



# Computational Biology Helpers

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# Agenda

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- 03 Use Cases
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# Problem Description



Many software engineers want to learn about computational biology but struggle to manage projects and understand how or why different algorithms are used.



# Our Motivation

Just like many other students learning computational Biology, we wanted to be able to see the algorithms in action without downloading anything to our computers



# Solution Architecture

# Technical Architecture

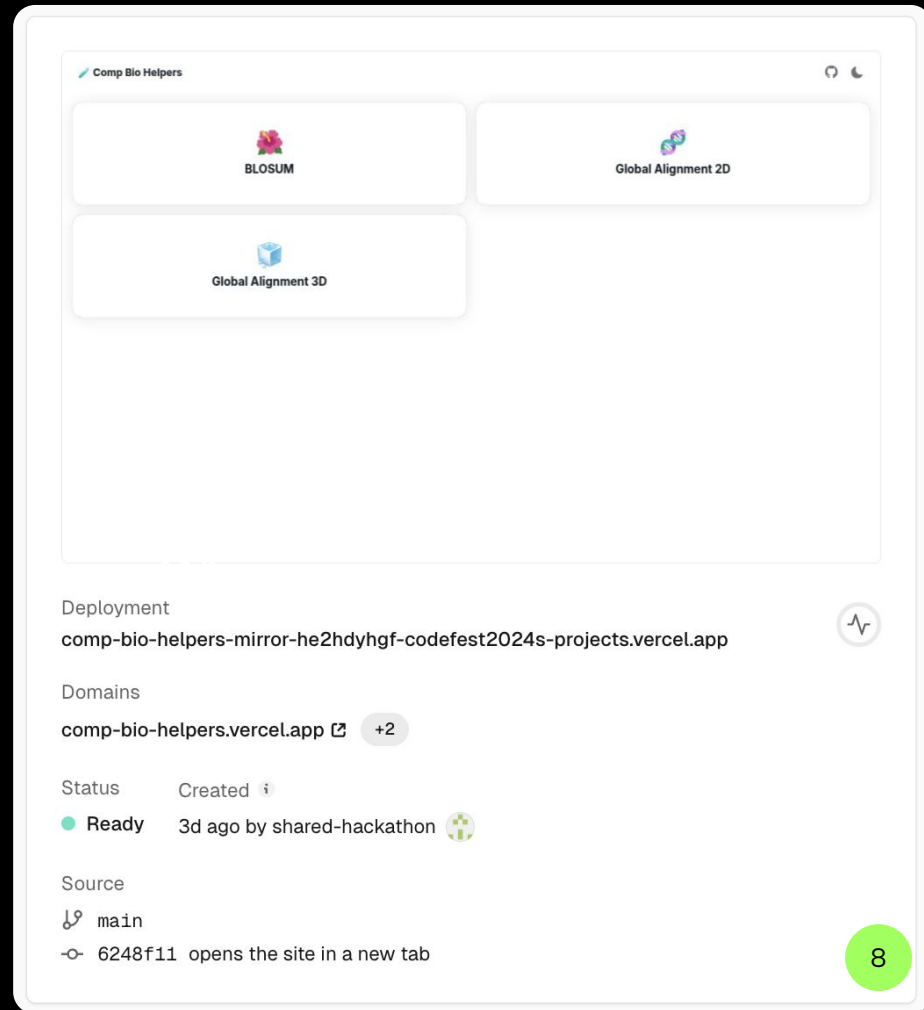
NEXT.js + NextUI

Vercel



## Our Deployment

1. Mirrored to a private github repository using Git Workflows
2. Hosted By Vercel
3. Custom domain purchased through Cloudflare
4. Deployment automatically updates when new code is pushed (CI/CD)







# Top Three Use Cases



# Use Case Overview

## BLOSUM Matrix

Lambda Value  
1

Calculate

Letter	A	B	C	D
A	0.42			
B	0.47	0.53		
C	-0.06	0.18	1.16	
D	0.34	-0.91	0.18	1.51

## 2D Global Alignment

Match Score  
1

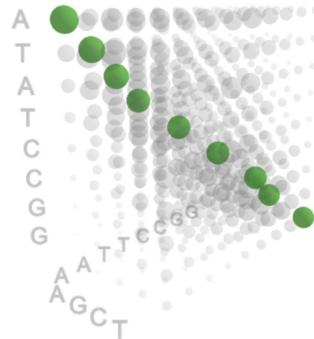
Mismatch Score  
-1

Gap Score  
-2

DP Table

	-	G	T	C
-	0	-2	-4	-6
G	-2	1	-1	-3
A	-4	-1	0	-2
T	-6	-3	0	-1

## 3D Global Alignment

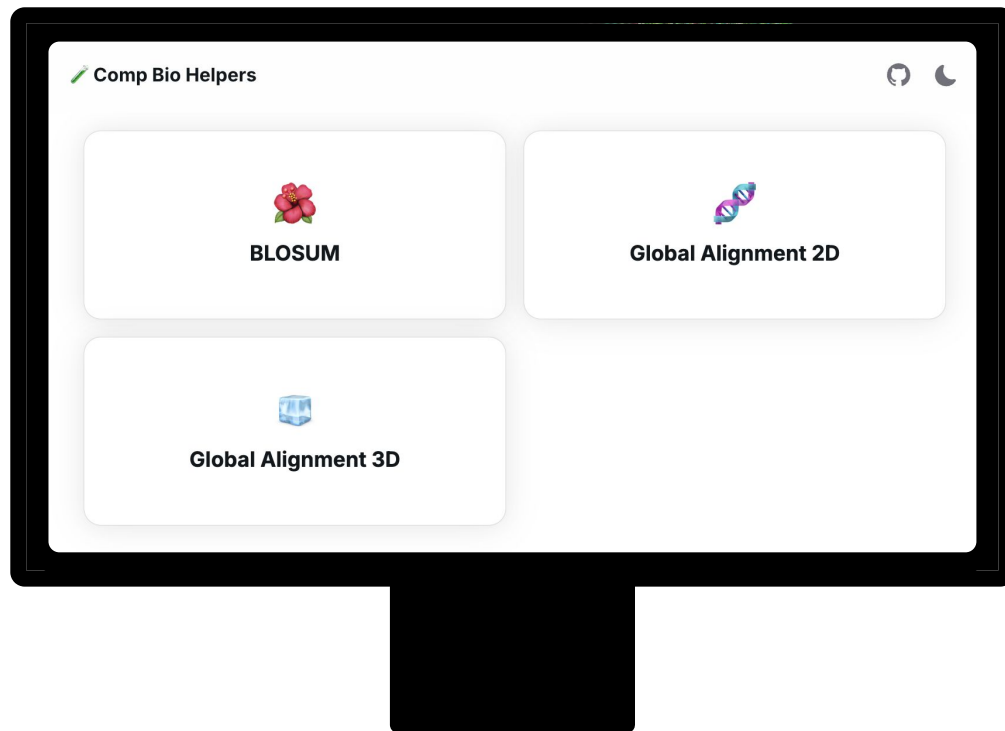




# Interactive Demo



[comp-bio-helpers.vercel.app](https://comp-bio-helpers.vercel.app)





# Connection To Class



# Usability Heuristics

Place User  
in Control

Reduce  
User's  
Memory

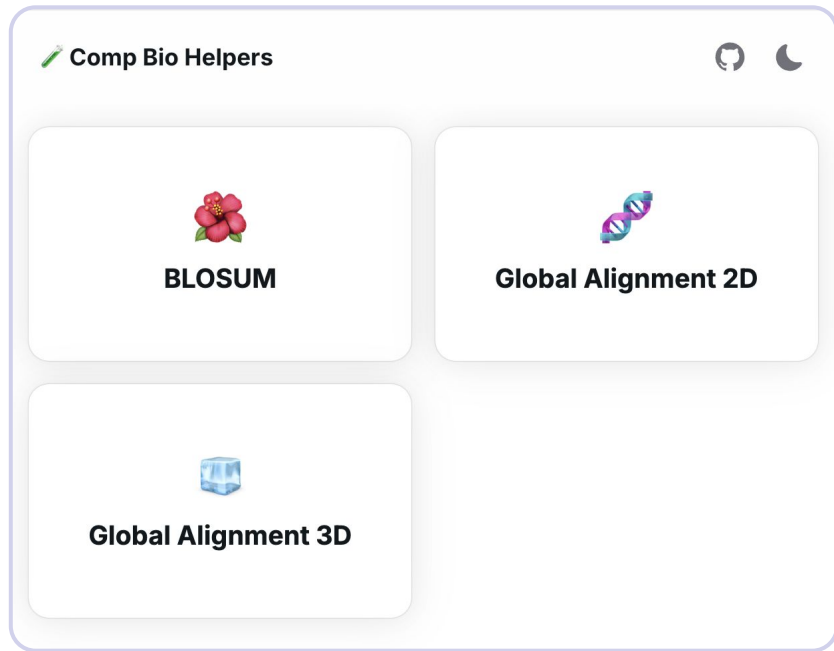
Make  
Interface  
Consistent



# Place User in Control

Home page has 3 tabs  
for quick, **easy access**

Light/Dark mode toggle  
for more **customization**





# Reduce User's Memory

The user **doesn't have to remember** the intermediate values of the BLOSUM Matrix calculation

Values are **automatically saved** when switching tabs

Comp Bio Helpers

Input Data   Q Values   P values matrix   BLOSUM Table

Enter BLOSUM block  
Enter block data with each character representing a cell

Add Block   Add Homework 1 Data

Column 1	Column 2	Column 3
A	B	C
D	E	F
A	B	C

Column 1	Column 2	Column 3	Column 4	Column 5
A	B	C	D	A
A	B	C	D	A





# Make Interface Consistent

The Alignment Table and  
Sequence Input user  
interface **remain  
consistent** between both  
2D and 3D Global  
Alignment

Alignment Table

Sequence	1	2	3	4	5	6	7	8	9
X	G	T	C	G	A	C	G	C	A
Y	G	A	T	T	A	C	-	-	A

Sequence 1  
GTCGACGCA

Sequence 2  
GATTACA

Match Score  
1

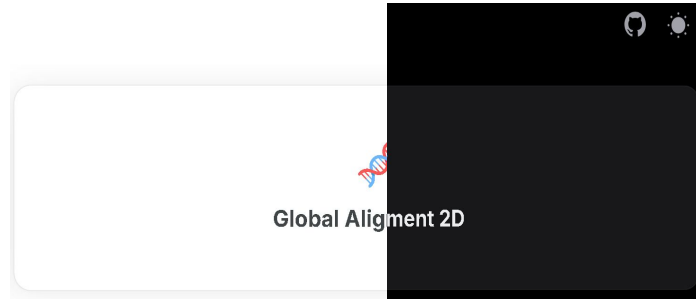
Mismatch Score  
-1

Gap Score  
-2

## HCI Design Principles | Part 2

### Visibility of system status (1)

- Visual cues for toggling mode
- Action is instant and reversible
- Light/dark mode have different images

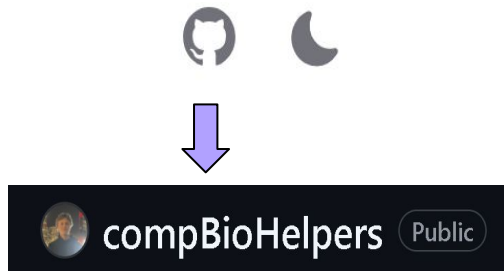


### Flexibility and Efficiency of use (7)

- Supports 2D and 3D visualizations
- More use cases for more user's needs, improving experience

### Help and documentation (10)

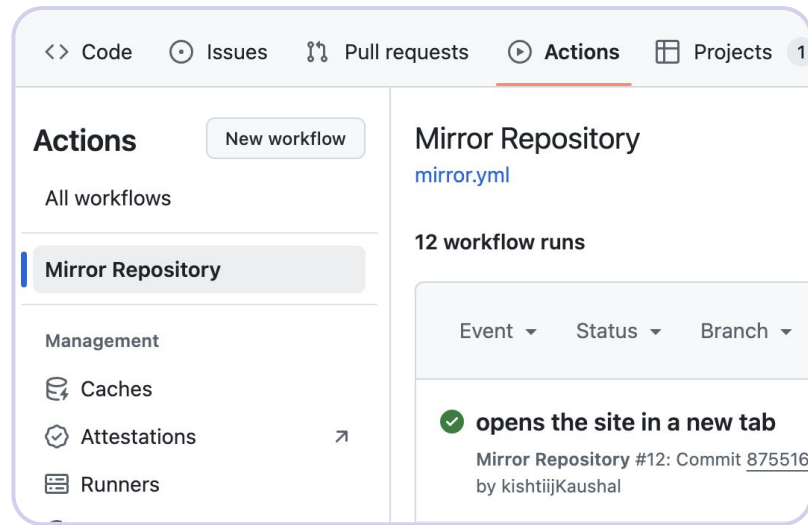
- GitHub icon links to repository
- Entry point for documentation
- One spot for all relevant information





# CI/CD Part 1

**Continuous Integration and Deployment** helped us to quickly iterate on new features and see their resulting changes without tedious processes

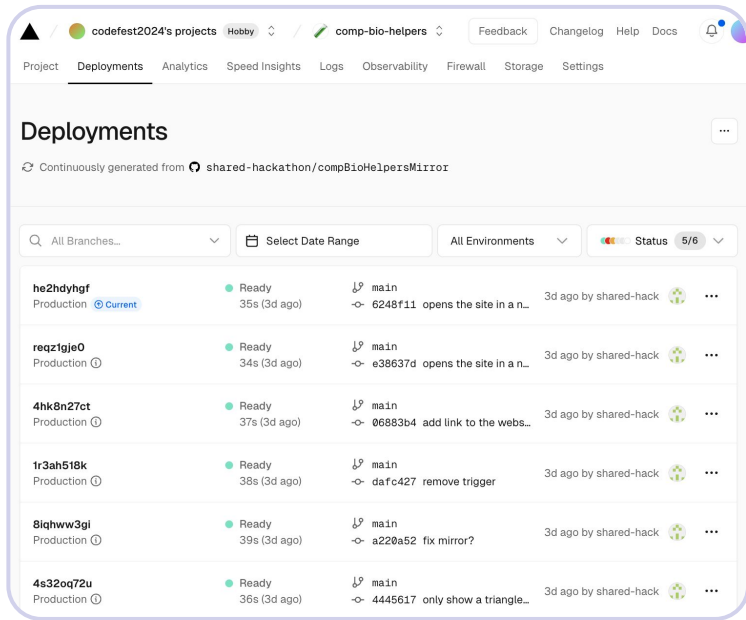


*Github Action to mirror the repository  
in preparation for Vercel*



# CI/CD Part 2

Once our infrastructure was set up, anyone could push a change to Github and see the live website update in <3 minutes with **no extra work needed**.



*Continuously Generated Deployments  
from our Github on Vercel*



# Related & Future Work



# Related Work

## 3D Alignment

A [Github Repository](#) for a python script that extends the Needleman-Wunsch algorithm to 3 sequences

## BLOSUM Matrix

A [Wikipedia Page](#) for how to calculate the matrix. There was no other published code or websites for how to implement the algorithm.

## 2D Alignment

An interactive [Github Pages](#) website for doing Global Alignment. Very useful but the interface is cluttered and confusing.



# Future of our project

Use multithreading to compute the alignments quickly

Make the user interface nicer and easier to navigate

Incorporate more computational biology algorithms and general Software Engineering Algorithms

Share solutions with team members and other users of the website



# Any Questions?