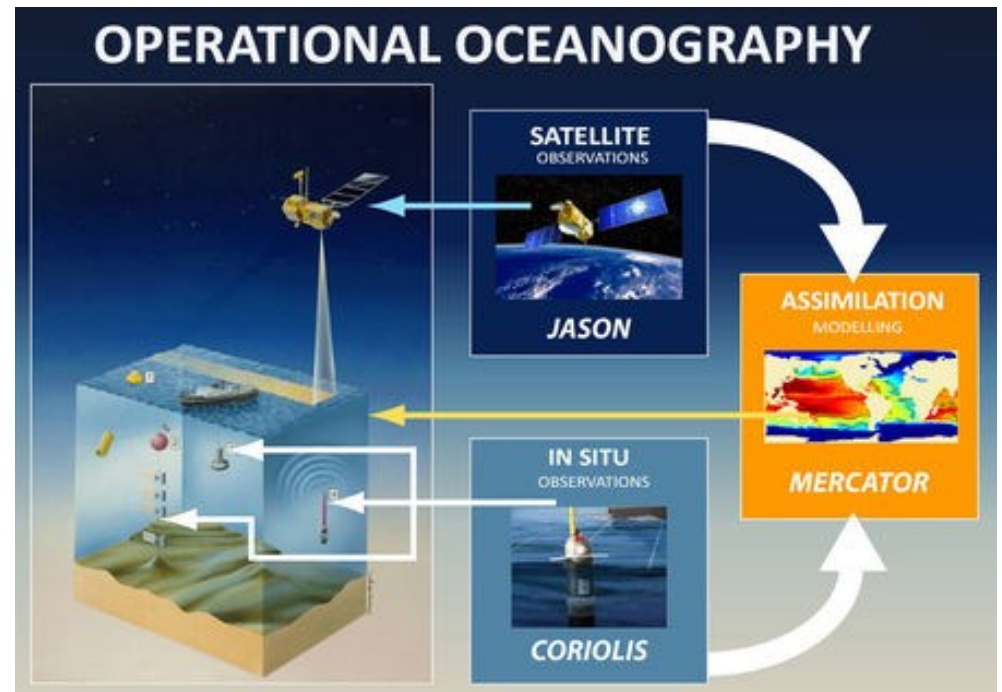


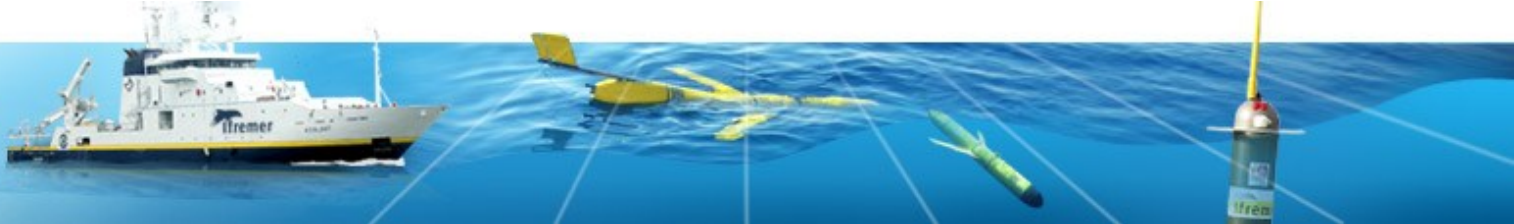
## An In-Situ Service For Operational Oceanography

**Goal:** In-situ data portal for operational oceanography

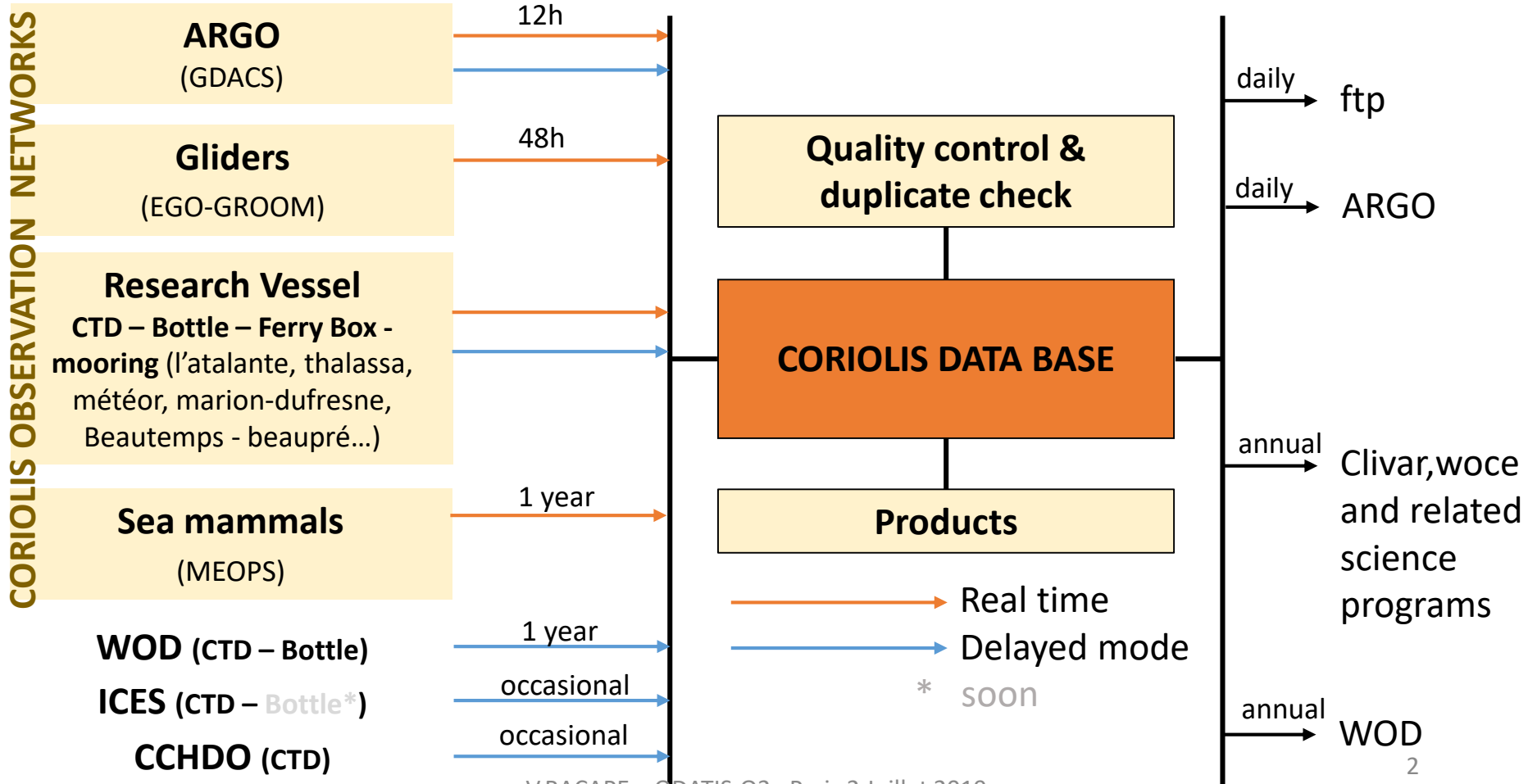
**Actors :** 7 French institutes contributing to the French operational oceanography program for the in-situ observations

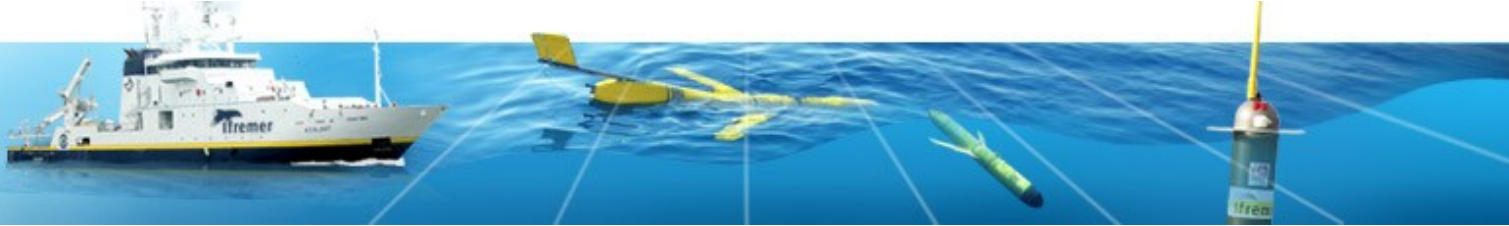
**Role :** Acquisition, collection, validation and dissemination of real-time and delayed mode in situ data for the global ocean.





## O<sub>2</sub> flux throughout the Coriolis Data Center





## QC code and O<sub>2</sub> units in the Coriolis Data Base

### QC CODE

Code	Meaning
0	No QC was performed
1	Good data
2	Probably good data
3	Bad data that are potentially correctable
4	Bad data
5	Value changed
6	Not used
7	Not used
8	Interpolated value
9	Missing value

### Units

**CORIOLIS DATA BASE**  
mL/L - μmol/L - μmol/kg

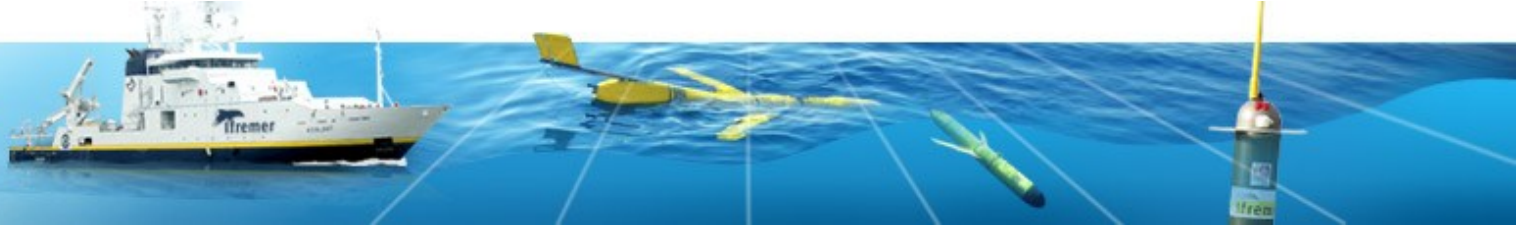
**Products**  
μmol/kg

### Variables

**DOX1**  
mL/L

**DOXY**  
μmol/L

**DOX2  
(\_ADJUSTED)**  
μmol/kg



## Duplicate check by Coriolis R&D

Nota Bene

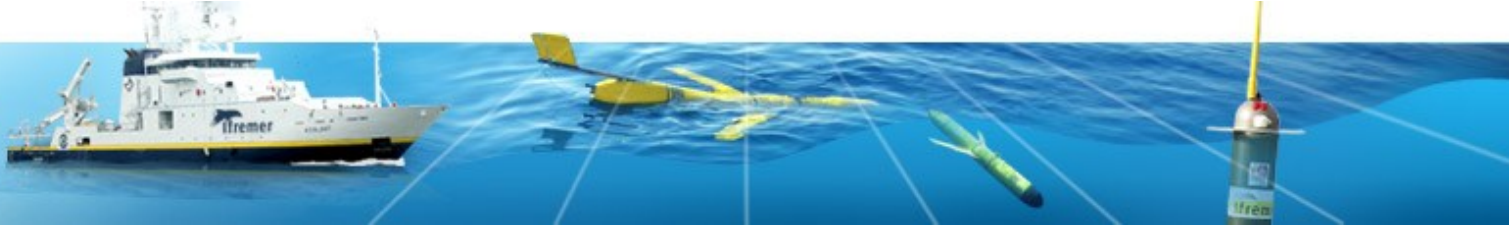
- All profiles with  $\Delta t$  and  $\Delta(x,y) < 15'$  are considered as a duplicate *Automatic Query*
  - Performed on all profiles in the coriolis data base
  - Statut undistributed (like quarantine) up to human decision
  - *Inconvenient* : require good metadata / doesn't take into consideration parameter values
- Frozen profiles test *return alert for human decision*
  - Performed on platform files
  - Test that complets previous query

In the Coriolis data base,  
1 **profile** is defined by  
**x,y,z,t,n parameters**

### Human decision

1/ priority for data coming from french source  
2/ priority to profile with the greatest number of parameters,  
to profile with original parameters...

Coriolis dissemination **by platform** = 1 file with all profiles from the same platform



## First O<sub>2</sub> Quality Control by Coriolis R&D

*Automatic Queries* → **As soon as data is loaded** (WOD, ICES, CCHDO, MEOP\*)

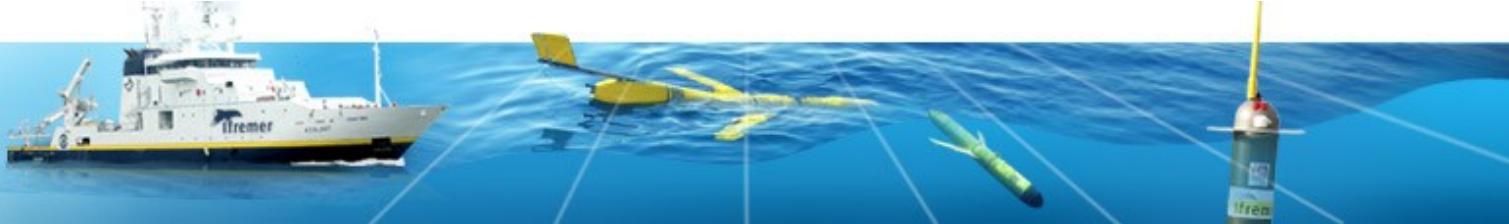
- **Check potential unit inversion**
- **Negative Pressure Test**  
DOX#\_QC = 4 if and only if PRES/DEPH < 0 dbar/m
- **P&T&S QC Test\*** *Only for μmol/kg*  
DOX#\_QC = 4/3/4 if and only if PRES\_QC or TEMP\_QC or PSAL\_QC = 4/3/Filled Value
- **Regional Range Test\***  
Any QC modification due to this test will be controlled later by an operator

**In progress**

*Alert controlled by an operator* (all sources / their application depend on the profile type)

- **Check :**
  - 1/ Unit number and their relationships
  - 2/ data&QC association / QC=0?
- **P&T&S QC test** for data in μmol/kg
- **Negative pressure test**
- **Regional Range Test**
- **Frozen Value test**
- **Spike test**
- **Frozen profile test** (for profile only)

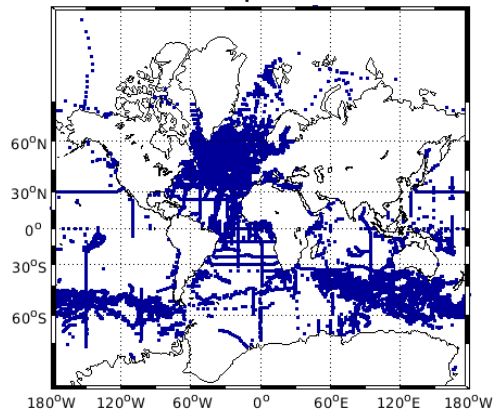
**In progress**



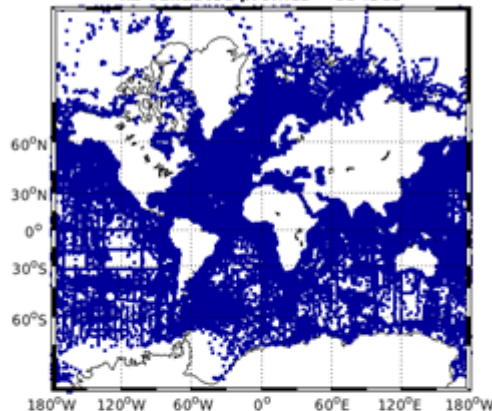
# O<sub>2</sub> VALIDATED PROFILES IN THE CORIOLIS DATA BASE

Work in progress

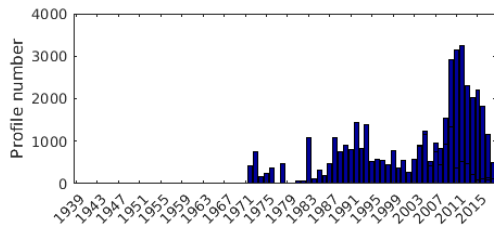
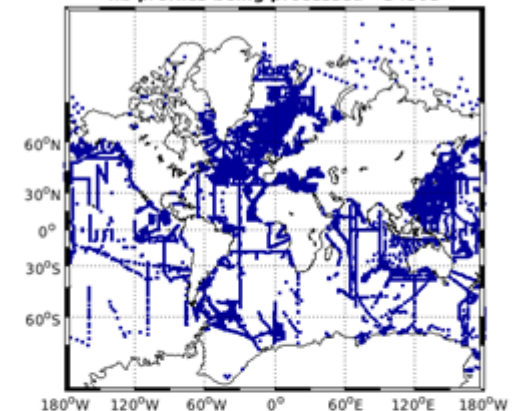
nb validated profiles = 41923



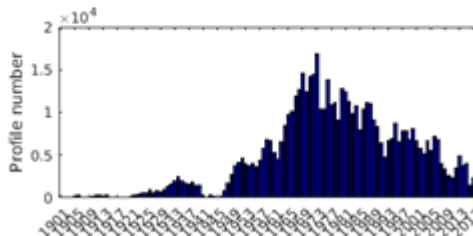
nb validated profiles = 554389



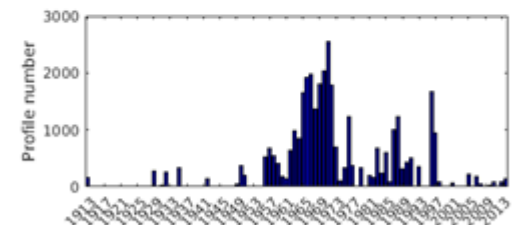
nb profiles being processed = 34305

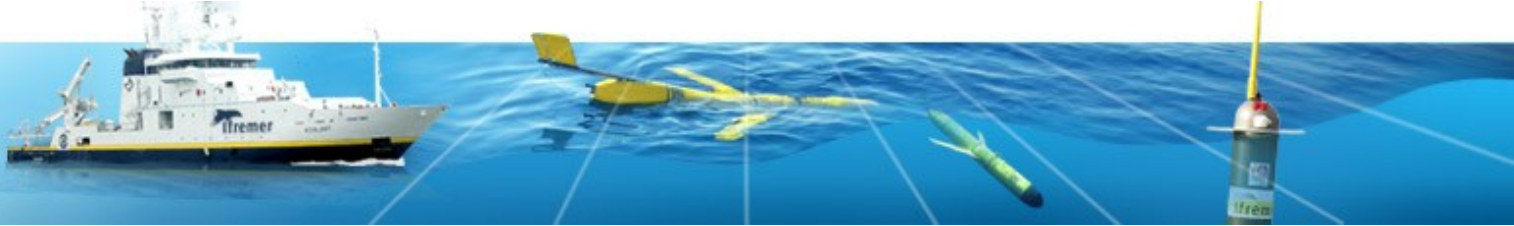


Including Argo float  
in DM



Including WOD  
CTD&BO





## O<sub>2</sub> Products

### Work in progress

- **INSITU\_GLO\_REP\_OBSERVATIONS\_013\_046**

Product of **Copernicus Marine Environment Monitoring Service** (<http://www.marineinsitu.eu/>)

**Availability** : September 2019

**Content** : All vertical profiles (CTD-BO-PF-SM-ML) validated by the first O<sub>2</sub> QC procedure  
(including ARGO floats in DM only)

**Validation** : First O<sub>2</sub> QC procedure

Saturation Test

Comparison with WOD18

**Unit** : μmol/kg

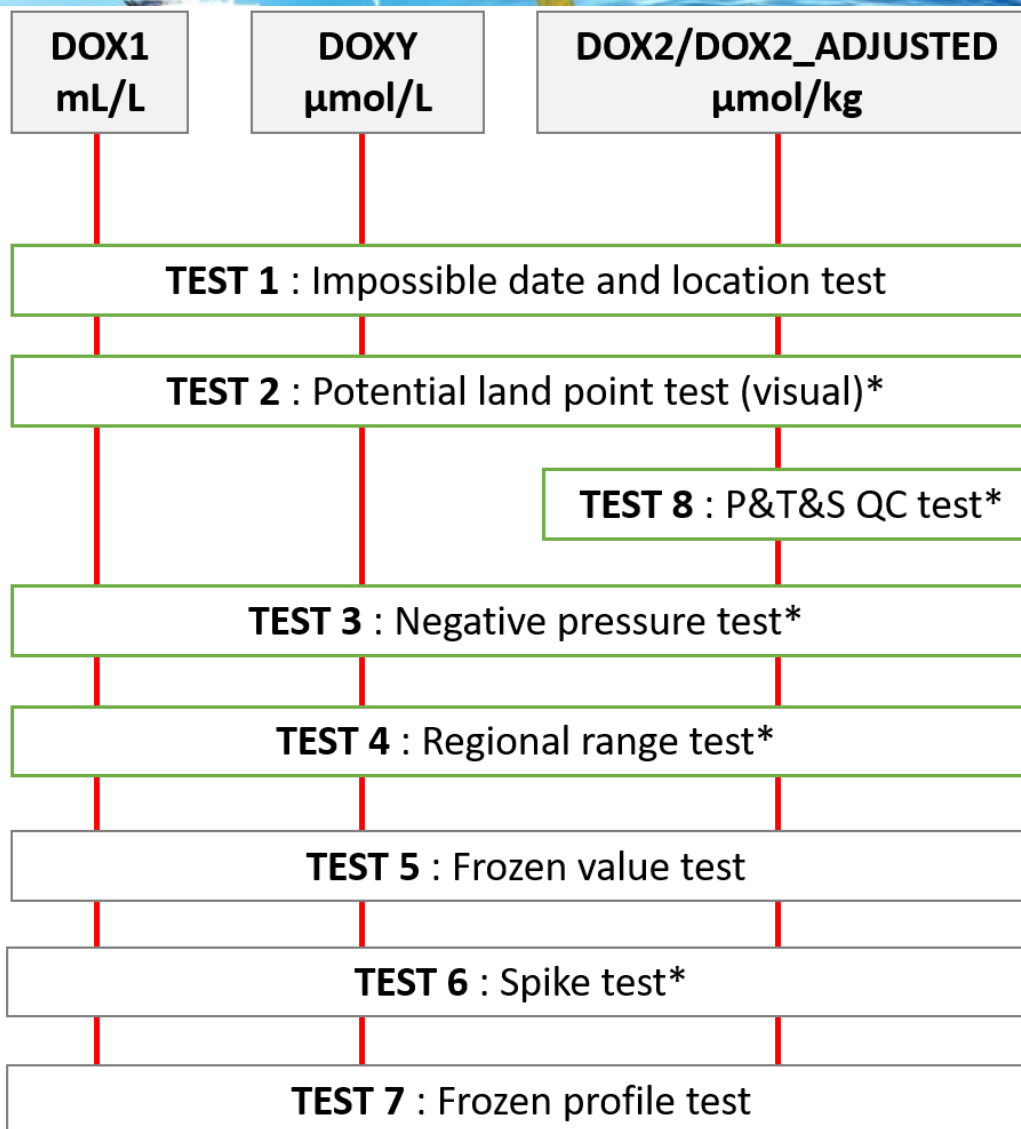
- Objective Analysis using ISAS-O2

**Content** : All vertical profiles (CTD-BO-PF-SM) validated by the first O<sub>2</sub> QC procedure  
(including ARGO floats in DM only)

**First guest** : WOD / home first guest using bottle from Glodap\_v2

**Starting** September 2019

**Unit** : μmol/kg



→ Profiles (CT, SM, ML and MO)

□ Isolated Samples (BO)

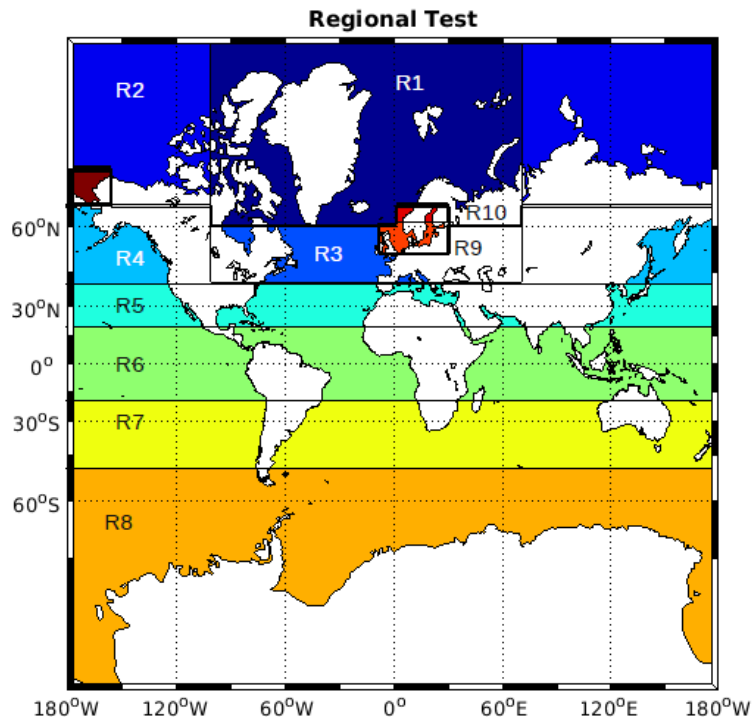
\* Tests applied in addition to ARGO recommendation (PF)





## Regional Range Test

Definition of the thresholds for the NRT-regional range test (conversion using  $\text{mean}(\rho) = 1.025 \text{ kg/L}$  and  $V(\text{O}_2) 44.6596 \text{ } \mu\text{mol/ml}$  (SCOR 142))



### Global Basin

R1 : 60°N to 90°N - 100°W to 70°E (ARCT-ATL)  
40 to 600  $\mu\text{mol/kg}$  | 41 to 615  $\mu\text{mol/L}$  | 0.9 to 13.8 mL/L

R2 : 65°N to 90°N - 70°E to 100°W (ARTC – PAC)  
40 to 600  $\mu\text{mol/kg}$  | 41 to 615  $\mu\text{mol/L}$  | 0.9 to 13.8 mL/L

R3 : 40°N to 60°N - 100°W to 70°E (ARCT-ATL)  
-5 to 600  $\mu\text{mol/kg}$  | -5 to 615  $\mu\text{mol/L}$  | -0.1 to 13.8 mL/L

R4 : 40°N to 65°N - 70°E to 100°W (ARTC – PAC)  
-5 to 600  $\mu\text{mol/kg}$  | -5 to 615  $\mu\text{mol/L}$  | -0.1 to 13.8 mL/L

R5 : 20°N to 40°N  
-5 to 500  $\mu\text{mol/kg}$  | -5 to 512.5  $\mu\text{mol/L}$  | -0.1 to 11.5 mL/L

R6 : 20°S to 20°N  
-5 to 400  $\mu\text{mol/kg}$  | -5 to 410  $\mu\text{mol/L}$  | -0.1 to 9.20 mL/L

R7 : 50°S to 20°S  
-5 to 500  $\mu\text{mol/kg}$  | -5 to 512.5  $\mu\text{mol/L}$  | -0.1 to 11.5 mL/L

R8 : 90°S to 50°S  
50 to 600  $\mu\text{mol/kg}$  | 51.25 to 615  $\mu\text{mol/L}$  | 1.15 to 13.8 mL/L

### Baltic Sea and north seas

R9 : 52°N to 60°N / 8°W to 30.34°E  
-5 to 27 mL/L

R10 : 60°N to 65.84°N / 1.3°E to 30.34°E  
-5 to 567  $\mu\text{mol/kg}$  | -5 to 581  $\mu\text{mol/L}$  | -0.1 to 13 mL/L

### Chukchi sea

R11 : 65°N to 73°N / 180°W to 155°W  
-5 to 780  $\mu\text{mol/KG}$  | -5 to 800  $\mu\text{mol/L}$  | -0.1 to 18 mL/L

# A method testing the statistical entropy change caused by the instrument

Based on a 2 step estimation of the [modified Akaike information criterion](#) (UEDA, 2009):

*UEDA, T. 2009. A simple method for the detection of outliers. Electronic Journal of Applied Statistical Analysis, 67-76*

- ➔ A vertical sliding window of 5 data centered on 1 potential outlier  $[x_{i-2} \ x_{i-1} \ x \ x_{i+1} \ x_{i+2}]$  constrained by distance between 2 samples  
 $[\Delta Z < 5\text{db} \ \text{for } Z > 10\text{db}] \ [\Delta Z < 50\text{bd} \ \text{for } 10 < Z < 100]$   
 $[\Delta Z < 200\text{dbar} \ \text{for } 100 < Z < 998] \ [\Delta Z < 500\text{dbar} \ \text{for } Z > 998\text{dbar}]$

First step ( $Ut_1$ ) = without the outlier  $[x_{i-2} \ x_{i-1} \ x_{i+1} \ x_{i+2}]$   
 $n(\text{total})=4$  ,  $ng(\text{good data})=4$ ,  $nb(\text{bad data})=0$

Second Step ( $Ut_2$ ) = **with the outlier**  $[x_{i-2} \ x_{i-1} \ x \ x_{i+1} \ x_{i+2}]$   
 $n(\text{total})=5$ ,  $ng=4$ ,  $nb=1$

**X is an outlier if  $dU > dU_{crit}$**

- ➔ How to estimate  $dU_{crit}$  ?  
 depending on parameter (accuracy),  
 on vertical region (natural variability)

T&S  $dU_{crit-posit} = 1,15 * 98^{th}$  percentil of  $dU$   
 $dU_{crit-neg} = 0,85 * 98^{th}$  percentil of  $dU$

O<sub>2</sub> window extension to 7 data (variability)  
 $dU_{crit} = 1,75 * 98^{th}$  percentil of  $dU$

(example for 100 data and 2 potential outliers)

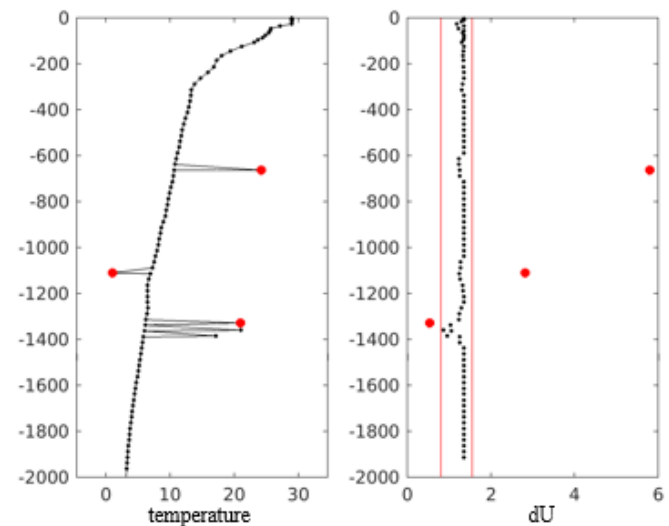
$$Ut = \frac{1}{2} AIC = ng \log(\sigma + 1) - \text{term 2}$$

$$\text{term 2} = nb - \frac{\log(n!)}{n} \sqrt{\sigma}$$

$$\sigma = \sqrt{\frac{\sum_2 (x_i - x)^2}{ng}}$$

$$dU = \text{abs}(Ut_1) - Ut_2$$

**$\Delta \log(\sigma + 1) - \text{term 2}$**



# A method based on vertical median and standard deviation

## By D. Dobbler

Based on human eye visual work:

➡ **where normally should the points be?**

A vertical **sliding median** is computed with its sliding window expressed in [dbar] and depending on vertical layers

If less than 5 points to compute median, the sliding window is extended to cover 5 points in the limitation of 500 dbar extension.

Depths [dbar]	Sliding window [dbar]
< 500	50
500 – 1200	200
> 1200	300

➡ **what's the variability of my data, depending on the vertical layer?**

- **Standard deviation** is computed on different vertical layers (**one value per layer**)
- The result is bounded by a given domain :

Pressions [dbar]	TEMP_std range [°C]	PSAL_std range [PSU]	DOXY_std range [micromole/kg]
< 10	= 8	=1.1	= 70
10 - 500	[0.5 6]	[0.1 0.9]	[2.5 50]
500 - 1200	[0.5 2]	[0.07 0.3]	[2.5 25]
> 1200	[0.5 2]	[0.07 0.3]	[2.5 25]

➡ **Is my point out of what I expect to see (i.e. : out of normal location +/- the variability) ?**

Test\_value= (PARAM – PARAM\_med > n\_std \* PARAM\_std ) in the following n\_std=1