Bioinformatics@IBPM: from atomic level to genome-scale data analysis, and the ELIXIR-Italy Training Platform

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The Biocomputing Lab at IBPM has a long-standing tradition in the study of biological macromolecules at the sequence, structure and functional level. Thanks to highly complementary professional profiles of its members, the expertise of the group ranges from structural bioinformatics to cancer genomics and best training practices in bioinformatics, from small molecule drug design to statistical analysis and integration of complex high-throughput sequencing (HTS) data sets, from biomarker discovery to software development. Genomics, transcriptomics, epigenomics, protein-RNA interactions data and protein 3D atomic structures are analysed both by employing state-of-the-art software and methods and by developing ad hoc computational strategies and pipelines for non-standard analyses. Results are exploited to gain knowledge on the systems under investigation (e.g., evolutionary relationships, 3D atomic structure and function inferences) and to design new molecules (protein, peptides and small compounds) endowed with desired biological properties.

A large part of these studies is carried out in close collaboration with experimental groups and is focussed on the understanding of, and development of new strategies against, diseases such as: cancer (e.g., identification of non-coding regulatory regions with oncogenic or oncosuppressor potential; definition of functional miRNA network modulated by reverse transcriptase inhibition; characterization of the interaction network of importin-β, a master regulator of mitosis overexpressed in many cancer types; design of ferritin variants as tissue-targeted carriers of diagnostic or therapeutic agents); Huntington’s disease (identification of drugs able to bind target proteins by virtual screening); mitochondrial diseases (design of rescuing peptides and peptide-mimetic compounds). Additionally, we are interested in the molecular mechanisms underlying parasitic diseases (we have developed an automated procedure to analyze point mutations associated with antibiotic resistance) and in the design of humanized variants of therapeutic antibodies.

The IBPM Biocomputing Lab coordinates the Training Platform of the ELIXIR Italian Node, which is involved in the design, development and delivery of bioinformatics training activities. ELIXIR is a pan-European Research Infrastructure that coordinates, integrates and sustains bioinformatics resources across member states, and enables users in academia and industry to access services that are vital for research in life sciences. In this context, the IBPM Biocomputing Lab has developed expertise in the science of learning and teaching, and educational psychology.

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