

## ***i*CluF**

Iterative Cluster Fusion (*i*CluF) is a Python-based tool that extracts and integrates commonalities from multiomic datasets and identifies clusters in an unsupervised manner. This method requires at least two datasets to integrate.

## **Download**

The software *i*CluF can be downloaded from <https://github.com/GudaLab/.....>

## **Running *i*CluF**

**Example 1:** To predict 3 clusters for cancer type “CHOL” with n\_iter (Number of iterations) = 7, use the following command-

`python iCluF_main.py CHOL 3 7`  
K (Number of clusters)  
Cancer type      Number of iterations

**Example 2:** To predict 4 clusters for cancer type “ACC” with n\_iter (Number of iterations) = 6, use the following command-

`python iCluF_main.py ACC 4 6`  
K (Number of clusters)  
Cancer type      Number of iterations

The predicted clusters are saved in the output folder `.data/output/Clusters`

Please choose a cancer type from the following list of 30 cancers-

['ACC', 'BLCA', 'BRCA', 'CESC', 'CHOL', 'COAD', 'DLBC', 'ESCA', 'GBM', 'HNSC', 'KICH', 'KIRC', 'KIRP', 'LAML', 'LGG', 'LIHC', 'LUAD', 'LUSC', 'MESO', 'PAAD', 'PCPG', 'PRAD', 'READ', 'SARC', 'STAD', 'TGCT', 'THCA', 'THYM', 'UCEC', 'UCS', 'UVM']

### ***Running iCluF on different dataset***

For running the algorithm on a dataset not in the list, the user needs to create a folder with the proper name in “`./data/input_data/TCGA_data`”. The format of the data types should be the same as given in the different cancer types.