上海交通大学自动化系
Department of Automation
Shanghai Jiao Tong University

系统控制与信息处理教育部重点实验室
Key Laboratory of System Control and Information Processing, Ministry of Education

生物信息系列学术报告会

报告人：**Rita Casadio**

单位： **University of Bologna, Italy**

地点：电院**2-410**会议室

(1) Bioinformatics and Computational Biology in the post-genomic era

时间： 2014-10-27 （周一） 10:00- 11:30

(2) The effect of disease-related variations on protein stability: a large-scale investigation

时间： 2014-10-29 （周三）10:00- 11:30

(3) Predicting the sub-cellular localisation of proteins

时间： 2014-10-31 （周五）10:00- 11:30

Biography:

RC got a degree in Physics at the University of Bologna in 1973 with full marks and laude. After her degree, RC got a research fellowship at the University of Bologna and worked in Bioenergetics. In 1978-1979 RC was Assistant Research Biochemistry at the Cardiovascular Research Institute of the University of California, San Francisco. She was then the recipient of an EMBO fellowship to work at the Department of Biophysics of the University of Osnabruck, Germany. Back to Italy, she worked at the University of Bologna as a researcher in Biophysics. In 1987 she got a permanent position as an Assistant Professor of Biophysics at the same University. Since 1993 she is the group leader of the Biocoputing Unit of the Interdepartmental Centre for Biotechnological Researches (CIRB) of the University of Bologna, Italy. In October 1/2001 RC became full professor of Biophysics in the same University. Presently she is interested in computer modelling of relevant biological processes, such as protein folding and modelling and her researches are devoted to different aspects of protein modelling, including prediction of secondary and tertiary structures with neural networks, hidden Markov models and genetic algorithms, molecular docking and drug design. One major field of research is the implementation and developments of tools out of machine-learning approaches for the prediction of secondary and tertiary structure of proteins from their amino acid residue sequences, particularly of membrane proteins and their transmembrane topology. Projects focus on the prediction of contact maps, of protein-protein and protein-DNA interaction, of the bonding state of cysteines and their topology. RC is the author of over 150 scientific papers and presented her work at several (over 280) national and international meetings (for details see http://www.biocomp.unibo.it/casadio/).

Abstract:

(1) Bioinformatics and Computational Biology in the post-genomic era

In the post-genomic era, Computer science well interplays with the empirical and theoretical methods of Natural Sciences, particularly biological sciences, with an un-precedent effort of accelerating breakthroughs in science and benefits to society. A shift of paradigm occurred, becoming feasible to unravel cell complexity thanks to an unprecedented technological advancement, allowing large-scale production of data. Simulation and modelling become global aiming at the whole organism behaviour and Bioinformatics and Computational Biology help in understanding basic mechanisms from molecular biology to systems/organismic biology in order to revolutionizing medicine and healthcare. Data acquired at molecular level from different species and/or individuals offer a unique opportunity to unravel not only the genetic content of different species, but also their trascriptome, proteome, interactome, reactome, and finally epigenome. Big volume of data of the different omics are analyzed at large and integrated in order to investigate our common origins, how we differentiated, and how diseases are inscribed in our genome, eventually in relation to environmental factors. Worldwide-integrated platforms for scientific computing implement new mathematical and statistical approaches, based on new computing paradigms. Therefrom, new ideas and/or re-organization of scientific efforts with a better collaboration among researchers in theoretical, computational, and experimental areas of investigation are in place. Focusing as a test case on the human genome, different important applications include genome annotation, human variability, alternative splicing and its regulation, epigenetics, functional genomics, cellular function and simulation, genomic medicine, SNPs and maladies.

(2) The effect of disease-related variations on protein stability: a large-scale investigation

The problem of annotating missense mutations is routinely addressed by considering the effect of variations on protein stability and/or on protein-protein, protein-nucleic acid interaction. It is therefore urgent to investigate whether the so-called disease-related variants are or not as stable as the native proteins, and discriminate among natural and disease-causing variants. Unfortunately, data on whether disease-related variants reach the same level of expression of the native ones are barely available and we therefore need developing computational approaches. Here we focus on mapping the OMIM and natural variations on the corresponding PDB structures of the human proteome and we statistically derive some rules of thumb to supplement a machine learning based approach capable of predicting whether the free energy change of folding is or not affected by a variation. By comparing with other methods based on different approaches we corroborate the notion that promoting protein instability is not the only source of disease and that other protein features are more important in assessing whether a variation is disease related or not.

(3) Predicting the sub-cellular localisation of proteins

Computational methods are invaluable when protein sequences, directly derived from genomic data, need functional and structural annotation. Subcellular localisation is a feature necessary for understanding the protein role and the compartment where the mature protein is active and very difficult to characterise experimentally. Mitochondrial proteins encoded on the cytosolic ribosomes carry specific patterns in the precursor sequence from where it is possible to recognise a peptide targeting the protein to its final destination. Here we discuss to which extent it is feasible to develop computational methods for detecting mitochondrial targeting peptides in the precursor sequences and benchmark our and other methods on the human mitochondrial proteins endowed with experimentally characterised targeting peptides. Furthermore we illustrate our newly implemented web server and its usage on the whole human proteome in order to infer mitochondrial targeting peptides, their cleavage sites and whether the targeting peptide regions contains or not arginine rich recurrent motifs. By this, we add some other 2800 human proteins to the 124 ones already experimentally annotated with a mitochondrial targeting peptide.