

# Guillaume J. Filion

guillaume.filion@gmail.com

*I am a computational biologist with over ten years of experience. My professional pledge is to remove the boundary between molecular biology and bioinformatics. To achieve this, I rely on a deep knowledge of molecular and cellular biology, on new computational and experimental methods, and on intimate collaborations with specialists. This unique strategy allows me to tackle questions that would otherwise be impossible to answer.*

**Citizenship:** French / Canadian.

**Birth date:** September 4, 1979.

## RESEARCH EXPERIENCE

**from 2012: Junior group leader,** Center for Genomic Regulation (Barcelona, Spain).

*My current focus is to understand how genome organization ties in with gene regulation. I am particularly interested in the implications for host-virus interactions. This requires new statistical and computational methods that are also developed within the team.*

**2008-2011: Post-doc,** Netherlands Cancer Institute (Amsterdam, The Netherlands).

*During my post-doc with Bas van Steensel, I redefined the *Drosophila* chromatin. Using genome-wide technologies and computational tools, I proposed a classification of chromatin in five basic states, going beyond euchromatin and heterochromatin.*

**2004-2007: PhD student,** Curie Institute (Paris, France).

*During my PhD with Pierre-Antoine Defossez, I discovered two new mammalian zinc finger proteins able to bind meCpGs (ZBTB4 and ZBTB38).*

## EDUCATION

**2003-2004: M2, Human Genetics**

Université Denis Diderot (Paris, France)

**2001-2003: M2, Molecular Biology**

Ecole Normale Supérieure (Lyon, France)

**2000-2001: L3 (BSc) Biology**

Concordia University (Montreal, Canada)

**1998-2000: L2 Biology**

Université Claude Bernard (Lyon, France)

## COMPETITIVE FUNDING

- 2019-2020 Plan Estatal.** 100 K€ for consumables.
- 2017-2019 Plan Estatal.** 120 K€ for consumables.
- 2015-2017 AGAUR.** 13 K€ for consumables.
- 2014-2019 ERC Synergy Grant.** 2.2 M€ distributed in salaries and consumables.
- 2012-2015 EpiGeneSys RISE1.** 150 K€ for a post-doc position.
- 2012-2016 Marie Curie Career Integration Grant.** 80 K€ for consumables.
- 2013-2016 FPI grant.** 100 K€ for a PhD position.
- 2013-2016 Plan Nacional.** 150 K€ for a post-doc position.

## PRIZES AND AWARDS

- 2012 RISE1 member of the EpiGeneSys network.**
- 2006 EMBO Short-Term mobility fellowship.**
- 2000 École Normale Supérieure de Lyon (first rank).**

## MEETING ORGANIZATION

- Statistics for genomics:** Spain, 2019
- 4D Synergy meeting:** Spain, 2016
- CRG annual symposium:** Spain, 2015
- EpiGeneSys meeting:** Spain, 2014

## EDITORIAL EXPERIENCE

- PLOS Computational Biology
- PLOS Genetics

## TEACHING EXPERIENCE

- 2018:** University Pompeu Fabra (Barcelona, Spain).  
Data visualization, L3 students (20 hours of class, creator of the course).
- 2014-2016:** Summer school SMTB (Russian, Spain).  
Experiments and lectures, highschool students (50+ hours of class, creator of the course).
- 2004-2007:** Université Denis Diderot (Paris, France).  
Mendelian genetics, L2 students (64 hours of class, teaching assistant).

## PRESENTATIONS AT MEETINGS (selection from 23)

**Pairing Meeting:** Canada, 2018  
**Nuclear Landscapes:** Poland, 2018  
**Bioinformatics: from algorithms to applications:** Russia, 2017  
**Gene Regulation by the Numbers:** Germany, 2017  
**Second Danube Epigenetics Conference:** Hungary, 2016  
**Intelligent Systems for Molecular Biology:** Ireland, 2015  
**Network Models in Cellular Regulation:** Spain, 2015  
**Statistical Methods for Post Genomic Data:** Germany, 2015  
**Society for Bioinformatics in Northern Europe:** Norway, 2014  
**EpiGeneSys meeting:** United Kingdom, 2013  
**Boheringer meeting:** Germany, 2012  
**Epigenetics, from bases to pathology:** France, 2011  
**EMBL Functional Genomics meeting:** Germany, 2010

## REVIEWING EXPERIENCE

I wrote peer reviews for academic journals including (but not limited to) Nature, Nature Biotechnology, Nature Methods, PNAS, Nature Communications, Genome Biology, Genome Research, PLOS Genetics, Cell Reports, Nucleic Acids Research, Bioinformatics, Biophysical Journal. The texts and statistics of my reviews are available at Publons (link below).

<https://publons.com/author/315077/guillaume-filion#stats>

In addition, I reviewed projects for organizations such as the European Research Council, the Agence Nationale pour la Recherche (France), the Polish Foundation for Science (Poland) and I was a member of the evaluation panel of the research institute IRI Life Sciences (Berlin, Germany) in 2017.

## SOFTWARE DEVELOPMENT

**2019: Sesame** <https://github.com/guillaume/sesame>

**2015: Zerone** <https://github.com/nanakiksc/zerone>

**2014: Seeq** <https://github.com/ezorita/seeq>

**2014: Starcode** <https://github.com/guillaume/starcode>

## COMMUNITY & OUTREACH ACTIVITIES

**2012-present:** Author of a blog on statistics and their application to biology  
<http://blog.thegrandlocus.com>

**2017:** Presentation at the Pint of Science festival  
Grizzly 72 Sports Bar (Barcelona, Spain)

**2016:** Presentation at the 9th Barcelona DataBeers  
Antiga Fàbrica Estrella Damm (Barcelona, Spain)

The \* symbol signifies shared corresponding author.

## RESEARCH ARTICLES

1. Lucic B, Chen HC, Kuzman M, Zorita E, Wegner J, Minnerker V, Roukos V, Benkirane M, Weng W, Schmidt M, Fronza R, Stadhouders R, Vlahovicek K, **Filion GJ\***, Lusic M, *Spatially clustered loci with multiple enhancers are frequent targets of HIV-1* **Nature Communications** in press (2019).
2. Pokusaeva V, Usmanova D, Putintseva E, Espinar L, Sarkisyan K, Mishin A, Bogatyreva N, Ivankov D, **Filion GJ**, Carey L, Kondrashov FA, *An experimental assay of the interactions of amino acids from orthologous sequences shaping a complex fitness landscape*, **PLOS Genetics** 15(4): e1008079. doi:10.1371/journal.pgen.1008079 (2019).
3. Cortini R, **Filion GJ**, *Theoretical principles of transcription factor traffic on folded chromatin*, **Nature Communications**, Vol. 9 p. 1740 doi:10.1038/s41467-018-04130-x (2018).
4. Chen HC, Zorita E, **Filion GJ**, *Using Barcoded HIV Ensembles (B-HIVE) for Single Provirus Transcriptomics*, **Current Protocols in Molecular Biology**, Vol. 122 e56 doi:10.1002/cpmb.56 (2018)
5. Vidal E, le Dily F, Quilez J, Stadhouders R, Cuartero Y, Graf T, Martí-Renom MA, Beato M, **Filion GJ**, *OneD: increasing reproducibility of Hi-C Samples with abnormal karyotypes*, **Nucleic Acids Research**, gky064 doi:10.1093/nar/gky064 (2018).
6. Abner E, Stoszko M, Zeng L, Chen HC, Izquierdo-Bouldstridge A, Konuma T, Zorita E, Fanunza E, Zhang Q, Mahmoudi T, Zhou MM, **Filion GJ**, Jordan A *A new quinoline BRD4 inhibitor targets a distinct latent HIV-1 reservoir for re-activation from other 'shock' drugs*, **Journal of Virology**, pii: JVI.02056-17 doi:10.1128/JVI.02056-17 (2018).
7. Stadhouders R, Vidal E, Serra F, Di Stefano B, Le Dily F, Quilez J, Gomez A, Collombet S, Berenguer C, Cuartero Y, Hecht J, **Filion GJ**, Beato M, Marti-Renom MA, Graf T, *Transcription factors orchestrate dynamic interplay between genome topology and gene regulation during cell reprogramming*, **Nature Genetics**, Vol. 50 pp. 238–249 doi:10.1038/s41588-017-0030-7 (2018).
8. **Filion GJ**, *Analytic combinatorics for computing seeding probabilities*, **Algorithms**, Vol. 11 doi:10.3390/a11010003 (2018).
9. Ferry L, Fournier A, Tsusaka T, Adelmant G, Shimazu T, Matano S, Kirsh O, Amouroux R, Dohmae N, Suzuki T, **Filion GJ**, Deng W, de Dieuleveult M, Fritsch L, Kudithipudi S, Jeltsch A, Leonhardt H, Hajkova P, Marto JA, Arita K, Shinkai Y, Defossez PA, *Methylation of DNA Ligase 1 by G9a/GLP Recruits UHRF1 to Replicating DNA and Regulates DNA Methylation*, **Molecular Cell**, Vol. 67 pp. 550–565 (2017).
10. Serra F, Baù D, **Filion GJ**, Marti-Renom MA, *Structural features of the fly chromatin colors revealed by automatic three-dimensional modeling*, **PLOS Computational Biology**, Vol. 13 e1005665. doi:10.1371/journal.pcbi.1005665 (2017).
11. Corrales-Berjano M, Rosado-Díez A, Cortini R, van Arensbergen J, van Steensel B, **Filion GJ**, *Clustering of Drosophila housekeeping promoters facilitates their expression*, **Genome Research**, Vol. 27 pp. 1153–1161 (2017).
12. Chen HC, Martinez JP, Zorita E, Meyerhans A, **Filion GJ**, *Position effects influence HIV latency reversal*, **Nature Structural and Molecular Biology**, Vol. 24 pp. 47–54 (2017).
13. Cuscó P, **Filion GJ**, *Zerone: a ChIP-seq discretizer for multiple replicates with built-in quality control*, **Bioinformatics**, Vol. 32 pp. 2896–902 (2016).

14. Corrales-Berjano M, Cuscó P, Usmanova DR, Chen HC, Bogatyreva NS, **Filion GJ**, Ivankov DN, *Machine Learning: How Much Does It Tell about Protein Folding Rates?*, **PLOS ONE**, Vol. 10 e0143166. doi:10.1371/journal.pone.0143166 (2015).
15. Zorita E, Cuscó P, **Filion GJ**, *Starcode: sequence clustering based on all-pairs search*, **Bioinformatics**, Vol. 31 pp. 1913–9 (2015).
16. le Dily F, Baù D, Pohl A, Vicent GP, Serra F, Soronellas D, Castellano G, Wright RH, Ballare C, **Filion G**, Marti-Renom MA, Beato M, *Distinct structural transitions of chromatin topological domains correlate with coordinated hormone-induced gene regulation*, **Genes & Development**, Vol. 19 pp. 2151–62 (2014).
17. van Bemmelen J, **Filion GJ**, Rosado A, Talhout W, de Haas M, van Welsem T, van Leeuwen F, van Steensel B, *A network model of the molecular organization of chromatin in Drosophila*, **Molecular Cell**, Vol. 49 pp. 759–71 (2013).
18. Steglich B, **Filion G**, van Steensel B, Ekwall K, *The inner nuclear membrane proteins Man1 and Ima1 link to two different types of chromatin at the nuclear periphery in S. pombe*, **Nucleus**, Vol. 3 pp. 77–87 (2012).
19. **Filion GJ**, van Bemmelen JG, Braunschweig U, Talhout W, Kind J, Ward LD, Brugman W, de Castro Genebra de Jesus I, Kerkhoven RM, Bussemaker H, van Steensel B, *Systematic protein location mapping reveals five principal chromatin types in Drosophila cells*, **Cell**, Vol. 143, pp. 212–24 (2010).
20. van Steensel B, Braunschweig U, **Filion GJ**, Chen M, van Bemmelen JG, Ideker T, *Bayesian network analysis of targeting interactions in chromatin*, **Genome Research**, Vol. 20, pp. 190–200 (2010).
21. Yamada D, Pérez-Torrado R, **Filion GJ**, Caly M, Jammart B, Devignot V, Sasai N, Ravasard P, Mallet J, Sastre-Garau X, Schmitz ML, Defossez PA, *The Human protein kinase HIPK2 phosphorylates and downregulates the methyl-binding transcription factor ZBTB4*, **Oncogene**, Vol. 28, pp. 2535–44 (2009).
22. Augui S, **Filion GJ**, Huart S, Nora E, Guggiari M, Maresca M, Sterwart AF, Heard E, *Sensing X chromosome pairs before X inactivation via a novel X-pairing region of the Xic*, **Science**, Vol. 318, pp. 1632–6 (2007).
23. **Filion GJ**, Fouvry L, Defossez PA, *Using reverse electrophoretic mobility shift assay to measure and compare protein-DNA binding affinities*, **Analytical Biochemistry**, Vol. 357, pp. 156–8 (2006).
24. **Filion GJ**, Zhenilo S, Salozhin S, Yamada D, Prokhortchouk E, Defossez PA, *A family of human zinc finger proteins that bind methylated DNA and repress transcription* **Molecular and Cellular Biology**, Vol. 26, pp. 169–81 (2006).
25. Defossez PA, Kelly KF **Filion GJ**, Perez-Torrado R, Magdinier F, Menoni H, Nordgaard CL, Daniel JM, Gilson E, *The human enhancer blocker CTC-binding factor interacts with the transcription factor Kaiso* **Journal of Biological Chemistry**, Vol. 280, pp. 43017–23 (2005).

## PREPRINTS UNDER REVISION

1. **Filion GJ**, Cortini R, Zorita E, *Calibrating seed-based heuristics to map short DNA reads* bioRxiv <https://doi.org/10.1101/619155v1> (2019).

## REVIEWS, BOOK CHAPTERS AND OPINION ARTICLES

1. Stadhouders R, **Filion GJ**, Graf, T, *Transcription factors and 3D genome conformation in cell fate decisions*, *Nature*, Vol. 569, pp. 345–354 (2019).
2. Quilez J, Vidal E, le Dily F, Serra F, Cuartero Y, Stadhouders R, Graf T, Martí-Renom MA, Beato M, **Filion GJ**, *Parallel sequencing lives, or what makes large sequencing projects successful*, *GigaScience*, gix100 doi:10.1093/gigascience/gix100 (2017).
3. Corrales-Berjano M, **Filion GJ**, *Modeling chromatin states*, *Epigenetics and Systems Biology* edited by Leonie Ringrose, pp. 25-43. Elsevier (2017).
4. **Filion GJ**, Betao M, *3D genome structure. Organization of the nucleus in space and time*, *FEBS Letters*, Vol. 589 pp. 28678 (2015).
5. **Filion GJ**, *The signed Kolmogorov-Smirnov test: why it should not be used*, *Gigascience*, Vol. 4 doi:10.1186/s13742-015-0048-7 (2015).
6. **Filion GJ**, van Steensel B, *Reassessing the abundance of H3K9me2 chromatin domains in embryonic stem cells*, *Nature Genetics*, Vol. 42, p. 4 (2010).
7. **Filion GJ**, Paul RE, Robert V, *Transmission and immunity: the importance of heterogeneity in the fight against malaria*, *Trends in Parasitology*, Vol. 22, pp. 345–8 (2006).