Kian Faizi

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Education

California Institute of Technology — Sep. 2021 – present
Ph.D. in Systems Biology — *Pasadena, CA*

University of California, San Diego — Aug. 2017 – June 2021
B.S. in Molecular Biology, Minor in Mathematics (GPA: 3.75) — *La Jolla, CA*

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

International School of Kuala Lumpur — Aug. 2013 – June 2017
I.B. Diploma, Earth Club President, Varsity Basketball Team Captain — *Kuala Lumpur, Malaysia*

Experience

Rotation Student — Sep. 2021 – Dec. 2021
Lab of Rob Phillips, Caltech — *Pasadena, CA*

- Studying microbial gene regulation using MPRAs and statistical mechanics

Lab Technician — Nov. 2019 – Sep. 2021
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 modeling
- Created a Python GUI for segmenting time-series images of root growth
- Helped develop algorithms for plant phenotyping from noisy 3D point clouds
- Built a pipeline for co-expression network analysis of scRNA-seq data to identify genetic targets for future crop engineering

Volunteer Research Assistant — Nov. 2018 – Nov. 2019
Lab of Patrick Hsu, Salk Institute for Biological Studies — *La Jolla, CA*

- Developed an automated pipeline to mine metagenomes for new orthologs of CRISPR-Cas13d, and searched over 20TB of sequence data
- Assisted in performing a pooled 150,000-guide Cas13d screen in K562s to optimize gRNA design

Publications

Branch-Pipe: Improving graph skeletonization around branch points in 3D point clouds.

- Illia Ziamtsov, **Kian Faizi**, and Saket Navlakha. *Remote Sensing.* (2021) doi:10.3390/rs13193802

Network design principles in the *Arabidopsis* root system.

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

Preprints

Deep learning of Cas13 guide activity from high-throughput gene essentiality screening.

- Jingyi Wei, Peter Lotfy, **Kian Faizi**, Hugo Kitano, Patrick D. Hsu, and Silvana Konermann. *bioRxiv.* (2021) doi:10.1101/2021.09.14.460134

Teaching

Undergraduate Instructional Apprentice | *UCSD* — Aug. 2020 – Dec. 2020

- For *Genetic Inquiry*, supervised by Stanley Lo

Posters and Presentations

Co-expression analysis of single-cell RNA-seq data | *Talk* Oct. 2020
- HDSI Research Conference

Mining Genomes for RNA-Targeting CRISPR Effectors | *Talk* Aug. 2019
- UCSD Summer Research Conference

Metagenomic Discovery of Type VI-D CRISPR Effectors | *Poster* June 2019
- UCSD Biology Student Research Showcase

Honors and Awards

Halicioglu Data Science Institute Scholarship Project Award | *UCSD* May 2021

DOE CSGF Honorable Mention | *Krell Institute* Apr. 2021

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 Wolfgang Busch

Eureka! Scholar | *$5,000* | *UCSD* June 2019
- Project: *Discovery and development of Type VI-D CRISPR effectors for transcriptome engineering applications*, proposed under Patrick Hsu

Provost Honors | *UCSD* quarterly

Professional Activities

Undergraduate Bioinformatics Club Member | *UCSD* Nov. 2017 – June 2021
- Collaborated with Illumina to develop digital resources for high school students interested in bioinformatics
- Helped organize the 2018 Faculty & Industry Bioinformatics Symposium
- Volunteered at the SD Science & Engineering Festival to teach the community about DNA sequencing technology

Skills

Laboratory: Cell/tissue culture, molecular cloning, CRISPR screens, optical microscopy
Computational: Image analysis, biologically-inspired algorithms, point clouds, GUI development
Languages: Python, bash, HTML/CSS/JavaScript
Organizational: Git, LaTeX, Linux/Unix systems
Libraries: NetworkX, matplotlib, seaborn, numpy, pandas, BLAST+