# Troy A. Brier

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## **PROFESSIONAL SUMMARY**

Chemist and software developer with a background in biological scientific computing. Experienced solving diverse problems in computational science settings enables the application of 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, ETEX, 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, 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

#### EXPERIENCE

Graduate/Postdoctoral Research Assistant | The Luthey-Schulten Group, Dept. of Chemistry at UIUC

Jan 2018 – present

- 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.
  - \* Organized 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 experiment.
  - \* Built a sequence alignment based pipeline to identify genetic motifs within a bacterial genome and predict transcriptional events.
  - \* Analyzed Illumina, Pacific Biosciences, and Oxford Nanopore Technologies RNA sequencing experiments.
  - \* Created tools to predicted transcription units, and visualize the RNA isofrom.
- 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 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 | The 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.

### **EDUCATION**

University of Illinois at Urbana-Champaign (UIUC) The College of New Jersey (TCNJ)

PhD in Chemistry BS in Chemistry (ACS-certified) Aug 2017 – Dec 2024 Aug 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*
- B. R. Gilbert, Z. R. Thornburg, T. A. Brier, J. A. Stevens, F. Grünewald, J. E. Stone, S. J. Marrink, Z. Luthey-Schulten, **Dynamics of Chromosome Organization in a Minimal Bacterial Cell**, *Frontiers in Cell and Developmental Biology 2023*
- 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