SILVIO BICCIATO

Curriculum vitae

PERSONAL INFORMATION

Family name	Bicciato
First name	Silvio
Nationality	Italian
Date of birth	08-02-1967
Phone	+39 059 205 5219
Email	silvio.bicciato@unimore.it
Web	http://personale.unimore.it/Rubrica/dettaglio/sbicciat

CURRENT POSITION

Full Professor of Industrial Bioengineering
University of Modena and Reggio Emilia – Dept. of Life Sciences and Center for Genome Research

EDUCATION

1993 – 1996	PhD, Chemical Engineering (automatic control of biochemical processes), School of Engineering, University of Padova (Padova, Italy)
1986 – 1992	BS, Chemical Engineering (automation of protein synthesis), School of Engineering, University of Padova, (Padova, Italy)

POST GRADUATE TRAINING AND FELLOWSHIP APPOINTMENTS

1998 – 2000	Research Fellow, Dept. of Chemical Engineering Processes – University of Padova, (Padova, Italy)
1996 – 1998	NATO-CNR Post-doctoral Associate – Bioinformatics and Metabolic Engineering Lab (Prof. Gregory N. Stephanopoulos) – MIT Massachusetts Institute of Technology (Cambridge, MA)

EMPLOYMENT

2016 – present	Full Professor of Industrial Bioengineering, Dept. of Life Sciences – University of Modena and Reggio Emilia (Modena, Italy)
2010 – 2016	Associate Professor of Industrial Bioengineering, Dept. of Life Sciences – University of Modena and Reggio Emilia (Modena, Italy)
2007 – 2010	Assistant Professor of Industrial Bioengineering, Dept. of Biomedical Sciences – University of Modena and Reggio Emilia (Modena, Italy)
2004 – 2007	Assistant Professor of Industrial Bioengineering, Dept. of Chemical Engineering Processes – University of Padova (Padova, Italy)
1998 – 2003	Research Associate, Dept. of Chemical Engineering Processes – University of Padova (Padova, Italy)

TEACHING

Class Lecturing

- University of Modena and Reggio Emilia – Dept. of Life Sciences: I am currently teaching the classes of "Bioinformatics" (BS Program in Biotechnologies), "Introduction to the Analysis of Biological Data" and "Functional Interpretation of Genomic data" (MS Program in Medical Biotechnologies), and "Applied Bioinformatics" (PhD Program in Molecular and Regenerative Medicine). I also chaired the classes of "Analysis Genomes: Methods and Applications" (MS Program in Medical Biotechnologies) and "Principles of Metabolic Engineering" (MS Program in Industrial Biotechnologies).
- University of Modena and Reggio Emilia – Dept. of Dept. of Physics, Informatics and Mathematics: I am currently

teaching the classes of "Bioinformatics" (MS Program in Informatics).

- University of Padova – School of Engineering: I chaired the classes of "Cellular Bioengineering" (MS Program in Bioengineering) and "Genomics for Bioengineering" (MS Program in Bioengineering).
- University of Milano-Bicocca: I chaired the class of "Functional Genomics" (MS Program in Molecular Immunology)

Student Training and Supervision of Postdoctoral Fellows

I trained more than 20 undergraduate students, 12 PhD students, and 14 postdocs. Of these, 7 have now independent positions in academic and research institutions in Italy, Europe, and US. I take pride in the fact that, despite the small dimension of my group, most of my post-docs managed to complete interesting work and obtain first author publications in leading journals. As Director of the MS Program in Industrial Biotechnologies (2012 – 2018), I supervised admissions, classes, international traineeships, and graduations of BS students.

School Organization and Chairing

I organized specific, problem-oriented, national and international hand-on training courses in Bioinformatics to support users across the life sciences (i.e., biologists, bench scientists, geneticists, biochemists, clinical specialists) in the use of methods and software for the analysis of high-throughput genomic data.

2012 Chair, 3rd Bioinformatics Training School (EuGESMA Cost Action: European Genomics and Epigenomics Study on MDS and AML) – Modena (Italy)
2011 Chair, 2nd Bioinformatics Training School (EuGESMA Cost Action: European Genomics and Epigenomics Study on MDS and AML) – Modena (Italy)
2010 Chair and lecturer, 1st Bioinformatics Training School (EuGESMA Cost Action: European Genomics and Epigenomics Study on MDS and AML) – Barcelona (Spain)
2007 Chair and lecturer, XXVI Annual School of the National Bioengineering Group: Computational Genomics and Proteomics – Bressanone (Bolzano, Italy)
2004 Chair and lecturer, Practical Course in Analysis of data from microarray platforms – Dept. of Oncological and Surgical Sciences – University of Padova (Padova, Italy)

INSTITUTIONAL RESPONSIBILITIES

2012 – present Head, Bioinformatics Core, Center for Genome Research – University of Modena and Reggio Emilia
2012 – 2018 Director, MS Program in Industrial Biotechnologies, Dept. of Life Sciences – University of Modena and Reggio Emilia
2012 – 2014 Member, Scientific Advisory Board, Dept. of Life Sciences – University of Modena and Reggio Emilia
2012 – 2014 Member, Permanent Ministry Committee for national evaluation of Assistant Professorships in Industrial Bioengineering – all Italian universities
2011 – 2012 Member, Board for the institution of the Dept. of Life Sciences – University of Modena and Reggio Emilia
2018 – present Grant review panelist, EEA and Norway Grants 2014-2021
2017 – present Grant review panelist, Bando FAS Salute 2014, Regione Toscana
2012 – present Grant review panelist, Italian SuperComputing Resource Allocation – ISCRA Grants, CINECA
2009 – present Grant review panelist, Italian Ministry for Education and Research
2010 – 2011 Grant review panelist, Swiss National Science Foundation
2009 – 2010 Grant review panelist, Regional Call for Medical Research, Regione Liguria

MEMBERSHIPS OF SCIENTIFIC SOCIETIES

2015 – present ISCB – International Society for Computational Biology

OTHER ACTIVITIES

- *Ad hoc* reviewer for career promotions and awards for Italian universities and research institutions.
- Member of the Editorial Board of Cancer Informatics.

- Reviewer activity: Regularly for Bioinformatics, BMC Bioinformatics, Nucleic Acids Research, Genome Biology, Nature Communications, Briefings in Bioinformatics, PLoS Computational Biology. Occasionally for Nature Methods, Cell Reports, Cell Systems, Biotechnology and Bioengineering, Metabolic Engineering, Blood, Cancer Informatics, Journal of Biotechnology.

PATENTS

2011 WO/2011/157294 – Compositions for use in treating or preventing cancer, breast cancer, lung cancer, ovarian cancer, metastasis, heart failure, cardiac remodeling, dilated cardiomyopathy, autoimmune diseases, or diseases or disorders related thereto

2010 WO/2010/083880 – Prognosis of breast cancer patients by monitoring the expression of two genes

RESEARCH

I started my lab in 2003. Throughout my career, I have pursued research lines that I considered innovative and used multidisciplinary approaches to push our research efforts in computational biology and bioinformatics significantly beyond the state of the art. In the last 15 years, I raised more than 2.1M € in research funds from national and international competitive grants. I created the Bioinformatics Core at the Center for Genome Research of the University of Modena and Reggio Emilia, an interdisciplinary group that includes computer scientists, molecular biologists, statisticians, biotechnologists, and engineers who cooperate in the generation and application of bioinformatics tools for the analysis of high-throughput molecular data. Currently, the team of the Bioinformatics Core consists of 1 assistant professor, 3 postdocs, 2 PhD students, and 4 MS students. The computing resources comprise a total of 248 processor cores, including a server for memory-intensive applications with 24TB disk space, 1TB of RAM memory, and 64 core processors. File storage is provided by network-attached storage units, which collectively offer access to over 130TB of usable file space. The Bioinformatics Core can also use HPC resources at CINECA, one of the largest computing centers in Europe, within the context of ELIXIR-IIB, the Italian node of the European Infrastructure for Bioinformatics.

On-going Grants

09/2015 – 08/2020 ERC Advanced Grant program H2020: *De novo generation of somatic stem cells by YAP/TAZ: regulation and mechanisms of cell plasticity* (Unit PI: S. Bicciato; Project PI: S. Piccolo; Project budget: 2.499.000,00 €; Unit budget: 260.000,00 €)

01/2012 – 12/2018 Italian Ministry of University and Scientific Research – ITALIAN FLAGSHIP PROJECTS – *EPIGEN: Epigenomics flagship project* (Unit PI: S. Bicciato; Project PI: G. Macino; Unit budget: 100.000,00 €)

Completed Grants

2011 –2018 Italian Association for Cancer Research (AIRC) – Special Program Molecular Clinical Oncology 5x1000: *Molecular basis for triple negative breast cancer metastasis: new tools for diagnosis and therapy* (Unit PI: S. Bicciato; Project PI: G. Del Sal; Project budget: 12.000.000,00 €; Unit budget: 500.000,00 €)

2015 –2018 CARIPLO Foundation: *RAN-translation of normal and expanded nucleotide repeats containing transcripts to neurotoxic polypetides* (Unit PI: S. Bicciato; Project PI: A. Poletti; Project budget: 330.000,00 €; Unit budget: 100.000,00 €)

2013 – 2018 JDRF – Type 1 Diabetes Research Funding and Advocacy – Strategic Research Agreement: *Islets specific aptamers by cell-selex and high throughput sequencing* (Unit PI: S. Bicciato; Project PI: P. Serafini; Project budget: 999.000,00 $; Unit budget: 30.000,00 $)

2015 – 2017 Italian Ministry of University and Scientific Research – ITALIAN FLAGSHIP PROJECTS – *EPIGEN: Study of mutant p53-dependent epigenetic modifications in HNSCC* (Unit PI: S. Bicciato; Project PI: G. Blandino; Project budget: 300.000,00 €; Unit budget: 89.000,00 €)

2013 – 2015 GENETHON France – Collaborative research project (PI: S. Bicciato; Unit budget: 60.000,00 €)

2012 – 2015 FIRB – Collaborative Research Project RBAP11T3WB: *RNA and nanotechnology in the control of neoplastic immunosuppression sustained by amino acid catabolism* (Unit PI: S. Bicciato; Project PI: U. Grohmann; Project budget: 1.709.000,00 €; Unit budget: 344.000,00 €)

2009 – 2013 EU – Cost Action BM0801 *European Genomics and Epigenomics Study on MDS and AML* (Unit PI: S. Bicciato; Project PI: K. Mills)

2008 – 2010 CARIMO Foundation – Grant for International Projects 2008: *Development of a bioinformatics framework for the analysis of complex biological systems: application to the study of myeloid differentiation* (PI: S. Bicciato; Project budget: 84.000,00 €)

2007 – 2010 PRIN – Collaborative Research Project 2007Y84HTJ: *A systems biology approach to reconstruct the networks of molecular interaction and the monocyte/macrophage activation process in response to inflammation under physiological conditions using omic technologies* (Unit PI: S. Bicciato; Project PI: C. Battaglia; Project budget: 110.255,00 €; Unit budget: 15.000,00 €)

2007 – 2010 CARIPARO Foundation – Grant of Excellence 2006: *A computational approach to the study of skeletal muscle genomic expression in health and disease* (PI: S. Bicciato; Project budget: 300.000,00 €)

2007 – 2009 PRIN – Collaborative Research Project 2005069853: *Immune response against prostate cancer: molecular basis for novel therapeutic strategies* (Unit PI: S. Bicciato; Project PI: F. Pagano; Project budget: 115.000,00 €; Unit budget: 29.000,00 €)

2006 – 2008 FIRB – Collaborative Research Project RBAU01935A: *Genome-wide analysis of accessory cells that control the immune response* (Unit PI: S. Bicciato; Project PI: V. Bronte; Unit budget: 40.000,00 €)

2004 – 2006 ONCOSUISSE 2004-2006: *Collaborative Cancer Research Project OCS 01517022004: Cancer genes involved in genetic progression of germinal center B cell lymphomas* (PI: F. Bertoni)

2003 – 2007 FIRB – Collaborative Research Project RBNE01TZZ8: *Biomolecules, fluids, systems and data handling in Bio-chip technology* (Unit PI: S. Bicciato; Project PI: G. De Bellis; Unit budget: 218.000,00 €)

Main Research Lines and Achievements

My principal research interest is the design and application of computational biology and bioinformatics methods to organize, analyze, compare, interpret, and visualize -omics data. From a methodological standpoint, my current research lines comprise the development of methods, resources and tools for i) integrative analysis of multi -omics and phenotypic data; ii) epigenomics and 3D genome; iii) computational systems biology; and iv) single cell genomics. From an applicative perspective, my research supported wet biologists in investigating the genomic bases of complex biological systems, with particular emphasis on onco-genomics, immunogenomics, and neurosciences. With some of these groups, we are operating like one extended laboratory, where we provide key support to bioinformatics analyses of -omics data. Following is a summary of my contributions in computational biology and basic life-science research.

1. **Integrative analysis of multi-omics and phenotype data.** We developed pioneering methods to merge different type of genomics data and -omics data with phenotype characteristics, clinical information, outcomes, and drug responses. Specifically:
   a. we designed tools for the batch retrieval from public repositories of raw data files and of any related meta-information, their local organization, the re-annotation of samples to create user-defined batches of data, the integrative analysis of data obtained from different platforms, and the sharing of data, meta-information, analysis flows and results (Ferrari et al., Bioinformatics 2007; Bisognin et al., BMC Bioinformatics 2009; Fallarino et al., Nat Med 2010);
   b. we constructed and analyzed in-silico databases of high throughput experimental data and clinical information (more than 6800 breast cancer samples and more than 1500 lung cancers), obtained from whole transcriptome sequencing and microarray assays. Gene expression profiling allowed stratifying cancers into molecularly and clinically different subtypes with distinct gene expression patterns and the identification, testing, and validation of prognostic and predictive signatures in cancer tissues (Adorno et al., Cell 2009; Cordenonsi et al., Cell 2011; Montagner et al., Nature 2012; Rustighi et al., EMBO Mol Med. 2014; Di Minin et al., Mol Cell. 2014; Enzo et al., EMBO J 2015; Turner et al., NPJ Breast Cancer. 2015; Sorrentino et al., Nat Commun. 2017; Santinon et al., EMBO J 2018; Ingallina et al., Nat Cell Biol. 2018; Poli et al., Nat Commun. 2018);

c. we implemented novel integrative approaches to complement gene expression data with other types of gene information, as copy number and chromosomal localization (Callegaro et al., Bioinformatics. 2006; Bicciato et al., Nucleic Acids Res. 2009; Ferrari et al., Bioinformatics. 2011; Lahti et al., Brief Bioinform. 2013) and the transcriptional landscape of non-coding RNAs (Tenedini et al., Cell Death Dis. 2010; Lionetti et al., Blood 2009; Martello et al., Cell 2010; Sales et al., Nucleic Acids Res. 2010; Ganci et al., Mod Pathol. 2017; Pruszko et al., EMBO Rep. 2017; Lo Sardo et al., Carcinogenesis. 2017);
d. we defined new procedures for the integrative analysis of gene expression, genome-wide binding sites, and genomic interactions data to elucidate the mechanisms of action of transcriptional regulators (see Bioinformatics for epigenomics and 3D genome);
e. we deployed web-based tools for the integrative analysis of genomic traits (mutational status and transcriptional activation) and drug responses in cancer (Taccioli et al., Oncotarget 2015; Caroli et al., Nucleic Acids Res. 2018).

2. **Development of methods, resources and tools.** The translation of ideas, formalisms, and models first into algorithms and codes and then their implementations into user-friendly and professional software solutions with increasing levels of sophistication are among our methodological aims. We coded:
   a. SIMCA, a computational procedure for marker identification and for classification of multiclass gene expression data through the application of disjoint principal component models (Bicciato et al., Bioinformatics 2003; Bicciato et al., Methods Inf Med. 2004);
   b. BCGA, an algorithm for automatic genotype calling based on the full course of real-time PCR data (Callegaro et al., Nucleic Acids Res. 2006);
   c. SODEGIR, a procedure to identify significant overlap of differentially expressed and genomic imbalanced regions in cancer datasets (Bicciato et al., Nucleic Acids Res. 2009);
   d. PREDA, an R package that builds on our previous LAP locally adaptive statistical procedure (Callegaro et al., Bioinformatics. 2006) to detect regional variations in genomics data (Ferrari et al., Bioinformatics. 2011).

   From a *developer* perspective, I perceive the gap between algorithms and codes designed by bioinformaticians and the need of wet biologists (the end *users*) to have friendly, flexible, and usable tools to explore molecular data. Thus, we developed, made available to the scientific community, and maintained user-friendly bioinformatics tools to handle and analyze large volumes of -omics data. Specifically, we designed:
   a. A-MADMAN (Bisognin et al., BMC Bioinformatics 2009), an open source web application which allows the retrieval, annotation, organization and meta-analysis of gene expression datasets obtained from Gene Expression Omnibus;
   b. UCbase 2.0, a platform-independent Web resource dedicated to the analysis of ultraconserved sequences (Lomonaco et al., Database 2015);
   c. APTANI, a computational tool to identify target-specific aptamers from HT-SELEX data and secondary structure information (Caroli et al., Bioinformatics 2015);
   d. WoPPER, a web tool integrating gene expression and genomic annotations to identify differentially expressed chromosomal regions in bacteria (Puccio et al., Nucleic Acids Res. 2017);
   e. MDP (Taccioli et al., Oncotarget 2015) and GDA (Caroli et al., Nucleic Acids Res. 2018), two web-based tools for Genomics and Drugs integrated Analysis that combine drug response data for >50,800 compounds with mutations and gene expression profiles across 73 cancer cell lines.

3. **Bioinformatics for epigenomics and 3D genome.** We developed and applied computational methods for the analysis of linear epigenomic marks and regulatory elements and their integration with transcriptional profiles in different physiological and pathological cellular systems (Coppe et al., Nucleic Acids Res. 2009; Poletti et al., PLoS One. 2015; Cavazza et al., Stem Cell Reports. 2016; Romano et al., Sci Rep. 2016; Hirsch et al., Nature 2017). We also introduced algorithmic approaches to superimpose chromosome conformation data to genome-wide maps of expression levels, epigenomic marks, regulatory elements, and transcription factor binding sites (Zanconato et al., Nat Cell Biol. 2015; Zanconato et al., Nat Med. 2018). We quantitatively compared the performances of Hi-C data analysis methods for the identification of multi-scale chromatin structures (Forcato et al., Nat Methods. 2017; Nicoletti et al., Curr Opin Biotechnol. 2018) and evidenced some crucial limitations of existing methods (e.g., their inefficacy in capturing subtle interaction patterns and changes in the chromatin architecture). Currently, in line with

projects to study the 3D genome organization in the nucleus, we are working on novel algorithms to analyze Hi-C data and study the dynamics of epigenetic landscapes.

4. **Computational systems biology.** We have been active in developing bioinformatics and computational biology approaches for reverse engineering and reconstruction of the cell regulatory landscape (Bicciato et al., Biotechnol Bioeng. 2003; Bicciato, Curr Opin Mol Ther. 2004; Biasiolo et al., Pac Symp Biocomput. 2010; Agnelli et al., Clin Cancer Res. 2011). Methodologically, we introduced the concept of the critical analysis of network components to inspect the transcriptional and post-transcriptional regulatory networks reconstructed from mRNA and microRNA expression data in pathological samples (Lionetti et al., Blood. 2009; Agnelli et al., Clin Cancer Res. 2011).
5. **Methods for single cell genomics.** Recent advances in single-cell techniques are providing exciting opportunities for dissecting cell heterogeneity and investigating cell identity, fate, and function. However, the analysis and modeling of single cell data -omics poses incredible computational challenges and needs entirely new bioinformatics techniques and methods. We are currently working on the development of i) new multi-dimensional approaches to extract, from the background noise, the higher-order information embedded into the 3D spatial, architectural and mutual organization of cells; ii) novel multi-scale algorithms to identify and model the molecular connections among cell regulatory circuits, dynamics and functional output; and iii) visualization tools to display and navigate cell atlases. Specifically, we are using machine-learning, deconvolution, and projection methods to associate variations in single cell gene expression profiles with specific regulatory mechanisms, define transcriptional fingerprints associated with tissues and phenotypes, and assess the spatial distribution of gene expression signatures within cellular subpopulations (Malecova et al., Nat Commun. 2018).
6. **Onco-genomics, immunogenomics, and neurosciences.** We applied tools and computational expertise to analyze genomics data from three main areas of research: onco-genomics, immunogenomics, and neurosciences. This inspired new interdisciplinary ideas and posed new bioinformatics challenges. Specifically, we supported the discovery that the transcription co-factor YAP and TAZ are important determinants of cancer and cancer metastasis (Cordenonsi et al., Cell 2011; Azzolin et al., Cell 2012; Azzolin et al., Cell 2014; Zanconato et al., Nat Cell Biol 2015), that these factors translate cell mechanics into coordinated changes of gene expression(Dupont et al., Nature 2011), and that their activation turns differentiated cells of different types into their corresponding somatic stem cells (Panciera et al., Cell Stem Cell 2016). We participated in the identification of novel metastasis inducing and suppressing mechanisms (Adorno et al., Cell 2009; Martello et al., Cell 2010; Montagner et al., Nature 2012) and in decoding layers of oncogene regulation (Rustighi et al., EMBO Mol Med. 2014; Di Minin et al., Mol Cell. 2014; Enzo et al., EMBO J. 2015; Sorrentino et al., Nat Commun. 2017; Santinon et al., EMBO J. 2018; Ingallina et al., Nat Cell Biol. 2018; Poli et al., Nat Commun. 2018). In the area of immunogenomics, we contributed to deciphering the role of the enzyme indoleamine 2,3-dioxygenase (IDO) in the immunosuppressive pathway of tryptophan catabolism (Orabona et al., Blood 2006) and its involvement in intracellular signaling events (Pallotta et al., Nat Immunol. 2011; Bessede et al., Nature 2014) and disease (Mondanelli et al., Immunity 2017; Mondanelli et al., Front Immunol. 2017; Orabona et al., JCI Insight. 2018). We contributed in the characterization of circulating inflammatory-type monocytes (Gallina et al., J Clin Invest. 2006) and of myeloid-derived suppressor cells (MDSCs MDSCs; Marigo et al., Immunity. 2010; Zoso et al., Eur J Immunol. 2014). We supported the discovery that a network of pro-tumor factors can be targeted to boost cancer immunotherapies (Marigo et al., Cancer Cell. 2016) and that mechanisms of iNKT cells might be harnessed for therapeutically reprogramming the tumor microenvironment in prostate cancer (Cortesi et al., Cell Rep. 2018). In the area of neurosciences, we contributed to the identification of signaling molecules involved in dampening the immune response during neuroinflammation, highlighting pathways that could be exploited therapeutically in chronic autoimmune diseases such as multiple sclerosis (Fallarino et al., Nat Med. 2010; Volpi et al., Neuropharmacology. 2016). Finally, we analyzed the transcriptional landscape of astrocytes differentiation and supported the characterization of a cellular system to study human disorders derived from developmental and functional impairment of astrocytes (Magistri et al., Eur J Neurosci. 2016).

BIBLIOMETRICS

- h-index (WoS): 37
- Total citations (WoS): 7773

- Number of publications (WoS): 180
- Number of publications on scientific journals as (co)first or (co)corresponding author: 16
- Total IF for publications on scientific journals: 1218
- Average for publications on scientific journals: IF: 9.7

The complete list of my (life sciences) publications is available in PubMed MyBibliography: https://www.ncbi.nlm.nih.gov/myncbi/browse/collection/44584334/?sort=date&direction=descending.

Book Chapters

- Battaglia C, Mangano E, **Bicciato S**, Frascati F, Nuzzo S, Tinagli, V, Bianchi C, Perego RA, Cifola I (2011). Molecular Portrait of Clear Cell Renal Cell Carcinoma: An Integrative Analysis of Gene Expression and Genomic Copy Number Profiling. In: Emerging Research and Treatments in Renal Cell Carcinoma. Robert J. Amato. p. 23-56, RIJEKA:InTech, ISBN: 9789535100225
- Bellazzi R, **Bicciato S**, Cobelli C, Di Camillo B, Ferrazzi F, Magni P, Sacchi L, Toffolo G (2011). Microarray Data Analysis: Gene Regulatory Networks. In: Cerutti S, Marchesi M. Advanced Methods of Biomedical Signal Processing. p. 473-488, Chicester:John Wiley and Sons Ltd, ISBN: 9780470422144.
- Bellazzi R, **Bicciato S**, Cobelli C, Di Camillo B, Ferrazzi F, Magni P, Sacchi L, Toffolo G (2011). Microarray Data Analysis: General Concepts, Gene Selection, and Classification. In: Cerutti S, Marchesi M. Advanced Methods of Biomedical Signal Processing. p. 443-471, Chicester:John Wiley and Sons Ltd, ISBN: 9780470422144
- **Bicciato S**, Bortoluzzi S, Metodi per l'analisi dei profili di espressione su scala genomica, in "Genomica e proteomica computazionale" a cura di R. Bellazzi, S. Bicciato, S. Cavalcanti, C. Cobelli e G.M. Toffolo, Patron Editore, 2007, ISBN: 8855529447
- Bellazzi R, **Bicciato S**, Cobelli C, Di Camillo B, Ferrazzi F, Magni P, Sacchi L, Toffolo G, Analisi di dati di DNA microarray: fondamenti, selezione di geni, classificazione, in "Metodi avanzati di elaborazione di segnali biomedici" a cura di S. Cerutti e C. Marchesi, Patron Editore, 2004, ISBN: 8855527681
- Bellazzi R, **Bicciato S**, Cobelli C, Di Camillo B, Ferrazzi F, Magni P, Sacchi L, Toffolo G, Analisi di dati di DNA microarray: reti di regolazione, in "Metodi avanzati di elaborazione di segnali biomedici" a cura di S. Cerutti e C. Marchesi, Patron Editore, 2004, ISBN: 8855527681
- **Bicciato S**, Di Bello C, Matrici di DNA per lo studio dell'espressione genica in "Analisi e Modifica di Biomolecole e di Cellule" a cura di E. Biondi, M. Grattarola, M. Stefanelli e V. Tagliasco, Patron Editore, 2000, ISBN: 8855525565