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   📍 Stanford, CA
3.9 GPA

🏆 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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in linkedin.com/in/tbencomo

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.

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