

Theresa Wohlever
5006 Valencia Drive
Toledo, OH 43623

February 21, 2023

Invitae Recruitment and Hiring Team
Invitae Corp.
1400 16th Street
San Francisco, CA 94103

Dear Invitae Recruitment and Hiring Team,

I am a seasoned remote Bioinformatics IT Manager who will quickly prove to be an asset to Invitae's mission. I have demonstrated success translating customer needs to clear software and analysis requirements for all U.S. based QIAGEN Digital Insight secondary analysis clients. I am well versed in the challenges associated with working from home every day brings. Today, I consistently leap over hurdles associated with managing remotely with acumen and grace.

I was early to flattening the covid19 curve when I became a fully remote employee in 2013. I left Boston, MA and continued my role at CLC bio, a QIAGEN company. My manager made it clear I was an essential asset to the team and ensured I was fully supported in this transition to continuously working from home.


Leadership asked If I would run my team through periods of my remote career with QIAGEN. I graciously accepted each instance with the understanding that a fully remote manager was not a permanent solution. I look back on those experiences with fondness. I enjoyed lifting up my [interim] reports to become their best selves resulting in high quality outcomes from California to Denmark to Romania.

Through my management experience, I learned I enjoy the thrill of successfully negotiating interpersonal conflict more than the thrill of finding an unintentional assignment (=) instead of evaluation (==). The art of translating clinician needs into feasible software requirements brings me more joy than convincing my shell to use JRE 1.8 for GATK. I find bringing together diverse individuals to overcome the impossible through their complementary strengths more rewarding than my accomplishments as an individual.

There are world class scientists who prefer disciplined deep work over leading a team. They often fear the challenges associated with navigating complex interpersonal relationships, but I embrace the challenge. Experience taught me excellence does not come through fear, but by ego-less pursuit of a clear vision. I'm not afraid of rooms where I am the least intelligent; I'm afraid of silencing voices with the most informed insight. I'm not afraid of shifting priorities; I'm afraid of failing to follow AGILE practices that enable effective response. I'm not afraid of hard choices; I'm afraid of paralyzing indecision. I'm not afraid of failure; I'm afraid of repeating the same mistakes and falling into complacent mediocrity.

Given my experience, demonstrated success, and passion for quality healthcare I will be a Bioinformatics Operations Manager who "consistently exceeds expectations" at Invitae.

Best wishes,


Theresa Wohlever

Theresa Wohlever

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Experienced remote Bioinformatics IT Manager with a passion for cultivating new talent and process improvement. Demonstrated success translating high profile client needs to clear software development requirements. *Seeking opportunities to grow into a Director role while furthering the mission of improved patient care* 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, Eclipse IDE, SQL
- *Internal Systems*: MS Teams, JIRA, Confluence, Jenkins, Salesforce

Research & Work History

Labcorp Toledo, OH

Bioinformatic IT Manager, Nov. 2021 - Present

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QIAGEN Digital Insights (QDI) Toledo, OH

Custom Services Manager, Jan. 2021 - Aug. 2021

- Lead transcontinental team of 4 bioinformaticians and 4 software engineers
- Set customer expectations regarding deliverables and timelines for custom service projects
- Obtain, allocate, and prioritize resources to meet customer expectations
- Sustain multimillion USD client partnerships via "White Glove" level of care

QIAGEN Bioinformatics Chicago, IL

Senior Bioinformatician, May 2016 - Jan. 2021

- Manage software releases for over 25 custom projects
- Manage multi-year projects for many high value clients
- Define requirements, scope, and Statement of Work (SOW) for custom bioinformatic solutions and services
- Communicate with clients and developers to define and implement project requirements
- Test, release, and support client use of custom bioinformatic software

QIAGEN Bioinformatics Chicago, IL

Senior Scientist, Oct. 2014 - Apr. 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
- 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
- Contribute to internal documentation for consistent quality support across the globally 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 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 support colleagues through support system transitions

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 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 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 cholerae*, HMP, *E. coli*, *Staphylococcus aureus*, and *Neisseria gonnorrhoea* 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
- Preliminary analysis of new sequencing technologies for assembly: Illumina (Solexa), 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, perform 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.

Leadership

- 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