

Oswaldo Zagordi

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Born: January 31st, 1979 – Napoli, Italy
Nationality: Italian
Languages: Italian (maternal language), English, French, German (basic)

Current position

Post-doc researcher, ETH Zurich
also affiliated to SIB, Swiss Institute of Bioinformatics

Areas of competence

Computational biology – bioinformatics – next-generation sequencing – high throughput sequencing data – Bayesian statistics – graphical models – scientific programming

Appointments held

Research

2008-present	ETH Zurich, post-doc
2007	Abdus Salam International Centre for Theoretical Physics (ICTP), visiting scientist

Teaching

2008-2009	ETH Zurich, Tutorials in Systems Biology for the Biotechnology Master program
2008-2009	ETH Zurich, Tutorials in Evolutionary Dynamics for the Computational biology and Bioinformatics Master program
2007-2008	ICTP, Trieste (Abdus Salam International Centre for Theoretical Physics), Tutorials in Statistical Mechanics for the Diploma course in Condensed Matter Physics
2005-2006	IPSIA Galvani, Trieste (Professional school), Substitute Physics Teacher

Students advised

- 2011 (ongoing) Rounak Vyas, Phylogenetic analysis of HIV in single host
Master thesis, Computational biology and Bioinformatics Master program, ETH Zurich
- 2010b Hoda Sharifian, Errors induced during PCR amplification
Master thesis, Computational biology and Bioinformatics Master program, ETH Zurich
- 2010a Arnab Bhattacharya, Performance optimizations and improved sampling techniques for Dirichlet Process Mixture models
Bachelor thesis, Birla Institute, Pilani, India
- 2009 Cem Sievers, Analysis of Polycomb Response Elements identified by PRC1 ChIP-Seq Experiments
Diploma thesis, Biotechnology, Technische Universität Braunschweig, Germany
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Education

- 2007, July PhD in Statistical and Biological Physics
Advisors: Prof. Riccardo Zecchina, Dr. Michele Leone
Dissertation: Statistical Physics Methods in Computational Biology
Statistical and Biological Physics Sector
International School of Advanced Studies (SISSA-ISAS), Trieste - Italy
- 2002, October MSc in Physics, 110/110 *cum laude*
Advisor: Prof. Luca Peliti
Dissertation: Stochastic models for spontaneous mutations in DNA
Università degli Studi di Napoli Federico II, Napoli - Italy
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Publications

Journal articles

- 2011 **Oswaldo Zagordi**, Arnab Bhattacharya, Nicholas Eriksson, Niko Beerenwinkel
ShoRAH: estimating the genetic diversity of a mixed sample from next-generation sequencing data
BMC Bioinformatics 12:119 (2011), **Highly accessed**
- 2010b **Oswaldo Zagordi**, Rolf Klein, Martin Däumer, Niko Beerenwinkel
Error correction of next-generation sequencing data and reliable estimation of HIV quasispecies
Nucleic Acids Research, vol. 38 pp. 7400-7409 (2010)
- 2010a **Oswaldo Zagordi**, Lukas Geyrhofer, Volker Roth, Niko Beerenwinkel
Deep sequencing of a genetically heterogeneous sample: local haplotype reconstruction and read error correction
Journal of Computational Biology vol. 17 (3) pp. 417-28 (2010)

- also in: *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology RECOMB 2009 LNCS* vol. 5541 pp. 345-358 (2009)
- 2009b Fahad Saeed, Ashfaq Khokhar, **Oswaldo Zagordi**, Niko Beerenwinkel
Multiple sequence alignment system for pyrosequencing reads
Proceedings of the 1st Bioinformatics and Computational Biology (BICoB 2009) conference LNBI vol. 5462, pp. 362-375, (2009)
- 2009a **Oswaldo Zagordi**, Alessandro Michelangeli
1D periodic potentials with gaps vanishing at $k = 0$
Memoirs on Differential Equations and Mathematical Physics vol. 47 pp. 133-158 (2009)
- 2006 Michele Leone, Andrea Pagnani, Giorgio Parisi, **Oswaldo Zagordi**
Finite size corrections to random Boolean networks
J. Stat. Mech. P12012 (2006)
- 2005 **Oswaldo Zagordi**, Jean R. Lobry
Forcing reversibility in the no strand-bias substitution model allows for the theoretical and practical identifiability of its 5 parameters from pairwise DNA sequence comparisons
Gene, vol. 347 (2) 175-182 (2005)

Conference proceedings

- 2010-2011 Sandhya Prabhakaran, Melanie Rey, **Oswaldo Zagordi**, Niko Beerenwinkel, Volker Roth
HIV-Haplotype Inference using a Constraint-based Dirichlet Process Mixture Model
NIPS Machine Learning in Computational Biology (MLCB 2010) workshop (extended abstract)
also: under revision for acceptance at the *28th International Conference on Machine Learning (ICML 2011)*
- 2009 **Oswaldo Zagordi**, Lukas Geyrhofer, Volker Roth, Niko Beerenwinkel
Deep sequencing of a genetically heterogeneous sample: local haplotype reconstruction and read error correction
Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology RECOMB 2009 LNCS vol. 5541 pp. 345-358 (2009)

Book chapters

- 2005 Demian Battaglia, Lorenzo Stella, **Oswaldo Zagordi**, Giuseppe E. Santoro, Erio Tosatti
Deterministic and Stochastic Quantum Annealing Approaches
Lecture Notes in Physics vol. 679 pp. 171-206

Talks

- 2011 SIB Scientific days 2011, January 31st, Biel/Bienne, Switzerland
- 2009b Advances in Statistical Modeling of High Dimensional Data, September 27th, Mu-

- nich, Germany
- 2009a RECOMB 2009, May 18th, Tucson (Arizona), USA
- 2008b Quasispecies: past, present and future 30th anniversary, VIII Jornada de Virologia, November 17th, Barcelona, Spain
- 2008a Biology, Computation and Information 2008, September 9th, Trieste, Italy

Other activities

Scientific

- 2008-present Main developer of the scientific software [ShoRAH](#) for the analysis of next-generation sequencing data.
- 2008-present Reviewer for the journals: *Bioinformatics*, *Human Genetics*, *New Journal of Physics*

Other

- 2005-2007 Member of the Editorial board of the SISSA house organ [SISSA News](#)
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Grants, honors & awards

- 2009b Travel fellowship RECOMB 2009, Tucson (Arizona) USA
- 2009a Abbott Swiss HIV Cohort Grant: 2nd prize 2009 with the project “Ultra-deep sequencing of HIV: a pilot study evaluating the benefit for predicting therapy outcome”
The 65,000 CHF grant from SHCS was rewarded by Abbott Swiss with additional 15,000 CHF
- 2003-2007 PhD fellowship, SISSA-ISAS, Trieste - Italy
- 2003 June - October: pre-doctoral fellowship, SISSA-ISAS, Trieste - Italy
Advisor: Prof. Giuseppe Santoro, Prof. Stefano Baroni
Research project: Classical diffusion and quantum mechanics in periodic potentials
- 2000-2001 Erasmus scholarship at Université Joseph Fourier Grenoble - France
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Statement of research

Next-generation sequencing

Inferring genetic diversity I am currently involved in the development, implementation and application of a novel method to analyse ultra high-throughput sequencing data. My interest lies in the application of these sequencing techniques to the detection and quantification of genetic diversity in heterogeneous

samples. Genetic heterogeneity is a key feature of some pathogen populations, particularly of retroviruses as HIV. High diversity of HIV population in a single host is correlated to treatment failure and poor prognosis. Thus, correctly assessing the present diversity is important in designing an effective therapy.

All studies that use next-generation sequencing techniques to detect genetic variants present in low frequency encounter the same difficulty: how to distinguish variants that are really present in the sample from those that appear only as an effect of the high error rate of the technology. I have designed a Bayesian model to correct the technical errors and infer the variants present in a genetically heterogeneous sample with high reliability. Together with other tools, this method is implemented in the software ShoRAH. I have applied the method to data obtained by collaborators at the Institut für Immunologie und Genetik, Kaiserslautern, in the context of HIV drug resistance testing. I have actively participated in the design of the experiments as these were supposed to validate the computational error correction.

My research goal is to extend the method I have developed in order to apply it to different biological systems. First, the computational methods devised so far need to be constantly updated. In fact, the technologies keep evolving and provide a constantly increasing amount of data also of different kind (*e.g.*, the paired-end approach now available for all major platforms allows for the phasing of genetic variants at longer distance). Since genetic diversity is relevant not only in viral infections, but also in bacterial ones and in cancer development, it will be important to test the applicability of NGS technologies in this directions as well.

ChIP-Seq I am currently involved in a project in epigenetics of *Drosophila* aiming at detecting Polycomb response elements by means of ChIP-Seq data. The goal is to find a minimal set of motives characterising the region where Polycomb-group proteins bind.

Other projects

Another project I am following involves the analysis of AFM (atomic force microscope) data for the characterisation of the response of proteins to external forces. These experiments are modeled with a type of Hidden Markov Model (HMM), a tool also used in sequence alignment.

References

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