

Supplementary Materials to Biomarker discovery from high-throughput data by connected network-constrained support vector machine (Figure S2)

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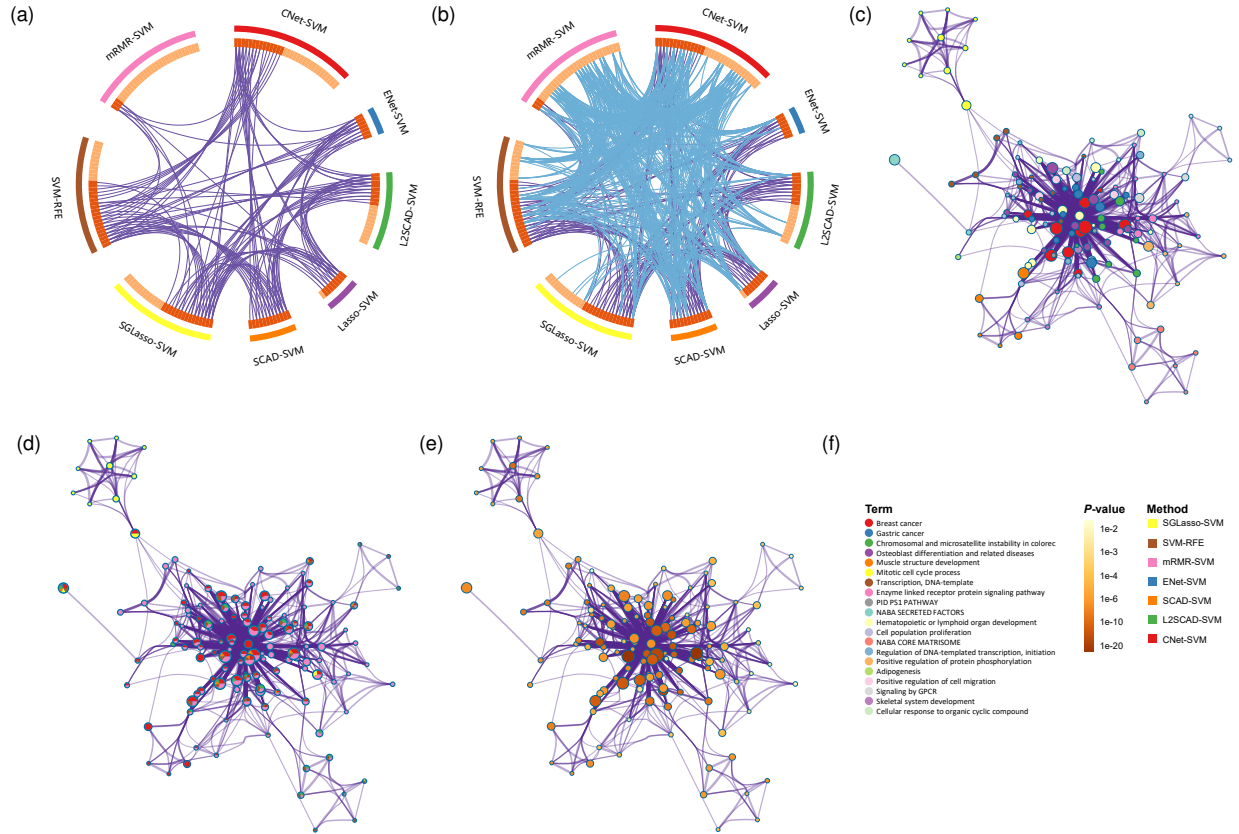


Figure 1: The functional enrichment analysis of biomarkers respectively identified by seven methods. (a) The same genes shared by multiple gene subsets are linked by purple lines. (b) The different genes where they fall into the same ontology term are linked by blue links. (c) The enriched ontology clusters are colored by cluster labels. (d) The same enrichment network, with nodes colored by P -value. (e) The same enrichment network, with nodes displayed as pies. (f) The legends for (c), (d) and (e).

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