

Guido Sanguinetti

CURRENT JOB POSITION AND ORGANIZATION

Professore Ordinario di Fisica Applicata (FIS/07), Scuola Internazionale di Studi Superiori Avanzati, Trieste.

PROFESSIONAL SUMMARY (research area of interest, with evidence, for the LS and PE macrosectors, of bibliometric indicators related to publications and citations, and, for the SH macrosector, of the quality and impact of publications;)

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 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
2004-2006 Post-doctoral Research Associate, Department of Computer Science, University of Sheffield, UK

AWARDS

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

DEGREE OF SUCCESS IN PREVIOUS ITALIAN/INTERNATIONAL PROJECTS

2019-2028 UKRI Centre for Doctoral Training in Biomedical Artificial Intelligence, EP/S02431X/1 PI and Director, University of Edinburgh (£6.5M)
2019 Leverhulme Trust Research grant RPG-2018-423 (£165K)
2017-18 Wellcome Trust, ISSF Award, Unravelling the interplay between chromatin and RNA processing from high throughput data sets, £41.000.
2016-18H2020 Marie Curie EF project 661179 MoDATS, £200K, PI (research fellow Dr Edward Wallace).
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.

2014 Procter & Gamble pump-priming funding, Molecular models of collagen production, £50K.
2012-15 FP7 Marie Curie/ EMBO advanced fellowship 299192 Epigene Informatics, £200K, PI (research fellow Dr Gabriele Schweikert) 2012-15.

2012-16 BBSRC BB/I024747/1 Computational reconstruction of stochastic regulation: from transcriptional modules to network remodelling, £37.000 International Award, to pump-prime research with Harvard Statistics (Prof. E. Airolidi)

2012-15 Microsoft Research, Machine learning methods for formal dynamical models: a systems biology case study (with Prof J. Hillston) £69.000, PhD studentship.

2011-14 Microsoft Research, Machine learning for systems biology: reconstructing the dynamics of plants' molecular clocks, £69.000, PhD studentship.

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).

2008-11 EPSRC EP/F009461/1 Advancing machine learning methodology for new classes of prediction problems, £85.491, P.I., with M. Girolami (Glasgow) and G Cawley (UEA)

BIBLIOMETRIC INDICATORS (Scopus)

Number of publications 147

Total number of citations 2853

H index 32

PUBLICATIONS (20)

Caravagna, Giulio, et al. "Subclonal reconstruction of tumors by using machine learning and population genetics." *Nature Genetics* 52.9 (2020): 898-907.

Chhatbar, Kashyap, et al. "Quantitative analysis questions the role of MeCP2 in alternative splicing." *Plos Genetics* 16(10) (2020):e1009087.

Argelaguet, Ricard, et al. "Multi-omics profiling of mouse gastrulation at single-cell resolution." *Nature* 576.7787 (2019): 487-491.

Kapourani, Chantriolnt-Andreas, and Guido Sanguinetti. "Melissa: Bayesian clustering and imputation of single-cell methylomes." *Genome biology* 20.1 (2019): 1-15.

Clark, Stephen J., et al. "scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells." *Nature communications* 9.1 (2018): 1-9.

Caravagna, Giulio, et al. "Detecting repeated cancer evolution from multi-region tumor sequencing data." *Nature methods* 15.9 (2018): 707-714.

Aslanzadeh, Vahid, et al. "Transcription rate strongly affects splicing fidelity and cotranscriptionality in budding yeast." *Genome research* 28.2 (2018): 203-213.

Tebaldi, Toma, et al. "HuD is a neural translation enhancer acting on mTORC1-responsive genes and counteracted by the Y3 small non-coding RNA." *Molecular cell* 71.2 (2018): 256-270.

Huang, Yuanhua, and Guido Sanguinetti. "BRIE: transcriptome-wide splicing quantification in single cells." *Genome biology* 18.1 (2017): 1-11.

Selega, Alina, et al. "Robust statistical modeling improves sensitivity of high-throughput RNA structure probing experiments." *Nature methods* 14.1 (2017): 83-89.

Van Nues, Rob, et al. "Kinetic CRAC uncovers a role for Nab3 in determining gene expression profiles during stress." *Nature communications* 8.1 (2017): 1-18.

Lagger, Sabine, et al. "MeCP2 recognizes cytosine methylated tri-nucleotide and di-nucleotide sequences to tune transcription in the mammalian brain." *PLoS genetics* 13.5 (2017): e1006793.

Kapourani, Chantriolnt-Andreas, and Guido Sanguinetti. "Higher order methylation features for clustering and prediction in epigenomic studies." *Bioinformatics* 32.17 (2016): i405-i412.

Milligan, Laura, et al. "Strand-specific, high-resolution mapping of modified RNA polymerase II." *Molecular systems biology* 12.6 (2016): 874.

Puchta, Olga, et al. "Network of epistatic interactions within a yeast snoRNA." *Science* 352.6287 (2016): 840-844.

Schnoerr, David, Ramon Grima, and Guido Sanguinetti. "Cox process representation and inference for stochastic reaction–diffusion processes." *Nature communications* 7.1 (2016): 1-11.

Huynh-Thu, Vân Anh, and Guido Sanguinetti. "Combining tree-based and dynamical systems for the inference of gene regulatory networks." *Bioinformatics* 31.10 (2015): 1614-1622.

Benveniste, Dan, et al. "Transcription factor binding predicts histone modifications in human cell lines." *Proceedings of the National Academy of Sciences* 111.37 (2014): 13367-13372.

Schweikert, Gabriele, et al. "MMDiff: quantitative testing for shape changes in ChIP-Seq data sets." *BMC genomics* 14.1 (2013): 826.

Zammit-Mangion, Andrew, et al. "Point process modelling of the Afghan War Diary." *Proceedings of the National Academy of Sciences* 109.31 (2012): 12414-12419.