

CURRICULUM VITAE

HHMI Janelia Farm Research Campus
19700 Helix Drive
Ashburn VA 20147

E-mail: wheelert@janelia.hhmi.org
Phone: (571) 449-6401
<http://www.nimbletwist.com>

EDUCATION

Postdoctoral Associate, HHMI Janelia Farm Research Campus Mentor: Sean Eddy	current
Ph.D. Computer Science, University of Arizona, Tucson <i>Efficient construction of accurate multiple alignments and large-scale phylogenies</i> Advisors: John Kececioglu (Computer Science) Mike Sanderson (Evolutionary Biology) Minor in Evolutionary Biology Minor Advisor: David Maddison (Evolutionary Biology)	2009
M. S. Computer Science, University of Arizona, Tucson Advisor: John Kececioglu	2006
B. A. Ecology and Evolutionary Biology, The University of Arizona, Tucson Minors in Anthropology and English Cum Laude	1995

HONORS AND AWARDS

NSF IGERT Comparative Genomics Fellowship, University of Arizona	2008-2009
NSF travel grant	2007
NSF IGERT Genomics Fellowship, University of Arizona	2004-2007
Phi Beta Kappa Inductee	1994

TEACHING EXPERIENCE

Instructor, University of Arizona. Computational Section of Functional and Evolutionary Genomics course Developed curriculum and homework, presented lectures, managed teaching assistant	2006 & 2008
---	-------------

PROFESSIONAL EXPERIENCE

Tree of Life Web Project (tolweb.org) <ul style="list-style-type: none">• Lead Architect and Developer on projects to convert Tree of Life Web Project (ToLWeb) content to a database-driven architecture, improve flexibility and accessibility of web interface, and develop tools to enable and encourage content contribution by biologists world-wide. ToLWeb is a collection of web pages that presents information about the diversity and evolutionary relationship of organisms.• Managed 1 full-time developer and 5 graduate research assistants.	2000 - 2003
Intuit, Inc. <ul style="list-style-type: none">• Designed and developed Telephony, Customer-Relationship-Management, Database Management and Automation applications for a 2500 person call center.• Taught classes on accounting and software support.• Managed team of 15.	1995 - 2000

SERVICE

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	2004 - 2005

PUBLICATIONS

1. Tanifuji, G. Onodera, N.T., Wheeler, T.J., Dlutek, M., Donaher, N., and Archibald, J.M. 2010. Complete nucleomorph genome sequence of the non-photosynthetic alga *Cryptomonas paramecium* reveals a core nucleomorph gene set. *Genome Biology and Evolution*. (doi: 10.1093/gbe/evq082)
2. Kececioğlu, J., Kim, E., and Wheeler, T. 2010. Aligning protein sequences with predicted secondary structure. *Journal of Computational Biology*, 17(3): 561-580. (selected as a "recommended read" for the Faculty of 1000 Biology)
3. Wheeler, T.J. 2009. Large-scale neighbor-joining with NINJA. *Proceedings of the 9th Workshop on Algorithms in Bioinformatics (WABI)*, 375-389. (cited 2 times)
4. Kim, E., Wheeler, T.J., and Kececioğlu, J.D. 2009. Learning models for aligning protein sequence with predicted secondary structure. *Proceedings of the 13th Conference on Research in Computational Molecular Biology (RECOMB)*, Springer-Verlag Lecture Notes in Bioinformatics 5541: 586-605.
5. Wheeler, T.J. and Kececioğlu, J.D. 2007. Multiple alignment by aligning alignments. *Proceedings of the 15th ISCB Conference on Intelligent Systems for Molecular Biology (ISMB)*, Bioinformatics, 23: i559-i568. (16% acceptance rate; cited >20 times)
6. Good, J.M., Hayden, C.A., and Wheeler T.J. 2006. Adaptive protein evolution and regulatory divergence in *Drosophila*. *Molecular Biology and Evolution*, 23(6): 1101-1103. (cited 9 times)
7. Hayden, C.A., Wheeler, T.J., and Jorgensen R.A. 2005. Evaluating and improving cDNA sequence quality with cQC. *Bioinformatics*, 21(24): 4414-4415. (cited 3 times)
8. Cutter, A.D, Good, J.M., Pappas, C.T., Saunders, M.A., Starrett, D.M., Wheeler T.J. 2005. Transposable element orientation bias in the *Drosophila melanogaster* genome. *Journal of Molecular Evolution*, 61(6): 733-741. (cited 8 times)

DISTRIBUTED SOFTWARE

1. Wheeler, T.J. and Maddison, D.R. 2010. NINJA: a Mesquite package for fast neighbor-joining phylogeny inference.
<http://nimbletwist.com/software/ninja/mesquite.html>
2. Wheeler, T.J. 2009. NINJA: software for large-scale neighbor-joining phylogeny inference.
<http://nimbletwist.com/software/ninja>
3. Wheeler, T.J. and Maddison, D.R. 2009. Opalescent: a Mesquite package for multiple sequence alignment.
<http://mesquiteproject.org/packages/opal>
4. Wheeler, T.J. and Kececioğlu, J.D. 2006. Opal: software for multiple sequence alignment by optimally aligning alignments.
<http://opal.cs.arizona.edu>
5. Maddison, D.R., Wheeler, T.J., and Maddison, W.P. 2006. Align: a Mesquite package for aligning sequence data.
<http://mesquiteproject.org>
6. Starrett, D.M., Wheeler, T.J., and Kececioğlu, J.D. 2005. AlignAlign: software for optimally aligning alignments.
<http://alignalign.cs.arizona.edu>
7. Hayden, C.A. and Wheeler, T.J. 2005. 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/>

TALKS

1. “Large-scale neighbor-joining with NINJA”. WABI, Philadelphia, Pennsylvania, September 12, 2009.
2. “Multiple alignment by aligning alignments”. ISMB, Vienna, Austria, July 23, 2007.
3. “Opal: Forming and polishing multiple alignments by optimally aligning subalignments”. NSF-IGERT Program in Genomics Fall Symposium, University of Arizona, Tucson, Arizona, December 6, 2006.
4. “Tree of Life Web Project: Implementing an Open-source Database and Toolset for Sharing Phylogenetic and Other Biological Information via the Web”. O’Reilly Bioinformatics Technology Conference, Tucson, Arizona, January 29, 2002.