Troy A. Brier, PhD

Computational Chemist · Biophysicist

1314 N. DuPont St, Wilmington, DE 19806

(+1) 732-859-9742 | troya.brier@gmail.com | troy-a-brier | T.A. Brier

Synthesize.Bio Recruitment Team

February 5, 2025

Synthesize.Bio
1940 5th Avenue West
Seattle, WA 98119

Job Application for Bioinformatics Data Engineer

To whom it may concern,

About Me

I am a physical chemist by training with a background in scientific computing focusing on biological systems. Specifically, I have integrated principles from chemistry, physics, and statistics to investigate diverse phenomena within bacterial cells, such as a regulatory mechanisms for stress response and the interplay between the transcriptome and proteome. In my career, I have achieved proficiency in a wide array of computational tools to design and implement analytical pipelines within multiple different environments (HPC, AWS, Docker, Conda) on various operating systems (Linix, MacOS, Windows) leveraging custom and pre-built software packages with standard coding languages (Python, R, Bash, etc). Additionally, I have developed skills in designing, managing, and contributing to exploratory multi-year projects that require flexibility, self-assessment, reproducibility, and publication-level documentation. I have extensive experience working in highly collaborative environments, domestically and internationally, and I am well practiced in presenting technical material to audiences of varying subject-matter expertise.

Why Synthesize.Bio?

My former experience has given me a deep appreciation for scientific innovation and the need for more efficient and accelerated methods to extend innovation beyond the laboratory and into the real world. Therefore, I am particularly drawn to Synthesize.Bio's mission to fundamentally change life sciences research and accelerate the pace of biomedical discovery. As a start-up in biomedical research, I am inspired by Synthesize.Bio's commitment to improve the accessibility of genomic data by reducing the known difficulties with producing and handling such data. Furthermore, Synthesize.Bio's dedication to empowering scientific exploration with AI/ML tools is appealing to me and aligns with my personal philosophy of wanting to push the boundaries of knowledge using computational innovation. I would welcome the opportunity to join your team to contribute to making the company's vision a reality.

Why Me?

As a computational chemist and biophysicist I would bring a deep understanding of fundamental biological principles, complemented by hands-on experience in scientific computing across diverse operating systems and environments. I have significant knowledge of Python and am proficient in R as tools to solve complex scientific questions including the processing and handling of multiple types of NGS data sets. Throughout my career I have worked with many different types and sizes of data sets, so I am confident in my capacity to adapt, manage, and utilize new data sets regardless of size for addressing challenging biological questions. While my AI/ML experience is limited, I very eager to learn more and employ it towards real world applications. My ability to achieve and communicate scientific discovery is exemplified through my publication and presentation record. In summary, I believe my problem-solving abilities, commitment to learning and integrating novel techniques across disciplines, and aptitude for collaboration makes me an ideal candidate for the **Bioinformatics Data Engineer** position at Synthesize.Bio.

Thank you for considering my application. I would welcome the opportunity to discuss my qualifications further.
Sincerely,

Troy A. Brier, PhD

Troy A. Brier

(732)-859-9742 | troya.brier@gmail.com | troy-a-brier | github.com/troyb2

Professional Summary

Chemist and software developer with a background in biological scientific computing. Experienced solving diverse problems in computational science settings applying novel techniques across domains. Skilled in the design and management of exploratory multi-year projects requiring flexibility, self-assessment mechanisms, and documentation suitable for publication. Proficient in presenting technical material to audiences with varying subject-matter expertise.

Technical Skills

Programming : Python, MATLAB, Bash, R, Tcl, LaTeX, C/C++, CUDA, HTML

Tools : Unix/Linux, MacOS, Windows, AWS, SVN, Git, SSH, Docker, Apptainer, slurm, Jupyter, VScode, MARTINI CG, NVIDIA DGX

Software : pandas, matplotlib, seaborn, numpy, scipy, biopython, cobra, HTSeq, pysam, Guppy, minimap2, PyTorch, sklearn, HDF5, VMD, MAFFT, Clustal, BLAST, deepTools, SAMtools, GROMACS, AMBERMD, NAMD, AlphaFold2

Theoretical Training : *Mathematics* — Probability Theory, Stochastic Processes, Information Theory, Numerical Analysis, Linear Algebra, ODEs | *Science & Engineering* — Biophysics, Systems Biology, Bioinformatics, Molecular Dynamics, Equil. and Nonequil. Statistical Physics and Thermodynamics, Quantum Mechanics, Chemical Kinetics

Selected Experiences

Graduate/Postdoctoral Research Assistant | *Luthey-Schulten Group*, Dept. of Chemistry at UIUC *January 2018 – December 2024*

- Constructed a stochastic kinetic model using data collected from super-resolution imaging experiments to simulate the sugar-stress response in *Escherichia coli*.
- Collaborated in the use of GPU-accelerated, hybrid stochastic-deterministic methods to simulate whole-cell models of bacteria that capture the reaction and diffusion of ∼10,000 biochemical components at the cell-scale.
  * Constructed a kinetic model of the nucleotide metabolism for a bacteria cell.
  * Curated genomics, transcriptomics, proteomics, metabolomics, and kinetic rates data.
  * Updated software/code for use on high performance GPU cluster.
- Developed a methodology to profile the bacterial transcriptome coupling bioinformatics and computational analysis of NGS experiments.
  * Built a sequence alignment based pipeline to identify genetic motifs and predict transcriptional events in bacteria
  * Analyzed Illumina, Pacific Biosciences, and Oxford Nanopore Technologies RNA sequencing experiments.
  * Created tools to predict transcription units and visualize the RNA isoforms.
- Assisted PI in preparation of grant materials to acquire federal funding: *NSF MCB 2221237* - $2.00M (proposal, annual reports) | *NSF MCB 1818344* - $1.50M (annual reports) | *NSF MCB 1840320* - $1.18M (annual reports).
- Maintained group's GPU cluster and website.
- Collaborated with industrial and academic partners, both domestic and international.
- Presented research results to broader scientific community at domestic and international conferences.
- Mentored junior graduate and undergraduate student researchers.

Seminar/Workshop Teaching Assistant | *Luthey-Schulten Group*, Dept. of Chemistry at UIUC *May 2024, October 2021, July 2019*

- NSF STC-QCB Advanced Computational Workshop 2024—Mentored junior graduate students to construct teaching material, installed software on supercomputer, and troubleshot errors during live tutorials.
- Online Hands-on Workshop on Computational Biophysics—Held virtual lecture for graduate students and post-doctoral and prepared tutorials run on AWS instances.
- Center for the Physics of Living Cells (CPLC) Summer School—Held lectures for graduate students and post-doctoral associates and prepared tutorials run on AWS instances.

Undergraduate Research Assistant | *The Baker Group*, Dept. of Chemistry at TCNJ *December 2014 – May 2017*

- Explored atomistic and coarse grained molecular dynamics simulations of membrane bound proteins
- Presented research results to broader scientific community at domestic conferences.
- Mentored junior undergraduate student researchers.

Education

University of Illinois at Urbana-Champaign (UIUC) — **PhD in Chemistry** — *August 2017 – December 2024*

The College of New Jersey (TCNJ) — **BS in Chemistry (ACS-certified)** — *August 2013 – May 2017*

Selected Publications (0000-0002-9530-6517)

T. A. Brier, J. E. Cournoyer, B. R. Gilbert, S. A. Glass, Y. Gao, Z. R. Thornburg, K. Goglin, G. John, T. Mamaghani, S. Shivakumar, Y. Yu, C. Fields, J. I. Glass, A. P. Mehta, Z. Luthey-Schulten, **Unraveling the Transcriptional Landscape within a Minimized Bacterium via Comparative Analysis**, *in preparation*

J. A. Stevens, F. Grünewald, P.A. Marco van Tilburg, M. König, B. R. Gilbert, T. A. Brier, Z. R. Thornburg, Z. Luthey-Schulten, S. J. Marrink, **Molecular Dynamics Simulation of an Entire Cell**, *Frontiers in Chemistry 2023*

Z. R. Thornburg, D. M. Bianchi, T. A. Brier, B. R. Gilbert, T. M. Earnest, M. C.R. Melo, N. Safronova, J. P. Sáenz, A. T. Cook, K. S. Wise, C. A. Hutchison III, H. O. Smith, J. I. Glass, Z. Luthey-Schulten, **Fundamental Behaviors Emerge from Simulations of a Living Minimal Cell**, *Cell 2022*

D. M. Bianchi, T. A. Brier, A. Poddar, M. S. Azam, C. K. Vanderpool, T. Ha, Z. Luthey-Schulten, **Stochastic Analysis Demonstrates the Dual Role of Hfq in Chaperoning *E. coli* Sugar Shock**, *Frontiers in Molecular Biosciences 2020*