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TECHNICAL SKILLS

Computational skills: Highly proficient with R, python, bash scripting, AWS, slurm, SGE, version control (git). Very experienced using sequencing analysis software tools for read alignment, genome assembly, variant calling, SV calling, transcriptome assembly/quantification, methylation analysis, metagenomics, public data access, etc. Competent with MATLAB, LaTeX, Adobe Illustrator.

Lab techniques: Expertise in DNA/RNA extraction and handling, NGS-based assays, nanopore library prep and sequencing (ONT), mammalian cell culture.

EDUCATION

Johns Hopkins University	Baltimore, MD
Ph.D. Biomedical Engineering	September 2022
Advisor - Dr. Winston Timp	
<i>Thesis: Nanopore sequencing for infectious disease applications</i>	
Johns Hopkins University	Baltimore, MD
B.S. Biomedical Engineering (major), French Literature (minor)	May 2016
B.A. Electrical Engineering (major)	

AWARDS AND HONORS

Doctoral Foreign Study Award 2018 – 2021
Three-year graduate fellowship awarded by the Canadian Institutes of Health Research (CIHR) providing special recognition and support to Canadian students pursuing a doctoral degree in a health-related field outside of Canada.
Title: Clinical infectious disease sequencing for antimicrobial resistance detection and antibiotic stewardship

Provost's Undergraduate Research Award (PURA) 2015
Supports and encourages Hopkins undergraduate students to engage in independent research, scholarly and creative projects.
Title: Methylation Sequencing on the MinION

Irini J. Maroulis Award 2015
Awarded each year to a female undergraduate student in the Johns Hopkins University Whiting School of Engineering for outstanding community service and outreach.

PUBLICATIONS

1. **Y. Fan**, A. N. Gale, A. Bailey, K. Barnes, K. Colotti, M. Mass, L. B. Morina, B. Robertson, R. Schwab, N. Tselepidakis, and W. Timp, “Genome and transcriptome of a pathogenic yeast, *Candida nivariensis*,” *G3: Genes, Genomes, Genetics*, vol. 11, no. 7, p. jkab137, 2021
2. J. Vornhagen, C. M. Bassis, S. Ramakrishnan, R. Hein, S. Mason, Y. Bergman, N. Sunshine, **Y. Fan**, C. L. Holmes, W. Timp, M. C. Schatz, V. B. Young, P. J. Simner, and M. A. Bachman, “A plasmid locus associated with *Klebsiella* clinical infections encodes a microbiome-dependent gut fitness factor,” *PLoS Pathogens*, vol. 17, no. 4, p. e1009537, 2021
3. S. Kovaka, **Y. Fan**, B. Ni, W. Timp, and M. C. Schatz, “Targeted nanopore sequencing by real-time mapping of raw electrical signal with uncalled,” *Nature Biotechnology*, vol. 39, no. 4, pp. 431–441, 2021
4. P. M. Thielen, S. Wohl, T. Mehoke, S. Ramakrishnan, M. Kirsche, O. Falade-Nwulia, N. S. Trovão, A. Ernlund, C. Howser, N. Sadowski, C. P. Morris, M. Hopkins, M. Schwartz, **Y. Fan**, V. Gniazdowski, J. Lessler, L. Sauer, M. C. Schatz, J. D. Evans, S. C. Ray, W. Timp, and H. H. Mostafa, “Genomic diversity of sars-cov-2 during early introduction into the baltimore–washington metropolitan area,” *JCI Insight*, vol. 6, no. 6, 2021
5. A. Gershman, T. G. Romer, **Y. Fan**, R. Razaghi, W. A. Smith, and W. Timp, “De novo genome assembly of the tobacco hornworm moth (*Manduca sexta*),” *G3: Genes, Genomes, Genetics*, vol. 11, no. 1, p. jkaa047, 2021
6. J. L. Drewes, A. Corona, U. Sanchez, **Y. Fan**, S. K. Hourigan, M. Weidner, S. D. Sidhu, P. J. Simner, H. Wang, W. Timp, M. Oliva-Hemker, and C. L. Sears, “Transmission and clearance of potential procarcinogenic bacteria during fecal microbiota transplantation for recurrent *Clostridioides difficile*,” *JCI Insight*, vol. 4, no. 19, 2019
7. P. D. Tamma, **Y. Fan**, Y. Bergman, G. Pertea, A. Q. Kazmi, S. Lewis, K. C. Carroll, M. C. Schatz, W. Timp, and P. J. Simner, “Applying rapid whole-genome sequencing to predict phenotypic antimicrobial susceptibility testing results among carbapenem-resistant *Klebsiella pneumoniae* clinical isolates,” *Antimicrobial Agents and Chemotherapy*, vol. 63, no. 1, pp. e01923–18, 2019
8. V. Beleva Guthrie, D. L. Masica, A. Fraser, J. Federico, **Y. Fan**, M. Camps, and R. Karchin, “Network analysis of protein adaptation: modeling the functional impact of multiple mutations,” *Molecular Biology and Evolution*, vol. 35, no. 6, pp. 1507–1519, 2018
9. P. D. Tamma, **Y. Fan**, Y. Bergman, A. C. Sick-Samuels, A. J. Hsu, W. Timp, P. J. Simner, B. C. Prokesch, and D. E. Greenberg, “Successful treatment of per-

sistent *Burkholderia cepacia* complex bacteremia with ceftazidime-avibactam,” *Antimicrobial Agents and Chemotherapy*, vol. 62, no. 4, pp. e02213–17, 2018

10. R. Luo, A. Zimin, R. Workman, **Y. Fan**, G. Pertea, N. Grossman, M. P. Wear, B. Jia, H. Miller, A. Casadevall, W. Timp, S. X. Zhang, and S. L. Salzberg, “First draft genome sequence of the pathogenic fungus *Lomentospora prolificans* (formerly *Scedosporium prolificans*),” *G3: Genes, Genomes, Genetics*, vol. 7, no. 11, pp. 3831–3836, 2017
11. J. J. Credle, C. Y. Itoh, T. Yuan, R. Sharma, E. R. Scott, R. E. Workman, **Y. Fan**, F. Housseau, N. J. Llosa, W. R. Bell, H. Miller, S. X. Zhang, W. Timp, and H. B. Larman, “Multiplexed analysis of fixed tissue rna using ligation in situ hybridization,” *Nucleic Acids Research*, vol. 45, no. 14, pp. e128–e128, 2017
12. A. L. Norris, R. E. Workman, **Y. Fan**, J. R. Eshleman, and W. Timp, “Nanopore sequencing detects structural variants in cancer,” *Cancer Biology & Therapy*, vol. 17, no. 3, pp. 246–253, 2016

PRESENTATIONS

Conference Talks

SFAF - Sequencing, Finishing and Analysis in the Future (2018) Santa Fe, NM
Title: Bacterial sequencing and assembly for analysis of antibiotic resistance genes and mutations

Nanopore Community Meeting (2017) New York, NY
Title: Bacterial DNA modifications

Poster Presentations

AGBT - Advances in Genome Biology and Technology (2020) Marco Island, FL
Title: Calling bacterial methylation signatures using nanopore sequencing

Genome Informatics (2019) Cold Spring Harbor Laboratory
Title: Genome assembly using R9 and R10 type ONT flowcells

ASM Next-Generation Sequencing (2018) Washington, D.C.
Title: Nanopore sequencing for AMR detection and characterization