

Theresa A. Wohlever

f.k.a. Theresa A. Hepburn

Citizen of The United States

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Experienced bioinformatician, at home with open source and commercial bioinformatics resources as well as combining analyses through scripting. Effective troubleshooter with excellent communication and organizational skills, who brings together these attributes to provide consistent, high level, quality bioinformatics support to biologists and bioinformaticians of varied backgrounds.

SPECIALIZED SKILLS

- Languages: Perl, R, bash/tcsh, C/C++, SQL, L^AT_EX
- Alignment/Assembly Software: CLC Assembly Cell, Newbler, ARACHNE, Velvet, BLAST, bwa
- Genomic Software: CLC Genomics Workbench, CLC Genomics Server, RDP, JalView, mothur, usearch/otupipe, AbundantOTU, RasMol, MOE
- Service Interfaces: JIRA, HelpSpot, Confluence

RESEARCH & WORK EXPERIENCE

CLC bio Cambridge, MA

Application Scientist, Jan. 2012 - Present

- Interpret, replicate, and propose solutions for a broad range of customer questions and problems
- Effectively and clearly communicate software issues with support team, developers, and customers
- Collaborate on research, drafting, and editing of customer facing text eg. Frequently Asked Questions (FAQ)

The Broad Institute of MIT and Harvard Cambridge, MA

Associate Computational Biologist, Jan. 2010 - Jan. 2012

- Developed and maintained 454 16S filtering and classification pipeline [Perl, L^AT_EX, R and mothur]
- Processed 16 ongoing 16S projects consisting of in house and external data
- Improved accuracy of 16S-based microbial diversity estimations
- Facilitated transition of the 16S pipeline to the Software Engineering team
- Installed, supported, and maintained group specific software - eg. mothur, RDP, usearch

The Broad Institute of MIT and Harvard Cambridge, MA

Bioinformatics Assembly Analyst, July 2007 - Jan. 2010

- Proposed, developed, and maintained 454 analysis pipeline reducing error and analyst time by 90% [Perl, L^AT_EX, and Gnuplot]: 322 genomes completed including *Brucella*, *Vibrio cholerae*, HMP, *E. coli*, *Staphylococcus aureus*, and *Neisseria ghonnorea* strains
- Trained the genome finishing team to utilize and upgrade bacterial analysis software
- Characterized and proposed solutions for failures in assembly, sequencing, library construction, and DNA sample preparation
- Preliminary analysis of new sequencing technologies for assembly: Illumina, Pacific Biosciences
- Mentored three junior analysts to successfully accomplish similar responsibilities

Rensselaer Polytechnic Institute Troy, NY

Undergraduate Research Assistant, May 2005 - July 2007

- Designed and implemented amino acid oligo classifier to predict small molecule binding propensity
- Collaborated with outside researchers on code development for atom type project
- Curated multiple datasets and performed descriptor calculations and model generation
- Webmaster for the Rensselaer Exploratory Center for Cheminformatics Research (RECCR)

EDUCATION

Rensselaer Polytechnic Institute Troy, NY

Bachelor of Science, August 2003 - May 2007

- *cum laude* 3.56/4.0
- Bioinformatics and Molecular Biology Major 3.29/4.0
- Computer Science Minor 3.70/4.0

PUBLICATIONS

- den Bakker HC, Desjardins CA, Griggs AD, Peters JE, Zeng Q, et al. *Evolutionary Dynamics of the Accessory Genome of Listeria monocytogenes*. **PLoS One**. 2013; 8(6): e67511. doi:10.1371/journal.pone.0067511.
- Anthony A. Fodor, Todd Z. DeSantis, Kristine M. Wylie, Jonathan H. Badger, Yuzhen Ye, Theresa Hepburn, Ping Hu, Erica Sodergren, Konstantinos Liolios, Heather Huot-Creasy, Bruce W. Birren, Ashlee M. Earl. *The “Most Wanted” Taxa from the Human Microbiome for Whole Genome Sequencing*. **PLoS One**. 2012; 7(7): e41294. doi: 10.1371/journal.pone.0041294.
- Jumpstart Consortium Human Microbiome Project Data Generation Working Group (2012). *Evaluation of 16S rDNA-Based Community Profiling for Human Microbiome Research*. **PLoS ONE**. 7(6): e39315. doi:10.1371/journal.pone.0039315.
- The Human Microbiome Project Consortium. *Structure, function and diversity of the healthy human microbiome*. **Nature**. 486, 207214 (14 June 2012) doi:10.1038/nature11234.
- The Human Microbiome Project Consortium. *A framework for human microbiome research*. **Nature**. 486, 215221 (14 June 2012) doi:10.1038/nature11209.
- Human Microbiome Jumpstart Reference Strains Consortium. *A catalog of reference genomes from the human microbiome*. **Science**. 2010 May 21;328(5981):994-9.
- Charles Bergeron, Theresa Hepburn, C. Matthew Sundling, Michael Krein, Bill Katt, Nagamani Sukumar, Curt M. Breneman, Kristin P. Bennett. *Prediction of peptide bonding affinity: kernel methods for nonlinear modeling*. **arXiv:1108.5397v1 [stat.ML]**. 2011 August.