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.

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Professional Experiences and Projects		
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 months)	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.

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. Under review at Genome Research.

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. J Monlong, C Meloche, G Rouleau, P Cossette, SL Girard, and G Bourque. 2015 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. P G Ferreira, P Jares, D Rico, G Gomez-Lopez, A Martinez-Trillos, N Villamor, 2014 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, and et al. Transcriptome and genome sequencing uncovers functional variation in humans. Nature.2013 P C t Hoen, et al., and Geuvadis Consortium. Reproducibility of highthroughput mRNA and small RNA sequencing across laboratories. Nature biotechnology.GTEx Consortium. The Genotype-Tissue Expression (GTEx) project. Nat 2013 Genet. 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

Scientific Presentations

registry data. BMJ.

2017	QUEBEC, CANADA, Montreal. Oral presentation, Human Genetics Dept. Research Day.
2017	Quebec, Canada, Quebec. Oral presentation, 6th Annual Canadian Human and Statistical Genetics Meeting.
2016	Spain, Barcelona. Poster presentation, European Society of Human Genetics conference. Best Poster Award candidate.
2016	Japan, Kyoto. Oral presentation, 13th International Congress of Human Genetics.
2015	Scotland, Glasgow. Poster presentation, European Society of Human Genetics conference.
2015	BC, Canada, Vancouver. Oral presentation, 4rd Annual Canadian Human and Statistical Genetics Meeting.

2014 UK, Cambridge.

Oral presentation, *Genome Informatics* 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.