B2A2

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```r
#library(mosaic)
#library(knitr)
#library(dplyr)
source("RBIB.R")
```

```
## Warning: Paket 'S4Vectors' wurde unter R Version 4.1.2 erstellt
```

```r
library(Biostrings)
```

Die Sequenzen sind:

```r
#Nukleotide
snuk = "CGATCCTGT"
tnuk = "CATCGCCTT"
#Aminosäuren
sam = "KIQYKREPNIPSVSLINSLFAWEIRDRI"
tam = "KAQYRRECMIFVWEINRL"
```

```r
M = getmat()
```

Globales Alignment der beiden Nukleotide:

```r
align(snuk, tnuk, M)
```

```
## Global PairwiseAlignmentsSingleSubject (1 of 1)
## pattern: CGATC-CTGT
## subject: C-ATCGCCTT
## score: 0
```

```
## [1] "Score: 0 , Matches:  6 , Missmatch:  2"
```

Lokales Alignment der beiden Nukleotide:

```r
align(snuk, tnuk, M, "local")
```

```
## Local PairwiseAlignmentsSingleSubject (1 of 1)
## pattern: [3] ATC
## subject: [2] ATC
## score: 3
```

```
## [1] "Score: 3 , Matches:  3 , Missmatch:  0"
```

Globales Alignment der beiden Aminosäuren:

```r
align(sam, tam, M)
```

```
## Global PairwiseAlignmentsSingleSubject (1 of 1)
## pattern: KIQYKREPNIPSVSLINSLFAWEIRDRI
## subject: KAQYRRECMIF-V--------WEIN-RL
```

```
## score: -16
```

```
## [1] "Score: -16 , Matches:  11 , Missmatch:  7"
```

Lokales Alignment der beiden Aminosäure:

```
align(sam, tam, M, "local")
```

```
## Local PairwiseAlignmentsSingleSubject (1 of 1)
## pattern: [1] KIQYKRE
## subject: [1] KAQYRRE
## score: 3
```

```
## [1] "Score: 3 , Matches:  5 , Missmatch:  2"
```

Aufgabe 2.4

Globales Alignment mit BLOSUM62:

```
blosum(sam, tam)
```

```
## Global PairwiseAlignmentsSingleSubject (1 of 1)
## pattern: KIQYKREPNIPSVSLINSLFAWEIRDRI
## subject: KAQYRRE--C----MI---FVWEI-NRL
## score: 47
```

```
## [1] "Score: 47 , Matches:  11 , Missmatch:  7"
```

Lokales Alignment mi BLOSUM62

```
blosum(sam, tam, "local")
```

```
## Local PairwiseAlignmentsSingleSubject (1 of 1)
## pattern: [1] KIQYKREPNIPSVSLINSLFAWEIRDRI
## subject: [1] KAQYRRE--C----MI---FVWEI-NRL
## score: 47
```

```
## [1] "Score: 47 , Matches:  11 , Missmatch:  7"
```