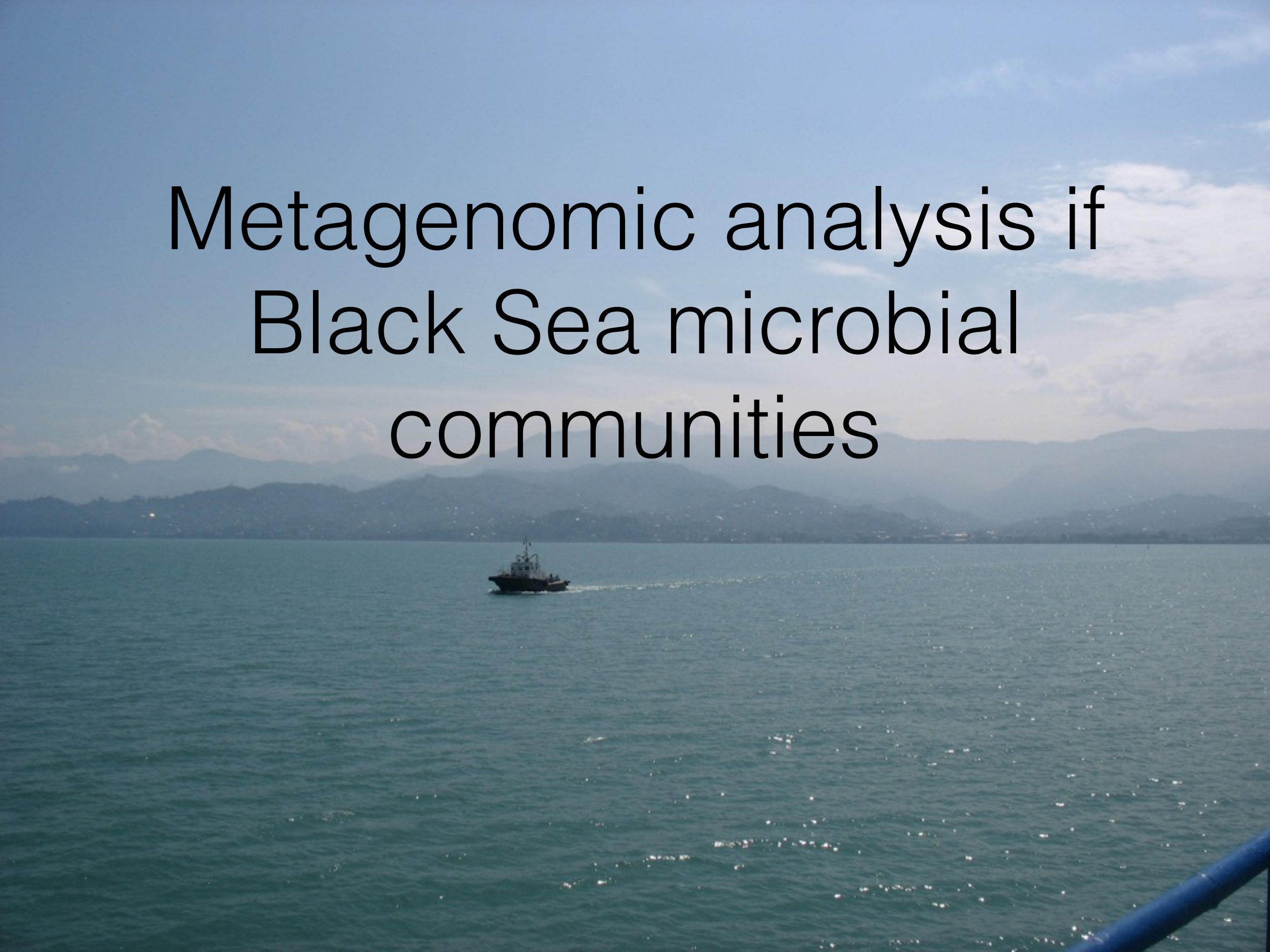
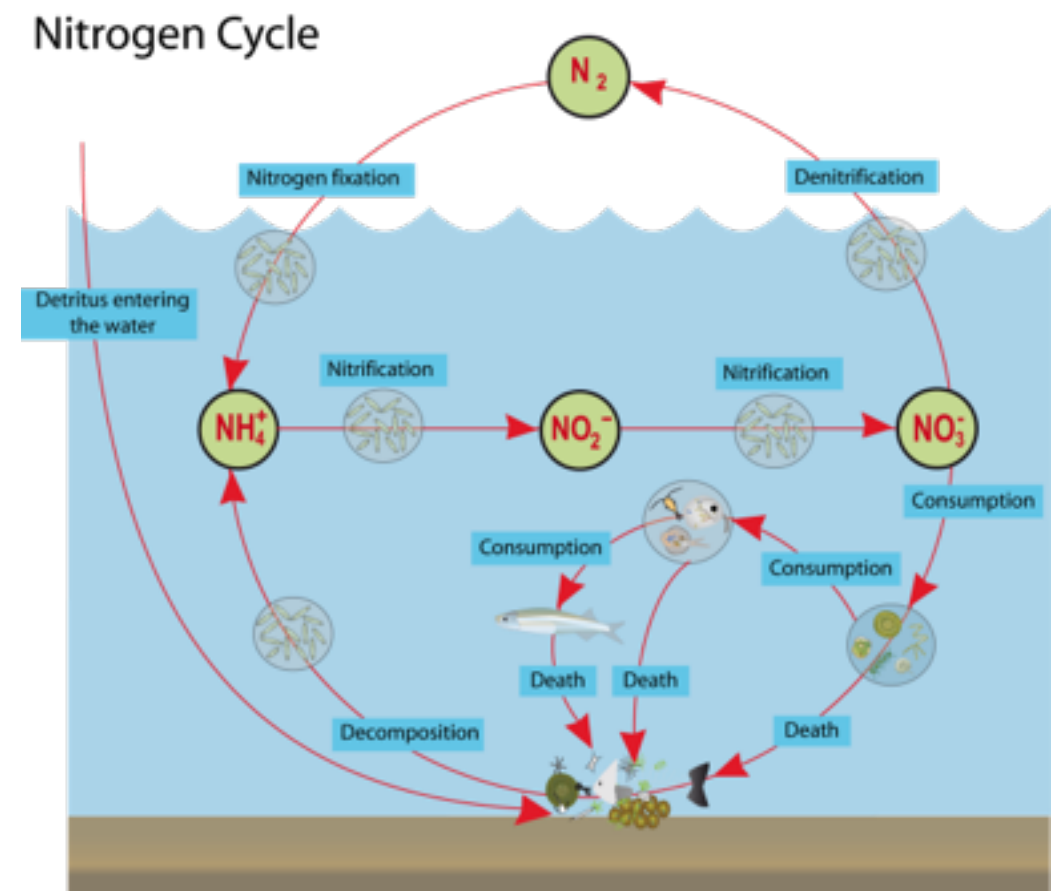


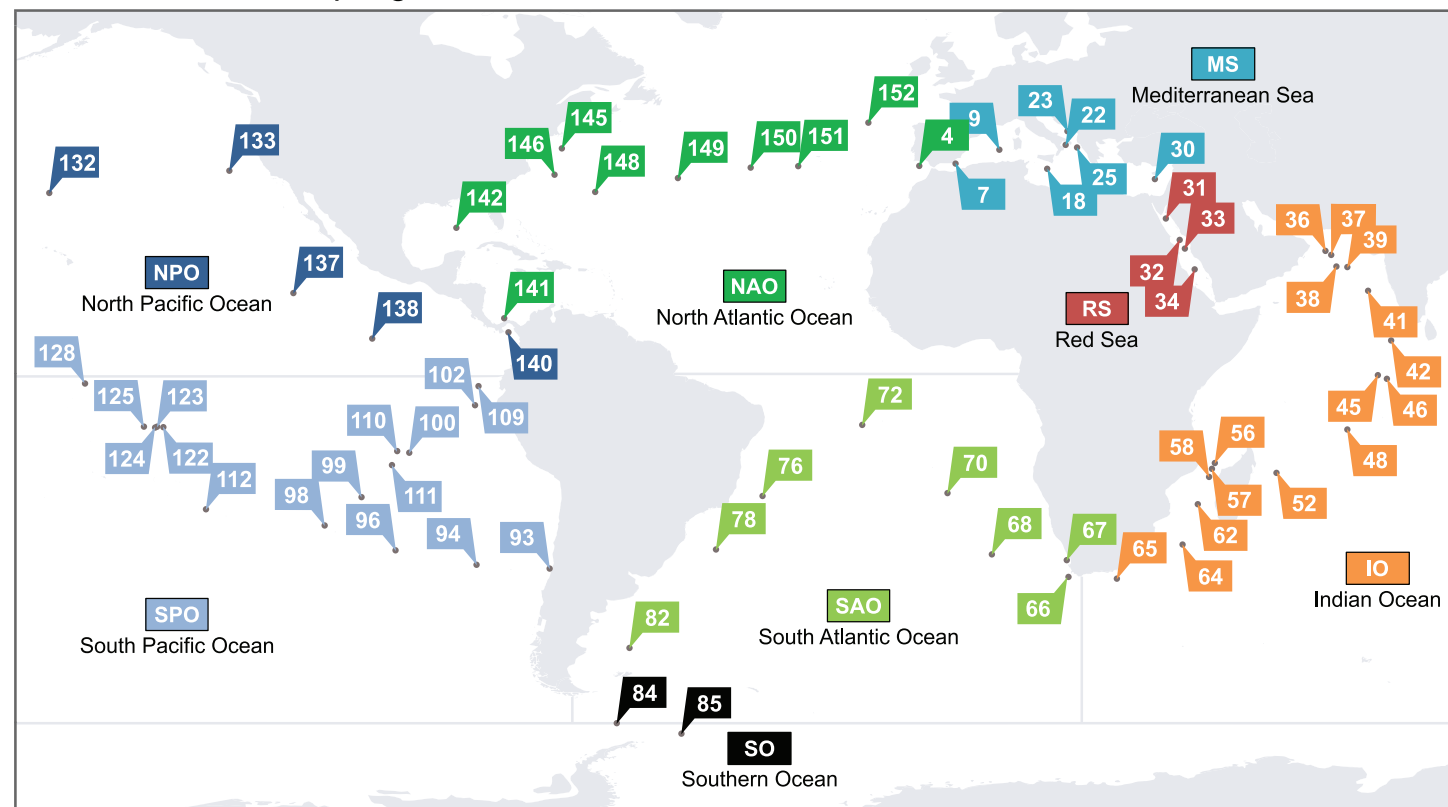
# Metagenomic analysis of Black Sea microbial communities



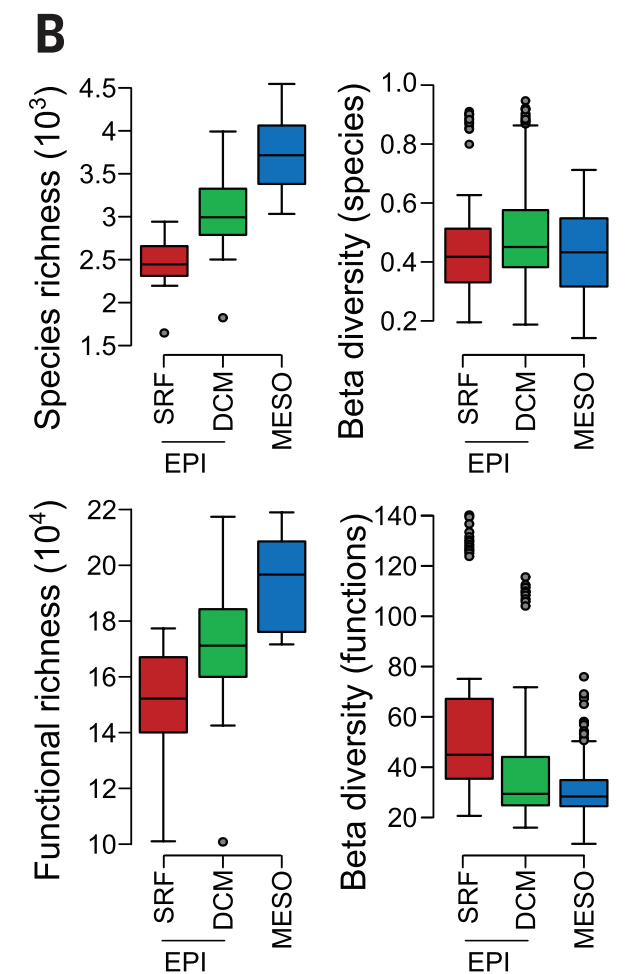
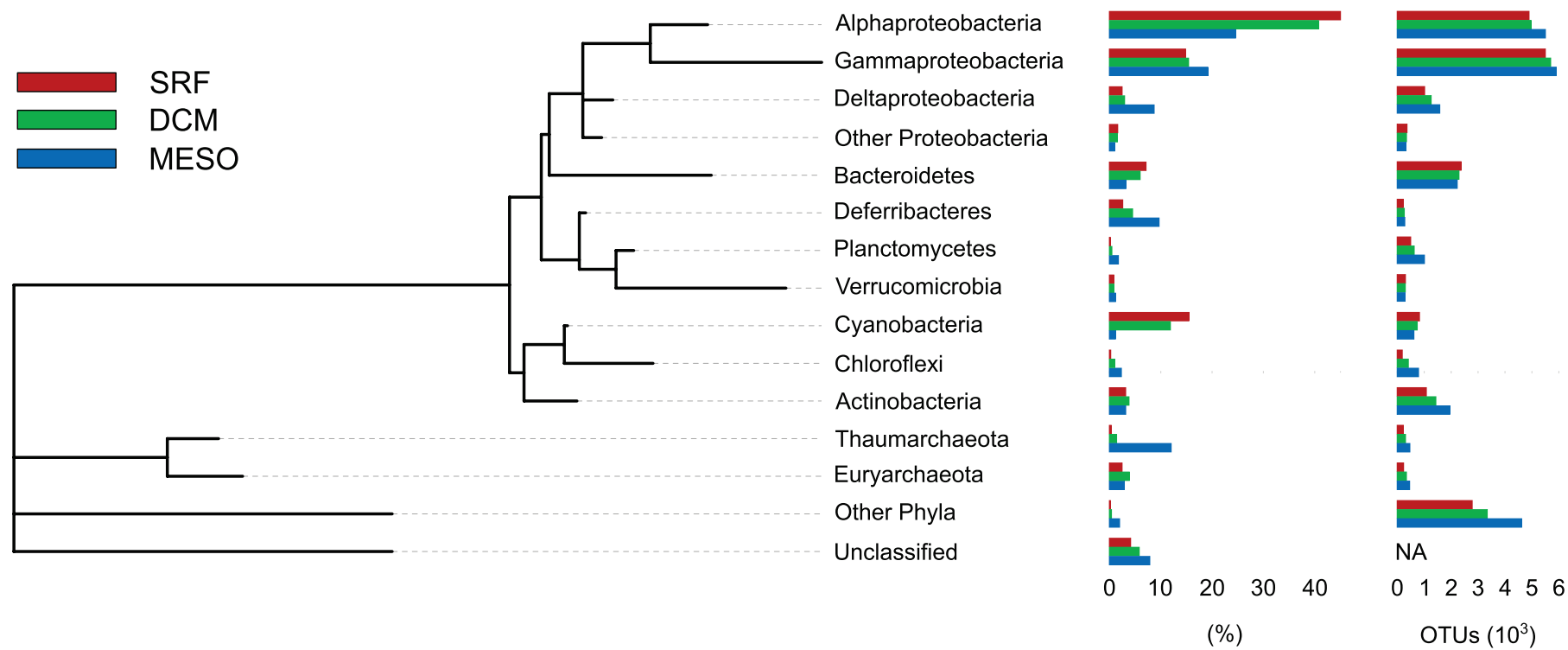
# Why is it important

- Integral to all major biochemical cycles, fluxes and processes that run in marine ecosystems
- ~99% of marine microorganisms cannot be cultured in the lab





■ SRF  
■ DCM  
■ MESO



**Sunagawa et al. 2015**



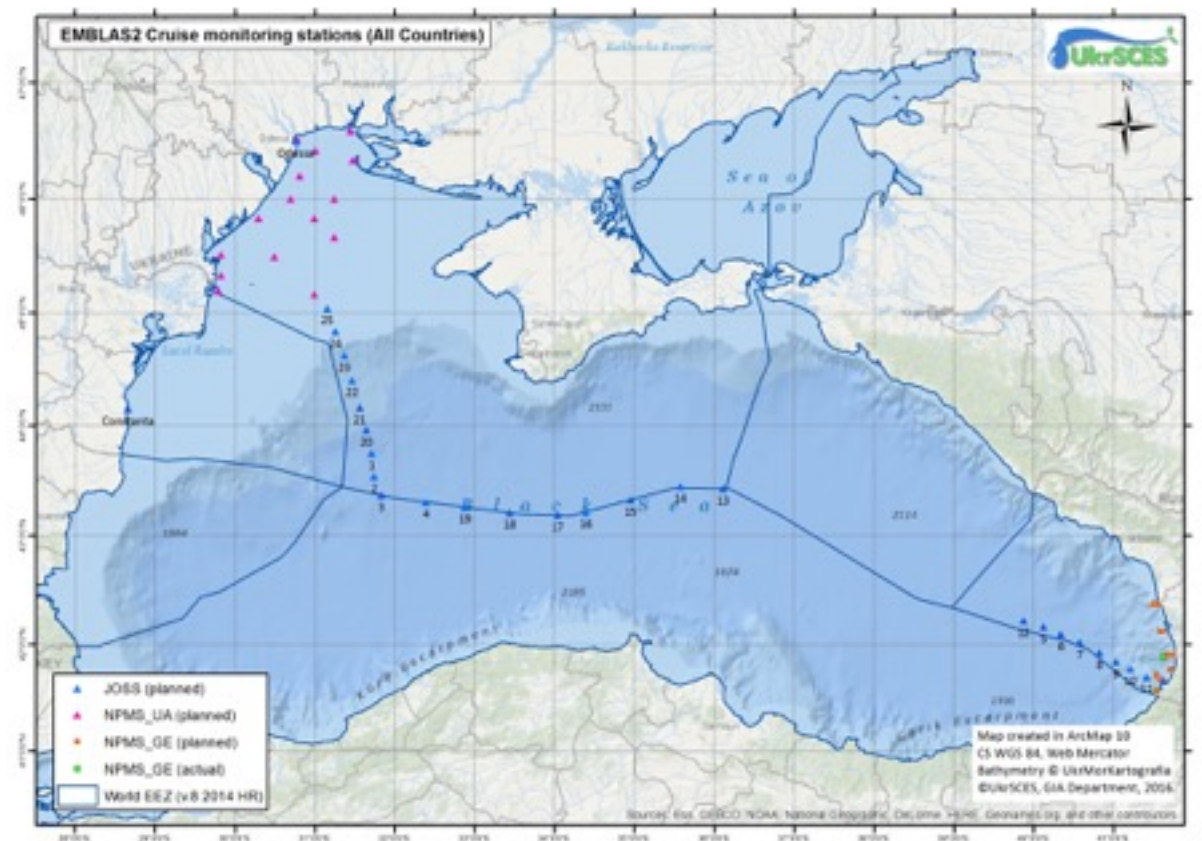
# What we want to do

69 sea water samples from 12 stations

30 sediment samples from 5 stations in May-June 2016.

16s Illumina sequencing, sequence assembly, gene prediction, metagenomic operational taxonomic units (mOTUs) identification, estimation of mOTU relative abundance and gene abundance in a community...

Correlate relative abundances of taxonomic and gene compositions with the data on environmental parameters, such as temperature, salinity, nutrient abundance, oxygen concentration and H<sub>2</sub>S concentration to discover specific gene and taxonomic patterns and possible adaptation of microbial communities





Thanks for attention!