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Education

- 2015 **Ph.D., Computer Science**, *University of Maryland*, College Park, MD, USA.
- 2009 **M.S., Computer Science**, *University of Maryland*, College Park, MD, USA.
- 2003 **B.S., Computer Science**, *Rochester Institute of Technology*, Rochester, NY, USA.
Honors computer science program.

Doctoral dissertation

- title *Computational Methods to Advance Phylogenomic Workflows*
- advisor Dr. Michael Cummings
- abstract Phylogenomics refers to the use of genome-scale data in phylogenetic analysis. There are several methods for acquiring genome-scale, phylogenetically-useful data from an organism that avoid sequencing the entire genome, thus reducing cost and effort, and enabling one to sequence many more individuals. In this dissertation we focus on one method in particular — RNA sequencing — and the concomitant use of assembled protein-coding transcripts in phylogeny reconstruction. Phylogenomic workflows involve tasks that are algorithmically and computationally demanding, in part due to the large amount of sequence data typically included in such analyses. This dissertation applies techniques from computer science to improve methodology and performance associated with phylogenomic workflow tasks such as sequence classification, transcript assembly, orthology determination, and phylogenetic analysis. While the majority of the methods developed in this dissertation can be applied to the analysis of diverse organismal groups, we primarily focus on the analysis of transcriptome data from Lepidoptera (moths and butterflies), generated as part of a collaboration known as “Leptree”.

Master's thesis

- title *The Lattice Project: A Multi-model Grid Computing System*
- advisor Dr. Michael Cummings
- abstract This thesis presents The Lattice Project, a system that combines multiple models of grid computing. Grid computing is a paradigm for leveraging multiple distributed computational resources to solve fundamental scientific problems that require large amounts of computation. The system combines the traditional “service” model of grid computing with the “desktop” model of grid computing, and is thus capable of utilizing diverse resources such as institutional desktop computers, dedicated computing clusters, and machines volunteered by the general public to advance science. The production grid system includes a fully-featured user interface, support for a large number of popular scientific applications, a robust grid-level scheduler, and novel enhancements such as a grid-wide file caching scheme. A substantial amount of scientific research has already been completed using The Lattice Project.

Professional and academic experience

- 2016–present **Bioinformatics Principal Investigator**, NBACC, Fort Detrick, MD, USA.
- 2015–2016 **Post-Doctoral Associate**, *University of Maryland*, College Park, MD, USA.
- 2004–2015 **Faculty Research Assistant**, *University of Maryland*, College Park, MD, USA.
Laboratory of Molecular Evolution, Center for Bioinformatics and Computational Biology.
- Performed molecular data analyses for the Leptree project, which seeks to understand the evolutionary relationships of moths and butterflies.
 - Lead developer of The Lattice Project, a multi-model grid computing system, featuring the GARLI web service found at molecularevolution.org.
- 2003–2016 **Course Instructor**, *Workshop on Molecular Evolution, Workshop on Genomics, and Workshop on Population and Speciation Genomics.*
- Duties included teaching, setting up the computing environment, providing scientific application support, and administering the workshop web site at evomics.org.
- 2005–2006 **GRE Test Preparation Instructor**, *Transemantics, Inc.*, Washington, D.C., USA.
- Designed and administered GRE test preparation courses.
- 2001–2003 **Software and Web Developer**, *Bureau Veritas e-Business*, Buffalo, NY, USA.
- Our group was responsible for all company web sites, both internal and external.

Publications

Book chapters

- [1] AL Bazinet and MP Cummings. The Lattice Project: a Grid research and production environment combining multiple Grid computing models. In MHW Weber, editor, *Distributed & Grid Computing — Science Made Transparent for Everyone. Principles, Applications and Supporting Communities*, chapter 1, pages 2–13. Rechenkraft.net, Marburg, 2008.
- [2] DS Myers, AL Bazinet, and MP Cummings. Expanding the reach of Grid computing: combining Globus- and BOINC-based systems. In E-G Talbi and AY Zomaya, editors, *Grids for Bioinformatics and Computational Biology*, Wiley Book Series on Bioinformatics: Computational Techniques and Engineering, chapter 4, pages 71–85. Wiley-Interscience, Hoboken, 2008.

Conference papers

- [3] Adam L. Bazinet and Michael P. Cummings. Computing the tree of life: Leveraging the power of desktop and service grids. *2011 IEEE International Symposium on Parallel and Distributed Processing Workshops and PhD Forum*, pages 1896–1902, 2011.

Journal articles

- [4] Jacquelyn S. Meisel, Daniel J. Nasko, Brian Brubach, Victoria Cepeda-Espinoza, Jessica Chopyk, Héctor Corrada-Bravo, Marcus Fedarko, Jay Ghurye, Kiran Javkar, Nathan D. Olson, Nidhi Shah, Sarah M. Allard, Adam L. Bazinet, Nicholas H. Bergman, Alexis Brown, J. Gregory Caporaso, Sean Conlan, Jocelyne DiRuggiero, Samuel P. Forry, Nur A. Hasan, Jason Kralj, Paul M. Luethy, Donald K. Milton, Brian D. Ondov, Sarah Preheim, Shashikala Ratnayake, Stephanie M. Rogers, M. J. Rosovitz, Eric G. Sakowski, Nils Oliver Schliebs, Daniel D. Sommer, Krista L. Ternus, Gherman Uritskiy, Sean X. Zhang, Mihai Pop, and Todd J. Treangen. Current progress and future opportunities in applications of bioinformatics for biodefense and pathogen detection: report from the Winter Mid-Atlantic Microbiome Meet-up, College Park, MD, January 10, 2018. *Microbiome*, 6(1):197, Nov 2018.
- [5] Adam L. Bazinet, Brian D. Ondov, Daniel D. Sommer, and Shashikala Ratnayake. BLAST-based validation of metagenomic sequence assignments. *PeerJ*, 6:e4892, May 2018.
- [6] Odile Loreille, Shashikala Ratnayake, Adam L. Bazinet, Timothy B. Stockwell, Daniel D. Sommer, Nadin Rohland, Swapan Mallick, Philip L.F. Johnson, Pontus Skoglund, Anthony J. Onorato, Nicholas H. Bergman, David Reich, and Jodi A. Irwin. Biological sexing of a 4000-year-old egyptian mummy head to assess the potential of nuclear dna recovery from the most damaged and limited forensic specimens. *Genes*, 9(3):135, March 2018.
- [7] Jessica A. Goodheart, Adam L. Bazinet, Ángel Valdés, Allen G. Collins, and Michael P. Cummings. Prey preference follows phylogeny: evolutionary dietary patterns within the marine gastropod group Cladobranchia (Gastropoda: Heterobranchia: Nudiobranchia). *BMC Evolutionary Biology*, 17(1):221, Oct 2017.

- [8] Adam L. Bazinet. Pan-genome and phylogeny of *Bacillus cereus sensu lato*. *BMC Evolutionary Biology*, 17(1):176, Aug 2017.
- [9] William T. White, Shannon Corrigan, Lei Yang, Aaron C. Henderson, Adam L. Bazinet, David L. Swofford, and Gavin J. P. Naylor. Phylogeny of the manta and devilrays (Chondrichthyes: mobulidae), with an updated taxonomic arrangement for the family. *Zoological Journal of the Linnean Society*, 2017.
- [10] Shannon Corrigan, Pierpaolo Maisano Delser, Corey Eddy, Clinton Duffy, Lei Yang, Chenhong Li, Adam L. Bazinet, Stefano Mona, and Gavin J.P. Naylor. Historical introgression drives pervasive mitochondrial admixture between two species of pelagic sharks. *Molecular Phylogenetics and Evolution*, 110:122–126, 2017.
- [11] Daniel H. Huson, Rewati Tappu, Adam L. Bazinet, Chao Xie, Michael P. Cummings, Kay Nieselt, and Rohan Williams. Fast and simple protein-alignment-guided assembly of orthologous gene families from microbiome sequencing reads. *Microbiome*, 5(1):11, 2017.
- [12] Adam L. Bazinet, Kim T. Mitter, Donald R. Davis, Erik J. Van Nieuwerkerken, Michael P. Cummings, and Charles Mitter. Phylotranscriptomics resolves ancient divergences in the Lepidoptera. *Systematic Entomology*, 2016.
- [13] Jerome C. Regier, Charles Mitter, Kim Mitter, Michael P. Cummings, Adam L. Bazinet, Winifred Hallwachs, Daniel H. Janzen, and Andreas Zwick. Further progress on the phylogeny of Noctuoidea (Insecta: Lepidoptera) using an expanded gene sample. *Systematic Entomology*, 42(1):82–93, 2016.
- [14] Jessica A. Goodheart, Adam L. Bazinet, Allen G. Collins, and Michael P. Cummings. Relationships within Cladobranhia (Gastropoda: Nudibranchia) based on RNA-Seq data: an initial investigation. *Royal Society Open Science*, 2(9), 2015.
- [15] Adam L. Bazinet and Michael P. Cummings. Subdividing long-running, variable-length analyses into short, fixed-length BOINC workunits. *Journal of Grid Computing*, 14(3):429–441, 2015.
- [16] Adam L. Bazinet, Derrick J. Zwickl, and Michael P. Cummings. A gateway for phylogenetic analysis powered by grid computing featuring GARLI 2.0. *Systematic Biology*, 2014.
- [17] Adam L. Bazinet, Michael P. Cummings, Kim T. Mitter, and Charles W. Mitter. Can RNA-Seq resolve the rapid radiation of advanced moths and butterflies (Hexapoda: Lepidoptera: Apoditrysia)? An exploratory study. *PLoS ONE*, 8(12):e82615, 12 2013.
- [18] Jerome C. Regier, Charles Mitter, Andreas Zwick, Adam L. Bazinet, Michael P. Cummings, Akito Y. Kawahara, Jae-Cheon Sohn, Derrick J. Zwickl, Soowon Cho, Donald R. Davis, Joaquin Baixeras, John Brown, Cynthia Parr, Susan Weller, David C. Lees, and Kim T. Mitter. A large-scale, higher-level, molecular phylogenetic study of the insect order Lepidoptera (moths and butterflies). *PLoS ONE*, 8(3):e58568, 03 2013.
- [19] Adam L. Bazinet and Michael P. Cummings. A comparative evaluation of sequence classification programs. *BMC Bioinformatics*, 13:92, 2012.

- [20] Jerome C Regier, Andreas Zwick, Michael P Cummings, Akito Y Kawahara, Soowon Cho, Susan Weller, Amanda Roe, Joaquin Baixeras, John W Brown, Cynthia Parr, Donald R Davis, Marc Epstein, Winifred Hallwachs, Axel Hausmann, Daniel H Janzen, Ian J Kitching, M Alma Solis, Shen-Horn Yen, Adam L Bazinet, and Charles Mitter. Toward reconstructing the evolution of advanced moths and butterflies (Lepidoptera: Ditrysia): an initial molecular study. *BMC Evol Biol*, 9:280, 2009.
- [21] Huyen Tue Dao, Adam L. Bazinet, Robin Berthier, and Ben Shneiderman. NASDAQ velocity and forces: An interactive visualization of activity and change. *J. UCS*, 14(9):1391–1410, 2008.
- [22] AL Bazinet, DS Myers, J Fuetsch, and MP Cummings. Grid Services Base Library: A high-level, procedural application programming interface for writing Globus-based Grid services. *Future Generation Comp Syst*, 23(3):517–522, 2007.

Preprints

- [23] Adam L. Bazinet, Brian D. Ondov, Daniel D. Sommer, and Shashikala Ratnayake. BLAST-based validation of metagenomic sequence assignments. *bioRxiv*, 2017.
- [24] Adam L Bazinet. Pan-genome and phylogeny of *Bacillus cereus sensu lato*. *bioRxiv*, 2017.

Technical reports

- [25] Jessica A. Goodheart, Adam L. Bazinet, Allen G. Collins, and Michael P. Cummings. Phylogeny of Cladobronchia (Gastropoda: Nudibranchia): a total evidence analysis using DNA sequence data from public databases. Technical report, University of Maryland, College Park, 2015.
- [26] Huyen Tue Dao, Adam L. Bazinet, Robin Berthier, and Ben Shneiderman. NASDAQ velocity and forces: An interactive visualization of activity and change. Technical Report HCIL-2007-29, University of Maryland, College Park, 2007.
- [27] Daniel S Myers and Adam L Bazinet. Intercepting arbitrary functions on Windows, UNIX, and Macintosh OS X platforms. *Institute for Advanced Computer Studies. University of Maryland, CS-TR-4585, UMIACS-TR-2004-28*, 2004.

Conferences, workshops, and symposia

- Jan 2019 Mid-Atlantic Microbiome Meet-up: Predictions and the Microbiome. Baltimore, MD, USA.
- Oct 2018 NVIDIA GPU Technology Conference. Washington, D.C., USA.
- July 2018 ISMB 2018. Chicago, IL, USA.
- Jan 2018 Winter Mid-Atlantic Microbiome Meet-up (M3). College Park, MD, USA.
- Nov 2017 Frontiers in Genomics Symposium: A Celebration of the Institute for Genome Sciences' 10th Anniversary. Baltimore, MD, USA.
- July 2017 ISCB DC RSG Bioinformatics, Genomics, and Computational Biology Workshop. College Park, MD, USA.
- June 2017 PacBio User Group Meeting. Baltimore, MD, USA.

June 2017 ASM Microbe. New Orleans, LA, USA.
May 2017 Workshop on Deep Learning. College Park, MD, USA.
May 2017 CAMI/M3 Workshop on Metagenomic Software Validation. College Park, MD, USA.
May 2017 CAMI Hackathon. College Park, MD, USA.
Nov 2016 M3 Workshop and Conference. College Park, MD, USA.
Sept 2016 SMRT Informatics Developers Conference. Gaithersburg, MD, USA.
June 2016 ASM Microbe. Boston, MA, USA.
Jan 2016 Workshop on Population and Speciation Genomics. Český Krumlov, Czech Republic.
Sept 2015 Methods and Analysis of Coevolution Across Scales: From Within Genomes to Disease and Environments. Smithsonian Institution, Washington, D.C., USA.
Jan 2015 Workshop on Molecular Evolution. Český Krumlov, Czech Republic.
Sept 2014 Genome-Scale Phylogenetics: Analysing the Data. Smithsonian Institution, Washington, D.C., USA.
Jan 2014 Workshop on Genomics. Český Krumlov, Czech Republic.
Nov 2013 Trinity and Tuxedo RNA-Seq Workshop. University of Virginia, Charlottesville, VA, USA.
May 2013 Frontiers in Phylogenetics: “Genome-Scale Phylogenetics”. Smithsonian Institution, Washington, D.C., USA.
Jan 2013 Workshop on Molecular Evolution. Český Krumlov, Czech Republic.
Jan 2013 Workshop on Genomics. Český Krumlov, Czech Republic.
Jan 2012 Workshop on Genomics. Český Krumlov, Czech Republic.
Oct 2011 Workshop on Genomics. Smithsonian Institution, Washington, D.C., USA.
Aug 2011 Workshop on Molecular Evolution. Colorado State University, Fort Collins, CO, USA.
July 2011 Workshop on Genomics. Colorado State University, Fort Collins, CO, USA.
May 2011 5th Workshop on Desktop Grids and Volunteer Computing Systems (PCGrid 2011). Anchorage, AK, USA.
Jan 2011 Workshop on Molecular Evolution. Český Krumlov, Czech Republic.
Jan 2011 Workshop on Genomics. Český Krumlov, Czech Republic.
Aug 2010 The 6th BOINC Workshop. King’s College, London, England.
July 2010 Workshop on Molecular Evolution. Woods Hole, MA, USA.
Mar 2010 GlobusWorld 2010. Argonne National Laboratory, Chicago, IL, USA.
Jan 2010 Workshop on Molecular Evolution. Český Krumlov, Czech Republic.
Sept 2009 9th Workshop on Algorithms in Bioinformatics (WABI 2009). University of Pennsylvania, Philadelphia, PA, USA.
July 2009 Workshop on Molecular Evolution. Woods Hole, MA, USA.
June 2009 Workshop on Molecular Evolution. Smithsonian Institution, Washington, D.C., USA.
Jan 2009 Workshop on Molecular Evolution. Český Krumlov, Czech Republic.
Nov 2008 GlobusWorld 2008. Austin, TX, USA.
July 2008 Workshop on Molecular Evolution. Woods Hole, MA, USA.

- Feb 2008 Workshop on Molecular Evolution.
Centers for Disease Control and Prevention, Atlanta, GA, USA.
- July 2007 Workshop on Molecular Evolution. Woods Hole, MA, USA.
- Sept 2006 GlobusWorld 2006. Washington, D.C., USA.
- July 2006 Workshop on Molecular Evolution. Woods Hole, MA, USA.
- Feb 2005 GlobusWorld 2005. Boston, MA, USA.
- July 2004 Workshop on Molecular Evolution. Woods Hole, MA, USA.
- July 2003 Workshop on Molecular Evolution. Woods Hole, MA, USA.

Presentations

- Mar 2014 *Lepidopteran phylogenomics using RNA-Seq.*
University of Maryland, College Park, MD, USA.
- Feb 2013 *Phylo-transcriptomics of Lepidoptera.*
Hollings Marine Laboratory, Charleston, SC, USA.
- Sept 2012 *The Lattice Project: a grid system for phylogenetics.*
University of Delaware, Newark, DE, USA.
- Nov 2011 *The Lattice Project: a grid system for phylogenetics.*
McDaniel College, Westminster, MD, USA.
- Feb 2011 *Applications of next-generation sequencing (NGS) to phylogenomics.*
National Institutes of Health, Bethesda, MD, USA.
- Nov 2009 *The Lattice Project: a multi-model grid computing system.*
Smithsonian Institution, Washington, D.C., USA.
- Jan 2007 *The Lattice Project: a computational grid system.*
University of Maryland University College, Adelphi, MD, USA.
- Oct 2006 *The Lattice Project: our efforts at grid computing.*
University System of Maryland, Adelphi, MD, USA.

■ Reviewing of manuscripts for journals

- *BMC Bioinformatics*
- *BMC Evolutionary Biology*
- *BMC Microbiology*
- *Current Microbiology*
- *European Journal of Clinical Microbiology & Infectious Diseases*
- *Frontiers in Microbiology*
- *Future Generation Computer Systems*
- *Genome Biology*
- *Infection, Genetics and Evolution*
- *Information Sciences*
- *Journal of Parallel and Distributed Computing*
- *PLOS Computational Biology*
- *PLOS ONE*
- *PeerJ*
- *Scientific Reports*

■ Mentoring and supervising

Graduate students

- 2015 Ashwin Moodumane, University of Maryland
- 2010 Jingxin Han, Bowie State University
- 2004 Deji Akinyemi, University of Maryland

Undergraduate students

- 2015–2016 Benjamin Ferraro, University of Maryland
- 2015–2016 Jordan Kiesel, University of Maryland
- 2014–2015 Kevin Young, University of Maryland
- 2015 Mara Meng Cai, University of Maryland
- 2014–2015 Yue (Monica) Zhu, University of Maryland
- 2010–2013 Yevgeny Deviatov, University of Maryland
- 2010–2012 Derrick Hinkle, University of Maryland
- 2010–2011 Philip Davis, University of Maryland
- 2009–2011 Barry Dutton, University of Maryland
- 2010 Kareem Johnson, Bowie State University
- 2010 Bradley Senft, University of Maryland
- 2008–2009 Pratik Khatavkar, Rochester Institute of Technology
- 2006–2007 Andrew Younge, Rochester Institute of Technology
- 2005–2006 Matthew Chan, Rochester Institute of Technology
- 2005–2006 Phuc (Phil) Huynh, University of Maryland

- 2005–2006 Danh Luong, Rochester Institute of Technology
- 2004–2005 Stephen McLellan, Rochester Institute of Technology
- 2004–2005 Christopher Milliron, Rochester Institute of Technology
- 2004 Jonathan Howard, University of Maryland

High school students

- 2014 Tonle Bloomer, Montgomery Blair High School
- 2014 Navid Chowdhury, Montgomery Blair High School
- 2014 Puriwat Lahpong, Montgomery Blair High School
- 2014 Dave Qin, Poolesville High School

Computer skills

- operating systems Mac OS X, MS Windows, CentOS, Red Hat Enterprise Linux, Ubuntu Linux, Yellow Dog Linux, other Unix-based operating systems
- languages ActionScript, Bash, C, C++, CSS, CUDA, HTML, JSP, Java, JavaScript, jQuery, LaTeX, Lisp, OCaml, OpenGL, PHP, Perl, Python, R, RDF/OWL, SQL, Visual Basic, XML
- software Action Method, Adobe CS, Adobe Flex Builder, Amazon EC2, Anaconda, Apache, Asana, BOINC, BibDesk, CVS, Condor, Cygwin, Drupal, Eclipse, Emacs, Git/GitLab, Globus Toolkit, Keynote, LibreOffice, MS Office, Mattermost, MySQL, OpenOffice, Overleaf, PBS/Torque/Maui, PostgreSQL, phpMyAdmin, R, SLURM, SVN, Shiny, Slack, Snake-make, Sun Grid Engine, TeXworks, Vim, VMware, VirtualBox, MS Visual Studio, Word-Press
- scientific software ABySS/Trans-ABySS, AliView, BEAST, BLAST, BWA, Bandage, BioPerl, Bowtie, Bracken, CARMA, CLARK, COGsoft, ClonalFrameML, Clustal W/X, Cufflinks, DIAMOND, DendroPy, Ensembl, FASTA, FigTree, GARLI, Glimmer, Gubbins, HaMStR, HMMER, Hawk-eye, IM, Infernal, Kraken, Krona, LAMARC, Lambda, MAFFT, MALT, MARXAN, MDIV, MEGAN, MG-RAST, MINIMUS, MUMmer, MUSCLE, Mash, MetAMOS, MetaPhyler, Migrate-N, ModelTest, MrBayes, NASP, NCBI resources, OrthoMCL, PAML, PATRIC, PAUP*, PHYLIP, PRANK, PhyML, Phycas, PhyloPythiaS, PhyloTreePruner, PhymmBL, Prokka, (Meta)QUAST, R packages (ape, genealogicalSorting, randomForest), RAIphy, RAXML, Roary, SAMtools, Scoary, SeaView, SplitsTree, Structure, T-Coffee, TopHat, Trinity, UniProt, Xander

Spoken languages

- English native speaker
- French limited working proficiency