Agilent Technologies

# AGILENT LUNCH SEMINAR

WEDNESDAY 10 JUNE | 1:00PM-2:00PM | BIG HALL

## ADVANCES IN METABOLOMICS RESEARCH

### Agilent Solutions for the Metabolomics

Speaker: Dr. Shaun Bilsborough, Mass Spectrometry Product Specialist, Agilent Technologies

*Abstract: Mass spectrometry profiling is used to determine the changes occurring in a biological system in response to different conditions, in order to better understand aberrations in the biochemical pathways involved. When the investigation focusses upon the metabolite-level, different methods, mass spectrometry platforms and analytical conditions are required due to the various chemical properties of the compounds of interest, leading to numerous data files for each biological replicate. More recently, the application of hyphenated techniques such as ion mobility have led to better separation of complex biological samples while the additional dimension has added another level of complexity. In this presentation, an overview of the required hardware for maximum coverage of the metabolome will be discussed together with the software solutions required for interpretation of complex data sets.*

### High-throughput metabolome profiling of cellular responses

Speaker: Prof. Uwe Sauer, Institute of Molecular Systems Biology, ETH Zurich

*Abstract: Metabolism is often the first responding molecular network to environmental changes and also the functional end point of many cellular responses. Since metabolite concentration data are crucial to understand cellular responses but monitoring metabolome changes is experimentally tedious and demanding, we developed a methodology for high-throughput metabolome profiling. Relying on the high mass resolution of a Agilent 6550 QTOF for compound annotation, this method is based on so-called flow injection analysis (FIA) in which samples are directly injected into the mass spectrometer without chromatographic separation. Thereby we achieve a throughput of one sample per minute for monitoring of relative concentration changes in 300-700 metabolites (Fuhrer et al. 2011 Anal Chem 83: 7074; Sevin & Sauer 2014, Nature Chem Biol 10: 266). This method is now routinely used for comparative studies in bacteria, yeast, cell lines or body fluids as a rapid hypothesis generator for detailed follow-up analyses. Here I will illustrate how the analytical speed can be exploited for hypothesis generation in large sample cohorts. One example is the construction of the first, yet unpublished gene-metabolite response network by analyzing the entire gene deletion library of E. coli with more than 30'000 measurements. In the other example we exploit high-throughput metabolomics in yeast kinase mutant collections to identify functionality of enzyme phosphorylation (Schulz et al 2014, Science Signaling 7:353).*

* Lunch included

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