



CHROMOSOME STRUCTURE DETERMINATION USING MODELING AND HI-C DATA

<http://gtpb.igc.gulbenkian.pt/bicourses/CSDM15/>

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**The Gulbenkian Training
Program in Bioinformatics**

Gulbenkian Institute, Oeiras.

Teachers from CNAG-CRG:

- François Serra
- Davide Baù
- Marc A. Marti-Renom

The sequence of a genome alone does not carry enough information to fully understand how genomic processes are carried out in the cell nucleus; to achieve this, the knowledge of the three-dimensional (3D) architecture of a genome is necessary. Advances in genomic technologies and the development of new analytical methods, such as 3C-based methods, have allowed getting insights at unprecedented resolution into how the genome is organized. In this course, participants will learn to use TADbit, a software for the analysis and modeling of Hi-C data.

More information about TADbit can be found at <http://www.3DGenomes.org>