Kevin Chau

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Education:

- University of California, San Diego, 2019
  - Biology, M.S. Candidate
- University of California, San Diego, 2018
  - Biology w/ Specialization in Bioinformatics, B.S.

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

- Experienced with numerous current bioinformatics tools such as BLAST, BWA, Kallisto, etc.
- Applied programming skills in personal recreations of some bioinformatics tools (e.g., Local/Global Sequence Alignment, De Bruijn graphs, etc.)

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

MISC

- Conversational in Spanish and Vietnamese

Previous Projects:

CO-EXPRESSION NETWORK AND ENRICHMENT TUTORIAL, R (WEIGHTEDNETANALYSISTUT)

- Fully-guided tutorial on the usage of WGCNA and Enrichr for the construction and analysis of gene co-expression networks
- Created as an easy-to-use Docker image that contains all necessary data and libraries
- Contains R Markdown notebook to guide the user through the analysis

CO-EXPRESSION NETWORK PIPELINE, R/BASH (WGCNA_pipeline)

- Weighted Gene Co-Expression Network Analysis
- Created genetic co-expression networks to find novel candidate genetic isoforms in autism pathogenesis
- Automated for use with SLURM Unix job scheduling system

SEQUENCE ALIGNMENT, PYTHON (ALIGNMENTALGORITHMS)

- Implementation of both Needleman-Wunsch (global alignment) and Smith-Waterman (local alignment) algorithms for amino acid sequence alignment

GENOME ANNOTATION BROWSER, PYTHON3, DJANGO (GENOME-ANNOTATION-TABLE)

- Implemented a genome browser web application using Python and Django
- Data curated from other students is compiled into SQLite3 database and presented to user through a web browser
- Browser elements presented using HTML and Javascript, through the Django framework

HUFFMAN COMPRESSION, C++ (HUFFMANCOMPRESSION)

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

Experience:

BIOINFORMATICS RESEARCH ASSISTANT, IAKOUCHEVA LAB

September 2016 – Present

- UCSD School of Medicine, Department of Psychiatry
- Exploring splicing isoform networks relative to gene co-expression in the context of psychiatric disorders
- Multi-dimensional analysis for data quality control
- Statistical analysis of large data sets, e.g. variant enrichment, Gene Ontology enrichment, redistribution calculations

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