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As a **computational biologist**, I develop novel statistical, machine learning and bioinformatics approaches to emerging **molecular biology** technologies. At SEMC-NYSBC, I build new computational methods to improve the center's **cryogenic electron microscopy (cryo-EM)** and other **structural biology** pipelines. My postdoctoral research focused on cryo-EM image processing, specifically addressing the modeling and integration of prior information. During my PhD, I implemented analyses of **chromosome conformation capture** and **chromatin immunoprecipitation** data that provided insight into the regulation of genomes through the organization of chromatin's higher-order structures.

Keywords: computational biology, machine learning, cryo-EM, 4D regulatory genomics

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Education

2019–24	Postdoctoral Researcher Yale University, New Haven, USA <i>Advisors:</i> Mark B Gerstein, Hemant D Tagare and Yong Xiong
2013–19	PhD in Computer Science, concentration in Bioinformatics (October 2019) McGill University, Montréal, CAN <i>Thesis:</i> High-resolution computational analysis of chromatin architecture and function <i>Advisors:</i> Mathieu Blanchette and Josée Dostie
2012–13	MSc in Bioinformatics (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
2006–11	BSc in Biomedical Toxicology, minor in Computer Science (February 2012) University of Guelph, Guelph, CAN <i>Thesis:</i> Molecular graph neural networks for toxicology <i>Advisor:</i> Stefan Kremer

Positions held

2025–Now	Adjunct Associate Research Scientist <i>Department of Biochemistry and Molecular Biophysics, Columbia University</i>
2024–Now	Computational Scientist <i>Simons Electron Microscopy Center, New York Structural Biology Center</i>
2021–25	Special Graduate Faculty <i>School of Computer Science, University of Guelph</i>
2019–24	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>
Fall 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 & Research Assistant <i>School of Computer Science, University of Guelph</i>

Publications

† co-first or -second authors

16. Meng R, Zhu W, Cameron CJF, Ni P, Zhou X, Ulammandak T, and Gerstein MB. Machine-learning models based on histological images from healthy donors identify imageQTLs and predict chronological age. *Proc Natl Acad Sci U S A*. DOI: [10.1073/pnas.2423469122](https://doi.org/10.1073/pnas.2423469122)
15. Cameron CJF, Seager SJH, Sigworth FJ, Tagare HD and Gerstein MB. REliable PIcking by Consensus (REPIC): a consensus methodology for harnessing multiple cryo-EM particle pickers. *Commun Biol*. DOI: [10.1038/s42003-024-07045-0](https://doi.org/10.1038/s42003-024-07045-0)
14. Zhang Y, Cameron CJF, and Blanchette M (2024) Posterior inference of Hi-C contact frequency through sampling. *Front Bioinform*, (3). DOI: [10.3389/fbinf.2023.1285828](https://doi.org/10.3389/fbinf.2023.1285828)
13. Rozowsky J, Gao J, Borsari B, [and 103 others, including Cameron CJF] (2023) The EN-TEx resource of multi-tissue personal epigenomes & variant-impact models. *Cell*, 186(7):1493-1511.e40. DOI: [10.1016/j.cell.2023.02.018](https://doi.org/10.1016/j.cell.2023.02.018)
12. Tsai P, Cameron CJF, Forni MF, Wasko RR, Naughton BS, Horsley V, Gerstein MB and Schlieker C (2022) 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](https://doi.org/10.1186/s13104-020-05106-1)
11. Amaya C, Cameron CJF[†], Devarkar SC[†], 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](https://doi.org/10.1016/j.jbc.2021.100937)
10. Ramiłowski 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*, 30:1060-1072. DOI: [10.1101/gr.254219.119](https://doi.org/10.1101/gr.254219.119)
9. 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](https://doi.org/10.1186/s13104-020-05106-1)
8. 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](https://doi.org/10.1038/s41467-020-14337-6)
7. 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](https://doi.org/10.1186/s13059-019-1913-y)
6. Prost JA[†], Cameron CJF[†] and Blanchette M. SACSANN: identifying sequence-based determinants of chromosomal compartments. *BioRxiv*. DOI: [10.1101/2020.10.06.328039](https://doi.org/10.1101/2020.10.06.328039)
5. 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](https://doi.org/10.1186/s12864-019-5532-5)
4. 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*. DOI: [10.1101/841494](https://doi.org/10.1101/841494)
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](https://doi.org/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](https://doi.org/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](https://doi.org/10.1186/1471-2105-11-S8-S4)

Peer-reviewed conference papers

2. Kirchhof M, Cameron CJF and Kremer SC (2021) **End-to-end chromosomal compartment prediction from reference genomes.** *IEEE BIBM*: 50-57. DOI: [10.1109/BIBM52615.2021.9669521](https://doi.org/10.1109/BIBM52615.2021.9669521)
1. Cameron CJF, Ma EYT and Kremer SC (2010) **Neural Grammar Networks for Toxicology.** *IEEE CIBCB* (Montréal, CAN): 1-8. DOI: [10.1109/CIBCB.2010.5510322](https://doi.org/10.1109/CIBCB.2010.5510322)

Conferences with abstract submission

15. Cameron CJF, 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*, Lyon, FRA
14. Cameron CJF, 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](https://doi.org/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](https://doi.org/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 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*, Chicago, USA
7. Cameron CJF, Dostie J and Blanchette M (2018) **Prediction of complete Hi-C contact maps from genomic sequence alone.** *RECOMB*, 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*, 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.** *RNA*, Kyoto, JPN
3. Cameron CJF, Dostie J and Blanchette M (2016) **Improved Hi-C Contact Maps by Adaptive Density Estimation.** *GLBIO/CCBC*, Toronto, CAN
2. Cameron CJF, Kaplan M, Drouin A and Blanchette M (2016) **Linking Transposable Elements to Chromatin Architecture in *Arabidopsis thaliana*.** *GLBIO/CCBC*, 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*, 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., Lanzuolo C. (eds) *Capturing Chromosome Conformation.* Methods in Molecular Biology, vol 2157. *Humana, New York, NY*. DOI: [10.1007/978-1-0716-0664-3_8](https://doi.org/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](https://doi.org/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](https://doi.org/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**, 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**, Holetown, BRB
1. (Aug 2016) **The 3D genome**. *Beijing Institute of Genomics (BIG) at the Chinese Academy of Sciences, Beijing, CHN*

Awards and scholarships

2017–19	Walter Sumner Fellowship, <i>Walter Sumner Foundation</i>
2018	Travel Fellowship Award for ISCB Student Council Symposium, <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 Hitschfeld Award - Computer Science, <i>McGill University</i>

Training and workshops

2024	Scipion for facilities, <i>National Center for Biotechnology</i> , Madrid, ESP
2024	MaxQuant Summer School , <i>Ludwig Maximilian University</i> , Munich, DEU
2023	LBMS cryo-EM Training Workshop Series 1-2 & 4, <i>Brookhaven National Laboratory</i> , Upton, USA
Spr 2023	LBMS on-demand training on screening EMs, <i>Brookhaven National Laboratory</i> , Upton, USA
Spr 2023	Compass Leadership & Management training and mentoring program
2020–22	CCTP/CIRTL teaching certification: Associate (2020) & Practitioner (2022)

Academic service

2016–25	Undergraduate and graduate student mentorship ($N = 25$)
2025	(IUCr) <i>Acta Crystallographica Section D</i> peer reviewer
2020–25	Intelligent Systems for Molecular Biology peer reviewer
2024	RECOMB peer reviewer
2023–24	<i>Nature Communications Biology</i> peer reviewer
2023	Bioinformatics Advances peer reviewer
2021–23	YPA symposium committee co-coordinator (2021–22) & member
Fall 2017	COMP 364: Computer Tools for Life Sciences co-instructor (with Oliver CG)