Building PWM

Task Name: pwm-build

Builds a position weight matrix from a multiple sequence alignment file.

Parameters:

in — semicolon-separated list of input MSA files. [String, Required]

out — output file. [String, Required]

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 build the matrix. [String, Optional, Default: “Berg and von Hippel”]

The following values are available:

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

Example:

```
ugene pwm-build --in=COI.aln --out=result.pwm
```