

Train Model

Run Model

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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 .npz  
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  
TGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTC  
ACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGAC  
TGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTC  
ACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGAC  
TG

DNA sequence 2

ACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGAC  
TGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTC  
ACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGAC  
TGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTC  
ACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGAC  
TG

Cancel

OK

saved\_model1



Ⓞ manual entry

- upload data file

DNA sequence 1

ACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGAC  
TGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTG  
ACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGAC  
TGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTG  
ACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGAC  
TG

ACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGAC  
TGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTG  
ACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGAC  
TGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTG  
ACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGAC  
TG

Cancel

OK

## Evaluation Parameters

Choose model

saved\_model1



Input sequences



manual entry



upload data file

Supported filetypes: .csv, .txt, and .npz

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[sample filepath here](#)



Cancel

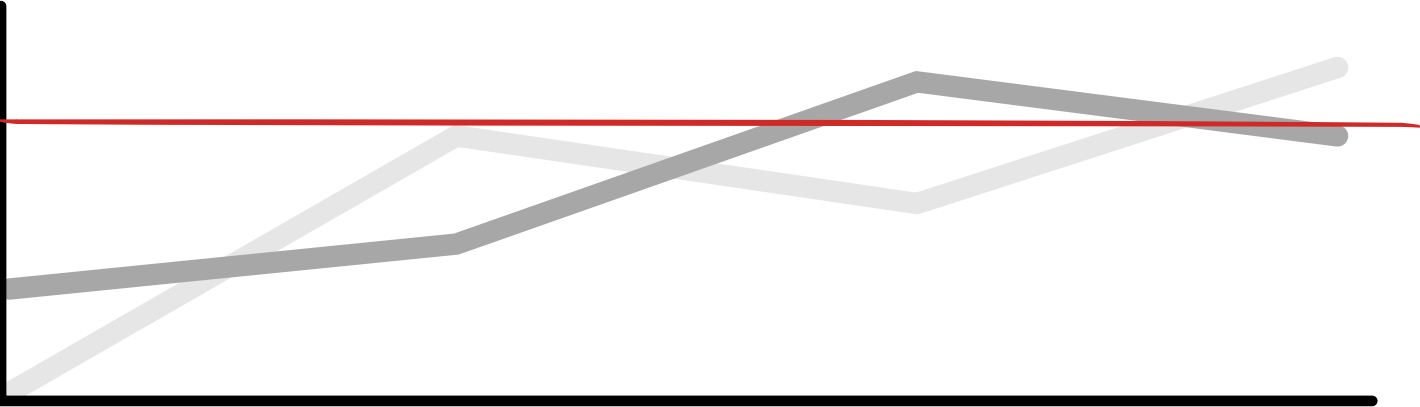
OK



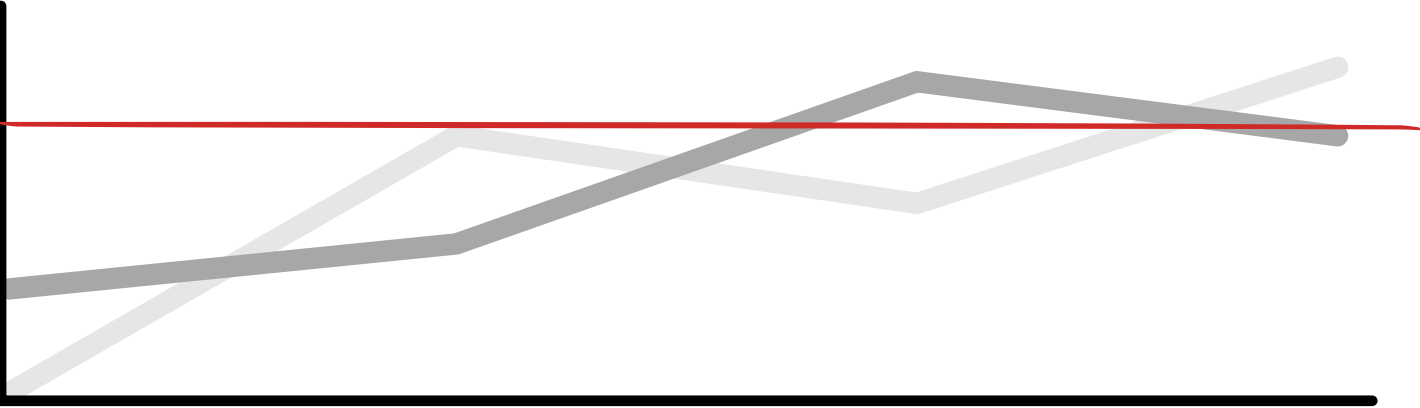
Output graph

Export As...

DNA sequence 1



DNA sequence 2



Threshold

93

Output graph

Export As...

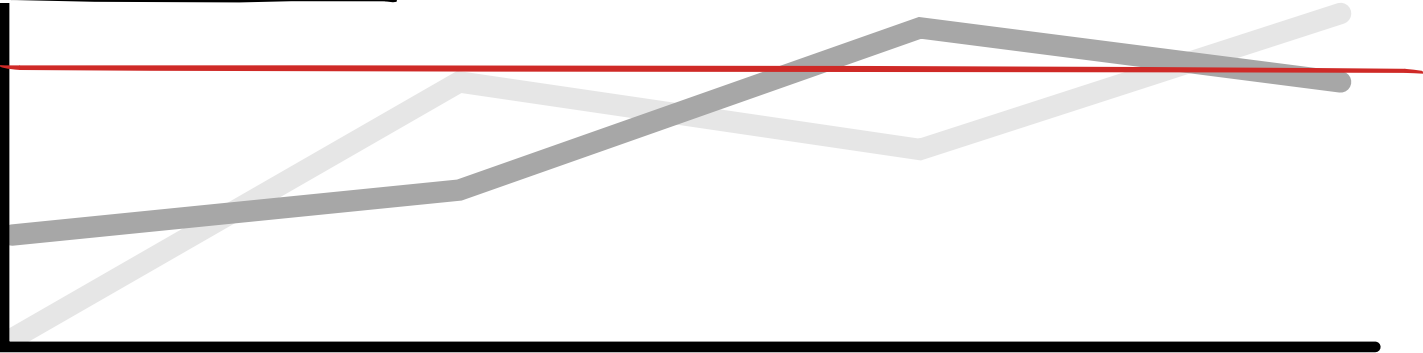
.png

.pdf

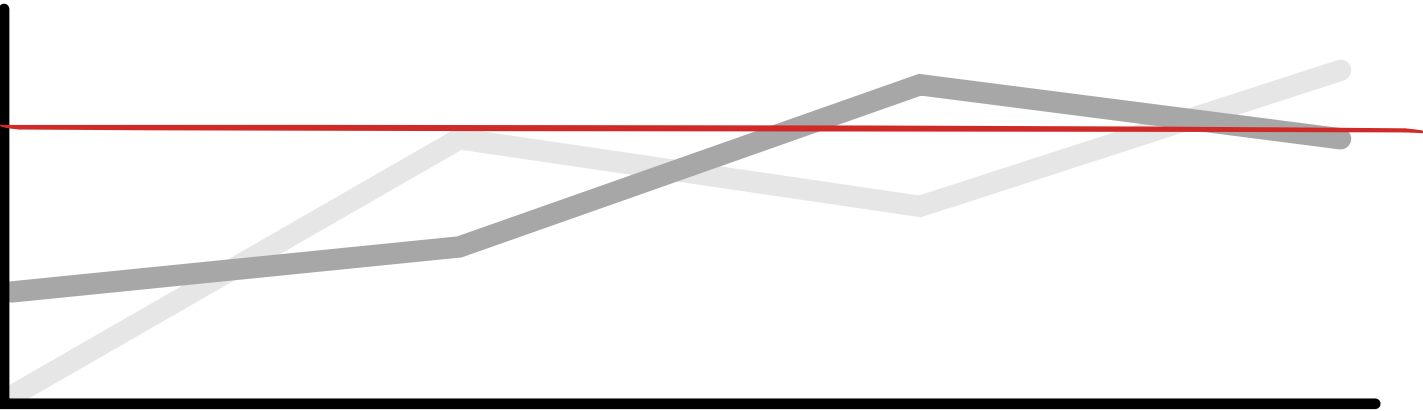
.svg

Threshold

93



DNA sequence 2



Output graph

Export As...

.png

.pdf

.svg

Threshold

93

Confirmation

Output saved to current directory.

OK

DNA sequence 2

