Dataset name: **Gene expression in microbial eukaryotic plankton communities**

|  |  |
| --- | --- |
| Parameters: | * **Sequencing data (fastq file)**
 |

PROJECT TITLE: **MOBYDICK**

Oceanographic cruise: **MOBYDICK**

Start date: **18/02/2018**

End date: **27/03/2018**

Project manager: **Bernard Quéguiner** bernard.queguiner@mio.osupytheas.fr

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 Geographic information: **Indian sector of the Southern Ocean**

 Latitude: **49.5°S – 52.5°S**

 Longitude: **67,0°E – 74.5°E**

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# OPERATIONS

## Sampling device(s)

Surface (10–15 m) rosette bottles (CTD Omics T).

## List of stations sampled

M2\_1, M4\_1, M3, M2\_2, M1, M4\_2, M2\_3, M3\_3

# INSTRUMENTS

Instrument Type: **Peristaltic pump**

Manufacturer: **Masterflex L/S**

Model: **Easy Load II**

Instrument Features / Calibration: **N/A**

# DESCRIPTION of PARAMETERS

## Measurement details

30 L of surface seawater (10 or 15m depth) were prefiltered through 60µm mesh and filtered onto a 0.8 µm Polycarbonate filter (142 mm). Each operation lasted 10 to 30 min depending on cell concentration (1 L min–1). The filters were placed into 15 mL Falcon tubes, preserved with RNAlater and stored at –80°C.

## Analytical procedure

Total environmental RNA will be extracted from the samples following standard protocols, which include poly-A selection to enrich eukaryotic RNA (Gilbert & Hughes, 2011). Complementary DNA will be synthesized from the extracted mRNA for the construction of paired-end Illumina libraries. The libraries will be sequenced on an Illumina Hiseq platform. Sequence data will be analyzed using established pipelines (Toseland *et al.*, 2014), including quality control (FastQC) of the raw sequencing reads and *de novo* assembly of sequence reads into contigs with the software Trinity. Coding sequences will be assigned to different metabolic pathways such as carbon metabolism (Caron *et al.*, 2016) using the KEGG (Kanehisa *et al.*, 2016) and NCBI databases. Comparison of normalized read counts from the different samples will identify differentially abundant genes among distinct foodwebs (Alexander *et al.*, 2015; Pearson *et al.*, 2015).

## Units

N/A

## Sensor precision

N/A

## Post-cruise data analysis/treatment required

N/A

## Estimated Date of Delivery

Winter 2020

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