

deepBlockAlign v1.0

Alignment parameters:

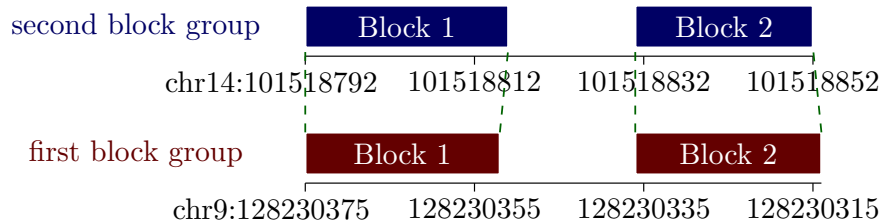
```
[Input]
date and time          Sun, 03 Feb 2013 02:01:22 +0100
first block group      CervixHelas3Rep2_cluster_15123
first file             /home/projects/users/sachin/frontier/putative_mirna//tmp3500query.tmp
second block group     bg_221
second file            /home/projects/users/sachin/frontier/bgs/mirbase.all.map.bgs.flagged.sig

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

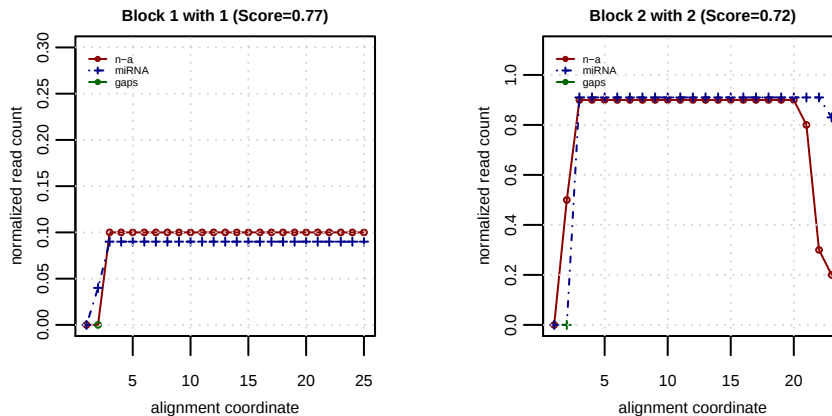
[Block alignment]
gap initialization penalty -2
gap extension penalty    -1
threshold for expression difference 1
match score             1
mismatch score          -1
profile shape difference penalty 1

[Block group information]
Entropy (first block group) 1.36
Reads (first block group) 10.00
% Unique reads (first block group) 100
Entropy (second block group) 0.51
Reads (second block group) 23.00
% Unique reads (second block group) 100
```

Block group alignment: CervixHelas3Rep2-cluster-15123-n-a(-) with bg-221-hsa-mir-487a-MI0002471(+) [Score: 0.83]



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)