Principal Investigator	**Francesca M Buffa**
Affiliation	IFOM, Milan
Title of the proposed project:	Using AI to build multi-omics clinical classifiers
Short description of the project	This project aims to develop and apply advanced computational methods to build multi-omics classifiers for clinical studies. It stems from a collaboration between Prof. Francesca Buffa and Prof. Salvatore Siena at Niguarda Hospital, who will co-supervise the project. The datasets will integrate transcriptomic and genomic profiles with pathology, imaging and other clinical data, enabling comprehensive multi-modal analysis. A diverse range of machine learning models will be explored, including ensemble methods such as XGBoost, deep learning architectures like variational autoencoders and generative adversarial networks (GANs), and graph neural networks (GNNs) to capture relational structures within and across data types. The goal is to uncover robust predictive features, improve patient stratification, and inform clinical decision-making.
Main research area for the project	Computational Biology
Second research area for the project	
3 key words for project	AI, multi-omics, machine learning
Main topic/s of the lab	Systems Biology, AI, omics, hypoxia, TME
Short description of the lab activity	Our research combines computational and multi-omics techniques to decode how biological networks are rewired in a disease like cancer, where cancer cells evolve and interact within a complex and dynamic microenvironment. We search for gene networks, and associated ‘signatures’, that enable us to understand how normal cells rewire their molecular circuits to become cancer cells, and how they respond to microenvironment characteristics, such as low oxygen levels (hypoxia), or signalling from non-cancer cells. This helps us to understand cancer evolution, heterogeneity, and to predict therapeutic strategies that are most appropriate.
Recent bibliography	Defining hypoxia in cancer: A landmark evaluation of hypoxia gene expression signatures. Di Giovannantonio M et al. Cell Genom. 2025 Feb 12;5(2):100764. doi: 10.1016/j.xgen.2025.100764. Epub 2025 Jan 31. Identification and validation of a machine learning model of complete response to radiation in rectal cancer reveals immune infiltrate and TGFβ as key predictors. Domingo E et al. EBioMedicine. 2024 Aug;106:105228. doi: 10.1016/j.ebiom.2024.105228. Epub 2024 Jul 16. New role of fat-free mass in cancer risk linked with genetic predisposition.

	Harris BHL et al. Sci Rep. 2024 Mar 27;14(1):7270. doi: 10.1038/s41598-024-54291-7. Metabolic symbiosis between oxygenated and hypoxic tumour cells: An agent-based modelling study. Jayathilake PG et al. PLoS Comput Biol. 2024 Mar 15;20(3):e1011944. doi: 10.1371/journal.pcbi.1011944. eCollection 2024 Mar. Single cell RNA-sequencing: A powerful yet still challenging technology to study cellular heterogeneity. Ke M et al. Bioessays. 2022 Nov;44(11):e2200084. doi: 10.1002/bies.202200084. Epub 2022 Sep 6.
Group composition	IFOM group: 2 postdoctoral researchers (1 joint with Bocconi), 1 PhD, 2 researchers predoc (one joint with Boccconi). Bocconi group: 1 assistant professor, 3 postdoctoral researchers (one in Oxford), 1 PhD, 2 predoc researcher assistants, and a variable number of interns/research students/visiting researchers.
Institutional page link	https://www.ifom.eu/en/cancer-research/researchers/francesca-buffa.php
Lab website link	https://www.ifom.eu/en/cancer-research/research-labs/research-lab-buffa.php
Social media links	https://uk.linkedin.com/in/francesca-buffa-578643b