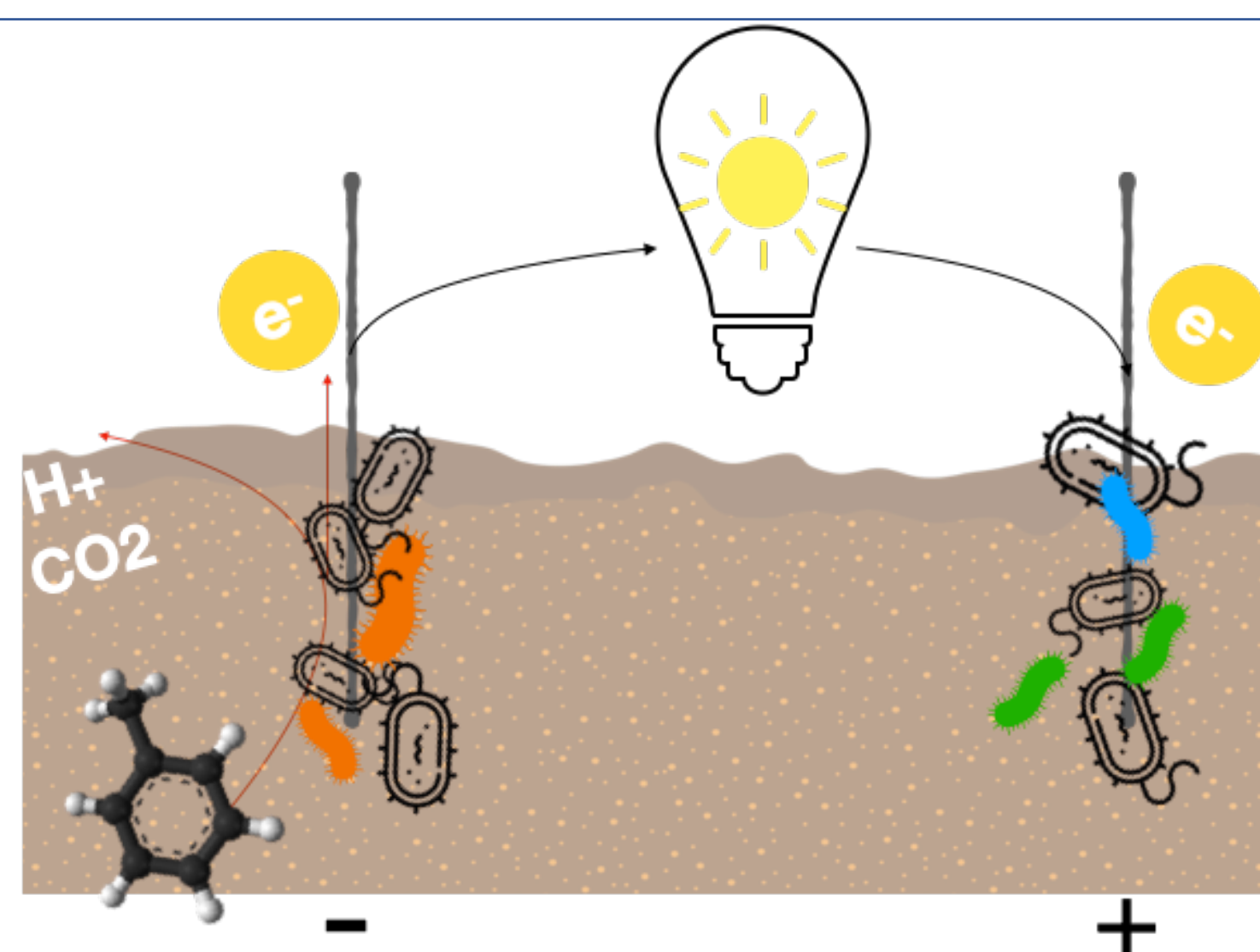


## Introduction

**Hydrocarbons (HC)** can be naturally degraded by microorganisms in the environment.

**Anaerobic** pathway for hydrocarbons degradation have been shown to occur in anoxic media such as soil sediment<sup>1</sup>, or groundwater<sup>2</sup>. The anaerobic oxidation of HC can be enhanced with an **electronic acceptor**, which catalyses the oxidation reaction and accelerate the process of degradation<sup>3</sup>. As pictured in Figure 1., Microbial Fuel Cell (MFC) rely on the presence of electrogenic bacteria at an anode. Therefore, communities that are to be found at the anode's side of this kind of system are of interest in remediation matter.

**Are *Geobacter*, a known electrogenic bacteria stimulated by the presence of anodes in polluted environment, capable of HC degradation?**



**Figure 1. Schema of a Microbial Fuel Cell (MFC)**

Organic matter is oxidized by microorganisms near or on the contact of the anode, producing an electron flow towards the cathode.

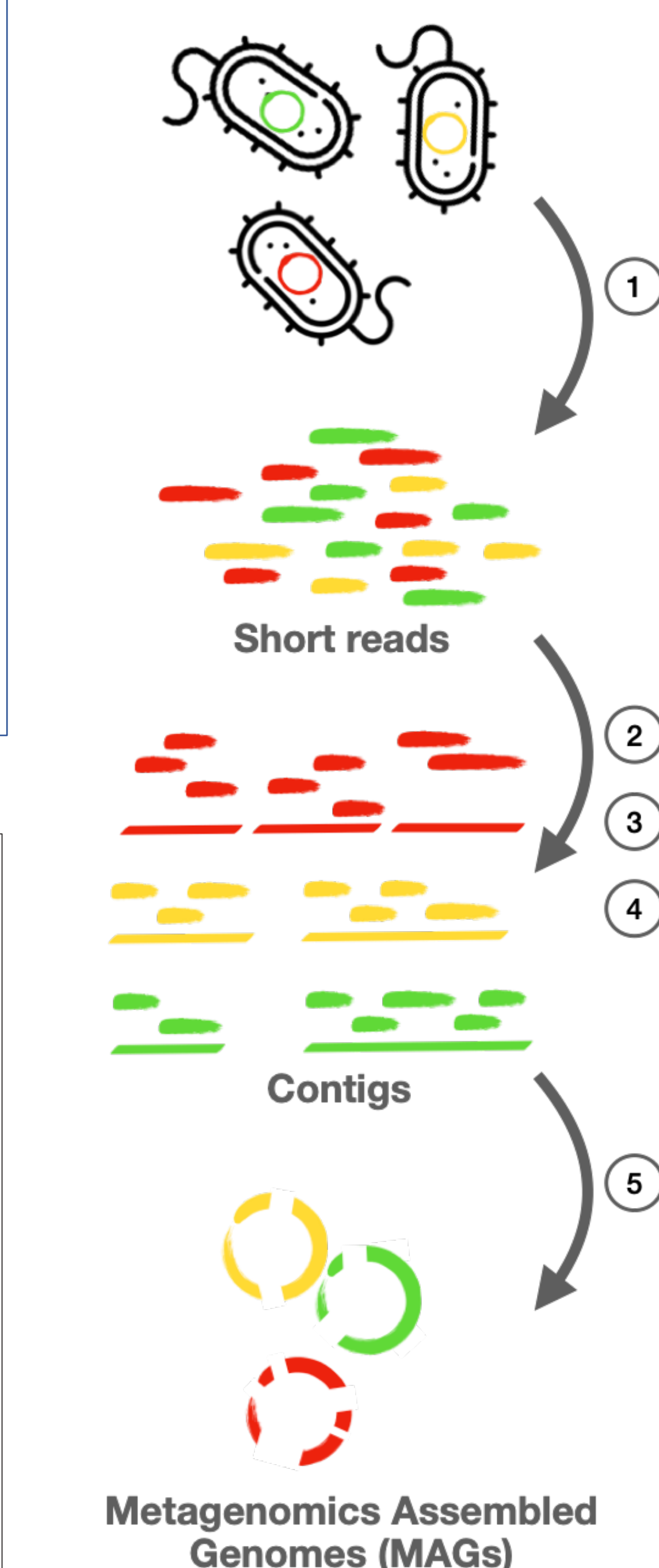
## Methods and Materials

MFC were set up in anaerobic polluted sediments. Metagenomics samples from the anode's side of the system were analysed using **Anvi'o metagenomics workflow**<sup>4</sup>, that uses several software (Figure 2.). **Anvi'o** is an open source tool for microbial 'omic analysis and visualisation. Gene clustering was then performed on *Geobacter* **Metagenomics Assembled Genomes (MAGs)** from anodes and known exoelectrogenic *Geobacters* species genomes with **Anvi'o pangenomics workflow**<sup>5</sup>.

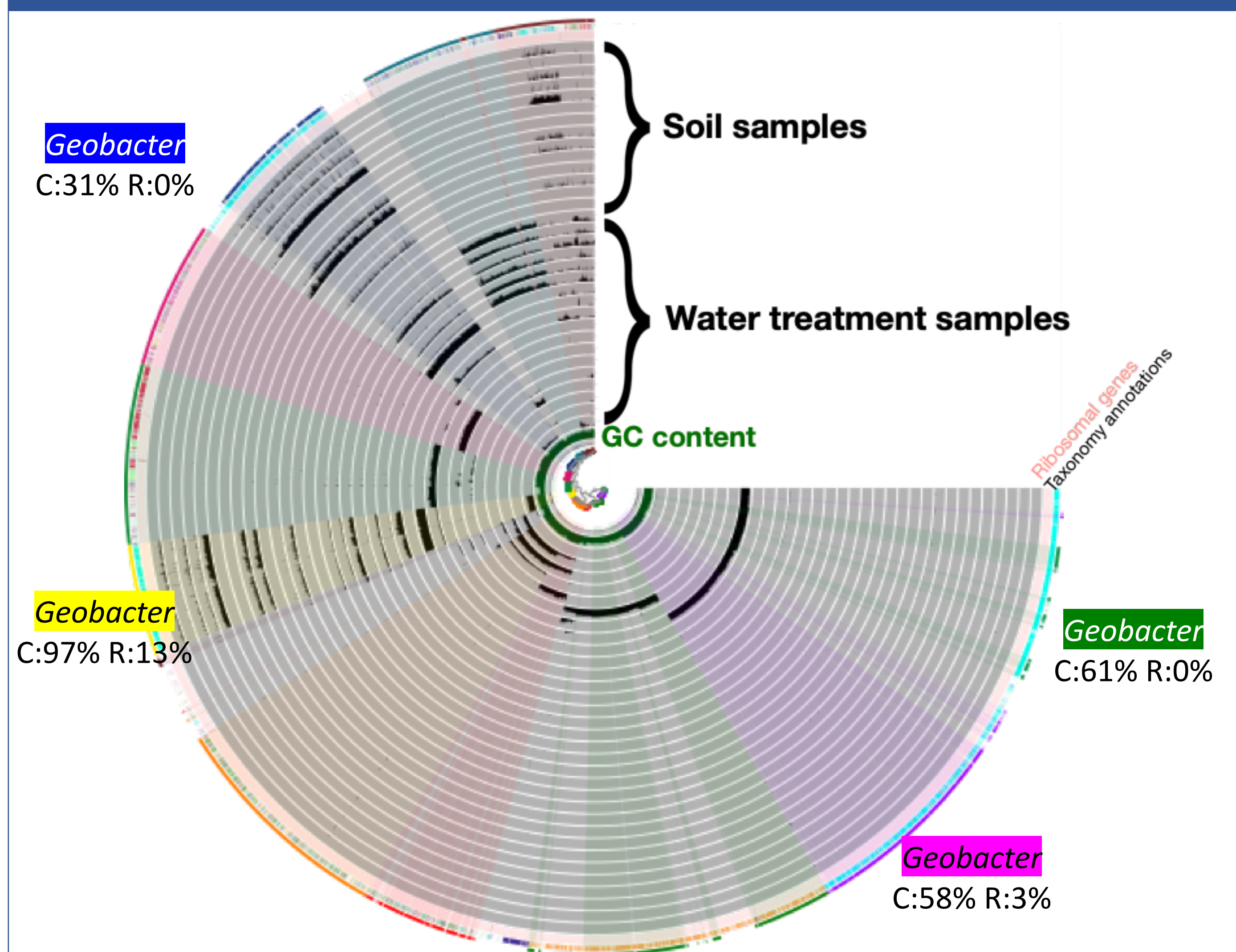
**Figure 2. Metagenomic workflow**

1. Shotgun sequencing
2. De novo assembly with **megahits**  
Overlapping reads are merged in contigs
3. Mapping with **bowtie2**  
Reads are aligned back to the contigs in order to compute gene coverage
4. Gene level taxonomy annotations with **centrifuge** and functional annotations of genes with **NCBI Clusters of Orthologous Group (COG)**
5. Binning with **binsanity** and hand refinement through **anvi'o** interactive interface  
Contigs are group based on sequence composition and GC content, and differential coverage

**Genomes from anodes' samples**



## Results

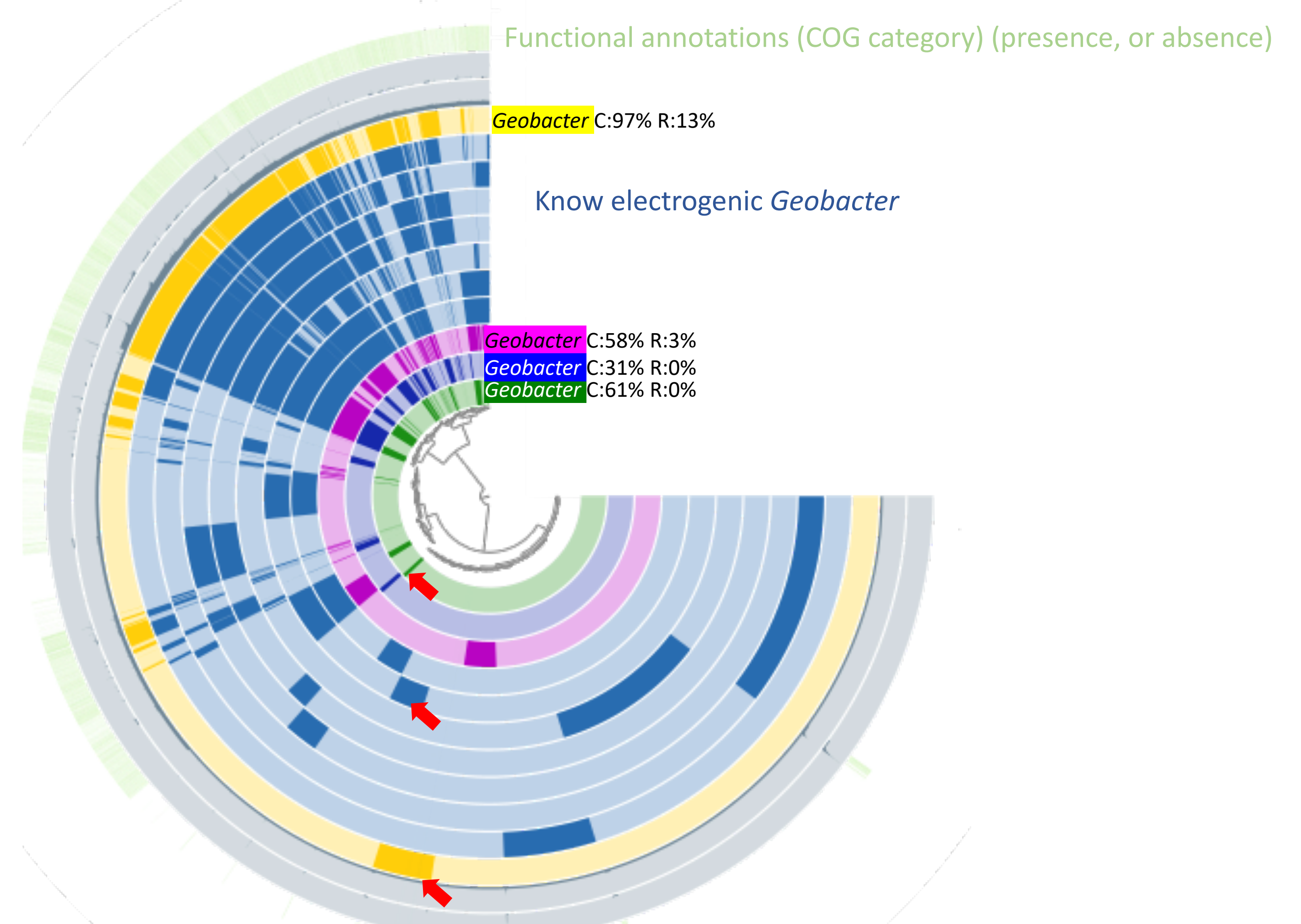


**Figure 3. Anvi'o interactive display of contigs**

Each highlighted coloured parts represent a bin (*i.e.* a group of contigs that aims to reconstitute a genome).

**C = Completion:** estimation of how complete the MAG is.

**R = Redundancy:** estimation of contamination



**Figure 4. Anvi'o interactive display of a pangenomics analysis of *Geobacter* MAGs combined with genomes of electrogenic *Geobacter***

Each blocs represent genes clustered. Some unique genes from the MAGs built in this study are pointed. ➔

No HC genes have been observed.

## Conclusion

*Geobacter* MAGs were recovered from anodes set in polluted sediments, but their ability to degrade HC anaerobically is yet to be demonstrated as no known HC degrading genes have been observed. Further studies could bring out evidence of HC degradation genes in these MAGs or other roles involved in the operation of MFC.

## Contact

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[https://github.com/ziphra/ecl\\_ampere\\_internship](https://github.com/ziphra/ecl_ampere_internship)

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