

Curriculum vitae -- Guido Sanguinetti

CURRENT JOB POSITION AND ORGANIZATION

Professore Ordinario di Fisica Applicata (FIS/07), Scuola Internazionale di Studi Superiori Avanzati, Trieste.
Honorary Professor of Informatics, School of Informatics, University of Edinburgh.

EDUCATION

DPhil in Mathematics, University of Oxford, 2004
Laurea in Fisica, Università degli Studi di Genova, 1998

PROFESSIONAL EXPERIENCE

2020- Professor of Applied Physics, SISSA, Trieste
2020, 2023 Panel member, ERC Synergy Grants PE6
2019-2020 Director, UKRI Centre for Doctoral Training in Biomedical AI, University of Edinburgh, UK
2019- Editor in Chief, De Gruyter *Statistical Applications in Genetics and Molecular Biology*
2017-2022 Professor of Computational Bioinformatics, University of Edinburgh, UK
2013-2017 Reader in Machine Learning, University of Edinburgh, UK
2010-2013 Lecturer in Machine Learning, University of Edinburgh, UK
2006-2010 Lecturer in Computer Science, University of Sheffield, UK

AWARDS (select)

2017, Best Poster Award, High Throughput Sequencing – Algorithms and Applications
2016, Best Paper Award, European Conference on Computational Biology
2013, Best Paper Award, International Conference on Quantitative Estimation of Systems
2012 PNAS Cozzarelli Prize in Engineering and Applied Sciences
1999 Franco Triccerri Memorial Prize for Laurea Thesis in Geometry or Mathematical Physics, Unione Matematica Italiana

MAJOR PROJECTS

2023-2027 AIRC IG27631 AI-driven integration of clinical and omics data for personalized treatment of myelodysplastic syndromes, Eur 750K, PI.
2019-2028 UKRI Centre for Doctoral Training in Biomedical Artificial Intelligence, EP/S02431X/1 PI and Director, University of Edinburgh (£6.5M)
2014-18 EPSRC EP/ L027208/1 Large scale spatio-temporal point processes: novel machine learning methodologies and application to neural multi-electrode arrays, £350K, sole PI.
2012-2017 ERC Starting Grant 306999 Machine Learning in Computational Science: formal and statistical models of biological systems, £1.1M, PI.
2010-14 BBSRC BB/I004777/1 Systems Understanding of Microbial Oxygen-Dependent and Independent Catabolism (SUMO2), £332.930, PI (part of EraSysBio consortium SUMO2 with Sheffield, Amsterdam, Stuttgart and Magdeburg).
2010-13 BBSRC BB/H01702X/1 Carbon monoxide and metal carbonyl CO-releasing molecules (CORMs) as novel antimicrobial agents - a systems approach to cellular targets and effects, £324.295, PI, with R. K. Poole (microbiology, Sheffield).

PUBLICATIONS (select recent)

Journal papers

1. El Kazwini, Nour and Sanguinetti, G. "SHARE-Topic: Bayesian interpretable modelling of single-cell multi-omics data", *Genome biology*, 25.55 (2024)
2. Zhang, Alex Chen-Yi, Rosa, A. and Sanguinetti, G. "Bottom up data integration in polymer models of chromatin organization", *Biophysical J.* 123(2) (2024)
3. Ocal, Kaan et al. "Model reduction for the Chemical Master Equation: an information theoretic approach", *J. Chem Phys* 158(11) 2023
4. Maniatis, Christos, et al. "SCRAPL: A Bayesian hierarchical framework for detecting technical associates in single-cell multi-omic data", *PLoS Computational Biology* 18.6 (2022)
5. Huang, Yuanhua and Sanguinetti, G. "BRIE2: Computational identification of splicing phenotypes from single-cell transcriptomic experiments", *Genome biology* 22.1 (2021)

6. Marangio, Paolo, et al. "SHIBUM-PMM: a robust statistical modeling approach for detecting RNA flexibility changes in high-throughput structure probing data." *Genome biology* 22.1 (2021): 1-21.
7. Kapourani, Chantriolnt-Andreas, et al. "scMET: Bayesian modeling of DNA methylation heterogeneity at single-cell resolution." *Genome biology* 22.1 (2021): 1-21.
8. Caravagna, Giulio, et al. "The MOBSTER R package for tumour subclonal deconvolution from bulk DNA whole-genome sequencing data." *BMC bioinformatics* 21.1 (2020): 1-11.
9. Caravagna, Giulio, et al. "Subclonal reconstruction of tumors by using machine learning and population genetics." *Nature Genetics* 52.9 (2020): 898-907.
10. Chhatbar, Kashyap, et al. "Quantitative analysis questions the role of MeCP2 as a global regulator of alternative splicing." *PLoS genetics* 16.10 (2020): e1009087.
11. Argelaguet, R., et al. Multi-omics profiling of mouse gastrulation at single-cell resolution. *Nature* **576**, 487–491 (2019)
12. Rule ME, et al Neural field models for latent state inference: Application to large-scale neuronal recordings. *PLoS Comput Biol* 15(11) (2019): e1007442
13. Kapourani, Chantriolnt-Andreas, and Guido Sanguinetti. "Melissa: Bayesian clustering and imputation of single-cell methylomes." *Genome biology* 20.1 (2019): 1-15.
14. Caravagna, Giulio, et al. "Detecting repeated cancer evolution from multi-region tumor sequencing data." *Nature methods* 15.9 (2018): 707-714.
15. M. Rule and G. Sanguinetti, Autoregressive Point-Processes as Latent State-Space Models: a Moment-Closure Approach to Fluctuations and Autocorrelations, *Neural Computation*, in press, 2018.
16. C-A Kapourani and G. Sanguinetti, BPRMeth: a flexible Bioconductor package for modelling methylation profiles, *Bioinformatics* 34(14), 2485-2486.
17. S.J. Clark et al, scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells, *Nature Communications*, 9(1), 71, 2018.
18. A. Georgoulas, J. Hillston and G. Sanguinetti , ProPPA: Probabilistic Programming for Stochastic Dynamical Systems, *ACM Trans. on Modelling and Computer Simulations (TOMACS)*, 28(1), 2018.
19. V. Aslandazeh, et al, Transcription rate strongly affects splicing fidelity and cotranscriptionality in budding yeast, *Genome Research* 28, 2018.
20. D. Schnoerr et al Efficient low-order approximation of first-passage time distributions, *Physical Review Letters* 119(21), 2017.
21. E. Bartocci et al Policy learning in continuous-time Markov decision processes using Gaussian Processes, *Performance Evaluation* 116, 2017.
22. Huang, Yuanhua, and Guido Sanguinetti. "BRIE: transcriptome-wide splicing quantification in single cells." *Genome biology* 18.1 (2017): 1-11.
23. S. Lagger, J C Connelly, G. Schweikert, et al, MeCP2 recognizes cytosine methylated tri-nucleotide and di-nucleotide sequences to tune transcription in the mammalian brain, *PLoS Genetics*, 13(5):e1006793, 2017
24. R. van Nues et al, Kinetic CRAC uncovers a role for Nab3 in determining gene expression profiles during stress, *Nature Communications*, 8(12), 2017.
25. D. Schnörr, G. Sanguinetti and R. Grima, Approximation and inference methods for stochastic biochemical kinetics - a tutorial review, *J. Phys. A: Mathematical and Theoretical*, 50 (9), 2017.
26. Selega, Alina, et al. "Robust statistical modeling improves sensitivity of high-throughput RNA structure probing experiments." *Nature methods* 14.1 (2017): 83-89.