

WeightsVis User's Guide

(Release 1.0)

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1 Visualization of the Weights

Since version 2.1 the weights matrix calculated by TICO is written to the file `tico.weights` in the output directory. The matrix can be visualized with the MATLAB® compiler generated tool `WeightsVis` which is provided in TICO2.1 complete package. The tool also is provided separately as a tarball which should be unpacked in the TICO-home directory or as independent »complete package« version.

The visualization of the positional weights (see figure) is realized in the form of a colored scheme. The colors represent the level of the weights of a trinucleotide at the respective position. High positive weights produce deep red areas in the plot, high negative weights produce deep blue ones, intermediate weights are represented by orange, yellow and green areas. A color scale displays the colors with the associated weight values.

The positions correspond to those in the *extract window* of TICO, which are aligned to the position of the candidate TIS denoted at position 0. The positions with negative value indicate the upstream region, the positions with positive value indicate the downstream region, respectively. Note that the last two positions of the sequences are not considered in the evaluation for they do not represent a trimer. So if for example the default values are used for up- and downstream extraction, the example sequences (output in `tis.seq` and `tis.altseq`) have the length 60, with the TIS candidates at position 31 (giving the first position the index 1). For the evaluation the trimer occurrences are counted for position 1-58. Additionally, to exclude boundary effects, the weights of the first and the last three positions are neglect. The latter positions are part of the weights matrix but are excluded from the visualization. So the visualization of a weights matrix calculated for the settings described above would show the position -27..0..24.

`WeightsVis` can be started from a script, adapting the necessary paths and setting some default parameters or the program may be called directly.

During invocation a flag with value 0 or 1 may be given to the script. The default value of the flag is 0. If the flag has value 1 the trinucleotide with maximum positive score is marked in the visualized matrix. Additionally the title and the labels of the axis may be altered in the starter script or during the direct invocation of the program.

Syntax for invocation with the starter script:

```
vis weights-file [max-flag]
```

Example for invocation with the bash-script:

```
vis /var/tmp/5793472968765/tico.weights
```

Example for invocation with the batch-script:

```
vis "c:\my documents\758943764892\tico.weights"
```

Note for invocation with the batch-script: The maxFlag cannot be given in the commandline, but may be altered in the batch script (vis.bat).

Syntax for invocation without the starter script:

```
WeightsVis oligos figure-title X-Label Y-Label weights-file max-flag
```

Example for invocation without the starter script:

```
WeightsVis ./oligos 'TICO-Weights' 'Position' 'Trinucleotide' ../123/tico.weights 0
```

Example for invocation with the batch-script:

```
vis.bat c:\var\tmp\5793472968765\tico.weights
```

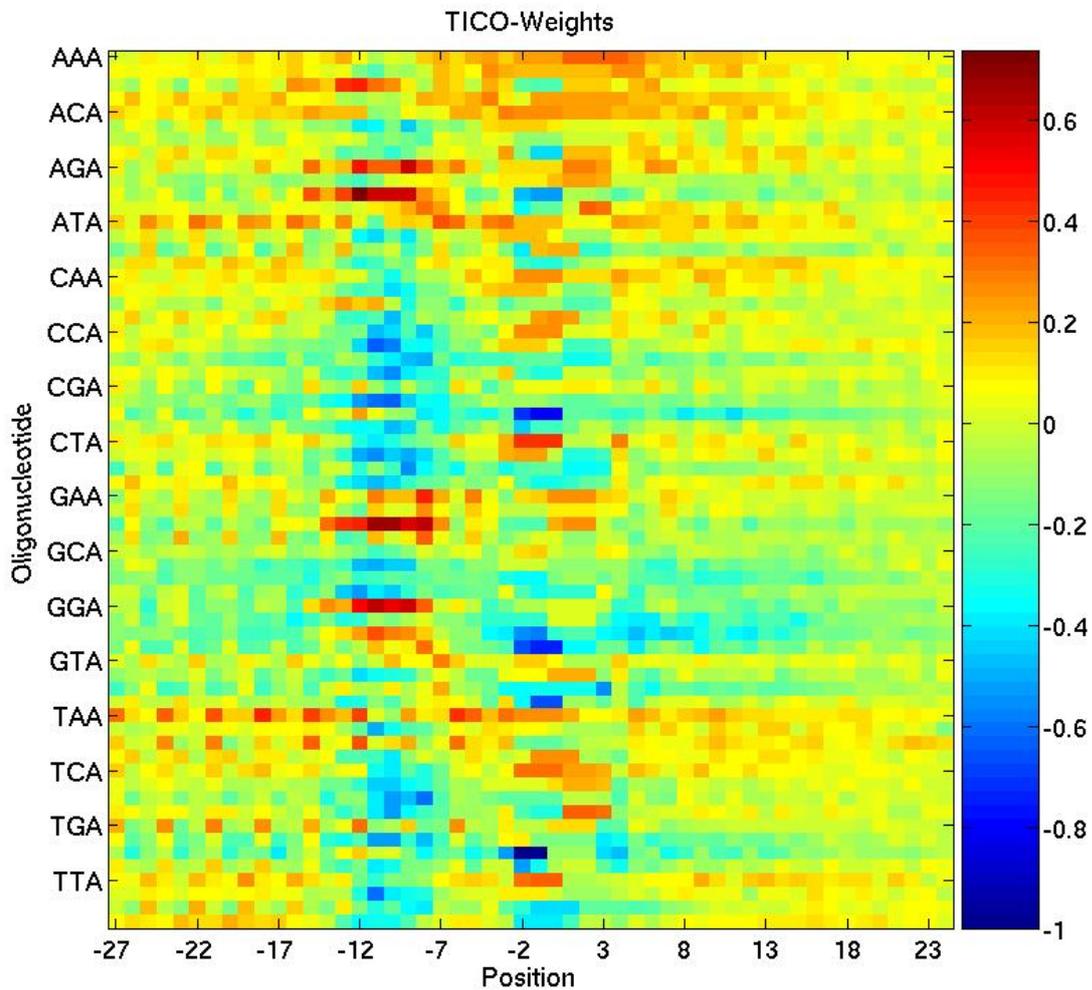


Figure 1: Visualization of the weights matrix calculated for *E. coli* using the default settings.