Epigenome marks interaction defines chromatin compartments

Elena Stavrovskaya, A.V. Favorov

Moscow State University, Leninskie gory 1-73, Moscow, 119992, Russia , stavrovskaya@gmail.com

Andrey A. Mironov

Institute for Information Transmission Problems , Bolshoy Karetny per. 19, Moscow, 127994, Russia mironov@bioinf.fbb.msu.ru

Vavilov Institute of Genral Genetics RAS , Gubkina str. 3, Moscow, 119333, Russia favorov@gmail.com

State Scientific Center Genetika , 1-st Dorozhniy pr., 1, Moscow, 117545, Russia

State Johns Hopkins University School of Medicine , 550 N Broadway ste 1103 Baltimore, MD 21205 USA

Study of 3D chromatin structure is important for the understanding of genome regulation and functioning. Experimental techniques like Hi-C give comprehensive information about chromosomal contacts, but they require high sequencing coverage and thus are expensive and not suitable for mass analysis. That makes development of computational methods for chromatin structure investigation a challenging problem.

The further analysis of Hi-C data revealed structural chromatin domains, which can be classified into two [1, 2] or even more [3] genome compartments, having different structural and functional characteristics. It is shown, that these compartments differ in epigenome landscape [3]. It allows using epigenomic data for chromatin structure prediction.

The epigenome landscape is determined by an interaction of epigenomic modifications. In this work, we use correlation as a measure of this interaction. We apply algorithm StereoGene, that allows fast calculation of correlation between two epigenome features along the genome. This method allows excluding the influence of a confounder. In addition, when analyzing a collection of tracks for the same tissue, the common confounder can be estimated computationally as the first principal component of the tracks.

We proved that the physical 3D structure of chromatin represented by the compartment annotation defines some local correlations between the epigenomic tracks. Thus, the compartment annotations can be defined from the epigenomic interaction landscape.

1. E.Lieberman-Aiden et al. (2009) Comprehensive mapping of long range interactions reveals folding principles of the human genome, *Science*, **326(5950):** 289–293**.**

2. J.P. Fortin and K.D. Hansen (2015) Reconstructing A/B compartments as revealed by Hi-C using long-range correlations in epigenetic data, *Genome Biology*, **16:**180.

3. S.S.P. Rao et al. (2014) A 3D Map of the Human Genome at Kilobase Resolution Reveals Principles of Chromatin Looping, *Cell*, **159:**1665–1680.