

Franck Picard

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Academic Positions

2020–Present	CNRS Research Director (DR1) , Lyon, Laboratoire de Biologie et Modélisation de la Cellule (LBMC)
2016–2020	CNRS Research Director (DR2) , Lyon, Laboratoire de Biométrie et Biologie Évolutive (LBBE)
2007–2016	CNRS Research Scientist (CRCN) , Lyon, Laboratoire de Biométrie et Biologie Évolutive (LBBE)
2005–2007	Postdoctoral Fellow , Université d'Évry · Évry, Statistics and Genome Laboratory
2002–2005	PhD Student , Université Paris-Sud / Orsay · Paris, Applied Mathematics and Computer Science

Coordination

2026–Present	Head of SCAI – Artificial Intelligence for Single-Cell Data Analysis , Lyon, Laboratoire de Biologie et Modélisation de la Cellule (LBMC)
2023–2027	Coordinator / PI, AI4scMed , Artificial Intelligence for Single-Cell Based Medicine, PEPR Santé Numérique
2014–2020	Head of the High Dimensional Statistics for Genomics Group , Lyon, Laboratoire de Biométrie et Biologie Évolutive

Education

2014	Habilitation à Diriger des Recherches (HDR) , Université de Lyon
2002–2005	PhD , Université Paris-Sud / Orsay
2001–2002	Master's Degree in Stochastic and Statistical Modelling , Université Paris-Sud / Orsay
1999–2002	Engineering Diploma , Institut National Agronomique Paris-Grignon · Paris

Grants (past 5 years)

2023–2027	AI4scMed , Artificial Intelligence for Single-Cell Based Medicine · PEPR Santé Numérique, Coordinator / PI
2024–2028	SpaceTranscriptomix , Machine Learning Methods to Identify Spatial Gene Networks · ANR, Co-PI with P. Bertolino, CRCL
2019–2024	SingleStatOmics , Statistics and Machine Learning for Single-Cell Genomics · ANR, PI
2021–2022	SpaceNet , Machine Learning for Spatial Transcriptomics · PlaScan, PI: P. Bertolino (CRCL), O. Gandrillon (LBMC)

Selected Publications

- F. Picard, V. Rivoirard, A. Roche, and V. M. Panaretos. PCA for point processes. *The Annals of Statistics*, 54(2):929 – 956, 2026
- A. Ozier-Lafontaine, C. Fourneaux, G. Durif, P. Arsenteva, C. Vallot, O. Gandrillon, S. Gonin-Giraud, B. Michel, and F. Picard. Kernel-based testing for single-cell differential analysis. *Genome Biology*, 25(1):114, 2024
- H. Van Assel, T. Espinasse, J. Chiquet, and F. Picard. A probabilistic graph coupling view of dimension reduction. In *Advances in Neural Information Processing Systems*, volume 35, pages 10696–10708. Curran Associates, Inc., 2022
- A. Bonnet, C. Lacour, F. Picard, and V. Rivoirard. Uniform deconvolution for poisson point processes. *Journal of Machine Learning Research*, 23(194):1–36, 2022
- F. Picard, P. Reynaud-Bouret, and E. Roquain. Continuous testing for Poisson process intensities: a new perspective on scanning statistics. *Biometrika*, 105(4):931–944, 2018

Supervision (past 5 years)

Current PhD Students

2026–2029	A. Galloy , Spatial Processes for Spatial Transcriptomics · 50%, with J.-F. Coeurjolly, LJK Grenoble
2024–2029	M. Guignandon , Sensitivity Analysis for Kernel Testing · 50%, with C. Helbert, ICJ Lyon
2024–2029	P. Rongierias , Self-Supervised Learning for Single-Cell Data Analysis · 25%, with T. Vayer, IRISA Rennes
2024–2027	B. Samson , Bioinformatics Approaches for the Study of Cellular Communications within Endocrine Tumors · 50%, with P. Bertolino, CRCL Lyon
2024–2027	L. Attwood , Kernel Methods for Spatial Data · 50%, with B. Michel, EC Nantes

Former PhD Students

2022–2026	N. Bourarach , Functional Dimension Reduction for Count Data · 30%, with V. Rivoirard and A. Roche, Université Paris-Dauphine
2021–2022	H. van Assel , Statistical Foundations of Stochastic Neighborhood Embedding · 50%, with A. Garivier, ENS Lyon
2019–2023	A. Ozier-Lafontaine , High-Dimensional Testing for Single-Cell Data Analysis · 50%, with B. Michel, EC Nantes
2018–2022	R. Belhakem , Functional Data Analysis · 30%, with V. Rivoirard and A. Roche, Université Paris-Dauphine; now Data Scientist, Quantmetry

Postdocs & Engineers

2023–2026	P. Arsenteva , Development of an R/Python Package for Kernel Testing, with B. Michel, EC Nantes
2023–2024	B. Samson , Development of a Nextflow Pipeline for Visium Data, with G. Durif and O. Gandrillon, ENS Lyon; P. Bertolino, CRCL
2023–2024	P. Lacroix , Calibration of Kernel Testing for Single-Cell Data Analysis, with B. Michel, EC Nantes, and V. Rivoirard, Université Paris-Dauphine; now Assistant Professor, Nantes University
2020–2022	M. Lepetit , Development of a Nextflow Pipeline for scRNA-Seq Data Analysis, with O. Gandrillon, ENS Lyon, and P. Bertolino, CRCL

Scientific Software (current)

pppca	Principal Component Analysis for replicated point-process data (R).
ktest	Kernel-based hypothesis testing (R and Python).
kAOV	Kernel hypothesis testing for general experimental designs (Python).
knit	Kernel Normalised Independence Test (Python).

Teaching (past 5 years)

2022–2026	Machine Learning for Biology , M1 Biosciences, ENS de Lyon (12h)
2022–2024	Statistics , L3 Biosciences, ENS de Lyon (30h)
2022	Model-Based Machine Learning , Master Mathématique en Action (12h)

Scientific and Academic Service (past 5 years)

Institutional Appointments

GdR BIMMM	GdR Bioinformatique Moléculaire: Modélisation et Méthodologie; Scientific Committee.
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Committees

Recruitment	CNRS CPJ (2025); INRAE CR (2023, 2024).
HCERES	President of the MAIAGE evaluation committee (2024).
HDR Reviews	N. Varoquaux (Grenoble, 2025), V. Brault (Grenoble, 2025), B. Hejblum (Bordeaux, 2024), C. Maugys-Rabusseau (Toulouse, 2022), M. Richard (Grenoble, 2022), C. Dalmasso (Évry, 2022), V. Pancaldi (Toulouse, 2021).
HDR Juries	P. Villoutreix (Marseille, 2026), T. Lagache (Institut Pasteur, 2023), R. Azaïs (Lyon, 2022).
PhD Reviews	F. Pittion (Grenoble, 2025), G.-J. Huizin (PSL, 2024), B. Hivert (Bordeaux, 2024), M. Gomtsyan (Paris-Saclay, 2023), A. Kotov (Paris-Saclay, 2023), M. Gautier (Bordeaux, 2021), G. Romano (Lancaster, 2021).
PhD Juries	E. Gachon (Bordeaux, 2026), L. Monnier (Paris-Saclay, 2025), B. Batardière (Paris-Saclay, 2024), F. Mifsud (Sorbonne Université, 2023), P. Lacroix (Orsay, 2022).

Conference Organization (past 5 years)

2025	Mathematics of Single-Cell Data Analysis , CIRM, Marseille, Organizer
2010–2025	Statistical Methods for Post-Genomic Data Analysis , European Annual workshop, Steering Committee
2022	Journées de Statistique , French Statistical Society Conference, Co-President of the Organizing Committee with A.-L. Fougères

Full Publication List

1. F. Picard, V. Rivoirard, A. Roche, and V. M. Panaretos. PCA for point processes. *The Annals of Statistics*, 54(2):929 – 956, 2026
2. M.-D. Ilie, A. Flores-Martinez, M. Chanal, M. Lepetit, B. Samson, A. Lehiani, A. Vasiljevic, L. Chinezu, E. Jouanneau, D. Bernard, O. Gandrillon, F. Picard, G. Raverot, and P. Bertolino. Mast cells act as pro-angiogenic and pro-tumorigenic players in pituitary gonadotroph tumors. *Neuro-Oncology*, 28(1):175–190, 2025
3. R. Belhakem, F. Picard, V. Rivoirard, and A. Roche. Minimax estimation of functional principal components from noisy discretized functional data. *Scandinavian Journal of Statistics*, 52(1):38–80, 2025
4. M. Ilie, M. Lepetit, M. Chanal, A. Vasiljevic, E. Jouanneau, O. Gandrillon, F. Picard, G. Raverot, and P. Bertolino. 8322 mast cells: a new player in gonadotroph tumors. *Journal of the Endocrine Society*, 8(Supplement_1):bva163–1271, 2024
5. A. Ozier-Lafontaine, C. Fourneaux, G. Durif, P. Arsenteva, C. Vallot, O. Gandrillon, S. Gonin-Giraud, B. Michel, and F. Picard. Kernel-based testing for single-cell differential analysis. *Genome Biology*, 25(1):114, 2024
6. C. Fourneaux, L. Racine, C. Koering, S. Dussurgey, E. Vallin, A. Moussy, R. Parmentier, F. Brunard, D. Stockholm, L. Modolo, et al. Differentiation is accompanied by a progressive loss in transcriptional memory. *BMC biology*, 22(1):58, 2024
7. C. Arpin, F. Picard, and O. Gandrillon. In silico single-cell metabolism analysis unravels a new transition stage of cd8 t cells 4 days post-infection. *ImmunoInformatics*, page 100038, 2024
8. M. Lepetit, M. D. Ilie, M. Chanal, G. Raverot, P. Bertolino, C. Arpin, F. Picard, and O. Gandrillon. scan1. 0: A reproducible and standardized pipeline for processing 10x single cell rnaseq data. *In Silico Biology*, (Preprint):1–11, 2023
9. J. Poulet-Benedetti, C. Tonnerre-Doncarli, A. L. Valton, M. Laurent, M. rard, N. Barinova, N. Parisi, F. Massip, F. Picard, and M. N. Prioleau. Dimeric G-quadruplex motifs-induced NFRs determine strong replication origins in vertebrates. *Nat Commun*, 14(1):4843, Aug 2023
10. H. Van Assel, T. Espinasse, J. Chiquet, and F. Picard. A probabilistic graph coupling view of dimension reduction. In *Advances in Neural Information Processing Systems*, volume 35, pages 10696–10708. Curran Associates, Inc., 2022
11. A. Bonnet, C. Lacour, F. Picard, and V. Rivoirard. Uniform deconvolution for poisson point processes. *Journal of Machine Learning Research*, 23(194):1–36, 2022
12. S. Zreika, C. Fourneaux, E. Vallin, L. Modolo, R. Seraphin, A. Moussy, E. Ventre, M. Bouvier, A. Ozier-Lafontaine, A. Bonnaïfoux, et al. Evidence for close molecular proximity between reverting and undifferentiated cells. *BMC biology*, 20(1):1–16, 2022

13. J. Käfer, A. Bewick, A. Andres-Robin, G. Lapetoule, A. Harkess, J. Caius, B. Fogliani, G. Gâteblé, P. Ralph, C. W. dePamphilis, et al. A derived zw chromosome system in amborella trichopoda, representing the sister lineage to all other extant flowering plants. *New Phytologist*, 233(4):1636–1642, 2022
14. J. Käfer, N. Lartillot, G. A. B. Marais, and F. Picard. Detecting sex-linked genes using genotyped individuals sampled in natural populations. *Genetics*, 218(2), 03 2021
15. J. E. Mold, L. Modolo, J. Hård, M. Zamboni, A. J. Larsson, M. Stenudd, C.-J. Eriksson, G. Durif, P. L. Ståhl, E. Borgström, et al. Divergent clonal differentiation trajectories establish cd8+ memory t cell heterogeneity during acute viral infections in humans. *Cell reports*, 35(8):109174, 2021
16. C. Brossas, A. L. Valton, S. V. Venev, S. Chilaka, A. Counillon, M. Laurent, C. Goncalves, B. Duriez, F. Picard, J. Dekker, and M. N. Prioleau. Clustering of strong replicators associated with active promoters is sufficient to establish an early-replicating domain. *EMBO J*, 39(21):e99520, 11 2020
17. H. Badouin, A. Velt, F. Gindraud, T. Flutre, V. Dumas, S. Vautrin, W. Marande, J. Corbi, E. Sallet, J. Ganofsky, S. Santoni, D. Guyot, E. Ricciardelli, K. Jepsen, J. Käfer, H. Berges, E. Duchêne, F. Picard, P. Hugueney, R. Tavares, R. Bacilieri, C. Rustenholz, and G. A. B. Marais. The wild grape genome sequence provides insights into the transition from dioecy to hermaphroditism during grape domestication. *Genome Biol*, 21(1):223, 09 2020
18. F. Massip, M. Laurent, C. Brossas, J. M. Fernández-Justel, M. Gómez, M.-N. Prioleau, L. Duret*, and F. Picard*. Evolution of replication origins in vertebrate genomes: rapid turnover despite selective constraints. *Nucleic acids research*, 47(10): 5114–5125, 2019
19. G. Durif, L. Modolo, J. E. Mold, S. Lambert-Lacroix, and F. Picard. Probabilistic count matrix factorization for single cell expression data analysis. *Bioinformatics*, 35(20):4011–4019, 2019
20. F. Picard, P. Reynaud-Bouret, and E. Roquain. Continuous testing for Poisson process intensities: a new perspective on scanning statistics. *Biometrika*, 105(4):931–944, 2018
21. A. Muyle, N. Zemp, C. Fruchard, R. Cegan, J. Vrana, C. Deschamps, R. Tavares, R. Hobza, F. Picard, A. Widmer, and G. A. B. Marais. Genomic imprinting mediates dosage compensation in a young plant XY system. *Nat Plants*, 4(9): 677–680, 09 2018
22. G. Durif, L. Modolo, J. Michaelsson, J. Mold, S. Lambert-Lacroix, and F. Picard. High dimensional classification with combined adaptive sparse pls and logistic regression. *Bioinformatics*, 2017
23. M. Giacomini, S. Lambert-Lacroix, and F. Picard. Minimax wavelet estimation for multisample heteroscedastic nonparametric regression. *Journal of Nonparametric Statistics*, pages 1–24, 2017
24. A. Muyle, J. Käfer, N. Zemp, S. Mousset, F. Picard*, and G. A. Marais*. Sex-detector: a probabilistic approach to study sex chromosomes in non-model organisms. *Genome biology and evolution*, 8(8):2530–2543, 2016
25. H. Lopez-Maestre, L. Brinza, C. Marchet, J. Kielbassa, S. Bastien, M. Boutigny, D. Monnin, A. E. Filali, C. M. Carareto, C. Vieira, et al. Snp calling from rna-seq data without a reference genome: identification, quantification, differential analysis and impact on the protein sequence. *Nucleic acids research*, 44(19):e148–e148, 2016
26. S. Ivanoff, F. Picard, and V. Rivoirard. Adaptive lasso and group-lasso for functional poisson regression. *Journal of Machine Learning Research*, 17(55):1–46, 2016
27. E. Bonafede, F. Picard, S. Robin, and C. Viroli. Modeling overdispersion heterogeneity in differential expression analysis using mixtures. *Biometrics*, 72(3):804–814, 2016
28. V. Viallon, S. Lambert-Lacroix, H. Hoefling, and F. Picard. On the robustness of the generalized fused lasso to prior specifications. *Statistics and Computing*, 26(1-2):285–301, 2016
29. F. Picard, J.-C. Cadoret, B. Audit, A. Arneodo, A. Alberti, C. Battail, L. Duret, and M.-N. Prioleau. The spatiotemporal program of dna replication is associated with specific combinations of chromatin marks in human cells. *PLoS genetics*, 10(5):e1004282, 2014
30. L. Modolo, F. Picard, and E. Lerat. A new genome-wide method to track horizontally transferred sequences: application to drosophila. *Genome biology and evolution*, 6(2):416–432, 2014
31. V. Miele, F. Picard, and S. Dray. Spatially constrained clustering of ecological networks. *Methods in Ecology and Evolution*, 5(8):771–779, 2014
32. O. Mestre, P. Domonkos, F. Picard, I. Auer, S. Robin, E. Lebarbier, R. Böhm, E. Aguilar, J. A. Guijarro, G. Vertchnik, et al. Homer: a homogenization software—methods and applications. *Időjárás*, 2013

33. M. Giacomini, S. Lambert-Lacroix, G. Marot, and F. Picard. Wavelet-based clustering for mixed-effects functional models in high dimension. *Biometrics*, 69(1):31–40, 2013
34. V. Miele, S. Penel, V. Daubin, F. Picard, D. Kahn, and L. Duret. High-quality sequence clustering guided by network topology and multiple alignment likelihood. *Bioinformatics*, 28(8):1078–1085, 2012
35. F. Picard, É. Lebarbier, E. Budinská, and S. Robin. Joint segmentation of multivariate gaussian processes using mixed linear models. *Computational Statistics & Data Analysis*, 55(2):1160–1170, 2011a
36. F. Picard, E. Lebarbier, M. Hoebeke, G. Rigai, B. Thiam, and S. Robin. Joint segmentation, calling, and normalization of multiple cgh profiles. *Biostatistics*, 12(3):413–428, 2011b
37. T. Vernoux, G. Brunoud, E. Farcot, V. Morin, H. Van den Daele, J. Legrand, M. Oliva, P. Das, A. Larrieu, D. Wells, et al. The auxin signalling network translates dynamic input into robust patterning at the shoot apex. *Molecular systems biology*, 7(1):508, 2011
38. M. A. Van de Wiel, F. Picard, W. N. Van Wieringen, and B. Ylstra. Preprocessing and downstream analysis of microarray dna copy number profiles. *Briefings in bioinformatics*, 12(1):10–21, 2010
39. H. Zanghi, F. Picard, V. Miele, and C. Ambroise. Strategies for online inference of model-based clustering in large and growing networks. *The Annals of Applied Statistics*, 4(2):687–714, 2010
40. F. Picard, V. Miele, J.-J. Daudin, L. Cottret, and S. Robin. Deciphering the connectivity structure of biological networks using mixnet. *BMC bioinformatics*, 10(6):S17, 2009
41. F. Picard, J.-J. Daudin, M. Koskas, S. Schbath, and S. Robin. Assessing the exceptionality of network motifs. *Journal of Computational Biology*, 15(1):1–20, 2008
42. J.-J. Daudin, F. Picard, and S. Robin. A mixture model for random graphs. *Statistics and computing*, 18(2):173–183, 2008
43. F. Picard, S. Robin, E. Lebarbier, and J.-J. Daudin. A segmentation/clustering model for the analysis of array cgh data. *Biometrics*, 63(3):758–766, 2007
44. M. Guedj, E. Della-Chiesa, F. Picard, and G. Nuel. Computing power in case-control association studies through the use of quadratic approximations: application to meta-statistics. *Annals of human genetics*, 71(2):262–270, 2007
45. C. Lubrano-Berthelie, B. Dubern, J.-M. Lacorte, F. Picard, A. Shapiro, S. Zhang, S. Bertrais, S. Hercberg, A. Basdevant, K. Clement, et al. Melanocortin 4 receptor mutations in a large cohort of severely obese adults: prevalence, functional classification, genotype-phenotype relationship, and lack of association with binge eating. *The Journal of Clinical Endocrinology & Metabolism*, 91(5):1811–1818, 2006
46. C. Govaerts, S. Srinivasan, A. Shapiro, S. Zhang, F. Picard, K. Clement, C. Lubrano-Berthelie, and C. Vaisse. Obesity-associated mutations in the melanocortin 4 receptor provide novel insights into its function. *Peptides*, 26(10):1909–1919, 2005
47. F. Picard, S. Robin, M. Lavielle, C. Vaisse, and J.-J. Daudin. A statistical approach for array cgh data analysis. *BMC bioinformatics*, 6(1):27, 2005
48. S. Srinivasan, C. Lubrano-Berthelie, C. Govaerts, F. Picard, P. Santiago, B. R. Conklin, and C. Vaisse. Constitutive activity of the melanocortin-4 receptor is maintained by its n-terminal domain and plays a role in energy homeostasis in humans. *Journal of Clinical Investigation*, 114(8):1158, 2004