

ADAM THRASH

Bioinformatics Research Associate

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EXPERIENCE

Research Associate II

Institute for Genomics, Biocomputing & Biotechnology

📅 April 2019 – Present

📍 Mississippi State University, Starkville, MS

- 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

Institute for Genomics, Biocomputing & Biotechnology

📅 August 2015 – April 2019

📍 Mississippi State University, Starkville, MS

- Analyze client/collaborator data with current bioinformatics software and pipelines
- Develop scripts to customize analyses
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PROGRAMS DEVELOPED

PAST

IGBB and USDA-ARS

In recent years, a bioinformatics method for interpreting genome-wide association study (GWAS) data using metabolic pathway analysis has been developed and successfully used to find significant pathways and mechanisms explaining phenotypic traits of interest in plants. However, the many scripts implementing this method were not straightforward to use, had to be customized for each project, required user supervision, and took more than 24 hours to process data.

PAST (Pathway Association Study Tool), a new implementation of this method, has been developed to address these concerns. PAST has been implemented as a package for the R language. Two user-interfaces are provided; PAST can be run by loading the package in R and calling its methods, or by using an R Shiny guided user interface. In testing, PAST completed analyses in approximately half an hour to one hour by processing data in parallel and produced the same results as the previously developed method. PAST has many user-specified options for maximum customization.

AWARDS & GRANTS

Innovation Award

USDA ARS

📅 2020

Team member on Innovation Award to further develop PAST (see Programs Developed)

SKILLS

Visualization Software Development

Writing Training Students

unix Git Differential Expression D3

Genome Assembly Emacs

orgmode Genome Assembly Annotation

LANGUAGES

Python ● ● ● ● ●

R ● ● ● ● ●

HTML ● ● ● ● ●

CSS ● ● ● ● ●

Javascript ● ● ● ● ●

Julia ● ● ● ● ●

C ● ● ● ● ●

EDUCATION

Ph.D., Computer Science

Mississippi State University

📅 May 2016 – August 2019

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. These attributes make PAST accessible to researchers interested in associating metabolic pathways with GWAS datasets to better understand the genetic architecture and mechanisms affecting phenotypes.

PAST is available on GitHub, Bioconductor, and at MaizeGDB.

Keanu

IGBB and 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 is a command-line tool for visualizing and exploring sample content in metagenomics data and makes viewing complex data easier.

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, with node size indicating abundance, or as a bilevel partition graph, with arc size indicating abundance. Keanu provides a simple means by which researchers can explore and visualize species present in sequence data generated from complex communities and environments.

Keanu is freely available at GitHub.

Quack

IGBB

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.

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
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M.S., Computer Science

Mississippi State University

📅 May 2014 – May 2016

Highlighted Coursework

- Essentials of Molecular Genetics
 - Genomes and Genomics
 - High Throughput Sequence Analysis
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Certificate, Computational Biology

Mississippi State University

📅 May 2016

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.

B.S., Summa Cum Laude, Software Engineering

Mississippi State University

📅 August 2010 – May 2014

REFERENCES

Available upon request.

PUBLICATIONS

Journal Articles

- Thrash, Adam, Federico Hoffmann, and Andy Perkins (July 2020). "Toward a more holistic method of genome assembly assessment". en. In: *BMC Bioinformatics* 21.S4, p. 249. ISSN: 1471-2105. DOI: 10.1186/s12859-020-3382-4. URL: <https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-020-3382-4> (visited on 10/30/2020).
- Tekedar, Hasan C. et al. (July 2020). "Identification of Antimicrobial Resistance Determinants in *Aeromonas veronii* Strain MS-17-88 Recovered From Channel Catfish (*Ictalurus punctatus*)". In: *Frontiers in Cellular and Infection Microbiology* 10, p. 348. ISSN: 2235-2988. DOI: 10.3389/fcimb.2020.00348. URL: <https://www.frontiersin.org/article/10.3389/fcimb.2020.00348/full> (visited on 10/30/2020).
- Thrash, Adam and Marilyn L Warburton (July 2020). "A Pathway Association Study Tool for GWAS Analyses of Metabolic Pathway Information". en. In: *Journal of Visualized Experiments* 161, p. 61268. ISSN: 1940-087X. DOI: 10.3791/61268. URL: <https://www.jove.com/video/61268/a-pathway-association-study-tool-for-gwas-analyses-metabolic-pathway> (visited on 10/30/2020).
- Thrash, Adam, Juliet D. Tang, et al. (Jan. 2020). "PAST: The Pathway Association Studies Tool to Infer Biological Meaning from GWAS Datasets". en. In: *Plants* 9.1, p. 58. ISSN: 2223-7747. DOI: 10.3390/plants9010058. URL: <https://www.mdpi.com/2223-7747/9/1/58> (visited on 10/30/2020).
- Rycroft, Taylor (2019). "AOPERA: A proposed methodology and inventory of effective tools to link chemicals to adverse outcome pathways". In: *ALTEX*. ISSN: 1868596X. DOI: 10.14573/altex.1906201. URL: <https://www.altex.org/index.php/altex/article/view/1300> (visited on 10/30/2020).
- Feugang, Jean M. et al. (Oct. 2019). "Exploring potential biomarkers for boar sperm cryopreservation using RNA-sequencing technology". en. In: *Theriogenology* 137, p. 135. ISSN: 0093691X. DOI: 10.1016/j.theriogenology.2019.05.073. URL: <https://linkinghub.elsevier.com/retrieve/pii/S0093691X19302122> (visited on 10/30/2020).
- Thrash, Adam, Mark Arick, Robyn A. Barbato, et al. (Mar. 2019). "Keanu: a novel visualization tool to explore biodiversity in metagenomes". en. In: *BMC Bioinformatics* 20.S2, p. 103. ISSN: 1471-2105. DOI: 10.1186/s12859-019-2629-4. URL: <https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-019-2629-4> (visited on 10/30/2020).
- Li, Hui et al. (June 2019). "Leveraging GWAS data to identify metabolic pathways and networks involved in maize lipid biosynthesis". en. In: *The Plant Journal* 98.5, pp. 853–863. ISSN: 0960-7412, 1365-313X. DOI: 10.1111/tpj.14282. URL: <https://onlinelibrary.wiley.com/doi/abs/10.1111/tpj.14282> (visited on 10/30/2020).
- Grover, Corrinne E, Mark A Arick, Adam Thrash, et al. (Jan. 2019). "Insights into the Evolution of the New World Diploid Cottons (*Gossypium*, Subgenus *Houzingenia*) Based on Genome Sequencing". en. In: *Genome Biology and Evolution* 11.1. Ed. by Bill Martin, pp. 53–71. ISSN: 1759-6653. DOI: 10.1093/gbe/evy256. URL: <https://academic.oup.com/gbe/article/11/1/53/5201035> (visited on 10/30/2020).
- Warburton, Marilyn L. et al. (Mar. 2018). "Genome-Wide Association and Metabolic Pathway Analysis of Corn Earworm Resistance in Maize". en. In: *The Plant Genome* 11.1, pp. 1–8. ISSN: 1940-3372, 1940-3372. DOI: 10.3835/plantgenome2017.08.0069. URL: <https://onlinelibrary.wiley.com/doi/abs/10.3835/plantgenome2017.08.0069> (visited on 10/30/2020).
- Thrash, Adam, Mark Arick, and Daniel G. Peterson (May 2018). "Quack: A quality assurance tool for high throughput sequence data". en. In: *Analytical Biochemistry* 548, pp. 38–43. ISSN: 00032697. DOI: 10.1016/j.ab.2018.01.028. URL: <https://linkinghub.elsevier.com/retrieve/pii/S0003269718300630> (visited on 10/30/2020).
- Grover, Corrinne E, Mark A Arick, Justin L Conover, et al. (Dec. 2017). "Comparative Genomics of an Unusual Biogeographic Disjunction in the Cotton Tribe (Gossypieae) Yields Insights into Genome Downsizing". en. In: *Genome Biology and Evolution* 9.12, pp. 3328–3344. ISSN: 1759-6653. DOI: 10.1093/gbe/evx248. URL: <https://academic.oup.com/gbe/article/9/12/3328/4669810> (visited on 10/30/2020).

Conference Proceedings

- Rice, Jonathan et al. (Sept. 2015). "Investigating genome similarity through cross mapping percentage". In: *Proceedings of the 6th ACM Conference on Bioinformatics, Computational Biology and Health Informatics*. BCB '15. Atlanta, Georgia: Association for Computing Machinery, pp. 543–544. ISBN: 9781450338530. DOI: 10.1145/2808719.2811456. URL: <https://doi.org/10.1145/2808719.2811456> (visited on 10/30/2020).