README ASAP SAS21

WP5 ASAP metadata SAS-Oden expedition 2021

Project title: Adaptive strategies of Arctic prokaryotes at extremely low growth rates – carbon cycling, respiration, biomass, production, gene expression, morphology (ASAP).

In this file you find the metadata related to samples collected for different projects of ASAP work package 5 (see Expedition Logbook file, (Expedition Report SWEDARCTIC : Synoptic Arctic Survey 2021 with icebreaker Oden (diva-portal.org)).
Note that this file needs to be used together with the Expedition Logbook file in which the device operation is coupled to date, time, geographical position and ocean depth.

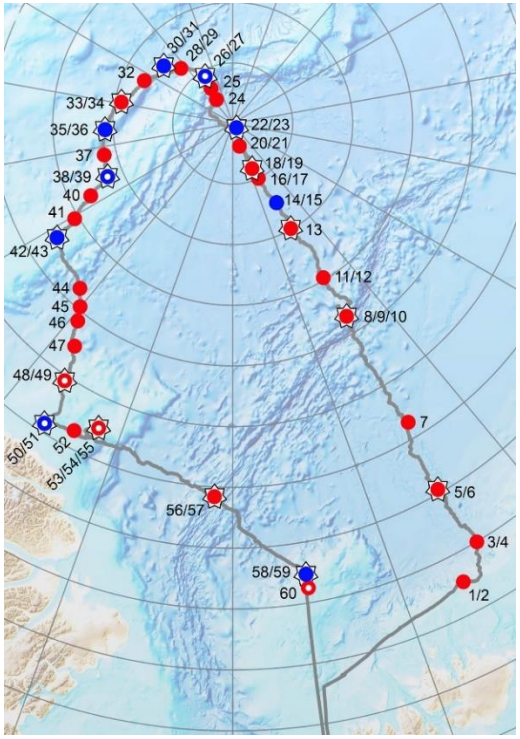

Figure 1. Mapp over expedition route with station codes.

Projects	Description
PROMAC	In this project, seawater was collected from duplicate Niskin-bottles at 4 different depths. The seawater was first prefiltered through a 1.2 µm Isopore-filters before subsequent study of prokaryotic maintenance activity.
SAS	In this project seawater was collected from 8 different depths for analyzing spatial variability in abundance and activity of prokaryotes contributing to the larger project objectives.
24hrIceSAS	This project is similar to SAS but at stations where ice sampling was performed including the Ice-seawater interface (ISI) was collected and analyzed for different variables.
RespirationQ10	In this project the temperature sensitivity of plankton respiration (Q10) in surface water was in two stations.
TCF	In this project, samples were analyzed from three different depths (10, 30 and 500 m) for determining the thymidine conversion factor (TCF)
IsotopeDilutionExpGrowth	In this project, samples were analyzed from 3 different depths (30, 50 and 300 m) for determining saturating concentration of ^{3}H-Thymidine
Note	Variables mentioned after projects name in each worksheet is separated by an underscore (_).

All sheets of this file

Column heading	Description
Cast	Cast number (1-19), a running number for each device operation performed at one station
Comments	Any comment to the sampling event
CTD_type	CTD used for collecting water samples
Depth	Depth from which water samples were collected (m)
Device_operation	A unique code consisting of the expedition abbreviation (SO21 = SAS-Oden 2021), the station number (1-60) and the cast number (a running number for each device operation performed at one station).
Environment	Classification of environment type sampled
Expedition_code	Expedition code for Synoptic Arctic Survey 2021
Leg	Leg number (1-7). When the ship's direction was fundamentally changed after a station, a new leg was started.
Niskin Bottle No.	Number of Niskin bottle sampled
Parameter	Parameter name
ParameterID	Parameter ID specific for the variable
Replicate	List of replicate samples
RunningNo.	Running number of the variable
SampleID	Unique sample ID for each variable, composed by Expedition_code, ParameterID and Running No.

Start_Date	Start of sampling (YYYY-MM-DD)
SampTime	Start time of CTD rosette sampling. If sub-sampling was extended markedly a range is reported.
Start_lat	Latitude (degree decimal minutes, DD MM.mm) at the start of the CTD cast
Start_lon	Longitude (degree decimal minutes, DD MM.mm) at the start of the CTD cast
Start_time	Start of sampling (UTC; hh:mm)
Station	Station number (1-60). These stations were reached by ship (36 stations) or by helicopter (24 stations). All stations in this file are ship stations.
Qcode	Quality code according to the quality code key reported by the EU-project Aquacosm.

Column headings common for PROMAC_ProkaryoticRespiration, SAS_PlanktonRespiration, Respiration_Q10, and 24hIceSAS_PlanktonRespiration.

Column heading	Description
SeawTemp	Sea water temerature in °C
IncTemp	Set temperature of the incubator (°C)
Salinity	CTD salinity values (in psu)
WellNo	Well number in the optode-incubator
OptodeNo	Serial number of optodes used for measuring oxygen concentration
StDatTim	Start date (YYYY-MM-DD) and time of the incubation (hh:mm) separated by T.
EnDatTim	End date (YYYY-MM-DD) and time of the incubation (hh:mm) separated by T
FanSpeed	Speed of the fan adjusted to maintain the set temperature of the incubator
RoomTemp	Room temperature where the incubation was done (°C)
Resp	Respiration rate in µmol O_2 dm^{-3} d^{-1}
95CIResp	95% confidence interval for the respiration rate estimate (regression of time series) in µmol O_2 dm^{-3} d^{-1}
OxConsP	Probability for type I error for the regression of oxygen and time
OxConsR2	Coefficient of determination for the regression of oxygen and time
OxyN	Number of oxygen sensor measuremnts
AirSat	Initial (n=20) air saturation during the experiment
Comment	Comment to the measurement.

Column headings common for PROMAC_Prokaryotic-Growth, SAS_Prokaryotic-Growth, 24hIceSAS_Prokaryotic-Growth, TCF_ThymidineUptake, and IsotopeDilutionExpGrowth

Column heading	Description
SampDay	Day of experiment (TCF_Growth project only)
SampType	Code differentiating between control and samples
SampVol	Starting sample volume for prokaryotic growth (cm^3)
IncStart	Incubation start time of samples after the addition of radioisotope (UTC; hh:mm)
IncEnd	Incubation end time of samples after the addition of radioisotope (UTC; hh:mm)
StrTemp	Storage temperature of the samples (°C)
ThymConc	Thymidine concentration (in nmol dm^{-1}) used for incubation. Only used in the IsotopeDilutionExpGrowth project
DPM	Disintegration per minute of tritium of the thymdine tracer
IncTime	Incubation time with thymidine tracer (decimal hours)
TCF	Thymidine conversion factor used (cells mol^{-1} [^{3}H-thymidine]). Determined in this study (TCF_ThymidineUptake and TCF_CellGrowth).
PrGrMe	Average procaryotic community growth (celler dm^{-3} d^{-1}) per depth
PrGrSE	Standard error of average procaryotic community growth (celler dm^{-3} d^{-1}) per depth
n_thy	Number of replicates for thymidine uptake per depth (Niskin bottle)

Column headings common for PROMAC_Prokaryotic-Abundance, SAS_Prokaryotic-Abundance, 24hIceSAS_Prokaryotic-Abundance and TCF_CellGrowth

Column heading	Description
SampType	Code differentiating between control and samples
VolFix	Volume of the water samples used for fixation (cm^3)
SampVol	Volume filtered for slide preparation (cm^3)
ForAdd	Amount of 37% formaldehyde added to the sample (cm^3)
StrTemp	Storage temperature of the samples after fixation (°C)
SampDay	Sampling day for the fixation of samples, meant only for TCF_CellGrowth-project
PrConc	Prokaryotic cell concentration (cells cm^{-3})
PrSDCon	Standarddeviation of prokaryotic cell concentration on the filter surface (cells cm^{-3})

PrNPic	Number of images per filter
PrCouCel	Number of cells counted
PrVol	Prokarotic average cell volume (µm^3)
PrSDVol	Standarddeviation of prokarotic average cell volume in the sample (µm^3)
AnaDat	Date of microscopic analysis

Column headings for Dissolved Organic Carbon (DOC), and Total Dissolved Phosphorus and Nitrogen (TDP-TDN)

Column heading	Description
StarFilt	Start time of the filtration (UTC; hh:mm)
StopFilt	Stop time of the filtration (UTC; hh:mm)
HClAdd	Amount of 1.2 M HCl added (µl), only used in the DOC estimation
StrTemp	Storage temperature of the samples (°C)
DOCBru	Brutto concentration of DOC before background correction (µmol dm^{-3})
DOC	DOC concentration after background correction (µmol dm^{-3})
TDPBru	Brutto concentration of TDP before background correction (µmol dm^{-3})
TDP	TDP concentration after background correction (µmol dm^{-3})
TDNBru	Brutto concentration of TDN before background correction (µmol dm^{-3})
TDN	TDN concentration after background correction (µmol dm^{-3})

Column headings for Scanning Electron Microscopy (SEM) for specific project: PROMAC_SEM, SAS_SEM, and 24hIceSAS_SEM

Column heading	Description
VolFil	Amount of volume used for filtration and concentration of sample (cm^3)
VolACon	Volume of the sample left after filtration and concentration (cm^3)
StrtFil	Start time of the filtration (UTC; hh:mm)
StopFil	Stop time of the filtration (UTC; hh:mm)
VolFix	Final volume of concentrated sample used for fixation (cm^3)
CtrTim	Centrifugation speed (× g) and time (minutes) used to pellet the cells
Fix2V	Volume of the fixative 2 used for the steps of fixation (µl)
IncAFix2	Incubation condition of the sample after adding fixative 2

Fix3V	Volume of fixative 3 used for long term storage (in µl)
StrTemp	Storage temperature of the samples (°C)
ImgN	Total number of scanned images in one sample in Scanning Electron Microscopy (SEM)
ObjN	Total number of unique objects found in all scanned images of a sample
ClShpStr	Different classes of cell shapes or structures identified in an image
ShpFqr	Total frequency distribution of respective class in scanned images of a single sample
CCFqr	Total frequency distribution of cell-cell interactions
CAgSFr	Total frequency distribution of complex extracellular aggregates attached to cell with a stalk-like tubules (prostheca)
SStrSFr	Total frequency distribution of Spherical Structures attached to cell with a stalk-like tubules (prostheca)
SStrFr	Total frequency distribution of Spherical Structures directly attached to cell
SStrPFr	Total frequency distribution of Spherical Structures with pili directly attached to cell
ExAgFr	Total frequency distribution of complex network of Extracellular Aggregates attached to cell
ExAgSFq	Total frequency distribution of complex network of Extracellular Aggregates attached to cell with stalk (prostheca)
PiliFq	Total frequency distribution of pili like structures attached to cell
PiliAFq	Total frequency distribution of pili like structures attached to all over surface of a cell
BlbFq	Total frequency distribution of membrane blebbing
EExMFq	Total frequency distribution of cells entrapped in a mesh of extracellular matrix
FlgFq	Total frequency distribution of flagella
VPsFqr	Total frequency distribution of presence of membrane vesicles like particles in the vicinity of a cell
CellDFq	Total frequency distribution of cell-division

Column headings for PROMAC_Metabarcoding_DNA and PROMAC_Transcriptomics_RNA

Column heading	Description
VolFilt	Amount of volume filtered through 0.2 µm Sterivex filter after prefiltration through 1.2µm filter (dm^3)
StarFilt	Start time of the filtration through 0.2 µm filter (hh:mm)
StopFilt	Stop time of the filtration through 0.2 µm filter (hh:mm)
TE buffer	Confirmation that Tris-EDTA buffer was added to the Sterivex filters
RNA later	Confimration that RNA later was added to the Sterivex filters
StrTemp	Storage temperature of the samples (°C)

Column headings for PROMAC_OMVs (Outer Membrane Vesicles)

Column heading	Description
PreFil	Whether collected seawater was prefiltered through 90 µm filter before proceeding for ultrafiltration
VolFilU	Total volume of water filtered by tangential-flow ultrafiltration (dm^3)
StarFilt	Start time of the filtration (UTC; hh:mm)
StopFilt	Stop time of the filtration (UTC; hh:mm)
NaOH	Whether 0.25 mol dm^{-3} NaoH was used for washing filters
VolConc	Volume of concentrated water collected after ultrafiltration (cm^3)
StrTemp	Storage temperature of the samples (°C)
XConc	Times OMV´s were concentrated from field value
PrtConc	Protein concentration (µg/cm^3) of extracted vesicle like particles based on BCA (Bicinchoninic Acid) method

Column headings for SAS_Prokaryotic-Culturing

Column heading	Description
Habitat	Habitat where the sample was collected
VolCryVi	Amount of water sample fixed for cryopreservation (cm^3)
GlycAdd	Amount of glycerol added to the sample for cryopreservation (cm^3)
StrTemp	Storage temperature of the samples (°C)

Quality codes

From Aquacosm QA & QC report D4.1: Deliverables | AQUACOSM

Flag Value	*Description*
V0	Valid value
V1	Valid value but comprised wholly or partially of below detection limit data
V2	Valid estimated value
V3	Valid interpolated value
V4	Valid value despite failing to meet some QC or statistical criteria
V5	In-valid value due to possible contamination (e.g., pollution source, laboratory contamination source.
V6	In-valid value due to non-standard sampling conditions (e.g., instrument malfunction, sample handling)
V7	Valid value but set equal to the detection limit (DL) because the measured value was below the DL
M1	Missing value because no value is available
M2	Missing value because invalidated by data originator
H1	Historical data that have not been assessed or validated