

Short CV of Rita Casadio

Educational Background: RC, after her degree in Physics at the University of Bologna, Italy, attended several courses both in Italy and abroad and acquired experience and theoretical background in different fields, such as Computer Science, Membrane and Protein Biophysics, Bioenergetics and Irreversible Thermodynamics.

Professional Experience: After working in Laboratories of Biophysics both in the United States and in Germany, in 1987 RC became Assistant Professor of Biophysics at the University of Bologna Italy. Since 1/10/2003 she is full professor of Biochemistry/Bioinformatics/Biophysics at UNIBO. RC worked in membrane and protein Biophysics (particularly with bacteriorhodopsin from *Halobacterium Halobium* and F1F0 ATPases from mesophilic organisms), both experimentally and theoretically. Presently she is interested in computer modelling of relevant biological processes, such as protein folding and modelling, protein-protein interaction, genome annotation, protein interaction networks, and SNPs search and annotation and their effect on protein stability. One major field of research is the development of specific software for problem solving of large scale analysis of biomedical and biotechnological data out of genome sequencing or experiments on proteomes and interactomes. Methods are based on neural networks, hidden Markov models, Support Vector Machines, conditional random fields and their combinations. Her researches are devoted to different aspects of protein structure prediction, including prediction of secondary and tertiary structure, membrane protein topology, protein function, protein-protein and protein-DNA interaction, protein reaction mechanisms in biological processes and de novo design of peptides/molecules (for details see <http://lipid.biocomp.unibo.it>). RC is the author of about 300 scientific papers and presented her work at several (over 300) national and international meetings (for details see <http://lipid.biocomp.unibo.it/casadio/cv.html>).

RC is the founder and the group leader of the Biocomputing Unit of the University of Bologna. The group became officially active in 1995, when the Interdepartmental Center for the Biotechnological Research of the University of Bologna supported the establishment of a Biocomputing Center. Since then research interests focus on different aspects of protein sequence analysis, mainly the implementation of predictive algorithms based on methods out of machine learning approaches. The results of these works have been selected several times for presentation at the International Forum of Bioinformatics "Intelligent Systems for Molecular Biology (**ismb**)". A method (CORNET) developed in the lab for the prediction of contact maps of proteins (a relevant step for the ab initio prediction of protein 3D structure) was scored the best of its category in the Critical Assessment of Techniques for Protein Structure Prediction (CASP) 4 (Asilomar, California, December 3-7, 2000) and at CASP5 (Asilomar, California, December 1-5, 2002). A method for predicting the topography of outer membrane proteins based on HMM and sequence profile was acknowledged with the SGI best award at **ismb02** (Edmonton, Canada, August 3-7, 2002). More recently a method for SNPs annotation deserved some attention (Selected for the [Human Mutation Virtual Issue "Evaluating Mutation Patogenicity"](#); Tavtigian SV and Greenblatt MS, eds; May 2010) and a method for protein functional annotation (BAR+) scored favourably at Critical Assessment of Protein Function Annotation (CAFA-1). The unit is also active in organising training courses on Bioinformatics (www.biocomp.unibo.it).

Scientific fields: LS2_10 Bioinformatics; LS1_1 Molecular interactions; LS2_13 Systems biology

Scientific Indicators of RC (ORCID: 0000-0002-7462-7039): H Index, 40 (SCOPUS); G INDEX, 77 (SCOPUS)

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