Hossam Zaki

(401) 855 5567 • hossam_zaki@brown.edu • hossam.computer
https://github.com/hossam-zaki

Education

Brown University **Providence, RI**
Bachelor of Science in Computer Science and Biology, *Expected Graduation: May 2022*

- **Related Coursework:** Computational Biology, Computer Vision, Software Engineering, Experimental VR, Practical System Skills, Deep Learning, 3D Computer Vision Using Deep Learning
- **Programming Languages:** Python, Java, Dart, SQL, HTML/CSS, Bash, Javascript, Swift, R
- **Librarys/Frameworks:** Node.js, Angular.js, Android Studio, Flutter, Pandas, Numpy, Tensorflow, Sklearn, PyTorch
- **Scholarships:** Jackie Robinson Foundation Scholar, Merck ACS Scholar

Work Experience

Broad Institute of MIT and Harvard **Remotely**
Undergraduate Researcher *June 2020 - August 2020*

- Researched effect of mutations in DNA repair genes on whole genome Structural Variants
- Developed algorithm using Python and R and analyzed data using various statistical tests
- Combined data from several databases including ICGC, PCAWG, Uniprot, Ensembl, and TCGA

Google **Remotely**
SPS Program Intern *June 2020 - August 2020*

- Worked with team to develop a real-time voting app using Java and HTML/CSS
- Tested app with several Googlers and gave presentation to several people in the Translate team

Wessel Lab at Brown University **Providence, RI**
Undergraduate Researcher *July 2017 - Present*

- Researched the effect of Sea Star Wasting Disease on the embryonic development of Sea Star and Sea Urchin
- Developed pipeline to search and find new genetic motifs in the RNA of germ-line cells using Python and the Knuth-Morris-Pratt algorithm
- Co-authored an abstract presented in Developmental Biology of the Sea Urchin Conference titled: "Bisphenol A exposure differentially affects echinoderm embryogenesis. Developmental Biology of the Sea Urchin"

Protein Data Bank of Europe **Cambridge, UK**
Software Engineering and Bioinformatics Intern *June 2019 - August 2019*

- Developed a pipeline to superpose protein structures in a UniprotKB Accession, cluster the proteins based on structure similarity, and show them visually on PyMol
- Designed Algorithm using Python and SQL and analyzed data using Hierarchical Clustering.
- Compiled the algorithm on over 47,000 Uniprot Accessions which included over 350,000 PDBe entries
- Co-authored and published a paper to Nucleic Acids Research titled "PDBe: Improved findability of Macromolecular structure data in the PDB"

Software Projects

Apollo | A Speech-to-Text Note-Taking App for Doctors
https://github.com/hossam-zaki/apollo | http://apollohealth.herokuapp.com/

- Utilized Google's Speech Recognition Library to capture appointment transcript, and used Knuth-Morris-Pratt to search for relevant details
- Encrypted patient data and appointment transcript using Google Tink
- User-tested with medical students at Brown Medical School, and doctors at Rhode Island Hospital

Computational Analysis of Sea Urchin Transcriptome
https://github.com/hossam-zaki/Sea_Urchin_Transcriptome_Analysis

- Developed pipeline to search for known genetic motifs in the transcriptome of the Sea Urchin, as well as discovering new motifs
- Implemented Knuth Morris Pratt Algorithm to linear-time pattern recognition as well as a Suffix Trie to search for the longest most common substring
- Currently developing a machine learning model to search for transcription factors

X-Ray Classification
Github Link Coming Soon...

- Built a neural network to classify X-Ray images in NIH Dataset and added in COVID-19 X-Rays
- Achieved an average of 65% True Positive Rate