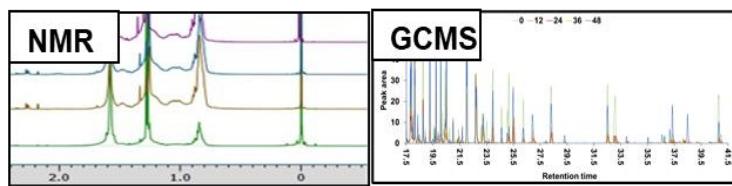
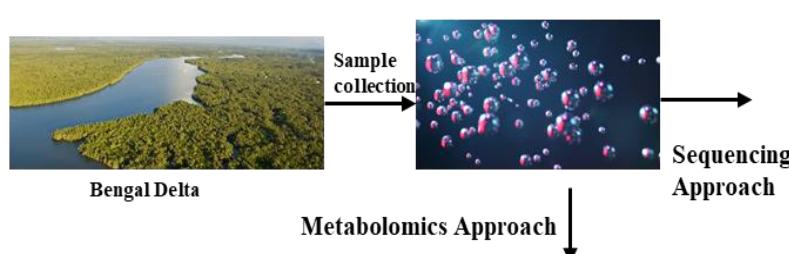
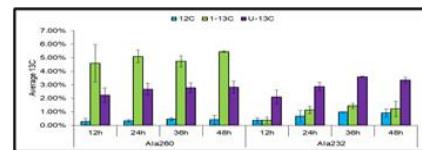
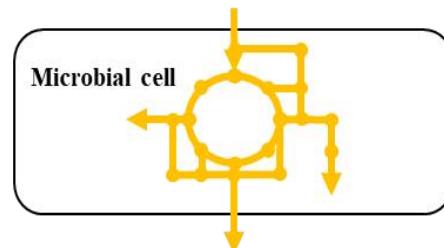


# Graphical Abstract -Statement of Research Interest

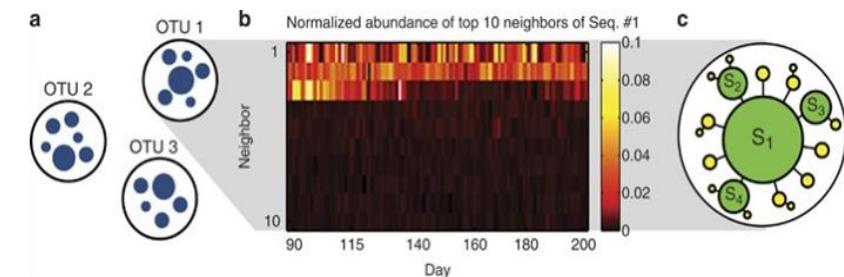


**Decoding metabolism**

- Genomics
- Transcriptomics
- Metabolomics
- Fluxomics



Flux analysis and Arsenic flow identification



Interpreting 16S metagenomic data and clustering to achieve sub-OUT resolution



**Statistical Analysis and data compilation**

## Statement of Research Interest

Project Title - Microbial cycling of arsenic in aquifers

Lead Supervisor IIT Kharagpur- Prof Pinaki Sar (Biotechnology)

Lead Supervisor University of Manchester - Prof Jon Lloyd (Earth & Environmental Sciences)

Water-bearing permeable rocks which forms underground layer is known as an Aquifer. It contains microbial community which dissolve arsenic in aquifers. Arsenic is present in earth crust in abundance of about 2-5ppm. Solubilization of As in aquifers can lead to major health manifestations in humans. As contaminated water is poisonous for human. It also causes cancer, Cardio vascular diseases and dermatitis in human population. Therefore, this As contaminated water becomes a leading problem in developing countries where drinking water treatment is rarely carried out. Hence studying microbial cycling of arsenic in aquifers will provide an alternative solution to the problem.

Water samples from As contaminated aquifers like from Bengal Delta Plains can be collected. These samples then can be analyzed for the presence of microbial community present in it which is involved in cycling of As.  $^{13}\text{C}$  based Metabolite profiling of these microbes can provide an insight of fluxes in microbes which in turn can help in understanding the flow of arsenic in microbial system. 16S rRNA gene amplification and sequencing of taken samples will provide data of microbial community involved in arsenic mobilization. We can also get information of microbes having arsenic uptake ability by whole genome sequencing approach which can help in bioremediation. Statistical analysis can be done using principal component analysis.

I have done my M.Tech final year project in the metabolomics field where I gained expertise in Gas chromatography–mass spectrometry (**GC-MS**), Nuclear Magnetic Resonance (**NMR**) and High performance liquid chromatography (**HPLC**). During my 2<sup>nd</sup> semester I took Next generation sequencing as a course and learned basics of sequencing. In my Metabolomics and systems biology course I gained expertise in statistical analysis i.e., Principal component analysis etc. using Metaboanalyst and R as well. I also possess knowledge of programming language like Python, SQLite and Django.

## **References**

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