

## Jean MONLONG

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## Education

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- 2012 – 2018** [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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- 2018 –** [UNIVERSITY OF CALIFORNIA SANTA CRUZ](#), Santa Cruz, USA.  
Postdoctoral researcher with Benedict Paten in the [Computational Genomics Lab](#), analyzing structural variation using [variation graphs](#).
- 2012 – 2018** [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.
- 2017** [CENTER FOR GENOMIC MEDICINE](#), Kyoto, Japan.  
(3 months) As part of an exchange program, I visited Dr. Matsuda's group and contributed to their ongoing sequencing projects to characterize Japanese genomes.
- 2017** [GENOMICS ENGLAND](#), London, UK.  
(1.5 month) Visiting the bioinformatics team lead by Dr. Rendon, I contributed to the curation of structural variant calls for their genome analysis pipeline.
- 2011 – 2012** [CENTER FOR GENOMIC REGULATION\(CRG\)](#), Barcelona, Spain.  
(1 year) 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** [UNIVERSITAT POLITÈCNICA DE CATALUNYA](#), Barcelona, Spain.  
(3 months) Study of the regularization of the generalized canonical correlation analysis.
- 2010** [NEOMADES](#)(Mobile software development), Bidart, France.  
(3 months) Implementation of a Java module of their principal product.
- 2010** [ENSIMAG](#), Grenoble, France.  
(1 month) 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, WDL, Snakemake, AWK, Perl, D3/Javascript/HTML/CSS.  
Git, Linux, High Performance Computing, LaTeX, R/Markdown, Emacs.  
Structural Variation, Bioinformatics, Genomics, Transcriptomics.

## Scholarships and Awards

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2019-2020	BioData Catalyst Fellow. National Heart, Lung, and Blood Institute, USA.
2018	Department Activity Award. Human Genetics Dept, McGill University.
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.
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.
2015	Excellence Award. Human Genetics Dept, McGill University.
2014	Best oral presentation. Human Genetics Dept's Research Day, McGill University.

## Publications

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2021	E Kuzmin, <b>J Monlong</b> , C Martinez, H Kuasne, CL Kleinman, J Ragoussis, G Bourque, and M Park. Inferring Copy Number from Triple-Negative Breast Cancer Patient Derived Xenograft scRNAseq Data Using scCNA. In <i>Mapping Genetic Interactions</i> , volume 2381, pages 285–303. Springer US, 2021.
2021	M Dankner, M Caron, T Al-Saadi, W Yu, V Ouellet, R Ezzeddine, SM Maritan, MG Annis, PU Le, J Nadaf, NS Neubarth, P Savage, D Zuo, CP Couturier, <b>J Monlong</b> , H Djambazian, H Altoukhi, G Bourque, J Ragoussis, RJ Diaz, M Park, M Guiot, S Lam, K Petrecca, and PM Siegel. Invasive growth associated with cold-inducible RNA-binding protein expression drives recurrence of surgically resected brain metastases. <i>Neuro-Oncology</i> , January 2021.
2020	J Sirén*, <b>J Monlong*</b> , X Chang*, AM Novak*, JM Eizenga*, C Markello, JA Sibbesen, G Hickey, P Chang, A Carroll, D Haussler, E Garrison, and B Paten. Genotyping common, large structural variations in 5,202 genomes using pangenomes, the giraffe mapper, and the vg toolkit. <i>bioRxiv</i> , 2020.
2020	Y Wang, JYP Park, A Pacis, RE Denroche, GH Jang, A Zhang, A Cuggia, C Domecq, <b>J Monlong</b> , ..., and G Zogopoulos. A Preclinical Trial and Molecularly Annotated Patient Cohort Identify Predictive Biomarkers in Homologous Recombination-deficient Pancreatic Cancer. <i>Clinical Cancer Research</i> , 2020.
2020	CP Couturier, S Ayyadhury, PU Le, J Nadaf, <b>J Monlong</b> , ..., J Antel, G Bourque, J Ragoussis, and K Petrecca. Single-cell RNA-seq reveals that glioblastoma recapitulates a normal neurodevelopmental hierarchy. <i>Nature Communications</i> , 2020.
2020	K Shafin, T Pesout, R Lorig-Roach, M Haukness, HE Olsen, ..., <b>J Monlong</b> , ..., KH Miga, P Carnevali, M Jain, and B Paten. Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. <i>Nature Biotechnology</i> , May 2020.
2020	G Hickey*, D Heller*, <b>J Monlong*</b> , JA Sibbesen, J Siren, J Eizenga, ET Dawson, E Garrison, AM Novak, and B Paten. Genotyping structural variants in pangenome graphs using the vg toolkit. <i>Genome Biology</i> , 2020.
2020	B Rodriguez-Martin, EG Alvarez, A Baez-Ortega, ..., <b>J Monlong</b> , ..., HH Kazazian, KH Burns, PJ Campbell, and JMC Tubio. Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , 2020.
2019	S Jessa, A Blanchet-Cohen, B Krug, M Vladioiu, M Coutelier, D Faury, B Poreau, N De Jay, S Hébert, <b>J Monlong</b> , ..., G Bourque, J Ragoussis, L Garzia, MD Taylor, N Jabado, and CL Kleinman. Stalled developmental programs at the root of pediatric brain tumors. <i>Nature Genetics</i> , 2019.

- 2019 J Grajcarek, **J Monlong**, Y Nishinaka-Arai, M Nakamura, M Nagai, S Matsuo, D Loughheed, H Sakurai, MK Saito, G Bourque, and K Woltjen. Genome-wide microhomologies enable precise template-free editing of biologically relevant deletion mutations. *Nature Communications*, 2019.
- 2018 **J Monlong**, P Cossette, C Meloche, G Rouleau, SL Girard, and G Bourque. Human copy number variants are enriched in regions of low mappability. *Nucleic Acids Research*, 2018.
- 2018 **J Monlong\***, SL Girard\*, ..., JL Michaud, G Rouleau, BA Minassian, G Bourque, and P Cossette. Global characterization of copy number variants in epilepsy patients from whole genome sequencing. *PLOS Genetics*, 2018.
- 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*, 2017.
- 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.
- 2017 **The GTEx Consortium**. Genetic effects on gene expression across human tissues. *Nature*, 2017.
- 2017 A Saha, et al., and **The GTEx Consortium**. Co-expression networks reveal the tissue-specific regulation of transcription and splicing. *Genome research*, 2017.
- 2017 F Yang, et al., and **The GTEx Consortium**. Identifying cis-mediators for trans-eQTLs across many human tissues using genomic mediation analysis. *Genome research*, 2017.
- 2017 X Li, et al., and **The GTEx Consortium**. The impact of rare variation on gene expression across tissues. *Nature*, 2017.
- 2017 MH Tan, et al., and **The GTEx Consortium**. Dynamic landscape and regulation of RNA editing in mammals. *Nature*, 2017.
- 2017 T Tukiainen, et al., and **The GTEx Consortium**. Landscape of X chromosome inactivation across human tissues. *Nature*, 2017.
- 2015 M Melé, PG Ferreira, F Reverter, DS DeLuca, **J Monlong**, M Sammeth, ..., and The GTEx Consortium. The human transcriptome across tissues and individuals. *Science*, 2015.
- 2015 **The GTEx Consortium**. The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. *Science*, 2015.
- 2015 D Pervouchine, S Djebali, A Breschi, CA Davis, PP 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*, 2015.
- 2014 **J Monlong**, M Calvo, PG Ferreira, and R Guigó. Identification of genetic variants associated with alternative splicing using sQTLseeker. *Nature Communications*, 2014.
- 2014 PG Ferreira, P Jares, D Rico, G Gomez-Lopez, A Martinez-Trillos, N Villamor, S Ecker, A Gonzalez-Perez, DG 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, PG Ferreira, **The Geuvadis Consortium**, T Lapalainen, ET 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\*, MR Friedlander\*, PA t Hoen\*, **J Monlong\***, MA Rivas\*, and et al. Transcriptome and genome sequencing uncovers functional variation in humans. *Nature*, 2013.
- 2013** PC 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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- 2019** NY, USA, Cold Spring Harbor Laboratory.  
**Oral** presentation, *Genome Informatics* conference.
- 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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- 2020** NY, USA, New York City.  
**Oral** presentation, *GSP-TOPMed Analysis Workshop*.
- 2019** TX, USA, Houston.  
**Oral** presentation, *GRC-GIAB Workshop* at ASHG.
- 2019** CA, USA, UC Davis.  
**Oral** presentation, *Northern California Computational Biology Symposium*.
- 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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- 2019-present** UNIVERSITY OF CALIFORNIA, SANTA CRUZ.  
Representative for the UCSC STEM Postdoc Association. Co-chair of the 2020 USPA Symposium.
- 2018** IRCM, MONTREAL.  
Gave a [short seminar about R Markdown](#) at the [Montreal Bioinformatics User Group](#).
- 2013-2018** MCGILL UNIVERSITY.  
Organizer and instructor of eight 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.