

Synoptic CB: Porewater DIC

August 2023 Samples

2025-10-25

Contents

0.1	Import Data Functions	2
0.2	Import Sample Data	2
0.3	Assessing Standard Curves - assessed on the instrument manually	3
0.4	CRM Check - Don't run chunk if no CRMs run	3
0.5	Assess Check Standards	3
0.6	Assess Blanks	4
0.7	Assess Duplicates	5
0.8	Sample Flagging - Are samples Within the range of the curve?	6
0.9	Visualize Data by Plot	7
0.10	Convert data from mg/L to uMoles/L	8
0.11	Check to see if samples run match metadata & merge info	8
0.12	Export Processed Data	8

```

##Setup - Change things here & write any notes

#identify section
cat("Setup Information")

## Setup Information

##### Run information - PLEASE CHANGE
Date_Run = "08/18/23" #Date that instrument was run
Run_by = "Stephanie J. Wilson" #Instrument user
Script_run_by = "Stephanie J. Wilson" #Code user
run_notes = " " #any notes from the run
samples <- c("GCW", "GWI", "MSM", "SWH") #whatever identifies your samples within the same names
samples_pattern <- paste(samples, collapse = "|")
#samples_pattern <- "GCW" #use this instead of the line above if you have only one site code
chks_name = "Chk_Std_" #what did you name your check standards?
crm_name = "CRM|crm" #what did you name your CRMS?

##### File Names - PLEASE CHANGE
#file path and name for raw summary data file
raw_file_name = c("Raw Data/TOCTN_COMPASS_Synoptic_DIC_202308_1.txt",
                 "Raw Data/TOCTN_COMPASS_Synoptic_DIC_202308_2.txt")

#file path and name for raw all peaks file
# raw_allpeaks_name = c("Raw Data/COMPASS_SynopticCB_PW_DIC_202308_1_allpeaks.txt",
#                       "Raw Data/COMPASS_SynopticCB_PW_DIC_202308_2_allpeaks.txt")

#file path and name of processed data file
processed_file_name = "Processed Data/COMPASS_SynopticCB_PW_Processed_DIC_202308.csv"

##### Log Files - PLEASE CHECK
#downloaded metadata csv - downloaded from Google drive as csv for this year
Raw_Metadata = "Raw Data/COMPASS_SynopticCB_PW_SampleLog_2023.csv"

#qaqc log file path for this year
#Log_path = "Raw Data/COMPASS_Synoptic_DIC_QAQClog_2023.csv"

```

```

##Set Up Code
##Read in metadata and create similar sample IDs for matching to samples

```

0.1 Import Data Functions

0.2 Import Sample Data

```
## Import Sample Data
```

```

## New names:
## New names:
## * `` -> '...14'

```

```
## # A tibble: 6 x 3
##   sample_name          ic_raw run_datetime
##   <chr>                <dbl> <chr>
## 1 GCW_202308_TR_LysB_10cm  28.1  8/19/2023 9:50:53 AM
## 2 GCW_202308_WC_LysA_10cm 162.   8/19/2023 10:08:13 AM
## 3 GCW_202308_WC_LysA_20cm 148.   8/19/2023 10:26:42 AM
## 4 GCW_202308_WC_LysA_45cm 170.   8/19/2023 10:44:08 AM
## 5 GCW_202308_WC_LysB_10cm 198.   8/19/2023 11:00:44 AM
## 6 GCW_202308_WC_LysB_20cm 165.   8/19/2023 11:18:50 AM
```

0.3 Assessing Standard Curves - assessed on the instrument manually

0.4 CRM Check - Don't run chunk if no CRMs run

```
## Assess the CRMs

## New names:
## New names:
## * `` -> '...14'

## [1] "IC crm has a % Difference <25% of expected - PROCEED"

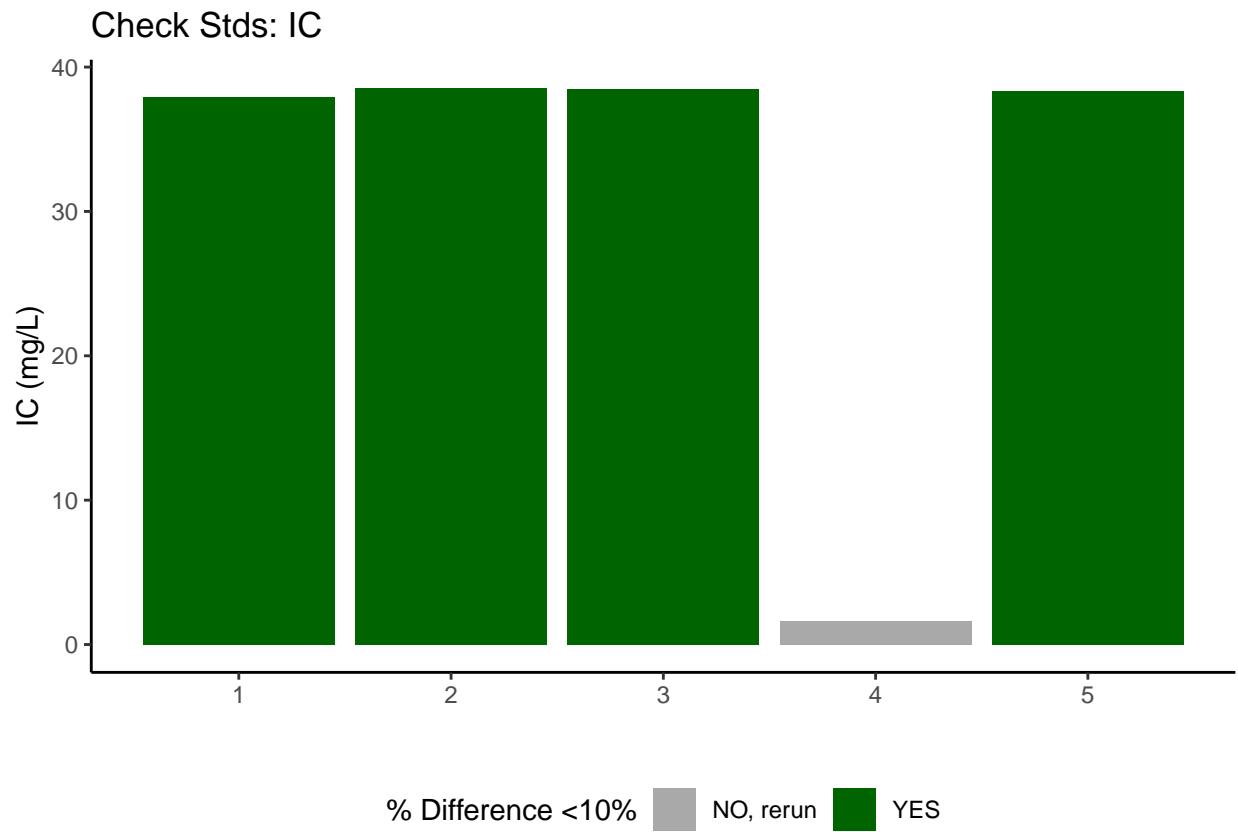
## Run mean = 23.1575

## Expected = 22.19
```

0.5 Assess Check Standards

```
## Assess the Check Standards
```

```
## New names:
## New names:
## * `` -> '...14'
```



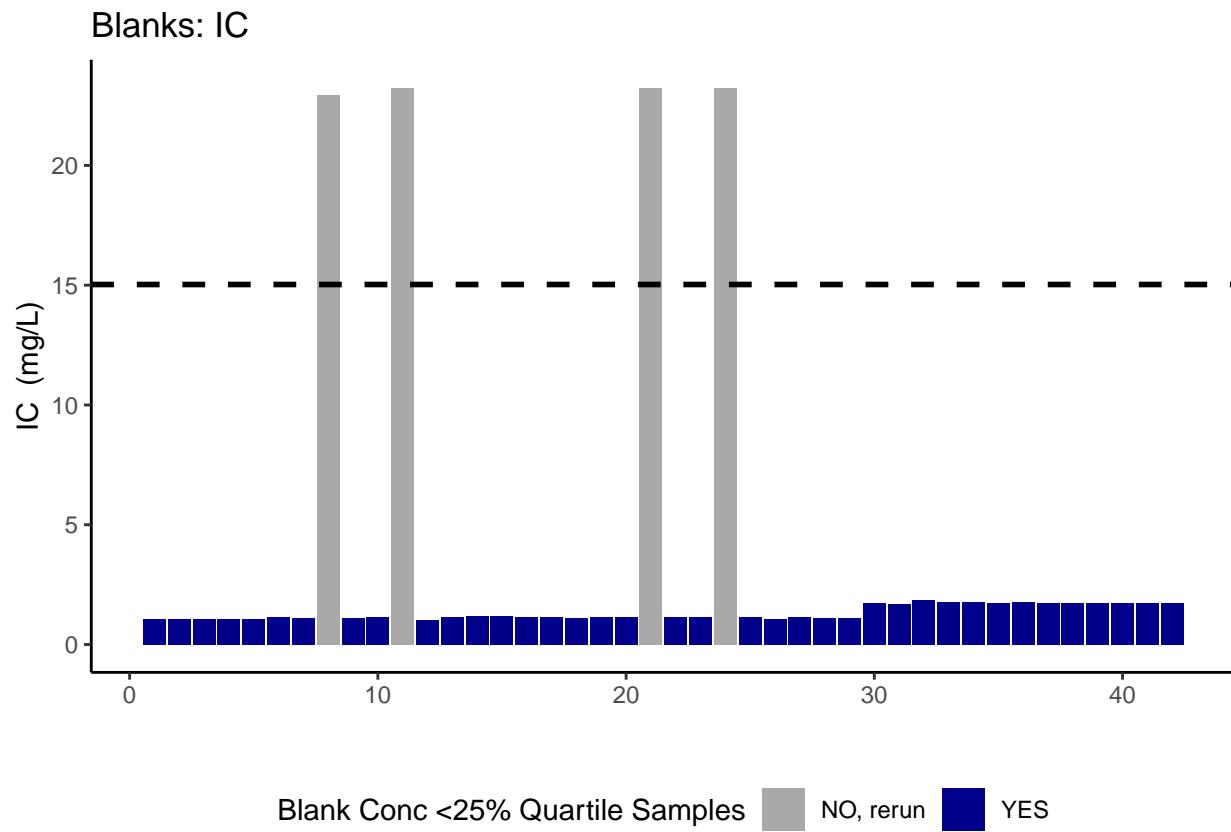
```
## [1] ">60% of IC Check Standards are within range of expected concentration"
```

0.6 Assess Blanks

```
## Assess Blanks
```

```
## New names:  
## New names:  
## * ' ' -> '...14'
```

```
## [1] ">60% of Carbon Blank concentrations are lower 25% quartile of samples"
```

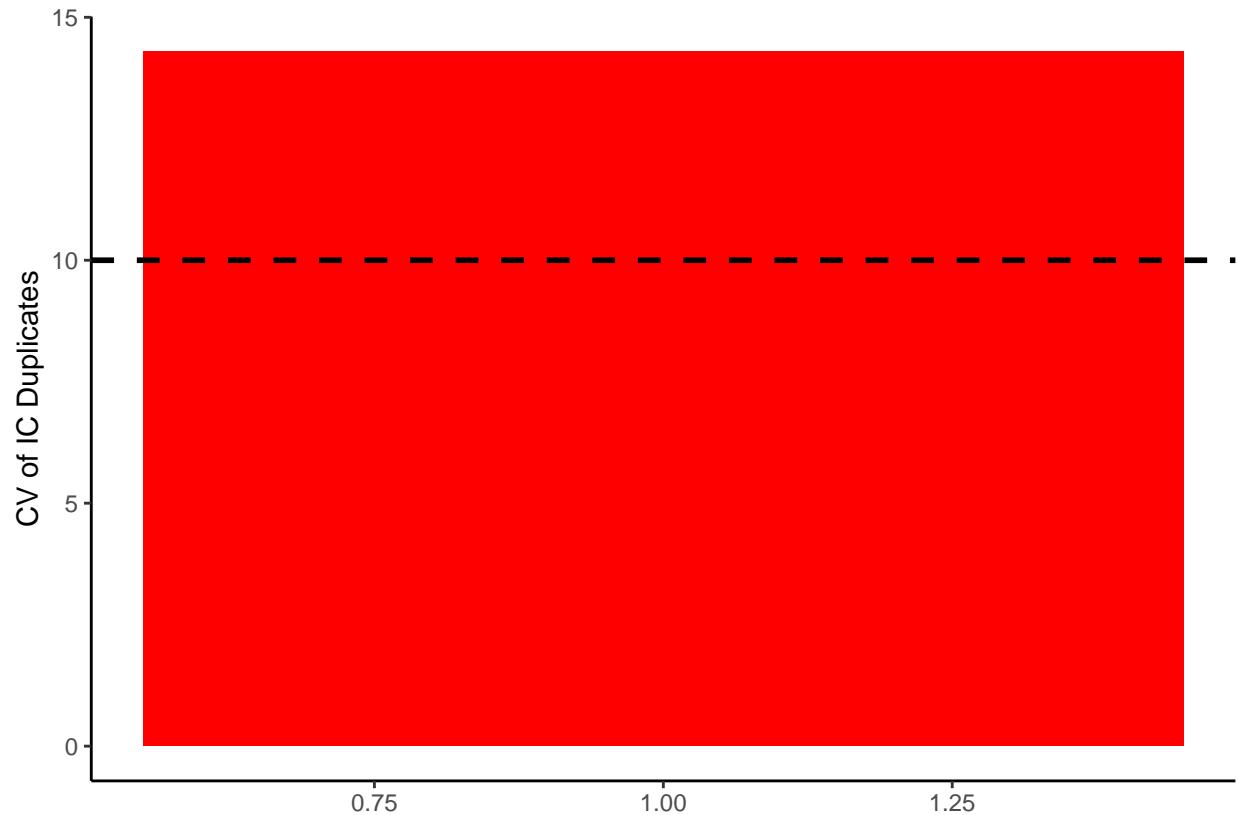


```
## carbon blanks:
```

```
## [1] 3.413595
```

0.7 Assess Duplicates

```
## Assess Duplicates
```

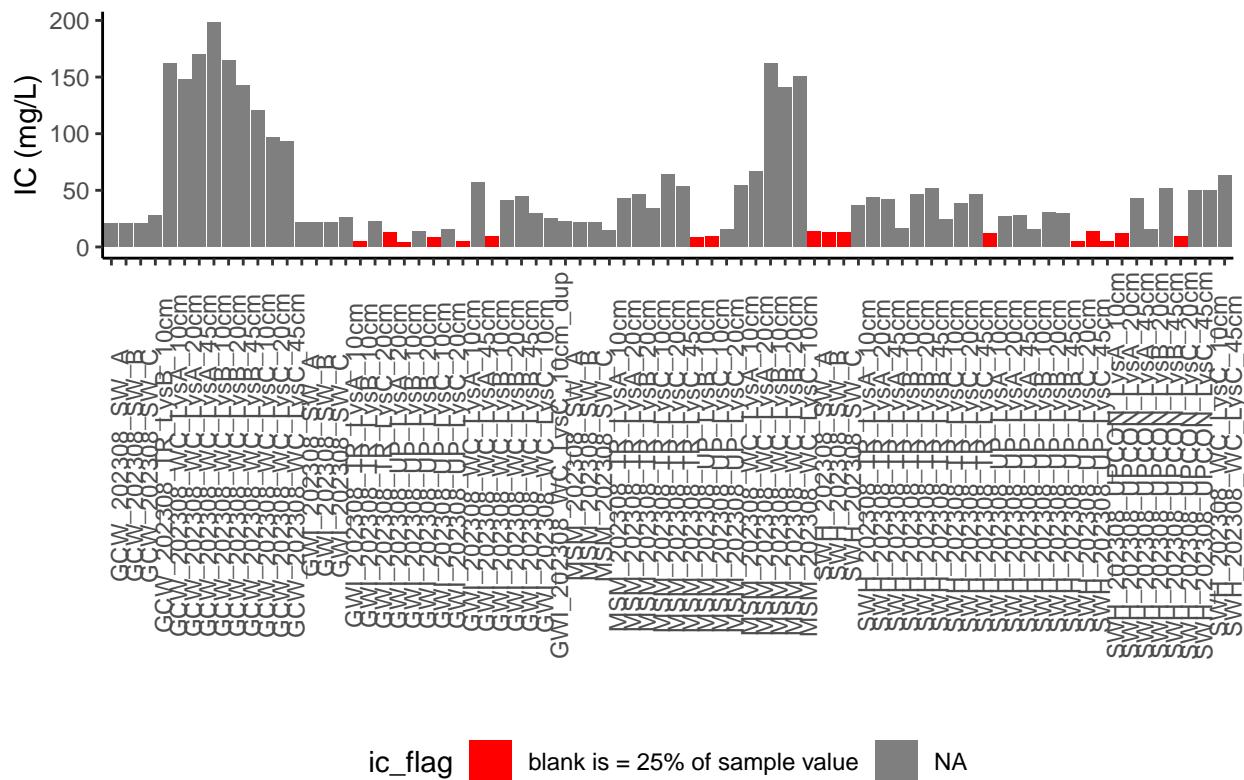


```
## [1] "<60% of Carbon Duplicates have a CV <10% - REASSESS"
```

0.8 Sample Flagging - Are samples Within the range of the curve?

```
## Sample Flagging
```

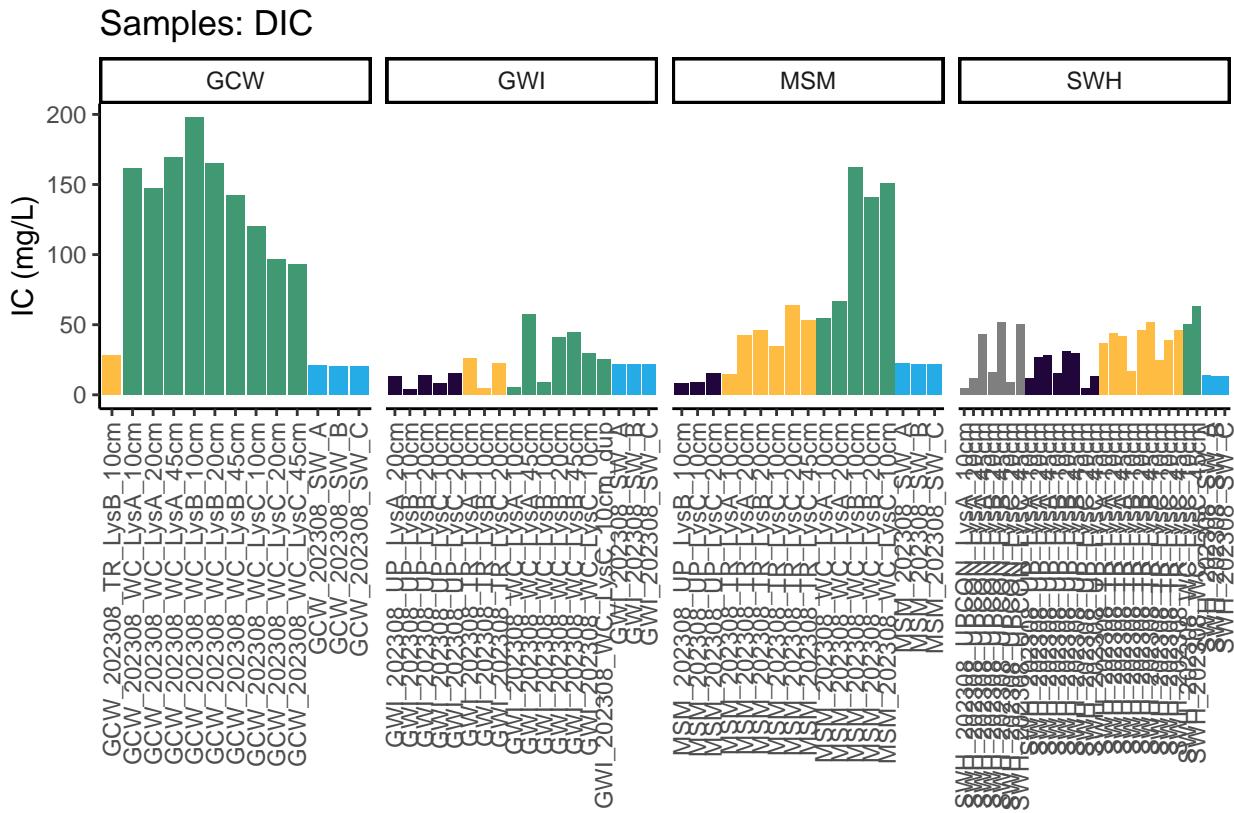
C: Grey = Within Range of Curve



0.9 Visualize Data by Plot

```
## Visualize Data

## Warning in rbind(c("GCW", "202308", "TR", "LysB", "10cm"), c("GCW", "202308", :
## number of columns of result is not a multiple of vector length (arg 1)
```



0.10 Convert data from mg/L to uMoles/L

0.11 Check to see if samples run match metadata & merge info

```
## Check Sample IDs with Metadata
## All sample IDs are present in metadata.
```

0.12 Export Processed Data

```
## Export Processed Data

## # A tibble: 6 x 18
##   Project      Region Site  Zone  Replicate Depth_cm Sample_ID Year Month Day
##   <chr>        <chr>  <chr> <fct> <chr>     <int> <chr>    <int> <int> <int>
## 1 COMPASS: Sy~ CB    SWH  UPCON A          10 SWH_2023~ 2023     8    23
## 2 COMPASS: Sy~ CB    SWH  UPCON A          20 SWH_2023~ 2023     8    23
## 3 COMPASS: Sy~ CB    SWH  UPCON A          45 SWH_2023~ 2023     8    23
## 4 COMPASS: Sy~ CB    SWH  UPCON B          20 SWH_2023~ 2023     8    23
## 5 COMPASS: Sy~ CB    SWH  UPCON B          45 SWH_2023~ 2023     8    23
## 6 COMPASS: Sy~ CB    SWH  UPCON C          20 SWH_2023~ 2023     8    23
## # i 8 more variables: Time <lgl>, Time_Zone <lgl>, ic_mgL <dbl>, ic_uM <dbl>,
## #   ic_flag <chr>, Analysis_runtime <chr>, Run_notes <chr>, Field_notes <chr>
## # end
```