# COMPASS: TEMPEST Discrete DOC Data QAQC

August 2024 run 2

2025-06-23

#### **Run Information**

```
#identify which section you are in
cat("Run Information")
```

## Run Information

```
#a link to the Gitbook or whatever protocol you are using for this analysis
  #steph will add this soon
#anything that needs to be changed do this in the first chunk
 Date Run = "09/05/24"
  Run_by = "Stephanie J. Wilson"
  Script_run_by = "Stephanie J. Wilson"
 run_notes = " "
  #file path and name for summary file
   raw_file_name = "tmp_doc_raw_data_2024/TMP_202408.txt"
  #file path and name for the all peaks file
   raw_allpeaks_name = "tmp_doc_raw_data_2024/TMP_202408_allpeaks.txt"
  #file path and name for processed data after QAQC
   processed_file_name = "tmp_doc_processed_data_2024/TMP_PW_DOC_Processed_202408a.csv"
#check standard concentrations - Update if running different checks:
   chk std c = 1
  chk_std_n = 1
#Log path
   Log_path = "tmp_doc_raw_data_2024/COMPASS_TMP_TOCTN_QAQClog_2024.csv"
```

#### Setup

Pull in active porewater tracking inventory sheet

## File already exists. No download needed.

### **Import Data Functions**

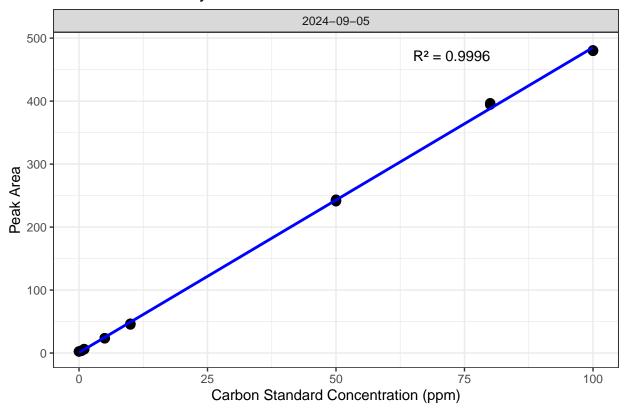
#### Import Sample Data

## Assessing standard Curves

## Assess the Standard Curve

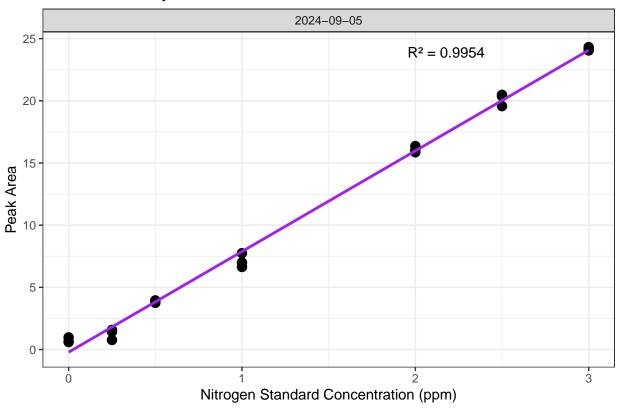
```
## New names:
## 'geom_smooth()' using formula = 'y ~ x'
## * '' -> '...18'
```

## NPOC Std Curve by Date



## 'geom\_smooth()' using formula = 'y ~ x'

## TN Std Curve by Date



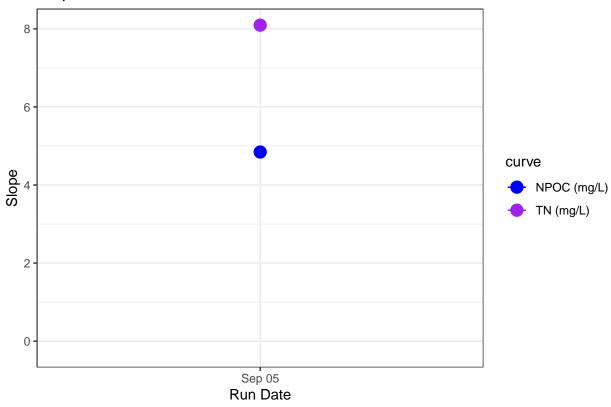
## Warning: Removed 19 rows containing missing values or values outside the scale range
## ('geom\_point()').

## Warning: Removed 19 rows containing missing values or values outside the scale range
## ('geom\_line()').

## 'geom\_line()': Each group consists of only one observation.

## i Do you need to adjust the group aesthetic?

## Slope Drift Assessment



- ## [1] "NPOC Curve r2 GOOD"
- ## [1] "TN Curve r2 GOOD"

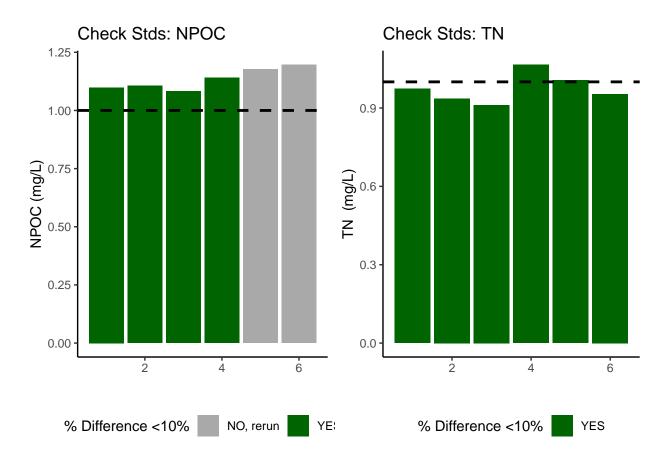
#### **Assess Check Standards**

## Assess the Check Standards

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

## [1] "Carbon Check Standard RSD within Range"

## [1] "Nitrogen Check Standard RSD within Range"



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

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

#### **Assess Blanks**

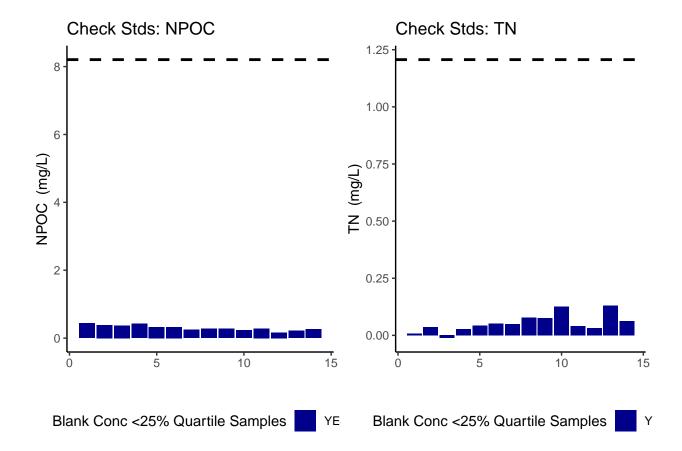
## Assess Blanks

## New names:

## \* '' -> '...14'

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

## [1] ">60% of Nitrogen Blank concentrations are below the lower 25% quartile of samples"



## carbon blanks:

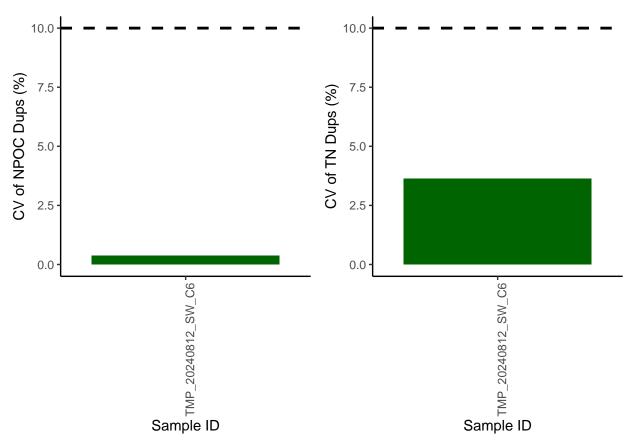
## [1] 0.3019643

## nitrogen blanks:

## [1] 0.05335857

#### Assess Duplicates - if there are any

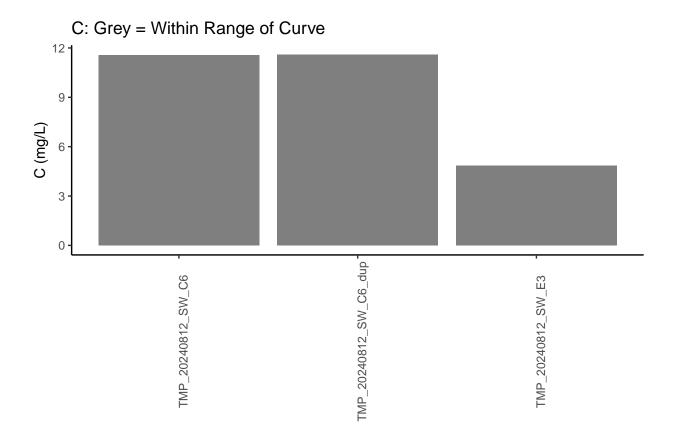
```
## Assess Duplicates
## # A tibble: 1 x 3
##
     sample_name
                        npoc_raw_dup tdn_raw_dup
     <chr>>
                               <dbl>
                                            <dbl>
## 1 TMP_20240812_SW_C6
                                11.6
                                            2.17
            sample_name npoc_raw tdn_raw
                                                 run_datetime npoc_flag tdn_flag
##
                                   2.097 9/5/2024 9:35:07 PM
## 1 TMP_20240812_SW_C6
                           11.55
    npoc_raw_dup tdn_raw_dup
##
## 1
                        2.171
            11.59
##
            sample_name npoc_raw tdn_raw
                                                 run_datetime npoc_flag tdn_flag
## 1 TMP_20240812_SW_C6
                           11.55
                                  2.097 9/5/2024 9:35:07 PM
##
     npoc_raw_dup tdn_raw_dup npoc_dups_cv npoc_dups_cv_flag tdn_dups_cv
## 1
            11.59
                        2.171
                                 0.3662456
                                                                 3.633469
##
     tdn_dups_cv_flag
## 1
## Warning: Using 'size' aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use 'linewidth' instead.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.
```

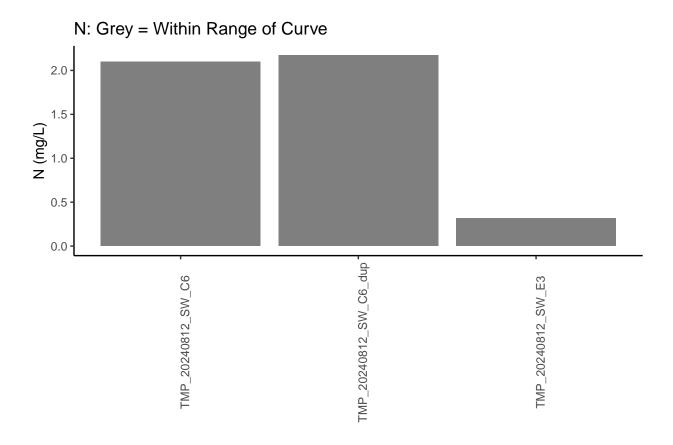


- ## [1] ">60% of Carbon Duplicates have a CV <10%"
- ## [1] ">60% of Nitrogen Duplicates have a CV <10%"

## Sample Flagging

## Sample Flagging



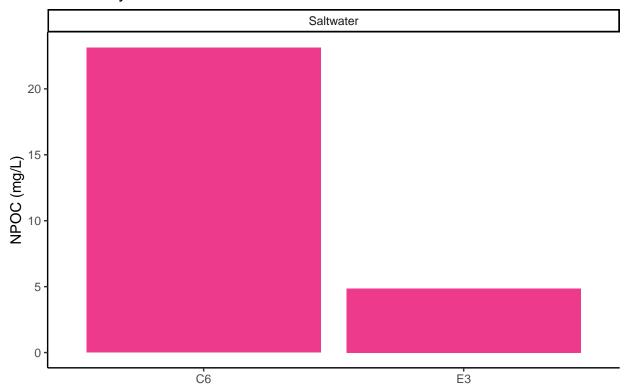


#### Visualize Data by Plot

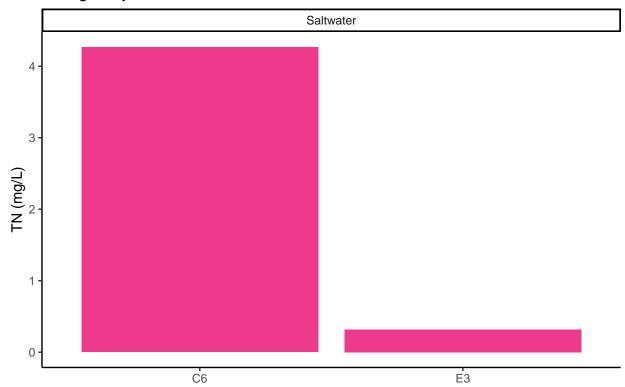
```
## Visualize Data
```

```
## Warning in rbind(c("TMP", "20240812", "SW", "C6"), c("TMP", "20240812", :
## number of columns of result is not a multiple of vector length (arg 1)
                  Date Plot Grid_Square Extra
##
     Site_Code
## 1
           TMP 20240812
                         SW
## 2
           TMP 20240812
                         SW
                                     C6
                                          dup
## 3
           TMP 20240812
                         SW
                                     E3
                                          TMP
    Site_Code
                  Date Plot Grid_Square Extra
                                                         sample_name npoc_raw
## 1
           TMP 20240812
                         SW
                                     C6
                                          TMP
                                                  TMP_20240812_SW_C6
                                                                      11.550
## 2
           TMP 20240812
                         SW
                                     C6
                                          dup TMP_20240812_SW_C6_dup
                                                                       11.590
## 3
          TMP 20240812 SW
                                     E3
                                          TMP
                                                   TMP_20240812_SW_E3
                                                                        4.861
    tdn_raw
                    run_datetime npoc_flag tdn_flag
## 1 2.0970 9/5/2024 9:35:07 PM
## 2 2.1710 9/5/2024 10:07:22 PM
## 3 0.3165 9/5/2024 10:38:39 PM
```

### Carbon by Plot



# Nitrogen by Plot



## Convert data from mg/L to uMoles/L

#### Add in/check metadata

#### **Export Processed Data**

## Export Processed Data

```
## # A tibble: 2 x 21
     Project plot grid Depth_cm sample_type Vial_ID date npoc_mgL npoc_uM
     <chr>
             <chr> <chr>
                            <dbl> <chr>
                                               <chr>
                                                                <dbl>
                                                                        <dbl>
##
                                                       <chr>>
## 1 <NA>
             <NA> <NA>
                               15 <NA>
                                               <NA>
                                                       <NA>
                                                                11.6
                                                                          963.
## 2 <NA>
                                               <NA>
                                                                          405.
             <NA> <NA>
                               15 <NA>
                                                       <NA>
                                                                 4.86
## # i 12 more variables: npoc_flag <chr>, tdn_mgL <dbl>, tdn_uM <dbl>,
       tdn_flag <chr>, Analysis_runtime <chr>, Run_notes <chr>,
       Evacuation_date_YYYMMDD <dbl>, Collection_Date_YYYYMMDD <dbl>,
## #
       Collection_Start_Time_24hrs <dbl>, Collection_End_Time_24hrs <dbl>,
## #
       EST_EDT <chr>, Volume_mL <dbl>
```

#end