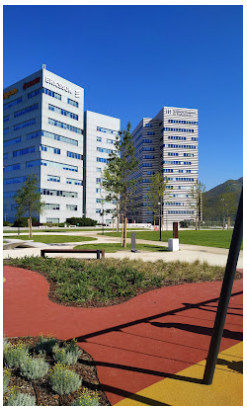
ISTITUTO ITALIANO DI TECNOLOGIA
INTEGRATIVE NUCLEAR ARCHITECTURE

the giovanni ARMENISE HARVARD foundation

Integrative Nuclear Architecture
Istituto Italiano di Tecnologia



Who we are:
The Armenise-Harvard Integrative Nuclear Architecture (INA) research line is located at the Center for Human Technologies (CHT@Erzelli), Istituto Italiano di Tecnologia in Genova. INA's mission is to investigate the 3D genome organisation plasticity and how multiple components of the nucleus influence gene regulation information across scales using imaging and genomics data, and implementing ad-hoc quantitative analysis and modelling tools..

More information at
https://www.iit.it/it/web/integrative-nuclear-architecture
https://www.iit.it/it/cht-erzelli
https://www.iit.it/it/home

What we offer:
We can offer up to 1 or 2 internships (depending on duration).
- ***Support:*** up to 800euro gross monthly.
- ***Requirements:*** statistics and probability, linear algebra, Python programming

Proposed internships:
Topic 1: Chromatin Imaging Data Analysis
This research project is related to the extension and application of our python library Chromatin IMaging Analysis tool (CIMA, unpublished), aimed at automatic processing and analysis of chromatin imaging data. Specifically, the project will focus on point-cloud data as thus obtained with Single-molecule localization microscopy (SMLM) experiments as OligoSTORM *(Nir*,Farabella* et al. PlosGen 2018),* aiming at developing and testing automated methods for the identification and decoding of imaged chromatin loci.
The project will require exploring varied density-based clustering methods (*e.g.,* DSCAN, OPTICS, and HDBSCAN) to enhancing signal detection and mitigating the molecular crowding problem that can occur in nuclear detection, coding the algorithmic implementation, and analysis of both synthetic and real data.

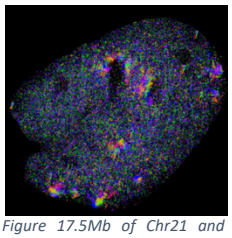


Figure 17.5Mb of Chr21 and 7.5Mb of Chr1 in male fibroblast cell line. Image acquired by Sarah Aufmkolk and Antonios Lioutas at Harvard Medical School.

Topic 2: Computational Genomics
This research project will focus on study statistical preferences of long non-coding RNAs in binding to the genome *(Farabella et al. Nat. Struct. Mol. Biol. 2021; Morf et al. Nat Biotechnol. 2019).* Specifically, the project aims at integrating a plethora of publicly available "omics" experiments as RNAseq with single-cell type deconvolution, Chip-seq of varied epigenetic markers, conformation capture experiments in a common frameworks to create a spatial genomics and transcriptomics dataset that will serve as the starting point to investigate changes in the network of interaction between lncRNAs and the chromatin (lncRNA-chromatin interactome) during neural differentiation, especially focusing on genomic location linked with neurodevelopmental disorders.

Requirements and Further Actions:
If interested, contact irene.farabella@iit.it