

Chromatin structure from high resolution microscopy: scaling laws and micro-phase separation

Recent advances in experimental fluorescence microscopy allow high accuracy determination (resolution of 50nm) of the 3D physical location of multiple (up to 10^2) tagged regions of the chromosome. We investigate publicly available microscopy data for two loci of the human genome obtained from multiplexed FISH methods for different cell lines and treatments. Inspired by polymer physics models, our analysis centers around distance distributions between different tags, aiming to unravel the chromatin conformational arrangements. We show that for any specific genomic site, there are (at least) two different conformational arrangements of chromatin, implying coexisting distinct topologies which we refer to as phase “ α ” and phase “ β ”. These two phases show different scaling behaviors: the former is consistent with a crumpled globule while the latter indicates a confined, but more extended conformation, as a looped domain. The identification of these distinct phases sheds light on the coexistence of multiple chromatin topologies and provides insights into the effects of cellular context and/or treatments on chromatin structure.

Auteur principal: M. REMINI, Loucif (L2C)

Co-auteurs: Prof. PARMEGGIANI, Andrea (L2C); Prof. CARLON, Enrico (KU Leuven); Dr WALTER, Jean-Charles (L2C); Dr PALMERI, John (L2C); M. SEGERS, Midas (KU Leuven)

Orateur: M. REMINI, Loucif (L2C)