

8. Übung

-8.1

```
> library(Biostrings)
> s1 <- "GAATC"
> s2 <- "CATAC"
> sigma <- nucleotideSubstitutionMatrix(match = 10, mismatch = -5, baseOnly = TRUE)
> sigma
      A  C  G  T
A 10 -5 -5 -5
C -5 10 -5 -5
G -5 -5 10 -5
T -5 -5 -5 10
> 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
> |
```

-8.2

```
> DNA
A DNAStringSet instance of length 317
width seq
[1] 1015 -----ATGGCTTTA...GTAAAAAAGAAAA-----names
[2] 1015 -----ATGGGAATA...ATTGAGAGAAGAAAAAG-----Rickettsia prowaz...
[3] 1015 -----ATGGGAATA...ATTGAGAGAAGAAAAAG-----Porphyromonas gin...
[4] 1015 -----ATGGGAATA...ATTGAGAGAAGAAAAAG-----Porphyromonas gin...
[5] 1015 -----ATGGCTATC...GTACGTCGTCGTGGTAAA-----Pasteurella multo...
... ..
[313] 1015 -----ATGGCAATT...GTACGTCGCGGTACTAAA-----Pectobacterium at...
[314] 1015 -----ATGCCTATT...ATTCGCGATCGTCGCGTCAAG-----Acinetobacter sp....
[315] 1015 -----ATGGGCATT...GTGCGTCGTCGCAAGAAGTCTTCCAAGCGGGTTCGCGTGGTTCGTCACTCT Thermosynechococc...
[316] 1015 -----ATGGCACTG...CTCCTAAGCCGCCACAAGCGGAAGAAG-----Bradyrhizobium ja...
[317] 1015 -----ATGGGCATT...ATCCGCCGTCGCAAGACGGCTTCGGGCGAGGT-----Gloeobacter viola...
```