ALMA MATER STUDIORUM
UNIVERSITÀ DI BOLOGNA

DIPARTIMENTO
DI FARMACIA
E BIOTECNOLOGIE

AVVISO DI SEMINARIO

Il giorno **1 Ottobre 2026**
alle ore **14.30**

Dr. Francesco Nicassio

Istituto Italiano di Tecnologia (IIT)
(Ospite: Prof.ssa Anna Maria Porcelli)

terrà un seminario in lingua inglese dal titolo:

Decoding Cancer Plasticity through Single-Cell Multi-Omics and Long-Read Transcriptomics

Area tematica: Cancer Biology

in presenza:
Aula 1 via Belmeloro 6, Bologna

e in streaming:
https://teams.microsoft.com/l/meetup-join/19%3aN09c0NIyEssBnF7ObCyDOQwkgDWm1qdd9f7F2nJV9fw1%40thread.tacv2/1631519544944?context=%7b%22Tid%22%3a%22e99647dc-1b08-454a-bf8c-699181b389ab%22%2c%22Oid%22%3a%225a941351-ef41-4aa4-8771-fa50a6d62ca1%22%7d

L' evento è organizzato nell'ambito del Corso di Dottorato in Biologia Cellulare e Molecolare/Colleghi e studenti sono cordialmente invitati

ABSTRACT

Cancer cells are not fixed entities. Even within a single tumour, individual cells can switch states; some proliferate rapidly, others invade tissue, and some lie dormant, evading therapy entirely. This plasticity is one of the greatest obstacles (unmet need) in cancer treatment, yet how it is regulated at the molecular level remains poorly understood.

We study this problem in triple-negative breast cancer (TNBC), one of the most aggressive subtypes with incomplete charaterization and limited therapeutic options. Using single-cell lineage tracing combined with multi-omics, we previously showed that tumour-initiating potential and drug tolerance are not randomly acquired, but rather they are pre-encoded within rare cell subpopulations that exist before any selective pressure (Nadalin et al., Nat Commun 2024). These pre-adapted clones share a common epigenetic program linked to a hybrid epithelial–mesenchymal state (hEMT), conserved across human tumours.

Here, we dissect the regulatory circuits that establish this plastic state, with a focus on non-coding RNAs and enhancers. By integrating histone-mark profiling, 3D chromatin interaction maps, and RNA–chromatin interaction data, we identify candidate lncRNAs engaged at hEMT-specific regulatory loci. We complement these maps with BRIGHT, a unique transcriptomic atlas of breast cancer based on long-read and native RNA sequencing that resolves previously unannotated isoforms, lncRNAs and enhancer-associated transcripts enriched in aggressive TNBC states. Finally, CRISPR-based functional screening moves from correlation to causation, revealing specific ncRNA and enhancer dependencies linked to plasticity and tumour-initiating potential.

Together, our work builds a new framework for understanding how non-coding regulatory networks drive aggressive cancer behaviour and where they create vulnerabilities that could be therapeutically targeted.

BIOGRAPHICAL SKETCH

After graduating in Biology at the University of Bari, Francesco Nicassio completed his PhD in Life Sciences at the European Institute of Oncology (IEO, Milan). He subsequently carried out postdoctoral and research activities at IFOM and IEO before joining IIT in 2012, where he established his independent research group. Since 2017, he has been coordinating the Center for Genomic Science, overseeing scientific strategy, infrastructure development, and personnel management, and in 2022 he was tenured as Senior Researcher. He is Director of the Center for Genomic Science (CGS) at IIT@SEMM in Milan, where he also leads the Genomic Science research line. He coordinates the RNA Technology Flagship at IIT, a cross-center program integrating RNA biology, RNA technologies, and translational research, and serves as faculty member at the European School of Molecular Medicine (SEMM).

FN scientific background is rooted in genomics and transcriptomics, with a long-standing focus on understanding gene regulation in cancer through the integration of experimental and computational approaches. His laboratory operates as a hybrid experimental–computational environment, integrating genomics, single-cell and multi-omic approaches, long-read sequencing technologies, and CRISPR-based functional genomics to dissect RNA-mediated regulatory mechanisms in physiological and disease-relevant contexts. A key aspect of his work is the development and implementation of advanced omics technologies, including native RNA sequencing and RNA modification profiling, to link regulatory complexity with biological and biomedical applications. In the context of cancer, these approaches are applied both to the development of RNA-based diagnostic strategies and to the dissection of regulatory networks underlying cancer plasticity, drug resistance, and disease progression.

Over the years, FN has made major contributions to RNA biology and cancer genomics. His work has been instrumental in uncovering fundamental mechanisms of microRNA regulation, including the discovery and characterization of Target-Directed microRNA Degradation (TDMD), and in developing circulating microRNA signatures with diagnostic potential in human cancer, implemented in research hospitals. More recently, his research has expanded toward multi-omic and single-cell approaches to study cancer evolution, spanning lineage tracing and integrative genomics, as exemplified by the work on the transcriptional, epigenetic and genetic determinants of cancer progression (Nadalin et al., 2024). In parallel, his laboratory has played an active role in advancing RNA sequencing technologies, particularly long-read and native RNA sequencing using Oxford Nanopore platforms, contributing analytical tools and benchmarking studies (Maestri et al., 2024) for RNA modification detection and transcriptome characterization.

Nicassio's research activity is supported by competitive funding from national and European agencies, including multiple Investigator Grants from the Italian Association for Cancer Research (AIRC), most recently awarded in 2025. He contributes to national and international initiatives on sequencing and genomics, including as a member of the European Genomic Data Infrastructure (GDI) project the Italian mirror group for the B1+Million Genomes initiative, and is actively involved in efforts aimed at defining best practices and standards for advanced sequencing technologies.