## **CURRICULUM VITAE**

#### PERSONAL INFORMATION

## Allegra Via









H-index: 21 Citations: 2379

Sex F | Date of birth 24/01/1968 | Nationality Italian | Status Separated, two children (born 1998 and 2001)

#### **CURRENT POSITIONS & ROLES**

Institute of Molecular Biology and Pathology (IBPM), National Research Council (CNR), Rome, IT

Research Scientist, 2016 -

#### **ELIXIR**

Co-lead of the ELIXIR-EXCELERATETrain-the-Trainer subtask, 2015 -Co-lead of Training Platform Task 4 (Capacity Building), ELIXIR Project Plan 2019 – 2021

#### **ELIXIR-IT**

Training Platform Coordinator, 2015 -

**University of Bologna, School of Science, Master Degree in Bioinformatics,** Laboratory of Bioinformatics 1 – Modulo 3, Bologna, IT

Adjunct professor, 2015 - 2019

**University of Bologna, School of Science, Master Degree in Bioinformatics,** Programming for Bioinformatics – Modulo 2, Bologna, IT

Adjunct professor, 2018 - 2019

**Sapienza University, Degree in Biological Sciences,** Laboratory of Bioinformatics, Rome, IT *Adjunct professor*, 2017 – 2019

Sapienza University, QuID group (Group for the Quality and Innovation of Teaching), Rome, IT Expert, 2017 -

# NATIONAL SCIENTIFIC QUALIFICATION

Associate Professor: Molecular Biology (05/E2 - SSD BIO/11) Associate Professor: Applied Physics (02/B3 - SSD FIS/07) Associate Professor: Biochemistry (05/E1 – SSD BIO/10)

#### WORK EXPERIENCE

## Dec 2016 - Research Scientist

Institute of Molecular Biology and Pathology, The National Research Council, Italy (IBPM-CNR)

• Research in protein structure, function and diseases; Cognitive and educational psychology and learning processes; teaching and training; undergraduate, graduate, and PhD student tutoring; bachelor and master degree thesis supervising; grant writing; collaboration coordination. Networking.

#### Jan 2016 – Dec 2016

### Research Associate (RTD)

Institute of Biomembrane and Bioenergetics, The National Research Council, Italy (IBIOM-CNR)

• Research in protein structure, function and diseases; Cognitive and educational psychology and learning processes; teaching and training; undergraduate, graduate, and PhD student tutoring; bachelor and master degree thesis supervising; grant writing; collaboration coordination. Networking.

#### Jan 2013 - Dec 2015

#### Research Associate (RTD)

Department of Physics, Sapienza University of Rome, Italy (http://www.phys.uniroma1.it/fisica/)

· Research in protein structure, function and diseases; teaching and training; undergraduate, graduate, and PhD student tutoring; bachelor and master degree thesis supervising; grant writing; collaboration coordination. Networking.

Sector Structural Bioinformatics and Computational Biology

#### Sept 2015 -

#### Training Coordinator of the ELIXIR Italian node (ELIXIR-IT)

• Coordination of ELIXIR-ITA training activities. ELIXIR (http://www.elixir-europe.org) is a distributed sustainable European infrastructure for life science information, supporting life science research and its translation to medicine, agriculture, bioindustries and society. ELIXIR-ITA (the Italian node of ELIXIR) is a Joint Research Unit with twelve member institutions (8 Universities including Sapienza, CNR, CRS4, INFN, CINECA)

Sector Training in Bioinformatics

#### Nov 2015 - Sep 2017

#### ELIXIR-IT Technical Coordinator for Sapienza University

• Coordination of ELIXIR-ITA research support activities for Sapienza Univeristy, Rome Sector Support to Bioinformatics research

#### Dec 2009 – Dec 2012

#### Research Associate (RTD)

Department of Biochemical Sciences, Sapienza University of Rome, Italy (http://wg.uniroma1.it/bio\_chem/sito\_biochimica/index.html)

• Research in protein structure, function and diseases; teaching and training; undergraduate, graduate, and PhD student tutoring; bachelor and master degree thesis supervising; grant writing; collaboration coordination. Networking.

Sector Structural Bioinformatics and Computational Biology

#### Dec 2007 - Nov 2009

#### Postdoc

Department of Biochemical Sciences, Sapienza University of Rome, Italy (http://w3.uniroma1.it/bio\_chem/sito\_biochimica/index.html)

• Research in protein structure and function. Protein phosphorylation. Linear motifs. Teaching. Undergraduate, graduate, and PhD student tutoring; grant writing. Sector Structural Bioinformatics and Computational Biology

#### Dec 2006 – Nov 2007

#### Postdoc

Department of Experimental Biology of Evolution, Alma Mater Studiorum Università di Bologna, Bologna, Italy (http://www.unibo.it/)

• Research in protein structure and function. Protein phosphorylation. Linear motifs. Neural networks. Modelling of biological systems. Teaching. Undergraduate, graduate, and PhD student tutoring. Contribution to grant writing.

Sector Bioinformatics and Computational Biology

#### Sep 2006 – Nov 2006

#### Postdoc

Department of Biology, University of Rome "Tor Vergata", Italy (http://www2.bio.uniroma2.it)

• Research in protein sequence, structure and function. Protein phosphorylation. Linear motifs. Neural networks. Modelling of biological systems. Teaching and teacher assistant. Undergraduate, graduate, and PhD student tutoring. Contribution to grant writing.

Sector Bioinformatics and Computational Biology

#### Sep 2003 - Aug 2006

#### Postdoc

Department of Biology, University of Rome "Tor Vergata", Italy (http://www2.bio.uniroma2.it)

• Research in protein sequence, structure and function. Protein phosphorylation. Linear motifs. Neural networks. Modelling of biological systems. Teaching and teacher assistant. Undergraduate, graduate, and PhD student tutoring. Contribution to grant writing.

Sector Bioinformatics and Computational Biology

#### May 2003 – Aug 2003 Posdoc

Department of Biology, University of Rome "Tor Vergata", Italy (http://www2.bio.uniroma2.it)

• Research in protein sequence, structure and function. Protein phosphorylation. Linear motifs. Modular domains. Modelling of biological systems. Teacher assistant. Undergraduate and graduate student tutoring. Contribution to grant writing.

Sector Bioinformatics and Computational Biology

#### Nov 1999 – Apr 2003

## PhD in Cellular and Molecular Biology

Department of Biology, University of Rome "Tor Vergata", Italy (http://www2.bio.uniroma2.it)

• Research in protein sequence, structure and function. Protein phosphorylation. Linear motifs. Modular domains. Modelling of biological systems. Teacher assistant. Undergraduate student tutoring.

Sector Bioinformatics and Computational Biology

### Feb 1998 - Oct 1999

### Postgraduate Fellowship

Department of Biology, University of Rome "Tor Vergata", Italy (http://www2.bio.uniroma2.it)

• Research in protein sequence, structure and function. Modular domains. Modelling of biological

Sector Bioinformatics and Computational Biology

#### **EDUCATION AND TRAINING**

### Apr 2003 PhD in Cellular and Molecular Biology

Department of Biology, University of Rome "Tor Vergata", Italy

- Thesis title: Protein structural study for the optimization and analysis of sequence functional motifs.
- Supervisor: Prof. Manuela Helmer-Citterich.

Sector Cellular and Molecular Biology, Bioinformatics and Computational Biology

#### Jul 1997

#### Master Degree in Physics

Department of Physics, Sapienza University, Rome, Italy

- Thesis Title: Analytical study of the Sherrington and Kirkpatrick spin-glass model.
- Supervisor: Prof. Giorgio Parisi.

Sector Mechanics, Dynamics, Quantum Mechanics, Mathematical Analysis, Condensed matter, Statistical Mechanics, Theoretical Physics, Spin-glasses

#### Aug 1994 – Jul 1995

#### Erasmus programme

Department of Mathematics, Université Paris VII, Paris, France

Sector Mathematical Analysis, Statistical Mechanics, Mathematical Methods applied to Physics.

#### **PERSONAL SKILLS**

#### Mother tongue

#### Other languages

English: Proficient in spoken and written language (C1/C2) French: Proficient in spoken and written language (C1/C2)

German: Basic communication skills (A1)

#### Programming&software

- UNIX/Linux, MacOSX
- Python programming
- Web programming (HTML, CGI)
- MySQL, PostgreSQL
- R scripting
- PyMOL, Chimera, SwissPDBviewer
- Docking packages (e.g. Autodock)
- Network analysis software (Cytoscape)
- Several Bioinformatics and Computational Biology software (e.g. local Blast+, ClustalW, Modeller, etc.)

#### Communication skills

- good communication skills gained through the experience as teacher, trainer and public speaker;
- experienced in scientific manuscript and grant writing;
- good public speaking skills acquired giving talks and seminars;
- good communication over distance skills acquired in conference calls;
- comfortable in speaking to interdisciplinary audiences about technical and scientific topics.

#### Organisational/managerial skills

- leadership (lead of the ELIXIR-IT Training Platform; co-lead of the ELIXIR-EXCELERATE Train the Trainer programme; co-chair of the ELIXIR-Carpentries Working Group)
- project coordination ability (coordination of ELIXIR Train the Trainer Subtask; coordination of the ELIXIR-IT Training Platform, WP PI in European and Italian Project)
- manuscript review management capability (as Editorial Board member and reviewer of scientific journals)
- network management (as Chair of BTN and ELIXIR-IIB Training Platform coordinator)
- workshop and course organisation skills (obtained co-organising a workshops, a conference and training courses)

#### Other skills

• passionate about working and engaging with others to achieve goals; adaptable; independent; team player; interested in community building; proactive; perfectionist; curious. Passionate about drawing, painting and writing.

Driving licence B

#### ADDITIONAL INFORMATION

#### Research projects

- Devon CNR 1997 (Target project in Biotechnology) Three-dimensional profiles: a new software and database for the analysis of protein function, stability and specificity (36 months) – **Participant**
- EU FP6 2000 ELM: The Eukaryotic Linear Motif Resource ELM: A new European Bioinformatics facility for revealing functional sites in modular proteins (id QLRI-CT-2000-00127) (36 months) - Participant
- TELETHON 2000: A multi-centre bioinformatic project for a systematic investigation of genes expressed in human skeletal muscle (id GPo101Y01) (36 months) - Participant
- AIRC 2001: Specificity of recognition and/or interaction in phospho-proteins (36 months) **Participant**
- FIRB 2001: Bioinformatica per la Genomica e la Proteomica (36 months) Participant
- MIUR FSSRIS 2002 (Fondo Speciale per lo Sviluppo della Ricerca di Interesse Strategico) GENEFUN: Geni e loro funzioni: un approccio integrato (24 months) – Participant
- FIRB 2003 LIBI: Laboratorio Internazionale di Bioinformatica (36 months) Participant
- TELETHON 2004: A bioinformatic approach for the identification of interactors of proteins involved in genetic diseases (id GGP04273) (24 months) – Participant
- AIRC 2005: A structural approach for the analysis of recognition specificity in phosphoproteins (36 months) - Participant
- EU FP7 2008 LEISHDRUG: Targeting the Leishmania kinome for the development of novel anti-parasitic strategies (36 months) - Participant
- KAUST (2008-2012): Computational Analysis of the Human Genome (48 months) -**Participant**
- Fondazione Roma (2009-2012): Rational approach to the specific inhibition of Plasmodium falciparum and Schistosoma mansoni (36 months) – Participant
- FIRB (2007-2013): Rete italiana di Bioinformatica (ITALBIONET) (60 months) Participant
- Progetto di Ateneo 2011: Identificazione di target molecolari in malaria e schistosomiasi e caratterizzazione delle loro interazioni con potenziali inibitori (12 months) - Principal Investigator
- PRIN 2012: Approccio integrato computazionale e sperimentale per lo studio di patologie umane (12 months) – Participant
- Progetto di Ateneo 2013: Characterisation of Plasmodium falciparum antigens triggering autoimmune response (12 months) – Principal Investigator
- ELIXIR-EXCELERATE (2014 2019): Grant funded by the European Commission within the Research

Infrastructures programme of Horizon 2020 following the ESFRI and European Council decision in 2014 to categorize ELIXIR as one of Europe's three priority new Research Infrastructures. Grant agreement number 676559 – Lead of the WP11 Train the Trainer subtask.

- ELIXIR Implementation Study on Learning Paths (2018 2019) Participant
- ELIXIR Project Plan 2019-2021 Co-lead of Task 4 "Capacity Building"
- ELIXIR Infrastructure for the Rare Disease-Community (2019-21) Co-PI of WP4
- PON Research and Innovation (2019 2023), "Centro Nazionale di Ricerca in Bioinformatica per le scienze Omiche" – Scientific coordinator of the Training Platform WP.

#### Main invited seminars

- 2019: Title: "Curriculum Development: considerations for education and training", Pan African Bioinformatics Network for H3Africa (H3ABioNet), Education summit, Cape Town, South Africa.
- 2018: Title: "The ELIXIR Italy Training Platform: supporting researchers and professionals in acquiring specialized computational and data management skills", GARR Conference on Data Revolution, Cagliari, IT
- 2018: Title: "ELIXIR: Safeguarding the results of life science research in Europe", EaPConnect e-Health workshop on Biomedical collaborations over National Research and Education networks: success stories and best practices, Istituto Superiore di Sanità, Rome,
- 2018: Title: "Cognitive psychology in the bioinformatics learning enterprise", ISMB COSI on Computational Biology Education, Chicago, US
- 2018: Title: "A critical look at competencies", ELIXIR workshop on ELIXIR Implementation Study on Learning Paths, Amsterdam, NL
- 2017: Title: "From knowledge, skills and abilities to learning paths: Using Mastery Rubrics for training", GOBLET AGM Workshop, Oeiras, PT
- 2017: Title: "Integrating protein-protein interaction and expression data for the identification of cellular targets in drug delivery", Workshop of the SIB group on "Computational and Systems Biology", Bologna, IT
- 2016: "Ten simple rules to make your teaching more effective", BITS 2016 Conference, University of Salerno, Fisciano (SA), IT
- 2016: "Role of structure-based homology modeling in biomolecular sciences", Scientific School on "Computational modeling for Life Sciences", Sardinian Scientific and Technological Park, Pula (CA), IT
- 2014: Title: "Computational approaches to the study of functional sites in biomolecules", Dept. of Experimental Medicine and Surgery, University of Rome "Tor Vergata", IT
- 2014: Title: "A computational approach for the study of therapeutic targets and their inhibitors in human pathogens", TAGC Inserm, Aix-Marseille Université, France.
- 2013: Title: "Best practices in programming for biological data management", The Genome Analysis Centre, Norwich, UK
- 2013: Title: "GOBLET", NextGenBug 31st meeting, ARK Genomics, Roslin, Edinburgh, UK
- 2012: Title: "A structural approach to the study of therapeutical targets and their inhibitors in human pathogens", Bi-national Israel-Italy meeting, Tel Aviv University, IL
- 2009: Title: "Cross-talking between human genome variations and their protein environment: a computational study", IRB Barcelona, SP
- 2008: Title: "Structural bioinformatics: a meeting-place for Biology and Physics", Alma Mater Università di Bologna, IT
- 2006: Title: "High-throughput protein functional annotation based upon local structure similarity", Genome Annotation: a BioSapiens Network of Excellence Initiative. 5<sup>th</sup> European Conference on Computational Biology (ECCB), IL
- 2001: Title: "Proteins: Structure, Function, Evolution", IUSS (Istituto Universitario di Studi Superiori), University of Pavia, IT
- 2001: Title: "The structure of Proteins", in the Course of "Problems in Biological Evolution"; Scuola di Genetica di Cortona, Associazione Genetica Italiana (AGI), Cortona, IT

- Honours and awards 2002 Telethon award
  - 2005 Telethon award

# organisation

Workshop and course • Organised the ELIXIR-EXCELERATE Train the Trainer course, Padova, Italy, 30-31 May, 2018

- Co-organised the ELIXIR Data Carpentry workshop, Milano, Italy, 14-15 Feb, 2018
- Co-organised the ELIXIR Software workshop, Napoli, Italy, 11-12 Feb, 2019
- Co-organised the ELIXIR-EXCELERATE Train the Trainer course, Stockholm, Sweden, 9-11
  Oct, 2018
- Co-organised the **ELIXIR-EXCELERATE Train the Trainer** course, Rome, I, 27-28 Sep, 2018
- Co-organised the Practical course on **Population Genomics: background and tools**, Naples, Italy, 21-27 Apr, 2018
- Co-organised the Software Carpentry Workshop, Paris, France, 28-29 Mar, 2018
- Co-organised the **ELIXIR-EXCELERATE Train the Trainer** course, Paris, FR, 26-27 Mar, 2018
- Co-organised the Software Carpentry Workshop, Milan, Italy, 22-23 Feb, 2018
- Co-organised the ELIXIR-EXCELERATE Train the Trainer, Lausanne, CH, 30-31 Jan, 2018
- Co-organised the practical course on Linux shell scripting for high-throughput biological data processing on supercomputers, Roma, IT, 16-17 Jan, 2018
- Co-organised the Curation workshop on molecular and causal interactions, Roma, IT, 5-7 Dec, 2017.
- Organised the ELIXIR-EXCELERATE Train the Trainer course, Salerno, IT, 27-29 Sep, 2017
- Co-organised the Elixir-IIB/NETTAB Tutorial on Biological Networks: data analysis, visualization and medical application, Palermo, IT, 18-19, Oct 2017
- Organised a Training course on Python for Life Scientists, Rome, IT, 11-15 September 2017
- Co-organised the training course on RNA-Seg data analysis, Milan, IT, 18-20 July 2017
- Co-organised a Workshop and a Summer School on **Advanced Computational Metagenomics**, Bari, IT, 19-23 June 2017
- Co-organised the EMBO Practical Course on Population Genomics: background and tools, Naples, IT, 18-26 May 2017.
- Co-organised the practical course on Computational approaches to the study of protein interactions and rational drug design, Padua, IT, 10-13 April 2017
- Local organiser for the ELIXIR All Hands meeting 2017, Rome, IT, ~400 participants, 20-23
  March 2017
- Local organiser for the NETTAB 2016 workshop on **Reproducibility, standards and SOP in bioinformatics**, CNR, Rome, IT, ~100 participants, October 2016
- Co-organised the NETTAB 2016 satellite Goblet/ELIXIR-IIB joint tutorial on **Train the Trainer**, CNR, Rome, IT, expected 20 participants, October 2016
- Co-organised the Education & Training special session of the NETTAB 2016 Workshop, CNR, Rome, IT, October 2016
- Co-organised the practical course on **Python for Life Scientists**, University of Bari, Bari, IT, expected 24 participants, September 2016
- Co-organised the practical course on **Exome analysis using Galaxy**, University of Milano-Bicocca, Milano, IT, expected 24 participants, September 2016
- Co-organised the 2<sup>nd</sup> ELIXIR-EXCELERATE **Train the Trainer** course, IGC, Oeiras, PT, (limited to) 8 participants, July 2016
- Co-organised the BITS 2016 satellite workshop on **Effective academic teaching**, University of Salerno, Fisciano (SA), IT, 20 participants, June 2016
- Co-organised and co-chaired the round table on **Teaching Bioinformatics: state-of-the-art** and new ideas at the BITS 2016 conference, University of Salerno, Fisciano (SA), IT, June 2016
- Co-organised the 1st ELIXIR-EXCELERATE Train the Trainer course, University of Cambridge, Cambridge, UK, (limited to) 10 participants, May 2016
- Co-organised the ELIXIR-IIB practical course on **NGS** for evolutionary biologists: from basic scripting to variant calling, CNR, Naples, IT, 24 participants, May 2016
- Co-chaired the ELIXIR-EXCELERATE Train the Trainer framework workshop, EBI, Hinxton, UK, January 2016
- Co-organised the ELIXIR-IIB practical course on Protein networks and systems biology.
  Università di Bologna, Bologna, IT, 24 participants, December 2015
- Co-organised the ELIXIR-IIB practical course on **NGS for evolutionary biologists: from basic scripting to variant calling**. CINECA Auditorium, Rome, IT, 24 participants, November 2015
- Organised the ELIXIR-IIB practical course on **Gene expression profiling with HTS: RNA-Seq data analysis**. CINECA Auditorium, Rome, IT, 24 participants, October 2015
- Co-organised the practical course on **Next Generation Sequencing data analysis**. PhD School in Biology and Molecular Medicine (BeMM), Rome, IT, 40 participants, October 2015

- Co-organised the practical course on Python for Life Scientists. The Genome Analysis Centre, Norwich, UK, 25 participants, 40h, October 2013 and April 2015
- Co-organised the workshop: Bioinformatics Training for Life Scientists: Showcases and Challenges from Tutors' Perspectives, Basel, CH, 40 participants, September 2012
- Local organising committee member of ECCB'08 (European Conference on Computational Biology), Cagliari, Sardinia, IT, > 400 participants, September 2008.

#### Memberships

#### Scientific Journal Editorial Boards:

- BMC Research Notes (http://www.biomedcentral.com/bmcresnotes)
- Structural Biology (http://www.hindawi.com/journals/sb/)
- The Scientific World Journal (http://www.hindawi.com/journals/tswj/)
- Advances in Bioinformatics (Special Issue) (http://www.hindawi.com/journals/abi/)
- Frontiers in Genetics (Research Topic) (http://www.frontiersin.org/systems\_biology)

#### **Conference Organising Committees:**

- ECCB (European Conference on Computational Biology)
- ISMB (International Conference on Intelligent Systems for Molecular Biology)
- BIRD (International Conference on Bioinformatics Research and Development)
- BIOINFORMATICS (http://www.bioinformatics.biostec.org)

#### Societies and Organisations:

- GOBLET (Global Organisation for Bioinformatics Learning Education and Training http://www.mygoblet.org) - Former secretary
- ISCB (International Society for Computational Biology http://www.iscb.org) Member
- SIB (Italian Society for Biochemistry) Member
- BTN (Bioinformatics Training Network http://www.biotnet.org) Chair
- BITS (Bioinformatics Italian Society http://www.bioinformatics.it) Member
- "Training portal" ELIXIR task force (http://www.elixir-europe.org)
- "e-learning and training" ELIXIR task force (<a href="http://www.elixir-europe.org">http://www.elixir-europe.org</a>)

### Reviewer Scientific Journals:

- Bioinformatics
- Bioorganic Chemistry
- BMC Bioinformatics
- BMC Research Notes
- Briefings in Bioinformatics
- Computational and Mathematical Methods in Medicine
- Database
- FEBS letters
- GENE
- Infection, Genetics, and Evolution
- Journal of Computational Biology and Bioinformatics Research
- Nucleic Acids Research
- PLoS Computational Biology
- PLoS ONE
- Proteins
- Proteomics
- Molecular BioSystem
- PeerJ
- Journal of Molecular Cell Biology

#### Research projects:

- Excellence project 2006, Fondazione Cariparo.
- Innovative health research 2012. EU

#### Attendance to training courses

 August 2005: BioMalPar (FP6 Malaria Initiative) "Introduction to Plasmodium Bioinformatics". Wellcome Trust Sanger Institute. Hinxton, Cambridge, UK.

- February 2003: 4th Bologna Winter School "Hot Topics in Structural Genomics", Bologna, IT
- June 1998: ISI (Institute for Scientific Interchange foundation) Euroconference on "Protein folding and structure prediction", Villa Gualino, Torino, IT

#### TEACHING AND TRAINING ACTIVITY

- Academic courses AA2005/2010: Metodi informatici della Biologia (Computational methods for Biology, 48h), MD in Bioinformatics, University of Rome "Tor Vergata", IT
  - AA2010/2013: Macromolecular structures (60h), MD in Engineering of Nanotechnology, Sapienza University of Rome, IT
  - AA2011/2012: Biochemistry (48h), MD in Physics of Biosystems, Sapienza University of Rome, IT
  - AA2013/2015: Macromolecular structures (60h), MD in Engineering of Nanotechnology, Sapienza University of Rome, IT
  - AA 2015/2019: Laboratory of Bioinformatics 1 Modulo 3 (30h) Master Degree in Bioinformatics, University of Bologna, Bologna, IT
  - AA 2017/2019: Laboratory of Bioinformatics Module 2 (24h). Degree in Biological Sciences, Sapienza University of Rome, Rome, IT
  - AA 2018/2019: Programming for Bioinformatics Modulo 2 (40h) Master Degree in Bioinformatics, University of Bologna, Bologna, IT

## examiners

- Member of the board of Since 2012: Course of Physics, B.Sc. in Pharmaceutical Biotechnology, Sapienza University of Rome, IT
  - Since 2010: Course of Bioinformatics and Proteomics, B.Sc. in Pharmaceutical Biotechnology, Sapienza University of Rome, IT
  - 2001-2005 Course of Bioinformatics, B.Sc. in Cellular and Molecular Biology and B.Sc. in Human Biology, University of Rome "Tor Vergata", IT
  - 2003-2005 Course of Molecular Bioinformatics, MDs in Cellular and Molecular Biology, in Human Biology, and in Bioinformatics, University of Rome "Tor Vergata", IT

# courses

- Lectures in academic AA 2002/2003: 8h in the Course of Bioinformatics, B.Sc. in Cellular and Molecular Biology and B.Sc. in Human Biology, University of Rome "Tor Vergata", Rome, IT
  - AA 2003/2005: 8h (each year) in the Course of Molecular Bioinformatics, MDs in Cellular and Molecular Biology, in Human Biology, and in Bioinformatics, University of Rome "Tor Vergata", Rome, IT

Second level masters • AA2013/2014: Programming and algorithms for Bioinformatics (24h), Master in BIOINFORMATICS: Biomedical and Pharmaceutical applications. Sapienza University of Rome, Rome, IT

# instructor

- Training experience as ELIXIR-Carpentries Instructor Training, Stockholm, SE, 3-4 Apr, 2019
  - EMBO Practical Course on Computational analysis of protein-protein interactions: Sequences, networks and diseases, Rome, 5-10 Nov, 2018
  - ELIXIR-EXCELERATE Train the Trainer course, Stockholm, SE, 9-11 Oct, 2018
  - ELIXIR-EXCELERATE Train the Trainer course, Rome, IT, 27-28 Sep, 2018
  - Software Carpentry Workshop, Paris, FR, 28-29 Mar, 2018
  - ELIXIR-EXCELERATE Train the Trainer course, Paris, FR, 26-27 Mar, 2018
  - Software Carpentry Workshop, Milan, IT, 22-23 Feb, 2018
  - ELIXIR-EXCELERATE Train the Trainer, Lausanne, CH, 30-31 Jan, 2018
  - Practical course on Linux shell scripting for high-throughput biological data processing on supercomputers, Rome, IT, 16-17 Jan, 2018
  - Carpentries Instructor Training (Train the Trainer) workshop, Online, 4-5 Dec, 2017
  - Carpentries Instructor Training (Train the Trainer) workshop, Utrecht, NL, 6-7 Nov, 2017
  - ELIXIR-EXCELERATE Train the Trainer course, Salerno, IT, 27-29 Sep, 2017.
  - ELIXIR-IIB practical course on Python for Life Scientists, Rome, IT, 11-15 Sept 2017
  - Carpentries Instructor Training (Train the Trainer) workshop, Online, 10-11 Jul, 2017
  - Carpentry Instructor Training (Train the Trainer) workshop, Online, 21-22 Feb, 2017
  - ELIXIR-EXCELERATE Train the Trainer course, University of Lausanne, CH, 16-18 Jan 2017
  - ELIXIR-EXCELERATE Train the Trainer course, University of Ljubljana, Faculty of Medicine, SE, 28-30 Nov, 2016

- ELIXIR-IIB practical course on Python for Life Scientists, University of Bari, Bari, IT, 26-30
  Sep, 2016
- RDA-CODATA Research Data Science Summer School, ICTP, Trieste, IT, Software Carpentry module, 1-4 Aug, 2016
- ELIXIR-EXCELERATE Train the Trainer course, IGC, Oeiras, PT, 10-15 Jul 2016
- Scientific School on "Computational modeling for Life Sciences", Sardinian Scientific and Technological Park, Pula (CA), IT, 6-10 June 2016
- RNA-seq data analysis workshop, University of Naples Federico II in collaboration with ELIXIR-IIB, Naples, IT, 6-10 Jun, 2016
- ELIXIR-IIB practical course on NGS for evolutionary biologists: from basic scripting to variant calling, CNR, Naples, IT, 2-5 May, 2016
- EMBO practical course on "Computational analysis of protein-protein interactions: Sequences, networks and diseases" (http://events.embo.org/16-protein-protein/), Budapest, HU, 30 May - 4 Jun, 2016
- ELIXIR-IIB practical course on "Protein networks and systems biology", University of Bologna, IT, 14-18 Dec, 2015
- ELIXIR-IIB practical course on "NGS for evolutionary biologists: from basic scripting to variant calling", CINECA Auditorium, Rome, IT, 23-27 Nov, 2015
- ELIXIR-IIB practical course on "Gene expression profiling with HTS: RNA-Seq data analysis",
  CINECA Auditorium, IT, 19-22 Oct, 2015
- PhD School in Biology and Molecular Medicine Training course on "Next Generation Sequencing data analysis", Sapienza University of Rome, Rome, IT, 5-7 Oct 2015
- EMBO practical course on Computational Analysis of Protein-Protein Interactions: From Sequences to Networks (http://events.embo.org/15-protein-protein/), TGAC, Norwich, UK, 28 Sept- 3 Oct, 2015
- 2<sup>nd</sup> level Master in Bioinformatics: Biomedical and Pharmaceutical applications, Course on "Programming and algorithms for Bioinformatics", Sapienza University of Rome, Rome, IT, (24h each year) in 2014 and 2015
- GTPB practical course on "Bioinformatics using Python for Biologists", Instituto Gulbenkian de Ciência, Oeiras, PT, (40h each year), 2010-2018
- TGAC practical course on "Python for Life Scientists", Norwich, UK, (40h each year), in 2013 and 2014
- Pasteur practical course on Proteomics and drug design", Institute Pasteur, Tunis, TN, (20h), Apr 2012
- Post-graduate training course on Bioinformatics applications", University of Rome "Tor Vergata", Rome, IT, (30h), 2000

#### Thesis supervisor

- 2010/2011: 2 thesis (G. Gonnelli and R. Lepore) in the MD in Bioinformatics, University of Rome "Tor Vergata", Rome, Italy.
- 2011/2012: 2 thesis (L. Lenci and F. Ruggeri) in the MD in Engineer of Nanotechnology, Sapienza University of Rome, Rome, IT
- 2014/2015: 1 thesis (I. Bonafede) in the MD in Engineer of Nanotechnology, Sapienza University of Rome, Rome, IT
- 2015/2016: 1 thesis (E. Micarelli) in the MD in Engineer of Nanotechnology, Sapienza University of Rome, Rome, IT
- 2017/2020: 1 PhD thesis (D. Staid) in the PhD School of Biochemistry, Sapienza University of Rome, Rome, IT

#### SCIENTIFIC PUBLICATIONS

### Scientific journals

- 1. Tractenberg ET, Lindvall JM, Attwood KA, Via A. Guidelines for curriculum development in higher education: How learning outcomes drive all decision-making. In preparation
- 2. Tractenberg ET, Lindvall JM, Attwood KA, Via A. (2019) The Mastery Rubric for Bioinformatics: supporting design and evaluation of career-spanning education and training. bioRxiv 655456. doi: https://doi.org/10.1101/655456.
- 3. Four simple recommendations to encourage best practices in research software

- Kuzak M, Harrow J, Jimenez RC, Martinez PA, Psomopoulos FE, Svobodová Vařeková R, Via A. (2018) Lesson development for Open Source Software best practices adoption. WSSSPE6.1, October 29, 2018. doi: 10.5281/zenodo.1420462.
- 5. **Via A**, Attwood TK, Fernandes PL, Morgan SL, Schneider MV, Palagi PM, Rustici G and Tractenberg RE (2017) A new pan-European Train-the-Trainer Programme for bioinformatics: Pilot results on feasibility, utility and sustainability of learning. Briefings in Bioinformatics. 2017 Sep 26. doi: 10.1093/bib/bbx112.
- 6. Morgan SL, Palagi PM, Fernandes PL, Koperlainen E, Dimec J, Marek D, Larcombe L, Rustici G, Attwood TK, Via A (2017) The ELIXIR-EXCELERATE Train-the-Trainer pilot programme: empower researchers to deliver high-quality training. F1000Research 2017, 6:1557. doi: 10.12688/f1000research.12332.1.
- 7. Jiménez RC, Kuzak M, Alhamdoosh M, Barker M, Batut B, Borg M, Capella-Gutierrez S, Chue Hong N, Cook M, Corpas M, Flannery M, Garcia L, Gelpí JL, Gladman S, Goble C, González Ferreiro M, Gonzalez-Beltran A, Griffin PC, Grüning B, Hagberg J, Holub P, Hooft R, Ison J, Katz DS, Leskošek B, López Gómez F, Oliveira LJ, Mellor D, Mosbergen R, Mulder N, Perez-Riverol Y, Pergl R, Pichler H, Pope B, Sanz F, Schneider MV, Stodden V, Suchecki R, Svobodová Vařeková R, Talvik HA, Todorov I, Treloar A, Tyagi S, van Gompel M, Vaughan D, Via A, Wang X, Watson-Haigh NS, Crouch S. (2017) .Four simple recommendations to encourage best practices in research software [version 1; peer review: 3 approved] F1000Research. doi: http://dx.doi.org/10.12688/f1000research.11407.1
- 8. Schiffthaler B, Kostadima M, the **NGS Trainer Consortium**, Delhomme N and Rustici G (2016) Training in High-Throughput Sequencing: Common Guidelines to Enable Material Sharing, Dissemination and Re-Usability. PLoS Computational Biology, 12(6): e1004937. doi: 10.1371/journal.pcbi.1004937.
- 9. Ison J, Rapacki K, Ménager H, Kalaš M, Rydza E, Chmura P, Anthon C, Beard N, Berka K, Bolser D, Booth T, Bretaudeau A, Brezovsky J, Casadio R, Cesareni G, Coppens F, Cornell M, Cuccuru G, Davidsen K, Vedova GD, Dogan T, Doppelt-Azeroual O, Emery L, Gasteiger E, Gatter T, Goldberg T, Grosjean M, Grüning B, Helmer-Citterich M, Ienasescu H, Ioannidis V, Jespersen MC, Jimenez R, Juty N, Juvan P, Koch M, Laibe C, Li JW, Licata L, Mareuil F, Mičetić I, Friborg RM, Moretti S, Morris C, Möller S, Nenadic A, Peterson H, Profiti G, Rice P, Romano P, Roncaglia P, Saidi R, Schafferhans A, Schwämmle V, Smith C, Sperotto MM, Stockinger H, Vařeková RS, Tosatto SC, de la Torre V, Uva P, Via A, Yachdav G, Zambelli F, Vriend G, Rost B, Parkinson H, Løngreen P, Brunak S. (2016) Tools and data services registry: a community effort to document bioinformatics resources. Nucleic Acids Res. 44(D1):D38-47. doi: 10.1093/nar/gkv1116.
- Lapatas V, Stefanidakis M, Jimenez RC, Via A, Schneider MV (2015) Data integration in biological research: an overview. J Biol Res (Thessalon). 22(1):9. doi: 10.1186/s40709-015-0022-5.
- 11. Attwood TK, Bongcam-Rudloff E, Brazas ME, Corpas M, Gaudet P, Lewitter F, Mulder N, Palagi PM, Schneider MV, van Gelder CW; **GOBLET Consortium** (2015) GOBLET: the Global Organisation for Bioinformatics Learning, Education and Training. PLoS Comput Biol. 11(4):e1004143. doi: 10.1371/journal.pcbi.1004281.
- 12. Via A, Zanzoni A (2015) A prismatic view of protein phosphorylation in health and disease. Front. Genet. doi: 10.3389/fgene.2015.00131.
- 13. **Via A,** Uyar B, Brun C, Zanzoni A. (2015) How pathogens use linear motifs to perturb host cell networks. Trends Biochem Sci. 40(1):36-48. doi: 10.1016/j.tibs.2014.11.001.
- 14. Di Marino D, Coletta A, D'Annessa I, Via A\*, Tramontano A. (2015) Characterization of the differences in the cyclopiazonic acid binding mode to mammalian and *P. falciparum* Ca<sup>2+</sup> pumps: a computational study. *PROTEINS:* Structure, Function and Bioinformatics. Jan 10. doi: 10.1002/prot.24734.
- 15. Dias RO, Via A, Brandão MM, Tramontano A, Silva-Filho MC. (2015) Digestive peptidase evolution in holometabolous insects culminated in a specialized group of enzymes in Lepidoptera. *Journal of Molecular Biology*. 58C:1-11. doi: 10.1016/j.ibmb.2014.12.009.
- 16. Corpas M, Jimenez RC, Bongcam-Rudloff E, Budd A, Brazas MD, Fernandes PL, Gaeta B, van Gelder C, Korpelainen E, Lewitter F, McGrath A, MacLean D, Palagi PM, Rother K, Taylor J, Via A, Watson M, Schneider MV, Attwood TK. (2015) The GOBLET training portal: a global repository of bioinformatics training materials, courses and trainers. Bioinformatics. 31(1):140-2. doi: 10.1093/bioinformatics/btu601
- 17. Fiorillo A, Di Marino D, Bertuccini L, Via A, Pozio E., Ilari A, Lalle M. (2014) The crystal structure of Giardia duodenalis g14-3-3 in the apo form reveals unique features of the 14-3-3 protein family. PLoS ONE. 9(3): e92902.
- Via A, Blicher T, Bongcam-Rudloff E, Brazas MD, Brooksbank C, Budd A, De Las Rivas J, Dreyer J, Fernandes PL, van Gelder C, Jacob J, Jimenez RC, Loveland J, Moran F, Mulder N, Nyrönen T, Rother K, Schneider MV, Attwood TK. (2013) Best practices in bioinformatics

- training for life scientists. Briefings in Bioinformatics. 14(5):528-37.
- 19. Jimenez RC, Albar JP, Bhak J, Blatter MC, Blicher T, Brazas MD, Brooksbank C, Budd A, De Las Rivas J, Dreyer J, van Driel MA, Dunn MJ, Fernandes PL, van Gelder CW, Hermjakob H, Ioannidis V, Judge DP, Kahlem P, Korpelainen E, Kraus HJ, Loveland J, Mayer C, McDowall J, Moran F, Mulder N, Nyronen T, Rother K, Salazar GA, Schneider R, Via A, Villaveces JM, Yu P, Schneider MV, Attwood TK, Corpas M. (2013) iAnn: an event sharing platform for the life sciences. Bioinformatics. 29(15):1919-1921.
- 20. Lepore R., Tramontano A., Via A. (2013) TIPs: a database of therapeutic targets in pathogens and associated tools. Bioinformatics. 29(14):1821-2.
- 21. Pillai D.R., Lau R., Khairnar K., Lepore R., Via A., Staines H.M., Krishna S. (2012) Artemether resistance in vitro is linked to mutations in PfATP6 in travellers returning with Plasmodium falciparum infections. Malar J. 11:131.
- 22. Caroli A., Simeoni S., Lepore R., Tramontano A., Via A. (2012) Investigation of a Potential Mechanism for the Inhibition of SmTGR by Auranofin and its implications for Plasmodium falciparum Inhibition. Biochem Biophys Res Commun. 417(1):576-81.
- 23. Dinkel H., Michael S., Weatheritt R.J., Davey N.E., Van Roey K., Altenberg B., Toedt G., Uyar B., Seiler M., Budd A., Jödicke L., Dammert M.A., Schroeter C., Hammer M., Schmidt T., Jehl P., McGuigan C., Dymecka M., Chica C., Luck K., Via A., Chatr-Aryamontri A., Haslam N., Grebnev G., Edwards R.J., Steinmetz M.O., Meiselbach H., Diella F., Gibson T.J. (2012) ELM-the database of eukaryotic linear motifs. Nucleic Acids Res. 40:D242-51
- 24. Schneider M.V., Walter P., Blatter M.C., Watson J., Brazas M.D., Rother K., Budd A., Via A., van Gelder C.W.G., Jacob J., Fernandes P., Nyronwn T., De Las Rivas J., Blicher T., Loveland J., McDowall J., Jones P., Bren Vaughan, Lopez R., Attwood T.K., Brooksbank C. (2012) Bioinformatics Training Network (BTN): A community resource for bioinformatics trainers. Brief Bioinform. 13(3):383-9.
- 25. Via A., De Las Rivas J., Attwood T.K., Landsman D., Brazas M.D., Leunissen J.A.M., Tramontano A., Schneider M.V. (2011) 10 simple rules for developing a short bioinformatics training course. PLoS Computational Biology. 7(10):e1002245.
- 26. Sayadi A., Briganti L., Tramontano A., Via A. (2011) Exploiting Publicly Available Biological and Biochemical Information for the Discovery of Novel Short Linear Motifs. PLoS One. 6(7): e22270.
- 27. Lepore A., Simeoni S., Raimondo D., Caroli A., Tramontano A., Via A. (2011) Identification of the Schistosoma mansoni Molecular Target for the Anti Malarial Drug Artemether. J Chem Inf Model. 51(11):3005-16.
- 28. Mancini E., Tammaro F., Baldini F., Via A., Raimondo D, George P., Audisio P., Sharakhov I, Tramontano A., Catteruccia F., della Torre A. (2011) Molecular evolution of a gene cluster of female serine proteases involved in reproductive processes of the malaria mosquito *Anopheles gambiae*. BMC Evolutionary Biology, 11, 72.
- 29. Dinkel H., Chica C., Via A., Gould C., Jensen L., Gibson T., Diella F. (2011) Phospho.ELM: a database of phosphorylation sites- update 2011 Nucleic Acid Research, 39:D261-D267.
- 30. Via A., Diella F., Gibson T.J., Helmer-Citterich M. (2011) From sequence to structural analysis in protein phosphorylation motifs. Frontiers in Bioscience, 16, 1261-1275.
- 31. Zanzoni A., Carbajo D., Diella F., Gherardini P.F., Tramontano A., Helmer-Citterich M., Via A. Phospho<sub>3</sub>D 2.0: An enhanced database of three-dimensional structures of phosphorylation sites (2011) Nucleic Acid Research, 39: D268-271.
- 32. Chinappi M.<sup>†</sup>, Via A.<sup>†</sup>, Marcatili P., Tramontano A. (2010) On the mechanism of chloroquine resistance in *Plasmodium falciparum*. PLoS ONE, 5(11), e14064.
- 33. Schneider MV., Watson J., Attwood T., Rother K., Budd A., McDowall J., Via A., Fernandes P., Nyronen T., Blicher T., Jones P., Blatter M-C., De Las Rivas J., Judge DP., van der Gool W. and Brooksbank C. (2010) Bioinformatics training: a review of challenges, actions and support requirements. Briefings in Bioinformatics, 11(6): 544-551.
- 34. Gould C.M., Diella F., Via A., Puntervoll P., Gemünd C., Chabanis-Davidson S., Michael S., Sayadi A., Bryne J.C., Chica C. et al. (2010) ELM: The status of the 2010 Eukaryotic Linear Motif Resource. Nucleic Acid Research, 38:D167-80.
- 35. Via A., Gould C.M., Gemünd C., Gibson T.J., Helmer-Citterich M. (2009) A structure filter for the Eukaryotic Linear Motif Resource. BMC Bioinformatics 2009, 10:351.
- 36. Diella F., Gould C., Chica C., Via, A., Gibson, T. (2008) Phospho.ELM: a database of phosphorylation sites update 2008. Nucleic Acid Res., 36:D240-D244.
- 37. Ausiello G., Gherardini P.F., Marcatili P., Tramontano A., Via A., Helmer-Citterich M. (2008) FunClust: a web server for the identification of structural motifs in a set non-homologous protein structures. BMC Bioinformatics, 9:S2
- 38. Ferraro E., Peluso D., Via A., Ausiello G., Helmer-Citterich M. (2007) SH3-Hunter: discovery of SH3 domain interaction sites in proteins. Nucleic Acid Res., 35:W451-W454.

- 39. Via A., Peluso D., Gherardini P.F., de Rinaldis E., Colombo T., Ausiello G., Helmer-Citterich M. (2007) 3dLOGO: a web server for the identification, analysis and use of conserved protein substructures. Nucleic Acid Res, 35:W416-9.
- 40. Via A., Gherardini F., Ferraro E., Ausiello G., Scalia Tomba G. and Helmer-Citterich M. (2007) False occurrences of functional motifs in protein sequences highlight evolutionary constraints. BMC Bioinformatics, 8(1):68.
- 41. Ausiello, G., Peluso, D., Via, A., Helmer-Citterich, M. (2007). Local comparison of protein structures highlights cases of convergent evolution in analogous functional sites. BMC Bioinformatics, 8:S24
- 42. Zanzoni A., Ausiello G., Via A., Gherardini P.F. and Helmer-Citterich M. (2006) Phospho<sub>3</sub>D: a database of three-dimensional structures of protein phosphorylation sites. Nucleic Acid Res., 35:D229-31.
- 43. Ferraro E., Via A., Ausiello G. and Helmer-Citterich M. (2006) A novel structure-based encoding for machine-learning applied to the prediction of SH3 domain specificity. Bioinformatics 22(19):2333-9.
- 44. Ferraro, E., Via A., Ausiello G. and Helmer-Citterich M. (2005) A neural strategy for the inference of SH<sub>3</sub> domain-peptide interaction specificity. BMC Bioinformatics, 6 Suppl 4: S<sub>13</sub>.
- 45. Ausiello G., Via A., Helmer-Citterich M. (2005) Query3d: a new method for high-throughput analysis of functional residues in protein structures. BMC Bioinformatics, 6 Suppl 4: S5.
- 46. Ausiello G., Zanzoni A., Peluso D., Via A., Helmer-Citterich M. (2005) pdbFun: Mass selection and fast comparison of annotated PDB residues. Nucleic Acids Res., 33: W133-W137.
- 47. Via A, Zanzoni A, Helmer-Citterich M. (2005) Seq2Struct: a resource for establishing sequence-structure links Bioinformatics, 21(4): 551-3.
- 48. Diella F., Cameron S., Gemund C., Linding R., Via A., Kuster B., Sicheritz-Ponten T., Blom N., Gibson TJ.(2004) Phospho.ELM: a database of experimentally verified phosphorylation sites in eukaryotic proteins. BMC Bioinformatics, 5(1):79.
- 49. Via A., Helmer-Citterich M. (2004) A structural study for the optimisation of functional motifs encoded in protein sequences. BMC Bioinformatics, 5(1):50.
- 50. Ferre' F., Via A., Ausiello G., Brannetti B., Zanzoni A. and Helmer-Citterich M. (2003) Development of computational tools for the inference of protein interaction specificity rules and functional annotation using structural information. Comparative and Functional Genomics, 4(4); 416-419.
- 51. Puntervoll P., Linding R., Gemund C., Chabanis-Davidson S., Ramu C., Mattingsdal M., Cameron S., Martin D.M.A., Ausiello G., Brannetti B., Costantini A., Ferre' F., Maselli V., Via A., Cesareni G., Diella F., Superti-Furga G., Wyrwicz L., McGuigan C., Gudavalli R., Letunic I., Bork P., Rychlewski L., Küster B., Helmer-Citterich M., Hunter W.N., Aasland R. and Gibson T. J. (2003) The ELM server: A new source for revealing short functional sites in modular eukaryotic proteins. Nucleic Acids Res., 31(13):3625-30.
- 52. Via A., Ferre' F., Brannetti B. e Helmer Citterich M. (2000) Protein surface similarities: a survey of methods to describe and compare protein surfaces. Cell Mol Life Sci., 57 (13-14):1970-7.
- 53. Via A., Ferre' F., Brannetti B., Valencia A. e Helmer Citterich M (2000) 3D view of the surface motif associated to the ploop structure: cis and trans cases of convergent evolution. J. Mol. Biol., 303 (4): 455-65.
- 54. Brannetti B., Via A., Cesareni G. e Helmer Citterich M. (2000) SH<sub>3</sub>-SPOT: an algorithm to predict preferred ligands to different members of sh<sub>3</sub> gene family. J. Mol. Biol., 298(2):313-328.

**Books** 

55. Via A., Rother K., Tramontano A. (2014) Managing your Biological Data with Python. Chapman and Hall/CRC. Taylor and Francis Group.

#### **Book chapters**

- 56. Via A., Tramontano A. (2011) Protein structural motifs: identification, annotation and use in function prediction. In Sequence and Genome Analysis II Methods and Applications. ISBN: 978-1463789138. iConcept Press. Retrieved from <a href="http://www.iconceptpress.com/books/sequence-and-genome-analysis-ii--methods-and-applications/">http://www.iconceptpress.com/books/sequence-and-genome-analysis-ii--methods-and-applications/</a>
- 57. Brannetti B.†, Via A.† (2002) Theoretical aspects of Protein Sequence Alignments. In *The Internet for Cell and Molecular Biologists* ed. A. Cabibbo, R.P. Grant, M. Helmer-Citterich, Horizon Scientific Press, pg. 73-87.
- 58. Via A. (2002) Practical aspects of Protein Sequence Analysis. In *The Internet for Cell and Molecular Biologists* ed. A. Cabibbo, R.P. Grant, M. Helmer-Citterich, Horizon Scientific Press, pg. 163-232.

59. † equally contributing authors

6o. \* corresponding author

The undersigned express their consent for the personal data provided to be processed, in compliance with the Legislative Decree 30 June 2003, n. 196, for the obligations related to the present application. The undersigned is aware that, pursuant to art. 76 of the D.P.R. n. 445 of the 28/12/2000, the false declarations, the falsity in the records and the use of false deeds are punished according to the penal code and the special laws in matter.

In accordance with the Italian DPR no. 445/2000, Italian the signature is not subject to authentication, this declaration must be accompanied by a photocopy of a identification document.

Rome, 09/05/2019