

Interests

Machine Learning, Bioinformatics

Education

2013–2017 **PhD, Bioinformatics and Systems Biology**, *University of California, San Diego*, La Jolla, CA.

2009–2012 **MS, Computer Science and Engineering**, *The Ohio State University*, Columbus, OH.

Thesis: *Application of biclustering algorithms to gene expression data.*

2004–2009 **BS, Biology**, *University of Michigan*, Ann Arbor, MI.

Minors: Mathematics and Computer Science.

Honors and Awards

2013–2016 **NIH National Library of Medicine Biomedical Informatics Training Grant Fellowship.**

Publications

Marina Caskey, Till Schoofs, Henning Gruell, Allison Settler, Theodora Karagounis, Edward F Kreider, Ben Murrell, Nico Pfeifer, Lilian Nogueira, Thiago Y Oliveira, et al. Antibody 10-1074 suppresses viremia in hiv-1-infected individuals. *Nature medicine*, 23(2):185, 2017.

Kemal Eren and Ben Murrell. RIFRAF: a frame-resolving consensus algorithm. 2017.

Kemal Eren, Steven Weaver, Robert Ketteringham, Morné Valentyn, Melissa Laird Smith, Venkatesh Kumar, Sanjay Mohan, Sergei L Kosakovsky Pond, and Ben Murrell. Full-Length Envelope Analyzer (FLEA): A tool for longitudinal analysis of viral amplicons. 2017.

Elise Landais, Ben Murrell, Bryan Briney, Sasha Murrell, Kimmo Rantalainen, Zachary T Berndsen, Alejandra Ramos, Lalinda Wickramasinghe, Melissa Laird Smith, Kemal Eren, et al. Hiv envelope glycoform heterogeneity and localized diversity govern the initiation and maturation of a v2 apex broadly neutralizing antibody lineage. *Immunity*, 47(5):990–1003, 2017.

Daniel T MacLeod, Nancy M Choi, Bryan Briney, Fernando Garces, Lorena S Ver, Elise Landais, Ben Murrell, Terri Wrin, William Kilembe, Chi-Hui Liang, et al. Early antibody lineage diversification and independent limb maturation lead to broad HIV-1 neutralization targeting the Env high-mannose patch. *Immunity*, 44(5):1215–1226, 2016.

Melissa Laird Smith, Ben Murrell, Kemal Eren, Caroline Ignacio, Elise Landais, Steven Weaver, Pham Phung, Colleen Ludka, Lance Hepler, Gemma Caballero, et al. Rapid

sequencing of complete env genes from primary HIV-1 samples. *Virus Evolution*, 2(2), 2016.

Mehmet Deveci, Onur Küçüktunç, Kemal Eren, Doruk Bozdağ, Kamer Kaya, and Ümit V. Çatalyürek. Querying co-regulated genes on diverse gene expression datasets via biclustering. In *Methods in Molecular Biology*, Methods in Molecular Biology, pages 1–20. Humana Press, 2015.

Ben Murrell, Steven Weaver, Martin D. Smith, Joel O. Wertheim, Sasha Murrell, Anthony Aylward, Kemal Eren, Tristan Pollner, Darren P. Martin, Davey M. Smith, Konrad Scheffler, and Sergei L. Kosakovsky Pond. Gene-wide identification of episodic selection. *Molecular Biology and Evolution*, 2015.

Kemal Eren, Mehmet Deveci, Onur Küçüktunç, and Ümit V. Çatalyürek. A comparative analysis of biclustering algorithms for gene expression data. *Briefings in Bioinformatics*, 2012.

Experience

2017–2018 **Machine Learning Research Engineer, Qeexo**, Pittsburgh, PA.

- Machine learning-based solutions for mobile devices and embedded platforms.

2013–2017 **Doctoral Candidate, UCSD Bioinformatics and Systems Biology**, San Diego, CA.

Adviser: Joel Wertheim.

- Statistical and computational models for viral sequence analysis.

Summer **Software Engineer, scikit-learn**.

2013 **Mentors:** Vlad Nicolae, Gaël Varoquaux.

- Funded by the Google Summer of Code.
- Implemented high-performance biclustering algorithms: Spectral Coclustering and Spectral Biclustering.
- Implemented biclustering scoring metrics.

2012–2013 **Software Engineer, Heidelberg Collaboratory for Image Processing**, Heidelberg, Germany.

Supervisor: Fred Hamprecht.

- Image processing algorithms and software.
- Developed object classification for the ilastik interactive learning and segmentation toolkit.

2009–2012 **Graduate Research Assistant, OSU HPC Laboratory**, Columbus, OH.

Adviser: Ümit V. Çatalyürek.

- Developed BiBench, a framework for validation of biclustering algorithms on simulated and real microarray datasets.
- Studied and updated the Correlated Patterns Biclustering (CPB) algorithm.
- Developed algorithms for sequence mapping using the Burrows Wheeler Transform on graphical processing units.

Summer **Software Engineer, Machine Intelligence Research Institute**.

2009 **Mentor:** Lucio de Souza Coelho.

- Funded by the Google Summer of Code.
- Contributed to OpenBiomind, an open source machine learning toolkit.
- Implemented denoising, features selection, and classification algorithms for block-related fMRI experimental data.

- 2008-2009 **Research Assistant, *Strategic Reasoning Group***, Ann Arbor, MI.
Adviser: Michael P. Wellman.
 - Developed an autonomous agent (MANX) for the Trading Agent Competition Market Design Challenge.
 - Development and testing for for the Trading Agent Competition Ad Auction Challenge.
- Summer **Research Assistant, *Columbia University Palmer Lab***, New York NY.
 2007 **Adviser:** Arthur G. Palmer.
 - Designed molecular animations for publication in electronic journals.
- Summer **Software Engineer, *Hyland Software***, Cleveland, OH.
 2007
 - Developed Electronic Content Management (ECM) software.
 - Developed a document generator for testing document indexing.
- 2005–2006 **Research Assistant, *Computational Biophysics Group***, Ann Arbor, MI.
Adviser: Ioan Andricioaei.
 - Collaborated on a computational model of a photoswitchable azobenzene crosslinker.

Expertise

- Statistics statistical learning, Bayesian modeling, hidden Markov models, Kalman filters.
- CS machine learning, image processing, optimization.
- Bioinformatics SMRT sequence analysis, phylogenetics, gene expression analysis, pipeline design.
- Programming Python (NumPy, SciPy, pandas, scikit-learn, etc.), Cython, Julia, STAN, C, R, Lisp, UNIX shell scripting, T_EX, GNU make, git, and others.
- Parallel CUDA, MPI, OpenMP, multiprocessing.