Ming-Ju Kuo

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Education

Technical University of Dresden, Dresden, Germany   *10/2016 – 09/2019*
MSc in Bioengineering

National Taiwan University (NTU), Taipei, Taiwan   *09/2010 – 06/2015*
BSc in Life Science and Geosciences (Double Major)
Relevant Coursework: *Computer Programming*

Fu Jen Catholic University, Taipei, Taiwan   *09/2020 – 06/2021*
Non-degree courses
Related Courses: *Linear Algebra, Discrete Math, Data Structures, Algorithms and Operating System*

Work Experience

Lyntics GmbH, Taipei, Taiwan   *04/2022 – Present*
Software Engineer
- Designing Restful APIs for the web application to handle complicated user permission logic.
- Cooperating with Front-end engineers to integrate React with well-defined APIs.
- Developing unit tests for APIs and integrating the tests with Bitbucket pipeline for CI.
- Deploying the microservice on AWS such as NGINX for web encryption and reverse proxy.

NZXT, Inc., Taipei, Taiwan   *12/2020 – 03/2022*
Software Development Engineer in Test
- Implemented end-to-end test automation for e-commerce website and web-based desktop application (CAM) with CucumberJS in TypeScript to ensure the quality of applications.
- Integrated GitHub Action CI workflow with TestRail and Slack API to report the daily test result.
- Designed the test cases to cover all the features as much as possible.

National Chiao Tung University, Hsinchu, Taiwan   *04/2020 – 07/2020*
Bioinformatician
- Constructed the single-cell analysis pipeline with Cell Ranger and Seurat.
- Applied dimensional reduction methods to visualize muti-dimensional single-cell data.

Publications

A Acevedo, Sara Ciucci, **MJ Kuo**, Claudio Durán, Carlo V Cannistraci. Measuring group-separability in geometrical space for evaluation of pattern recognition and embedding algorithms (**IEEE Access**)

Research

Master Thesis
Correlation-based detection of activation/repression transcription factor regulation from gene expression
- Predicted the regulatory types of transcription factors by using various correlation-based methods (Pearson, Spearman and distance correlation, etc.).
- Benchmarked the correlation-based method and network-based algorithms (Bayesian and Boolean networks) for gene regulatory types prediction from transcriptomics data.

Lab Projects
PC-corr Application for Developmental Gene Expression Pattern Analysis
- Unfolded the gene expression patterns from gene expression profiles by PCA.
- Constructed the gene regulatory network from PCA results through PC-corr methods.

Extracurricular Experience

University Sport Team

- Varsity Male Soft Tennis Team at NTU

Volunteer

- Eden Social Welfare Foundation