******************** INFORMATION *****************************

Graph-based Hub Gene Selection Technique using Protein Interaction Information: Application to Sample Classification

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************************* PREREQUISITES ***********************

Python 2.7+
sklearn
matplotlib 2.0+
mpl_toolkits
numpy 1.10+
Cytoscape
##

This is the readme file that contains the guidelines and information of the uploaded supplementary materials.

- **1. MOO-based clustering**:- This folder contains the python code of the proposed MOO-based clustering. Once you open the folder, compile the projects as follows.
    - cd examples
        - Write the **PATH DESCRIPTION** of the dataset in line number 28 of the *main.py*
    - *python main.py <initial_population_size> <number_of_generation>*

    - *Output:-*
        - Generate a file named '*non_dominated_solutions.txt*' that contains all the cluster information

- **2. Modified Goldberg Algorithm**:- This folder contains the modified Goldberg Algorithm.
- **3. Significant_genes_expression_values.py** :- Obtain the gene expression values of the selected genes.
- **4. all_classifiers.py :** Implementation of four classifiers (SVM, Random Forest, kNN, and ANN) with 10-fold cross validation