ERIC CHEUNG

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I am a biochemist who worked as a Research Assistant in the Lobo Lab. My interests lie in the development of algorithms and usage of readily available biological data to understand complex biological systems. I enjoy the interdisciplinary aspect of my research and plan to pursue further education in bioinformatics.

RESEARCH EXPERIENCE

Laboratory of Dr. Daniel Lobo **Baltimore, MD**
Undergraduate Research Assistant & Web Developer Nov 2017 – Feb 2020

- Curated planarian worm gene expression profiles from published sources into a SQL database
- Designed and maintained a custom website using Tripal toolkit for public access to the database
- Created semi-automated tools for transferring data between PlangexQ and Plangex formats
- Develop the PlangexQ tool for standardized curation of planarian worm gene expression
- Setup website server and video card test server

EXPERIENCE

Hunan Manor **Silver Spring, MD**
Assistant Manager Sept 2015 – Present

- Aided in the creation of new menus; printing, and ordering menu paper and covers
- Redesigned website and online experience to improve tele-ordering process
- Maintain positive attitude and professionalism in stressful situations

EDUCATION

University of Maryland, Baltimore County **Baltimore, MD**
B.S. in Biochemistry and Molecular Biology (GPA: 3.473) 2015-2019

SKILLS

Laboratory: Cell Culture, PCR, Western Blot
Programming: Java, C++, Python, PHP, SQL, Drupal

RELATED EXPERIENCE

- **Database System**

- Developed normalized ER diagrams, setup databases using MySQL, and accessed data using C++

- **Data Analytics**

- Extracted data from MySQL databases and used ThinkStats library for analysis of information

CONFERENCES

- Undergraduate Research and Creative Achievement Day (URCAD) Apr 2018, Apr 2019
- Summer Undergraduate Research Fest 2018 (SURF) Aug 2018

PUBLICATION

- Roy, Joy et al. “Curation and annotation of planarian gene expression patterns with segmented reference morphologies.” *Bioinformatics (Oxford, England)* vol. 36,9 (2020): 2881-2887. doi:10.1093/bioinformatics/btaa023