

## Christopher John Frederick Cameron, PhD

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<sup>2</sup> 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

### Contact information

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### Education

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

### Positions held

|                  |  |
|------------------|--|
| <b>2019–Now</b>  | <b>Postdoctoral Associate</b><br><i>Department of Molecular Biophysics and Biochemistry, Yale University</i> |
| <b>2021–Now</b>  | <b>Special Graduate Faculty</b><br><i>School of Computer Science, University of Guelph</i>                   |
| <b>2013–19</b>   | <b>Graduate Research Assistant</b><br><i>School of Computer Science, McGill University</i>                   |
| <b>Fall 2017</b> | <b>Course Lecturer</b><br><i>School of Computer Science, McGill University</i>                               |
| <b>2013–17</b>   | <b>Teaching Assistant</b><br><i>School of Computer Science, McGill University</i>                            |
| <b>2012–13</b>   | <b>Graduate Service &amp; Research Assistant</b><br><i>School of Computer Science, University of Guelph</i>  |
| <b>2008–12</b>   | <b>Undergraduate Research Assistant</b><br><i>School of Computer Science, University of Guelph</i>           |

## Journal publications

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

14. [Cameron CJE](#), Seager SJH, Sigworth FJ, Tagare HD and Gerstein MB. **REPIC — an ensemble learning methodology for cryo-EM particle picking**. *BioRxiv*. DOI:[110.1101/2023.05.13.540636](#)
13. Leng J, [Cameron CJE](#), Oh S, Khurana E, Noonan JP and Gerstein MB. **LESSeq: local event-based analysis of alternative splicing using RNA-Seq data**. *BioRxiv*. DOI:[10.1101/841494](#)
12. Prost JA<sup>†</sup>, [Cameron CJE](#)<sup>†</sup> and Blanchette M. **SACSANN: identifying sequence-based determinants of chromosomal compartments**. *BioRxiv*. DOI:[10.1101/2020.10.06.328039](#)
11. Rozowsky J, Gao J, Borsari B, [and 103 others, including [Cameron CJE](#)]. **The EN-TEEx resource of multi-tissue personal epigenomes & variant-impact models**. *Cell*, 186(7):1493-1511.e40. DOI:[10.1016/j.cell.2023.02.018](#)
10. Tsai P, [Cameron CJE](#), Forni MF, Wasko RR, Naughton BS, Horsley V, Gerstein MB and Schlieker C. **Dynamic quality control machinery that operates across compartmental borders mediates the degradation of mammalian nuclear membrane proteins**. *Cell Rep*, 41(8):111675. DOI:[10.1186/s13104-020-05106-1](#)
9. Amaya C, [Cameron CJE](#)<sup>†</sup>, Devarkar SC<sup>†</sup>, Seager SJH, Gerstein MB, Xiong Y and Schlieker C (2021) **Nodal modulator (NOMO) is required to sustain endoplasmic reticulum morphology**. *JBC*, 297(2):100937. DOI:[10.1016/j.jbc.2021.100937](#)
8. Ramilowski J, Yip CW, Agrawal S, [and 115 others, including [Cameron CJE](#)] (2020) **Functional Annotation of Human Long Non-Coding RNAs via Molecular Phenotyping**. *Genome Res*, 30:1060-1072. DOI:[10.1101/gr.254219.119](#)
7. [Cameron CJE](#), 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 CJE](#)] (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 CJE](#), 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 CJE](#)<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 CJE](#), 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 CJE](#), 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 CJE](#) 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 CJE](#) 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 CJE](#), 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

15. [Cameron CJE](#), Seager SJH, Sigworth FJ, Tagare HD and Gerstein MB (2023) **REPIC — an ensemble learning methodology for cryo-EM particle picking**. *MLCSB COSI at ISMB/ECCB 2023*, Lyon, FRA
14. [Cameron CJE](#), Seager SJH, Sigworth FJ, Tagare HD and Gerstein MB (2023) **REPIC — an ensemble learning methodology for cryo-EM particle picking**. *3DEM GRC/GRS*, Newry, USA

13. [Cameron CJF](#), Seager SJH, Sigworth FJ, Tagare HD and Gerstein MB (2023) **REPIC — an ensemble learning methodology for cryo-EM particle picking**. *BPS*, San Diego, USA. DOI:[10.1016/j.bpj.2022.11.914](#)
12. [Cameron CJF](#), Sigworth FJ, Gerstein MB, and Tagare HD (2023) **MIDLS — membrane detection in cryo-EM using deep level sets**. *BPS*, San Diego, USA. DOI:[10.1016/j.bpj.2022.11.913](#)
11. [Cameron CJF](#), Seager 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., 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

5. (Aug 2023) **Reliable protein identification in cryo-EM images by machine-learning consensus**. *New York Structural Biology Center*, NYC, USA
4. (Aug 2023) **Reliable protein identification in cryo-EM images by machine-learning consensus**. *Spanish National Research Council*, Madrid, ESP
3. (Jul 2017) **The future of Hi-C**. *Birds of a Feather panel discussion at ISMB/ECCB 2017*, Prague, CZE
2. (Apr 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*, Holotown, BRB
1. (Aug 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>                      |

## Training and workshops

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|-----------------|---|
| <b>2023</b>     | LBMS cryo-EM Training Workshop Series 1-2 & 4, <i>Brookhaven National Laboratory</i> , Upton, USA                         |
| <b>Spr 2023</b> | LBMS on-demand training on screening EMs, <i>Brookhaven National Laboratory</i> , Upton, USA                              |
| <b>Spr 2023</b> | <a href="#">Compass</a> Leadership & Management training and mentoring program  |
| <b>2020–Now</b> | <a href="#">CCTP/CIRTL</a> teaching certification: <a href="#">Associate (2020)</a> & <a href="#">Practitioner (2022)</a> |

## Academic service

|                  |  |
|------------------|--|
| <b>2016–Now</b>  | <a href="#">Undergraduate and graduate student mentorship</a> ( $N = 21$ )                                 |
| <b>2024</b>      | <a href="#">RECOMB</a> peer reviewer   |
| <b>2023</b>      | <a href="#">Nature Communications Biology</a> peer reviewer  |
| <b>2023</b>      | <a href="#">Bioinformatics Advances</a> peer reviewer  |
| <b>2020–23</b>   | <a href="#">Intelligent Systems for Molecular Biology (ISMB)</a> peer reviewer                             |
| <b>2021–23</b>   | <a href="#">YPA symposium</a> committee co-coordinator (2021–22) & member                                  |
| <b>Fall 2017</b> | <a href="#">COMP 364: Computer Tools for Life Sciences</a> co-instructor (with <a href="#">Oliver CG</a> ) |