

Simone Rubinacci

Resume

<http://srubinacci.github.io> *
Genopode, UNIL-Sorge, 1015, Ecublens, CH
rubinacci.simone@gmail.com
+41 78 233 44 70



Personal statement

I am a postdoctoral researcher at the Systems and Population Genetics Group, University of Lausanne. My research is mainly focused in the development of statistical methods for genotype imputation and haplotype phasing.

Education and Relevant Research Activities

11/2019–now **Postdoctoral researcher in Statistical and Population Genomics**, Research interests: imputation and phasing methods, GWAS, eQTL.
Department of Computational Biology, University of Lausanne, CH

10/2015–05/2020 **DPhil in Statistical and Population Genomics**, Modelling and development of IMPUTE5 imputation method using the Positional Burrows-Wheeler Transform.
Department of Statistics, University of Oxford, UK

03/2015–10/2015 **Research assistant**, *Analysis off-lattice and in-lattice simulation traces using spatio-temporal logics*.
Department of Computer Science, University of Milano-Bicocca, Italy

10/2012–03/2015 **Msc in Computer Science**, Thesis: *Noisy Random Boolean Networks dynamics for cellular differentiation*.
Department of Computer Science, University of Milano-Bicocca, Italy

01/2014–08/2014 **Research assistant**, *Development of biological models in the Chaste modelling environment*.
Department of Computer Science, University of Oxford, UK

Teaching Experience

01/2017–02/2018 **Teaching Assistant**, *TA for doctoral students (DTC)*, University of Oxford.
Statistics course. Gibbs sampling and Stochastic Differential Equations

10/2016–02/2018 **Tutor (teaching support)**, *Tutor for doctoral students (DTC)*, University of Oxford.
Courses: C++ Programming, Introduction to Linux, Shell scripting, Statistics

Training and Other Research Experience

- 03/2019–06/2019 **Research Visit**, Department of Computational Biology, University of Lausanne, Switzerland.
- 12/2016–07/2016 **Academy for PhD Training in Statistics (APTS)**.
3-week programme for advanced statistical studies in Cambridge, Oxford and Durham.
- 07/2016–10/2016 **Research Project**, *Efficient approaches to simulating cell-based models of epithelial tissues*, Department of Computer Science, University of Oxford, UK.
- 03/2016–06/2016 **Research Project**, *Phasing methods on large scale datasets using rare variants*, Department of Statistics, University of Oxford, UK.
- 10/2015–03/2016 **Systems Biology Centre for Doctoral Training**.
University of Oxford, UK. <http://www.sysbiodtc.ox.ac.uk/>

Awards

- 08/2020 **ASHG 2020 Epstein Trainee Awards for Excellence in Human Genetics Research (postdoctoral category)**, *Semifinalist*.
- 01/2014 **EXTRA Scholarship Award**.

Publications

Journal Articles

Simone Rubinacci, Alex Graudenzi, Giulio Caravagna, Giancarlo Mauri, James Osborne, Joe Pitt-Francis, and Marco Antoniotti. Cognac: a chaste plugin for the multiscale simulation of gene regulatory networks driving the spatial dynamics of tissues and cancer. *Cancer informatics*, 14:CIN–S19965, 2015. doi:10.4137/CIN.S19965.

Anisa Rula, Matteo Palmonari, Simone Rubinacci, Axel-Cyrille Ngonga Ngomo, Jens Lehmann, Andrea Maurino, and Diego Esteves. Tisco: Temporal scoping of facts. *Journal of Web Semantics*, 2018. doi:10.1016/j.websem.2018.09.002.

Submitted Papers

John E Gorzynski, Hannah N De Jong, David Amar, Chris R Hughes, Alexander Ioannidis, Rob Bierman, Darren Liu, Yosuke Tanigawa, Amy Kistler, Jack Kamm, Jaehee Kim, Lorenzo Cappello, Norma F. Neff, Simone Rubinacci, Olivier Delaneau, Massa J. Shoura, Kinya Seo, Anna Kirillova, Archana Raja, Shirley Sutton, ChunHong Huang, Malaya Kumar Sahoo, Kalyan C. Mallemapati, Gonzalo Montero-Martin, Kazutoyo Osoegawa, David Jimenez-Morales, Nathaniel Watson, Nathan Hammond, Ruchi Joshi, Marcelo Fernandez-Vina, Jeffrey W. Christle, Matthew T. Wheeler, Phil Febbo, Kyle Farh, Gary Schroth, F Desouza, Julia Palacios, Julia Salzman, Benjamin A. Pinsky, Manuel A Rivas, Carlos D. Bustamante, Euan A. Ashley, and Victoria N. Parikh. High-throughput sars-cov-2 and host genome sequencing from single nasopharyngeal swabs. *medRxiv*, 2020. doi:10.1101/2020.07.27.20163147.

Simone Rubinacci, Olivier Delaneau, and Jonathan Marchini. Genotype imputation using the positional burrows wheeler transform. *bioRxiv*, 2020. doi:10.1101/797944.

Simone Rubinacci, Diogo Ribeiro, Robin Hofmaister, and Olivier Delaneau. Efficient phasing and imputation of low-coverage sequencing data using large reference panels. *bioRxiv*, 2020. doi:10.1101/2020.04.14.040329.