Freddy Cliquet

Computational biologist

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Citizenship: France

Education

2007–2011   **Ph.D. in Computer Science**, *Université de Nantes*.
- Title: *From MS/MS spectra to protein identification - interpretation of data from shotgun protein analysis in an unsequenced organism.*
- Advisors: Guillaume Fertin and Dominique Tessier

2006–2007   **Master Degree in Computer Science**, *Université de Tours*.
- Thesis subject: *Creation of a visual classification method to sort files.*
- Advisor: Gilles Venturini

2004–2007   **Engineer Degree in Computer Science**, *École polytechnique universitaire de Tours*.

2002–2004   **DUT in Computer Science**, *Université Paris-Sud, Institute of Technology*, Orsay.

Languages

English   **fluent**   French   **native**

Research experience

2015-present, Institut Pasteur

Research engineer
Advisors: Thomas Bourgeron at the Human genetics and cognitive functions unit and Benno Schwikowski at the Systems biology lab

- Development of a Cytoscape app to visualize and analyze genetic variants within protein-protein interaction networks.
- Processing, analysis and data management of whole-exome sequencing, whole-genome sequencing and SNParray data in a study of autism in the Faroe islands (300 individuals) and in a European IMI2 project (1000 individuals).

2012-2014, Institut Pasteur & 2015, Karolinska Institutet

Postdoctoral fellow
Advisors: Benno Schwikowski at the Institut Pasteur and Janne Lehtiö at the Karolinska Institutet

- Development of a tool to transfer identifications between experiments using a 2D alignment method for mass spectrometry data separated by iso-electric focusing and liquid chromatography.

2007-2011, Université de Nantes & INRA Nantes

PhD student

Advisors: Guillaume Fertin at the Université de Nantes on the Computer Science aspect and Dominique Tessier at the INRA Nantes on the Biology/Proteomics aspect.

- Development of a tool to identify peptides using mass spectrometry data for the analysis of unsequenced species.
- Development of a pipeline to improve identification performances through various filtering and heuristics.

Skills

Genomics

- Quality Control of SNParray, Whole-Genome Sequencing and Whole-Exome Sequencing (plink, peddy)
- Variant calling (GATK, Freebayes)
- Structural variant calling (ERDS, cn.mops, XHMM)
- Annotation (VEP, vcfanno)
- Data management (Gemini, contribution to the integration of clinical data in PaDaWaN)
- Analysis (Polygenic Risk Score, Burden, Transmission Desequilibrium Test)

Proteomics - mass spectrometry

- Raw data processing (peak picking, spectra deconvolution)
- MS/MS spectra identification (MS-GFDB, Mascot, Sequest)
- Alignment of LC-MS and IEF-LC-MS data

Software & Pipeline development

- Languages (Java, Python, SQL, XML, R, C/C++)
- Build tools (Maven, Make)
- Source management (Gitlab, Subversion)
- Pipeline (Snakemake, Make)

System administration

- Setup and configuration of a cluster of 40 linux machines.
- Cluster manager (Warewulf)
- Workload manager (Slurm, SGE)
- Storage (ZFS, NFS, MooseFS)

Publications and presentations

Articles

- **F. Cliquet**, A. Mathieu, T. Kergrohen, T. Rolland, G. Dumas, R. Delorme, B. Schwikowski, and T. Bourgeron. Gravity: a tool to analyze genetic variants in individuals using gene networks. *to be submitted*, 2017.

- **F. Cliquet**, C. Carton, C. Leblond, G. Huguet, T. Mathieu, T. Kergrohen, J. Buratti, N. Lemière, R. Toro, M. Rastam, I.C. Gillberg, B. Regnault, R. Delorme, M. Lathrop, J.F. Deleuze, A. Bolland, C. Gillberg, and T. Bourgeron. The genetic architecture of autism in the Faroe Islands. *in progress*, 2017.

- C. Loucoubar, A.V. Grant, JF. Bureau, I. Casademont, N.A. Bar, A. Bar-Hen, M. Diop, J. Faye, F.D. Sarr, A. Badiane, JF. Trape, **F. Cliquet**, B. Schwikowski, M. Lathrop, R. Paul, and A. Sakuntabhai. Detecting multi-way epistasis in family-based association studies. *Briefings in bioinformatics*, 18(3):394–402, 2016.

Conference publications (peer-reviewed)

- **F. Cliquet**, G. Fertin, I. Rusu, and D. Tessier. Proper alignment of MS/MS spectra from unsequenced species. In *Proceedings of the International Conference on Bioinformatics and Computational Biology (BIOCOMP'10)*, volume 2, pages 766–772, Las Vegas, United-States, 2010. CSREA Press.

- **F. Cliquet**, G. Fertin, I. Rusu, and D. Tessier. Comparison of spectra in unsequenced species. In *Proceedings of the 4th Brazilian Symposium on Bioinformatics (BSB 2009): Advances in Bioinformatics and Computational Biology*, volume 5676 of *LNCS*, pages 24–35, Porto Alegre, Brazil, 2009.

Seminars

- **F. Cliquet**, A. Mathieu, T. Kergrohen, T. Rolland, G. Dumas, R. Delorme, B. Schwikowski, and T. Bourgeron. Gravity: a tool to analyze genetic variants in individuals using gene networks. *GenMed Labex annual seminar*, 2017.

- **F. Cliquet**, R.M.M. Branca, J. Lehtiö, and B. Schwikowski. 2D alignment of IEF-LS-MS data - application on the consortium data. *GlycoHIT FP7 meeting, Westport, Ireland*, 2013.

- **F. Cliquet**, R.M.M. Branca, J. Lehtiö, and B. Schwikowski. 2D alignment of IEF-LS-MS data - benchmarking. *GlycoHIT FP7 meeting, Tel-Aviv, Israel*, 2013.

- **F. Cliquet**, R.M.M. Branca, J. Lehtiö, and B. Schwikowski. 2D alignment of IEF-LS-MS data - early steps. *GlycoHIT-China joint meeting, Changsha, China*, 2012.

- **F. Cliquet**, R.M.M. Branca, J. Lehtiö, and B. Schwikowski. Using isoelectric focusing and liquid chromatography data to improve peptide identification. *Mass Spectrometry in Biotechnology and Medicine summer school, Dubrovnik, Croatia*, 2012.

- **F. Cliquet**, G. Fertin, I. Rusu, and D. Tessier. SIFpackets: a framework for protein identification in unsequenced species. *Workgroup Bio-Informatique Ligérienne (BIL)*, 2010.

- **F. Cliquet**, G. Fertin, I. Rusu, and D. Tessier. Comparaison de spectres MS/MS pour des organismes non séquencés (Comparison of MS/MS spectra for unsequenced species). at the *Biopolymers interaction Assemblies unit of the INRA*, 2009.

Posters

- **F. Cliquet**, A. Mathieu, T. Kergrohen, T. Rolland, G. Dumas, R. Delorme, B. Schwikowski, and T. Bourgeron. Gravity: a tool to analyze genetic variants in individuals using gene networks. In *American Society of Human Genetics*. Orlando, 2017.

- **F. Cliquet**, A. Mathieu, T. Kergrohen, T. Rolland, G. Dumas, R. Delorme, B. Schwikowski, and T. Bourgeron. Gravity: a tool to analyze genetic variants in individuals using gene networks. In *Journées départementale Neurosciences, Institut Pasteur*. Paris, 2017.

- **F. Cliquet**, A. Mathieu, T. Kergrohen, T. Rolland, G. Dumas, R. Delorme, B. Schwikowski, and T. Bourgeron. Visualizing multiple hits in autism spectrum disorders using whole genome sequencing and protein-protein interaction network. In *International Meeting for Autism Research (IMFAR)*. San Francisco, 2017.

- **F. Cliquet**, G. Dumas, T. Rolland, A. Mathieu, J. Buratti, C. Carton, J. Van Gils, S. Calderari, R. Delorme, B. Schwikowski, and T. Bourgeron. Tackling the genetic heterogeneity of autism. In *Journées C3BI, Institut Pasteur*. Montpellier, 2015.

- **F. Cliquet**, G. Dumas, T. Rolland, A. Mathieu, J. Buratti, C. Carton, J. Van Gils, S. Calderari, R. Delorme, B. Schwikowski, and T. Bourgeron. Tackling the genetic heterogeneity of autism. In *Journées Départementales Génomes et Génétique, Institut Pasteur*. Gif sur Yvette, 2015.

- **F. Cliquet**, R.M.M. Branca, J. Lehtiö, and B. Schwikowski. A computational approach to enable label-free deep proteomic analysis. In *Journées Départementales Génomes et Génétique, Institut Pasteur*. Paris, 2013.

- **F. Cliquet**, G. Fertin, I. Rusu, and D. Tessier. Comparison of spectra in unsequenced species. In *9ème Journées Ouvertes Biologie Informatique Mathématiques (JOBIM 2009) (Yearly French conference on bioinformatic)*. Nantes, 2009.

- **F. Cliquet**, G. Fertin, I. Rusu, and D. Tessier. Comparaison de spectres MS/MS : analyse de l'algorithme SpectralAlignment (Comparison of MS/MS spectra: analyze of the SpectralAlignment algorithm). In *9ème Journées Ouvertes Biologie Informatique Mathématiques (JOBIM 2008) (Yearly French conference on bioinformatic)*. Lille, 2008.

- **F. Cliquet**, G. Fertin, I. Rusu, and D. Tessier. Identification de spectres MS/MS pour des organismes non séquencés (Identification of MS/MS spectra for unsequenced species). In *Journée des Doctorants (Ph.D. students day of Université de Nantes)*. Nantes, 2009.

Teaching experience

2017   **Bioinformatics of PPI for wet lab scientists**, *C3BI, Institut Pasteur*.
- Cytoscape practical work (3h)

2015 and 2016   **Lecturer in the Bioinformatics Master 2 program**, *Université Paris Diderot*.
- Introduction to Bioinformatics for Proteomics & Systems Biology (10h)

2010–2011   **Teaching Assistant (ATER)**, *Université de Nantes*.
- Informatics and internet certification for L1 in Sciences (40h)
- Introduction to algorithmic and programming for L1 in Biology (56h)

Reviewing

Conferences   **ISMB/ECCB, ICCABS, ISBRA, GIW**.

Journals   **PLOS one, BMC Bioinformatics**.

Organizing activities for conferences and meetings

JOBIM 2009   Member of the organization committee of the 9th edition of the Yearly French conference on bioinformatics. Nantes, 9 to 11 June 2009.

References

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