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## MAM : Methylation Analysis of Microalgae.

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Microalgae are defined as unicellular or pluricellular undifferentiated organisms, eukaryotes or prokaryotes living in water. In some situations, phytoplankton proliferates, causing harmful algal blooms with considerable economic losses for aquaculture, fishing and tourism. [1]. Epigenetics plays an important role in the adaptation and proliferation processes of microalgae. Thanks to MinION Oxford Nanopore technology (ONT), which allows the sequencing of native DNA molecules without the need for bisulfite treatment, many tools for methylation detection have been developed by the scientific community. However, these algorithms are complicated to use for researchers with a background in biology and therefore require the implementation of automated, standardized and user-friendly solutions. In addition, the tools used for ONT are often updated and require regular monitoring to use them properly. Also, there is rarely information on the resources needed for the tool, tutorials explaining how the tool works, examples of analyses and test data sets. Finally, these tools are not designed for non-model organisms, but rather for mammals or bacteria. Finally, most of the methylation analysis tools are based on a reference model but this model is rarely adapted to the species of interest.

In this context, the objective of the work is to build a reusable pipeline for the analysis of methylations in microalgae. For our project, we were able to design a model from Methyseq Illumina sequencing data of *Prymnesium parvum*. Between the multitude of tools capable of identifying the positions of epigenetic modifications from Nanopore sequencing reads we chose two: Megalodon [2] and DeepSignal [3], [4]. Both tools work with a neural network and require a reference model to identify epigenetic modifications of sequences. We were able to compare the different results of these tools in order to select the "best" one according to the needs. In the future, it will be necessary to automate the data treatment processes in order to respect the FAIR principles (findable, accessible, interoperable and reusable).

### References

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