KEVIN MOYUNG

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EDUCATION

Duke University *Durham, NC*
Ph.D in Computational Biology and Bioinformatics *Aug 2019 - Present*
Advisors: David MacAlpine and Alex Hartemink

University of California, San Diego *La Jolla, CA*
B.S. in Biology: Bioinformatics *Sep 2015 - Jun 2019*

EXPERIENCE

MacAlpine Lab, Duke University *Durham, NC*
Research Rotation *Apr 2020 - Jul 2020*

· Profiled nucleosomal and sub-nucleosomal changes using MNase-seq data of mutant Saccahromyces cerevisiae samples.

Xie Group, Duke University *Durham, NC*
Research Rotation *Jan 2020 - Mar 2020*

· Developed statistical and computational approaches to study chromatin remodeling and transcriptomic changes in T cell memory formation by leveraging bulk RNA-seq and ATAC-seq data in mice.

Wray Lab, Duke University *Durham, NC*
Research Rotation *Sep 2019 - Nov 2019*

· Analyzed single-cell RNA-seq data during the early development of sea urchin embryos.
· Identified novel transcription factors that could illuminate uncovered aspects of the developmental gene regulatory network in the Lytechinus Variegatus species.

Insel Lab, UC San Diego *La Jolla, CA*
Research Intern *Nov 2016 - May 2019*

· Helped develop and implement an RNA-seq analysis pipeline using bioinformatics tools such as Kallisto and EdgeR.
· Reduced RNA-seq analysis time through automation via batch scripts.
· Assisted with analysis of RNA-seq data from multiple projects at the Insel lab.
· Analyzed RNA-seq data for differential gene expression of G-protein coupled receptors in solid tumors.
· Mined and visualized data for mutations, copy number variation and gene expression using TCGA and GTEX public databases, incorporating tools from UCSC Xena.
· Developed methods and best practices for removing batch effects in gene expression data, including for publicly available data such as TCGA.

Ferring Research Institute, Inc. *San Diego, CA*
Bioinformatics Intern *Jun 2018 - Aug 2018*

- Developed and optimized machine learning models to stratify non-muscle invasive bladder cancer patients into various molecular and prognostic subgroups.
- Performed survival analysis on overall survival and tumor progression derived from molecular gene signatures.
- Developed and optimized a cross-platform analysis pipeline for high dimensional RNA-seq and Microarray datasets.

Aduro Biotech, Inc. *Berkeley, CA*
Immune Monitoring and Biomarker Development Intern *Jun 2017 - Sep 2017*

- Optimized data mining from the prediction of immunogenic peptides using NetMHC 4.0 and Epitope Prediction using R.
- Built a graphical user interface in Python that quickly mines the PubMed database for article abstracts.
- Developed a database to store and access ELISPOT and high dimensional clinical data using SQL and Access.

Karin Lab, UC San Diego *La Jolla, CA*
Lab Assistant *Jan 2016 - May 2017*

- Performed Polymerase Chain Reactions (PCR) on over 100 strains of mice.
- Optimized PCR workflow using new reagents.
- Generated data from amplified DNA via Gel Electrophoresis.

PUBLICATIONS

GPCRs show widespread differential mRNA expression, frequent mutation and copy number variation in solid tumors
PLOS Biology (2019)

Krishna Sriram, Kevin Moyung, Ross Corriden, Hannah Carter, Paul Insel

Detection and quantification of GPCR mRNA: An assessment and implications of data from high-content methods
ACS Omega (2019)

Krishna Sriram, Shu Z. Wiley, Kevin Moyung, Matthew W. Gorr, Cristina Salmern, Jordin Marucut, Randall P. French, Andrew M. Lowy, Paul A. Insel

ABSTRACTS

New insights from The Cancer Genome Atlas: Implications for GPCR expression in cell compartments in solid tumors
The FASEB Journal (2020)

Krishna Sriram, Kevin Moyung, Paul A. Insel

Solid tumors have frequent mutation, copy number variation and differential mRNA expression of GPCRs: Are such GPCRs functional oncogenes
Cancer Research (2018)

Krishna Sriram, Kevin Moyung, Ross Corriden, Paul Insel

HRH1: A novel GPCR drug target in pancreatic cancer
The FASEB Journal (2018)

Alyssa Rodriguez, Krishna Sriram, Kevin Moyung, Paul A. Insel

AWARDS AND HONORS

NSF Graduate Research Fellowship Program (Honorable Mention, 2021)
UC San Diego Provost Honors (2017, 2018)

SKILLS

Programming Languages	R, Python, Bash, C++, Java, MATLAB
Bioinformatics	RNA-seq, DNA-seq, MNase-seq, ATAC-seq, Survival Analysis
Machine Learning	Clustering, Supervised Learning, Principal Component Analysis
Tools	Git, Vim, RStudio
Laboratory Techniques	PCR, Gel Electrophoresis

LEADERSHIP AND EXTRACURRICULARS

Computational Biology and Bioinformatics Recruitment Committee *Durham, NC*
Chair *Nov 2020 - Present*

· Planned and hosted of a virtual recruitment week for prospective PhD students during the 2021 application cycle.

Computational Biology and Bioinformatics Recruitment Committee *Durham, NC*
Member *Oct 2019 - Feb 2020*

· Contributed to the planning and execution of recruitment events for PhD applicants to the Duke Computational Biology and Bioinformatics program.
· Led an after-hours social for interviewees

The Undergraduate Bioinformatics Club (UBIC) *La Jolla, CA*
Community Service Chair *Sep 2017 - Jun 2018*

· Created a Sequence a Monster activity for elementary, middle, and high school students at the San Diego Science and Engineering Festival to teach children about DNA, genotypes, and phenotypes.
· Built a Lego Sequencer using Arduino and Python.
· Led a committee of undergraduate bioinformatics students to plan and host quarterly outreach programs and events.

The Undergraduate Bioinformatics Club (UBIC) *La Jolla, CA*
Bioinformatics Expo Chair *Mar 2017 - Jun 2017*

· Led a team of committee members to plan and successfully execute an industry and academia symposium for undergraduate bioinformatics students with over 80 attendees.
· Coordinated with distinguished speakers such as Dr. Pavel Pevzner, Dr. Trey Ideker, Dr. Hannah Carter, and Dr. Terry Gaasterland.

RELEVANT COURSEWORK

Genome Tools and Technologies
Computational Sequence Biology
Advanced Bioinformatics Lab
Advanced Tools in Bioinformatics
Probability and Statistics for Bioinformatics
Design and Analysis of Algorithms
Advanced Data Structures
Linear Algebra
Introduction to Machine Learning
Molecular Sequence Analysis
Biological Databases
Introduction to Mathematical Statistics

INTERESTS

Volleyball, Weightlifting, Tennis, Music Production, Bouldering