

# The EBI Metagenomics Portal - a free to use analysis platform for metagenomic data

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Metagenomics, the analysis of genetic material from microbial communities inhabiting different environments, is an exciting and fast-growing field of research. Metagenomic analyses have recently been successfully applied to a variety of areas, including agriculture, food manufacture and spoilage, bioenergy production, the elucidation of antibiotic resistance mechanisms, and animal and human health.

With the increased popularity of the method and the diminishing cost of sequencing, data volumes are becoming increasingly cumbersome to process, analyse and navigate. More often than not, the computational overhead is the bottleneck of a metagenomics experiment. To help alleviate this situation, we have brought together a cross-disciplinary team of computer scientists, bioinformaticians, statisticians and biologists to produce the EBI Metagenomics Portal. Some of the recent technical developments necessary to deal with the 10 terabytes of sequence data from the first phase of the Tara Oceans project processed by the Portal will be presented. The functional and taxonomic composition of this flagship project, although vast in size, can be summarised in a just 5 files, amounting to only a few megabytes.

The EBI Metagenomics Portal (<https://www.ebi.ac.uk/metagenomics/>), a free to use, analysis and archiving resource for the metagenomics research community. Covering data submission, archiving and sharing functions, community standards-compliant meta-data curation, and rich functional and taxonomic diversity analyses, the service has attracted a growing user base world-wide. The website provides access to analysis results for tens of billions of sequences, drawn from from thousands of runs from hundreds of different projects across disparate biomes. An overview of the features of the website will also be presented, describing the data submission and analysis processes, and highlighting the ways in which it can be used to interrogate and compare metagenomic samples.