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PROJECT INFO	
Title of the proposed project:	RNAseq-Driven Machine Learning framework for Predicting Immunotherapy Response
Short description of the project	Immune checkpoint inhibitors have transformed the therapeutic landscape of oncology by enabling durable responses across multiple tumor types, yet only a subset of patients derives meaningful benefit, and available biomarkers such as PD-L1 expression and tumor mutational burden provide limited predictive accuracy across tumor types and clinical contexts. Similar challenges apply to breast cancer, where response to systemic therapy remains incompletely predicted by conventional clinicopathological and single-analyte biomarkers. The project focuses on developing and validating predictive models of anti-cancer treatment outcome by integrating whole-exome sequencing, bulk RNA sequencing, and single-cell RNA sequencing across several malignancies. This multi-layered approach also enables dissection of tumor biology, deconvoluting transcriptomic signatures into their cellular constituents and linking genomic alterations to the transcriptional states of malignant and immune compartments underlying sensitivity or resistance. The primary modeling goal is stratification of patients into progression-free survival risk groups using time-to-event frameworks, reflecting the clinical relevance of durable disease control. Where RECIST-based response classifications are available, these will serve as an additional supervised target within a complementary binary classification framework. By combining genomic and transcriptomic features in a unified machine learning approach, the study aims to generate clinically actionable models that improve patient stratification while providing mechanistic insight into determinants of response.
Main research area for the project	Computational biology
Second research area for the project	Cancer genomics
3 key words for the project	Transcriptomics, Machine Learning, Advanced Solid Tumors, Immunotherapy response

LAB INFO	
Main topic/s of the lab	Computational biology.
Short description of the lab activity	At the Data Science Unit, we apply mathematical and computational approaches to address a central challenge in cancer genomics: identifying which patients are likely to have a favorable prognosis and respond to specific therapies. Leveraging genomic and transcriptomic data, we develop

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	machine learning-based prognostic and predictive models to stratify patients into distinct risk groups. Our work focuses primarily on key clinical settings, including breast cancer (HR+/HER2- early-stage and triple-negative), immunotherapy across multiple cancer types, and acute myeloid leukemia (AML).
Recent bibliography	DOI: 10.1038/s41467-026-71607-5 DOI: 10.1016/j.esmoop.2026.106064 DOI: 10.1016/j.esmoop.2025.105875 DOI: 10.1016/j.esmoop.2025.105847 DOI: 10.1016/j.annonc.2025.03.005 DOI: 10.1038/s41591-024-03346-3 DOI: 10.1016/S0140-6736(24)00054-0 DOI: 10.1007/s10549-024-07292-z DOI: 10.1016/j.esmoop.2023.101608 DOI: 10.1016/j.annonc.2021.08.2153 DOI: 10.15252/emmm.202013598
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Institutional page link	https://www.research.ieo.it/research-and-technology/technological-units/data-science-unit/