

# R Dev Exercise

## Data Science, R Shiny, R Data Manipulation

In this file <https://bio-test-data.s3.amazonaws.com/Demo/RShiny/Homo+sapiens.csv> you will find a table with gene symbols, gene synonyms, GO (gene ontology) terms, etc.

Write an R shiny app with the following behaviour:

1. A user can enter a gene symbol or a GO term in an input box.
2. As the user types, autocomplete results are shown.
3. If a gene is selected: show its gene symbol, gene synonyms, Ensembl ID, and GO terms.
4. If a GO term is selected: show the associated genes. And for each gene, show its gene symbol, gene synonyms, Ensembl ID, and GO terms.

Please share your full code as well as suggestions on how to improve the user experience.