**ATGPred-FL**

**# 1 Description**

Autophagy is a conservative ‘self-eating’ process during biological evolution. Accurately identification of autophagy proteins (ATGs) is crucially important to reveal their biological functions. Here, we developed the first machine learning-based software that enables the classification of proteins into ATGs or non-ATGs. ATGPred-FL, which identifies ATGs using feature representation learning scheme and support vector machine algorithm. It has the potential to facilitate future computational work in this field.

Webserver and datasets available at:

http://lab.malab.cn/~acy/ATGPred-FL/

**# 2 Requirements**

Before running, please make sure the following packages are installed in Python environment:

joblib==1.1.0

numpy==1.21.5

pandas==1.3.5

python==3.8.5

scikit-learn==1.0.2

For convenience, we strongly recommended users to install the Anaconda Python 3.8.5

(or above) in your local computer.

**# 3 Running**

Changing working dir to ATGPred-master, and then running the following command:

python ATGPred.py -i test.fasta -o prediction\_results.csv

-i: input file in fasta format

-o output file name