# A new algorithm for finding network motifs

**Abstract**

Complex networks are studied across many fields of science and are particularly important to unders tand biological processes. Motifs in networks are small connected sub-graphs that occur significantly in higher frequencies than in random networks. They have recently gathered much attention as a use ful concept to uncover structural design principles of complex networks. Existing algorithms for findi ng network motifs are extremely costly in CPU time and memory consumption and have practically r estrictions on the size of motifs.
We present a new algorithm (Kavosh), for finding k-size network motifs with less memory and CPU ti me in comparison to other existing algorithms. Our algorithm is based on counting all k-size sub-grap hs of a given graph (directed or undirected). We evaluated our algorithm on biological networks of E. coli and S.
cereviciae, and also on non-biological networks: a social and an electronic network.
The efficiency of our algorithm is demonstrated by comparing the obtained results with three well-k nown motif finding tools. For comparison, the CPU time, memory usage and the similarities of obtain ed motifs are considered. Besides, Kavosh can be employed for finding motifs of size greater than eig ht, while most of the other algorithms have restriction on motifs with size greater than eight.