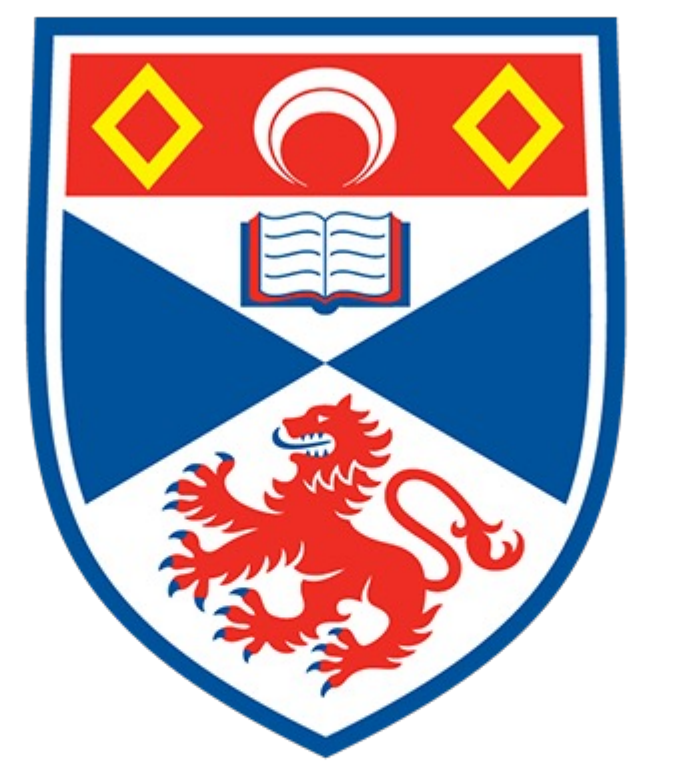


# The Diversity and Evolution of Micro-organisms in Hydrothermal Vents

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## Introduction

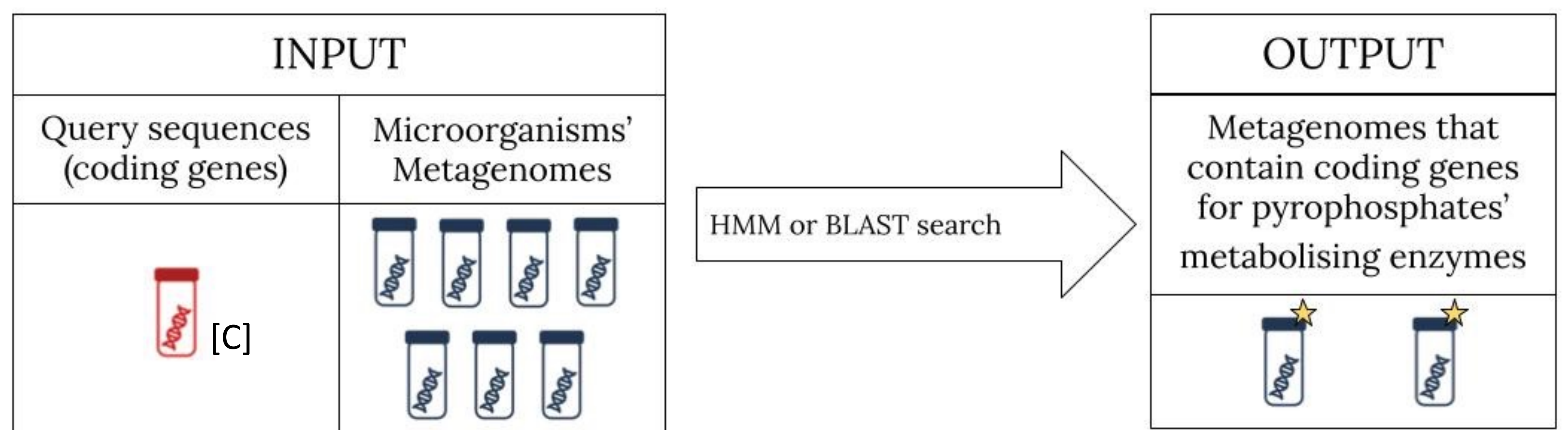
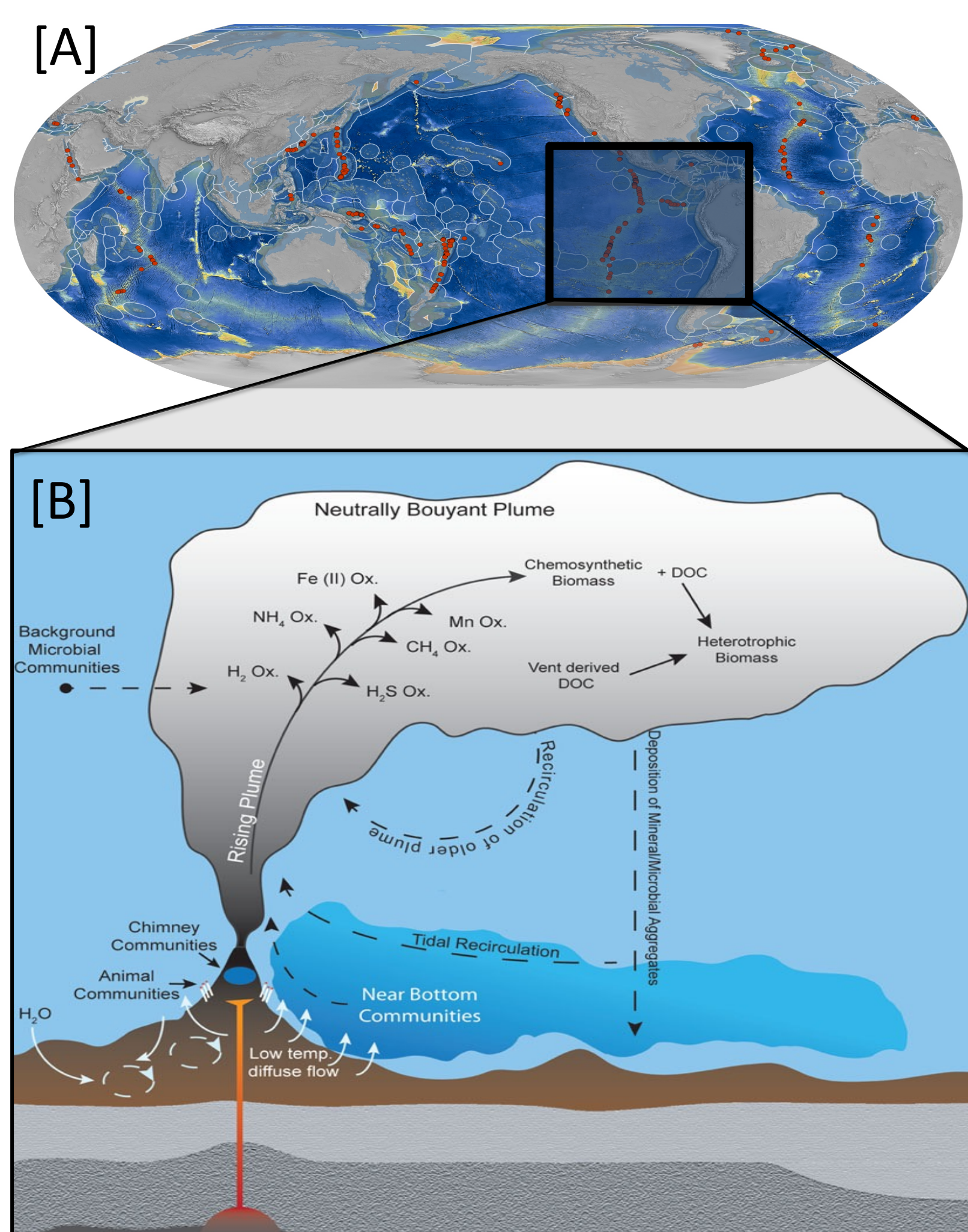
Deep-sea hydrothermal vents, first discovered in 1977 [1], are characterised by being unique ecological niches, with harsh biological parameters, that contain nutrients released from geothermal waters warmed by the volcanic activity present under the seafloor [2]. The emergence of diffuse fluids from high-temperature hydrothermal fluids mixed with cold deep seawater produces a gradation in pH, temperature, and energy sources, generating, depending on said local geochemical conditions, different habitats and microbial communities [2].

## Pyrophosphates as a source of energy

Pyrophosphates (PPi) during the 1960's, started to be considered a primitive source of energy in early stages of life [3] as an alternative to ATP when it was found that photosynthetic bacterial membrane-bound inorganic pyrophosphatase (PPase) was the main pathway to catalyse light-induced phosphorylation of Pi into Ppi [4][5]. Because of the membrane-bound PPase also being a Na<sup>+</sup> pump, the abundance of Na<sup>+</sup> in hydrothermal vents, mimicking the Archean Earth biocological conditions, introduced the question of whether microorganisms found in such environments also employ PPi as their energy source.

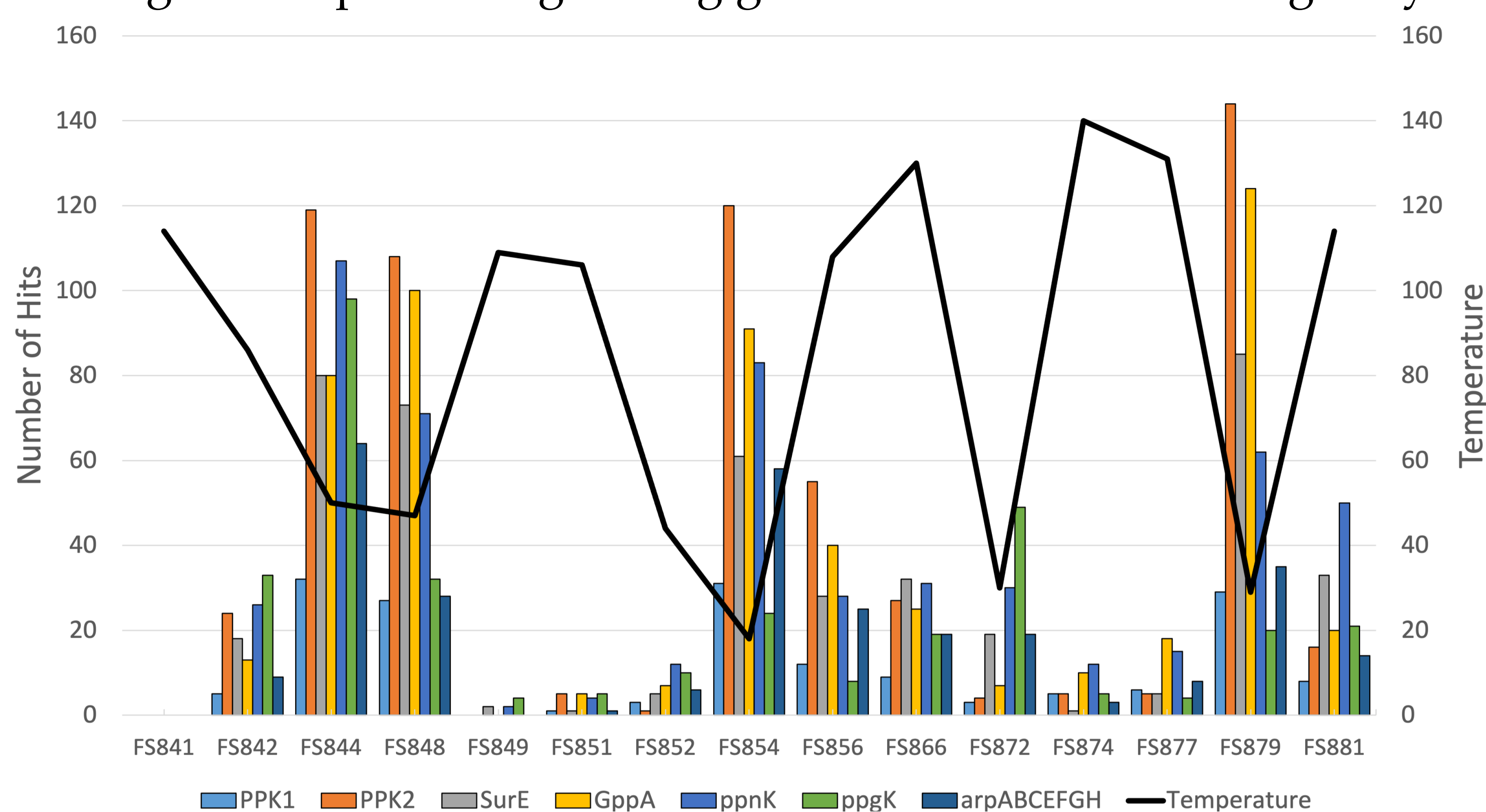
## HMM and BLAST: Search for homologies

The first step to interrogate whether microorganisms in hydrothermal vents employ PPi as their energy source is through either an HMM search or by performing a BLAST. These two methods, its employment being dependent on the type of the input data, are used to find homologous sequences between the query sequences of a selection of 7 different PPi and the metagenomes of microorganisms in hydrothermal vents, 15 collected from the Mid-Cayman Rise and 16 from Juan de Fuca Ridge. The result from either of those searches is the list of which metagenomes do possess genes that code for PPi' metabolising enzymes.

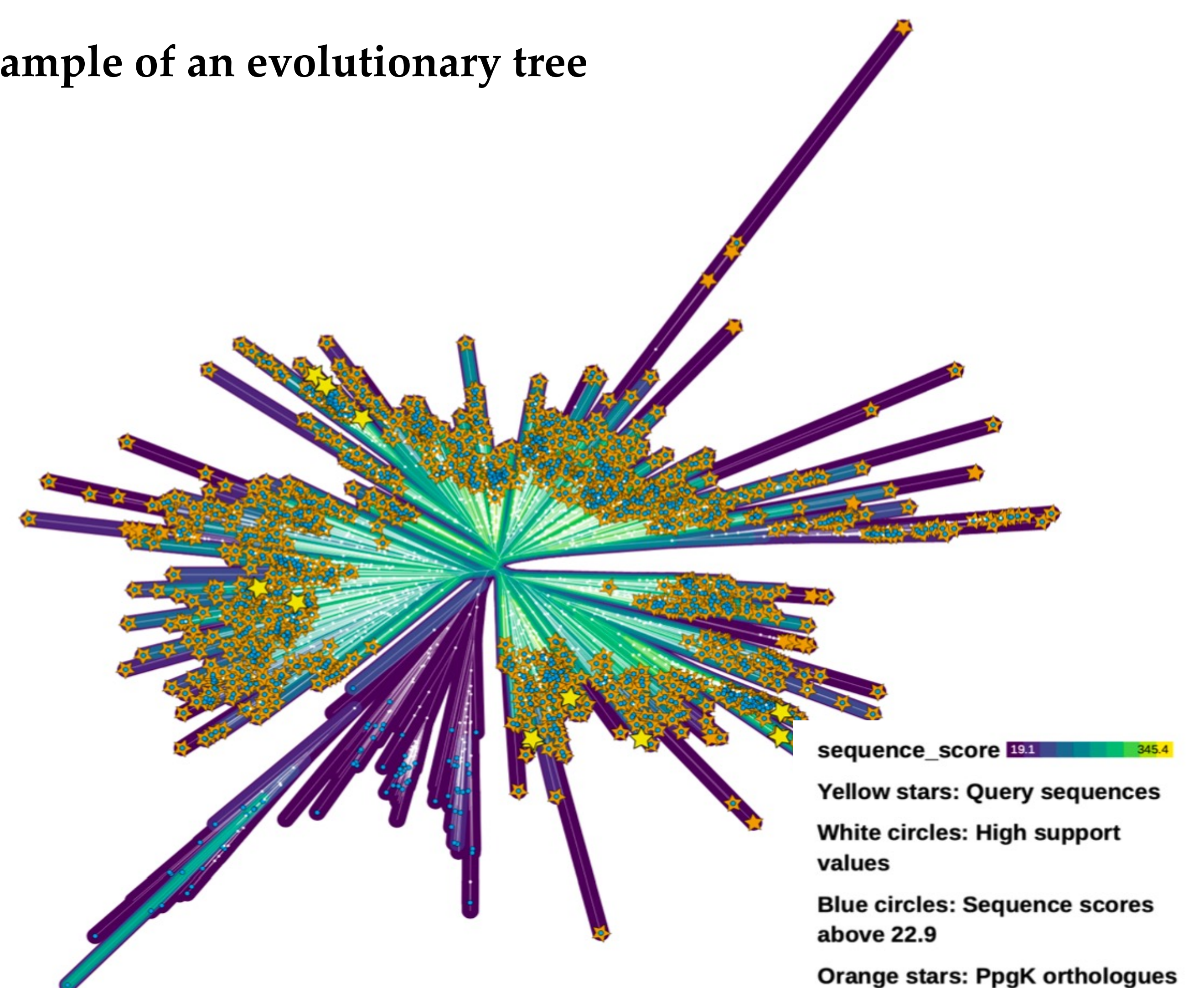


## Statistical analysis of HMM and BLAST hits

The output indicated that in almost all samples there were hits of microorganisms possessing coding genes for PPi' metabolising enzymes:



## Example of an evolutionary tree



## Evolutionary and Reconciliation trees

As the NCBI indicates, the hits obtained could be used as already conclusive, but this research checked the results by producing an evolutionary tree, in which it was noticed that some of the branches were phylogenetically far from the query sequences, meaning that those hits were not that closely related to the PPi sequences and entailing the possibility of those metagenomes not having said coding genes; consequently, those branches were not included as actual orthologues. Reconciliation trees were computed to unravel the origin of the studied coding genes and how they evolved. The results obtained suggested that microorganisms in the sampled hydrothermal vents employ metabolising enzymes that emerged in early stages of life.

## General Conclusion

Based on the results obtained, most of the microorganisms in the sampled hydrothermal vents do possess in their metagenomes coding genes for pyrophosphates' metabolising enzymes that, according to the reconciliation trees ran, emerged in early stages of life.

## Acknowledgements

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