

# deepBlockAlign v1.0

## Alignment parameters:

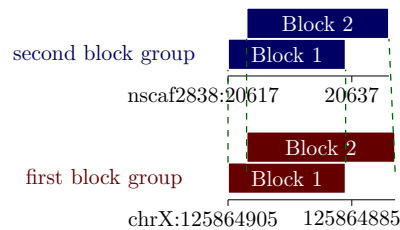
```
[Input]
date and time          Sun, 03 Feb 2013 02:04:00 +0100
first block group      CervixHelas3Rep2_cluster_15885
first file             /home/projects/users/sachin/frontier/putative_mirna//tmp3500query.tmp
second block group     bg_110
second file            /home/projects/users/sachin/frontier/bgs/mirbase.all.map.bgs.flagged.sig

[Block group alignment]
distance weight        1
block weight           1
gap penalty            -1

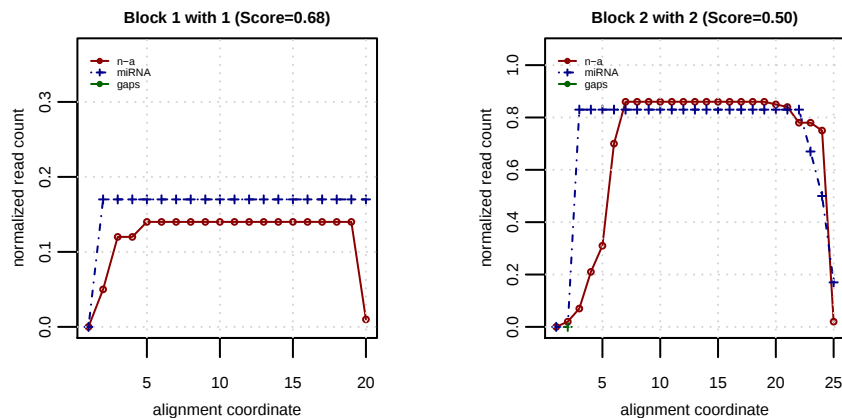
[Block alignment]
gap initialization penalty -2
gap extension penalty    -1
threshold for expression difference 1
match score             1
mismatch score          -1
profile shape difference penalty 1

[Block group information]
Entropy (first block group) 2.55
Reads (first block group) 10.12
% Unique reads (first block group) 0
Entropy (second block group) 0.65
Reads (second block group) 12.00
% Unique reads (second block group) 100
```

**Block group alignment:** CervixHelas3Rep2-cluster-15885-n-a(-) with bg-110-bmo-mir-2813-2-MI0012436(+) [Score: 0.73]



## Block alignment:



**Citation:** Langenberger, D\*, Pundhir, S\*, Ekstrøm, C.T., Stadler, P.F., Hoffmann, S., and Gorodkin, J.(2012). deepBlockAlign: A tool for aligning RNA-seq profiles of read block patterns. *Bioinformatics*, **28**(1),17-24. (\*equal contribution)