JOHN HAWKINS

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EDUCATION

The University of Texas at Austin, Austin, TX, USA
    Ph.D. in Computational Science, Engineering and Mathematics, 2018
    Investigations in Integrative and Molecular Bioscience
    Committee: William H. Press (Co-Supervisor), Ilya J. Finkelstein (Co-Supervisor),
    George Biros, Ron Elber, Oscar Gonzalez, Edward Marcotte

The University of Texas at Austin, Austin, TX, USA
    M.S. in Computational Science, Engineering and Mathematics, 2014
    Supervisors: William H. Press, Ilya J. Finkelstein

Walla Walla University, Walla Walla, WA, USA
    B.S.E in Mechanical Engineering, 2010
    B.S. in Mathematics, 2010
    B.A. in Humanities, 2010

RESEARCH INTERESTS

Computational molecular biology, integrative biology, high-throughput DNA sequencing, high-dimensional analysis, machine learning, mathematical modeling, visualization

TECHNICAL SKILLS

- Python, R, MATLAB, C++
- Basic bench skills: pipetting, gels, DNA sequencing prep, plasmid transformation, etc.
- LaTeX, Jupyter, Matplotlib, ggplot
- Adobe Illustrator, Inkscape, Adobe Photoshop, GIMP
- Linux, Windows, and Mac
- Bash, makefiles, compilers, version control systems (Git, SVN)
- Software developer for (see github.com/hawkjo):
    - CHAMP alignment software
    - FREE barcodes generation and decoding software
    - Mismatching Isoform eXon Remover (MIXR)
    - NucleaSeq processing software

LANGUAGES

Fluent in English and Spanish, introductory German, French, and Japanese.

RESEARCH EXPERIENCE

German Cancer Research Center (DKFZ), Heidelberg, Germany, 2020-Present
(Postdoctoral Fellow with Oliver Stegle)

- **Decoding Context-Dependent Genetic Networks *in vivo***
  Leading computational biologist for a multi-lab ERC project to uncover context-dependent genetic networks *in vivo* in Drosophila and Arabidopsis, using a combination of single-cell techniques, gene editing, and phenotypic readouts in whole-organism tissues.

- **Error-correcting DNA Barcodes for Long Read Single-Cell Assays**
  Expanded my previous work on FREE divergence indel-correcting DNA barcodes to randomly selected single-cell assay barcodes in the context of high-error long read sequencing, for full-transcript inquiries in high-throughput assays at the single-cell level.

The University of Texas at Austin, Austin, TX, USA, 2011-2019
(with William H. Press and Ilya J. Finkelstein)

- **Binding and Cleavage Profiles of multiple CRISPR Systems**
  Profiled the binding affinity and cleavage rate of several natural and engineered CRISPR proteins across thousands to millions of DNA sequences using our Chip Hybridized Association Mapping Platform (CHAMP) and Nuclease digestion and sequencing (NucleaSeq). Performed the first such binding assay on the entire human exome. Identified current best CRISPR systems for binding or cleavage applications.

- **Indel-correcting DNA Barcodes for High-Throughput Sequencing**
  Defined Fill/truncated Right End Edit (FREE) divergence to correctly measure errors in DNA barcodes, proved required properties of FREE divergence, generated error-correcting FREE barcodes, experimentally validated FREE barcodes error-correcting properties.

- **Registration of Sequenced DNA and TIRF Microscope Images**
  Developed novel method for aligning DNA sequencing information with total internal reflection fluorescence (TIRF) microscope images. Method uses two-step algorithm: rough alignment with Fourier methods in image space and precision "constellation" alignment with linear least squares in puncta space.

- **Bat Transcriptome Assembly, Annotation, and Evolutionary Analysis**
  Assembled transcriptomes of 12 bats using both public and new sequencing data. Found orthologous gene families with an additional 6 bats with genomic data, filtered using multiple syntenic analyses, exon structure, and the novel Mismatching Isoform eXon Remover (MIXR) algorithm. Performed phylogenetic and positive selection analyses.

The University of Texas at Austin, Austin, TX, USA, 2009
  (with Ron Elber and James Chelikowsky)

- **"Tex" Moncrief Computational and Applied Mathematics Intern**
  Developed single-mutation protein flow network for simple protein-folding model.
  Extended real space density functional theory MATLAB code to process a much larger
  sets of initial conditions.

PUBLICATIONS

Journal Articles

- Kuo, Y., Jung, C., Chen, Y., Kuo, H, Zhao, O., Nguyen, T., Rybarski, J. R., Hong, S., Chen, Y., Wylie, D. D., **Hawkins, J. A.**, Walker, J. N., Shields, S. W. J., Brodbelt, J. S., Petty, J. T., Finkelstein, I. J., Yeh, H. (Accepted). Massively Parallel Selection of NanoCluster Beacons. *Advanced Materials.*

- Eslami-Mossallam, B., Klein, M., van der Smagt, C., van der Sanden, K., Jones, S. K., **Hawkins, J. A.**, Finkelstein, I.J. & Depken, M. (2022). A kinetic model predicts SpCas9 activity, improves off-target classification, and reveals the physical basis of targeting fidelity. *Nature communications,* 13(1), 1-10.

- **Hawkins, J. A.***, Jones, S. K.*, Johnson, N. V., Jung, C., Hu, K., Rybarski, J. R., Chen, J. S., Doudna, J. A., Press, W. H., and Finkelstein, I. J. (2021). Massively parallel kinetic profiling of natural and engineered CRISPR nucleases. *Nature Biotechnology*, 39(1), 84-93.

- Press, W. H. & **Hawkins, J. A.** (2020). Likelihood Models for Forensic Genealogy. *arXiv preprint arXiv:2010.02985*.

- Press, W. H., **Hawkins, J. A.**, Jones, S. K., Schaub, J. M., & Finkelstein, I. J. (2020). HEDGES error-correcting code for DNA storage corrects indels and allows sequence constraints. *Proceedings of the National Academy of Sciences*, *117*(31), 18489-18496.

- **Hawkins, J. A.,** Kaczmarek, M. E., Müller, M. A., Drosten, C., Press, W. H., & Sawyer, S. L. (2019). A metaanalysis of bat phylogenetics and positive selection based on genomes and transcriptomes from 18 species. Proceedings of the National Academy of Sciences, 116(23), 11351-11360.

- **Hawkins, J. A.**, Jones, S. K., Finkelstein, I. J., and Press, W. H. (2018). Indel-correcting DNA barcodes for high-throughput sequencing. Proceedings of the National Academy of Sciences, 201802640.

- **Hawkins, J. A.***, Jung, C.*, Jones, S. K.*, Xiao, Y., Rybarski, J. R., Dillard, K. E., Hussmann, J., Saifuddin, F. A., Savran, C. A., Ellington, A. D., Ke, A., Press, W. H.,

Finkelstein, I. J. (2017). Massively parallel biophysical analysis of CRISPR-Cas complexes on next generation sequencing chips. Cell, 170(1), 35-47.

- Stabell, A. C., **Hawkins, J. A.**, Li, M., Gao, X., David, M., Press, W. H., & Sawyer, S. L. (2016). Non-human primate schlafen11 inhibits production of both host and viral proteins. PLoS pathogens, 12(12), e1006066.

- Ng, M., Ndungo, E., Kaczmarek, M. E., Herbert, A. S., Binger, T., Kuehne, A. I., Jangra, R. K., **Hawkins, J. A.**, Gifford, R. J., Biswas, R., Demogines, A., James, R. M., Yu, M., Brummelkamp, T. R., Drosten, C., Wang, L., Kuhn, J. H., Müller, M. A., Dye, J. M., Sawyer, S. L., Chandran, K. (2015). Filovirus receptor NPC1 contributes to species-specific patterns of ebolavirus susceptibility in bats. Elife, 4, e11785.

- **Hawkins, J. A.**, Rittenhouse, J. L., Soper, L. M., & Rittenhouse, R. C. (2008). Use of the Primitive Unit Cell in Understanding Subtle Features of the Cubic Closest-Packed Structure. Journal of Chemical Education, 85(1), 90-92.

Patents

- Hawkins, J. A., Press, W. H., Finkelstein, I. J., (2018). Error-correcting DNA Barcodes. US Patent Application No. 62/660,531. Patent pending.

- Finkelstein, I., Hawkins, J. A., Jung, C., Jones Jr., S. K., Rybarski, J., Saifuddin, F. A., Savran, C., Ellington, A. D., Press, W. H., (2018). Chip Hybridized Association-Mapping Platform and Methods of Use. US Patent Application No. 62/519,502. Patent pending.

ORAL AND POSTER PRESENTATIONS

- Massively parallel kinetic profiling of natural and engineered CRISPR nucleases. Oral Presentation. Harvard Genome Engineering Seminar Series @HMS. Cambridge, MA, USA, March 2021.

- High-throughput Profiling of DNA Binding and Cleavage by Engineered Cas9 Variants and Cas12a. Poster. 2019 Annual Meeting of Biophysical Society (BPS). Baltimore Convention Center, Baltimore, MD, USA, March 2019.

- Explorations in Computational Molecular Biology. Oral presentation. Ivo Babuska Forum Series. The University of Texas at Austin, Austin, TX, USA, February 2019.

- Free Divergence Error-Correcting DNA Barcodes. Oral Presentation. Computational and Applied Mathematics Colloquium. Rice University, Houston, TX, USA, September 2018.

- Indel-Correcting DNA Barcodes for High-Throughput Sequencing. Poster. 2018 Annual Meeting of the Society for Mathematical Biology (SMB). The University of Sydney, Sydney, NSW, Australia, July 2018.

- Indel-Correcting DNA Barcodes for High-Throughput Sequencing. Poster. International Physics of Living Systems Annual Meeting (iPoLS). Rice University, Houston, TX, USA, June 2018.

- Free Divergence Error-Correcting DNA Barcodes. Oral presentation. ICES Seminar. The University of Texas at Austin, Austin, TX, USA, January 2018.

- Free Divergence Error-Correcting DNA Barcodes. Oral Presentation. BioTacos Seminar Series. The University of Texas at Austin, Austin, TX, USA, November 2017.

- Massively Parallel Biophysical Analysis of a CRISRP-Cas Complex on Next Generation Sequencing Chips. Byte Club. Oral Presentation. The University of Texas at Austin, Austin, TX, USA, September 2017.

- Context-Tolerant, Error-Correcting DNA Codes. Poster. The 23rd International Conference on DNA Computing and Molecular Programming (DNA23). The University of Texas at Austin, Austin, TX, USA, September 2017.

- Massively Parallel Biophysical Analysis of a CRISRP-Cas Complex on Next Generation Sequencing Chips. Poster. Biophysics Day. The University of Texas at Austin, Austin, TX, USA, May 2017.

- Massively Parallel Biophysical Analysis of a CRISRP-Cas Complex on Next Generation Sequencing Chips. Poster. 5th Annual Big Data in Biology Symposium. The University of Texas at Austin, Austin, TX, USA, May 2017.

- Massively Parallel Biophysical Analysis of a CRISRP-Cas Complex on Next Generation Sequencing Chips. Poster. Molecular Biosciences Retreat. The University of Texas at Austin, Austin, TX, USA, March 2017.

- Massively Parallel Biophysical Analysis of a CRISRP-Cas Complex on Next Generation Sequencing Chips. Oral Presentation. Physics of Living Systems Biophysics Retreat. Camp Lone Star, La Grange, TX, USA, March 2017.

- Massively Parallel DNA-Binding Protein Profiling. Oral Presentation. ICES Seminar. The University of Texas at Austin, Austin, TX, USA, April 2016.

- Massively Parallel Target Profiling of the CRISPR Cascade Complex. Oral Presentation. BioTacos Seminar Series. The University of Texas at Austin, Austin, TX, USA, February 2016.

TEACHING EXPERIENCE

The University of Texas at Austin, Austin, TX, USA, 2013-2016

Teaching Assistant

Statistical and Discrete Methods for Scientific Computing, William H. Press
Postgraduate course introducing a variety of statistical concepts and methods, such as high-dimensional analysis, multiple hypothesis testing, Bayesian inference, MCMC methods, mixture models, and model selection. I attended and assisted with all classes, and I lectured on a bonus topic each Friday.

Problem Solving: Molecular Biology/Epidemiology, Marc S. Lewis
Undergraduate course introducing biology students to the high-throughput and computational methods of modern biology, such as online biological and biomedical databases, homology search, and developing creative, testable hypotheses. I attended and assisted with some classes.

Public Policy and the Digitally Native Technologist, William H. Press
Undergraduate course to help science students understand and influence science and technology public policy. Topics covered included big data, net neutrality, patent trolls, and mathematics and computer literacy education. I attended and assisted with all classes.

Mentor

McNair Scholars Program Mentor
I mentored a first-generation college student, a double-major biochemistry and computer science planning to pursue a Ph.D. I advised him on his academic trajectory and guided him on small research projects with impact on our real-world research.

Japanese Exchange and Teaching (JET) Program, Hikone, Shiga, Japan, 2011

Teacher

English
High-school English in Hikone Higashi High School, a Super Science track high school for students preparing for a future in science. I taught classes and helped prepare them for writing science papers and applying to English speaking universities.

AWARDS AND HONORS

- Computational Science, Engineering, and Mathematics Fellowship, The University of Texas at Austin, 2015.
- Palme d'Organism Science Film Competition First Prize, The University of Texas at Austin, 2017.
- Engineer of the Year, Walla Walla University, 2010.
- Solomon Scholarship for Interdisciplinary Excellence, Walla Walla University, 2010.
- Mathematics scholarship, Walla Walla University, 2010.
- Engineering scholarship, Walla Walla University, 2010.
- Honors Program scholarship, Walla Walla University, 2010.

PROFESSIONAL AFFILIATIONS

Society for Industrial and Applied Mathematics (SIAM)

Biophysical Society (BPS)

American Association for the Advancement of Science (AAAS)