

DEXA: User Manual

A Novel Python-Integrated Model for Advancing the Deciphering of Differential Gene Expression Patterns

Overview:

DEXA (Differential Gene Expression Analysis) is a Python-based tool designed for the robust analysis of RNA-seq data, facilitating the identification of differentially expressed genes. This user manual provides a step-by-step guide on how to set up and utilize DEXA effectively.

Step 1: Set Up the Computer System

Ensure that Python is installed on your system. If not, download and install Python from the official website: Python Downloads: <https://www.python.org/downloads/>

Step 2: Import Required Python Modules

DEXA relies on a few Python modules for its functionality. You can install these modules using the following commands:

```
Pip install pandas
```

```
pip install numpy==1.18
```

```
pip install scipy==1.1.0
```

```
pip install xlrd==1.2.0
```

```
pip install openpyxl
```

Note: Python Modules are specified with the versions for the ease of users

Alternatively, consider installing Anaconda, a distribution that includes many commonly used Python libraries: Anaconda Downloads: <https://www.anaconda.com/download>

Step 3: Set Working Directory

Navigate to the directory where your input data is located, or where you want the output files to be generated. This can be done using the cd command:

```
cd /path/to/your/directory
```

Step 4: Run the DEXA Command Line Tool

Execute the DEXA command-line tool by entering the following command:

```
python3 DEXA.py <input_file.xlsx>
```

Replace <input_file.xlsx> with the path to your input Excel file containing the Count matrix data.

```
(base) samarth@samarth-HP-EliteOne-800-G6-24-All-in-One-PC:~/Downloads/L2FC scrip
t$ python3 L2FC.py '/home/samarth/Downloads/L2FC script/Sample Data.xlsx'

*****
                        Welcome to
                        DEXA: Differential Expression Analysis
*****

Documentation Link: https://github.com/ICAR-BIOINFORMATICS/L2FC
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Opening file: /home/samarth/Downloads/L2FC script/Sample Data.xlsx
Number of replications: 3
1. Calculating Log 2 Fold Change Values...
2. Calculating p-values...
3. Calculating expressions...
4. Saving the output file 1...
File saved: /home/samarth/Downloads/L2FC script/Sample Data_results.xlsx
5. Filtering the results...
6. Saving the gene list...
File saved: /home/samarth/Downloads/L2FC script/Sample Data_gene_list.xlsx
Execution finished...
```

Figure 1: Working View of DEXA

Outputs

DEXA will generate two output files in the working folder:

- Gene_Values_File.xlsx: Comprehensive overview of all gene values, including log2fold change values and corresponding p-values.
- Significantly_Expressed_Genes_File.xlsx: Categorization of highly expressed significant genes into categories such as Positive Regulators, Negative Regulators, Activators, and Deactivators.
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Contact Information

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Feel free to reach out for any queries or feedback regarding the DEXA tool. Happy analyzing!