

deepBlockAlign v1.0

Alignment parameters:

```

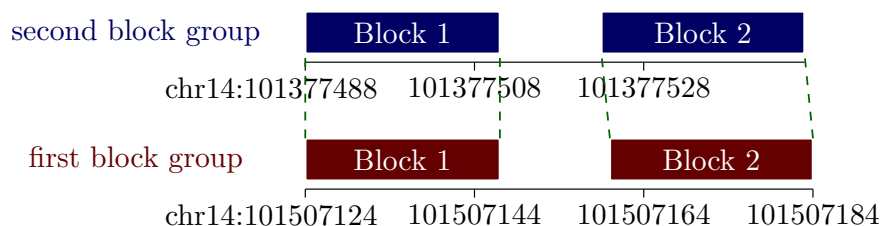
[Input]
date and time          Sun, 03 Feb 2013 01:52:56 +0100
first block group      BreastMcf7Rep2_cluster_3598
first file             /home/projects/users/sachin/frontier/putative_mirna//tmp3000query.tmp
second block group     bg_195
second file            /home/projects/users/sachin/frontier/bgs/mirbase.all.map.bgs.flagged.sig

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

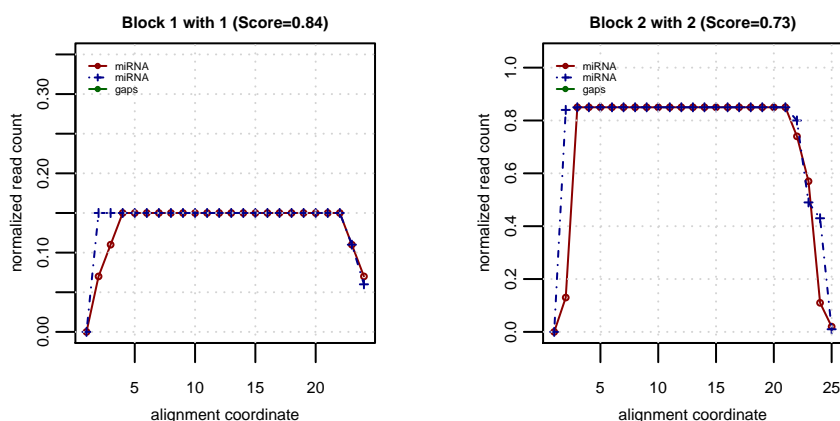
[Block alignment]
gap initialization penalty -2
gap extension penalty   -1
threshold for expression difference 1
match score            1
mismatch score        -1
profile shape difference penalty 1

[Block group information]
Entropy (first block group) 1.36
Reads (first block group)   26.75
% Unique reads (first block group) 15
Entropy (second block group) 0.71
Reads (second block group)  79.00
% Unique reads (second block group) 100
  
```

Block group alignment: BreastMcf7Rep2-cluster-3598-hsa-mir-376a-1(+) with bg-195-hsa-mir-370-MI0000778(+) [Score: 0.85]



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)