4.1.1) Seq 1 : AATCG   Match: +1
        Seq 2 : AACG   Mismatch: -1
        Seq 3 : CG   Gap: -2
        Seq 4 : AA

Progressives Alignment

1. paarweises Alignment

Seq 1: A ATC G   Seq 1: A AT CG   Seq 1: A ATCG
Seq 2: A A – C G   Seq 3: – – – C G   Seq 4: A A – – –

$p = 1/5 = 0,2$ $p = 3/5 = 0,6$ $p = 3/5 = 0,6$

Seq 2: A ACG   Seq 2: A ACG   Seq 3: C G
Seq 3: – – C G   Seq 4: AA – –   Seq 4: A A

$p = 2/4 = 0,5$ $p = 2/4 = 0,5$ $p = 2/2 = 1$

2. Distanzmatrix

	S1	S2	S3	S4
S1	/	0,2	0,6	0,6
S2	0,2	/	0,5	0,5
S3	0,6	0,5	/	1
S4	0,6	0,5	1	/

3. Guide Tree mit UPGMA

	S3	S4	X
S3	0	1	0,55
S4	0		0,55
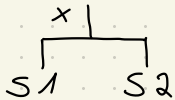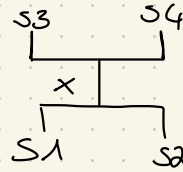
Seq 1   A ATC G
Seq 2   A A – C G
Seq 3   – – – C G
Seq 4   A A – – –

4.1.2) Konsens Alignment

```
w   A A T C G              Match   +1
x   A A — C G              Mismatch −1
y   — . − − C G            Gap      1
z   A A — − −
```

$\longrightarrow$ A A — C G

4.1.3) Sum −of− Pairs− Score: $\sigma(w \times y z) = \sigma(w,x) + \sigma(w,y) + \sigma(w,z) +$
$$\sigma(x,y) + \sigma(x,z) + \sigma(y,z)$$
$$= 2 - 4 - 4 - 1 - 1 - 7 = 0$$

4.2) siehe Ü4_Phylogenetischer Baum. jpg
und AView. pdf