

Bence M. Kotis

BIOMEDICAL ENGINEER/DATA WRANGLER

San Diego, CA

☎ (619)433-9232 | ✉ bence@kotis.me | 🏠 www.bencekotis.com | 📺 [wickdchromosome](https://www.youtube.com/channel/UCwv31111111111111111111)

Skills

Programming languages Python, R, bash, JS, C/C++
Web development/IT Languages HTML/CSS, AWS serverless, 5+ years of solid Linux experience
Languages English, Hungarian

Experience

The Scripps Research Institute

[La Jolla, CA, USA](#)

SOFTWARE ENGINEER/DATA WRANGLER

Nov. 2018 - Present

- Designed and built high performance data analysis pipelines and software tools for analyzing and visualizing large genomic datasets
- Built and currently maintaining physical and virtual Linux servers according to dbGAP data storage guidelines

The Daily Orange

[Syracuse, NY, USA](#)

IT MANAGER

2017 - 2018

- Increased site uptime from frequent daily crashes to 99.9% yearly uptime
- Optimized site to withstand more than 8x normal load without loss in performance
- Maintained company webserver, IT infrastructure
- Maintained Wordpress plugins abandoned by the community that the site is using to ensure site reliability
- Provided 24/7 instant tech support through Slack channel for 50 employees to find and fix bugs on site
- Trained Assistant IT Manager in website maintenance and IT infrastructure

Syracuse University

[Syracuse, NY, USA](#)

HENDERSON LAB

2017 - 2018

- Designed a plugin that tracks and follows biological cells in real time with 90%+ accuracy, using the MicroManager Matlab API and a tracking algorithm called ACTIVE
- Designed an algorithm that tracks biological cells using visible light microscopy (without the need to pre-stain) using a combination of image filtering and geometric projections and a tracking algorithm called ACTIVE in Matlab
- Made tracking algorithm Linux and OSS compatible

Projects

Genetic outlier detection webapp

AWS SERVERLESS, R, JS, PYTHON

- A webapp that finds abnormally expressed genes (likely responsible for rare genetic diseases for example) in an individual, based on gene expression data
- The webapp runs on AWS lambda with an R layer, along with some nodeJS and Python wrapping functions
- Interactive result visualization is done using matplotlib, plotly

Slack load monitoring app

C++, LINUX, WEBHOOKS, SLACK

- A systemd daemon for Linux that monitors load averages, ram usage
- Daemon sends Slack notifications if an alert or warning is set off

Education

Syracuse University

[Syracuse, NY, USA](#)

B.S. IN BIOMEDICAL ENGINEERING

Sep. 2014 - May. 2018

- Started and completed first year as an entrepreneurship student