The study of genetic material sampled directly from marine environmental sources is still in its infancy, but is rapidly expanding. To prevent that processing and analysis of these samples becomes a bottleneck, where data production is faster than the speed users are able to make use of it, there is an urgent need to establish dedicated data management e-infrastructure and bioinformatics pipelines specialized for marine research. While EBI has developed EBI-metagenomics, a generic pipeline, which aims to provide insights into the phylogenetic diversity as well as the functional and metabolic potential of the samples, the Norwegian node has developed Meta-pipe in the direction coupled with marine bioprospecting. In this pilot project the two pipelines will be harmonized in terms of interoperability in order to establish long-term sustainable service platforms and build a user community for marine metagenomics analysis in ELIXIR.

**Deliverables**

[1] Harmonizing existing metagenomics pipelines (EBI-metagenomics and Meta-Pipe) to ensure interoperability.

[2] Assess specialized databases such as Merops, Panther and SFLD (Structure Function Linkage-Database) to evaluate whether these can enrich the output further.


[4] Report on gap analysis related to establishment of reference genomes for the marine environment. Also includes a workshop with ESFRI initiatives, EU FP7 projects and other appropriate groups/networks to discuss current status and needs of marine reference genomes.


**Status**

[1] Specific intermediate pipeline steps has been identified where components needs to be improved or developed, such as pre-processing and removing 16S sequences before assembly. Additionally, assessing new databases as mentioned in [2] and implementing Interproscan in Meta-pipe is in progress.

[3] EMBL-EBI Embassy Cloud services has been used to set up a virtual cluster with 15 nodes total and a shared NFS file system. To experiment with the possibilities this cloud service provides, a Blast job against UniprotKB using Slurm as a scheduler has been computed successfully.


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EBI Metagenomics Portal
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www.ebi.ac.uk/support/metagenomics