Report on Ontology Enrichment Analysis App

The Gene Ontology Enrichment Analysis Shiny app is designed to perform enrichment analysis for a predefined set of genes associated with cancer. Users can either utilize a predefined list of genes or input their own gene lists. The app provides insights into the biological significance of these genes through Gene Ontology (GO) enrichment analysis, focusing on three categories:

1. **Biological Process (BP)**
2. **Cellular Component (CC)**
3. **Molecular Function (MF)**

The results are visualized as bar plots, highlighting the top 10 enriched GO terms based on user-selected categories.

Methods Used

1. **Data Preparation:**
    - The app begins by defining a list of genes known to be upregulated in cancer. These genes are represented by their symbols (e.g., TP53, BRCA1) and converted to their corresponding Entrez IDs using the `AnnotationDbi` package.
2. **User Input Handling:**
    - Users can choose between using a predefined gene list or uploading their own. If uploading, they can enter genes in either Gene Symbol or Ensembl ID formats.
    - The app checks the validity of the input and converts the provided gene symbols or IDs to Entrez IDs.
3. **Enrichment Analysis:**
    - The core enrichment analysis is performed using the `TCGAanalyze_EAcomplete` function from the `TCGAbiolinks` package, which evaluates the significance of the input gene list against the GO terms.
    - The analysis is segmented by ontology type (BP, CC, MF) based on user selection.
4. **Visualization:**
    - Results are presented as bar plots, generated by the `TCGAvisualize_EAbarplot` function, allowing users to visually interpret the significance of the enriched GO terms.

Challenge

- The **TCGAanalyze_EAcomplete** function relies on internet access to query external resources (e.g., TCGA, KEGG). Network timeouts, certificate errors, or server outages can disrupt functionality.
- **Solution:** Use local gene list when possible.