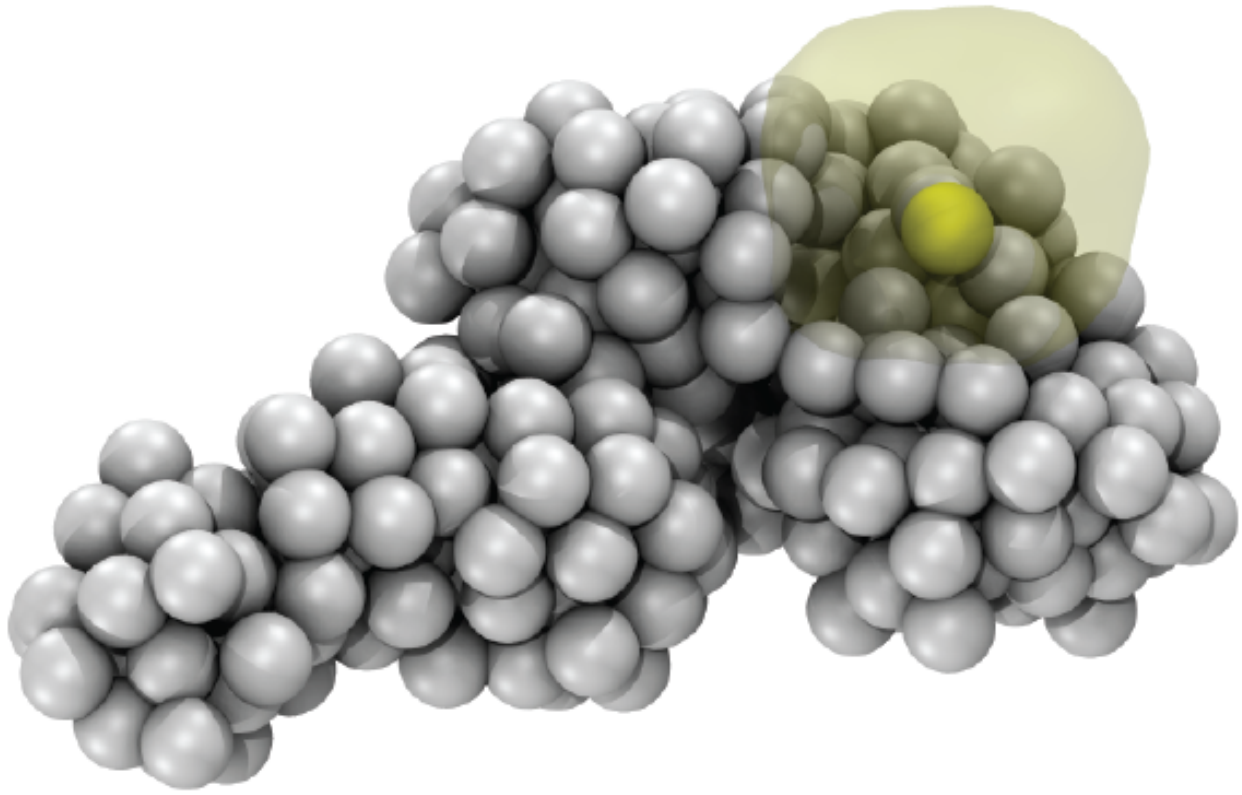
Gulbenkian
Training
Programme in
Bioinformatics

3DAROC22

3C-data Analysis and 3D Chromatin Folding

November 22nd-25th 2022



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 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 (see for example: http://hic.umassmed.edu/welcome/welcome.php or http://www.aidenlab.org/data.html).

In this course, participants will learn to use TADbit, a software designed and developed to manage all dimensionalities of the 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. Although the TADbit software is central in this course, alternative software will be discussed for each part of the analysis.

Course website
http://gtpb.igc.gulbenkian.pt/bicourses/2022/3DAROC22

Instructors

Marc Marti-Renom
Centro Nacional de Análisis Genómico and Center for Genomic Regulation, Barcelona, ES

Marco Di Stefano
Institute of Human Genetics Centre National Recherche Scientifique, University of Montpellier, Montpellier, FR.

David Castillo
Centro Nacional de Análisis Genómico and Center for Genomic Regulation, Barcelona, ES

. . .

GTPB Organiser

Pedro L. Fernandes
Instituto Gulbenkian de Ciência
Oeiras, PT

. . .

Sponsorship

OEIRAS VALLEY PORTUGAL
MUNICÍPIO OEIRAS

BioData.pt elixir PORTUGAL
Co-financiado por: CRESC ALGARVE 2020 Lisb@20 20 PORTUGAL 2020

cost EUROPEAN COOPERATION IN SCIENCE & TECHNOLOGY

GULBENKIAN SCIENCE