

Kian Faizi

xxx-xxx-xxxx | kfaizi@ucsd.edu | kianfaizi.com | github.com/kfaizi

EDUCATION

University of California, San Diego

Aug. 2017 – May 2021

B.S. Molecular Biology, Minor in Mathematics (GPA: 3.76)

La Jolla, CA

- Selected coursework: Bioinformatics, Biophysics, Computational Linear Algebra, Gene Regulation, Genome Editing, Modeling, Statistics, Stochastic Processes

International School of Kuala Lumpur

Aug. 2013 – May 2017

I.B. Diploma, Earth Club President, Varsity Basketball Team Captain

Kuala Lumpur, Malaysia

RESEARCH EXPERIENCE

Lab Technician

Nov. 2019 – present

Lab of Wolfgang Busch, Salk Institute for Biological Studies

La Jolla, CA

- Investigated cost-performance trade-offs in the *Arabidopsis* root system using high-throughput phenotyping and graph-theoretic approaches
- Developed a Python GUI to segment time-series images of roots grown on agar plates; produced and analyzed approximately 1500 images
- Built a pipeline for co-expression network analysis of scRNA-seq data to identify root growth genes, in order to aid crop engineering efforts
- Measured ground-truth angles and radii from 3D point cloud data to aid development of phenotyping software

Volunteer Research Assistant

Nov. 2018 – Nov. 2019

Lab of Patrick Hsu, Salk Institute for Biological Studies

La Jolla, CA

- Created an automated pipeline to search over 20Tb of metagenome sequences for novel orthologs of Cas13d, an RNA-targeting CRISPR effector
- Assisted in conducting a pooled 150,000-guide CRISPR-Cas13d screen in K562s to study gRNA efficiency

TEACHING EXPERIENCE

Instructional Apprentice: Genetic Inquiry

Aug. 2020 – Dec. 2020

Supervised by Dr. Stanley Lo, UCSD

PUBLICATIONS

Curve skeleton extraction from 3D point clouds for high-throughput plant phenotyping.

- Illia Ziamtsov, **Kian Faizi**, and Saket Navlakha. *In prep.*

Network design principles in the *Arabidopsis* root system.

- Kian Faizi**, Matthieu Platre, Arjun Chandrasekhar, Saket Navlakha, and Wolfgang Busch. *In prep.*

A pooled CRISPR-Cas13d screen reveals guide RNA design principles.

- Silvana Konermann, **Kian Faizi**, Peter Lotfy, and Patrick Hsu. *In prep.*

POSTERS AND PRESENTATIONS

Co-expression analysis of single-cell RNA-seq data | *Talk*

Oct. 2020

- Presented at the annual HDSI Research Conference

Mining Genomes for RNA-Targeting CRISPR Effectors | *Talk*

Aug. 2019

- Presented at the annual UCSD Summer Research Conference

Metagenomic Discovery of Type VI-D CRISPR Effectors | *Poster*

June 2019

- Presented at the annual UCSD Biology Student Research Showcase

HONORS AND AWARDS

- Halicioglu Data Science Institute Scholarship** | \$2,500 / UCSD Dec. 2019
- Project: *Single-cell transcriptomics and web mining for rapid reverse genetics in plants*, proposed under Dr. Busch
- Eureka! Research Scholarship for Biological Sciences** | \$5,000 / UCSD June 2019
- Project: *Discovery and development of Type VI-D CRISPR effectors for transcriptome engineering applications*, proposed under Dr. Hsu
- Provost Honors** | UCSD quarterly
- First Place Solo Performance** | *Sunway National Poetry Slam, Malaysia* Apr. 2016

PROFESSIONAL ACTIVITIES

- Member, Undergraduate Bioinformatics Club** | UCSD Nov. 2017 – present
- Collaborated with Illumina to develop digital resources for high school students interested in bioinformatics
 - Helped organize the 2018 Faculty & Industry Bioinformatics Symposium
 - Volunteered in the club booth at SDSEF to educate the community about DNA sequencing technology

SKILLS

Laboratory: Cell/tissue culture, molecular cloning, CRISPR screens, lentiviral transduction, optical microscopy
Languages: Python, bash, JavaScript, HTML/CSS, R, Perl
Organizational: Git, L^AT_EX, conda, vim, Unix systems
Libraries: BLAST+, pandas, NumPy, ScanPy, matplotlib, NetworkX