Position: PhD students in computational biology.

About the positions:

We are looking for 2 PhD students to join our lab at IFOM.
One PhD student will be working on the computational reconstruction and analysis of enhancer-gene regulatory networks altered in cancer. The second PhD student will be recruited together with a collaborator at IFOM and will be working on the characterization of gene modules involved in defining pluripotency and totipotency characteristics of stem cells.

The successful candidates will work primarily on the analysis of functional genomics data: namely genome-wide data obtained from next generation sequencing technologies, including gene expression (e.g. RNA-seq), chromatin marks (e.g. ChIP-seq) and chromatin folding (e.g. Hi-seq) data. The development of new methods and tools for data analysis is expected to be part of the research activity as well.
English is the working language at the institute.

About the lab:

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

We are a computational biology group focused on the study of epigenetics and transcriptional regulation of genome functionality. Our expertise and specific interest is the role of 3D chromatin organization in regulating transcription and epigenetics modifications.
Examples of current ongoing projects include:
1) Altered enhancer-genes regulatory network in cancer. We are working on the identification of non-coding mutations in cancer altering the complex regulatory network of genes and their non-coding regulatory elements (promoters and enhancers).
2) Genomics data analysis methods. We are working on novel algorithms for the analysis of functional genomics data, in particular for epigenetics marks (ChIP-seq data) and 3D chromatin architecture (Hi-C data).
3) Short range chromatin loops. We are working on identifying and characterizing short-range chromatin loops involved in regulating transcription, by using high-resolution genome-wide chromatin architecture data.
4) Experimental techniques for chromatin architecture. Together with a collaborator we are working on the development of a novel experimental technique for characterizing chromatin accessibility in different normal and pathological conditions.
5) Characterizing gene circuits controlling cell identity. Together with collaborators we are working to identify transcriptional and epigenetics regulatory modules involved in cell identity definition, with particular focus on those defining pluripotency and totipotency characteristics of stem cells.

What we offer

- Enrollment in an internationally recognized PhD program in Fundamentals of Cancer Biology (https://www.ifom.eu/en/training/phd-cancer-biology.php)
- International and interdisciplinary research environment
- A competitive fellowship

Required skills:

- Proficiency in scripting environments for statistics and data analysis (preferenatially 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:

- Experience in functional genomics data analysis and especially in Next Generation Sequencing data
- Research experience in an interdisciplinary environment
- Previous work experience in an international/multi-cultural environment
- Previous publications in peer-reviewed journals
- Expertise in statistical methods and algorithms development in the context of biological systems

Contact details:

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

Selected publications:

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

1. 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*, IN PRESS
2. 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 Research 2017*, IN PRESS
3. 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.
4. 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.
5. **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.
6. **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.
7. 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.