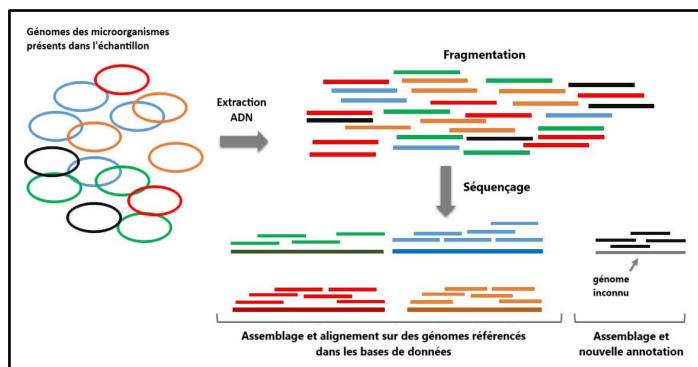


## Metagenomics, a powerful tool to explore microbial marine diversity

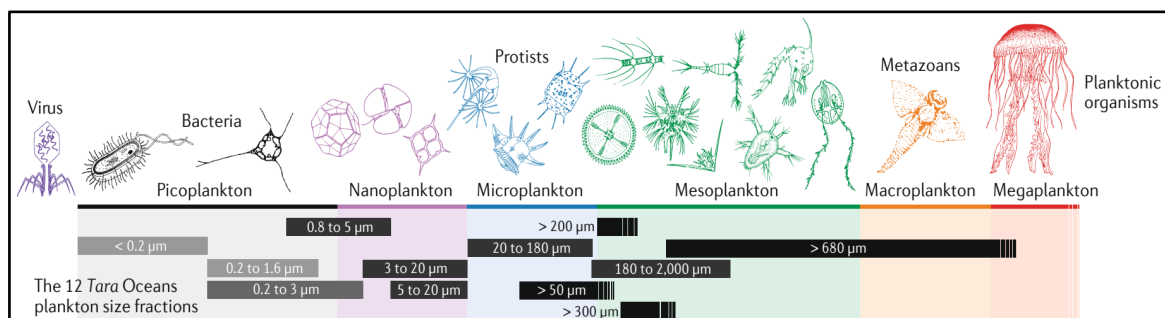
To unravel the diverse and often unknown microbial communities, the Tara Oceans Foundation conducted global expeditions using metagenomics. This high-throughput approach consisted in sequencing DNA from entire plankton communities (shotgun sequencing) directly from environmental samples, bypassing the traditional need to culture organisms. This shotgun sequencing was followed by genome reconstruction of the marine plankton, using *de novo* assembly for unknown species, and mapping to a reference genome for known species (Fig. 1).

Data from the Tara Oceans's metagenomics analysis revealed an exceptional diversity of species (Fig. 2), and resolved a key ecological puzzle: how plankton communities maintain such high diversity in nutrient-poor oceanic environments. Researchers discovered that plankton exchange essential metabolites, such as amino acids and B-group vitamins, highlighting the cooperative and interconnected relationships between oceanic microbial communities.

However, important questions remain, including the mechanisms by which these metabolites are exchanged.



**Fig.1:** Genomic sequencing process (France Génomique. *Métagénomique shotgun.*)



**Fig.2:** Diversity of marine plankton. (Giordano, N. et al. 2024)

Thank you to Odile Lecompte for giving us interesting insights into environmental metagenomics!

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