Troy A. Brier, PhD

Computational Chemist · Biophysicist

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Rajant Health Inc Recruitment Team

March 31, 2025

Rajant Health Inc
200 Chesterfield Parkway
Malvern, PA 19355

Job Application for Computational Biologist

To whom it may concern,

About Me

I am a physical chemist by training with a background in scientific computing, specializing on biological systems. Specifically, I have integrated principles from chemistry, physics, and statistics to investigate diverse phenomena within bacterial life, such as 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 computing environments (HPC, AWS, Docker, Conda) on various operating systems (Linux, MacOS, Windows) leveraging both custom and pre-built software 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, both domestically and internationally, and I am well practiced in presenting technical material to audiences of varying subject-matter expertise.

Why Rajant Health Inc?

My former experience has given me a deep appreciation for scientific innovation and the need for more efficient and accelerated methods to translate innovation from the laboratory into real-world impact. I am motivated by the Rajant Health Inc's mission to revolutionize health discovery on a global scale. I am particularly drawn to Rajant Health Inc's perspective that health should be proactive and personalized through innovation in diagnostics, therapeutics, and communication. I appreciate the stress on the emphasis on deciphering complex relationships within data, and the insights that can emerge from such analysis. I am excited at the opportunity to join the Rajant Health Inc team and contribute to its vision with my computational skills.

Why Me?

As a computational chemist and biophysicist, I would bring a deep understanding of biological research complemented by hands-on experience in scientific computing across diverse computing systems and environments. I have significant knowledge of Python and am proficient in R as tools to solve complex scientific questions including developing custom code for simulation and data analysis. Throughout my career I have worked with many data sets of varying types and sizes, and I am confident in my capacity to adapt, manage, and utilize new data sets to address challenging questions, regardless of data size. Most relevant to the position is my previous experience with NGS sequencing data from varying methodologies (Illumina, PacBio, and ONT), where I integrated various software and algorithms to compare and predict complex relationships between the data sets. This included comparing proteomic data to the results to better understand transcriptome-proteome relationships. Of the job-listing requirements my AI/ML experience is currently foundational. I have experience applying pre-built AI/ML approaches such as AlphaFold2 to aid in discovery. While I have no appreciable experience in constructing AI/ML solutions, I am very eager to learn and employ them towards real world applications. In summary, I believe my problem-solving abilities, commitment to learning and integrating novel techniques across disciplines, and aptitude for collaboration make me an ideal candidate for the **Computational Biologist** position at Rajant Health Inc.

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 computational scientist with an expertise in biological scientific computing. Experienced applying novel computational techniques to diverse scientific challenges. Skilled in the design and management of exploratory multi-year projects requiring flexibility, self-assessment mechanisms, and documentation suitable for publication. Adept at conveying complex 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, JIRA, 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 bacterial cell.
  * Curated genomics, transcriptomics, proteomics, metabolomics, and kinetic rates from experiments/databases.
  * 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 lectures for graduate students and post-doctoral researchers and prepared tutorials to 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 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*