

Master project 2020-2021

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Project

Computational genomics

Project Title:

Role of macroH2A histone variant in three-dimensional genomics context

Keywords:

Chromatin, macroH2A, HiC, Histone, R, NGS

Summary:

Chromosome conformation capture (C-)techniques allow to assess the nuclear architecture and distribution of chromatin in unprecedented level and have boosted the growth of nuclear organization field during the recent years (1). A large number of different variants of C-techniques including Hi-C and , Hi-ChIP have become routine in basic research, this has led to the creation of a massive amount of data stored in different public databases. Our laboratory has particular interest for years in the study of a particular histone variant called macroH2A (2). Histone variants replace canonical histones in a sub-fraction of the core structural units of chromatin, the nucleosomes. Recently, we demonstrated surprising impact of macroH2A on nuclear organization and heterochromatin architecture (3). The proposal of this master project is to investigate the role of macroH2A and other heterochromatin regulators, through the integration of the data created by our laboratory (Hi-C, HiChIP, ChipSeq, RNAseq) with those present in public databases. Specifically, we will address the following questions: 1. To evaluate association of macroH2A with respect to self-interacting genomic regions such as topological associated domains (TADs) and genome compartments. 2. To modify a framework of our previously created tool (regioner (4)) to allow its application in a three-dimensional genomics context. 3. To create, pipelines and bioinformatics tools to query and visualize such a complex mass of data. Technically we will mainly use resources in R (Bioconductor) and Python, in Linux environment. High Performance Computer calculation will be carried out at CSUC (www.csuc.cat).

References:

1 - Grob S., Cavalli G. (2018) Technical Review: A Hitchhiker's Guide to Chromosome Conformation Capture. In: Bemer M., Baroux C. (eds) Plant Chromatin Dynamics. Methods in Molecular Biology, vol 1675. Humana Press, New York, NY. 2 - Post-Translational Modifications of H2A Histone Variants and Their Role in Cancer. Corujo D, Buschbeck M. Cancers (Basel). 2018 Feb 27;10(3). 3 - MacroH2A histone variants maintain nuclear organization and heterochromatin architecture. Douet J, Corujo D, Malinverni R, Renaud J, Sansoni V, Posavec Marjanović M, Cantariño N, Valero V, Mongelard F, Bouvet P, Imhof A, Thiry M, Buschbeck M. J Cell Sci. 2017 May . 4 - regioneR: an R/Bioconductor package for the association analysis of genomic regions based on permutation tests. Gel B, Díez-Villanueva A, Serra E, Buschbeck M, Peinado MA, Malinverni R. Bioinformatics. 2016 Jan 15.

Expected skills::

Experience in programming languages (preferably R). Basic knowledge of NGS data and Linux operating system. Enthusiasm to answer biological questions.

Possibility of funding::

To be discussed

Possible continuity with PhD: :

To be discussed

Comments:

This project will be co-supervised by Roberto Malinverni and Marcus Buschbeck
