



Mickaël CANOUIL

Biostatistician, Ph.D.

*The best thing about being a statistician is that you get to
play in everyone's backyard
– John Tukey*

Experience

- Jan. 2016 – **Head of the Biostatistic Team (CNRS / Pasteur Institute Lille)**, UMR CNRS 8199 - *Integrated Genomics and Metabolic Diseases Modeling*, Lille, Activities: Genome-wide association studies, experimental design, -omics data analysis, methodological developments, consortium work package lead analyst, team management.
Nov. 2018 Headed by Pr. P. Froguel.
- Sept. 2012 – **Biostatistician (CNRS)**, UMR CNRS 8199 - *Integrated Genomics and Metabolic Diseases Modeling*, Lille, Activities: Genome-wide association studies, experimental design, -omics data analysis, methodological developments.
Dec. 2015 Headed by Pr. P. Froguel.
- Nov. 2011 – **Biostatistician**, *The French Institute of Science and Technology for Transport, Development and Networks (IFSTTAR) - UMRESTTE - UMR T 9405*, Bron, Activities: Analysis of a mobility and accident study in secondary-school pupils.
Dec. 2011 Supervised by Dr. M. Haddak.
- Jan. 2011 – **Biostatistician (Internship)**, *Hospices Civiles de Lyon - Biostatistics Unit - UMR CNRS 5558*, Lyon, Activities: Development of a non-parametric (on time) clustering algorithm for longitudinal data.
Jun. 2011 Supervised by Pr. R. Ecochard et Dr. C. Genolini.
- Mar. 2010 – **Biostatistician (Internship)**, *Laboratory of Biometry and Evolutionary Biology (LBBE) - UMR CNRS 5558*, Lyon, Activities: Mathematical modelling of nosocomial rotavirus infections in pediatric ward.
Jun. 2010 Supervised by Dr. C. Kribs-Zaleta.

Main Activities In The Last Job Position

- Data Analysis** I've been analysing omics (SNP, CpG, expression, metabolites, etc.) data within numerous projects related to metabolic diseases. These projects involve collaborations with national and international consortia like CKDgen, CHARGE, IMIDIA, DIRECT or more recently RHAPSODY. My contribution covers GWA analyses, differential methylation/expression analyses, rare variants analyses, disease progression modelling, genetic epidemiology and meta-analyses.
- Team Management** I've been managing a team of three junior statisticians. My role is to provide guidance regarding choices of statistical methodologies for analysing the data and code (mainly in R) optimisation for implementing these methodologies.
- Research** My main research interests are **mixed models**, more recently extended to joint models. **Joint model**, especially the **joint likelihood approach** implemented in the R package *JM* was studied in the context of Type 2 Diabetes incidence and fasting glucose progression (associated by diagnosis definition) using SNPs as biomarkers of interest [Canouil et al., 2018].

Education

- Oct. 2014 – **Doctor of Philosophy (Ph.D.) in BioStatistics**, *University of Lille 2*, Lille, "Development and Application of Statistical Methods for Multi-Omics Studies in Type 2 Diabetes: Beyond the Genome-Wide Association Studies Era".
Sept. 2017
Supervised by Pr. P. Froguel and Dr. G. Rocheleau
- Sept. 2009 – **Master's Degree in Biostatistics, Bioinformatics and Genomics**, *University Claude Bernard Lyon 1*, Lyon, Specialised in Biostatistics.
Jul. 2011
- Sept. 2006 – **Bachelor's Degree in Biology**, *University Claude Bernard Lyon 1*, Lyon, Specialised in Mathematics and Informatics for Biology.
Jul. 2009

Computer Skills

- Basic** C, SQL
- Intermediate** JULIA, LUA, PERL, PYTHON, SAS
- Advanced** R (Shiny, Rmarkdown, etc.), HTML, CSS, LATEX, MARKDOWN
- Environment** DOCKER, UNIX, WINDOWS

Languages

- French** Native
- English** Fluent / Full Professional Proficiency
- Spanish** Elementary proficiency

Awards

- 2015 **Funding Allocation SFD-Lilly**, *French speaking Diabetes Society (SFD)*, Bordeaux, Detection of new genomic variants associated with fasting blood glucose and incidence of type 2 diabetes simultaneously.

R Packages

- snpEnrichment **R package implementing a method for calculating an enrichment statistic of a set of SNP within a GWA signal.**
Mickaël Canouil and Loïc Yengo (2013)
<https://cran.r-project.org/package=snpEnrichment>
- clere **R package implementing the CLERE methodology.**
Loïc Yengo, Julien Jacques, Christophe Biernacki and Mickaël Canouil (2014)
<https://cran.r-project.org/package=clere>

Communications

Oral Presentations

- **Julia for Intensive Scientific Computing** (*half-day workshop available on GitHub*)
Mickaël Canouil
National Days of Higher Education and Research Software Developpement - JDEV, Bordeaux, France (2015)
- **Longitudinal Genetic Modelling: Revisiting Associations of SNPs Associated with Blood Fasting Glucose in Normoglycemic Individuals**
Mickaël Canouil, Ghislain Rocheleau, Loïc Yengo and Philippe Froguel
Statistical Methods for Post Genomic Data - SMPGD, Lille, France (2016)
- **R and Databases** (*two-days training available on GitHub*)
Mickaël Canouil
URFIST - University of Bordeaux, Bordeaux, France (2018)

Poster Presentations

- **Application of Joint Models in Genetic Association Studies**
Ghislain Rocheleau, Mickaël Canouil, Loïc Yengo and Philippe Froguel
International Genetic Epidemiology Society - IGES, Baltimore, United-States (2015)
- **Single Nucleotide Polymorphisms Associated With Fasting Blood Glucose Trajectory And Type 2 Diabetes Incidence: A Joint Modelling Approach**
Mickaël Canouil, Philippe Froguel and Ghislain Rocheleau
International Genetic Epidemiology Society - IGES, Toronto, Canada (2016)
- **Single Nucleotide Polymorphisms Associated With Fasting Blood Glucose Trajectory And Type 2 Diabetes Incidence: A Joint Modelling Approach**
Mickaël Canouil, Philippe Froguel and Ghislain Rocheleau
4th Symposium European Genomic Institute for Diabetes (E.g.i.d), Lille, France (2016)
- **Variants Génétiques Associés à la Trajectoire de la Glycémie à Jeun et à l'Incidence du Diabète de Type 2: Une Approche par Modèle Joint (CA-075)**
Mickaël Canouil, Philippe Froguel and Ghislain Rocheleau
Annual Congress of Société Francophone du Diabète (SFD), Lille, France (2017)

Publications

- [Abderrahmani et al., 2018] Abderrahmani, A., Yengo, L., Caiazzo, R., Canouil, M., Cauchi, S., Raverdy, V., Plaisance, V., Pawlowski, V., Lobbens, S., et al. (2018). Increased hepatic PDGF-AA signaling mediates liver insulin resistance in obesity associated type 2 diabetes.
- [Baumeier et al., 2017] Baumeier, C., Saussenthaler, S., Kammel, A., Jähnert, M., Schlüter, L., Hesse, D., Canouil, M., Lobbens, S., Caiazzo, R., et al. (2017). Hepatic DPP4 DNA methylation associates with fatty liver. 66(1):25–35.
- [Bonnetfond et al., 2017] Bonnetfond, A., Yengo, L., Dechaume, A., Canouil, M., Castelain, M., Roger, E., Allegaert, F., Caiazzo, R., Raverdy, V., et al. (2017). Relationship between salivary/pancreatic amylase and body mass index: a systems biology approach. 15(1):37.
- [Canouil et al., 2018] Canouil, M., Balkau, B., Roussel, R., Froguel, P., and Rocheleau, G. (2018). Jointly modelling single nucleotide polymorphisms with longitudinal and time-to-event trait: An application to type 2 diabetes and fasting plasma glucose. 9.
- [Carrat et al., 2017] Carrat, G. R., Hu, M., Nguyen-Tu, M.-S., Chabosseau, P., Gaulton, K. J., van de Bunt, M., Siddiq, A., Falchi, M., Thurner, M., et al. (2017). Decreased STARD10 expression is associated with defective insulin secretion in humans and mice. 100(2):238–256.
- [Feitosa et al., 2018] Feitosa, M. F., Kraja, A. T., Chasman, D. I., Sung, Y. J., Winkler, T. W., Ntalla, I., Guo, X., Franceschini, N., Cheng, C.-Y., et al. (2018). Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570k individuals across multiple ancestries. 13(6):e0198166.
- [Karamitri et al., 2018] Karamitri, A., Plouffe, B., Bonnetfond, A., Chen, M., Gallion, J., Guillaume, J.-L., Hegron, A., Boissel, M., Canouil, M., et al. (2018). Type 2 diabetes-associated variants of the MT2 melatonin receptor affect distinct modes of signaling. 11(545):eaan6622.
- [Mahajan et al., 2018a] Mahajan, A., Taliun, D., Thurner, M., Robertson, N. R., Torres, J. M., Rayner, N. W., Payne, A. J., Steinthorsdottir, V., Scott, R. A., et al. (2018a). Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. page 1.
- [Mahajan et al., 2018b] Mahajan, A., Wessel, J., Willems, S. M., Zhao, W., Robertson, N. R., Chu, A. Y., Gan, W., Kitajima, H., Taliun, D., et al. (2018b). Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. 50(4):559–571.
- [Ndiaye et al., 2017] Ndiaye, F. K., Ortalli, A., Canouil, M., Huyvaert, M., Salazar-Cardozo, C., Lecoeur, C., Verbanck, M., Pawlowski, V., Boutry, R., et al. (2017). Expression and functional assessment of candidate type 2 diabetes susceptibility genes identify four new genes contributing to human insulin secretion. 6(6):459–470.
- [Sung et al., 2018] Sung, Y. J., Winkler, T. W., de Las Fuentes, L., Bentley, A. R., Brown, M. R., Kraja, A. T., Schwander, K., Ntalla, I., Guo, X., et al. (2018). A large-scale multi-ancestry genome-wide study accounting for smoking behavior identifies multiple significant loci for blood pressure. 102(3):375–400.

- [Verbanck et al., 2017] Verbanck, M., Canouil, M., Leloire, A., Dhennin, V., Coumoul, X., Yengo, L., Froguel, P., and Poulain-Godefroy, O. (2017). Low-dose exposure to bisphenols a, f and s of human primary adipocyte impacts coding and non-coding RNA profiles. 12(6):e0179583.
- [Yengo et al., 2016] Yengo, L., Jacques, J., Biernacki, C., and Canouil, M. (2016). Variable clustering in high-dimensional linear regression: The r package clere. 8(1):92–106. bibtex: RJ-2016-006.

As co-first author in the following articles:

- [Ndiaye et al., 2017]
- [Verbanck et al., 2017]
- [Abderrahmani et al., 2018]

Interests

- Movies / TV-Shows / Japanese Animation
- Data visualisation (IMDb rating on GitHub)
- Board games
- Hiking
- A little bit of reading (fantastic novel)