Updated 25 September 2019

Outline of pre-conference workshop at MEWE2019 (Hiroshima, Japan)

Prospects for multi-omics methods in the microbial ecology of water engineering

Description on topics of the workshop

Over the last 15 years new methods for high throughput assaying of different kinds of biomolecules have become mainstream techniques in many areas of the life sciences. These include surveying mRNA levels using sequencing based transcriptomics (RNA-Seq), surveying protein or metabolites levels using high resolution mass spectrometry and the use of next generation sequencing for genome-wide genotyping or genome assembly. The combined use of one or more of these omics techniques on the same set of samples has become known as *multi-omics* or *integrative omics*.

In the context of microbial ecology, these approaches are increasingly being applied to the systematic study of composition and function in complex microbial communities [1,2]. This is particularly urgent given that culture-based approaches for biochemical and physiological characterisation are not readily applicable to many member taxa due to our lack of detailed knowledge of relevant culture conditions. When combined with experimental manipulation or observational designs, and underpinned by rigorous statistical bioinformatics, multi-omics data has tremendous potential to identify the molecular and cellular mechanisms underpinning the function state of complex microbial communities *in situ*.

For example, recent progress in this area in the MEWE context includes *1*) the recent demonstration that strains of *Ca.* Accumulibacter can perform denitrification in microaerobic conditions [3]; *2*) mechanistic insights from coupled metagenome-metatranscriptome studies into the ecobiology of microbial fuel cells [4]; *3*) studies of full scale EBPR plants using combined metagenome-metatranscriptome analysis [5] and *4*) emerging use of whole community metabolomics and proteomics on activated sludge communities [6,7,8].

Despite the potential of multi-omics methods, there remain many obstacles to their more routine use, including high cost, the complexity of sample handling and extractions, the need to implement and operate complex bioinformatics workflows, challenges with developing rigorous methods for independently testing predictions obtained from these analyses and developing modelling approaches suitable for these complex data [9]. Furthermore how we can make use of these new methods to study full-scale systems and real world problems remains an open but critical question.

Tentative program and time schedule

The workshop will involve a series of short presentations followed by a discussion session.

1000-1130 Short talks (15 min per presenter)

1 Introduction and overview of multi-omics. Rohan Williams (SCELSE)
2 From 16S amplicon sequencing to genome-resolved metagenomics. Per Halkjær Nielsen (AAU)
3 Coupled metagenomics and metatranscriptomics. Trina McMahon (UW-Madison), Shun'ichi Ishii (JAMSTEC)
4 Bringing in proteomics and metabolomics. Yu Ke (PKU).
5 Bringing in modelling approaches. Aljoscha Wahl (TU Delft)

1130-1300 Lunch break

At a local resturant or cafe of your choice (no lunch is provided).

1300-1500 Discussion session

The discussion session will be split into the following sections:

1300-1400. Technical and practical issues

- *Nuts-and-bolts startup issues in multiomics, both wet and dry lab.*
- *Lessons learned from laboratory scale studies.*
- *Testing predictions from multi-omics studies.*
- *Integration of multi-omics data with modelling approaches.*

1400-1500. Translational aspects

- *Potential for performing multi-omics in full scale systems*
- *Future prospects for collaborative consortia and IWA task groups*

Workshop organizer / primary contact

Rohan Williams (lsirbhw@nus.edu.sg)
Singapore Centre for Environmental Life Science Engineering (SCELSE)
National University of Singapore

Registration

Open to all participants of MEWE2019. Prior registration appreciated but not mandatory. Walk-in participants are most welcome.

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