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ABSTRACT

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Short talk: "The Role of PolyComb and RNA Polymerase 2 in Promoter-Centred 3D Chromatin Contact Networks"

Despite the increasing number of studies mapping 3D chromatin interaction networks, there are surprisingly few network analyses performed on these datasets. In current approaches the network topology is rarely considered, safe for the identification and characterization of highly connected chromatin fragments. Assortativity is a property that is widely used in social networks to detect whether nodes with similar features tend to be connected. We propose to use assortativity to combine the epigenetic landscape in a specific cell type or sample with the chromatin interaction network mapped by any sequence based method. To illustrate our method, we analyse two chromatin interaction datasets for mouse embryonic stem cells, which were generated with two different very recent promoter capture HiC methods (PCHiC and HiCap) which produce chromatin interaction networks that are strongly enriched for interactions containing at least one promoter. These datasets define networks of interactions amongst promoters and between promoters and other genomic loci, presumably distal regulatory elements. We calculate the presence of a MeDIP and ChIP-seq collection of 79 chromatin features (including 3 cytosine modifications, 13 histone marks and chromatin-related proteins) in the chromatin fragments that constitute the nodes of the network. We find PolyComb Group proteins and associated histone marks to be the most important factors in both datasets. Remarkably, we observe higher assortativity of actively elongating forms of RNA Polymerase 2 compared to the inactive forms of polymerase in promoter-other end interactions only, suggesting an important role for active elongation in promoter-enhancer contacts.

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