

**Michael Alberda** [malberda15@gmail.com](mailto:malberda15@gmail.com) | 2087612179 | Boise, ID | <https://github.com/malberda>

## Education

**Boise State University**  
*BS Computer Science*

Boise, ID  
*August 2021 | May 2023*

**University of Idaho**  
*BS Mathematics - Computation Option, GPA: 3.5*

Moscow, ID  
*September 2017 | May 2021*

## Experience

**Tap Network LLC**      Boise, ID      *Software Intern*      *January 2022 | Ongoing*

- Work with developers and other interns to create documentation for existing codebase

**Dr. Neuhaus**      Moscow, ID      *Grader*      *September 2019 | September 2020*

- Cleanly and correctly grade all homework and deliver on time to the professor

**Treasure Valley YMCA**      Boise, ID      *Head Lifeguard*      *June 2016 | September 2017*

- Work with other lifeguards to maintain a clean and safe place of business and engage with patrons to secure a happy and healthy YMCA

## Skills

**Proficient Programming Languages:** C, C++, Java, Linux Shell

**Familiar Programming Languages:** TypeScript, JavaScript, HTML, Python, Unity

**Other Relevant Skills:** Scrum and Agile Development, Git Workflow

## Projects

**Reduction of States in a Finite Automaton C**      <https://github.com/malberda/cs385finalproject>  
Demonstration of the concept of reducing states in a finite automaton.

**Optimal Binary Search Tree JavaScript**      <https://github.com/malberda/project-395>  
Created a simple visual demonstration of an optimal binary search trees creation and maintenance

**CPU Scheduling Simulation Java**      <https://github.com/malberda/CPUSchedulingEmulator>  
Emulate a simple CPU and its scheduling of processes using Java and a cache system

**School Database Manipulation SQL**      <https://github.com/malberda/BSU-HU-CS-310-Final-Project>  
Create a database and manipulate data from it in order to simulate a schools database.

**Data Structures Bioinformatics Java**      <https://github.com/malberda/BTree-BIOINFORMATICS>  
Create a B-Tree that stores and performs operations on a series of excerpts of the human genome.  
Implement a cache in order to speed up processing while searching the genome for frequencies of specific substrings.