Bioinformatic Toolkit March 26 Software Plan Documents

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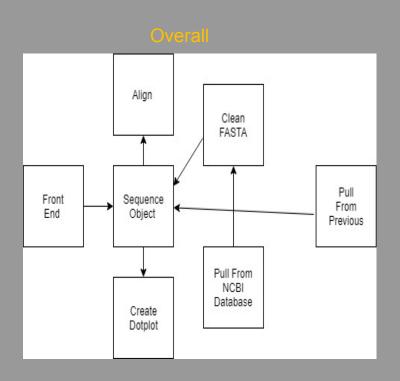
Software Requirements Specification

- 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.
 - a. Preconditions: None
- 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.
 - a. Preconditions: None
- 3. Create user interface. This use case allows the user to access all of the features easily.
 - a. Preconditions: None
- 4. Support Fasta format Allows user to input their information in the FASTA format
 - a. none
- Allow user input for grading similarity, this changes the way the alignment in use case one is performed based on user input
 - a. Preconditions: Align DNA This Changes the settings on which DNA is aligned so the basic alignment should be possible before this is completed

Software Requirements Specification

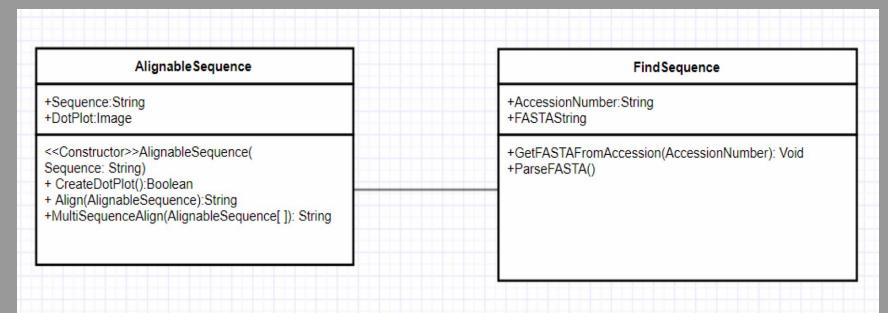
- Users can select different grading matrices changes the way the alignment in use case one is performed based on user input
 - Preconditions: Alignment, this changes the settings on which a protein is aligned so the basic alignment should be possible before this is completed
- 2. Pull from the NCBI online database to gain sequence
 - a. 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. Allow users to save and export alignments Allows users to save the results of their alignments
 - a. Preconditions: Align DNA, it will save the output of this user story so it needs to be completed.
- Allow users to perform basic multi sequence alignments, allows the user to perform alignments on more than two sequences
 - Preconditions: Align DNA, this needs to be completed as this will use this to bootstrap the multi sequence.
 Alignments
- 5. Optimize search time, this improves the ability of the user to find and access their previous results
 - a. Preconditions: Allow Users to save alignments as this will allow them to access their saved alignments

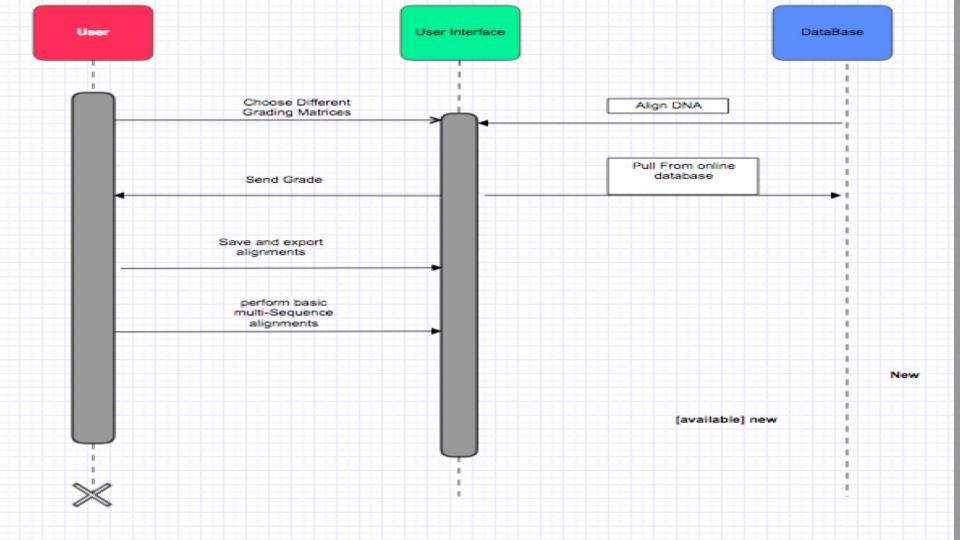
High Level Design Document



BioInformatic Toolkit Align Create Dotplot MultiSequence Save to Database Retrieve Sequence Pull From NCBI Database

Class Diagram





Configuration Management Plan

Team Responsibilities.

Member Name₽	Git User ID₽	Responsibility₽
Patrick Tessmer ₽	pattezz₽	Front end, front end test,
		Software Architecture
		documentation₽
		Back end, Back End Testing₽
4	Jghoffer28₽	Front end, front end test,
John Hoffer⊬	₽	documentation, ₽
42		Back end, Back End Testing₽
Wei Mao√	yasutsunap₽	Front end, front end test,
43		documentation, ₽
		Back end, Back End Testing₽
Yang Sun√	yanggggr₽	Front end, front end test,
43		documentation, ₽
		Back End Testing

Version Release Plan

Version Number or Label₽	Features /Bug fixes Included in version.	Remarks₽	Ç
ę.	4	₽	42
ą.	43	₽	+
φ	43	.₽	4
₽.	4	₽.	+

Sprint Plan

Week Of	Sprint Tasks
	User Story 1, User Story 3
9-Apr	User Story 2, User Story 4, User Story 5
	User Story 6, User Story 7
23-Apr	User Story 8
26-Apr	Demonstration #2
	TAs inspect Meeting Minutes document and record absences.
	User Story 9
7-May	User Story 10
10-May	Final Demonstration
	TAs inspect Meeting Minutes document and record absences.