

Supplementary Figures

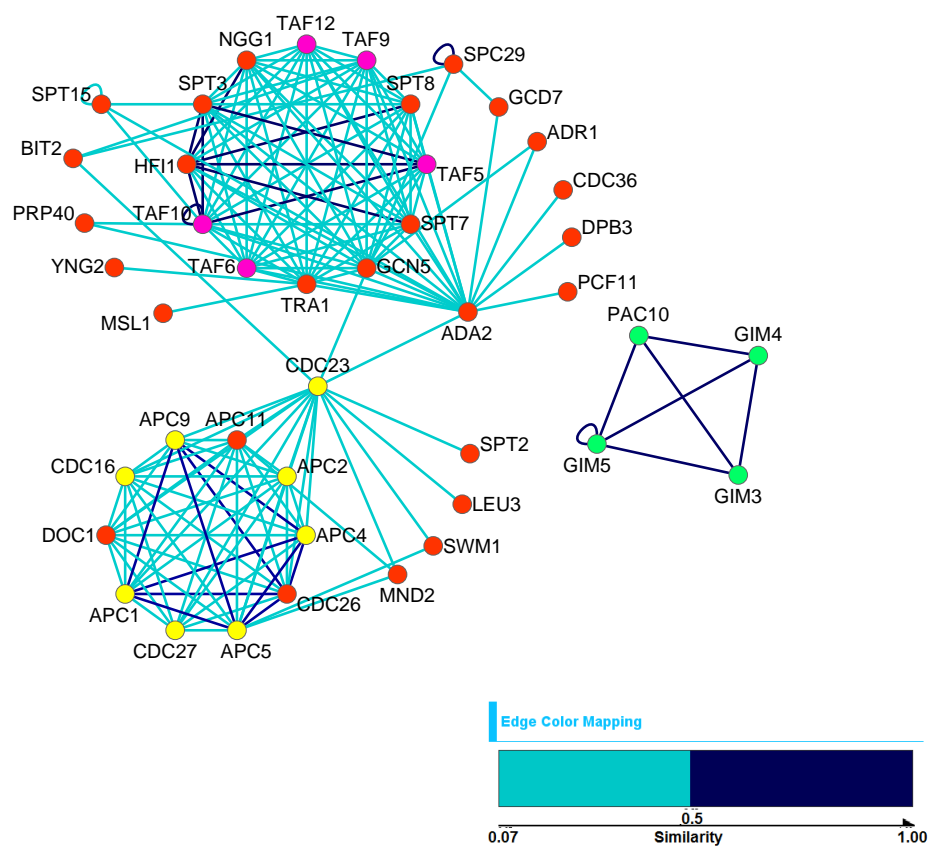


Figure 1: Figure of a cluster predicted by PROCOMOSS using Lin semantic similarity measure with molecular function annotation. Yellow colored nodes represent proteins Apc1, Apc2, Apc4, Apc5, Apc9, Cdc16, Cdc23, Cdc27 that are component of Anaphase-promoting complex, cyclosome, pink colored nodes represent some portion of TFIID complex, green nodes represents protein GIM2, GIM3, GIM4, and PAC10 which constitute the Gim protein complex. Edges has two colors, here violet colored edge signifies semantic similarity between two proteins connected with that edge is higher than 0.500 whereas the proteins connected with blue colored edge have similarity less than 0.500.

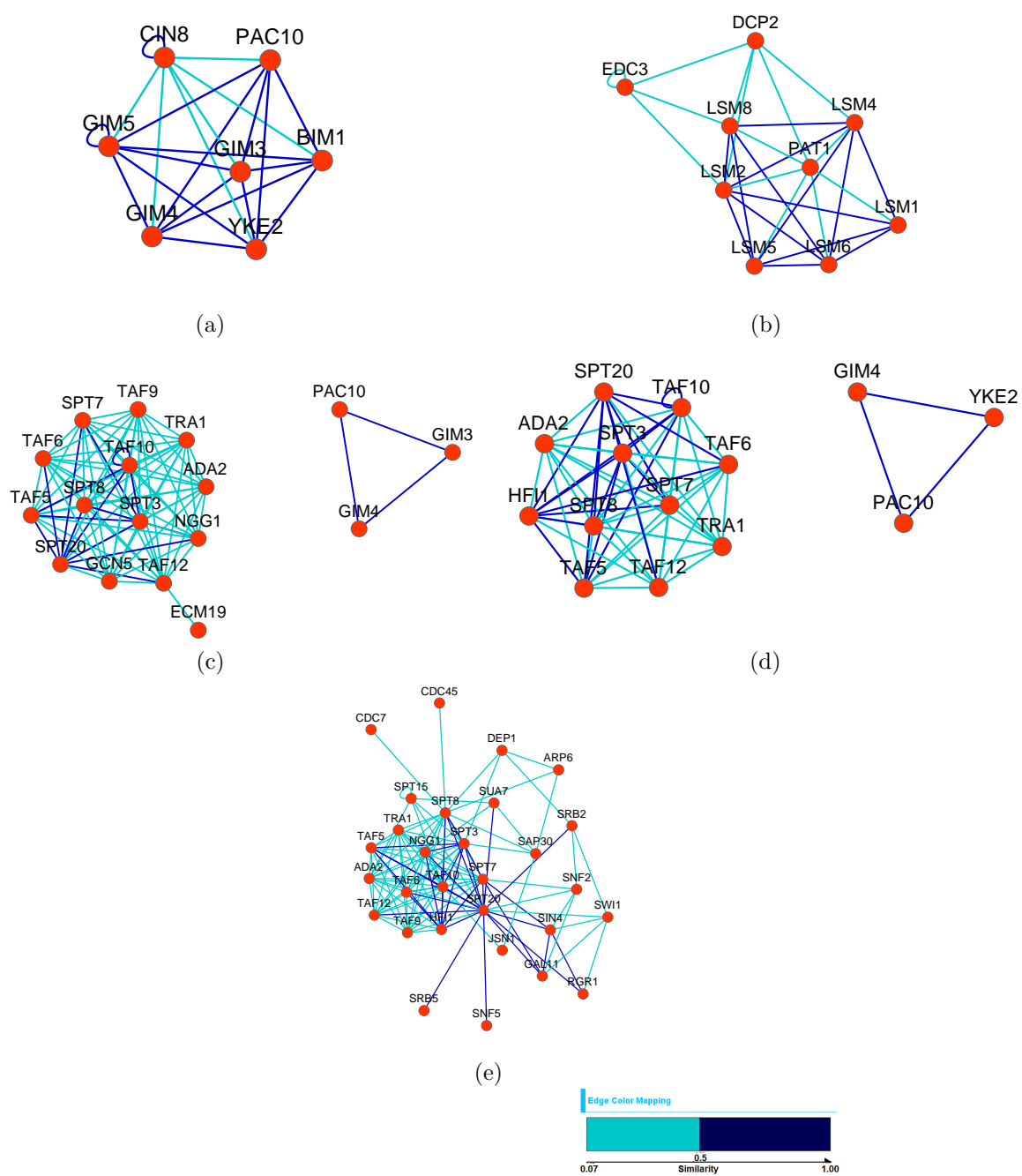


Figure 2: Figure of some clusters identified by PROCOMOSS using Lin semantic similarity measure in MIPS dataset

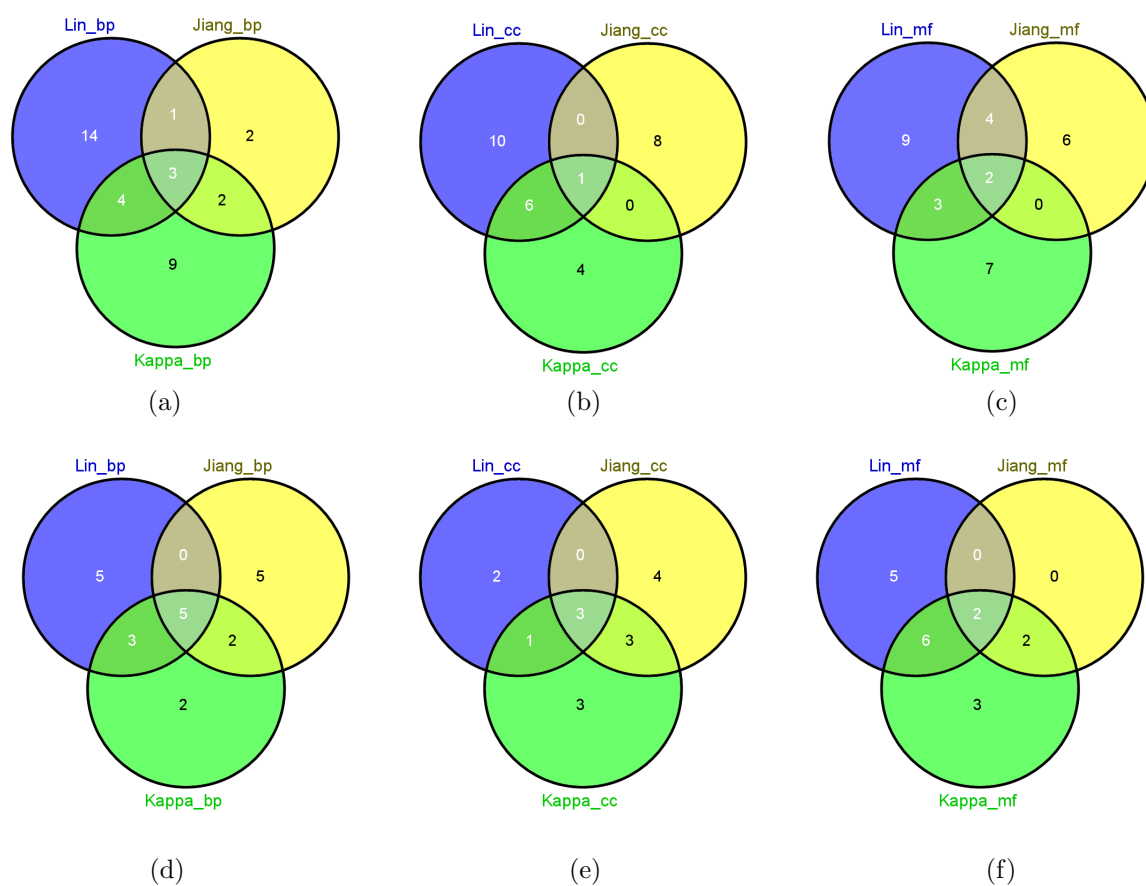


Figure 3: Venn diagram of predicted complexes which has greater than 60 percent of common proteins in some of the resulting cluster. Complexes are identified by PROCOMOSS using Lin, jiang, and kappa measures in DIP and MIPS dataset. Figure (a) represents Venn diagram of complexes predicted by Lin, Jiang and Kappa measures using biological process annotation. (b) and (c) describes the same using cellular component and molecular function respectively. Similarly (d), (e) and (f) represent the same in MIPS dataset.