

TOMAS BENCOMO

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Biomedical data scientist passionate about using informatics to improve our understanding and treatment of human disease. I am currently applying to MD-PhD programs. My research interests focus on using bioinformatics to elucidate disease biology and building tools to aide physician decision-making. I'm also interested in open science and science education.

EDUCATION

BS	Stanford University, Computer Science Concentration in Biocomputation GPA: 3.99	June 2021
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HONORS AND AWARDS

Stanford Bio-X Summer Research Grant Funding for undergraduate research in the Dermatology department	2020
Tau Beta Pi Member Joined the engineering honors society in 2020	2020
Stanford VPUE Conference Grant Award to present research at Society For Investigative Dermatology Annual Meeting	2020
Mayo Clinic Summer Undergraduate Research Fellowship Fellow studying glioblastoma in the Precision NeuroTherapeutics Program	2018 & 2019
TGen Helios Scholar High school intern in the Helios Program at TGen	2016
Helios Symposium Poster Award Winner Awarded for a top 10 poster at the intern symposium	2016

EXTRACURRICULARS

Tau Beta Pi Honors Society Board – Academic Co-Chair Organize academic development events and lead the Peer Mentorship Program	2020 – 2021
Computer Science Peer Mentor Advise and mentor underclassmen considering a major in Computer Science	2020 – 2021

RESEARCH EXPERIENCE

Research Associate, Lee Lab, Stanford Medicine

2021 – present

Advisor: Carolyn Lee MD, PhD

- Worked as the lab bioinformatician
- Investigated skin cancer genes using single cell sequencing
- Performed a meta-analysis of publicly available non-melanoma datasets
- Studied metabolic reprogramming caused by non-coding mutations in metabolic genes
- Mentored undergraduate trainees

Undergraduate Researcher, Lee Lab, Stanford Medicine

2017 – 2021

Advisor: Carolyn Lee MD, PhD

- Characterized novel genes implicated in skin cancers using multi-omics data
- Examined survival data to find biomarkers for squamous cell carcinoma (SCC)
- Applied single cell RNA-sequencing to study SCCs with perineural invasion
- Analyzed proteomics data to identify novel interactors for melanoma oncogene RAC1
- Developed NGS analysis pipelines and deployed on SLURM HPC cluster
- Assisted with experimental design and grant applications
- Used sequencing approaches to investigate molecular basis of rare skin diseases

Summer Undergraduate Research Fellow, Swanson Lab, Mayo Clinic

2018-2019

Advisor: Kristin Swanson, PhD

- Analyzed MRI data to study blood brain barrier disruption in glioblastoma (GBM)
- Investigate sex-specific visual features of GBM on MRI
- Trained machine learning models to predict drug distribution in the brain from MRI
- Built prognostic models using radiomics data to predict patient survival
- Created data processing pipelines to process MR images and test registration methods
- Integrated processing pipelines with lab's codebase

Helios Scholar, Translational Genomics Research Institute

2016

Advisor: Seungchan Kim PhD and Gil Speyer PhD

- Redesigned the lab's EDDY algorithm to use NVIDIA's CUDA API
- Wrote C code and implemented memory optimizations to exploit GPU parallelism
- Helped secure \$200,000 Compute 4 the Cure grant from NVIDIA
- Achieved 500x speedup; the algorithm can now analyze previously impossible datasets

PUBLICATIONS

Conference Abstracts

Somatic Mutation of the OXA1L 5'UTR enables Cutaneous Squamous Cell Carcinoma

Angela Mah, Jasmine Garcia, Dane Sessions, **Tomas Bencomo**, Ashley Amado, Ankit Srivastava, Carolyn Lee

Plenary Session - Society For Investigate Dermatology 2021 Annual Meeting

Molecular Profiling of Cutaneous C-Group Non-Langerhans Cell Histiocytoses

Rebekah Wieland, **Tomas Bencomo**, Carolyn Lee, RYANNE BROWN

United States and Canadian Academy of Pathology 2021 Annual Meeting

Sex Differences In GBM Patient Survival As A Function of Extent Of Surgical Resection and Cycles of Adjuvant Temozolomide During Standard Of Care Regimens

Julia Lorence, **Tomas Bencomo**, Haylye White, Cassandra Rickertsen, Susan Massey, Kyle Singleton, Andrea Hawkins-Daarud, Sandra Johnston, Alyx Porter, Maciej Mrugala, Bernard Bendok, Leland Hu, Joshua Rubin, Kristin Swanson

Society for Neuro-Oncology 2020 Annual Meeting

Rac1-interacting proteins are prognostic factors for melanoma survival

Marten CG Winge, **Tomas Bencomo**, M. Peter Marinkovich, Carolyn S. Lee

Society For Investigative Dermatology 2020 Annual Meeting

Sex differences in GBM treatment: an observational study

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.

3rd Annual Celebration of Women's Health Research – Sexx as a Biological Variable

Sex Differences in Tumor Location Incidence in Newly Diagnosed Glioblastoma Patients

Lorence J., **Bencomo T.**, White H., Rickertsen C.R., De Leon G., Singleton K., Bendok B., Porter A. B., Rubin J. B., Swanson K. R.

Society for Neuro-Oncology 2019 Annual Meeting

Modeling the interface between non-invasive imaging and drug distribution

Ranjbar, Sara; **Bencomo, Tomas**; Jackson, Pamela R; Randall, Elizabeth; Regan, Micheal; Abdelmoula, Walid M; Lopez, Begona GC; Massey, Susan Christine; He, Lihong; Macura, Slobodan; Hu, Leland; Agar, Jefferey N; Sarkaria, Jann; Agar, Nathalie; Swanson, Kristin R.

CSBC/PS-ON 2019 Annual Investigators Meeting

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

Tomas Bencomo, Andrea Hawkins-Daarud, Kyle Singleton and Kristin R. Swanson.

CSBC/PS-ON 2018 Annual Investigators Meeting

GPU-accelerated differential dependency network analysis

Gil Speyer, Juan Rodriguez, **Tomas Bencomo** and Seungchan Kim

Euromicro International Conference on Parallel, Distributed and Network-Based Processing 2018

LANGUAGES

English: Native Language

Spanish: Intermediate Proficiency

TECHNICAL SKILLS

Programming: R, Python, Java, C, C++

Biostatistics: Regression modeling, machine learning, survival analysis, experimental design

Bioinformatics: Variant calling, RNA-Seq & scRNA-Seq analysis, data visualization

Computing: Snakemake, Docker, Unix, Bash, HPC, scikit-learn, pandas, tidyverse