Enes Dilber

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EDUCATION

UNIVERSITY OF MICHIGAN
Ph. D. Candidate in Statistics
Advisor: Jonathan Terhorst
August 2018 - Apr 2023 (Expected) | Ann Arbor, MI

MIDDLE EAST TECHNICAL UNIVERSITY
BS in Statistics, Minor in Computer Engineering
September 2014 - June 2018 | Ankara, Turkey

EXPERIENCE

ANCESTRY.COM | Population Geneticist, Intern
June 2021 – August 2021 | Lehi, UT
- Ancestry has a massive DNA data collection. They use their DNA data to create a reference panel to estimate the ethnicities of the customers by a Hidden Markov Model along the genome. Their model performs well on average. But it occasionally does misassignments. **The focus of my project was to understand the patterns of those misassignments**.
- Developed reproducible machine learning programs to detect the patterns of misassignments. My findings helped the company to increase the performance of ethnicity estimates. Moreover, the programs can be used in the future after each update on the ethnicity estimate model to assess their performance by analyzing the misassignment patterns.
- Used the following methods; Probability theory, Bayesian statistics, Clustering, Change point detection and Data visualization.
- Used the following tools; AWS, Jupyter-Notebook with python kernel and Confluence for documentation.

UNIVERSITY OF MICHIGAN | Teaching and Research Assistant
September 2018 – Present | Ann Arbor, MI
- Assisted (Lab instructor and Grader) Statistical Computing, Introduction to Data Science and Introduction to Theoretical Statistics courses.
- Funded as a Research Assistant to do Statistical Genetics research.

DISSERTATION PROJECTS

INFERRING THE DEMOGRAPHIC HISTORY Ongoing
- Estimate history of population size changes, migrations, and other demographic events affecting a set of populations by using a fast approximate method.
- Extend this method to infer phylogenies which helps to model evolutionary processes of viruses.

ROBUST DETECTION OF NATURAL SELECTION 2021
- Derive new likelihood-based methods for detecting natural selection which are robust to confounding by fluctuations in effective population size. At the core of this method is a novel probabilistic model of tree imbalance, which generalizes Kingman's coalescent to allow certain aberrant tree topologies to arise more frequently than is expected under neutrality.
- **Open source software of the method** and **paper results** are available on github.
- Manuscript accepted by **Genetics**.

COURSEWORK

Statistics Department:
- Statistical Inference
- Probability Theory
- Data Science in Python
- Statistical Genetics
- Bayesian Statistics
- Stochastic Process
- Analysis of Multivariate Data

Computer Engineering Department:
- Algorithms And Data Structures
- Data Management And File Structures
- Computer Vision
- Deep Learning
- Data Mining

Mathematics Department:
- Advanced Calculus in Statistics
- Linear Algebra

COMPUTER SKILLS

Proficient at the following python packages;
- Numpy • JAX • Keras
- msprime • tskit
- sckit-learn • pandas • re

Familiar with the following python packages;
- TensorFlow • PyTorch
- NLTK • PySpark

Proficient at base R and Tidyverse packages such as;
- ggplot2 • dplyr • tidyr • purr

Genetics research software;
- SLiM 3 • BEAST 2

Other research tools;
- slurm • The Jupyter Notebook • Bash
- Markdown • LaTeX • SQL

PUBLIC REPOSITORIES

bim
Software to detect natural selection on whole genome sequences.

pyslurm
Python wrapper for the slurm. It also provides useful functions to visualize and analyze batch jobs in the cluster.

AWARDS

2021 Best **Poster** Award in MSSISS
2018 Promotion to direct Doctor of Philosophy track
2018 Ranked 1st among Statistics graduates
2014-2018 Dean's High Honor List