

Taming Errors for Peptides with Post-Translational Modifications; Bioinformatics Interest Group

Presenters

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Coordinators

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The Bioinformatics for MS Interest Group produced a workshop for the 2014 ASMS meeting in Baltimore. The meeting began by introducing Sangtae Kim (Sangtae.Kim@pnnl.gov), a staff scientist at Pacific Northwest National Laboratory who is known for his work with generating functions, particularly the one in the MS-GF+ search engine.

The workshop topic focused on errors in posttranslational modification (PTM) annotation. The use of database search engines for identification of PTMs is common practice in most proteomics labs, but these identifications have been plagued by errors from two key sources. Karl Clauser highlighted the elevation of false discovery rates that results from allowing more degrees of freedom in identification, such as allowing for “blind PTM” searches or permitting too many modifiable sites in some peptides. Karl Mechtler emphasized localization, the challenge of associating PTMs with the appropriate residue when multiple modifiable sites may be found in a peptide. The discussion was initiated by a mock debate about which of these two error sources needed most attention and continued with questions and comments from the audience. Approximately 200 people attended the interest group meeting, and we enjoyed an insightful discussion.



This panoramic photo illustrates the size of the audience for the workshop, showing Karl Mechtler during his opening oration.



This photo shows the two organizers (Tabb and Käll) at the left, with the two speakers (Mechtler and Clauser) in the middle, with the new organizer (Kim) at the right.