3DAROC16
3C-based data analysis and chromatin reconstruction

October 10th – 14th 2016

Course Description

3C-based methods, such as Hi-C, produce a huge amount of raw data as pairs of DNA reads that are in close spatial proximity in the cell nucleus. Overall, those interaction matrices have been used to study how the genome folds within the nucleus, which is one of the most fascinating problems in modern biology. The rigorous analysis of those paired-reads using computational tools has been essential to fully exploit the experimental technique, and to study how the genome is folded in the space. Currently, there is a clear expansion on the wealth of data on genome structure with the availability of many datasets of Hi-C experiments down to 1Kb resolution (*). In this course, participants will learn to use TADbit, a software designed and developed to manage all the dimensionalties of Hi-C data:

1D - Map paired-end sequences to generate Hi-C interaction matrices
2D - Normalize matrices and identify constitutive domains (TADs, compartments)
3D - Generate populations of structures which satisfy the Hi-C interaction matrices
4D - Compare samples at different time points

Participants can bring specific biological questions and/or their own 3C-based data to analyze during the course. At the end of the course, participants will be familiar with the TADbit software and will be able to fully analyze Hi-C data.

Note: Although the TADbit software is central in this course, alternative software will be discussed for each part of the analysis.

(*) Examples:
http://hic.umassmed.edu/welcome/welcome.php
http://promoter.bx.psu.edu/hi-c/view.php
http://www.aidenlab.org/data.html

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The participation fee will be reduced for three candidates (see the course website http://gtpb.igc.gulbenkian.pt/3DAROC16)