

Theresa Wohlever

née Hepburn

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Experienced remote Bioinformatics IT Manager with a passion for cultivating talent and improving process. Demonstrated success translating high profile client needs into a clear vision and effective delivery. **Seeking opportunities to drive positive impact in healthcare** through emphasizing team focused values, AGILE philosophy, and a growth mindset.

Specialized Experience

I demonstrate familiarity with the following resources listed left to right from greatest proficiency to least

- *NGS Data*: Illumina, Pacific Biosciences, 454, Ion Torrent, Oxford Nanopore, SOLiD, Complete Genomics
- *Genomic Software*: CLC Genomics/Biomedical Workbench, CLC Assembly Cell, CLC Servers, IGV, BLAST, Newbler, bwa, ARACHNE, Velvet, maq, RDP, JalView, mothur, usearch/otupipe, AbundantOTU, nucmer
- *Programming*: bash/tcsh, Perl, R, \LaTeX , git, svn, Visual Studio Code, Eclipse IDE, SQL
- *Internal Systems*: MS Teams, JIRA, Confluence, Jenkins, Salesforce

Research & Work History

Labcorp Diagnostics, Data Science, AI, Clinical Bioinformatics

Bioinformatics IT Manager, November 2021 - Present

- Identify and implement process improvement aligned with industry best practices within bioinformatic scope of clinical assay development, deployment, and production support
- Drive AGILE adoption for ~20 person team of biologists, bioinformaticians, and software engineers
- Develop Tableau Dashboard based on PostgreSQL database populated for production lab QC monitoring

QIAGEN Digital Insights (QDI), Custom Solutions and Services

Interim Custom Services Manager, January 2021 - August 2021

- Managed transcontinental team of 4 bioinformaticians and 4 software engineers
- Sustain multimillion USD client partnerships via 'White Glove' level of care
- Obtain, allocate, and prioritize resources to delight customers and retain talent
- Align with Account Management on feasibility and forecast for projects with 2 weeks LOE to >2 years

QIAGEN Bioinformatics, Custom Solutions

Senior Bioinformatician, May 2016 - January 2021

- Manage multi-year projects for U.S. based high value clients
- Define requirements, scope, and Statement of Work (SOW) for custom bioinformatic solutions and services
- Communicate with clients, Key Account Managers, and developers to define and complete project goals
- Manage testing, release, and support client use of custom bioinformatic software for >25 custom projects

CLC bio, a QIAGEN Company, Advanced Genomics Applications

Senior Scientist, October 2014 - April 2016

- 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 fulfill analysis objectives
- Partner with R&D, Product Management, sales, and marketing for process improvement
- Establish and revise systems and protocols for customer engagement (SalesForce)
- Improve internal resources enabling consistent quality support across the globally integrated team

CLC bio, Customer Support

Application Scientist, January 2012 - October 2014

- Interpret, replicate, and propose solutions for a broad range of customer questions and problems
 - Troubleshoot and guide assessment 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 CLC Workbench, CLC Server, and CLC 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

- Mentor and train junior support colleagues

The Broad Institute of MIT and Harvard, Microbial Systems and Communities

Associate Computational Biologist, January 2010 - January 2012

- Develop and maintain 454 16S filtering and classification pipeline [Perl, L^AT_EX, R, mothur]
- Process 16 ongoing 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
- Install, support, and maintain group specific software [mothur, RDP, usearch, JalView, etc.]

The Broad Institute of MIT and Harvard, Assembly Computation and Development Core

Bioinformatics Assembly Analyst, July 2007 - January 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 gonnorea* 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 misassemblies 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
- Mentor three junior analysts to successfully accomplish similar responsibilities
- Assess new sequencing technologies for de novo assembly: Illuminia (Solexa), Pacific Biosciences

Rensselaer Polytechnic Institute, Rensselaer Exploratory Center for Cheminformatics Research

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, perform descriptor calculations, and model generation
- Webmaster for the Rensselaer Exploratory Center for Cheminformatics Research (RECCR)

Teaching Experience

Rensselaer Polytechnic Institute, Advising and Learning Assistance Center

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, RPI Biology Department

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, Bioinformatics and Molecular Biology
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

Scrum Alliance, Concepts and Beyond
CSPO, October 2022

- Certified Scrum Product Owner (CSPO)
- Certificant ID: 001426943 Certification Active through: 06 October 2024

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.

Leadership

- 2023: Labcorp Labratorian of the Year
- 2019 - 2023: Lucas County Child Services Foster Parent
- 2007-2012: Association for Women in Science (AWIS) Active Member; MA
- 2007-2009: Ubuntu Local Community (LoCo) Team Member; MA
- 2006: Archer Center Leadership Conference Host; RPI
- 2005-2007: Women's Mentor Program: Mentor; RPI
- 2005-2007: Society of Biological Sciences: Secretary/Webmaster; RPI

Awards and Honors

- 2007: Beta Beta Beta Biological Honors Society
- 2003-2007: RPI Dean's List
- 2003-2007: Rensselaer Medal