**MODA User Manual**

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1. Introduction

Multi-Omics Data Integration and Analysis (MODA) offers a free platform for researchers to seamlessly integrate and analyze multi-omics data. Leveraging Genome-Scale Metabolic Network (GSMN), machine learning coefficients, and the Copy Number Profile Matching (CPM) algorithm, our tool not only facilitates a more comprehensive integration of metabolomics with other omics but also uncovers novel molecules based on deep learning. With a focus on extracting key modules and identifying hub molecules with significant expression fluctuations, our tool provides researchers with an advanced and robust solution for in-depth analysis and interpretation of multi-omics data.

1. Manual
   1. Predicted Metabolic Flux
      1. Set Parameter

output\_folder: 'PRADall'

input\_folder: 'PRADall'

2.1.2 Input files

Parameters (Example: \_OPTIONS\_.xlsx) # Downloaded example data and revised information based on your project

Template (Example: \_TEMPLATE\_.xls) # Downloaded example data and revised information based on your project

RNA-seq profile (Example: PRAD\_RNAseq\_FPKM all data.txt) # Downloaded example profile and tidied your data

* 1. Integration Multi-omics data
     1. Set Parameter
        1. Embedding

depth: 2 # default: 2, suggestion: 1-4;

dataSet: 'PRAD' # Your project name;

agg\_func: 'MEAN' # default;

epochs: 30 # default: 30, suggestion: 20-60;

b\_sz: 50 # default: 50, suggestion: 32-128;

seed: 777 # default;

cuda: False # default: False, suggestion: True/False;

learn\_method: 'sup' # default;

unsup\_loss: 'normal' # default;

name: 'debug' # default;

num\_layers: 2 # default;

hidden\_emb\_size: 128 # default;

gcn: False # default;

loss\_mean\_inital: 100 # default;

weight: 3 # default;

* + - 1. Module detection

project: 'PRAD' # Your project name;

community\_top: 8 # default;

over\_community\_num: 8 # default;

step\_size: 0.01 # default;

threshold: 0.01 # default;

method: 'CPM' # default;

dimension: 4 # default;

numIter: 2 # default;

power: 2 # default;

inflation: 2 # default;

c\_num: 2 # default;

spectral\_k: 40 # default;

* + 1. Input files

Seed nodes (Example: seed node.csv) # Downloaded example profile and tidied your data

Node Features (Example: node\_feature.csv) # Downloaded example profile and tidied your data