Integrative bioinformatics for Trans-omics networks representation and image analysis

Project Description

The aim of this proposal is to define novel integrative bioinformatics tools to provide a global view of different biological data sources and to unravel control systems of the cells. These tools will support the representation and analysis of biological processes by leveraging trans-omics networks, deep learning techniques and imaging analysis.

The collection of biological data serves as a means to catalog the elements of life, but to truly understand a system, it requires the integration of these data using mathematical and relational models. These models can mechanistically describe the relationships between the components of the system, including the control systems of the cells and imaging data.

Through advanced analysis of these datasets, we have made significant progress in understanding biological regulations, uncovering both generic rules and exceptions to these rules. These generic rules are observed as trends in the data, but there are often variations that deviate from these patterns.

To overcome the limitations of comprehensiveness and information gaps in interactions across multiple omic layers, we propose a trans-omics approach. This approach involves constructing a network structure that represents the biochemical trans-omics network, capturing causality and the input-output relationships at a molecular level. By incorporating control systems of the cells and imaging data into this network, we can gain deeper insights into biological processes.

Deep learning techniques offer promising tools for integrating multi-omics datasets and conducting various analyses based on the trans-OWAS approach and trans-omics representations. These techniques enable the identification of complex patterns and relationships within the integrated data, allowing us to uncover novel insights into cellular control systems and imaging analysis.

Prospective Students

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

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

Prof. Antonio M. Rinaldi (DIETI-UNINA)
Dr. Alberto Luini (IEOS-CNR)
Dr. Seetharaman Parashuraman (IEOS-CNR)

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.

References

Kamdar, M. R., Fernández, J. D., Polleres, A., Tudorache, T., & Musen, M. A. (2019). Enabling web-scale data integration in biomedicine through linked open data. NPJ digital medicine, 2(1), 1-14.

Kang, M., Ko, E., & Mersha, T. B. (2022). A roadmap for multi-omics data integration using deep learning. Briefings in Bioinformatics, 23(1)

Lin, Z., Li, X., Zhan, X., Sun, L., Gao, J., Cao, Y., & Qiu, H. (2017). Construction of competitive endogenous RNA network reveals regulatory role of long non-coding RNAs in type 2 diabetes mellitus. Journal of cellular and molecular medicine, 21(12), 3204-3213

Ohno-Machado, L., Sansone, S. A., Alter, G., Fore, I., Grethe, J., Xu, H., ... & Kim, H. E. (2017). Finding useful data across multiple biomedical data repositories using DataMed. Nature genetics, 49(6), 816-819

Subramanian, I., Verma, S., Kumar, S., Jere, A., & Anamika, K. (2020). Multi-omics data integration, interpretation, and its application. Bioinformatics and biology insights, 14

Vidal, M. E., Endris, K. M., Jozashoori, S., Karim, F., & Palma, G. (2019). Semantic data integration of big biomedical data for supporting personalised medicine. In Current Trends in Semantic Web Technologies: Theory and Practice (pp. 25-56). Springer, Cham

Yugi, K., Kubota, H., Hatano, A., & Kuroda, S. (2016). Trans-omics: how to reconstruct biochemical networks across multiple 'omic'layers. Trends in biotechnology, 34(4), 276-290

Yugi, K., Kubota, H., Toyoshima, Y., Noguchi, R., Kawata, K., Komori, Y., ... & Kuroda, S. (2014). Reconstruction of insulin signal flow from phosphoproteome and metabolome data. Cell reports, 8(4), 1171-1183