

Curriculum vitae

PERSONAL INFORMATION **Pier Luigi Martelli**

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Sex Male | Date of birth 07/01/1972 | Nationality Italian

EDUCATION AND TRAINING

- 1998–2001 **PhD in Physics** EQF level 8
University of Bologna, Bologna (Italy)
Thesis title: Hybrid systems of HMMs and Neural Networks for protein structure prediction.
- 1991–1997 **Master Degree in Physics** EQF level 7
University of Bologna, Bologna (Italy)
Thesis title: Prediction of Foldons in proteins

WORK EXPERIENCE

- 31/03/2017–Present **Licenced for Full Professorship in Biochemistry (BIO/10) from the ASN national committee**
- 23/05/2016–Present **Director of the International Master in Bioinformatics**
University of Bologna (Italy)
- 01/10/2006–31/01/2015 **Assistant professor in Biochemistry (BIO/10)**
University of Bologna, Bologna (Italy)
Research activity in Computational Biology and Bioinformatics at the Biocomputing Group of the University of Bologna.
Lecturer for the "In silico biology" course at the International Master Degree in Bioinformatics
- 01/10/2005–30/09/2006 **Contract Researcher (Young Researcher contract) for the FIRB2003 Project "LIBI: International Laboratory of Bioinformatics".**
University of Bologna, Bologna (Italy)
- 01/08/2003–31/07/2006 **Contract Researcher (Assegno di Ricerca) for the FIRB2001 Project "Bioinformatics for Genomics an Proteomics"**
University of Bologna, Bologna (Italy)
- 02/05/2002–30/04/2006 **Fellow Researcher. Fellowship from the CNR Target Project on Molecular Genetics**
National Council for Research (CNR), Roma (Italy)
- 01/03/2001–28/02/2002 **Fellow Researcher**
INBB Consortium- Istituto Nazionale di Biostrutture e Biosistemi, Roma (Italy)

ADDITIONAL INFORMATION

Teaching activities

- Academic Year 2000-2001: Course module "Modellistica Molecolare" at University of Ferrara, Degree in Biology.
- April 2003: Special Course on "HMMs, Basics and applications to molecular biology" at Bioinformatics Group of Sanofi-Synthelabo (Labège, Toulouse, Francia)
- Academic Years 2002-2006: Course on "Fisica Computazionale Applicata alle Macromolecole" at University of Trento, Degree in Biomedical Physics and Technology
- April 2006: Assistant to the course "Pills of Bioinformatics". Universidad Tecnica Particular de Loja (Ecuador)
- Academic Years 2004-2008: Special Course on "Probabilistic models for biological sequences" at Complutense University in Madrid (Spain), Master in Bioinformatics.
- January 2012: Special course in "Basic and Advanced Bioinformatics" at Sultan Qabus University (Muscat, Oman)
- October 2012: Lectures on "Programming in Perl for NGS data analysis". RGB NET (Cost Action) Training School on "Rabbit and Pig Genome analysis" (Norwich, UK)
- June 2013: Lectures on "NGS Data Analysis" at the training school of PON project "Applicazione di biotecnologie molecolari e microrganismi protecnologici per la caratterizzazione e valorizzazione delle filiere lattiero-casearia e prodotti da forno di produzioni tipiche." (S. Margherita al Belice, AG)
- 2006-current: Teaching activity at the International Master Degree in Bioinformatics of the University of Bologna (courses: Bio-medical databases, Elements of Computational Biology, Models of Biological Systems, Systems and In Silico Biology, Laboratory of Bioinformatics, Programming for Bioinformatics)

Research Activity

Protein folding and theoretical molecular Biophysics

Since 1996, PLM has been involved in theoretical investigations on problems related to the protein folding by means of computational tools, mainly based on neural networks and genetic algorithms. In particular, the analysis of the predictive properties of feed-forward neural networks enabled the definition of an entropic criterion for selecting segment in alpha-helical structure that are likely to be the nucleation sites for the protein folding.

Development of tools for the prediction of protein structure and function

Since 1997 PLM is involved in the design and development of tools based on machine learning techniques for the prediction of structural and functional features of proteins, starting from their residue sequences. In particular, PLM designed and implemented hybrid systems of neural networks (NN) and hidden Markov models (HMM) able also to elaborate the information contained in sequence profiles out of multiple sequence alignments. These tools have been adopted for developing predictors for -) the topology of membrane proteins, both with alpha-helical and beta-barrel structures; -) the bonding state of cysteine residues in proteins; -) the presence and localization of GPI-anchors; -) the presence and localization of target peptides and signal peptides.

He contributed to the development of the Bologna Annotation Resource (BAR)

Prediction of the relationship between SNPs and diseases

PLM collaborated in the implementation of SNPs&GO, a tool based on SVM for predicting whether a residue mutation is conducive to human disease. For the first time, this tool exploits the information contained in functional annotations encoded with the Gene Ontology terms. Several independent evaluations assessed that SNPs&GO is one of the best performing tools, among those available for the specific task at hand.

Prediction of the subcellular localization of eukaryotic proteins

PLM collaborated in the implementation of BaCellO, a decision tree of support vector machines (SVM) able to discriminate up to four different localization in animals and fungi and up to five localizations in plants. BaCellO represents the state of the art in the prediction of subcellular localization of eukaryotic proteins.

NGS data analysis in a Systems Biology context

PLM participated in different projects involving the analysis of NGS data on DNA and RNA of different species (human, *Triticum aestivum*, pig). In particular, he applied his expertise in structural and functional annotation of gene products and in characterization of the effect of variations.

He also participated to the development of NET-GE, a tool for functional enrichment, useful to target pathways shared by groups of genes (carrying variations or differentially expressed)

Protein modeling and investigations on the structure-function relationship

PLM studies the structure-function relationship using tools for protein modelling, molecular dynamics simulations, and molecular docking. In collaboration with experimental groups PLM achieved the following results: -) the computation of the three-dimensional models of proteins from thermophilic organisms, in order to elucidate the features conducive to thermostability; -) the modelling and dynamic simulations of enzymes immobilized in membranes in bioreactors, in order to study the effects of immobilization on the structural stability; -) the simulation of the destabilizing effect of the double mutation at positions 7 and 14 on the sperm whale myoglobin; -) the simulation of the mobility of tryptophan residues in the beta-galactosidase from *Sulfolobus solfataricus* and the correlation with its fluorescence emission properties; -) the discovery and characterization of a fusogenic peptide in the glycoprotein H of *Herpes simplex virus*; -) the modelling of the C-terminal segment of the subunit B of the glyceraldehyde-3-phosphate dehydrogenase from *Spinacea olearia*; this peptide is particularly important for the regulation of the enzyme in relation to dark/light metabolisms.

Editorial activity Since 2017 he is member of the Editorial Board of "Computation"

PLM acts as reviewer for the many Journals, among which: Bioinformatics, PLoS Computational Biology, PLoS One, BMC Bioinformatics, BMC Genomics, BMC Systems Biology, Amino acids, Proteins, BioSystems, Journal of Genetics

Present and Past Collaborations

- University of Copenhagen (Denmark): Prof. Anders Krogh
- BIOSAPIENS EU Consortium
- Sabanci University and Acibadem University (Turkey): Prof. Ugur Sezerman
- CAS-MPG Partner Institute for Computational Biology in Shanghai (China): Dr. Christine Nardini
- CHIRON Vaccines SpA: Dr. Giulio Ratti
- CNR Institute for Protein Biochemistry and Enzymology in Naples: Prof. Mosè Rossi
- CNR Institute for Biomembranes and Bioenergetics in Bari: Prof. Graziano Pesole
- Second University of Napoli: Prof. Gustavo Damiano Mita, Prof. Gaetano Irace
- University of Milano-Bicocca: Prof. Paolo Tortora
- University of Rome "La Sapienza": Prof. Anna Tramontano
- University of Ferrara: Prof. Carlo Bergamini
- Quilmes University (Argentina): Prof. Gustavo Parisi

Institutional appointments

Since 2015: the coordinator of the group "Computational and Systems Biology" of the Italian Society of Biochemistry and Molecular Biology (SIB), affiliated to FEBS.

Since 2014: member of the panel "Biological sciences" of the Commission for the evaluation of the research activity (VRA) at the University of Bologna.

Since 2014: member of the Research commission of the Department BiGeA of the University of Bologna.

2011-2015: coordinator of the Bologna University Unit for the PRIN Project "Integration of experimental and computational approaches for the study of human pathologies". (National coordinator: Prof. Anna Tramontano).

Honours and awards The paper: **Martelli PL, Fariselli P, Krogh A and Casadio R (2002) A sequence-profile-based HMM for predicting and discriminating beta barrel membrane proteins- *Bioinformatics* 18: S46-S53** presented at the 10th International Conference on "Intelligent Systems for Molecular Biology" (ISMB02), Edmonton Canada, 3-7/8/2002 won the SGI best paper award

Bibliometry SCOPUS (June 2017):

Documents: 101, Total number of citations: 2354, h-index: 28

- Capriotti E, Martelli PL, Fariselli P, Casadio R. Blind prediction of deleterious amino acid variations with SNPs&GO (2017) Hum Mutat. (in press)
- Xu Q, Tang Q, Katsonis P, Lichtarge O, Jones D, Bovo S, Babbi G, Martelli PL, Casadio R, Lee GR, Seok C, Fenton AW, Dunbrack RL Jr. Benchmarking predictions of allostery in liver pyruvate kinase in CAG14. (2017) Hum Mutat. (in press)
- Savojardo C., Martelli P.L., Fariselli P., Casadio R. SChloro: directing Viridiplantae proteins to six chloroplastic sub-compartments. (2017) Bioinformatics (in press)
- Savojardo C, Fariselli P, Martelli PL, Casadio R. IS-PRED4: Interaction Sites PREDiction in protein structures with a refining grammar model. (2017) Bioinformatics 33:1656-1663
- Zuntini R, Cortesi L, Calistri D, Pippucci T, Martelli PL, Casadio R, Capizzi E, Santini D, Miccoli S, Medici V, Danesi R, Marchi I, Zampiga V, Fiorentino M, Ferrari S, Turchetti D. BRCA1 p.His1673del is a pathogenic mutation associated with a predominant ovarian cancer phenotype (2017) Oncotarget 8:22640-22648.
- Sazzini M., De Fanti S., Cherubini A., Quagliariello A., Profiti G., Martelli P.L., Casadio R., Ricci C., Campieri M., Lanzini A., Volta U., Caio G., Franceschi C., Spisni E., Luiselli D. Ancient pathogen-driven adaptation triggers increased susceptibility to non-celiac wheat sensitivity in present-day European populations (2016) Genes and Nutrition 23 (11): art. no. 15,.
- Jiang, Y., Oron, T.R., et al. An expanded evaluation of protein function prediction methods shows an improvement in accuracy(2016) Genome Biology, 17 (1), art. no. 184, .
- Savojardo, C., Fariselli, P., Martelli, P.L., Casadio, R. INPS-MD: A web server to predict stability of protein variants from sequence and structure(2016) Bioinformatics, 32 (16), pp. 2542-2544.
- Martelli, P.L., Fariselli, P., Savojardo, C., Babbi, G., Aggazio, F., Casadio, R. Large scale analysis of protein stability in OMIM disease related human protein variants(2016) BMC Genomics, 17, art. no. 397, .
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- Di Lena, P., Martelli, P.L., Fariselli, P., Casadio, R. NET-GE: A novel NETWORK-based Gene Enrichment for detecting biological processes associated to Mendelian diseases(2015) BMC Genomics, 16 (8), art. no. S6, .
- Martelli, P.L., Savojardo, C., Fariselli, P., Tasco, G., Casadio, R. Computer-based prediction of mitochondria-targeting peptides(2015) Mitochondrial Medicine, 1, pp. 305-320.
- Fariselli, P., Martelli, P.L., Savojardo, C., Casadio, R. INPS: Predicting the impact of non-synonymous variations on protein stability from sequence(2015) Bioinformatics, 31 (17), pp. 2816-2821.
- Savojardo, C., Martelli, P.L., Fariselli, P., Casadio, R. TPpred3 detects and discriminates mitochondrial and chloroplastic targeting peptides in eukaryotic proteins (2015) Bioinformatics, 31 (20), pp. 3269-3275.
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Protein Engineering, Design and Selection, 28 (5), pp. 127-135.

- Martelli, P.L., Savojardo, C., Fariselli, P., Tasco, G., Casadio, R. Computer-based prediction of mitochondria-targeting peptides (2015) *Methods in Molecular Biology*, 1264, pp. 305-320.
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- Capriotti, E., Calabrese, R., Fariselli, P., Martelli, P.L., Altman, R.B., Casadio, R. WS-SNPs&GO: a web server for predicting the deleterious effect of human protein variants using functional annotation. (2013) *BMC genomics*, 14 Suppl 3, art. no. S6, .
- Di Lena, D., Wu, G., Martelli, P.L., Casadio, R., Nardini, C. MIMO: An efficient tool for molecular interaction maps overlap (2013) *BMC Bioinformatics*, 14, art. no. 159, .
- Indio, V., Martelli, P.L., Savojardo, C., Fariselli, P., Casadio, R. The prediction of organelle-targeting peptides in eukaryotic proteins with Grammatical-Restrained Hidden Conditional Random Fields (2013) *Bioinformatics*, 29 (8), pp. 981-988.
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- Piovesan, D., Martelli, P.L., Fariselli, P., Proffiti, G., Zauli, A., Rossi, I., Casadio, R. How to inherit statistically validated annotation within BAR+ protein clusters (2013) *BMC Bioinformatics*, 14 (SUPPL.3), art. no. S4, .
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- Savojardo, C., Fariselli, P., Piovesan, D., Martelli, P.L., Casadio, R. Machine-learning methods to predict protein interaction sites in folded proteins (2012) *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, 7548 LNBI, pp. 127-135.
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Exploring copy number variation in the rabbit (*Oryctolagus cuniculus*) genome by array comparative genome hybridization (2012) *Genomics*, 100 (4), pp. 245-251.

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- Fontanesi, L., Galimberti, G., Calò, D.G., Fronza, R., Martelli, P.L., Scotti, E., Colombo, M., Schiavo, G., Casadio, R., Buttazoni, L., Russo, V. Identification and association analysis of several hundred single nucleotide polymorphisms within candidate genes for back fat thickness in Italian large white pigs using a selective genotyping approach (2012) *Journal of Animal Science*, 90 (8), pp. 2450-2464.
- Casadio, R., Vassura, M., Tiwari, S., Fariselli, P., Luigi Martelli, P. Correlating disease-related mutations to their effect on protein stability: A large-scale analysis of the human proteome (2011) *Human Mutation*, 32 (10), pp. 1161-1170.
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- Savojardo, C., Fariselli, P., Martelli, P.L., Shukla, P., Casadio, R. Prediction of the bonding state of cysteine residues in proteins with machine-learning methods (2011) *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, 6685 LNBI, pp. 98-111.
- Savojardo, C., Fariselli, P., Alhamdoosh, M., Martelli, P.L., Pierleoni, A., Casadio, R. Improving the prediction of disulfide bonds in Eukaryotes with machine learning methods and protein subcellular localization (2011) *Bioinformatics*, 27 (16), art. no. btr387, pp. 2224-2230.
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- Pierleoni, A., Martelli, P., Casadio, R. PredGPI: A GPI-anchor predictor (2008) *BMC Bioinformatics*, 9, art. no. 392, .
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