CAB201 Programming Principles - Semester 2, 2019

# *Project – Genomic Sequence Retrieval – Part 2*

# *Feedback*

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| Section | Score | Value in CAB201 grade |
| *Part II* | 94/100 | 28.2/30% |

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| **Penalties**  If the statement of completeness, self-reflection is incomplete or missing, the student will lose marks | | | **Part I Marks Lost:** |
| **0/-30** |
| *Statement of Completeness* | Missing | 0/-7 | |
| Incomplete (up to -6) | 0/-6 | |
| **Total** | **0/-7** | |
| *Self-Reflection* | Missing | 0/-3 | |
| Incomplete | 0/-1.5 | |
| **Total** | **0/-3** | |
| *Progress Report* | Missing | 0/-20 | |
| Incomplete | 0/-15 | |
| **Total** | **0/-20** | |
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| *Feedback: The statement and the report are thorough.* | | | |

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| **Code Quality**  To score points in this section, the student must follow the code quality guidelines as specified in the C# Coding Style Guide on Blackboard | **Part I Marks Available:** |
| **18/30** |
| Maintained consistent, clear, and meaningful standard in variable and method naming. No magic numbers. | 2/3 |
| Well structured – consistent and appropriate white spacing, line length, indentation, and separation into files within the project (i.e. one class per file) | 2/2 |
| Well commented – class header comment at beginning of each class, comment before every method, and in-line comments to explain complex or not easily discernible code. In-line comments are not excessive. | 2/4 |
| The DRY principle (Don’t repeat yourself) is followed where appropriate | 2/3 |
| Methods are single purpose and clear | 2/4 |
| Classes are well designed, with high cohesion and low coupling | 4/8 |
| Classes are separated into reusable modules where appropriate | 2/3 |
| Exceptions are thrown and handled appropriately | 2/3 |
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| *Feedback: Some attempt at OOP/OOD.* | |

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| Basic Functionality  To score marks in this section, your program must be able to be run from the command line with the appropriate arguments. | | | Part I Marks Available: |
| 15/15 |
| *Basic Output* | The program displays the data from the file | 1/1 | |
| The program displays the appropriate line | 1/1 | |
| The correct amount of information is displayed, e.g. only the relevant entries | 1/1 | |
| The correct level, provided as a command line flag ***-levelN***, is executed | 1/1 | |
| The program **does not** store the whole file in memory, instead it accesses the file on disk | 5/5 | |
| **Total:** | **9/9** | |
| *Error Handling* | A clear error message is displayed when an incorrect number of arguments is provided | 2/2 | |
| A clear error message is provided when an incorrect flag is provided (e.g. not -level1, etc.) | 2/2 | |
| A clear error message is provided when the input file doesn’t exist, or is incorrectly formatted | 2/2 | |
| **Total:** | **6/6** | |
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| *Feedback: Basic functionality is satisfactory.* | | | |

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| Part II  To score marks in this section, your program must be able to run levels 1-3. | | | Marks Available: |
| **6**1/55 |
| *Level 4* | The program creates a file as specified by the command line arguments | 2/2 | |
| The index file contains a list of all the sequence ids with the appropriate byte-offset | 5/5 | |
| The searching program makes use of the created index file to execute a number of queries | 5/5 | |
| A clear error message is provided when the index file does not exist | 1/1 | |
| Clear error messages are provided when the query file cannot be found, or when a bad query is given, like in Level 3 | 2/2 | |
| **Total:** | **15/15** | |
| *Level 5* | The program correctly locates and prints the id (and only the id) of every matching sequence | 10/10 | |
| A clear error message is provided when the sequence does not exist | 4/5 | |
| **Total:** | **14/15** | |
| *Level 6* | The program correctly locates and prints the id (and only the id) from every matching metadata line. | 15/15 | |
| A clear error message is provided when the keyword does not exist | 4/5 | |
| **Total:** | **19/20** | |
| *Level 7* | The program correctly decodes the expression given, identifies any matching sequences and prints out the corresponding id (and only the id). | 5/+5 | |
| A clear error message is provided when the sequence does not exist | 4/+5 | |
| **Total:** | 9/+10 | |
| *Progress Report* | Statement of completeness 2.5  Self-reflection 2.5 | **4/5** | |
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| *Feedback: Level 4-7 implementations render satisfactory outputs.* | | | |