

BiLTR is a simple, easy-to-use, and efficient program for siRNA efficacy prediction. It has the two features:

- To predict knockdown efficacy of siRNAs
- To test the performance of BiLTR: BiLTR will show the Pearson correlation coefficient between predicted values and experimental values.

I. Data format:

- To predict knockdown efficacy of siRNAs. In dataset file, each line contains each siRNA sequence.

For example: file "Predicted.txt" has three siRNA sequences:

```
GACGCCAAAAACAUAAGA
ACGCCAAAAACAUAAGAA
AAAACAUAAGAAAGGCC
```

- To test the performance of BiLTR. In dataset file, each line contains a siRNA sequence and its knockdown efficacy.

For example: file "Testing.txt" has four siRNA sequences.

```
CUAAUAUGUAAUUGAUUUAU 46.2
AAUAUGUAAUUGAUUUAUAC 38.4
CAAUCCUUUCAAUUUUAUCU 36.4
CAGACCAAAAUAAAUAAGAA 52.2
```

II. Compiler: Please make a folder on your computer and download files on our server to your folder.

On windows:

- Please download the dev-cpp software at the website address: <http://www.bloodshed.net/devcpp.html> and install dev-cpp environment.
- Double click to run "BiLTR.dev" file. On the dev-cpp environment, please press Ctrl+F9 or the compile button to compile and produce "BiLTR.exe" file

On Mac:

Please launch the command or Terminal and type the following command:

```
g++ -g Tensor\ Regression.cpp main.cpp -o BiLTR
```

III. Using: Please go to the folder containing downloaded files and run one of the following commands:

- **Windows:** BiLTR.exe filename arg
- **Linux or Mac OS:** ./BiLTR filename arg

where "filename" is the file name of siRNA dataset. The "arg" is an integer number. If the "arg" parameter is set by zero, the BiLTR is used to predict. In the other cases, the BiLTR is used to test.

For example:

- Using BiLTR to predict knockdown efficacy of siRNAs in the "Predicted.txt" file on Linux : `./BiLTR Predicted.txt 0`
- Using BiLTR to test its performance with the "Testing.txt" file on the Linux:
`./BiLTR Testing.txt 1`