

Jean MONLONG

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Education

- 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

- 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).

Scholarships and Awards

- 2017** Student Exchange Support Program. JASSO, Japan.
- 2017** Graduate Mobility Award. Graduate and Postdoctoral Studies, McGill University.
- 2017** Oral Presentation, Honorable Mention. Human Genetics Dept's Research Day, McGill University.
- 2015 & 2017** Excellence award. Human Genetics Dept, McGill University.
- 2013-2016** Graduate Research Enhancement and Travel Award funding attendance to five international conferences. Human Genetics Dept, McGill University.
- 2014** Best oral presentation. Human Genetics Dept's Research Day, McGill University.

Selected Publications

- 2017 F Hamdan, CT Myers, P Cossette, P Lemay, D Spiegelman, A Dionne-Laporte, C Nassif, O Diallo, **J Monlong**, ..., BA Minassian, and JL Michaud. High Rate of Recurrent De Novo Mutations in Developmental and Epileptic Encephalopathies. *American journal of human genetics*.
- 2017 **J Monlong**, 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. *bioRxiv*.
- 2017 M Arseneault*, **J Monlong***, ..., 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. *Scientific Reports*.
- 2015 **J Monlong**, C Meloche, G Rouleau, P Cossette, SL Girard, and G Bourque. Human copy number variants are enriched in regions of low-mappability. *bioRxiv*.
- 2015 M Melé, P G Ferreira, F Reverter, D S DeLuca, **J Monlong**, M Sammeth, ..., and The GTEx Consortium. The human transcriptome across tissues and individuals. *Science*.
- 2015 **The GTEx Consortium**. The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. *Science*.
- 2015 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, **J Monlong**, ..., C Notredame, R Guigo, and TR Gingeras. Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. *Nature Communications*.
- 2014 **J Monlong**, M Calvo, P G Ferreira, and R Guigó. Identification of genetic variants associated with alternative splicing using sQTLseeker. *Nature Communications*.
- 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*.
- 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*.
- 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*.

Other Publications as part of the Geuvadis and GTEx consortia

- 2017 Ashis Saha, et al., and **The GTEx Consortium**. Co-expression networks reveal the tissue-specific regulation of transcription and splicing. *Genome research*.
- 2017 Fan Yang, et al., and **The GTEx Consortium**. Identifying cis-mediators for trans-eQTLs across many human tissues using genomic mediation analysis. *Genome research*.
- 2017 Xin Li, et al., and **The GTEx Consortium**. The impact of rare variation on gene expression across tissues. *Nature*.
- 2017 Meng How Tan, et al., and **The GTEx Consortium**. Dynamic landscape and regulation of RNA editing in mammals. *Nature*.

2017	Taru Tukiainen, et al., and The GTEx Consortium . Landscape of X chromosome inactivation across human tissues. <i>Nature</i> .
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. <i>PloS one</i> .
2013	P C t Hoen, et al., and The Geuvadis Consortium . Reproducibility of high-throughput mRNA and small RNA sequencing across laboratories. <i>Nature biotechnology</i> .
2013	The GTEx Consortium . The Genotype-Tissue Expression (GTEx) project. <i>Nat Genet</i> .

Selected Scientific Presentations

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

Other Scientific Presentations

2017	QUEBEC, CANADA, Montreal. Oral presentation, Human Genetics Dept. Research Day.
2016	SPAIN, Barcelona. Poster presentation, <i>European Society of Human Genetics</i> conference. Best Poster Award candidate.
2015	SCOTLAND, Glasgow. Poster presentation, <i>European Society of Human Genetics</i> conference.
2014	QUEBEC, CANADA, Montreal. Oral presentation, Human Genetics Dept. Research Day.
2014	BRITISH COLUMBIA, CANADA, Victoria. Poster presentation at the <i>3rd Annual Canadian Human and Statistical Genetics Meeting</i> .
2014	NEW MEXICO, USA, Santa Fe. Poster presentation at the <i>Mobile Genetic Elements and Genome Evolution</i> Keystone conference.
2013	QUEBEC, CANADA, Esterel. Poster presentation at the <i>2nd Annual Canadian Human and Statistical Genetics Meeting</i> .
2013	MONTANA, USA, Big Sky. Poster presentation at the <i>Mobile DNA in Mammalian Genomes</i> FASEB conference.
2011	SPAIN, Barcelona. Poster presentation at the <i>XIIIth Spanish Biometry Conference and 3rd Ibero-American Biometry Meeting</i> .

Other Activities

- 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.