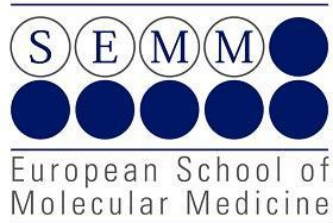


AVAILABLE POSITIONS

<b>Principal Investigator</b>	YINXIU ZHAN
<b>Institute of Affiliation</b>	IEO

PROJECT INFO	
Title of the proposed project:	RNAseq-Driven Machine Learning framework for Predicting Immunotherapy Response
Short description of the project	<p>Immune checkpoint inhibitors have transformed the therapeutic landscape of oncology by enabling durable responses across multiple tumor types. Despite these advances, only a subset of patients derives meaningful clinical benefit, and currently available biomarkers, including PD-L1 expression and tumor mutational burden (TMB), provide limited predictive accuracy and reproducibility across different tumor types and clinical contexts.</p> <p>The project focuses on developing and validating predictive models of immunotherapy outcome based on the integration of RNA sequencing and DNA sequencing data. The primary modeling goal is the stratification of patients into progression-free survival (PFS) risk groups using time-to-event frameworks, reflecting the clinical relevance of durable disease control as the key measure of immunotherapy benefit. When RECIST-based response classifications are available, these will be incorporated as an additional supervised target, enabling a complementary binary classification framework. By combining transcriptomic and genomic features within a unified machine learning approach, the study aims to generate clinically actionable models that improve patient stratification.</p>
Main research area for the project	Computational biology
Second research area for the project	Cancer genomics
3 key words for the project	Immunotherapy response, machine learning, survival analysis

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 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	LB Bielo et al 2026, ESMO open; D. Mattavelli et al 2026 ESMO open
Group composition	4 fellows, 1 PhD, 2 postdocs



2026 spring call PhD selections

## AVAILABLE POSITIONS

Institutional page link

<https://www.research.ieo.it/research-and-technology/technological-units/data-science-unit/>