

CURRICULUM VITAE

Andrew D. Thrasher, PhD

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EDUCATION

PhD	University of Notre Dame Computer Science and Engineering Research Area: Novel methods for massive biological datasets leveraging distributed computing.	Notre Dame, IN	2011 – 2013
MS	University of Notre Dame Computer Science and Engineering	Notre Dame, IN	2009 – 2013
BA	Anderson University Majors: Computer Science, Mathematics, and Physics	Anderson, IN	2005 – 2009

PROFESSIONAL EXPERIENCE

St. Jude Children's Research Hospital Senior Software Engineer	Memphis, TN	2013 – present
<ul style="list-style-type: none">• Interface with scientists in a variety of fields to implement and analyze various genomic datasets leveraging distributed computing resources• Implemented automation of computational analyses to enable clinical genomics platform (Bash, Perl, Python, SQL, R)• Primary responsibility for clinical genomics automation and processing which has generated over 2PB of data in less than two years. Oversee the development lifecycle in this environment. Interface with a variety of stakeholders including senior leadership, laboratory personnel, clinic personnel, and research departments.• Primary responsibility for handling processing of genomic data from 3000 cancer survivors.		
University of Notre Dame Graduate Assistant	Notre Dame, IN	2009 – 2013
<ul style="list-style-type: none">• Implemented novel bioinformatics applications leveraging distributed computing resources and frameworks and contributed to a leading distributed computing set of tools. (Perl, SQL, C, R)• Led laboratory sessions and problem sessions for Fundamentals of Computing II and Discrete Mathematics		
Battelle National Biodefense Institute (BNBI) / National Biodefense Analysis and Countermeasures Center (NBACC) Summer Research Associate	Frederick, MD	2011
<ul style="list-style-type: none">• Developed methods for high-throughput detection of bacterial pathogens from next generation sequencing data. Utilizing maximal exact match signatures, this method		

detected and classified bacterial pathogens in complex, environmental DNA samples. This method was faster, produced a more precise taxonomical classification, and was more sensitive than competing methods. (**Perl**)

Software Research Center

Anderson, IN

2007 - 2009

Project Manager

- Managed development projects and staff for internal and external client projects including software that handled all incoming packages to campus and software used across campus to create the master course schedule. (**C++**, **VB**, **HTML**, **SQL**)

PROFICIENCIES

- Perl, Bash, SQL, C/C++, C#, VB.NET, Python, R
- Linux (RHEL), Windows and OSX operating systems
- PostgreSQL, SQL Server, MySQL
- Distributed computing, bioinformatics, data analytics
- Business analysis, software design and architecture, technical leadership, research

PUBLICATIONS

- Zhaoming Wang, Carmen L. Wilson, John Easton, **Andrew Thrasher**, Heather Mulder, Qi Liu, Dale J. Hedges, Shuoguo Wang, Michael Rusch, Michael Edmonson, Shawn Levy, Jennifer Q. Lanctot, Eric Caron, Kyla Shelton, Kelsey Currie, Matt Lear, Aman Patel, Celeste Rosencrance, Ying Shao, Bhavin Vadodaria, Donald Yergeau, Yadav Sapkota, Russell J. Brooke, Wonjong Moon, Evadnie Rampersaud, Xiaotu Ma, Ti-Cheng Chang, Stephen V. Rice, Cynthia Pepper, Xin Zhou, Xiang Chen, Wenan Chen, Angela Jones, Braden Boone, Mathew J. Ehrhardt, Mathew J. Krasin, Rebecca M. Howell, Nicholas S. Phillips, Courtney Lewis, Deokumar Srivastava, Chimene A. Kesserwan, Gang Wu, Kim E. Nichols, James R. Downing, Melissa M. Hudson, Yutaka Yasui, Leslie L. Robison, Jinghui Zhang, *Genetic Risk for Subsequent Neoplasms among Long-term Survivors of Childhood Cancer in the St. Jude Lifetime Cohort*, Journal of the American Medical Association, *under review*.
- Michael Rusch, Joy Nakitandwe, Sheila Shurtleff, Scott Newman, Zhaojie Zhang, Michael Edmonson, Mathew Parker, Yuannian Jiao, Xiaotu Ma, Jiali Gu, Michael Walsh, Jared Becksfort, **Andrew Thrasher**, Yongjin Li, James McMurry, Erin Hedlund, Aman Patel, John Easton, Donald Yergeau, Bhavin Vadodaria, Ruth Tatevossian, Susana Raimondi, Dale Hedges, Xiang Chen, Rose McGee, David Ellison, Tanja Gruber, James Downing, and Jinghui Zhang, *Clinical Cancer Genomic Profiling by “Total Sequencing” of Whole Genome, Whole Exome and Transcriptome*, Nature Communications, *under review*.
- Zhaoming Wang, Carmen L. Wilson, John Easton, Dale Hedges, Qi Liu, Gang Wu, Michael Rusch, Michael Edmonson, Shawn Levy, Jennifer Q. Lanctot, Eric Caron, Kyla

Shelton, Kelsey Currie, Matthew Lear, Heather L. Mulder, Donald Yergeau, Celeste Rosencrance, Bhavin Vadodaria, Yadav Sapkota, Russell J. Brooke, Wonjong Moon, Evadnie Rampersaud, Xiaotu Ma, Shuoguo Wang, Ti-Cheng Chang, Stephen Rice, **Andrew Thrasher**, Aman Patel, Cynthia Pepper, Xin Zhou, Xiang Chen, Wenan Chen, Angela Jones, Braden Boone, Deo Kumar Srivastava, Chimene A. Kesserwan, Kim E. Nichols, James R. Downing, Melissa M. Hudson, Yutaka Yasui, Leslie L. Robison and Jinghui Zhang, *Germline mutations in cancer predisposition genes and risk for subsequent neoplasms among long-term survivors of childhood cancer in the St. Jude Lifetime Cohort*, AACR Annual Meeting, 2017.

- **Andrew Thrasher**, Zhaoming Wang, Heather Mulder, Dale Hedges, Ti-Cheng Chang, Celeste Rosencrance, John Easton, Leslie Robison, and Jinghui Zhang, *Saliva is a good alternative DNA source for whole genome and/or whole exome sequencing*, American Society of Human Genetics, 2016.
- Elizabeth M Azzato, Michael Rusch, Sheila Shurtleff, Joy Nakitandwe, Zhaojie Zhang, Dale Hedges, Scott Newman, Michael Edmonson, **Andrew Thrasher**, Jared Becksfort, Chimene Kesserwan, Susana Raimondi, Kim E Nichols, David W Ellison, Jinghui Zhang, and James Downing, *Clinical Utilization of Whole-Genome, Whole-Exome and Transcriptome Sequencing Integrative Analysis for Pediatric Oncology Molecular Diagnostics*, Journal Of Molecular Diagnostics, Volume 18, Issue 6, 2016.
- Zhaoming Wang, Yutaka Yasui, Kirsten K. Ness, Carmen L. Wilson, Deo Kumar Srivastava, Michael Rusch, **Andrew Thrasher**, Melissa M. Hudson, Jinghui Zhang, and Leslie L. Robison, *Telomere Length and Accelerated Aging in Adult Survivors of Childhood Cancer: a report from the St. Jude Lifetime Cohort*, International Congress Of Human Genetics (ICHG), 2016.
- Michael Rusch, Joy Nakitandwe, Zhaojie Zhang, Michael N. Edmonson, Matthew Parker, Xiaotu Ma, Jared Becksfort, **Andrew Thrasher**, Yongjin Li, Erin Hedlund, Aman Patel, John Easton, Donald Yergeau, Bhavin Vandoria, Xiang Chen, Tanja A. Gruber, Rose McGee, David Ellison, Sheila Shurtleff, James R Downing, and Jinghui Zhang, *Molecular diagnosis for pediatric cancer through integrative analysis of whole-genome, whole-exome and transcriptome sequencing*, American Association for Cancer Research (AACR) Annual Meeting, 2016.
- **Andrew Thrasher**, Zachary Musgrave, Brian Kachmarck, Douglas Thain and Scott Emrich, *Scaling Up Genome Annotation Using MAKER and Work Queue*, Int. J. of Bioinformatics Research and Applications (ICCABS 2012 Special Issue), Volume 10, Issue 4-5, 2014
- Dinesh Rajan, **Andrew Thrasher**, Badi' Abdul-Wahid, Jesus A Izaguirre, Scott Emrich, and Douglas Thain, *Case Studies in Designing Elastic Applications*, 13th IEEE/ACM International Symposium on Cluster, Cloud and Grid Computing (CCGrid), 2013

- **Andrew Thrasher**, Zachary Musgrave, Douglas Thain and Scott Emrich, Shifting the Bioinformatics Computing Paradigm: A Case Study in Parallelizing Genome Annotation Using MAKER and Work Queue, 2nd IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS), 2012
- Christopher Moretti, **Andrew Thrasher**, Li Yu, Michael Olson, Scott Emrich and Douglas Thain, A Framework for Scalable Genome Assembly on Clusters, Clouds, and Grids, Transactions on Parallel and Distributed Systems, Volume 23, Issue 12, 2012.
- Karine Megy, Scott J Emrich, Daniel Lawson, David Campbell, Emmanuel Dialynas, Daniel ST Hughes, Gautier Koscielny, Christos Louis, Robert M MacCallum, Seth N Redmond, Andrew Sheehan, Pantelis Topalis, Derek Wilson and the **VectorBase Consortium**, VectorBase: improvements to a bioinformatics resource for invertebrate vector genomics, Nucleic Acids Research, Volume 40, Issue D1
- Peter Bui, Li Yu, **Andrew Thrasher**, Rory Carmichael, Irena Lanc, and Douglas Thain, Scripting distributed scientific workflows using Weaver, Concurrency and Computation: Practice and Experience, Volume 24, Issue 15, 2012.
- Li Yu, Christopher Moretti, **Andrew Thrasher**, Scott Emrich, Kenneth Judd, and Douglas Thain, Harnessing Parallelism in Multicore Clusters with the All-Pairs, Wavefront, and Makeflow Abstractions, Journal of Cluster Computing, September, 2010.
- **Andrew Thrasher**, Rory Carmichael, Peter Bui, Li Yu, Douglas Thain, and Scott Emrich, Taming Complex Bioinformatics Workflows with Weaver, Makeflow, and Starch, 5th Workshop of Workflows in Support of Large-Scale Science, at Supercomputing 2010
- **Andrew Thrasher**, Irena Lanc, Douglas Thain, and Scott Emrich, Makeflow for Bioinformatics, 2010 International conference on Intelligent Systems for Microbiology, Boston, MA.

REFERENCES

Michael Rusch (901-595-7075, michael.rusch@stjude.org)

Director of Bioinformatics Software Development, Computational Biology
St. Jude Children's Research Hospital

Scott Emrich, PhD (574-631-0353, semrich@nd.edu)

Research Assistant Professor, Computer Science and Engineering
University of Notre Dame

Gang Wu, PhD (901-595-8126, gang.wu@stjude.org)

DNA Group Lead, Computational Biology
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