

Adam Thrash

Bioinformatics Software Developer

@ adam@adamthrash.com

cv.adamthrash.com

adamthrash

Knoxville, TN

Experience

Computer Specialist

February 2021 — Present

Institute for Genomics, Biocomputing & Biotechnology

- Analyze client/collaborator data with current bioinformatics software and pipelines
- Develop custom reports to better visualize and explain complex data
- Develop scripts to customize analyses
- Develop software to meet needs of collaborators
- Draft manuscripts and assist with manuscript production
- Train student workers as needed
- Develop training material for the [Atlas supercomputing cluster](#)
- Lead training workshops for the [Atlas supercomputing cluster](#)
- Support USDA-ARS researchers on the [Atlas supercomputing cluster](#)

Research Associate II

April 2019 — February 2021

Institute for Genomics, Biocomputing & Biotechnology

- Analyze client/collaborator data with current bioinformatics software and pipelines
- Develop custom reports to better visualize and explain complex data
- Develop scripts to customize analyses
- Develop software to meet needs of collaborators
- Draft manuscripts and assist with manuscript production
- Train student workers as needed

Research Associate I

August 2015 — April 2019

Institute for Genomics, Biocomputing & Biotechnology

- Analyze client/collaborator data with current bioinformatics software and pipelines
- Develop scripts to customize analyses
- Develop software to meet needs of collaborators
- Draft manuscripts and assist with manuscript production
- Assist with training student workers as needed

Education

PhD, Computer Science

August 2019

Mississippi State University

Dissertation

A machine learning approach to genome assessment

An exploration of current methods of genome assembly assessment, where these methods fall short, and how machine learning can be used to model expert knowledge for genome assessment

Highlighted Coursework

- Machine Learning
- Visual Data Analysis with R
- Data Information and Visualization
- Directed Individual Study of Genome Assembly

MS, Computer Science

May 2016

Mississippi State University

Highlighted Coursework

- Essentials of Molecular Genetics
- Genomes and Genomics
- High Throughput Sequence Analysis

Certificate, Computational Biology

This certificate requires students to take a combination of five computer science and biological sciences courses to build their understanding of how to combine the two disciplines.

BS, Software Engineering

May 2014

Mississippi State University

Languages

Programming	Web	Markup
Python	HTML	LaTeX
R	Javascript	Markdown
Rust	CSS	orgmode

Programs

PAST

 IGBB/PAST

 Institute for Genomics, Biocomputing & Biotechnology

 USDA-ARS

In recent years, a method for interpreting genome-wide association study (GWAS) data using metabolic pathway analysis was developed and successfully used to find significant pathways and mechanisms explaining phenotypic traits of interest in plants. The scripts implementing this method were both difficult to use and slow to run, sometimes taking longer than 24 hours. PAST (Pathway Association Study Tool), a new implementation of this method, has been developed to address these concerns and implemented as a package for the R language. Two user-interfaces are provided—console and R Shiny application. PAST completed analyses in approximately half an hour to one hour and produced the same results as the previously developed method. Thus, to promote a powerful new pathway analysis methodology that interprets GWAS data to find biological mechanisms associated with traits of interest, we developed a more accessible, efficient, and user-friendly tool. PAST is available on GitHub, Bioconductor, and at MaizeGDB.

Keanu

 IGBB/keanu

 Institute for Genomics, Biocomputing & Biotechnology

 US Army ERDC

One of the main challenges when analyzing complex metagenomics data is the fact that large amounts of information need to be presented in a comprehensive and easy-to-navigate way. In the process of analyzing FASTQ sequencing data, visualizing which organisms are present in the data can be useful, especially with metagenomics data or data suspected to be contaminated. Keanu, a tool for exploring sequence content, helps a user to understand the presence and abundance of organisms in a sample by analyzing alignments against a database that contains taxonomy data and displaying them in an interactive web page. The content of a sample can be presented either as a collapsible tree or as a bilevel partition graph. Keanu is freely available at GitHub.

Quack

 IGBB/quack

 Institute for Genomics, Biocomputing & Biotechnology

The quality of data generated by high-throughput DNA sequencing tools must be rapidly assessed in order to determine how useful the data may be in making biological discoveries; higher quality data leads to more confident results and conclusions. Due to the ever-increasing size of data sets and the importance of rapid quality assessment, tools that analyze sequencing data should quickly produce easily interpretable graphics. Quack addresses these issues by generating information-dense visualizations from FASTQ files at a speed far surpassing other publicly available quality assurance tools in a manner independent of sequencing technology. Quack is freely available at GitHub.

Skills

Communication

- data visualization
- writing documentation
- creating training materials and leading workshops
- writing manuscripts

Technical

- software and analysis pipeline development in high-performance computing environments
- data organization
- project management via git
- reproducible projects via orgmode, software containers, and LMOD

Bioinformatics

- differential expression and functional analysis
- genome assembly and annotation

Awards and Honors

Featured Article

 2023

 G3: Genes | Genomics | Genetics

A high-quality chromosome-level genome assembly of rohu carp, Labeo rohita, and its utilization in SNP-based exploration of gene flow and sex determination

Best Paper Published in 2020

 2021

 ALTEX

AOPERA: A proposed methodology and inventory of effective tools to link chemicals to adverse outcome pathways

Innovation Award

 2020

 USDA-ARS

Team member on Innovation Award that received \$25,000 to continue work on PAST

Publications

- Poudel, S.; Jia, L.; Arick, M.A., II; Hsu, C.-Y.; **Thrash, A.**; Sukumaran, A.T.; Adhikari, P.; Kiess, A.S.; Zhang, L. 2023. *In silico prediction and expression analysis of vaccine candidate genes of Campylobacter jejuni*, *Poultry Science*. DOI: [10.1016/j.psj.2023.102592](https://doi.org/10.1016/j.psj.2023.102592)
- Arick, M.A., II; Grover, C.E.; Hsu, C.-Y.; Magbanua, Z.; Pechanova, O.; Miller, E.R.; **Thrash, A.**; Youngblood, R.C.; Ezzell, L.; Alam, M.S.; Benzie, J.A.H.; Hamilton, M.G.; Karsi, A.; Lawrence, M.L.; Peterson, D.G. 2023. *A high-quality chromosome-level genome assembly of rohu carp, Labeo rohita, and its utilization in SNP-based exploration of gene flow and sex determination*, *G3: Genes, Genomes, Genetics*. DOI: [10.1093/G3JOURNAL/JKAD009](https://doi.org/10.1093/G3JOURNAL/JKAD009)
- Grover, C.E.; Arick, M.A.; **Thrash, A.**; Sharbrough, J.; Hu, G.; Yuan, D.; Snodgrass, S.; Miller, E.R.; Ramaraj, T.; Peterson, D.G.; Udall, J.A.; Wendel, J.F. 2022. *Dual Domestication, Diversity, and Differential Introgression in Old World Cotton Diploids*, *Genome Biology and Evolution*. DOI: [10.1093/gbe/evac170](https://doi.org/10.1093/gbe/evac170)
- Warburton, M.L.; Jeffers, D.; Smith, J.S.; Scapim, C.; Uhdre, R.; **Thrash, A.**; Williams, W.P. 2022. *Comparative Analysis of Multiple GWAS Results Identifies Metabolic Pathways Associated with Resistance to A. flavus Infection and Aflatoxin Accumulation in Maize*, *Toxins*. DOI: [10.3390/toxins14110738](https://doi.org/10.3390/toxins14110738)
- Poudel, S.; Li, T.; Arick, M.A.; Hsu, C.-Y.; **Thrash, A.**; Sukumaran, A.T.; Adhikari, P.; Kiess, A.S.; Zhang, L. 2022. *Complete Genome Sequences of Four Campylobacter jejuni Strains Isolated from Retail Chicken Meat and Broiler Feces*, *Microbiology Resource Announcements*. DOI: [10.1128/mra.00898-22](https://doi.org/10.1128/mra.00898-22)
- Tekedar, H.C.; Arick, M.A., II; Hsu, C.-Y.; **Thrash, A.**; Blom, J.; Lawrence, M.L.; Abdelhamed, H. 2020. *Identification of Antimicrobial Resistance Determinants in Aeromonas veronii Strain MS-17-88 Recovered From Channel Catfish (Ictalurus punctatus)*, *Frontiers in Cellular and Infection Microbiology*. DOI: [10.3389/fcimb.2020.00348](https://doi.org/10.3389/fcimb.2020.00348)
- Thrash, A.**; Hoffmann, F.; Perkins, A. 2020. *Toward a more holistic method of genome assembly assessment*, *BMC Bioinformatics*. DOI: [10.1186/s12859-020-3382-4](https://doi.org/10.1186/s12859-020-3382-4)
- Thrash, A.**; Warburton, M.L. 2020. *A pathway association study tool for gwas analyses of metabolic pathway information*, *Journal of Visualized Experiments*. DOI: [10.3791/61268](https://doi.org/10.3791/61268)
- Rycroft, T.E.; Foran, C.M.; **Thrash, A.**; Cegan, J.C.; Zollinger, R.; Linkov, I.; Perkins, E.J.; Garcia-Reyero, N. 2020. *AOPERA: A proposed methodology and inventory of effective tools to link chemicals to adverse outcome pathways*, *Altex*. DOI: [10.14573/altex.1906201](https://doi.org/10.14573/altex.1906201)
- Thrash, A.**; Tang, J.D.; Deornellis, M.; Peterson, D.G.; Warburton, M.L. 2020. *PAST: The pathway association studies tool to infer biological meaning from GWAS datasets*, *Plants*. DOI: [10.3390/plants9010058](https://doi.org/10.3390/plants9010058)
- Li, H.; **Thrash, A.**; Tang, J.D.; He, L.; Yan, J.; Warburton, M.L. 2019. *Leveraging GWAS data to identify metabolic pathways and networks involved in maize lipid biosynthesis*, *Plant Journal*. DOI: [10.1111/tpj.14282](https://doi.org/10.1111/tpj.14282)
- Thrash, A.**; Arick, M., II; Barbato, R.A.; Jones, R.M.; Douglas, T.A.; Esdale, J.; Perkins, E.J.; Garcia-Reyero, N. 2019. *Keanu: A novel visualization tool to explore biodiversity in metagenomes*, *BMC Bioinformatics*. DOI: [10.1186/s12859-019-2629-4](https://doi.org/10.1186/s12859-019-2629-4)
- Grover, C.E.; Arick, M.A., II; **Thrash, A.**; Conover, J.L.; Sanders, W.S.; Peterson, D.G.; Frelichowski, J.E.; Scheffler, J.A.; Scheffler, B.E.; Wendel, J.F. 2019. *Insights into the evolution of the New World diploid cottons (Gossypium, subgenus houzienia) based on genome sequencing*, *Genome Biology and Evolution*. DOI: [10.1093/gbe/evy256](https://doi.org/10.1093/gbe/evy256)
- Thrash, A.**; Arick, M., II; Peterson, D.G. 2018. *Quack: A quality assurance tool for high throughput sequence data*, *Analytical Biochemistry*. DOI: [10.1016/j.ab.2018.01.028](https://doi.org/10.1016/j.ab.2018.01.028)
- Warburton, M.L.; Womack, E.D.; Tang, J.D.; **Thrash, A.**; Smith, J.S.; Xu, W.; Murray, S.C.; Williams, W.P. 2018. *Genome-wide association and metabolic pathway analysis of corn earworm resistance in Maize*, *Plant Genome*. DOI: [10.3835/plantgenome2017.08.0069](https://doi.org/10.3835/plantgenome2017.08.0069)
- Grover, C.E.; Arick, M.A.; Conover, J.L.; **Thrash, A.**; Hu, G.; Sanders, W.S.; Hsu, C.-Y.; Naqvi, R.Z.; Farooq, M.; Li, X.; Gong, L.; Mudge, J.; Ramaraj, T.; Udall, J.A.; Peterson, D.G.; Wendel, J.F. 2017. *Comparative Genomics of an Unusual Biogeographic Disjunction in the Cotton Tribe (Gossypieae) Yields Insights into Genome Downsizing*, *Genome Biology and Evolution*. DOI: [10.1093/gbe/evx248](https://doi.org/10.1093/gbe/evx248)
- Rice, J.; Dees, K.; Perkins, A.; **Thrash, A.** 2015. *Investigating genome similarity through cross mapping percentage*, *BCB 2015 - 6th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics*. DOI: [10.1145/2808719.2811456](https://doi.org/10.1145/2808719.2811456)