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Microsoft Teams



Prof. **Michele Ceccarelli**

DIETI - Università di Napoli Federico II

www.docenti.unina.it/michele.ceccarelli

Computational Biology: Large scale data analysis to understand the molecular bases of human diseases

Abstract: The availability of high-throughput technologies in the life sciences, and in particular for molecular biology, and their large-scale analysis gives the opportunity to pursue significant biomedical discoveries by associating molecular features to biological status and phenotypes such as stage and type of diseases, prognosis, response to of therapies, and others. The data are typically scattered over a plethora of both public and private repositories and are represented using a large number of different formats as they represent multiple levels of molecular information (as for example DNA mutation, DNA copy, DNA methylation, mRNA, miRNA, and protein expression). This situation makes searching and mining for the extraction of new knowledge from the complete set of available data a novel great challenge for the computational science community. For example, projects such as The Cancer Genome Atlas (TCGA) and the International Cancer Genome Consortium (ICGC) make available comprehensive

genomic data sets on human cancers, representing multiple levels of data for thousands of patients.

The integrative analysis of these datasets has fostered the selection and discovery of novel and accurate biomarkers that can be used for disease diagnosis and prognosis, for predicting therapeutic responses and for developing therapies or to mark a specific stage of the developmental process. Furthermore, information derived from aberrant pathways and network activities facilitates the detection of diagnosis and treatment, the identification of novel drug targets, the classification of disease types and the prediction of outcomes. I will report recent research lines that exploited the availability of large-scale datasets for a better understanding of the molecular basis of one of the most aggressive forms of brain tumors and how this effort can improve diagnosis and patient management toward the use of personalized medicine.

Michele Ceccarelli is Full Professor of Computer Science and Engineering at University of Naples "Federico II", Italy, he is also Principal Investigator of the Bioinformatics and Computational Biology Laboratory at the BIOGEM Research Center in Italy. Michele has given contributions to the field of systems biology and cancer genomics, developing novel tools and algorithms for gene expression data analysis, gene network analysis and identification of structural genomic alterations. He was involved in the TCGA Pan Glioma Analysis Working Group participating to the discovery of novel biologically and clinically relevant glioma subtypes. His current research activity is focused in the development of computational tools for the immunological characterization of cancer.

Info: **Michele Ceccarelli** - tel. 081 7683787 – michele.ceccarelli@unina.it



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