

assignment 7 Rebekka Trenkle

1 Paarweises Alignment

Figure 1: Screenshot of the executed code with result

```
1 # import package
2 library(Biostrings)
3
4 # create strings for the sequences to be aligned
5 s1 <- "GAATC"
6 s2 <- "CATAAC"
7
8 # create the nucleotide substitution matrix called sigma. This can only be symmetric
9 sigma <- nucleotideSubstitutionMatrix(match = 10, mismatch = -5, baseOnly = TRUE)
10 sigma
11 # change entries in sigma to zero, that it matches the one from the lecture
12 sigma[1,3] <- 0
13 sigma[2,4] <- 0
14 sigma[3,1] <- 0
15 sigma[4,2] <- 0
16 sigma
17
18 # perform the alignment using the function from the package Biostrings
19 # https://www.rdocumentation.org/packages/Biostrings/versions/2.40.2/topics/pairwiseAlignment
20 # change the values for gapopening and gapExtension to -4 to match the lecture
21 alignment <- pairwiseAlignment(s1, s2, substitutionMatrix = sigma, gapOpening = -4,
22                                gapExtension = -4, scoreOnly = FALSE)
23 alignment # shows the aligned sequences
```

22:40 (Top Level) R Script

Console Terminal Jobs

```
~/
> alignment
> # change the values for gapopening and gapExtension to -4 to match the lecture
> alignment <- pairwiseAlignment(s1, s2, substitutionMatrix = sigma, gapOpening = -4, gapExtension = -4, scoreOnly = FALSE)
> alignment
Global PairwiseAlignmentssinglesubject (1 of 1)
pattern: GA-ATC
subject: CATA-C
score: 9
> |
```

Figure 2: Closer look at the aligned sequences

```
> alignment
Global PairwiseAlignmentssinglesubject (1 of 1)
pattern: GA-ATC
subject: CATA-C
score: 9
|
```

2 Multiples Alignment

Figure 3: Screenshot of a snippet of the aligned sequences. Sequences used: example data from the DECIPHER package, aligned with the alignTranslation function.

