DGEAR-Web Dashboard Manual

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Differential Gene Expression Analysis Resource (DGEAR)

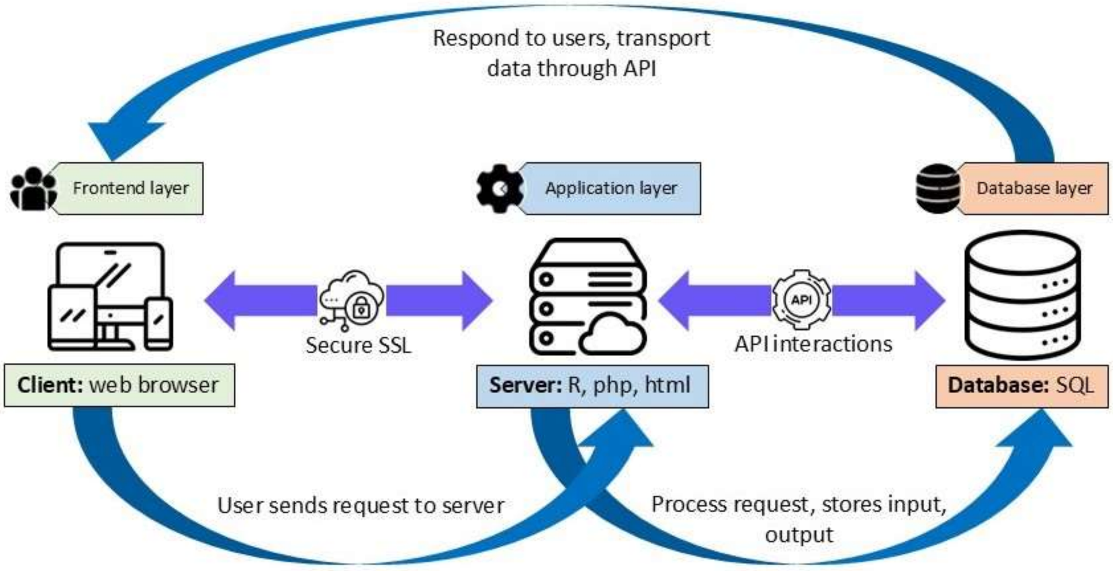
Introduction

Welcome to **DGEAR-Web**, an intuitive web-based platform for **ensemble-based differential gene expression analysis**. DGEAR empowers researchers, scientists, and users from varied backgrounds to perform complex DEG (Differentially Expressed Genes) predictions from gene expression data through a user-friendly, GUI-driven environment.

Architecture Overview

DGEAR-Web is designed with the following key principles:

- **Cross-Platform Compatibility:** Accessible across Windows, macOS, Linux, and mobile devices through any modern web browser.
- **User-Friendly Interface:** Easy-to-navigate graphical interface with buttons, forms, and menus, ensuring usability without prior programming knowledge.
- **Accessibility:** Opens up bioinformatics analysis to users with minimal technical expertise.
- **Efficiency and Time-Saving:** Streamlined workflows minimize manual intervention, speeding up the data preprocessing and analysis process.

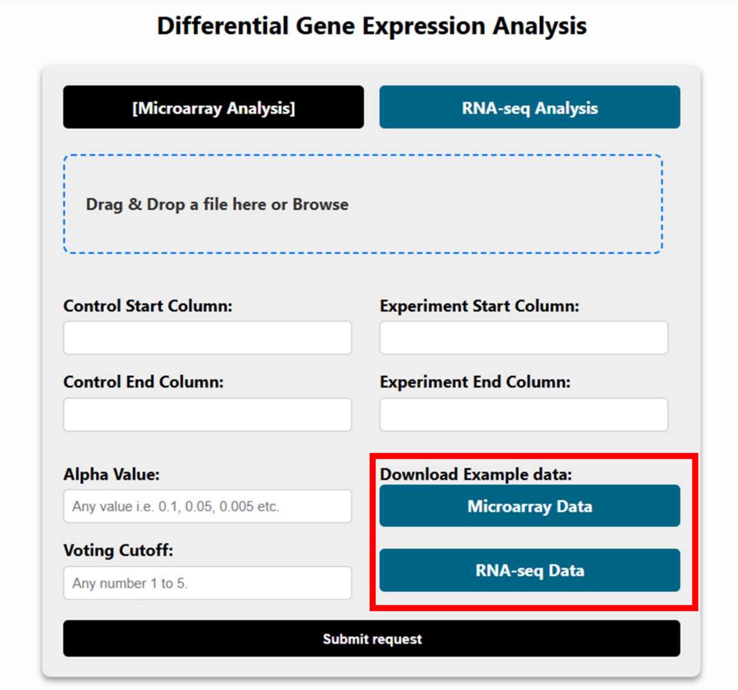


Key Features

- **Upload and Analyze Gene Expression Data:** Simple file upload mechanism.
- **Customizable Input Parameters:** Define control/experimental groups, significance level (alpha), and ensemble voting cutoff.
- **Visual Outputs:** Generate plots, results summaries, and downloadable data.
- **Result Exploration:** Interactive browsing and download options for outputs.

Data Format and Example Data

- Before uploading your data, please check your data formatting.
- To check if your data is compatible with the DGEAR you can download example data from the site it self



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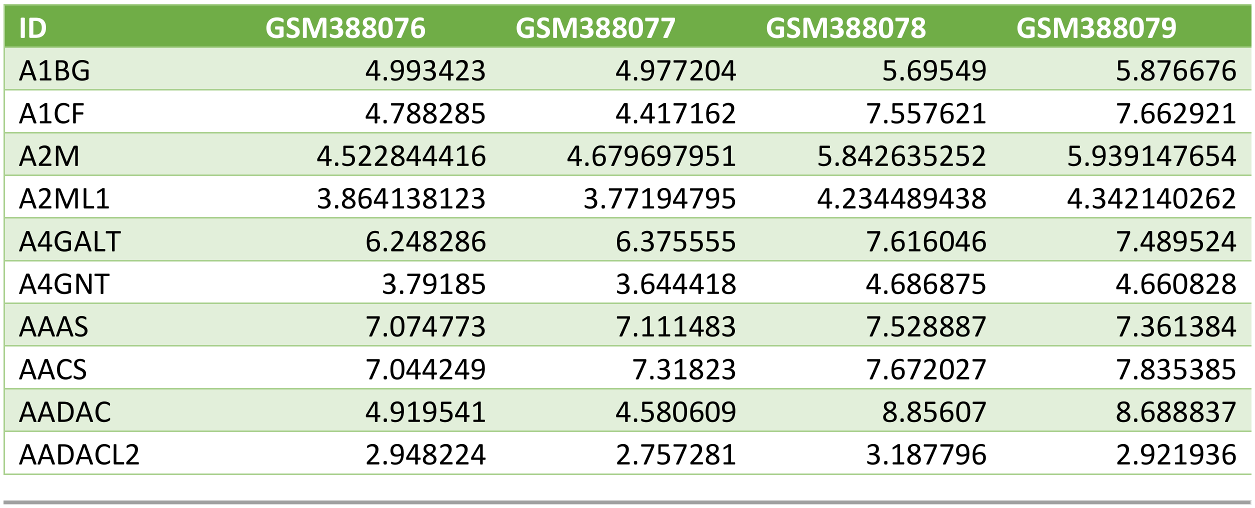
1. Microarray Example Data

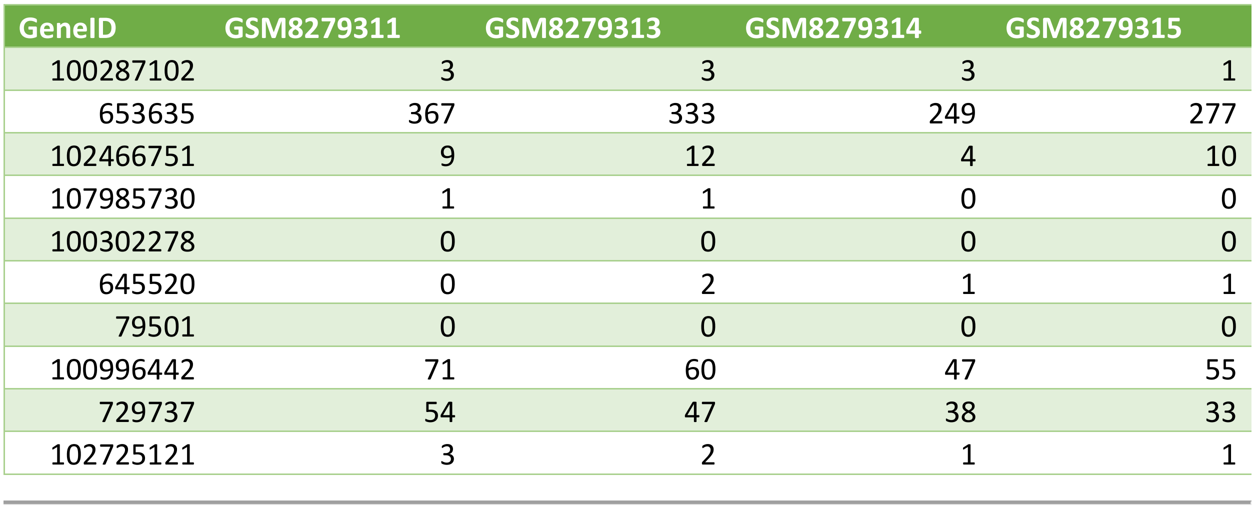
- Here is a snip-shot of the microarray example data



ID	GSM388076	GSM388077	GSM388078	GSM388079
A1BG	4.993423	4.977204	5.69549	5.876676
A1CF	4.788285	4.417162	7.557621	7.662921
A2M	4.522844416	4.679697951	5.842635252	5.939147654
A2ML1	3.864138123	3.77194795	4.234489438	4.342140262
A4GALT	6.248286	6.375555	7.616046	7.489524
A4GNT	3.79185	3.644418	4.686875	4.660828
AAAS	7.074773	7.111483	7.528887	7.361384
AACS	7.044249	7.31823	7.672027	7.835385
AADAC	4.919541	4.580609	8.85607	8.688837
AADACL2	2.948224	2.757281	3.187796	2.921936

2. RNA-seq Example Data

- Here is a snip-shot of the RNA-seq example data



GeneID	GSM8279311	GSM8279313	GSM8279314	GSM8279315
100287102	3	3	3	1
653635	367	333	249	277
102466751	9	12	4	10
107985730	1	1	0	0
100302278	0	0	0	0
645520	0	2	1	1
79501	0	0	0	0
100996442	71	60	47	55
729737	54	47	38	33
102725121	3	2	1	1

User Manual

1. Opening the Web Tool

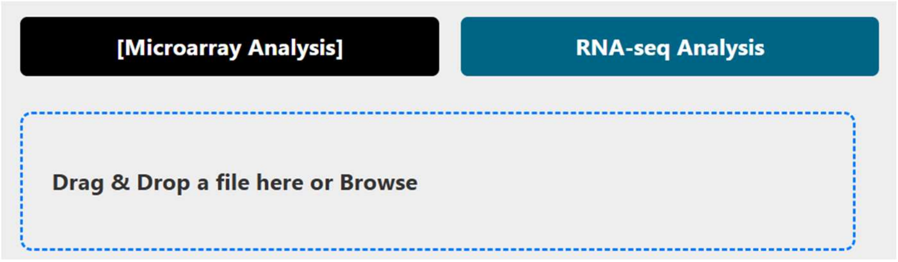
- Visit the DGEAR-Web homepage at https://compbiosysnbu.in/DGEAR/ .
- The landing page provides an overview of the tool, its purpose, and how to navigate it.

2. Navigation

- Use the **navigation panel** located at the top (or bottom) of the page.
- Key sections include:
    - **Home**
    - **Analysis**
    - **Results**
    - **Contact**

3. Uploading Data

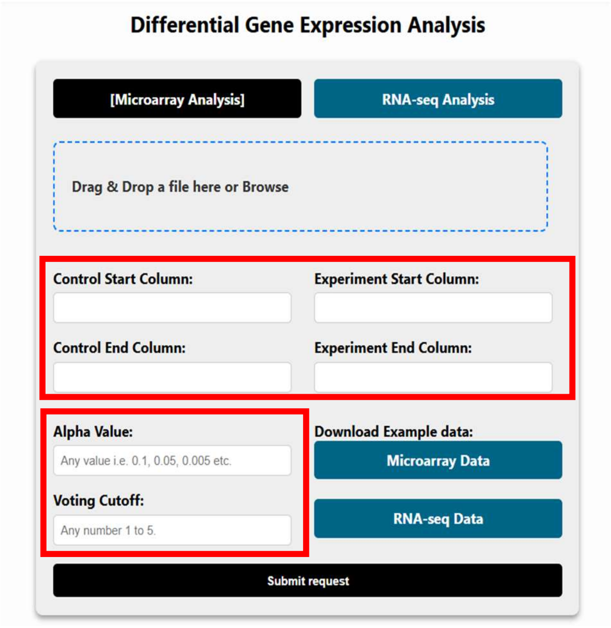
- Go to the **Analysis** tab.
- Chose Microarray analysis or RNA-seq analysis as your need.
- Drag and drop or click to select a gene expression file (supported formats: `.tsv`, `.txt`).



4. Setting Input Parameters

- After uploading, configure the following:
    - **Compare Column Range:** Indicate the range or list of columns corresponding to your samples. Suppose you have 4 samples; and you want to compare first 2 with the last 2 in that case Control Start Column: 1; Control End Column: 2; Experiment Start Column: 3; Experiment End Column: 4
    - **Alpha Value:** Set the significance threshold for statistical testing (default example: 0.05).

  - **Voting Cutoff:** Define the minimum number of methods supporting a gene as differentially expressed. For Microarray analysis 1 to 5 and for RNA-seq you can select 1 to 3



Differential Gene Expression Analysis

Control Start Column:

Experiment Start Column:

Control End Column:

Experiment End Column:

Alpha Value: Any value i.e. 0.1, 0.05, 0.005 etc.

Voting Cutoff: Any number 1 to 5.

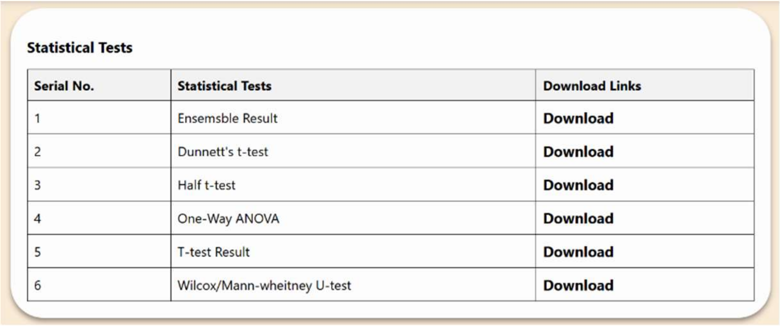
Download Example data:

5. Submitting and Processing the Request

- Click **Submit Request** to initiate the differential expression analysis.
- The system will process the data and apply the ensemble-based framework.

6. Exploring Results

- After processing, the **Results Page** will become accessible.
- You can:
  - View summary plots (e.g., Volcano plots, MA plots).
  - Download DEG lists and other result files.

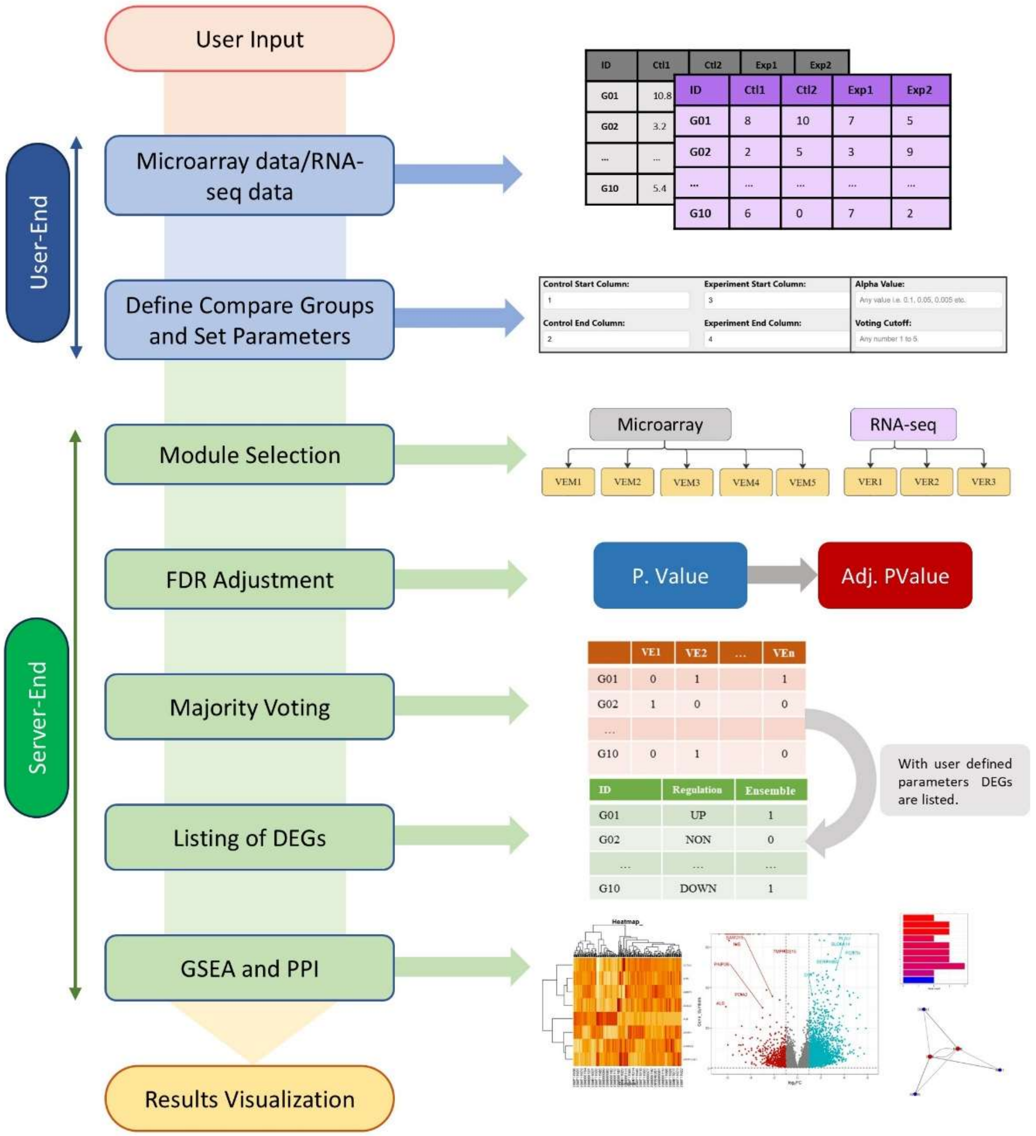


Statistical Tests

Serial No.	Statistical Tests	Download Links
1	Ensemsble Result	**Download**
2	Dunnett's t-test	**Download**
3	Half t-test	**Download**
4	One-Way ANOVA	**Download**
5	T-test Result	**Download**
6	Wilcox/Mann-wheitney U-test	**Download**

DGEAR Algorithm

DGEAR, an ensemble model with a modified majority voting algorithm is implemented. Multiple statistical tests i.e. Student's t-test, one-way ANOVA, Dunnett's t-test, half t-test, and Wilcoxon/Mann-Whitney U-test were employed for the microarray data and linear modeling, negative binomial distribution-based modeling and empirical Bayes method were employed for the RNA-seq data. After multiple hypothesis testing and FDR correction, outcomes from individual test were transformed into logical vectors, and through majority voting the Differentially.



ID	Ctl1	Ctl2	Exp1	Exp2
G01	10.8			
G02	3.2			
...	...			
G10	5.4			

ID	Ctl1	Ctl2	Exp1	Exp2
G01	8	10	7	5
G02	2	5	3	9
...	...	...	...	...
G10	6	0	7	2

Control Start Column: 1
Experiment Start Column: 3
Alpha Value: Any value i.e. 0.1, 0.05, 0.005 etc.
Control End Column: 2
Experiment End Column: 4
Voting Cutoff: Any number 1 to 5.

	VE1	VE2	...	VEn
G01	0	1		1
G02	1	0		0
...				
G10	0	1		0

ID	Regulation	Ensemble
G01	UP	1
G02	NON	0
...	...	...
G10	DOWN	1

With user defined parameters DEGs are listed.

Important Notes

- Ensure your uploaded gene expression file is formatted correctly (genes as rows, samples as columns).
- Input parameters must be set carefully to reflect the experimental design.
- Internet connection is required for using the web-based platform.

Project Background

DGEAR-Web was developed as part of the academic project titled: **"To Develop an Ensemble Framework for Differential Expression Analysis"** submitted to the **University of North Bengal** in partial fulfillment for the award of **Master of Science in Bioinformatics** by **Koushik Bardhan (Batch: 2022-2023)** under the guidance of **Dr. Chiranjib Sarkar**, Department of Bioinformatics, University of North Bengal, West Bengal, India.

Support

For any issues, bugs, or suggestions, please refer to the **Contact** the project team through the provided communication channels on the platform.

Happy Researching with DGEAR-Web!