POSTDOCTORAL POSITIONS IN COMPUTATIONAL BIOLOGY

Francesco Ferrari
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IFOM, Milan, Italy (http://www.ifom.eu)

ABOUT THE POSITIONS

We are looking for postdoctoral researchers with expertise in computational biology to join our computational genomics group at IFOM, Milan, Italy. We are especially looking for outstanding motivated ambitious candidates, with a proven track record of experience and publications in the field of genomics and computational biology, interested in working in an international and competitive research environment.

The successful candidate will work primarily on the analysis of genomics data: namely genome-wide data obtained by high throughput sequencing based techniques, including gene expression (e.g. RNA-seq, single cell RNA-seq), chromatin marks (e.g. ChIP-seq), chromatin 3D architecture (e.g. Hi-C) and whole genome sequencing data. The development of new methods and tools for data analysis is expected to be part of the postdoctoral research activity as well.

English is the working language at IFOM.

REQUIRED SKILLS

- PhD or equivalent degree in Bioinformatics, Statistics, Biophysics, Computer Science, Molecular Biology or other related fields.
- Previous research experience in the field of genomics and computational biology
- Experience in functional genomics data analysis and especially in Next Generation Sequencing data
- Track record of publications in peer-reviewed journals
- Proficiency in scripting environments for statistics and data analysis (preferentially R/Bioconductor, or alternatively Matlab)
- Proficiency in at least one scripting or programming language (PERL, Python or C/C++)
- Excellent communication skills (English is the working language at the institute)

ADDITIONAL DESIRED SKILLS

- Research experience in an interdisciplinary environment
- Previous work experience in an international/multi-cultural environment
- Strong publication track record
- Expertise in statistical methods and algorithms development in the context of biological systems

WHAT WE OFFER

- An international and interdisciplinary research environment
- An internationally competitive salary commensurate with the experience level of the candidates
- Dedicated support for settling in Milan by "IFOM welcome office" for foreign national research scholars

CONTACT DETAILS

To apply send your cover letter, complete CV and contact information for at least two academic references to francesco.ferrari@ifom.eu with '[POSTDOC POSITION]' and your name in the subject line.

ABOUT THE LAB Computational genomics - Francesco Ferrari lab - IFOM, Milan, Italy (http://www.ifom.eu)

We are a computational genomics group especially interested in studying the role of chromatin 3D organization in regulating genome functionality. Our expertise is particularly focused on the use of 3D chromatin architecture data, obtained by Hi-C and other high throughput techniques derived from chromosome conformation capture (3C). We also use functional genomics data, mainly derived from transcriptomics and epigenomics techniques based on next generation sequencing (NGS). We adopt these 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 Topological Associated Domains (TADs), or Lamina Associated Domains (LADs).

On a finer scale, instead, we study distal regulatory elements (enhancers) and their epigenetic or genetic alterations in genetics diseases and cancer. 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.

ONGOING RESEARCH PROJECTS

1. **Altered enhancer-genes regulatory network in cancer.** We are working on the characterization of non-coding mutations in cancer altering the complex regulatory network of genes and their non-coding regulatory elements (promoters and enhancers).
2. **Heterochromatin alterations in aging and diseases.** Together with a collaborator we are working on a novel experimental technique for characterizing chromatin accessibility in different normal and pathological conditions. We are applying it to study heterochromatin structure changes in aging and diseases.
3. **Chromatin architecture data analysis methods.** We are working on novel computational biology methods for the analysis of functional genomics data, in particular for epigenetics marks (ChIP-seq data) and 3D chromatin architecture (Hi-C data).
4. **Single cells resolution definition of transcriptional circuits.** Together with collaborators we are leveraging single cells genomics data to identify transcriptional and epigenetics regulatory modules activated in different processes with heterogenous or rare cell sub-populations. For example characterizing tumor infiltrating immune cells or, in other projects, the circuits governing cell identity and pluripotency.

SELECTED PUBLICATIONS (* co-first authors; § co-last/co-corresponding authors)

1. Pal K, Forcato M§, **Ferrari F§**. Hi-C analysis: from data generation to integration (Review article) *Biophysical Reviews*, 2018 Dec 20 [Epub ahead of print]. doi: 10.1007/s12551-018-0489-1.
2. Forcato M, Nicoletti C, Pal K, Livi CM, **Ferrari F§**, Bicciato S§. Comparison of computational methods for the analysis of Hi-C data. *Nature Methods*, 2017 Jul;14(7):679-685.
3. Puccio S, Grillo G, Liciulli F, Severgnini M, Liuni S, Bicciato S, De Bellis G, **Ferrari F§,** Peano C§. WoPPER: Webserver for Position Related data analysis of gene Expression in Prokaryotes. *Nucleic Acids Res.*, 2017 Apr 29.
4. De Los Angeles A*, **Ferrari F***, Fujiwara Y, Mathieu R, Lee S, Lee S, Tu H, Ross S, Chou S, Nguyen M, Wu Z, Theunissen TW, Powell BE, Imsoonnthornruksa S, Chen J, Borkent M, Krupalnik V, Lujan E, Wernig M, Hanna JH, Hochedlinger K, Pei D, Jaenisch R, Deng H, Orkin SH, Park PJ, Daley GQ. Failure to Replicate the STAP Cell Phenomenon. *Nature*, 2015 Sep 24;525(7570):E6-9.
5. Biagioli M*, **Ferrari F***, Mendenhall EM, Zhang Y, Erdin S, Vijayvargia R, Vallabh SM, Solomos N, Manavalan P, Ragavendran A, Ozsolak F, Lee JM, Talkowski ME, Gusella JF, MacDonald ME, Park PJ, Seong IS. Htt CAG repeat expansion confers pleiotropic gains of mutant huntingtin function in chromatin regulation. *Hum Mol Genet.*, 2015 May 1;24(9):2442-57. Epub 2015 Jan 8.
6. **Ferrari F**, Alekseyenko AA, Park PJ, Kuroda MI. Transcriptional control of a whole chromosome: emerging models for the molecular basis of dosage compensation. (Review article) *Nature Structural and Molecular Biology*, 2014 Feb;21(2):118-25.
7. **Ferrari F***, Plachetka A*, Alekseyenko AA*, Jung YL, Ozsolak F, Kharchenko PV, Park PJ, Kuroda MI. "Jumpstart and gain" model for dosage compensation in Drosophila based on direct sequencing of nascent transcripts. *Cell Reports*, 2013 Nov 14;5(3):629-636.
8. Apostolou E*, **Ferrari F***, Walsh RM, Bar-Nur O, Stadtfeld M, Cheloufi S, Stuart HT, Polo JM, Ohsumi TK, Borowsky ML, Kharchenko PV, Park PJ, Hochedlinger K. Genome-wide interactions of the *Nanog* locus in pluripotency, differentiation and cellular reprogramming. *Cell Stem Cell*, 2013 Jun 6;12(6):699-712.