Rafael Ramon Bravo

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Research Focus: Integrating mechanistic modeling of cancer with patient data and developing computational tools that make these methods accessible to other researchers.

EDUCATION

PhD, Integrated Mathematical Oncology | 2018–2024
University of South Florida & Moffitt Cancer Center | Advisor: Alexander Anderson
Dissertation: *3D Organ-Scale Models of Tumor Growth and Treatment*

MS, Computer Science | 2013–2015
University of California, Davis | Advisor: Jeffrey Schank
Master's Thesis: *Exploring the evolution of multicellularity from single-cells using agent-based simulated ecosystem*

BS, Computer Science | 2009–2013
Rutgers University–New Brunswick
Dickinson Carr Scholar (merit scholarship)

RESEARCH EXPERIENCE

Postdoctoral Fellow | 2024–2026

Oden Institute for Computational Engineering and Sciences, The University of Texas at Austin | PI: Tomas Yankeelov

Developed a hierarchical Bayesian model of tumor growth and treatment response using longitudinal clinical trial data to infer patient-specific parameters and predict treatment response in held-out patients. Fit a PDE model to glioblastoma MRI to estimate patient-specific migration-to-proliferation ratios and investigate their associations with survival, radiomics, and molecular data.

Doctoral Research | 2019–2024

Moffitt Cancer Center, Integrated Mathematical Oncology Department | PI: Alexander Anderson

Developed a 3D organ-scale, cell-resolution agent-based model of NSCLC initiation to investigate how normal tissue density shapes tumor growth and evolution. Extended the model to investigate biomarker- versus imaging-based tumor detection for adaptive therapy. Built a 2D GBM model linking local growth rates to MRI intensity.

Programmer | 2016–2018

Moffitt Cancer Center, Integrated Mathematical Oncology Department | PI: Alexander Anderson

Developed the Hybrid Automata Library (HAL), a spatial cancer modeling framework, and designed Cancer Crusade, a crowdsourced cancer modeling game.

Master's Thesis | 2014–2015

University of California, Davis | Advisor: Jeffrey Schank

Modeled the evolution of multicellularity in an agent-based ecosystem where cells physically bond and interconnect neural networks.

Research Assistantship | 2013–2014

University of California, Davis | PI: Amanda E. Guyer

Supported development of a research pipeline and maintenance of research servers.

Summer Internship | 2013

OHSU Center for Spatial Systems Biomedicine | PI: Xiaolin Nan

Combined stochastic Ras membrane dynamics with a differential equation model of the MAPK pathway to study Ras clustering.

Undergraduate Research | 2012

Rutgers University–New Brunswick | PI: David Axelrod

Developed a published agent-based model of stochastic cell dynamics in human colon crypts, calibrated to biopsy measurements of cell populations. Used the model to simulate colon cancer initiation and compare chemotherapy and radiation schedules in silico.

Undergraduate Research | 2012

Rutgers University–New Brunswick | PI: Dario Pompili

Programmed and built an autonomous submarine for adaptive sampling.

Undergraduate Project | 2009

Rutgers University–New Brunswick

Developed a portable water filtration prototype for rural Thailand with a four-student team.

DEVELOPED SOFTWARE

Hybrid Automata Library (HAL): Primary developer of a published spatial agent-based and PDE modeling framework with integrated visualization. Java, OpenGL, Swing.

Bayesian Framework: Developed a general framework for hierarchical Bayesian inference of global and patient-specific parameters. Python, JAX, NumPyro.

Cancer Crusade: Designed and developed a citizen science game where players treat an agent-based tumor model. C#, Unity.

Python Automata Library (PAL): Developed a high-performance Python version of HAL. Python, Numba, Pygame.

TECHNICAL SKILLS

Programming: Python, Java, JavaScript, C, C++, C#, Bash, Clojure, MATLAB, NetLogo

Scientific Computing: JAX, NumPyro, NumPy, SciPy, Pandas, Numba, Matplotlib, Seaborn

Modeling: Agent-based models, PDE/ODE models, hierarchical Bayesian inference, parameter estimation, longitudinal patient data, medical imaging and molecular data integration

AI-Assisted Research: Software development, research automation, and scientific writing.

PUBLICATIONS

Peer-Reviewed Publications

Kapteyn, M. G., Chaudhuri, A., Lima, E. A. B. F., Pash, G., **Bravo, R.**, Willcox, K. E., Yankeelov, T. E., & Hormuth II, D. A. (2026). TumorTwin: a Python framework for patient-specific digital twins in oncology. *BMC Medical Informatics and Decision Making*, 26, 237.

West, J., Rentzeperis, F., Adam, C., **Bravo, R.**, Luddy, K. A., Robertson-Tessi, M., & Anderson, A. R. (2024). Tumor-immune metaphenotypes orchestrate an evolutionary bottleneck that promotes metabolic transformation. *Frontiers in Immunology*, 15, 1323319.

Marzban, S., Srivastava, S., Kartika, S., **Bravo, R.**, Safriel, R., Zarski, A., Anderson, A. R., Chung, C. H., Amelio, A. L., & West, J. (2024). Spatial interactions modulate tumor growth and immune infiltration. *NPJ Systems Biology and Applications*, 10(1), 106.

Schenck, R. O., Kim, E., **Bravo, R.**, West, J., Leedham, S., Shibata, D., & Anderson, A. R. (2022). Homeostasis limits keratinocyte evolution. *Proceedings of the National Academy of Sciences*, 119(35), e2006487119.

Bravo, R., Baratchart, E., West, J., Schenck, R. O., Miller, A. K., Gallaher, J., Gatenbee, C. D., Basanta, D., Robertson-Tessi, M., & Anderson, A. R. (2020). Hybrid Automata Library: A flexible platform for hybrid modeling with real-time visualization. *PLoS Computational Biology*, 16(3), e1007635.

Gatenbee, C. D., Schenck, R. O., **Bravo, R.**, & Anderson, A. R. (2019). EvoFreq: visualization of the Evolutionary Frequencies of sequence and model data. *BMC Bioinformatics*, 20(1), 710.

El-Kenawi, A., Gatenbee, C., Robertson-Tessi, M., **Bravo, R.**, Dhillon, J., Balagurunathan, Y., Berglund, A., Vishvakarma, N., Ibrahim-Hashim, A., Choi, J., Luddy, K., Gatenby, R., Pilon-Thomas, S., Anderson, A. R., Ruffell, B., & Gillies, R. (2019). Acidity promotes tumour progression by altering macrophage phenotype in prostate cancer. *British Journal of Cancer*, 121(7), 556–566.

Bravo, R., & Axelrod, D. E. (2013). A calibrated agent-based computer model of stochastic cell dynamics in normal human colon crypts useful for in silico experiments. *Theoretical Biology and Medical Modelling*, 10(1), 66.

Preprints and Manuscripts Under Review

Bravo, R., Robertson-Tessi, M., Antonia, S., Gray, J., Beg, A., Gatenby, R., Schabath, M. B., & Anderson, A. R. (2025). The impact of normal tissue density on tumor growth and evolution in a 3D whole-tumor model of lung cancer. *bioRxiv. doi:10.1101/2025.09.25.676637. (under review)*

Bravo, R., Hormuth II, D. A., Lima, E. A. B. F., Tercan, B., Aguilar, B., & Yankeelov, T. E. (2026). Estimating glioblastoma migration-to-proliferation ratio from single time-point MRI data via radial density distribution. *Submitted to PLOS Computational Biology.*

West, J., Park, D., Harmon, C., Williamson, D., Ashcroft, P., Maestrini, D., Ardaseva, A., **Bravo, R.**, Sahoo, P., Khong, H., Luddy, K., & Robertson-Tessi, M. (2018). Evolutionary exploitation of PD-L1 expression in hormone receptor positive breast cancer. *bioRxiv*, 454447.

Manuscripts in Preparation

Bravo, R., Pettit, J., Petersen, B., Doucette, C., Edery, D., Faissol, D., Robertson-Tessi, M., & Anderson, A. R. (2026). Learning protocols for optimal cancer treatment: Humans versus machine.

Bravo, R., Prasad, S., Robertson-Tessi, M., & Anderson, A. R. (2026). Investigating the impact of cancer imaging vs blood biomarkers for monitoring adaptive therapy in an imaging-scale model.

Bravo, R., Ravi, H., Gatenby, R., Natarajan, R., & Anderson, A. R. (2026). MRI sequences correlate with GBM invasion and survival.

PRESENTATIONS AND AWARDS

Society for Mathematical Biology Annual Meeting | 2025 | Contributed talk: Testing the feasibility of estimating the migration to proliferation rate ratio in glioblastoma from single time-point MRI data

Integrated Mathematical Oncology Workshop | 2023 | Winning Team: Steering Cancer Extinction in MBC Using an Integrative Toxicity Metric

USNCCM17 | 2023 | Minisymposium talk: The Impact of Normal Tissue Density on Tumor Growth and Evolution in a 3D Whole-Tumor Model of Lung Cancer

AACR Annual Meeting | 2023 | Poster: The impact of normal tissue density on tumor growth and evolution in a 3D whole-tumor model of lung cancer

Society for Mathematical Biology Annual Meeting | 2023 | Poster Award: Using MRI scans to predict tumor margin propagation in GBM under immunotherapy

MathOnc23 | 2023 | Contributed talk: Investigating the impact of normal tissue density on the effectiveness of Adaptive Therapy in an imaging-scale model

Society for Mathematical Biology Annual Meeting | 2021 | Contributed talk: Investigating the impact of tissue density on tumor growth and evolution in a 3D whole-organ model of lung cancer

MENTORING EXPERIENCE

IMO High School Internship Program | 2017–2023

Philip Axelrod | 2017: 3D agent-based model of tumor spheroid response to acidosis.

Rajat Doshi | 2018: ODE model of adaptive therapy without a cost of resistance.

Edon Palenchar | 2019: 3D agent-based model of fibroblast-tumor interactions.

Saanvi Prasad | 2022–2023: Adaptive therapy in a 3D spatial model.