

INSTRUCTION

There are three file folders in this demo. The 'data' file is used to store the features data.

The 'sequence feature' file is a demo for sequence feature extraction.

The 'zcurve feature' file is a demo for z-curve feature extraction.

Take BS-EC as an example:

1. Use 'sequence feature' program to extract BS and EC sequence features, respectively.
2. Use 'zcurve feature' program to extract BS and EC z-curve features, respectively.
3. After all features data above have been calculated, put them into the 'data' file folder.
4. Execute 'demo_testbsecoli.m' for calculation, and then results will be obtained.

Organism abbreviated name in the code should be changed if other calculation is required.

Take BS-AB as an example, 'BS' is used for training, 'EC' is replaced by 'AB' in this new model. All 'ecoli' in the code should be replaced by 'ab'.

AB is the short for Acinetobacter baylyi ADP1.

BS is short for Bacillus subtilis 168.

EC is short for Escherichia coli MG1655.

There is a limit on the number of file. The 'sequence feature' and 'zcurve feature' matlab programs can be downloaded at the website of our laboratory:

<http://www.csssk.net/download>.