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# Higher-order interactions in human chromosomes: finding topologically associated domains via network community detection

In this post-genome sequence era, the investigation of the genomic interactions on top of the identified sequence is of great importance. There exist nontrivial structural properties in the interactions, despite the fact that the sequence itself is a topologically simple one-dimensional structure. In particular, topologically associated domains (TADs), representing the group or modular structures, are crucial substructures of chromosome interactions. As the weighted network structures effectively capture the genomic interactions, the identification of TADs naturally corresponds to finding the modular or community structures in the genomic interaction network. In this work, we suggest a systematic way to identify TADs using network community identification algorithms. As a concrete example, we take a representative genomic interaction data called the Hi-C map and apply algorithms for network community detection, in particular, with the tunable resolutions parameter that enables us to find TADs with various resolutions. For validity of our method, we compare several known biological markers for the TAD boundary, such as the enrichment of transcriptional repressor CTCF, with our systematically identified TADs

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