



**META-OMICS IN ENVIRONMENTAL ENGINEERING RESEARCH.
THEORY, STATISTICS, AND DATA INTERPRETATION.
May 14, 2019.**

High throughput meta-omics methods are being routinely used to probe microbial community structure and function in environmental engineering research. While this makes the microbial world more accessible, robust and rational data interpretation is not straightforward. Further, the technologies underpinning these methods are also changing at a rapid pace; this can make hypothesis-appropriate methodological choices also very challenging. The objectives of this workshop are (1) to outline best practices for method selection and data interpretation for microbial community structure and function characterization and (2) to identify imminent technological advances that may influence the choice of molecular methods in the near future.

The intended learning outcomes of the workshop are as follows: Participants should be able (1) pick the appropriate meta-omic method for their research questions, (2) identify data analysis approaches best suited to their method of choice, (3) understand the limitations of each method and associated data, and (4) incorporate a working knowledge of upcoming changes in meta-omics methods into their planned research. Participants will be provided with virtual resources and reference materials, including a virtual machine containing pre-installed software, example data and tutorials/resources, to assist them as they begin to explore the meta-omic techniques independently.

Participants should be using or plan to use meta-omics methods with working understanding of microbiology and statistics.

Organizers:

Christopher Anderson, Northeastern University
Zihan Dai, University of Glasgow
Christopher Lawson, University of Wisconsin, Madison
Ameet Pinto, Northeastern University
Jacob Price, University of Wisconsin, Madison
Maria Sevillano, Northeastern University
Varun Srinivasan, Brown and Caldwell
Ryan Ziels, University of British Columbia

WHY ARE YOU ATTENDING THIS WORKSHOP?



[Word cloud generated on worditout.com]

PARTICIPANT OVERVIEW

Who?

Junior Researcher

Senior PhD

Post-doc

Faculty/PI

Can program in?

R

Python/Perl

C(++)

Micro-expertise

None

Expert

Intermediate

Beginner

UNIX-comfort

Expert

Intermediate

Challenges?

Beginner

Fast changes

Data interpretation

Method choice

UNIX Proficiency

SCHEDULE

09:00 am Introduction Ameet Pinto

SESSION 1**SEQUENCING METHODS AND THEIR APPLICATIONS FOR COMMUNITY STRUCTURE**

09:10 am Understanding sequencing platforms Ameet Pinto

09:20 am Amplicon sequencing Zihan Dai

09:35 am Metagenomics Varun Srinivasan

SESSION 2**APPLICATIONS TO ASSESS COMMUNITY FUNCTION**

09:50 am Stable Isotope Probing with Metagenomics and Metatranscriptomics
Ryan Ziels

10:00 am Stable Isotope Probing with Metaproteomics and Amino Acid Tagging
Christopher Lawson

SESSION 3**STATISTICAL METHODS AND THEIR APPLICATIONS**

10:15 am Statistical considerations for 'omic data analyses Jacob Price

10:30am Network Analyses Maria Sevillano

BREAK (15 MINUTES)**SESSION 4****GROUP ACTIVITY AND POST-WORKSHOP RESOURCES OVERVIEW**

11:00 am Group activity Ryan Ziels
Please form groups of 5-8 around poster boards.
Two prompts: Wastewater or Drinking Water
Christopher Lawson

11:40 am Virtual Environments and Containers for
Reproducible Research Christopher Anderson

SESSION 5: WHAT LIES AHEAD

11:55 am Keep an eye on this Ameet Pinto

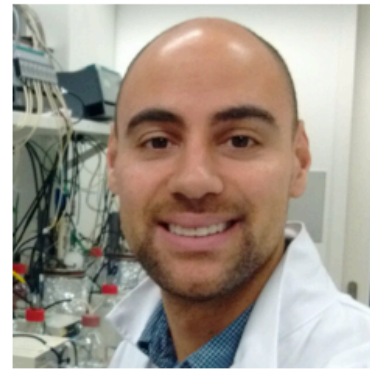
WORKSHOP ORGANIZERS



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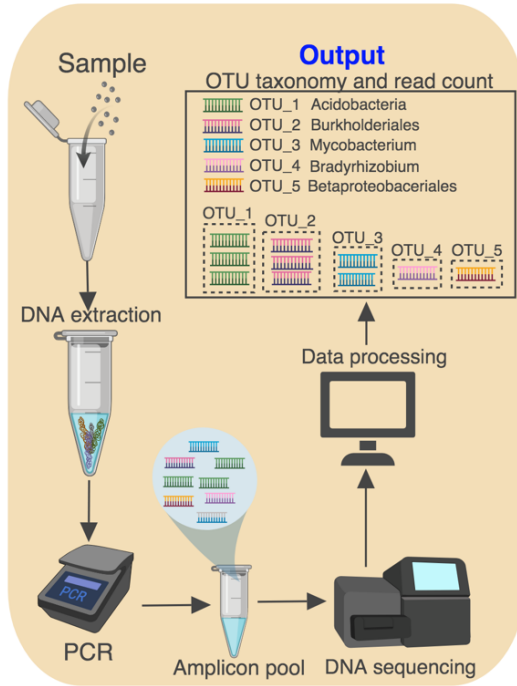
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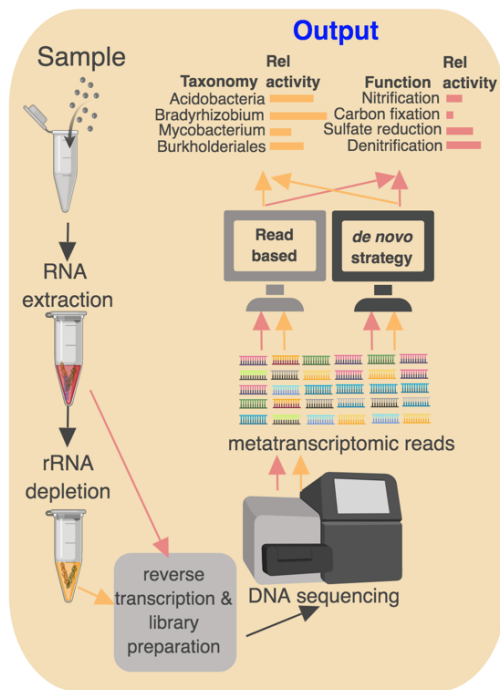
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KEY METHODS

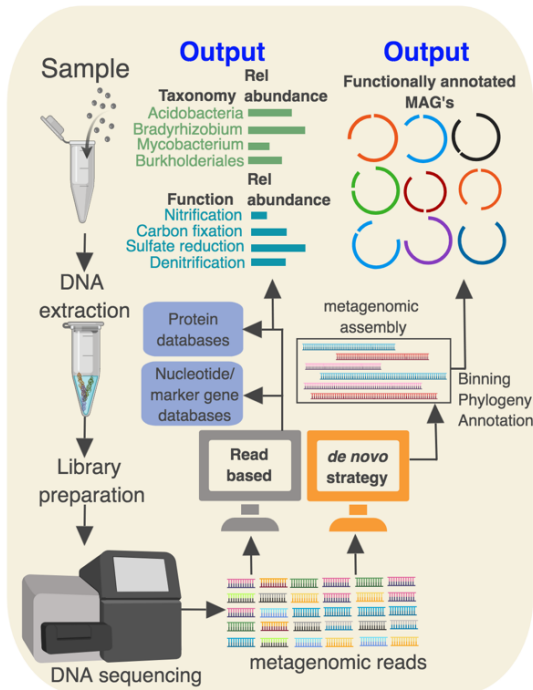
Amplicon Sequencing



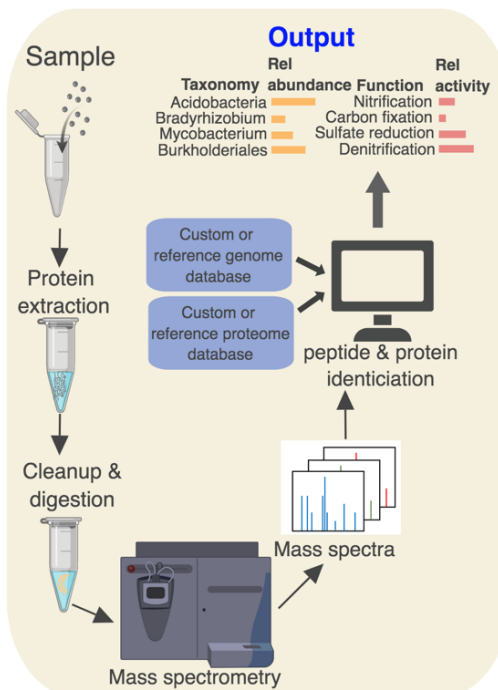
Metatranscriptomics



Metagenomics



Metaproteomics



METHOD APPLICATION CHEAT SHEET

Method	Input	Output							
		How many?	Who is there?	What they can do?	Who is active?	What function is active?	Who is growing?	Who is assimilating?	Pathway fluxes
Flow cytometry	Cells	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
qPCR	DNA	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/> With label	<input type="checkbox"/>
	RNA	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Functional gene	<input type="checkbox"/>	<input checked="" type="checkbox"/> With label	<input type="checkbox"/>
Amplicon sequencing	DNA	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/> With label	<input type="checkbox"/>
	RNA	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Functional gene	<input type="checkbox"/>	<input checked="" type="checkbox"/> With label	<input type="checkbox"/>
Meta-genomics	DNA	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> With label	<input type="checkbox"/>
		<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Meta-genomics + transcriptomics	DNA	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> With label	<input type="checkbox"/>
	RNA	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> With label	<input type="checkbox"/>
Meta-genomics + proteomics	DNA	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> With label	<input type="checkbox"/>
	Protein	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> With label	<input checked="" type="checkbox"/> With label
Meta-genomics + Metabolomics	DNA	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> With label	<input type="checkbox"/>
	Metabolites	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> With label	<input checked="" type="checkbox"/> With label

WORKSHOP NOTES

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