Mark Evan Fornace, PhD

Lawrence Berkeley National Laboratory

Alvarez fellow, Mathematics group, AMCR division (2025-)
Postdoctoral researcher, Mathematics group, AMCR division (2023-2025)
Projects:

- Row and column subset selection using nuclear score maximization (efficient interpolative decompositions of dense, sparse, and implicit matrices using randomized linear algebra)
- Interpolative decompositions of tensor data (approximate dense, sparse, or CP format tensors using matricized column selection and randomized sketching techniques)
- Principled reduced order models of reversible discrete-space Markov chains using nuclear score selection (construction of macrostate models of theoretically guaranteed error using a marked chain approach)
- Tensor-based models for nucleic acid thermodynamics (development of a new paradigm for secondary structure analysis enabling higher accuracy, unified algorithms, and GPU implementations)

California Institute of Technology

Postdoctoral scholar, Biology & Biological Engineering (2022-2023)
Doctor of Philosophy, Chemistry (2013-2022. Cumulative GPA 4.1) Thesis: *Computational methods for simulating and parameterizing nucleic acid secondary structure thermodynamics and kinetics.*
Selected coursework: statistical physics, quantum chemistry, nuclear chemistry, thermodynamics of natural systems (also served as TA in quantum chemistry, introduction to bioengineering)
Projects:

- Unified dynamic programming framework for nucleic acid secondary structure analysis: recursions, evaluation algebras, operation orders (enhanced physical models [coaxial and dangle stacking], dramatic speedups [20-120x for test tube analysis], scalability [e.g., 30,000 nt complexes])
- Computational parametrization of equilibrium and kinetic nucleic acid secondary structure models via massive (i.e., >20 million CPU hours) molecular dynamics simulation and Gaussian process regression (computational framework replacing patchwork multi-decade experimental parameterization process)
- Efficient stochastic algorithms for simulation of nucleic acid hybridization kinetics (complexity reduction, enabling simulation of systems of practical interest with order-of-magnitude speedups)
- Automated coarse-graining of nucleic acid hybridization kinetics for complex and test tube ensembles (automatic generation of low-dimensional kinetic models governing large molecular systems)
- Non-negative least squares algorithms for spectral unmixing of fluorescent images of mRNA expression with hybridization chain reaction (HCR) (enable robust multiplexed bioimaging using fluorophores with strongly overlapping excitation and emissions spectra)
- Convolution-based methods for single molecule dot detection and colocalization in images of fluorescent HCR expression (enable single-molecule imaging in whole-mount vertebrate embryos)
- Re-architecture, improvement, and cloud-based implementation of NUPACK, a growing software suite for the analysis and design of nucleic acid structures, devices, and systems (NUPACK web app usage in 2023: 240,000 user sessions, 5,100,000 screen minutes, 4,400,000 page views)
- Embedded mean field theory for ab initio multiscale electronic structure calculations using density functional theory (DFT) (principled cost reduction by calculating energetic terms using different density functionals, basis sets, and Coulombic repulsion treatments)

University of Chicago:

Bachelor of Science in Chemistry (2009-2013. Cumulative GPA 3.74. Major GPA 3.84)
Bachelor of Science with Honors in Geophysical Sciences
Selected coursework: organic chemistry, physical chemistry, inorganic chemistry, computational chemistry, biological diversity, ecology and evolution, numerical analysis

Research experience:

- Mathematics group, Lawrence Berkeley National Laboratory (2023-, Supervisor: James Sethian)
- Pierce lab, Caltech (2015-2023, PI: Niles Pierce)
- Miller lab, Caltech (2013-2015, PI: Thomas F. Miller III)
- Origins lab, University of Chicago (2011-2013, PI: Nicolas Dauphas)
- Plasma mass spectrometry lab, University of Maryland (2011, PI: Bill McDonough)

Selected presentations:

- "Rank reduction of graph Laplacians via column selection." *Copper Mountain Conference on Iterative Methods*, Copper Mountain, Colorado (2024).
- "Low-rank approximation via determinantal point processes." *High-Dimensional Scientific Computing Seminar*, University of California, Berkeley (2024).
- "Theoretical methods for nucleic acid secondary structure thermodynamics and kinetics." *Applied Mathematics Seminar*, Lawrence Berkeley Laboratory and University of California, Berkeley (2022).
- "Theoretical methods for nucleic acid secondary structure thermodynamics and kinetics." *Biophysics Seminar*, Simon Fraser University (2022).
- "NUPACK: molecular programming in the cloud." *DNA28 Conference*, University of Mexico (2022).
- "Computational investigations of nucleic acid thermodynamics." *Center for Molecular and Cellular Medicine Seminar*, California Institute of Technology (2021).
- "Improved methods for predicting the thermodynamics of nucleic acids." *Molecular Programming Project Workshop*, California Institute of Technology (2019).

Subject matter expertise:

- Applied mathematics: Numerical linear algebra, randomized algorithms, Markov chains, Gaussian processes, dynamic programming algorithms
- Computational biology: nucleic acid analysis and design, fluorescence image analysis
- Computational chemistry: statistical mechanics, molecular dynamics, electronic structure

Computational skills:

- Experienced programming in C++20 and Python 3; working knowledge of Docker, CMake, MPI, OpenMP, git, zsh/bash, C, Fortran, Mathematica, MATLAB, LaTeX
- Past experience using Kubernetes, OpenStack, PBS-based clusters (government and academic), and AWS cloud computing services (EC2, DynamoDB, CloudWatch, S3)

Awards and funding:

- Alvarez postdoctoral fellowship (LBNL; accepted, 2025)
- "Combinatorial optimization and inference using randomized numerical linear algebra" (team member for DOE randomized algorithms FOA; encouraged by LBNL & DOE; pending, 2025)
- "Rank structured reduction of spatiotemporal data" (team member for DOE data reduction FOA; encouraged by LBNL & DOE; not offered, 2024)
- Schmidt AI for Science postdoctoral fellowship (University of Chicago; offered and declined, 2023)
- "Computational parameterization of nucleic acid secondary structure models" (team member for NSF INSPIRE opportunity; awarded, 2016)
- NSF graduate research fellowship program honorable mention (2014)

Research artifacts:

- NUPACK 4 hybrid cloud web application
- NUPACK 4 C++/Python module with extensive user guide
- HCR Imaging Python module containing Dot Detection 2.0 and Unmix 1.0 packages with user guide
- Nuclear score maximization package for efficient and parallelized column selection in C++
- Public Github contributions: `dask-jetstream` (XSEDE Jetstream scheduling using dask and Kubernetes), `lilwil` (C++ unit testing framework), `rebind` (bindings between C++, Python, Rust)

Publications:

[1] Y. Zhang, M. Fornace, and M. Lindsey, "Fast and accurate interpolative decompositions for general, sparse, and structured tensors," *arXiv [math.NA]*, Mar. 24, 2025.

[2] M. Fornace and M. Lindsey, "Column and row subset selection using nuclear scores: Algorithms and theory for Nystrom approximation, CUR decomposition, and graph Laplacian reduction," Jul. 1, 2024.

[3] N. Pierce, M. Fornace, R. M. Murray, E. Winfree, and L. Qian, "Molecular programming for biological circuit design," Analog Computing for Science Workshop, research rep., 2024.

[4] S. J. Schulte, M. E. Fornace, J. K. Hall, G. J. Shin, and N. A. Pierce, "HCR spectral imaging: 10-plex, quantitative, high-resolution RNA and protein imaging in highly autofluorescent samples," en, *Development*, vol. 151, 4 Feb. 15, 2024.

[5] M. E. Fornace, J. Huang, C. T. Newman, N. J. Porubsky, M. B. Pierce, and N. A. Pierce, "NUPACK: Analysis and design of nucleic acid structures, devices, and systems," en, *ChemRxiv*, Nov. 11, 2022.

[6] M. E. Fornace, "Computational methods for simulating and parameterizing nucleic acid secondary structure thermodynamics and kinetics," 2022.

[7] M. E. Fornace, N. J. Porubsky, and N. A. Pierce, "A unified dynamic programming framework for the analysis of interacting nucleic acid strands: Enhanced models, scalability, and speed," *ACS Synth. Biol.*, vol. 9, pp. 2665–2678, 10 2020.

[8] H. M. T. Choi, M. Schwarzkopf, M. E. Fornace, A. Acharya, G. Artavanis, J. Stegmaier, A. Cunha, and N. A. Pierce, "Third-generation in situ hybridization chain reaction: Multiplexed, quantitative, sensitive, versatile, robust," *Development*, vol. 145, dev165753, 12 2018.

[9] A. W. Heard, N. Dauphas, I. L. Hinz, J. E. Johnson, M. Blanchard, E. E. Alp, M. Y. Hu, J. Zhao, B. Lavina, M. E. Fornace, J. Y. Hu, M. Roskosz, C. Kin I Sio, N. X. Nie, and B. Baptiste, "Isotopic constraints on the nature of primary precipitates in archean–early paleoproterozoic iron formations from determinations of the iron phonon density of states of greenalite and 2L- and 6L-ferrihydrite," en, *ACS Earth Space Chem.*, vol. 7, pp. 712–727, 4 Apr. 20, 2023.

[10] A. Heard, N. Dauphas, I. L. Hinz, J. E. Johnson, M. Blanchard, E. E. Alp, M. Y. Hu, J. Zhao, B. Lavina, M. E. Fornace, J. Hu, and B. Baptiste, "Constraints on the nature of primary precipitates in archean iron formations from spectroscopic and theoretical determinations of the equilibrium iron isotopic behavior of greenalite and ferrihydrite," en, *AGUFM*, vol. 2022, PP52B–03, 2022.

[11] M. Blanchard, N. Dauphas, M. Y. Hu, M. Roskosz, E. E. Alp, D. C. Golden, C. K. Sio, F. L. H. Tissot, J. Zhao, L. Gao, R. V. Morris, M. Fornace, A. Floris, M. Lazzeri, and E. Balan, "Reduced partition function ratios of iron and oxygen in goethite," en, *Geochim. Cosmochim. Acta*, vol. 151, pp. 19–33, Feb. 2015.

[12] M. E. Fornace, J. Lee, K. Miyamoto, F. R. Manby, and T. F. Miller 3rd, "Embedded mean-field theory," en, *J. Chem. Theory Comput.*, vol. 11, pp. 568–580, 2 Feb. 10, 2015.

[13] N. Dauphas, H. Kobayashi, M. Fornace, and H. Tang, "Chronological and dynamical constraints on the accretion of mars," en, *LPI Contrib.*, p. 1305, 1719 Mar. 1, 2013.