

TOMAS BENCOMO

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Computer science student interested in biomedical informatics and medicine. I'm passionate about using informatics to improve our understanding and treatment of diseases. I plan to pursue an MD-PhD, seeking to better translate informatics research to improve patient care. My research interests include applying informatics to better understand disease biology, building tools to improve physician decision-making, and evaluating new medical interventions. I'm an advocate for open science and reproducible research.

EDUCATION

BS	Stanford University, Computer Science Concentration in Biocomputation	2021
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HONORS AND AWARDS

Mayo Clinic Summer Undergraduate Research Fellowship	2018/2019
Research Fellow in the Precision NeuroTherapeutics Innovation Program at Mayo Clinic	

TGen Helios Symposium Top 10 Poster Presentations	2016
One of the top 10 posters presented at the intern research symposium out of 50 posters	

TGen Helios Scholar	2016
Recipient of the Helios Scholarship, a summer internship program funded by the Helios Education Foundation	

RESEARCH EXPERIENCE

Mayo Clinic, Phoenix AZ	2018/2019
Summer Undergraduate Research Fellow, Dr. Kristin R. Swanson	
Summer 2019	

- Studied multiparametric MR imaging to understand and predict drug distribution in glioblastoma
- Worked on prognostic risk models for GBM patients using tumor size and location
- Built data pipelines to register, normalize, extract feature data, and measure tumors in MR images
- Tested registration methods to identify optimal method for image to atlas registration
- Fit statistical models to analyze survival data and identify prognostic factors
- Presented lecture on best statistical practices for survival analysis

Summer 2018

- Investigated sex differences in glioblastoma MR imaging
- Analyzed multimodal MRI using machine learning techniques to identify sex differences
- Implemented image preprocessing functionality to the lab's imaging pipeline with Python and the SimpleElastix imaging library
- Extracted insightful data from MRI using custom feature generation pipeline

Stanford University School of Medicine, Stanford CA

2017-present

Undergraduate Researcher, Dr. Carolyn Lee

- Characterized new genes implicated in epithelial cancers
- Analyze multi-level omics data to profile target genes
- Examined TCGA data to identify genetic predictors of survival in epithelial cancers
- Used computational drug repurposing to identify drugs with predicted efficacy in squamous cell carcinoma
- Developed RNASeq and WES pipelines for Sherlock HPC cluster
- Experimentally validated repurposed drugs in organotypic tissue models

Translational Genomics Research Institute, Phoenix AZ

2016-2017

Helios Scholar, Dr. Gil Speyer

- Redesigned the Biocomputing Lab's EDDY algorithm to use NVIDIA's CUDA API
- Wrote C/C++ code and implemented memory optimizations to exploit GPU parallelism
- Helped secure \$200,000 Compute 4 the Cure grant from NVIDIA
- EDDY-GPU achieved 500x speedups and the ability to analyze datasets previously impossible to analyze

PUBLICATIONS

Tomas Bencomo, Andrea Hawkins-Daarud, Kyle Singleton and Kristin R. Swanson, "The Same But Different: Identifying Distinct Imaging Ecologies in Male and Female Glioblastomas," 2018 CSBC/PS-ON Annual Investigators Meeting, 2018.

Gil Speyer, Juan Rodriguez, **Tomas Bencomo** and Seungchan Kim, "GPU-accelerated differential dependency network analysis", PDP 2018, Cambridge, UK, Mar 21-23, 2018.

PRESENTATIONS

Research Talk, "MRI-MALDI: Can We Predict Drug Distribution from MRI," Mayo Clinic, 2019.

Research Talk, "Best Practices For Survival Analysis," Mayo Clinic, 2019.

Research Talk, "Investigating Sex Differences In Glioblastoma MR Imaging," Mayo Clinic, 2018.

Poster Presentation, "Optimizing EDDY-GPU to Improve Accuracy and Performance" Helios Scholars Symposium, 2016.

SKILLS

Languages: Python, R, Java, C++, C, SQL

Packages and Libraries:

Python: pandas, numpy, scikit-learn, matplotlib, seaborn, simpleitk, simpleelastix

R: dplyr, ggplot2, tidyr, mice, survival, rms, bioconductor

Technologies: Machine Learning, Statistics, Bioinformatics, Imaging Informatics, HPC and GPGPU Computing, Data Engineering