Curriculum Vitae of Piero Fariselli

Contacts

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Current Position

Full Professor at Department of Medical Sciences, University of Torino, Italy

National Scientific Qualification as Full Professor (ASN-2016)

– General Biochemistry (Bio/10 - 05/E1)
– Applied Physics (Fis/07 - 02/D1)
– Theoretical Physics of the Matter (Fis/03 - 01/B2)
– Computer Science (Inf/01 - 01/B1)

Educational Background

- Master Degree in Physics at the University of Bologna in 1991 with full marks and a thesis on "Neural networks for the prediction of secondary structure of proteins".
- Ph.D. in Biophysics at the University of Genova in 1996 with a thesis on "Ab initio methods for the structural an functional characterization of proteins"

Academic Appointments in Italy

- 2016-2018 Associate Professor, University of Padova
- 2001-2016 Researcher. University of Bologna
- 1999-2001 Contract researcher at the Department of Biology University of Bologna
- 1999-2000 Lecturer of Molecular Modelling at the University of Ferrara
- 1998-2000 Lecturer of Model of Biological System at the University of Bologna

Academic Appointments abroad

- 2018 and 2004. Visiting Researcher at the Bioinformatics Centre Department of Biology, University of Copenhagen (Prof. Anders Krogh).
- 2013 and 2008. Visiting Researcher at the Center for Misfolding and Diseases, Department of Chemistry University of Cambridge, UK (Prof. Michele Vendruscolo).
- 2013. Visiting Researcher at the Computational Biology Group, Computer Laboratory, University of Cambridge, UK (Prof. Pietro Liò).
- 2005. Visiting Lecturer at the Bioinformatics Group, University College of London, (Prof. David Jones).
- 2001 and 1999. Visiting Researcher at the Protein Design Group, CNB, Cantoblanco Madrid, (Prof. Alfonso Valencia).
- 1994 and 1995. Visiting PhD at the Protein Design Group, EMBL Heidelberg, (Prof. Chris Sander)

Bibliometric indices

Co-authors of more than 140 peer-reviewed publications, some of them are listed here:
SCOPUS: https://scholar.google.it/citations?user=W7Z7PPYAAAAJ&hl=en
PubMed: https://www.ncbi.nlm.nih.gov/pubmed/?term=fariselli+p[Bau]
- SCOPUS: h-index=33, number of paper=146, number of citations= 6053
- ISI WOS: h-index =30, number of paper=145, number citations=5163
- Google SCHOLAR: h-index=42, i10-index=90, number of citations= 8688

Awards

- Listed among the *Top Italian Scientists* on the bases of my research activity in Computational Biology and Bioinformatics (http://www.topitalianscientists.org).
- Four papers has been highlighted and reccomended by "Faculty of 1000, Biology" (http://www.facultyof1000.com/).
- A method, BAR (Bologna Annotation Resource), has been evaluated one of the best annotation tools at the "Critical Assessment of protein Function Annotation algorithms" (CAFA 1, 2010-2011) http://www.nature.com/nmeth/journal/v10/n3/full/nmeth.2340.html
- A method for predicting the topology of outer membrane proteins based on HMM and sequence profile has been acknowledged with the SGI best award at ismb02 (Edmonton, Canada, August 3-7, 2002).
- A method (CORNET) for the prediction of contact maps of proteins (a relevant step for the ab initio prediction of protein 3D structure) has been scored the best of its category in the Critical Assessment of Techniques for Protein Structure Prediction (CASP) 4 (Asimolar, California, December 3-7, 2000) and at CASP5 (Asilomar, California, December 1-5, 2002).

Current research topics

Developing computational methods to tackle biomedical problems, design and implementation of Machine-learning models for biomedical analysis.

Funds

Italian funds:
- PRIN 2017: "Integrative tools for defining the molecular basis of the diseases: computational and experimental methods for protein variant interpretation" (PI)
- BIRD 2017 -University of Padova: BIRD179335,. "Development of computational methods for the interpretation of pets and livestock genomes: the case study of the canine genome." (PI)
- PRIN 2004: "Modelling su larga scala di proteasi e loro interazioni con inibitori specifici". (PI)

International projects:
- EBA-PRISM: Evolutionary-based approach for predicting protein interaction sites and residue mutation impact. Italian-Israelel Cooperation 2017-2019 (PI).
- FP6 Specific Targeted Research Project TargetHerpes LSHGCT-2006-037517, with In BioDec. (Participant)
- BioSapiens Network of Excellens, FP6-2002-LIFESCIHEALTH: A European Network for Integrated Genome Annotation, in particlar for the generation of DAS (Distributed-

Annotation-Server) for the membrane protein annotation, and Tumor annotation. (Parrticipant)

- BIOWULF 2000- Speeding-up Biocomputing applications using a commodity-based parallel computer EU. (Participant)
- ESPRIT, 4PQ-1998-DRUG: Supercomputing Drug Design for Industrial and Academic Partnership; (Participant)