Diogo M. Camacho

+1 617 945 4383 | diogo.camacho.2008@gmail.com | diogocamacho | diogocamacho

Qualifications and research interests

Highly effective and experienced executive in Computational System Biology and Machine Learning, focusing on the development and implementation of computational platforms in biotech/pharma. Adept strategist and operational leader, interested in the application of computational tools in the drug discovery, disease biology characterization, large data analytics for biology, while focusing on bridging the gap between the wet and dry labs. Extensive experience in bringing novel data solutions to the organization, to extend data utilization to empower ML models.

Leadership Skills

Servant Leadership | Mentorship | Operational Leadership | Team Building | Communication | Interdisciplinary Collaboration | External Partnerships | Board Communication

Technical Skills

Machine learning | Deep learning | Multi-omics data analyses | R/Bioconductor | Python | AWS | Git

Education

Virginia Polytechnic Institute and State University *Blacksburg, VA*
Ph.D. in Genetics, Bioinformatics, and Computational Biology

Faculdade de Ciencias da Universidade de Lisboa *Lisboa, Portugal*
B. Sc. in Biochemistry

Experience

42 Bio LLC *Sudbury, MA*
Founder / Owner *March 2024 - Present*

42 Bio is a Computational Systems Biology and Machine Learning consulting firm, focusing on bringing computational solutions and strategical insights to its clients.

Cellarity *Boston, MA*
Vice President, Computational and Data Sciences *July 2022 - February 2024*

Cellarity is leading the discovery of novel chemical entities that can modulate cell behavior phenotypes through single cell technologies. In my role:

- Core member of R&D Leadership Team
- Implementation of vision, strategy, and operational framework for department
- Lead team of computational biologists, machine learning, and data scientists to deliver against program objectives
- Lead of PLatform Core Team, setting strategic and operational frameworks for the implementation of Cellarity computational platform
- Interfacing with external partners, board members, and founding VC partners on computational approaches at Cellarity

Rheos Medicines *Boston, MA*
Senior Director, Computational Biology and Bioinformatics *November 2020 - July 2022*

Rheos was a Precision Medicine company focused on integrating multi-omics data (transcriptomics and metabolomics) in the identification of novel targets for auto-immune disorders. In my role:

- Led implementattion of MetPM platform, Rheos' computational platform for precision medicine
- Implementation of Computational Biology and Bioinformatics strategy within the company
- Development of novel algorithm for patient stratification based on metabolic pathway representations
- Cross-functional integration of Computational Biology into programs at different stages of development

- Managed interactions with computational CROs to ensure on time delivery of work
- Led and managed relationships with ML CROs for implementation of Rheos' Knowledge Graph
- Communication of computational developments to board members, founding VC partners, and corporate partners

Wyss Institute @ Harvard University *Boston, MA*
Lead, Predictive BioAnalytics Initiative, Advanced Technology Team *July 2016 - November 2020*

The Wyss Institute of Harvard University is focusing on translating discoveries done in the lab into tangible applications. In my role:

- Founding member of the Predictive BioAnalytics Initiative
- Developed and implemented the research strategy for the Initiative, focusing on enabling ML/AI capabilities
- Managed and mentored staff scientists, post-doctoral fellows, graduate students, and interns
- Secure research funding through federal grants with DARPA, NIH
- Hands-on development of algorithms and computational approaches

Evelo Biosciences *Cambridge, MA*
Senior Scientist, Computational Systems Biology Lead *January 2015 - April 2016*

First employee of Evelo Biosciences. Deeply involved in the build out of the computational and data infrastructure capabilities for the organization, above and beyond the scope of my role. As the lead Computational Systems Biologist:

- Implemented diverse tools for analysis of high throughput data (transcriptomics, RNA-seq, metabolomics)
- Implemented a 16S rDNA sequencing analysis pipeline
- Development of a novel algorithm for the identification of microbiome-focused therapies through sequence-based analyses

- Responsible for the interface with IT provider to delineate and expand computational capabilities of the company, from general to research needs

Ember Therapeutics *Cambridge, MA*
Principal Scientist, Computational Systems Biology Lead *January 2014 - December 2014*

Ember Therapeutics was focused on the identification of small molecules to modulate energy expenditure, which is implicated in weight loss and improved metabolic health. In my role:

- Responsible for the implementation of muti-omics analytical pipelines (RNA-seq, metabolomics)
- Implementation of a knowledge-based and data-driven approach for construction of screening libraries for recombinant proteins, small peptides, and RNAi therapeutic efforts
- Implementation of analytical strategies (QC, statistical analyses, hit-calling) for high throughput screens
- Responsible for the interface with IT provider to delineate and expand computational capabilities of the company, from general to research needs

Pfizer, Inc *Cambridge, MA*
Senior Research Scientist, Computational Sciences Center of Emphasis *January 2011 - January 2014*

I was a member of the Computational Sciences Center of Emphasis at Pfizer, providing computational support across different preclinical programs at the organization, from cardiovascular disease to pain management and drug repositioning efforts. Some of the functions of the role included:

- Development and implementation of a network analysis tool for the characterization of differential networks in healthy and diseased populations under the scope of metabolic diseases
- Development and implementation of a methodology for metabolite set enrichment analysis for metabolomics data
- Involved in the analysis of a multi-omics data set for the characterization of the mechanism of action of a lead molecule for the Metabolic Diseases Research Unit

Howard Hughes Medical Institute @ Boston University *Boston, MA*
Post-doctoral Fellow *July 2007 - January 2011*

Post-doctoral training with Dr. James Collins at Boston University, focusing on the application of machine learning and network inference approaches in biomedicine.

Awards and Grants

Molecular circuits in the hematopoietic stem cell niche (NIH) *$415,000*
co-Investigator *9/1/20*

Synergistic Discovery and Design (DARPA) *$2,000,000*
co-PI *9/1/17*

Publications

- Valeri, JA, Soenksen, LR, Collins, KM, Ramesh, P, Cai, G, Powers, R, Angenent–Mari, NA, **Camacho, DM**, Wong, F, Lu, TK, Collins, JJ (2023), BioAutoMATED: An end-to-end automated machine learning tool for explanation and design of biological sequences, *Cell Systems*, 14, 525 [PubMed]
- Sperry, MM, Novak, R, Keshari, V, Dinis, ALM, Cartwright, MJ, **Camacho, DM**, Paré, JF, Super, M, Levin, M, Ingber, DE (2022), Enhancers of host immune tolerance to bacterial infection discovered using linked computational and experimental approaches, *Adv Sci* [PubMed]
- Gazzaniga, FS, **Camacho, DM**, Wu, M, Palazzo, MFS, Dinis, ALM, Grafton, FN, Cartwright, MJ, Super, M, Kasper, DL, Ingber, DE (2021), Harnessing Colon Chip technology to identify commensal bacteria that promote host tolerance to infection, *Frontiers in Cellular and Infection Microbiology*, 11, 105 [PubMed]
- Bein, A, ,Fadel, CW, Swenor, B, Cao, W, Powers, RK, **Camacho, DM**, Naziripour, A, Parsons, AW, LoGrande, NT, Sharma, S, Kim, S, Jalili-Firoozinezhad, S, Grant, J, Breault, DT, Iqbal, J, Ali, A, Denson, LA, Moore, SR, Prantil-Baun, R, Goyal, G, Ingber, DE (2022), Nutritional deficiency recapitulates intestinal injury associated with environmental enteric dysfunction in patient-derived Organ Chips, *Nature Biomed Eng* [PubMed]
- Bojar, D, Powers, RK, **Camacho, DM**, Collins, JJ (2020), Deep-Learning Resources for Studying Glycan-Mediated Host-Microbe Interactions, *Cell Host & Microbe*, 29, 132-144 [PubMed]
- Valeri, J, Collins, KM, Ramesh, P, Alcantar, M, Lepe, BA, Lu, TK, **Camacho, DM** (2020), Sequence-to-function deep learning frameworks for engineered riboregulators, *Nature Communications*, 11, 5058 [PubMed]
- Jalili-Firoozinezhad, S, Gazzaniga, FS, Calamari, EL, **Camacho, DM**, Fadel, C, Nestor, B, Cronce, MJ, Tovaglieri, A, Levy, O, Gregory, KE, Breault, DT, Cabral, JMS, Kasper, DL, Novak, R, Ingber, DE (2019), A complex human gut microbiome cultured in an anaerobic intestine-on-a-chip, *Nature Biomedical Engineering*, 3, 520-531 [PubMed]
- Tovaglieri, A, Sontheimer-Phelps, A, Geirnaert, A, Prantil-Baun, R, **Camacho, DM**, Chou, DB, Jalili-Firoozinezhad, S, de Wouters, T, Kasendra, M, Super, M, Cartwright, M, Richmond, CA, Breault, DT, Lacroix, C, Ingber, DE (2019), Species-specific enhancement of enterohemorrhagic *E. coli* pathogenesis mediated by microbiome metabolites, *Microbiome*, 7, 43 [PubMed]
- **Camacho, DM**, Collins, KM, Powers, RK, Costello, JC, Collins, JJ (2018), Next-generation machine learning for biological networks, *Cell*, 173, 1581-1592 [PubMed]
- Musah, S, Dimitrakakis, N, **Camacho, DM**, Church, GM, Ingber, DE (2018), Directed differentiation of human induced pluripotent stem cells into mature kidney podocytes and establishment of a Glomerulus Chip, *Nature Protocols*, 13, 1662-1685 [PubMed]
- Paandey, SP, Winkler, JA, Li, H, **Camacho, DM**, Collins, JJ, Walker, GC (2014), Central role for RNase YbeY in Hfq-dependent and Hfq-independent small-RNA regulation in bacteria, *BMC Genomics*, 15, 121 [PubMed]
- Galagan, JE, Minch, K, Peterson, M, Lyubetskya, A, Azzizi, E, Sweet, L, Gomes, A, Rustad, T, Dolganov, G, Glotova, I, Abeel, T, Mawhinney, C, Kennedy, A, Allard, R, Brabant, W, Krueger, A, Jaini, S, Honda, B, Yu, W-H, Hickey, M, Zucker, J, Garay, C, Weiner, B, Sisk, P, Stolte, C, Winkler, J, Van de Peer, Y, Iazzetti, P, **Camacho, D**, Dreyfuss, J, Liu, Y, Dorhoi, A, Mollenkopf, H-J, Drogaris, P, Lamontagne, J, Zhou, Y, Piquenot, J, Park, ST, Raman, S, Kaufmann, S, Mohney, R, Chelsky, D, Moody, B, Sherman, D, Schoolnik, G (2013), The Mycobacterium tuberculosis regulatory network and hypoxia, *Nature*, 499, 178-183 [PubMed]
- Belenky, P, **Camacho, D**, Collins, JJ (2013), Fungicidal drugs induce a common oxidative-damage cellular death pathway, *Cell Reports*, 3, 350-358 [PubMed]
- Marbach, D, Costello, JC, Kuffner, R, Vega, N, Prill, RJ, **Camacho, DM**, Allison, KR, the DREAM5 Consortium, Kellis, M, Collins, JJ, Stolovitzky, G (2012), Wisdom of crowds for robust gene network inference, *Nature Methods*, 9, 796-804 [PubMed]
- Dwyer, DJ, **Camacho, DM**, Callura, JM, Kohanski, MA, Collins, JJ (2011), Antibiotic-induced bacterial cell death exhibits physiological and biochemical hallmarks of apoptosis, *Molecular Cell*, 46, 561-572 [PubMed]

- Modi, SR, **Camacho, DM**, Kohanski, MA, Collins, JJ (2011), Functional characterization of bacterial sRNAs using a network biology approach, *Proc. Natl. Acad. Sci. USA*, 108, 15522-15527 [PubMed]
- **Camacho, DM**, Collins, JJ (2009), Systems biology strikes gold, *Cell*, 137, 24-26 [PubMed]
- **Camacho, D**, Vera-Licona, P, Laubenbacher, R, Mendes, P (2007), Comparison of existing reverse engineering methods by use of an in silico system, *Ann. N. Y. Acad. Sci.*, 1115, 73-89 [PubMed]
- Mendes, P, **Camacho, D**, de la Fuente, A (2005), Modelling and simulation for metabolomics data analysis, *Biochem. Soc. Trans.*, 33, 1427-1429 [PubMed]
- **Camacho, D**, de la Fuente, A, Mendes, P (2005), The origin of correlations in metabolomics data, *Metabolomics*, 1, 53-63 [Link]
- Martins, AM, **Camacho, D**, Shuman, J, Sha, W, Mendes, P, Shulaev, V (2004), A systems biology study of two distinct growth phases of *Saccharomyces cerevisiae* cultures, *Curr. Genomics*, 5, 649-663 [Link]

Patents

- Methods for detecting cellular transitions (US Provisional, 63/612,266)
- Disease detection systems and methods (US Providional, 63/612,320)
- Systems and methods for predicting compounds associated with transcriptional signatures (US Non-provisional, 18/539,190; International PCT, PCT/US2023/083922)
- Contrastive systems and methods (US Non-provisional, 18/539,204; International PCT, PCT/US2023/083934)
- Complex Human Gut Microbiome Cultured in an Anaerobic Human Gut-on-A-Chip (US20240002808A1)
- Riboregulators and methods of use thereof (International PCT, PCT/US2020/064695)
- Compositions and methods for treating fungal infections (WO2014130922A1)