



Integrative Bioinformatics for trans-omics networks representation and analysis

Project Description

The aim of this proposal is to define novel integrative bioinformatics tools to give a global view of different biological data sources and to support biological process representation and analysis by means of trans-omics networks and deep learning techniques.

Collection of biological data is a method to catalogue the elements of life but the understanding of a system requires the integration of these data under mathematical and relational models that can describe mechanistically the relationships between their components. Analyses on these datasets advanced our understanding of biological regulations by providing “generic rules yet with several exceptions”. These generic rules are observed as a trend. On the other hand, the trans-omics approach tries to overcome the lack of comprehensiveness and the information gap regarding interaction across multiple omic layers. A network structure of a biochemical trans-omics network directly involves causality and the input–output relationship at a molecular level. Deep learning techniques are promising tools to allow the integration of multi-omics data sets and to perform different analyses based on trans-OWAS approach and trans-omics representations.

Prospective Students

Possible candidates are expected to have different backgrounds in artificial intelligence, big data and bioinformatics.

Supervisor(s), Lab/Group details, other additional info

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The **COmputational System BIOlogy (COSMO) lab** has been established through the joint efforts of the Department of Electrical Engineering and Information Technology (DIETI) at University in Naples Federico II (UNINA) and the Molecular and Cell Biology group at the CNR, IEOS, Naples. It is led by Dr. Alberto Luini (CNR-IEOS) and Prof. Antonio M. Rinaldi (UNINA-CNR-IEOS). The Lab develops methods for the analysis of cellular molecular networks of interest and focuses on uncovering and analyzing the control systems operating in the cell and in particular in the transport pathways and integrative bioinformatics approaches and bioimages analysis. The research topics on which the Lab intends to investigate require the use of innovative computational intelligence techniques in the field of systems biology. This view is focused on understanding cell regulation on a global and more holistic level. The regulation of the transport system is similar in design to the regulation of other complex systems, both biological and artificial, and can best be described on the basis of a set of concepts, collectively referred to as control theory, which were originally developed in the field of engineering for the management of complex machines and were subsequently applied to biological systems. Moreover, the use of knowledge-driven frameworks able to integrate



big multi-omics data into a knowledge structure enabling the exploration and discovery of novel biological patterns and associations using trans-omics network reconstruction and multi-omics analysis. This research will rely on techniques for the identification of control systems in the cell based on perturbations on cellular events. These perturbations, which can be of various kinds (thermal, pharmacological, genetic, etc.), change the pattern of gene expression and the signaling cascades. The data obtained from these perturbations are too complex (thousands of signals per experiment) and require computational approaches for their analysis. In addition, the study of trans-ome-wide association (trans-OWAS) connecting phenotypes with trans-omics networks that reflect both genetic and environmental factors can characterize complex diseases and support novel approaches for precision medicine.

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