



**UNIVERSITÀ
DI TRENTO**

**Dipartimento di
Biologia Cellulare,
Computazionale e Integrata**



Organizers:

**Marta Biagioli
Fulvio Chiacchiera**

Epigenetics Mondays Seminars

Every Monday from May 10th till June 14th

Online seminar, registration required

May 17th @ 2:00PM

Francesco Ferrari, PhD

IFOM, the FIRC Institute of Molecular Oncology

IGM-CNR, Institute of Molecular Genetics -CNR, Pavia

From chromatin 3D organization to transcription regulation

The three-dimensional (3D) organization of chromatin within the cell nucleus is crucial for regulating genome functionality. The knowledge of its role has greatly advanced thanks to the development of novel imaging and molecular biology techniques.

My research group is especially interested in studying the role of chromatin 3D organization in regulating genome functionality in physiological and pathological conditions, with a special focus on cancer. We commonly integrate multiple types of functional genomics data from transcriptomics, epigenomics 3D chromatin organization techniques based on high-throughput sequencing. We leverage omics data to gain mechanistic insights into transcription regulation at different levels.

On a large scale, we investigate mechanisms for the coordinated regulation of large chromatin domains in physiological and disease conditions. These involve, for example, the organization of the genome in distinct structural domains, such as Topologically Associating Domains (TADs), or Lamina Associated Domains (LADs). We investigate their reorganization as well as heterochromatin dynamics in cancer and other diseases. On a finer scale, instead, we study distal regulatory elements (enhancers) and their epigenetic or genetic alterations in cancer and other diseases. In this context, we leverage chromatin 3D organization data to refine the association of distal regulatory elements and their target genes, to characterize the functional role of enhancers in epigenetics and gene expression regulation, within the broader gene regulatory network.

I will discuss recent work from my research group and in particular how the development of specific computational biology solutions has been instrumental to address unanswered biological questions.