

Dr G. Sanguinetti, Laurea (Genoa), DPhil (Oxon)

Brief highlights

- Founding director of UKRI CDT in Biomedical Artificial Intelligence
- Internationally leading expert in bioinformatics/ data science
- More than 80 peer reviewed publications, including *Science*, *Nature Methods*, *Nature Communications*, *PNAS*, *Bioinformatics*, *J. Am. Stat. Ass.*, *NIPS*
- Recipient of ERC Starting Grant 2012-17
- Recipient of research funds worth in excess of £10M since 2010 from ERC, EPSRC, BBSRC, EC and industry
- PNAS Cozzarelli Prize in Applied Science and Engineering 2012
- Best paper award at ECCB 2016 (major bioinformatics conference with >1200 attendees)

1 General

FULL NAME: Guido Sanguinetti

DATE OF BIRTH: 11 March 1974

EDUCATION AND QUALIFICATIONS:

- 1994-1998 University of Genova; Laurea in Fisica, 110/110 cum laude. Thesis title: Mirror symmetry on string theories compactified on K3 surfaces (supervisor Prof Ugo Bruzzo).
- 1998-2002 University of Oxford; DPhil in Mathematics. Thesis title: Complex geometry of dual isomonodromic deformations (supervisor Dr Nicholas M. J. Woodhouse).
- 2014, Italian National habilitation (level A, Professore Ordinario), disciplinary sector INF01 (Informatics and Computer Science)

CURRENT APPOINTMENT:

- 08/2017 - Personal Chair of Computational Bioinformatics, School of Informatics, University of Edinburgh.
- 01/17 - Associate Faculty, Wellcome Trust Centre for Cell Biology, University of Edinburgh.
- 06/17- Associate Faculty, MRC Institute of Genetics and Molecular Medicine, University of Edinburgh.

PREVIOUS APPOINTMENTS:

- 08/2013- 07/2017 Reader in Machine Learning, School of Informatics, University of Edinburgh.
- 04/10-07/13 Lecturer in Machine Learning (grade 8), School of Informatics, University of Edinburgh
- 09/08-04/10 Lecturer in Systems Biology (grade 8), Dept of Chemical and Process Engineering and Dept of Computer Science, University of Sheffield
- 09/06-09/08 Lecturer in Computer Science (grade 8) at the University of Sheffield
- 09/04-09/06 Research Associate in the Department of Computer Science, University of Sheffield.

SCHOLARSHIPS AND AWARDS

- Journal of Physics A: Mathematical and Theoretical "Highlights of 2017" for the paper *Approximation and inference methods for stochastic biochemical kinetics*, with D. Schnoerr and R. Grima.
- HiT-Seq 2017 Best Poster Award (with student Y. Huang).
- ECCB 2016 Best paper Award at the 15th European Conference on Computational Biology (with student A. Kapourani), The Hague, 2016 (>1200 attendees, >400 submissions)
- QEST Best Paper Award, 10th International Conference on Quantitative Evaluation of Systems (QEST), Buenos Aires, 2013.
- 2012 PNAS Cozzarelli Prize, Class III (Engineering and Applied Science), for the paper *Point Process Modelling of the Afghan War Diary*, by A. Zammit-Mangion et al. (corresponding author). First time the award was given to an informatician.
- Nominated for Best Teacher Award, Edinburgh University Student Association, 2011
- Exceptional Contribution Award, University of Sheffield (2007)
- Keely Senior Scholar, Wadham College, Oxford (2000-01)
- University of Oxford DPhil scholarship (1999-2001)
- Italian Mathematical Union 'F. Tricerri' memorial prize for best Laurea thesis (1999)
- 2017 *Chinese Government Award for Outstanding Self-financed PhD Student Abroad* awarded to former PhD student Dr Y. Huang.
- 2012 *IET Doctoral Dissertation Award in Automation and Control* awarded to former PhD student Dr A. Zammit-Mangion.

2 Professional and external development activities (select)

- Invited seminars at >20 institutions in the UK, US, Italy, Germany, Sweden and France, including (select since 2012) MIT, Harvard, Sloan-Kettering Cancer Center, EBI, Cambridge MRC Biostatistics Unit, Oxford Computer Science, Oxford Physiology and Genetics, Imperial College London Biology and Computer Science, Ludwig-Maximilians University Munich, Technische Universitat Berlin, Saarland University, Chalmers University Gothenburg, SISSA, University of Trento, IMT Lucca, University of Pisa, Glaxo-Smith-Kline, Microsoft Research, Xerox Research Centre Europe.
- Invited speaker at >20 international conferences/ workshops/ summer schools, including (select since 2012) Wellcome Trust Conference on Computational RNA Biology (Hinxton, 2016), 13th Int'l conference on Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB, Stirling, 2016), Krupp Symposium on Precision Medicine (Munich, 2016), Third Workshop of the EPSRC Network on Computational Statistics and Machine Learning (Edinburgh 2016), 15th Int'l Conference on Runtime Verification (RV15, Vienna, 2015, tutorial speaker), Epigen Summer School (Udine, 2015), Seventh Int'l Workshop on Machine Learning and Systems Biology (MLSB, Berlin, 2013).
- Organisation of several international workshops including Workshop on Statistical Modelling in Epigenomics and Gene Regulation (Harvard 2015), 2014 Bayes Lectures on Spatio-temporal Modelling (Edinburgh 2014), Fourth Int'l Workshop on Machine Learning in Systems Biology (Edinburgh 2010).
- Senior Programme Committee / Area chair for several conferences including International Conference on Machine Learning (ICML) 2017, European Conference on Machine Learning (ECML) 2016, Computational Methods in Systems Biology (CMSB) 2016, 2017 and 2018 (Program Co-Chair), Quantitative Evaluation of Systems (QEST) 2017.
- 2018- Editor in Chief, *Statistical Applications in Genetics and Molecular Biology*
- 2012-2018 Associate Editor, *Statistical Applications in Genetics and Molecular Biology*
- PhD examiner for 21 candidates in 12 institutions in 5 countries (UK, Italy, Germany, Sweden, Finland)
- Associate Editor, *Statistical Applications in Genetics and Molecular Biology*.

- Member, IAPR Technical Committee 20 (Bioinformatics).
- Reviewer for the BBSRC, EPSRC, MRC, Wellcome Trust, Royal Society, Medical Research Council Scotland, ERC, National Science Foundation (NSF) USA, Rumanian Research Council, Austrian Research Council (FWF), Swiss Research Council (SNF).
- Reviewer for >20 international journals, including *Nature Reviews Genetics*, *Nature Protocols*, *Proceedings of the National Academy of Sciences*, *Genetics*, *Genome Biology*, *Bioinformatics*, *IEEE Trans. on Pattern Analysis and Machine Intelligence*, *IEEE Trans. Signal Processing*, *IEEE Trans. Neural Networks*, *J. Mach. Learn. Res.*.

3 Teaching

- 2016 invited lecturer for PhD course on Bayesian Machine Learning (20 hrs), Department of Computer Science, Technical University of Vienna.
- 2015 invited lecturer for PhD course on Bayesian Machine Learning (20 hrs), Department of Computer Science, University of Pisa.
- 2014, invited lecturer for PhD course on Machine Learning for Systems Biology (12 hrs), CIBIO, University of Trento.
- 2010/11-2012/13, Bioinformatics 2 (MSc level 11 course). Nominated for EUSA (Edinburgh University Students' Association) best teacher award (2011)
- 2011/12 Informatics 2B: Introduction to learning. Nominated for EUSA best course award
- 2006-10 Network Performance Analysis and Bioinformatics (University of Sheffield)
- Supervision of MSc/ final year students: over fifteen students successfully supervised.
- Supervision of PhD students: eight completed as primary supervisor (G. Skolidis, 2011, H.M.S. Asif, 2012, A. Ocone 2013, Z. Liu 2014, D. Trejo-Banos 2015, T. Mayo 2017, Y. Huang 2017, A. Selega 2018). Four completed as joint supervisor (C. Penfold, 2008, A. Zammit-Mangion 2012, D. Schnoerr 2016, A. Georgoulas 2016). Currently supervising four PhD students (A. Kapourani, M. Michaelidis, E. Scher and C. Maniatis)

4 Management and administration

- 2018- Chair, Academic Steering Committee, EPSRC Centre for Doctoral Training in Data Science, University of Edinburgh.
- 2017-18 Convenor, MSc Board of Examiners, School of Informatics, University of Edinburgh.
- 2013- Member, Informatics Equality and Diversity Committee, School of Informatics, University of Edinburgh.
- 2011-12 Year Organiser, UG2 Informatics, University of Edinburgh.
- 2010-12 Member of Academic Board, Centre for Systems Biology at Edinburgh, University of Edinburgh.
- 2007-10 Head of Machine Learning Research Group, Department of Computer Science, University of Sheffield.
- 2006-09 Director of MSc course Software Systems and Internet Technology, University of Sheffield.

5 Research

Active grants

- UKRI Centre for Doctoral Training in Biomedical Artificial Intelligence, EP/S02431X/1, £6.8M (PI and Director)
- Leverhulme Trust, RPG-2018-423, Stochastic reactions in crowded cells: theories, inference, and implications, £169,400 PI
- MRC Health Data Research UK, Scottish Substantive Site, £5M (co-investigator)

Past Grants

- Wellcome Trust, ISSF Award, Unravelling the interplay between chromatin and RNA processing from high throughput data sets, £41.000, 2017-2018.
- H2020 Marie Curie EF project 661179 MoDATS, £200K, PI (research fellow Dr Edward Wallace), 2016-18.
- EPSRC EP/ L027208/1 Large scale spatio-temporal point processes: novel machine learning methodologies and application to neural multi-electrode arrays., ~ £350K, sole PI, 2014-17.
- ERC Starting Grant 306999 Machine Learning in Computational Science: formal and statistical models of biological systems, £1.1M, sole PI, 2012-17.
- Procter & Gamble pump-priming funding, Molecular models of collagen production, £50K, 2014.
- FP7 Marie Curie/ EMBO advanced fellowship 299192 Epigene Informatics, £200K, PI (research fellow Dr Gabriele Schweikert) 2012-15.
- 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. Airoldi)
- Microsoft Research, Machine learning methods for formal dynamical models: a systems biology case study (with Prof J. Hillston) £69.000, PhD studentship, 2012-15.
- Microsoft Research, Machine learning for systems biology: reconstructing the dynamics of plants' molecular clocks, £69.000, PhD studentship 2012-15.
- BBSRC BB/I004777/1 Systems Understanding of Microbial Oxygen-Dependent and Independent Catabolism (SUMO2), £332.930 2010-2013, PI (part of EraSysBio consortium SUMO2 with Sheffield, Amsterdam, Stuttgart and Magdeburg).
- 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 2010-2013, PI, with R. K. Poole (microbiology, Sheffield).
- EPSRC EP/F009461/1 Advancing machine learning methodology for new classes of prediction problems, £85.491 2008-11, P.I., with M. Girolami (Glasgow) and G Cawley (UEA)
- Department of Health, HTD Advanced Lifestyle Monitoring Systems, £155.710, 2008-09, co-investigator (with Prof M. Hawley)
- EU FP7 PASCAL2 Network of Excellence, Sheffield Site Manager (2008-2010)

6 Publications

Books and book chapters

1. V.-A. Huynh-Thu and **G. Sanguinetti**, (eds) Gene regulatory networks, in *Methods in Molecular Biology* series, Springer, 2018.
2. N.D. Lawrence, M. Girolami, M.Rattray and **G. Sanguinetti** (eds), Learning in Computational Systems Biology, MIT press (2009)
3. A. Ruttor, **G. Sanguinetti** and M. Opper, Approximate inference for stochastic reaction systems, to appear in Lawrence et al, Learning in Computational Systems Biology, MIT press (2009)
4. V. Kadiramanathan, **G. Sanguinetti**, M. Girolami and M. Niranjan (eds), Pattern Recognition in Bioinformatics, Lecture Notes in Bioinformatics, Springer (2009)
5. J. Noirel, **G. Sanguinetti** and P.C. Wright, Network-based integration of high-throughput data, to appear in S. Choi, Systems Biology of Signalling Networks, Springer (2010)

Journal Papers

1. C.-A. Kapourani and **G. Sanguinetti**, Melissa: Bayesian clustering and imputation of single cell methylomes, *Genome Biology*, 20:61, 2019.
2. Inma Spiteri, Giulio Caravagna, GD Cresswell, A Vatsiou, D Nichol, A Acar, L Ermini, K Chkhaidze, B Werner, R Mair, E Brognaro, Roel GW Verhaak, **G Sanguinetti**, SGM Piccirillo, C Watts, A Sottoriva, Evolutionary dynamics of residual disease in human glioblastoma, *Annals of Oncology*, 30(3), 456-463, 2019.
3. G. Caravagna *, Y. Giarratano, D. Ramazzotti, I. Tomlinson, **G. Sanguinetti** * and A. Sottoriva *, Detecting repeated cancer evolution in human tumours from multi-region sequencing data, *Nature Methods*, 15, 707-714 2018 (*= joint corresponding author).
4. 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.
5. T. Tebaldi et al., HuD Is a Neural Translation Enhancer Acting on mTORC1-Responsive Genes and Counteracted by the Y3 Small Non-coding RNA, *Mol. Cell*, 71(2), 256-270, 2018.
6. C-A Kapourani and **G. Sanguinetti**, BPRMeth: a flexible Bioconductor package for modelling methylation profiles, *Bioinformatics* 34(14), 2485-2486.
7. S.J. Clark, R. Argelaguet, C-A. Kapourani, et al, scNMT-seq enables joint profiling of chromatin accessibility DNA methylation and transcription in single cells, *Nature Communications*, 9(1), 71, 2018.
8. 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.
9. V. Aslandazeh, Y. Huang, **G. Sanguinetti** and J. Beggs, Transcription rate strongly affects splicing fidelity and cotranscriptionality in budding yeast, *Genome Research* 28, 2018.
10. D. Schnoerr, B. Cseke, R. Grima and *G. Sanguinetti*, Efficient low-order approximation of first-passage time distributions, *Physical Review Letters* 119(21), 2017.
11. E. Bartocci, L. Bortolussi, T. Bradzil, D Milios and **G. Sanguinetti** Policy learning in continuous-time Markov decision processes using Gaussian Processes, *Performance Evaluation* 116, 2017.
12. Y. Huang and **G. Sanguinetti**, BRIE: transcriptome-wide splicing quantification in single cells, *Genome Biology*, 18(1), 2017.
13. , S. Lagger, J C Connelly, G. Schweikert, S. Webb, J. Selfridge, B. H Ramsahoye, M. Yu, C. He, **G. Sanguinetti**, L C Sowers, M. D Walkinshaw and A. Bird, MeCP2 recognizes cytosine methylated tri-nucleotide and di-nucleotide sequences to tune transcription in the mammalian brain, *PLOS Genetics*, 13(5):e1006793, 2017
14. R. van Nues, G. Schweikert, E. de Lau, A. Selega, I. Iosub, P. Wadsworth, **G. Sanguinetti** and S. Granneman, Kinetic CRAC uncovers a role for Nab3 in determining gene expression profiles during stress, *Nature Communications*, 8(12), 2017.
15. 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.
16. A. Selega, C. Sirocchi, I. Iosub, S. Granneman* and **G. Sanguinetti***, Robust statistical modelling improves sensitivity of high-throughput RNA structure probing experiments, *Nature Methods*, 14(1), 83-89, 2017 (*= joint corresponding author).
17. B. Cseke, D. Schnörr, M. Opper and **G. Sanguinetti**, Expectation propagation for continuous time stochastic processes, *J. Phys. A: Mathematical and Theoretical*, 49:494002 2016.
18. A. Selega and **G. Sanguinetti**, Trends and Challenges in Computational RNA Biology, *Genome Biology* 17:253, 2016.
19. S. Lukauskas, R. Visintainer, **G. Sanguinetti** and G. Schweikert, DGW: an exploratory data analysis tool for clustering and visualisation of epigenomic marks, *BMC Bioinformatics*, 17(Suppl 16):447, 2016.
20. Y. Huang and **G. Sanguinetti**, Statistical modeling of isoform splicing dynamics from RNA-seq time series data, *Bioinformatics*, 32(19), 2965-2972, 2016

21. C-A Kapourani and **G. Sanguinetti**, Higher order methylation features for clustering and prediction in epigenomic studies, *Bioinformatics* 32(17), i405-i412, 2016 (ECCB2016 best paper award)
22. L. Milligan, V-A. Huynh Thu, C. Delan-Forino, A. Tuck, E. Petfalski, R. Lombrana Pascual, **G. Sanguinetti***, G. Kudla*, and D. Tollervey*, Strand-specific, high-resolution mapping of modified RNA polymerase II, *Molecular Systems Biology*, 12(6) 2016 (*=joint corresponding author)
23. A. Georgoulas, J. Hillston and **G. Sanguinetti**, Unbiased Bayesian inference for population Markov jump processes via random truncations, *Statistics and Computing*, DOI 10.1007/s11222-016-9667-9, 2016.
24. D. Schnoerr, R. Grima and **G. Sanguinetti**, Cox process representation and inference for stochastic reaction-diffusion processes, *Nature Communications* 7, 11729, 2016.
25. O. Puchta, B. Cseke, H. Czaja, D. Tollervey, **G. Sanguinetti** and G. Kudla, Network of epistatic interactions within a yeast snoRNA, *Science* 352 (6287), 840-844, 2016
26. L.K. Wareham, R. Begg, H.E. Jesse, J.W. van Beilen, S. Ali, D. Svistunenko, S. McLean, K.J. Hellingwerf, **G. Sanguinetti** and R.K. Poole, Carbon Monoxide Gas Is Not Inert, but Global, in Its Consequences for Bacterial Gene Expression, Iron Acquisition, and Antibiotic Resistance, *Antioxidants and Redox Signaling*, epub ahead of print, 2016
27. L. Bortolussi, D. Milios and **G. Sanguinetti**, Smoothed model checking for uncertain continuous-time Markov chains, *Information and Computation* 247, 235-253, 2016.
28. L. Holyoake, S. Hunt, **G. Sanguinetti**, G. M. Cook, M.J. Howard, M.L. Rowe, R.K. Poole and M. Shepherd, CydDC-mediated reductant export in *Escherichia coli* controls the transcriptional wiring of energy metabolism and combats nitrosative stress, *Biochem. J.*, 473(6), 693-701, 2016
29. D. Barrass, J. Reid, Y. Huang, R. D. Hector, **G. Sanguinetti**, J. D. Beggs and S. Granneman, Transcriptome-wide RNA processing kinetics revealed using extremely short 4tU labeling, *Genome Biology* 16(1), 1-17, 2015
30. B. Cseke, A. Zammit-Mangion, T. Heskes and **G. Sanguinetti**, Sparse approximations in spatio-temporal point process models, *J. Am. Stat. Ass.*, published online 22/12/2015
31. D. Schnoerr, **G. Sanguinetti** and R. Grima, Comparison of different moment-closure approximations for stochastic chemical kinetics, *Journal of Chemical Physics* 143 (18), 185101, 2015
32. F. Lauria, T. Tebaldi, L. Lunelli, P.Struffi, P. Gatto, A. Pugliese, M. Brigotti, L. Montanaro, Y. Ciribilli, A. Inga, A.Quattrone, **G. Sanguinetti** and G. Viero, RiboAbacus: a model trained on polyribosome images predicts ribosome density and translational efficiency from mammalian transcriptomes, *Nucleic Acids Research*, 43 (22), e153, 2015.
33. D. Trejo-Banos, A.J. Millar and **G. Sanguinetti**, A Bayesian approach for structure learning in oscillating regulatory networks, *Bioinformatics*, 31 (22), 3617-3624, 2015.
34. J. L. Wilson, S. McLean, R. Begg, **G. Sanguinetti** and R.K. Poole, Analysis of transcript changes in a heme-deficient mutant of *Escherichia coli* in response to CORM-3 [Ru (CO) 3 Cl (glycinate)], *Genomics Data* 5, 231-234, 2015
35. E. Bartocci, L. Bortolussi, L. Nenzi and **G. Sanguinetti**, System design of stochastic models using robustness of temporal properties, *Theor. Comp. Sci.* 587, 3-25, 2015.
36. J. L. Wilson, L. K. Wareham, S. McLean, R. Begg, S. Greaves, B. E. Mann, **G. Sanguinetti** and R. K. Poole, CO-Releasing Molecules Have Nonheme Targets in Bacteria: Transcriptomic, Mathematical Modeling and Biochemical Analyses of CORM-3 [Ru (CO) 3Cl (glycinate)] Actions on a Heme-Deficient Mutant of *Escherichia coli*, *Antioxidants and Redox Signalling* 23(2), 148-162, 2015 featured on issue cover
37. K.J. Denby, M.D. Rolfe, E. Crick, **G. Sanguinetti**, R.K. Poole and J. Green, Adaptation of anaerobic cultures of *Escherichia coli* K12 in response to environmental trimethylamine-N-oxide, *Env. Microbiology* 17(7) 2477-2491, 2015.
38. V.-A. Huynh-Thu and **G. Sanguinetti**, Combining tree-based and dynamical systems for the inference of gene regulatory networks, *Bioinformatics* 31 (10), 2015.

39. T. Mayo, G. Schweikert and **G. Sanguinetti**, M3D: a kernel-based test for spatially correlated changes in methylation profiles, *Bioinformatics* 31(6), 809-16, 2015. Associated Bioconductor tool at <http://bioconductor.org/packages/release/bioc/html/M3D.html> (1887 downloads from 986 individual IP addresses as of 22/07/15)
40. D. Schnoerr, **G. Sanguinetti** and R. Grima, Validity conditions for moment closure approximations in stochastic chemical kinetics. *Journal of Chemical Physics*, 141(8), 2014
41. D. Benveniste, H.-J. Sonntag, **G. Sanguinetti***, and D. Sproul*, Transcription factor binding predicts histone modifications in human cell lines, *Proc. Natl Acad. Sci. USA (PNAS)*, 111(37), 13367-13372, 2014 (*= joint corresponding author)
42. D. Schnoerr, **G. Sanguinetti** and R. Grima, The Complex Chemical Langevin Equation, *Journal of Chemical Physics*, 141, 024103, 2014.
43. K. Bettenbrock, H. Bai, M. Ederer, J. Green, K. J. Hellingwerf, M. Holcombe, S. Kunz, M. D. Rolfe, **G. Sanguinetti**, O. Sawodny, P. Sharma, S. Steinsiek and R. K. Poole, Towards a systems level understanding of the oxygen response of *Escherichia coli*, *Adv. Micr. Phys.* 64, 65-114, 2014.
44. G. Schweikert, B. Cseke, T. Clouaire, A. Bird and **G. Sanguinetti** MMDiff: quantitative testing for shape changes in ChIP-Seq data sets, *BMC Genomics* 14(1), 826 (2013). Associated Bioconductor tool at <http://bioconductor.org/packages/release/bioc/html/MMDiff.html> (3040 downloads from 1557 individual IP addresses as of 22/07/15).
45. G. Skolidis and **G. Sanguinetti**, Semi-supervised Multi-task Learning with Gaussian Processes, *IEEE Trans. Neur. Netw.* 24(12), 2101-2112 (2013).
46. H.M.S. Asif and **G. Sanguinetti**, Simultaneous clustering and inference of transcriptional dynamics in gene regulatory networks, *Stat. Appl. Gen. Mol. Biol.* 12(5), 545-557 (2013).
47. R. I. Menzies, A. Zammit-Mangion, L. M. Hollis, R. J. Lennen, M. A. Jansen, D. J. Webb, J. J. Mullins, J. W. Dear, **G. Sanguinetti** and M. A. Bailey, An anatomically unbiased approach for analysis of renal BOLD magnetic resonance images, *Am. J. Physiol.*, 305(6) F845-F852 (2013)
48. A. Ocone, A.J. Millar and G. Sanguinetti, Hybrid Regulatory Models: a statistically tractable approach to model regulatory network dynamics, *Bioinformatics*, 29(7), 910-916 (2013).
49. S McLean, R Begg, HE Jesse, BE Mann, **G. Sanguinetti** and RK Poole, Analysis of the bacterial response to Ru (CO) 3Cl (glycinate)(CORM-3) and the inactivated compound identifies the role played by the ruthenium compound and reveals sulfur-containing species as a major target of CORM-3 action, *Antiox. Redox. Signal.* 19(17), 1999-2012 (2013)
50. A. Zammit-Mangion, M. A. Dewar, V. Kadiramanathan and **G. Sanguinetti**, Point Process Modelling of the Afghan War Diary, *Proceedings of the National Academy of Sciences of the USA (PNAS)*, 109(31) 12414-19 (2012).
51. M. D. Rolfe, A. Ocone, M. R. Stapleton, S. Hall, E. W. Trotter, R. K. Poole, **G. Sanguinetti** and J. Green, Systems analysis of transcription factor activities in environments with stable and dynamic O₂ concentrations, *Royal Society Open Biology*, 2:120091 (2012)
52. G. Skolidis, K. Hansen, **G. Sanguinetti** and M. Rupp, Multi-task Learning for pKA prediction, *Journal of Computer Aided Modelling and Design*, 26(7) 883-895 (2012)
53. A. Zammit-Mangion, **G. Sanguinetti** and V. Kadiramanathan, Variational Estimation in Spatiotemporal Systems from Continuous and Point-Process Observations, *IEEE Transactions on Signal Processing*, 60(7), 3449-3459 (2012)
54. G. Skolidis and **G. Sanguinetti**, A Case Study on Meta-Generalising: A Gaussian Processes Approach, *Journal of Machine Learning Research* 13 (Mar), 691-721, (2012)
55. A. I. Graham, **G. Sanguinetti**, N. Bramall, C. W. McLeod and R. K. Poole, Dynamics of a starvation-to-surfeit shift: A transcriptomic and modelling analysis of the bacterial response to zinc reveals transient behaviour of the Fur and SoxS regulators, *Microbiology*, 158(1), 284-292 (2012)
56. G. Skolidis and **G. Sanguinetti**, Bayesian Multitask Classification with Gaussian Process Priors, *IEEE Transaction on Neural Networks*, 22(12), 2011-2021 (2011)

57. E. W. Trotter, M. D. Rolfe, A. M. Hounslow, C. J. Craven, M. P. Williamson, **G. Sanguinetti**, R. K. Poole and J. Green, Reprogramming of Escherichia coli K-12 Metabolism during the Initial Phase of Transition from an Anaerobic to a Micro-Aerobic Environment, *PLoS One* 6(9) (2011)
58. A. Ocone and **G. Sanguinetti**, Reconstructing transcription factor activities in hierarchical transcription network motifs, *Bioinformatics* 27(20):2873-9 (2011).
59. I. Bellantuono, **G. Sanguinetti** and W. N. Keith, Progeroid syndromes: models for stem cell aging?, *Biogerontology*, 13(1), 63-75 (2011).
60. M. Filippone and **G. Sanguinetti**, Approximate Inference of the Bandwidth in Multivariate Kernel Density Estimation, *Computational Statistics and Data Analysis*, 55(12), 3104-3122 (2011).
61. A. Kuwabara, A. Backhaus, R. Malinowski, M. Bauch, L. Hunt, T. Nagata, N. Monk, **G. Sanguinetti**, and A. Fleming, A shift towards smaller cell size via manipulation of cell cycle gene expression acts to smoothen Arabidopsis leaf shape, *Plant Physiology*, 156: 2196-2206 (2011)
62. A. Zammit-Mangion, K. Yuan, V. Kadirkamanathan, M. Niranjana and **G. Sanguinetti**, Online Variational Inference for State-Space Models with Point-Process Observations, *Neural Computation* 23(8), 1967-1999 (2011)
63. H.M. S. Asif and **G. Sanguinetti**, Large-scale learning of combinatorial transcriptional dynamics from gene expression, *Bioinformatics*, 27(9), 1277-1283 (2011)
64. M. D. Rolfe, A. Ter Beek, A. I. Graham, E. W. Trotter, H. M. Shahzad Asif, **G. Sanguinetti**, J. Teixeira de Mattos, R. K. Poole, and J. Green, Transcript profiling and inference of Escherichia coli K-12 ArcA activity across the range of physiologically relevant oxygen concentrations, *Journal of Biological Chemistry*, 286, 10147-10154 (2011)
65. M. Filippone and **G. Sanguinetti**, A Perturbative Approach to Novelty Detection in Autoregressive Models, *IEEE Transactions on Signal Processing*, 59(3), 1027-1036 (2011)
66. H.M. S. Asif, M. Rolfe, J. Green, N. D. Lawrence, M. Rattray and **G. Sanguinetti**, TFInfer: A Tool for Probabilistic Inference of Transcription Factor Activities, *Bioinformatics*, 26(20), 2635-2636 (2010)
67. M. Opper and **G. Sanguinetti**, Learning combinatorial transcriptional dynamics from gene expression data, *Bioinformatics*, 26(13) 1623-1629 (2010)
68. S. McLean, L. A. H. Bowman, **G. Sanguinetti**, R. C. Read and R. K. Poole, Peroxynitrite toxicity in Escherichia coli K-12 elicits expression of oxidative stress responses, and protein nitration and nitrosylation, *Journal of Biological Chemistry*, 285: 20724-20731 (2010)
69. M. Shepherd, **G. Sanguinetti**, G. M. Cook and R. K. Poole, Compensations for diminished terminal oxidase activity in Escherichia coli: cytochrome bd-II-mediated respiration and glutamate metabolism, *Journal of Biological Chemistry*, 285: 18464-18472 (2010)
70. M. A Dewar, V. Kadirkamanathan, M. Opper and **G. Sanguinetti**, Parameter estimation and inference for stochastic reaction-diffusion systems: application to morphogenesis in D. melanogaster, *BMC Systems Biology* 4:21 (2010)
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1. D. Milios, D. Schnoerr and **G. Sanguinetti** Probabilistic Model Checking for Continuous Time Markov Chains via Sequential Bayesian Inference, QEST 2018
2. M. Michaelidis, J. Hillston and **G. Sanguinetti** Statistical abstraction for multi-scale spatio-temporal systems, QEST 2017
3. E. Bartocci, L. Bortolussi, T. Brazdil, D. Milios and **G. Sanguinetti** Policy learning for time-bounded reachability in Continuous-Time Markov Decision Processes via doubly-stochastic gradient ascent, QEST 2016
4. M. Michaelidis, D. Milios, J. Hillston and **G. Sanguinetti** Property-driven State-Space Coarsening for Continuous Time Markov Chains, QEST 2016
5. L. Bortolussi, D. Milios and **G. Sanguinetti**, U-check: Model Checking and Parameter Synthesis under Uncertainty, QEST 2015
6. L. Bortolussi, D. Milios and **G. Sanguinetti**, Efficient stochastic simulation of systems with multiple time scales via statistical abstraction, CMSB 2015
7. D. Trejo-Banos, A.J. Millar and **G. Sanguinetti**, Experimental design for inference over the *A. thaliana* circadian clock network, CMSB 2015
8. E. Bartocci, L. Bortolussi and **G. Sanguinetti**, Data-driven Statistical Learning of Temporal Logic Properties, FORMATS 2014: 23-37

9. L. Bortolussi and **G. Sanguinetti**, A Statistical Approach for Computing Reachability of Non-linear and Stochastic Dynamical Systems. QEST 2014: 41-56
10. A. Georgoulas, J. Hillston, D. Milios and **G. Sanguinetti**, Probabilistic Programming Process Algebra. QEST 2014: 249-264
11. A. Georgoulas, J. Hillston and **G. Sanguinetti**, ABC-Fun: A Probabilistic Programming Language for Biology. CMSB 2013: 150-163
12. B Cseke, M Opper and **G. Sanguinetti**, Approximate Inference in Latent Diffusion Processes from Continuous Time Observations, Advances in Neural Information Processing Systems (NIPS) 2013 (spotlight presentation, top 5% of submissions)
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