RV *INVESTIGATOR*

HYDROCHEMISTRY DATA PROCESSING REPORT

Voyage:	IN2026_V01
Chief Scientist	Dr. Linda Armbrecht
Voyage title:	Cook Ice Ecosystems and Sediments (COOKIES)
Report compiled by:	Narendra Pati and Pavie Nanthasurasak

Table of Contents

Executive Summary

Voyage Objectives

Recent modelling identifies the Cook Ice Shelf as exceptionally vulnerable to climate change, with a projected ice mass loss of approximately 14 Gt per year over the next two centuries. Despite the regional importance of this area, there remains a critical lack of oceanographic, bathymetric, biological, and paleo-data. Such information is vital for reconstructing the evolution and sensitivity of the Wilkes Subglacial Basin, particularly as the Cook and Ninnis Glaciers drain 60 percent of the ice held within this vast sector.

This study addresses these data gaps through three primary objectives: characterizing marine ecosystem composition within the Cook Glacier region during past warming periods over the last million years; assessing the relationships between benthic biodiversity and population genetic signatures with regional productivity and ice-sheet history; and determining the geological and palaeoceanographic conditions that have influenced the spatial distribution of marine life across the Cook region. From February 9th 2026 onwards, the main area of operation was moved to Dibble glacier region until the end of the voyage.

To achieve these goals, the voyage utilizes a suite of specialized instruments across the continental rise, slope, and shelf. Seafloor mapping is conducted using multibeam echo sounders and the sub-bottom profiler to characterize bathymetry and sediment thickness. These tools are essential for identifying optimal sampling sites, while a towed magnetometer is utilized during transits to provide broader geological context of the seafloor.

Water column properties are analysed using a CTD and Niskin rosette for physical data and genomics, which also features a downward-facing camera to capture seafloor imagery. A specialized trace metal rosette is used for micronutrient sampling, while ocean dynamics are monitored through ADCP and Argo float deployments. Additionally, the underway seawater intake line allows for the continuous collection of microbial, eDNA, and plankton data during transit.

Sediment records are retrieved through a range of coring methods, including multicores for the sediment-water interface, Kasten cores for stratigraphy, and piston cores to capture long-term glacial history. Benthic biodiversity is characterized using a deep-towed camera system with an integrated eDNA sampler, complemented by an epibenthic sled for the collection of physical specimens.

General Hydrochemistry Information

For this voyage, CTD samples were collected and analysed for nutrients, dissolved oxygen, and salinity while underway (UWY), Trace metal rosette (TMR), porewaters (Core, from Multicore and Kasten core) and incubation (INC) samples were collected and analysed for nutrients by the on-board Hydrochemistry team. Please refer to Hydrochemistry output section for more detail on sample types and analyses. Additionally, Thermosalinograph (TSG) samples were continuously

collected throughout the voyage, with on-board measurements of their salinity used to calibrate the ship's underway system.

Please cite the following manuscript when reporting or publishing data for silicate, phosphate, nitrate+nitrite (NO_x) and nitrite:

Rees, C., L. Pender, K. Sherrin, C. Schwanger, P. Hughes, S. Tibben, A. Marouchos, and M. Rayner. (2018) "*Methods for reproducible shipboard SFA nutrient measurement using RMNS and automated data processing*."

Limnol. Oceanogr: Methods, 17(1): pp. 25-41.

doi:10.1002/lom3.10294

If publishing ammonium data, please cite the following:

Rees, C., Janssens, J., Sherrin, K., Hughes, P., Tibben, S., McMahon, M., McDonald, J., Camac, A., Schwanger, C. and Marouchos, A., (2021*) "Method for Reproducible Shipboard Segmented Flow Analysis Ammonium Measurement Using an In-House Reference Material for Quality Control."*

Frontiers in Marine Science, 8.

doi:10.3389/fmars.2021.581901

The final hydrology dataset, data processing report, analytical methods, related log sheets and processing notes can be obtained from the CSIRO data centre. Please visit CSIRO data trawler, should there be any inquiries on hydrology data please contact CSIRO data centre at NCMI_DataLibrarians@csiro.au.

Itinerary and Voyage track

Table 1: Voyage itinerary

	Depart	Arrive
Port	Hobart	Hobart
Date	02/01/2026	25/02/2026
Time	1500	0800

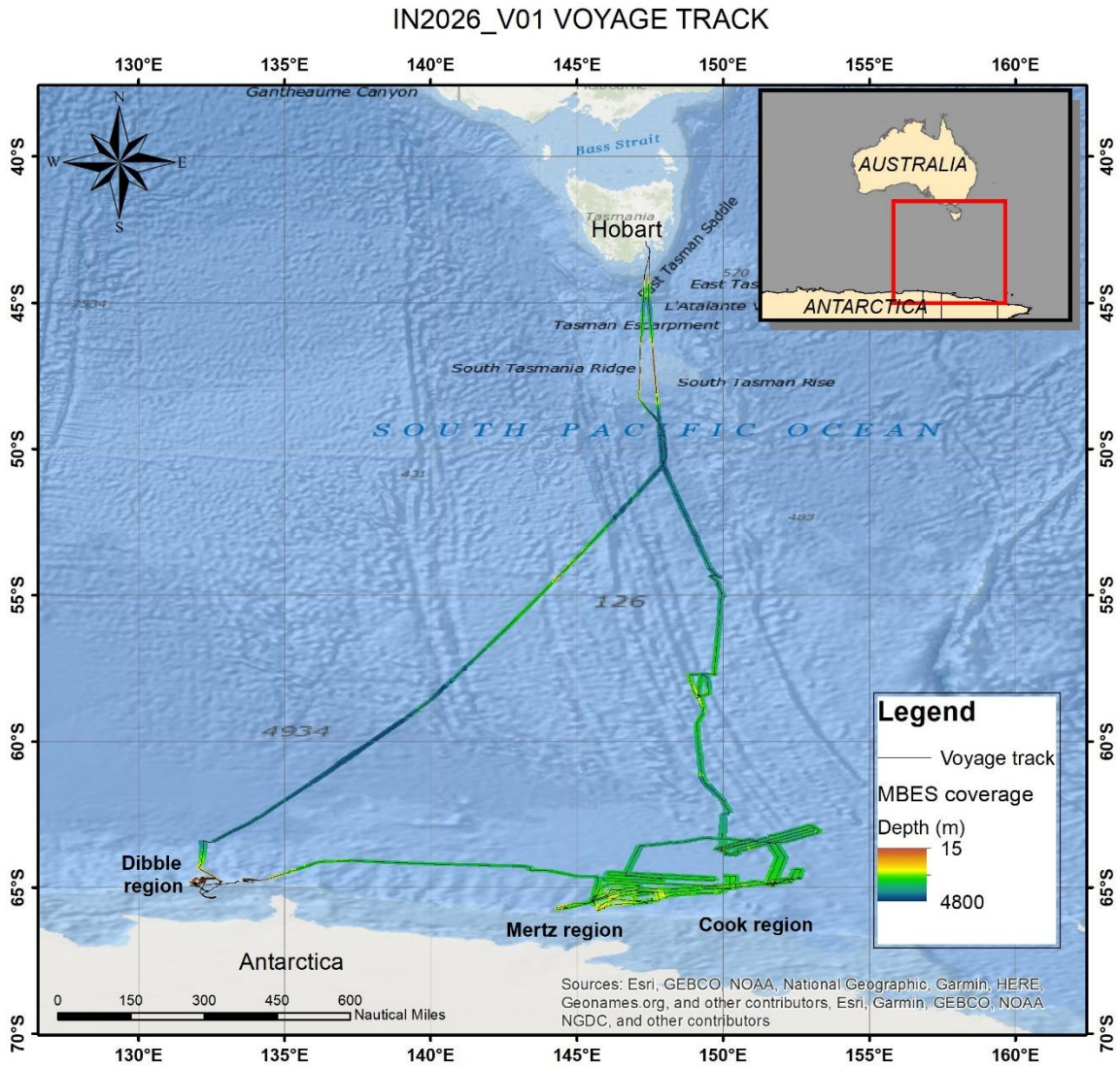

Figure 1. Voyage map of IN2026_V01.

Key personnel list

Table 2: Key Personnel list on IN2026_V01

Name	Role	Organisation
Linda Armbrecht	Chief Scientist	UTAS
Claire Grubb	Voyage Manager	CSIRO
Narendra Pati	Hydrochemist	CSIRO
Pavie Nanthasurasak	Hydrochemist	CSIRO

Sample Summary

Sample Type and Number Assayed

Table 3: Hydrochemistry sample type and analysis summary for IN2026_V01

Analysis	Instrument	Sample source/type	Number of samples
Nutrients	Seal AA500	Conductivity-Temperature-Depth (CTD) Underway (UWY) Trace metal rosette (TMR) Porewater (Core) Incubation (Inc)	336 42 126 480 13
Salinity	Guidline Autosal	Conductivity-Temperature-Depth (CTD) Thermosalinograph (TSG)	336 51
Dissolved oxygen (DO)	Scripps automated titration	Conductivity-Temperature-Depth (CTD)	336

CTD sample (Conductivity, Temperature, Depth)

Table 4: CTD summary for IN2026_V01

Rosette type	36
Niskin Bottle size	12 L
Number of deployments	37
Number of deployments sampled for hydrochemistry analyses	30
CTD sampling order	Dissolved Oxygen (DO) → Nutrients → Salinity
Sample bottle	DO: 140 mL glass iodine determination flasks with glass stopper Nutrient: 50 mL HDPE with screw cap lids Salinity: 200 mL volume OSIL bottles made of type II glass (clear) with disposable plastic insert and plastic screw cap
Sample log	CTD deployment paper log sheet and CAP Deployment Log Editor version 1.4.5
Sample preparation	No additional preparation, analysed as neat
Sampling personnel (hydrochemistry)	Narendra Pati and Pavie Nanthasurasak
Sampling personnel (science party)	Jan Jansen, Amaranta Focardi, Gina Paroz, Amy Wells, Amy Leventer, Talia Hawkes, Sally Lau, Katherine Prata, Timothy Nugroho, Izzy White, Ana Gomes, Rebecca Knight, Lucinda Duxbury, Jan Strugnell, Dr. Gary Mitchell, Luca Zurli, Luca Magri and Sarah Jessop

Underway sample (UWY)

Table 5: UWY summary for IN2026_V01

UWY source	Instrument clean seawater line supplying the pCO2 instrument in the underway laboratory
Sample bottle	Nutrient: 10 mL PP tube with screw cap lids
Sample log	UWY log sheet and UWY Samples Event Logs (available on CSIRO data trawler)
Sample preparation	No additional preparation, analysed as neat
Sampling personnel (hydrochemistry)	N/A
Sampling personnel (science party)	Amaranta Focardi, Gina Paroz, Amy Leventer, Fiorenza Torricella

Thermosalinograph sample (TSG)

Table 6: TSG summary for IN2026_V01

TSG source	Instrument clean seawater line supplying the pCO2 instrument in the underway laboratory
Sample bottle	200 mL volume type I (clear) borosilicate bottle with rubber liner lid and aluminium crimp cap
Sample log	TSG Samples Event Logs (available on CSIRO data trawler)
Sample preparation	No additional preparation, analysed as neat
Sampling personnel (hydrochemistry)	Narendra Pati and Pavie Nanthasurasak
Sampling personnel (science party)	N/A

Trace Metal Rosette (TMR)

Table 7: TMR summary for IN2026_V01

Rosette type	12
Niskin Bottle size	12 L
Number of deployments	12
Number of deployments sampled for hydrochemistry analyses	12
Sample bottle	Nutrient: 50 mL HDPE with screw cap lids
Sample log	TMR deployment log sheet
Sample preparation	No additional preparation, analysed as neat
Sampling personnel (hydrochemistry)	N/A
Sampling personnel (science party)	Amy Wells, Talia Hawkes, Noah Menner

Porewaters (Core)

Table 8: Core summary for IN2026_V01

Core source	Sediment core (Multi-core and Kasten core)
Sample bottle	Nutrient: 10 mL PP tube with screw cap lids
Sample log	Core log sheet
Sample preparation	Multicore: Centrifuged at 4200 rpm for 30 minutes, filtered through 0.45 µm Polyethersulfone (PES) filter, and diluted with LNSW 10 times. Kasten core: Filtered through Core Solution Sampler (CSS, Rhizon, 5 cm porous membrane, 0.15 µm pore size) and diluted with LNSW 10 times. Samples from both cores measured too high for certain nutrients were diluted further with LNSW by Hydrochemistry team. Please refer to Core log sheet for dilution factors.
Sampling personnel (hydrochemistry)	N/A
Sampling personnel (science party)	Amy Wells, Talia Hawkes, Noah Menner

Incubation (Inc)

Table 9: Inc summary for IN2026_V01

Inc source	Incubation tank
Sample bottle	Nutrient: 10 mL PP tube with screw cap lids
Sample log	Incubation log sheet
Sample preparation	Filtered with 0.45 µm HDPE filter
Sampling personnel (hydrochemistry)	N/A
Sampling personnel (science party)	Amaranta Focardi

Data Processing Overview

The sample meta-data, measured bottle salinity results, dissolved oxygen assay results and the nutrient assay raw data are processed using the CSIRO-developed program HyPro. This processing generates the final hydrology dataset. An overview of this process is illustrated below (fig.2).

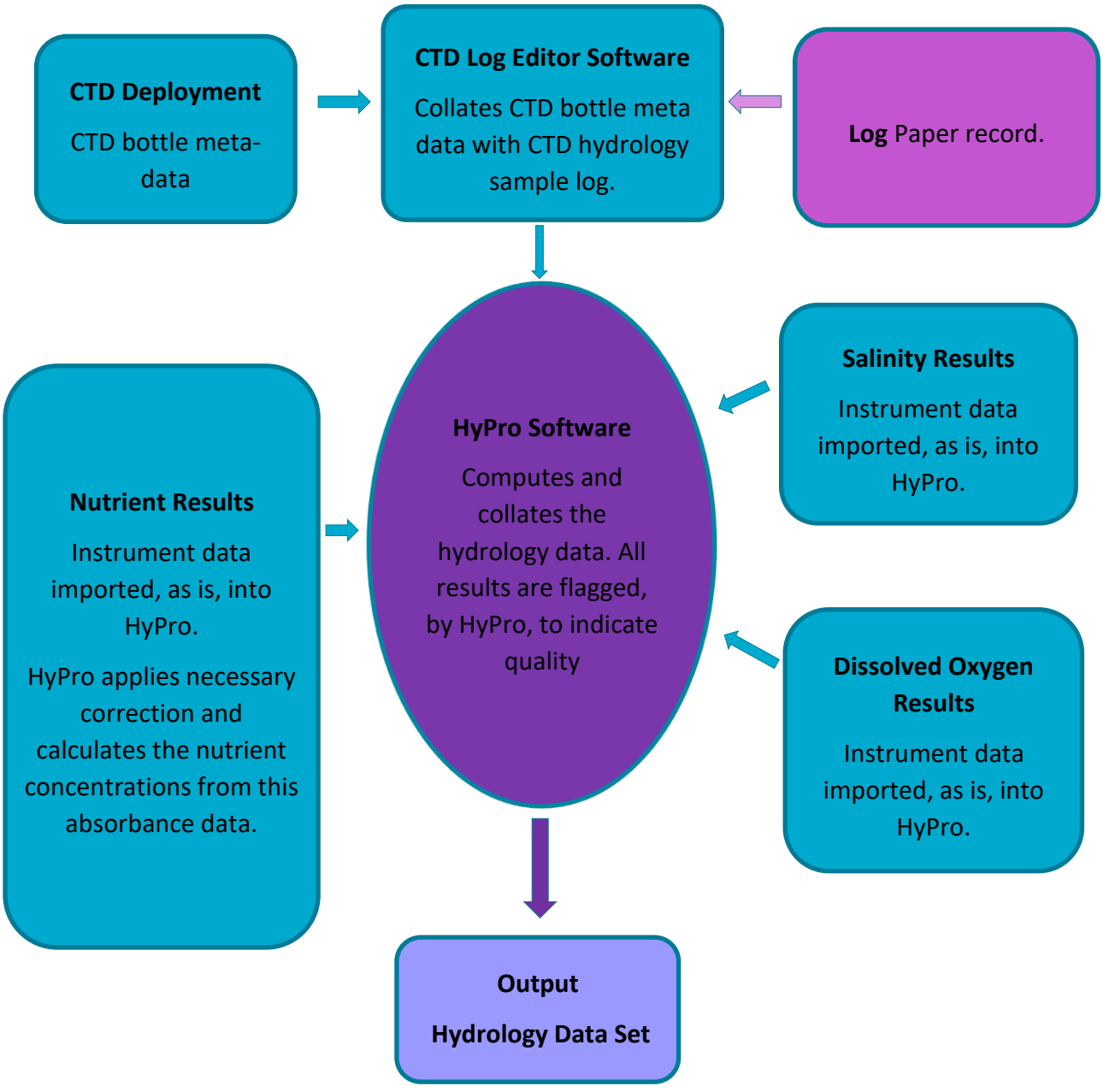

Figure 2. Conventional Hydrology Data Processing Flow Diagram.

Salinity

Salinity Measurement Parameters

Table 10. Salinity Measurement Parameters

Details	
HyPro Version	5.9
Instruments	Guildline Autosal Laboratory Salinometer 8400(B) – SN 72873. Bath temperature 24.0°C
Software	Ocean Scientific International Ltd (OSIL) Data Logger ver 1.2
Hydrochemistry Methods	Sampling: Salinity - WI_Sal_001, TSG – WI_Sal_004 Analysis: SOP 006
Accuracy	± 0.001 practical salinity units (PSU)
Reference Material	OSIL IAPSO – Batch P167, use by 21st February 2026, K_{15} = 0.99988 and Batch P168, use by 1st December 2026, K_{15} = 0.99993.
Sample Container	CTD: 200 mL volume OSIL bottles made of type II glass (clear) with disposable plastic insert and plastic screw cap. TSG: 200 mL volume type I (clear) borosilicate bottle with rubber liner lid and aluminium crimp cap.
Sample Storage	Stored in salinometer lab for minimum of 8 hrs for temperature equilibration before measurement
Analyst	Narendra Pati and Pavie Nanthasurasak

Salinity Method

Salinity samples were measured on a Guildline Autosal 8400B, operated in accordance with the manufacturer's technical manual. The measured value is recorded with an OSIL data logger.

Practical salinity (S) is defined as the ratio (K_{15}) of the electrical conductivity of seawater measured at 15°C, 1 atm to that of a potassium chloride (KCl) solution of mass fraction 32.4356 x 10^{-3}.

Before each lot of sample measurements, the Autosal is calibrated with standard seawater (OSIL, IAPSO) with a known K_{15} ratio. A fresh bottle of OSIL standard is used for each calibration, and calibration is performed at least once per run.

Method summary: The salinity sample is collected in a 200 mL glass bottle. The bottle is rinsed three times with sample, then filled from the bottom, via a polytetrafluoroethylene (PTFE) straw, until overflowing. The bottle is removed from the straw, and the sample is decanted to allow a headspace of approximately 25 cm^3. A dry plastic insert is fitted, the bottle inverted and rinsed with ultra-pure water, wiped dry, capped and stored upside down until analysis. To measure, the salinometer cell is flushed three times with the sample and then measured after the third and fourth flush. The OSIL data logger software captures the conductivity ratio and calculates the practical salinity.

The output from the data logger is imported into HyPro and linked with the CTD deployment meta-data.

CTD Salinity vs Bottle Salinity

For this voyage, the difference between the unprocessed (uncorrected) CTD value and the measured bottle value is generally less than 0.03 PSU. The larger differences are often observed in shallow samples, where sudden changes in the thermohaline profile occurs. Occasionally, these discrepancies may also be attributed to mismatches between the CTD downcast and upcast profiles. CTD sensor data were recorded on the downcast, while bottle samples were collected on the upcast.

The unprocessed CTD values are adjusted (corrected) by DAP using the salinity bottle results. The corrected values are not reported in the hydrology set. Please refer to IN2026_V01 CTD data on CSIRO marlin metadata system for corrected sensor data.

OSIL Salinity Standard

For each salinity analysis conducted on this voyage, the instrument was calibrated with OSIL standard seawater, lot P167 (PSU = 34.995) and P168 (PSU = 34.997). Please note that OSIL batch P168 standard was used for the last analysis run in which the analysis date was after the expiry date of Batch P167 standard.

The mean measured value for the P167 OSIL standard seawater across the voyage was:

Mean = 34.9951 PSU SD = 0.00013 n = 18

The mean measured value for the P168 OSIL standard seawater across the voyage was:

Mean = 34.9971 PSU SD = 0.00000 n = 1

Dissolved Oxygen

Dissolved Oxygen Measurement Parameters

Table 11. Dissolved oxygen measurement parameters.

Details	
HyPro Version	5.9
Instrument	Scripps Automated Photometric Oxygen System
Software	Scripps Institution of Oceanography (SIO)
Hydrochemistry Methods	Sampling: WI_DO_001 Analysis: SOP 005
Titrant	60 g/L Sodium Thiosulphate
Primary standard	0.0125244 N Potassium Iodate
Accuracy	± 0.5 µmol L^{-1}
Sample Container type	140 mL glass iodine determination flasks with glass stopper
Sample Storage	Samples stored in the hydrochemistry lab until analysis within 72 hrs.
Analyst	Narendra Pati and Pavie Nanthasurasak

Dissolved Oxygen Method

Scripps Institution of Oceanography (SIO) method is used for dissolved oxygen analysis. The method is based on the whole bottle modified Winkler titration of Carpenter (1965) with modifications by Culberson *et al* (1991).

Method summary: The sample is collected in an iodine determination flask of known volume. To the sample, 1 mL of manganese (II) chloride solution is added, followed by 1 mL of alkaline iodide solution. The flask is then stoppered and inverted at least 30 times. Dissolved oxygen in the sample oxidizes an equivalent amount of Mn (II) to Mn (IV) which forms a precipitate. Just before titration, the sample is acidified, reducing Mn (IV) back to the divalent state and liberating an equivalent amount of iodine. The iodine is titrated with a standardised thiosulphate solution using a Metrohm Dosimat fitted with a 1 mL burette. The titration endpoint is determined by measuring the decrease in the UV absorption at 365 nm.

The thiosulphate solution is standardised by with a 10 mL aliquot of potassium iodate primary standard. A blank correction is also determined from the difference between two titres of consecutive additions of 1 mL aliquots of potassium iodate to the same blank sample. The standardisation is conducted at least once every 24 hours, when samples are being assayed.

The output from the SIO instrument software is imported into HyPro and collated with the CTD deployment meta-data.

CTD Dissolved Oxygen vs Bottle Dissolved Oxygen

For this voyage, the difference between the unprocessed (uncorrected) CTD value and the measured bottle value is generally less than 17 µmol L^{-1}. The larger differences are often observed in shallow samples, where sudden changes in the thermohaline profile occurs. Occasionally, these discrepancies may also be attributed to mismatches between the CTD downcast and upcast profiles. CTD sensor data were recorded on the downcast, while bottle samples were collected on the upcast.

The unprocessed CTD values are adjusted (corrected) by DAP using the dissolved oxygen bottle results. The corrected values are not reported in the hydrology set. Please refer to IN2026_V01 CTD data on CSIRO marlin metadata system for corrected sensor data.

Dissolved Oxygen Instrument titrant: thiosulphate normality and blank correction

The variation in thiosulphate concentration remains within the QC parameter of less than 0.0005 N between standardisations. The blank correction, which accounts for oxidisable species in the reagents and in the Milli-Q water that is added to the KIO_3 aliquot before the titration, is used in the calculation of the thiosulphate normality.

The mean normality of thiosulphate for this voyage was:

Mean: 0.245425 N SD: 0.00020 n = 18

The mean blank concentration was:

Mean: 0.0005 mL SD: 0.00013 n = 18

Nutrients

Nutrient Measurement Parameters

Table 12. Nutrient measurement parameters analysed with Seal AA500 segmented flow analyser. All instrument parameters, reagent batches, and instrument events are logged for each analysis run. This information is available on request.

Details					
Instrument	Seal AA500 segmented flow analyser				
HyPro version	5.9				
Operating Software	AACE 8.06 Alpha 32				
Hydrochemistry Sampling Method	WI_Nut_001				
Hydrochemistry analysis method	SOP001	SOP002	SOP003	SOP003	SOP004
Nutrients analysed	Silicate ($SiO4^{4-}$)	Phosphate (PO_4^{3-})	Nitrate + Nitrite (NO_x)	Nitrite (NO_2^-)	Ammonium (NH_4^+)
Top concentration (µmol L^{-1})	140.0	3.0	42.0	1.4	2.0
Method detection limit (MDL) (µmol L^{-1})	0.2	0.02	0.02	0.02	0.02
Stock standards	Phosphate and Nitrite made on 24th of November 2025. Silicate, Nitrate, and Ammonium made on 1st of December 2025. Prepared for open ocean concentration in 1L HDPE bottle.				
Intermediate standards	Prepared every 72 hours in 30 mL polypropylene tubes. Reused after acid wash with 10% hydrochloric acid solution.				
Working standards	Prepared every 48-72 hours in 30 mL polypropylene tubes. Reused after acid wash with 10% hydrochloric acid solution.				
Reference Material	KANSO RMNS lot CP and CR (occasionally to verify ammonium measurement)				

Sample Container	CTD and TMR: 50 mL HDPE with screw cap lids. Reused after acid wash with 10% hydrochloric acid solution. UWY, Core and Inc: 10 mL PP tube with screw cap lids. One-time use.
Sample Storage	< 4 hours at room temperature after collection or < 12 hours at 4°C after collection, samples returned to room temperature prior to analysis.
Sample preparation	CTD, TMR, and UWY: No filtration. Core: Samples from Multicore – centrifuged at 4200 rpm for 30 minutes, filtered through 0.45 µm Polyethersulfone (PES) filter, and diluted with LNSW 10 times. Samples from Kasten core – filtered through Core Solution Sampler (CSS, Rhizon, 5 cm porous membrane, 0.15 µm pore size) and diluted with LNSW 10 times. Inc: Filtered with 0.45 µm HDPE filter
Analysts	Narendra Pati and Pavie Nanthasurasak

Nutrient Methods

Nutrient samples are analysed using a Seal AA500 segmented flow auto-analyser, equipped with 1 cm flow-cells for colorimetric measurements. Seal fluorescence detector was used for ammonium measurement.

Silicate (SOP001): colourimetric, molybdenum blue method. Based on Armstrong et al. (1967). Silicate in seawater is reacted with acidified ammonium molybdate to produce silicomolybdic acid. Tartaric acid is added to remove the phosphate molybdic acid interference. Tin (II) chloride is then added to reduce the silicomolybdic acid to silicomolybdous acid and its absorbance is measured at 820 nm.

Phosphate (SOP002): colourimetric, molybdenum blue method. Based on Murphy and Riley (1962) with modifications from the NIOZ-SGNOS[1] Practical Workshop 2012 optimizing the antimony catalyst/phosphate ratio and the reduction of silicate interferences by pH. Phosphate in seawater forms a phosphomolybdenum complex with acidified ammonium molybdate. It is then reduced by ascorbic acid and its absorbance is measured at 880 nm.

Nitrate (SOP003): colourimetric, Cu-Cd reduction – naphthylenediamine method. Based on Wood et.al (1967). Nitrate is reduced to nitrite by first adding an ammonium chloride buffer then sending it through a copper - cadmium column. Sulphanilamide is added under acidic conditions to form a diazo compound. This compound is coupled with 1-N-naphthly-ethylenediamine di-hydrochloride to produce a magenta azo complex, and its absorbance is measured at 540 nm.

Nitrite (SOP003): colourimetric, naphthylenediamine method. As per nitrate method without the copper cadmium reduction column and buffer. Absorbance measured at 540 nm.

Ammonium (SOP004): fluorescence, ortho-phtaldiadehyde method. Based on Kérouel and Aminot (1997). Ammonium reacted with ortho-phtaldialdehyde and sulphite at a pH of 9.0-9.5 to produce an intensely fluorescent product. Its emission is measured at 460 nm after excitation at 370 nm.

SOP methods can be obtained from the CSIRO Oceans and Atmosphere Hydrochemistry Group.

[1] Royal Netherlands Institute for Sea Research – Study Group on Nutrient Standards.

HyPro Processing Summary for Nutrients

After a run, the raw absorbance and fluorescence data is exported from the instrument and processed by HyPro. For each analyte, HyPro re-constructs the peak traces and defines peak window, which corresponds to the plateau region used to determine the peak heights. HyPro then constructs the calibration curve and applies corrections for carry-over, baseline, and sensitive drifts, refractive index then the nutrient concentrations for each sample are calculated. The corrections are quantified using dedicated solutions included in every run.

HyPro applies specific criteria to identify suspect calibration points, noisy peaks, method detection limits above the nominal threshold, and duplicate sample results that do not match.

Suspect calibration points are given less weight when fitting the calibration curve. The cut-off limits for acceptable calibration data are as followed:

- ±0.5% of the concentration of the top standard for silicate and nitrate+nitrite (as per WOCE[1]).
- 0.02 µmol L^{-1} for phosphate, nitrite, and ammonium.

HyPro classifies data quality as good, suspect, or bad and flags the results accordingly. The Flag key can be found in Appendix, Data Quality Flag Key. Missing or suspect nutrient data is listed in Appendix, Missing or Suspect Nutrient Data.

[1] World Ocean Circulation Experiment

Table 13. HyPro 5.9 Processing Parameters. All instrument parameters and reagent batches and operation events are logged for each analysis run. This information is available on request.

Result Details	Silicate	Phosphate	Nitrate + Nitrite	Nitrite	Ammonium
Data Reported as	µmol L^{-1}	µmol L^{-1}	µmol L^{-1}	µmol L^{-1}	µmol L^{-1}
Calibration Curve fit	Linear	Linear	Quadratic	Quadratic	Linear
# of points in Calibration	7	7	7	7	7
Forced through zero	N	N	N	N	N
Matrix correction	N	N	N	N	N
Blank correction	N	N	N	N	N
Refractive Index Blank (RIB) correction	Y	Y	Y	Y	Y
Peak window defined by	HyPro	HyPro	HyPro	HyPro	HyPro
Carryover correction	Y	Y	Y	Y	Y
Baseline drift correction	Y	Y	Y	Y	Y
Sensitivity drift correction	Y	Y	Y	Y	Y
Data Adjusted for RMNS variance	N	N	N	N	N
Medium of Standards	Low nutrient seawater (LNSW) collected in June 2024. Sub-lot passed through a 5-micron filter (filtered in September 2025) and stored in 20 L carboys in the hydrochemistry laboratory at 20°C.				
Medium of Baseline	18.2 MΩ water. Dispensed from the Milli-Q IQ 7010 system.				
Duplicate samples	CTD: Niskin fired at the greatest depth for each CTD deployment were analysed in duplicate. Single samples were analysed for remaining depths.				
Note	The reported data is not corrected to the RMNS. Per deployment RMNS data is provided in supporting document.				

Refractive Index Blank (RIB) measurement and correction

The refractive index blank (RIB) is an optical interference caused by the difference in refraction between seawater and Milli-Q water. This effect alters light transmission and scattering within the flow cell, resulting in baseline shifts and potential underestimation or overestimation in absorbance measurements during colorimetric analysis (Kirkwood, D.S., 1996). Please note that refractive index blank is not applicable for fluorescence detection.

To quantify RIB, the non-coloured reagent method was employed. In this approach, Milli-Q water and LNSW were analysed using the complete reagent set described in the Nutrients Method section above, except for the colour-generating chemicals. Specifically, 1-N-naphthyl-ethylenediamine dihydrochloride was omitted for NOx and NO2, while ammonium molybdate was excluded for silicate and phosphate. No RIB effect was observed for ammonium channel.

At the end of an analysis run, the full suite of reagents was switched to the non-coloured reagent setup, and the percentage difference between Milli-Q water and LNSW was recorded for each channel using AACE software. This percentage was then converted into concentration values using a proportional ratio calculation, where the highest calibrant nominal concentration and its corresponding peak height percentage were used as reference points.

The average RIB values from multiple nutrient analysis runs overtime are presented in Table 14. RIB value was entered into HyPro where nutrient data was corrected.

Table 14. Average refractive index blank (RIB) offset value for each channel used for correction on this voyage (Units: µmol L^{-1}, n = 4).

Silicate	Phosphate	Nitrite	Nitrate + Nitrite
0.06405 ± 0.1109	0.02643 ± 0.0054	0.01146 ± 0.0027	0.02316 ± 0.0234

Accuracy - Reference Material for Nutrient in Seawater (RMNS)

Descriptive statistics are used to ascertain the accuracy and precision of the analysis from the repetitive measurement of the RMNS for silicate, phosphate, NOx, nitrite and ammonium in seawater.

For this voyage, Japanese KANSO certified RMNS lot CP was assayed in triplicates in each run to monitor accuracy (Table 15). RMNS CM were only analysed in the characterisation (run nut001) run as additional accuracy monitoring at the start of the voyage without samples. RMNS CR was assayed occasionally throughout the voyage as accuracy monitoring for ammonium measurement. An internal bulk quality control (BQC) was also analysed in each analysis run.

The GO-SHIP criteria (Hyde *et al.*, 2010), Appendix, GO-SHIP Specifications, specifies using 1-3% of full scale (depending on the nutrient) as acceptable limits of accuracy.

KANSO publishes the RMNS nutrient values in µmol kg^{-1}. These are converted to µmol L^{-1} at 21°C. NO_x is derived by summing the NO_3 and NO_2 values.

Table 15. RMNS certified concentrations ± expanded uncertainty (U) at 21°C. Units: µmol L^{-1}

RMNS	Silicate	Phosphate	Nitrite	Nitrate + Nitrite	Ammonium
Lot CR	14.3389 ± 0.3073	0.4035 ± 0.0143	0.9935 ± 0.0717	6.5856 ± 0.2356	0.9730 ± 0.1536
Lot CP	62.5687 ± 0.3072	1.7951 ± 0.0184	0.3175 ± 0.0717	25.7136 ± 0.3789	NA
Lot CM	102.9169 ± 0.5120	2.4372 ± 0.0307	0.0184 ± 0.0061	34.0169 ± 0.3134	NA

Table 16. RMNS CP statistics for of this voyage. Units: µmol L^{-1}

RMNS CP	Silicate	Phosphate	Nitrite	Nitrate + Nitrite	Ammonium
Mean	63.2	1.81	0.316	25.8	NA
Standard deviation	0.3	0.01	0.005	0.2	NA

Table 17. RMNS CR statistics for of this voyage. Units: µmol L^{-1}

RMNS CR	Silicate	Phosphate	Nitrite	Nitrate + Nitrite	Ammonium
Mean	14.5	0.407	1.00	6.51	0.986
Standard deviation	0.1	0.002	0.01	0.03	0.015

RMNS plots

The measured RMNS values for each nutrient analysis run on this voyage is shown in plots below. The green, pink, and red contour lines represent 1%, 2% and 3% or 1*MDL, 2*MDL and 3*MDL (MDL = 0.02 µmol L^{-1}) deviation from the RMNS certified mean value. The blue line is the manufacturer's expanded uncertainty of the certified value. The measured RMNS values per CTD deployments are provided in supporting document available on CSIRO data trawler.

For this voyage, results for RMNS lot CP and CR show high agreement with certified values, with calculated results falling within the expanded uncertainty. The plot of RMNS lot CP and CR analysed in each channel are shown in figure 3 to figure 7.

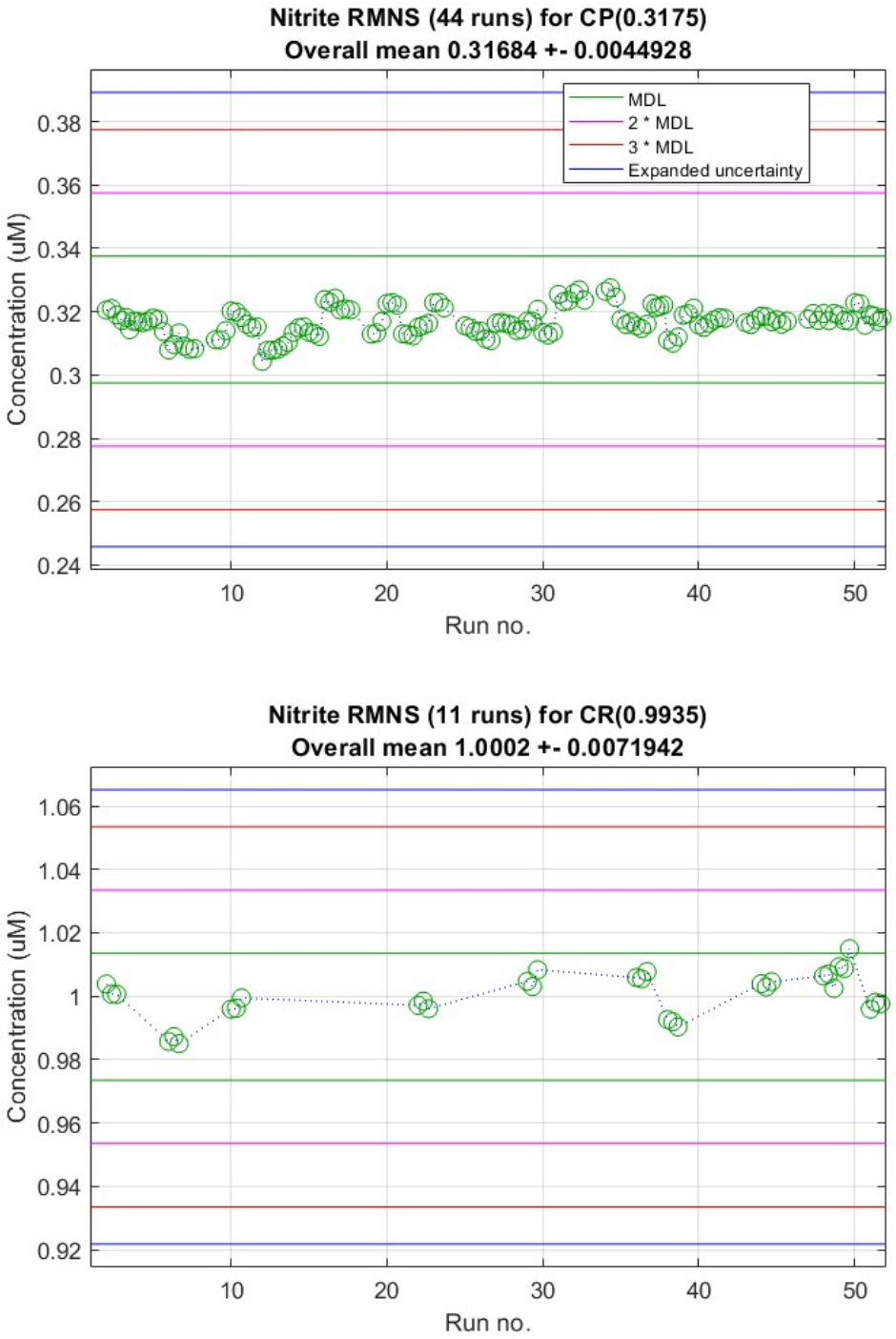

Figure 3. Nitrite RMNS lot CP and CR plot. Units: µmol L^{-1}.

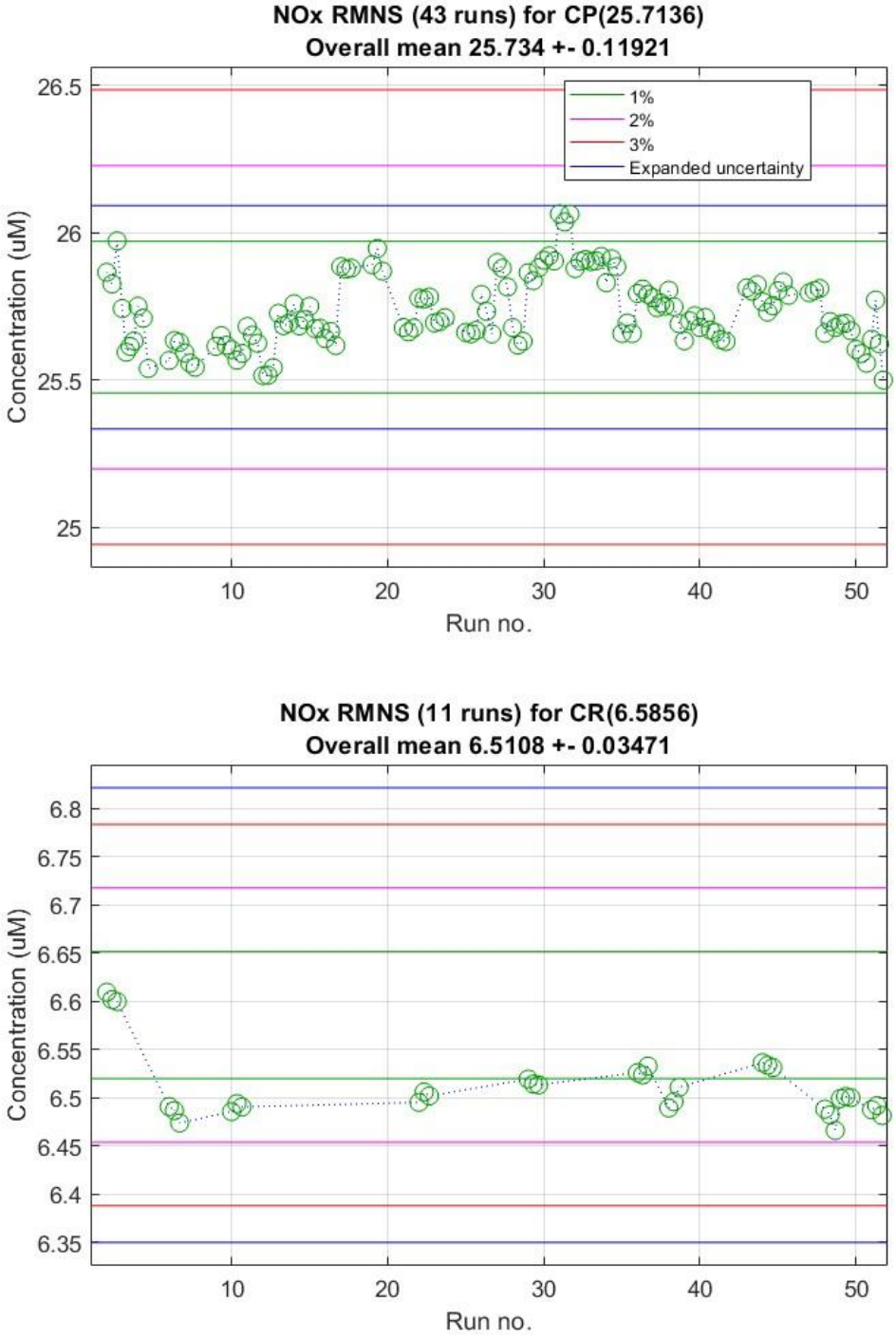

Figure 4. Nitrate + Nitrite (NOx) RMNS lot CP and CR plot. Units: µmol L^{-1}.

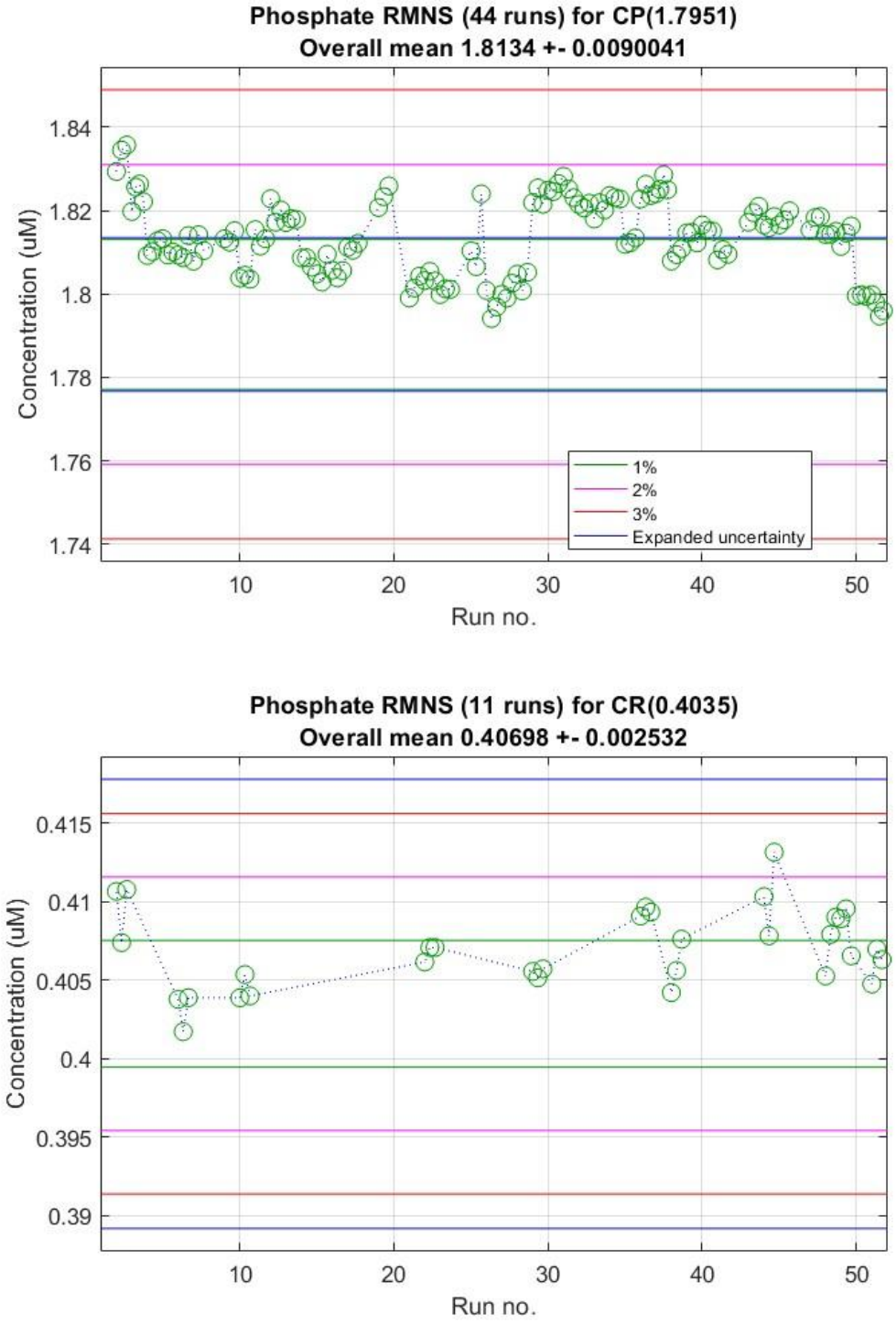

Figure 5. Phosphate RMNS lot CP and CR plot. Units: Units: µmol L^{-1}.

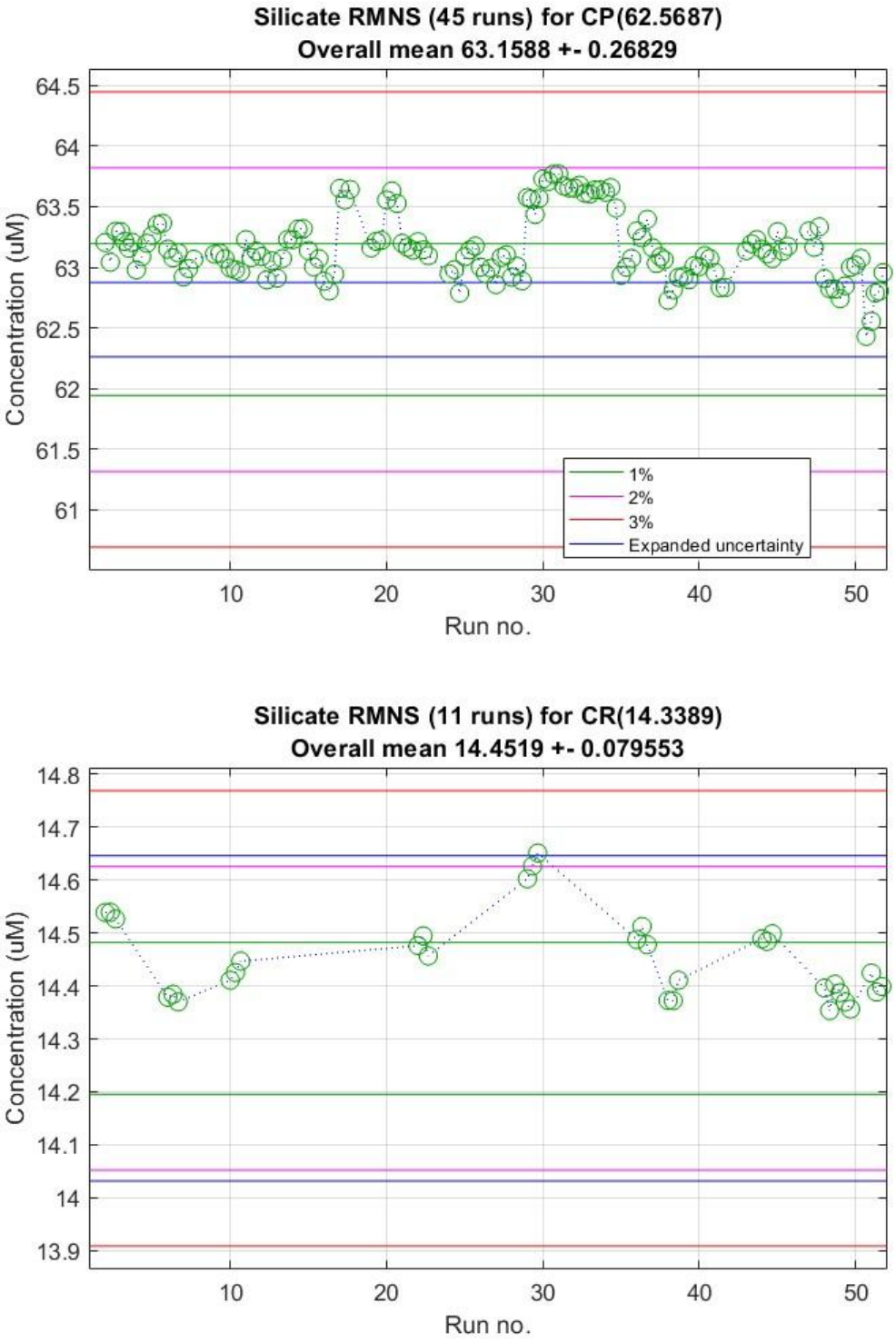

Figure 6. Silicate RMNS lot CP and CR plot. Units: Units: µmol L^{-1}.

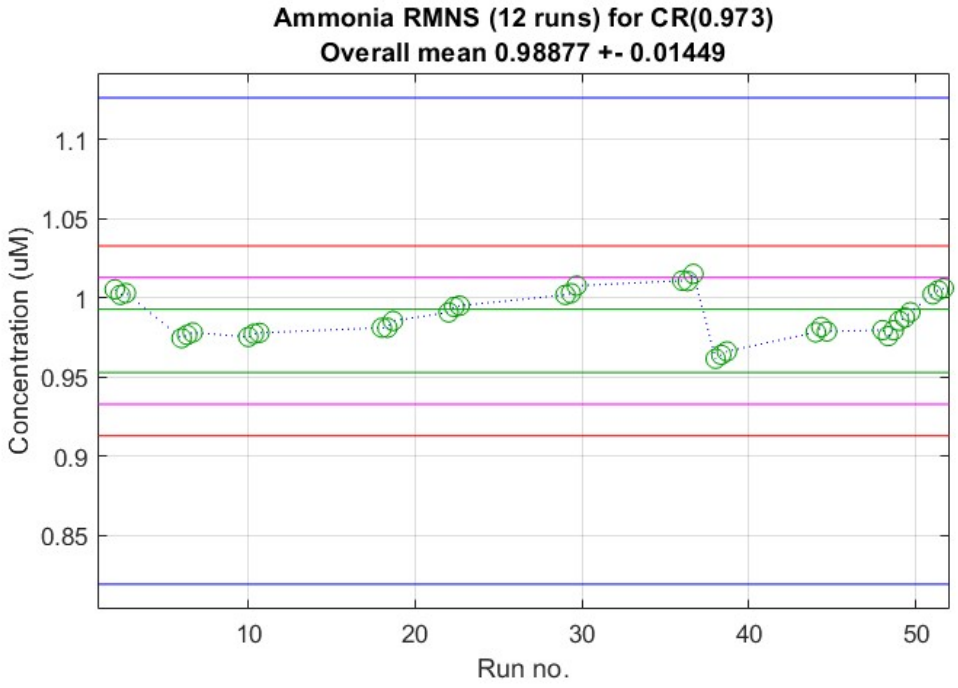

Figure 7. Ammonium RMNS lot CR plot. Units: Units: µmol L^{-1}.

Measurement Uncertainty

The CSIRO hydrochemistry method measurement uncertainty (MU) has been calculated for each nutrient based on the variation in the calibration curve, calibration standards, pipette and glassware calibration, and precision of the RMNS over time (Armishaw 2003).

Table 18. CSIRO Hydrochemistry nutrient analysis uncertainty values. Units: µmol L^{-1}

Calculated Measurement Uncertainty at 1 µmol L^{-1}				
Silicate	**Phosphate**	**Nitrite**	**Nitrate + Nitrite**	**Ammonium**
±0.017	±0.024	±0.140	±0.019	±0.30

The reported uncertainty is an expanded uncertainty using a coverage factor of 2 giving a 95% level of confidence.

Method Detection Limit for Nutrients

The method detection limit (MDL) is defined as three times the standard deviation (SD) of the LNSW results (National Association of Testing Authorities 2013). The MDL is used to assess the precision of the analysis at low nutrient concentrations.

Table 19. AA500 auto analyser MDL statistics for this voyage. The mean and standard deviation are calculated from every analytical run performed over the voyage. Units: µmol L^{-1}.

MDL	Silicate	Phosphate	Nitrite	Nitrate + Nitrite	Ammonium
Nominal MDL	**0.2**	**0.02**	**0.02**	**0.02**	**0.02**
Mean	0.03	0.005	0.003	0.011	0.003
Standard deviation	0.02	0.003	0.002	0.007	0.002

Sampling Precision

Sampling precision is typically determined using the CTD test deployment (CTD 1) where multiple bottles are fired the same depth, each of which is then sampled as replicates for hydrochemistry nutrient analysis. The mean and standard deviation of nutrients analysed on test deployment is shown in table 20.

Duplicate nutrient samples are also collected from the greatest depth of subsequent CTD deployments. For nutrients analysis, the sampling precision is considered good if the difference from the mean of duplicate measurements is less than the nominal method detection limit (Table 19). The exception is for NO_x (nitrate+nitrite), which uses the limit of 0.06 µmol L^{-1}. Duplicate samples that exceed the limit are flagged. These are tabulated in Appendix, Data Quality Flag Key.

Table 20. Test cast deployment at 1000 dbar. Bottle rosette position (RP) 1-36. Units: µmol L^{-1}. * = value below detection limit.
Please note that negative value observed with Nitrite is suspected to be potentially due to reference matrix (low nutrients seawater) used on the autoanalyser containing consistent background concentration that is higher than the samples. On this voyage, Nitrite concentration in open ocean samples is generally approaching zero below 500 dbar.

Replicates	Silicate	Phosphate	Nitrite	Nitrate + Nitrite	Ammonium
Mean	23.2	1.97	-0.008*	28.7	0.000*
Standard deviation	0.043	0.004	0.002	0.154	0.002

Temperature

Hydrochemistry lab and nutrient analyser

Ambient conditions in the hydrochemistry laboratory and on the segmented flow analyser were monitored at the following locations:

- Hydrochemistry lab temperature: positioned in close proximity to the autoanalyser
- Nutrient sample pump temperature: positioned on the pump tubes where nutrient samples and reagents are introduced into the analyser

Temperature data was measured using Ruuvi temperature logger and monitored in Grafana. A time series plot of hydrochemistry laboratory temperature plot throughout the voyage is shown below. A complete log of temperature is available upon request through CSIRO data centre. The average analyser pump temperature of the analyser during each nutrients analysis is provided in supporting documents available on CSIRO data trawler.

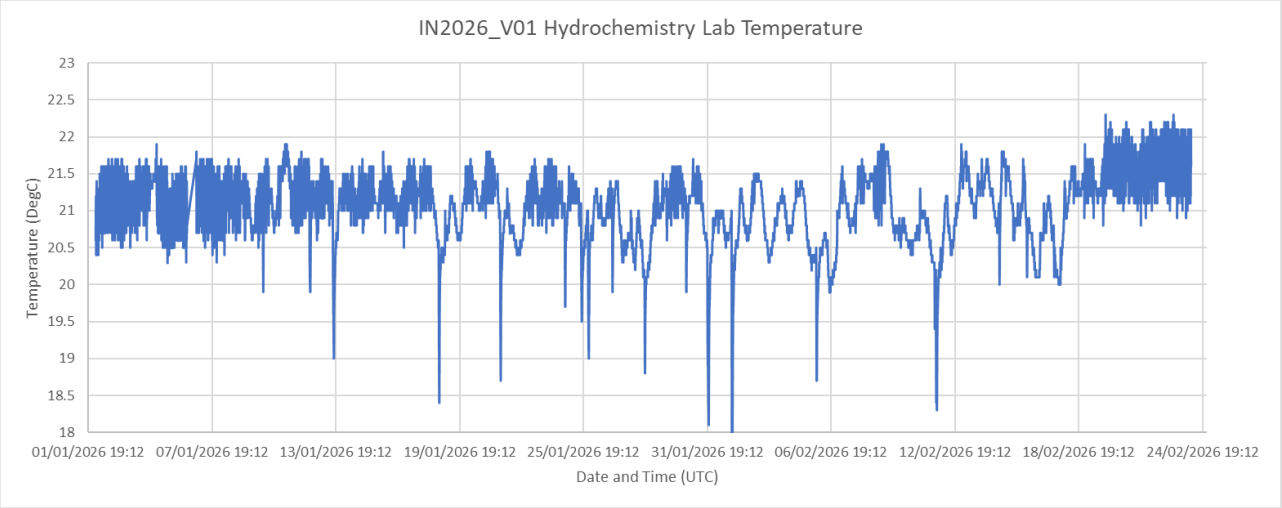

Figure 8. Hydrochemistry lab Ruuvi sensor; scale is 18°C to 23°C, mean: 21.1°C, SD: 0.5°C.

Salinity laboratory

Ambient conditions in the salinity laboratory were monitored using a Ruuvi temperature logger positioned near the area where sample crates were stored. Temperature data was recorded and visualised in Grafana. A time series plot of salinity lab temperature throughout the voyage is shown below. A complete log of temperature is available upon request through CSIRO data centre.

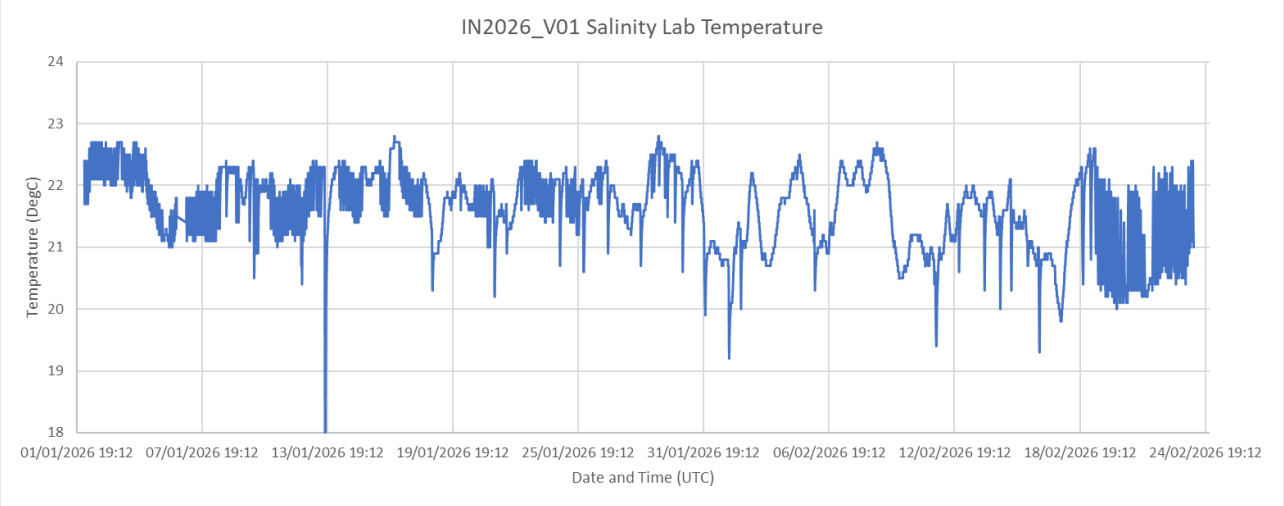

Figure 9. Salinity lab Ruuvi sensor; scale is 18°C to 24°C, mean: 21.6°C, SD: 0.6°C.

Appendix

Salinity: Reference material used

OSIL IAPSO Standard Seawater		
Batch	P167	P168
Use by date	21 February 2026	1 December 2026
K_{15}	0.99988	0.99993
PSU	34.995	34.997

Nutrients: RMNS correction

The submitted nutrient results do NOT have RMNS corrections applied. The measured RMNS value per CTD deployment is provided in supporting document available on CSIRO data trawler.

How to use the RMNS for correction

Ratio = Certified RMNS Concentration/Measured RMNS Concentration in each run

Corrected Concentration = Ratio x Measured Nutrient Concentration

How to use the RMNS for smoothing

Ratio = Average RMNS Concentration across voyage/Measured RMNS Concentration in each run

Corrected Concentration = Ratio x Measured Nutrient Concentration

Missing or Suspect Salinity Data

Data is flagged based on CTD sampling log notes, observations during analysis, and examination of depth profile plots (Appendix, Data Quality Flag Key).

CTD	RP	Flag	Reason for Flag
NA	NA	NA	NA

Missing or Suspect Dissolved Oxygen Data

Data is flagged based on CTD sampling log notes, observations during analysis, and examination of depth profile plots (Appendix, Data Quality Flag Key).

CTD	RP	Flag	Reason for Flag
1	21	69	Data is suspect, marked by operator. Potential outlier from the rest of the bottles though still under offset limit. Cause is unknown.
1	35	133	Data is bad, marked by operator. Analysis error, solution was not stirring during titration.
2	8	133	Data is bad, marked by operator. Sampling error, lid was put in upside down. Sample is compromised.
25	27	133	Data is bad, marked by operator. Sampling error, the Niskin bottle was already opened prior to sampling. No alternate bottle with the same depth was available.

Missing or Suspect Nutrient Data

Data is flagged based on CTD sampling log notes, observations during analysis, and examination of depth profile plots (Appendix, Data Quality Flag Key).

Note: Within the .csv file many ammonium and nitrite samples with concentration near zero may be flagged 63 – below nominal detection limit and may be reported as a negative value. For ammonium, this is due to the baseline (Milli-Q water) becoming slightly contaminated due to air quality in the laboratory. For Nitrite, this is due to reference matrix (low nutrients seawater) containing consistent background concentration that is higher than the samples. These ammonium and nitrite samples are not reported in this table.

CTD / sample	RP	Analyte	Flag	Reason for Flag
Core005	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core041	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.

Core051	NA	NOx, NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core052	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core060	NA	NOx, NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core061	NA	NOx	65	Data is suspect, marked by software; however, data for this sample is BAD. Operator was unable to change the flag in the software. Absorbance peak cannot be accurately measured due to prior off-scale sample interference. The sample is also repeated with ID core081 and significant difference in value was found. Data is inconclusive due to value discrepancy.
Core061	NA	NH_4^+	129	Data is bad, marked by software. Absorbance peak cannot be accurately measured due to prior off-scale sample interference.
Core062	NA	NH_4^+	133	Data is bad, marked by operator. Absorbance peak cannot be accurately measured due to prior off-scale sample interference.
Core063	NA	NH_4^+	133	Data is bad, marked by operator. Absorbance peak cannot be accurately measured due to prior off-scale sample interference.
Core064	NA	NH_4^+	133	Data is bad, marked by operator. Absorbance peak cannot be accurately measured due to prior off-scale sample interference.
Core081	NA	NOx	133	Data is bad, marked by operator. Sample is a repeat of core061 and significant difference in value was found. Data is inconclusive due to value discrepancy.
Core081	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.

Core097	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core098	NA	NH_4^+	133	Data is bad, marked by operator. Absorbance peak cannot be accurately measured due to prior off-scale sample interference.
Core098	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core102	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core103	NA	NH_4^+	133	Data is bad, marked by operator. Absorbance peak cannot be accurately measured due to prior off-scale sample interference.
Core105	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core105	NA	NOx	65	Data is suspect, marked by software. Absorbance peak shape, measured by the instrument, is marginally outside set limits.
Core106	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core107	NA	NOx, NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core110	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core111	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core112	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.

Core130	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core131	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core131	NA	NH_4^+	133	Data is bad, marked by operator. Absorbance peak cannot be accurately measured due to prior off-scale sample interference.
Core134	NA	NH_4^+	133	Data is bad, marked by operator. Absorbance peak cannot be accurately measured due to prior off-scale sample interference.
Core135	NA	NH_4^+	133	Data is bad, marked by operator. Absorbance peak cannot be accurately measured due to prior off-scale sample interference.
Core137	NA	NH_4^+	133	Data is bad, marked by operator. Absorbance peak cannot be accurately measured due to prior off-scale sample interference.
CTD 4	1	SiO_4	69	Data is suspect, marked by software. Duplicate data is outside of set limits.
CTD 5	5	SiO_4	65	Data is suspect, marked by software. Absorbance peak shape, measured by the instrument, is marginally outside set limits.
CTD 5	8	SiO_4	65	Data is suspect, marked by software. Absorbance peak shape, measured by the instrument, is marginally outside set limits.
Core 144	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 147	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 188	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.

Core 189	NA	NH_4^+	133	Data is bad, marked by operator. Absorbance peak cannot be accurately measured due to prior off-scale sample interference.
Core 190	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 192	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 197	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 198	NA	NH_4^+	133	Data is bad, marked by operator. Absorbance peak cannot be accurately measured due to prior off-scale sample interference.
Core 199	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 200	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 201	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 202	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 203	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 204	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 205	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.

Core 206	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 207	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 208	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 209	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 211	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 214	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 221	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 223	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 228	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core254	NA	SiO_4	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core253	NA	SiO_4	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 303	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.

Core 309	NA	NOx, NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 311	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 314	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 346	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 351	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 357	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
CTD 35	1	NOx	69	Data is suspect, marked by software. Duplicate data is outside of set limits.
CTD 36	1	NO_2	69	Data is suspect, marked by software. Duplicate data is outside of set limits.
Core 406	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 406	NA	NOx	133	Data is bad, marked by operator. The peak shape and plateau deviated from the standards, blockage from potential sediment in the sample was suspected. The value cannot be measure accurately.
Core 407	NA	NH_4^+	133	Data is bad, marked by operator. Absorbance peak cannot be accurately measured due to prior off-scale sample interference.
Core 411	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.

Core 412	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 412	NA	NOx	133	Data is bad, marked by operator. The peak shape and plateau deviated from the standards, blockage from potential sediment in the sample was suspected. The value cannot be measure accurately.
Core 413	NA	NH_4^+	133	Data is bad, marked by operator. Absorbance peak cannot be accurately measured due to prior off-scale sample interference.
Core 415	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 427	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 427	NA	NOx	133	Data is bad, marked by operator. There was a spike in the middle of the peak plateau, the value cannot be measured accurately.
Core 431	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 455	NA	NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 469	NA	NOx, NH_4^+	129	Data is bad, marked by software. Off-scale sample. Absorbance peak exceeds the maximum value that can be measured by instrument.
Core 470	NA	NH_4^+	133	Data is bad, marked by operator. Absorbance peak cannot be accurately measured due to prior off-scale sample interference.

Data Quality Flag Key

Flag	Description	

0	Data is GOOD	
63	Nutrients only.	Data below nominal detection limit.
65	Data is SUSPECT.	Nutrients only: Absorbance peak shape, measured by the instrument, is marginally outside set limits.
69	Data is SUSPECT.	Duplicate data is outside of set limits (software). Data point is an outlier on the depth profile plot (operator). Tagged by software or operator
79	Data is SUSPECT.	Nutrients only. Measured Method Detection Limit (MDL) for the analysis run is greater than the nominal MDL. All samples in that run tagged.
129	Data is BAD.	Nutrients Only. Absorbance peak exceeds the maximum value that can be measured by the instrument.
133	Data is BAD.	Set by operator.
134	Data is BAD.	Nutrients Only. Absorbance peak shape of calibrant, measured by the instrument, is outside of set limits (software).
141	NO Data.	Used in netcdf results file. Not used in csv results file.

GO-SHIP Specifications

Salinity

Accuracy of 0.001 is possible with Autosal™ salinometers and concomitant attention to methodology. Accuracy with respect to one particular batch of standard Seawater can be achieved at better than 0.001 PSS-78. A precision of approximately 0.0002 PSS-78 is possible following the methods of Kawano with great care and experience. Air temperature stability of ± 1°C is very important and should be recorded[2].

Dissolved Oxygen

Target accuracy is that 2 sigma (standard deviation) should be less than 0.5% of the highest concentration found in the ocean. Precision or reproducibility (2 sigma) is 0.08% of the highest concentration found in the ocean.

$Si(OH)_4$

Approximately 1-3% accuracy[1], 0.2% precision[3], full scale.

PO_4

Approximately 1-2% accuracy[1], 0.4% precision[3], full scale.

NO_3

Approximately 1% accuracy[1], 0.2% precision[3], full scale.

Notes

[1] If no absolute standards are available then accuracy should be taken to mean the reproducibility presently obtainable in the better laboratories.

[2] Keeping constant temperature in the room where salinities are determined greatly increases their quality. Also, room temperature during the salinity measurement should be noted for later interpretation if queries occur. Additionally, monitoring and recording the bath temperature is also recommended. The frequent use of IAPSO Standard Seawater is endorsed. To avoid the changes that occur in Standard Seawater, the use of the most recent batch is recommended. The bottles should also be used in an interleaving fashion as a consistency check within a batch and between batches.

[3] Developments of reference materials for nutrients are underway that will enable improvements in the relative accuracy of measurements and clearer definition of the performance of laboratories when used appropriately and the results are reported with the appropriate meta-data.

References

Armishaw, P. (2003) "*Estimating measurement uncertainty in an afternoon. A case study in the practical application of measurement uncertainty*." Accred Qual Assur, 8: pp. 218-224

Armstrong, F.A.J., Stearns, C.A., and Strickland, J.D.H. (1967) *"The measurement of upwelling and subsequent biological processes by means of the Technicon Autoanalyzer and associated equipment,"* Deep-Sea Res., 14: pp.381-389. doi: 10.1016/0011-7471(67)90082-4

Hood, E.M. (2010). *"Introduction to the collection of expert reports and guidelines."* The GO-SHIP Repeat Hydrography Manual: A Collection of Expert Reports and Guidelines. IOCCP Report No 14, ICPO Publication Series No. 134, Version 1, 2010.

Hydes, D., Aoyama, M., Aminot, A., Bakker, K., Becker, S., Coverly, S., Daniel, A.G., Dickson, O., Grosso, R., Kerouel, R., van Ooijen, J., Sato, K., Tanhua, T., Woodward, E.M.S., and Zhang, J.Z. (2010). *"Determination of dissolved nutrients (N, P, Si) in seawater with high precision and inter-comparability using gas-segmented continuous flow analysers."* The GO-SHIP Repeat Hydrography Manual: A Collection of Expert Reports and Guidelines. IOCCP Report No 14, ICPO Publication Series No. 134, Version 1, 2010. (UNESCO/IOC)

Kérouel, R., and Aminot, A. (1997) *"Fluorometric determination of ammonia in sea and estuarine waters by direct segmented flow analysis".* Mar. Chem., 57: pp. 265-275. doi: 10.1016/S0304-4203(97)00040-6

Kirkwood, D. S. (1996) "*Nutrient Analyses in Seawater Using Autoanalyzers: Refractive Index and Other Sources of Error*", *Marine Chemistry, 52*(1), 1-10. [DOI: 10.1016/0304-4203(95)00086-0]

Murphy, J. And Riley, J.P. (1962)"*A Modified Single Solution Method for the Determination of Phosphate in Natural Waters"*, Anal. Chim. Acta, 27: p.30. doi: 10.1016/S0003-2670(00)88444-5

Rees, C., L. Pender, K. Sherrin, C. Schwanger, P. Hughes, S. Tibben, A. Marouchos, and M. Rayner. (2018) "*Methods for reproducible shipboard SFA nutrient measurement using RMNS and automated data processing*." Limnol. Oceanogr: Methods, 17(1): pp. 25-41. doi:10.1002/lom3.10294

Wood, E.D., Armstrong, F.A.J., and Richards, F.A. (1967) *"Determination of nitrate in seawater by cadmium-copper reduction to nitrite."* Journal of the Marine Biological Association of U.K. 47: pp. 23-31.