

TRAVIS WHEELER
CURRICULUM VITAE
(updated October, 2017)

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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 methods and models in sequence search/alignment, and 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

Assistant Chair, Dept of Computer Science, University of Montana	2016 – current
Assistant Professor, Dept of Computer Science, University of Montana	2014 – current
Partner, Nimbletwise Consulting (Bioinformatics Consulting)	2016 – current
Senior Research Scientist, HHMI Janelia Farm Research Campus	2011 – 2014
Postdoctoral Associate, HHMI Janelia Farm Research Campus	2009 – 2011
Mentor: Sean Eddy	
Tree of Life Web Project (tolweb.org)	2000 – 2003
<ul style="list-style-type: none">Lead Architect and Developer of Tree of Life Web Project (tolweb.org); 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">Developed Telephony, Customer-Relationship-Management, Database Management, and Automation applications for a 2500 person call center.	

EDUCATION

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	

FUNDING

UM CBSD CoBRE Pilot grant – “Reducing error in sequence annotation” \$50K direct	Jan 2017 – Dec 2017
NIH R15 – “Improved protein-DNA models for translated sequence search with profile Hidden Markov models” \$300K direct	Apr 2017 – Mar 2020
UM CBSD CoBRE Junior Investigator grant – “Methods for fast bio-sequence comparison with profile hidden Markov models” \$450K direct	Aug 2017 – July 2020

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. **Skyline: 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. Skylign 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://hmmer.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

Assistant Chair, Dept of Computer Science, U. Montana.	2016 – present
General Education Committee, member	2016 – present
Reviewer: Bioinformatics, Database, BMC Bioinformatics, Science, PLoS One, ACM-BCB, GLBIO, IEEE, Genome Atlantic, 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