

Hyrum D. Carroll, PhD

Center for Computational Science
Department of Computer Science
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Full-Time Professional Positions

2011–present **Assistant Professor** — Department of Computer Science
Middle Tennessee State University, Murfreesboro, Tennessee

2008–2011 **Postdoctoral Fellow** — National Center for Biotechnology Information
National Institutes of Health, Bethesda, Maryland

Part-Time Professional Positions

2015–present **Special Volunteer** — National Center for Biotechnology Information
National Institutes of Health, Bethesda, Maryland

2012–2015 **Scientific Visitor** — National Center for Biotechnology Information
National Institutes of Health, Bethesda, Maryland

2011 **Instructor** — *Theoretical and Applied Bioinformatics* (Spring Semester)
Foundation for Advanced Education in the Sciences Graduate School, Bethesda, Maryland

2007 **Instructor** — *Introduction to Computer Systems* (Summer Term)
Department of Computer Science, Brigham Young University, Provo, Utah

Education

2005–2008 **Doctorate of Philosophy**, Computer Science
Brigham Young University, Provo, Utah
Dissertation: *Biologically Relevant Multiple Sequence Alignment*

2003–2004 **Master of Science**, Computer Science
Brigham Young University, Provo, Utah
Thesis: *A Trace-Driven Simulator For Palm OS Devices*

1997–2002 **Bachelor of Science**, Computer Engineering
Brigham Young University, Provo, Utah

Funding

2016 Optimization and accessibility of the ecoTTC database
Co-PI, Funded by the Health and Environmental Sciences Institute, \$20,000.00

2013 Identification of Fragmentary Greek Papyri
PI, Funded by MTSU, \$7,350.41

Publications (Names of advised students are underlined)

Peer-reviewed Journal Articles

1. **H.D. Carroll**, A.C. Williams, A.G. Davis, and J.L. Spouge. 2015. Improving Retrieval Efficacy of Homology Searches using the False Discovery Rate. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* **12**, 531–537. ([web](#), [pdf](#))
2. B.T. Grimes, A.K. Sisay, **H.D. Carroll**, and A.B. Cahoon. 2014. Deep sequencing of the tobacco mitochondrial transcriptome reveals expressed ORFs and numerous editing sites outside coding regions. *BMC Genomics* **15**:31. ([web](#), [pdf](#))
3. T. O'Connor, K. Sundberg, **H. Carroll**, M. Clement, and Q. Snell. 2010. Analysis of long branch extraction and long branch shortening. *BMC Genomics* **11**(Suppl 2):S14. ([web](#), [pdf](#))
4. **H.D. Carroll**, M.G. Kann, S.L. Sheetlin, and J.L. Spouge. 2010. Threshold Average Precision (TAP- k): A Measure of Retrieval Efficacy Designed for Bioinformatics. *Bioinformatics* **26**:14, 1708–1713. ([web](#), [pdf](#))
5. K. Clement, N. Gustafson, A. Berbert, **H. Carroll**, C. Merris, A. Olsen, M. Clement, Q. Snell, J. Allen, and R.J. Roper. 2010. PathGen: A Transitive Gene Pathway Generator. *Bioinformatics* **26**:3, 423–425. ([web](#), [pdf](#))
6. **H. Carroll**, A.R. Teichert, J. Krein, K. Sundberg, Q. Snell, and M. Clement. 2009. An open source phylogenetic search and alignment package. *International Journal of Bioinformatics Research and Applications* **5**:3, 349–364. ([web](#), [pdf](#))
7. K. Sundberg, T. O'Connor, **H. Carroll**, M. Clement, and Q. Snell. 2008. Parsimony accelerated Maximum Likelihood searches. *International Journal of Computational Biology and Drug Design* **1**:1, 74–87. ([web](#), [pdf](#))
8. **H.D. Carroll**, P.G. Ridge, M.J. Clement, and Q.O. Snell. 2007. Phylogenies Scores for Exhaustive Maximum Likelihood and Parsimony Scores Searches. *International Journal of Bioinformatics Research and Applications* **3**:4, 493–503. ([web](#), [pdf](#))
9. **H. Carroll**, W. Beckstead, T. O'Connor, M. Ebbert, M. Clement, Q. Snell, and D. McClellan. 2007. DNA Reference Alignment Benchmarks Based on Tertiary Structure of Encoded Proteins. *Bioinformatics* **23**:19, 2648–2649. ([web](#), [pdf](#))

Peer-reviewed Conference Articles

10. A.C. Williams, A. Santarsiero, C. Meccariello, G. Verhasselt, **H.D. Carroll**, J.F. Wallin, D. Obbink, and J. Brusuelas. 2015. Proteus: A Platform for Born Digital Critical Editions of Literary and Subliterary Papyri. In *2015 Digital Heritage* **2**, 453–456. ([web](#), [pdf](#))
11. A.C. Williams, **H.D. Carroll**, J.F. Wallin, J. Brusuelas, L. Fortson, A. Lamblin, and H. Yu. 2014. Identification of Ancient Greek Papyrus Fragments Using Genetic Sequence Alignment Algorithms. In *10th IEEE International Conference on e-Science* **2**, 5–10. ([web](#), [pdf](#))
12. A.C. Williams, J.F. Wallin, H. Yu, M. Perale, **H.D. Carroll**, A. Lamblin, L. Fortson, D. Obbink, C.J. Lintott, and J.H. Brusuelas. 2014. A Computational Pipeline for Crowdsourced Transcriptions of Ancient Greek Papyrus Fragments. In *IEEE International Conference on Big Data*, 100–105. ([web](#), [pdf](#))
13. **H.D. Carroll**, A.C. Williams, A.G. Davis, and J.L. Spouge. 2013. False Discovery Rate for Homology Searches. In *Advances in Bioinformatics and Computational Biology*, J. C. Setubal, and N. F. Almeida (Eds.) **8213**, 194–201. ([web](#), [pdf](#))

14. **H. Carroll**, M. Clement, Q. Snell, and D. McClellan. 2009. ChemAlign: Biologically Relevant Multiple Sequence Alignment Using Physicochemical Properties. In *Proceedings of the IEEE International Conference on Bioinformatics & Biomedicine*, 70–73. ([web](#), [pdf](#))
15. T. O'Connor, K. Sundberg, **H. Carroll**, M. Clement, and Q. Snell. 2009. Analysis of Long Branch Extraction. In *International Conference on Bioinformatics and Computational Biology*, 489–495. ([pdf](#))
16. K. Sundberg, **H. Carroll**, Q. Snell, and M. Clement. 2008. Incomparability of results between phylogenetic search programs. In *International Conference on Bioinformatics and Computational Biology*, 81–84. ([pdf](#))
17. N. Rungta, **H. Carroll**, E. Mercer, R. Roper, M. Clement, and Q. Snell. 2007. Analyzing Gene Relationships for Down Syndrome with Labeled Transition Graphs. In *Proceedings of Formal Methods in Computer Aided Design*, 216–219. ([web](#), [pdf](#))
18. **H. Carroll**, M. Ebbert, M. Clement, and Q. Snell. 2007. PSODA: Better Tasting and Less Filling Than PAUP. In *Proceedings of the 4th Biotechnology and Bioinformatics Symposium*, 74–78. ([pdf](#))
19. J.L. Krein, A.R. Teichert, **H.D. Carroll**, M.J. Clement, and Q.O. Snell. 2007. PsodaScript: Applying Advanced Language Constructs to Open-source Phylogenetic Search. In *Proceedings of the 4th Biotechnology and Bioinformatics Symposium*, 89–94. ([pdf](#))
20. K. Sundberg, T. O'Connor, **H. Carroll**, M. Clement, and Q. Snell. 2007. Using Parsimony to Guide Maximum Likelihood Searches. In *Proceedings of the 7th IEEE International Conference on Bioinformatics and Bioengineering II*, 774–779. ([web](#), [pdf](#))
21. **H. Carroll**, P. Ridge, M. Clement, and Q. Snell. 2006. Effects of Gap Open and Gap Extension Penalties. In *Proceedings of the Third Biotechnology and Bioinformatics Symposium*, 19–23. ([pdf](#))
22. P. Ridge, **H. Carroll**, D. Sneddon, M. Clement, and Q. Snell. 2006. Large Grain Size Stochastic Optimization Alignment. In *Proceedings of the Sixth IEEE Symposium on Bioinformatics and Bio-Engineering*, 127–134. ([web](#), [pdf](#))
23. **H. Carroll**, Q. Snell, M. Clement, and K. Crandall. 2005. Phylogenetic Analysis on Large Sequence Data Sets. In *Proceedings of the Second Biotechnology and Bioinformatics Symposium*, 20–24. ([pdf](#))
24. **H. Carroll**, J.K. Flanagan, and S. Baniya. 2005. A Trace-Driven Simulator For Palm OS Devices. In *Proceedings of IEEE International Symposium on Performance Analysis of Systems and Software*, 157–166. ([web](#), [pdf](#))

Dissertation, Thesis and Book Review

25. **H.D. Carroll**. December 2008. Biologically Relevant Multiple Sequence Alignment. Ph.D. dissertation, Brigham Young University. ([pdf](#))
26. **H. Carroll**. 2008. Dynamic homology and phylogenetic systematics: a unified approach using POY. *Cladistics* **24**:6, 1071–1072. ([web](#), [pdf](#))
27. **H.D. Carroll**. December 2004. A Trace-Driven Simulator for Palm OS Devices. Master's thesis, Brigham Young University. ([pdf](#))

Presentations:

1. “False Discovery Rate for Homology Searches,” *BSB 2013*, Recife, Brazil, Nov. 2013.
2. “Pairwise Sequence Alignment with PSI-GLOBAL,” Computational Science PhD Program Seminar Series at *Middle Tennessee State University*, Murfreesboro, TN, Oct. 2011.
3. “Domain-aware Alignment with PSI-GLOBAL: Combining the best of PSI-BLAST and GLOBAL,” *National Center for Biotechnology Information*, Bethesda, MD, Jun. 2011.

4. "PSI-GLOBAL: Domain-inspired Alignment & PaSA: Pathway-aware SNP Associations," *Middle Tennessee State University*, Murfreesboro, TN, Feb. 2011.
5. "Threshold Average Precision (TAP- k): A Measure of Retrieval Designed for Bioinformatics," *BioLINK*, Boston, MA, Jul. 2010.
6. "Better Tasting and Less Filling Than PAUP," *BIOT 2007*, Colorado Springs, CO, Oct. 2007.
7. "Using parsimony to guide maximum likelihood searches," *IEEE BIBE 2007*, Boston, MA, Oct. 2007.
8. "Effects of Gap Open and Gap Extension Penalties," *BIOT 2006*, Provo, UT, Oct. 2006.
9. "Large Grain Size Stochastic Optimization Alignment," *IEEE BIBE 2006*, Washington D.C., Oct. 2006.
10. "A Trace-Driven Simulator For Palm OS Devices," *IEEE ISPASS 2005*, Austin, TX, Mar. 2005.

Works in Preparation:

1. C.M. Klinger, L. Paoli, R. Newby, M.Y. Wang, **H.D. Carroll**, J.D. Leblond, C.J. Howe, J.B. Dacks, B. Cahoon, R.G. Dorrell, and E.H. Richardson. 2016. Promiscuous origins and corrective selection underpin the evolution of transcript editing across dinoflagellate plastid lineages. *Molecular Biology and Evolution*. (Under review).
2. **H.D. Carroll**, A.G. Davis, and R. Seipelt-Thiemann. 2017. Gene Family Visualization Server. *In preparation*.
3. **H.D. Carroll**, J.L. Spouge, and M.W. Gonzalez. 2017. The MultiDomainBenchmark Suite: A Multiple-domain Query and Subject Database Suite. *In preparation*.
4. **H.D. Carroll**, S.L. Sheetlin, M.W. Gonzalez, and J.L. Spouge. 2017. PSI-SemiGLOBAL: The Best of PSI-BLAST and GLOBAL. *In preparation*.
5. A.B. Cahoon, **H.D. Carroll**, M.Y. Wang, R.C. Ewool, and R.F. Al-Tobasei. 2017. Analysis of the *Karenia Brevis* Transcriptome. *In preparation*.

Academic Awards

2014	Second place MTSU Scholars Week graduate poster competition
2013	Third place MTSU Scholars Week undergraduate poster competition
2007	BYU Research Presentation Award
2006	BIOT Best Student Paper Award

Professional Activities

2014	BIOT Conference Program Committee Member
2013	BIOT Conference Program Committee Member
2012	NIH Career Symposium Speaker
2012	BIOT Conference Program Committee Member
2012	HiCOMB Conference Program Committee Member
2011	International Society for Computational Biology Member
2010	Invited Speaker at BioLINK (SIG of Intelligent Systems for Molecular Biology)
2009–2010	NIH Career Symposium Steering Committee Member
2007	BIBE Conference Program Committee Member
2007	BIBE Conference Reviewer
2007	BIOT Conference Reviewer
2006	BIOT Conference Reviewer

Service (By organization, then reverse chronological order)

Computer Science Department:

Scholarship Committee, Webmaster, Algorithms and Data Structures (CSCI 3110) Course Coordinator, Faculty Senate Representative, Facilities Planning Committee, Strategic Planning Committee, Invited presentation: “How to Flip a Class”, Faculty Search Committee (twice), Lab Director Search Committee, Student Advisory Committee, External Advisory Board Committee, Chair Search Committee

Computational Science PhD Program:

Executive Council Member, Student Evaluation Committee Head, Self Study [5-year report] Committee Member, PhD Qualifying Exam Committee Reader (six times), PhD Qualifying Exam Committee Head (twice), Faculty Search Committee (twice)

College of Basic and Applied Sciences:

Research Committee Member, Biology (Genomicist) Faculty Search Committee

Middle Tennessee State University:

Faculty Salary Report Committee, XSEDE Campus Champion, Academic Appeals Committee, Assistant Faculty Advisor for Latter-Day Saints Student Association (LDSSA) (a university-wide club)

Community:

Volunteer for “We Build Tech: Code Camp Program”, Invited guest speaker for Technology Explorer Post, Assisted with class website at Scales Elementary School

Miscellaneous

Skills: Perl, C++, C, Python, Bash, FORTRAN, Java
Languages: Native English speaker and fluent in Portuguese