

CURRICULUM VITAE

Damon H. May
Bioinformatics Analyst
Computational Biology Program
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Educational Background

2014- University of Washington, Seattle, Washington. PhD Candidate, Department of Genome Sciences
2005 University of Washington, Seattle, Washington. MS, Computer Science & Engineering
1998 Yale University, New Haven, Connecticut. BS with Distinction, Computer Science

Professional Positions

2012-2014 Bioinformatics Analyst, Optides Program (Olson Lab), Fred Hutchinson Cancer Research Center, Seattle, Washington
2005-2012 Scientific Software Engineer, Computational Biology Program (McIntosh Lab), Fred Hutchinson Cancer Research Center, Seattle, Washington
2004-2005 Senior Development Manager, Oracle Supplier Network, Oracle Corporation, Seattle, WA
2002-2004 Senior Principal Consultant, eXtension Management Services, Oracle Corporation, Seattle, WA
2001-2002 Development Manager, Oracle Exchange Platform, Oracle Corporation, Redwood Shores, CA
1998-2001 Applications Engineer and Project Leader, Manufacturing Applications, Oracle Corporation, Redwood Shores, CA

Awards / Fellowships

2015 National Defense Science and Engineering Graduate (NDSEG) Fellowship
2015 National Science Foundation Graduate Research Fellowship Honorable Mention

Publications in Refereed Journals

1. **May D**, Tamura K, Noble W. Param-Medic: Automatic inference of optimal mass spectrometry search parameters. J Proteome Res. 2017. DOI: 10.1021/acs.jproteome.7b00028.
2. Timmins-Schiffman E, **May D**, Mikan M, Riffle M, Frazar C, Harvey H, Noble W, Nunn B. Critical decisions in metaproteomics: Achieving high confidence protein annotations in a sea of unknowns. ISME J. 2016. DOI: 10.1038/ismej.2016.132
3. **May DH**, Timmins-Schiffman E, Mikan MP, Harvey HR, Borenstein E, Nunn BL, Noble WS. An alignment-free 'metapeptide' strategy for metaproteomic characterization of microbiome samples using shotgun metagenomic sequencing. J Proteome Res. 2016. DOI: 10.1021/acs.jproteome.6b00239

4. Chen R, Dawson D, Pan S, Ottenho N, de Wilde R, Wolfgang C, **May DH**, Crispin D, Lai L, Lay A, Waghray M, Wang S, McIntosh M, Simeone D, Maitra A, Brentnall T. Proteins associated with pancreatic cancer survival in patients with resectable pancreatic ductal adenocarcinoma. *Laboratory Investigation*. 2015;95:43-55
5. Pan S, Chen R, Tamura Y, Crispin DA, Lai, LA, **May DH**, McIntosh MW, Goodlett DR, Brentnall TA. Quantitative Glycoproteomics Analysis Reveals Changes in N-Glycosylation Level Associated with Pancreatic Ductal Adenocarcinoma. *J Proteome Res*. 2014;13(3):1293-1306
6. **May DH**, Navarro S, Ruczinski I, Hogan J, Ogata Y, Schwarz Y, Levy L, Holzman T, McIntosh MW. Metabolomic profiling of urine: response to a randomised, controlled feeding study of select fruits and vegetables, and application to an observational study. *Br J Nutr*. 2013;110(10):1760-70
7. Herbrich SM, Cole RN, West KP, Schulze K, Yager JD, Groopman JD, Christian P, Wu L, O'Meally RN, **May DH**, McIntosh MW, Ruczinski I. Statistical inference from multiple iTRAQ experiments without using common reference standards. *J Proteome Res*. 2013;12(2):594-604
8. Pan S, Tamura Y, Chen R, **May D**, McIntosh MW and Brentnall TA. Large-scale quantitative glycoproteomics analysis of site-specific glycosylation occupancy. *Mol BioSyst*. 2012;8(11):2850-6
9. Bates JG, Salzman J, **May D**, Garcia PB, Hogan GJ, McIntosh M, Schlissel MS, Brown PO. Extensive gene-specific translational reprogramming in a model of B cell differentiation and Abl-dependent transformation. *PLoS One*. 2012;7(5):e37108
10. Pan S, Chen R, Stevens T, Bronner MP, **May D**, Tamura Y, McIntosh MW, Brentnall TA. Proteomics portrait of archival lesions of chronic pancreatitis. *PLoS One*. 2011;6(11):e27574
11. Pan S, Chen R, Crispin DA, **May D**, Stevens T, McIntosh MW, Bronner MP, Ziogas A, Anton-Culver H, Brentnall TA. Protein alterations associated with pancreatic cancer and chronic pancreatitis found in human plasma using global quantitative proteomics profiling. *J Proteome Res*. 2011;10(5):2359-76
12. **May D**, Pan S, Crispin D, Lai K, Bronner MP, Hogan J, Hockenbery DM, McIntosh MW, Brentnall T, Chen R. Investigating neoplastic progression of ulcerative colitis with label-free comparative proteomics. *J Proteome Res*. 2010;10(1):200-9
13. Chen R, Crispin DA, Pan S, Hawley S, McIntosh MW, **May D**, Anton-Culver H, Ziogas A, Bronner MP, Brentnall TA. Pilot study of blood biomarker candidates for detection of pancreatic cancer. *Pancreas*. 2010;39(7):981-8
14. Reimel BA, Pan S, **May DH**, Shaffer SA, Goodlett DR, McIntosh MW, Yerian LM, Bronner MP, Chen R, Brentnall TA. Proteomics on fixed tissue specimens - A Review. *Curr Proteomics*. 2009;6(1):63-69
15. **May D**, Law W, Fitzgibbon MP, Fang Q, McIntosh M. A software platform for rapidly creating computational tools for mass spectrometry-based proteomics. *J Proteome Res*. 2009;8(6):3212-7
16. Fang Q, Strand A, Law W, Faca VM, Fitzgibbon MP, Hamel N, Houle B, Liu X, **May DH**, Poschmann G, Roy L, Stühler K, Ying W, Zhang J, Zheng Z, Bergeron JJ, Hanash S, He F, Leavitt BR, Meyer HE, Qian X, McIntosh MW. Brain-specific proteins decline in the cerebrospinal fluid of humans with Huntington disease. *Mol Cell Proteomics*. 2009;8(3):451-66
17. **May D**, Liu Y, Law W, Fitzgibbon M, Wang H, Hanash S, McIntosh M. Peptide sequence confidence in accurate mass and time analysis and its use in complex proteomics experiments. *J Proteome Res*. 2008;7(12):5148-56
18. Martin DB, Holzman T, **May D**, Peterson A, Eastham A, Eng J, and McIntosh M. MRMer: An interactive open-source and cross-platform system for data extraction and visualization of multiple reaction monitoring experiments. *Mol Cell Proteomics*. 2008;7(11):2270-8

19. Fitzgibbon M, Law W, **May D**, Detter A, McIntosh M. Open-source platform for the analysis of liquid chromatography-mass spectrometry (LC-MS) data. *Methods Mol Biol.* 2008;428:369-82.
20. **May D**, Fitzgibbon M, Liu Y, Holzman T, Eng J, Whiteaker J, Paulovich A, McIntosh M. A platform for accurate mass and time analyses of mass spectrometry data. *J Proteome Res.* 2007;6(7):2685-94
21. Bellew M, Coram M, Fitzgibbon M, Igra M, Randolph T, Wang P, **May D**, Eng J, Fang R, Lin CW, Chen J, Goodlet D, Whiteaker J, Paulovich A, McIntosh M. A suite of algorithms for the comprehensive analysis of complex protein mixtures using high-resolution LC-MS. *Bioinformatics.* 2006;22(15):1902-9

Selected Scientific Posters

1. **May D**, Tamura K, Noble W. Param-Medic: breathing new life into MS/MS database search. Presented at the American Society for Mass Spectrometry 65th Conference on Mass Spectrometry and Allied Topics, Indianapolis, IN. June 4-8, 2017.
2. **May D**, Navarro S, Ruczinski I, Hogan J, Ogata Y, Schwarz Y, Levy L, Holzman T, Lampe J, McIntosh M. Profiling metabolomic changes in urine in response to a controlled feeding study of select fruits and vegetables. Presented at the USHUPO 8th Annual Conference, San Francisco, CA. Mar 4-7, 2012.
3. **May D**, Liu Y, Law W, Fitzgibbon M, Wang H, Hanash S, McIntosh M. Probability assignment and protein inference for accurate mass and time analysis: using high-resolution LC-MS data in complex MS/MS experiments. Presented at the HUPO 7th Annual World Congress, Amsterdam, Netherlands. Aug 16-20, 2008.
4. **May D**, Fitzgibbon M, McIntosh M. Accurate mass and time methods with extensively fractionated data. Presented at the HUPO 6th Annual World Congress, Seoul, South Korea. October 6-10, 2007.
5. **May D**, Fitzgibbon M, McIntosh M. Post-Acquisition Mass Calibration and Filtering of High-Resolution Mass Spectrometry Data. Presented at USHUPO 3rd Annual Conference, Seattle, WA. March 5-8, 2007.

Distributed (Published) Software

(Accessible at proteomics.fhcrc.org)

1. Mass spectrometry in-silico peptide characterization tool (msInspect): a suite of software for quantitative signal processing of high-resolution mass spectrometry data, distributed beginning 2005.
2. Qurate: A platform for visual inspection of quantitative mass spectrometry experiments.
3. msInspect/AMT: a suite of tools for Accurate Mass and Time analysis of LC-MS peptide data
4. Sixgill: a tool for constructing peptide databases from shotgun metagenomic sequencing
5. Param-medic: a tool for inferring mass error in MS/MS experiments

Scientific Presentations

- 2016 Investigating metaproteomes with databases of translated metagenomic sequencing reads. Cascadia Proteomics Symposium. Seattle, WA, July 11, 2016

- 2012 Metabologna: Metabolomic Profiling of Urine in Response to a Controlled Feeding Study of Fruits, Soy, and Vegetables. Metabolomics User Group Seminar Series, Institute of Translational Health Sciences. Seattle, WA, February 1, 2012
- 2007 Accurate Mass and Time Analysis Techniques Applied to Extensively Fractionated Data. Human Proteome Organization 6th Annual World Conference. Oral presentation at colloquium: "Technology and Strategy for Proteomic Analysis". Seoul, South Korea, October 9, 2007

Teaching

- 2014 Keynote talk: Nature's Drugs. Northwest Association for Biomedical Research BioExpo (high school science fair). Seattle, WA, May 22, 2014
- 2010 Advanced Proteomics Data Analysis Course (taught with three other instructors). Instituto Nacional de Proteómica, Barcelona, Spain, January 25-28, 2012
- 2007-2008 Software Methods for LC-MS Data Analysis. Mass Spectrometry-Based Proteomics Course. Fred Hutchinson Cancer Research Center, Seattle, WA. (annual internal course)
- 2007 CPAS (Comparative Proteomics Analysis System) Analysis Overview. ICBC Bioinformatics Workshop, International Cancer Biomarker Consortium. Seoul, South Korea, October 5, 2007

Book Chapter

Fitzgibbon M, Law W, **May D**, Detter A, and McIntosh M. Open-source platform for the analysis of liquid chromatography-mass spectrometry (LC-MS) data. Chapter in Clinical Proteomics in the Methods in Molecular Biology series, Humana Press, 2007, Edited by Antonia Vlahou.