

Defne Surujon

145 Englewood Ave, unit 35
Brighton, MA 02135

defnesurujon@gmail.com
[Github](#) [LinkedIn](#)

413-262-3729

Overview

Accomplished computational biologist with over 4 years of industry experience in clinical diagnostics. Strong foundation in microbial genomics, 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: *Computational Approaches in Infectious Disease Research: Towards Improved Diagnostic Methods*

Amherst College, BA in Biochemistry and Mathematics, *summa cum laude*

2010-2014

Thesis: *Creating an rdeA-/fbxA- double knockout to investigate intracellular signalling processes in D. discoideum*

Software and code

- [ShinyOmics](#) (R): a browser-based visualization application for 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 2024-Current)

- 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)

- Application of machine learning and predictive modeling in bacterial fitness and adaptive outcome
- 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 Opijnen 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 Opijnen 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 Opijnen 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)