**Hong Kong Metropolitan University**

**Jockey Club STEAM Education Resources Sharing Scheme**

**Sequencing Alignment**

Sequencing alignment is an important bioinformatics technique in identifying the source of unknown DNA sequences. Local alignment is one of the dynamic programming applications to find out the most similar part between two DNA sequences and return you with an alignment score. The Smith-Waterman algorithm is a local alignment algorithm used for this purpose. Let’s try it out!

Rules

1. Diagonal : Add match or mismatch score
2. Left: Add gap penalty
3. Up: Add gap penalty
4. All negative number round to zero
5. Take the maximum number

Scoring system

Match: +1

Mismatch: -2

Gap penalty: -2

|  |  |  |
| --- | --- | --- |
|  |  | T |
|  |  |  |
| T |  |  |

|  |  |  |
| --- | --- | --- |
|  |  | C |
|  |  |  |
| T |  |  |

**Level 1**

Sequence A: GC

Sequence B: GC

Scoring system

Match: +1

Mismatch: -2

Gap penalty: -2

|  |  |  |  |
| --- | --- | --- | --- |
|  |  | G | C |
|  |  |  |  |
| G |  |  |  |
| C |  |  |  |

Result: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**Level 2**

Sequence A: ATGC

Sequence B: TGC

Scoring system

Match: +1

Mismatch: -2

Gap penalty: -2

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  |  | A | T | G | C |
|  |  |  |  |  |  |
| T |  |  |  |  |  |
| G |  |  |  |  |  |
| C |  |  |  |  |  |

Result: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**Level 3**

Sequence A: GTCCTA

Sequence B: GTCTA

Scoring system

Match: +1

Mismatch: -2

Gap penalty: -2

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | G | T | C | C | T | A |
|  |  |  |  |  |  |  |  |
| G |  |  |  |  |  |  |  |
| T |  |  |  |  |  |  |  |
| C |  |  |  |  |  |  |  |
| T |  |  |  |  |  |  |  |
| A |  |  |  |  |  |  |  |

Result: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**Level 4**

Sequence A: BEWARE

Sequence B: BEAR

Scoring system

Match: +3

Mismatch: -3

Gap penalty: -2

Scoring system

Match: +3

Mismatch: -3

Gap penalty: -2

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | B | E | W | A | R | E |
|  |  |  |  |  |  |  |  |
| B |  |  |  |  |  |  |  |
| E |  |  |  |  |  |  |  |
| A |  |  |  |  |  |  |  |
| R |  |  |  |  |  |  |  |

Result: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**Level 5**

Scoring system

Match: +3

Mismatch: -3

Gap penalty: -2

Sequence A: CHLOROPLAST

Sequence B: ROAST

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | C | H | L | O | R | O | P | L | A | S | T |
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| R |  |  |  |  |  |  |  |  |  |  |  |  |
| O |  |  |  |  |  |  |  |  |  |  |  |  |
| A |  |  |  |  |  |  |  |  |  |  |  |  |
| S |  |  |  |  |  |  |  |  |  |  |  |  |
| T |  |  |  |  |  |  |  |  |  |  |  |  |

Result: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_