

Process Deliverable I (3%) (Connor)

The submission for this deliverable will depend on the specific SE process model your team plans to use to complete the group project (as described in your project proposal).

Scrum: submit notes (include each teammate) from *at least weekly* scrum meetings.

Meeting 1 (Sept 30 – Oct 4)

1. Member: Connor Brodish
 - What I did? Completed work towards project milestone 1
 - What I need to do next? Look at requirements for project milestone 2 and get familiar with the computational biology interface
 - What is blocking me? 2 midterm exams next week and a project due this weekend
2. Member: Kishitij Kaushal
 - What I did? Completed work towards PM1
 - What I need to do next? Learn more about the project
 - What is blocking me? Systems Project
3. Member: Eli Bullock-Papa
 - What I did? Addressed errors in BLOSUM table calculations; finalized sequence input handling.
 - What I need to do next? Begin implementing algorithm switching functionality for different alignment methods.
 - What is blocking me? Understanding algorithm switching complexities; awaiting feedback on initial calculation accuracy.
4. Member: Ryan Zhang
 - What I did? Reviewed project requirements for global alignment visualization; completed a preliminary assessment of interview data for project insights.
 - What I need to do next? Start coding basic global alignment logic; outline initial design for the visualization interface.
 - What is blocking me? Time constraints with other coursework; managing tasks for PaxHistoria project.

Meeting 2 (Oct 7 – Oct 11)

1. Member: Connor Brodish
 - What I did? Delegated as scrum master, began collecting scrum meeting info
 - What I need to do next? Choose meeting style and inform group of next milestone due date
 - What is blocking me? Performed worse than expected on 1 midterm, feeling less productive as a result
2. Member: Kishitij Kaushal
 - What I did? Learned about the algorithms we are using.
 - What I need to do next? Learn more about the project
 - What is blocking me? Assignments
3. Member: Eli Bullock-Papa

- What I did? Addressed errors in BLOSUM table calculations; finalized sequence input handling.
 - What I need to do next? Begin implementing algorithm switching functionality for different alignment methods.
 - What is blocking me? Understanding algorithm switching complexities; awaiting feedback on initial calculation accuracy.
4. Member: Ryan Zhang
- What I did? Developed basic code for global alignment; began initial design for alignment visualization.
 - What I need to do next? Expand visualization to include interaction features like zoom and highlight.
 - What is blocking me? Balancing time between development tasks and analyzing interview data.

Meeting 3 (Oct 14 – Oct 18)

1. Member: Connor Brodish
- What I did? Was sick for most of the week, could not work
 - What I need to do next? Begin brainstorming requirements for the system
 - What is blocking me? Now behind on assigned work, even with granted extensions
2. Member: Kishitij Kaushal
- What I did? Started working on the project
 - What I need to do next? Check out what PM2 is.
 - What is blocking me? Midterm next week
3. Member: Eli Bullock-Papa
- What I did? Implemented preliminary algorithm switching functionality; fixed minor BLOSUM calculation bugs.
 - What I need to do next? Work on enhancing the visualization of BLOSUM results and integrating it with the global alignment interface.
 - What is blocking me? Understanding visualization library options; limited documentation on computational biology-specific requirements.
4. Member: Ryan Zhang
- What I did? Refined global alignment code; added basic interaction functionality to the visualization.
 - What I need to do next? Improve the UI layout for user-friendly visualization; connect visualization output to algorithm results.
 - What is blocking me? Finalizing UI options; limited resources on interactive visualization best practices for biology applications.

Meeting 4 (Oct 21 – Oct 25)

1. Member: Connor Brodish
- What I did? Completed the midterm for this class, so was unable to get ahead on milestone 2 work.
 - What I need to do next? Decide tasks for milestone 2, split up work

- What is blocking me? Busy time of the semester, general course work challenges
2. Member: Kishitij Kaushal
 - What I did? Completed the midterm
 - What I need to do next? Start working on PM2
 - What is blocking me? Midterms and projects due next week
 3. Member: Eli Bullock-Papa
 - What I did? Enhanced visualization of BLOSUM results; completed the basic integration with global alignment interface.
 - What I need to do next? Start user testing for interface usability; address any feedback on alignment accuracy.
 - What is blocking me? Gathering feedback promptly; balancing time with additional project responsibilities.
 4. Member: Ryan Zhang
 - What I did? Finished connecting visualization output to algorithm results; tested UI layout for functionality and accessibility.
 - What I need to do next? Gather user feedback on visualization features; improve interaction based on test results.
 - What is blocking me? Limited time for thorough testing; awaiting more detailed feedback from initial users

Meeting 5 (Oct 28 – Nov 1)

1. Member: Connor Brodish
 - What I did? Created a document for submission. Finalized tasked work for milestone 2
 - What I need to do next? Submit milestone 2 when all parts are completed
 - What is blocking me? Midterm this week, presenting discussion on Friday
2. Member: Kishitij Kaushal
 - What I did? Started working on PM2
 - What I need to do next? Submit PM2 and start working towards PM3
 - What is blocking me? Three midterms and systems project due this week
3. Member: Eli Bullock-Papa
 - What I did? Completed user testing for the BLOSUM and global alignment interface; addressed initial feedback on interface usability and alignment accuracy.
 - What I need to do next? Implement additional functionality to customize alignment parameters; improve error handling for invalid input sequences.
 - What is blocking me? Waiting on clarification from the professor regarding specific alignment parameter configurations.
4. Member: Ryan Zhang
 - What I did? Collected and reviewed user feedback on visualization features; made adjustments to interaction elements based on test results.
 - What I need to do next? Finalize visualization adjustments and optimize performance; start preparing documentation for the visualization module.

- What is blocking me? Managing project deadlines for other classes; awaiting further feedback on the most recent UI updates.

Requirements Analysis (6%)

Based on the results of your requirements elicitation, goals for your project, and course materials, please complete the following tasks:

1. Provide an example of five hypothetical non-functional requirements for your system. Be sure to include the specific type of requirement discussed in class, with each requirement coming from a unique category. (Connor)
 - Usability: The page should reformat to keep text, graphs, and pictures visible always, supporting any window layout (full screen, half, etc.).
 - Reliability: A user should be able to save the current state of an algorithm to load it at a later point in time without resetting progress.
 - Performance: When performing an algorithm, a progress bar should show current progress in percentage done and should take at most 1 minute(s) to complete.
 - Supportability: a user should be able to switch algorithms quickly and hassle-free, and the system should remember the last one they used.
 - Implementation/constraints: Setup must be run using a website.
2. Provide an example of five hypothetical functional requirements for your system.
 - **BLOSUM Matrix Generation:** The system shall allow users to compute a BLOSUM scoring matrix and display the matrix values. Users should be able to input specific amino acid pairs and retrieve their substitution score based on the selected BLOSUM matrix.
 - **Global Sequence Alignment Computation:** The system shall enable users to input two protein or DNA sequences and compute the optimal global alignment using algorithms like Needleman-Wunsch. The system should output both the aligned sequences and an alignment score.
 - **Interactive Visualization of Sequence Alignment:** The system shall visually represent the alignment of two sequences in a side-by-side or stacked format, with gaps and matching or mismatching bases or amino acids highlighted. Users should be able to interact with this visualization, such as by highlighting specific regions of interest.
 - **Dynamic Selection of Alignment Algorithms:** The system shall provide users with a choice of different sequence alignment algorithms (e.g., Needleman-Wunsch for global, Smith-Waterman for local) and allow users to switch between these algorithms to compare results. Each algorithm's results should be displayed and saved for comparison.
 - **Customizable Parameter Input for Algorithm Configuration:** The system shall provide an interface for users to set various algorithm parameters, such as gap penalties or scoring matrices, and visualize the impact of these settings on the alignment output and score. Parameters should be configurable before computation begins.

3. Write five formal use cases for your system and provide use case or sequence diagrams to represent each use case.

Use Case 1: Compute BLOSUM Matrix

Description: Allows the user to compute a BLOSUM matrix by selecting specific amino acid pairs.

Primary Actor: User

Preconditions: The user has navigated to the BLOSUM matrix calculation page.

Main Flow:

- The user selects amino acid pairs and inputs custom scoring values
- The system calculates the BLOSUM matrix based on the input values
- The system displays the calculated BLOSUM matrix to the user

Use Case 2: Perform Global Sequence Alignment

Description: Allows the user to perform a global alignment on two sequences.

Primary Actor: User

Preconditions: The user has accessed the sequence alignment page and has the sequences ready.

Main Flow:

- The user inputs two sequences and selects the alignment algorithm (e.g., Needleman-Wunsch).
- The system performs the alignment using the selected algorithm.
- The system displays the aligned sequences along with an alignment score.

Use Case 3: Interactive Visualization of Sequence Alignment

Description: Enables the user to view and interact with a visual representation of the sequence alignment.

Primary Actor: User

Preconditions: The user has completed an alignment and visualization data is available.

Main Flow:

- The user selects the option to visualize the alignment.
- The system generates a visual representation, highlighting matches, mismatches, and gaps.
- The user interacts with the visualization, such as zooming in, panning, or highlighting specific regions.

Use Case 4: Switch Alignment Algorithms

Description: Allows the user to select different algorithms (e.g., Needleman-Wunsch, Smith-Waterman) for sequence alignment.

Primary Actor: User

Preconditions: The user has accessed the alignment interface and completed at least one alignment.

Main Flow:

- The user selects a different alignment algorithm from a dropdown menu.
- The system updates the algorithm and re-aligns the sequences.
- The system displays the new alignment and corresponding score.

Use Case 5: Customize Parameters for Alignment Configuration

Description: Allows the user to adjust parameters, such as gap penalties, for customized alignment.

Primary Actor: User

Preconditions: The user has accessed the alignment settings and has prior knowledge of parameter settings.

Main Flow:

- The user navigates to the settings section and adjusts parameters (e.g., gap penalty).
- The system validates the parameters.
- The system applies the parameters to the alignment and displays the updated result.

Requirements Specification (6%)

Based on the results of your requirements elicitation, goals for your project, and course materials, please complete the following tasks:

1. Write four user stories from the perspective of at least two different actors. Provide the acceptance criteria for these stories.
2. For each user story mentioned above, estimate the amount of effort needed to complete relevant subtasks using function points. Explain your answer.

User Story 1: Compute BLOSUM Matrix

As a user, I want to compute a BLOSUM matrix by selecting amino acid pairs and inputting scoring values so that I can generate a substitution matrix for sequence alignment.

Acceptance Criteria:

- The user can select amino acid pairs and input custom scoring values.
- The system calculates and displays the BLOSUM matrix.
- The system provides an error message for invalid input values.

Effort Estimation (Function Points):

- Input amino acid pairs: 3 FP (External Input)
- Display calculated matrix: 5 FP (External Output)
- Validation and error handling: 2 FP (Internal Logic)
- Total: 10 FP

Explanation: Moderate complexity in user input handling and matrix calculation but straightforward output display.

User Story 2: Perform Global Sequence Alignment

As a user, I want to align two sequences globally using an algorithm of my choice (e.g., Needleman-Wunsch) so that I can view optimal alignment and score.

Acceptance Criteria:

- The user can input two sequences.
- The system performs the selected global alignment algorithm.
- The aligned sequences and score are displayed.

Effort Estimation (Function Points):

- Sequence input fields: 3 FP (External Input)
- Alignment calculation: 8 FP (Internal Logic)
- Display results and alignment score: 5 FP (External Output)
- Total: 16 FP

Explanation: High complexity due to sequence processing and algorithmic calculation, combined with result display.

User Story 3: Switch Alignment Algorithms

As a user, I want to switch between alignment algorithms so that I can compare results from different approaches.

Acceptance Criteria:

- The user can select from multiple alignment algorithms.
- The system performs alignment using the chosen algorithm.
- Results are updated based on the selected algorithm.

Effort Estimation (Function Points):

- Algorithm selection field: 3 FP (External Input)
- Recalculation with chosen algorithm: 8 FP (Internal Logic)
- Updated result display: 4 FP (External Output)
- Total: 15 FP

Explanation: Complexity comes from recalculating alignment with different algorithms and updating the results.

User Story 4: Manage User Access (Admin)

As an admin, I want to manage user permissions and data access so that I can control who can use the system features.

Acceptance Criteria:

- Admin can view a list of all users.
- Admin can grant or revoke access to different features.
- Changes to user permissions are saved and take effect immediately.

Effort Estimation (Function Points):

- Display user list: 4 FP (External Output)
- Modify user permissions: 6 FP (Internal Logic)
- Save and apply changes: 3 FP (Internal Logic)
- Total: 13 FP

Explanation: Moderate complexity due to the need for a user interface, permission modification, and immediate application of changes