**Bioinformatic toolkit**

**Software Requirements Specification**

**For PC**

**Version 1.0**

**Revision History**

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| **Date** | **Version** | **Description** | **Author** |
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**Software Requirements Specification**

**1.**                  **Introduction**

**1.1**               **Purpose**

The purpose of this project is to create a toolkit that takes the functions on several bioinformatic tools already available and to combine them in a single program that is more use friendly than those already in existence with the design constraint that the user interface be green. These functionalities are the alignment of DNA RNA and proteins with the users choice of scoring systems or matrices. To create dot Plot representations of the relationship between strands and to preform basic multisequence alignments. All while allowing the user to pull form the NCBI database to make access to information that the user may want to analyze easier.

**1.2**               **Scope**

The Scope of this document is to describe the requirements that the customers our TA’s asked for in the Bioinformatic Toolkit Project that will be completed by this group for the final demonstration on May 10th

**1.3**               **Definitions, Acronyms and Abbreviations**

FASTA is a data format used in bioinformatic to store Sequences of DNA, RNA or Proteins

**1.4**               **References**

**1.5**               **Overview**

The remainder of this document is organized into three sections an overview of the requirements that have been asked for, the specific details of the requirements and a final section that

**2.**                  **Overall Description**

**2.1**               **Use-Case Model Survey**

1. Align DNA, RNA, Proteins This Use case is the core of the project and will provide the user with the best alignment for two sequences of the same type that are provided by the user.

2. Create Graphical Representation This Use case allows the user to create a graphical representation of the relationships between two different sequences or gain the information available by comparing the sequence to itself.

3. Create User interface This use case allows the user to access all of the features easily

4. Pull From online database scrapes the NCBI Database to gain sequence

5. Allow User Input for grading similarity changes the way the alignment in use case one is performed based on user input

6. Users can select different grading matrices changes the way the alignment in use case one is performed based on user input

7.Support Fasta format Allows user to input their information in the FASTA format

8. allow users to save and export alignments Allows users to save the results of their alignments

9.allow users to preform basic multisequence alignments allows the user to preform alignments on more than two sequences

10.Optimize search Time Improves the ability of the user to find and access their previous results

**2.2**               **Assumptions and Dependencies**

This Project is fairly Independent the dependencies that exist within the project are between that user stories 5, 6, 7 modify user story 1 and that user story 4 is reliant on the NCBI database an online database of government information that will be scraped.

**3.**                  **Specific Requirements**

**3.1**               **Use-Case Reports**

**3.1.1 Align DNA, RNA, Proteins**

**Description:** The User will be able to input two Sequences of DNA, RNA or Proteins and have the program give the user the best alignment of the sequences.

**Actors:** User

**Preconditions:** None

**3.1.2 Create Graphical Representation**

**Description:** The User will be able to input two Sequences of DNA, RNA or Proteins and have the program give the user the Dotplot of the sequences or the Dotplot of the sequence vs itself.

**Actors:** User

**Preconditions:** None

**3.1.3 Create User Interface**

**Description:** Allows the user to easily access all functions of the program with a green theme

**Actors:** User

**Preconditions:** None

**3.1.4 Pull From online database**

**Description:** The User will be able to enter an accession number and have the program scrape the NCBI database for the DNA RNA or Protein Sequence associated with it.

**Actors:** User

**Preconditions:** Support FASTA Format. The NCBI database Has its data in the FASTA format this means that the program must support it to allow this to function properly

**3.1.5 Allow User Input for grading similarity**

**Description:** The User will be able to set the grading scheme used to align DNA or RNA This will not affect proteins

**Actors:** User

**Preconditions:** Align DNA This Changes the settings on which DNA is aligned so the basic alignment should be possible before this is completed

**3.1.6 Allow User To Change Grading Matrix**

**Description:** The User will be able to set the grading scheme for proteins by selecting a scoring matrix or Uploading their own. This will only affect proteins not DNA or RNA complements 3.1.5

**Actors:** Use

**Preconditions:** Align This Changes the settings on which a protein is aligned so the basic alignment should be possible before this is completed

**3.1.7 Allow User Input for grading similarity**

**Description:** The User will be able to set the grading scheme used to align DNA or RNA This will not affect proteins

**Actors:** User

**Preconditions:** Align DNA This Changes the settings on which DNA is aligned so the basic alignment should be possible before this is completed

**Preconditions:** Align This Changes the settings on which a protein is aligned so the basic alignment should be possible before this is completed

**3.1.8 Allow Users to save alignments**

**Description:** The User will be able to Save their previous Alignments for later access

**Actors:** User

**Preconditions:**  Align DNA it will save the output of this user story so it needs to be completed.

**3.1.9 Preform Basic Multisequence Alignment**

**Description:** The User will be able Align More than two sequences

**Actors:** User

**Preconditions:**  Align DNA needs to be completed as this will use this to bootstrap the multisequence Alignments

**3.1.10 Optimize search Time**

**Description:** The User will be able to Search their previous alignments efficiently

**Actors:** User

**Preconditions:**  Allow Users to save alignments as this will allow them to access their saved alignments

**3.2**               **Supplementary Requirements**

There is one supplementary specification not include in any of the Use cases which is to Make the User interface have a green theme

**4.**                  **Supporting Information**

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