Gene Ontology (GO) analysis

1. Input a group of Gene IDs or promoter sequences
   All Inputs: ID1, ID2, ID3, ID4, ID5
   GO1: ID1, ID2, ID5
   GO2: ID1, ID2, ID5
   GO3: ID1, ID2
   Calculating how many GOs were related to the input gene group, and each GO probability could be shown. (sequence input format would skip this step)

Selecting all input Gene IDs or genes involved in interesting GO for further analysis.

Promoter extraction

3. TSS(+1)
   -2500 to +500 (the range could be defined by users) is extracted as promoter sequence.
   (sequence input format would skip this step)

Using transcription factor binding profiles from PLACE, TRANSFAC public release 7.0, AGRIS, and JASPER for TFBSs scanning.

TF binding sites detection

4. MATCH
   - TRANSFAC, PLACE, AGRIS, JASPER
   - TFBS
   - TFBS
   - TFBS
   - TFBS
   - TFBS
   - TFBS

Co-occurrence of TFBSs recognition

5. Recognizing a TFBS that co-occur in a group of gene promoters.

Combinatorial TFBSs identification

6. The threshold of combinatorial support and confidence should be set. Additionally, users could consider distance between combinatorial transcription factors to filter less significant results.

Distance constraint

7. With distance constraint
   - TFBS1
   - TFBS2
   - TFBS2
   - 40 bp
   - 20 bp
   - 700 bp
   - 40 bp