

Software Requirements Specifications
for
JAX Front-end Project

Version 1.0 approved

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Revision History

Name	Date	Reason For Changes	Version
Sarah Crane	2-11-25	Initial Draft	1.0
	2-16-25	Preliminary Draft	1.1

1. Introduction

1. Introduction

In this section, you will find information about this document, its purpose and intended audience, the scope of the project, terms used throughout, and references.

1.1 Purpose

This software requirements specification document (SRS hereafter) will lay out the requirements of the Jackson Laboratories Front-End project for Northeastern's Spring 2025 Portland campus CS5500: Software Engineering course. It will detail the goals for the project that the team intends to accomplish, including both functional and non-functional requirements, as determined by the client and the team members. This document is intended as a reference for the students responsible (listed above) and for Professor Cantrell, the course instructor.

1.2 Project Scope

GeneWeaver is an application that allows for gene comparison and analysis. It comprises a database of gene sets and a set of analysis tools. GeneWeaver is an open-source project; all the code is available on GitHub for users to run locally. There is also a web application, which is easier and quicker to use. The broad purpose of the software is to allow users to search for gene sets and compare them with other gene sets based on specified criteria. Users are able to search for or add gene sets, add them to their projects, run analysis tools on them, and share them with other users. This project will be focused on implementing and improving several of the analysis tools in the web application. One will be the GeneSet graphs, which is intended to show how closely linked genesets are.

1.3 Definitions, Acronyms, and Abbreviations

Gene set: a list of genomic features, free text descriptive content, ontology annotations, and gene association scores [1]

Jax: Jackson Laboratories, the client on this project

MoSCoW Method: M - *Must have*, S - *Should have*, C - *Could have*, W - *Won't have*. [2]

SRS: Software Requirements Specification [3]

1.4 References

[1] "Genes and genesets," Genes and GeneSets - GeneWeaver,

<https://thejacksonlaboratory.github.io/geneweaver-docs/concepts/genes-and-genesets/#genomic-features-genes> (accessed Feb. 14, 2025).

[2] "MoSCow method." Wikipedia, https://en.wikipedia.org/wiki/MoSCoW_method (accessed Feb. 16, 2025).

[3] "IEEE Recommended Practice for Software Requirements Specifications," in *IEEE Std 830-1998*, vol., no., pp.1-40, 20 Oct. 1998, <https://ieeexplore.ieee.org/document/720574> (accessed Feb. 16, 2025).

1.5 Overview

(Describe what the rest of the SRS will contain and explain how it is organized.)

2. Overall Description

2. Overall Description

2.1 Product Perspective

2.2 Product Functions

2.3 User Characteristics

GeneWeaver is meant for use by researchers, particularly genomics researchers, educators, and students. In general, its intended users are scientists. These users may have coding knowledge (they may be able to run GeneWeaver locally) or they may not (in which case they can use the web application). They have statistical knowledge that enables them to run the analysis tools.

2.4 Constraints

2.5 Assumptions and Dependencies

3. Specific Requirements

3. Specific Requirements

3.1 External Interface Requirements

3.1.1 User Interfaces

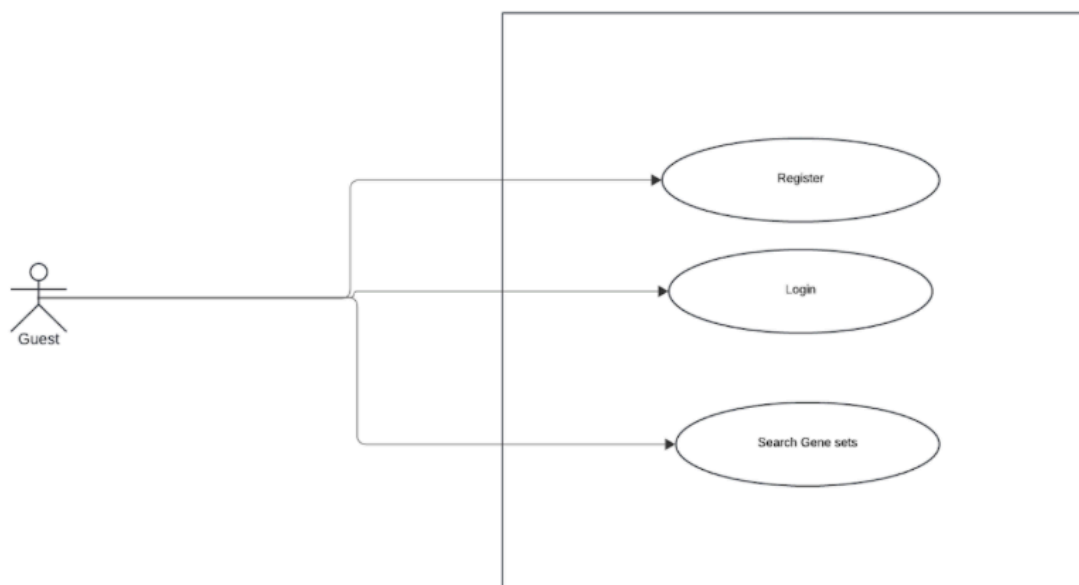
3.1.2 Hardware Interfaces

3.1.3 Software Interfaces

3.1.4 Communications Interfaces

3.2 Functional Requirements

3.2.1 User story 1



As a guest user, we want to browse and explore publicly available gene sets and documentation so that we can understand the platform's capabilities before deciding to register.

3.2.1.1 Feature 1.1 - Public Browsing of Gene Sets

3.2.1.1.1 Introduction/Purpose of feature

This feature enables **Guest** users to discover and explore the publicly available gene sets in GeneWeaver. Its primary goal is to provide a clear entry point for new or casual visitors who wish to learn about the system's offerings without creating an account.

3.2.1.1.2 Priority/MoSCoW

Priority: Must Have (M)

The ability for guests to browse publicly available gene sets is fundamental to encouraging new users to explore the platform and potentially register for full functionality.

3.2.1.1.3 Associated Functional Requirements

3.2.1.1.3.1 List 1 ...

3.2.1.1.3.2 List 2 ...

3.2.1.2 Feature 1.2

3.2.1.2.1 Introduction/Purpose of feature

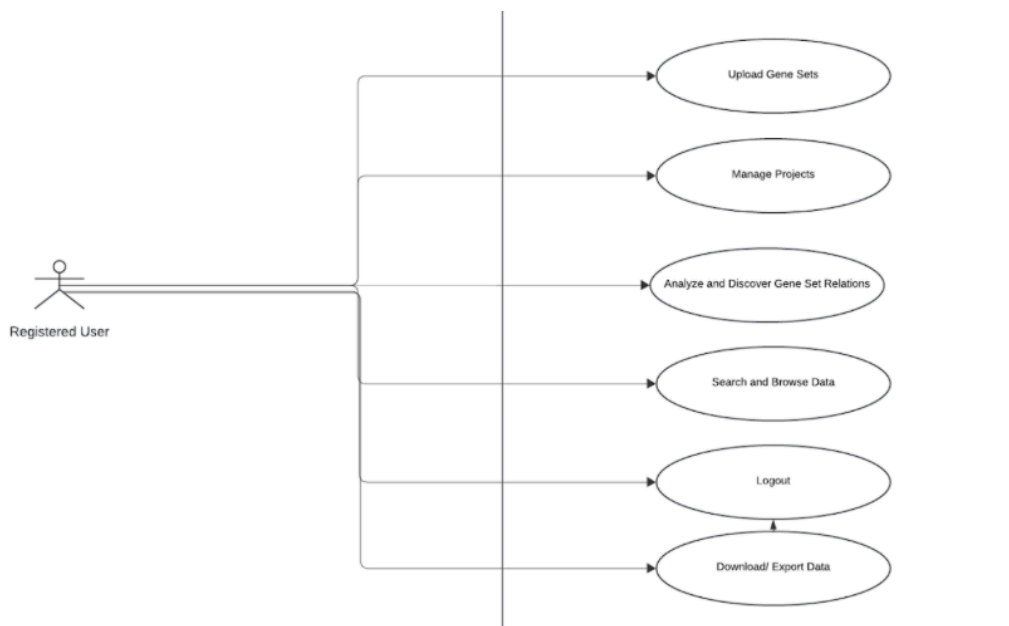
3.2.1.2.2 Priority/MoSCoW

3.2.1.2.3 Associated Functional Requirements

3.2.1.2.3.1 List 1

3.2.1.2.3.2 List 2 ...

3.2.2 User Story 2



3.2.2.1 Feature 1.1 - Registered User

3.2.2.1.1 Introduction/Purpose of feature

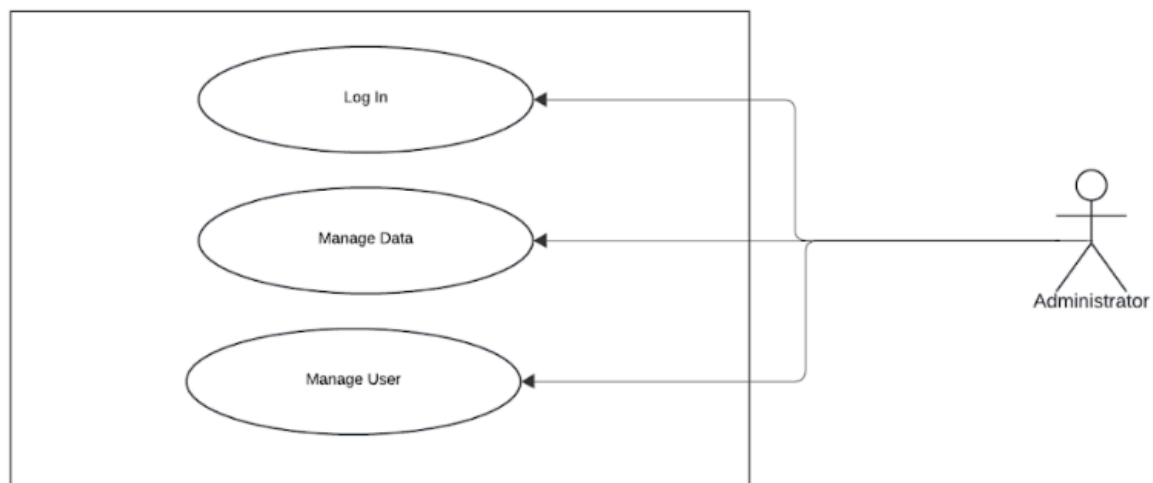
As a **registered user**, we want to upload and organize gene sets, so we can easily manage and analyze my research data.

3.2.2.1.2 Priority/MoSCoW

Priority: Must Have (M)

The ability for guests to browse publicly available gene sets is fundamental to encouraging new users to explore the platform and potentially register for full functionality.

3.2.3 User Story 3



3.2.3.1 Feature 1.1 - Administrator

3.2.3.1.1 Introduction/Purpose of feature

As an **administrator**, we want to manage user accounts and data submissions, so that the system remains secure and reliable for all users.

The feature would be an administrative control page.

3.2.3.1.2 Priority/MoSCoW

Priority: Must Have (M)

The system shall allow administrators to review, approve, or disable user accounts and provide tools to monitor and remove problematic datasets.

3.3 Nonfunctional Requirements

3.3.1 Configuration

3.3.2 Etc. (Add more, see SRS class slides for inspo.)

3.4 Design Constraints

3.5 Software System Attributes

The Geneset Graph Tool in GeneWeaver is expected to exhibit the following software system attributes to ensure its effectiveness, usability, and reliability.

1. **Reliability:** The system should consistently provide accurate and reproducible gene set relationships, ensuring correctness in graph generation and analysis. It must handle errors gracefully without data corruption or unexpected failures.
2. **Scalability:** The system should support increasing numbers of gene sets and complex graph structures without significant degradation in performance. It should be able to accommodate large-scale datasets used in genomics research.

4. Usability: The user interface should be intuitive, allowing researchers to easily navigate, interpret, and manipulate gene set graphs with minimal training. Clear visualization and well-labeled elements should enhance the user experience.
5. Security: The tool should protect gene set data from unauthorized access and ensure data integrity. If applicable, authentication mechanisms will be in place for restricted functionalities.

Appendixes

(Add and label as needed, some suggestions noted below. Will add doc links if kept.)

Appendix A: Glossary

Appendix B: Analysis Models

(Place to add diagrams etc.)

Appendix C: Issues List

(Could be used to include/document TBD elements of project, pending decisions, conflicts, etc.)