

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

- NGS Data: Illumina, 454, Ion Torrent, SOLiD, Pacific Biosciences, Complete Genomics, Helicos
- Programming: Perl, R, bash/tcsh, C/C++, SQL, L^AT_EX
- Genomic Software: CLC Genomics Workbench, CLC Assembly Cell, CLC Servers, Biomedical Genomics Workbench, Ingenuity Variant Analysis, RDP, JalView, mothur, usearch/otupipe, AbundantOTU, Newbler, ARACHNE, Velvet, BLAST, bwa, nucmer,
- Service Interfaces: JIRA, HelpSpot, Confluence, Salesforce, ServiceCloud

RESEARCH & WORK EXPERIENCE

QIAGEN Bioinformatics Chicago, IL

Senior Scientist, Oct. 2014 - Present

- Analyze, define, and resolve complex scientific and technical issues from scientist and clinician users
- Enable users to successfully harness CLC and Ingenuity product lines to meet their advanced needs
- Modify and establish procedures to promptly and comprehensively meet customer needs
- Partner with global R&D, product management, sales, and marketing teams to improve processes
- Establish and revise systems and protocols the team uses for customer engagement

CLC bio Cambridge, MA

Application Scientist, Jan. 2012 - Oct. 2014

- 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

The Broad Institute of MIT and Harvard Cambridge, MA

Associate Computational Biologist, Jan. 2010 - Jan. 2012

- Develop and maintain 454 16S filtering and classification pipeline [Perl, L^AT_EX, R, mothur]
- Process 16 ongoing 16S projects consisting of in-house and external data
- Improved accuracy of 16S-based microbial diversity estimations
- Facilitate transition of the 16S pipeline to the Software Engineering team

The Broad Institute of MIT and Harvard Cambridge, MA

Bioinformatics Assembly Analyst, July 2007 - Jan. 2010

- Propose, develop, and maintain 454 analysis pipeline reducing error and analyst time by 90% [Perl, L^AT_EX, and Gnuplot]: 322 genomes completed including *Brucella*, *Vibrio cholerea*, HMP, *E. coli*, *Staphylococcus aureus*, and *Neisseria ghonnorea* strains
- Train the genome finishing team to utilize and upgrade bacterial analysis software
- Characterize and propose solutions for sequencing, library construction, and DNA sample failures
- Preliminary analysis of new sequencing technologies for assembly: Illumina, Pacific Biosciences

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, 207–214 (14 June 2012) doi:10.1038/nature11234.
- The Human Microbiome Project Consortium. *A framework for human microbiome research*. **Nature**. 486, 215–221 (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.