Luca Albergante

Personal data

First Name	**Luca**	Last Name	**Albergante**
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Academic career

September 2016 – present **Postdoctoral research fellow in Bioinformatics and Systems Biology**. Computational Systems biology of Cancer group, INSERM Unit 900, Institut Curie, Paris, France

My responsibilities in the computational systems biology of cancer team (led by E Barillot and A Zinovyev) include the analysis of biological data (particularly single cell RNA-Seq), the development of machine learning algorithms to identify large-scale trends in biological big data, the supervision of undergraduate students, the preparation of scientific manuscripts, the presentation of my work in international conferences, and the delivery of tutorial and courses focused on computational systems biology. To this end, I have been using R and C++ in a parallel and distributed computing environment. I also made extensive use of version control and virtualization tools (GitHub and Docker).

June 2018 – July 2018 **Visiting Research Scholar**. Pinello Group, Center for Cancer Research, Massachusetts General Hospital, Boston, USA

As a part of my research activity, I visited the group of L Pinello to discuss novel methodologies to analyze and visualize single cell data.

October 2017 – November 2017 **Visiting Research Scholar**. Kharchenko group, Department of Biomedical Informatics, Harvard Medical School, Boston, USA

As a part of my research activity, I visited the group of P Kharchenko to discuss novel approaches to analyze single cell data.

August 2011 – August 2016 **Postdoctoral research fellow in Theoretical Systems Biology**. Division of Computational Biology and Division of Cell and Developmental Biology, School of Life Sciences, University of Dundee, Dundee, UK

My responsibilities in the theoretical systems biology team (led by T Newman) included the analysis of diverse complex biological data (networks, ChIP-Seq, images, epidemiological data), the development of statistical approaches to validate mathematical models, the supervision of B.Sc./M.Sc./Ph.D. students, the preparation of scientific manuscripts, the presentation of my work in international conferences, and the delivery of tutorial and courses focused on computational statistics. To this end, I have been using R in a parallel and distributed computing environment. I also collaborated with the Centre for Anatomy & Human Identification to design novel machine learning approaches for the analysis of anatomical and forensic data.

March 2014 – February 2016 **Lecturer in Statistics and Data Analysis.** School of Science and Engineering, University of Dundee, Dundee, UK

As a fixed-term lecturer, my responsibilities included the design and delivery of several courses on statistics and data analysis to B.Sc. and M.Sc. students in Anatomy, Forensic anthropology, and Engineering. The courses included hand-on workshops focused on the use of Excel and R as tools to test statistical hypothesis testing and, more broadly, to perform data analysis.

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

As a fixed-term lecturer, my responsibilities included the design and delivery of several courses on Algorithms and Statistics to B.Sc. and M.Sc. students in Mathematics and to B.Sc. students in Biology. The courses were focused on practical issues related to algorithm design and analysis, and statistical analysis. Hands-on tutorials with C, MATLAB, R or Excel were included in the courses.

November 2008 – June 2009	**Visiting research scholar**. Non-Standard Computation group, Department of Computer Science, University of York, York, UK

As part of my Ph.D. research activity, I spent several months in York to collaborate with experimental biologists. I also researched complex systems modeling and analysis using both mathematical and computational approaches.

EDUCATION

November 2006 – December 2010	**Ph.D. in Mathematics and Statistics for Computational Sciences**. Department of Mathematics, University of Milan, Milan, Italy

The research of my Ph.D., supervised by J Timmis (University of York) and G Naldi (University of Milan), focused on two main areas: the design and analysis of immune inspired algorithms and the development of mathematical models of infection. My Ph.D. training included exams on stochastic processes, statistics, computational biology, mathematical modeling, and sensitivity analysis. My Ph.D. thesis presents a model of experimental visceral leishmaniasis developed using stochastic Petri nets. The model is extensively validated via biological data either obtained from the literature or provided by the group of P Kaye (University of York). The robustness of the model was explored using sensitivity analysis.

October 1997 – October 2006	**Combined B.Sc. and M.Sc. in Computer Science** (5+ year program). Graduated *magna cum laude*. Department of Computer Science, University of Milan, Italy. 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).

During my university studies, I attended courses covering different aspects of computer science, including procedural and object-oriented programming, physics, computer architecture, operating systems, calculus, probability theory, statistics, networking, serial and parallel algorithms, programming language theory, cryptography, and information theory. My master thesis was centered on public key cryptography. In 2004/2005, I attended and passed all the 4 semesters of the Cisco System Networking Academy (CSNA).

# PUBLICATIONS - "&" DENOTES EQUAL CONTRIBUTION

1. Liu D, Albergante L, Horn D, Newman T. **A VSG Hierarchy During African Trypanosome Infections: A Feint Attack By Parasites**, 2018, Scientific Reports; 8, 10922 – In this article, I contributed to develop a statistical approach aimed at studying the cellular processes that contribute to the heterogeneity of variant surface glycoproteins (VSG) during an infection.

2. Palmer S, Albergante L, CC Blackburn, Newman TJ, **Further discussion on the immunological model of carcinogenesis**, 2018, PNAS; 115 (19), E4319-E4321

3. Palmer S, Albergante L, CC Blackburn, Newman TJ, **Thymic involution and rising disease incidence with age**, 2018, PNAS; 115 (8) 1883-1888 – In this article, I used statistical analysis on epidemiological data derived from different sources to show how a mathematical model based on immunosenescence is able to correctly describe the incidence of different infectious diseases and cancers. A press release for this article is available: http://bit.ly/2E8PymR

4. Liu D & Albergante L, Newman TJ, **Universal attenuators and their interactions with feedback loops in gene regulatory networks**, 2017, Nucleic Acid Research; 45(12), 7078–7093 – In this article, I used network analysis and statistics to study the role of regulatory cascades in gene networks. The analysis highlights the evolutionary pressures acting on these networks and provides new concepts to explore the emergence of heterogeneity in bacteria and cancer cells.

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 – In this article, I developed the bioinformatics pipeline to study the binding profile of 53BP1 using ChIP-Seq data. I also developed the necessary computational tools to explore the connections between this profile and the prediction of a mathematical model of DNA replication. The article highlights the strong connection of 53BP1 with unreplicated DNA and shows how the propensity of different genomic areas to present DNA replication problems can be theoretically predicted.

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 – In this article, I contributed to the development of a mathematical model of DNA replication errors based on probability theory and I developed the necessary computational and statistical methods to test the predictions of the model using genomic data. The article shows how DNA replication is optimized to limit the number of replications errors, which, however, are shown to be almost inevitable in human cells.

7. <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 drug-treated tumour populations using high-throughput analysis of karyotypic heterogeneity**, 2015, Convergent Science Physical Oncology; 1(2):025001 – In this article, I used image analysis on spectral karyotypes in combination with multidimensional statistics to study the heterogeneity of cancer cell lines before and after a drug treatment.

9. <u>Albergante L</u>, Blow JJ & Newman TJ, **Buffered Qualitative Stability explains the robustness and evolvability of transcriptional networks**, 2014, eLife; 3:302863 – In this article, I used mathematical modelling, network theory and statistical data analysis to study the robustness of gene networks. The article shows how robustness is able to explain many topological features of gene networks and highlighted the peculiar structure of gene regulation in cancer. A press release for this article is available: http://bit.ly/1T9yoH1

10. 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 – In this article, I developed a statistical approach to study a peculiar bias in gene mutations observed across different cancers. This bias can be explained using an evolutionary perspective that stresses the importance of non-mutated genes for the survival of cancer cells. A press release for this article is available: http://bit.ly/23JOhUe

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 – In this article, I presented the analysis of a Petri net model that I developed to study experimental visceral leishmaniasis. The model integrates biological data obtained from various sources and is extensively studied with statistical and computational approaches. The predictions of the models shed light on the dynamics of the infection and suggest new immune-based therapeutic options.

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 – In this article, I presented an immune-inspired algorism that allows discussion forums to self-manage.

13. <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, This article presents ElPiGraph, a flexible tool to discover complex trajectories in data distributions that I developed in collaborations with

other theoretical and computational researchers. Exemplary applications are presented in the context of biology and astronomy.

16. 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, This article present STREAM, a tool to discover and visualize trajectories in single cell data and to explore their biological significance. I contributed to STREAM by developing key parts of the trajectory discovery procedure.

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

1. <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
10. 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.
18. 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
19. 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 PhD Students, College of Life Sciences, University of Dundee, Dundee, UK
20. 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
21. 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)

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.

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.

THESIS SUPERVISION/CONTRIBUTION

2017-2018 **Supervisor** of Louis Faure (M.Sc.). As supervisor I provided guidance on the analytical approaches to study single cell data. Especially in the context of pseudotime analysis.

2013-2016 **Statistical, mathematical and statistical supervision** of the Ph.D. projects of Rana Al 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.

2013-2015 **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** for Marco Frank (B.Sc.), DRM and cryptographic methods: a reasoned review. Computer science curriculum, University of Milan.

TEACHING

2018 **Transcriptomique et épigénomique en cellule unique: théorie et pratique (sincellTE / Ecole thématique CNRS)**, Lecturer (Pseudotime reconstruction and cell cycle), Station Biologique Roscoff, Roscoff, France (graduate course – 3 hours).

2017 **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).

2015-2016 **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).

2010-2011 **Mathematical and statistical methods**, Lecturer (Introduction to probability theory and statistics), Biology curriculum, University of Milan, Italy (Undergraduate course – 40 hours).

2010- **Algorithms**, Lecturer (Algorithm design and implementation in MATLAB, essential bioinformatics,

2011	computational intelligence approaches), Mathematics curriculum, University of Milan, Italy (Undergraduate and graduate course – 44 hours).
2008-2009	**Algorithms**, Lecturer (Algorithm design and implementation in C), Mathematics curriculum, University of Milan, Italy (Undergraduate course – 24 hours).
2007-2008	**Algorithms**, Lecturer (Algorithm design and implementation in C), Mathematics curriculum, University of Milan, Italy (Undergraduate course – 24 hours).
2007-2008	**Cryptography**, Teaching assistant, Computer science curriculum, University of Milan, Italy (Graduate course – 10 hours).
2007-2008	**Information theory**, Teaching assistant, Computer science curriculum, University of Milan, Italy (Graduate course – 6 hours).

TECHNICAL SKILLS

Programming and Algorithm Design	I have an extensive experience in analyzing and designing single processor, parallel and distributed algorithms. I have a theoretical and practical knowledge of various general-purpose and scientific-oriented programming languages (C, C++, Java, R, Python, and MATLAB). I have an advanced knowledge of R as a tool for (bio)statistics, data analysis, simulations and interactive interface design (via Shiny). I have teaching experience with C, MATLAB and R. I have experience using version control systems (GitHub) and virtual machine deployment (Docker).
Applied Statistics / Machine Learning	I have a theoretical and practical knowledge of various statistical and machine learning techniques, including univariate and multivariate statistics, A/B testing, supervised and unsupervised clustering, manifold learning, feature selection, and regression. I have teaching experience in theoretical and computational statistics, and experience in designing and delivering applied statistics courses using R and Excel.
Mathematical Modeling	I have a theoretical and practical knowledge of various mathematical and computational techniques to build and validate models, including Markov processes, UML, differential equations, agent-based modeling, Petri nets, and sensitivity analysis.
Biostatistics and Biological Data Analysis	I have an extensive theoretical and practical knowledge of analysis (bash/R/Bioconductor) and visualization (ggplot/Shiny) of large biological big data. I have been analyzing images, bulk and single cell genomic data, molecular data, and epidemiological data.
Databases	I have a theoretical and practical knowledge of SQL and database development in both Oracle and MySQL.
Networking	I successful passed the CISCO System Network Academy (CSNA) and I have a theoretical and practical knowledge of network configuration management (with CISCO and SOHO appliances).

OTHER WORK EXPERIENCE

2015-2016	**Graphic designer**. I designed the flyer for several of international art exhibitions organized in Milan, Roma and Florence.
2014	**Translator**. 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.
2007-2009	**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.
2004	**Cisco System Networking Academy (CSNA)**, Department of Computer Science, Università degli Studi di Milano (Milan, Italy).
2001-2002	**Office Employee**, Servizio Istruzione e Formazione Professionale del Comune di Novara. Office worker in the Education Offices of the municipality of Novara