THE TADBIT AND TADKIT SOFTWARE FOR MODELING AND ANALYZING 3D GENOMES.

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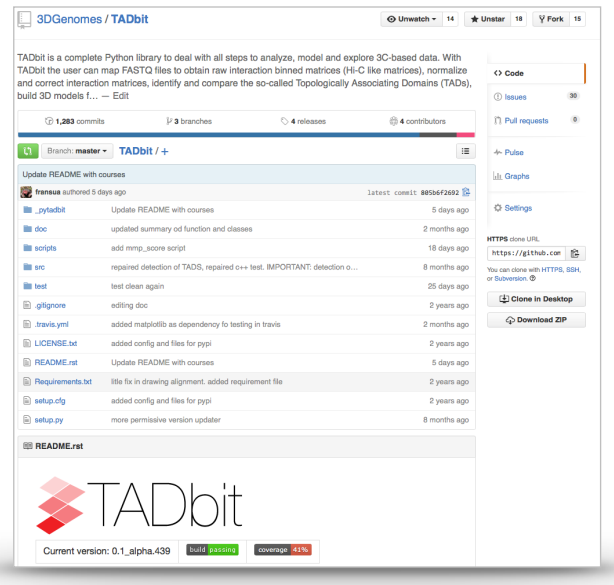
The sequence of a genome alone is insufficient to characterize many genomic processes carried out in the cell nucleus. To achieve this, the knowledge of the three-dimensional architecture of a genome is necessary. Advances in genomic technologies and the development of new analytical methods, such as Chromosome Conformation Capture (3C) and its derivatives, allow now to gain insights into how the genome is organized. We have developed TADbit, a computational pipeline for the three-dimensional analysis and modeling of genomic regions, as well as TADkit a general genome browser with capability to connect 1D (genomic), 2Ds (epigenomic) and 3D (modeling) datasets. TADbit and TADkit are available as open-source code at http://www.3DGenomes.org.

TADbit

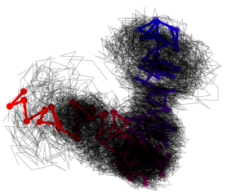
http://3DGenomes.org/tadbit



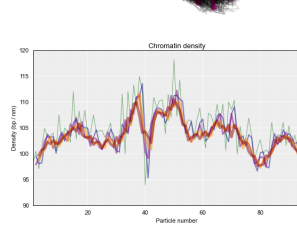
TADkit

http://3DGenomes.org/tadkit

Map analysis



Model building



Model analysis

ANGULARJS by Google

https://github.com/angular/angular.js

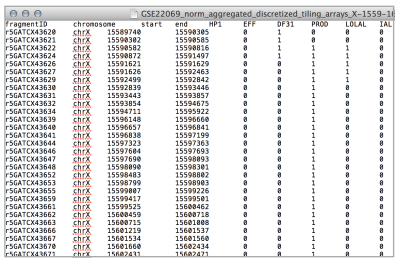
Data-Driven Documents

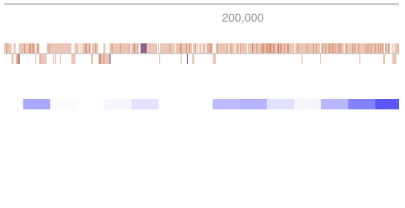
https://github.com/mbostock/d3

THREE.js

https://github.com/mrdoob/three.js

TADbit → THREE.js





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centre nacional d'anàlisi genòmica
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CRG Centre for Genomic Regulation

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erc

HFSP