Theresa Wohlever
1555 Barrington Dr.
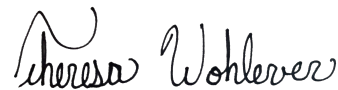Wexford, PA 15090

December 20, 2023

Katz Admissions
3950 Roberto Clemente Dr.
Pittsburgh, PA 15260

Dear Katz Admissions,

A week of persistent phone calls, emails, and a healthy dose of pleading finally resulted in transferring 300 pages of my children's medical history to our new pediatrician. We haven't attempted the records from talk therapy, occupational therapy, speech therapy, or psychiatry. It's not urgent; we're on waiting lists. As an adoptive parent of former foster youth with trauma history, I am familiar with the challenges of coordinating healthcare. This is considered best in class. Within the scope of IT, contemporary healthcare is trapped in the class of 1984. Joining in "Two Minutes Hate" is tempting; instead I will direct my passion to lowering the hurdle for children like ours to access appropriate care. My primary post-graduate goal is to make dramatic improvement in healthcare IT as a Product Manager.

While my formal education is in bioinformatic software development, my most fulfilling successes are connecting cross-functional teams to symbiotic solutions. Pursuit of productive collaboration by courageously and tactfully working through crucial conversations is my cultivated strength. My role in professional services taught me how easy it is to immediately commit "yes" to client requests. However, transparency and integrity prove higher value long-term benefits over positive yet fleeting social encounters. When scope, schedule, and budget are out of balance, all parties are dissatisfied. I aim to align these fronts within Healthcare IT by leveraging my strength as patient advocate, technical translator, and project manager with the skills I gain through the Katz Business school to become an impactful Product Manager.

Best wishes,

Theresa Wohlever

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 Product Management opportunities to drive positive impact in healthcare systems (EHR)** through emphasizing team focused values, AGILE philosophy, and continuous learning.

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

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, LaTeX, 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, 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 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