# GeneScope

-"Explore Differential Gene Expression with GeneScope."

Done by Team:Ladybugs

# Problem Statement

**Gene Expression Explorer:**Use NCBI's public GEO repository to analyze biomedical data.For example, select a microarray or RNA-seq dataset comparing healthy vs disease samples and build a classifier or visualization.teams might use Python libraries(Pandas,Scipy) find differentially expressed genes and present a simple web interface where users can query genes of intrest.This project leverages open genomics data for a bilogically meaningful analysis

# Solution

- It supports both types of data microarray and RNA-seq.
- For advanced visualization uses python libraries.
- It can handle large datasets simultaneously and it can analyze multiple datasets.
- An interface that respond to user input in real-time.

# Benefits

-Broad Dataset Compatibility

-Advanced and Interactive Visualizations

-Multi Dataset Analysis

-Accessible From Any Device

-It can built both classification and visualization

# Techincal Architecture

Frontend : HTML,CSS,Javascript,React

Backend:Python

Libraries:Pandas,Scipy,Seaborn,GEOparse

# Testing and Validation

**Functional Testing:**
All interactive elements, including forms and navigation links, were tested for proper functionality.

**Performance Metrics:**
The application demonstrates fast load times and efficient performance across devices.

**User Feedback:**
Initial user testing indicates a positive reception regarding usability and design aesthetics.

# GeneScope

Use NCBI's public GEO repository to analyze biomedical data. Select microarray or RNA-seq datasets comparing healthy vs disease samples, build classifiers, and discover differentially expressed genes through our intuitive web interface for biologically meaningful analysis.

Q  **Start Gene Analysis**          **Browse GEO Datasets**

### GEO Repository

Access NCBI's comprehensive Gene Expression Omnibus database

### Microarray & RNA-seq

Analyze both microarray and RNA-sequencing datasets

### Differential Expression

Compare healthy vs disease samples to find significant genes

### Classification Models

Build and validate classifiers for biomedical predictions

# Test Result Snapshot:

| Test Case | Expected Result | Actual Result | Status |
|---|---|---|---|
| Form Submission w/Valid Data | Success message shown | ✅ As expected | Passed |
| Mobile View (iPhone/Pixel) | Responsive layout renders | ✅ Responsive | Passed |
| Page Load Time < 2s | Loads in 1.4s on 4G | ✅ Fast | Passed |
| Broken Link Check (404 errors) | No errors found | ✅ None found | Passed |

# Key Features

-Upload or fetch GEO datasets

-Preprocess gene expression matrices

-Differential expression analysis

-Interactive visualizations(Volcano, Heatmap)

# Conclusion

GeneScope is a powerful yet user-friendly web tool developed by NCBI to simplify differential gene expression analysis using public datasets from the GEO repository. By integrating robust R-based packages like GEOquery and limma, it enables researchers to quickly identify genes that are differentially expressed between experimental conditions such as healthy vs diseased samples.

# Team Members

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# Thank YOU