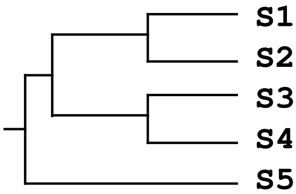
Step a: Compute pairwise alignments between all sequences to calculate the distance matrix

```
S1   ATCTCGAGA
S2   ATCCGAGA
S3   ATGTCGACGA
S4   ATGTCGACAGA
S5   ATTCAACGA
```

S1	-				
S2	.11	-			
S3	.20	.30	-		
S4	.27	.36	.09	-	
S5	.30	.33	.20	.27	-
	S1	S2	S3	S4	S5

Step b: Calculate tree (guide tree) from the distance matrix



Step c: Progressive alignment: align following the guide tree

Step c.1: align S1 with S2

```
S1   ATCTCGAGA
S2   ATC-CGAGA
```

Step c.2: align S3 with S4

```
S3   ATGTCGAC-GA
S4   ATGTCGACAGA
```

Step c.3: align α(S1,S2) with α(S3,S4)

```
S1   ATCTCGA--GA
S2   ATC-CGA--GA
S3   ATGTCGAC-GA
S4   ATGTCGACAGA
```

Step c.4: align α(S1,S2, S3, S4) with S5

```
S1   ATCTCGA--GA
S2   ATC-CGA--GA
S3   ATGTCGAC-GA
S4   ATGTCGACAGA
S5   AT-TCAAC-GA
```

Fig. 2
Duret & Abdeddaïm
Bioinformatics - a practical approach