



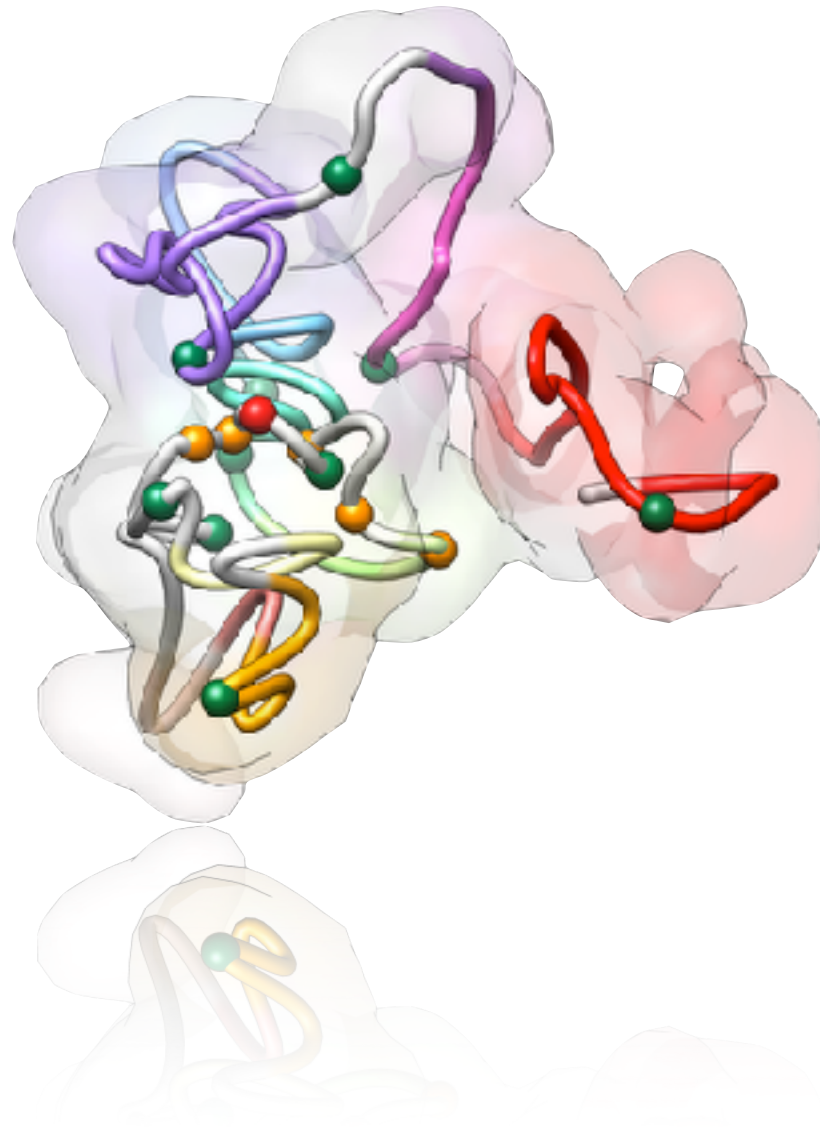
3DAROC18: 3C-based data analysis and 3D reconstruction of chromatin folding

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Structural Genomics Group

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FlexServ

FlexServ: Protein Flexibility Server

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Last most-relevant publications

- Prediction and validation of protein intermediate states from structurally rich ensembles and coarse-grained simulations [Nat Commun](#)
- Long-timescale dynamics of the Drew-Dickerson dodecamer. [Nucleic Acids Res](#)
- BIGNASim: a NoSQL database structure and analysis portal for nucleic acids simulation data. [Nucleic Acids Res](#)

MuG: Multiscale Complex Genomics

<http://www.multiscalegenomics.eu/MuGVRE/>



Multiscale
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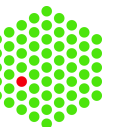
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Course outline

Theory · Examples · Practice

Day 1

Overview to structure determination (Marc)

3D modeling of the genomes and genomic domains (Marc)

Introduction to linux & python (David)

NGS and data handling (David)

Hi-C data (David)

Day 2

Summary Day 1 (François)

Chromatin structure and Hi-C data (Marc)

Integrative modeling applied to chromatin (Marc)

Biological applications (I) (Marc)

Hi-C contact matrices (François)

Day 3

Summary Day 2 (David)

Biological applications (II) (Marc)

Compartment detection and analysis (François)

Topologically Associated Domains (François)

Comparison between experiments (François)

Day 4

Summary Day 3 (François)

Biological applications (III) (Marc)

3D modeling of real Hi-C data with TADbit (David)

3D Analysis and visualization (David)

Final wrap-up (Marc)

Day 5

Summary Day 4 (Marc)

Multiscale Genomics: from genomes to structures (Marc)

Nucleosome positioning & Dynamics (Diana)

Coarse-Grained DNA (Jürgen)

Chromatin Dynamics (Jürgen)