Theresa Wohlever

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Experienced bioinformatician, proficient 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 researchers 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, LaTeX, gcc, git, svn, SQL
- *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 advanced customer 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
- Contribute to internal documentation for consistent quality support across the globaly integrated team

CLC bio Cambridge, MA
Application Scientist, Jan. 2012 - Oct. 2014

- Interpret, replicate, and propose solutions for a broad range of customer questions and problems
  - Troubleshoot and guide assessmentt of *de novo* assembly and read mapping results
  - Provide basic recommendations for transcriptomic related workflows, ie. RNA-Seq
  - Outline steps to accomplish variant detection and downstream analysis goals
  - Troubleshoot issues with the Workbench, Server, and Command Line Tools
- 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, LaTeX, 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, LaTeX, and Gnuplot]: 322 genomes completed including *Brucella*, *Vibrio cholerea*, HMP, *E. coli*, *Staphlyococcus 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
  - Resolve mis-assemblies due to repeat structure and sequencing/cloning bias
  - Recommend sequencing technology, library type, and coverage for extreme GC genomes
  - Quickly identify and alert sequencing and projects teams to mislabeled DNA
  - Diagnose contaminant sequence sources as collaborators or Broad lab process
- Preliminary analysis of new sequencing technologies for assembly: Illuminia, Pacific Biosciences

Rensselaer Polytechnic Institute Troy, NY
Undergraduate Research Assistant, May 2005 - July 2007

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

Teaching Experience

Rensselaer Polytechnic Institute Troy, NY
Residence Hall Learning Assistant Coordinator, January 2005 - May 2007

- Coordinator of 9 Learning Assistants
- Acted as an academic resource for 150 freshmen college students by holding workshops, office hours, and personally distributing newsletters
- Gained crisis management and paraprofessional counseling skills while ensuring the safety and well-being of the students in the residence hall

Rensselaer Polytechnic Institute Troy, NY
Teaching Assistant for Intro. to Cell Biology, January 2005 - May 2006

- Presented course material and guided 15 students in an introductory cell biology lab

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.

Contributed Posters

- "Efficient High Throughput Bacterial Assembly with Automated Plasmid Identification," (2009) Sequencing, Finishing and Analysis in the Future (FINTF), Santa Fe, New Mexico.
- "Efficient High Throughput Bacterial Assembly with Automated Plasmid Identification," (2009) Advances in Genome Biology and Technology (AGBT), Marco Island, Florida.
- "TAE Augmented scoring functions: Two approaches, atom and surface based." (2007) 234th ACS National Meeting, Boston, MA.
- "Realizing Prospective QSAR through data fusion and modern descriptors." (2007) 234th ACS National Meeting, Boston, MA.
- "Bio- and chem-Informatics: Where do the twain meet?" (2007) 234th ACS National Meeting, Boston, MA.

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