

## Jean MONLONG

740, Dr. Penfield Avenue, Room 4200

H3A 0G1 Montreal, Canada

Email: [jean.monlong@mail.mcgill.ca](mailto:jean.monlong@mail.mcgill.ca)

Webpage: <https://jmonlong.github.io/>

## Education

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- 2012 – now** [MCGILL UNIVERSITY](#), Montreal, Canada.  
**PhD in the Human Genetics Department** in [Guillaume Bourque's Lab](#).
- 2010 – 2011** [UNIVERSITAT POLITÈCNICA DE CATALUNYA](#), Barcelona, Spain.  
**Master in Statistic and Operations Research** as an exchange student in the Faculty of Mathematics and Statistics.
- 2008 – 2010** [ENSIMAG](#), Grenoble, France.  
**Computer Science and Mathematics** course with specialization in **Bioinformatics**.
- 2006 – 2008** [LYCÉE MICHEL MONTAIGNE](#), Bordeaux, France.  
Preparatory classes for entrance to the Grandes Écoles. Mathematics and Physics.

## Professional Experiences and Projects

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- 2017**  
(3 months) [CENTER FOR GENOMIC MEDICINE](#), Kyoto, Japan.  
As part of an exchange program, I visited Dr. Matsuda's group and contributed to their ongoing sequencing projects to characterize Japanese genomes.
- 2017**  
(1.5 month) [GENOMICS ENGLAND](#), London, UK.  
Visiting the bioinformatics team lead by Dr. Rendon, I contributed to the curation of structural variant calls for their genome analysis pipeline.
- 2012 – now** [BOURQUE LAB](#), [McGill Genome Centre](#), Montreal, Canada.  
PhD project. Implementation of a [CNV detection method](#) for whole-genome sequencing that can deal with repeat-rich regions. Application to large cohorts of normal and disease genomes.
- 2011 – 2012**  
(1 year) [CENTER FOR GENOMIC REGULATION\(CRG\)](#), Barcelona, Spain.  
Graduation project in [Roderic Guigó's group](#). Comparison of splicing activity and [detection of splicing QTLs](#) from RNA-Seq experiments. Participation in the [Geuvadis](#) and [GTEx](#) projects.
- 2011**  
(3 months) [UNIVERSITAT POLITÈCNICA DE CATALUNYA](#), Barcelona, Spain.  
Study of the regularization of the generalized canonical correlation analysis.
- 2010**  
(3 months) [NEOMADES](#)(Mobile software development), Bidart, France.  
Implementation of a Java module of their principal product.
- 2010**  
(1 month) [ENSIMAG](#), Grenoble, France.  
Breast cancer modelization and Bayesian estimation of the overdiagnosis rate. Collaboration with La Tronche's hospital (Grenoble).

## Expertise

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R, Java, C, Bash, Python, AWK, Perl, D3/Javascript/HTML/CSS.

Git, Linux, High Performance Computing, LaTeX, R/Markdown, Emacs.

Bioinformatics, Genomics, Transcriptomics.

## Scholarships and Awards

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- 2017** Student Exchange Support Program. JASSO, Japan.
- 2017** Graduate Mobility Award. Graduate and Postdoctoral Studies, McGill University.

<b>2017</b>	Oral Presentation, Honorable Mention. Human Genetics Dept's Research Day, McGill University.
<b>2015 &amp; 2017</b>	Excellence award. Human Genetics Dept, McGill University.
<b>2013-2016</b>	Graduate Research Enhancement and Travel Award funding attendance to five international conferences. Human Genetics Dept, McGill University.
<b>2014</b>	Best oral presentation. Human Genetics Dept's Research Day, McGill University.

## Publications

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<b>2017</b>	<b>J Monlong</b> , SL Girard, C Meloche, M Cadieux-dion, DM Andrade, RG Lafreniere, M Gravel, D Spiegelman, C Boelman, F Hamdan, JL Michaud, G Rouleau, BA Minassian, G Bourque, and P Cossette. Genome-wide characterization of copy number variants in epilepsy patients. <i>bioRxiv</i> , 2017.
<b>2017</b>	M Arseneault*, <b>J Monlong*</b> , ..., M Lathrop, G Bourque, and Y Riazalhosseini. Loss of chromosome Y leads to down regulation of KDM5D and KDM6C epigenetic modifiers in clear cell renal cell carcinoma. <i>Scientific Reports</i> , 2017.
<b>2017</b>	F Hamdan, CT Myers, P Cossette, P Lemay, D Spiegelman, A Dionne-Laporte, C Nassif, O Diallo, <b>J Monlong</b> , ..., BA Minassian, and JL Michaud. High Rate of Recurrent De Novo Mutations in Developmental and Epileptic Encephalopathies. <i>American journal of human genetics</i> , 2017.
<b>2017</b>	Ashis Saha, et al., and <b>The GTEx Consortium</b> . Co-expression networks reveal the tissue-specific regulation of transcription and splicing. <i>Genome research</i> , 2017.
<b>2017</b>	Fan Yang, et al., and <b>The GTEx Consortium</b> . Identifying cis-mediators for trans-eQTLs across many human tissues using genomic mediation analysis. <i>Genome research</i> , 2017.
<b>2017</b>	Xin Li, et al., and <b>The GTEx Consortium</b> . The impact of rare variation on gene expression across tissues. <i>Nature</i> , 2017.
<b>2017</b>	Meng How Tan, et al., and <b>The GTEx Consortium</b> . Dynamic landscape and regulation of RNA editing in mammals. <i>Nature</i> , 2017.
<b>2017</b>	Taru Tukiainen, et al., and <b>The GTEx Consortium</b> . Landscape of X chromosome inactivation across human tissues. <i>Nature</i> , 2017.
<b>2015</b>	<b>J Monlong</b> , C Meloche, G Rouleau, P Cossette, SL Girard, and G Bourque. Human copy number variants are enriched in regions of low-mappability. <i>bioRxiv</i> , 2016.
<b>2015</b>	M Melé, P G Ferreira, F Reverter, D S DeLuca, <b>J Monlong</b> , M Sammeth, ..., and The GTEx Consortium. The human transcriptome across tissues and individuals. <i>Science</i> , 2015.
<b>2015</b>	<b>The GTEx Consortium</b> . The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. <i>Science</i> , 2015.
<b>2015</b>	D Pervouchine, S Djebali, A Breschi, C A Davis, P P Barja, A Dobin, A Tanzer, J Lagarde, C Zaleski, L See, M Fastuca, J Drenkow, H Wang, G Bussotti, B Pei, S Balasubramanian, <b>J Monlong</b> , ..., C Notredame, R Guigo, and TR Gingeras. Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. <i>Nature Communications</i> , 2015.
<b>2014</b>	<b>J Monlong</b> , M Calvo, P G Ferreira, and R Guigó. Identification of genetic variants associated with alternative splicing using sQTLseeker. <i>Nature Communications</i> , 2014.

- 2014 P G Ferreira, P Jares, D Rico, G Gomez-Lopez, A Martinez-Trillos, N Villamor, S Ecker, A Gonzalez-Perez, D G Knowles, **J Monlong**, ..., E Campo, and R Guigo. Transcriptome characterization by rna sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. *Genome research*, 2014.
- 2014 L Greger, J Su, J Rung, P G Ferreira, **The Geuvadis Consortium**, T Lappalainen, E T Dermitzakis, and A Brazma. Tandem RNA chimeras contribute to transcriptome diversity in human population and are associated with intronic genetic variants. *PloS one*, 2014.
- 2013 T Lappalainen, M Sammeth\*, M R Friedlander\*, P A t Hoen\*, **J Monlong\***, M A Rivas\*, and et al. Transcriptome and genome sequencing uncovers functional variation in humans. *Nature*, 2013.
- 2013 P C t Hoen, et al., and **The Geuvadis Consortium**. Reproducibility of high-throughput mRNA and small RNA sequencing across laboratories. *Nature biotechnology*, 2013.
- 2013 **The GTEx Consortium**. The Genotype-Tissue Expression (GTEx) project. *Nat Genet*, 2013.
- 2011 A. Seigneurin, O. Francois, J. Labarere, P. Oudeville, **J. Monlong**, and M. Colonna. Overdiagnosis from non-progressive cancer detected by screening mammography: stochastic simulation study with calibration to population based registry data. *BMJ*, 2011.

### Selected Scientific Presentations

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- 2017 QUEBEC, CANADA, Quebec.  
**Oral** presentation, *6th Annual Canadian Human and Statistical Genetics Meeting*.
- 2016 JAPAN, Kyoto.  
**Oral** presentation, *13th International Congress of Human Genetics*.
- 2015 BC, CANADA, Vancouver.  
**Oral** presentation, *4rd Annual Canadian Human and Statistical Genetics Meeting*.
- 2014 UK, Cambridge.  
**Oral** presentation, *Genome Informatics* conference.

### Other Scientific Presentations

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- 2017 QUEBEC, CANADA, Montreal.  
**Oral** presentation, Human Genetics Dept. Research Day.
- 2016 SPAIN, Barcelona.  
**Poster** presentation, *European Society of Human Genetics* conference. Best Poster Award candidate.
- 2015 SCOTLAND, Glasgow.  
**Poster** presentation, *European Society of Human Genetics* conference.
- 2014 QUEBEC, CANADA, Montreal.  
**Oral** presentation, Human Genetics Dept. Research Day.
- 2014 BRITISH COLUMBIA, CANADA, Victoria.  
**Poster** presentation at the *3rd Annual Canadian Human and Statistical Genetics Meeting*.
- 2014 NEW MEXICO, USA, Santa Fe.  
**Poster** presentation at the *Mobile Genetic Elements and Genome Evolution* Keystone conference.

- 2013** QUEBEC, CANADA, Esterel.  
**Poster** presentation at the *2nd Annual Canadian Human and Statistical Genetics Meeting*.
- 2013** MONTANA, USA, Big Sky.  
**Poster** presentation at the *Mobile DNA in Mammalian Genomes* FASEB conference.
- 2011** SPAIN, Barcelona.  
**Poster** presentation at the *XIIIth Spanish Biometry Conference and 3rd Ibero-American Biometry Meeting*.

## Other Activities

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- 2013-2017** MCGILL UNIVERSITY.  
 Organizer and instructor of seven full-day *Introduction to R and Bioinformatics* workshops for Human Genetics graduate students.
- 2014-2017** MCGILL UNIVERSITY.  
 VP Communications at the [Human Genetics Student Society](#).
- 2017** UNIVERSITÉ DE MONTREAL.  
 Participated to a Bio-Hackaton. Our 24h project was to detect extending filaments from 3D cell imaging.
- 2017** IRCM, MONTREAL.  
 Gave a [short seminar about the Gviz package](#) at the [Montreal Bioinformatics User Group](#).
- 2016** KYOTO, JAPAN.  
 Instructor at the *4th Kyoto Course and Symposium on Bioinformatics for Next Generation Sequencing with Applications in Human Genetics*.
- 2015** UNIVERSITÉ DE MONTREAL.  
 Participated to a Bio-Hackaton. Our 24h project was to develop interactive visualization of gene expression in cancer samples.
- 2014** MCGILL UNIVERSITY.  
 Teaching Assistant for the *Advanced Statistical Concepts in Genetic and Genomic Analysis* course.
- 2014** MCGILL UNIVERSITY.  
 Organizer of a four-days *R and Bioinformatics* workshop for System Biology graduate students.