1 Needleman-Wunsch

```
python nw.py Files\example1.fasta Files\example2.fasta Files\example3.fasta
```

```
The score for this alignment is: 56
```

```
AC.TGG.TCA
.CAGGG.TCA
CCAGGGACCA
```

2 Smith-Waterman

```
python sw.py Files\example1.fasta Files\example2.fasta Files\example3.fasta
```

```
The aligned portion of the sequences is bounded by |
All nucleotides outside of these bounds are only there to show the entire sequence,
and there is no alignment between the sequences outside of these bounds.
```

```
The score for this alignment is: 66
```

```
A|C.TGG.TCA|
 |CAGGG.TCA|
C|CAGGGACCA|
```