# 10 Exercise solutions – Progressing alignment

## 1. Linkage clustering method for progressive alignment

Select two alignments from the three alignments,  $A^1 = s^1$ ,  $A^2 = s^2$ ,  $s^3$ , and  $A^3 = s^4$ ,  $s^5$ , for clustering.

Pairwise scores

	$s^1$	$s^2$	$s^3$	$s^4$	$s^5$
$s^1$	-	2	3	1	6
$\begin{array}{c c} s^1 \\ \hline s^2 \\ \hline s^3 \\ \end{array}$		-	-	4	5
			-	3	4
$\frac{s^4}{s^5}$				-	-
$s^5$					-

(a) Use the average linkage.

**Solution:**  $A^2$  and  $A^3$ :  $S(A^1, A^2) = 2.5$ ,  $S(A^1, A^3) = 3.5$ ,  $S(A^2, A^3) = 4$ 

(b) Use the maximum linkage.

**Solution:**  $\mathcal{A}^1$  and  $\mathcal{A}^3$ :  $S(\mathcal{A}^1, \mathcal{A}^2) = 3$ ,  $S(\mathcal{A}^1, \mathcal{A}^3) = 6$ ,  $S(\mathcal{A}^2, \mathcal{A}^3) = 5$ 

(c) Use the minimum linkage.

**Solution:**  $\mathcal{A}^2$  and  $\mathcal{A}^3$ :  $S(\mathcal{A}^1, \mathcal{A}^2) = 2$ ,  $S(\mathcal{A}^1, \mathcal{A}^3) = 1$ ,  $S(\mathcal{A}^2, \mathcal{A}^3) = 3$ 

## 2. Linear progressive alignment

Construct an MSA from seq1, seq2, seq3 and a phylogenetic tree by using the progressive alignment method specified below.

seq1: AGCT
seq2: ACT

seq3: AGCAT
seq2 seq1 seq3

- Clustering: Linear clustering
- Aligning method: Pair-guided alignment
- Aligning order: Use the specified tree
- Pairwise DP: Global alignment with linear gap penalty
- DP scoring scheme: match (10), mismatch (-5), gap penalty (10)
- (a) What is the aligning order that can be defined by the given tree?

### **Solution:**

- 1: Seq2 & Seq1
- 2: Seq1 & Seq3
- (b) Solve the first pairwise alignment.

### Solution:

- Seq2: A-CT
- Seq1: AGCT
- (c) Solve the second pairwise alignment.

### **Solution:**

- Seq1: AGC-T
- Seq3: AGCAT
- (d) Find the optimal MSA by combining the first and the second alignments.

#### Solution:

- Seq1: AGC-T
- Seq2: A-C-T
- Seq3: AGCAT
- (e) What is the SP score of the optimal MSA?

#### **Solution:**

- Seq1 & Seq2: 20
- Seq1 & Seq3: 30
- Seq2 & Seq3: 10
- SP: 60