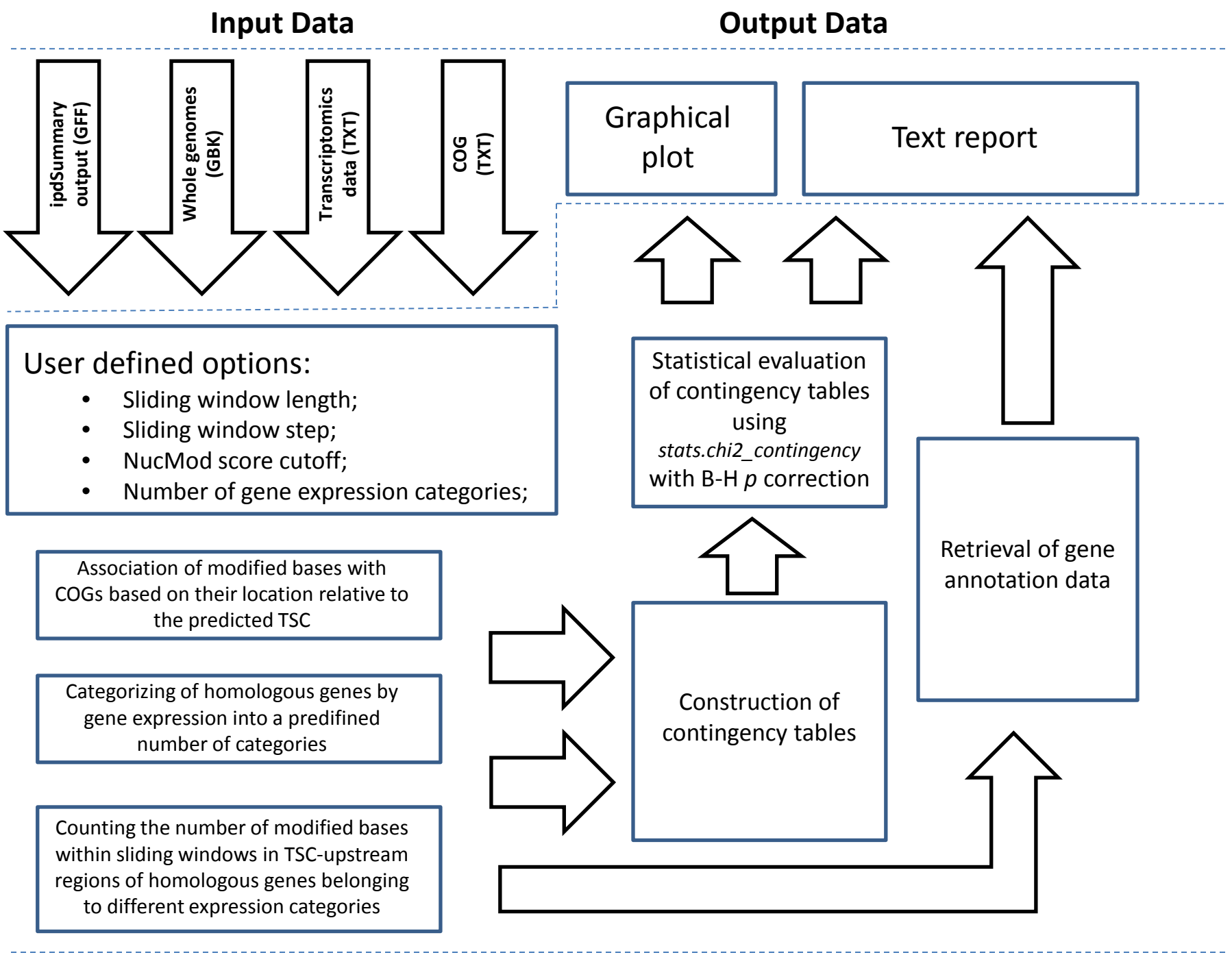
Input Data
Output Data
ipdSummary output (GFF)
Whole genomes (GBK)
Transcriptomics data (TXT)
COG (TXT)
Graphical plot
Text report
User defined options:
Sliding window length;
Sliding window step;
NucMod score cutoff;
Number of gene expression categories;
Statistical evaluation of contingency tables using stats.chi2_contingency with B-H p correction
Retrieval of gene annotation data
Association of modified bases with COGs based on their location relative to the predicted TSC
Categorizing of homologous genes by gene expression into a predifined number of categories
Counting the number of modified bases within sliding windows in TSC-upstream regions of homologous genes belonging to different expression categories
Construction of contingency tables