Julien Gagneur

Born 4 Sep 1977 in Avignon, France
French nationality

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Google scholar citations / h-index
ORCID

8,590 / 39
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Education

École Centrale Paris (F)
2004

PhD in Applied Mathematics
Algorithms for the decomposition of biomolecular networks

École Normale Supérieure de Cachan (F)
2000

Master in Applied Mathematics
Machine Learning and Signal Processing

École Centrale Paris (F)
2000

'Grande École' Engineering Degree
Major in Applied Mathematics

Positions

Technical University of Munich
Munich (D)
Feb 2020 - Today

Full Professor
Computational Molecular Medicine
Faculty of Informatics
Secondary affiliation at the Faculty of Medicine

Helmholtz Center Munich
Munich (D)
Nov 2019 - Today

Group leader
Institute of Computational Biology

Technical University of Munich
Munich (D)
Jan 2016 - Jan 2020

Assistant Professor (Tenure track)
Computational Biology
Faculty of Informatics

Gene Center, LMU
Munich (D)
Jul 2012 - Dec 2015

Group leader
Computational Genomics
Department of Biochemistry

European Molecular Biology Laboratory
Heidelberg (D)
Jan 2008 - Jun 2012
Jun 2005 - Dec 2007

Staff scientist
Genome Biology Unit
Lars Steinmetz laboratory (functional genomics)
High-throughput functional genomics center

Cellzome AG
Biotech, Heidelberg (D)
Jul 2002 - May 2005

Research scientist
PhD student (until May 2004)

Lion Bioscience
Bioinformatic company, Heidelberg (D)
Sep 2001 - Jun 2002

PhD student

Epigene Biotech start-up, Paris (F) Oct 2000 - Aug 2001	**Bioinformatician**

Teaching

TUM, Munich (D) 2021 - today 1 semester / year (67.5 hours)	**Machine Learning for Regulatory Genomics** Master students in Bioinformatics, CS, Physics
TUM, Munich (D) 2017 - today 1 semester / year (67.5 hours)	**Statistical Methods for Systems Genetics** Master students in Bioinformatics, CS, Physics
TUM, Munich (D) 2016 - today 1 semester / year (67.5 hours)	**Data Analysis and Visualization in R** Data science good practices: get and organize data, visualize and draw hypotheses, hypothesis testing, regression Bachelor and Master students in Bioinformatics, CS, Medicine, Business and Economy
LMU, then TUM, Munich (D) 2013 - 2018 1 semester / year (84 hours)	**Statistical modeling and machine learning** Fundamentals of machine learning from a probabilistic point of view Master students in Bioinformatics, Physics, and Statistics
QBM, Munich (D) 2014-today 2 x 4 hours / year	**High-dimensional data analysis + quantitative genetics** PhD students of the graduate School QBM
LMU, Munich (D) 2013 1 semester / year (24 hours)	**Transcriptional regulation** Experiments and quantitative models. Master students in Bioinformatics and Biochemistry
École Centrale Paris (F) 2005 - 2007 20 hours / year	**Mathematical modeling of metabolism** Enzyme kinetics and Flux Balance Analysis Master students in Applied Mathematics
Workshops and 'summer' schools 2013 - today Typically 3-5 hours each	2017 Summer school e:Med SEED (on diagnosis of rare disorders by RNA-seq) 2015 Winterschool *Genetic and Clinical Epidemiology*, Munich; 2013 RNASeq analysis using BioConductor, Recife; 2013 EMS Autumn School on Computational Aspects of Gene Regulation, Będlewo

Community

Journal reviewer	American Journal of Human Genetics, Bioinformatics, BMC Bioinformatics, eLife, Genome Biology, Molecular Systems Biology, Nature Communications, Nature Genetics, Nucleic Acids Research, PLoS Computational Biology, PLoS Genetics, Science

Conference organizer / scientific committee	*Kipoi Monthly Seminar*, Online seminar series, Since Oct 2020; *European Bioconductor Developer Meeting*, Munich, 2018; *International Conference on Systems Biology*, Lyon, 2018; *European Conference on Computational Biology*, Athens, 2018; *Statistical Methods for Post Genomic Data*, Munich, 2015; *Systems Genetics Workshop* at ICSB conference, Heidelberg, 2011; *Statistical and dynamical models in biology and medicine*, Heidelberg 2010, Göttingen 2011, Stuttgart 2012, and Dresden 2013
Open source software	We are frequently contributing open source software, and often to the Bioconductor project (listed at `https://www.gagneurlab.in.tum.de/index.php?id=31`). We are also a driving group behind the model repository for genomics Kipoi (`https://kipoi.org`)

External funding

€ 965,100 out of € 20,000,000 (2020-2025)	GHGA, German Human Genome-Phenome Archive, Deutsche Forschung Gemeinschaft. Coordinated by Oliver Stegle, DKFZ.
€ 295,620 (2020-2023)	perMIM, Personalized medicine for mitochondrial diseases, German Federal Ministry of Education and Research. Coordinated by Holger Prokisch, TUM.
€ 234,883 (2020-2023)	CLINSPECT-M. Clinical Mass Spectrometry Center Munich, German Federal Ministry of Education and Research. Coordinated by Bernhard Kuester, TUM.
€ 273,500 (2020-2022)	Research network in Computational Life Science VALE, German Federal Ministry of Education and Research. Cooperation with Matthias Heinig, HMGU and Stephan Hutter, Munich Leukemia Labor.
€ 188,000 out of € 11,718,000 (2019-2023)	SFB/Transregio 267: non-coding RNA in the cardiovascular system), Deutsche Forschung Gemeinschaft. Coordinated by Stefan Engelhardt, TUM, and Stefanie Dimmeler, Frankfurt University
€ 309,000 out of € 847,000 (as coordinator, 2019-2023)	Research network in Computational Life Science MERGE (Model Exchange for Regulatory GEnomics), German Federal Ministry of Education and Research. Cooperation with Oliver Stegle, DKFZ and Michael Ziller, MPI for Psychiatry.
€ 270,000 out of € 3,032,000 (2018-2021)	Research network in Machine Learning MechML (From Machine Learning to mechanistic modeling: Functional predictions in genomics and medicine), German Federal Ministry of Education and Research. Coordinated by Fabian Theis, Helmholtz Center, and Oliver Stegle, DKFZ.
€ 163,000 out of € 451,000 (as coordinator, 2017-2019)	Research network in Systems medicine AbCD-Net (Aberrant transcriptome influencing risk of Common Diseases), *e:Med*, German Federal Ministry of Education and Research. Cooperation with Heribert Schunkert, German Heart Center and Michael Ziller, MPI for Psychiatry.

€ 50,000 (2017-2019)	KONWIHR Computational methods for mapping of regulatory elements from large-scale RNA-sequencing compendia, High-Performance Computing grant from the Kompetenznetzwerk für wissenschaftliches Höchstleistungsrechnen in Bayern.
€ 6,000 (2017-2018)	Travel grant for scientific exchange with the Steinmetz lab, Stanford University, *e:Med*, BaCaTec Bavaria California Technology.
€ 241,000 (2015-2018)	Innovation Action SOUND (Statistical multi-Omics UNDerstanding of Patient Samples), *Horizon 2020*, European Commission. I was coordinating one work package. Topic: Statistical methods integrating transcriptome, metabolome, and organism phenotypes for the analysis of genetic disorders.
€ 449,000 out of € 2,000,000 (as coordinator, 2014-2018)	Junior network in Systems medicine mitOmics (Identifying molecular bases of mitochondrial disorders by personalized omics), *e:Med*, German Federal Ministry of Education and Research. Cooperation with Fabiana Perocchi, Helmholtz Zentrum (mitochondrial biology) and Tobias Haack, TUM (human genetics).

Invited lectures and oral presentations in conferences

1. Pinpointing disease-causing regulatory genetic variants by multi-omics and machine learning, IBSE 3rd International Symposium, IIT Madras, Chennai, Jan 2022
2. Detection of aberrant splicing events in RNA-seq data, NEC lab Europe, Heidelberg, Jan 2022
3. What has AI to do with it? AI in genomics: the present and the future, Annual meeting of the European Society of Human Genetics (ESHG), Vienna, Aug 2021
4. Genetic diagnosis of Mendelian disorders using RNA sequencing, Boston Children's Hospital, Boston, Jan 2021
5. Cracking the regulatory code with Deep Learning, VIB (Vlaams Instituut voor Biotechnologie), Ghent, Oct 2020
6. Pinpointing disease-causing regulatory genetic variants by multi-omics and machine learning, Institute IMAGINE, APHP University Paris, Paris, Jan 2020
7. Modeling the regulatory code: From basic biology to clinical research, University of Saarbruecken, Germany, Jan 2020
8. Pinpointing disease-causing regulatory genetic variants by multi-omics and machine learning, EMBO workshop Precision Health: Molecular Basis, Technology and Digital Health, Heidelberg, Nov 2019
9. Pinpointing disease-causing regulatory genetic variants by multi-omics and machine learning, Curie Institute, Paris, Oct 2019
10. Modeling the regulatory code: From basic biology to clinical research, Institute of Pharmacy and Molecular Biotechnology, University of Heidelberg, Germany, Apr 2019
11. *When the outlier is the signal: Denoising autoencoders to pinpoint causes of rare diseases, SMPGD 2019 Statistical Methods for Postgenomic Data, Barcelona, Spain, Jan 2019
12. Kipoi: Accelerating the community exchange and reuse of predictive models for regulatory genomics, Center for Genomic Regulation, Barcelona, Spain, Jan 2019
13. Pinpointing disease-causing regulatory genetic variants by multi-omics and machine learning, Universitätsklinikum, Tübingen, Germany, Dec 2018
14. Pinpointing disease-causing regulatory genetic variants by multi-omics and machine learning, Symposium Computational Biology, now and then, Helmholtz Zentrum, Munich, Germany, Nov 2018
15. Pinpointing disease-causing regulatory genetic variants by multi-omics and machine learning, Roche Advanced Analytics Network (RAAN) day, Roche Diagnostics, Mannheim, Germany, Nov 2018
16. * Kipoi: Accelerating the community exchange and reuse of predictive models for regulatory genomics, ASHG 18, annual meeting of the American Society of Human Genetics, San Diego, USA, Oct 2018
17. Pinpointing disease-causing regulatory genetic variants by multi-omics and machine learning, Department of Genetics, University of Stanford, USA, Oct 2018
18. Deciphering the gene regulatory code: from modelling to applications to genetic diseases, University of Basel, Switzerland, Apr 2018
19. Cracking the gene regulatory code: from modelling to applications to genetic diseases, Technical University of Munich, Germany, Mar 2018
20. Proteome- and transcriptome-wide analysis of human tissues reveals genetic determinants of protein expression, Genomic Regulation 2018, Haute-Nendaz, Switzerland, Mar 2018
21. Genetic basis of gene regulation: Genome-wide models and applications to diagnosis, Max Planck Institute for Biophysical Chemistry, Göttingen, Germany, Nov 2017

22. * Genetic diagnosis of rare disorders by multi-omics analysis, EMBO | EMBL Symposium: From Single- to Multiomics: Applications and Challenges in Data Integration, Heidelberg, Germany, Nov 2017
23. Genetic basis of gene regulation: genome-wide models and applications to diagnosis, Institute of Computational Biology, Helmholtz Zentrum, Munich, Germany, Jul 2017
24. Genetic basis of gene regulation: genome-wide models and applications to diagnosis, Seminar series C3BI of Institut Pasteur, Paris, France, Jun 2017
25. Genetic basis of gene regulation: genome-wide models and applications to diagnosis, Luxembourg Centre for Systems Biomedicine, Luxembourg, Mar 2017
26. * Sequence features explain most of the mRNA stability variation across genes in yeast, Systems Biology: Global regulation of genex expression, Cold Spring Harbor Laboratory, USA, Mar 2017
27. Genetic basis of gene regulation: genome-wide models and applications to diagnosis, MPI Psychiatry, Munich, Germany, Dec 2016
28. Modeling gene expression from genetic data, Molecular Life of Stem Cells, Ljubljana, Slovenia, Sep 2016
29. Novel approaches for genetic diagnosis of rare disorders, Latsis Symposium on personalized medicine, ETH, Zürich, Switzerland, Jun 2016
30. * Genome-wide generalized additive models, SMPGD 2016 Statistical Methods for Postgenomic Data, Lille, France, Feb 2016
31. * Genetic determinants of RNA metabolism in fission yeast (and a bit in human), Ringberg conference of the gene center of the LMU and the BioM Biotech Cluster Development GmbH and the Biocluster, Ringberg, Germany, Jan 2016
32. Statistical Model for Signal Detection and Bias Correction in ChIP-Seq Data, University of Lyon I, Lyon, France, Nov 2015
33. * Determinants of RNA metabolism in the S. pombe genome, LyonSysBio 2015, Lyon, France, Nov 2015
34. Identification of novel causal genes in rare diseases - A Bayesian approach, e:Med 2015, DKFZ, Heidelberg, Germany, Oct 2015
35. Systems genetics of gene regulation: Two studies, University of Mainz, Germany, Oct 2015
36. * Determinants of RNA metabolism in the Schizosaccharomyces pombe genome, Statistical Modeling of Epigenomics and Gene Regulation, Harvard, Aug 2015
37. Negative feedback buffers effects of regulatory variants & Determinants of RNA metabolism in the S. pombe genome University of Edinburgh, Edinburgh, UK, Jun 2015
38. Negative feedback buffers effects of regulatory variants & Determinants of RNA metabolism in the S. pombe genome European Bioinformatics Institute, Hinxton, UK, Jun 2015
39. Statistical Model for Signal Detection and Bias Correction in ChIP-Seq Data, European Bioconductor Developer Meeting, EMBL, Heidelberg, Germany, Jan 2015
40. * Negative feedback buffers effects of regulatory variants EMBO Conference "From Functional Genomics to Systems Biology", Heidelberg, Germany, Nov 2014
41. Genome-wide models of gene expression, Max Planck Institute of Biochemistry, Munich, Germany, Aug 2014
42. Exploiting genotype-environment interactions to identify causal mediating pathways, 4th Workshop of Genetic Epidemiology, Grainau, Germany, May 2014
43. Of cis, trans and feedback regulation: Dissecting local regulation in yeast, Systems Genetics and Evolution of non-human (model) organisms, Ascona, Switzerland, May 2014

44. Of cis, trans and feedback regulation: Dissecting local regulation in yeast, SMPGD 2014 Statistical Methods for Postgenomic Data, Paris, France, Jan 2014
45. Course on RNASeq analysis using BioConductor, Satellite of X-meeting BSB 2013, Recife, Brazil, Nov 2013
46. Genome Annotation, and Systems genetics: Of genotype, gene expression and phenotypes, EMS Autumn School on Computational Aspects of Gene Regulation, Będlewo, Poland, Oct 2013
47. Inferring Causal Molecular Intermediates from Omics Data in the Context of Genetic and Environmental Variations, Workshop on Statistical Methods for Bioinformatics, Göttingen, Germany, Oct 2013
48. Model-based Gene Set Analysis and Systems genetics with environment, ETH, Seminar for statistics, Zürich, Switzerland, Sep 2013
49. * Inferring Causal Molecular Intermediates from Omics Data in the Context of Genetic and Environmental Variations, Workshop on Statistical Genomics and Data Integration for Personalized Medicine, Ascona, Switzerland, May 2013
50. Model-based Gene Set Analysis, 5th International Conference of the ERCIM on computing and statistics (ERCIM 2012), Oviedo, Spain, Dec 2012
51. * Environmentally persistent genetic associations with gene expression reveal pathways mediating genetic signals to phenotype EMBO Conference "From Functional Genomics to Systems Biology", Heidelberg, Germany, Nov 2012
52. * Joint models of gene expression and global phenotypes in the context of genetic and environmental variations, 22nd Annual Workshop on Mathematical and Statistical Aspects of Molecular Biology, Berlin, Germany, Apr 2012
53. * Model-based Gene Set Analysis, SMPGD 2012 Statistical Methods for Postgenomic Data, Lyon, France, Jan 2012
54. Genome-wide models of gene expression, German Cancer Research Center (DKFZ), Heidelberg, Germany, Nov 2011
55. Antisense transcription increases gene expression variability, Biotec institute, Dresden, Germany, Mar 2011
56. Of bidirectional promoters and antisense transcription, Department of Biology, Columbia University, New-York, USA, Mar 2011
57. Of bidirectional promoters and antisense transcription, Max Planck Institute for Molecular Genetics, Berlin, Germany, Nov 2010
58. Of bidirectional promoters and antisense transcription, Charité, Universit?tsmedizin Berlin, Germany, Apr 2010
59. Technological advances in genomics and their impact for personalized medicine, Oberwolfach Workshop Statistical Issues in Prediction: what can be learned for individualized predictive medicine?, Oberwolfach, Germany, Jan 2010
60. * genomeIntervals and Model-Based Gene-Set Analysis, Bioconductor, European Developers' Meeting 2010, Manchester, UK, Jan 2010
61. Gene list analysis by causative sets identification, Workshop Statistical Methods in Bioinformatics, Munich, Germany
62. Genome-wide analysis of allele-specific expression, Max Planck Institute for Molecular Genetics, Berlin, Germany, Feb 2008
63. Algorithms for the decomposition of biomolecular networks, Computer Science and Artificial Intelligence Laboratory, MIT, Boston, USA, 2006

64. Modular decomposition of protein-protein interaction networks, CNRS Marseille-Luminy, Marseille, France, 2004

* contributed talk.

Publications

[1] Francisca Rojas Ringeling, Shounak Chakraborty, Caroline Vissers, Derek Reiman, Akshay M. Patel, Ki-Heon Lee, Ari Hong, Chan-Woo Park, Tim Reska, **Julien Gagneur**, Hyeshik Chang, Maria L. Spletter, Ki-Jun Yoon, Guo-li Ming, Hongjun Song, and Stefan Canzar. Partitioning RNAs by length improves transcriptome reconstruction from short-read RNA-seq data. *Nature Biotechnology*, pages 1–10, 2022.

[2] Žiga Avsec, Melanie Weilert, Avanti Shrikumar, Sabrina Krueger, Amr Alexandari, Khyati Dalal, Robin Fropf, Charles McAnany, **Julien Gagneur**, Anshul Kundaje, and Julia Zeitlinger. Base-resolution models of transcription-factor binding reveal soft motif syntax. *Nature Genetics*, 53(3):354–366, 2021.

[3] Alexander Karollus, Žiga Avsec, and **Julien Gagneur**. Predicting mean ribosome load for 5'utr of any length using deep learning. *PLOS Computational Biology*, 17(5):e1008982, 2021.

[4] Christian Mertes, Ines F. Scheller, Vicente A. Yépez, Muhammed H. Çelik, Yingjiqiong Liang, Laura S. Kremer, Mirjana Gusic, Holger Prokisch, and **Julien Gagneur**. Detection of aberrant splicing events in RNA-seq data using FRASER. *Nature Communications*, 12(1):529, 2021.

[5] Vicente A. Yépez, Christian Mertes, Michaela F. Müller, Daniela Klaproth-Andrade, Leonhard Wachutka, Laure Frésard, Mirjana Gusic, Ines F. Scheller, Patricia F. Goldberg, Holger Prokisch, and **Julien Gagneur**. Detection of aberrant gene expression events in RNA sequencing data. *Nature Protocols*, 16(2):1276–1296, 2021.

[6] David R. Murdock, Hongzheng Dai, Lindsay C. Burrage, Jill A. Rosenfeld, Shamika Ketkar, Michaela F. Müller, Vicente A. Yépez, **Julien Gagneur**, Pengfei Liu, Shan Chen, Mahim Jain, Gladys Zapata, Carlos A. Bacino, Hsiao-Tuan Chao, Paolo Moretti, William J. Craigen, Neil A. Hanchard, and Brendan Lee. Transcriptome-directed analysis for Mendelian disease diagnosis overcomes limitations of conventional genomic testing. *The Journal of Clinical Investigation*, 131(1), 2021.

[7] Benjamin Krämer, Rainer Knoll, Lorenzo Bonaguro, Michael ToVinh, Jan Raabe, Rosario Astaburuaga-García, Jonas Schulte-Schrepping, Kim Melanie Kaiser, Gereon J. Rieke, Jenny Bischoff, Malte B. Monin, Christoph Hoffmeister, Stefan Schlabe, Elena De Domenico, Nico Reusch, Kristian Händler, Gary Reynolds, Nils Blüthgen, Gudrun Hack, Claudia Finnemann, Hans D. Nischalke, Christian P. Strassburg, Emily Stephenson, Yapeng Su, Louis Gardner, Dan Yuan, Daniel Chen, Jason Goldman, Philipp Rosenstiel, Susanne V. Schmidt, Eicke Latz, Kevin Hrusovsky, Andrew J. Ball, Joe M. Johnson, Paul-Albert Koenig, Florian I. Schmidt, Muzlifah Haniffa, James R. Heath, Beate M. Kümmerer, Verena Keitel, Björn Jensen, Paula Stubbemann, Florian Kurth, Leif E. Sander, Birgit Sawitzki, Janine Altmüller, Angel Angelov, Anna C. Aschenbrenner, Robert Bals, Alexander Bartholomäus, Anke Becker, Matthias Becker, Daniela Bezdan, Michael Bitzer, Conny Blumert, Ezio Bonifacio, Peer Bork, Bunk Boyke, Helmut Blum, Nicolas Casadei, Thomas Clavel, Maria Colome-Tatche, Markus Cornberg, Inti Alberto De La Rosa VelÃązquez, Andreas Diefenbach, Alexander Dilthey, Nicole Fischer, Konrad Förstner, Sören Franzenburg, Julia-Stefanie Frick, Gisela Gabernet, **Julien Gagneur**, Tina Ganzenmueller, Marie Gauder, Janina Geißert, Alexander Goesmann, Siri Göpel, Adam Grundhoff, Hajo Grundmann, Torsten Hain, Frank Hanses, Ute Hehr, André Heimbach, Marius Hoeper, Friedemann Horn, Daniel Hübschmann, Michael Hummel, Thomas Iftner, Angelika Iftner, Thomas Illig, Stefan Janssen, Jörn Kalinowski, René Kallies, Birte Kehr, Andreas Keller, Oliver T. Keppler, Sarah Kim-Hellmuth, Christoph Klein, Michael Knop, Oliver Kohlbacher, Karl Köhrer, Jan Korbel, Peter G. Kremsner, Denise Kühnert, Ingo Kurth, Markus Landthaler, Yang Li, Kerstin U. Ludwig, Oliwia Makarewicz, Federico Marini, Manja Marz, Alice C. McHardy, Christian Mertes, Maximilian Münchhoff, Sven Nahnsen, Markus Nöthen, Francine Ntoumi, Peter Nürnberg, Stephan Ossowski, Jörg Overmann, Silke Peter, Klaus Pfeffer, Isabell Pink, Anna R. Poetsch, Ulrike Protzer, Alfred Pühler, Nikolaus Rajewsky, Markus Ralser, Kristin Reiche, Olaf Rieß, Stephan Ripke, Ulisses Nunes da Rocha, Philip Rosenstiel, Antoine-Emmanuel Saliba, Leif Erik

Sander, Birgit Sawitzki, Simone Scheithauer, Philipp Schiffer, Jonathan Schmid-Burgk, Wulf Schneider, Eva-Christina Schulte, Joachim L. Schultze, Alexander Sczyrba, Mariam L. Sharaf, Yogesh Singh, Michael Sonnabend, Oliver Stegle, Jens Stoye, Fabian Theis, Thomas Ulas, Janne Vehreschild, Thirumalaisamy P. Velavan, Jörg Vogel, Sonja Volland, Max von Kleist, Andreas Walker, Jörn Walter, Dagmar Wieczorek, Sylke Winkler, John Ziebuhr, Anna C. Aschenbrenner, Joachim L. Schultze, and Jacob Nattermann. Early IFN-alpha signatures and persistent dysfunction are distinguishing features of NK cells in severe COVID-19. *Immunity*, 54(11):2650–2669.e14, 2021.

[8] Jun Cheng, Muhammed Hasan Çelik, Anshul Kundaje, and **Julien Gagneur**. MTSplice predicts effects of genetic variants on tissue-specific splicing. *Genome Biology*, 22(1):94, 2021.

[9] Žiga Avsec@, Roman Kreuzhuber, Johnni Israeli, Nancy Xu, Jun Cheng, Avanti Shrikumar, Abhimanyu Banerjee, Daniel S. Kim, Thorsten Beier, Lara Urban, Anshul Kundaje@, Oliver Stegle@, and **Julien Gagneur**@. The Kipoi repository accelerates community exchange and reuse of predictive models for genomics. *Nature Biotechnology*, 2019.

[10] Leonhard Wachutka*, Livia Caizzi*, **Julien Gagneur**@, and Patrick Cramer@. Global donor and acceptor splicing site kinetics in human cells. *eLife*, 2019.

[11] Jun Cheng, Thi Yen Duong Nguyen, Muhammed Hasan Çelik, Žiga Avsec, and **Julien Gagneur**. CAGI5 splicing challenge: Improved exon skipping and intron retention predictions with MMSplice. *Human Mutation*, 2019.

[12] Gökcen Eraslan*, Žiga Avsec*, **Julien Gagneur**@, and Fabian J. Theis@. Deep learning: New computational modeling techniques for genomics. *Nature Reviews Genetics*, 2019.

[13] Jun Cheng, Thi Yen Duong Nguyen, Kamil J Cygan, Muhammed Hasan Çelik, William Fairbrother, Žiga Avsec, and **Julien Gagneur**. Modular modeling improves the predictions of genetic variant effects on splicing. *Genome Biology*, 2019.

[14] Basak Eraslan, Dongxue Wang, Mirjana Gusic, Holger Prokisch, Björn M Hallstrjöm, Mathias Uhlén, Anna Asplund, Fredrik Pontén, Thomas Wieland, Thomas Hopf, Hannes Hahne@, Bernhard Kuster@, and **Julien Gagneur**@. Quantification and discovery of sequence determinants of protein per mRNA amount in 29 human tissues. *Molecular Systems Biology*, 2019.

[15] Dongxue Wang, Basak Eraslan, Thomas Wieland, Björn M Hallstrjöm, Thomas Hopf, Daniel Paul Zolg, Jana Zecha, Anna Asplund, Li-Hua Li, Chen Meng, Martin Frejno, Tobias Schmidt, Karsten Schnatbaum, Mathias Wilhelm, Fredrik Pontén, Mathias Uhlén, **Julien Gagneur**, Hannes Hahne@, and Bernhard Kuster@. A deep proteome and transcriptome abundance atlas of 29 healthy human tissues. *Molecular Systems Biology*, 2019.

[16] Felix Brechtmann, Christian Mertes, Agne Matuseviciute, Vicente A. Yépez, Žiga Avsec, Maximilian Herzog, Daniel M. Bader, Holger Prokisch, and **Julien Gagneur**. OUTRIDER: A Statistical Method for Detecting Aberrantly Expressed Genes in RNA Sequencing Data. *The American Journal of Human Genetics*, 103(6):907–917, 2018.

[17] Beate Hagl, Benedikt D. Spielberger, Silvia Thoene, Sophie Bonnal, Christian Mertes, Christof Winter, Isaac J. Nijman, Shira Verduin, Andreas C. Eberherr, Anne Puel, Detlev Schindler, Jürgen Ruland, Thomas Meitinger, **Julien Gagneur**, Jordan S. Orange, Marielle E. van Gijn, and Ellen D. Renner. Somatic alterations compromised molecular diagnosis of dock8 hyper-ige syndrome caused by a novel intronic splice site mutation. *Scientific Reports*, 8(1):16719, 2018.

[18] Vicente A. Yépez, Laura S. Kremer, Arcangela Iuso, Mirjana Gusic, Robert Kopajtich, Eliška Koňaříková, Agnieszka Nadel, Leonhard Wachutka, Holger Prokisch, and **Julien Gagneur**. OCR-Stats: Robust estimation and statistical testing of mitochondrial respiration activities using Seahorse XF Analyzer. *PLOS ONE*, 13(7):e0199938, 2018.

[19] Georg Stricker, Mathilde Galinier, and **Julien Gagneur**. GenoGAM 2.0: scalable and efficient implementation of genome-wide generalized additive models for gigabase-scale genomes. *BMC Bioinformatics*, 19(1):247, 2018.

[20] Ashiq Hussain, Atefeh Pooryasin, Mo Zhang, Laura F. Loschek, Marco La Fortezza, Anja B. Friedrich, Catherine-Marie Blais, Habibe K Üçpunar, Vicente A. Yépez, Martin Lehmann, Nicolas Gompel, **Julien Gagneur**, Stephan J. Sigrist, and Ilona C. Grunwald Kadow. Inhibition of oxidative stress in cholinergic projection neurons fully rescues aging associated olfactory circuit degeneration in Drosophila. *eLife*, 2018.

[21] Žiga Avsec, Mohammadamin Barekatain, Jun Cheng, and **Julien Gagneur**. Modeling positional effects of regulatory sequences with spline transformations increases prediction accuracy of deep neural networks. *Bioinformatics*, 2017.

[22] Jun Cheng, Kerstin C. Maier, Žiga Avsec, Petra Rus, and **Julien Gagneur**. Cis-regulatory elements explain most of the mRNA stability variation across genes in yeast. *RNA*, 2017.

[23] Hai Wei, Bo Yan, **Julien Gagneur**@, and Barbara Conradt@. Caenorhabditis elegans CES-1 Snail Represses pig-1 MELK Expression To Control Asymmetric Cell Division. *Genetics*, 206(4):2069–2084, 2017.

[24] Laura S. Kremer, Daniel M. Bader, Christian Mertes, Robert Kopajtich, Garwin Pichler, Arcangela Iuso, Tobias B. Haack, Elisabeth Graf, Thomas Schwarzmayr, Caterina Terrile, Eliška Koňaříková, Birgit Repp, Gabi Kastenmüller, Jerzy Adamski, Peter Lichtner, Christoph Leonhardt, Benoit Funalot, Alice Donati, Valeria Tiranti, Anne Lombes, Claude Jardel, Dieter Gläser, Robert W. Taylor, Daniele Ghezzi, Johannes A. Mayr, Agnes Rötig, Peter Freisinger, Felix Distelmaier, Tim M. Strom, Thomas Meitinger, **Julien Gagneur**@, and Holger Prokisch@. Genetic diagnosis of Mendelian disorders via RNA sequencing. *Nature Communications*, 8:15824 EP –, 2017.

[25] Maximilian Witzel, Daniel Petersheim, Yanxin Fan, Ehsan Bahrami, Tomas Racek, Meino Rohlfs, Jacek Puchałka, Christian Mertes, **Julien Gagneur**, Christoph Ziegenhain, Wolfgang Enard, Asbjørg Stray-Pedersen, Peter D Arkwright, Miguel R Abboud, Vahid Pazhakh, Graham J Lieschke, Peter M Krawitz, Maik Dahlhoff, Marlon R Schneider, Eckhard Wolf, Hans-Peter Horny, Heinrich Schmidt, Alejandro A Schäffer, and Christoph Klein. Chromatin-remodeling factor SMARCD2 regulates transcriptional networks controlling differentiation of neutrophil granulocytes. *Nature Genetics*, 49(5):742–752, 2017.

[26] Georg Stricker, Alexander Engelhardt, Daniel Schulz, Matthias Schmid, Achim Tresch, and **Julien Gagneur**. GenoGAM: Genome-wide generalized additive models for ChIP-seq analysis. *Bioinformatics*, 2017.

[27] **Julien Gagneur**, Caroline Friedel, Volker Heun, Ralf Zimmer, and Burkhard Rost. Bioinformatics advances biology and medicine by turning big data troves into knowledge. *Informatik-Spektrum*, 40(2):153–160, 2017.

[28] Margaux Michel*, Carina Demel*, Benedikt Zacher, Björn Schwalb, Stefan Krebs, Helmut Blum, **Julien Gagneur**@, and Patrick Cramer@. TT-seq captures enhancer landscapes immediately after T cell stimulation. *Molecular Systems Biology*, 2017.

[29] Samira Ait-El-Mkadem, Manal Dayem-Quere, Mirjana Gusic, Annabelle Chaussenot, Sylvie Bannwarth, Bérengère François, Emmanuelle C. Genin, Konstantina Fragaki, Catharina L.M. Volker-Touw, Christelle Vasnier, Valérie Serre, Koen L.I. van Gassen, Françoise Lespinasse, Susan Richter, Graeme Eisenhofer, Cécile Rouzier, Fanny Mochel, Anne De Saint-Martin, Marie-Thérèse Abi Warde, Monique G.M. de Sain-van der Velde, Judith J.M. Jans, Jeanne Amiel, Ziga Avsec, Christian Mertes, Tobias B. Haack, Tim Strom, Thomas Meitinger, Penelope E. Bonnen, Robert W. Taylor, **Julien Gagneur**, Peter M. van Hasselt,

Agnès Rötig, Agnès Delahodde, Holger Prokisch, Sabine A. Fuchs, and Véronique Paquis-Flucklinger. Mutations in MDH2, Encoding a Krebs Cycle Enzyme, Cause Early-Onset Severe Encephalopathy. *The American Journal of Human Genetics*, 100(1):151–159, 2017.

[30] Benedikt Zacher@, Margaux Michel, Björn Schwalb, Patrick Cramer, Achim Tresch@, and **Julien Gagneur**@. Accurate Promoter and Enhancer Identification in 127 ENCODE and Roadmap Epigenomics Cell Types and Tissues by GenoSTAN. *PLOS ONE*, 12(1):e0169249, 2017.

[31] Leonhard Wachutka and **Julien Gagneur**. Measures of RNA metabolism rates: Toward a definition at the level of single bonds. *Transcription*, 8(2):75–80, 2017.

[32] Saumya Gupta, Aparna Radhakrishnan, Rachana Nitin, Pandu Raharja-Liu, Gen Lin, Lars M Steinmetz, **Julien Gagneur**, and Himanshu Sinha. Meiotic Interactors of a Mitotic Gene TAO3 Revealed by Functional Analysis of its Rare Variant. *G3*, 2016.

[33] Björn Schwalb, Margaux Michel, Benedikt Zacher, Katja Frühauf, Carina Demel, Achim Tresch, **Julien Gagneur**@, and Patrick Cramer@. TT-seq maps the human transient transcriptome. *Science*, 352(6290):1225–8, 2016.

[34] Philipp Eser, Leonhard Wachutka, Kerstin C Maier, Carina Demel, Mariana Boroni, Srignanakshi Iyer, Patrick Cramer@, and **Julien Gagneur**@. Determinants of RNA metabolism in the Schizosaccharomyces pombe genome. *Molecular systems biology*, 12(2):857, 2016.

[35] Julia Glas, Sebastian Dümcke, Benedikt Zacher, Don Poron, **Julien Gagneur**, and Achim Tresch. Simultaneous characterization of sense and antisense genomic processes by the double-stranded hidden Markov model. *Nucleic Acids Research*, 44(5):e44–e44, 2016.

[36] Tobias B. Haack, Christian Staufner, Marlies G. Köpke, Beate K. Straub, Stefan Kölker, Christian Thiel, Peter Freisinger, Ivo Baric, Patrick J. McKiernan, Nicola Dikow, Inga Harting, Flemming Beisse, Peter Burgard, Urania Kotzaeridou, Joachim Kühr, Urban Himbert, Robert W. Taylor, Felix Distelmaier, Jerry Vockley, Lina Ghaloul-Gonzalez, Johannes Zschocke, Laura S. Kremer, Elisabeth Graf, Thomas Schwarzmayr, Daniel M. Bader, **Julien Gagneur**, Thomas Wieland, Caterina Terrile, Tim M. Strom, Thomas Meitinger, Georg F. Hoffmann, and Holger Prokisch. Biallelic Mutations in NBAS Cause Recurrent Acute Liver Failure with Onset in Infancy. *The American Journal of Human Genetics*, 7, 2015.

[37] S Gupta, A Radhakrishnan, R.L. Pandu, Gen Lin, LM Steinmetz, **Julien Gagneur**, and Himanshu Sinha. Temporal expression profiling identifies pathways mediating effect of causal variant on phenotype. *PLoS Genetics*, 11, 2015.

[38] Daniel M Bader, Stefan Wilkening, Gen Lin, Manu M Tekkedil, Kim Dietrich, Lars M Steinmetz, and **Julien Gagneur**. Negative feedback buffers effects of regulatory variants. *Molecular systems biology*, 11:785, 2015.

[39] Benedikt Zacher, Michael Lidschreiber, Patrick Cramer, **Julien Gagneur**@, and Achim Tresch@. Annotation of genomics data using bidirectional hidden Markov models unveils variations in Pol II transcription cycle. *Molecular systems biology*, 10(12):768, 2014.

[40] Aatish Bhatia, Anupama Yadav, **Julien Gagneur**, Chenchen Zhu, Lars M Steinmetz, Gyan Bhanot, and Himanshu Sinha. Yeast Growth Plasticity Is Regulated by Environment Specific Multi-QTL Interactions. *G3*, 2014.

[41] Raeka S Aiyar, Maria Bohnert, Stéphane Duvezin-Caubet, Cécile Voisset, **Julien Gagneur**, Emilie S Fritsch, Elodie Couplan, Karina von der Malsburg, Charlotta Funaya, Flavie Soubigou, Florence Courtin, Sundari Suresh, Roza Kucharczyk, Justine Evrard, Claude Antony, Robert P St Onge, Marc Blondel, Jean-Paul di Rago, Martin van der Laan, and Lars M Steinmetz. Mitochondrial protein sorting as a therapeutic target for ATP synthase disorders. *Nature communications*, 5:5585, 2014.

[42] Stefan Wilkening, Gen Lin, Émilie S Fritsch, Manu M Tekkedil, Simon Anders, Raquel Kuehn, Michelle Nguyen, Raeka S Aiyar, Michael Proctor, Nikita A Sakhanenko, David J Galas, **Julien Gagneur**, Adam Deutschbauer, and Lars M Steinmetz. An Evaluation of High-Throughput Approaches to QTL Mapping in Saccharomyces cerevisiae. *Genetics*, 2013.

[43] Daniel Schulz, Bjoern Schwalb, Anja Kiesel, Carlo Baejen, Phillipp Torkler, **Julien Gagneur**, Johannes Soeding, and Patrick Cramer. Transcriptome Surveillance by Selective Termination of Noncoding RNA Synthesis. *Cell*, 155(5):1075–1087, 2013.

[44] **Julien Gagneur***, Oliver Stegle*, Chenchen Zhu, Petra Jakob, Manu M Tekkedil, Raeka S Aiyar, Ann-Kathrin Schuon, Dana Pe'er, and Lars M Steinmetz. Genotype-environment interactions reveal causal pathways that mediate genetic effects on phenotype. *PLoS Genetics*, 9(9):e1003803, 2013.

[45] Jonathan J M Landry, Paul Theodor Pyl, Tobias Rausch, Thomas Zichner, Manu M Tekkedil, Adrian M Stütz, Anna Jauch, Raeka S Aiyar, Gregoire Pau, Nicolas Delhomme, **Julien Gagneur**, Jan O Korbel, Wolfgang Huber, and Lars M Steinmetz. The genomic and transcriptomic landscape of a HeLa cell line. *G3*, 3(8):1213–24, 2013.

[46] Stefan Wilkening, Manu M Tekkedil, Gen Lin, Émilie S Fritsch, Wu Wei, **Julien Gagneur**, David W Lazinski, Andrew Camilli, and Lars M Steinmetz. Genotyping 1000 yeast strains by next-generation sequencing. *BMC Genomics*, 14(1):90, 2013.

[47] Fernando Izquierdo-Carrasco, **Julien Gagneur**, and Alexandros Stamatakis. Trading Memory for Running Time in Phylogenetic Likelihood Computations. *2012 Bioinformatics conference, Vilamoura, Portugal*, 2012.

[48] Maïlis Bietenhader, Alexandre Martos, Emmanuel Tetaud, Raeka S Aiyar, Carole H Sellem, Roza Kucharczyk, Sandra Clauder-Münster, Marie-France Giraud, François Godard, Bénédicte Salin, Isabelle Sagot, **Julien Gagneur**, Michelle Déquard-Chablat, Véronique Contamine, Sylvie Hermann-Le Denmat, Annie Sainsard-Chanet, Lars M Steinmetz, and Jean-Paul di Rago. Experimental relocation of the mitochondrial ATP9 gene to the nucleus reveals forces underlying mitochondrial genome evolution. *PLoS Genetics*, 8(8):e1002876, 2012.

[49] Sebastian Bauer, Peter N Robinson, and **Julien Gagneur**. Model-based gene set analysis for Bioconductor. *Bioinformatics*, 27(13):1882–1883, 2011.

[50] Elodie Couplan, Raeka S Aiyar, Roza Kucharczyk, Anna Kabala, Nahia Ezkurdia, **Julien Gagneur**, Robert P St Onge, Bénédicte Salin, Flavie Soubigou, Marie Le Cann, Lars M Steinmetz, Jean-Paul di Rago, and Marc Blondel. A yeast-based assay identifies drugs active against human mitochondrial disorders. *Proc Natl Acad Sci USA*, 2011.

[51] Zhenyu Xu*, Wu Wei*, **Julien Gagneur***, Sandra Clauder-Münster, Milosz Smolik, Wolfgang Huber, and Lars M Steinmetz. Antisense expression increases gene expression variability and locus interdependency. *Molecular Systems Biology*, 7(1):468, 2011.

[52] Sebastian Bauer*, **Julien Gagneur***@, and Peter N Robinson@. GOing Bayesian: model-based gene set analysis of genome-scale data. *Nucleic Acids Research*, 38(11):3523–3532, 2010.

[53] Robert P. Zinzen*, Charles Girardot*, **Julien Gagneur***, Martina Braun, and Eileen E. M. Furlong. Combinatorial binding predicts spatio-temporal cis-regulatory activity. *Nature*, 462(7269):65–70, 2009.

[54] Stephanie A Blandin, Rui Wang-Sattler, Marina Lamacchia, **Julien Gagneur**, Gareth Lycett, Ye Ning, Elena A Levashina, and Lars M Steinmetz. Dissecting the genetic basis of resistance to malaria parasites in Anopheles gambiae. *Science*, 326(5949):147–50, 2009.

[55] **Julien Gagneur**, Himanshu Sinha, Fabiana Perocchi, Richard Bourgon, Wolfgang Huber, and Lars M Steinmetz. Genome-wide allele- and strand-specific expression profiling. *Molecular Systems Biology*, 5(1), 2009.

[56] Zhenyu Xu*, Wu Wei*, **Julien Gagneur**, Fabiana Perocchi, Sandra Clauder-Münster, Jurgi Camblong, Elisa Guffanti, Francoise Stutz, Wolfgang Huber, and Lars M. Steinmetz. Bidirectional promoters generate pervasive transcription in yeast. *Nature*, 457(7232):1033–1037, 2009.

[57] Katarzyna Oktaba, Luis Gutiérrez, **Julien Gagneur**, Charles Girardot, Aditya K Sengupta, Eileen E M Furlong, and Jürg Müller. Dynamic regulation by polycomb group protein complexes controls pattern formation and the cell cycle in Drosophila. *Developmental Cell*, 15(6):877–89, 2008.

[58] Raeka S Aiyar, **Julien Gagneur**, and Lars M Steinmetz. Identification of mitochondrial disease genes through integrative analysis of multiple datasets. *Methods*, 46(4):248–55, 2008.

[59] Yannick Haudry, Hugo Berube, Ivica Letunic, Paul-Daniel Weeber, **Julien Gagneur**, Charles Girardot, Misha Kapushesky, Detlev Arendt, Peer Bork, Alvis Brazma, Eileen E M Furlong, Joachim Wittbrodt, and Thorsten Henrich. 4DXpress: a database for cross-species expression pattern comparisons. *Nucleic Acids Research*, 36(Database issue):D847–53, 2008.

[60] Fabiana Perocchi, Lars J Jensen, **Julien Gagneur**, Uwe Ahting, Christian von Mering, Peer Bork, Holger Prokisch, and Lars M Steinmetz. Assessing systems properties of yeast mitochondria through an interaction map of the organelle. *PLoS Genet*, 2(10):e170, 2006.

[61] **Julien Gagneur***, Lior David*, and Lars M Steinmetz. Capturing cellular machines by systematic screens of protein complexes. *Trends in Microbiology*, 14(8):336–9, 2006.

[62] **Julien Gagneur** and Georg Casari. From molecular networks to qualitative cell behavior. *FEBS Letters*, 579(8):1867–71, 2005.

[63] Tewis Bouwmeester, Angela Bauch, Heinz Ruffner, Pierre-Olivier Angrand, Giovanna Bergamini, Karen Croughton, Cristina Cruciat, Dirk Eberhard, **Julien Gagneur**, Sonja Ghidelli, Carsten Hopf, Bettina Huhse, Raffaella Mangano, Anne-Marie Michon, Markus Schirle, Judith Schlegl, Markus Schwab, Martin A Stein, Andreas Bauer, Georg Casari, Gerard Drewes, Anne-Claude Gavin, David B Jackson, Gerard Joberty, Gitte Neubauer, Jens Rick, Bernhard Kuster, and Giulio Superti-Furga. A physical and functional map of the human TNF-alpha/NF-kappa B signal transduction pathway. *Nature Cell Biology*, 6(2):97–105, 2004.

[64] **Julien Gagneur*** and Steffen Klamt*. Computation of elementary modes: a unifying framework and the new binary approach. *BMC Bioinformatics*, 5:175, 2004.

[65] **Julien Gagneur@**, Roland Krause, Tewis Bouwmeester, and Georg Casari. Modular decomposition of protein-protein interaction networks. *Genome Biol*, 2004.

[66] **Julien Gagneur@**, David B Jackson, and Georg Casari. Hierarchical analysis of dependency in metabolic networks. *Bioinformatics*, 19(8):1027–34, 2003.

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