

## Christopher John Frederick Cameron, PhD

<sup>1</sup> Program in Computational Biology and Bioinformatics, Yale University

<sup>2</sup> 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

### Contact information

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### Education

<b>2019–Now</b>	<b>Postdoctoral Researcher</b> Yale University, New Haven, USA <i>Advisors:</i> Mark Gerstein, Yong Xiong and Hemant Tagare
<b>2013–19</b>	<b>PhD in Computer Science, concentration in Bioinformatics</b> (October 2019) McGill University, Montréal, CAN <i>Thesis:</i> High-resolution computational analysis of chromatin architecture and function <i>Advisors:</i> Josée Dostie and Mathieu Blanchette
<b>2012–13</b>	<b>MSc in Bioinformatics</b> (February 2014) University of Guelph, Guelph, CAN <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>2006–11</b>	<b>BSc in Biomedical Toxicology, minor in Computer Science</b> (February 2012) University of Guelph, Guelph, CAN <i>Thesis:</i> Molecular graph neural networks for toxicology <i>Advisor:</i> Stefan Kremer

### Positions held

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

## Journal publications

<sup>†</sup> co-first or -second authors

12. 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](#)
11. 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](#)
10. Amaya C, [Cameron CJF](#)<sup>†</sup>, Devarkar SC<sup>†</sup>, Seager SJH, Gerstein MB, Xiong Y and Schlieker C. **Nodal modulator is required to sustain endoplasmic reticulum morphology**. *In submission at eLife*. DOI:[10.1101/2021.01.28.428001](#)
9. Prost JA<sup>†</sup>, [Cameron CJF](#)<sup>†</sup> 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<sup>†</sup>, [Cameron CJF](#)<sup>†</sup>, 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. **ABCNet: predicting chromosomal compartments directly from reference genomes**. *In preparation for IEEE BIBM 2021*.
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, CAN): 1-8. DOI:[10.1109/CIBCB.2010.5510322](#)

## Conferences with abstract submission

10. [Cameron CJF](#), Tagare H, 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**. *2014 CSHL Conference on Epigenetics & Chromatin*, 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., 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 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*, Hometown, BRB
1. (August 2016) **The 3D Genome**. *Beijing Institute of Genomics (BIG) at the Chinese Academy of Sciences*, Beijing, CHN

#### Awards and scholarships

<b>2017–19</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, <i>Mitacs/Japan Society for the Promotion of Science</i>
<b>2013–14</b>	Grad Excellence Award in Computer Science, <i>McGill University</i>
<b>2013–14</b>	Walter Hirschfeld Award - Computer Science, <i>McGill University</i>

#### Academic service

<b>2021–22</b>	<a href="#">YPA symposium</a> committee member (2021) & co-coordinator (2022)
<b>2020–Now</b>	<a href="#">CCTP completion</a> & <a href="#">CIRTL</a> associate
<b>2020</b>	<a href="#">Intelligent Systems for Molecular Biology (ISMB)</a> peer reviewer
<b>Fall 2017</b>	<a href="#">COMP 364: Computer Tools for Life Sciences</a> co-instructor (with <a href="#">Oliver CG</a> )
<b>2016–Now</b>	<a href="#">Undergraduate and graduate student mentorship</a> ( $N = 14$ )