


# TOMAS BENCOMO

Computer science student passionate about using informatics to improve our understanding and treatment of human disease. After undergrad I hope to further develop my skills as an MD-PhD student. My research interests focus on using bioinformatics to elucidate disease biology and building tools to aide physician decision-making. I'm an advocate for open science, reproducible research, and science education.





## EDUCATION

- 2017  
|  
2021
- Stanford University**  
B.S. in Computer Science, Biocomputation  
3.9 GPA
-  Stanford, CA





## HONORS AND AWARDS

- 2018  
|  
2019
- Mayo Clinic Summer Undergraduate Research Fellowship**  
Fellow in the Precision NeuroTherapeutics Program
- 2016
- TGen Helios Scholar**  
Scholar in the Helios Program at TGen
- 2016
- Helios Symposium Poster Award Winner**  
Poster Award Winner at Intern Symposium

## RESEARCH EXPERIENCE

- 2017  
|  
present
- Lab Bioinformatician**  
Lee Lab, Stanford Medicine  
 Stanford, CA
    - Characterize new genes implicated in epithelial cancers
    - Analyze multi-level omics data (TCGA and GEO) to identify genes of interest
    - Examine survival data to find biomarkers for squamous cell carcinoma (SCC)
    - Identify drugs with predicted efficacy for SCC via computational drug repurposing
    - Build NGS processing pipelines and deploy on SLURM HPC cluster
    - Help design experiments and develop grant applications
- 2018 &  
2019
- Summer Undergraduate Research Fellow**  
Swanson Lab, Mayo Clinic  
 Phoenix, AZ
    - Used magnetic resonance imaging (MRI) to understand blood brain barrier disruption in glioblastoma
    - Investigated glioblastoma sex differences using MRI
    - Trained models to predict drug levels in the brain using MRI
    - Developed prognostic risk models using radiomics data
    - Built data pipelines to process MR images and tested different registration methods
    - Integrated processing pipelines with lab's codebase

## CONTACT INFO

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## SKILLS

Experienced in bioinformatics, biostatistics, and imaging informatics. I use R and Python to analyze biomedical datasets. I'm a fan of Git, RMarkdown, and Jupyter for creating reproducible analyses.

2016  
|  
2017



**Helios Scholar**

Mentor: Dr. Gil Speyer, TGen

📍 Phoenix, AZ

- Redesigned the 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
- Achieved 500x speedups; the algorithm can now analyze previously impossible datasets



**PUBLICATIONS**

2019



**Sex differences in GBM treatment: an observational study**

3rd Annual Celebration of Women’s Health Research – Sexx as a Biological Variable. Lorence J., **Bencomo T.**, White H., Rickertsen C.R., De Leon, G. Singleton K. W., Daruud-Hawkins A., Bendok B. R., Porter A. B., Mrugala M. M., Rubin J.B., and Swanson K. R.

2018



**The Same But Different: Identifying Distinct Imaging Ecologies in Male and Female Glioblastomas**

CSBC/PS-ON Annual Investigators Meeting. **Tomas Bencomo**, Andrea Hawkins-Daarud, Kyle Singleton and Kristin R. Swanson

2018



**GPU-accelerated differential dependency network analysis**

PDP 2018. Gil Speyer, Juan Rodriguez, **Tomas Bencomo** and Seungchan Kim



**PRESENTATIONS**

2019



**MRI-MALDI: Can We Predict Drug Distribution from MRI**

SURF 2019 Project

2019



**Best Practices For Survival Analysis**

Biostatistics Workshop  
Available on my Github

2018



**Investigating Sex Differences in Gliblastoma MR Imaging**

SURF Project 2018

2016



**Optimizing EDDY-GPU to Improve Accuracy and Performance**

Helios Scholars Symposium Poster