

Boris Hejblum

Research faculty in Biostatistics
(*Chargé de Recherche*)

French, 34 years old
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Research experience

- 2021–present **Faculty Researcher (*Chargé de Recherche*)** in Biostatistics, tenured, Inserm U1219 *Bordeaux Population Health* research center, *SISTM* team, Bordeaux (France).
- 2016–2021 **Associate Professor (*Maître de Conférences*)** in Biostatistics, tenured, ISPED *Bordeaux School of Public Health*, Bordeaux University, Bordeaux (France).
- 2016 **Postdoctoral Research Associate**, Department of Biostatistics, Harvard School of Public Health, Boston (USA).
- 2015–2016 **Postdoctoral Research Fellow**, Department of Biostatistics, Harvard School of Public Health, Boston (USA).
- 2011–2015 **Research Assistant** (Ph.D. student), Inserm U897 *Biostatistics team*, Bordeaux (France).
- Apr.–Sept. **Research Assistant** (Masters intern), Inserm U897 *Biostatistics team*, Bordeaux (France).
- 2011 Development of dynamic statistical models applied to the epidemiology of myocardial infarction.
- May–Jul. **Statistician Assistant** (Masters intern), *AltraBio* (start-up in biotechnologies), Lyon (France).
- 2011 Analysis of transcriptomics data of preclinical trials.

Education

- 2011–2015 **Ph.D. in Biostatistics**, ISPED *Bordeaux School of Public Health*, Bordeaux University.
Integrative analysis of high-dimensional data applied to vaccine research.
Advisors: Pr. Rodolphe Thiébaud (rodolphe.thiebaud@u-bordeaux.fr),
François Caron (caron@stats.ox.ac.uk)
- 2008–2011 **Master of Science (M.Sc.) in Statistics** (*diplôme d'ingénieur*), ENSAI, National School for Statistics and Information Analysis (*École Nationale de la Statistique et de l'Analyse de l'Information*), Rennes (France). Specialization in biostatistics, with high honors.
- 2011 **Master of Science (M.Sc.) in Statistics and Econometrics**, Department of Mathematics, University of Rennes 1, Rennes (France). Dual degree partnership in conjunction with studies at ENSAI (additional education focused on scientific research).
- 2009 **Bachelor of Science (B.Sc.) in Mathematics** (*licence de mathématiques*), Pierre and Marie Curie University – Paris 6 (UPMC), Paris (France). In conjunction with studies at ENSAI (dual curriculum, remote learning).
- 2006–2008 **Post-Secondary Preparatory Classes** (*Classes Préparatoires aux Grandes Écoles – CPGE*), Lycée Hoche, Versailles (France). University-level courses required in preparation for competitive exams into top universities, engineering, and graduate schools (France's *Grandes Écoles*). Major in Mathematics and Physics.
- 2006 **High school diploma**, Lycée Richelieu, Rueil-Malmaison (France). With high honors.

Teaching experience

- 2019 - present **International Ph.D. course**, Graduate School of Health and Medical Sciences, University of Copenhagen, (Denemark).
- Bayesian methods in biomedical research (graduate class, 3.5 days per year)
- 2018 - present **Ph.D. courses**, Bordeaux University (France).
- R for development & performance (graduate class, 18h per year)
 - Basics for data science using R (graduate class, 12h per year)
- 2019 - present **Master in Public Health**, ISPED, Bordeaux University (France).
- omics data analysis (graduate class, 20h per year)
 - data visualisation (undergraduate class, 4h)
- 2021 - present **Master in numerical sciences & bio-health**, École Centrale Nantes (France).
- Statistical learning in high-dimension (graduate class, 2h per year)
- 2016 - 2021 **Associate Professor**, Bordeaux University, France.
- Ph.D. courses:
- Introduction to Bayesian analysis for biometric research (graduate class, 18h per year)
- Master in Public Health Data Science & Master in Biostatistics courses:
- likelihood estimation and multivariate regression (graduate class, 30h per year)
 - factor methods for multivariate data analysis (graduate class, 30h per year)
 - Bayesian analysis and sampling methods (graduate class, 30h per year)
 - omics data analysis (graduate class, 20h per year)
 - sparse Partial Least Squares methods (graduate class, 7h per year)
 - ANOVA regression (graduate class, 7.5h per year)
 - hypothesis testing (graduate class, 30h per year)
 - advanced R (undergraduate class, 15h per year)
- 2012 - 2014 **Teaching Assistant**, Bordeaux University, France.
- Master in Public Health and Master in Biostatistics courses:
- MCMC methods for Bayesian analysis (graduate class, 12h)
 - sparse Partial Least Squares methods (graduate class, 5h)
 - basic statistics (undergraduate class 16h)
 - logistic regression (undergraduate class, 12h)
 - R software (undergraduate class 9h)

Scientific supervision

Postdoctoral researchers

- Laura Villain (2019 – 2021: 100%)
- Hung Van Tran (2019: 50%)

Ph.D. students

- Kalidou Ba (2022 – ... : 50%)
- Benjamin Hivert (2020 – ... : 50%)
- Paul Freulon (2019 – 2022: 50%)
- Marine Gauthier (2018 – 2021: 50%)
- Soufiane Ajana (2017 – 2019: 15%)
- Stephanie Chan (2016: 15%)

Interns

- Arthur Hughes (M2 internship 2023: 75%)
- Maud Perpère (M1 internship 2023: 100%)
- Emma Avisou (M1 internship 2021: 100%)
- Clément Bonnet (M1 internship 2021: 100%)
- Benjamin Hivert (M2 master thesis 2020: 100%)
- Anthony Devaux (M2 master thesis 2019: 100%)
- Aaron Sonabend (PhD research visit 2019: 100%)
- Victor Gasque (M1 internship 2019: 50%)

- Thomas Ferte (M2 master thesis 2019: 100%)
- Marine Gauthier (M2 master thesis 2018: 100%)
- Roxane Coueron (M2 master thesis 2018: 50%)
- Paul Tauzia (M2 master thesis 2017: 50%)
- Chariff Alkhasim (M2 master thesis 2015: 50%)
- Damien Chimits (M2 master thesis 2014: 50%)
- Lise Cahuzac (M1 internship 2013: 50%)

Grants & funding

- 2016-2024 **Participant** ANRS LabEx Programme “Vaccine Research Institute” (VRI).
- 2023-2027 **Participant** PEPR *Santé Numérique*, axis “Statistical and AI based Methods for Advanced clinical Trials Challenges in digital Health” (funding 1 PhD student).
- 2023-2027 **Participant** PEPR *Santé Numérique*, axis “multiScale AI for SingleCell-based precision MEDicine” (funding 50% of 1 PhD student).
- 2018-2020 **Principal Investigator** of the Inria associate-team DESTRIER: “DEfining Surrogacy of early Transcriptomics foR vacclnE Response” (36K€ over 3 years)
- 2020-2024 **Participant** (genomics-statistics referent) in the EU H2020 Framework Programme “IP-cure-B” (*Im-mune profiling to guide host-directed interventions to cure HBV infections*).
- 2018-2020 **Principal Investigator** of the Inria associate-team SWAGR: “Statistical Workforce for Advanced Genomics using RNA-seq” (36K€ over 3 years)
- 2019-2022 **Participant** (computational statistics referent) in the ANR-18-CE36-0004 “DyMES” (*Dynamic Models for Epidemiological Longitudinal Studies of Chronic Diseases*).
- 2019-2021 **Principal Investigator** of the Technology Development Action from Inria Bordeaux Sud-Ouest “VASI” (*Visualization and Analysis Solutions for Immunologists*): 2 year support for a software engineer.
- 2018-2020 **Teaching discharge** for research at Inria Bordeaux Sud-Ouest: 96h per year.
- 2017-2020 **Participant** (RNA-seq analysis referent) in the Transcan-2 ERA-NET “GLIOMA-PRD” (*Multi-parametric analysis of the evolution and progression of low grade glioma*): support for a post-doctoral researcher for 2 years.
- 2016-2019 **Participant** (réfèrent statistique en grande dimension) au *Research and Innovation Programme* n°634479 de EU H2020 EYE-RISK (*Systems medicine for identifying risk factors, molecular mechanisms and therapeutic approaches for age-related macular degeneration*).
- 2016 **Recipient** of a travel grant from the Harvard Program in Quantitative Genomics (PQG) to attend the ENAR conference.
- 2011 **Recipient** of a Ph.D. grant from the EHESP (*École des Hautes Études en Santé Publique*, Rennes, France) – ranked 1st.

Research expertise

Statistical genomics & high dimensional data: I have a strong interest in models for high dimensional data. I am familiar with the multiple testing issue and potential strategies to face it. I have worked on sparse Partial Least Squares methods, and with other dimension reduction approaches such as the random forests or the LASSO. I have analyzed gene expression data in a clinical trial context and I am familiar with the specificities of this kind of data, such as preprocessing.



























Artificial Intelligence for health: I have developed various artificial intelligence approaches to solve biomedical data analysis bottlenecks. In particular, I am working on machine learning approaches to automate the processing of flow and mass cytometry measurements, and also on automated medical diagnosis from both structured data and free text medical notes in English, French and Chinese through language agnostic algorithms.

Electronic Health Records: I am currently developing models to perform probabilistic record linkage to match electronic health records without using identifier variables, and to predict disease phenotype from electronic health record data, with application in infection and rheumatoid arthritis.

Bayesian nonparametric models: I am interested in statistical learning methods such as nonparametric Bayesian mixture of skew distributions for the clustering of large cell populations.

Evidence synthesis causal analysis: I studied stochastic modeling of life-course health data. The developed idea was to explore potential causal factors of myocardial infarction by relating the drift of a degradation process with metadata from the literature.

Software development & maintenance

- 2023 **citcdf:** an  package for performing Conditional Independence Testing Through Conditional Cumulative Distribution Function Estimation. Available on GitHub . *Co-creator & maintainer.*
- 2022 **CytOpT:** an  package for automatic gating transfer in cytometry data using optimal transport with domain adaptation. Uses Python code.. Available on CRAN, development version on GitHub . *Co-creator & maintainer.*
- 2020 **dearseq:** an  package for Differential Expression Analysis for RNA-seq data through a robust variance component test. Available on , development version on GitHub . *Co-creator & maintainer.*
- 2019 **vici:** an interactive  Shiny application for accurate estimation of vaccine induced cellular immunogenicity with bivariate linear modeling. Available online or locally from the CRAN, development version on GitHub . *Creator & maintainer.*
- 2019 **marqLevAlg:** an  package for (parallelized) optimization of convex multiparametric functions. Available on CRAN, development version on GitHub . *Contributor.*
- 2019 **foodingraph:** an  package for displaying weighted undirected food networks from adjacency matrices. Available on CRAN, development version on GitHub . *Co-creator.*
- 2019 **phenotypr:** an  package for probabilistic phenotyping patients from electronic health records using both diagnosis codes and natural language processed medical notes. Available on CRAN, development version on GitHub . *Creator & maintainer.*
- 2017 **ludic:** an  package for probabilistic record linkage using diagnosis codes. Available on CRAN, development version on GitHub . *Co-creator & maintainer.*
- 2017 **cytometree:** an  package for automatic gating and annotation of flow-cytometry data. Available on CRAN, development version on GitHub . *Co-creator & maintainer.*
- 2017 **sslcov:** an  package for covariance semi-supervised learning. Available on GitHub . *Co-creator.*
- 2016 **tcsaseq:** an  package for longitudinal RNA-seq data analysis at the gene set level. Available on GitHub . *Co-creator & maintainer.*
- 2017 **kernscr:** an  package for survival analysis by gene sets in presence of competing risks. Available on CRAN, development version on GitHub . *Co-creator & maintainer.*
- 2015 **NPflow:** an  package for clustering of large cell populations with Dirichlet process mixture of skew-Normal and skew-t distributions. Uses C++ code to speed up computation.. Available on CRAN, development version on GitHub . *Co-creator & maintainer.*
- 2014 **TcGSA:** an  package for longitudinal gene-expression data from microarrays at the gene set level. Available on CRAN, development version on GitHub . *Creator & maintainer.*

Active international research collaborations

Denis Agniel, *Rand Corporation, Statistics group, Santa Monica (CA, USA), Associate Statistician.*

Tianxi Cai, *Harvard TH Chan School of Public Health, Department of Biostatistics, Boston (MA, USA), Professor.*

Layla Parast, *University of Texas at Austin, Austin (TX, USA), Associate Professor.*

Research visits abroad

- 2018-2019 **MRC Biostatistics Unit, Cambridge University**, Cambridge (United-Kingdom)
(2×3 weeks) invited by Sylvia Richardson, Professor.
- 2018 **Rand Corporation, Statistics group**, Santa Monica (CA, USA)
(1 week) invited by Denis Agniel, Associate Statistician.
- 2016-2017 **Harvard University, Department of Biostatistics**, Cambridge (MA, USA)
(2×1 week) invited by Tianxi Cai, Professor.
- 2013-2014 **University of Oxford, Department of Statistics**, Oxford (United-Kingdom)
(3×1 week) invited by François Caron, Research Fellow.
- 2012 **Benaroya Research Institute**, Chaussabel Laboratory, Seattle (WA, USA)
(1 month) invited by Damien Chaussabel, Director of Systems Immunology.
- 2011 **Baylor Institute for Immunology Research**, Dallas (TX, USA).
(1 month)

Scientific evaluation

- 2023 **Member of the Scientific Committee for the 2023 Channel Network Conference of the International Biometrics Society.**
- 2021 **Member of the PhD defense committee of Shaima Belhechmi, Université Paris-Saclay.**
- 2021 **Reviewer for the ANRT**, (*Association Nationale de la Recherche Technologique*).
- 2021 **Member of the Scientific Committee for the 42nd ISCB conference.**
- 2021 **Member of the Pharm. D. defense committee of Blandine Malbos, Université d'Angers.**
- 2019 **Invited member of the PhD defense committee of Soufiane Ajana, Université de Bordeaux.**

Reviewer for international peer-reviewed scientific journals

Annals of Applied Statistics, Bayesian Analysis, BioData Mining, Bioinformatics, Biometrics, Cell Reports Methods, Cancer Reports, Computational Statistics Data Analysis, Journal of Open Source Software, Journal of Statistical Computation and Simulation, PLOS Computational Biology, Scientific Reports, STAT, Statistics in Medicine, Statistical Applications in Genetics and Molecular Biology, WIREs Applications in Genetics and Molecular Biology

Academic responsibilities

- 2023–present **Member of the Organizing Committee for the next annual conference of the French Statistical Society (SFdS).**
- 2021–present **French Biometric Society correspondent to the Channel Network region of the International Biometrics Society.**
- 2019–present **Member of the Bureau of the French Biometric Society (*Société Française de Biométrie*) – webmaster.**
- 2019 **Co-organizer of the Bordeaux Statistics Seminar series** (quarterly).
- 2017–present **Organizer of the Public Health Department Biostatistics Seminar series** (biweekly).
- 2018 **Co-organizer of the workshop in honor of Daniel Commenges' 70th birthday.**
- 2012–2014 **Founder of the ISPED Ph.D. students (weekly) seminar.**
- 2009–2010 **President (formerly Secretary General) of the ENSAI Business Networking Forum.**
Responsible for organizing the yearly networking event between companies and ENSAI students
- 2009 **Vice President of the ENSAI Student Council.**
Organize and coordinate associative activities and social life at the school

Publications

▷ Books:

Desquilbet L, Granger S, Hejblum BP, Legrand A, Pernot P & Rougier N. *Vers une recherche reproductible : Faire évoluer ses pratiques*. Urfist de Bordeaux, 2019.

▷ Preprints:

Bigot J, Freulon P, Hejblum BP & Leclaire A. On the potential benefits of entropic regularization for smoothing wasserstein estimators. *arXiv* 2210.06934, 2022. DOI: 10.48550/arXiv.2210.06934

Hejblum BP, Ba K, Thiébaut R & Agniel D. Neglecting normalization impact in semi-synthetic RNA-Seq data simulation generates artificial false positives. *bioRxiv* 2022.05.10.490529, 2022. DOI: 10.1101/2022.05.10.490529

Hivert B, Agniel D, Rodolphe T & Hejblum BP. Post-clustering difference testing: Valid inference and practical considerations. *arXiv* 2210.13172, 2022. DOI: 10.48550/arXiv.2210.13172

Gauthier M, Agniel D, Thiébaut R & Hejblum BP. Distribution-free complex hypothesis testing for single-cell RNA-seq differential expression analysis. *bioRxiv* 2021.05.21.445165, 2021. DOI: 10.1101/2021.05.21.445165

Villain L, Ferté T, Thiébaut R & Hejblum BP. Gene set analysis for time-to-event outcome with the generalized berk-jones statistic. *bioRxiv* 2021.09.07.459329, 2021. DOI: 10.1101/2021.09.07.459329

Hejblum BP, Kunzmann K, Lavagnini E, Hutchinson A, Robertson DS, Jones SC & Eckes-Shephard AH. Realistic and robust reproducible research for biostatistics. *Preprints* 2020060002, 2020. DOI: 10.20944/preprints202006.0002.v1

▷ Published or in press: (* indicates equal contribution)

Freulon P, Bigot J & Hejblum BP. CytOpT: Optimal Transport with Domain Adaptation for Interpreting Flow Cytometry data. *Annals of Applied Statistics* 17(2):1086-1104, 2023. DOI: 10.1214/22-A0AS1660

Collin A, Hejblum BP, Vignals C, Lehot L, Thiébaut R, Moireau P & Prague M. Using population based kalman estimator to model COVID-19 epidemic in france: Estimating the effects of non-pharmaceutical interventions on the dynamics of epidemic. *International Journal of Biostatistics*, 2023. DOI: 10.1515/ijb-2022-0087

Thiébaut R, Hejblum B, Mougin F, Tzourio C & Richert L. ChatGPT and beyond with artificial intelligence (AI) in health: Lessons to be learned. *Joint Bone Spine* 90(5):105607, 2023. DOI: 10.1016/j.jbspin.2023.105607

Agniel D, Hejblum BP, Thiébaut R & Parast L. Doubly-robust evaluation of high-dimensional surrogate markers. *Biostatistics* in press, 2022. DOI: 10.1093/biostatistics/kxx005

Ferté T, Jouhet V, Greffier R, Hejblum BP & Thiébaut R. The benefit of augmenting open data with clinical data-warehouse EHR for forecasting SARS-CoV-2 hospitalizations in Bordeaux area, France. *JAMIA open* ooac086, 2022. DOI: 10.1093/jamiaopen/ooac086

Richert L, Lelièvre J, Lacabaratz C, Hardel L, Hocini H, Wiedemann A, Lucht F, Poizot-Martin I, Bauduin C, Diallo A, Rieux V, Durand M, Hejblum BP, Launay O, Thiébaut R, Lévy Y, on behalf of the ANRS VRI01 Study group. T-cell immunogenicity, gene expression profile and safety of four heterologous prime-boost combinations of HIV vaccine candidates in healthy volunteers - results of the randomized multi-arm phase I/II ANRS VRI01 trial. *Journal of Immunology* 208(12):2663-2674, 2022. DOI: 10.4049/jimmunol.2101076

Rinchai D, Deola S, Zoppoli G, Ahamed Kabeer BS, Taleb S, Pavlovski I, Maacha S, Gentilcore G, Toufiq M, Mathew L, Liu L, Vempalli FR, Mubarak G, Lorenz S, Sivieri I, Cirmena G, Dentone C, Cuccarolo P, Giacobbe D, Baldi F, Garbarino A, Cigolini B, Cremonesi P, Bedognetti M, Ballestrero A, Bassetti M, Hejblum BP, Augustine T, Van Panhuys N, Thiébaut R, Branco R, Chew T, Shojaei M, Short K, Feng C, PREDICT-19 consortium, Zughaier SM, De Maria A, Tang B, Ait Hssain A, Bedognetti D, Grivel J, Chaussabel D. High-temporal resolution profiling reveals distinct immune trajectories following the first and second doses of COVID-19 mRNA vaccines. *Science Advances* 8(45):eabp9961, 2022. DOI: 10.1126/sciadv.abp9961

Acar N, Merle BMJ, Ajana S, He Z, Grégoire S, Hejblum BP, Martine L, Buaud B, Bron AM, Creuzot-Garcher CP, Korobelnik J, Berdeaux O, Jacqmin-Gadda H, Bretillon L, Delcourt C, for the Biomarkers of Lipid Status And

metabolism in Retinal ageing (BLISAR) Study Group. Predicting the retinal content in omega-3 fatty acids for age-related macular-degeneration. *Clinical and Translational Medicine* 11(7):e404, 2021. DOI: 10.1002/ctm2.404

Lefèvre-Arbogast S, Hejblum BP, Helmer C, Klose C, Manach C, Low DY, Urpi-Sarda M, Andres-Lacueva C, González-Domínguez R, Aigner L, Altendorfer B, Lucassen PJ, Ruigrok SR, De Lucia C, Du Preez A, Proust-Lima C, Thuret S, Korosi A & Samieri C. Early signature in the blood lipidome associated with subsequent cognitive decline in the elderly: A case-control analysis nested within the three-city cohort study. *EBioMedicine* 64:103216, 2021. DOI: 10.1016/j.ebiom.2021.103216

Lévy Y, Wiedemann A*, Hejblum BP*, Durand M, Lefebvre C, Surénaud M, Lacabartz C, Perreau M, Foucat E, Déchenaud M, Tisserand P, Blengio F, Hivert B, Gauthier M, Cervantes-Gonzalez M, Bachelet D, Laouénan C, Bouadma L, Timsit J, Yazdanpanah Y, Pantaleo G, Hocini H & Thiébaut R. CD177, a specific marker of neutrophil activation, is associated with coronavirus disease 2019 severity and death. *iScience* 24(7):102711, 2021. DOI: 10.1016/j.isci.2021.102711

Colas C, Hejblum B, Rouillon S, Thiébaut R, Oudeyer P, Moulin-Frier C & Prague M. EpidemiOptim: A toolbox for the optimization of control policies in epidemiological models. *Journal of Artificial Intelligence Research* 71:479-519, 2021. DOI: 10.1613/jair.1.12588

Zhang HG*, Hejblum BP*, Weber G, Palmer N, Churchill S, Szolovits P, Murphy S, Liao K, Kohane I & Cai T. ATLAS: An automated association test using probabilistically linked health records with application to genetic studies. *Journal of the American Medical Informatics Association* 28(12):2582-2592, 2021. DOI: 10.1093/jamia/ocab187

Ferte T, Cossin S, Schaevebeke T, Barnette T, Jouhet V & Hejblum BP. Automatic phenotyping of electronic health record: PheVis algorithm. *Journal of Biomedical Informatics* 117:103746, 2021. DOI: 10.1016/j.jbi.2021.103746

Ajana S, Cougnard-Grégoire A, Colijn J, Merle BM, Verzijden T, Jong P, Hofman A, EYE-RISK Consortium, Vingerling J, Hejblum BP, Korobelnik J, Meester-Smoor M, Jacqmin-Gadda H, Klaver C, Delcourt C. Predicting progression to advanced age-related macular degeneration from clinical, genetic and lifestyle factors using machine learning. *Ophthalmology* 128(4):587-597, 2021. DOI: 10.1016/j.optha.2020.08.031

Philipps V, Hejblum BP, Prague M, Commenges D & Proust-Lima C. Robust and efficient optimization using a marquardt-levenberg algorithm with r package marqLevAlg. *The R Journal* 13(2):365-379, 2021. DOI: 10.32614/RJ-2021-089

Lin L & Hejblum BP. Bayesian mixture models for cytometry data analysis. *Wiley Interdisciplinary Reviews: Computational Statistics* 13:e1535, 2021. DOI: 10.1002/wics.1535

Bouadma L, Wiedemann A, Patrier J, Surenaud M, Wicky P, Foucat E, Diehl J, Hejblum BP, Sinnah F, Montmollin E, Lacabartz C, Thiébaut R, Timsit J & Lévy Y. Immune alterations during SARS-CoV-2-related acute respiratory distress syndrome. *Journal of Clinical Immunology* 40:1082-1092, 2020. DOI: 10.1007/s10875-020-00839-x

Lhomme E, Hejblum BP, Lacabartz C, Wiedemann A, Lelièvre J, Lévy Y, Thiébaut R & Richert L. Analyzing cellular immunogenicity in vaccine clinical trials: A new statistical method including non-specific responses for accurate estimation of vaccine effect. *Journal of Immunological Methods* 477:112711, 2020.

Gauthier M, Agniel D, Thiébaut R & Hejblum B. Dearseq: A variance component score test for RNA-seq differential analysis that effectively controls the false discovery rate. *NAR Genomics and Bioinformatics* 2(4):lqaa093, 2020. DOI: 10.1093/nargab/lqaa093

Wiedemann A, Foucat E, Hocini H, Lefebvre C, Hejblum BP, Durand M, Krüger M, Keita AK, Ayoub A, Mély S, Fernandez J, Touré A, Fourati S, Lévy-Marchal C, Raoul H, Delaporte E, Koivogui L, Thiébaut R, Lacabartz C, Lévy Y, PostEboGui Study Group. Long-lasting severe immune dysfunction in ebola virus disease survivors. *Nature Communications* 11:3730, 2020. DOI: 10.1038/s41467-020-17489-7

Chan SF, Hejblum BP, Chakraborty A & Cai T. Semi-supervised estimation of covariance with application to phenome-wide association studies with electronic medical records data. *Statistical Methods in Medical Research* 29:455-465, 2020. DOI: 10.1177/0962280219837676

Hejblum BP, Alkhassim C, Gottardo R, Caron F & Thiébaut R. Sequential dirichlet process mixture of skew t-distributions for model-based clustering of flow cytometry data. *Annals of Applied Statistics* 13(1):638-660, 2019. DOI: 10.1214/18-AOAS1209

Ajana S, Niyazi A, Bretillon L, Hejblum BP, Jacqmin-Gadda H & Cécile D. Benefits of dimension reduction in penalized regression methods for high dimensional grouped data: A case study in low sample size. *Bioinformatics* 35:3628-3634, 2019. DOI: 10.1093/bioinformatics/btz135

Thiébaud R, Hejblum BP, Hocini H, Bonnabau H, Skinner J, Montes M, Lacabaratz C, Richert L, Palucka K, Banchereau J & Levy Y. Gene expression signatures associated with immune and virological responses to therapeutic vaccination with dendritic cells in HIV-infected individuals. *Frontiers in Immunology* 10:874, 2019. DOI: 10.3389/fimmu.2019.00874

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Hejblum BP, Cui J, Lahey LJ, Cagan A, Sparks JA, Sokolove J, Cai T & Liao KP. Association between anti-citrullinated fibrinogen antibodies and coronary artery disease in rheumatoid arthritis. *Arthritis Care & Research* 70:1113-1117, 2018. DOI: 10.1002/acr.23444

Commenges D, Alkassim C, Gottardo R, Hejblum BP & Thiébaud R. Cytometree: A binary tree algorithm for automatic gating in cytometry analysis. *Cytometry: Part A* 93(11):1132-1140, 2018. DOI: 10.1002/cyto.a.23601

Sinnott JA, Cai F, Yu S, Hejblum BP, Hong C, Kohane IS & Liao KP. PheProb: probabilistic phenotyping using diagnosis codes to improve power for genetic association studies. *Journal of the American Medical Informatics Association* 25(10):1359-1365, 2018. DOI: 10.1093/jamia/ocy056

Lefèvre-Arbogast S, Gaudout D, Bensalem J, Letenneur L, Dartigues J, Hejblum BP, Féart C, Delcourt C & Samieri C. Pattern of polyphenol intake and the long-term risk of dementia in older persons. *Neurology*, 2018. DOI: 10.1212/WNL.0000000000005607

Hejblum BP, Weber GM, Liao KP, Palmer NP, Churchill S, Shadick NA, Szolovits P, Murphy SN, Kohane IS & Cai T. Probabilistic record linkage of de-identified research datasets with discrepancies using diagnosis codes. *Scientific Data* 6:180298, 2018. DOI: 10.1038/sdata.2018.298

Neykov M, Hejblum BP & Sinnott JA. Kernel machine score test for pathway analysis in the presence of semi-competing risks. *Statistical Methods in Medical Research* 27(4):1099-1114, 2018. DOI: 10.1177/0962280216653427

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▷ Oral communications: (* indicates invited talks)

- Mexico 2022* Hejblum B, Parast L, Agniel D, Transcriptomics: a potential early surrogate for vaccine response ?, *BIRS-CMO 22w5184*, Oaxaca.
- Latvia 2022 Hejblum B, Gauthier M, Ba K, Thiébaut R, Agniel D, Distribution-free complex hypothesis testing for single-cell RNA-seq differential expression analysis, *31st International Biometric Conference*, Riga.
- France 2022* Hejblum B, Machine learning approaches for the analysis of bulk and single-cell RNA-seq data, *4th GenMed workshop on Medical Genomics*, Paris.
- Germany 2022* Hejblum B, Teaching Bayesian statistics during a pandemic, *German Association for Medical Informatics, Biometry and Epidemiology (GMDS) Teaching & Didactics workshop*, Saarbrücken.
- France 2021* Hejblum B, Collin A, Wittkop L, Dutartre D, Clairon Q, Moireau P, Thiébaut R, Hejblum B, Leveraging random effects to estimate the impact of NPIs on epidemic dynamics across French regions, *8th Channel Network Conference of the International Biometric Society*, Paris.
- France 2021* Hejblum B, Clustering of flow cytometry data using non parametric Bayesian modeling, *Séminaire LMBA*, Vannes.
- France 2021* Hejblum B, Distribution-free complex hypothesis testing for single-cell RNA-seq differential expression analysis, *Statistical Methods for Post-Genomic Data (SMPGD) – 2021*, online.
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- France 2019* Hejblum B, Gauthier M, Thiébaut R, Agniel D, Controlling Type-I error in RNA-seq differential analyses through a variance component score test with an application to tuberculosis infection, *Séminaire de l'équipe de Statistique de l'Institut de Recherche MATHématique de Rennes (IRMAR)*, Rennes.
- UK 2019* Hejblum B, Kirk PDW, Scaling up nonparametric Bayesian clustering with MCMC for big data applications, *12th International Conference of the ERCIM WG on Computational and Methodological Statistics*, Londres.
- Taiwan 2019* Hejblum B, Gauthier M, Thiébaut R, Agniel D, A variance component score test applied to RNA-Seq differential analysis, *3rd EcoSta Conference*, Taichung.
- France 2019 Hejblum B, Lhomme E, Thiébaut R, Richert L, VICI: a Shiny app for accurate estimation of Vaccine Induced Cellular Immunogenicity with bivariate modeling, *UseR! 2019*, Toulouse.
- France 2018* Hejblum B, Gauthier M, Thiébaut R, Agniel D, Controlling type-I error and false discoveries in RNA-seq differential analyses through a variance component score test, *Bioinfo-Biostat GenoToul Annual Day*, Toulouse.
- Spain 2018 Hejblum B, Agniel D, A variance component score test for RNA-seq differential analysis in vaccine trials, *29th International Biometric Conference*, Barcelona.
- UK 2017* Hejblum B, Alkhassim, Gottardo, Caron, Thiébaut, Dirichlet Process Mixtures of Multivariate Skew t-distributions for Unsupervised Clustering of Cell Populations from Flow-Cytometry Data, *BSU invited Seminar*, Cambridge.
- Spain 2017 Hejblum B, Agniel D, Type I error and false discovery rate control in RNA-seq differential analyses through a variance component score test, *38th Annual Conference of the International Society for Clinical Biostatistics*, Vigo.
- USA 2016 Hejblum B, Agniel D, Time-course Gene Set Analysis of longitudinal RNA-seq data, *ENAR 2016 Spring Meeting*, Austin (TX).
- Italy 2014 Hejblum B, Caron F, Thiébaut R, Bayesian analysis of time-course flow cytometry data with Dirichlet process mixture modeling, *27th International Biometric Conference*, Florence.

- France 2014 Hejblum B, Genuer R, Thiébaut R, Variable selection in high-dimensional dataset: comparison of sPLS with other approaches in an HIV vaccine trial, *8th International Conference on Partial Least Squares and Related Methods*, Paris.
- France 2014* Hejblum B, Caron F, Thiébaut R, Bayesian nonparametric modeling of flow cytometry data with Dirichlet process mixtures, *Ph.D. students working group of the LSTA (Laboratoire de Statistique Théorique et Appliquée) in Paris 6 University*, Paris.
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- Norway 2012 Hejblum B, Skinner J, Thiébaut R, Application of Gene Set Analysis of Time-Course gene expression in a HIV vaccine trial, *33rd Annual Conference of the International Society for Clinical Biostatistics*, Bergen.

▷ [Written communications](#)

- USA 2015 Hejblum B, Cai T, Weber G, Probabilistic Patient Linkage Algorithms for PIC-SURE, *BD2K all Hands Meeting 2015*, Bethesda (MD).
- UK 2014 Hejblum B, Caron F, Thiébaut R, Hierarchical Analysis of Time-Course Flow Cytometry Data with Dirichlet Process Mixture Modeling, *Medical Research Council Conference on Biostatistics in celebration of the MRC Biostatistics Unit's centenary year*, Cambridge.