

## Report on workshop convened by Lipid Mass Spectrometry and Lipidomics Interest Group

64<sup>th</sup> ASMS 2016, San Antonio

“Lipidomics in the Era of Systems Biology: The Big Fat Challenges”

### chairs:

A/Prof Christer Ejsing (University of Southern Denmark)

A/Prof Todd Mitchell (University of Wollongong)

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The original proposal for this workshop is stated below:

“There is a growing interest in using lipidomics for systems biology studies for understanding the molecular underpinnings of cellular processes and mechanisms of diseases. This workshop will focus on key challenges in integrating lipidomics with other -omics technologies, and how computational strategies can be designed to support meaningful insights into (patho)physiological processes. The discussion will be led by a panel of experts who will invite opinion from participants on current solutions and challenges in using lipidomics for systems biology studies of lipid function in both basic and clinical sciences.”

The workshop was held on Tuesday June 7<sup>th</sup> (5:45-7:00 pm) and was attended by approximate 135 conference delegates.

Both **A/Prof Christer Ejsing** and **A/Prof Todd Mitchell** facilitated the workshop and verbal discussions. **A/Prof Christer Ejsing** kicked off the workshop by giving a short overview of the topic and the challenges that the field is facing. Subsequently, two invited speakers, **Dr. Robert Ahrends** (Leibniz Institute for Analytical Sciences, Germany) and **A/Prof John M. Asara** (Beth Israel Deaconess Medical Center, Boston), gave presentations about their experiences and challenges in using lipidomics for systems biology studies. **A/Prof Todd Mitchell** finished off the workshop by giving an overview of the key challenges that had been discussed during the workshop and the possible solutions to address these.

**Dr. Robert Ahrends** (Leibniz Institute for Analytical Sciences, Germany) spoke about their recent efforts to combine lipidomics, proteomics and metabolomics. His contribution prompted the audience to consider the following questions:

- What is the best approach for collecting and preparing samples for analysis by three types of -omics techniques?
- How do you document the performance of an integrated multi-omics workflow?
- How do you recapitulate remodelling of cell biological processes using interaction and metabolic networks?

**A/Prof John M. Asara** (Beth Israel Deaconess Medical Center, Boston) shared their recent attempts to do systems biology studies by also combining lipidomics, proteomics and metabolomics. This prompted discussion on the following questions:

- Do lipidomics software applications produce meaningful outputs that can be used for systems biology studies?
- What data formats are applicable for systems biology studies (absolute quantification, intensity profiling)?
- What type of statistics should be applied for multi-omics studies?