

## Annalisa Barla

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**Education**      **PhD in Computer Science** (CICLO XVII). University of Genoa, Italy. 30/5/2005.  
*A general framework for Image Kernel Engineering.*  
Thesis Supervisor: Prof. Alessandro Verri.

**Laurea Degree in Physics** (MsC equivalent). University of Genoa, Italy. 19/09/2001.  
*Rappresentazione dati nella teoria statistica dell'apprendimento.* (Data Representation  
in statistical learning theory).  
Mark: 110/110. Thesis Supervisor: Prof. Alessandro Verri.

**Current Position**      Since 01/2012  
**Assistant Professor in Computer Science** (Ricercatore)  
Institution: DISI - University of Genoa, Italy.

**Research Experience**      1/2011-12/2011  
**Post-Doctoral Research Fellowship** (Assegno di Ricerca)  
Main Duties: Study and development of methods for feature selection and classification  
for genomic and proteomic data. Coordination of the Computational Biology team  
within the SlipGURU group (CS Department, University of Genoa)  
Institution: DISI - University of Genoa, Italy.

1/2009-12/2010  
**Post-Doctoral Research Fellowship** (Assegno di Ricerca)  
Main Duties: Focus on sparsity-inducing methods for signature identification in the  
context of Health-e-Child FP6 project. Coordination of the Computational Biology  
team within the SlipGURU group (CS Department, University of Genoa)  
Institution: DISI - University of Genoa, Italy.

01/2007-12/2008  
**Post-Doctoral Research Fellowship** (Assegno di Ricerca)  
Main Duties: research and development activities related to the Health-e-Child FP6  
project for the analysis of Paediatric Gliomas genomic data.  
Institution: DISI - University of Genoa, Italy.

08/2006-12/2006  
**Post-Doctoral Fellowship**  
Main Duties: research and development activities related to the Health-e-Child FP6  
project for the analysis of Paediatric Gliomas genomic data.  
Institution: DISI - University of Genoa, Italy.

08/2006-12/2006  
**Visiting Researcher**  
Main Duties: Problems of feature selection and predictive proling in DNA microarray  
and proteomics data.  
Supervisor: Dr. Cesare Furlanello.  
Institution: ITC-IRST (now FBK-IRST), Trento, Italy.

04/2005-07/2006

**Post-Doctoral Fellowship** (borsa AIRC Associazione Italiana Ricerca sul Cancro)  
Main Duties: Problems of feature selection and predictive profiling in DNA microarray and proteomics data.

Supervisor: Dr. Cesare Furlanello.

Institution: ITC-IRST (now FBK-IRST), Trento, Italy.

10/2004-02/2005

**Pre-doctoral Research Fellowship/Internship**

Main Duties: Problems of tumour detection in 3d CT-scans

Institution: Siemens Corporate Research, Princeton, NJ, USA.

01/2002-09/2004

**Pre-doctoral Research Fellowship**

Main Duties: Kernel Methods for Image content understanding Institution: CNR/INFM (INFM funded Project MAIA), Italy.

## Research

**Research Interests:** data integration, gene signature identification

Following an MSc in Physics with a thesis on data representation in statistical learning theory, I attained a PhD in Computer Science with a research project on machine learning and kernel engineering for images.

During my PhD years I focused on supervised machine learning methods, especially Support Vector Machines for binary and one-class classification and I designed novel kernel functions tailored on the specific representation of the data at hand. The results of my research were presented at several international conferences (including ECCV 2002) and published on a journal paper [Odone et al. IEEE Transactions on Image Processing, 2005].

An internship on medical imaging in the Integrated Data Systems Department headed by Dr. Comaniciu, at Siemens Corporate Research (Princeton, NJ, USA) led me to develop an interest in evidence-based medicine.

Right after my graduation I joined Dr. Furlanellos Lab at ITC-IRST, now Fondazione Bruno Kessler (Trento, Italy), where I had the opportunity to start my research on computational biology in a group with long-standing experience in the field. The time at Dr. Furlanellos Lab allowed me to acquire the expertise needed for a careful design of selection-bias aware data analysis frameworks [G. Jurman et al. Bioinformatics, 2008]. I learned how to deal with DNA microarray data and I started a new research line on mass-spectrometry proteomic data [M. Cannataro et al. IEEE Trans. on Nanobiosciences, 2007; Barla et al Briefings in Bioinformatics, 2008]. Moreover, I had the opportunity to become familiar with distributed computing facilities and computationally intensive algorithms.

The FP6 Integrated Project Health-e-Child IST-2004-02774919 gave me the opportunity to join the group in Genova in 2006. Since then, I am a research fellow at the Computer Science Department of the University of Genova, in Prof. A. Verri Statistical Learning and Image Processing group (<http://slipguru.disi.unige.it>). Capitalizing on the expertise acquired in Trento, I initiated a research line in computational biology, and I am now the person in charge of the computational biology unit. My research is placed at the intersection of statistical learning and computational biology. In particular, I am interested in developing regularization methods that guarantee robust and unbiased results and possibly exploit the available knowledge on the given prob-

lem. My responsibilities and activities include: investigating novel machine learning methods and designing the protocols for high-throughput data analysis, leading and contributing to the software development, and managing the unit research projects.

My unit collaborates with different groups active in medical and biological research: Dr. Varesio, Molecular Biology Lab, Istituto Giannina Gaslini, Genova, Italy Dr. Cama and Dr. Capra, Neuro-oncology unit, Istituto Giannina Gaslini, Genova, Italy Dr. Mosci, Ophthalmology, E.O. Ospedali Galliera, Genova, Italy Dr. M. Scala, Istituto Scientifico Tumori, Genova, Italy. For all these research projects, I dealt with the entire processing pipeline, from data normalization or pre-processing to the knowledge extraction phase and to the in-silico validation step. The results of this research were published on international renowned journals [Fardin et al. BMC Bioinformatics, 2009; J. of Biomed. and Biotech., 2010; Molecular Cancer, 2010; Mosci et al. 2009 Europ. Journ. Ophthalm.].

The analysis of biological data is characterized by a large amount of features representing each given example (high-dimensionality) and a relatively small number of samples. Traditional statistical tools were developed and studied to adapt in the opposite scenario, where the samples outnumber many times the variables, so different approaches have to be explored. In particular, there is a broad class of methods for feature selection that has been at the centre of researchers attention in the recent years, since this step is necessary to select the most informative variables at hand. My current interest is on sparsity-enforcing regularization methods, exploiting different penalties to achieve sparse models depending only on few and relevant variables, with the main goal of modelling complex biological systems. Such methods should possibly allow for the integration of different data types and be flexible enough to incorporate all the available biological prior knowledge.

## Major Accomplishments

- My PhD project focused on kernel methods for images. In this context, I designed novel and effective kernel functions tailored on the specific representation of the data at hand that allowed for a content-based classification of images. I also proved their effectiveness on different real dataset, publishing the results of my research in journals [Odone et al. IEEE Trans. on Image Processing, 2005] and conferences (ECCV 2002; ICPR 2002; ICIAP 2003; ICIP2002).
- The time at Dr. C. Furlanello's lab in Trento represented the possibility to apply my expertise in machine learning to a very interesting and yet tricky field: the analysis of molecular high-throughput data. I learned how to deal with DNA microarray data, I participated to the design of selection-bias aware frameworks [G. Jurman et al. Bioinformatics, 2008] and I started a new research line on mass-spectrometry proteomic data [Cannataro et al. IEEE Trans. on Nanobiosc. 2007; Barla et al. Brief. In Bioinf. 2008].
- With the Health-e-Child project, I had the opportunity to form and lead a unit of four researchers within Prof. A. Verris group, with the aim of studying machine learning methods for computational biology. Together with my coworkers, I carried on successful collaborations with biologists and MDs, gaining enough interdisciplinary knowledge to understand their fundamental biological questions and to cast such issues into a valid and robust statistical framework. Our results have been published on relevant journals in the field [Fardin et al. BMC Bioinformatics 2009; Fardin et al. J. of Biomed. and Biotech. 2010a; Fardin et al. 2010b Molecular Cancer]. Moreover, in the Pediatric Glioma study (Health-e-

Child project) our results have also undergone a biological validation phase that confirmed their validity [paper in preparation].

**Involvement in projects and grants**

2012-2013: NGS  
Role: Investigator.  
Funding: 100k€, Fondazione CARIGE.

2010-2013: Modelli e metodi computazionali nello studio della fisiologia e patologia di reti molecolari di controllo in ambito oncologico.  
Role: Investigator.  
Funding: 180k€, Compagnia di San Paolo.

2007-2009: Modelli e Metodi Computazionali Innovativi per la Biologia Molecolare in Ambito Oncologico.  
Role: Investigator for TEMA1 (analysis of molecular data in pediatric gliomas)  
Funding: 190k€, Compagnia di San Paolo.  
<http://crac.disi.unige.it/projects/sanpaolo.html>

2006-2010: IST-2004-02774919 EU Integrated Project: Health e-child.  
Role: Task leader: Novel knowledge discovery methods (T13.2), Genomics Data Analysis (T13.5)  
Funding: 890k€, EU (FP6).  
<http://www.health-e-child.org>

2006-2009: FIRB project RBIN04PARL: Learning Theory and Engineering Applications.  
Role: leader for bioinformatic research  
Funding: 605k€, MIUR.  
<http://slipguru.disi.unige.it/Research/LEAP>

2002-2005: INFN Project MAIA (Medicine and Architecture Image Analysis).  
Role: collaborator  
Funding: 505k€, (PRA) INFN, Istituto Nazionale di Fisica della Materia.

2002-2005: FIRB Project: ASTAA (Statistical learning: theory, algorithms and applications).  
Role: collaborator  
Funding: 170k€, MIUR.  
<http://slipguru.disi.unige.it/Research/ASTA>

## Publications

Indexes associated to my publications are:  
total citations: 400 - h-index: 9  
(January 2013 - source: Google Scholar)

## Full Papers

G. Zycinski, **A. Barla**, M. Squillario, T. Sanavia, B. Di Camillo and A. Verri  
Knowledge Driven Variable Selection (KDVS) - a new approach to enrichment analysis  
of gene signatures obtained from high-throughput data.  
Source Code for Biology and Medicine 8:2, 2013 - doi:10.1186/1751-0473-8-2

C. De Ambrosi, **A. Barla**, L. Tortolina, N. Castagnino, R. Pesenti, A. Verri, A.  
Ballestrero, F. Patrone and S. Parodi.  
Parameter Space Exploration within Dynamic Simulations of Signaling Networks  
Mathematical Biosciences and Engineering, 10 (01) , 2013.

L. Baldassarre, L. Rosasco, **A. Barla** and A. Verri.  
Multi-Output Learning via Spectral Filtering.  
Machine Learning, 2012 - i.f. 1.742

B.Di Camillo, T. Sanavia, M. Martini, G.Jurman, F. Sambo, **A. Barla**, M.Squillario,  
C. Furlanello, G. Toffolo, C. Cobelli.  
Effect of size and heterogeneity of samples on biomarker discovery: synthetic and real  
data assessment.  
Plos One, 7, 2012 - i.f. 4.411

C. Mosci, F. B. Lanza, **A. Barla**, S. Mosci, J. Hrault, L. Anselmi, M. Truini.  
Comparison of Clinical Outcomes for Patients with Large Choroidal Melanoma after  
Primary Treatment with Enucleation or Proton Beam Radiotherapy  
Acta Ophthalmologica, 2012 - i.f. 2.809

M. Squillario and **A. Barla**.  
A procedure for functional characterization of potential biomarkers from heterogeneous  
molecular data: Alzheimers as a case study.  
BMC Medical Genomics 2011, 4:55 - i.f. 3.77

P. Fardin, **A. Barla**, S. Mosci, L. Rosasco, A. Verri, R. Versteeg, H. N. Caron, J. J.  
Molenaar, I. Ora, A. Eva, M. Puppo and L. Varesio.  
A biology-driven approach identifies the hypoxia gene signature as a predictor of the  
outcome of neuroblastoma patients.  
Molecular Cancer, 9:185, 2010. - i.f. 4.16

P. Fardin, A. Cornero, **A. Barla**, S. Mosci, M. Acquaviva, L. Rosasco, C. Gambini, A.  
Verri, L. Varesio  
Identification of multiple hypoxia signatures in neuroblastoma cell lines by l1-l2 regu-  
larization and data reduction.  
Journal of Biomedicine and Biotechnology, 2010. - i.f.1.75

P. Fardin, **A. Barla**, S. Mosci, L. Rosasco, A. Verri, L. Varesio  
The l1-l2 regularization framework unmasks the hypoxic signature hidden in the tran-  
scriptome of a set of heterogeneous neuroblastoma cell lines.  
BMC Genomics, October 2009. - i.f. 3.76

C. Mosci, S. Mosci, **A. Barla**, S. Squarcia, P. Chauvel, A. Iborra  
Proton Beam radiotherapy of uveal melanoma: the italian patients treated in Nice,  
France

European Journal of Ophtalmology, 2009 - i.f. 1.018

**A. Barla**, G. Jurman, S. Riccadonna, M. Chierici, S. Merler, and C. Furlanello.  
Machine learning methods for predictive proteomics.  
Briefings in Bioinformatics 2008 9: 119-128 - .f. 7.329

G. Jurman, S. Merler, **A. Barla**, A. Galea, C. Furlanello.  
Algebraic stability indicators for ranked lists in molecular profiling.  
Bioinformatics , 24(2):258-264, 2008 - i.f. 7.329

M. Cannataro, **A. Barla**, R. Flor, A. Gallo, G. Jurman, S. Merler, S. Paoli, G. Tradigo,  
P. Veltri, and C. Furlanello  
A grid environment for high-throughput proteomics.  
IEEE Trans. on Nanobiosciences, 6(2):117-123, 2007 - i.f. 1.705

F. Odone, **A. Barla** and A. Verri.  
Building Kernels from Binary Strings for Image Matching.  
IEEE Trans. on Image Processing. Feb 2005 - i.f. 2.848

**Conference Proc.** G. Zycinski, **A. Barla**, A. Verri.  
SVS: Data and knowledge integration in computational biology.  
Proceedings of IEEE EMBC 2011, Boston, USA

**A. Barla**, G. Jurman, R. Visintainer, M. Squillario, M. Filosi, S. Riccadonna, C.  
Furlanello.  
A machine learning pipeline for discriminant pathways identification.  
Proceedings of CIBB2011, ISBN: ISBN online 9788890643705. Gargnano, Italy.

L. Baldassarre, **A. Barla**, L. Rosasco.  
Vector Field Learning with Spectral Filtering.  
Proc. of ECML-PKDD, Barcelona, Spain. Sept, 2010.

A Barla, L Baldassarre, N Noceti, F Odone.  
Learning How to grasp objects.  
Proc. of ESANN, European Symposium on Artificial Neural Networks 2010.

**A. Barla** and M. Ferrante.  
Deployment of a regularized feature selection framework on an overlay desktop grid  
Proc. of HiBi09 High Performance Computational Systems Biology, October 2009.

N. Noceti, B. Caputo, C. Castellini, L. Baldassarre, **A. Barla**, L. Rosasco, F. Odone  
and G. Sandini  
Towards a theoretical framework for learning multi-modal patterns for embodied agents.  
Proc. of Image Analysis and Processing - ICIAP 2009, 15th International Conference.  
2009.

L. Baldassarre, **A. Barla**, B. Gianesin, M. Marinelli  
Vector Valued Regression for Iron Overload Estimation  
Proc. of 19th International Conference on Pattern Recognition. ICPR - Tampa, FL,  
Dec 2008.

S. Mosci, **A. Barla**, A. Verri, and L. Rosasco.  
Finding structured gene signatures.  
IEEE Proc. of Workshop on Data Mining in Functional Genomics (IEEE International

Conference on Bioinformatics and Biomedicine), Nov 2008.

**A. Barla**, S. Mosci, L. Rosasco and A. Verri.  
A method for robust variable selection with significance assessment.  
Proc. of ESANN, European Symposium on Artificial Neural Networks 2008.

**A. Barla**, B. Irler, S. Paoli, G. Jurman, S. Merler, and C. Furlanello.  
Semisupervised multiband segmentation for predictive proteomic analysis.  
Proc. of Congress of European Proteomics Association, Valencia, Feb, 2007.

**A. Barla**, B. Irler, S. Merler, G. Jurman, S. Paoli, and C. Furlanello.  
Proteome profiling without selection bias.  
In Proceedings of IEEE-CMBS 2006.

F. Odone, **A. Barla**, E. Franceschi and A. Verri.  
Web tools to support image classification.  
In Proceedings of Electronic Imaging. San Jose, CA, USA. January 2005.

F. Odone, **A. Barla** and A. Verri.  
Histogram intersection kernel for image classification.  
In Proceedings of ICIP 2003, Barcelona, Spain. September 2003.

**A. Barla**, F. Odone and A. Verri.  
Old Fashioned State-of-the-Art Image Classification.  
In Proceedings of ICIAP 2003, Mantova, Italy. September 2003.

**A. Barla**, F. Odone and A. Verri.  
Hausdorff Kernel for 3D Object Modeling and Recognition.  
INFMeeting 2002.

**A. Barla** and F. Odone.  
Kernel-based 3D Object Representation.  
In Proceedings of ICANN, LNCS 2415, p. 1195 ff, 2002

**A. Barla**, E. Franceschi, F. Odone and A. Verri.  
Image kernels.  
In Proceedings of the International Workshop on Pattern Recognition with Support Vector Machines, satellite event of ICPR 2002, LNCS 2388, p. 83 ff, 2002.

**A. Barla**, F. Odone and A. Verri.  
Hausdorff Kernel for 3D Object Acquisition and Detection.  
In European Conference on Computer Vision, LNCS 2353, pp 20 – 33, 2002.

**Short Papers**  
**Oral Comm.**  
**Posters**

M. Squillario, C. Malattia, C. Basso, **A. Barla**.  
A molecular based subtyping in juvenile idiopathic arthritis (JIA)  
19th Annual ECCB/ISMB - International Conference on Intelligent Systems for Molecular Biology and 10th European Conference on Computational Biology, 2011.

M. Squillario, S. Masecchia, G. Zycinski, **A. Barla**.  
Uncovering Candidate Biomarkers for Alzheimer's and Parkinson's Diseases with Regularization Methods and Prior Knowledge, Neuro-Degenerative Diseases - Elect. Proceedings of AD/PD 2011, Barcelona, Spain, 8 (Supp. 1) , 2011.

**A. Barla**, S. Masecchia, M. Squillario.



L1-L2 regularization framework for Alzheimer's molecular characterization.  
ISMB - 18th Annual International Conference on Intelligent Systems for Molecular Biology, 2010.

S. Mascelli, A. Raso, P. Nozza, S. Pignatelli, R. Biassoni, **A. Barla**, S. Mosci, L. Rosasco, A. Verri, G. Wittenberg, K. Noy, C. Mircean, D. Fasulo, G. Morana, C. Milanaccio, A. Cama, V. Capra, V, M. L. Garrè.  
Specific gene expression signatures of low-grade gliomas (LGG).  
Neuro-Oncology, 12 (6) , pp.II23–II23, 2010.

S. Mascelli, A. Raso, P. Nozza, S. Pignatelli, R. Biassoni, **A. Barla**, S. Mosci, L. Rosasco, A. Verri, G. Wittenberg, K. Noy, C. Mircean, D. Fasulo, G. Morana, C. Milanaccio, A. Cama, V. Capra, V, M. L. Garrè.  
Low-grade gliomas: identification of specific gene expression profiles.  
Haematol-Hematol J, 95 (7) , pp.S2–S3, 2010.

B. Di Camillo , M. Martini, T. Sanavia, G. Jurman, F. Sambo, **A. Barla**, M. Squillario, C. Furlanello, G. Toffolo, C. Cobelli.  
Effect of size and heterogeneity of samples on biomarker discovery: synthetic and real data assessment.  
ECCB European Conference on Computational Biology, Ghent, Belgium, 2010.

M. Squillario, S. Masecchia , **A. Barla**.  
Functional characterization of Parkinson by high-throughput data analysis with l1l2 regularization.  
ECCB European Conference on Computational Biology, Ghent, Belgium, 2010.

**A. Barla**, S. Mosci, L. Rosasco, A. Verri, P. Fardin, A. Cornero, M. Acquaviva, L. Varesio.  
Combining l1-l2 regularization with biological prior for multi-level hypoxia signature in Neuroblastoma  
Workshop on Machine Learning in Systems Biology, 2010.

T. Sanavia, **A. Barla**, B. Di Camillo, S. Mosci, G. Toffolo.  
Function-based analysis of microarray data via l1-l2 regularization  
ISMB/ECCB Stockholm, Sweden. July 2009.

## Book Chapters

**A. Barla**, G. Jurman, R. Visintainer, M. Squillario, M. Filosi, S. Riccadonna, C. Furlanello.  
A machine learning pipeline for discriminant pathways identification A Systems Biology Approach.  
Editor: N. Kasabov. Springer Handbook of Bio- and Neuroinformatics (to appear, 2012)

S. Parodi, L. Tortolina, N. Castagnino, C. De Ambrosi, **A. Barla**, F. Patrone, A. Ballestrero.  
Dynamic simulations of pathways downstream of TGF-beta, Wnt and EGF-family growth factors, in colorectal cancer, including mutations and treatments with onco-protein inhibitors.  
Editors: A. dOnofrio, Z. Agur, P. Cerrai and A. Gandolfi. New Challenges for Cancer Systems Biomedicine. Springer Verlag - SIMAI Lecture Notes (to appear, 2012)

**A. Barla**, S. Riccadonna, G. Jurman, and C. Furlanello.  
Classificazione predittiva per il profiling proteomico.

Genomica e Proteomica Computazionale, volume 26 of CNR - Gruppo Nazionale di Bioingegneria, pages 227-244, Patron editore, 2007.

## Teaching Activity

2005-2010: co-supervisor for PhD students (S. Mosci, L. Baldassarre, S. Masecchia, G. Zycinski), MSc students (B. Irlor, S. Pongiglione) and BSc students (L. Gemme).

2011/2012 - **Lecturer** (Professore a contratto).

Introduction to Computer Science (Fondamenti di Informatica)

6 credits, 60h.

I year - Corso di Laurea in Scienze dell'Architettura.

Facoltà di Architettura e Ingegneria. Univ. Genova

2010/2011 - **Lecturer** (Professore a contratto).

Introduction to Computer Science (Fondamenti di Informatica)

6 credits, 87 students, 60h.

I year - Corso di Laurea in Scienze per il Progetto Integrato T.A.P.

Facoltà di Architettura e Ingegneria. Univ. Genova

2009/2010 - **Lecturer** (Professore a contratto).

Introduction to Computer Science (Fondamenti di Informatica)

4 credits, 97 students, 40h.

I year - Corso di Laurea in Tecniche per la Pianificazione Urbanistica Territoriale e Ambientale Facoltà di Architettura e Ingegneria. Univ. Genova

2005/2006 - **Lecturer** (Professore su invito).

Statistical Machine Learning, 3 credits, 8h.

<http://ict.unitn.it/program/exams/courses/21417-statistical-machine-learning>

PhD Course, ICT - Information and Communication Technology Doctoral School, Univ. Trento

2003/2004, 2006/2007, 2007/2008, 2008/2009, 2009/2010 - **Monographic lectures and Teaching Assistant** (Lezioni frontali ed esercitazioni in laboratorio)

Statistical Learning (Apprendimento Statistico), 15 h/AY.

Computer Science MsC (Corso di Laurea Specialistica in Informatica), Univ. Genova

2008/2009, 2009/2010 - **Monographic lectures and Teaching Assistant** (Lezioni frontali ed esercitazioni in laboratorio)

Mathematical Foundations of Statistical Learning (Fondamenti matematici per l'Apprendimento Statistico), 10h/AY.

Math MsC (Corso di Laurea Specialistica in Matematica), Univ. Genova

2008/2009 - **Project Supervisor** (G. Chiusano (1 e 2), M. Strumia)

Laboratorio Specialistico 1 e 2, 15h/AY

Computer Science MsC (Corso di Laurea in Informatica), Univ. Genova

2003/2004 - **Monographic lectures and Teaching Assistant** (Lezioni frontali ed esercitazioni in laboratorio)

Computer Vision 2 (Visione Computazionale 2), 10h. Computer Science MsC (Corso di Laurea in Informatica), Univ. Genova

2002/2003 **Teaching Assistant** Esercitazioni in laboratorio

Computer Vision 1 (Visione Computazionale 1), 10h.

Computer Science MsC (Corso di Laurea in Informatica), Univ. Genova

## **Professional Activities**

### **Oral Presentations (Refereed Conferences)**

IEEE ISBM 2011 - 19th Annual International Conference on Intelligent Systems for Molecular Biology and 10th European Conference on Computational Biology, Boston, MA, USA.  
CIBB 2011 - Eighth International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics  
MLSB 2010 - Fourth International Workshop on Machine Learning in Systems Biology, Edinburgh, UK  
ISMB 2010 - International Conference on Intelligent Systems for Molecular Biology, Boston, MA, USA  
MGED11 - 11th International Meeting of MGED, September 2008, Riva del Garda  
BITS 2009 - Bioinformatics Italian Society Meeting, Genova  
BIBM 2008 - IEEE International Conference on Bioinformatics and Biomedicine, Philadelphia, PA, USA  
ESANN 2008 - European Symposium on Artificial Neural Networks, 23 April 2008, Bruges, Belgium  
ICIP 2003- International Conference on Image Processing Barcelona, Spain

### **Oral Presentations (Non-Refereed Conferences)**

SONO 2008 - XXXIII Riunione Societ Oftalmologica Nord-Occidentale, Genova

### **Workshop/Conference Organization**

11/2011 Workshop on Different aspects of mathematical modeling applied to systems biology, DISI, Genova  
11/2011 I Giornata Ligure di Bioinformatica, DISI, Genova  
06/2007 a journey through computation, Oratorio San Filippo Neri, Genova  
09/2006 Third Bioinformatics Meeting on Machine Learning for Microarray Studies of Disease: biomarker selection. Oratorio San Filippo Neri, Genova

### **Invited Seminars**

11/2011 Parameter space exploration within dynamic simulations of signaling networks. Workshop on Different aspects of mathematical modeling applied to systems biology, DISI, Genova.  
11/2011 A computational procedure for functional characterization of potential marker genes from molecular data: Alzheimer's as a case study.  
I Giornata Ligure di Bioinformatica. Genova, Italy.  
05/05/2011 Alzheimer's microarray data analysis.  
European Brain Research Institute (EBRI) Rita Levi- Montalcini, Roma, Italy  
2006-2010: Health-e-Child Project: updates on task status (Toledo, Spain - Paris, France - Archamps, France).  
08/10/2005 Correlation-aware feature selection  
Second Bioinformatics Meeting on Machine Learning for the Microarray Studies of Disease 2005. Wannsee, Germany.  
05/2005 Kernels for Images.  
Trento, Italy. ITC-IRST.  
09/2004 A general framework for Image Kernel Engineering.  
Siemens Corporate Research, Princeton NJ USA.

### **Reviewing**

I have contributed to the revision process for submitted papers for: Plos One, BMC Genomics, Briefings in Bioinformatics, Pattern Recognition.

### **Program Committee Member**

IJCAI-13 - 23rd International Joint Conference on Artificial Intelligence - Beijing,

China

IDAMAP 2012 - Intelligent Data Analysis in bioMedicine And Pharmacology - Pavia, Italy

**Software Development:** I contributed to the implementation of code for data pre-processing, data statistical analysis and data visualization using the R package, Matlab, C/C++ and Python.

**Distributed Computing:** I used different distributed computing infrastructures (grid/ cloud/cluster) and I am familiar with the main distributed computing environments.

**General Computer Skills:** I am proficient in dealing with the main operating systems across platforms (Linux/Mac/Win). I wrote code and developed several webpages, using HTML combined with CSS or adopting CMS (Content Management Systems) such as Joomla and Wordpress. I also implemented graphical using Photoshop/GIMP.

**Language Skills** Excellent knowledge of written and spoken English. Basic knowledge of French.