Weight Matrix

The Weight Matrix plugin is a tool for solving the problem of a sequence annotating. As well as for the SITECON, the main use case of the plugin is recognition of potential transcription factor binding sites on basis of the data about conservative conformational and physicochemical properties revealed with the binding sites sets analysis.

The Weight Matrix contains a lot of position frequency matrices (PFM 's) and position weight matrices (PWM 's, also known as position specific score matrices — PSSM 's). The matrices came from two wide-known open archives: JASPAR, which contains frequency matrices, and UniPROBE containing weight matrices.

Also the Weight Matrix plugin provides a tool for creating specific position frequency and weight matrices from an existing alignment or from a file with several sequences. The created matrix can be used as a profile for the search as well as the JASPAR and UNIPROBE ones.

To search for transcription factor binding sites in a DNA sequence select the Analyze Search TFBS with matrices context menu item. The Weight matrix search dialog will appear:

용 Weight Matrix S	Search		? ×			
Matrix: Score: Search JASPAR da Weight algorithm Strands Both strands			View matrix			
 Direct strand 		1 -	199950			
 Reverse complement strand 						
Matrix	Minimal score	Algorithm	Load list Save list Load folder Clear list			
Range Clear results Sa Results found: 0.	Matrix ave as annotations	Strand Score				
	Add to queue	Search Close	Help			

In the search dialog you must specify a file with PWM or PFM. You can do so by pressing the browse button and selecting the file.

Also you can use the special interface to choose a JASPAR matrix by pressing the Search JASPAR database button.

Alternative way to specify the position weight/frequency matrix is to create a specific one from an alignment or a file with several sequences with the *build* a new matrix tool.

After the profile (the matrix) is loaded, you can adjust the threshold value. The threshold sets the minimal identity score for a result to pass. The more the result score is, the more it is homologically related to the aligned region. By changing the threshold you can filter low- scoring results.

If the loaded matrix is a position frequency matrix, you must also specify the algorithm to build the corresponding position weight matrix which will represent the transcription factor. There are four algorithms available.

Weight algorithm	Berg and von Hippel 🛛 👻
-Strands	Berg and von Hippel
Suanus	Log-odds
 Both strand 	Match
O bourbuand	NLG
O Direct stress	

Also you can add a selected matrix with the specified *Minimal score* and the *Algorithm* to the matrices list. To do it, select the matrix and other options and press the *Add to queue* button. The plugin will search with all matrices specified in the list.

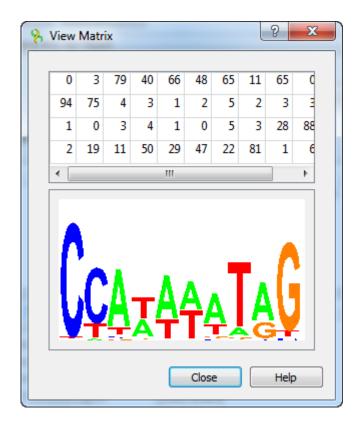
You can use the Save list button to export the list of matrices to a *.csv file. Later the list can be loaded from the file using the Load list button.

The rest options are standard sequence search options: the strand and the sequence region where to search for matches.

After specifying the necessary options press the Search button. The found results will appear in the dialog table. The corresponding results identity scores are in the Score column.

Range 🔍 🔻	Matrix	Strand	Score
199944199949	9 MA0271.1.pfm	Direct strand	31.26%
199943199948	3 MA0271.1.pfm	Direct strand	62.39%
199942199947	7 MA0271.1.pfm	Direct strand	53.92%
199941199946	5 MA0271.1.pfm	Direct strand	26.86%
199940199945	5 MA0271.1.pfm	Direct strand	26.86%
199939199944	+ MA0271.1.pfm	Direct strand	14.07%
199938199943	3 MA0271.1.pfm	Direct strand	57.69%

Also you can see the matrix by using the View matrix button:



The regions found by the weight matrix algorithm can be saved as annotations to the DNA sequence in the Genbank format by pressing the Save as annotations button.

After saving, the file with resulting annotations will be automatically added to the current project, and the annotations will be added to the original sequence.

Note that in case of selecting JASPAR or UNIPROBE matrix, the resulting annotations will contain the given matrix properties.

🗞 Weight Matrix S	earch	8 23			
Matrix: C:/work/ug	gene/data/position_weight_matrix/JASPAR/plants/MA0044.1.pfm				
Score:	Create Appotation	85%			
Search JASPAR D	% Create Annotation	View matrix			
Weight algorithm	▼ Save annotation(s) to				
Both strands	Existing table Create new table	•			
 Direct strand Reverse com 	✓ Annotation parameters Group name <auto></auto>	199950			
Matrix MA0044.1.pfm	Annotation name misc_feature	Load list			
	Create Cancel Help Save list				
		Clear list			
Range	Matrix Strand Score	*			
199824199832	2 MA0044.1.pfm Direct strand	85.35%			
199397199405	5 MA0044.1.pfm Direct strand	85.75%			
19897519898	3 MA0044.1.pfm Direct strand	85.29% 👻			
Clear results Sa	ave as annotations				
Results found: 1379.					
	Add to queue Search Close	Help			

See also:

- Searching JASPAR DatabaseBuilding New Matrix