

# FLUXestimator

A webserver to estimate cell-/sample-wise metabolic fluxome by using scRNA-seq or general transcriptomics data

ABOUT

Step1-1: Select species.

 Select Species

Homo Sapiens

Mus Musculus

Other Organisms

 Select Network

M171

M171\_NAD

KEGG

GGSL

Glucose-TCAcycle

Glucose-Glutaminolysis

## Step1

### Select species and metabolic (sub)networks

Please select the species of your data and to-be-analyzed metabolic network in the left boxes.

#### Homo sapiens Glucose-TCAcycle

**Glucose-TCAcycle:** This metabolic network is formed by glycolysis, pentose phosphate and TCA cycle pathways in human, which covers essential metabolites in fueling energy production and cell growth. This model focuses on a closed system of metabolism that assumes the major source of glucose are for feeding the energy production and biosynthesis. The network includes 65 genes of 45 enzymes. We reconstructed this network into 15 modules and 12 intermediate metabolites.

 Position

Step 1: Select Species And Network

Step 2: Upload Data

Step 3: Parameters

Step 4: Submit Task

Step 5: Check Results

Step1-2: Select metabolic networks.



Select Species

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Step2

Upload input data

Step2-1: Choose input data.

Choose File

No file chosen

Upload

Step2-4: Upload input data.

The input of scFEA is a scRNA-seq or general transcriptome data, in which each row is one gene and each column is one sample. TPM (or CPM/FPKM) normalized data is recommended. scFEA webserver accepts comma-(.csv), space-(.txt), tab-(.txt) delimited input files. Please make sure the input data is in a matrix form and contains row/column names. Both gene symbol and Ensembl gene ID are accepted. For a large data set, we recommend to only upload gene expression data of the scFEA metabolic genes that will be used for flux computation. The maximal input file size should be smaller than **500MB**. For a large data set, we recommend to only upload gene expression data of the scFEA metabolic genes that will be utilized for flux computation ([scFEA human genes](#), [scFEA mouse genes](#)). See more details in [Tutorial](#). Note: it may take a few minutes to upload a data > 100MB.

You can choose or download example input data files below.

Choose Example File

Download Example File

Step2-2: Choose input data.

HNSCC\_Fib\_expr\_counts.csv

文件名(N): HNSCC\_Fib\_expr\_counts.csv

打开(O)

Step2-3: Confirm input data.



### Step3

#### Select Species

Homo Sapiens

Mus Musculus

Other Organisms

#### Select Network

M171

M171\_NAD

KEGG

GGSL

Glucose-TCAcycle

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## Imputation

scFEA utilizes MAGIC for a data imputation. We recommend this step for snRNA-seq or drop-seq data that have a high sparsity level.

Step3-1: Perform imputation.

- ☒ Perform imputation  
☐ Not perform imputation

## Normalization

- ☐ Log(x+1)  
☒ CPM  
☐ Log(CPM+1)  
☐ No Normalization

Step3-2: Normalization by CPM.

#### Position

Step 1: Select Species And Network

Step 2: Upload Data

Step 3: Parameters

Step 4: Submit Task

Step 5: Check Results

### Step4


## Submit Task

Make sure you have finished step1 to step3 before you submit your tasks.

Step4: Submit task.

Submit Task




 Select Species

Homo Sapiens

Mus Musculus

Other Organisms

 Select Network

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GGSL

Glucose-TCAcycle

Glucose-Glutaminolysis

Step4

Submit Task

Make sure you have finnished step1 to step3 before you submit your tasks.

Submit Task


Step5

Check Your Result

Make sure you have submit your task, and it is finnished.

My Results

Step5: Check the result.

 Position

Step 1: Select Species And Network

Step 2: Upload Data

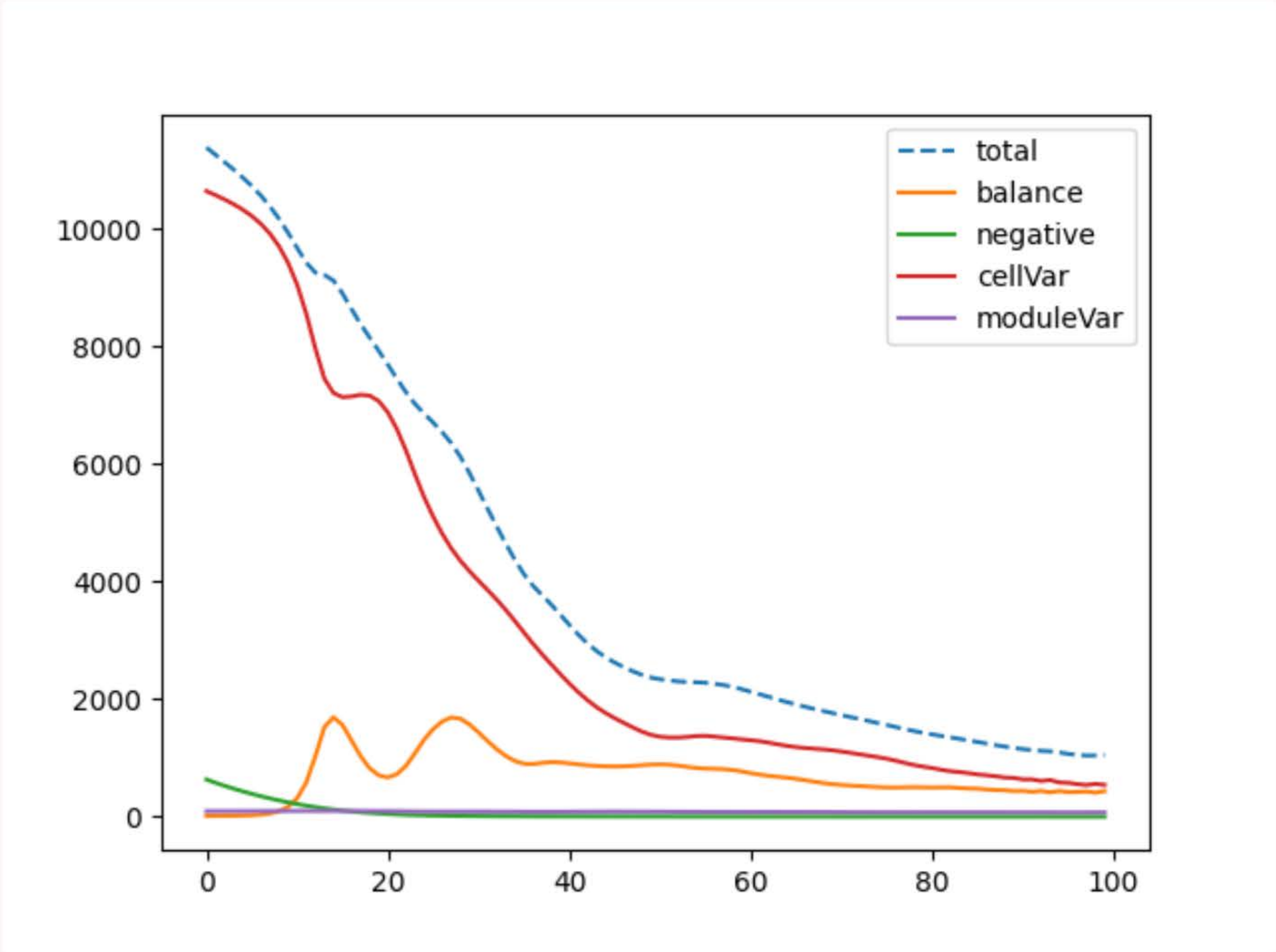
Step 3: Parameters

Step 4: Submit Task

Step 5: Check Results



Curve of loss



Step6: Check the output files.

Input data	Expression profile of metabolic genes extracted from the input file that was used in the analysis.	HNSCC_Fib_expr_counts_scFEA_input.csv
Output files	Imputed sample-wise metabolomics profile	HNSCC_Fib_expr_counts_metabolites.csv
	Predicted sample-wise metabolic flux	HNSCC_Fib_expr_counts_flux.csv
Module information	scFEA.Glucose-TCAcycle.human.moduleinfo.csv	scFEA.Glucose-TCAcycle.human.moduleinfo.csv
	scFEA.Glucose-TCAcycle.human.v1.symbols.gmt	scFEA.Glucose-TCAcycle.human.v1.symbols.gmt