Curriculum Vitae

Maxime Caron
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Working experience

CHU Sainte-Justine
August 2015 – Today

Bioinformatician

- Genomic data analysis of pediatric cancers (sequencing, expression, methylation and regulation).
- Research, development and integration of bioinformatic modules (sample clustering and classification, tumor purity estimation, copy number detection, deconvolution).
- Participation in writing papers/grants.
- Bioinformatic support for collaborators and staff/students.

Mcgill University (MUGQIC)
October 2012 – August 2015

Bioinformatics IT consultant

- Main data analyst for the Canadian Epigenome Mapping Center (EMC) part of the International Human Epigenome Consortium (IHEC).
- Development of next generation sequencing pipelines (wgb-seq, chip-seq, rna-seq, atac-seq, capture-methylseq, rrb-seq, smallrna-seq).
- Quality control of processed IHEC data.
- Downstream analyses for collaborators and clients, knowledge transfer to colleagues and students.
- Participation in writing papers/grants.

Genome Quebec (MUGQIC)
June 2011 – October 2012

Bioinformatician

- Development of next generation sequencing pipelines for the center and clients (chip-seq, rna-seq, exome-seq).
- Development of bioinformatics and statistical analysis software (R, perl, shell, java).
- Downstream analyses for collaborators and clients, knowledge transfer to colleagues and students.
- Support for clients before, during and after analyses.

Prognomix
April 2008 – May 2011

Bioinformatician

- GWAS of thousands of individuals genotyped using high density SNP arrays (Affymetrix).
- Management and quality control of data.
- Research and development of bioinformatic pipelines and methods (fine and coarse grain stratification (pca), association analyses (plink), empirical statistical models (bootstrap, crossvalidation), machine learning models (linear regression, neural networks)).
- Management of the bioinformatics cluster (IBM Blade Center, 6 servers/48 cores, SAN storage).
- Installation and management of the job submission system (Sun Grid Engine).

Education

- M.Sc. in Bioinformatics (University of Montreal 2009).
- B.Sc. in Bioinformatics (University of Montreal 2006).

Publications

1. Caron M, St-Onge P, Drouin S, Richer C, Sontag T, *et al*. Very long intergenic non-coding RNA expression profiles are associated to specific childhood acute lymphoblastic leukemia subtypes. **PLoS One, November 2018.**
Designed and implemented the study, worked on downstream analyses/graphs and wrote the manuscript. Estimated contribution 80%.

2. Neveu B, **Caron M**, Lagace K, Richer C, Sinnett D. Genome wide mapping of ETV6 binding sites in pre-B leukemic cells. **Scientific Reports, Sept 2018.**
Processed ChIP-seq data and worked on downstream analyses/graphs. Estimated contribution 40%.

3. Gioia R, Drouin S, Ouimet M, **Caron M**, St-Onge P, *et al*. LncRNAs downregulated in childhood acute lymphoblastic leukemia modulate apoptosis, cell migration, and DNA damage response. **Oncotarget, Aug 2017.**
Generated RNA-seq processed data. Estimated contribution 10%.

4. Audet-Walsh É, Dufour CR, Yee T, Zouanat FZ, Yan M, Kalloghlian G, Vernier M, *et al.* **Genes Dev, July 2017.**
Implemented a ChIP-seq pipeline, generated processed data and worked on downstream analyses/graphs. Estimated contribution 5%.

5. Lajoie M, Drouin S, **Caron M**, St-Onge P, Ouimet M, *et al*. Specific expression of novel long non-coding RNAs in high-hyperdiploid childhood acute lymphoblastic leukemia. **PLoS One, Mar 2017.**
Performed RNA-seq downstream analyses. Estimated contribution 15%.

6. Ramsay L, Marchetto MC, **Caron M**, Chen SH, Busche S, *et al*. Conserved expression of transposon-derived non-coding transcripts in primate stem cells. **BMC Genomics, Feb 2017.**
Implemented a RNA-seq pipeline, generated processed data and provided guidance. Estimated contribution 15%.

7. Ouimet M, Drouin S, Lajoie M, **Caron M**, St-Onge P, Gioia R, Richer C, Sinnett D. A childhood acute lymphoblastic leukemia-specific lncRNA implicated in prednisolone resistance, cell proliferation, and migration. **Oncotarget, Jan 2017.**
Performed RNA-seq downstream analyses. Estimated contribution 20%.

8. Ecker S, Chen L, Pancaldi V, Bagger FO, Fernández JM, *et al*. Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. **Genome Biol, Jan 2017.**
Implemented the epigenetic sequencing pipelines and generated processed data as part of the CEEHRC/IHEC consortium. Quality control and submission to EGA. Estimated contribution 3%.

9. Bujold D, Morais DA, Gauthier C, Côté C, **Caron M**, *et al*. The International Human Epigenome Consortium Data Portal. **Cell Systems, Nov 2016.**
Implemented the epigenetic sequencing pipelines and generated processed data as part of the CEEHRC/IHEC consortium. Quality control and submission to EGA. Estimated contribution 15%.

10. Chen L, Ge B, Casale FP, Vasquez L, Kwan T, *et al*. Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. **Cell, Nov 2016.**
Implemented the epigenetic sequencing pipelines and generated processed data as part of the CEEHRC/IHEC consortium. Estimated contribution 3%.

11. Tahmasebi S, Jafarnejad SM, Tam IS, Gonatopoulos-Pournatzis T, Matta-Camacho E, *et al*. Control of embryonic stem cell self-renewal and differentiation via coordinated alternative splicing and translation of YY2. **Proc Natl Acad Sci U S A, Nov 2016.**
Implemented a ChIP-seq pipeline, generated processed data and implicated in downstream analyses/graphs. Estimated contribution 5%.

12. Morin A, Kwan T, Ge B, Letourneau L, Ban M, Tandre K, **Caron M**, *et al*. Immunoseq: the identification of functionally relevant variants through targeted capture and sequencing of active regulatory regions in human immune cells. **BMC Med Genomics, Sep 2016.**

Participated in the implementation of an Exome-seq pipeline and generated processed data. Estimated contribution 10%.

13. Deblois G, Smith HW, Tam IS, Gravel SP, **Caron M**, *et al*. ERRα mediates metabolic adaptations driving lapatinib resistance in breast cancer. **Nat Communications, Jul 2016.**
Implemented a ChIP-seq pipeline, generated processed data and implicated in downstream analyses/graphs. Estimated contribution 10%.

14. Audet-Walsh É, Papadopoli DJ, Gravel SP, Yee T, Bridon G, **Caron M**, *et al*. The PGC-1α/ERRα Axis Represses One-Carbon Metabolism and Promotes Sensitivity to Anti-folate Therapy in Breast Cancer. **Cell Rep, Feb 2016.**
Implemented a ChIP-seq pipeline, generated processed data and implicated in downstream analyses/graphs. Estimated contribution 10%.

15. Busche S, Shao X, **Caron M**, Kwan T, Allum F, *et al*. Population whole-genome bisulfite sequencing across two tissues highlights the environment as the principal source of human methylome variation. **Genome Biology, Dec 2015.**
Implemented a WGBS pipeline, generated processed data and implicated in downstream analyses/graphs. Estimated contribution 25%.

16. Aarabi M, San Gabriel MC, Chan D, Behan NA, **Caron M**, *et al*. High-dose folic acid supplementation alters the human sperm methylome and is influenced by the MTHFR C677T polymorphism. **Hum Mol Genet, Nov 2015.**
Implemented a RRBS pipeline, generated processed data and implicated in downstream analyses/graphs. Estimated contribution 10%.

17. Dyke SO, Cheung WA, Joly Y, Ammerpohl O, Lutsik P, Rothstein MA, **Caron M**, *et al*. Epigenome data release: a participant-centered approach to privacy protection. **Genome Biology, Jul 2015.**
Implemented the epigenetic sequencing pipelines and generated processed data. Estimated contribution 10%.

18. Allum F, Shao X, Guénard F, Simon MM, Busche S, **Caron M**, *et al*. Characterization of functional methylomes by next-generation capture sequencing identifies novel disease-associated variants. **Nat Communications, May 2015.**
Implemented a Methyl-seq capture pipeline, generated processed data and implicated in downstream analyses/graphs. Estimated contribution 15%.

19. McGraw S, Zhang JX, Farag M, Chan D, **Caron M**, *et al*. Transient DNMT1 suppression reveals hidden heritable marks in the genome. **Nucleic Acids Res, Feb 2015.**
Implemented a RRBS pipeline, generated processed data and implicated in downstream analyses/graphs. Estimated contribution 20%.

20. Adoue V, Schiavi A, Light N, Almlöf JC, Lundmark P, Ge B, Kwan T, **Caron M**, *et al*. Allelic expression mapping across cellular lineages to establish impact of non-coding SNPs. **Mol Syst Biol, Oct 2014.**
Implemented a RNA-seq/ChIP-seq pipeline, generated processed data and implicated in downstream analyses/graphs. Estimated contribution 10%.

21. Magnus N, Garnier D, Meehan B, McGraw S, Lee TH, **Caron M**, Bourque G, *et al*. Tissue factor expression provokes escape from tumor dormancy and leads to genomic alterations. **Proc Natl Acad Sci U S A, Mar 2014.**
Implemented a RRBS pipeline, generated processed data and implicated in downstream analyses/graphs. Estimated contribution 5%.

22. Kleinman CL, Gerges N, Papillon-Cavanagh S, Sin-Chan P, Pramatarova A, *et al*. Fusion of TTYH1 with the C19MC microRNA cluster drives expression of a brain-specific DNMT3B isoform in the embryonal brain tumor ETMR. **Nat Genetics, Jan 2014.**
Implemented a RNA-seq pipeline and generated processed data. Estimated contribution 5%.

23. Grundberg E, Meduri E, Sandling JK, Hedman AK, Keildson S, *et al*. Global analysis of DNA methylation variation in adipose tissue from twins reveals links to disease-associated variants in distal regulatory elements. **Am J Hum Genet, Nov 2013.**
Performed downstream analyses. Estimated contribution 3%.

24. De Guire V*, **Caron M***, Scott N, Ménard C, Gaumont-Leclerc MF, Chartrand P, Major F, Ferbeyre G. Designing small multiple-target artificial RNAs. **Nucleic Acids Res. 2010 Jul.** *Contributed equally.
Designed and implemented the computational approach (meta heuristic using a genetic algorithm), implicated in downstream analyses/graphs. Estimated contribution 50%.

Posters, workshops and others

1. Next generation sequencing workshop *(RNA-Seq, Methyl-Seq, ChIP-Seq).* CRRF (Research center on fertility and reproduction) CHU Sainte-Justine (2017).

2. Busche S, **Caron M**, Kwan T, Forgetta V, Ge B, Westfall S, Qi J, Simon MM, Bell J, MuTHER Consortium, UK10K Consortium, Richards B, Bourque G, Lathrop M, Deloukas P, Spector T, Pastinen T, Grundberg E. *Full resolution DNA methylome analysis in multiple tissues from twins.* American Society Human Genetics 2013. Poster

3. Morin A, Kwan T, Tandre K, Eloranta M, Arsenault V, **Caron M**, Letourneau L, Bourque G, Laprise C, Montpetit A, Syvanen AC, Ronnblom L, Lathrop M, Pastinen T. *ImmunoSeq: Discovery of novel rare variants implicated in autoimmune and inflammatory diseases by targeting regulatory regions in immune cells.* American Society Human Genetics 2013. Poster

4. Next-generation sequencing workshop *(RNA-Seq, Methyl-Seq, ChIP-Seq).* Genome Quebec Workshop 2012.

5. LaBoissiere S, Montpetit A, **Caron M**, Bourgey M, Voisin G, Bourque G. Note technique d'application Genome Québec: RNA profiling using Next-Generation Sequencing technologies 2012.
http://gqinnovationcenter.com/documents/technicalNotes/technicalNotes_GQ11.pdf. Technical Note

Scholarships

1. FRQS (2018-2021)
2. FESP University of Montreal (2006-2007)