*i*CluF

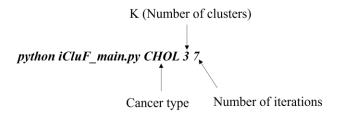
Iterative Cluster Fusion (*i*CluF) is a Python-based tool that extracts and integrates commonalities from multiomic datasets and identifies clusters in an unsupervised manner. This method requires at least two datasets to integrate.

Download

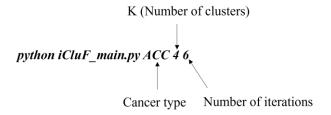
The software iCluF can be downloaded from https://github.com/GudaLab/.....

Running iCluF

Example 1: To predict 3 clusters for cancer type "CHOL" with n_iter (Number of iterations) = 7, use the following command-



Example 2: To predict 4 clusters for cancer type "ACC" with n_{i} ter (Number of iterations) = 6, use the following command-



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', '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.