Brandon **Saint-John, Ph. D.**

COMPUTER SYSTEMS ENGINEER 2 · BIOINFORMATICS ENGINEER
Berkeley, CA, USA
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Skills

Bioinformatics	Experience with several standard genomics data formats (FASTA/Q, BAM, BED, GTF). Experience with common bioinformatics tools (UCSC Genome Browser, samtools, bedtools, DNA/RNA aligners, assemblers, etc.). Also includes several formats for long-read sequencing such as FAST5 and POD5. Familiar with sequencing databases like NCBI, GTEx, TCGA, and others. Knowledgeable about sequencing technologies, genetics, and molecular biology techniques.
Programming Languages	Strongly proficient with Python and Rust. Proficient with shell scripting. Working knowledge of C/C++, all in a Unix-based environment.
Linux Software Development	Proficient with Linux. Proficient in Git and GitHub for source code management. Developed containerized applications using Docker and QEMU for scalable and portable environments. Familiar with developing CI/CD systems using GitHub Actions
Scientific Programming	10+ years of experience in developing and maintaining applications using Python with object-oriented programming and standard scientific programming libraries such as numpy, scipy, scikit-learn, polars (similar to Pandas). Experienced with visualization of genomic data with matplotlib and seaborn. 5+ years experience using Rust to accelerate scientific software and personal projects.
Interpersonal Skills	Regularly work in an interdisciplinary environment with molecular biologists to develop tools that incorporate experimental workflows as well as feedback for the design of interfaces to pipelines.

Experience

Computer Systems Engineer 2 — Berkeley, CA, USA

LAWRENCE BERKELEY NATIONAL LABORATORY — March 2026 -

- Validated and benchmarked new versions of bioinformatics tools for inclusion in production sequencing and analysis pipelines
- Built a CI/CD system to provide automated test for a widely used bioinformatics suite both internally and worldwide.

Postdoctoral Research Scientist — Berkeley, CA, USA

LAWRENCE BERKELEY NATIONAL LABORATORY — Oct 2023 - Oct 2025

- Spearheaded computational approaches for a national-security-associated project to develop portable, pathogen-agnostic detection technologies funded by the Defense Threat Reduction Agency. Developed computational pipelines based on standards for evaluating portable VIS/NIR spectrometers.
- Engineered a machine-learning pipeline to process, filter, and build models using scikit-learn, xgboost, and H2O AutoML for classification of multi-wavelength spectroscopy datasets for the Shimadzu SolidSpec 3700, custom embedded spectroscopy devices, and Synchrotron-based Fourier-Transform Infrared Spectroscopy from the Advanced Light Source Beamline 1.4
- Reverse-engineered proprietary spectroscopy data formats from Thermo Fisher-based software to extract embedded bright-field images, enabling integration of custom Python FTIR software packages.
- Built GUI software using Rust and slint for embedded ARM devices, empowering non-technical researchers to troubleshoot device problems.
- Standardized preprocessing and quality assurance of spectroscopy data into a reusable library using Python, polars, pandas, and scikit-learn.
- Established SOPs and experiments for spectroscopic instrument standardization and evaluating machine-learning pipeline accuracy

- Authored clear monthly report updates for our Program Managers, translating scientific milestones and next-step plans
- Implemented a Cell Painting assay using confocal laser microscopy to visualize stains for studying the innate immune response and the effects of LPS and LTA on cell morphology

Graduate Student Researcher

Santa Cruz, CA, USA

University of California, Santa Cruz

2016 - 2023

- Built a fast and memory-efficient toolkit using Python and Rust to analyze data and visualize results with numpy, scipy, matplotlib and seaborn for signal processing of Oxford Nanopore long-read sequencing data
- Trained Gaussian Mixture Models for machine learning-based approach to detect kmer signal differences using Rust and scikit-learn
- Architected reusable pipelines using Rust, Bash, and Docker to provide easy-to-use workflows for analyzing specific regions and training models for different modifications
- Tested and maintained toolkit, automatically generated documentation, and compiled binaries with continuous integration using GitHub Actions
- Analyzed differential RNA junction usage from single-cell RNA-seq of AL and PM mouse brain cells in collaboration, mapping pseudo-bulk RNA-seq reads with the STAR aligner and quantifying RNA junction usage with the lab-developed tool MESA.
- Developed the MESA tool that detects differentially used, statistically significant junctions between two cell types using Fisher's exact test in Python.

Education

Ph. D. in Biomolecular Engineering and Bioinformatics

Santa Cruz, CA, USA

University of California, Santa Cruz

2016 - 2023

- Dissertation: Application of Long-Read Sequencing to Modified Nucleotides for Detecting Chromatin Accessibility

Bachelor of Science in Biochemistry

Charlottesville, VA, USA

University of Virginia

2012 - 2016

Presentations

Towards Agnostic Identification of Pathogens using Machine Learning of Hyperspectral Data

Fort Lauderdale, FL

Defense Threat Reduction Agency CBD S&T Conference

December 2-5, 2024

Talk presented as part of the AI-powered Diagnostics session

Publications

Bai, G., Dhillon, N., Felton, C., Meissner, B., **Saint-John, B.**, Shelansky, R., Meyerson, E., Hrabeta-Robinson, E., Hodjat, B., Boeger, H., & Brooks, A. N. (2025). SMAdd-seq: probing chromatin accessibility with small molecule DNA intercalation and nanopore sequencing. *Nucleic Acids Research*, *53*(14), gkaf671. https://doi.org/10.1093/nar/gkaf671

Beale, H. C., Tse, V., Lee, J. Y., Akutagawa, J., Mavura, Y., **Saint-John, B.**, Cheney, A., Mulligan, D. R., Chacaltana, G., Gutierrez, M., Tenney, J., Shieh, J. T., Martin, P.-M., Yip, T., Hodoglugil, U., Fay, A. J., Brooks, A. N., Van Ziffle, J., Stone, M. D., … Slavotinek, A. (2025). A novel splice site variant in DEGS1 leads to aberrant splicing and loss of DEGS1 enzyme activity, a VUS resolved. *Medrxiv*. https://doi.org/10.1101/2025.04.04.25325118

Brooks, A., **Saint-John, B.**, Boeger, E., Hinrich Robinson, & Shelansky, R. (2021,). *Methods for Determining Bound and Unbound Regions in Nucleic Acid Molecules and Systems for Practicing Same*.

Pardo-Palacios, F. J., Wang, D., Reese, F., Diekhans, M., Carbonell-Sala, S., Williams, B., Loveland, J. E., De Maria, M., Adams, M. S., Balderrama-Gutierrez, G., **Saint-John, B.**, & others. (2024). Systematic assessment of long-read RNA-seq methods for transcript identification and quantification. *Nature Methods*, *21*(7), 1349–1363.

Saint-John, B., Bandela, M., Gadde, M., Inman, J., Zwart, P., & Mukundan, H. (n.d.). Detection of Innate Immune signatures using synchrotron FTIR spectromicroscopy. *In Preparation*.

Saint-John, B., Wolf-Yadlin, A., Jacobsen, D. E., Inman, J. L., Gart, S., Keener, M., McMurray, C., Snijders, A. M., Mukundan, H., Kubicek-Sutherland, J. Z., & Brown, J. B. (2025). Reagent-free Hyperspectral Diagnosis of SARS-CoV-2 Infection in Saliva Samples. *ECS Sensors Plus*, *4*(1), 14601. https://doi.org/10.1149/2754-2726/ad9c92

Sakkos, A., **Saint-John, B.**, Tyml, T., Myskova, E., Aureli, L., Inman, J. L., Snijders, A., Mouncey, N. J., Mukundan, H., & Schulz, F. (2025). Agnostic Capture of Pathogens for Detection and Diagnostics of Emerging Threats. *Submitted*.