

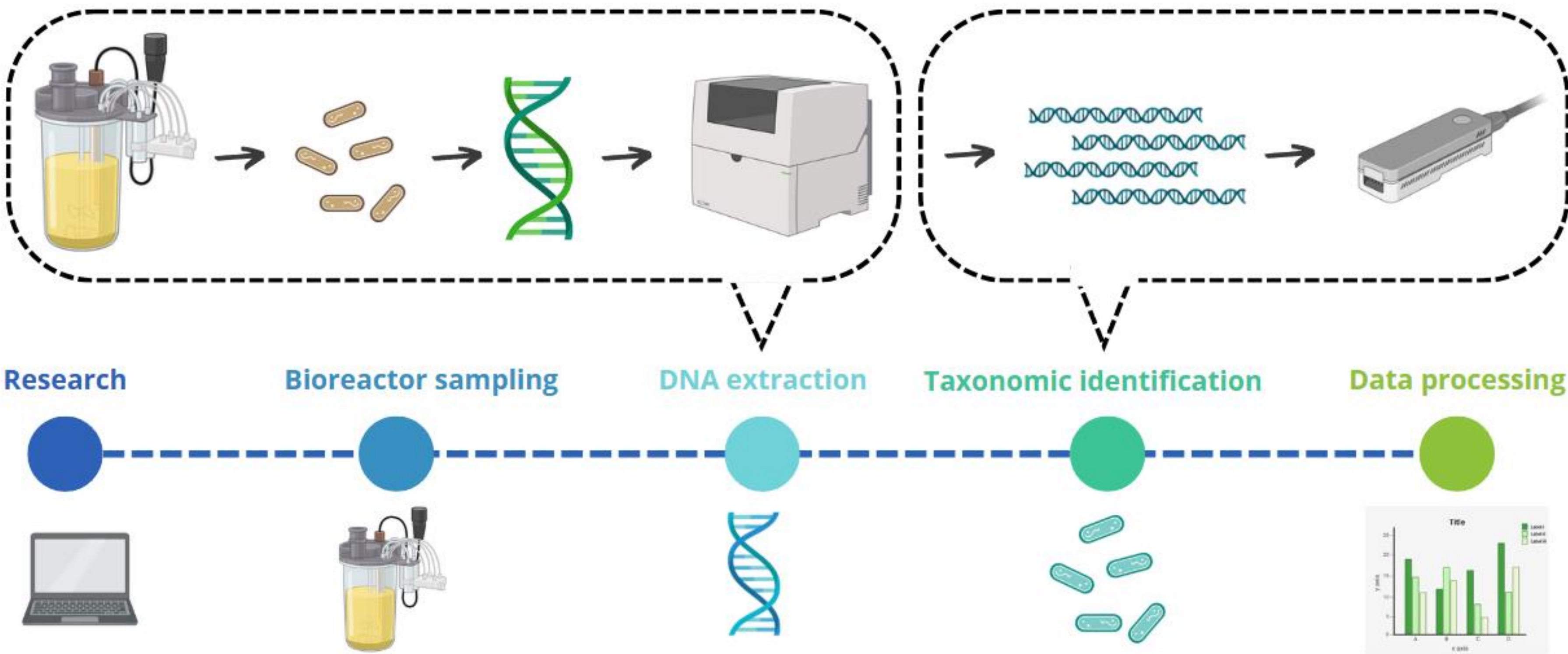
BACTERIAL COMMUNITY CHARACTERIZATION IN VOLATILE FATTY ACID PRODUCTION FROM INDUSTRIAL WASTE

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Introduction

Starch-rich waste is a by-product of the food industry and can become raw material for high-value biotechnological processes, such as the production of volatile fatty acids (VFAs) (Lee *et al.*, 2014).
VFAs are short-chain fatty acids used as low-cost carbon sources that play a crucial role in the circular bioeconomy, valorizing waste and reducing its environmental impact. VFAs can be generated from a wide variety of organic wastes through bacterial **anaerobic fermentation** (Llamas *et al.*, 2020).
It is known the composition and behavior of the bacterial community during fermentation can give high impact to the production of VFAs/PHA. It is highly desired by the work fields to understand the bacterial community in order to obtain high controllability of the fermentation process. This study characterizes the **bacterial communities** responsible for the production of VFAs with various process conditions, such as pH, temperature and substrate/inoculum ratio. To identify bacterial species, molecular level characterization method is implemented via metagenomic DNA sequencing using **Oxford Nanopore sequencing**. The shift of key VFA producing bacterial genera, such as *Clostridium* and *Bacteroides*, will allow us to understand the dynamic of fermentation involved and maximize the performance of the process, contributing to more controllable VFAs/PHA production by using waste streams.

Methodology



With the objective of **characterizing** the bacterial communities responsible for the production of VFAs present in starch-based industrial wastes, the following method was developed. After planning the method and taking samples from the semi-continuous fermentation running in the bioreactor, DNA extraction took place. **DNA extraction** was carried out using specific kits for this procedure and carrying out quality, quantity and length **controls** of the DNA. Next, for the **taxonomic identification** of the bacterial communities, a **DNA library** was created and the DNA was sequenced using **Oxford nanopore sequencing devices**. After this process, the **data** obtained will be processed for its study.

Figure 1. Methodology for analysing bacterial communities in volatile fatty acid production from industrial waste.

Expected results

The expected results to be obtained are a relative quantitative measurements of bacterial communities composed by different species that evolve throughout the fermentation process.
By using the proposed metagenomic method, we expect to create high quality and comprehensible big data to characterize bacterial community by using fermenting starch-rich wastes samples.
The big data then would be processed by inhouse pipeline **StrainScope**. By using this method, we hope to link the switch of bacterial species to the production of VFAs. Furthermore, we plan to link the phenotypes of bacterial species to explain the impact of fermentation conditions on VFAs production.

Applications

VFA are of great importance in the market due to their wide applicability. Its applications are shown in Figure 2 (Samaniego and Pedroza-Sandoval, 2013). The optimization of this process thanks to the knowledge of the bacterial communities present in the industrial waste throughout the fermentation process will allow the production of bioproducts such as VFAs in greater quantity, higher quality and at a lower cost.
The results of this project can be reflected in the creation of **new bacterial communities** that can be used as **inocula** for a wide variety of objectives in new fermentations.

References

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3. Lee, W. S. *et al.* (2014). Chemical Engineering Journal (Lausanne, Switzerland : 1996), 235, 83–99.

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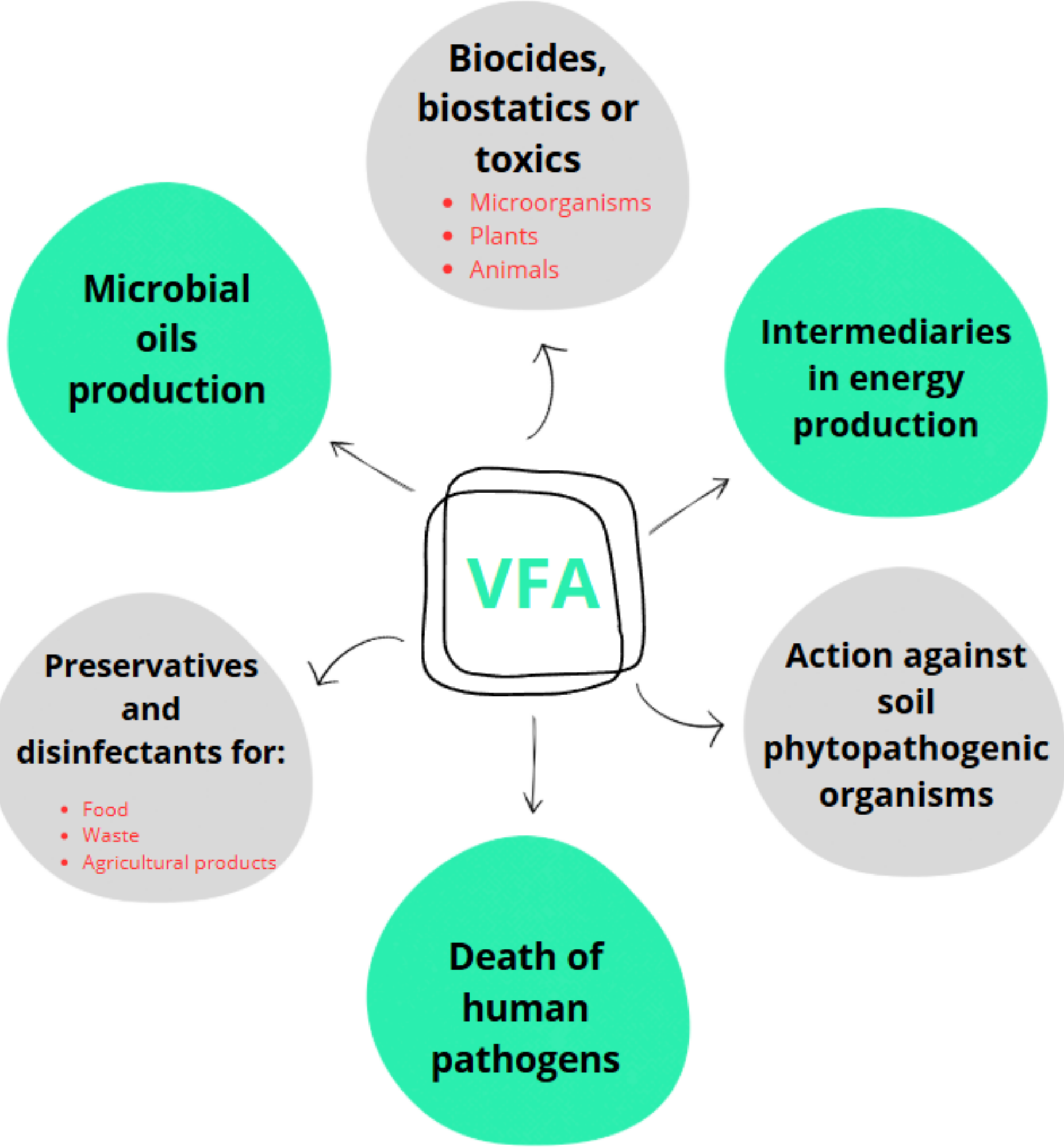


Figure 2. Applications of the VFAs (Samaniego and Pedroza-Sandoval, 2013).