# ALEXANDER FENG

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# **EDUCATION**

### UCSD JACOBS SCHOOL OF ENGINEERING

LA JOLLA, CA

Bioengineering – Bioinformatics B.S.

- Graduated: Spring 2018
- Core Computer Science courses: Advanced data structures, discrete math, object-oriented design, design and analysis of algorithms, computer organization and systems programming

## PROJECTS

Discord bot

Summer 2018 – Ongoing

- Uses RESTful API requests to pull data based on user commands and present data to the user
- Allows users to interact with social and statistical features
- Tools used: Python, RESTful API requests, Discord

External survey extraction and database sync

Summer 2018 – Fall 2018

- Refactored tools used to extract survey data by integrating RESTful API requests against external survey source
- Updated relational database to house newly formatted data and prepare it for metadata analysis
- Tools used: Python, PostgreSQL, RESTful API requests

Differential gene analysis of papillary renal cancer

*Spring 2017* 

- Organized data of 40 cancer patients in various stages of PRCC and used differential gene analysis to identify genes of interest
- Additionally, utilized DAVID to associate functions with possible correlation with cancer
- Tools used: R, DESeq2, DAVID

Glucose 6-phosphate dehydrogenase model

Winter 2016

- Modeled enzymatic activity of glycolysis and its relation to G6PDH
- Methods/skills used: enzymatic networking, network modeling

### SKILLS AND PROFICIENCIES

Languages: Python, Java, C++, C#, PostgreSQL, JavaScript, HTML

Additional skills/experience: Unit testing, data structures, object-oriented design, databases, API requests, algorithm design, discrete math, Git, Unity, Linux development

# WORK EXPERIENCE

UCSD DEPARTMENT OF PEDIATRICS: KNIGHT LAB

LA JOLLA, CA

Software Developer

April 2018 – October 2018

- Expanded American Gut participant portal website infrastructure
- Designed scripts to query American Gut database and handle participant data
- Designed unit tests to ensure quality and consistency of scripts
- Explored analysis of human gut microbial communities