European School of Molecular Medicine

2026 spring call PhD selections

AVAILABLE POSITIONS

Principal Investigator	MARTIN SCHAEFER
Institute of Affiliation	IEO

PROJECT INFO	
Title of the proposed project:	Modelling immunotherapy response in cancer
Short description of the project	This project aims at systematically understanding which molecular factors predict best response to immunotherapy. We will develop machine learning approaches for predicting immunotherapy response by integrating public and in-house multi-omics datasets. The project will leverage large public cohorts to train and benchmark predictive models, which will then be systematically transferred and validated on deeply phenotyped IEO patient cohorts. A central goal is to identify which data modalities (e.g., genomics, transcriptomics, epigenomics, tumor microenvironmental features) contribute most to predictive and prognostic performance, to uncover potential biases in current approaches (such as overreliance on genomic features), and to define robust multi-modal signatures of treatment response. The successful candidate will work at the interface of computational biology, machine learning, and cancer genomics, contributing both to method development and biological insight. The work will be done in close collaboration with computational and clinical researchers.
Main research area for the project	Computational biology
Second research area for the project	
3 key words for the project	Immunotherapy, machine learning, multi-modal biomarkers

LAB INFO	
Main topic/s of the lab	Epigenomics, network biology, machine learning, computational cancer biology
Short description of the lab activity	The lab of Martin Schaefer develops and applies computational methods to study genomic organization and gene regulation in cancer, with a particular focus on epigenetic and copy number alterations. It integrates multi-omics data (e.g., DNA methylation, copy number, transcriptomics) using machine learning, including explainable AI, to identify cancer drivers and disentangle selection from background variation. A central aim is to understand tumor evolution and uncover clinically relevant biomarkers and vulnerabilities. The work bridges network biology and precision oncology, supporting improved interpretation of patient data with the goal of making clinical impact.
Recent bibliography	• Heery R, Schaefer MH. Systematic identification of regions where DNA methylation is correlated with transcription refines regulatory logic in normal and tumour tissues. Nucleic Acids Research. 2025 Oct 14;53(18):gkaf949.

	• Blumenthal DB, Lucchetta M, Kleist L, Fekete SP, List M, Schaefer MH. Emergence of power law distributions in protein-protein interaction networks through study bias. Elife. 2024 Dec 11;13:e99951. • Alfieri F, Caravagna G, Schaefer MH. Cancer genomes tolerate deleterious coding mutations through somatic copy number amplifications of wild-type regions. Nature Communications. 2023 Jun 16;14(1):3594.
Institutional page link	https://www.research.ieo.it/research-and-technology/principal-investigators/martin-schaefer/
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Video link	https://www.youtube.com/watch?v=CZkQmMb1q60