## 1 FEBRUARY AT 11.30 A.M. Room B109 | Povo 2



## A SECOND-GENERATION OF GENETIC-VULNERABILITY-MAPS IN CANCER CELLS

## FRANCESCO IORIO

IORIO GROUP, COMPUTATIONAL BIOLOGY RESEARCH CENTRE



## HUMAN TECHNOPOLE – MI

In the pursuit of systematically identifying new therapeutic targets for cancer, various approaches have been explored in pre-clinical drug discovery. Some of these approaches involve large-scale chemical or functional-genomics screens of extensively characterised human cancer cell lines (CLs), with a focus on correlating molecular features - often cancer driver (epi)genomic events - with drug sensitivity and vulnerabilities. These efforts have generated extensive public datasets encompassing thousands of CLs, their comprehensive characterisations, and responses to individual gene inactivation through CRISPR-Cas9 genome editing. This has laid the groundwork for the collaborative **Cancer Dependency Map project**, aiming to **catalog all intra-cellular cancer dependencies**, i.e., genes essential for cancer cell survival. This endeavour has led to the **identification of drug response markers**, **synthetic lethality cases**, **and genome-scale prioritisation of novel therapeutic targets**. I will introduce our recent contributions in this field, including dedicated computational tools, a second generation of prioritised **cancer therapeutic targets**, and new data modalities shaping the future of **cancer dependency maps**.





UNIVERSITÀ DI TRENTO

Department of Cellular, Computational and Integrative Biology - CIBIO