
- -4pc - -4pc

Name

`aacode3` -- Produce a weighted matrix from a FASTA file

`aacode3`

```
aacode [[-l[-i[-e-b]]]][-w #][-d #][-t tmpdir][-m output_matrix][-p output_pinfo]  
{file.txt}
```

Description

aacode3 takes as input a FASTA file of protein sequences. It will output a matrix of word weights based on the weighting scheme selected. Additionally, it produces a `.pinfo` file that maps the protein IDs to the elements of the matrix.

aacode3 uses a `wordsize` to generate the output matrix. When the `-d` option is specified, this `wordsize` becomes a window size, and the `wordsize` is (window-wildcards).

Options

* 0.60+1em

* 0.60+1em `-l` use LBA weighting

* 0.60+1em `-i` use IPF weighting

* 0.60+1em `-e` use log-entropy weights

* 0.60+1em `-b` use binary weights

* 0.60+1em `-w #` window/word size

* 0.60+1em `-d #` number of "wildcards"

* 0.60+1em `-t tmpdir` directory to store unmerged files in. This has to be as least as large as you expect your output matrix to be.

* 0.60+1em `-m output_matrix` filename to save the output matrix as. Defaults to `file.matrix`

* 0.60+1em `-p output_pinfo` filename to save the output pinfo as. Defaults to `file.pinfo`

* 0.60+1em `file.txt` The input FASTA file. This argument is required, and must have a `.txt` extension.

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