

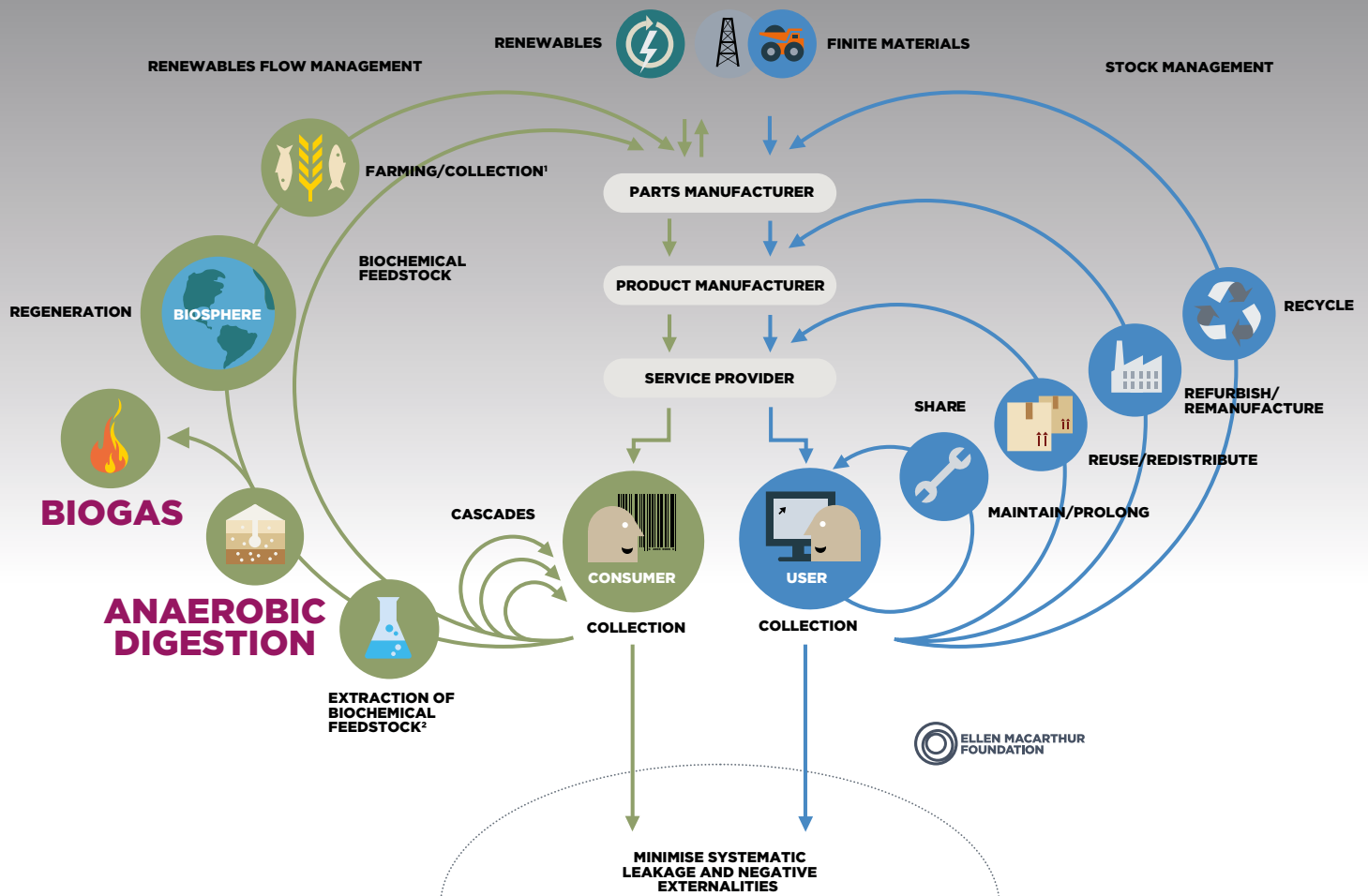
# AD&BIORESOURCES NEWS

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## ALL SYSTEMS GO



## ANAEROBIC DIGESTION CENTRAL TO \$34TRN TRANSITION OPPORTUNITY

**CHP: HOW YOU KEEP YOUR MOTOR RUNNING EFFICIENTLY**

**APPRECIATION: AD CHAMPION CLARE LUKEHURST OBE**

**NORTHERN IRELAND CAN BE A BIOMETHANE POWERHOUSE**

**BIOINFORMATICS COULD UNLOCK GREATER BIOGAS PRODUCTION**

# BIOINFORMATICS COULD UNLOCK GREATER BIOGAS PRODUCTION



With recent improvements in sequencing technology, **Sarah Forrester** considers how this might inform the process of anaerobic digestion in the coming years.

Wastewater treatment plants perform anaerobic digestion at a large scale. This process utilises microbes to breakdown organic material from treated waste and generate methane, which can then be repurposed for renewable energy purposes downstream. However, until recently, despite the process being facilitated by a community of microbes acting together, our understanding of what was happening within a digester at a biological level was limited. Improvements have instead largely been driven through incremental changes to operational procedure.

However, that might be about to change. Bioinformatics is a field that brings together genetics and technology, and it is primarily used to apply mathematics and statistics to interpret complex biological data. One area of bioinformatics that has become increasingly popular in both industry and research institutions is DNA sequencing. This technique allows us to identify which organisms are present in a sample, and their relative levels of abundance. Sequencing allows us to identify multiple organisms simultaneously from the complex communities of microbes from within an anaerobic digester in one sample, as opposed to having to sample lots of different organisms separately using multiple samples.

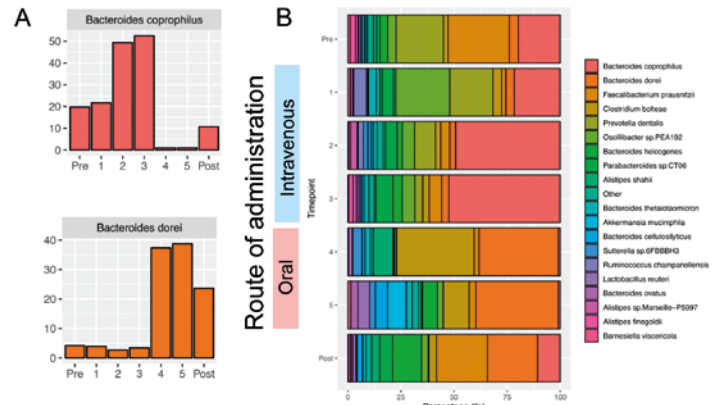
A microbiome is defined as the collective genome of all microbes within a community, and they are often biologically complex systems like the microbiome existing within an anaerobic digester. Other well studied microbiomes include the human skin and the soil microbiomes, which researchers have interrogated using sequencing data and bioinformatic analysis to understand the microbial dynamics within their biological system.

We can learn from these approaches and apply the same principles to learn more about what is present in our digester samples. In a previous EBNet webinar <https://ebnet.ac.uk/ebnet-rc22-bigdata/> we heard from two researchers that were both using large datasets and bioinformatics to understand the biology underpinning their systems <https://youtu.be/1QH0JKOX0Xw>.

Dr Sophie Nixon from the University of Manchester was interested in the diversity of microbial life in extreme environments and described how she used bioinformatics to mine sequence data and understand which microbes were present in samples taken from deep boreholes in Greenland <https://bit.ly/snix0222>.

Sophie showed how DNA sequencing could be used to identify the high number of species present in her samples. From this she also determined how many species were active, and that the profiles of microbial communities above and below the permafrost were distinct from each other. Her research highlighted that many low abundance species were often highly active. A species abundance is often used to rank its relative importance to the functionality of a community. The most dominant species are presumed to contribute the most, whereas these findings suggest that we need to reconsider the importance of lower abundance species in our communities too.

Dr Umer Ijaz from the University of Glasgow also presented his research <https://bit.ly/Ijaz0222>. With a background that is primarily computational rather than biological, he presented how his research focused on using



Example of how community profiling can have impact. Adapted from <https://wellcomeopenresearch.org/articles/7-50/v1> with permission. We used metagenomics to construct the microbes in the gut of a patient with a chronic infection. We were able to see species responding to antibiotics administered through different routes. In this patient we were able to see the displacement of *Bacteroides coprophilus* by another species *Bacteroides dorei* following the switching to a different treatment regimen.

mathematical and statistical knowledge to disentangle large complex biological datasets.

Umer's focus was on how to create and develop software to enable researchers like Dr Sophie Nixon to gain biological understanding through the development and application of statistical methods. His methods have been applied to a wide variety of systems such as biomedical ones, like the human gut microbiome, but also environmental biotechnology systems such as wastewater treatment.

Despite differences in their use cases of bioinformatics and the methods they used to deal with their big biological datasets, both agreed that one of the biggest challenges was gaining access to training resources and emphasised the importance of being part of a bioinformatics focused community. Bioinformatics as a field has evolved quickly, and has been pushed forward by technological advances and a decrease in the cost of sequencing. This rapid decrease in cost has allowed us to test hypotheses using experiments we would until recently not have thought possible. However, as a result, there are many researchers who do not have the training and the computational skills needed to generate the kinds of data described by Dr Sophie Nixon or Dr Umer Ijaz, or the analytical ability to understand it.

One of the key advantages of bioinformatics is that analyses performed are often bespoke and can be highly tailored to answer specific scientific questions. However, the downside to this is that this requires high bioinformatic skill. A key focus of the EBNet Bioinformatics Working group is to build a community interested in the application of bioinformatics to environmental biotechnology. Another focus is to facilitate access to training. To this end, we showcased free bioinformatics training available with our "Why Bioinformatics training is important?" The slides and associated links to training can be found here <https://bit.ly/3Qceewa>.

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