



CONSORTIUM  
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### Coordination

**Sylvain Foissac**  
UMR GenPhySE  
sylvain.foissac@inrae.fr

### Key words

Spatial genomics  
Hi-C  
Chromosome conformation  
Chromatin structure

### INRAE units involved

[GenPhySE](#)  
[GABI](#)  
[Get-PlaGE](#)  
[MIAT](#)  
[IPS2](#)

### Partnerships

CNRS  
INSERM  
Centro de Regulación Genómica  
(CRG), Barcelone

## An interdisciplinary network for 3D genomics

Within cell nuclei, the genome's three-dimensional structure strongly impacts the way it functions. Improving our understanding of the links between the 3D structure of the genome and its functioning is methodologically challenging and calls for dialogue between different disciplines.

### Context and challenges

Inside the nuclei of animal or plant cells, the three-dimensional structure of the genome strongly impacts its functioning, affecting key processes such as cell differentiation and embryonic development and the organism's survival. We know that the 3D structures that regulate these processes are organised hierarchically at various scales. However, little is known about the multi-scale dynamics of these structures and their interactions, and this limits our understanding of the links between genome structure and function.

Recent advances in molecular biology have made it possible to change the way in which the spatial organisation of chromosomes is studied, thanks to Hi-C (High-throughput chromosome conformation capture) DNA sequencing technology.

However, the data generated by this technology is difficult to analyse, largely because of its particular matrix format which is generated from the distances between genome loci. As a result, the identification of significant differences between sets of large matrices, for example, constitutes a considerable methodological challenge.



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## Goals

CHROCONET (CHROmatin CONformation NETwork) will bring together an interdisciplinary community and stimulate scientific discussion on the comparative analysis of 3D genomics data.

The nature of the project and the issues at stake call for collaboration between different fields. The consortium therefore includes members from several complementary disciplines:

- cell biology and molecular genetics for data production and interpretation of results;
- mathematics and statistics for the development of methodologies relating, in particular, to the modelling and statistical validity of planned tests;
- bioinformatics for the processing of sequencing data, software implementation and organisation of data, metadata and results.

Building on this original collaboration, the CHROCONET consortium aims to improve Hi-C data analysis methods to achieve a better understanding of the links between the 3D structure of the genome and its functioning.

## Research units involved and partnerships

INRAE scientific division	INRAE research units	Expertises
<b><u>Animal Genetics</u></b>	<u>GenPhySE</u>	Bioinformatics, animal genomics, cell biology
	<u>GABI</u>	Cellular biology, molecular biology
	<u>Get-PlaGE</u>	Molecular biology, biotechnology
<b><u>Mathematics and Digital Technologies</u></b>	<u>MIAT</u>	Statistics, biostatistics, mathematics, computer science, machine learning
<b><u>Plant Biology and Breeding</u></b>	<u>IPS2</u>	Cell biology, plant genomics
External partners		Expertises
CNRS		Statistics, biostatistics, bioinformatics
INSERM		Bioinformatics
Centro de Regulación Genómica (CRG), Barcelona		Molecular and cellular biology

