2016 AMSM Workshop Report
Bioinformatics: Challenges & Opportunities in Proteogenomics (Bioinformatics for MS)
Monday June 6, 2016
Sam Payne and Meena Choi, Presiding

Estimated Attendance: 75-100

Summary of Program and Discussion

The aim of the workshop was to discuss new developments in Proteogenomics to try and spur greater desire to understand and integrate multiple omics datasets. We had invited two speakers, each with recent exciting work in proteogenomics, and asked them to speak about how they see the field evolving in the near future. To help frame the discussion, Sam Payne gave a historical perspective of work in proteogenomics.

David Fenyo talked about working with clinical collaborators in the context of experiments for which one often has access to individualized genomic and transcriptomic data. Pedro Navarro spoke about identifying immunopeptides, and how proteogenomic work in that field could help simplify and improve the spectrum identification problem.

After the brief talks on these two topic areas, we opened the discussion with the following set of questions:

- Why do you need both genomics/transcriptomics and proteomics data?
- Is proteogenomics simply searching against personalized protein databases?
- Are nonsynonymous mutations useless in proteogenomics?
- Should all human proteomics experiments utilize a personalized genome?
- Why do we (proteomics experts) care more about genomics, not the vice versa?
- What are the existing software tools? Do they work well?
- Deep learning has successfully been applied to several recent genomics and transcriptomics integration studies. Will it also benefit proteogenomics?

In addition to these questions, there was quite a bit of discussion about pragmatic issues, wondering in what contexts and for what experiments might proteogenomics be useful. The audience participation was high, with a several audience members acting as ad-hoc panelists and answering questions.