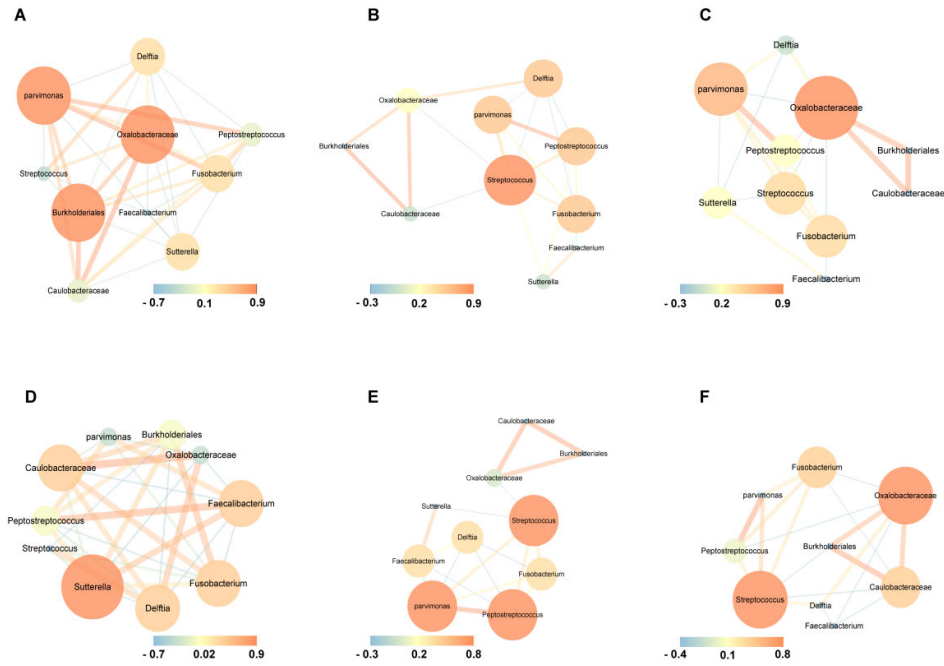


**Scheme 1.** Abundance change analysis of CRC stage-specific biomarkers. A: CRC stage I; B: CRC stage II; C: CRC stage III. Abundance change differences were compared using one-way ANOVA with Kruskal–Wallis test, \*,  $p < 0.05$ ; \*\*,  $p < 0.01$ ; \*\*\*,  $p < 0.001$ .





**Scheme 3.** Co-occurrence and co-excluding interaction networks of CRC stage-specific markers showing profiles of microbiome in adjacent-tumor site and off-tumor site during CRC progression. (A). Co-occurrence and co-excluding interaction networks in adjacent-tumor site at CRC stage I. (B). Co-occurrence and co-excluding interaction networks in adjacent-tumor site at CRC stage II. (C). Co-occurrence and co-excluding interaction networks in adjacent-tumor site at CRC stage III. (D). Co-occurrence and co-excluding interaction networks in off-tumor site at CRC stage I. (E). Co-occurrence and co-excluding interaction networks in off-tumor site at CRC stage II. (F). Co-occurrence and co-excluding interaction networks in off-tumor site at CRC stage III. Bacteria pairs with Spearman rank correlation  $> 0.2$  or  $< -0.2$  are represented in the network. Edges represent co-occurrence or co-excluding interaction relationships between bacteria pairs. Cytoscape v3.7.2 was used for co-occurrence and co-excluding interaction network construction. The size of the nodes corresponds to edge degree.