

**Ph.D. in Information Technology:
Palluzzi Final Dissertation**

DEIB Seminar Room

March 6th, 2017

2.00 pm

Ph.D. presentation and discussion:

Fernando PALLUZZI – XXVIII Cycle

“Novel Genome-Scale Data Models and Algorithms for Molecular Medicine and Biomedical Research”

Advisor: Prof. **Gaetano Ivan Dellino**, PhD (IEO, Istituto Europeo di Oncologia)

Abstract:

Genomes are complex systems, and not just static and monolithic entities. They represent the ensemble of the hereditary information of an organism or, in evolutionary terms, of a species. Sequencing sciences offered through the last two decades the possibility to dive into this complexity. This scientific revolution led to a series of paradigm changes, and the collateral need of efficient technical and methodological innovations. However, this process was not gradual, exposing genome research to an explosive data deluge, thus causing a series of bottlenecks: technological, computational, and methodological, due to the existence of efficient data reduction and analysis algorithm, capable of capturing the informative portion of genomic complexity. In the last years, there have been huge efforts towards the generation of unified standards and databases, ontologies, integrated platforms, integrative methodologies, to provide a strong theoretical background, capable of capturing true biological variation, often masked behind marginal synergic processes. The goal of this thesis was to shed light on this last problem, trying to expose a unifying theoretical foundation needed to approach the study of genome complexity.

PhD Committee:

Prof. **Barbara Pernici**, DEIB – Politecnico di Milano

Prof. **Davide Cittaro**, Ospedale San Raffaele

Prof. **Pier Giuseppe Pelicci**, Istituto Europeo di Oncologia