Train Model   Run Model

Train Model   **Run Model**

Use random data

Load data...

Select Transcription Factor

Select transcription factor (TF) to be associated with the model from the list below:

TF1
TF2
TF3
TF4
etc. ...

Cancel   OK

Select file

Supported filetypes: .csv, .txt, and .npy
Go to url for github docs for example file formats.

[sample filepath here]

Cancel   Train model with this data

Select Transcription Factor

Select transcription factor (TF) to be associated with the model from the list below:

TF1
TF2
TF3
TF4
etc. ...

Cancel   OK

Training model progress

```
[ 0 / 5 ] [ 0 / 1500 ] Loss: _____, etc.
[ 0 / 5 ] [ 100 / 1500 ] Loss: _____, etc.
[ 0 / 5 ] [ 200 / 1500 ] Loss: _____, etc.
[ 0 / 5 ] [ 300 / 1500 ] Loss: _____, etc.
[ 0 / 5 ] [ 400 / 1500 ] Loss: _____, etc.
.
.
.
```

Complete

Evaluation Parameters

Choose model | saved_model1 ▼ |

Input sequences   ◉ manual entry   ○ upload data file

(DNA sequence inputs can only be a max length of 300 b.p.)

DNA sequence 1

```
ACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGAC
TGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTG
ACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGAC
TGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTG
ACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGAC
TG
```

DNA sequence 2

```
ACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGAC
TGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTG
ACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGAC
TGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTG
ACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGAC
TG
```

Cancel   OK

Evaluation Parameters

Choose model | saved_model1 ▼ |

Input sequences ◯ manual entry ◉ upload data file

Supported filetypes: .csv, .txt, and .npy
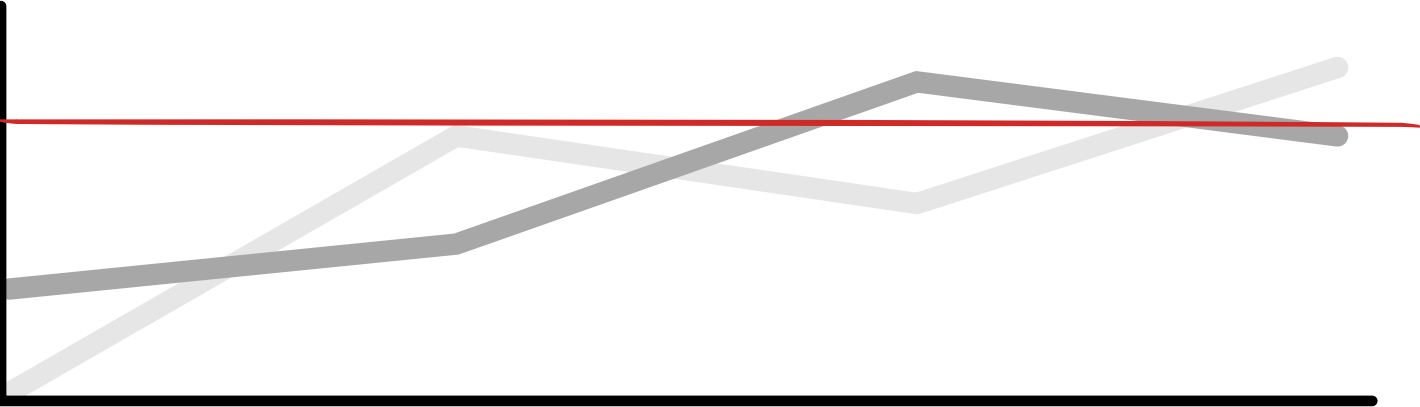Go to url for github docs for example file formats.
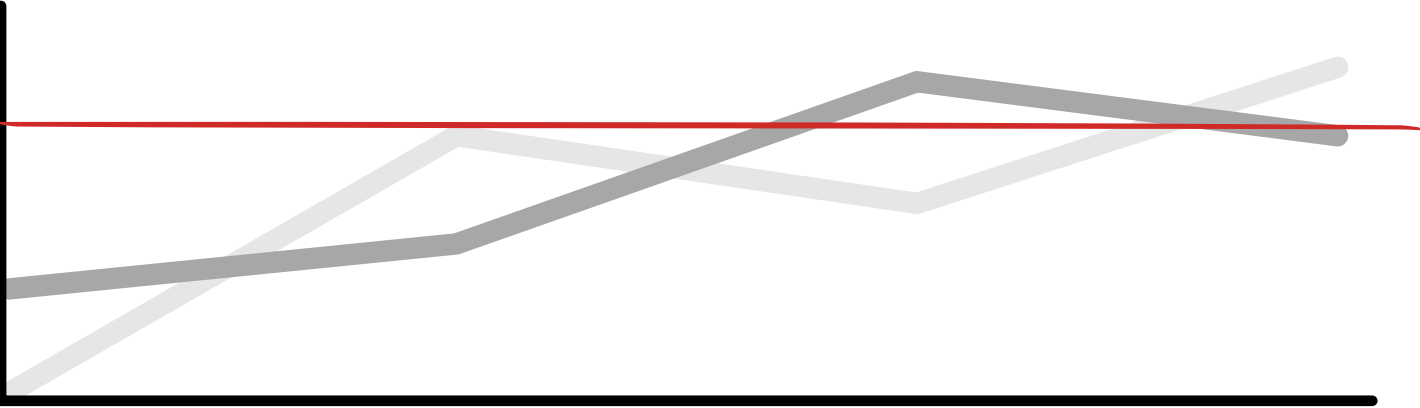
| sample filepath here | 📂

Cancel   OK

Output graph

Export As...

DNA sequence 1
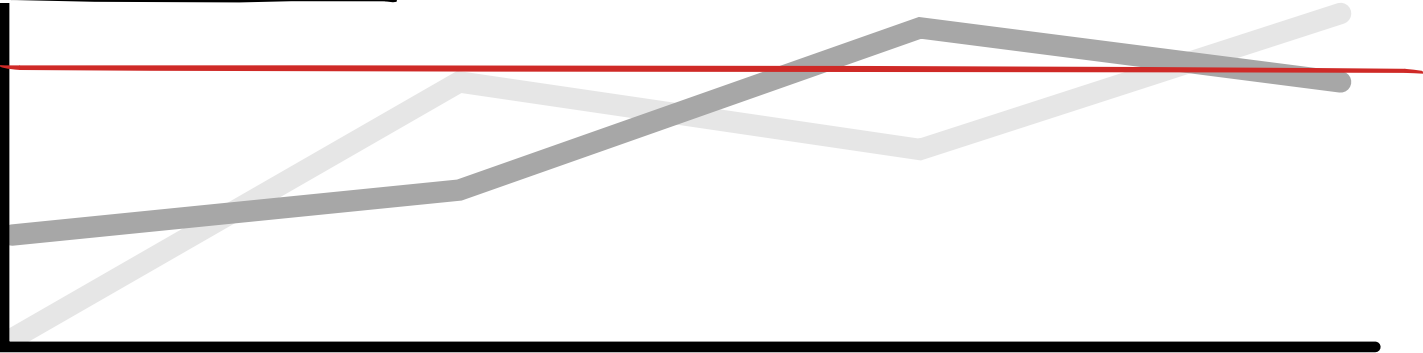
DNA sequence 2

Threshold

Output graph

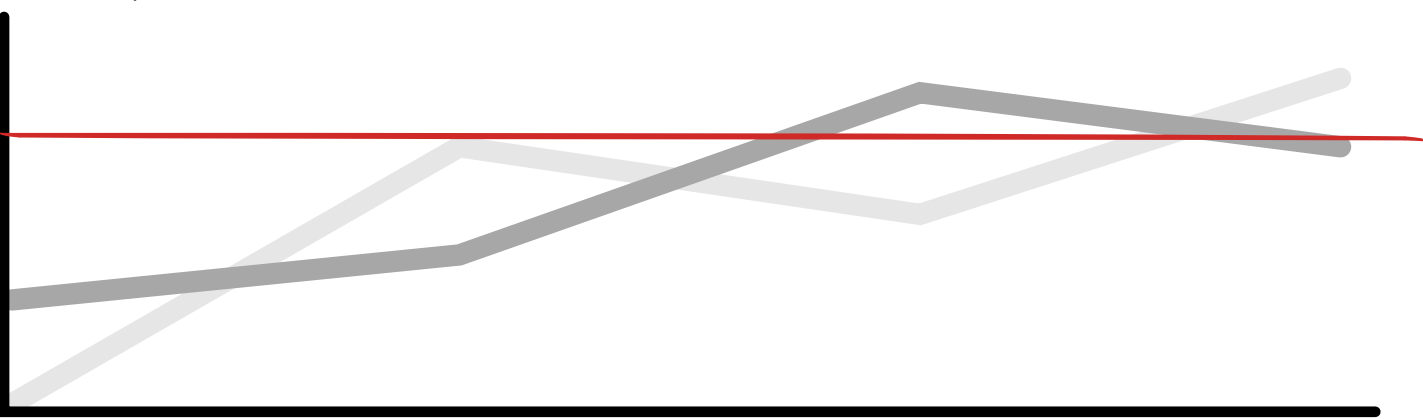## Export As...

.png

.pdf

.svg

Threshold

DNA sequence 2

Output graph

Export As...
- .png
- .pdf
- .svg

Confirmation

Output saved to current directory.

OK

DNA sequence 2