**Microarray Analysis Pipeline - Shiny Interface**

**Overview**

The **Microarray Analysis Pipeline** is a **Shiny-based web application** that provides an interactive interface for analyzing microarray data. It allows users to:

* **Upload CEL files** and assign sample groups
* **Perform quality control (QC) analysis** with various plots
* **Run differential expression analysis** and visualize results
* **Download results** for further analysis

This pipeline is designed to simplify the microarray data analysis process for researchers and bioinformaticians.

**Features**

* **Data Upload:** Supports uploading multiple **CEL files** and assigning experimental groups.
* **Quality Control:** Generates **RNA degradation plots, boxplots, MA plots, and density plots**.
* **Differential Expression Analysis:** Displays results in a **table format** and provides interactive **volcano plots and heatmaps**.
* **Downloadable Results:** Users can download processed data and analysis results in CSV format.
* **User-Friendly Interface:** Built using **Shiny and Shiny Dashboard**, making it accessible via a web browser.

**Installation & Dependencies**

The application requires **R** and several **Bioconductor** and **CRAN** packages.

**Required R Packages**

The following packages are installed automatically if they are missing:

* shiny
* shinydashboard
* DT
* plotly

Ensure you have **Bioconductor** installed before running the application.

To install dependencies manually, run:

if (!requireNamespace("BiocManager", quietly = TRUE))

install.packages("BiocManager")

required\_packages <- c("shinydashboard", "DT", "plotly")

for (package in required\_packages) {

if (!requireNamespace(package, quietly = TRUE))

BiocManager::install(package)

}

**How to Run the Application**

1. **Install dependencies** (if not already installed).
2. **Ensure the script microarray\_pipeline.R** is in the same directory as app.R.
3. Open R and set the working directory to the folder containing the app.
4. Run the following command in R:
5. library(shiny)
6. runApp("app.R")
7. The application will launch in your default web browser.

**Usage Guide**

**1️. Upload Data**

* Click on the **"Upload Data"** tab.
* Upload your **CEL files** (raw microarray data).
* Assign groups (e.g., **control** vs. **treatment**).
* Specify an output directory.
* Click **"Run Analysis"** to start the pipeline.

**2️. Quality Control**

* Navigate to the **"Quality Control"** tab.
* View diagnostic plots such as:
  + **RNA degradation plots**
  + **Box plots**
  + **MA plots**
  + **Density plots**

**3️. View and Download Results**

* Go to the **"Analysis Results"** tab.
* Select a comparison and view:
  + **Differential expression table**
  + **Volcano plot**
  + **Heatmap of top 25 differentially expressed genes**
* Download the results as a **CSV file**.

**File Structure**

📂 Microarray-Analysis-Pipeline

│-- 📄 app.R # Main Shiny app

│-- 📄 microarray\_pipeline.R # Core microarray analysis functions

│-- 📁 data/ # (Optional) Example dataset

│-- 📁 microarray\_results/ # Output directory (generated after running analysis)

**Troubleshooting**

* **Application doesn't launch?**
  + Ensure you have installed all dependencies.
  + Run sessionInfo() in R to check for missing packages.
* **No results appear after clicking "Run Analysis"?**
  + Verify that your **CEL files are correctly uploaded** and **groups are assigned**.
  + Check if microarray\_pipeline.R is present in the directory.
* **Plots not displaying properly?**
  + Ensure you have **plotly** installed correctly using install.packages("plotly").