**Note that in order to take an argument for whether or not the user wanted the matrix and alignments printed, I added two more args to the end of the arguments list. If they are both 1, then the matrix and alignments print out. IE:**

$ myaligner -s -1 -m 1 -g -1 TTCGGGAA TTCGGCTAC **1 1**

**Part 1 test 1:**

seq1 = "TTCGGGAA"

seq2 = "TTCGGCTAC"

mismatchScore = -1

matchScore = 1

gapPenalty = -1

Results:

Matrix:

[[[0, 'right'], [-1, 'down'], [-2, 'down'], [-3, 'down'], [-4, 'down'], [-5, 'down'], [-6, 'down'], [-7, 'down'], [-8, 'down']], [[-1, 'right'], [1, 'diag'], [0, 'diag'], [-1, 'down'], [-2, 'down'], [-3, 'down'], [-4, 'down'], [-5, 'down'], [-6, 'down']], [[-2, 'right'], [0, 'diag'], [2, 'diag'], [1, 'down'], [0, 'down'], [-1, 'down'], [-2, 'down'], [-3, 'down'], [-4, 'down']], [[-3, 'right'], [-1, 'right'], [1, 'right'], [3, 'diag'], [2, 'down'], [1, 'down'], [0, 'down'], [-1, 'down'], [-2, 'down']], [[-4, 'right'], [-2, 'right'], [0, 'right'], [2, 'right'], [4, 'diag'], [3, 'diag'], [2, 'diag'], [1, 'down'], [0, 'down']], [[-5, 'right'], [-3, 'right'], [-1, 'right'], [1, 'right'], [3, 'diag'], [5, 'diag'], [4, 'diag'], [3, 'down'], [2, 'down']], [[-6, 'right'], [-4, 'right'], [-2, 'right'], [0, 'diag'], [2, 'right'], [4, 'right'], [4, 'diag'], [3, 'diag'], [2, 'diag']], [[-7, 'right'], [-5, 'diag'], [-3, 'diag'], [-1, 'right'], [1, 'right'], [3, 'right'], [3, 'diag'], [3, 'diag'], [2, 'diag']], [[-8, 'right'], [-6, 'right'], [-4, 'right'], [-2, 'right'], [0, 'right'], [2, 'right'], [2, 'diag'], [4, 'diag'], [4, 'diag']], [[-9, 'right'], [-7, 'right'], [-5, 'right'], [-3, 'diag'], [-1, 'right'], [1, 'right'], [1, 'diag'], [3, 'right'], [3, 'diag']]]

Alignment:

TTCGG-GAA

TTCGGCTAC

Alignment Cost:

3

**Part 1 test 1:**

seq1 = "TTCGGGAA"

seq2 = "TTCGGCTAC"

mismatchScore = -11

matchScore = 5

gapPenalty = -2

Results:

Matrix:

[[[0, 'right'], [-2, 'down'], [-4, 'down'], [-6, 'down'], [-8, 'down'], [-10, 'down'], [-12, 'down'], [-14, 'down'], [-16, 'down']], [[-2, 'right'], [5, 'diag'], [3, 'diag'], [1, 'down'], [-1, 'down'], [-3, 'down'], [-5, 'down'], [-7, 'down'], [-9, 'down']], [[-4, 'right'], [3, 'diag'], [10, 'diag'], [8, 'down'], [6, 'down'], [4, 'down'], [2, 'down'], [0, 'down'], [-2, 'down']], [[-6, 'right'], [1, 'right'], [8, 'right'], [15, 'diag'], [13, 'down'], [11, 'down'], [9, 'down'], [7, 'down'], [5, 'down']], [[-8, 'right'], [-1, 'right'], [6, 'right'], [13, 'right'], [20, 'diag'], [18, 'diag'], [16, 'diag'], [14, 'down'], [12, 'down']], [[-10, 'right'], [-3, 'right'], [4, 'right'], [11, 'right'], [18, 'diag'], [25, 'diag'], [23, 'diag'], [21, 'down'], [19, 'down']], [[-12, 'right'], [-5, 'right'], [2, 'right'], [9, 'diag'], [16, 'right'], [23, 'right'], [21, 'down'], [19, 'down'], [17, 'down']], [[-14, 'right'], [-7, 'diag'], [0, 'diag'], [7, 'right'], [14, 'right'], [21, 'right'], [19, 'down'], [17, 'down'], [15, 'down']], [[-16, 'right'], [-9, 'right'], [-2, 'right'], [5, 'right'], [12, 'right'], [19, 'right'], [17, 'down'], [24, 'diag'], [22, 'diag']], [[-18, 'right'], [-11, 'right'], [-4, 'right'], [3, 'diag'], [10, 'right'], [17, 'right'], [15, 'down'], [22, 'right'], [20, 'down']]]

Alignment:

TTCGG--GA-A

TTCGGCT-AC-

Alignment Cost:

20

**Part 1 test 3:**

seq1 = " TAGCTTCGA"

seq2 = " TCGCTTAGC"

mismatchScore = -1

matchScore = 1

gapPenalty = -1

Results:

Matrix:

[[[0, 'right'], [-1, 'down'], [-2, 'down'], [-3, 'down'], [-4, 'down'], [-5, 'down'], [-6, 'down'], [-7, 'down'], [-8, 'down'], [-9, 'down']], [[-1, 'right'], [1, 'diag'], [0, 'down'], [-1, 'down'], [-2, 'down'], [-3, 'diag'], [-4, 'diag'], [-5, 'down'], [-6, 'down'], [-7, 'down']], [[-2, 'right'], [0, 'right'], [0, 'diag'], [-1, 'diag'], [0, 'diag'], [-1, 'down'], [-2, 'down'], [-3, 'diag'], [-4, 'down'], [-5, 'down']], [[-3, 'right'], [-1, 'right'], [-1, 'diag'], [1, 'diag'], [0, 'down'], [-1, 'diag'], [-2, 'diag'], [-3, 'diag'], [-2, 'diag'], [-3, 'down']], [[-4, 'right'], [-2, 'right'], [-2, 'diag'], [0, 'right'], [2, 'diag'], [1, 'down'], [0, 'down'], [-1, 'diag'], [-2, 'down'], [-3, 'diag']], [[-5, 'right'], [-3, 'diag'], [-3, 'diag'], [-1, 'right'], [1, 'right'], [3, 'diag'], [2, 'diag'], [1, 'down'], [0, 'down'], [-1, 'down']], [[-6, 'right'], [-4, 'diag'], [-4, 'diag'], [-2, 'right'], [0, 'right'], [2, 'diag'], [4, 'diag'], [3, 'down'], [2, 'down'], [1, 'down']], [[-7, 'right'], [-5, 'right'], [-3, 'diag'], [-3, 'right'], [-1, 'right'], [1, 'right'], [3, 'right'], [3, 'diag'], [2, 'diag'], [3, 'diag']], [[-8, 'right'], [-6, 'right'], [-4, 'right'], [-2, 'diag'], [-2, 'right'], [0, 'right'], [2, 'right'], [2, 'diag'], [4, 'diag'], [3, 'down']], [[-9, 'right'], [-7, 'right'], [-5, 'right'], [-3, 'right'], [-1, 'diag'], [-1, 'right'], [1, 'right'], [3, 'diag'], [3, 'right'], [3, 'diag']]]

Alignment:

TAGCTTCGA

TCGCTTAGC

Alignment Cost:

3

**Part 1 test 4:**

seq1 = " TAGCTTCGA"

seq2 = " TCGCTTAGC"

mismatchScore = -11

matchScore = 5

gapPenalty = -1

Results:

Matrix:

[[[0, 'right'], [-1, 'down'], [-2, 'down'], [-3, 'down'], [-4, 'down'], [-5, 'down'], [-6, 'down'], [-7, 'down'], [-8, 'down'], [-9, 'down']], [[-1, 'right'], [5, 'diag'], [4, 'down'], [3, 'down'], [2, 'down'], [1, 'diag'], [0, 'diag'], [-1, 'down'], [-2, 'down'], [-3, 'down']], [[-2, 'right'], [4, 'right'], [3, 'down'], [2, 'down'], [8, 'diag'], [7, 'down'], [6, 'down'], [5, 'diag'], [4, 'down'], [3, 'down']], [[-3, 'right'], [3, 'right'], [2, 'down'], [8, 'diag'], [7, 'down'], [6, 'down'], [5, 'down'], [4, 'down'], [10, 'diag'], [9, 'down']], [[-4, 'right'], [2, 'right'], [1, 'down'], [7, 'right'], [13, 'diag'], [12, 'down'], [11, 'down'], [10, 'diag'], [9, 'down'], [8, 'down']], [[-5, 'right'], [1, 'diag'], [0, 'down'], [6, 'right'], [12, 'right'], [18, 'diag'], [17, 'diag'], [16, 'down'], [15, 'down'], [14, 'down']], [[-6, 'right'], [0, 'diag'], [-1, 'down'], [5, 'right'], [11, 'right'], [17, 'diag'], [23, 'diag'], [22, 'down'], [21, 'down'], [20, 'down']], [[-7, 'right'], [-1, 'right'], [5, 'diag'], [4, 'down'], [10, 'right'], [16, 'right'], [22, 'right'], [21, 'down'], [20, 'down'], [26, 'diag']], [[-8, 'right'], [-2, 'right'], [4, 'right'], [10, 'diag'], [9, 'down'], [15, 'right'], [21, 'right'], [20, 'down'], [26, 'diag'], [25, 'down']], [[-9, 'right'], [-3, 'right'], [3, 'right'], [9, 'right'], [15, 'diag'], [14, 'down'], [20, 'right'], [26, 'diag'], [25, 'down'], [24, 'down']]]

Alignment:

T-AGCTT--CGA

TC-GCTTAGC--

Alignment Cost:

24