

## Francesco Sambo

---

### CONTACT INFORMATION

Department of Information Engineering  
University of Padova  
via Gradenigo 6/a, 35131 Padova, Italy

Voice: +39 049 827 7918  
E-mail: [sambofra@dei.unipd.it](mailto:sambofra@dei.unipd.it)  
WWW: [www.dei.unipd.it/~sambofra](http://www.dei.unipd.it/~sambofra)

### RESEARCH INTERESTS

- Stochastic local search, multi-objective optimization and evolutionary computation, with applications to reverse engineering of gene regulatory networks and to optimal design of experiments
- Data mining, machine learning, feature selection and Bayesian Networks, with applications to genetic markers selection from genome-wide data and to integration of genetic and phenotypic markers in the pathogenesis of complex diseases
- Big Data handling, with applications to storage and fast retrieval of genetic data

### EDUCATION

**Ph.D.** in Information Engineering, University of Padova, April 2010  
Thesis: *Advanced Algorithms for Genomic Data Analysis*  
Advisor: Prof. Silvana Badaloni

**Laurea Specialistica** (M.S.) in Computer Engineering, University of Padova, October 2006  
Thesis: *Distributed Computing, a Multi-Agent approach*  
Advisor: Prof. Carlo Ferrari  
Grade: 107/110

**Laurea Triennale** (B.S.) in Computer Engineering, University of Padova, September 2004  
Thesis: *A Local Search solution for a problem of FEM grids partitioning*  
Advisor: Prof. Geppino Pucci  
Grade: 103/110

### PROFESSIONAL APPOINTMENTS

**Postdoctoral Research Associate** *January 2014 - present*  
Department of Information Engineering, University of Padova, Italy  
Advisor: Prof. Barbara Di Camillo

**Postdoctoral Research Associate** *January 2012 - December 2013*  
Department of Information Engineering, University of Padova, Italy  
Advisor: Prof. Gianna Maria Toffolo

**Postdoctoral Research Associate** *January 2010 - December 2011*  
Department of Information Engineering, University of Padova, Italy  
Advisor: Prof. Silvana Badaloni

**Visiting Researcher** *October 2008 - July 2009*  
Institut des Recherches Interdisciplinaires et de Développements en Intelligence Artificielle, Université Libre de Bruxelles, Brussels, Belgium  
Advisors: Prof. Thomas Stützle and Prof. Marco Dorigo

## REFEREE ACTIVITY **Journals**

BMC Bioinformatics, PLoS ONE, International Journal of Approximate Reasoning, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Medical & Biological Engineering & Computing, IEEE Transactions on Biomedical Engineering, Diabetes Research and Clinical Practice.

## **Conferences**

World congress of the International Fuzzy Systems Association (IFSA 2009), International Conference on Swarm Intelligence (ICSI 2011), AAAI Conference on Artificial Intelligence (AAAI 2014).

## **Program Committees**

International Workshop on Intelligent Data Analysis in BioMedicine and Pharmacology (IDAMAP 2010), European Conference on Artificial Intelligence (ECAI 2014).

## TEACHING

### **Teaching Assistant**

*2007 - present*

Courses: *Artificial Intelligence, Foundations of Artificial Intelligence* and *Intelligent Systems* (Prof. Silvana Badaloni, University of Padova).

Topics: Machine Learning, Artificial Neural Networks, Support Vector Machines, Stochastic Local Search algorithms, applications of Artificial Intelligence to Computational Genomics.

## RESEARCH PROJECTS - FUND RAISING

### **Project writing**

Contribution in writing the proposal for the European funded FP7 project MOSAIC (MOdels and Simulation techniques for discovering diAbetes Influence factors, 2013 - 2015) and for the University of Padova funded projects BiD-Algo (Big Data Algorithmics, 2013 - 2014) and Neuroimaging Genetics: Models and Methods to Integrate Brain Phenotype and Genotype (2014 - 2015).

### **Participation to international projects**

Active participation to the European funded FP7 projects SUMMIT (SURrogate markers for Micro- and Macro-vascular hard endpoints for Innovative diabetes Tools, 2009 - 2014) and MOSAIC, writing deliverables, milestones and partner and work package reports, organizing plenary meetings and work package workshops and coordinating work package activities.

## SKILLS

### **Technical Skills**

Programming languages: C, C++, Java, MATLAB, R, elements of Python and HTML

Operating Systems: Mac OS X, Linux, Windows

Computational skills: big data handling, code profiling and optimization, parallel programming

### **Language Skills (CEFR level)**

Italian: native speaker (C2)

English: advanced (C1)

French: intermediate (B1)

Author lists denoted using "with" are alphabetical.

### Journal Papers

- [1] **Bayesian Network structure learning: hybridizing complete search with independence tests.** With Badaloni S and Venco F. *AI Communications*, Accepted for publication.
- [2] Costello JC, Heiser LM, Georgii E, Gnen M, Menden MP, Wang NJ, Bansal M, Ammad-ud-din M, Hintsanen P, Khan SA, Mpindi JP, NCI DREAM Community (with Sambo F), Kallioniemi O, Honkela A, Aittokallio T, Wennerberg K, Collins JJ, Gallahan D, Singer D, Saez-Rodriguez J, Kaski S, Gray JW, Stolovitzky G. **A community effort to assess and improve drug sensitivity prediction algorithms.** *Nature Biotechnology*, doi:10.1038/nbt.2877 (Epub ahead of print).
- [3] Sambo F, Di Camillo B, Toffolo G, Cobelli C. **Compression and fast retrieval of SNP data.** *Bioinformatics*, 30(21):3078-3085, 2014.
- [4] Sambo F, Malovini A, Sandholm N, Stavarachi M, Forsblom C, Mäkinen V-P, Harjutsalo V, Lithovius R, Gordin D, Parkkonen M, Saraheimo M, Thorn LM, Tolonen N, Wadén J, He B, Österholm A-M, Tuomilehto J, Lajer M, Salem RM, McKnight AJ, Tarnow L, Panduru NM, Barbarini N, Di Camillo B, Toffolo GM, Tryggvason K, Bellazzi R, Cobelli C, Groop P-H. **Novel genetic susceptibility loci for diabetic end stage renal disease identified through robust Naive Bayes classification.** *Diabetologia*, 57(8):1611-1622, 2014.
- [5] Sambo F, Borrotti M, Mylona K. **A coordinate-exchange two-phase local search algorithm for the D- and I-optimal design of split-plot experiments.** *Computational Statistics and Data Analysis* 71:1193-1207, 2014.
- [6] Di Camillo B, Sambo F, Toffolo G, Cobelli C. **ABACUS: an entropy based cumulative bivariate statistic robust to rare variants and different direction of genotype effect.** *Bioinformatics* 30(3):384-391, 2014.
- [7] Aghaeepour N, Finak G, the FlowCAP Consortium, the DREAM Consortium (with Sambo F), Hoos H, Mosmann TR, Gottardo R, Brinkman RR, Scheuermann RH. **Critical assessment of automated flow cytometry analysis techniques.** *Nature Methods* 10(3):228-238, 2013.
- [8] Sambo F, Trifoglio E, Di Camillo B, Toffolo G, Cobelli C. **Bag of Naïve Bayes: biomarker selection and classification from Genome-Wide SNP data.** *BMC Bioinformatics* 13(Suppl 14):S2, 2012.
- [9] **Qualitative Reasoning for Biological Network Inference from Systematic Perturbation Experiments.** with Badaloni S and Di Camillo B. *IEEE / ACM Transactions on Bioinformatics and Computational Biology* 9(5):1482-1491, 2012.
- [10] Sambo F, Montes de Oca M A, Di Camillo B, Toffolo G, Stützle T. **MORE: Mixed Optimization for Reverse Engineering. An application to modeling biological networks response via sparse systems of nonlinear differential equations.** *IEEE / ACM Transactions on Bioinformatics and Computational Biology* 9(5):1459-1471, 2012.
- [11] Di Camillo B, Sanavia T, Martini M, Jurman G, Sambo F, Barla A, Squillario M, Furlanello C, Toffolo G, Cobelli C. **Effect of size and heterogeneity of samples on biomarker discovery: synthetic and real data assessment.** *PLoS ONE* 7(3):e32200, 2012.

### Conference Proceedings Full Papers

- [12] Jøsang A, Sambo F. **Inverting Conditional Opinions in Subjective Logic.** In: *Proc. of the 20th International Conference on Soft Computing (MENDEL 2014)*, in press.
- [13] **A tag-based recommender system.** with De Caro P and Pini MS. In: Menegatti E, Berns K, Michael N and Yamaguchi H (eds.) *Proc. of the 13th International Conference on Intelligent Autonomous Systems (IAS 2014)*. Advances in Intelligent Systems and Computing. Springer / Verlag, in press.
- [14] Fico G, Cancela J, Arredondo MT, Dagliati A, Sacchi L, Segagni D, Millana AM, Fernandez-Llatas C, Traver V, Sambo F, Facchinetti A, Verdú J, Guillén A, Bellazzi R, Cobelli C. **User Requirements for Incorporating Diabetes Modeling Techniques in Disease Management Tools.** In: *6th European Conference of the International Federation for Medical and Biological Engineering*. IFMBE Proceedings, vol. 45, pp. 992-995. Springer International Publishing, 2015.
- [15] Dagliati A, Sacchi S, Bucalo M, Segagni D, Zarkogianni K, Martinez Millana A, Cancela J, Sambo F, Fico G, Meneu Barreira MT, Cerra C, Nikita K, Cobelli C, Chiovato C, Arredondo MT, Bellazzi R. **A Data Gathering Framework to Collect Type 2 Diabetes Patients Data.** In: *Proc. of the IEEE International Conference on Biomedical Health Informatics (BHI 2014)*, pp. 244-247. IEEE press, 2014.

- [16] **On hybridizing complete Bayesian Network structure search with independence tests.** with Badaloni S and Venco F. In: Mancini, T., Oddi, A. (eds.) *Experimental Evaluation of Algorithms for Solving Problems with Combinatorial Explosion 2012*. CEUR Workshop Proceedings, CEUR-WS.org, in press.
- [17] Sambo F, Di Camillo B. **Minimizing time when applying Bootstrap to contingency tables analysis of Genome-Wide data.** In: Hamadi, Y., Schoenauer, M. (eds.) *Learning and Intelligent Optimization*. Lecture Notes in Computer Science, vol. 7219, pp. 175-189. Springer Berlin / Heidelberg, 2012.
- [18] **Redefinition of Mutual Information in the Fuzzy Sets framework for Computational Genomics.** with Badaloni S, Falda M and Massignan P. In: Madani, K., Dourado, A., Rosa, A. and Filipe, J. (eds.) *Computational Intelligence*. Studies in Computational Intelligence, vol. 343, pp. 73-83. Springer Berlin / Heidelberg, 2011. Best paper award.
- [19] Sambo F, Di Camillo B. **Qualitative reasoning on systematic gene perturbation experiments.** In: Rizzo, R., Lisboa, P. J. G. (eds.) *Computational Intelligence Methods for Bioinformatics and Biostatistics*. Lecture Notes in Bioinformatics, vol. 6685, pp. 135-146. Springer Berlin / Heidelberg, 2011.
- [20] Sambo F, Montes de Oca M A, Di Camillo B and Stützle T. **On the difficulty of inferring gene regulatory networks: A study of the fitness landscape generated by relative squared error.** In: Collet, P., Monmarché, N., Legrand, P., Schoenauer, M., Lutton, E. (eds.) *Artificial Evolution*, Lecture Notes in Computer Science, vol. 5975, pp. 74-85. Springer Berlin / Heidelberg, 2010. Third best presentation award.
- [21] **Addressing temporally constrained Delivery Problems with the Swarm Intelligence approach.** with Badaloni S, Falda M and Zanini L. In: W. Burgard, R. Dillmann, C. Plagemann, and N. Vahrenkamp (eds.) *Intelligent Autonomous Systems 10*. Baden-Baden, Germany: IOS Press, pp. 264-271, 2008.

### Book Chapters

- [22] Sambo F, Sanavia T, Di Camillo B. **Integration of Genetic Variation as External Perturbation to Reverse Engineer Regulatory Networks from Gene Expression Data.** In: De La Fuente A (ed). *Gene Network Inference*. Springer Berlin Heidelberg, pp. 107-118, 2013.
- [23] Sambo F, Ferrazzi B, Bellazzi R. **Probabilistic modelling with Bayesian Networks.** In: Carson E, Cobelli C (eds). *Modelling Methodology for Physiology and Medicine, 2nd ed.* Elsevier, Oxford (UK), pp.257-280, 2013.
- [24] Di Camillo B, Castiglioni I, Sambo F, Gilardi MC, Toffolo GM. **Methods for discovery and integration of genetic and neuroimaging biomarkers.** In: Fato MM, Gilardi MC, Schenone A. *Neuroinformatica*. Gruppo Nazionale di Bioingegneria, vol. 30. Bologna: Pàtron, 2011.

### Conference proceedings short papers and abstracts

- [25] Di Camillo B, Sambo F, Toffolo G, Cobelli C. **A pathway cumulative SNP association analysis robust to rare variants and different direction of genotype effect.** In: *Proceedings of RE-COMB/ISCB Conference on Regulatory and Systems Genomics*. Toronto, Ontario. November 8-12, 2013.
- [26] Sambo F, Malovini A, Sandholm N, Stavarachi M, Forsblom C, Harjutsalo V, Lajer M, Tarnow L, Bellazzi R, Cobelli C, Groop PH on behalf of the FinnDiane Study Group. **End Stage Renal Disease in Type 1 Diabetes: a novel susceptibility locus identified by robust Naïve Bayes classification.** In: *Proceedings of the symposium "Diabetes - a Threat to Mankind"*. Helsinki, Finland. June 7-8, 2013. Second best poster award.
- [27] Sambo F, Malovini A, Sandholm N, Stavarachi M, Forsblom C, Harjutsalo V, Lajer M, Tarnow L, Bellazzi R, Cobelli C, Groop PH on behalf of the FinnDiane Study Group. **Advances in the genetics of diabetic end stage renal disease: new susceptibility loci detected by robust Nave Bayes classification.** In: *Proceedings of the 26th annual meeting of the European Study Group on Diabetic Nephropathy*. Castelldefels, Spain. May 24-25, 2013.
- [28] Sambo F, Trifoglio E, Di Camillo B, Toffolo G, Cobelli C. **Genome-Wide data analysis with a Bootstrap Ensemble of Nave Bayes Classifiers.** In: *Proceedings of the 3rd Congress of the Italian Group on Bioengineering*. Rome, Italy. June 26-29, 2012.

- [29] Sambo F, Trifoglio E, Di Camillo B, Toffolo G, Cobelli C. **Bag of Naïve Bayes: biomarker selection and classification from Genome-Wide SNP data.** In: *Clinical Bioinformatics. 11th Workshop on Network Tools and Applications in Biology NETTAB2011.* Pavia, Italy. Oct 12-14, 2011.
- [30] Sambo F, Di Camillo B, Toffolo G, Vella A, Cobelli C. **Potential Role of GLP1R in the Pathogenesis of Type 2 Diabetes Identified Using Bayesian Networks.** In: *Proceedings of the 4th International Congress on Prediabetes and the Metabolic Syndrome.* Madrid, Spain, April 6-9, 2011. *Journal of Diabetes*, 3 (s1), pp. 42-281
- [31] Sambo F, Di Camillo B, Toffolo G, Vella A, Cobelli C. **Type 2 Diabetes: Bayesian Network Modelling of Genetic and Phenotypic Traits.** In: *Proceedings of the 4th International Conference on Advanced Technologies & Treatments for Diabetes.* London, UK, February 16-19, 2011. *Diabetes Technology and Therapeutics*, 13 (2), pp. 173-293
- [32] Sanavia T, Sambo F, Grassi A, Di Camillo B, Toffolo G. **Gene Network inference by significance analysis on genotype/phenotype data.** In: *Proceedings of the 3rd Joint Conference on Systems Biology, Regulatory Genomics, and Reverse Engineering Challenges.* New York City, Nov 16 - 20, 2010. Honourable Mention for Best Performer (fourth place) in the DREAM5 challenge: Systems Genetics Challenge.
- [33] **Fuzzy Mutual Information for Reverse Engineering of Gene Regulatory Networks.** with Badaloni S, Falda M and Massignan P. In: *Proceedings of the International Conference on Fuzzy Computation ICFC09.* Madeira, Portugal, Oct. 5-7 2009. pp. 25-30, 2009.
- [34] Sambo F, Di Camillo B, Falda M, Toffolo G, Badaloni S. **CNET: an algorithm for the inference of gene regulatory interactions from gene expression time series.** In: *Proceedings of the 14th Workshop on Intelligent Data Analysis in medicine and Pharmacology IDAMAP09.* Verona, Italy. July 19 2009, pp. 23-28, 2009.
- [35] Sambo F, Di Camillo B, Toffolo G. **CNET: an algorithm for Reverse Engineering of Causal Gene Networks.** In: *Bioinformatics Methods for Biomedical Complex Systems Applications. 8th Workshop on Network Tools and Applications in Biology NETTAB2008.* Varenna, Italy. May 19-21 2008, pp. 134-136, 2008.
- [36] Sambo F, Di Camillo B, Falda M, Toffolo G, Badaloni S. **Evaluation of local reliability of gene networks inferred from time series expression data.** In: *RECOMB Satellite on Regulatory Genomics and Systems Biology.* Boston, MA. Oct 29 - Nov 2 2008. Abstract Book, p. 121, 2008.
- [37] Sambo F, Di Camillo B, Toffolo G. **Role of network structure and experimental design on the performance of two Reverse Engineering methods.** In: *Proceedings of the 7th European Conference on Computational Biology ECCB2008.* Cagliari, Italy. September 2008.
- [38] **Scale-free structure and topological properties in reverse engineering of gene regulatory networks.** with Badaloni S and Falda M. In: *Proceedings of Workshop Italiano su Vita Artificiale e Computazione Evolutiva WIVACE2008.* Venezia, Italy. September 2008.

#### Doctoral symposia and consortia

- [39] Sambo F. **Stochastic Local Search Strategies for Reverse Engineering of Gene Regulatory Networks.** In: *LS-DS 2009: Doctoral Symposium on Engineering Stochastic Local Search Algorithms.* Technical Report TR/IRIDIA/2009-024, IRIDIA, Universit Libre de Bruxelles, Brussels, Belgium, August 2009, pp. 61-65, 2009. Third best poster award.
- [40] Sambo F. **Advanced algorithms for genomic data analysis.** In: *11th Conference on Artificial Intelligence in Medicine AIME 2007 - Doctoral Consortium Working Notes.* Amsterdam, The Netherlands, July 7-11, 2007.

#### Ph.D. Thesis

- [41] Sambo F. **Advanced Algorithms for Genomic Data Analysis.** Ph.D. Thesis. University of Padova, Italy. 2010.