

Kevin Chau

8861 Villa La Jolla Drive, Apartment 23, La Jolla, CA 92037

kkhaichau@gmail.com | (408) 497-4165 | www.linkedin.com/in/kevinkhaichau | kkchau.github.io

Education:

- University of California, San Diego, 2017
 - Biology w/ Specialization in Bioinformatics, B.S. Candidate

Skills and Qualifications:

LABORATORY TECHNIQUES

- Able to prepare and analyze affinity chromatography columns and size exclusion columns
- Able to perform and analyze gel electrophoresis and Western Blots

BIOINFORMATICS

- Used BLAST and ClustalOmega in laboratory coursework to query DNA/protein sequences and alignment
- DAVID tool to annotate large sets of genes
- Built recreations of some genomic assembly tools for bioinformatics coursework

PROGRAMMING LANGUAGES

- Java, C, and C++ were used as tools in learning basic data structures through UCSD coursework
- Learned Python and R independently in order to process large clinical and laboratory datasets
- Learned HTML and CSS to build personal website and host personal web-based projects

Projects:

SPLICEFORM CLUSTERING, PYTHON/R

- Parsed clinical datasets containing mutation and splicing data from autism patients in Python
- Used R (Weighted Gene Co-Expression Network Analysis package) in order to analyze the data
- Created genetic coexpression networks to find novel candidate genetic isoforms in autism pathogenesis

DIFFERENTIAL COEXPRESSION NETWORK ANALYSIS, PYTHON

- Parse clinical datasets containing expression profiles of brain highly-expressed genes and isoforms
- Built pairwise coexpression networks and annotated using DAVID in order to find functional clusters
- Performed differential network analysis on coexpression networks to find significant genetic groupings

HUFFMAN COMPRESSION, C++

- Compression program that can compress files up to 10MB in size to approximately 50% in size.
- Utilizes personal implementations of a Huffman binary tree and BitStream manipulators.

GENOME ANNOTATION TABLE WEB APP, PYTHON/HTML/JAVASCRIPT

- Used the Django web framework to build
- Created a table that lists annotations for an un-annotated organism
- Annotations from BLAST, Pfam, Prosite, KEGG, Gene Ontology databases

SEQUENCE ALIGNMENT, PYTHON

- Implemented both Needleman-Wunsch and Smith-Waterman algorithms for global and local sequence alignments
- Aligns sequences from fasta-format files using either PAM250 or BLOSUM62 scoring matrices along with user-input affine-gap penalties
- Needleman-Wunsch also optimized with Hirschberg linear-space algorithm

Experience:

BIOINFORMATICS RESEARCH ASSISTANT, IAKOUCHEVA LAB

September 2016 – Present

- UCSD School of Medicine, Department of Psychiatry
- Research based on investigating genetic basis of psychiatric diseases such as autism spectrum disorder
- Use Python and R in order to perform statistical analysis of relevant gene transcripts
- Handle large data sets of mutations and transcripts
- Extensive reading of scientific literature in order to look for novel/relevant techniques to employ in lab

HOUSE MANAGER HEAD LEAD, UCSD OPERATIONS

May 2015 – Present

- Learned to provide friendly customer service and further strengthened communication skills.
- Assisted clients (student and non-student) in planning and coordinating meetings.
- General maintenance of the UCSD Price Center including troubleshooting audio/visual equipment.
- As head lead, trained all new employees and fostered a cohesive and efficient working environment