

deepBlockAlign v1.0

Alignment parameters:

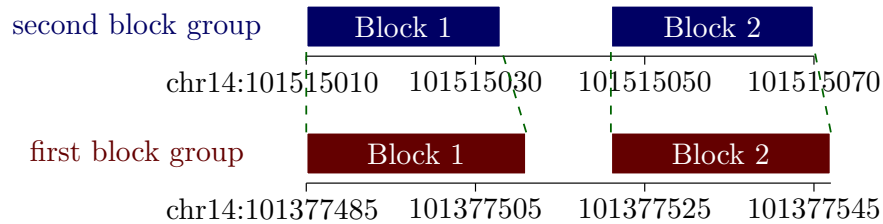
```
[Input]
date and time          Sun, 03 Feb 2013 01:54:47 +0100
first block group      LungAg04450Rep1_cluster_3939
first file             /home/projects/users/sachin/frontier/putative_mirna//tmp3000query.tmp
second block group     bg_219
second file            /home/projects/users/sachin/frontier/bgs/mirbase.all.map.bgs.flagged.sig

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

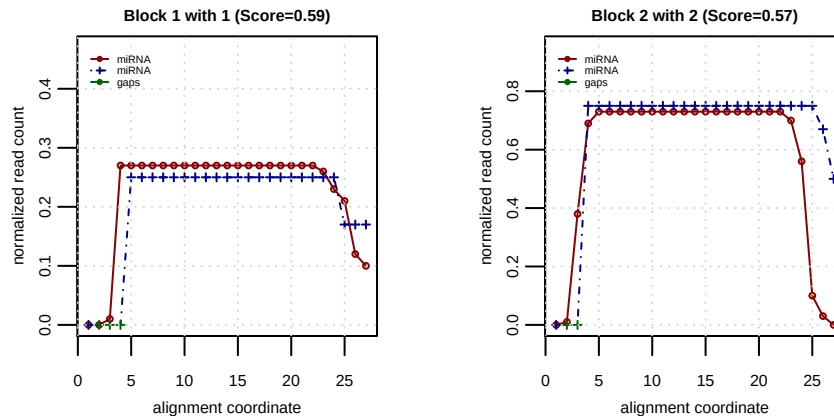
[Block alignment]
gap initialization penalty -2
gap extension penalty    -1
threshold for expression difference 1
match score             1
mismatch score          -1
profile shape difference penalty 1

[Block group information]
Entropy (first block group) 1.95
Reads (first block group) 1159.33
% Unique reads (first block group) 99
Entropy (second block group) 0.81
Reads (second block group) 12.00
% Unique reads (second block group) 100
```

Block group alignment: LungAg04450Rep1-cluster-3939-hsa-mir-370(+) with bg-219-hsa-mir-544a-MI0003515(+) [Score: 0.72]



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)