est Cases- Brute Force and general checks					
me of test	Description	Given Input File(s)	Expected Output	Actual Output	Pass/Fail Date Completed
			ATGTAGTGTATAAAGTACATGCA	ATGTAGTGTAT	
T 04 (D.::-)	Dans the annument of a second of an O	just given strings currently "ATGTAGTGTATAAAGTACATGCA	ATGTAGTACATGCA	ATGTAGTACAT	
T-01 (Run)	Does the program run to completion?	ATGTAGTACATGCA"	Score: 15		Pass 4/8/2019
Γ-02 (Input)	Take in input correctly?	GUI takes in any files, ex. large genome sequence files	Aligned strings and score	aligned strings a	pass 4/10/19
		just given strings currently "ATGTAGTGTATAAAGTACATGCA ATGTAGTACATGCA"	ATGTAGTGTATAAAGTACATGCA ATGTAGTACATGCA Score: 15 Screen reader support enabled.	ATGTAGTGTAT ATGTAGTACAT Score: 15 Screen reader si	
T-03 (Edge Case Input small file runtime)	how does it run with a simple sequence?				Pass 4/8/2019
T-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 ig	r pass 4/24/19
Γ-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
		just given strings currently "ATGTAGTGTATAAAGTACATGCA ATGTAGTACATGCA"			
T-06 (Output Print)	Print correct output?		Score: 15	score: 15	Pass 4/8/2019
Γ-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	Pass 4/24/2019
		light = "ACCTCACCC"	ACGTCAGG	ACGTCAGGG	
T-08 (Different Lengths of input)	Can the code handle one sequence shorter than the other and align them efficiently?	list1 = "ACGTCAGGG" list2= "ACGTCCAG"	ACGTCCA-G Score: 5	ACGTCCA-G Score: 5	Pass, can handle 4/8/2019
T-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,		
T-010 (Invalid characters)	What if it runs into a P?	invalidCharacterTest1.txt, invalidCharacterTest2.txt	an error to check	GUI ignores it ur	
7-011 (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	
T-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 bac	Pass 4/1/2019
T-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
1-010 (i Gricot matori input)	what should the score be if the two input sequences are exactly the same	list1 = "AAAAAAAAA"	Guore. 9	J. J	pass 4/15/2019
TTT-013.2 (Completely different strings)	What if the two input strings are completely different?	list2= "GGGGGGGG"	score:-9	Score: 9	pass 4/25/2019
					4/24/2019
II 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	
st Cases- Needleman-Wunsch	can you broak the corpy making the socies extremely small or extremely large:	any mparimos, parimaron- o, miomaron1, yap2	Juli printo ocoro	Jun printo 30016	7/24/2019
	Decariation	Civan Innut File(a)	Expected Output	Actual Outroot	Page/Feil Pate Commisted
Name of test	Description	Given Input File(s)	Expected Output	Actual Output	Pass/Fail Date Completed
		ATGTAGTGTATAAAGTACATGCA ATGTAGTACATGCA			
T-014 (Run)	Does the program run to completion?		score: -4	score: -4	pass 4/24/2019
T-015 (Edge Case Input large sequence runtime)	how does it run with a larger sequence?	largeGenomeTest1.txt, largeGenomeTest2.txt	Score: 95710	Memory Error-ta	kes a lot of ram 4/24/2019
T-016 (Runtime)	How long does it run? Is this efficient?	largeGenomeTest1.txt, largeGenomeTest2.txt	Score: 95710		
·		list1 = "ACGTCAGGG"		ACGTCAGGG ACGTCCAG	
T-017 (Different Lengths of input)	Can the code handle one sequence shorter than the other and align them efficiently?	list2= "ACGTCAG"	score: 5	Score: 5	pass 4/24/2019
T-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
	and the series are the series and should the series	ATGTAGTGTATAAAGTACATGCA		,52.5.0	7,27,2019
		ATGTAGTACATGCA			
T-019 (Edge Case Input small file runtime)	how does it run with a simple sequence?		score: -4	score: -4	pass 4/24/2019
TT-013.2 (Completely different strings)	what if strings are completely different	list1 = "AAAAAAAAA" list2= "GGGGGGGGG"	score: -9	score: -9	pass 4/24/2019
ant Canana Cunandiu					
st Cases- Greedy					
ame of test	Description	Given Input File(s)	Expected Output	Actual Output	Pass/Fail Date Completed
T-020 (Run)	Does the program run to completion?	list1 = "ACGTCAGGG" list2 = "ACGTCAGGC"	Score: 8	Score:8	pass 4/15/2019
					fail 4/25/2019
T-021 (Edge Case Input large sequence runtime)	how does it run with a larger sequence?	largeGenomeTest1.txt, largeGenomeTest2.txt	Score: 95710	crash	
T-022 (Runtime)	How long does it run? Is this efficient?	largeGenomeTest1.txt, largeGenomeTest2.txt	Score: 95710	crash	fail 4/25/2019
T-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
T-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
TT-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
TT-013.2 (Completely different strings)	what if the strings are completely different?	list1= "AAAAAA", list2= "GGGGGG"	score: -6	score: 0	- 4/24/2019
. 3.3.2 (Sampletory amorate anniga)	mach and durings are completely difference:	/ ******* 1000000	555.5	30010.0	7/27/2019
st Cases- Random					
me of test	Description	Given Input Files	Expected Output	Actual Output	Pass/Fail Date Completed
ine of eac	Description	ATGTAGTGTATAAAGTACAATGCA ATGTAGTACATAAAGTCCGCTGCA	Expedied Output	Score:	Date Completed
T-026 (Run)	Does the program run to completion?		score: 14	14	pass 4/24/2019
T-027 (Edge Case Input large sequence runtime)	how does it run with a larger sequence?	largeGenomeTest1.txt, largeGenomeTest2.txt	score: 95710		pass 4/24/2019
T-028 (Runtime)	How long does it run? Is this efficient?	largeGenomeTest1.txt, largeGenomeTest2.txt	score: 95710	score: 30448	pass 4/24/2019
, ,					·
TT-029 (Different Lengths of input)	Can the code handle one sequence shorter than the other and align them efficiently?	list1= "AAAGTCCCAAAAA" list2= "AAAGGTCAAAAA" list1 = "AAAAAAAAAAAAAAAAAA"	score: 4	score: 4	pass 4/24/2019
		list2 = "AAAAAAAAAAAAAAAAA"	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			pass	4/24/2019
TT-013.2 (Completely different strings)	what if the sequences are completely different?	liet1= "AAAAAAAAAAAAAAAA Iiet2= "GGGGGGGGG			pass	4/24/2019
11-013.2 (completely uniferent samgs)	what if the sequences are completely different:	iisti- www.www., iisiz- ooooooo	addddddddstale19	score: -19	pass	4/24/2019
(nown 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. Als	so, may give the us	4/9/19			
arge files or same length both return the minimum value in the code (brute for	rce) Updated brute force is better at handling large files		4/24/19 4/9/19			
Timestamp to record runtime	GUI has it		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	The (county)	During (e.j. the beath of the first energy is the beat	the file and the standard to t			
Algorithm Prute Force	Time (seconds)	Runtime (n is the length of the first sequence, m is the leng				
Brute Force		0.440652 Best Case: O(n^2) or O(nm), Worst Case: O(n^3)	AGTCTA, AGTTA Alignment: AGT-TA, Score: 3 ATGTAGTGTATAAAGTACATGCA			
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						
12						
10 —						
8 —						
spuc						
6 ————————————————————————————————————						
e e						
2						
0						
Brute Force Needleman-Wunsch	h Greedy Random					
Ale	orithm					
Alg	OHGHII					