i>Advisor:</i> Stefan Kremer

## Journal publications

\*co-first authors

6. Bonetti A., Agostini F., Hashimoto K., Suzuki A.M., Pascarella G., Gimenez J., Arner E., Cameron C.J.F., et al. (2018) **RADICL-seq, a novel methodology for identifying genome-wide RNA-chromatin interactions.** *In preparation for submission to Nature Genetics.*
5. Cameron C.J.F., Dostie J., and Blanchette M. (2018) **Estimating DNA-DNA interaction frequency from Hi-C data at restriction-fragment resolution.** *In review at Genome Biology.* doi:10.1101/377523
4. Wang X.Q.D.\*, Cameron C.J.F.\*, 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 P.J.R., Gytz H., Hussain F., Cameron C.J.F., Paquette D., Blanchette M., Dostie J., Nagar B., and Akavia U.D. (2018) **Double-Stranded Biotinylated Donor Enhances Homology-Directed Repair in Combination with Cas9 Monoavidin in Mammalian Cells.** *The CRISPR Journal*, **1**(6). doi:10.1089/crispr.2018.0045
2. Malina A. Cameron C.J.F., Robert F., Blanchette M., Dostie J., and Pelletier J. (2015) **PAM multiplicity marks genomic target sites as inhibitory to CRISPR/Cas9 editing.** *Nature Communications*, **6**:10124. doi:10.1038/ncomms10124
1. Ma E.Y.T., Cameron C.J.F., and Kremer S.C. (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 C.J.F., Ma E.Y.T., and Kremer S.C. (2010) **Neural Grammar Networks for Toxicology.** *In Computational Intelligence in Bioinformatics and Computational Biology (CIBCB), 2010 IEEE Symposium on:* 1-8. doi:10.1109/CIBCB.2010.5510322

## Conferences with abstract submission

9. Cameron C.J.F., Dostie J., and Blanchette M. (2018) **Prediction of complete Hi-C interaction matrices from sequence-based determinants.** *IRIC 2018 Annual Symposium*, Montréal, Canada
8. Cameron C.J.F., 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 C.J.F., Dostie J., and Blanchette M. (2018) **Prediction of complete Hi-C contact maps from genomic sequence alone.** *RECOMB 2018*, Paris, France
6. Cameron C.J.F., 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 C.J.F., 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. Cameron C.J.F., Blanchette M., De Hoon M., and Dostie J. (2016) **Identifying ncRNA Drivers of Architectural Change in Chromatin.** *RNA2016*, Kyoto, Japan
3. Cameron C.J.F., Dostie J., and Blanchette M. (2016) **Improved Hi-C Contact Maps by Adaptive Density Estimation.** *GLBIO/CCBC 2016*, Toronto, Canada
2. Cameron C.J.F., Kaplan M., Drouin A., and Blanchette M. (2016) **Linking Transposable Elements to Chromatin Architecture in *Arabidopsis thaliana*.** *GLBIO/CCBC 2016*, Toronto, Canada
1. Cameron C.J.F., 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. Cameron C.J.F., 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 S.A., Cameron C.J.F., and Kremer S.C. (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

<b>2017-2019</b>	Walter Sumner Fellowship, <i>Walter Sumner Foundation</i>
<b>2018</b>	Travel Fellowship Award for ISCB Student Council Symposium, <i>ISCB SCS</i>
<b>2017</b>	Graduate Research Enhancement and Travel Award, <i>McGill University</i>
<b>2017</b>	Graduate Mobility Award, <i>McGill University</i>
<b>2016</b>	Mitacs Globalink Research Award - Japan Society for the Promotion of Science (JSPS), <i>Mitacs/JSPS</i>
<b>2013-2014</b>	Grad Excellence Award in Computer Science, <i>McGill University</i>
<b>2013-2014</b>	Walter Hitschfeld Award - Computer Science, <i>McGill University</i>

## Summary of teaching activities

<b>Fall 2017</b>	COMP 364: Computer Tools for Life Sciences, <i>McGill University</i> (with C.G. Oliver)
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