

**TRAVIS WHEELER**  
**CURRICULUM VITAE**  
(updated October 17, 2016)

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### RESEARCH INTERESTS

Design of algorithms and statistical methods for sequence analysis in computational genomics; implementation of those methods in software. Particular emphasis on sensitive homology search, and relevant algorithms that can scale at high speed to genomic and metagenomic datasets. Application of these methods to biology-motivated topics, especially those involving transposable elements and regulatory elements.

### PROFESSIONAL EXPERIENCE

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| Assistant Professor, Dept of Computer Science, University of Montana   | 2014 - current |
| Senior Research Scientist, HHMI Janelia Farm Research Campus   | 2011 - 2014    |
| Postdoctoral Associate, HHMI Janelia Farm Research Campus<br>Mentor: Sean Eddy   | 2009 - 2011    |
| Tree of Life Web Project ( <a href="http://tolweb.org">tolweb.org</a> )  | 2000 - 2003    |
| <ul style="list-style-type: none"><li>• Lead Architect and Developer of Tree of Life Web Project (<a href="http://tolweb.org">tolweb.org</a>); 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.</li><li>• Managed 1 full-time developer and 5 graduate research assistants.</li></ul> |                |
| Intuit, Inc.   | 1995 - 2000    |
| <ul style="list-style-type: none"><li>• Developed Telephony, Customer-Relationship-Management, Database Management, and Automation applications for a 2500 person call center.</li></ul>   |                |

### 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. **The Dfam database of repetitive DNA families.** Hubley, R., Finn, R.D., Clements, J., Eddy, S.R., Jones, T.A., Bao, W., Smit, A.F.A., Wheeler, T.J. 2016. *Nucleic Acids Research*, 44:D81-89. (doi:10.1093/nar/gkv1272)
2. **A call for benchmarking transposable element annotation methods.** Hoen, D.R., Hickey, G., Bourque, G., Casacuberta, J., Cordaux, R., Feschotte, C., Fiston-Lavier, A-S., Hua-Van, A., Hubley, R., Kapusta, A., Lerat, E., Maumus, F., Pollock, D.D., Quesneville, H., Smit, A., Wheeler, T.J., Bureau, T.E., Blanchette, M. 2015. *Mobile DNA*, 6:13. (doi:10.1186/s13100-015-0044-6)

3. **HMMER web server: 2015 update.** Finn, R.D., Clements, J., Arndt, W., Miller, B.L., Wheeler, T.J., Schreiber, F., Bateman, A., and Eddy, S.R. 2015. *Nucleic Acids Research*, 43:gkv397. (doi:10.1093/nar/gkv397)
4. **Skygln: 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” ; cited 10 times)
5. **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; cited 13 times)
6. **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 47 times)
7. **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; cited 8 times)
8. **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 32 times)
9. **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; cited 7 times)
10. **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 37 times)
11. **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)
12. **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 120 times)
13. **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 22 times)
14. **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)
15. **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 19 times)

#### SOFTWARE, WEBSITES, AND DATABASES

1. HMMER web server.  
<http://www.ebi.ac.uk/Tools/hmmer/>  
Finn, R.D., Clements, J., Arndt, W., Miller, B.L., Wheeler, T.J., Schreiber, F., Bateman, A., and Eddy, S.R. 2015.
2. Skygln 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.

3. nhmmer: a DNA-DNA sequence homology search tool based on profile hidden Markov models, in the HMMER3 framework.  
**<http://hmmmer.org> (included in the HMMER3.1 release)**  
Wheeler, T.J. and Eddy, S.R. 2012.
4. 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.
5. 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.
6. NINJA: software for large-scale neighbor-joining phylogeny inference.  
**<http://nimbletwist.com/software/ninja>**  
Wheeler, T.J. 2009.
7. Opalescent: a Mesquite package for multiple sequence alignment.  
**<http://mesquiteproject.org/packages/opal>**  
Wheeler, T.J. and Maddison, D.R. 2009.
8. Opal: software for multiple sequence alignment by optimally aligning alignments.  
**<http://opal.cs.arizona.edu>**  
Wheeler, T.J. and Kececioglu, J.D. 2006.
9. Align: a Mesquite package for aligning sequence data.  
**<http://mesquiteproject.org>**  
Maddison, D.R., Wheeler, T.J., and Maddison, W.P. 2006.
10. AlignAlign: software for optimally aligning alignments.  
**<http://alignalign.cs.arizona.edu>**  
Starrett, D.M., Wheeler, T.J., and Kececioglu, J.D. 2005.
11. 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, Science, PLoS One, ACM-BCB, OICR, NSF.	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