Identifying chromosome domains at multiple scales and their hierarchy

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The spatial organization of the genome has a fundamental implication on the life of the cell. With the advent of chromosome conformation capture technique and genome sequencing, the problem of identifying domain structures from the pairwise interactions in the genome has received much attention over the past decade. However, existing methods rely on differently prepared data and algorithms to find domains at specific scales. Here we develop a unified method for finding the domain solutions at multiple scales. The scale of the domains is tuned by a single parameter, which controls the model's prior preference to a less fragmented domain solution. We find a family of domain solutions at varying scales, revealing an interesting structure of hierarchy between the domains at small and large scales. We successfully validate the domain solutions by comparing to appropriate bio-markers, and furthermore show that our method work as well as each of the previous methods at the corresponding scale.