EMBL

Location:	**EMBL Rome, Italy**
Category:	**Master internship**
Duration:	**Minimum of 6 months, up to one year**
Closing Date:	**October 15th 2019**
Starting Date:	**Can be arranged with the selected candidate**

The EMBL Epigenetics and Neurobiology Unit in Monterotondo (near Rome, Italy) is seeking a highly motivated student to join the Bioinformatics Services of EMBL Rome and the Boulard group for a Master internship.

Project

Epigenetics define biochemical modifications that are independent of the DNA sequence such as DNA methylation and histone modifications. Methylation of specific histone residues has been shown to influence gene expression. Abnormalities in histone modifications or transcription factor (TF) binding are frequently observed in cancer. Innovative clinical trials targeting writers or erasers of histone modifications are currently under development. However, the gold standard method for epigenomic profiling, namely ChIP-seq, has failed to show differences in chromatin modification upon treatment by these new epi-drugs. Over 30 years ago, the ChIP protocol was introduced and has been widely-used by the community to screen for TFs or histone modifications genome-wide without spike-in controls. Recent developments and enhancements of ChIP-seq with enzyme-tethering and spike-in methods such as DamID, ChEC-seq, or Cut&Run, both at bulk and single-cell level offer investigation of genomic loci at an unprecedent precision. The recent genomic revolution arising from these technologies however still lack solid bioinformatics foundations and benchmarking due to their recent development.

The selected candidate, under the supervision of Nicolas Descostes and Mathieu Boulard, will be in charge of developing methodologies for processing and analyzing Cut&Run and Cut&Tag data. The work will involve benchmarking and analysis of publicly available but also internally produced data sets.

These methodologies will have to be integrated in a pipeline. The candidate will have the opportunity to learn how to perform bioinformatics using one of the most powerful High Performance Computing (HPC) system in Europe but also, according to progression, to be initiated to the use of singularity dockers and conda environment. The work will be performed with Snakemake.

Profile

Background in Bioinformatics, Physics, Mathematics, Computer Sciences or other related disciplines are welcome.

The Candidate should have a solid training in programming (at least two-three courses of 30 hours with equivalent time of coding).

The candidate will have to demonstrate that he or she conducted projects (in Java, C, R, Python or others) within the context of classes at University. Experience in project in R will be a plus.

Knowledge in genome biology would be a key advantage.

Good communication skills in English is compulsory.

Benefit

The selected candidate will be provided a small stipend and accommodation.

Application

CV and motivation letter should be sent to nicolas.descostes@embl.it.