BIOGRAPHY

Antonio Colaprico, PhD graduated from University of Sannio, Italy, earning his Bachelor's degree and Master's degree in Telecommunication Engineering in 2005 and 2011, respectively. In July 2014, he defended his PhD thesis entitled 'Integrative analysis on colon and lung cancer with identification of master regulators microRNA--gene networks' supervised by Prof. Michele Ceccarelli. The PhD was awarded jointly by the the University of Sannio and BIOGEM (Biotechnology and Molecular Genetics Research Centre), Ariano Irpino (AV), Italy.

In October 2014, Antonio joined the Machine Learning Group (MLG) of the Université libre de Bruxelles (ULB) and the Interuniversity Institute of Bioinformatics in Brussels (IB)² as a postdoctoral researcher under the supervision of Prof. Gianluca Bontempi.

In July 2017, he started to work as an Assistant Scientist with Prof. Maria Figueroa in the Department of Human Genetics, Sylvester Comprehensive Cancer Center, University of Miami (USA). Dr. Colaprico is currently Assistant Scientist with Prof. Xi (Steven) Chen in the Department of Public Health Sciences, Division of Biostatistics, University of Miami (USA)

Dr. Colaprico is actively developing a number of software tools with his collaborators such as TCGAbiolinks, TCGAbiolinksGUI, SpidermiR, CancerSubtypes and MoonlightR.

His research activities are focused on the development of innovative integrated bioinformatics methods and applications with the aim of modelling complex systems in biology and improving molecular diagnosis. He is first and co-author of several scientific publications, in high impact factor journals including Nucleic Acid Research, Gastroenterology, Cell and Immunity.

Title: ***Bioinformatics tools to integrate and understand aberrant genomic and epigenomic changes associated with cancer***

Abstract

Technological advances and public databases like The Genomic Data Commons (GDC), The Encyclopedia of DNA Elements (ENCODE), and The NIH Roadmap Epigenomics Mapping Consortium (roadmap) have provided unprecedented opportunities to interrogate the epigenomes of normal and tumor tissues with high resolution. Performing integrated analyses of molecular datasets along with clinical information, has been shown to improve the prognostic and predictive accuracy for cancer phenotypes if compared to clinical features alone. This highlights the importance of developing bioinformatic tools and/or computational software able to easily integrate and analyze these data.

Among the tools providing integrative analyses we present the R/Bioconductor package TCGAbiolinks that integrates DNA methylation and gene expression data to identify differentiated promoter regions affecting the gene expression, and the R/Bioconductor package MoonlightR for the identification of driver genes (oncogenes and tumor suppressor) is crucial in the cancer treatment.

We identified 'moonlight' drivers playing a dual role in different context elucidating their molecular mechanism, with impact on prognosis, resistance to treatment, as well as to guide therapeutic decisions in direction of personalized therapy.

PUBLICATIONS

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