



ALIGNET: A WEB APPLICATION FOR MAPPED NGS READS USING OPEN-SOURCE GENOME BROWSER LIBRARIES

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BACKGROUND OF THE STUDY

Read mapping

- type of **sequence alignment** that involves determining the **position** of reads relative to the reference, then mapping these reads to identify regions of similarity
- essential in understanding the **functional**, **structural**, and **evolutionary** relationship between sequences (Mount, 2001).
- help in detecting **genomic variances**, which is essential in the study of **medicine** and **phylogenics** (Trapnell & Salzberg, 2009; Wiltgen, 2019)



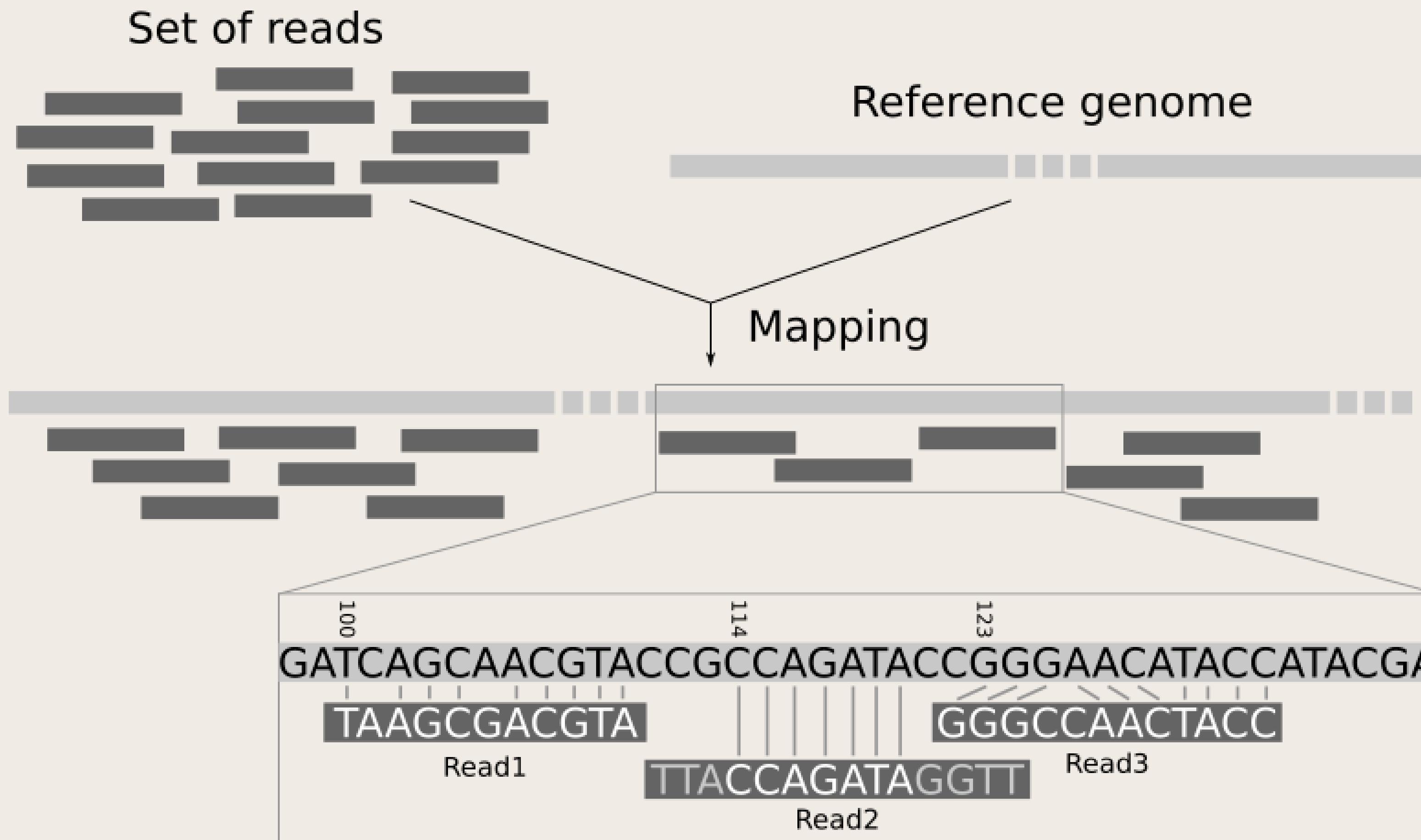


Figure 1. Short-read mapping



STATEMENT OF THE PROBLEM

- Developing a web application that specializes in **visualizing mapped reads** addresses the problem of use complexity with existing genome browsers.
 - Integrating **open-source libraries** may also help address these challenges and maximize their use.
 - The open-source web application may also serve as a **starting point** for developing other related applications.
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OBJECTIVES OF THE STUDY

- to integrate a **built-in library** containing genome references;

- to develop a **visual interface** for accessing and navigating mapping results;

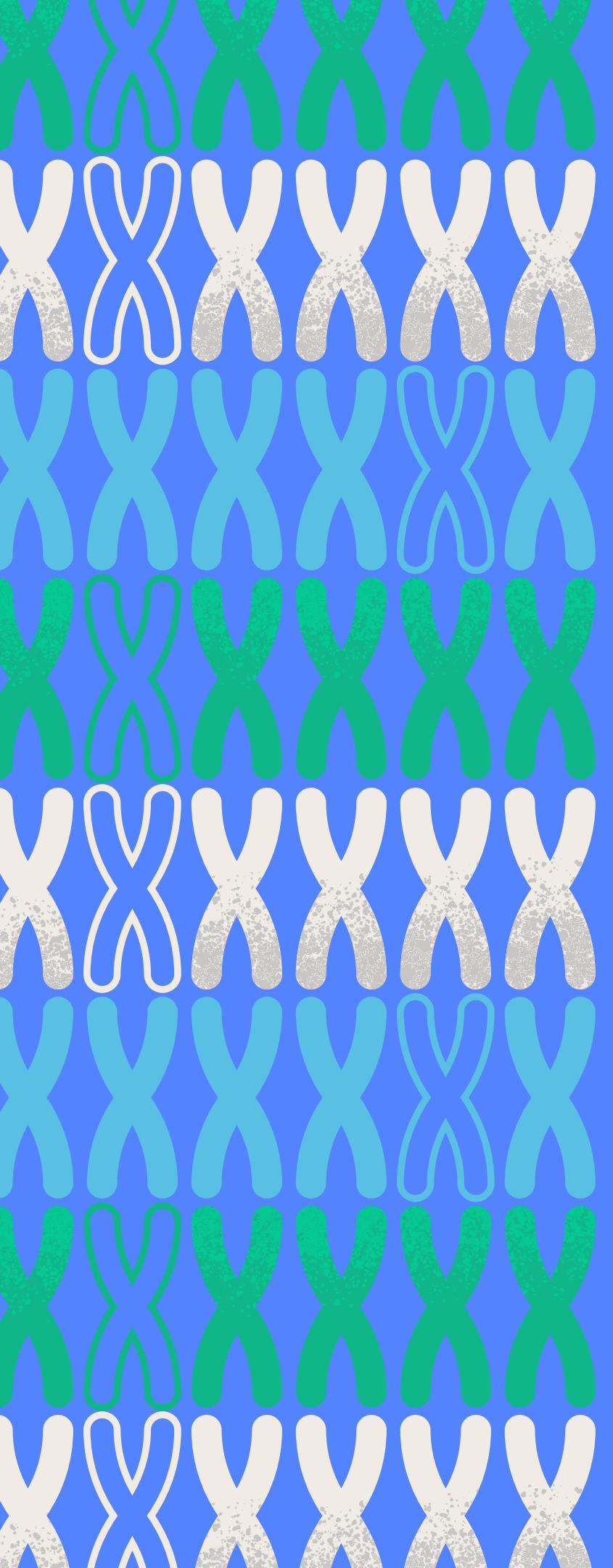
- to integrate existing open-source **genome browser libraries**; and

- to implement **user system features**, such as log-in and sign-up, in order to protect sensitive user data

METHODOLOGY

Development and Deployment

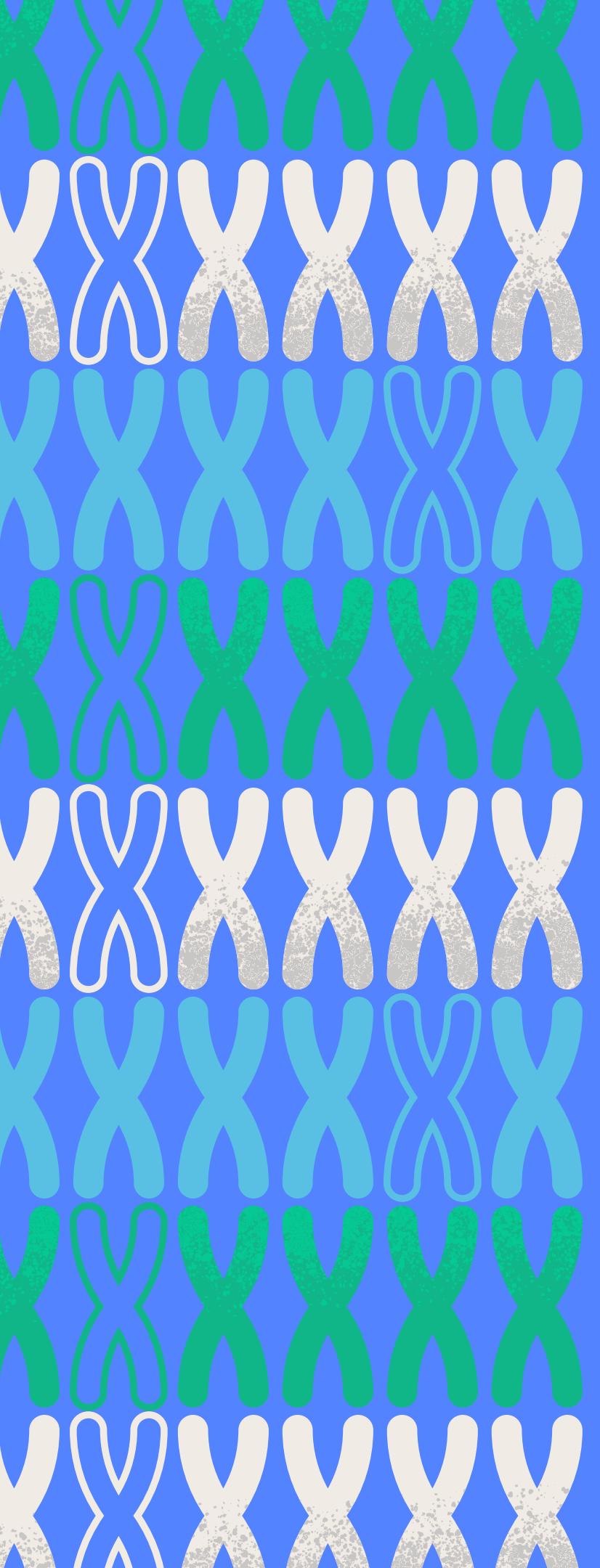
- **Back-end:** Django, Django REST Framework, Swagger, django-allauth
- **Front-end:** NextJS, TailwindCSS, IGV.js, NextAuth, shadcn
- **Database:** SQLite
- **Deployment:** DigitalOcean, Duck DNS, nginx



METHODOLOGY

Application Features

- Google single sign-on (SSO)
- CRUD functionality for references and reads files
- Genome visualizer interface
- File sharing
- Audit logs



RESULTS & DISCUSSION

The web application has been successfully deployed and is accessible through <http://alignet.duckdns.org/>. The API endpoints and admin interface may be accessed separately through <http://alignet.duckdns.org/swagger> and <http://alignet.duckdns.org/admin> respectively.



RESULTS & DISCUSSION

The **System Usability Scale (SUS)** was used to determine the usability of the application within its target users. The respondents comprise of biology students and professionals in the field of biology and bioinformatics from **UPLB**.



RESULTS & DISCUSSION

	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Q9	Q10	Score
Tester 1	4	1	5	1	4	1	5	1	5	1	95.00

Figure 2. SUS distribution and mean scores of testers
(Registered Microbiologist)

RESULTS & DISCUSSION

	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Q9	Q10	Score
Tester 1	5	1	5	2	5	1	5	1	5	1	97.50
Tester 2	5	1	5	2	5	1	5	1	4	1	95.00
Tester 3	4	1	5	1	4	2	5	1	4	1	90.00
Tester 4	5	3	4	2	5	1	3	2	3	3	72.50
Tester 5	5	2	5	1	5	1	5	2	4	2	90.00

Mean: 89.00

Figure 3. SUS distribution and mean scores of testers from the BS Biology program, majoring in Genetics, Cell and Molecular Biology, or Microbiology

CONCLUSION

The study was able to **accomplish its objectives** evident in the implemented features in the web application. Additional features such as file sharing and audit logs to encourage collaboration while maintaining user and file privacy have also been implemented.

The study as also able to achieve its goal of **providing accessibility** through deployment and delivering a **user-friendly experience**, as supported by the computed SUS score of **95.00** and **89.00**.

RECOMMENDATION

- Host the web application through a **paid server** with better virtual resources
- Adding a **help center** to brief first-time users
- Support **other visualizing layouts** aside from the current linear
- Implement **progress indicators** for file upload and download



THANK YOU!

References

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