LUCA ALBERGANTE

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Location:	Paris, Île-de-France, France

Phone: +33769047408 Nationality: Italian

LinkedIn www.linkedin.com/in/lucaalbergante

GitHub www.github.com/Albluca

Website albergante.netlify.com

OVERVIEW

I am a data scientist with 8+ years of experience in applying computational modelling, machine learning, and bioinformatics to characterize a broad range of biological phenomenon using different types of data, including NGS, imaging, and networks. I have an extensive experience in applying and developing machine learning algorithms (mainly in R, MATLAB and C/C++) and producing interactive visualizations. I taught university level courses on statistics, data analysis, programming and bioinformatics in English and Italian.

WORK EXPERIENCE WITH HIGHLIGHTS

September 2016Postdoctoral research fellow in Bioinformatics and Systems biology,- presentInstitut Curie, Paris, France (Supervisors: Andrei Zinovyev / Emmanuel Barillot)

Key responsibilities:

- Analyze clinical/non-clinical bulk/single-cell NGS data using established and novel computational statistics and machine learning approaches
- Develop software packages (implementing novel algorithms and providing interactive visualizations) to explore complex datasets
- Supervise and manage students
- Presents in international conferences to theoretical and experimental researchers
- Write research papers and projects
- Teach bioinformatics to researchers and students
- Organize scientific events

Key achievements:

- Management of up to 4 concurrent projects in collaboration with up to 10 researchers
- Analysis of several (>20) single cell RNA-Seq datasets obtained from local and international collaborators (Patient-derived xenografts, mouse tissues, Xenopus embryos) and public resources (human and murine cell lines)
- Contribution to the development of ElPiGraph (an algorithm to derive principal graph approximators of high-dimensional data) and ROMA (an algorithm to quantify the activity of genetic pathways)
- Development of 4 R packages (ElPiGraph, ElPiCycle, rROMA, rROMADash) designed to analyze and visualize biological data
- Contribution to the development of the STREAM python package
- Preparation of 7 scientific manuscripts (3 already published in international journals) and 3 students projects

- Contribution to the preparation of 4 research projects
- Presentation in international institution/conferences (6 talks / 5 posters)
- Supervision of 2 master students with projects focused on the analysis of single cell RNA-Seq
- Contribution to the organization of an international single cell conference

Key skills acquired:

- Advanced data manipulation, analysis, and interactive visualization using R, C++, ggplot2, Shiny, and several Bioconductor packages in a single-machine and distributed parallel environment
- Analysis of patient- and cell line-derived single cell RNA-Seq data
- Version control and collaborative coding via GitHub
- Software virtualization via Docker

June 2018 – **Visiting research scientist.** Center for cancer research, Massachusetts general July 2018 hospital, Boston, USA (Host: Luca Pinello)

Key responsibilities:

• Contribute to the development of STREAM, a python package designed to infer cellular dynamics from single cell RNA-Seq data

October 2018 – **Visiting research scientist.** Department of Biomedical Informatics, Harvard November 2018 medical school, Boston, USA (Host: Peter Kharchenko)

Key responsibilities:

• Explore the application of principal graphs to the analysis of single cell RNA-Seq data

August 2011 –Postdoctoral research fellow in Theoretical systems biology, School of
August 2016August 2016Life sciences, University of Dundee, Dundee, UK (Supervisor: Tim Newman)

Key responsibilities:

- Analyze non-clinical NGS, genetic mutations, anatomical, epidemiological data using established and novel computational statistics and machine learning approaches
- Provide statistical guidance to support experimental biological research
- Design and implement novel algorithms and statistical approaches to explore complex data
- Design and test novel mathematical/computational model to explore biological processes
- Supervise and manage students
- Present in international conferences to theoretical and experimental researchers
- Write research papers and projects

Key achievements:

- Management of up to 5 concurrent projects in collaboration with up to 6 researchers
- Preparation of 12 scientific manuscripts (11 already published in international journals)
- Presentation in international institution/conferences (14 talks / 15 posters)
- Supervision of 3 Ph.D. students and 1 M.Sc. student. Co-supervision of 1 postdoc
- Development of several R scripts to analyze networks, ChIP-Seq, and images
- Implementation of a complete bioinformatics pipeline to study the study bulk ChIP-Seq experiments in HeLa cells

Key skills acquired:

- Data analysis using MATLAB, R, ggplot2 and several Bioconductor packages in a single-machine and distributed computing environment
- Genome sequence alignment
- Analysis of bulk RNA-Seq, ChIP-Seq, location of genomic features, networks, images (karyotypes), and cancer incidence data

- Supervision of student activities and scientific project management
- Statistical analysis of human anatomical features

March 2014 – **Lecturer in Statistics and Data analysis**, School of Science and engineering, University of Dundee, Dundee, UK

Key responsibilities:

• Design and teach courses and hand-on tutorials on statistics and data analysis to B.Sc. and M.Sc. students in Anatomy, Forensic anthropology, and Engineering

Key achievements:

• Teaching and supervision of classes of up to 30 students

Key skills acquired:

- Preparation of interactive tutorials to teach data analysis using R and Excel
- Preparation of handouts via R Markdown file

November 2007 – Lecturer in Algorithms and Statistics, Department of Mathematics, July 2011 University of Milan, Milan, Italy

Key responsibilities:

• Design and teach courses on Algorithms and Statistics to B.Sc. and M.Sc. students in Mathematics and to B.Sc. students in Biology

Key achievements:

• Teaching and supervision of classes of up to 300 students

Key skills acquired:

- Preparation of interactive tutorials to teach programming using MATLAB, R and C
- University teaching

November 2008 – **Visiting research scholar.** Department of Computer science, University of June 2009 York, York, UK (Host: Jon Timmis)

Key responsibilities:

• Interact with experimental biologists to develop a computational model of leishmaniasis

Key achievements:

• Development of a Petri net model of leishmaniasis

Key skills acquired:

• Effective cross-disciplinary communication

EDUCATION

November 2006 –
 Ph.D. in Applied Mathematics. Department of Mathematics, University of Milan, Milan, Italy (Supervisors: Jon Timmis & Giovanni Naldi)

Key objectives:

- Design and analysis of immune inspired algorithms
- Mathematical modelling of immunological aspects of leishmaniasis
- Acquire competencies in stochastic processes, statistics, computational biology, mathematical modeling, and sensitivity analysis

Key outcomes:

• My Ph.D. thesis, focused on the development and analysis of a Petri net model of experimental

visceral leishmaniasis

• Publication of 5 scientific articles

Ostalsan 1007	Combined B.Sc. and M.Sc. in Computer Science (5+ year program).
December 2006	Graduated magna cum laude. Department of Computer Science, University of
Detember 2000	Milan, Italy.

Highlights and notes:

- During my university studies, I attended courses on Procedural and Object-oriented programming (including BASIC, Fortran, Pascal, C, Assembly, Prolog, Java), Physics, Computer architecture, Operating systems, Calculus, Probability theory, Statistics, Networking, Serial and parallel algorithms, Programming language theory, Cryptography, and Information theory
- During the course of my studies, I worked part-time and took two breaks to attend the mandatory Italian National Service (1 year) and the Cisco Systems Networking Academy (1 year).
- In 2004/2005, I attended and passed all the 4 semesters of the Cisco System Networking Academy (CSNA)
- My master thesis was centered on public key cryptography

TECHNICAL SKILLS SUMMARY

- 10+ years of experience in analyzing and designing single processor, parallel and distributed algorithms
- Theoretical and practical knowledge of various general-purpose and scientific-oriented programming languages including C, C++, Java, R, Python, and MATLAB
- 8+ years of experience using R as a tool for (bio)statistics, data analysis, simulation and interactive interface design (via Shiny)
- 4+ years of experience in teaching algorithms using C, MATLAB and R
- 2+ years of experience using version control systems (GitHub) and virtual machine deployment (Docker)
- 10+ years of experience applying various statistical and machine learning techniques, including univariate and multivariate statistics, A/B testing, supervised and unsupervised clustering, manifold learning, feature selection, dimensionality reduction and regression
- 3+ years of experience teaching theoretical and computational statistics, and designing and delivering applied statistics courses using R and Excel
- 4+ years of experience applying various mathematical and computational techniques to build and validate models, including Markov processes, UML, differential equations, agent-based modeling, Petri nets, and sensitivity analysis
 - 7+ years of experience applying data analysis (bash/R/Bioconductor) and producing interactive visualization (ggplot/Shiny) from biological big data.
- 7+ years of experience analyzing images, bulk and single cell genomic data, molecular data, and epidemiological data.
- 2+ years of experience using SQL
- **Databases** 1+ year of experience developing databases (Oracle and MySQL)
 - Successfully passed the CISCO System Network Academy (CSNA)
- **Networking** Theoretical and practical knowledge of network configuration management (with CISCO and SOHO appliances).

Programming and Algorithm Design

> Applied Statistics / Machine Learning

Mathematical Modeling

Biostatistics and Biological Data Analysis

LANGUAGES

Italian	Excellent (Mother tongue).
English	Excellent . Excellent proficiency in spoken and written English.
French	Intermediate. Intermediate knowledge of spoken and written French.
Spanish	Basic . Basic knowledge of spoken and written Spanish.
Japanese	Basic . Basic knowledge of spoken and written Japanese.

$\begin{array}{l} PUBLICATIONS \text{-} ``&'' \text{ denotes equal contribution} \\ (\sim\!120 \text{ citations / H-index 6}) \end{array}$

- 1. Liu D, <u>Albergante L</u>, Horn D, Newman T. **A VSG Hierarchy During African Trypanosome** Infections: A Feint Attack By Parasites, 2018, Scientific Reports; 8, 10922
- 2. Palmer S, <u>Albergante L</u>, CC Blackburn, Newman TJ, **Further discussion on the immunological model** of carcinogenesis, 2018, PNAS; 115 (19), E4319-E4321
- 3. Palmer S, <u>Albergante L</u>, CC Blackburn, Newman TJ, **Thymic involution and rising disease incidence** with age, 2018, PNAS; 115 (8) 1883-1888
- 4. Liu D & <u>Albergante L</u>, Newman TJ, **Universal attenuators and their interactions with feedback** loops in gene regulatory networks, 2017, Nucleic Acid Research; 45(12), 7078–7093
- 5. Moreno A, Carrington TJ, <u>Albergante L</u>, Al Mamum M, Haagensen EJ, Komseli E, Gourgolis VG, Newman TJ & Blow JJ, **Unreplicated DNA remaining from unperturbed S phases passes through mitosis for resolution in daughter cells**, 2016, PNAS; 113 (39) E5757-E5764
- 6. Al Mamum M & <u>Albergante L</u>, Moreno A, Blow JJ, Newman TJ, **Inevitability and containment of** replication errors as eukaryotic genome sizes increase from Megabase to Gigabase, 2016 PNAS; 113 (39) E5765-E5774
- <u>Albergante L</u>, Liu D, Palmer S, Newman TJ, Insights into Biological Complexity from Simple Foundations, 2016, in M.C. Leake (ed.), Biophysics of Infection, Advances in Experimental Medicine and Biology 915.
- 8. Dayal JHS & <u>Albergante L</u>, Newman TJ, South A, **Quantitation of multiclonality in control and drugtreated tumour populations using high-throughput analysis of karyotypic heterogeneity**, 2015, Convergent Science Physical Oncology; 1(2):025001
- 9. <u>Albergante L</u>, Blow JJ & Newman TJ, **Buffered Qualitative Stability explains the robustness and** evolvability of transcriptional networks, 2014, eLife; 3:302863
- Tinti M, Dissanayake K, Synowsky S, <u>Albergante L</u>, MacKintosh C, **Identification of 2R-ohnologue** gene families displaying the same mutation-load skew in multiple cancers, 2014, Open Biology; 4(5):140029
- 11. <u>Albergante L</u>, Timmis J, Beattie L, Kaye PM, **A Petri net model of granulomatous inflammation: implications for IL-10 mediated control of** *Leishmania donovani* **infection**, 2013, PLoS Computational Biology; 9(11):e1003334
- 12. <u>Albergante L</u>, **Automatic Management of Forums via Artificial Immune Systems**, 2011, International Journal of Autonomous and Adaptive Communications Systems (IJAACS), Vol. 4, No. 2
- <u>Albergante L</u>, Timmis J, Andrews PS, Beattie L, Kaye PM, A Petri Net Model of Granulomatous Inflammation, 2010, in Hart E, McEwan C, Timmis J, Hone A, eds., International Conference on Artificial Immune Systems (ICARIS), Vol. 6209 of Lecture Notes in Computer Science, Springer, pp. 1–3.
- 14. <u>Albergante L</u>, **Wireless Discussion Forums: Automatic Management via Artificial Immune Systems**, 2008, International Symposium on Performance Evaluation of Computer and Telecommunication Systems, 2008. (SPECTS 2008), pp. 74–81.

PUBLICATIONS UNDER REVIEW - "&" DENOTES EQUAL CONTRIBUTION

- 15. <u>Albergante L</u>, Mirkes EM, Chen H, Martin A, Faure L, Barillot E, Pinello L, Gorban AN, Zinovyev A, **Robust and scalable learning of complex dataset topologies via ElPiGraph**, 2018, arXiv
- Chen H, <u>Albergante L</u>, Hsu JY, Lareau CA, Lo Bosco G, Guan J, Zhou S, Gorban AN, Bauer DE, Aryee MJ, Langenau DM, Zinovyev A, Buenrostro JD, Yuan GC, Pinello L, **STREAM: Single-cell Trajectories Reconstruction, Exploration And Mapping of omics data**, 2018, bioRxiv

ORAL PRESENTATIONS

- 1. Robust and scalable learning of complex data topologies via ElPiGraph and applications to single-cell data modeling, 2018, Center for Cancer Research, Massachusetts General Hospital, Boston, USA
- 2. **Reconstructing gene dynamics via single-cell snapshot data**, 2018, Journées Scientifiques & Médicales de l'Institut Curie, Institut Curie, Paris, France
- 3. **Finding a way into biology with manifold learning**, 2017, Department of Biomedical Informatics, Harvard Medical School, Boston, USA
- 4. Single cell data analysis methodology: overdispersion, pseudotime, deconvolution and beyond, 2017, Single Cell Genomic Workshop, Institut du Cerveau et de la Moelle épinière (ICM), Paris, France
- 5. Characterising transcriptional programs in high-dimensional space using principal graphs and single-cell RNA-Seq, 2017, ABS4NGS meeting, AgroParis Tech, Paris, France
- 6. Robustness and evolutionary optimization in cell survival: examples from gene regulation and DNA replication, 2016, Department of Mathematics, University of Dundee, UK
- 7. Robust design of biological processes, 2016, Institut Curie, Paris, France
- 8. **Network robustness of biological Systems: from genes to cells**, 3rd journée Bio & Math sur la Montagne, 2015, Collège de France, Paris, France
- 9. **Uncovering cancer heterogeneity via computer-assisted karyotyping**, Dundee Medical Image Analysis Workshop, 2015, University of Dundee, UK
- 10. Network biology: finding simplicity beneath complexity, 2014, University of York, UK
- 11. Robustness in interaction systems: lessons from biology, 2014, School of Computing, University of Dundee, UK
- 12. The three R's of biology: Robustness, Randomness and Recognition, 2014, Third Systems Biology Workshop, University of Dundee, UK
- 13. Robustness and evolvability explain the structure of genetic networks, 2014, Biomathematics Seminar, Imperial College, London, UK
- 14. Buffered Qualitative Stability explains why transcriptional networks are robust and evolvable, 2013, Quantitative Methods in Gene Regulation, Cambridge, UK
- 15. Robustness and evolvability determine the organization of transcriptional networks, 2013, 14th International Conference on Systems Biology (ICSB2013), Copenhagen, Denmark
- 16. How gene networks tick: the BQS theory of evolvable robustness, 2013, Second Systems Biology Workshop, University of Aberdeen, UK
- 17. **Duality Between Data and Process: an Enriched Categorical Point of View**, 2010, International Category Theory Conference (CT2010), Genoa, Italy.
- 18. Granuloma formation in Leishmaniasis: a complex immunological response, 2010, University of York, York, UK.
- 19. How Conscious Can the Immune System Be?, 2010, 8th European Conference on Philosophy and Computing (E-CAP 2010). Contributing author. Presented by C Porcelluzzi.
- 20. **Identity in the Real World**, 2009, 7th European Conference on Philosophy and Computing (E-CAP 2009). Presented with M Casu.

POSTERS PRESENTATIONS

- <u>Albergante L</u>, Gorban A, Zinovyev A, Barillot E, Complex data structure discovery and analysis of large biological datasets via ElPiGraph, 2018, 26th Conference on intelligent Systems for Molecular Biology (ISMB2018), Chicago, USA
- 2. <u>Albergante L</u>, Gorban A, Zinovyev A, Barillot E, **Complex data structure discovery and analysis of large biological datasets via ElPiGraph**, 2018, Single-Cell Revolution (BITS2018 satellite), Turin, Italy
- 3. Faure L, Barillot E, Zinovyev A, <u>Albergante L</u>, Gene Network Inference from pseudotime ordered scRNAseq data, 2018, BITS2018, Turin, Italy
- 4. <u>Albergante L</u>, Gorban A, Zinovyev A, Barillot E, **Single cell transcriptional dynamics reconstruction via manifold learning with Elastic Principal Graphs (ElPiGraph)**, 2017, Single Cell Analyses, Cold Spring Harbor Laboratories, Cold Spring Harbor, USA
- 5. <u>Albergante L</u>, Gorban A, Zinovyev A, Barillot E, **Transcriptional dynamics reconstruction via single cell transcriptomics and principal graphs**, 2017, Single Cell Genomic Workshop, Institut du Cerveau et de la Moelle épinière (ICM), Paris, France
- 6. <u>Albergante L</u>, Zinovyev A, Barillot E, **Cell cycle characterization and discovery using principal** graphs, 2017, Keystone Simposia – Single Cell Omics (E3), Stockholm, Sweden
- 7. Liu D, Newman TJ, <u>Albergante L</u>, Newman TJ, **Universal attenuators and their interactions with feedback loops in gene regulatory networks**, 2016, ISCB Latin America, Buenos Aires, Argentina
- 8. Liu D, <u>Albergante L</u>, Newman TJ, **A modular view of gene regulatory networks: universal attenuators and feedback loops,** 2016, Advanced Lecture Course on Systems Biology (SysBio), Innsbruck, Austria
- 9. Liu D, <u>Albergante L</u>, Newman TJ, **A modular view of gene regulatory networks: universal attenuators and feedback loops,** 2016, Topical Research Meeting Physical Principles of Biological and Active Systems, University of Edinburgh, Edinburgh, UK
- Barfoot S, <u>Albergante L</u>, Wilkinson CM, Craniofacial Sexual Dimorphism in Southeast Asia: Assessing the Viability of 11 Craniometric Measurements for Sex Determination in Archaeological Context, 2016, For the love of death: Human Osteoarchaeology in Southeast Asia and the Pacific, University of Philippines, Quezon City, Philippines
- 11. Donnelly L, Meadows H, <u>Albergante L</u>, Black S, **A novel methodology for regional superficial pattern quantification on the hand dorsum,** 2015, The Anthropology of Hands Conference, University of Kent, Canterbury, UK
- 12. Al Mamun M, <u>Albergante L</u>, Moreno A, Blow JJ, Newman TJ, **From yeast to human: evolutionary transition of DNA repair for larger genomes,** 2015, College of Life Sciences Research Symposium, Crieff, UK
- 13. Stratton H, <u>Albergante L</u>, Meadows H, Black S, **Dorsal hand feature analysis: An aid to forensic human identification**, 2014, Scottish student forensic research Symposium, University of Strathclyde, Glasgow, UK (1st prize winner)
- 14. Vein pattern quantification using network analysis: An investigation of spatial regions of the hand dorsum for forensic utility, 2014, Scottish Student Forensic Research Symposium. University of Strathclyde, Glasgow, UK
- 15. Liu D, <u>Albergante L</u>, Newman TJ, **Long transcriptional cascades may contribute to regulation of heterogeneity and plasticity in microorganisms and cancer**, 2014, College of Life Sciences Research Symposium, Crieff, UK
- 16. <u>Albergante L</u>, Blow JJ & Newman TJ, **How gene networks tick: the BQS theory of evolvable robustness**, 2013, College of Life Sciences Research Symposium, Crieff, UK
- 17. <u>Albergante L</u>, Blow JJ & Newman TJ, **Robustness and evolvability determine the structure of transcriptional networks**, 2013, 5th Annual SULSA Conference, Edinburgh, UK.
- Stratton H, <u>Albergante L</u>, Meadows H, Black S, **Dorsal hand feature analysis: An aid to forensic human identification**, 2013, International policing conference, Scottish Institute for police research, Edinburgh, UK
- Stratton H, <u>Albergante L</u>, Meadows H, Black S, **Dorsal hand feature analysis: An aid to forensic human identification**, 2013, Poster session for 2nd year Ph.D. Students, College of Life Sciences, University of Dundee, Dundee, UK
- 20. Stratton H, Albergante L, Meadows H, Black S, Dorsal hand feature analysis: An aid to forensic

human identification, 2013, International policing conference, Scottish Institute for police research, Edinburgh, UK

Stratton H, <u>Albergante L</u>, Meadows H, Black S, **Dorsal hand feature analysis: An aid to forensic human identification**, 2013, Winter meeting of the "British association for human identification", Manchester, UK (1st prize winner)

THESIS SUPERVISION/CONTRIBUTION

2017-2019 **Supervisor** of Louis Faure (M.Sc.) and Johnathan Bac (M.Sc.). As supervisor I provided guidance on the analytical approaches to study single cell RNA-Seq. Especially in the context of pseudotime analysis.

Statistical, mathematical and statistical supervision of the Ph.D. projects of Rana Al

2013-2016 Mamun and of Dianbo Liu. Both projects involved a combination of mathematical modelling, computational simulations and statistical data analysis to explore complex biological processes such as DNA replication and gene regulation.

Supervision of network analysis of the veins pattern on the hand for the projects of Harriet

- Stratton (Ph.D.) and of Lindsay Donnely (M.Sc.). Harriet's project was shortlisted for the Research
 Project of the Year category of the Times Higher Education Award (2014) and was awarded the
 Queen's anniversary prize for higher and further education (2013/2014).
- 2009 **Co-Supervisor** of the B.Sc thesis of Marco Frank entitled *DRM and cryptographic methods: a reasoned review.* Computer science curriculum, University of Milan.

TEACHING

- Transcriptomique et épigénomique en cellule unique: théorie et pratique (sincellTE /
- 2018 **Ecole thématique CNRS)**, Lecturer (Pseudotime reconstruction and cell cycle), Station Biologique Roscoff, Roscoff, France (graduate course 3 hours).
- Modélisation et ingénierie pour les systèmes biologiques, Lecturer (Design principles of biological networks), Institut de Technologie et d'innovation, PSL Research University Paris, France (graduate course 4 hours).
- 2017 **Research Methods (CA32002)**, Lecturer (Workshop: applied statistics with R), Forensics and anatomy curriculum, University of Dundee, UK (Undergraduate course 2 hours).
- 2016 **Research Methods (CA32002)**, Lecturer (Workshop: applied statistics with R), Forensics and anatomy curriculum, University of Dundee, UK (Undergraduate course 2 hours).
- 2015- **Research Methods (CE50028)**, Lecturer (Applied statistics with Excel workshops), Civil engineering curriculum, University of Dundee, UK (Undergraduate course 25 hours).
- 2015 **Research Methods (CA32002)**, Lecturer (Workshop: applied statistics with R), Forensics and anatomy curriculum, University of Dundee, UK (Undergraduate course 2 hours).
- 2015 **Statistical Data Analysis: a Primer**, Lecturer (Computational statistics and data analysis with R), Forensics and anatomy curriculum, University of Dundee, UK (Graduate course 15 hours).
- 2014 **A Primer in Statistics for Researchers**, Lecturer (Computational statistics and data analysis with R), Forensics and anatomy curriculum, University of Dundee, UK (Graduate course 9 hours).
- 2010- Mathematical and statistical methods, Lecturer (Introduction to probability theory and
- 2011 statistics), Biology curriculum, University of Milan, Italy (Undergraduate course 40 hours).
- 2010- Algorithms, Lecturer (Algorithm design and implementation in MATLAB, essential bioinformatics,
- 2010-2011 computational intelligence approaches), Mathematics curriculum, University of Milan, Italy (Undergraduate and graduate course – 44 hours).
- Algorithms, Lecturer (Algorithm design and implementation in C), Mathematics curriculum,
 University of Milan, Italy (Undergraduate course 24 hours).
- Algorithms, Lecturer (Algorithm design and implementation in C), Mathematics curriculum,
 University of Milan, Italy (Undergraduate course 24 hours).
- 2007- Cryptography, Teaching assistant, Computer science curriculum, University of Milan, Italy
 2008 (Graduate course 10 hours).

2007- Information theory, Teaching assistant, Computer science curriculum, University of Milan, Italy
 2008 (Graduate course - 6 hours).

REVIEWING

I reviewed articles for Algorithms, Applied Sciences, Processes, Bioinformatics, Plos One, Computation, Future Internet, Molecules, and Multiscale Modeling and Simulation. I also wrote for the British Society for Cell Biology (BSCB) Newsletter.

ADDITIONAL WORK EXPERIENCE

- 2015- Graphic designer. I designed the flayer for several of international art exhibitions organized in2017 Milan, Roma and Florence.
- 2014 **Translator (Italian to Engligh)**. RAW: Pictures from liquid days by Corradi C., curated by Mola A.; 2014, Ed. Blurb
- 2010-2011 **Web Programmer**. Freelance web programmer on PHP/MySQL architectures.
- 2007- **ICT Manager**, Servizi e Consulenze Doganali di Albergante Glauco & C. s.a.s. Manager of the computer infrastructure of a SOHO company working in international transports.
- 2001- **Office Employee**, Servizio Istruzione e Formazione Professionale del Comune di Novara. Office 2002 worker in the Education Offices of the municipality of Novara