Journal Club Abstract Research Center for Mathematics on Chromatin Live Dynamics (RcMcD)

Three-dimensional chromatin structure generated by the IMP combined with 5C data Soya Shinkai

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Abstract:

3C-based assays have revealed three-dimensional organization of chromosomes. With 5C data of a 500-kb region on human chromosome 16, containing the α -globin locus, Baù *et al* focused on a computational generation of the three-dimensional folding of the chromatin domain. The α -globin gene is expressed in K562 cells and silenced in lymphoblastoid cells. The computational chromatin models can reproduce the known looping interactions between the α -globin genes and their distal regulatory elements.

Their work is the first one to uncover a three-dimensional folding as a result of genome interactions with 5C and a computational method at a megabase scale.

References:

1. Baù D, Sanyal A, Lajoie BR, Capriotti E, Byron M, Lawrence JB, Dekker J, Marti-Renom MA. The three-dimensional folding of the α -globin gene domain reveals formation of chromatin globules. Nat Struct Mol Biol. 2011 Jan;18(1):107-114.