JOHN T. PRINCE

Curriculum vitae

https://github.com/jtprince/portfolio

POSITIONS

Senior Platform Engineer
Aug 2020 – present. Engineering department, Owlet Baby Care, Lehi, Utah.
- Collaborating on and implementing schema-first Open API 3 endpoints
- Modification and implementation of endpoint monitoring
- Codefresh CI/CD modifications and enhancements
- Rewriting Python test suites used in microservices
- On-call duties monitoring dozens of kubernetes deployments and services
- Optimizing gunicorn and kubernetes health check parameters for microservices with investigation/presentation in Seaborn

Senior Data Engineer (Technical lead and Manager)
Apr 2019 – Aug 2020. Engineering department, 3plCentral, American Fork, Utah.
- Led new data engineer team to create event driven data platform in AWS
- Event driven processing system using Kafka and Faust (async python)
- Multi-tenant relational database to serve as data warehouse
- Order-volume dashboard and inventory reporting flask-based REST APIs (served with AWS Fargate)
- Middleware (authorization) using AWS lambda and JSON web tokens
- Product sunset analysis of ~3000 rdl (xml+sql) files
- Created or modified much of our team's gitlab CI/CD pipeline

Data Scientist & Senior Software Engineer
Sep 2014 – Apr 2019. Technology and Engineering departments, Doba Inc and CruxConnect, Lehi, Utah.
- Designed and implemented CruxConnect Product and Elasticsearch Indexing Models
- Designed and implemented out-of-stock forecasting algorithm (custom non-uniform Holt Winters triple exponential with probabilistic model for low counts).
- Parallel processing with async and utilizing AWS serverless architecture
- Migration of legacy web service to Django/python
- Integration of AWS tools (dynamodb, SQS, lambda, etc) into Doba platform
- Design and implement various RESTful APIs and integrations

Assistant Professor of Chemistry and Biochemistry
Mar 2010 – Aug 2014. Department of Chemistry and Biochemistry, Brigham Young University, Provo, Utah.
- Proteomics and lipidomics using high mass accuracy mass spectrometry
- Label-free quantitative analysis involving extensive software and algorithmic development
- Computational biology and bioinformatics

HHMI Research Specialist (Post-doctoral)
May 2008 – Feb 2010. Department of Chemistry and Biochemistry, University of Colorado, Boulder, Colorado.
  • Mass spectrometric identification of transient protein complexes in melanoma
  • Advisor: Natalie Ahn, HHMI, Past-President of *U.S. Human Proteome Organization*

EDUCATION

PhD in Molecular Biology (Bioinformatics track)
Aug 2001 – May 2008. Institute for Cellular and Molecular Biology (ICMB), Center for Systems and Synthetic Biology, University of Texas (UT), Austin, Texas.
  • Thesis: Integration and Validation of Mass Spectrometry Proteomics Data Sets
  • Advisor: Edward Marcotte, NIH Director's Pioneer Award Recipient
  • Bioinformatics and Computational Biology Track
  • GPA 4.0/4.0

Bachelor of Science in Microbiology
Dec 2000. Department of Biology and Agriculture, Brigham Young University (BYU), Provo, Utah.
  • Minor in Chemistry
  • Graduated *Magna Cum Laude* (3.9/4.0)
  • National Merit Scholar

ANALYTIC AND PROGRAMMING EXPERIENCE

https://github.com/jtprince/portfolio

  • 19+ years total programming experience
  • 7 years enterprise software development experience
  • Dozens of open source projects (> 300,000 downloads) and thousands of scripts
  • Custom analytic solutions dealing with massive, high dimensional data sets
  • Cloud based event-driven solutions
  • Design and implementation of several REST APIs
  • Behavior driven development, DRY, beautiful code

SIGNIFICANT OPEN-SOURCE SOFTWARE

As primary package author
  • django-gtin-fields [repo]
  • mspire [pubmed, rewrite]
  • rubabel [pubmed, repo]
  • mspire-molecular_formula [repo]
  • obi-warp [pubmed, repo, R integration]
  • histogram [repo]
  • rserve-simpler [repo]

As advisor
  • metriculator [pubmed, repo]
  • mspire-simulator [pubmed, repo]
  • JAMSS [pubmed, repo]
  • massifquant [pubmed, part of XCMS R package]
  • lipid classifier [pubmed, repo]

Peer Reviewed Publications (33 total)

First author publications typically indicate primary authorship (i.e., most responsible for work). Last author publications indicate primary advisorship (i.e., most responsible for overall direction and guidance)

Computationally Focused Publications (21)

These publications are focused primarily on computational methods and/or demonstrate significant algorithmic or programming accomplishment.

Probabilistic Generation of Mass Spectrometry Molecular Abundance Variance for Case and Control Replicates. Prince JT, Smith R. *Journal of Proteome Research* **2017**, 16:2429–2434. (after-hours personal project)

Current controlled vocabularies are insufficient to uniquely map molecular entities to mass spectrometry signal. Smith R, Taylor RM, Prince JT. *BMC Bioinformatics* **2015**, 16 Suppl 7:S2.

A coherent mathematical characterization of isotope trace extraction, isotopic envelope extraction, and LC-MS correspondence. Smith R, Prince JT, Ventura D. *BMC Bioinformatics* **2015**, 16 Suppl 7:S1.

Automated structural classification of lipids by machine learning. Taylor RM, Miller RH, Miller RD, Porter M, Dalgleish J, Prince JT. *Bioinformatics* **2015**, 31:621–5.

LC-MS alignment in theory and practice: a comprehensive algorithmic review. Smith R, Ventura D, Prince JT. *Briefings in Bioinformatics* **2015**, 16:104–17.

JAMSS: proteomics mass spectrometry simulation in Java. Smith R, Prince JT. *Bioinformatics* **2015**, 31:791–3.

Massifquant: open-source Kalman filter based XC-MS isotope trace feature detection. Conley CJ, Smith R, Torgrip RJ, Taylor RM, Tautenhahn R, Prince JT. *Bioinformatics* **2014**, 30:2636–43.

Proteomics, lipidomics, metabolomics: A mass spectrometry tutorial from a computer scientist's point of view. Smith R, Mathis AD, Ventura D, Prince JT. *BMC Bioinformatics* **2014**, 15:1–14.

Mspire-Simulator: LC-MS Shotgun Proteomic Simulator for Creating Realistic Gold Standard Data. Noyce AB, Smith R, Dalgleish J, Taylor RM, Erb KC, Okuda N and Prince JT. *Journal of Proteome Research* **2013**, 12:5742–9.

Metriculator: quality assessment for mass spectrometry-based proteomics. Taylor RM, Dance J, Taylor RJ, Prince JT. Bioinformatics **2013**, 29:2948–9.

Controlling for confounding variables in MS-omics protocol: why modularity matters. Smith R, Ventura D, Prince JT. Smith R, Ventura D, Prince JT. *Briefings in Bioinformatics* **2014**, 15:768–70.

Rubabel: Wrapping OpenBabel with Ruby. Smith R, Williamson R, Ventura D, Prince JT. *Journal of Cheminformatics* **2013**, 5:35.

Statistical Agglomeration: Peak Summarization for Direct Infusion Lipidomics. Smith R, Anthonymuthu TS, Ventura D, Prince JT. *Bioinformatics* **2013**, 29:2445–51.

Resolving Double Disulfide Bond Patterns in SNAP25B Using Liquid Chromatography-Ion Trap Mass Spectrometry. Ogawa N, Taylor RM, Woodbury DJ, Prince JT. *Journal of Mass Spectrometry* **2013**, 48:660–8.

Novel Algorithms and the Benefits of Comparative Validation . Smith R, Ventura D, Prince JT. *Bioinformatics* **2013**, 29:1583–5.

Integrating shotgun proteomics and mRNA expression data to improve protein identification. Ramakrishnan SR, Vogel C, Prince JT, Li Z, Penalva LO, Myers M, Marcotte EM, Miranker DP, Wang R. *Bioinformatics* **2009**, 25:1397–403.

mspire: Mass spectrometry proteomics in Ruby. Prince JT and Marcotte EM. *Bioinformatics* **2008**, 24:2796–7.

Chromatographic alignment of ESI-LC-MS datasets by bijective interpolated dynamic time warping. Prince JT and Marcotte EM. *Analytical Chemistry* **2006**, 78:6140–52.

A fast course filtering method for peptide identification by mass spectrometry. Ramakrishnan SR, Rui M, Nakorchevskiy AA, Prince JT, Willard WS, Xu W, Marcotte EM, Miranker DP. *Bioinformatics* **2006**, 22:1524–31.

Mass spectrometry of the M. smegmatis proteome: protein expression levels correlate with function, operons, and codon bias. Wang R, Prince JT, Graham DE, Marcotte EM. *Genome Research* **2005**, 15:1118–26.

The need for a public proteomics repository. Prince JT, Carlson MW, Wang R, Lu P, Marcotte EM. *Nature Biotechnology* **2004**, 22:471–2.

PEER REVIEWED COMPUTATIONAL APPLICATION PUBLICATIONS (11)

These publications are focused primarily on the elucidation of biological phenomena, but they demonstrate application of computational methods (typically in the analysis of mass spectrometry data).

Imbalanced sphingolipid signaling is maintained as a core proponent of a cancerous phenotype in spite of metabolic pressure and epigenetic drift. Speirs MMP, Swensen AC, Chan TY, Jones PM, Holman JC, Harris MB, Maschek JA, Cox JE, Carson RH, Hill JT, Andersen JL, Prince JT, Price JC. *Frontiers in Oncotarget* **2019**, 10:449–79.

Yersinia pseudotuberculosis BarA-UvrY Two-Component Regulatory System Represses Biofilms via CsrB. Schachterle JK, Stewart RM, Schachterle MB, Calder JT, Kang H, Prince JT, Erickson DL. *Frontiers in Cellular Infection Microbiology* **2018**, 8:323.

Whole blood and urine bioactive Hepcidin-25 determination using liquid chromatography mass spectrometry. Swensen AC, Finnell JG, Matias C, Gross AJ, Prince JT, Watt RK, Price JC. *Analytical Biochemistry* **2017**, 517:23–30.

Structures of the Gβ-CCT and PhLP1-Gβ-CCT complexes reveal a mechanism for G-protein β-subunit folding and Gβγ dimer assembly. Plimpton RL, Cuéllar J, Lai CW, Aoba T, Makaju A, Franklin S, Mathis AD, Prince JT, Carrascosa JL, Valpuesta JM, Willardson BM. *Proceedings of the National Academy of Sciences of the United States of America* **2015**, 112:2413–8.

The genomes, proteomes and structure of three novel phages that infect the Bacillus cereus group and carry putative virulence factors. Grose JH, Belnap DM, Jensen JD, Mathis AD, Prince JT, Merrill B, Burnett SH, Breakwell DP. *Journal of Virology* **2014,** 88:11846–60.

Insulin increases ceramide synthesis in skeletal muscle. Hansen ME, Tippetts TS, Anderson MC, Holub ZE, Moulton ER, Swensen AC, Prince JT, Bikman BT. *Journal of Diabetes Research* **2014,** 2014:765784.

A Comprehensive protein-protein interactome for yeast PAS kinase 1 reveals direct inhibition of respiration through the phosphorylation of Cbf1. DeMille D, Bikman BT, Mathis AD, Prince JT, Mackay JT, Sowa SW, Hall TD, Grose JH. *Molecular Biology of the Cell* **2014**, 25:2199–215.

Programmed Cell Death Protein 5 Interacts with the Cytosolic Chaperonin CCT to Regulate β-tubulin Folding. Tracy CM, Gray AJ, Cuellar J, Shaw TS, Howlett AC, Taylor RM, Prince JT, Ahn NG, Valpuesta JM, Willardson BM. *The Journal of Biological Chemistry* **2014**, 289:4490–502.

Mitochondrial fission mediates ceramide-induced metabolic disruption in skeletal muscle. Smith ME, Tippetts TS, Brassfield ES, Tucker BJ, Ockey A, Swensen AC, Anthonymuthu TS, Washburn TD, Kane DA, Prince JT, Bikman BT. Biochemical Journal **2013** 456:427–39.

AICAR Inhibits Ceramide Biosynthesis in Skeletal Muscle. Erickson KA, Smith ME, Anthonymuthu TS, Evanson MJ, Brassfield ES, Hodson AE, Bressler MA, Tucker BJ, Thatcher MO, Prince JT, Hancock CR and Bikman BT. *Diabetology & Metabolic Syndrome* **2012**, 4:45.

Sequence and structural characterization of great salt lake bacteriophage CW02, a member of the T7-like supergroup. Shen PS, Domek MJ, Sanz-García E, Makaju A, Taylor RM, Hoggan R, Culumber MD, Oberg CJ, Breakwell DP, Prince JT, Belnap DM. *J Virology* **2012** 86:7907–17.

Computationally Related Presentations

Enterprise software development from a biochemistry professor's point of view. JT Prince. University of Montana Computer Science Department. **2019**, Sep. (invited)

Definitive Network Reconstruction of the Yeast PAS Kinase Network via Mass Spectrometry Proteomics and Phosphoproteomics. A Mathis, TS Anthonymuthu, S Morley, T Southwick, D DeMille, J Grose, J Adebayo, S Warnick, JT Prince. US Human Proteome Organization Conference. **2012**, Mar.

Metriculator:Quality Assessment for Mass Spectrometry Based Proteomics. RM Taylor, J Dance, JT Prince. US Human Proteome Organization Conference. **2012**, Mar.

The Dynamic Proteome: Capturing proteome-wide protein-protein interactions. *BYU Microbiology & Molecular Biology Seminar.* **2010**, Oct. (invited)

The Open Proteomics Database (OPD) and publishing mass spectrometry based protein identifications. *The Paris Committee on Guidelines for Proteomic Data Publication.* **2005**, May. (invited)

Computationally Related Posters

Label-Free Inter-Smple Replicate Similarity Metrics for LC-MS Data Using Intra-Sample Information. Smith R, Ventura D, Prince JT. *61St American Society for Mass Spectrometry Conference.* **2013**, Jun.

Robust Lipid Fragmentation Modeling to Identify Global Lipid Changes during Epithelial-Mesenchymal Transition (EMT). Coutu B, Alexander K, Hansen M, Prince JT. *61St American Society for Mass Spectrometry Conference.* **2013**, Jun.

Novel Reconstruction of the Per-ARNT-Sim Kinase Network via Mass Spectrometry. Mathis A, Anthonymuthu TS, Morley S, Southwick T, Taylor RM, DeMille D, Adebayo J, Chetty V, Grose J, Warnick S, Prince JT. World HUPO Congress. **2012**, Sep.

Development of an Efficient, Integrated Proteomic Search Engine "Corymb". D Shah, J Pagaduan, J Clegg, RM Taylor, JT Prince. World HUPO Congress. **2012**, Sep.

Mspire-Simulator: LC-MS Simulator for Creating Realistic Gold Standard Data. Noyce AB, Dalgleish J, Taylor RM, Erb KC, Okuda N and Prince JT. World HUPO Congress. **2012**, Sep.

Measure and Model the Dynamic Proteome. Prince JT. *LDS Life Science Research Symposium.* **2010**, Jul.

Concatenated or Separate?: Using sample bias validation to decide between competing database search strategies and meta-engines. Prince JT, Marcotte EM. *56th American Society of Mass Spectrometry Conference.* **2008**, Jun.

Bias in Large Scale Mass Spectrometry Proteomics Protein/Peptide Identification Error Estimates. Prince JT, Marcotte EM. *Keystone Symposium (Cell Signaling and Proteomics).* **2007**, Mar.

Chromatographic Alignment of Multi-Dimensional Mass Spectra using Interpolated Dynamic Time Warping. Prince JT, Marcotte EM. *53rd American Society of Mass Spectrometry Conference.* **2005**, Jun.

Analysis and Identification of Proteins in Human Placental Mitochondria. Prince JT, Fuqua B, Johnson J, Marcotte EM. *Keystone Symposium (Proteomics and Applications).* **2003**, Mar.

Courses Taught

Student ratings range from 1– 8 where 1 is "exceptionally poor", 6 is "good", 7 is "very good", and 8 is "exceptionally good". Ratings are listed as (course/instructor).

CHEM689R. Computational Proteomics (Graduate lvl Special Topics) (1 time: 7.0/7.5)
CHEM391. Technical Writing for Chemists and Biochemists (3 times: 6.8/7.5, 7.5/7.8, 7.1/7.9)
CHEM481. Biochemistry (3 times: 6.7/7.2 most recently)

4.2 of 5 on rate my professors

Leadership, Societies & Review

Reviewer (ad-hoc), Bioinformatics. 2011 – 2014.
Reviewer (ad-hoc), Analytical Chemistry. 2011 – 2014.
Reviewer (ad-hoc), Journal of Proteome Research. 2011 – 2014.
Co-Founder and Co-Director of SciRuby and Vice President of Ruby Science Foundation. 2011 – 2014.
Member, Human Proteome Organization. 2011 – 2014.
Member, U.S. Human Proteome Organization. 2010 – 2014.
Member, Colorado Biological Mass Spectrometry Society. 2008 – 2010.
Member, American Society for Mass Spectrometry. 2005 – 2006.
Founder, Cell and Molecular Biology Graduate Student Association. 2004. University of Texas, Austin, Texas.
Member, Society for Computational Biology. 2002 – 2005. University of Texas, Austin, Texas.
Member, Golden Key National Honor Society. 2000 – Present.
Vice President, Health Occupations Students of America. 1999 – 2000. Brigham Young University Chapter, Provo, Utah.

Honors & Awards

Whitney M. Young Jr. 2008. Capitol Area Council, Austin, Texas. For "outstanding service by an adult individual … for demonstrated involvement in the development and implementation of Scouting opportunities for youth from … low-income urban backgrounds."
Department of Energy Scholarship (Proteomics and Applications). 2003. Keystone Symposium, Keystone, Colorado.
ICMB Research Assistantship. 2001. Institute for Cellular and Molecular Biology, University of Texas, Austin, Texas.
ICMB Graduate Fellowship Award (Supplementary). 2001 – 2005. Institute for Cellular and Molecular Biology, University of Texas, Austin, Texas.
Cancer Research Center Summer Fellowship. 1999. Brigham Young University, Provo, Utah.
Office of Research and Creative Activities Scholarship. 1999. Brigham Young University, Provo, Utah.
Trustees Scholarship (Full Tuition). 1994. Brigham Young University, Provo, Utah.
National Merit Scholarship. 1994. Manor High School, Manor, Texas.
Robert Byrd Scholarship. 1994. Manor High School, Manor, Texas.
Applied Materials Scholarship. 1994. Manor High School, Manor, Texas.
1st in High School Class. 1994. Manor High School, Manor, Texas.
Eagle Scout Award. 1993. Boy Scouts of America, Baton Rouge, Louisiana.

Professional Development

Intro to Machine Learning: Language Processing. 2019. Dec. AICamp. Tensorflow, google cloud, and language interfaces.

Genomics in Education Workshop. 2012. 14 hours. DNA Learning Center of Cold Spring Harbor Laboratory and iPlant Collaborative, held at BYU. Training on integrating wet lab and bioinformatics tools in a classroom setting.

The Art and Craft of Mixed Models. 2011. June 15 – 17. Summer Institute of Applied Statistics, BYU.

Writing Matters Seminar. 2011. June 20 – 24. University Writing & Dept of English, BYU.

Volunteer Experience

Co-founder 2018 – 2020. Community in Dialogue: Members and Former members of the Church of Jesus Christ of Latter-day Saints, BYU Dept of Religious Education, Provo, Utah.

Scout Leader (11yr old) 2014 – 2015. Troop 1376, Boy Scouts of America, Provo, Utah.

Scoutmaster 2011 – 2014. Troop 1376, Boy Scouts of America, Provo, Utah.

Assistant Scoutmaster 2010. Troop 1376, Boy Scouts of America, Provo, Utah.

Den Leader 2008 – 2009. Troop 364, Boy Scouts of America,.

Scoutmaster 2002 – 2007. Troop 100, Boy Scouts of America, Austin, Texas.

Tutor, Organic Chemistry Winter 1998. Brigham Young University, Provo, Utah.

CONTACT

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Lehi, UT 84043

(801) 636-4847
jprince@owletcare.com
jtprince@gmail.com

REFERENCES

Each of the individuals listed below have extensive experience with my work and character.

Rob Smith, PhD
Former student and scientific collaborator
Assistant Professor of Computer Science and CEO of Prime Labs
(National Science Foundation CAREER Award recipient)
robert.smith@mso.umt.edu
1-406-243-2886

> "John is a rare breed. He couples broad scientific expertise (as an expert programmer, bioinformatician, and chemist) with a personality that makes him enjoyable to work with. I've worked with John extensively on open source bioinformatics tools, academic research papers, and grants. He is probably the most clever programmer I know. Watching him solve problems is fascinating because I always learn some new technique." (LinkedIn Recommendation)

Dusty Chadwick
Backend software engineering teammate at Doba Inc. and CruxConnect
AWS, Serverless Cloud architect, former CTO of Room Choice
me@dchadwick.com
1-801-610-9855

> "John is so incredibly dynamic that he naturally becomes an informative resource on just about any topic. He is never satisfied by not having fully researched a topic to the point that he understands it at an expert level. … As our lead data scientist, we regularly engaged his personality for data understanding as well as his investigational skills in helping to define our core architecture around elasticsearch and heavy data transactions. … Working with him to develop our next generation platform, it was exciting to see him build code through OOP in a way that felt organic and evolutionary. He was able to grow this codebase easily and mutate it as the platform changed." (LinkedIn Recommendation)

Ben Reece
Former CTO of Doba Inc.
Sr. Software Engineer at BambooHR
1-559-927-3323

> "John is the man you want on your team when you need to tackle an especially challenging problem, particularly one that requires significant research. He's very thorough in his approach, and when he's happy with his solution, rest assured that it's clean, elegant, and well-presented." (LinkedIn Recommendation)

Brian Sevy
My product manager (Business Intelligence) and Product Leader at 3plCentral
Product Leader
1-916-799-6195

Erik Cornelsen
Team member on my Data Science/Engineering team at 3plCentral
Data Engineer at 3plCentral
1-801-361-5685

Cody Holdaway
Team member on my Data Science/Engineering team at 3plCentral
Data Science Engineer at 3plCentral
1-801-361-5685

Jeff Fischer
My engineering manager at Doba Inc. and CruxConnect
Senior Software Engineer and Engineering Manager at Crux Connect
1-801-361-5685

Jason Weir
(My current manager at Owlet)
Former co-worker and frequent UI pair at Doba Inc. and CruxConnect
Engieering Manager at Crux Connect and Platform Manager at Owlet Baby Care
1-801-471-7163

Paul Barker
CEO of the fledgling company for which I frequently perform pro-bono ETL work
CEO of XT Outfitters
1-801-360-8695

Greg Burton
My Department Chair when I left BYU
Professor Emeritus
gburton@chem.byu.edu

*I've had an excellent working relationship with all of my supervisors, colleagues, and co-workers and believe that I have earned their trust and respect. **As appropriate for a given employment opportunity**, feel free to seek a reference from anyone at any of the institutions where I've worked, and I am happy to provide additional referrals on request.*