

**EUROPEAN
CURRICULUM
VITAE
FORMAT**



PERSONAL INFORMATION

Name **BABBI GIULIA**
Address **Via Aldini 16, Cesena (FC), 47521 ITALY**
Telephone **+39 333 4486207**
E-mail **giulia.babbi3@unibo.it**
giubabbi@gmail.com
Nationality Italian
Date of birth 03/01/1991
Sex Female, she/her

EDUCATION AND TRAINING

- Dates 2015 – 2019
- Title of qualification awarded PhD in Earth, Life and Environmental Science – Curriculum Biology
SSD BIO/10 Subject: Computational Biology
Supervisor: Prof. Pier Luigi Martelli
- Organization providing education and training School of Science (Dept. of Biological, Geological and Environmental sciences)
Alma Mater Studiorum – University of Bologna
- Thesis Title The biological complexity of the genotype-phenotype relation: from genes and proteins to phenotypes and diseases (in humans)

- Dates 2013 – 2015
- Title of qualification awarded Master's Degree in Bioinformatics - LM6
- Final Evaluation 110/110 cum laude
- Organization providing education and training Alma Mater Studiorum – University of Bologna
- Thesis Title Analysing the association between protein variants and human diseases (SSD BIO/10)

- Dates 2010 – 2013
- Title of qualification awarded Bachelor's Degree in Biotechnology
- Final Evaluation 110/110 cum laude
- Organization providing education and training Alma Mater Studiorum – University of Bologna
- Thesis Title Annotation of the human membrane proteome with BAR+ (SSD BIO/10)

WORK EXPERIENCE

- Dates From December 2020
 - Occupation or position held Junior assistant professor (RTD-A) (SSD: BIO/10)
 - Name and address of employer Department of Pharmacy and Biotechnology (FaBiT) – University of Bologna, Via Belmeloro, 6, 40126 Bologna (BO), ITALY
 - Project European project H2020-CIRCLES: “Controlling mIcRobiomes CircuLations for bEtter food Systems”.
 - Main activities and responsibilities Implementation of a computational infrastructure for the management of omics data produced with "high throughput" tools, development of bioinformatics tools for data analysis, integration and interpretation.

- Dates January 2020-November 2020
 - Occupation or position held Research Fellow
 - Name and address of employer Department of Pharmacy and Biotechnology (FaBiT) – University of Bologna, Via Belmeloro, 6, 40126 Bologna (BO), ITALY
 - Project PRIN 2017, project: “Protein Bioinformatics for Human Health”
 - Main activities and responsibilities Curation of databases and tools devoted to the elucidation of the relations between protein variations, diseases and phenotypes. Implementation of novel computational tools for large-scale prediction/annotation of protein function and features.

- Dates April 2018 – July 2018
 - Occupation or position held Bioinformatician - Internship as PhD student
 - Name and address of employer GRIB – IMIM, PRBB, C/Dr. Aiguader, 88, 08003 – Barcelona, SPAIN
 - Supervisor Prof. Laura I. Furlong, - Pompeu Fabra University (UPF)
 - Main activities and responsibilities Updating online webservers, integration of platforms for the analysis of high volume of data, development of new tools and feature for existing resources in the field of gene-disease associations studies, with a specific interest in DisGeNet database.

- Dates January 2015 – July 2015
 - Occupation or position held Bioinformatician – Thesis Internship
 - Name and address of employer Bologna Biocomputing Group – University of Bologna Via S.Giacomo 9/2 – 40126 Bologna (BO), ITALY
 - Supervisor Prof. Rita Casadio, University of Bologna
 - Main activities and responsibilities Bioinformatics for the annotation of genomic variations data; implementation of a platform for genome analysis and SNPs annotation. Integration of different bioinformatics tools to annotate genomic variations in terms of molecular consequence, with proteomic and transcriptomic data. Mapping of diseases-related variations on the human genome, and statistical validation of the outcomes.

- Dates January 2013 – July 2013
 - Occupation or position held Biotechnologist – Thesis Internship
 - Name and address of employer Bologna Biocomputing Group – University of Bologna Via S.Giacomo 9/2 – 40126 Bologna (BO), ITALY
 - Supervisor Prof. Rita Casadio, University of Bologna

- Main activities and responsibilities

Analysis of the outcomes of BAR+, the Bologna Annotation Resource tool developed by the Bologna Biocomputing Group. Comparison among the curated BAR+ annotation with other databases to demonstrate the increasing quality of the data obtained with the implemented annotation in comparison with not curated experimental data. Modelling of protein complexes of particular interest.

OTHER ADVANCED COURSES ATTENDED

Advanced school: Bologna Winter School 2022
 “Structural Bioinformatics in the era of AlphaFold2” – On line event, February 9-25, 2022

Advanced school: Bologna Winter School 2021
 “Bioinformatics for Discovery in Structural and Functional Biology” – On line event, February 9-19, 2021

Advanced one week-school: Bologna Winter School 2020
 “What can we learn from protein structure?” – Bologna, February 17-21, 2020

Advanced one week-school: Bologna Winter School 2018
 “Big Data and Bioinformatics” – Bologna, February 12-16, 2018

Advanced one week course: “Protein modelling and docking” – Bologna, February 5-9, 2018
 Prof. Allegra Via – University of Bologna

Advanced course: "Cracking the disease code: mapping genomes to pathogenesis pathways"– Bologna, May 29 - June 1, 2017
 Prof. Yana Bromberg -Department of Biochemistry and Microbiology - Rutgers University, New Brunswick, NJ (USA)

Advanced one week-school: Bologna Winter School 2017:
 “Revisiting Bioinformatics Foundations” – Bologna, February 13-17, 2017

Advanced one week course: “Protein protein interaction and docking” – Bologna, February 2-10, 2017
 Prof. Allegra Via – University of Bologna

Prof. Ugur Sezerman – Acibadem University – Advanced Course: Network based analysis of omics data to study the affected pathways in disease aetiology – Bologna, February 29 - March 4, 2016

Advanced one week-school: Bologna Winter School 2016:
 “In Silico Markers for Precision Medicine” – Bologna, February 22-26, 2016

Advanced one week training course: “Protein Network and System Biology” – Bologna, December 14-18, 2015, ELIXIR-ITA

Advanced course: "Cracking the disease code: mapping genomes to pathogenesis pathways" – Bologna, May 28 - June 5, 2015
 Prof. Yana Bromberg -Department of Genetics - Rutgers University, New Brunswick (NJ, USA)

Advanced course: "Omics & multi-omics" – Bologna, March 2-5, 2015
Dr. Christine Nardini - Department of Molecular Systems Biology - CAS-MPG
Partner Institute for Computational Biology, Shanghai

Advanced one week-school: Bologna Winter School 2015:
"NGS data, Bioinformatics and New Molecular Scenarios" – Bologna, February
2-6, 2015

Advanced Course in NGS data analysis: "Nucleotide Sequences Homology
Modelling in the Next Gen Sequencing Era", September 22-26, 2014
Prof. Cédric Notredame - Centro de Regulacio Genomica - Barcelona.

Advanced course: "Pattern Recognition in Bioinformatics", May 5-9, 2014
Prof. Hong-Bin Shen - Computational and Systems Biology Group - Shanghai
Jiao Tong University.

Advanced one week-school: Bologna Winter School 2014:
"Bioinformatics for Biological Complexity" – Bologna, February 10-14, 2014

Advanced course: "Introduction to Bioinformatics" – Bologna, February 3-7,
2014
Prof. Arthur Lesk - Biochemistry and Molecular Biology - PennState University

SEMINARS ATTENDED

Seminar: Towards the application of quantum computing in computational
biology, online event, May 13, 2021
Prof. Pier Luigi Martelli – Organized by University of Pisa

Webinar: Introducing the new UniProt Disease Portal, 19 October, 2020

Galaxy-ELIXIR webinar series: FAIR data and Open Infrastructures to tackle
the COVID-19 pandemic
"Introduction to Galaxy and the Galaxy workflows for SARS-CoV-2 data
analysis" April 30, 2020
"Galaxy-ELIXIR webinar series: Genomics/Variant Calling" May 7, 2020

Seminars: Biomedical Informatics Research Programme - Retreat IMIM
"RNA sequencing of archived neonatal dried blood spots from extremely
preterm newborns" – Prof. Robert Castelo
"The human endogenous metabolome as a pharmacology baseline for drug
Discovery" – Prof. Jordi Mestres
"Text mining of clinical notes from PSMAR electronic health records" – Prof
Laura Furlong
"The role of RNA processing alterations in disease" – Prof. Eduardo Eyras
" Signaling bias in GPCR drug discovery" – Prof. Jana Selent
IMIM, PRBB Barcelona, July 4, 2018

Seminar: "Dementia" Prof. Miguel Angel Mayer
IMIM, PRBB Barcelona, May 15, 2018

Seminar: "DisGeNET: A discovery platform to support translational research on
human diseases" – Prof Laura Furlong
ECTB 2018, PRBB Barcelona, April 17, 2018

Seminar: "Towards a structure/function simulation of a cancer cell"
Bologna, September 26, 2017
Prof. Trey Ideker – Institute for Genomic Medicine, UCSD USA

Workshop: Workshop of the SIB group "Computational and Systems Biology",
Bologna, June 28, 2017

Advanced seminar: "Evolution of the metabolic biodiversity in plant organisms",
Bologna, May 11, 2017
Prof. Annalisa Tassoni – Organized by the Department of BiGeA, University of Bologna

Advanced seminar: "The self-consistency test for measuring bias in prediction protein destabilization upon mutation. Finding multi-dimensional epistasis in high-throughput data", Bologna, April 21, 2017
Prof. Dmitry Ivankov – Center for Genomic Regulation, Barcelona (ES)

Seminar: "La diffusione della disinformazione scientifica: l'eco della rete",
Bologna, April 11, 2017
Prof. Pierluigi Contucci, Dott. Giuseppe Profiti, Prof. Marco Ciardi _Organized by "Accademia delle Scienze", University of Bologna

Advanced seminar: "Towards the understanding of the genetic bases of complex adaptations in the human genome", Bologna, 19 October 2016
Prof. Jaume Bertranpetit – Organized by the Department of BiGeA, University of Bologna

Advanced Lecture: "Biclustering Algorithms for Biomedical Data Analysis",
Bologna, June 14, 2016
Prof. Sara Madeira, Eurias Fellow

Advanced seminar: "Models of growth and population dynamics",
Bologna, June 14, 2016,
Prof. Stefano Goffredo – Department of BiGeA, University of Bologna

Advanced seminar: "The animal mitochondrial genome: adaptation and evolution", Bologna, June 13, 2016,
Prof. Marco Passamonti – Department of BiGeA, University of Bologna

Advanced seminar: "Genomic approaches to the study of adaptation of populations in response to selective pressures", Bologna, April 29, 2016,
Prof. Marco Sazzini – Department of BiGeA, University of Bologna

RESEARCH ACTIVITY

PARTICIPATION IN PROJECTS

- Dates November 2019 - ongoing
- International project CIRCLES "Controlling mIcRobiomes CircuLations for bEtter food Systems"
funded by the European Union's Horizon 2020 research and innovation programme

- Occupation or position held Junior Researcher responsible of the development of bioinformatics tools for data analysis, integration and interpretation and of the management of a computational infrastructure for omics data produced with "high throughput" tools
- Dates July 2020 – October 2020
 - International project Collaboration with NASA Ames Research Center, Space Biosciences Branch for the Human Research Program
- Occupation or position held Collaboration for the analysis and annotation of human and mouse genetic variations for the investigation of markers of sensitivity to radiation
- Dates July 2020 - ongoing
 - International experiment The Critical Assessment of protein Function Annotation algorithms
- Occupation or position held Participant making computational predictions
- Dates February 2019 - ongoing
 - International project ELIXIR, an intergovernmental organisation that brings together life science resources from across Europe
- Occupation or position held Part of the Bioschemas community supported by ELIXIR
- Dates November 2016 - ongoing
 - International experiment Critical Assessment of Genome Interpretation
- Occupation or position held Participant making computational predictions
- Dates November 2019 - ongoing
 - National project National project: PRIN 2017: "Protein Bioinformatics for Human Health"
- Occupation or position held Research fellow involved in the analysis of the relations between protein variations, diseases and phenotypes, contributing in the implementation of novel computational tools for large-scale prediction/annotation of protein function and features.

MEMBERSHIP IN COMMITTEE

- Occupation or position held Member of the local organizing committee of:
 - Events National Conference on: WebPro - Proteins on the Web 2021- on line conference, Protein Group of SIB (Italian Society of Biochemistry and Molecular Biology, 20-21 May 2021
- Occupation or position held Member of the local committee of:
 - Events Advanced school: Bologna Winter School 2022: "Structural Bioinformatics in the era of AlphaFold2" - on line event, February 9-25, 2022
 - Advanced school: Bologna Winter School 2021: "Bioinformatics for Discovery in Structural and Functional Biology" - on line event, February 9-19, 2021
 - Advanced one week-school: Bologna Winter School 2020: "What can we learn from protein structure?" – Bologna, February 17-21, 2020
 - Advanced one week-school: Bologna Winter School 2019 "Data Science for Bioinformatics" - Bologna, February 18-22, 2019
 - Advanced one week-school: Bologna Winter School 2018: "Big Data and

Bioinformatics” – Bologna, February 12-16, 2018

Advanced one week-school: Bologna Winter School 2017: “Revisiting Bioinformatics Foundations” - Bologna, February 13-17, 2017

National Conference on: Proteine 2016: “Dissecting the Biological Complexity at the Molecular level” – Bologna, March 30- April 1, 2016

Advanced one week-school: Bologna Winter School 2016: “In Silico Markers for Precision Medicine” – Bologna, February 22-26, 2016

• Occupation or position held

- Dates
- Journal

Topic Editor

2022-ongoing

Frontiers in Genetics – MDPI

Topic: Omics Integration and Network Medicine to Decipher Human Complex Diseases

PRIZES AND AWARDS

- Dates
- International award

2019

The image of the article “Benchmarking predictions of allostery in liver pyruvate kinase in CAG14” has been selected as cover image for the Human Mutation Special Issue: the Critical Assessment of Genome Interpretation (CAGI)

- Dates
- National award

2021

Winner of the SIB scholarship “Borsa di partecipazione al 45 Virtual FEBS Congress”

- Dates
- National award

2017

Second classified at the 3MT competition, University of Bologna

CONFERENCES

ORAL PRESENTATIONS

International Conference: CAGI 2022: “Predicting the effects of missense variations and the case of MTHFR deficiency”, Berkeley, California (USA), remote attendance, May 14-16, 2022

International Conference: ISMB/ECCB 2021: “Physico-chemical and structural features of pathogenic and benign human protein missense variations collected from HUMSAVAR and ClinVar”, virtual event, remote attendance, July 25 - 30, 2021

National Conference: BITS 2021, Annual Meeting of the Bioinformatics Italian Society: “A large-scale analysis of human protein missense variations collected from HUMSAVAR and ClinVar”, virtual event, remote attendance, July 01-02, 2021

National Conference: SIB 2021 Congress Virtual Edition, “Analysis of the Huntingtin solvent accessible surface”, remote attendance, 23-24 September 2021

International Conference: R2B OnAir – Research to Business is the International Exhibition on Industrial Research and Skills for Innovation: “Bioinformatic tools and services for the analysis of biological big data”, virtual event, remote attendance, 10-12 June, 2020

National Conference: BBCC2017 Bioinformatics and Computational Biology Conference: “From phenotypes to molecular mechanisms and pathways” – Naples, Italy, December 18-20, 2017

International Conference: NGS 2017: structural variation and population genomics: “eDGAR: a webserver for analysing the relationship among genes and polygenic diseases” – Barcellona (Spain), April 3-5, 2017

Local session of the International Competition: 3MT competition - University of Bologna: “Organizing the knowledge for genome editing”– Bologna (Italy), March 28, 2017

National Conference on: Proteine 2016: “Dissecting the Biological Complexity at the Molecular level” – Bologna (Italy), March 30- April 1, 2016

International Conference on: CAGI 2016:” Predicting the effect of variations on NPM-ALK functional activity and binding affinity with Hsp90.” – San Francisco (USA), March 25-27, 2016

POSTER PRESENTATIONS

Babbi G, Savojardo C, Martelli PL, Casadio R. (2021) *The peculiar solvent accessible surface of Huntingtin*. FEBS OPEN BIO 11, 474-474 - FEBS conference 2021, virtual event, remote attendance, July 03-08, 2021

Babbi G, Martelli PL, and Casadio R. (2020) *Identifying biological functions underlying phenotypes using PhenPath*, F1000Research 2020, 9(ISCB Comm J):1328, doi: 10.7490/f1000research.1118374.1 - Bioinformatics and Computational Biology Conference (BBCC) Naples, remote attendance 16-18 November, 2020

Babbi G, Martelli PL, Savojardo C, Baldazzi D, Tavella T and Casadio R. (2020) *eDGAR+: a data resource of annotated gene-variant-disease relations*, International conference “Intelligent Systems for Molecular Biology” (ISMB), virtual event, remote attendance, 13-16 July, 2020

Babbi G, Garcia L, Gray A, Martelli PL, Casadio R. (2020) *eDGAR and PhenPath resources join the Bioschemas Profiles*, ELIXIR All Hands meeting, remote attendance 8-10 June, 2020 published on F1000Research 2020, 9 (ELIXIR):569, doi: 10.7490/f1000research.1118004.1

Babbi G, Martelli PL, Bovo S, Casadio R (2018) *From diseases and phenotypes to processes and pathways*, Congress of the Italian Federation of Life Sciences societies (FISV) 2018 congress, Rome, 18-21 September, 2018

Babbi G, Martelli PL, Profiti G, Bovo S, Savojardo C, Casadio R. (2017) *eDGAR: a webserver for analysing the relationship among genes and polygenic diseases*. International Conference, NGS 2017: structural variation and population genomics”, pp. 46 – 47 - Barcellona, Spain, April 3-5, 2017

Babbi G, Martelli PL, Profiti G, Bovo S, Savojardo C and Casadio R. (2017) *Analysing the relations among genes and polygenic diseases with eDGAR*, Joint 25th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB) and 16th European Conference on Computational Biology (ECCB) 2017 published on F1000Research 2017, 6: 1532 (doi: 10.7490/f1000research.1114767.1)

Babbi G, Martelli PL, Profiti G, Casadio R. *Analysing OMIM disease-related variations: a large-scale investigation at the chromosome level* Proceedings of IWWBIO 2016 – 4th International Work-Conference on Bioinformatics and

ABSTRACTS

Scicchitano D, Palladino G, Brigidi P, Laczny C, Halder R, De Cesare A, Manfreda G, Martelli PL, **Babbi G**, Turroni S, Candela M, Rampelli S (2022) Resistome and xenobiome temporal dynamics in poultry production chain: the CIRCLES project – Yakult Symposium 2022, Milan, Italy, 13-14 October, 2022

Hitrec T, Tinganelli W, Negrini M, **Babbi G**, Squarcio F, Simoniello P, Cenacchi G, Grillini M, Papa V, Morganti A, Romani , Compagnone M, Marchesano V, Helm A, Piscitiello E, Occhinegro A, Taddei L, Luppi M, Amici R, Sioli M, Zoccoli A, Durante M, Cerri M. (2022) *Molecular mechanism for synthetic torpor-induced radioprotection: HIBRAD preliminary results* – 47th Annual Meeting of the European Radiation Research Society (ERRS 2022), Catania, Italy, 21-24 September, 2022

Palladino G, Scicchitano D, Brigidi P, Laczny C, Halder R, Trevisi P, Luise D, De Cesare A, Manfreda G, Martelli PL, **Babbi G**, Turroni S, Candela M, Rampelli S. (2022) *Resistome and xenobiome temporal dynamics in poultry and swine production chains: the CIRCLES project* - Federation of European Microbiological Societies (FEMS) Conference in Balgrade, Serbia, 30 June – 2 July, 2022

Savojardo C, Martelli PL, **Babbi G**, Anteghini M, Manfredi M, Madeo G, Capriotti E, et al. (2021) *SB4ER: An ELIXIR Service Bundle for Epidemic Response*. BioHackrXiv. March 25.

Hitrec T, Tinganelli W, Romani F, Simoniello P, Squarcio F, Luppi M, Compagnone G, Morganti AG, **Babbi G**, Martelli PL, Casadio R, Amici R, Negrini M, Zoccoli A, Durante M and Cerri M. (2020) *Effetti molecolari indotti dall'irraggiamento di roditori in torpore sintetico*, SIRR 2020 (XIX Convegno Nazionale della Società Italiana per le Ricerche sulle Radiazioni) 10-12 November, 2020

Savojardo C, Martelli PL, **Babbi G**, Tartari G, Baldazzi D and Casadio R. (2020) *A Bologna Biocomputing pipeline combining multiple tools for protein functional annotation in CAFA4*, International conference “Intelligent Systems for Molecular Biology” (ISMB), 13-16 July, 2020

Savojardo C, Martelli PL, Fariselli P, **Babbi G** and Casadio R. (2018) *INPS and INPS-3D: sequence- and structure-based prediction of protein stability change upon single-point variations*, Conference on the Critical Assessment of Genome Interpretation (CAGI5), Chicago, July 5-7, 2018

Babbi G, Profiti G, Martelli PL and Casadio R. (2018) *From phenotypes to molecular mechanisms and pathway. Informal proceeding of the Human Genetic Variation and Disease*, Gordon Research Conference, University of New England, June 10 - 15, 2018

Martelli PL, **Babbi G**, Profiti G and Casadio R. (2018) *Predicting protein-protein interaction sites with computational approaches*. Proteine 2018, University of Verona, May 20 -30, 2018

Babbi G, Martelli PL, Bovo S, Casadio R. (2018), *EDGAR and PhenPath, from diseases and phenotypes to processes and pathways. Poster at the Human Genetic Variation and Disease*, Gordon Research Conference, University of New England, June 10 - 15, 2018

Andreoletti G, Hoskins RA, Moulton J, Brenner SE, **The Cagi Participants**.

(2017) *Findings from the Fourth Critical Assessment of Genome Interpretation, a community experiment to evaluate phenotype prediction*. International Conference “NGS 2017: structural variation and population genomics”, pp. 55 – 56 - Barcellona, Spain, April 3-5, 2017

Babbi G, Martelli PL, Profiti G, Bovo S, Savojardo C and Casadio R. (2017), *Analysing the relations among genes and polygenic diseases with eDGAR*. Proceedings of the 59th Congress of the Italian Society of Biochemistry of Molecular Biology (SIB 2017), Caserta, September 20 – 22, 2017

Babbi G, Martelli PL, Profiti G, Bovo S, Savojardo C, Casadio R. (2017) *Analysing the relations among genes and polygenic diseases with eDGAR*. BITS, Proceedings of the 14th Annual Meeting of the Bioinformatics Italian Society, p. 134-135. Cagliari, July 5-7, 2017

Bovo S, **Babbi G**, Martelli PL, Casadio R. (2016) *Liver pyruvate kinase (L-PYK): predict the effects of missense mutations on kinase activity and allosteric regulation*. Conference on the Critical Assessment of Genome Interpretation (CAGI4), 25-27 March 2016, San Francisco, California, USA.

Babbi G, Martelli PL, Bovo S, Casadio R. (2016) *Predicting the effect of variations on protein functional activity and interaction*. Conference on the Critical Assessment of Genome Interpretation (CAGI4), 25-27 March 2016, San Francisco, California, USA.

Bovo S, Martelli PL, **Babbi G**, Casadio R. (2016) *Discriminating sick from healthy individuals by annotating exome variations*. Conference on the Critical Assessment of Genome Interpretation (CAGI4), 25-27 March 2016, San Francisco, California, USA.

Babbi G, Martelli PL, Bovo S, Casadio R. (2016) *Predicting the effect of variations on NPM-ALK functional activity and binding affinity with Hsp90*. Conference on the Critical Assessment of Genome Interpretation (CAGI4), 25-27 March 2016, San Francisco, California, USA.

Martelli PL, **Babbi G**, Bovo S, Casadio R. (2016) *Mapping of OMIM diseases and their associated genes in the chromosome space: addressing the complexity of polygenic disorders*. – Conference book, Gordon Research Conference - Human Single Nucleotide Polymorphisms & Disease - Mount Holyoke College, South Hadley, MA - June 12-17, 2016

Diquigiovanni C, Bergamini C, Evangelisti C, Costanzini A, Isidori F, Anbunathan H, Bowcock A, Casadio R, **Babbi G**, Rhoden KJ, Lenaz G, Fato R, Seri M, Romeo G, Bonora E. *Mutation in MYO1F cause familial non-medullary thyroid cancer (FNMTC)*. European Human Genetics Conference. Barcelona, Spain. May 21-24, 2016.

ATTENDED CONFERENCES

Elixir All-Hands meeting 2021, virtual conference, 1-11 June 2021

BIOHACKATHON-EUROPE - ELIXIR, virtual hackathon, 9-13 November 2020

Interoperability F2F meeting – ELIXIR, virtual hackathon, 11-12 May, 2020

National Conference: From molecules to complex biological functions: The computational method – Bologna (Italy), July 12, 2016

International Symposium on: The impact of Genomic Deep Sequencing from Pediatric Research and Clinical Practice – Bologna (Italy), 19-20

November 2015

58th National Meeting of the Italian Society of Biochemistry and Molecular Biology – Urbino (Italy), September 14-16, 2015

PUBLICATIONS

- Indexes
H index: 8, as to Scopus 28th October 2022
Citations: 197, as to Scopus 28th October 2022
Cumulative Impact Factor 2021: 116.024, as to Web of Science 28th October 2022
Cumulative Impact Factor Five Year: 128.386, as to Web of Science 28th October 2022
Peer-reviewed journal articles: 23
ORCID 0000-0002-9816-4737
- Dates
Research activity from 2016
Leave of absence: 16th March – 16th August 2019 (maternity)
22nd May – 22nd October 2022 (maternity)

PEER-REVIEWED JOURNAL ARTICLES

2022

Savojardo C, Baldazzi D, **Babbi G**, Martelli PL, Casadio R (2022) “*Mapping human disease-associated enzymes into Reactome allows characterization of disease groups and their interactions*”, Sci Rep 12, 17963.

DOI: 10.1038/s41598-022-22818-5

Citations [Scopus]: 0

Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology

Journal Impact Factor 2021 [web of science]: 4.997

Journal Impact Factor Five Year [web of science]: 5.516

Quartile and subject [web of science]: Q2 in MULTIDISCIPLINARY SCIENCES

Babbi G, Savojardo C, Baldazzi D, Martelli PL, Casadio R (2022) “*Pathogenic variation types in human genes relate to diseases through Pfam and InterPro mapping*”, Front Mol Biosci, Sep 16;9:966927.

DOI: 10.3389/fmolb.2022.966927

Citations [Scopus]: 0

Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology

Journal Impact Factor 2021 [web of science]: 6.113

Journal Impact Factor Five Year [web of science]: 6.122

Quartile and subject [web of science]: Q1 in BIOCHEMISTRY & MOLECULAR BIOLOGY

Cekanaviciute E, Tran D, Nguyen H, Lopez Macha A, Pariset E, Langley S, **Babbi G**, Malkani S, Penninckx S, Schisler J, Tin N, Karpen G, Costes SV (2022) “*Mouse Genomic Associations with Ex Vivo Sensitivity to Simulated Space Radiation*”, Life Sciences in Space Research, in press, preprint on BioRxiv

DOI: 10.1016/j.lssr.2022.07.006

Citations [Scopus]: 0

Subject Area [Scopus]: Agricultural and Biological Sciences

Journal Impact Factor 2021 [web of science]: 2.73

Journal Impact Factor Five Year [web of science]: 3

Quartile and subject [web of science]: Q2 in ASTRONOMY & ASTROPHYSICS and Q3 in BIOLOGY

Savojardo C, **Babbi G**, Baldazzi D, Martelli PL, Casadio R (2021) “*A Glance into MTHFR Deficiency at a Molecular Level*”. Int. J. Mol. Sci., 23, 167.

DOI: 10.3390/ijms23010167

Citations [Scopus]: 1

Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology
Journal Impact Factor 2021 [web of science]: 6.208
Journal Impact Factor Five Year [web of science]: 6.628
Quartile and subject [web of science]: Q1 in BIOCHEMISTRY & MOLECULAR BIOLOGY

2021

Savojardo C, **Babbi G**, Martelli PL and Casadio R (2021) *Mapping OMIM Disease-Related Variations on Protein Domains Reveals an Association Among Variation Type, Pfam Models, and Disease Classes*. Front. Mol. Biosci. 8:617016.

DOI: 10.3389/fmolb.2021.617016

Citations [Scopus]: 3

Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology

Journal Impact Factor 2021 [web of science]: 6.113

Journal Impact Factor Five Year [web of science]: 6.122

Quartile and subject [web of science]: Q1 in BIOCHEMISTRY & MOLECULAR BIOLOGY

Babbi G, Savojardo C Martelli PL, Casadio R. (2021) "*Huntingtin: a protein with a peculiar solvent accessible surface*". Int. J. Mol. Sci. 2021, 22:6.

DOI: 10.3390/ijms22062878

Citations [Scopus]: 2

Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology

Journal Impact Factor 2021 [web of science]: 6.208

Journal Impact Factor Five Year [web of science]: 6.628

Quartile and subject [web of science]: Q1 in BIOCHEMISTRY & MOLECULAR BIOLOGY

2020

Babbi G, Baldazzi D, Martelli PL, Savojardo C, Casadio R (2020), "*Highlighting human enzymes active in different metabolic pathways and diseases: the case study of EC 1.2.3.1 and Alpha-Aminoacidic Semialdehyde Dehydrogenase*", Biomedicines. Vol. 8, pp.250-262

DOI: 10.3390/BIOMEDICINES8080250

Citations [Scopus]: 0

Journal Impact Factor 2021 [web of science]: 4.757

Journal Impact Factor Five Year [web of science]: 5.225

Quartile and subject [web of science]: Q2 in BIOCHEMISTRY & MOLECULAR BIOLOGY

2019

Savojardo C, **Babbi G**, Bovo S, Capriotti E, Martelli P and Casadio R (2019), "*Are machine learning based methods suited to address complex biological problems? Lessons from CAGI-5 challenges*", Human Mutation. Vol. 40(9), pp. 1455-1462.

DOI: 10.1002/humu.23784

Citations [Scopus]: 4

Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology

Journal Impact Factor 2021 [web of science]: 4.7

Journal Impact Factor Five Year [web of science]: 5.535

Quartile and subject [web of science]: Q2 in GENETICS & HEREDITY

Clark WT, Kasak L, Bakolitsa C, Hu Z, Andreoletti G, **Babbi G**, Bromberg Y, Casadio R, Dunbrack R, Folkman L, Ford CT, Jones D, Katsonis P, Kundu K, Lichtarge O, Martelli PL, Mooney SD, Nodzak C, Pal LR, Radivojac P, Savojardo C, Shi X, Zhou Y, Uppal A, Xu Q, Yin Y, Pejaver V, Wang M, Wei L, Moulton J, Yu GK, Brenner SE and LeBowitz JH (2019), "*Assessment of predicted enzymatic activity of alpha-N-acetylglucosaminidase variants of unknown significance for CAGI 2016*", Human Mutation., sep, 2019. Vol. 40(9), pp. 1519-

1529.

DOI: 10.1002/humu.23875

Citations [Scopus]: 5

Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology

Journal Impact Factor 2021 [web of science]: 4.7

Journal Impact Factor Five Year [web of science]: 5.535

Quartile and subject [web of science]: Q2 in GENETICS & HEREDITY

Monzon A, Carraro M, Chiricosta L, Reggiani F, Han J, Ozturk K, Wang Y, Miller M, Bromberg Y, Capriotti E, Savojardo C, **Babbi G**, Martelli PL, Casadio R, Katsonis P, Lichtarge O, Carter H, Kousi M, Katsanis N, Andreoletti G, Moulton J, Brenner S, Ferrari C, Leonardi E and Tosatto S (2019), "*Performance of computational methods for the evaluation of pericentriolar material 1 missense variants in CAGI-5*", Human Mutation. Vol. 40(9), pp. 1474-1485.

DOI: 10.1002/humu.23856

Citations [Scopus]: 4

Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology

Journal Impact Factor 2021 [web of science]: 4.7

Journal Impact Factor Five Year [web of science]: 5.535

Quartile and subject [web of science]: Q2 in GENETICS & HEREDITY

Savojardo C, Petrosino M, **Babbi G**, Bovo S, Corbi-Verge C, Casadio R, Fariselli P, Folkman L, Garg A, Karimi M, Katsonis P, Kim P, Lichtarge O, Martelli P, Pasquo A, Pal D, Shen Y, Strokach A, Turina P, Zhou Y, Andreoletti G, Brenner S, Chiaraluce R, Consalvi V and Capriotti E (2019), "*Evaluating the predictions of the protein stability change upon single amino acid substitutions for the FXN CAGI5 challenge*", Human Mutation. Vol. 40(9), pp. 1392-1399.

DOI: 10.1002/humu.23843

Citations [Scopus]: 12

Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology

Journal Impact Factor 2021 [web of science]: 4.7

Journal Impact Factor Five Year [web of science]: 5.535

Quartile and subject [web of science]: Q2 in GENETICS & HEREDITY

Cline M, **Babbi G**, Bonache S, Cao Y, Casadio R, de la Cruz X, Díez O, Gutiérrez-Enríquez S, Katsonis P, Lai C, Lichtarge O, Martelli P, Mishne G, Moles-Fernández A, Montalban G, Mooney S, O'Conner R, Ootes L, Özkan S, Padilla N, Pagel K, Pejaver V, Radivojac P, Riera C, Savojardo C, Shen Y, Sun Y, Topper S, Parsons M, Spurdle A and Goldgar D (2019), "*Assessment of blind predictions of the clinical significance of BRCA1 and BRCA2 variants*", Human Mutation. Vol. 40(9), pp. 1546-1556.

DOI: 10.1002/humu.23861

Citations [Scopus]: 11

Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology

Journal Impact Factor 2021 [web of science]: 4.7

Journal Impact Factor Five Year [web of science]: 5.535

Quartile and subject [web of science]: Q2 in GENETICS & HEREDITY

Kasak L, Hunter JM, Udani R, Bakolitsa C, Hu Z, Adhikari AN, **Babbi G**, Casadio R, Gough J, Guerrero RF, Jiang Y, Joseph T, Katsonis P, Kotte S, Kundu K, Lichtarge O, Martelli PL, Mooney SD, Moulton J, Pal LR, Poitras J, Radivojac P, Rao A, Sivadasan N, Sunderam U, Saipradeep VG, Yin Y, Zaucha J, Brenner SE and Meyn MS (2019), "*CAGI SickKids challenges: Assessment of phenotype and variant predictions derived from clinical and genomic data of children with undiagnosed diseases*", Human Mutation., sep, 2019. Vol. 40(9), pp. 1373-1391.

DOI: 10.1002/humu.23874

Citations [Scopus]: 5

Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology

Journal Impact Factor 2021 [web of science]: 4.7

Journal Impact Factor Five Year [web of science]: 5.535

Quartile and subject [web of science]: Q2 in GENETICS & HEREDITY

Zhang J, Kinch L, Cong Q, Katsonis P, Lichtarge O, Savojardo C, **Babbi G**, Martelli P, Capriotti E, Casadio R, Garg A, Pal D, Weile J, Sun S, Verby M, Roth F and Grishin N (2019), "*Assessing predictions on fitness effects of missense variants in calmodulin*", Human Mutation. Vol. 40(9), pp. 1463-1473. DOI: 10.1002/humu.23857

Citations [Scopus]: 9

Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology

Journal Impact Factor 2021 [web of science]: 4.7

Journal Impact Factor Five Year [web of science]: 5.535

Quartile and subject [web of science]: Q2 in GENETICS & HEREDITY

Voskanian A, Katsonis P, Lichtarge O, Pejaver V, Radivojac P, Mooney S, Capriotti E, Bromberg Y, Wang Y, Miller M, Martelli P, Savojardo C, **Babbi G**, Casadio R, Cao Y, Sun Y, Shen Y, Garg A, Pal D, Yu Y, Huff C, Tavtigian S, Young E, Neuhausen S, Ziv E, Pal L, Andreoletti G, Brenner S and Kann M (2019), "*Assessing the performance of in silico methods for predicting the pathogenicity of variants in the gene CHEK2, among Hispanic females with breast cancer*", Human Mutation. Vol. 40(9), pp. 1612-1622. DOI: 10.1002/humu.23849

DOI: 10.1002/humu.23849

Citations [Scopus]: 4

Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology

Journal Impact Factor 2021 [web of science]: 4.7

Journal Impact Factor Five Year [web of science]: 5.535

Quartile and subject [web of science]: Q2 in GENETICS & HEREDITY

Pejaver V, **Babbi G**, Casadio R, Folkman L, Katsonis P, Kundu K, Lichtarge O, Martelli P, Miller M, Moulton J, Pal L, Savojardo C, Yin Y, Zhou Y, Radivojac P and Bromberg Y (2019), "*Assessment of methods for predicting the effects of PTEN and TPMT protein variants*", Human Mutation. Vol. 40(9), pp. 1495-1506.

DOI: 10.1002/humu.23838

Citations [Scopus]: 7

Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology

Journal Impact Factor 2021 [web of science]: 4.7

Journal Impact Factor Five Year [web of science]: 5.535

Quartile and subject [web of science]: Q2 in GENETICS & HEREDITY

Babbi G, Martelli P and Casadio R (2019), "*PhenPath: A tool for characterizing biological functions underlying different phenotypes*", BMC Genomics. Vol. 20 DOI: 10.1186/s12864-019-5868-x

DOI: 10.1186/s12864-019-5868-x

Citations [Scopus]: 7

Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology

Journal Impact Factor 2021 [web of science]: 4.558

Journal Impact Factor Five Year [web of science]: 4.93

Quartile and subject [web of science]: Q2 in GENETICS & HEREDITY, Q2 in BIOTECHNOLOGY & APPLIED MICROBIOLOGY

Savojardo C, **Babbi G**, Martelli P and Casadio R (2019), "*Functional and structural features of disease-related protein variants*", International Journal of Molecular Sciences. Vol. 20(7)

DOI: 10.3390/ijms20071530

Citations [Scopus]: 8

Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology

Journal Impact Factor 2021 [web of science]: 6.208

Journal Impact Factor Five Year [web of science]: 6.628

Quartile and subject [web of science]: Q1 in BIOCHEMISTRY & MOLECULAR BIOLOGY

2018

Diquigiovanni C, Bergamini C, Evangelisti C, Isidori F, Vettori A, Tiso N, Argenton F, Costanzini A, Iommarini L, Anbunathan H, Pagotto U, Repaci A, **Babbi G**, Casadio R, Lenaz G, Rhoden K, Porcelli A, Fato R, Bowcock A, Seri M, Romeo G and Bonora E (2018), "*Mutant MYO1F alters the mitochondrial network and induces tumor proliferation in thyroid cancer*", International Journal of Cancer. Vol. 143(7), pp. 1706-1719

DOI: 10.1002/ijc.31548

Citations [Scopus]: 24

Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology

Journal Impact Factor 2021 [web of science]: 7.316

Journal Impact Factor Five Year [web of science]: 6.842

Quartile and subject [web of science]: Q1 in ONCOLOGY

2017

Daneshjou R, Wang Y, Bromberg Y, Bovo S, Martelli P, **Babbi G**, Lena P, Casadio R, Edwards M, Gifford D, Jones D, Sundaram L, Bhat R, Li X, Pal L, Kundu K, Yin Y, Moul J, Jiang Y, Pejaver V, Pagel K, Li B, Mooney S, Radivojac P, Shah S, Carraro M, Gasparini A, Leonardi E, Giollo M, Ferrari C, Tosatto S, Bachar E, Azaria J, Ofran Y, Unger R, Niroula A, Vihinen M, Chang B, Wang M, Franke A, Petersen B-S, Pirooznia M, Zandi P, McCombie R, Potash J, Altman R, Klein T, Hoskins R, Repo S, Brenner S and Morgan A (2017), "*Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges*", Human Mutation. Vol. 38(9), pp. 1182-1192.

DOI: 10.1002/humu.23280

Citations [Scopus]: 25

Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology

Journal Impact Factor 2021 [web of science]: 4.7

Journal Impact Factor Five Year [web of science]: 5.535

Quartile and subject [web of science]: Q2 in GENETICS & HEREDITY

Xu Q, Tang Q, Katsonis P, Lichtarge O, Jones D, Bovo S, **Babbi G**, Martelli P, Casadio R, Lee G, Seok C, Fenton A and Dunbrack R (2017), "*Benchmarking predictions of allostery in liver pyruvate kinase in CAGI4*", Human Mutation. Vol. 38(9), pp. 1123-1131.

DOI: 10.1002/humu.23222

Citations [Scopus]: 10

Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology

Journal Impact Factor 2021 [web of science]: 4.7

Journal Impact Factor Five Year [web of science]: 5.535

Quartile and subject [web of science]: Q2 in GENETICS & HEREDITY

Babbi G, Martelli P, Profiti G, Bovo S, Savojardo C and Casadio R (2017), "*eDGAR: A database of disease-gene associations with annotated relationships among genes*", BMC Genomics. Vol. 18

DOI: 10.1186/s12864-017-3911-3

Citations [Scopus]: 34

Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology

Journal Impact Factor 2021 [web of science]: 4.558

Journal Impact Factor Five Year [web of science]: 4.93

Quartile and subject [web of science]: Q2 in GENETICS & HEREDITY, Q2 in BIOTECHNOLOGY & APPLIED MICROBIOLOGY

2016

Martelli P, Fariselli P, Savojardo C, **Babbi G**, Aggazio F and Casadio R (2016), "*Large scale analysis of protein stability in OMIM disease related human protein variants*", BMC Genomics. Vol. 17

DOI: 10.1186/s12864-016-2726-y

Citations [Scopus]: 22

Subject Area [Scopus]: Biochemistry, Genetics and Molecular Biology

Journal Impact Factor 2021 [web of science]: 4.558

Journal Impact Factor Five Year [web of science]: 4.93
Quartile and subject [web of science]: Q2 in GENETICS & HEREDITY, Q2 in BIOTECHNOLOGY & APPLIED MICROBIOLOGY

PERSONAL SKILLS AND COMPETENCES

MOTHER TONGUE	Italian		
OTHER LANGUAGES	English	French	
• Reading skills	C1	B1	
• Writing skills	C1	B1	
• Verbal skills	C1	A2	
• Certification	B2– Exam during bachelor's degree 11/01/2013	B1 – Exam during bachelor's degree 10/01/2013	
• Social skills and competences	Activities carried out while researching, and participation to national and international projects gave me the opportunity to work in team several times. In particular, during the internships and the PhD program I worked in a heterogeneous team composed by Bioinformaticians, Physicists and Computer Scientists. These experiences gave me the possibility to establish relations with people with different backgrounds, acquiring knowledge and skills necessary for interdisciplinary communication, team working, and project planning.		

RESEARCH FIELDS AND TECHNICAL SKILLS

I'm able to apply Bioinformatics/Computational-Biology techniques for the development of tools for data mining. In particular I have skills in the analysis of different kinds of biological data and in the integration/interpretation of results from a Systems Biology point of view. I implemented databases and computational infrastructures to store and analyse high volume of data; I collaborated in implementing predictors for the effect of protein variants, and I used these tools in international experiments. I have experience in building pipelines for the characterization of genes, proteins and biological processes, curating their annotation and integrating resources from other primary databases.

General informatics skills

Knowledge of:

- Windows and Ubuntu as Operative Systems;
- Office and OpenOffice suites.

Computational Biology

- Protein 3D modelling
- Protein sequence comparison and analysis
- Functional annotation of bio sequences and variants
- Modeller and PyMol for protein structure homology modelling and protein structure inspection
- Databases, standards and ontologies for bioinformatics (HGNC,

- dbSNP, OMIM, HPO, GO terms, ClinVar, Humsavar, DisGeNet, PDB)
- Database implementation with PostgreSQL, SQLite and MySQL for database management
- HMMER for biosequence analysis using profile HMM
- Cytoscape for graph analysis
- Chimera and Rasmol for protein model visualization
- Python and its libraries (such as Biopython and Web2Py)
- Java and its libraries for XML parsing
- Handling XML, OBO and OWL file
- JSON format and graph visualization with D3js
- DataTables plug-in for jQuery
- CSS and Javascript for HTML documents
- R for the analysis of biological data

Experimental skills

- Biochemical techniques such as protein extraction and purification, enzymatic activity measurement, electrophoresis and blotting
- Molecular Biology techniques such as DNA extraction and purification, PCR, electrophoresis, blotting, analysis of polymorphism (RFLP)
- Recombinant DNA technology for Plant/Industrial/Animal biotechnologies

TEACHING EXPERIENCE

- | | |
|--|--|
| <ul style="list-style-type: none"> • Dates | From October 2022 |
| <ul style="list-style-type: none"> • Occupation or position held | Responsible of the module 2 of the course PROTEOMES, INTERACTOMES AND BIOLOGICAL NETWORKS (22 hours, SSD: BIO/10) at the first cycle degree programme in Genomics |
| <ul style="list-style-type: none"> • Name and address of employer | Department of Pharmacy and Biotechnology (FaBiT) – University of Bologna, Via Belmeloro, 6, 40126 Bologna (BO), ITALY |
| <ul style="list-style-type: none"> • Main activities and responsibilities | By the end of the course, students have the basic knowledge of the experimental techniques for analysing proteins expressed in a biological system and their interactions. Among the others, activities include Bash scripting and Python programming; information retrieval in web available databases; analysis of protein structure and protein-protein complexes; analysis and visualization of biological networks. |
| <ul style="list-style-type: none"> • Dates | October 2020 |
| <ul style="list-style-type: none"> • Occupation or position held | Teaching tutor of Laboratory of Bioinformatics 2 (SSD: BIO/10) at the Second cycle degree programme in Bioinformatics (LM-06) |
| <ul style="list-style-type: none"> • Name and address of employer | Department of Pharmacy and Biotechnology (FaBiT) – University of Bologna, Via Belmeloro, 6, 40126 Bologna (BO), ITALY |
| <ul style="list-style-type: none"> • Main activities and responsibilities | The main topics of the course include simple linear classifiers and machine learning approach, and their interpretation/evaluation.
It requires knowledge of the libsvm package for SVM development, of cross-validation procedure, of scoring indices like confusion matrix, sensitivity, specificity, accuracy, Matthews correlation coefficient. |

- Dates
 - November 2015 – July 2016
 - November 2016 – July 2017
 - November 2017 – July 2018
 - November 2018 – July 2019
- Occupation or position held
 - Teaching tutor of Laboratory of Bioinformatics 1 (SSD: BIO/10) at the Second cycle degree programme in Bioinformatics (LM-06)
- Name and address of employer
 - Alma Mater Studiorum – University of Bologna
 - School of Science (BiGeA), Via Selmi 3 – 40126 Bologna (BO), ITALY
- Main activities and responsibilities
 - The main topics are the problems of protein 3D-structure modelling following the building by homology approach, tools for the analysis of protein sequences, sequence alignments, Hidden Markov Models for the recognition and modelling of protein domains. The lectures required the knowledge of programming language (Python) and many software packages (RasMol, Procheck, jCe, Modeller, HMMER).
- CoSupervisor
 - “Toolkit for differential analysis of microbiome data” (SSD: BIO/10), presented by Óscar San José Rodríguez, 2022, at the Second cycle degree programme in Bioinformatics (LM-06)

ADDITIONAL INFORMATION

MEMBERSHIPS

Member of the Italian Society of Biochemistry and Molecular Biology (SIB) – from 2015

From 2022 Representative of the Young Section Committee for the Group Computation and System Biology

Member of the International Society for Computational Biology in 2016

Ambassador of the Italian Regional Student Group of the International Society For Computational Biology (ISCB-RSG) from 2015 to 2017