
Aligning Sequences

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Obtaining the sequences

Search the web for AGRE1_RAT Adhesion G protein-coupled receptor E2 protein. Download the protein sequence.

```
ratptnfile = bmes.downloadurl('https://www.uniprot.org/uniprot/Q5Y4N8.fasta', 'rat.agre1.ptn.fasta')
```

```
% also find and download the human protein, AGRE1_HUMAN
humptnfile = bmes.downloadurl('https://www.uniprot.org/uniprot/Q14246.fasta')
```

```
ratptnfile =
```

```
    'C:/Users/ahmet/AppData/Local/Temp/bmes/rat.agre1.ptn.fasta'
```

```
humptnfile =
```

```
    'C:/Users/ahmet/AppData/Local/Temp/bmes/
httpswww.uniprot.orguniprotQ14246.fasta'
```

Reading fasta file

```
ratptn = fastaread(ratptnfile)
```

```
ratptn =
```

```
    struct with fields:
```

```
    Header: 'sp|Q5Y4N8|AGRE1_RAT Adhesion G protein-coupled receptor
E2 OS=Rattus norvegicus OX=10116 GN=Adgre1 PE=2 SV=1'
```

```
    Sequence:
```

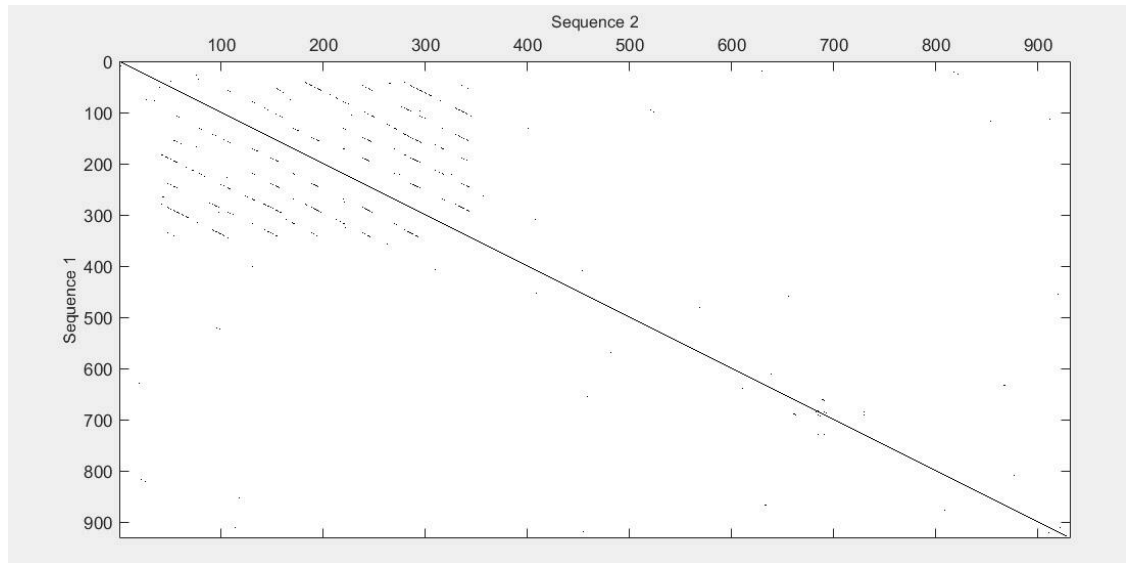
```
    'MWGFWLLLFWGFSGTHRWGMTTLAILGQRLNGVNECQDTTTCPAYATCTDTTESYYCTCKQGFLPSNGQTNFQGPGEVCQ'
```

Self-dot-plot

use window size=10, match filter 5 to filter out noise.

```
seqdotplot(ratptn, ratptn, 10, 5)
```

*Warning: Match matrix has more points than available screen pixels.
Scaling image by factors of 1 in X and 2 in Y.*



Sequence alignments

```
ratptn = fastaread(ratptnfile);  
humptn = fastaread(humptnfile);
```

Local alignment

```
[score, align] = swalign(ratptn, humptn, 'alphabet', 'aa')
```

score =

1.2933e+03

align =

3×938 char array

```
      'MWGFWLLLFWGFSGTHRW-  
GMTTLAILGQRLNGVNECQDTTTCPAYATCTDTTESYYCTCKQGFLPSNGQTNFQGPVVECQDVNECLRSDSPCGSNSVCTN  
S-  
WKLRMNSHVVGTVTGERKEDFSKPIVYTLQHIQPKQKSERVICVSWNTDVEDGRWTPSGCETVEASEHTVCSCNRMTNLA
```

Global alignment

$M =$

Columns 1 through 13

	4	-1	-2	-2	0	-1	-1	0	-2	-1	-1
-1	-1										
	-1	5	0	-2	-3	1	0	-2	0	-3	-2
2	-1										
	-2	0	6	1	-3	0	0	0	1	-3	-3
0	-2										
	-2	-2	1	6	-3	0	2	-1	-1	-3	-4
-1	-3										
	0	-3	-3	-3	9	-3	-4	-3	-3	-1	-1
-3	-1										
	-1	1	0	0	-3	5	2	-2	0	-3	-2
1	0										
	-1	0	0	2	-4	2	5	-2	0	-3	-3
1	-2										
	0	-2	0	-1	-3	-2	-2	6	-2	-4	-4
-2	-3										
	-2	0	1	-1	-3	0	0	-2	8	-3	-3
-1	-2										
	-1	-3	-3	-3	-1	-3	-3	-4	-3	4	2
-3	1										
	-1	-2	-3	-4	-1	-2	-3	-4	-3	2	4
-2	2										
	-1	2	0	-1	-3	1	1	-2	-1	-3	-2
5	-1										
	-1	-1	-2	-3	-1	0	-2	-3	-2	1	2
-1	5										
	-2	-3	-3	-3	-2	-3	-3	-3	-1	0	0
-3	0										
	-1	-2	-2	-1	-3	-1	-1	-2	-2	-3	-3
-1	-2										
	1	-1	1	0	-1	0	0	0	-1	-2	-2
0	-1										
	0	-1	0	-1	-1	-1	-1	-2	-2	-1	-1
-1	-1										
	-3	-3	-4	-4	-2	-2	-3	-2	-2	-3	-2
-3	-1										
	-2	-2	-2	-3	-2	-1	-2	-3	2	-1	-1
-2	-1										
	0	-3	-3	-3	-1	-2	-2	-3	-3	3	1
-2	1										
	-2	-1	3	4	-3	0	1	-1	0	-3	-4
0	-3										
	-1	0	0	1	-3	3	4	-2	0	-3	-3
1	-1										
	0	-1	-1	-1	-2	-1	-1	-1	-1	-1	-1
-1	-1										
	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	-4
-4	-4										

Columns 14 through 24

-2	-1	1	0	-3	-2	0	-2	-1	0	-4
-3	-2	-1	-1	-3	-2	-3	-1	0	-1	-4
-3	-2	1	0	-4	-2	-3	3	0	-1	-4
-3	-1	0	-1	-4	-3	-3	4	1	-1	-4
-2	-3	-1	-1	-2	-2	-1	-3	-3	-2	-4
-3	-1	0	-1	-2	-1	-2	0	3	-1	-4
-3	-1	0	-1	-3	-2	-2	1	4	-1	-4
-3	-2	0	-2	-2	-3	-3	-1	-2	-1	-4
-1	-2	-1	-2	-2	2	-3	0	0	-1	-4
0	-3	-2	-1	-3	-1	3	-3	-3	-1	-4
0	-3	-2	-1	-2	-1	1	-4	-3	-1	-4
-3	-1	0	-1	-3	-2	-2	0	1	-1	-4
0	-2	-1	-1	-1	-1	1	-3	-1	-1	-4
6	-4	-2	-2	1	3	-1	-3	-3	-1	-4
-4	7	-1	-1	-4	-3	-2	-2	-1	-2	-4
-2	-1	4	1	-3	-2	-2	0	0	0	-4
-2	-1	1	5	-2	-2	0	-1	-1	0	-4
1	-4	-3	-2	11	2	-3	-4	-3	-2	-4
3	-3	-2	-2	2	7	-1	-3	-2	-1	-4
-1	-2	-2	0	-3	-1	4	-3	-2	-1	-4
-3	-2	0	-1	-4	-3	-3	4	1	-1	-4
-3	-1	0	-1	-3	-2	-2	1	4	-1	-4
-1	-2	0	0	-2	-1	-1	-1	-1	-1	-4
-4	-4	-4	-4	-4	-4	-4	-4	-4	-4	1

M = eye(size(M))*2-1

M =

Columns 1 through 13

1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1
-1	-1									
-1	1	-1	-1	-1	-1	-1	-1	-1	-1	-1
-1	-1									
-1	-1	1	-1	-1	-1	-1	-1	-1	-1	-1
-1	-1									
-1	-1	-1	1	-1	-1	-1	-1	-1	-1	-1
-1	-1									
-1	-1	-1	-1	1	-1	-1	-1	-1	-1	-1
-1	-1									
-1	-1	-1	-1	-1	1	-1	-1	-1	-1	-1
-1	-1									
-1	-1	-1	-1	-1	-1	1	-1	-1	-1	-1
-1	-1									
-1	-1	-1	-1	-1	-1	-1	1	-1	-1	-1
-1	-1									
-1	-1	-1	-1	-1	-1	-1	-1	1	-1	-1
-1	-1									
-1	-1	-1	-1	-1	-1	-1	-1	-1	1	-1
-1	-1									
-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	1
-1	-1									
-1	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1

[illegible]

Columns 14 through 24

[illegible]

```
[score, align] =  
    nwalign(ratptn,humptn,'alphabet','aa','scoringmatrix',M)
```

-123

3x937 char array

'MWGFWLLLFWGFSGTHRWGMTTLAILGQRLNGVNECQDTTTTCPAYATCTDTTESYYCTCKQGFLPSNGQTNFQGPVVECQ
S-
WKLRLMNSHVVGTVTGERKEDFSKPIVYTLQHIQPKQKSERVICVSWNTDVEDGRWTPSGCETVEASETHTVCSNRMTNLA
'
'MRGFNLLLFWGCCVMHSEGHIRPTRKPNNTKG-
NNCRDSTLCPAYATCTNTVDSYYCACKQGFLSSNGQNHFKDPGVRCKDIDECQSPQPCGPNSSCKNLSGRYKCSCLDGFSS
N-----YSC----FC--N-----PGF-----ES-S-S---G-HLS-FQ--GLKA--
SCEDIDECTEMCPINSTCTNTPGSYFCTCHPGFAPSNGQLNFTDOGVECRDIDECRODPSTCGPNSICTNALGSYSCGCIAG