

TRAVIS WHEELER
CURRICULUM VITAE
(updated October, 2018)

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RESEARCH INTERESTS

The Wheeler lab designs algorithms and statistical methods for sequence analysis in computational genomics, and develops high-quality implementations of those methods for incorporation into highly-used software pipelines and web services. We are particularly focused on the alignment of biological sequences and the accompanying problem of searching for similar sequences within large-scale biological sequence databases. This work addresses concerns of speed (developing algorithmic and engineering techniques to accelerate sequence alignment), sensitivity (developing models to improve recognition of similarity between highly divergent sequences, even in the face of sequencing error), and reliability (developing approaches that reduce the propensity of highly sensitive methods to make erroneous claims, especially in the context of confounding factors). We apply our methods to the analysis and understanding of interesting biological phenomena, particularly transposable elements, conserved non-coding sequence, and surprising features of genomes such as dual-coding exons.

PROFESSIONAL EXPERIENCE

Assistant Professor, Department 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	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

NIH R01 – “Understanding Prevalent and Highly Conserved Dual-Coding Exons in Animals” \$625K direct	Aug 2019 – Jul 2023 (submitted Oct 2018; in review)
NIH R01 – “Reducing false sequence annotation due to alignment overextension and repetitive sequences” \$1.2M direct	Apr 2019 – Mar 2024 (submitted June 2018; in review)
NIH U24 – “Dfam: sustainable growth, curation support, and improved quality for mobile element annotation” (Co-PI with Arian Smit and Robert Hubley at ISB) Total \$1.9M direct; Wheeler lab portion: \$302K direct	Jul 2018 – Jun 2023 (active)
UM CBSD CoBRE Junior Investigator grant – “Methods for fast bio-sequence comparison with profile hidden Markov models” \$450K direct	Aug 2017 – July 2020 (active)
NIH R15 – “Improved protein-DNA models for translated sequence search with profile Hidden Markov models” \$300K direct	Apr 2017 – Mar 2020 (active)
UM CBSD CoBRE Pilot grant – “Reducing error in sequence annotation” \$50K direct	Jan 2017 – Dec 2017

PUBLICATIONS (Wheeler lab members underlined; citation count as of Oct 13 2018)

1. **15 years of PhosphoSitePlus®: Integrating posttranslationally modified sites, disease variants and isoforms.** Hornbeck, P., Kornhauser, J., Latham, V., Murray, B., Nandhikonda, V., Nord, A., Skrzypek, E., Wheeler, T., Zhang, B., and Gnad, F. 2018. Nucleic Acids Research. (in review)
2. **ULTRA: A Model Based Tool to Detect Tandem Repeats.** Olson, D. and Wheeler, T.J. 2018. Proceedings of the 2018 ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB), 37-46. (doi:10.1145/3233547.3233604)
3. **Splice-Aware Multiple Sequence Alignment of Protein Isoforms.** Nord, A., Hornbeck, P., Carey, K., and Wheeler, T.J. 2018. Proceedings of the 2018 ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB), 200-210. (doi:10.1145/3233547.3233592)
4. **Integration of protein phosphorylation, acetylation, and methylation data sets to outline lung cancer signaling networks.** Grimes, M., Hall, B., Foltz, L., Levy, T., Rikova, K., Gaiser, J., Cook, W., Smirnova, E., Wheeler, T., Clark, N.R., Lachmann, A., Zhang, B., Hornbeck, P., Maayan, A., and Comb, M. 2018. Science Signaling, 11:eaq1087. (doi:10.1126/scisignal.aq1087)
5. **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; cited 57 times)
6. **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; cited 38 times)
7. **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; cited 331 times)
8. **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” ; cited 95 times)
9. **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 118 times)
10. **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 121 times)

11. **Estimating the Accuracy of Multiple Alignments and its Use in Parameter Advising.** DeBlasio, D., Wheeler, T., and Kececioğlu, 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 21 times)
12. **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)
13. **Aligning protein sequences with predicted secondary structure.** Kececioğlu, 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 10 times)
14. **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 63 times)
15. **Learning models for aligning protein sequence with predicted secondary structure.** Kim, E., Wheeler, T.J., and Kececioğlu, 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; cited 2 times)
16. **Multiple alignment by aligning alignments.** Wheeler, T.J. and Kececioğlu, 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 196 times)
17. **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 24 times)
18. **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; cited 4 times)
19. **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. ULTRA: software for labeling tandem repeat regions in genomic sequence. Currently being incorporated into RepeatMasker (<http://repeatmasker.org>), which is used in annotation of nearly all newly sequenced organisms.
<https://github.com/TravisWheelerLab/ULTRA>
Olson, D. and Wheeler, T.J. 2018
2. Mirage: Software for splice-aware multiple sequence alignment of protein isoforms. Currently being incorporated into the PhosphositePlus web service (<https://www.phosphosite.org/>).
<https://github.com/TravisWheelerLab/Mirage>
Nord, A. and Wheeler, T.J. 2018
3. phmmer: a protein-DNA sequence homology search tool based on profile hidden Markov models, in the HMMER3 framework.
<https://github.com/TravisWheelerLab/hmmer> (develop branch)
Shands, W., Krause, G., and Wheeler, T.J. 2018
4. 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.

5. 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.
6. 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.
7. 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.
8. 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.
9. NINJA: software for large-scale neighbor-joining phylogeny inference.
<http://nimbletwist.com/software/ninja>
Wheeler, T.J. 2009.
10. Opalescent: a Mesquite package for multiple sequence alignment.
<http://mesquiteproject.org/packages/opal>
Wheeler, T.J. and Maddison, D.R. 2009.
11. Opal: software for multiple sequence alignment by optimally aligning alignments.
<http://opal.cs.arizona.edu>
Wheeler, T.J. and Kececioglu, J.D. 2006.
12. Align: a Mesquite package for aligning sequence data.
<http://mesquiteproject.org>
Maddison, D.R., Wheeler, T.J., and Maddison, W.P. 2006.
13. AlignAlign: software for optimally aligning alignments.
<http://alignalign.cs.arizona.edu>
Wheeler, T.J., Starrett, D.M., and Kececioglu, J.D. 2005.

SERVICE

Assistant Chair, Dept of Computer Science, U. Montana.	2016 – 2018
General Education Committee, member	2016 – 2018
Reviewer: Bioinformatics, Database, BMC Bioinformatics, Science, PLoS One, ACM-BCB, GLBIO, IEEE-TCBB, 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