

Giovanna AMBROSINI



Nationality **Date of birth**
Italian and Swiss 29/04/1967

Contact

- Rue du Centre 9
CH-1025 Saint -Sulpice
- giovanna.ambrosini@epfl.ch
- +41.79.658.33.44

Keywords

Data analysis
Genomics
Biostatistics
Project management
Team management
Software design
Web development
Teaching

Languages

	Italian	Native
	English	Fluent
	French	Fluent
	German	Basic
	Greek	Basic

Bioinformatician and Data Analyst

PROFESSIONAL EXPERIENCE

- current - [Swiss Federal Institute of Technology in Lausanne, EPFL](#) 
- 2020 EPFL/SV PTECH BICC, EPFL/SV ISREC UPBRI, CH-1015 Lausanne
Activity: Analysis of next-generation genome sequencing data, statistics and bioinformatics training for biologists
Customized analysis of next-generation sequencing data (ChIP-seq, RNA-seq, Exome-seq, Bisulfite-seq, TempO-Seq), with a particular focus on cancer data
Software development and data management
Statistical consulting and supervision of data analysis pipelines
- 2020 - [Swiss Federal Institute of Technology in Lausanne, EPFL](#) 
- 2007 CH-1015 Lausanne
Activity: Software development and algorithm design for the analysis of next-generation genome sequencing data
Responsible for the development and maintenance of the group software tools
Participation in important collaborations with other research groups at EPFL
Teaching assistant
- 2007 - [Swiss Institute for experimental Cancer Research, ISREC](#) 
- 2002 CH-1066 Epalinges (Lausanne)
Activity: Software development and contribution to research projects
- 2002 - [Creative Electronics Systems SA, CES SA](#) 
- 2000 CH-1212 Grand Lancy 1, Geneva
Activity: Development of the system and support software for the company products (Linux Architect)
- 2000 - [Lightning Instrumentation SA](#) 
- 1999 CH-1010 Lausanne
Activity: Software Engineer
- 1999 - [The European Organization for Nuclear Research, CERN, EPD Division](#) 
- 1995 CH-1211 Geneva
Activity: Development and coordination of Data Acquisition Systems
Team coordination and software design and implementation

MAIN ACHIEVEMENTS AND COMPETENCES

- Manage SW development projects of up to 10 people
- Data management and statistical analysis
- Develop SW tools for the analysis of large genome sequencing data
- Acquired technologies:
 - programming languages (C, C++, Fortran, Perl, Python, Bash, PHP, HTML)
 - software tools (R, Git, CVS, make, cmake, MySQL, Bowtie, BWA, BAMTools)
 - operating systems (Linux, Solaris, LynxOS, OS-9, PowerUNIX, WindowsNT)

EDUCATION

- 1995 Ph.D. in Physics, University of Pavia, Italy

MAIN PROJECTS



Software development and data analysis for computational biology (20 years)

Software Development and Data Management

- The Breast Cancer (BC) Epigenomics Track Hub: online exploration and visualization tool for public cancer data;
- Comprehensive all-against-all transcription factor binding motif benchmarking study;
- The ChIP-Seq project: tools for the analysis of ChIP-seq data and other types of mass genome annotation data;
- The PWMTools project: set of tools for deriving and evaluating DNA binding models described as position weight matrices (PWMs). The PWMTools Web service also includes a tool to scan genomes of common model organisms with PWMs (PWMScan);
- The SNP2TFBS project: Web resource providing information about the predicted effects of single nucleotide polymorphisms (SNPs) on transcription factor binding;
- The Signal Search Analysis (SSA) SW: set of analysis tools used for sequence motif discovery and characterization;
- The Tagger project: tools and Web resources for fast mapping of short sequences to genomes;
- The Eukaryotic Promoter Database (EPD): a collection of eukaryotic promoters.

Data Analysis, training and consulting

- Customized analysis and data processing of next-generation sequencing data (RNA-seq, ChIP-seq, Exome-seq, TempO-Seq, etc.) for different research groups from Swiss schools of higher education and research institutes ([EPFL](#), [UNIL](#), [CHUV](#));
- Statistics and bioinformatics training for biologists;
- Statistical advice (longitudinal data analysis, sample size, and application of statistical tests for statistical inference).

Current collaboration

- Collaboration with the research group led by Prof. Cathrin Brisken (EPFL, Lausanne). The lab studies the role of steroid hormones in human breast growth and differentiation, and how they contribute to breast cancer development.

Former collaborations

- Participation in the Transcription Factor Motif benchmarking initiative of the COST (European Cooperation in Science and Technology) Action CA15205, GREEKC (Gene regulation Ensemble Effort for the Knowledge Commons);
- Participation in the SystemX.ch project led by Prof. Emmanouil Dermitzakis on the study of chromatin 3D interactions as important mediators of genetic effects on gene expression;
- Participation in the SMiLE-seq project led by Prof. Bart Deplancke (EPFL, Lausanne) aimed at characterizing the DNA binding specificities of transcription factors;
- Participation in the SystemX.ch project on 'modeling of KRAB/KAP-mediated epigenetic regulation' led by Prof. Didier Trono (EPFL, Lausanne);
- Participation in the study on the mechanisms regulating Nuclear Factor I genomic binding with Prof. Nicolas Mermod's group (EPFL, Lausanne);
- Development of ZNF-Site, a Web interface to search genomes for zinc finger nuclease target and off-target sites, with Anton McCaffrey's group (University of Iowa).

Events organization

- Organization of the Computational Genomics Journal Club biweekly meetings at EPFL.

Former activities (teaching and events organization)

- Organization of the Functional Genomics biweekly meeting series at EPFL.
- Teaching assistant for the SIB training course series "Chip-seq data analysis: from quality check to motif discovery and more", academic years 2015/2016/2017/2018/2020;
- Lab assistant for Bioinformatics I and Topics in Bioinformatics I at EPFL, Lausanne, academic years 2005/2006, 2007/2008, 2008/2009, 2009/2010, 2010/2011, and 2016/2017.

RECENT PUBLICATIONS

1. *Contraceptive progestins with androgenic properties stimulate breast epithelial cell proliferation.*
EMBO Molecular Medicine 2021. DOI: 10.15252/emmm.202114314
M Shamseddin, F De Martino, C Constantin, V Scabia, et al.
2. *Intraductal xenografts show lobular carcinoma cells rely on their own extracellular matrix and LOXL1.*
EMBO Molecular Medicine 2021. DOI: 10.15252/emmm.202013180
G Sflomos, L Battista, P Aouad, F De Martino, V Scabia, et al.
3. *Insights gained from a comprehensive all-against-all transcription factor binding motif benchmarking study.*
Genome biology 21, 2020. DOI: 10.1186/s13059-020-01996-3
G Ambrosini, I Vorontsov, D Penzar, R Groux, Oriol Fornes, et al.
4. *The secreted protease Adamts18 links hormone action to activation of the mammary stem cell niche.*
Nature Commun. 2020. DOI: 10.1038/s41467-020-15357-y
D Ataca, P Aouad, C Constantin, C Laszlo, M Beleut, M Shamseddin, et al.
5. *Common genetic variants associated with Parkinson's disease display widespread signature of epigenetic plasticity.*
Scientific Reports 2019. DOI: 10.1038/s41598-019-54865-w
A Sharma, N Osato, H Liu, S Asthana, TC Dakal, G Ambrosini, P Bucher, I Schmitt, U Wüllner.
6. *EPD in 2020: enhanced data visualization and extension to ncRNA promoters.*
Nucleic Acids Res. 2020. DOI: 10.1093/nar/gkz1014
P. Meylan, R. Dreos, G. Ambrosini, R. Groux, P. Bucher.
7. *Chromatin 3D interactions mediate genetic effects on regulatory networks.*
Science 2019. DOI: 10.1126/science.aat8266
O Delaneau, M Zazhytska, C Borel, C Howald, S Kumar, H Ongen, K Popadin, D Marbach, G Ambrosini, et al.
8. *PWMScan: a fast tool for scanning entire genomes with a position-specific weight matrix.*
Bioinformatics, Volume 34, Issue 14, 15 July 2018. DOI : 10.1093/bioinformatics/bty127
G. Ambrosini, R. Groux, P. Bucher.
[F1000Prime recommended.](#)
9. *MGA repository: a curated data resource for ChIP-seq and other genome annotated data.*
Nucleic Acids Res. 2018. DOI : 10.1093/nar/gkx995
R. Dréos, G. Ambrosini, R. Groux, R. C. Périer, P. Bucher.
10. *Local Regulatory Networks Across Two Tissues and Applications to Analyze Rare Non-coding Variants.*
Clinical Chemistry and Laboratory Medicine 2017, 55, S76
O Delaneau, K Popadin, M Zazhytska, S Kumar, G Ambrosini, A Gschwind, et al.
11. *SMiLE-seq identifies binding motifs of single and dimeric transcription factors.*
Nature methods 2017. DOI: 10.1038/nmeth.4143
A. Isakova, R. Groux, M. Imbeault, P. Rainer, D. Alpern R. Dainese, G. Ambrosini, D. Trono, P. Bucher, B. Deplancke.
12. *Intra-and inter-chromosomal chromatin interactions mediate genetic effects on regulatory networks.*
bioRxiv, 2017, 171694. DOI: 10.1101/171694
O Delaneau, M Zazhytska, C Borel, C Howald, S Kumar, H Ongen, K Popadin, D Marbach, G Ambrosini, et al.
13. *The eukaryotic promoter database in its 30th year: focus on non-vertebrate organisms.*
Nucleic Acids Res. 2017. DOI: 10.1093/nar/gkw1069
R. Dreos, G. Ambrosini, R. Groux, R. Cavin Périer, P. Bucher.
14. *SNP2TFBS - a database of regulatory SNPs affecting predicted transcription factor binding site affinity.*
Nucleic acids research 2016. DOI: 10.1093/nar/gkw1064
S. Kumar, G. Ambrosini, P. Bucher.
15. *The ChIP-Seq tools and web server: a resource for analyzing ChIP-seq and other types of genomic data.*
BMC genomics 2016. DOI: 10.1186/s12864-016-3288-8
G. Ambrosini, R. Dreos, S. Kumar, P. Bucher.

For the complete publication list, please refer to Google Scholar.