

Searching for TFBS with PFM

Task Name: pfm-search

Searches for transcription factor binding sites (TFBS) with position weight matrices (PWM) converted from input position frequency matrices (PFM) 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 PFM. [String, Required]

out — output Genbank file.

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

type — type of the matrix. [Boolean, Optional, Default: false]

The following values are available:

- true (dinucleic type)
- false (mononucleic type)

Dinucleic matrices are more detailed, while mononucleic ones are more useful for small input data sets.

algo — algorithm used to convert a PFM to a PWM. [String, Optional, Default: "Berg and von Hippel"]

The following values are available:

- Berg and von Hippel
- Log-odds
- Match
- NLG

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 pfm-search --seq=in.fa --matrix=MA0265.1.pfm;MA0266.1.pfm --out=res.gb
```