**Project 3**

**Gene Expression Analysis of Normal vs. Tumor Samples in Colorectal Cancer**

**Objective:** Compare expression profiles to identify up- and downregulated genes in colorectal cancer.

**Data Source:**

* GEO (Gene Expression Omnibus) dataset, e.g., **GSE25070** (colon normal vs tumor samples).

**Steps:**

1. Download expression matrix from GEO (Series Matrix File).
2. Use **GEO2R (online tool)** to perform differential expression analysis.
3. Identify top 20 upregulated and 20 downregulated genes.
4. Perform functional enrichment (GO/KEGG) using **DAVID** or **Enrichr**.
5. Visualize results (volcano plot, bar graph of pathways).

**Deliverables:**

* Gene lists (CSV)
* Plots (volcano, pathway bar chart)
* Report highlighting key genes/pathways relevant in colorectal cancer