

INSERM workshop
Capturing chromosomes conformation :
Toward a 3D view of genome regulation

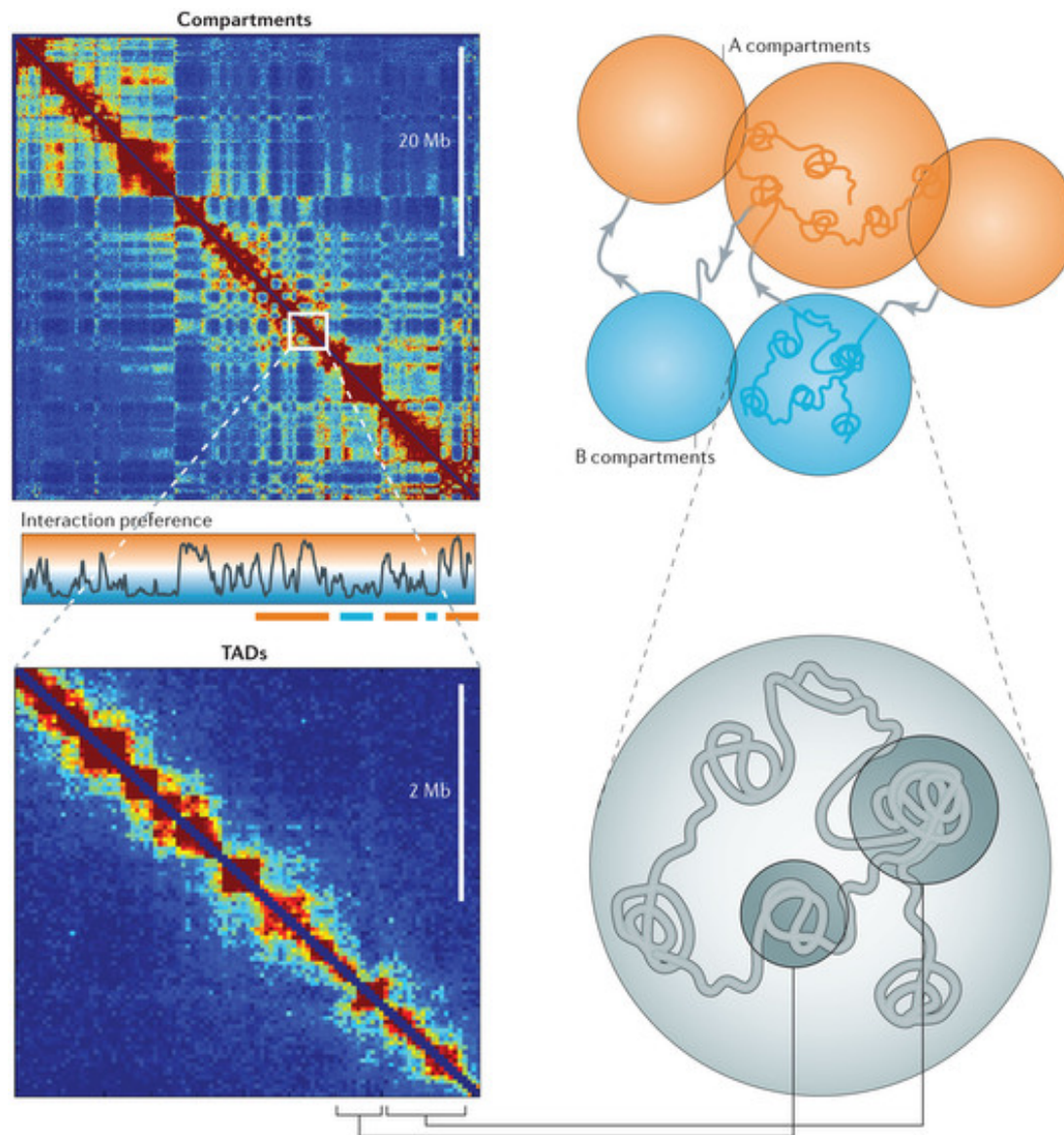
Outline of the presentation

- 1) Download and extraction of data.
Alignment with the software bowtie2.
- 2) Building of contacts maps, visualisation and Normalization.
- 3) Computation of Genomic distance laws.
- 4) Computation of correlation matrices, detection of compartments and TADs.
- 5) Filtering of the different events of a Hi-C/3C library.
Opened questions.

Outline of the Thursday session (9h30 - 12h30)

- 1) Computation of correlation matrices.
Detection of compartments with the eigen vectors decomposition.

- 2) Detection of Topological Associated Domains (TADs) with the Directional Index tool



Nature Reviews | **Genetics**

Exploring the three-dimensional organization of genomes: interpreting chromatin interaction data

Job Dekker Marc A. Marti-Renom Leonid A. Mirny

Nature Reviews Genetics 14,390–403 (2013) doi:10.1038/nrg3454

Computation of correlation matrice:

- Computation of matrices of expected values taking into account the effect of Genomic distance laws.

→ *The idea behind :*

to remove the effect of polymer behavior and detect more specific behaviors

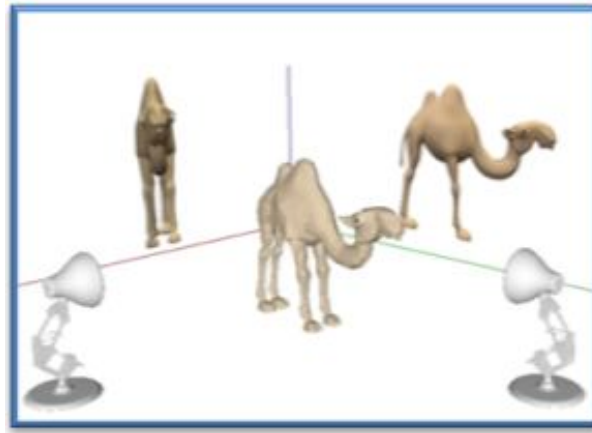
- Computation of correlation matrice :

→ *The idea behind :*

compute the Pearson coefficient between each line and column.

It will give the information of which vectors have the same patterns of contacts and thus supposed to be in close proximity.

Eigen vectors decomposition:



The idea behind :

We project a mathematical object in a lower dimension space and keep a certain content of the information initially present.

In our case : we will project the matrice on different axes (eigen vectors).

It was shown that the first eigen vector contains the information about the compartment partition of the genome.

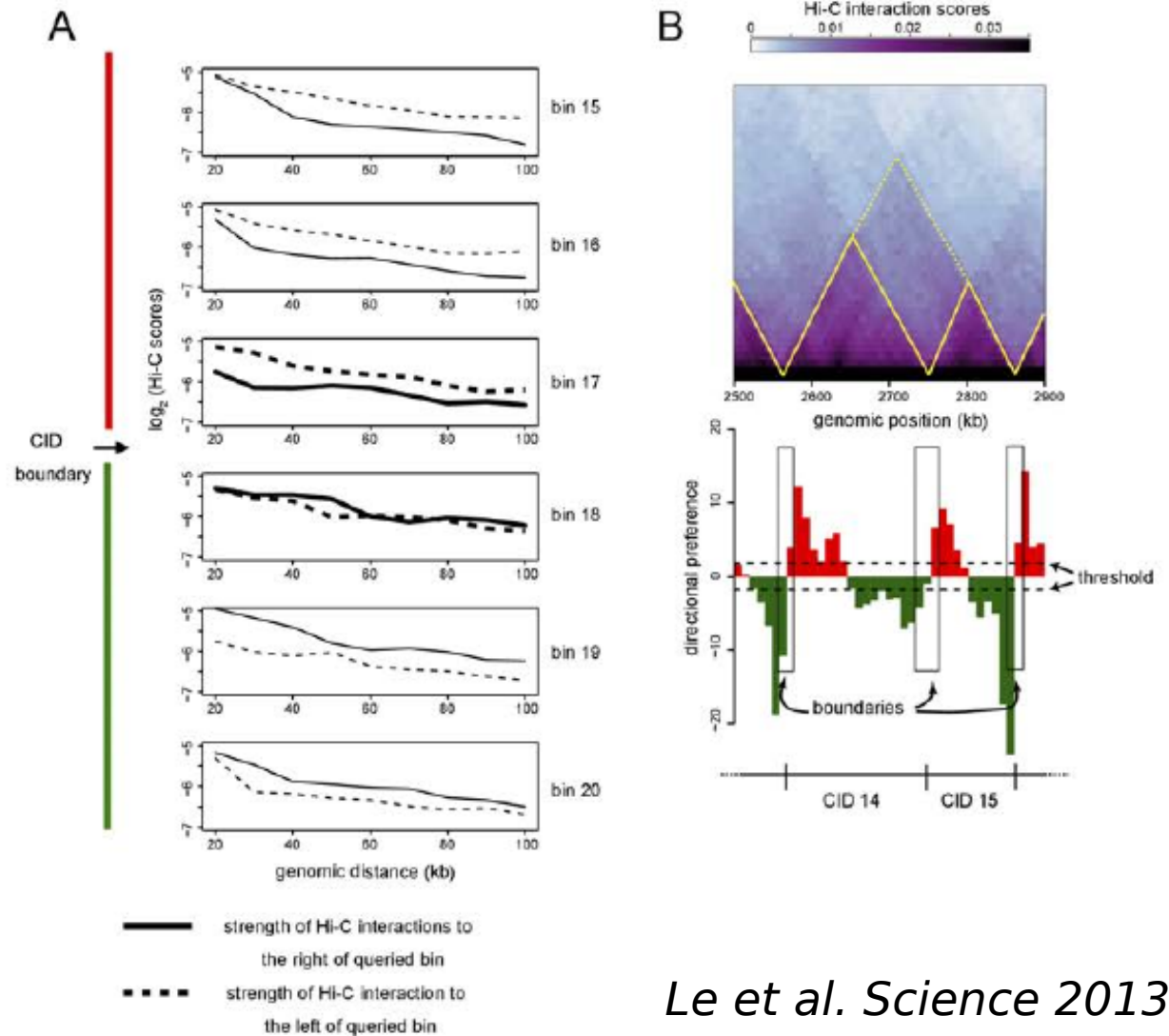
Exercise / practical part:

Plot the first eigen vector for the chromosome of your choice.

Can we observe compartments change between different cell types ?

2) Detection of Topological Associated Domains (TADs) with the Direction Index tool

Directional Index tool :



Le et al. Science 2013.

The idea behind :

A paired t-test method is applied between right and left vectors to detect change in direction of contacts at certain bins of the contacts map.

Exercise / practical part:

Plot the Directional Index for the chromosome of your choice.

Can we observe TADs change between different cell types ?