

## Test Report for Part2 Assignment CAB201

Name: Phuong Nam Ly

Student number: n10098097

I separate the test into 4 main parts for four levels. Input should be entered in the command line. The Expected Output will be a screenshot from the input file while the Actual Output will be a screenshot of the console output. Comment will explain how I evaluate and justify **my statement of completeness** and **self-assessed CRA**.

Test structure

Category	
Input	
Expected Output	
Actual Output	
Comment	

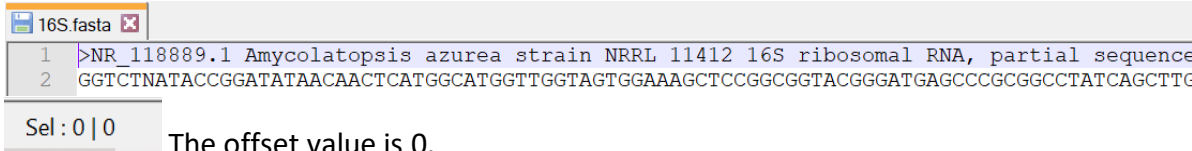
### Level 4 Functionalities (15 marks)

I use the IndexSequence project to create the indexed file, and then put it in the Debug folder of A1.new to use it for the Search project.

**Criteria:** The program for indexing creates a file as specified by the command line arguments (2 marks)

**Criteria:** The index file contains appropriate data (5 marks)

Test 4.1: Test the index program

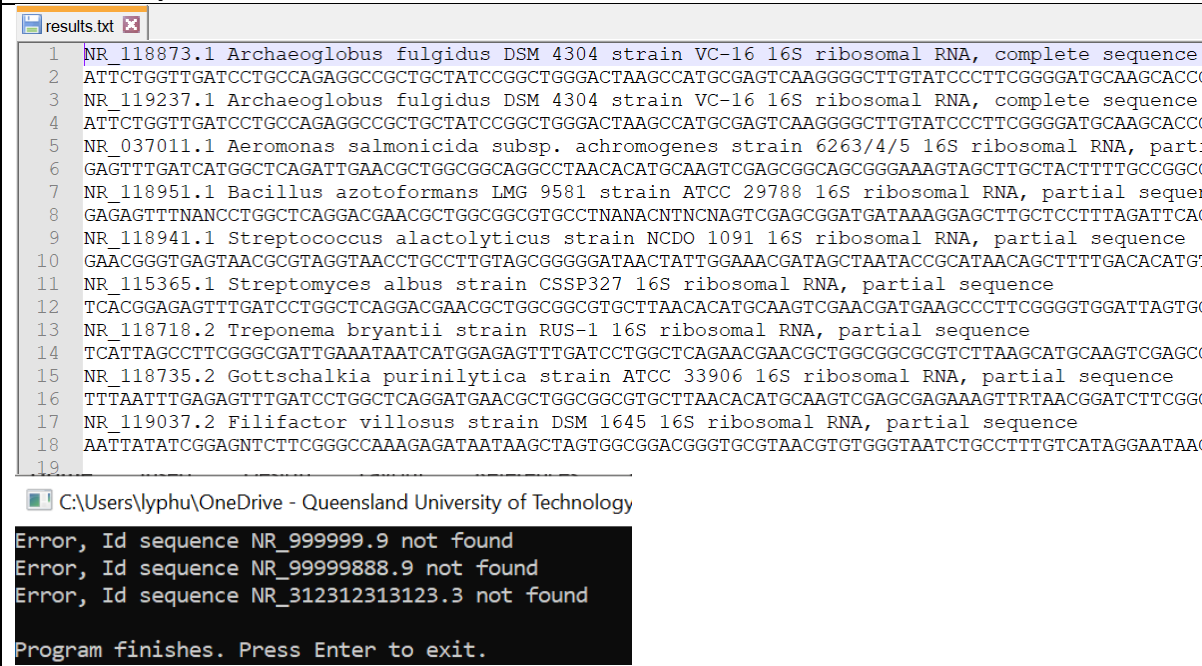
Category	Create a file that displays the correct data
Input	16S.fasta 16S.index
Expected Output	<p>The expected offset for an id sequence can be verified by bolding the texts prior to the id sequence and checking the "Sel" value at the right bottom corner.</p> <p>Examples:</p> <p>For checking the first sequence, NR_118889.1:</p>  <p>The offset value is 0.</p> <p>For checking the sequence, &gt;NR_118899.1:</p>

<div>16S.fasta</div> <pre> 1 &gt;NR_118889.1 Amycolatopsis azurea strain NRRL 11412 16S ribosomal RNA, partial sequence 2 GGTCTNATACCGGATATAACAACCTCATGGCATGGTTGGTAGTGGAAGCTCCGGCGGTACGGGATGAGCCCGCGGCCTATCAGCTTGT 3 &gt;NR_118899.1 Actinomyces bovis strain DSM 43014 16S ribosomal RNA, partial sequence 4 GGGTGAGTAACACGTGAGTAACCTGCCCCNNACTTCTGGATAACCGCTTGAAAGGGTNGCTAATACGGGATATTTTGGCCTGCTCGCA </pre> <div>Sel : 1,389   3</div> <p>The offset value is 1389.</p>	
<b>Actual Output</b>	
<div>16S.index</div> <pre> 1 NR_118889.1 0 2 NR_118899.1 1389 3 NR_074334.1 2841 4 NR_118873.1 2841 5 NR_119237.1 2841 6 NR_118890.1 4606 7 NR_044838.1 6033 8 NR_118908.1 7572 </pre>	
<b>Comment</b>	The indexing program creates the indexed file which contains the appropriate data. 7 marks are obtained.

**Criteria:** The program for searching creates a file that contains the appropriate data (5 marks)

Test 4.2: Test the searching program (Successful run)

<b>Category</b>	Create a file that displays the correct data
<b>Input</b>	-level4 16S.fasta 16S.index query.txt results.txt
<b>Expected Output</b> Provided query.txt file	

<pre> 1 NR_115365.1 2 NR_118873.1 3 NR_999999.9 4 NR_118941.1 5 NR_99999888.9 6 NR_037011.1 7 NR_118951.1 8 NR_119237.1 9 NR_312312313123.3 10 NR_118718.2 11 NR_118735.2 12 NR_119037.2 13 14 15 16 17 18 19 20 </pre>	<p>The output file contains all the id sequences except (NR_999999.9, NR_99999888.9, NR_312312313123.3) with the corresponding DNA sequence.</p>
<b>Actual Output</b>	
	
<b>Comment</b>	<p>The output file contains all 9 id sequences with the corresponding DNA lines. 5 marks are obtained</p>

**Criteria:** Clear error message is provided when the index file does not exist (1 mark)


Test 4.3: Test the index program (Unsuccessful run)

<b>Category</b>	Provide appropriate warning
-----------------	-----------------------------

<b>Input</b>	RandomName.fasta 16S.index
<b>Expected Output</b>	Appropriate warning is given through the console.
<b>Actual Output</b>	The input file RandomName.fasta does not exist or it is incorrectly formatted Program finishes. Press Enter to exit.
<b>Comment</b>	The appropriate warning is given. 1 mark is obtained

**Criteria:** Clear error message is provided when the query file does not exist or is incorrectly formatted (2 marks)

Test 4.4: Test the searching program (Unsuccessful run)

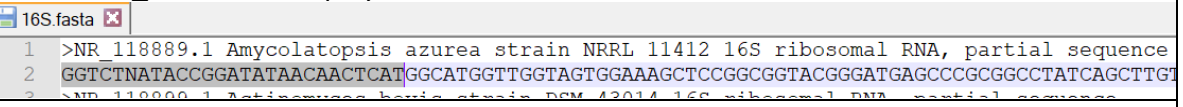
<b>Category</b>	Provide appropriate warning
<b>Input</b>	-level4 16S.fasta 16S.index RandomName.txt results.txt
<b>Expected Output</b>	Appropriate warning is given through the console.
<b>Actual Output</b>	 C:\Users\lyphu\OneDrive - Queensland University of Technology\Bachelor\CAB201\Assignment\Final The input file RandomName.txt does not exist or it is incorrectly formatted Program finishes. Press Enter to exit.
<b>Comment</b>	The appropriate warning is given. 1 mark is obtained

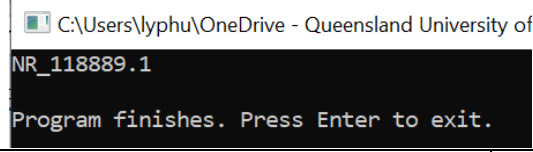
**All level 4 functionalities are achieved. 15 marks are obtained.**

## Level 5 Functionalities (15 marks)

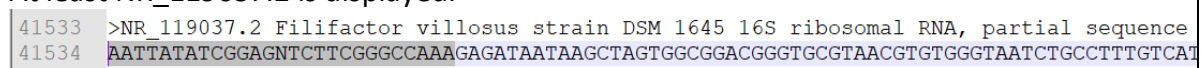
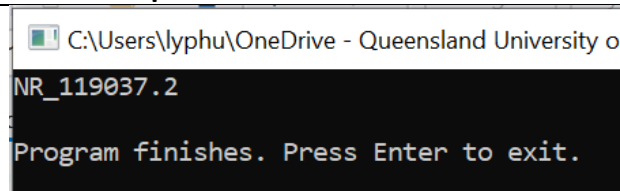
**Criteria:** The program prints the appropriate data (10 marks)

Test 5.1: Test the searching program with the expected output including the first id sequence (Successful run)

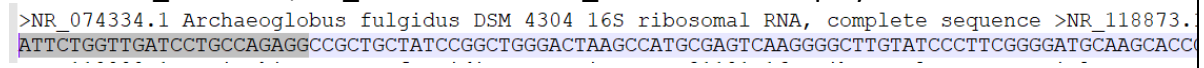
<b>Category</b>	Display the correct data
<b>Input</b>	-level5 16S.fasta GGTCTNATACCGGATATAACAACATCAT
<b>Expected Output</b>	At least NR_11889.1 is displayed. 
<b>Actual Output</b>	

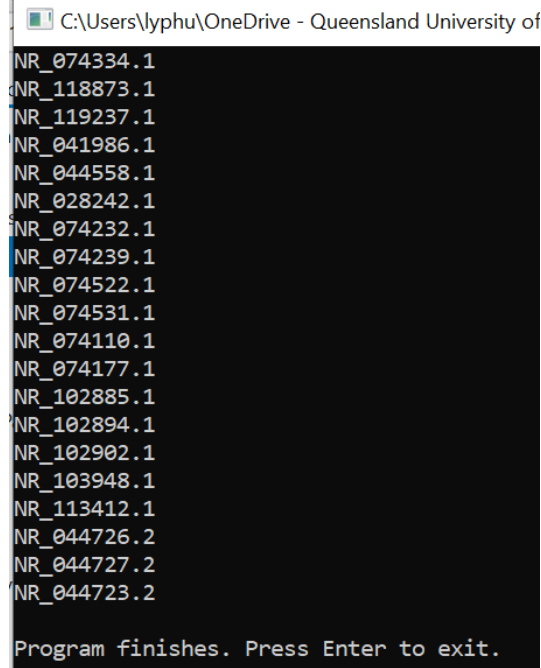
	
<b>Comment</b>	The correct sequence id is displayed. 3 marks are given.

Test 5.2: Test the searching program with the expected output including the last id sequence (Successful run)

<b>Category</b>	Display the correct data
<b>Input</b>	-level5 16S.fasta AATTATATCGGAGNTCTTCGGGCCAAA
<b>Expected Output</b> At least NR_119037.2 is displayed. 	
<b>Actual Output</b>	
	
<b>Comment</b>	The correct sequence id is displayed. 3 marks are given.

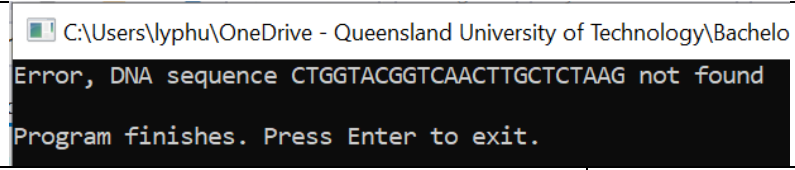
Test 5.3: Test the searching program with the expected output including the id sequences on the same metadata line (Successful run)

<b>Category</b>	Display the correct data
<b>Input</b>	-level5 16S.fasta ATTCTGGTTGATCCTGCCAGAGG
<b>Expected Output</b> At least NR_074334.1, NR_118873.1 and NR_119237.1 are displayed. 	
<b>Actual Output</b>	

	
<b>Comment</b>	The correct id sequences are displayed. 4 marks are given.

**Criteria:** Clear error message is provided sequence does not exist (5 mark)

Test 5.4: Test the searching program (Unsuccessful run)

<b>Category</b>	Provide appropriate warning
<b>Input</b>	-level5 16S.fasta CTGGTACGGTCAACTTGCTCTAAG
<b>Expected Output</b> Appropriate warning is given through the console.	
<b>Actual Output</b> 	
<b>Comment</b>	The appropriate warning is given. 5 marks is obtained

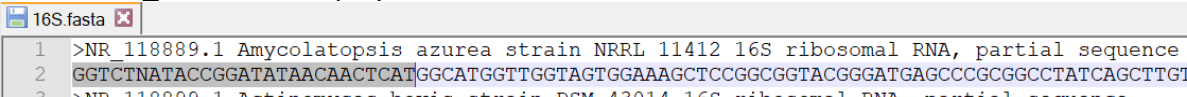
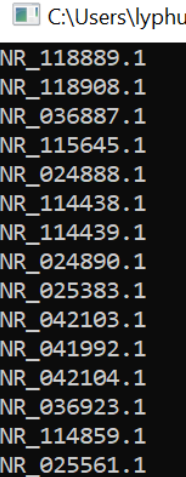
**All level 5 functionalities are achieved. 15 marks are obtained.**

## Level 6 Functionalities (20 marks)

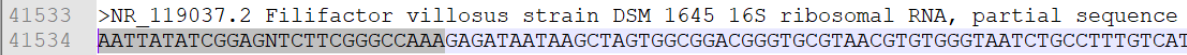
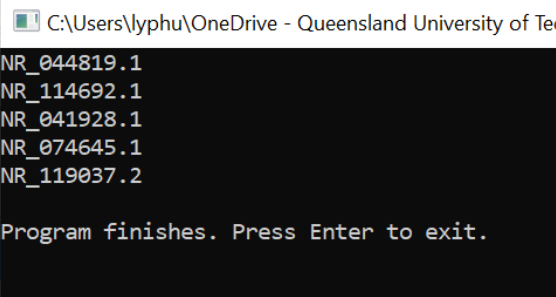
**Criteria:** The program prints the appropriate data (15 marks)

Test 6.1: Test the searching program with the expected output including the first id sequence (Successful run)

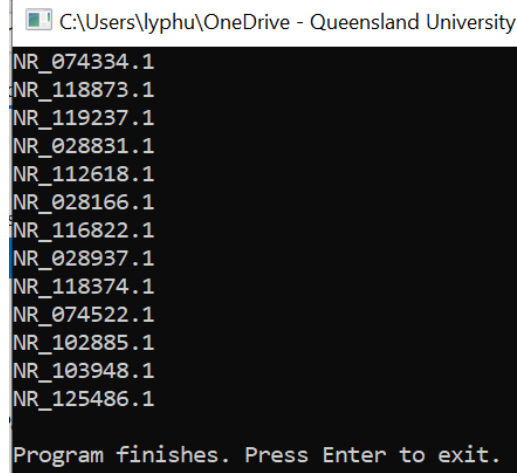
<b>Category</b>	Display the correct data
-----------------	--------------------------

<b>Input</b>	-level6 16S.fasta Amycolatopsis
<b>Expected Output</b> At least NR_11889.1 is displayed.	
	
<b>Actual Output</b> 	
<b>Comment</b>	The correct id sequences are displayed. 5 marks are given.

Test 6.2: Test the searching program with the expected output including the last id sequence (Successful run)

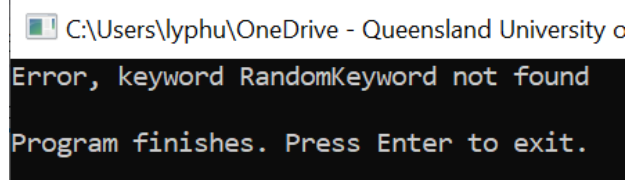
<b>Category</b>	Display the correct data
<b>Input</b>	-level6 16S.fasta Filifactor
<b>Expected Output</b> At least NR_119037.2 is displayed.	
	
<b>Actual Output</b> 	
<b>Comment</b>	The correct id sequences are displayed. 5 marks are given.

Test 6.3: Test the searching program with the expected output including the id sequences on the same metadata line (Successful run)

<b>Category</b>	Display the correct data
<b>Input</b>	-level6 16S.fasta Archaeoglobus
<b>Expected Output</b> At least NR_074334.1, NR_118873.1 and NR_119237.1 are displayed. >NR_074334.1 Archaeoglobus fulgidus DSM 4304 16S ribosomal RNA, complete sequence >NR_118873.1 ATTCTGGTTGATCCTGCCAGAGGCCGCTGCTATCCGGCTGGGACTAAGCCATGCGAGTCAAGGGGCTTGTATCCCTTCGGGGATGCAAGCACCO	
<b>Actual Output</b> 	
<b>Comment</b>	The correct id sequences are displayed. 5 marks are given.

**Criteria:** Clear error message is provided keyword does not exist (5 mark)

Test 6.4: Test the searching program (Unsuccessful run)

<b>Category</b>	Provide appropriate warning
<b>Input</b>	-level6 16S.fasta RandomKeyword
<b>Expected Output</b> Appropriate warning is given through the console.	
<b>Actual Output</b> 	
<b>Comment</b>	The appropriate warning is given. 5 marks is obtained.

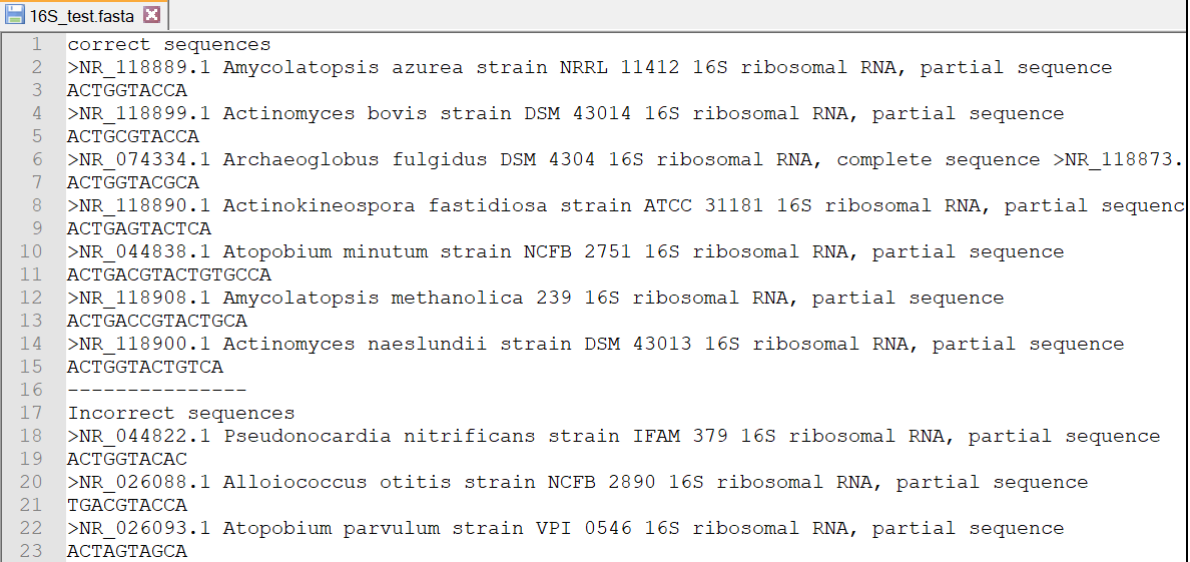
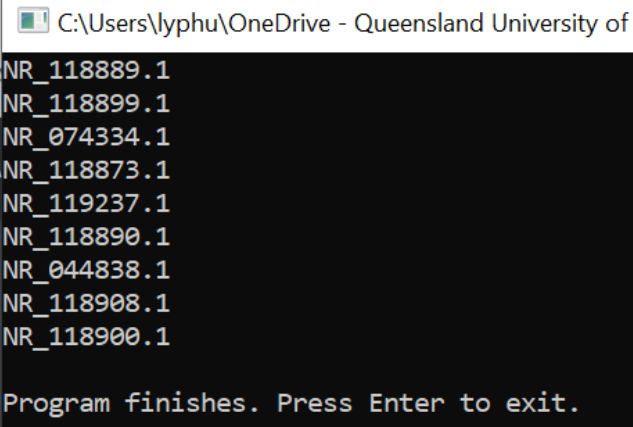
**All level 6 functionalities are achieved. 20 marks are obtained.**

## Level 7 Functionalities (10 marks)

**Criteria:** The program prints the appropriate data (5 marks)

Test 7.1: Test the searching program with a custom fasta file, in which we create correct and incorrect sequences for testing (Successful run)



<b>Category</b>	Display the correct data
<b>Input</b>	-level7 16S_test.fasta ACTG*GTAC*CA
<b>Expected Output</b> 16S_test is included as below. The program should ignore the incorrect sequences and output the correct sequences.	
	
<b>Actual Output</b> 	
<b>Comment</b>	The correct id sequences are displayed. 5 marks are given.

**Criteria:** Clear error message is provided sequence does not exist (5 mark)

Test 7.2: Test the searching program (Unsuccessful run)

<b>Category</b>	Provide appropriate warning
<b>Input</b>	-level7 16S_test.fasta AACC*GGTT*AC
<b>Expected Output</b> 16S_test is included as below. Appropriate warning is given through the console.	

<pre> 1 correct sequences 2 &gt;NR_118889.1 Amycolatopsis azurea strain NRRL 11412 16S ribosomal RNA, partial sequence 3 ACTGGTACCA 4 &gt;NR_118899.1 Actinomyces bovis strain DSM 43014 16S ribosomal RNA, partial sequence 5 ACTGCGTACCA 6 &gt;NR_074334.1 Archaeoglobus fulgidus DSM 4304 16S ribosomal RNA, complete sequence &gt;NR_118873. 7 ACTGGTACGCA 8 &gt;NR_118890.1 Actinokineospora fastidiosa strain ATCC 31181 16S ribosomal RNA, partial sequenc 9 ACTGAGTACTCA 10 &gt;NR_044838.1 Atopobium minutum strain NCFB 2751 16S ribosomal RNA, partial sequence 11 ACTGACGTACTGTGCCA 12 &gt;NR_118908.1 Amycolatopsis methanolica 239 16S ribosomal RNA, partial sequence 13 ACTGACCGTACTGCA 14 &gt;NR_118900.1 Actinomyces naeslundii strain DSM 43013 16S ribosomal RNA, partial sequence 15 ACTGGTACTGTCA 16 ----- 17 Incorrect sequences 18 &gt;NR_044822.1 Pseudonocardia nitrificans strain IFAM 379 16S ribosomal RNA, partial sequence 19 ACTGGTACAC 20 &gt;NR_026088.1 Alloiococcus otitis strain NCFB 2890 16S ribosomal RNA, partial sequence 21 TGACGTACCA 22 &gt;NR_026093.1 Atopobium parvulum strain VPI 0546 16S ribosomal RNA, partial sequence 23 ACTAGTAGCA </pre>	
<p><b>Actual Output</b></p> <pre> C:\Users\lyphu\OneDrive - Queensland University of Technology\l Error, Wild card sequence AACC*GGTT*AC not found Program finishes. Press Enter to exit. </pre>	
<p><b>Comment</b></p>	<p>The appropriate warning is given. 5 marks is obtained.</p>

**All level 7 functionalities are achieved. 10 marks are obtained.**

In total, 50 marks for L4-6 and 10 marks for L7 = 60 marks should be obtained.