



## 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. INA is an active member of the FANTOM6 collaborative project and of the Center of Genome Imaging.

More information at

- <https://ina.iit.it/it/>
- <https://www.iit.it/it/cht-erzelli>
- <https://www.iit.it/it/home>



### What we offer:

We can offer up to 2 or 3 internships (depending on duration).

- **Support:** up to 800euro gross monthly.
- **Requirements:** statistics and probability, linear algebra, Python programming
- **Plus:** Knowledge of version control systems (e.g., GitHub)

### Proposed internships:

#### Topic 1: Chromatin Imaging Data Analysis: detection

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project is related to the extension and application of our python library Chromatin IMaging Analysis tool (CIMA, unpublished), aimed at automatic processing and analysis of chromatin imaging data.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 improving varied density-based (e.g., DSCAN and HDBSCAN) clustering and network-based community identification methods (e.g. Louvain method) that have been tested for signal detection (Piacere et, al. in preparation), coding the algorithmic implementation, and analysis of both synthetic and real data.

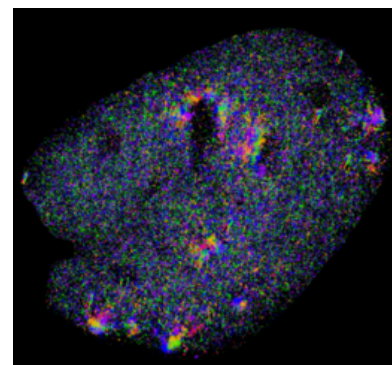
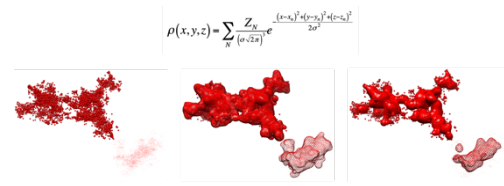


Figure 17.5Mb of Chr21 and 7.5Mb of Chr1 in male fibroblast cell line. Image acquired by Sarah Aufmkolk and Antonios Lioutas at Harvard Medical School.

### Topic 2: Chromatin Imaging Data Analysis: classification

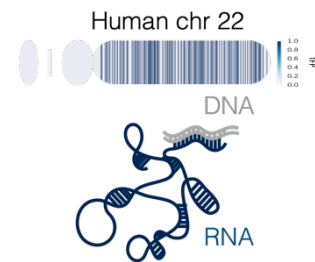
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(SMLM) experiments as OligoSTORM (Nir\*,Farabella\* et al. *PlosGen* 2018), aiming at implementing classification methods of imaged chromatin loci. The project will require the testing of representation methods for 3D points cloud object, testing varied classifiers to define chromatin loci sub-types, and the implementation of 3D alignment strategies for 3D object comparison, coding the algorithmic implementation, and testing it on of both synthetic and real data.



### Topic 3: 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) via triplex-formation. Specifically, the project aims at acquiring a multi-omics view of the lncRNA-chromatin interactome, integrating bioinformatic predictions, RADICL-seq and publicly available conformation capture experiment. The creation of this common framework s 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. The project is part of the FANTOM6 collaborative efforts, a worldwide collaborative project aiming at identifying all functional elements in mammalian genomes.



### **Requirements and Further Actions:**

If interested, contact [irene.farabella@iit.it](mailto:irene.farabella@iit.it)