

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:

TOOLS

- Experienced with numerous current bioinformatics tools (e.g. RSEM, STAR, DESeq2, Kallisto, Sleuth, BLAST)
- Utilized Docker containerization to create a RNA-seq co-expression network analysis walkthrough
- Used Django to create a genome annotation browser to display compiled annotations of a previously un-annotated organism
- Git version control system used to track and store all projects

PROGRAMMING LANGUAGES

- Java, C, and C++ used as tools in learning basic data structures through UCSD coursework
- Extensive use of Python, R, and Bash in order to process large clinical and laboratory datasets
- Some experience with SQL to query online biological datasets, e.g. UCSC

Misc

- Conversational in Spanish and Vietnamese

Previous Projects:

CO-EXPRESSION NETWORK AND ENRICHMENT TUTORIAL, DOCKER, 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

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

Experience:

BIOINFORMATICS INTERN, J. CRAIG VENTER INSTITUTE

June 2018 – Present

- Under mentorship of Dr. Richard Scheuermann, currently performing a meta-analysis of gene co-expression networks in the context of host immune response to viral infections
- Applied network theory concepts (clustering, network heat diffusion) to elucidate novel pathways in human immune response to influenza virus infection
- Integration and analysis of multiple host response factor datasets was done mainly in R and Bash on a Sun Grid Engine computing cluster

BIOINFORMATICS RESEARCH ASSISTANT, UC SAN DIEGO DEPARTMENT OF PSYCHIATRY

September 2016 – Present

- Under mentorship of Dr. Lilia Iakoucheva, currently exploring the novelty of splicing isoform networks relative to gene co-expression and protein-protein interaction networks in the context of psychiatric disorders
- Utilized and compared RNA-seq processing pipelines (RSEM/STAR/DESeq2; Kallisto/Sleuth) to create a gene pleiotropy map of normal human neurodevelopment
- Extensive use of R and Bash scripting in the statistical analysis of those large data sets, e.g. variant enrichment, Gene Ontology enrichment, and multi-dimensional analysis, and is performed on the XSEDE Comet computing cluster utilizing the SLURM job scheduler