BIEMANN MEDAL

2015 Recipient: Michael J. MacCoss

Award Lecture: 4:45 pm, Tuesday, Hall 5, level 1

Dr. Michael J. MacCoss has made a number of contributions of serious and long lasting impact to the field of proteomics. Chief among these is software development that has greatly facilitated proteomics. Dr. MacCoss' philosophy on making software freely available and continually supporting this software so that it enables others has greatly benefitted the proteomic sciences.

Bioinformatics tools developed by the MacCoss laboratory facilitate many different aspects of mass spectrometry data analysis. This includes tools for liquid chromatography mass spectrometry (LC-MS) feature finding, spectrum library searching, peak detection, post-processors for peptide database searching, and more. An important early contribution from his lab, the Percolator algorithm, improved peptide identifications from proteomic analyses through semi-supervised machine learning (Käll *et al.* "Semi-supervised learning for peptide identification from shotgun proteomics datasets," *Nature Methods*, 2007). Percolator became widely adopted partially because of its use of a liberal open source license that encouraged companies to build on Percolator and incorporate into commercial packages (e.g. Mascot and Proteome Discoverer). Another high-impact contribution from the MacCoss laboratory is the development and continued support of an integrated set of software tools called Skyline (MacLean *et al.* "Skyline: an open source document editor for creating and analyzing targeted proteomics experiments*"* *Bioinformatics*, 2010; available from http://skyline.maccosslab.org). Critically, Skyline is a vendor-neutral toolset, thus enabling methods to be easily transferred and tested across labs, even those that utilize different instrument platforms. Dr. MacCoss has also substantially advanced the new area of data-independent MS analyses. His key contribution in this area has been to develop a multiplexed strategy to better isolate noise and improve signal detection and therefore sensitivity through observational coherence (Egertson *et al.*, *Nature Methods* 2013).

One of the most recent projects championed by Dr. MacCoss is a nonprofit to provide a cost effective mechanism for labs to backup, share, visualize, and analyze data on the cloud called The Chorus Project (http://chorusproject.org). They are working with developers in academic labs and companies to offer tools to our community that can process mass spectrometry data stored within Chorus. The hope is to provide a platform where all labs have access to the latest analysis tools and published data can be easily reanalyzed.

Dr. MacCoss is professor in the Department of Genome Sciences, University of Washington, Seattle.

2015 RESEARCH AWARDS

Award Presentation: 4:45 pm, Tuesday, Hall 5

The Research Awards are fully funded by Thermo Scientific and Waters Corporation in the amount of $35,000 each.

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