

Education

- 2005–2007 **Ph.D. in Molecular Medicine**, *University of Milano*, Milano.
- 1996–2002 **Degree in Pharmaceutical Biotechnology**, *University of Milano*, Milano, Evaluation: 103/110.
- 1995 **Maturità scientifica**, *Istituto Salesiano S.Ambrogio*, Milano, Final evaluation: 49/60.

Ph.D. Thesis

- Title *Identification of deregulated metabolic pathways by transcriptomic analysis in renal cell carcinoma samples*
- Supervisor Dr.ssa Cristina Battaglia
- Description A bioinformatics approach based on pathway analysis is proposed in this work, in order to identify common deregulated pathways in samples from renal cell carcinoma samples.

Master thesis

- Title *Study on the structure-function relationship of KAAT1, a Na⁺/K⁺ dependent amino acid transporter*
- Supervisor Prof. Franca V. Sacchi
- Description A structure-function relationship study on the KAAT1 amino acid transporter from *Manduca sexta* using functional expression in *Xenopus laevis* oocytes.

Attended courses

- March 2006 **6th Bioinformatics course**, *European School of Genetic Medicine*, Bertinoro di Romagna, Italy.
- June 2008 **NuGO Hands-on microarray data analysis course**, *University of Maastricht*, Maastricht, The Netherlands.

Work experience

- 2008–current **Bioinformatics work on microarray data for the University of Florence**, *Department of Pharmacology, University of Florence*, Florence.
Research fellowship in Dr.Duccio Cavalieri's group to work on data analysis techniques for microarray data, especially regarding pathway analysis and database integration, on the fields of immunology and nutrigenomics.
- 2004–March 2009 **Bioinformatics work in the field of solid state tumors at Dr. Cristina Battaglia's laboratory**, *Centre of excellence CISI, University of Milano*, Milano.
Data analysis of renal cell carcinoma data obtained through microarray experiments.
- 2003–2004 **Cellular and molecular biology research on mouse neuronal development at Dr. Vania Broccoli's laboratory**, *DIBIT, San Raffaele Scientific Park, Segrate*, Milano.
Investigation of the expression of the ARX gene in primary cultured neurons.
- 2002–2003 **Work at Prof. Marco Parenti's laboratory on the function of caveolin-1 in neuronal development**, *DiMeSAB, University of Milano-Bicocca*, Monza.
Analysis of the CAV-1 protein expression in cell cultures mimicking different neuronal development states.

Miscellaneous experience

- April 2008 Participant and speaker at the **DC-THERA Annual Meeting** (Athens, Greece)
- June 2008 Teacher at the **NuGO hands-on microarray data analysis course** (Maastricht, The Netherlands) on the subject of pathway analysis
- November 2008 Speaker at the **I-ATLAS 2008: International Workshop on Gene Signalling Pathway Analysis and Representation for the Dendritic Cell** (Firenze, Italy) with the talk "Eu.Gene - a bioinformatic environment to query microarray databases with a pathway based logic"

Computer skills

OS	Linux, Unix, Windows	scientific	Affymetrix GCOS, GTYPE, CNAT, CNAG
programming	Python, PyQt, R	scripting	PHP (basic), Bash
typography	L ^A T _E X	image processing	Photoshop, GIMP
web design	XHTML, CSS	office suites	Openoffice.org, Microsoft Office
bioinformatics	functional annotation, pathway analysis, gene expression		

Languages

Italian	Native
English	Very good
Japanese	Basic

Interests

- Developmental biology I'm interested in how neurons mature and differentiate into their adult form.
- Pathway analysis Recently I have developed interest in the analysis of differentially regulated pathways in microarray data sets, as a viable alternative to traditional gene-based approaches.
- Bioinformatics Bioinformatics and related topics are very interesting for me, in particular the aspects related to data integration and pathway analysis.
- Web 2.0 The so-called *semantic web* technology is one of my main technology-related interests, even more so because of its use in modern bioinformatics

Publications

- Luca Beltrame, Lisa Rizzetto, Raffaele Paola, Philippe Rocca-Serra, Luca Gambineri, Cristina Battaglia, and Duccio Cavalieri. Using pathway signatures as means of identifying similarities among microarray experiments. *PLoS ONE*, 4(1):e4128, 2009.
- A. Callegaro, R. Spinelli, L. Beltrame, S. Bicciato, L. Caristina, S. Censuales, G. De Bellis, and C. Battaglia. Algorithm for automatic genotype calling of single nucleotide polymorphisms using the full course of TaqMan real-time data. *Nucleic Acids Res.*, 34(7):e56, 2006.
- Ingrid Cifola, Clelia Peano, Marco Severgnini, Roberta Spinelli, Luca Beltrame, Silvano Bosari, Ester Fasoli, Silvio Bicciato, and Cristina Battaglia. Poster: Integration of whole-genome SNP mapping and transcriptional data in the human metastatic renal carcinoma Caki-1 cell line. In *9th International Congress of the European Association for Cancer Research*, Budapest, Czech Republic, July 2006.
- Ingrid Cifola, Roberta Spinelli, Luca Beltrame, Clelia Peano, Ester Fasoli, Stefano Ferrero, Silvano Bosari, Stefano Signorini, Francesco Rocco, Roberto Perego, Vanessa Proserpio, Francesca Raimondo, Paolo Mocarrelli, and Cristina Battaglia. Genome-wide screening of copy number alterations and loh events in renal cell carcinomas and integration with gene expression profile. *Molecular Cancer*, 7:6+, January 2008.
- F. Raimondo, M. Verga, S. Ferrero, I. Cifola, R. Spinelli, L. Beltrame, C. Peano, C. Bianchi, V. Angeloni, F. Rocco, F. Magni, A. Di Fonzo, V. Proserpio, M. Galli-Kienle, C. Battaglia, P. Mocarrelli, and M. Pitto. Poster: Integration of genome wide molecular analysis and subcellular proteomics for renal cell carcinoma biomarker identification. In *2nd annual conference of the Italian Proteomic Association*, Acitrezza (Catania), Italy, 2007.

R. Spinelli, I. Cifola, S. Ferrero, L. Beltrame, P. Mocarrelli, and C. Battaglia. Assessment of common regions and specific footprints of dna copy number aberrations across multiple affymetrix SNP mapping arrays. In *Fourth International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics*, Portofino, Italy, 2007.

M. Zampieri, I. Cifola, D. Basso, R. Spinelli, L. Beltrame, C. Peano, C. Battaglia, and S. Bicciato. A computational procedure for the integrative analysis of genomic data at the single sample level. In *10th Symposium on Computer applications in biotechnology*, Cancún, Mexico, 2007.