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SUMMARY: Engineering leader with over twenty years experience who is *passionate about creating powerful and usable software that betters the human condition.*

EXPERIENCE: **Navio**   Portland, OR (remote)
(selected) *Head of Engineering*   Jul 2019 – Dec 2022
- Founding engineer at this seed stage **healthtech** startup that helps cancer patients better understand and keep track of their own care while gathering valuable real world data (RWD) and outcomes to improve care for all.
- Architected and led development of Navio's **no-code SaaS** for engaged patient experiences. Includes: patient, provider, admin and analyst UXs; SMS/email reminders and notifications with rich iCal-based scheduling; no-code UI and experience builder; EHR, HIE and medical records integrations; medical ontology; medication adherence and tracking; patient-reported outcomes (PROs); surveys.
- Responsible for overall **technical strategy and product direction**; hiring and remotely leading a team of 8 engineers (mix of on-staff and contract).
- Owned technical compliance, and aided in fundraising and acquisition diligence.

Myriad Genetics   San Francisco, CA (remote from Portland, OR)
Director of Software Engineering   Aug 2018 – Jul 2019
- Led development of "Counsyl Complete" insurance pricing estimation and **healthcare provider workflow** tools, cited as key asset in $375M acquisition of Counsyl by Myriad Genetics.
- **Hired and led** teams of up to 15 software engineers across multiple geographic locations and technology stacks. Developed technical roadmaps and product plans. Ran SCRUMs/sprints. Shipped software on time.

Counsyl, Inc   South San Francisco, CA (remote from Portland, OR)
Director, Software Engineering   March 2018 – Aug 2018
Engineering Manager, Senior Engineering Manager   Jan 2017 – March 2018
Software Engineer, Senior Software Engineer   Nov 2013 – Jan 2017
- Pivotal technical role on pricing strategy team that created **insurance cost estimates** system to solve critical reimbursement challenges.
- Developed pricing estimation **algorithms** and **user interface**, tightly integrated with existing in-house insurance billing software on Python, Django, Postgres, ElasticSearch, REST, React/Redux stack. Knew nothing about healthcare billing when beginning this project.
- Architected and integrated multiple internal and third-party APIs for insurance benefits, claims filing, genetic testing results.
- **Lead engineer for multiple teams** of up to 6 software engineers to make 4 rounds of backend and experience enhancements to this estimation system over 3

years, each shipping on time, and resulting in up to 25% increase in patient satisfaction.
– Implemented **WebGL/Javascript/HTML5** robot teaching tool for **high-throughput DNA sequencing lab**. Used to train/visualize paths of Staubli robot arms.

Thetus Corp.   Portland, OR
Lead Software Developer, Senior Software Developer   Feb 2010–Oct 2013
– Software architecture and development in semantic knowledge modeling for geospatial / **intelligence analyst notebook** software; large scale data architecture. Led of teams of 4-6 engineers. Java, Javascript, Flash/Actionscript, bespoke RDF Triple Store, Postgres.

Proteome Software   Portland, OR
Staff Scientist   May 2008–Feb 2010
– Designed, architected and led development of **rich web service** for quality control of scientific instrumentation data. **Flex**, Flash, **Java**, Hibernate, MySQL, REST/JSON, **Amazon Cloud AWS** hosted. Concept to product in three months.
– Developed, maintained and debugged Java Swing protein identification software.
– **Managed** in-house and contract developers; optimized Java Swing data analysis UI for protein identification.

Mayo Clinic Proteomics Research Center (MPRC)   Rochester, MN
Senior Analyst Programmer, Analyst Programmer   August 2003–April 2008
– **Hired and led a team** of bioinformatics developers; helped secure >$3M in grants.
– Authored three and co-authored four peer-reviewed articles on analysis of mass spectrometry data with a focus on **algorithms** for **biomarker discovery** by LC-MS.
– Developed open source, object-oriented library (libmprc) in **C++** & **R** for analyzing terabyte-scale **high-resolution mass spectrometry** datasets.
– Led development of protein identification workflow system using **Java**/Servlets, **GWT**, JMS, Groovy, **Hibernate**/Oracle, Grid Engine.
– Developed **3D OpenGL** LC-MS chromatogram visualization tool used for quality control.

Sequel Genetics, Inc.   Pittsburgh, PA
Software Group Leader, Programmer   May 2000 – May 2002
– Established Sequel's informatics team. Hired and managed developers.
– Designed and built mass spectrometry data analysis/visualization tool for Sequel's proprietary peptide-mass-signature genotyping process in **C++, Java Swing**

EDUCATION: BS in **Biological Sciences and Computer Science**   Carnegie Mellon Univ. May 2001
Honors: Merck Computational Biology Summer Scholar, 1999.

PERSONAL PROJECTS:

Bluetooth Low Energy (BLE) bus arrival display, E-paper screen, ARM MCU, custom circuit board layout (PCB), firmware, javascript host software.

Open Source C++ Bluetooth Low Energy SDK. Used in commercial projects.

Music Looping Pedal: hardware and python plugin for Ableton.

PUBLICATIONS: *A method for automatically interpreting mass spectra of ^{18}O labeled isotopic clusters.*
(selected)   Mason CJ, Therneau TM, Eckel-Passow JE, Johnson KL, Oberg AL, Olson JE, Nair KS, Muddiman DC, and Bergen HR III. **Molecular and Cellular Proteomics** 2007, 6:305-318.

Regression analysis for comparing protein samples with $^{16}O/^{18}O$ stable-isotope labeled mass spectrometry. Eckel-Passow JE, Oberg AL, Therneau TM, Mason CJ, Mahoney DW, Johnson KL, Olson JE and Bergen HR III. **Bioinformatics** 2006 22(22):2739-2745.

Reproducibility of Retention Time using a Splitless nanoLC Coupled to an ESI-FTICR Mass Spectrometer. Mason CJ, Johnson KL, Muddiman DC. **Journal of Biomolecular Techniques** 2005 16:414-422.

Analysis of the Low Molecular Weight Fraction of Serum by LC-DualESI-FT-ICR Mass Spectrometry: Precision of Retention Time, Mass, and Amplitude. Johnson KL, Mason CJ, Muddiman DC, Eckel JE. **Analytical Chemistry** 2004 Sep 1;76(17):5097-103. (co-first author)

Detection of genetic variants of transthyretin by liquid chromatography-dual electrospray ionization fourier-transform ion-cyclotron-resonance mass spectrometry. Nepomuceno AI, Mason CJ, Muddiman DC, Bergen HR 3rd, Zeldenrust SR. **Clinical Chemistry** 2004 Sep;50(9):1535-43.

Detection of cystic fibrosis mutations by peptide mass signature genotyping. Malehorn DE, Telmer CA, McEwen SB, An J, Kinsey AD, Retchless AC, Mason C, Vieta WM, Jarvik JW. **Clinical Chemistry** 2003 Aug;49(8):1318-30.

PRESENTATIONS: *Introduction to Mass Spectrometry Based Proteomics.* Christopher J Mason. Invited Presentation. Eastern North American Region/**International Biometric Society**. March 2007.

RAAMS: An algorithm for automatically interpreting mass spectra of ^{18}O labeled isotopic clusters. Mason CJ; Eckel-Passow JE; Johnson KL; Therneau TM; Oberg AL; Muddiman DC; Bergen, HR III. Poster. **American Society for Mass Spectrometry**, 2006.

Informatics Techniques for Biomarker Discovery in Serum using LC-FT-ICR Mass Spectrometry. Mason CJ; Hawkridge AM; Muddiman DC; Johnson KL; Oberg AL. Oral Presentation. **American Society for Mass Spectrometry**, 2004.