ENVIRONMENTAL BIOTECHNOLOGY NETWORK

Bioinformatics Training WG

[Bioinformatics Training for Microbial Environmental Biotechnologies](#) (BioInf WG)

Led by [Prof James Chong](#), University of York

The goal of this WG is to develop opportunities for stakeholders to engage with bioinformatics pipelines for understanding microbial community dynamics. In particular it aims to provide insight into the potential of 'omics techniques in Environmental Biotechnology and the design of these types of experiment, and to develop online training resources for analysis and visualisation of the resulting data.
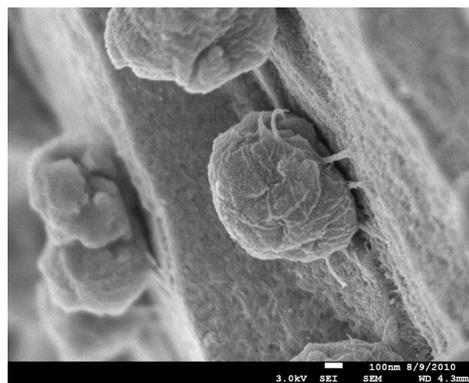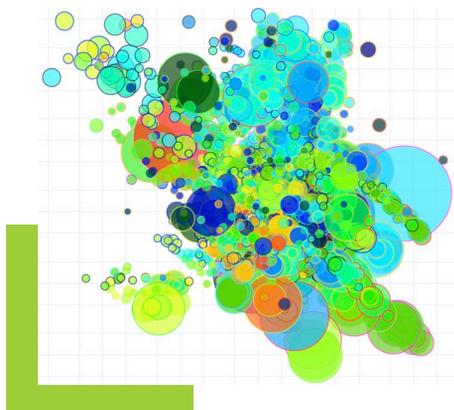
ACTIVITY SYNOPSIS

This WG led with two very popular webinars:

Webinar '*Why bioinformatics training is important*'
Webinar '*Using Big Data Approaches to Understand Microbial Communities*'

The WG has provided speakers for EBNet-supported sessions at several events, including two *European Biosolids and Organic Resources* conferences. In [2019](#) EBNet hosted a session on 'Converting Genetic information into Action – Progress and Problems', with presentations from Prof James Chong, University of York; Dr Claudio Avignone-Rossa, University of Surrey; Dr Chris Quince, University of Warwick; Dr Pawel Sierocinski, University of Exeter; Prof Rafaella Villa, De Montfort University; and Tom Taylor from Yorkshire Water wrapping up the session with an industry perspective. In [2022](#) we supported a session on 'Bioinformatics' with presentations by James Chong and Sarah Forrester, York; Pawel Sierocinski, Exeter; Stefano Campanero, Padova; David Inman and Lindsey Gove, Anglian Water. EBNet also sponsored the Student and Young Professionals' [Poster Awards](#) at these events.

The group coordinated a cross-WG meeting that led to an interdisciplinary workshop and follow-on proposals for UKRI Networks. Together with the Anaerobic Digestion, Anaerobic Fermentation and Bioelectrochemical Systems WG, it co-Led the [New Biomethane workshop](#).

ACTIVITY SYNOPSIS ctd

EBNet has supported two proof-of-concept (POC) projects and a Business Interaction Voucher (BIV) in this area:

POC202101 [Faecal pollution source tracking and quantitative microbial risk assessment methods for a suitcase laboratory](#)
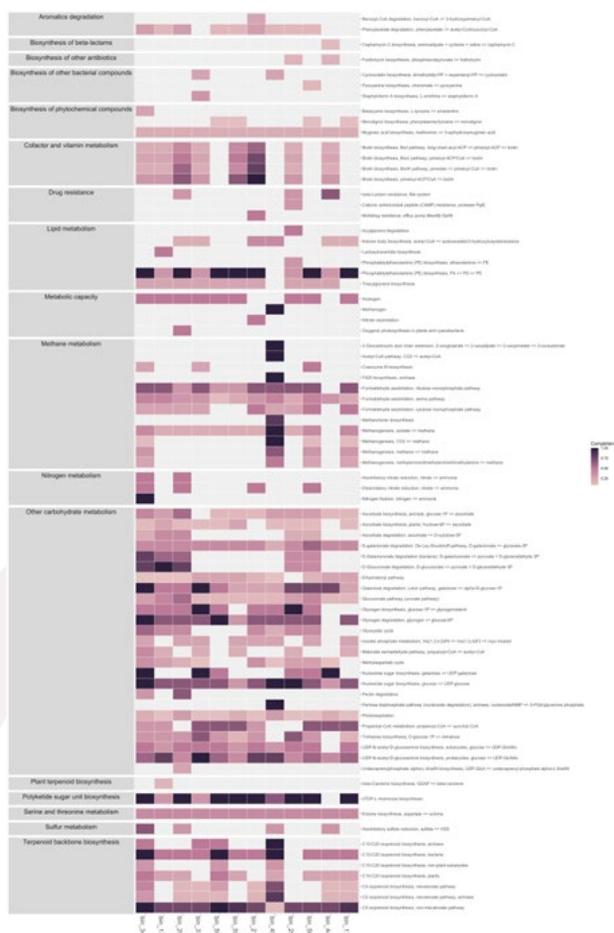
POC202112 [Real-time monitoring of Anaerobic Digestion microbial community as a foaming risk prediction method](#)

BIV202001 [Determination of microbial communities of laboratory anaerobic digestion tanks and impact of the CreChar additive on the microbial community dynamics](#)

WG members are also involved in the UKRI-funded Industrial Doctoral Landscape Award BIO-BOOST: Harnessing Wastewater Treatment Biotechnological Potential, a partnership between the Universities of York and Newcastle, the Environment Agency, UK Water Industry Research, Oxford Nanopore Technologies and Waters Corp.

The WG hosted a 6-month virtual training placement *Bioinformatics for Microbial Community Analysis* for an ECR from the University of Southampton. EBNet also put the WG into contact with the *Oracle for Research* program 2023, leading to an [Oracle Fellowship](#) for Prof Chong and US$100k support in cash, Cloud credits and technical collaboration – all of which helped underpin subsequent proposals.

The WG's training activities are continuing to go forward in the UKRI-funded [Cloud-SPAN](#): Specialised analyses for environmental 'omics with Cloud-based High Performance Computing led by Prof Chong, and the [Digital Research Skills Catalyst](#) led by Prof Emma Rand.

WG Outreach Publication

[Bioinformatics could unlock greater biogas production](#), by Sarah Forrester, University of York. EBNet Corner, AD & Bioresources News, Issue 53 Summer 2022

For more information see the WG **[Webpage](#)**, **[News](#)** tag and YouTube **[Playlist](#)**

Dr Dana Ofiteru
Newcastle University
POC202112

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UKRI Biotechnology and Biological Sciences Research Council

Real-time monitoring of anaerobic digestion microbial communities as a foaming risk prediction method

"This EBNet PoC showed us the power of collaboration with the university and the potential of using multi-omics for understanding the pervasive foaming phenomena in the digester we are operating. While there is still a long way until the industry will be able to make routinely such analyses, we are proud to be one of the first AD companies in the UK who embarked on this path".
Stefan Weitz & Darren Smith, BioConstruct NewEnergy Ltd.

AIM

Decomposition of the organic wastes generated by humans (estimated to be 105 billion tonnes/year) releases methane and other harmful greenhouse gases (GHG) directly into the atmosphere. Methane is a much more potent GHG than CO_2, and simply by managing organic wastes more effectively we can cut global GHG emissions.

Anaerobic digestion (AD) is a 'ready-to-use' technology which can prevent methane emissions and generate biogas, bio-fertilisers and other valuable bio-products. One major concerns for AD companies is foaming, which has a significant impact on process efficiency and operational costs. Foaming is a manifestation of instability in the AD process, and microorganisms are the main functional body ensuring AD performance. Therefore, foaming mechanisms need to be explored at the microbial community level. Industry is keen to have a way to predict foaming as it affects productivity, can damage infrastructure and is dangerous for operators.

We propose to use microbial community fingerprinting through low-cost metagenomics (to answer, "who is there?") and metaproteomics (to answer, "what are they doing?") to provide data in real time for the risk prediction and control of foaming in AD. For the first time, we are going to apply this method for monitoring a full scale AD treating mixed waste.

RESULTS

Our samples were collected the end of October 2021, from two similar reactors which received the same type of feed: one going through a foaming event and one without foaming.

Due to the complexity of the samples, DNA extraction proved challenging. Firstly, we used the third-generation sequencing technology provided by MinION (Oxford Nanopore Technologies). This generates longer reads and should improve the metagenome assembly. Due to the challenging extraction, we also sequenced the samples through Illumina, a second-generation sequencing technology which generates shorter reads.

Metagenomic data analysis showed that the microbial communities in the two reactors differ significantly. Some common species between the two plants had significantly higher relative abundance in the foaming reactor. Metaproteomics also confirmed the presence of these putative foam-forming bacteria and identified numerous flagellin proteins that are markers for filamentous bacteria which are known to cause foam.

Our results are a first step towards using a combined 'omics approach in studying foaming in industrial reactors treating complex mixed waste.

FURTHER ACTIVITY:
Work is underway to analyse a second set of samples. The results have been shared with other researchers for application of more advanced bioinformatics tools. This work is ongoing and we will soon have a fuller picture of possible microbial markers for foaming in AD.

Professor David Werner
Newcastle University
POC202101

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Environmental Biotechnology

UKRI Engineering and Physical Sciences Research Council

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Faecal Pollution Source Tracking & Quantitative Microbial Risk Assessment methods for a Suitcase Laboratory

"The workshop was an opportunity for me to refresh some molecular biology techniques and, most importantly, to learn and update myself on more recent techniques in the field. I also had the chance to meet other researchers from across Africa and to begin to build a network of researchers for future collaborations. Thank you for being very supportive and for investing your time and experience into building capacity on the African continent."

George Mangse, Lecturer at Nile University of Nigeria,
on molecular microbiology training with the suitcase laboratory at the Addis Ababa Water and Sewerage Authority
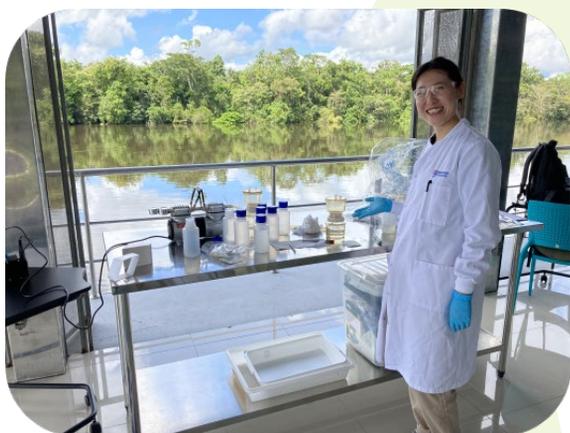
AIM

Using a suitcase laboratory that contains the MinION sequencing device of Oxford Nanopore Technologies, over 100 comprehensive water microbiome data sets have been collected from around the globe. This desk study exploits the global data for the development of multivariate data analysis tools which facilitate faecal pollution source attribution and related quantitative microbial risk assessments by suitcase laboratory users. The goal is to enable the wider uptake of an affordable suitcase laboratory for molecular water microbiology in environmental surveying and wastewater treatment biotechnology applications around the world.

RESULTS

Newcastle University researchers have developed an innovative '**Lab in a Suitcase**', a portable water testing lab, that can be used to comprehensively screen water samples for faecal pollution and waterborne hazards. This suitcase laboratory brings advanced genetic testing methods within reach of water, sanitation and hygiene (WASH) researchers working in low- and middle-income countries. It is also suitable for rapid onsite water quality testing by WASH professionals around the world who run sewage treatment works, manage livestock on farms, assess bathing waters and provide humanitarian aid to communities displaced by natural or human-made disasters.

The Newcastle University researchers developed a protocol for quantitative microbial risk assessment (QMRA) which uses data generated with the suitcase laboratory to rapidly assess risks of contracting gastrointestinal diseases from water that is polluted with faecal matter.

Researchers designed and delivered a hands-on training workshop. The suitcase laboratory was used to detect genetic markers for human sewage pollution in the urban river Ouseburn. Results were obtained within 3 hours of sampling. In Ethiopia, trainees gained hands-on experience in analysing river water and wastewater samples

Determination of microbial communities of laboratory anaerobic digestion tanks and impact of Crechar® additive on community dynamics

"Our collaboration with Prof Chong and his group has been instrumental in making the first steps towards building a pipeline for analysis of microbial communities in anaerobic digestion. This will help us to further develop our expertise in this area, and ultimately will allow us to optimise our CreChar product. I am looking forward to continuing our collaboration with Prof. Chong, possibly within the remit of his new Cloud SPAN project". Dr Adam Ostrowski, Carbogenics Ltd.

AIM

Carbogenics Ltd has developed a novel carbon additive CreChar® intended to increase the stability and process efficiency of Anaerobic Digestion plants. CreChar® is expected to facilitate microbial interactions, biofilm development and increases in the abundance of essential microbial taxa. Carbogenics recently acquired a MinION sequencer from Oxford Nanopore Technologies and obtained a large quantity of genomics data from various experimental reactors. However, very little information is available on the microorganisms commonly found in AD, and the MinION technology is very young and currently not supported by user-friendly analysis software. Carbogenics managed to process approx 30% of the obtained data, but lacked the expertise required to unlock all the information in the datasets. The company wanted to partner with Prof James Chong's group at the University of York, who are leaders in development of the tools for AD metagenomics.

"I hope our analyses will provide useful insights that can be used by Carbogenics to further develop its products. Working together has demonstrated a clear need for more accessible training to boost microbial community analysis expertise in small companies who are developing exciting innovations on limited budgets and short time-scales. I hope our Cloud-SPAN project will help to address that need". Professor James Chong, University of York

https://cloud-span.york.ac.uk

RESULTS

Cutting-edge DNA sequencing technologies such as Oxford Nanopore Technologies' MinION sequencer are democratising science and making DNA sequencing routinely possible in nontraditional settings such as SMEs and micro-businesses. However, the expertise and computational hardware required to make full use of this data currently trails our ability to generate it.

Our collaboration supported the interpretation of Carbogenics' in-house generated data using University of York high performance computing (HPC) infrastructure and expertise. In addition to providing biological insights into how Carbogenics' CreChar® additive supports the productivity of anaerobic digestion, the data analysis carried out in this project will allow Carbogenics to further refine its products.

As well as directly supporting Carbogenics' investigations, our project has highlighted a skills (and infrastructure) gap that we think can be filled though on-line training and HPC resources.

'I am an Environmental Biotechnologist because...'

Selected examples from EBNet ECR Conferences in 2023 and 2024

I am fascinated by using bioinformatics and metagenomics to decode complex microbial communities, unlocking insights that can drive innovations in environmental sustainability.

Annabel Cansdale, University of York

I am an environmental Biotechnologist because I believe in the power of microbes and genetics to develop environmentally friendly products.

Mingaile Jackson, Northumbria University

I am an environmental biotechnologist because I analyse microbial diversity in different environments using DNA technologies and bioinformatics to obtain microbial profiles and relevant descriptions of all the microorganisms (including viruses) in a certain environment.

Beatriz Delgado Corrales, Northumbria University

I am fascinated by the phylogenetic and functional diversity of environmental microorganisms. My research determines the specific functional roles of microorganisms within the context of the environments they inhabit, to understand the healthy functioning of a given ecosystem.

Lauren Messer, University of Stirling

I am an environmental biotechnologist as I practice bioinformatics and biochemistry approaches to solve bioremediation, and enzyme design to promote sustainable chemistries. I am passionate about how we can use biology as a tool to repair the damage done to the planet and technologies that are regenerative and distributive in a low carbon economy. Systems thinking is the core of what I do and am determined to make science and technology as sustainable as possible.

Camilla Pang, Pangscape Ltd

I am an environmental biotechnologist because I am most interested in antagonistic microbial interactions (such as with parasites, pathogens or predators) and how these interactions can be investigated and combined with novel technologies and techniques for the betterment of human and environmental health.

Ayo Ogundero, University of Glasgow

I am investigating how we can use natural processes in riparian buffer zones to remediate agricultural non-point source pollution. I look at how soils, microbes and plants interact but mainly focus on microbial genetic analysis. I hope to identify promising natural bacteria that can be introduced to improve contaminant degradation rates.

Freya Thornley, Newcastle University

I am a bioinformatics PDRA working on biofilter datasets, focusing on 18S rRNA, which represents eukaryotes, and 16S rRNA, which represents bacteria. My goal is to analyse the community profile, with a particular focus on identifying taxa that are correlated with pathogens. Investigating the interplay between eukaryotes and bacteria offers insights into fundamental ecological processes and the complex microbial networks that underpin environmental systems.

Uzma Uzma, University of Glasgow