

**TRAVIS WHEELER
CURRICULUM VITAE**

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RESEARCH INTERESTS

Design of algorithms and statistical methods for sequence analysis in computational genomics; implementation of those methods in distributed software. Particular emphasis on homology search, and relevant algorithms that can scale to genomic datasets.

PROFESSIONAL EXPERIENCE

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| Assistant Professor, Dept of Computer Science, University of Montana | current |
| Postdoctoral Associate, HHMI Janelia Farm Research Campus
Mentor: Sean Eddy | 2009 - 2014 |
| Tree of Life Web Project (tolweb.org) | 2000 - 2003 |
| <ul style="list-style-type: none">• Lead Architect and Developer on conversion of Tree of Life Web Project (ToLWeb) content to a database-driven, modern web architecture; developed tools to enable and encourage distributed contribution of content. ToLWeb is a collection of web pages that present information about the diversity of organisms in the context of their evolutionary relationship.• Managed 1 full-time developer and 5 graduate research assistants. | |
| Intuit, Inc. | 1995 - 2000 |
| <ul style="list-style-type: none">• Designed and developed Telephony, Customer-Relationship-Management, Database Management and Automation applications for a 2500 person call center.• Managed team of 15. | |

EDUCATION

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| Ph.D. Computer Science, University of Arizona, Tucson | 2009 |
| Efficient construction of accurate multiple alignments and large-scale phylogenies | |
| Advisors: John Kececioglu (Computer Science) | |
| Mike Sanderson (Evolutionary Biology) | |
| Minor in Evolutionary Biology | |
| Minor Advisor: David Maddison (Evolutionary Biology) | |
| M. S. Computer Science, University of Arizona, Tucson | 2006 |
| Advisor: John Kececioglu | |
| B. A. Ecology and Evolutionary Biology, University of Arizona, Tucson | 1995 |
| Minors in Anthropology and English | |
| Cum Laude, Phi Beta Kappa | |

PUBLICATIONS

1. **Skylign: a tool for creating informative, interactive logos representing sequence alignments and profile hidden Markov models.** Wheeler, T.J., Clements, J., Finn, R.D. 2014. *BMC Bioinformatics*, 15:7. (doi:10.1186/1471-2105-15-7; distinguished as a “Highly Accessed Article”)
2. **nhmmer: DNA homology search with profile HMMs.** Wheeler, T.J., Eddy, S.R. 2013. *Bioinformatics*, 29(19):2487–2489. (doi: 10.1093/bioinformatics/btt403; among the top 20 most read *Bioinformatics* articles during September 2013)
3. **Dfam: a Database of Repetitive DNA Based on Profile Hidden Markov Models.** Wheeler, T.J., Clements, J., Eddy, S.R., Hubley, R., Jones, T.A., Jurka, J., Smit, A.F.A, and Finn, R.D. 2012. *Nucleic Acids Research*, 41:D70–D82. (doi: 10.1093/nar/gks1265; selected as an NAR “Featured Article”; cited 10

times)

4. **Estimating the Accuracy of Multiple Alignments and its Use in Parameter Advising.** DeBlasio, D., Wheeler, T., and Kececioglu, J. 2012. Proceedings of the 16th Conference on Research in Computational Molecular Biology (RECOMB), Springer-Verlag Lecture Notes in Bioinformatics 7262, 45-59. (doi: 10.1007/978-3-642-29627-7_5) (15% acceptance rate)
5. **Complete nucleomorph genome sequence of the non-photosynthetic alga *Cryptomonas paramecium* reveals a core nucleomorph gene set.** Tanifuji, G. Onodera, N.T., Wheeler, T.J., Dlutek, M., Donaher, N., and Archibald, J.M. 2010. Genome Biology and Evolution, 3:44-54. (doi: 10.1093/gbe/evq082; cited 20 times)
6. **Aligning protein sequences with predicted secondary structure.** Kececioglu, J., Kim, E., and Wheeler, T. 2010. Journal of Computational Biology, 17(3): 561-580. (doi: 10.1089/cmb.2009.0222; selected as a "recommended read" for the Faculty of 1000 Biology)
7. **Large-scale neighbor-joining with NINJA.** Wheeler, T.J. 2009. Proceedings of the 9th Workshop on Algorithms in Bioinformatics (WABI), 375-389. (doi: 10.1007/978-3-642-04241-6_31; cited 30 times)
8. **Learning models for aligning protein sequence with predicted secondary structure.** Kim, E., Wheeler, T.J., and Kececioglu, J.D. 2009. Proceedings of the 13th Conference on Research in Computational Molecular Biology (RECOMB), Springer-Verlag Lecture Notes in Bioinformatics, 5541: 586-605. (doi: 10.1007/978-3-642-02008-7_36)
9. **Multiple alignment by aligning alignments.** Wheeler, T.J. and Kececioglu, J.D. 2007. Proceedings of the 15th ISCB Conference on Intelligent Systems for Molecular Biology (ISMB), Bioinformatics, 23: i559-i568. (doi: 10.1093/bioinformatics/btm226; 16% acceptance rate; cited 90 times)
10. **Adaptive protein evolution and regulatory divergence in *Drosophila*.** Good, J.M., Hayden, C.A., and Wheeler T.J. 2006. Molecular Biology and Evolution, 23(6): 1101-1103. (doi: 10.1093/molbev/msk002; cited 20 times)
11. **Evaluating and improving cDNA sequence quality with cQC.** Hayden, C.A., Wheeler, T.J., and Jorgensen R.A. 2005. Bioinformatics, 21(24): 4414-4415. (doi: 10.1093/bioinformatics/bti709)
12. **Transposable element orientation bias in the *Drosophila melanogaster* genome.** Cutter, A.D, Good, J.M., Pappas, C.T., Saunders, M.A., Starrett, D.M., Wheeler T.J. 2005. Journal of Molecular Evolution, 61(6): 733-741. (doi: 10.1007/s00239-004-0243-0; cited 17 times)

SOFTWARE AND DATABASES

1. Skygign Logo server: a tool for creating informative, interactive logos representing sequence alignments and profile hidden Markov models.
<http://skylign.org>
Wheeler, T.J., Clements, J., Finn, R.D. 2013.
2. nhmmer: a DNA-DNA sequence homology search tool based on profile hidden Markov models, in the HMMER3 framework.
<http://hmmer.org> (included in the HMMER3.1 release, May 2013)
Wheeler, T.J. and Eddy, S.R. 2012.
3. Dfam: a Database of Repetitive DNA Based on Profile Hidden Markov Models.
<http://dfam.org>
Wheeler, T.J., Clements, J., Eddy, S.R., Hubley, R., Jones, T.A., Jurka, J., Smit, A.F.A, Finn, R.D. 2012.
4. Ninja: a Mesquite package for fast neighbor-joining phylogeny inference.
<http://nimbletwist.com/software/ninja/mesquite.html>
Wheeler, T.J. and Maddison, D.R. 2010.
5. NINJA: software for large-scale neighbor-joining phylogeny inference.
<http://nimbletwist.com/software/ninja>
Wheeler, T.J. 2009.
6. Opalescent: a Mesquite package for multiple sequence alignment.

<http://mesquiteproject.org/packages/opal>

Wheeler, T.J. and Maddison, D.R. 2009.

7. Opal: software for multiple sequence alignment by optimally aligning alignments.

<http://opal.cs.arizona.edu>

Wheeler, T.J. and Kececioğlu, J.D. 2006.

8. Align: a Mesquite package for aligning sequence data.

<http://mesquiteproject.org>

Maddison, D.R., Wheeler, T.J., and Maddison, W.P. 2006.

9. AlignAlign: software for optimally aligning alignments.

<http://alignalign.cs.arizona.edu>

Starrett, D.M., Wheeler, T.J., and Kececioğlu, J.D. 2005.

10. cQC - cDNA Quality Control: A tool for resolving putative sequencing errors in single-pass cDNA, based on genomic sequence.

<http://genomics.arizona.edu/software/cQC/>

Hayden, C.A. and Wheeler, T.J. 2005.

SERVICE

Reviewer: Bioinformatics, Database, BMC Bioinformatics	2011 - present
Board member, Phi Beta Kappa Association of Greater Tucson	2006 - 2009
Vice President, Phi Beta Kappa Association of Greater Tucson	2007 - 2008
Computer Science Faculty Recruiting Committee, University of Arizona	2004 - 2005

HONORS AND AWARDS

NSF travel grant (IGERT Principal Investigators Meeting, Washington DC)	2009
NSF IGERT Comparative Genomics Fellowship, University of Arizona	2008-2009
NSF travel grant (ISMB, Vienna)	2007
NSF IGERT Genomics Fellowship, University of Arizona (1 year & 6 month renewals)	2006-2007
NSF IGERT Genomics Fellowship, University of Arizona (2 year fellowship)	2004-2005
Phi Beta Kappa Inductee	1994