**DeepAc4C**

**# 1 Description**

N4-acetylcytidine (ac4C) is the only acetylation modification that has been charac-terized in eukaryotic RNA, and is correlated with various human diseases. DeepAc4C, which identifies ac4C us-ing con-volutional neural networks (CNNs) using hybrid features composed of physico-chemical patterns and a distributed representation of nucleic ac-ids.The proposed model achieved better and more balanced performance than existing predictors.

Webserver and datasets available at:

<http://lab.malab.cn/~wangchao/softs/DeepAc4C/>

**# 2 Requirements**

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

gensim==3.4.0

pandas==1.0.3

tensorflow==2.3.0

python==3.7.3

biopython==1.7.8

numpy==1.19.2

For convenience, we strongly recommended users to install the Anaconda Python 3.7.3

(or above) in your local computer.

**# 3 Running**

Changing working dir to DeepAc4C-master, and then running the following command:

python DeepAc4C.py -i ./sequence/input\_query.fasta -o prediction\_results.csv

-i: input file in fasta format

-o output file name