Searching for TFBS with Weight Matrices

Task Name: pwm-search

Searches for transcription factor binding sites (TFBS) with position weight matrices (PWM) and saves the regions found as annotations.

Parameters:

seq — semicolon-separated list of input sequence files to search TFBS in. [String, Required]

matrix — semicolon-separated list of the input PWM. [String, Required]

out — output Genbank file.

name — name of the annotated regions. [String, Optional, Default: “misc_feature”]

min-score — minimum percentage score to detect TFBS. [Number, Optional, Default: 85]

strand — strands to search in. [Number, Optional, Default: 0]

The following values are available:

- 0 (both strands)
- 1 (direct strand)
- -1 (complement strand)

Example:

```
ugene pwm-search --seq=input.fa --matrix=Aro80.pwm;Aft1.pwm --out=res.gb
```