

# Curriculum Vitae

## Hyrum D. Carroll, PhD

TSYS School of Computer Science  
Columbus State University  
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### 1 Education

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- Jan 2005–Aug 2008 **Doctorate of Philosophy**, Computer Science  
Brigham Young University, Provo, Utah  
Dissertation: *Biologically Relevant Multiple Sequence Alignment*
- Jan 2003–Dec 2004 **Master of Science**, Computer Science  
Brigham Young University, Provo, Utah  
Thesis: *A Trace-Driven Simulator For Palm OS Devices*
- Jun 1997–Dec 2002 **Bachelor of Science**, Computer Engineering  
Brigham Young University, Provo, Utah  
GPA: 3.71/4.00

### 2 Academic and Significant Work Experience

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- Jul 2020–present **Associate Professor** — TSYS School of Computer Science  
Columbus State University, Columbus, GA
- Aug 2017–Jun 2020 **Assistant Professor** — TSYS School of Computer Science  
Columbus State University, Columbus, GA
- Aug 2015–May 2019 **Special Volunteer** — Nat'l Ctr for Biotechnology Information  
National Institutes of Health, Bethesda, MD
- Aug 2011–May 2017 **Assistant Professor** — Department of Computer Science  
Middle Tennessee State University, Murfreesboro, TN
- May 2012–Aug 2015 **Scientific Visitor** — Nat'l Ctr for Biotechnology Information  
National Institutes of Health, Bethesda, MD
- Sep 2008–Jul 2011 **Postdoctoral Fellow** — Nat'l Ctr for Biotechnology Information  
National Institutes of Health, Bethesda, MD

Spring 2011            **Instructor** — *Theoretical and Applied Bioinformatics*  
Fndn. for Adv. Edu. in the Sciences Grad. School, Bethesda, MD

Summer 2007           **Instructor** — *Introduction to Computer Systems*  
Dept. of Computer Science, Brigham Young University, Provo, UT

### 3 Fields of Special Interest within Discipline

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- Automatic Assessment Systems (autograders)
- Robotics
- Bioinformatics / Computational Biology

### 4 Professional Membership

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Nov 2018–present      **Association of Computing Machinery**

### 5 Service to the Community

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Nov 2020–present      **Russell County HS's Program & Software Development**, Recorder  
Nov 2017–Mar 2020    **FIRST LEGO League - Veterans Mem. MS**, Technical Coach  
Dec 2018–Apr 2019    **FIRST LEGO League Jr. - Double Churches ES**, Head Coach  
Oct 2018–Apr 2019    **FIRST LEGO League - Double Churches ES**, Head Coach  
May 2018                **NIH Career Symposium**, Panel Speaker  
Mar 2018                **FIRST Robotics Competition**, Robot Inspector  
Jan 2018                **FIRST LEGO League**, Robot Judge

### 6 Major Committees and Assignments

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#### **TSYS School of Computer Science**

Aug 2019–present      **Program Assessment Committee**, member  
Aug 2019–present      **Plagiarism Task Force**, member  
Aug 2019–present      **Website Task Force**, member  
Aug 2018–present      **CPSC 1301K Course Coordinator**, member  
Aug 2019–Aug 2020    **Undergraduate Program Committee**, chair  
Jul 2019–Aug 2020    **ACM Student Chapter**, faculty advisor  
Jul 2019–Jul 2020    **Graduate Admissions Committee**, member  
Aug 2018–Aug 2019    **Graduate Program Committee**, member  
Apr 2018–Jun 2018    **IT Support Specialist Search Committee**, member  
Aug 2017–Aug 2018    **Undergraduate Program Committee**, member

#### **Turner College of Business**

Jul 2020–present      **Curriculum Committee**, chair  
Aug 2019–Jul 2020    **Curriculum Committee**, member  
Aug 2017–July 2019   **Strategic Planning Committee**, member

## Columbus State University

Aug 2020–present    **Information Technology Advisory Committee**, member  
Apr 2020–May 2023    **Faculty Senate**, senator  
Jul 2020–Jun 2021    **Faculty Senate**, Executive Secretary  
Aug 2019–Aug 2020    **Information Technology Advisory Committee**, chair  
Apr 2019–May 2020    **Faculty Senate**, alternate  
Mar 2018–Mar 2020    **Graduate & Faculty Research Conf. Adv. Cmte.**, member

## 7 Professional Growth and Development

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### Certifications

Oct 2017                    **Quality Matters, 5<sup>th</sup> Edition**, MarylandOnline, Inc.  
Dec 2018                    **Quality Matters, 6<sup>th</sup> Edition**, MarylandOnline, Inc.

## 8 Professional Activities

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### Publications (Names of advised students are underlined)

#### Peer-reviewed Journal Articles

1. **H.D. Carroll**, J.L. Spouge, and M. Gonzalez. 2019. [MultiDomainBenchmark: a multi-domain query and subject database suite](#). *BMC Bioinformatics* **20**:77. (pdf)
  - [Scimago Journal Rank \(BMC Bioinformatics 2018\)](#): **Q1**
2. C.M. Klinger, L. Paoli, R.J. Newby, M.Y. Wang, **H.D. Carroll**, J.D. Leblond, C.J. Howe, J.B. Dacks, C. Bowler, A.B. Cahoon, R.G. Dorrell, and E. Richardson. 2018. [Plastid Transcript Editing across Dinoflagellate Lineages Shows Lineage-Specific Application but Conserved Trends](#). *Genome Biology and Evolution* **10**:4, 1019–1038. (pdf)
  - [Scimago Journal Rank \(Genome Biology and Evolution 2018\)](#): **Q1**
3. **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. (pdf)
4. 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. (pdf)
5. 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. (pdf)
6. **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. (pdf)
7. 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. (pdf)

8. **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. ([pdf](#))
9. 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. ([pdf](#))
10. **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. ([pdf](#))
11. **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. ([pdf](#))

#### Peer-reviewed Conference Articles

12. [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. ([pdf](#))
13. [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 *10<sup>th</sup> IEEE International Conference on e-Science* **2**, 5–10. ([pdf](#))
14. [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. ([pdf](#))
15. **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. ([pdf](#))
16. **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. ([pdf](#))
17. 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](#))
18. 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](#))
19. 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. ([pdf](#))
20. **H. Carroll**, M. Ebbert, M. Clement, and Q. Snell. 2007. PSODA: Better Tasting and Less Filling Than PAUP. In *Proceedings of the 4<sup>th</sup> Biotechnology and Bioinformatics Symposium*, 74–78. ([pdf](#))

21. 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 4<sup>th</sup> Biotechnology and Bioinformatics Symposium*, 89–94. ([pdf](#))
22. K. Sundberg, T. O'Connor, **H. Carroll**, M. Clement, and Q. Snell. 2007. [Using Parsimony to Guide Maximum Likelihood Searches](#). In *Proceedings of the 7<sup>th</sup> IEEE International Conference on Bioinformatics and Bioengineering II*, 774–779. ([pdf](#))
23. **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](#))
24. 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 BioEngineering*, 127–134. ([pdf](#))
25. **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](#))
26. **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. ([pdf](#))

#### Dissertation, Thesis, Book Review and Posters

27. H. Fleenor, and **H.D. Carroll**. 2020. Creating an OER Collection of Automatically Scored Practice Exercises for Computer Science 1. *ACM Special Interest Group on Computer Science Education (SIGCSE)*.
28. **H.D. Carroll**. 2018. [Computer Programs Grading Computer Programs](#). *CSU's Faculty and Staff Recognition Ceremony*. ([pdf](#))
29. A.B. Cahoon, **H. Carroll**, M.Y. Wang, R.J. Newby, R.F. Al-Tobasei, R.C. Ewool, D. Evangelista, C.D. Stanley, and J. Leblond. 2015. [Production of a complete library of the plastid derived transcripts of \*Karenia brevis\* and phylogenetic analysis of 6 proteins adds to the complex story of dinoflagellate endosymbiosis](#). *Botany 2015*.
30. F.H. Gebreyesus, and **H.D. Carroll**. 2014. [RNA-seq Analysis of the Maize Leaf Using de-novo Genome Assemblies](#). *MTSU Scholars' Week*. ([pdf](#))
31. [A.C. Williams](#), J.F. Wallin, and **H.D. Carroll**. 2014. [Identification of Ancient Greek Papyrus Fragments Using Genetic Sequence Alignment Algorithms](#). *MTSU Scholars' Week*. ([pdf](#))
32. [A.C. Williams](#), [A.G. Davis](#), and **H.D. Carroll**. 2013. [False Discovery Rates for Iterative Database Searching](#). *MTSU Scholars' Week*. ([pdf](#))
33. **H.D. Carroll**, M.G. Kann, S.L. Sheetlin, and J.L. Spouge. 2010. [Threshold Average Precision \(TAP-k\): A Retrieval Efficacy Measure for Bioinformatics](#). *Intelligent Systems for Molecular Biology*. ([pdf](#))
34. **H.D. Carroll**. December 2008. [Biologically Relevant Multiple Sequence Alignment](#). Ph.D. dissertation, Brigham Young University. ([pdf](#))
35. **H. Carroll**. 2008. [Dynamic homology and phylogenetic systematics: a unified approach using POY](#). *Cladistics* **24**:6, 1071–1072. ([pdf](#))

36. **H.D. Carroll.** December 2004. [A Trace-Driven Simulator for Palm OS Devices.](#)  
Master's thesis, Brigham Young University. ([pdf](#))

## Grants Funded

- Jun 2020–Dec 2020 **Quality Matters Course Improvement**  
PI, Funded by Columbus State University, \$1,500.00
- May 2019–Jun 2020 **Textbook Transformation for CS Foundation Courses**  
Co-PI, Funded by Affordable Learning Georgia - USG, \$30,000.00
- Jan 2019–Dec 2019 **Code Problems Repository**  
PI, Funded by Affordable Learning Georgia - USG  
\$1,600.00
- Jan 2019–May 2019 **Local Automatic Assessment Server for Computer Science 1**  
PI, Funded by Columbus State University  
\$2,491.53
- Aug 2016–Mar 2017 **Optimization and accessibility of the ecoTTC database**  
Co-PI, Funded by Health & Environmental Sciences Ins.  
\$20,000.00
- Nov 2013–May 2014 **Identification of Fragmentary Greek Papyri**  
PI, Funded by Middle Tennessee State University  
\$7,350.41

## Presentations

- Nov 2013 “False Discovery Rate for Homology Searches,” *BSB 2013*, Recife, Brazil
- Oct 2011 “Pairwise Sequence Alignment with PSI-GLOBAL,” Computational Science  
PhD Program Seminar Series at *MTSU*, Murfreesboro, TN
- Jun 2011 “Domain-aware Alignment with PSI-GLOBAL: Combining the best of PSI-  
BLAST and GLOBAL,” *National Center for Biotechnology Information*,  
Bethesda, MD
- Feb 2010 “PSI-GLOBAL: Domain-inspired Alignment & PaSA: Pathway-aware SNP  
Associations,” *MTSU*, Murfreesboro, TN
- Jul 2010 “Threshold Average Precision (TAP- $k$ ): A Measure of Retrieval Designed for  
Bioinformatics,” *BioLINK*, Boston, MA
- Oct 2007 “Better Tasting and Less Filling Than PAUP,” *BIOT 2007*, Colorado Springs,  
CO
- Oct 2007 “Using parsimony to guide maximum likelihood searches,” *IEEE BIBE 2007*,  
Boston, MA
- Oct 2006 “Effects of Gap Open and Gap Extension Penalties,” *BIOT 2006*, Provo, UT
- Oct 2006 “Large Grain Size Stochastic Optimization Alignment,” *IEEE BIBE 2006*,  
Washington D.C.
- Mar 2005 “A Trace-Driven Simulator For Palm OS Devices,” *IEEE ISPASS 2005*,  
Austin, TX

## Professional Activities

2020 LeadCSU  
Jun 2019 Reviewer, NAR Genomics and Bioinformatics  
Dec 2018 Reviewer, Nucleic Acids Research  
Feb 2018 Reviewer, Nucleic Acids Research  
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 Intel. Sys. 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