

Defne Surujon

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Overview

Accomplished computational biologist with 5 years of industry experience in clinical diagnostics. Strong foundation in multi-omics data analysis, microbial genomics, transcriptomics, short and long read sequencing analysis, pathogen detection and antimicrobial susceptibility prediction in microbial genomics data.

Education

Boston College , PhD in Biology	2016-2021
PhD in Biology, defended Jan 11, 2021	
Thesis: <i>Computational Approaches in Infectious Disease Research: Towards Improved Diagnostic Methods</i>	
Amherst College , BA in Biochemistry and Mathematics, <i>summa cum laude</i>	2010-2014
Thesis: <i>Creating an rdeA-/fbxA- double knockout to investigate intracellular signalling processes in D. discoideum</i>	

Software and code

- [ShinyOmics](#) (R): a browser-based visualization application for multi-omics data
- BFClust ([MATLAB](#), [Python](#)): Package for large-scale clustering of biological sequences
- R&D code ([Python](#)): In vitro adaptive evolution data processing and analysis

Research and Work Experience

DAY ZERO DIAGNOSTICS | Boston, MA

Senior Research Scientist, Computational Biology (January 2021-October 2025)

- Working with the regulatory affairs team, drafted a technical overview of DZD's species ID algorithm and reference database as a Q-Submission to the FDA
- Designed a bioinformatics pre-processing and quality control pipelines for MicrohmDB (genomic AST training database) and MicroRefDB (species ID reference database)
- Worked with the Software Engineering team to develop DZD's database pre-processing, bioinformatics, build and deployment pipelines for species ID. Established an automated, versioned and reproducible database build and validation process.
- Planned and executed R&D for the latest major update on Keynome ID, DZD's species ID algorithm, reducing the turn-around-time per sample to <30min and adding interpretability to the Keynome ID numeric output
- Supported the product engineering, molecular assay development and clinical teams in data analysis, interpretation, and experimental design
- Continued CLIA proficiency certification and operational support for EpiXact; DZD's outbreak detection service
- Hired, trained and managed 2 direct reports on R&D projects
- Led clinical data processing operations for 1 year

BOSTON COLLEGE | Boston, MA

PhD Student – Microbial Systems Biology Laboratory (June 2016-January 2021)

- Demonstration that transcriptomic entropy is a strong predictor of bacterial fitness ([Nat. Comm. 2020](#))
- Analysis and interpretation of transcriptomics, genomics, metabolomics and Tn-Seq data, tooling development for visualization and exploratory analysis of multi-omics datasets ([BMC Bioinfo. 2020](#))
- Microfluidic device design, manufacturing and application in antimicrobial susceptibility testing
- Mentored 3 undergraduate students, teaching wet-lab and computational SOPs, guiding experimental design, giving constructive feedback on experimental outcomes and scientific communication

USDA HUMAN NUTRITION RESEARCH CENTER ON AGING | Boston, MA

Research Technician - Obesity Metabolism Laboratory (June 2014-June 2016)

- Developed data tools for the analysis and visualization of high-dimensional data such as microarray, intestinal microbial diversity and untargeted metabolomics

- Performed immunohistochemistry, 16S microbiome sequencing and analysis, qRT-PCR and gene expression analysis, and indirect calorimetry experiments
- Maintained cell cultures, multiple colonies of mice, genotyping animals, performing metabolic and microbiome profiling experiments
- Ensured cleanliness and safety compliance of lab, managed inventory of consumables, trained lab members on SOPs

Patents

Forecasting bacterial survival-success and adaptive evolution through multiomics stress-response mapping and machine learning. Patent Number [11591634](#).

Selected Publications

- Rosconi, F., Rudmann, E., Li, [and 8 others including **Surujon D**]. A bacterial pan-genome makes gene essentiality strain-dependent and evolvable. *Nat Microbiol* 7, 1580–1592 (2022). <https://doi.org/10.1038/s41564-022-01208-7>
- Zhu Z*, **Surujon D***, Ortiz-Marquez J C, Wood S, Huo W, Isberg R R , Bento J and van Opijken T. Entropy of a bacterial stress response is a generalizable predictor for fitness and antibiotic sensitivity. *Nat Commun* 11, 4365 (2020). <https://doi.org/10.1038/s41467-020-18134-z>
- Wood S, Zhu Z, **Surujon D**, Rosconi F, Ortiz-Marquez J C, and van Opijken T. 2019 A pan-genomic perspective on the emergence, maintenance and predictability of antibiotic resistance. Cham: Springer International Publishing; 2020. p. 169–202. https://doi.org/10.1007/978-3-030-38281-0_8
- **Surujon D**., van Opijken T. ShinyOmics: collaborative exploration of omics-data. *BMC Bioinformatics* 21, 22 (2020). <https://doi.org/10.1186/s12859-020-3360-x>
- **Surujon D**, Ponty Y, Clote P. Small-World Networks and RNA Secondary Structures. *Journal of Computational Biology*. 2018 Oct 31;26(1):16–26.

* Equal contribution

Selected Oral Presentations

- *Computational approaches in infectious disease research and diagnostics. Amherst College Biology Weekly Seminar. November 2023. Amherst MA.
- Direct bacterial species identification from blood for rapid sepsis diagnostics. Boston Bacterial Meeting. June 2022. Boston, MA.
- Entropy of a bacterial stress response is a generalizable predictor for fitness and antibiotic sensitivity. Genome Informatics. November 2019. Cold Spring Harbor, NY.
- *Entropy is a generalizable predictor for bacterial fitness. MIT PLS Short Talks. October 2019. Cambridge, MA.
- ShinyOmics: A Browser-Based Tool for Collaborative Exploration of Omics-Data. Systems Biology and Antibacterial Resistance Program Annual Meeting. September 2019. Galveston, TX.

* Invited talk

Community Involvement and Service

- **Day Zero Diagnostics Diversity Equity Inclusion Committee** (July 2021 – August 2022): Committee member involved in putting together resources for hiring managers, outreach to local organizations that support DEI efforts, organizing quarterly company-wide events around DEI issues.
- **Boston Bacterial Meeting Organizing Committee** (November 2019-January 2024): Operational support for arranging breakout sessions, coordination with panelists, evaluating submitted abstracts, design and editing of abstract book, fundraising
- **Science on Tap Organizer** (June 2018-June 2020): Organizer of the student-run summer seminar series Science on Tap at Boston College
- **PreLights** (July 2019-Current): [Contributing author](#) for The Company of Biologists preprint highlight website
- **Ad hoc reviewer** for Journal of Open Source Software, European Conference on Computational Biology
- **Guest Lecturer** at Boston College. BIOL6110 Advanced Genetics (2016-2019), BIOL3150 Introduction to Genomics(2020)