

Mission

Translational Bioinformatics is an emergent field of health informatics that addresses the application of the scientific discoveries and technological innovations from the laboratories to the clinical practice. In the last decade, this area has seen a rising interest among the scientific community due to the development of Next Generation Sequencing (NGS) techniques that allowed the availability of increasingly voluminous amounts of genomic data. In this context, the main objective of the TBLab is the research of techniques, algorithms, services and infrastructures that are able to produce and provide new clinical knowledge from genomic and biomedical data. The aim of the TBLab is to identify, at molecular level, what are the key players, such as microRNA (miRNA), messenger RNA (mRNA), proteins, molecular compounds, and their interactions involved in the development of specific pathologies, like cancer and other chronic-degenerative diseases having an high impact on the social, economic and healthcare domain. The understanding of these mechanisms allows to translate, by means of services deployed on ad-hoc IT infrastructures taking into account the fundamental requirements about privacy and security, the results of the in silico analysis to the clinical practice, because this kind of knowledge is at the basis of the development of personalized diagnostic, prognostic and therapeutic treatments.

Fields of application

Application domains of TBLab consist in the study of molecules (miRNA, mRNA, protein) and their interactions in the regulatory mechanisms that are involved in cancer and chronic and degenerative diseases, in the identification of biomarkers for diagnostic and prognostic purposes for the "personalized medicine". In the healthcare domain, the goal of TBLab is to make available the results of those studies through the development of IT services and architectures.

Research themes

The main research themes of TBLab are artificial intelligence, knowledge organization and management, machine learning. The research activity is focused on the design and implementation of classification and clustering algorithms based on several computational approaches such as self-organizing neural networks, deep learning, probabilistic topic models. These algorithms are used to analyze genomic sequences, gene expression values, molecular compounds structures. Moreover, self-organizing neural networks are adopted to develop a miRNA-target predictor. As for knowledge organization and management, the research activity addresses the definition of an ontology of services and application in bioinformatics and biomedical domains in order to provide the functionalities of the decision support systems to the workflow management systems. Other research activities are focused on the design and implementation of a prototypal distributed IT architecture that allows to integrate and make available several algorithms and services, such as alignment and mapping of NGS data, statistical methods for the generation and analysis of gene expression values, gene enrichment methods for the functional annotation of differentially expressed miRNA and mRNA molecules.