Haolong Li

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EDUCATION

EPFL
MSc in Computational Science and Engineering
Aug. 2022 - Present
Lausanne, Switzerland
GPA: 5.13 / 6.0

HARBIN INSTITUTE OF TECHNOLOGY
BS in Statistics
Aug. 2018 - July. 2022
Harbin, China
GPA: 90.4/100
Ranking: 2 / 20

LINKS

Github: **Tachi-67**
LinkedIn: **Haolong Li**

COURSEWORK

EPFL
Software Engineering
Software Development Project
Applied Data Analysis
(Top 20% in final exam)
Machine Learning
(Top 20% in final exam)
Large-scale data science for real-world data
Data visualization
Algorithms

HIT
Stochastic Processes
Mathematical Statistics
Real Analysis
Functional Analysis
Numerical Linear Algebra

SKILLS

PROGRAMMING
Python • Kotlin • Java • CSS • JavaScript • Shell • R • LaTeX • C++
Familiar:
Git • Android • Hadoop • HiveQL • Spark

EXPERIENCE

COOK4ME | SDP Course Project Contributor & Scrum Master
Feb. 2023 - Present | EPFL, CH
Repo link here
- Full-stack developer: Designed features with Jetpack Compose & Kotlin in the pattern of **MVVM**; Established **instrumented testing**; Reviewed pull requests for other team members.
- Worked with **continuous integration**.
- Worked in a fashion inspired by the **Scrum** development process.

GENDER LENS | ADA Course Project Contributor
Sep. 2022 – Jan. 2023 | EPFL, CH
Repo link here
- Worked on the **CMU Movie Summary Corpus** with **Python** to obtain insights over gender inequalities in the movie industry.
- **Preprocessed** the data (reformatting data, dealing with abnormal data points, dropping less representative data, etc.) for further analysis.
- Analysed the evolution of gender inequalities by investigating the gender composition in the movie industry over time, proposing an mathematical explanation and inferring the conclusions.
- Tasked with the **final data-story page** implementation.

RESEARCH

NATIONAL UNIVERSITY OF SINGAPORE | Student Researcher
June 2021 – Sep. 2021 | Singapore
- Implemented 3 algorithms (EM, MM, AI-REML) to conduct variance component estimation in LMM with R. Evaluated outputs with simulated replicates.
- Used PLINK, a tool for genome-wide association study (GWAS) analysis, to conduct quality control and association analysis in order to filter the data and finally obtain results (possible SNPs) of the association analysis.

HARBIN INSTITUTE OF TECHNOLOGY | Student Researcher
Sep. 2021 – July 2022 | Harbin, CN
- Implemented 2 algorithms (BBKNN, MNN) for batch effect correction for single cell data
- Proposed an algorithm in Python for batch effects correction for single cell data.
- Integrated pancreas datasets from different sources for numerical experiments and verified correction results against existing algorithms.

AWARDS

2021	top 10%	People's Scholarship
2020	top 10%	People's Scholarship
2019	top 10%	People's Scholarship