

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 helped analyzing 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** **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***, and et al. 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, et al., 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 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**, and et al. 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**, and et al. 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. *Nature*.

- 2014 L Greger, J Su, J Rung, P G Ferreira, **The Geuvadis consortium**, T Lapalain, 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*.
- 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 **GTEEx Consortium**. The Genotype-Tissue Expression (GTEx) project. *Nat Genet*.

Selected Scientific Presentations

- 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

- 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

- 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 of 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.