Test Cases- Brute Force and general checks

Name of test	Description	Given Input File(s)	Expected Output	Actual Output	Pass/Fail	Date Completed
TTT-01 (Run)	Does the program run to completion?	just given strings currently "ATGTAGTGTATAAAGTACATGCA ATGTAGTACATGCA"	ATGTAGTGTATAAAGTACATGCA ATGTAGTACATGCA Score: 15	ATGTAGTGTAT, ATGTAGTACAT, Score: 15	Pass	4/8/2019
TTT-02 (Input)	Take in input correctly?	GUI takes in any files, ex. large genome sequence files	Aligned strings and score	aligned strings an	pass	4/10/19
TTT-03 (Edge Case Input small file runtime)	how does it run with a simple sequence?	just given strings currently "ATGTAGTGTATAAAGTACATGCA ATGTAGTACATGCA"	ATGTAGTGTATAAAGTACATGCA ATGTAGTACATGCA Score: 15 Screen reader support enabled.	ATGTAGTGTAT, ATGTAGTACAT, Score: 15 Screen reader su	Pass	4/8/2019
TTT-04 (Input Handling)	Is input file formatted correctly? No strange characters or letters inside?	invalidCharacterTest1.txt, invalidCharacterTest2.txt	continues and ignores strange character	continues and ign	pass	4/24/19
TTT-05 (Edge Case Input large sequence runtime)	how does it run with a larger sequence?	largeGenomeTest1.txt, largeGenomeTest2.txt	Score: 85131	Score: 85131	pass	4/24/2019
TTT-06 (Output Print)	Print correct output?	just given strings currently "ATGTAGTGTATAAAGTACATGCA ATGTAGTACATGCA"	Score: 15	score: 15	Pass	4/8/2019
TTT-07 (Runtime)	How long does it run? Is this efficient?	largeGenomeTest1.txt, largeGenomeTest2.txt	Time stamp will print how long it takes to run	Time stamp will p	Pass	4/24/2019
TTT-08 (Different Lengths of input)	Can the code handle one sequence shorter than the other and align them efficiently?	list1= "ACGTCAGGG" list2= "ACGTCCAG"	ACGTCAGGG ACGTCCA-G Score: 5	ACGTCAGGG ACGTCCA-G Score: 5	Pass, can handle	4/8/2019
TTT-09 (Valid different characters)	Can the code handle characters that occur in genomes that aren't A, C, T, or G?	validStrangeCharacterTest1.txt, validStrangeCharacterTest2.txt	GUI will handle it: a method changes it to an A, G, T, o	Not enough time	----	4/24/2019
TTT-010 (Invalid characters)	What if it runs into a P?	invalidCharacterTest1.txt, invalidCharacterTest2.txt	an error to check	GUI ignores it un	Pass	4/24/2019
TTT-011 (GUI and Backend connect correctly)	do the two connect their input and output correctly	any file combo	gets output from backend file	gets output from	Pass	4/10/2019
TTT-012 (GUI only allows txt files)	GUI input only allows txt files to be entered by the user, not just any file	any file other than .txt	takes the file and stores it as variables for the back en	does so, but bacl	Pass	4/1/2019
TTT-013 (Perfect match input)	What should the score be if the two input sequences are exactly the same	list1= "ACGTCAGGG" list2= "ACGTCAGGG"	Score: 9	Score: 9	pass	4/15/2019
TTT-013.2 (Completely different strings)	What if the two input strings are completely different?	list1= "AAAAAAAAA" list2= "GGGGGGGGG"	score:-9	---	----	4/24/2019
						4/24/2019
GUI Test	can you break the GUI by making the scores extremely small or extremely large?	any input files, but match= 5, mismatch= -1, gap= -2	still prints score	still prints score	pass	4/24/2019

Test Cases- Needleman-Wunsch

Name of test	Description	Given Input File(s)	Expected Output	Actual Output	Pass/Fail	Date Completed
TTT-014 (Run)	Does the program run to completion?	ATGTAGTGTATAAAGTACATGCA ATGTAGTACATGCA	score: -4	score: -4	pass	4/24/2019
TTT-015 (Edge Case Input large sequence runtime)	how does it run with a larger sequence?	largeGenomeTest1.txt, largeGenomeTest2.txt	Score: 95710	Memory Error-takes a lot of ram		4/24/2019
TTT-016 (Runtime)	How long does it run? Is this efficient?	largeGenomeTest1.txt, largeGenomeTest2.txt	Score: 95710	Memory Error-takes a lot of ram		4/24/2019
TTT-017 (Different Lengths of input)	Can the code handle one sequence shorter than the other and align them efficiently?	list1= "ACGTCAGGG" list2= "ACGTCCAG"	score: 5	ACGTCAGGG ACGTCCAG-- Score: 5	pass	4/24/2019
TTT-018 (Perfect match input)	What should the score be if the two input sequences are exactly the same	list1= "ACGTCAGGG" list2= "ACGTCAGGG"	score: 9	score: 9	pass	4/24/2019
TTT-019 (Edge Case Input small file runtime)	how does it run with a simple sequence?	ATGTAGTGTATAAAGTACATGCA ATGTAGTACATGCA	score: -4	score: -4	pass	4/24/2019
TTT-013.2 (Completely different strings)	what if strings are completely different	list1= "AAAAAAAAA" list2= "GGGGGGGGG"	score: -9	score: -9	pass	4/24/2019

Test Cases- Greedy

Name of test	Description	Given Input File(s)	Expected Output	Actual Output	Pass/Fail	Date Completed
TTT-020 (Run)	Does the program run to completion?	list1 = "ACGTCAGGG" list2 = "ACGTCAGGC"	Score: 8	Score:8	pass	4/15/2019
TTT-021 (Edge Case Input large sequence runtime)	how does it run with a larger sequence?	largeGenomeTest1.txt, largeGenomeTest2.txt	Score: 95710	-	----	4/24/2019
TTT-022 (Runtime)	How long does it run? Is this efficient?	largeGenomeTest1.txt, largeGenomeTest2.txt	Score: 95710	-		4/24/2019
TTT-023 (Different Lengths of input)	Can the code handle one sequence shorter than the other and align them efficiently?	list1= "AAAGTCCC" list2= "AAAGGTC"	Score: 1	Score: 1	pass	4/24/2019
TTT-024 (Perfect match input)	What should the score be if the two input sequences are exactly the same	list1 = "ACGTCAGGG" list2 = "ACGTCAGGG"	Score: 9	Score: 9	pass	4/15/2019
TTT-025 (Edge Case Input small file runtime)	how does it run with a simple sequence?	list1 = "ACGTCAGGG" list2 = "ACGTCAGGC"	Score: 8	Score: 8	pass	4/15/2019
TTT-013.2 (Completely different strings)	what if the strings are completely different?	list1= "AAAAAA", list2= "GGGGGG"	score: -6	score: 0	-	4/24/2019

Test Cases- Random

Name of test	Description	Given Input Files	Expected Output	Actual Output	Pass/Fail	Date Completed
TTT-026 (Run)	Does the program run to completion?	ATGTAGTGTATAAAGTACAATGCA ATGTAGTACATAAAGTCCGCTGCA	score: 14	Score: 14	pass	4/24/2019
TTT-027 (Edge Case Input large sequence runtime)	how does it run with a larger sequence?	largeGenomeTest1.txt, largeGenomeTest2.txt	score: 95710	score: 30448	pass	4/24/2019
TTT-028 (Runtime)	How long does it run? Is this efficient?	largeGenomeTest1.txt, largeGenomeTest2.txt	score: 95710	score: 30448	pass	4/24/2019
TTT-029 (Different Lengths of input)	Can the code handle one sequence shorter than the other and align them efficiently?	list1= "AAAGTCCCAAAAA" list2= "AAAGGTCAAAAA"	score: 4	score: 4	pass	4/24/2019
TTT-030 (Perfect match input)	What should the score be if the two input sequences are exactly the same	list1 = "AAAAAAAAAAAAAAAAAAAA" list2 = "AAAAAAAAAAAAAAAAAAAA"	score: 19	score: 19	pass	4/24/2019
TTT-031 (Edge Case Input small file runtime)	how does it run with a simple sequence?	ATGTAGTGTATAAAGTACAATGCA ATGTAGTACATAAAGTCCGCTGCA	score: 14	score: 14	pass	4/24/2019
TTT-013.2 (Completely different strings)	what if the sequences are completely different?	list1= "AAAAAAAAAAAAAAAAAAAA", list2= "GGGGGGGGGGGGGGGGGGGG	score: -19	score: -19	pass	4/24/2019

Known Issues							
Name of Issue	**How it was resolved**	**Date resolved**	**Date Found**				
Mismatch characters- Brute Force does not check for if a character is invalid	GUI checks for invalid characters with parsing files	4/23/19	4/8/19				
Does not check for valid characters that are anything but AGCorT	not enough time to resolve		4/8/19				
What should the numerical values for the score?	Researcher found example values: match 1, mismatch -1, gap -2. Also, may give the us	4/9/19	4/9/19				
Large files or same length both return the minimum value in the code (brute force)	Updated brute force is better at handling large files	4/24/19	4/9/19				
Timestamp to record runtime	GUI has it	4/24/19	4/24/2019				
NW algorithm not running to completion	Fixed and running	4/24/19	4/15/2019				
Greedy runs into issues if second string shorter than first			4/24/2019				
Brute Force does not work if second string is shorter than first			4/24/2019				
Greedy does not print out a score when strings are completely different			4/24/2019				
Brute Force complete mismatch score is always -2			4/24/2019				

Runtime Table and Graph

Algorithm	Time (seconds)	Runtime (n is the length of the first sequence, m is the length of the second)	Input that lead to the correct alignment
Brute Force	0.440652	Best Case: O(n^2) or O(nm), Worst Case: O(n^3)	AGTCTA, AGTTA Alignment: AGT-TA, Score: 3
Needleman-Wunsch	0.678185	O(nm)	ATGTAGTGTATAAAGTACATGCA ATGTAGTACATGCA Score: -4
Greedy	0.001	Best Case: O(n^2) or O(nm), Worst Case: O(n^3)	ACGTCAGGG ACGTCAGGC Score: 8
Random	11.16014	O(n^2)	ATGTAGTGTATAAAGTACAATGCA ATGTAGTACATAAAGTCCGCTGCA Score: 14

Time (seconds) vs. Algorithm