

# Maurizio Rinaldi

Researcher ID: C-7378-2009

## EDUCATION

He obtained the Degree in Physics in 1996, at the Milan University, Italy with a grade of 110 cum laude. In 1991 he got the PhD degree in Elementary Particles Physics, ISAS (International School for Advanced Studies), Trieste, Italy. From 1990 to 1993 he was appointed a postdoctoral fellowship, in the Mathematical and Physics Department of the Harvard University, Cambridge (MA), USA under the supervision of Prof. Arthur Jaffe, where he also was Teaching Assistant in Mathematics, Department of Mathematics. From 1993 to 1995 he enjoyed a postdoctoral fellowship, Mathematics Department, University of Milan, Italy. He worked in various areas in geometry, analysis and mathematical physics.

## UNIVERSITY CAREER

2000-2015	Associate professor, Department of Pharmaceutical Sciences (formerly Faculty of Pharmacy), University of Piemonte, Novara, Italy
1995-1999	University researcher in Mathematical Analysis, Faculty of Mathematical, Physical and Natural Sciences, University of Trieste, Trieste, Italy.

## MAIN FIELDS OF INTEREST

1. Topology and geometry of 3d-structures
2. Machine learning
3. Simulation of complex phenomena
4. Genome-wide data analysis

## CURRENT ISSUES OF RESEARCH

### 1. TOPOLOGY AND GEOMETRY OF POLYMERS AND PROTEINS

Proteins are an intriguing example of 3D structures consisting of a large number of points with connections, but many other interesting objects can be found. The study of their geometry and topological properties can be implemented also by using computer algebra systems. In particular beside graphical representations one could implement algorithms to compute topological

invariants (e.g. link polynomials) and geometric invariants.

## 2. MACHINE LEARNING

We use a variety of different data mining and multivariate data analysis techniques, particularly a wide range of cluster analysis and pattern recognition methods, and a wide range of classification algorithms. The further use of genetic algorithms makes it possible to optimize the technique at hand. We apply these techniques to data of biological, medical or pharmaceutical origin.

## 3. SIMULATION OF COMPLEX PHENOMENA

Life sciences traditionally offer a wide range of problems whose solutions escape traditional methods. In many biological situations, for instance the construction of ad hoc dynamical models allows a better understanding, and can lead to quite interesting results. The models could result in systems of complex equations (e.g. non linear difference equation) and the search for their solutions requires the development of new mathematical skills. A wide use of emerging numerical techniques is often extremely helpful to find good approximations of the solutions. Also computer simulation models of complex phenomena allow very often to gain some insight and to deepen understanding and forecasting ability.

## 4. HIGH THROUGHPUT DATA ANALYSIS

Microarray is a multiplex technology used in molecular biology and medicine in order to measure differential gene expression or microRNA profiling. Statistics play a fundamental role in experiment design and gene expression profile, which requires handling of large amount of data. This is just one example of a high-throughput technique that deserves a particular treatment of data.

### TOP FIVE PAPERS

1. Comoglio F. e Rinaldi M. *Rknots: Topological Analysis of Knotted Proteins, Biopolymers and 3D Structures*, R package version 1.3.1 (2015), <https://CRAN.R-project.org/package=Rknots>
2. Comoglio F, Rinaldi M: *A Topological Framework for the Computation of the HOMFLY Polynomial and its Application to Proteins*. PLoS ONE , 6(4):e18693, 04, 2011
3. Busacca S, Germano S, De Cecco L, Rinaldi M, Comoglio F, Favero F, Murer B, Mutti L, Pierotti M, e Gaudino G. *MicroRNA Signature of Malignant Mesothelioma with Potential Diagnostic and prognostic implications*. AMERICAN JOURNAL OF RESPIRATORY CELL AND MOLECULAR BIOLOGY, 42:312-319, 2010

4. Locatelli M, Gindro R, Travaglia F, Coisson JD, Rinaldi M, and Arlorio M: *Study of the DPPH-scavenging activity: Development of a free software for the correct interpretation of data.* FOOD CHEMISTRY, 114:889-897, 2009
5. Rinaldi M, Sgarro A, and Invernizzi S. *Moduli di Matematica e Statistica* . Zanichelli, 2000.

## **AWARDS**

Awarded from the Bok Derek Center of Teaching and Learning of the Harvard University with the Certificate of Distinction in Teaching (for the teaching of mathematics).