

Julien Gagneur

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Born 4 Sep 1977 in Avignon, France gagneurlab.in.tum.de
French nationality gagneur@in.tum.de

Education

École Centrale Paris (F) 2004	PhD in Applied Mathematics <i>Algorithms for the decomposition of biomolecular networks</i>
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) Jan 2016 - Today	Assistant Professor 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 Automated decomposition of metabolic networks and application to the analysis of metabolic fluxes
Epigene Biotech start-up, Paris (F) Oct 2000 - Aug 2001	Bioinformatician Design of histological sample database; Gene expression data analysis

Teaching

TUM, Munich (D) 2017 - today 1 semester / year (67.5 hours)	Statistical Methods for Systems Genetics Master students in Bioinformatics and CS
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, conclude (statistical testing). Bachelor and Master students in Bioinformatics and CS
LMU, then TUM, Munich (D) 2013 - today 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 Theory and practical. 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 <i>Genetic and Clinical Epidemiology</i> , Munich; 2013 RNASeq analysis using BioConductor, Recife; 2013 EMS Autumn School on Computational Aspects of Gene Regulation, Będlewo

Community

Journal reviewer	Bioinformatics, BMC Bioinformatics, Molecular Systems Biology, Nature Communications, Nucleic Acids Research, PLoS Computational Biology, PLoS Genetics
Conference organizer / scientific committee	<i>European Bioconductor Developer Meeting</i> , Munich, 2018; <i>International Conference on Systems Biology</i> , Lyon, 2018; <i>European Conference on Computational Biology</i> , Athens, 2018; <i>Statistical Methods for Post Genomic Data</i> , Munich, 2015; <i>Systems Genetics Workshop</i> at ICSB conference, Heidelberg, 2011; <i>Statistical and dynamical models in biology and medicine</i> , Heidelberg 2010, Göttingen 2011, Stuttgart 2012, and Dresden 2013
Open source software	MGSA, genomeIntervals, cellGrowth, GenoGAM, OUTRIDER, STAN (R/Bioconductor), CONCISE, Kipoi, wBuild (python, github)

External funding

- € 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. Formal confirmation pending.
- € 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 AbCDNet (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 am 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, 2014-2017) 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. Deciphering the gene regulatory code: from modelling to applications to genetic diseases, University of Basel, April 2018
2. Cracking the gene regulatory code: from modelling to applications to genetic diseases, Technical University of Munich, March 2018
3. Proteome- and transcriptome-wide analysis of human tissues reveals genetic determinants of protein expression, Genomic Regulation 2018, Haute-Nendaz, March 2018
4. Genetic basis of gene regulation: Genome-wide models and applications to diagnosis, Max Planck Institute for Biophysical Chemistry, Goettingen, November 2017
5. * Genetic diagnosis of rare disorders by multi-omics analysis, EMBO | EMBL Symposium: From Single- to Multiomics: Applications and Challenges in Data Integration, Heidelberg, November 2017
6. Genetic basis of gene regulation: genome-wide models and applications to diagnosis, Institute of Computational Biology, Helmholtz Zentrum, Munich, July 2017
7. Genetic basis of gene regulation: genome-wide models and applications to diagnosis, Seminar series C3BI of Institut Pasteur, Paris, June 2017
8. Genetic basis of gene regulation: genome-wide models and applications to diagnosis, Luxembourg Centre for Systems Biomedicine, Luxembourg, March 2017
9. * Sequence features explain most of the mRNA stability variation across genes in yeast, Systems Biology: Global regulation of gene expression, Cold Spring Harbor Laboratory, March 2017
10. Genetic basis of gene regulation: genome-wide models and applications to diagnosis, MPI Psychiatry, Munich, Dec 2016
11. Modeling gene expression from genetic data, Molecular Life of Stem Cells, Ljubljana, Slovenia, Sep 2016
12. Novel approaches for genetic diagnosis of rare disorders, Latsis Symposium on personalized medicine, ETH, Zürich, Switzerland, Jun 2016
13. * Genome-wide generalized additive models, SMPGD 2016 Statistical Methods for Postgenomic Data, Lille, France, Feb 2016
14. * 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
15. Statistical Model for Signal Detection and Bias Correction in ChIP-Seq Data, University of Lyon I, Lyon, France, Nov 2015
16. * Determinants of RNA metabolism in the *S. pombe* genome, LyonSysBio 2015, Lyon, France, Nov 2015
17. Identification of novel causal genes in rare diseases - A Bayesian approach, e:Med 2015, DKFZ, Heidelberg, Germany, Oct 2015
18. Systems genetics of gene regulation: Two studies, University of Mainz, Germany, Oct 2015
19. * Determinants of RNA metabolism in the *Schizosaccharomyces pombe* genome, Statistical Modeling of Epigenomics and Gene Regulation, Harvard, Aug 2015
20. Negative feedback buffers effects of regulatory variants & Determinants of RNA metabolism in the *S. pombe* genome University of Edinburgh, Edinburgh, UK, Jun 2015
21. Negative feedback buffers effects of regulatory variants & Determinants of RNA metabolism in the *S. pombe* genome European Bioinformatics Institute, Hinxton, UK, Jun 2015

22. Statistical Model for Signal Detection and Bias Correction in ChIP-Seq Data, European Bioconductor Developer Meeting, EMBL, Heidelberg, Germany, Jan 2015
23. * Negative feedback buffers effects of regulatory variants EMBO Conference "From Functional Genomics to Systems Biology", Heidelberg, Germany, Nov 2014
24. Genome-wide models of gene expression, Max Planck Institute of Biochemistry, Munich, Germany, Aug 2014
25. Exploiting genotype-environment interactions to identify causal mediating pathways, 4th Workshop of Genetic Epidemiology, Grainau, Germany, May 2014
26. Of cis, trans and feedback regulation: Dissecting local regulation in yeast, Systems Genetics and Evolution of non-human (model) organisms, Ascona, Switzerland, May 2014
27. Of cis, trans and feedback regulation: Dissecting local regulation in yeast, SMPGD 2014 Statistical Methods for Postgenomic Data, Paris, France, Jan 2014
28. Course on RNASeq analysis using BioConductor, Satellite of X-meeting BSB 2013, Recife, Brazil, Nov 2013
29. Genome Annotation, and Systems genetics: Of genotype, gene expression and phenotypes, EMS Autumn School on Computational Aspects of Gene Regulation, Będlewo, Poland, Oct 2013
30. 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
31. Model-based Gene Set Analysis and Systems genetics with environment, ETH, Seminar for statistics, Zürich, Switzerland, Sep 2013
32. * 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
33. Model-based Gene Set Analysis, 5th International Conference of the ERCIM on computing and statistics (ERCIM 2012), Oviedo, Spain, Dec 2012
34. * 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
35. * 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
36. * Model-based Gene Set Analysis, SMPGD 2012 Statistical Methods for Postgenomic Data, Lyon, France, Jan 2012
37. Genome-wide models of gene expression, German Cancer Research Center (DKFZ), Heidelberg, Germany, Nov 2011
38. Antisense transcription increases gene expression variability, Biotec institute, Dresden, Germany, Mar 2011
39. Of bidirectional promoters and antisense transcription, Department of Biology, Columbia University, New-York, USA, Mar 2011
40. Of bidirectional promoters and antisense transcription, Max Planck Institute for Molecular Genetics, Berlin, Germany, Nov 2010
41. Of bidirectional promoters and antisense transcription, Charité, Universit?tsmedizin Berlin, Germany, Apr 2010

42. 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
43. * genomeIntervals and Model-Based Gene-Set Analysis, Bioconductor, European Developers' Meeting 2010, Manchester, UK, Jan 2010
44. Gene list analysis by causative sets identification, Workshop Statistical Methods in Bioinformatics, Munich, Germany
45. Genome-wide analysis of allele-specific expression, Max Planck Institute for Molecular Genetics, Berlin, Germany, Feb 2008
46. Algorithms for the decomposition of biomolecular networks, Computer Science and Artificial Intelligence Laboratory, MIT, Boston, USA, 2006
47. Modular decomposition of protein-protein interaction networks, CNRS Marseille-Luminy, Marseille, France, 2004

* contributed talk.

Publications

- [1] Vicente A. Yépez, Laura S. Kremer, Arcangela Iuso, Mirjana Gusic, Robert Kopajtich, Eliška Koňářková, 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.
- [2] 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.
- [3] 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*, in press.
- [4] Žiga Avsec, Mohammadamin Barekatin, Jun Cheng, and **Julien Gagneur**. Modeling positional effects of regulatory sequences with spline transformations increases prediction accuracy of deep neural networks. *Bioinformatics*, 2017.
- [5] 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.
- [6] 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.
- [7] Laura S. Kremer, Daniel M. Bader, Christian Mertes, Robert Kopajtich, Garwin Pichler, Arcangela Iuso, Tobias B. Haack, Elisabeth Graf, Thomas Schwarzmayr, Caterina Terrile, Eliška Koňářková, 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.
- [8] Maximilian Witzel, Daniel Petersheim, Yanxin Fan, Ehsan Bahrami, Tomas Racek, Meino Rohlf, 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.
- [9] 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.
- [10] **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.
- [11] 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.

- [12] 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.
- [13] 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.
- [14] Leonhard Wachutka and **Julien Gagneur**. Measures of rna metabolism rates: Toward a definition at the level of single bonds. *Transcription*, page e1257972, 2016.
- [15] 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.
- [16] 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.
- [17] 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.
- [18] 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.
- [19] Tobias B. Haack, Christian Stauffer, 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 Kühn, 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.
- [20] 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.
- [21] 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.
- [22] 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.

- [23] 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.
- [24] 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.
- [25] 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.
- [26] 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.
- [27] **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.
- [28] 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.
- [29] 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.
- [30] Fernando Izquierdo-Carrasco, **Julien Gagneur**, and Alexandros Stamatakis. Trading Memory for Running Time in Phylogenetic Likelihood Computations. *2012 Bioinformatics conference, Vilamoura, Portugal*, 2012.
- [31] Mailis 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.
- [32] Sebastian Bauer, Peter N Robinson, and **Julien Gagneur**. Model-based gene set analysis for Bioconductor. *Bioinformatics*, 27(13):1882–1883, 2011.
- [33] 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.
- [34] 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.

- [35] 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.
- [36] 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.
- [37] 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.
- [38] **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.
- [39] 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.
- [40] 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.
- [41] 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.
- [42] 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.
- [43] 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.
- [44] **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.
- [45] **Julien Gagneur** and Georg Casari. From molecular networks to qualitative cell behavior. *FEBS Letters*, 579(8):1867–71, 2005.
- [46] Tewis Bouwmeester, Angela Bauch, Heinz Ruffner, Pierre-Olivier Angrand, Giovanna Bergamini, Karen Coughton, 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.
- [47] **Julien Gagneur*** and Steffen Klamt*. Computation of elementary modes: a unifying framework and the new binary approach. *BMC Bioinformatics*, 5:175, 2004.
- [48] **Julien Gagneur***@, Roland Krause, Tewis Bouwmeester, and Georg Casari. Modular decomposition of protein-protein interaction networks. *Genome Biol*, 2004.
- [49] **Julien Gagneur***@, David B Jackson, and Georg Casari. Hierarchical analysis of dependency in metabolic networks. *Bioinformatics*, 19(8):1027–34, 2003.

* equal contribution
@ corresponding (also when last)