Scan2a

Program for aligning two aminoacid sequences using a sequential search for most significant similarity regions.

Example of output:

```
L:146         Sequence  HEMOGLOBIN BETA HUMAN
vs C:\example_data\seq1.fa
Total 1 sequences produce 1 significant alignment(s).

[DD]      1, S:      21.664, L:       146 HEMOGLOBIN BETA NILE CROCODILE
**************************************************************************
[DD] Sequence:      1(     1), S:       21.664, L:       146 HEMOGLOBIN BETA
NILE CROCODILE
Summ of block lengths: 124, Alignment bounds:
On first  sequence: start        7, end        146, length 140
On second sequence: start        7, end        146, length 140
Block of alignment: 6
    1 P:        7         7 L:       2, G: 100.51, W:     10, S:2.64676
    2 P:       14        14 L:       7, G:  83.27, W:     20, S:5.05147
    3 P:       24        24 L:      99, G:  78.57, W:    225, S:20.0317
    4 P:      128       128 L:       7, G:  94.76, W:     30, S:5.80101
    5 P:      137       137 L:       2, G:  92.46, W:      8, S:2.4219
    6 P:      140       140 L:       7, G:  82.12, W:     19, S:4.97651
      1 vhltpeEKsavtaLWGKVNVdevGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPKV
        ......||.....||0||7|...|||||0|8|9||||07|9||7|||8|000|9|0|0||
      1 asfdphEKqligdLWHKVDVahcGGEALSRMLIVYPWKRRYFENFGDISNAQAIMHNEKV

     61 KAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKLHVDPENFRLLGNVLVCVLAHHFGK
        7|||||||07|08070|||08800||0||7|||8|||||||||8|||79890|||0|90|
     61 QAHGKKVLASFGEAVCHLDGIRAHFANLSKLHCEKLHVDPENFKLLGDIIIIVLAAHYPK

    121 EFtppvqAAYQKVVagVAnALAHKYH
        8|.....|||||7|..||.|||07||
    121 DFglechAAYQKLVrqVAaALAAEYH
....
```

Where:

1-st line is the header:

```
[DD] Sequence:      1(     1), S:       21.664, L:       146 HEMOGLOBIN BETA
NILE CROCODILE
```

[DD]	No sence, used for output compatibility on nucleotide sequence alignment.
Sequence: 1(1)	Order number of sequence from a query set which is submitted to alignment. In brackets is an order number for alignment of this sequence (if it resulted in more than one alignment). Variants: 4(5) - the fifth alignment of the fourth sequence from a set
S	Score of this alignment.
L	Length of this query sequence
HEMOGLOBIN BETA NILE CROCODILE	Name of this query sequence

Additional information about alignment:

```
Summ of block lengths: 124, Alignment bounds:
On first  sequence: start        7, end        146, length 140
On second sequence: start        7, end        146, length 140
```

| length | The length covered by alignment, in target and query sequences appropriately. |

List of alignment blocks:

```
Block of alignment: 6
   1 P:          7          7 L:        2, G: 100.51, W:     10, S:2.64676
   2 P:         14         14 L:        7, G:  83.27, W:     20, S:5.05147
```

Block of alignment: 6 - Number of blocks in this alignment. Each line below defines an appropriate block. Detailed description of a line from this list is shown further:

```
   1 P:          7          7 L:        2, G: 100.51, W:     10, S:2.64676
```

1	Block number.
P: 7 7	Positions of similarity block' start in target and query sequences appropriately. In this case - from the seventh position in both sequences.
L: 2	Length of this similarity block.
G: 100.51	Homology of this similarity block.
W: 10	Weight of this similarity block (the arithmetic sum of symbols' similarity calculated from the given similarity matrix).
S:2.64676	Score of this similarity block.

Alignment:

```
1 vhltpeEKsavtaLWGKVNVdevGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPKV
  ......||.....||0||7|...|||||0|8|9||||07|9||7|||8|000|9|0|0||
1 asfdphEKqligdLWHKVDVahcGGEALSRMLIVYPWKRRYFENFGDISNAQAIMHNEKV
```

1 line - The target sequence itself. Capital letters correspond to blocks of similarity, lower case - not aligned regions.
2 line - Separator line. Separator line symbols: "|" - perfect coincidence between symbols. Figures means the degree of symbols' similarity. Vary from 0 up to 9. 0 - no similarity, 9 - maximal similarity.
3 line - The query sequence itself. Capital letters correspond to blocks of similarity, lower case - not aligned regions.