Curriculum Vitae of Piero Fariselli

Contacts

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Current Position
Full Professor at University of Torino

Educational Background

- Master Degree in Physics at the University of Bologna in 1991 with full marks. Thesis on "Neural networks for the prediction of the 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 Assitant Professor. University of Bologna
- 1999-2001 Fixed-term 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)

Publications and Bibliometric indices

Co-authors of more than 150 peer-reviewed publications, some of them are listed here:
- **PubMed**: http://www.ncbi.nlm.nih.gov/pubmed/?term=fariselli+p[au]
- **Scopus:** http://www.scopus.com/authid/detail.url?authorId=7004658043
- **WOS**: http://www.webofscience.com/wos/author/record/HNJ-5136-2023
- **Scholar**: https://scholar.google.com/citations?user=W7Z7PPYAAAAJ&hl=en
- Current Biobliometric indices are:
  - SCOPUS: h-index=42, number of paper=188, number of citations= 8230
  - WOS: h-index=39, number of paper=174, number of citations= 7821
  - Google SCHOLAR: h-index=50, i10-index=122, number of citations= 12735

Awards

- In 2022, have been listed by Research.com, a prominent academic platform for scientists, among the leading scientists in the area of engineering & technology (https://research.com/u/piero-fariselli).
- I have been listed among the *Top Italian Scientists* on the bases of my research activity in Computational Biology and Bioinformatics (http://www.topitalianscientists.org).
- Four papers have been highlighted and recommended by "Faculty of 1000, Biology" (http://www.facultyof1000.com/).
- A method I contributed to develop, 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).

Projects
Ongoing projects
- BRAINTEASER (2021-2024) : BRinging Artificial INTelligencE home for a better cAre of amyotrophic lateral sclerosis and multiple SclERosis. Call H2020-SC1-DTH-2020-1 Personalised early risk prediction, prevention and intervention based on Artificial Intelligence and Big Data technologies (WP leader)
- GenoMed4All (2021-2024): Genomics and Personalized Medicine for all though Artificial Intelligence in Haematological Diseases. Call H2020-SC1-FA-DTS-2020-1. AI for Genomics and Personalised Medicine (Task leader)
- INTERVENE(2021-2025): . International consortium for integrative genomics prediction, Call H2020-SC1-FA-DTS-2020-1. AI for Genomics and Personalised Medicine (Local AI leader)
- PRIN 2017 (2019-2023, Ministry of Education, University and Research of Italy, grant for Research Projects of National Relevance (PRIN 2017 project code: 201744NR8S); Integrative tools for defining the molecular basis of the diseases: computational and experimental methods for protein variant interpretation (Project Coordinator)

I have been involved is several projects as a relevant player, among them:

Italian projects:

- BIRD-Unipd 2016: Development of computational methods for the interpretation of pets and livestock genomes: the case study of the canine genome.
- PRIN 2010: Approccio integrato computazionale e sperimentale per lo studio di patologie umane.
- PRIN 2004 Modelling su larga scala di proteasi e loro interazioni con inibitori specifici.
- PRIN 2003. Implementazione di un web server per confrontare le strutture proteiche di organismi termofili e mesofili.
- PRIN 2002. Sviluppo ed implementazione di algoritmi per la predizione della struttura di proteine.

International projects:

- EBA-PRISM - Evolutionary-based approach for predicting protein interaction sites and residue mutation impact (Italian-Israeli Collaboration 2017-2019).
- FP6 Specific Targeted Research Project TargetHerpes LSHGCT-2006-037517, with In BioDec
- 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.
- BIOWULF 2000- Speeding-up Biocomputing applications using a commodity-based parallel computer EU.
- ESPRIT, 4PQ-1998-DRUG: Supercomputing Drug Design for Industrial and Academic Partnership;

Research

Main current research topics

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

- Machine learning applications in Biology and Medicine;
- Development of AI-based tools for prognosis predictions;
- Development of computational tools for biomolecule feature predictions;
- Computational biological sequence analyses;
- Development of software for Bioinformatic applications
- Modeling of complex systems.