

# Synoptic\_CB\_Nutrients\_2023\_AnalysisTemplate

July 2023

2025-06-25

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##Run Information

```
cat("Run Information: Input by User") #lets you know what section you're in
```

## Run Information: Input by User

```
#set the run date & user name
run_date <- "20240114"
sample_year <- 2023
sample_month <- 07
user <- "Stephanie Wilson"
```

```
#identify the files you want to read in
```

```
#read in as a list to accomodate ultiple runs in a month
```

```
NOx_files <- c("Raw Data/SEAL_COMPASS_Synoptic_NOx_July2023_1.csv",
              "Raw Data/SEAL_COMPASS_Synoptic_NOx_July2023_2.csv",
              "Raw Data/SEAL_COMPASS_Synoptic_NOx_July2023_3.csv")
NH3_PO4_files <- c("Raw Data/SEAL_COMPASS_Synoptic_NH3_PO4_July2023_1.csv",
                  "Raw Data/SEAL_COMPASS_Synoptic_NH3_PO4_July2023_2.csv",
                  "Raw Data/SEAL_COMPASS_Synoptic_NH3_PO4_July2023_3.csv")
```

```
# Define the file path for QAQC log file - NO Need to change just check year
```

```
file_path <- "Raw Data/SEAL_COMPASS_Synoptic_QAQC_Log_2023.csv"
final_path <- "Processed Data/COMPASS_Synoptic_Nutrients_202307.csv"
```

```
#record any notes about the run or anything other info here:
```

```
run_notes <- "<60% of NOx blaks are lower 25% quartile of samples - REASSESS
Duplicate CVs out of range most likely due to low concentrations making small values high percentages"
```

```
#Set up file path for metadata
```

```
#downloaded metadata csv - downloaded from Google drive as csv for this year
```

```
#https://docs.google.com/spreadsheets/d/1HCAN0_q6y17x0RUXVzID09hVal-RfwWc/edit?usp=sharing&ouid=10899
Raw_Metadata = "Raw Data/COMPASS_SynopticCB_PW_SampleLog_2023.csv"
```

##Setup

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

## 0.1 Import Data & Clean

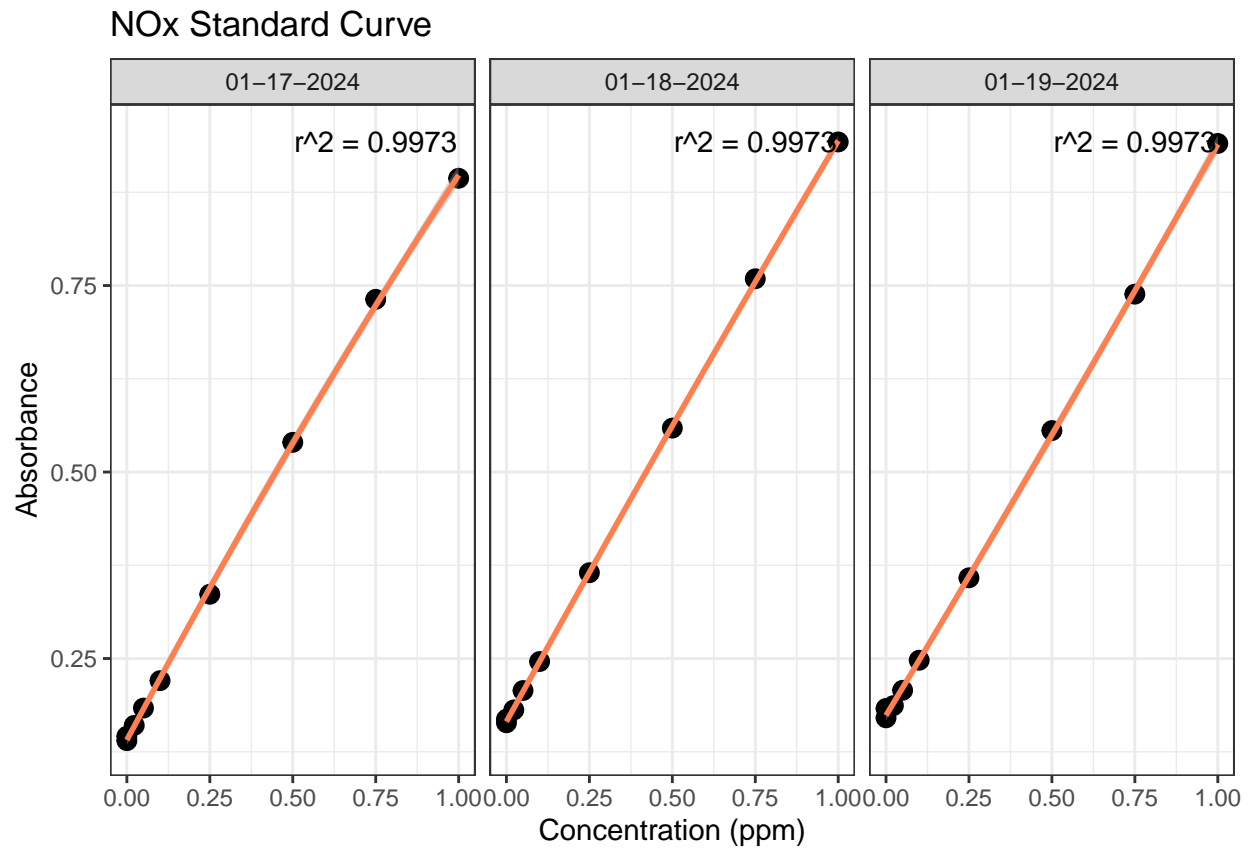
## 0.2 Assessing standard Curves

```
#Pull out standards data
```

```
## Assess Standard Curves
```

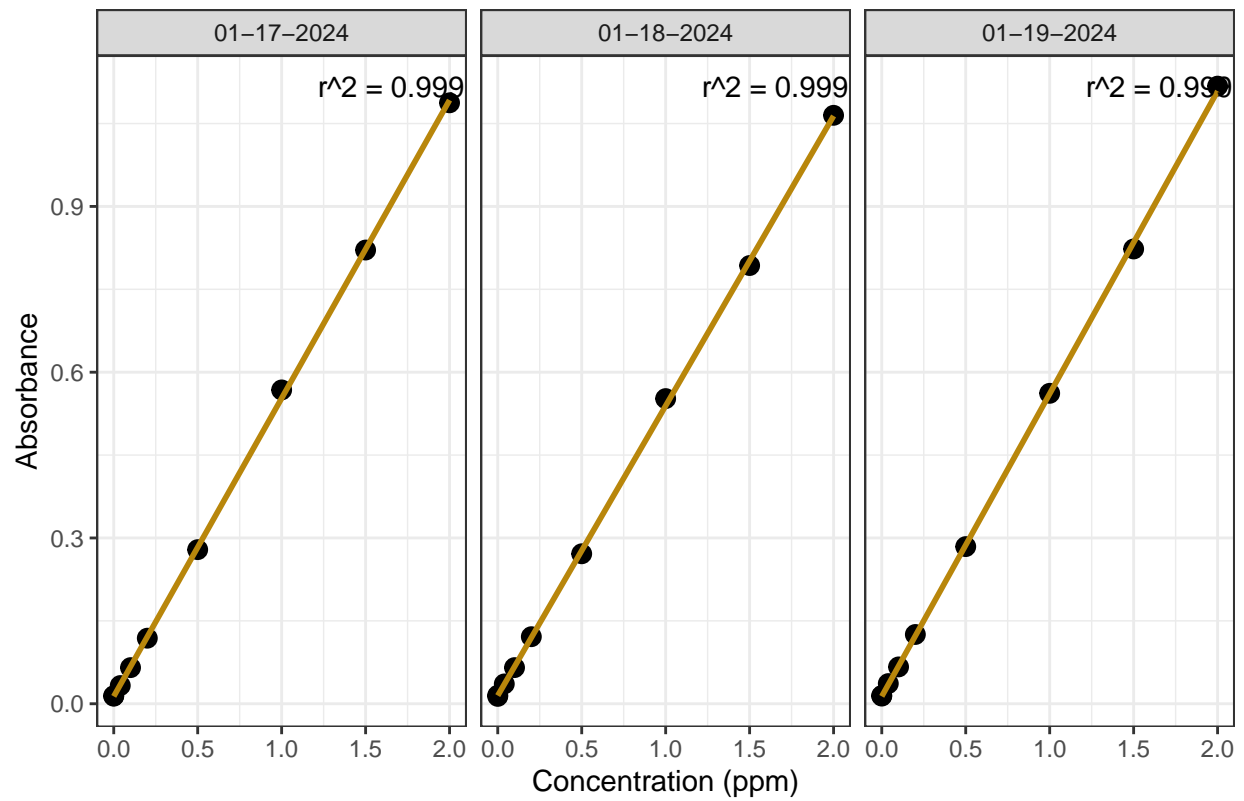
```
#Plot standards data
```

```
## Assess Standard Curves
```



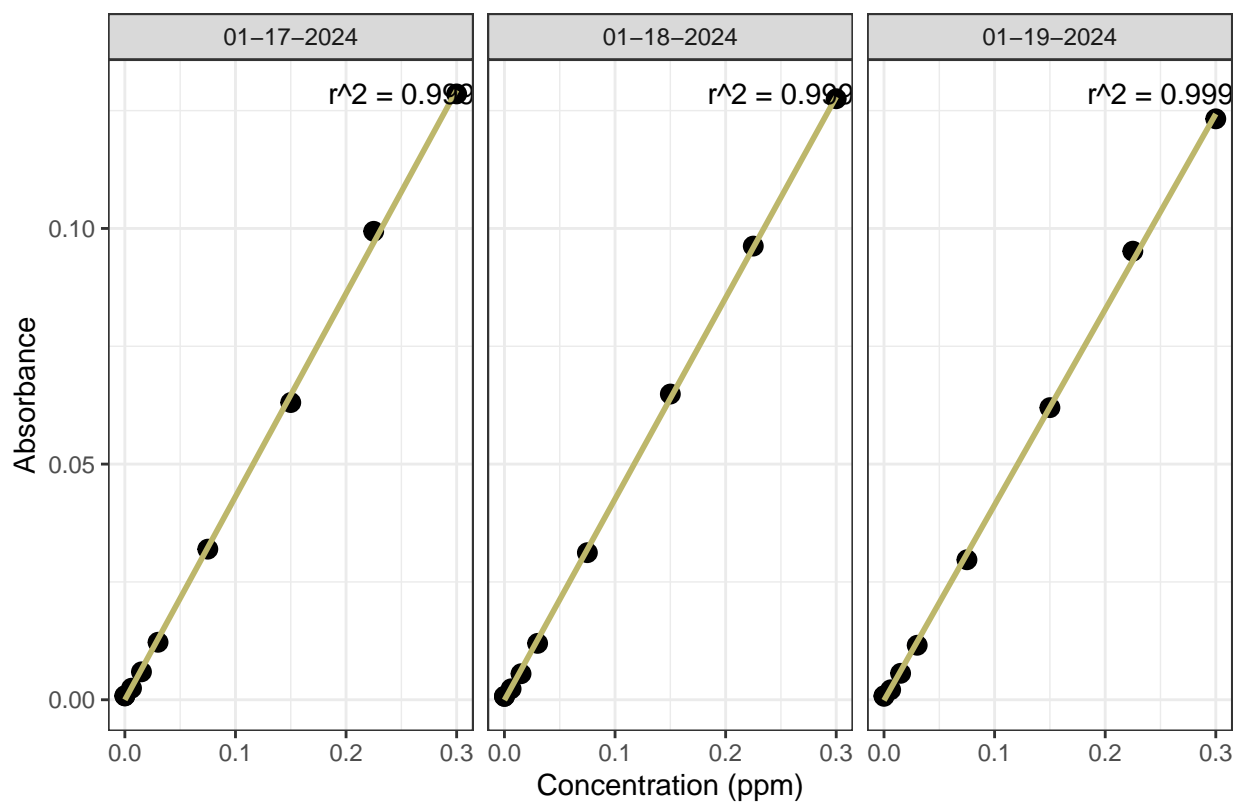
```
## 'geom_smooth()' using formula = 'y ~ x'
```

## NH3 Standard Curve



```
## 'geom_smooth()' using formula = 'y ~ x'
```

## PO4 Standard Curve



```
## [1] "NOx Curve r2 GOOD - PROCEED"
```

```
## [1] "NH3 Curve r2 GOOD - PROCEED"
```

```
## [1] "PO4 Curve r2 GOOD - PROCEED"
```

```
## [1] "QAQC log file exists and has been read into the code."
```

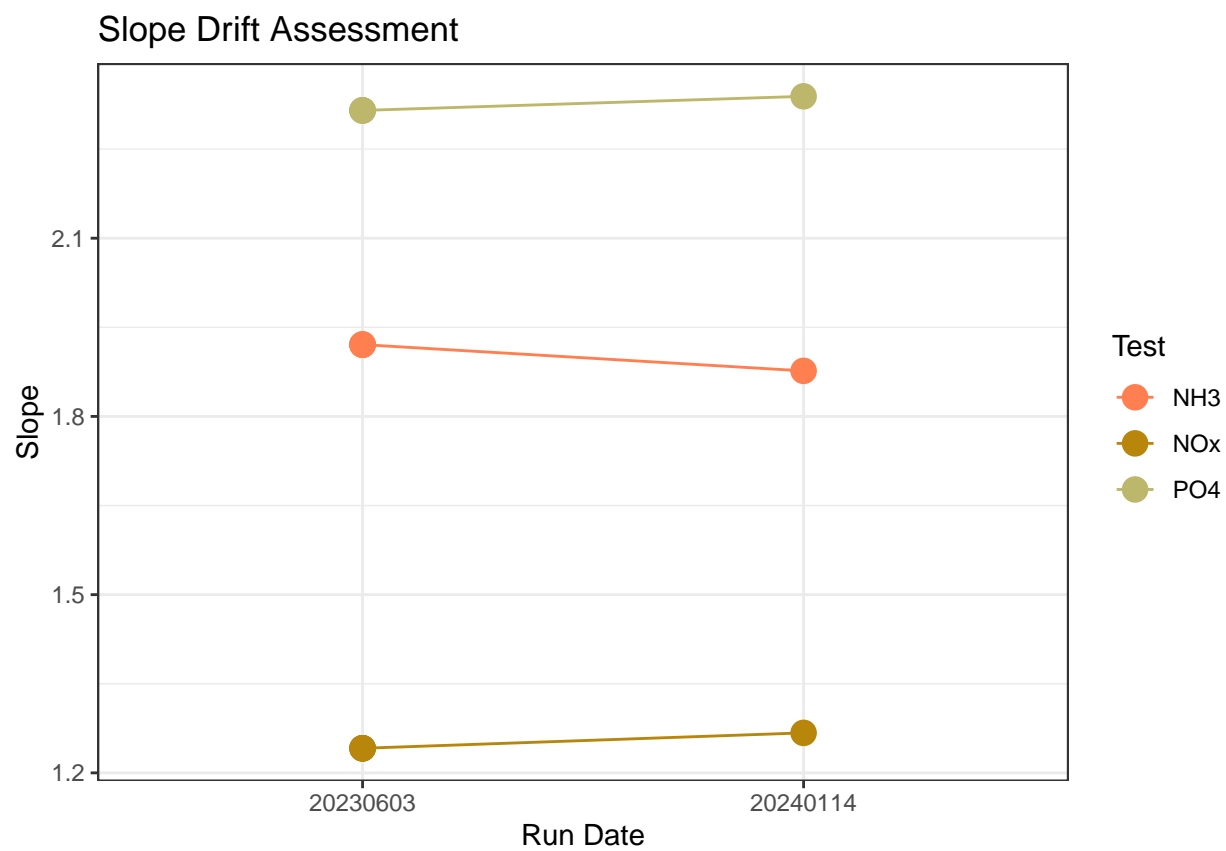


Table 1: Average Slope by Analyte

Test	avg_slope
NH3	1.912
NOx	1.247
PO4	2.320

### 0.3 Dilution Corrections - ensure the latest dilution is kept

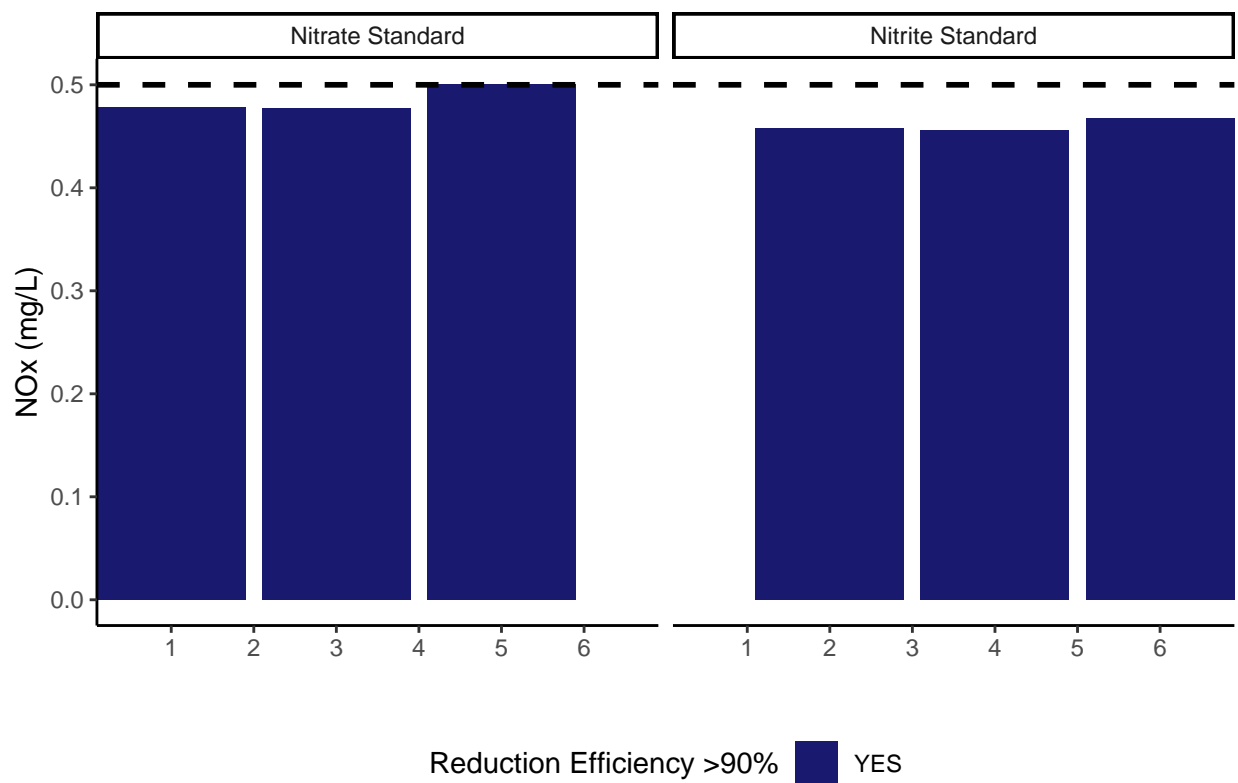
```
## Dilution Corrections
```

```
## Duplicated samples: MSM_202307_UP_LysC_20cm, MSM_202307_TR_LysA_20cm, MSM_202307_TR_LysB_10cm, MSM_202307_TR_LysC_10cm
```

```
## Dilution Present, Need to Correct
```

```
#Check NOx Reduction Efficiency
```

```
## Assess Reduction Efficiency
```



```
## [1] "Mean NOx Reduction Efficiency <95% - REASSESS"
```

```
## [1] 94.57947
```

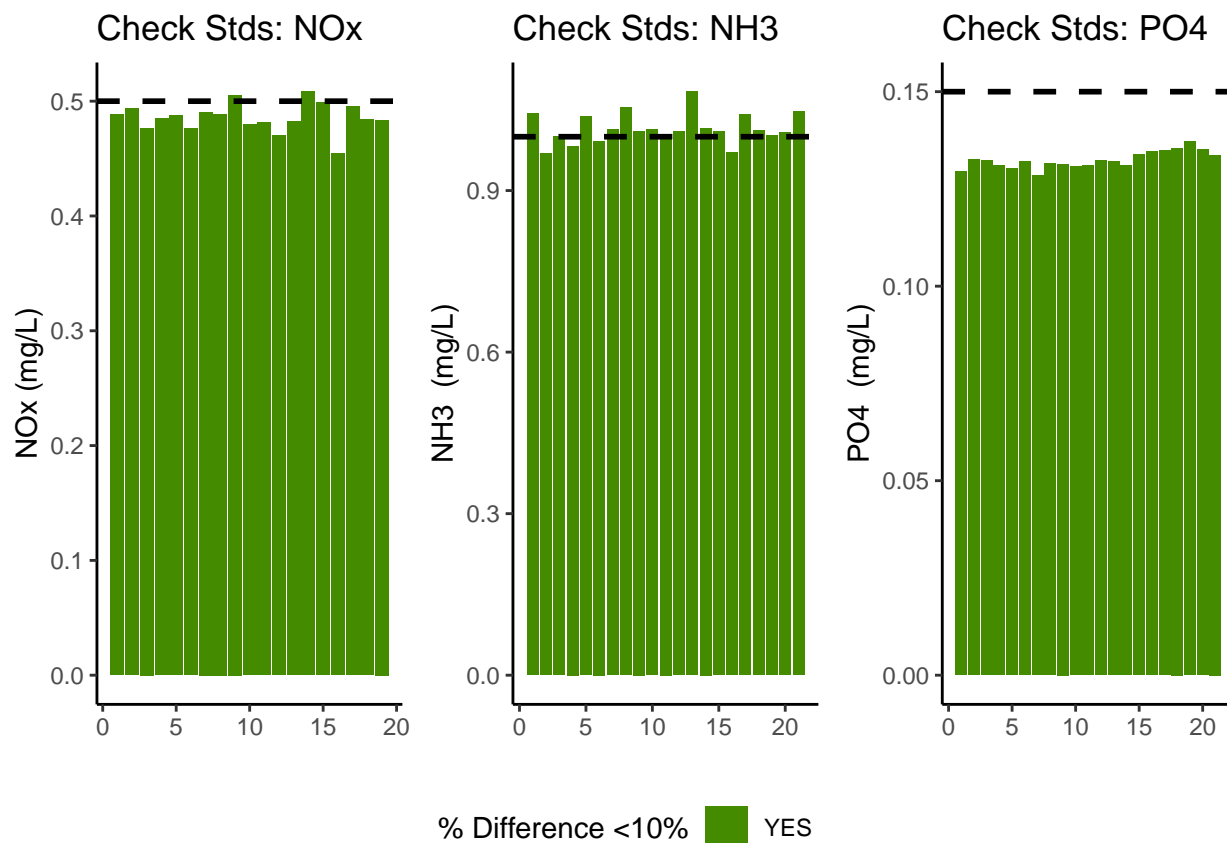
## 0.4 Analyze the Check Standards

```
## Analyze Check Standards
```

```
## [1] "NOx Check Standard RSD within Range - PROCEED"
```

```
## [1] "NH3 Check Standard RSD within Range - PROCEED"
```

```
## [1] "PO4 Check Standard RSD within Range - PROCEED"
```



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

```
## [1] ">60% of NH3 Check Standards are within range of expected concentration - PROCEED"
```

```
## [1] ">60% of PO4 Check Standards are within range of expected concentration - PROCEED"
```



## 0.5 Analyze Blanks

```
## Assess Blanks
```

```
## [1] "<60% of NOx blaks are lower 25% quartile of samples - REASSESS"
```

```
## [1] ">60% of NH3 Blank concentrations are lower than the lower 25% quartile of samples - PROCEED"
```

```
## [1] ">60% of PO4 Blank concentrations are lower than the lower 25% quartile of samples- PROCEED"
```

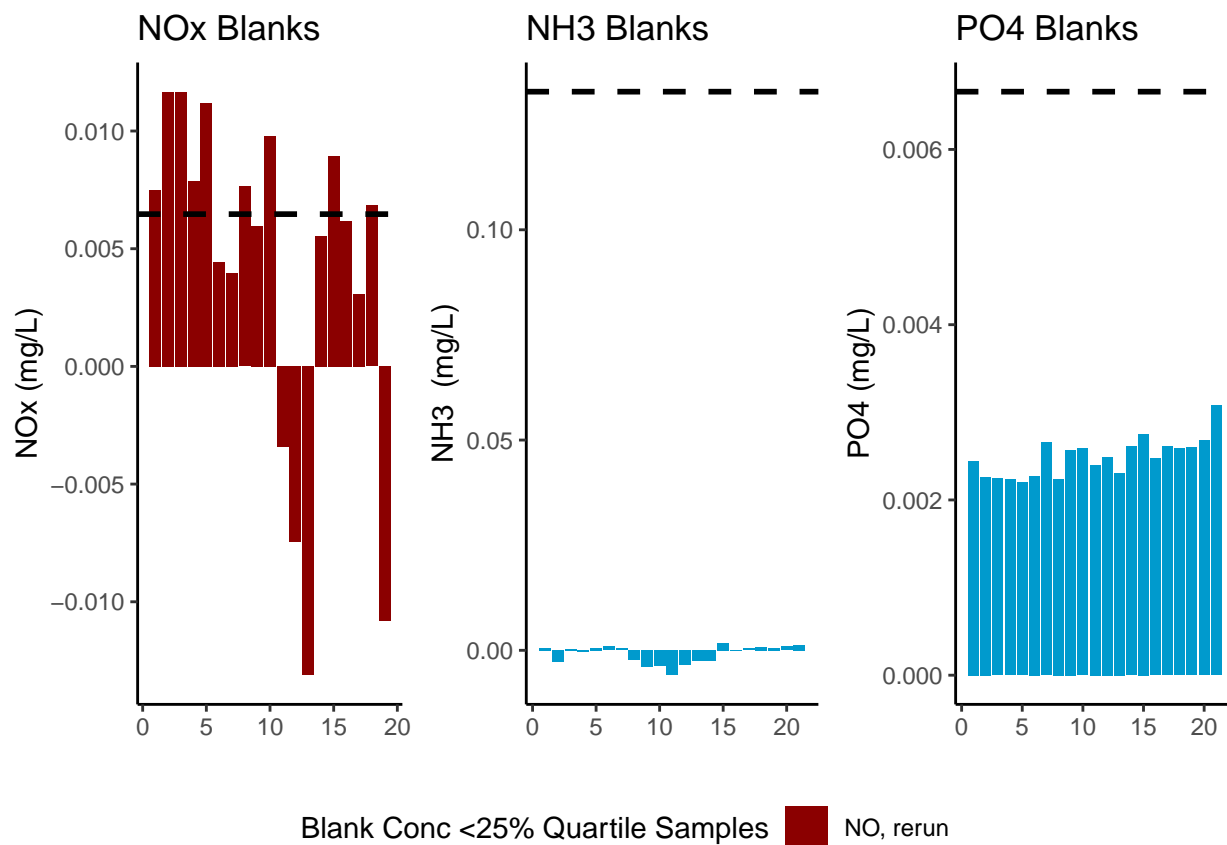


Table 2: Mean Concentration of Blanks

Test	Blank_Mean_Conc
NOx	0.0041
NH3	-0.0009
PO4	0.0025

## 0.6 Analyze Duplicates

```
## Analyze Duplicates
```

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

```
## [1] ">60% of NH3 Duplicates have a CV <10% - PROCEED"
```

```
## [1] "<60% of PO4 Duplicates have a CV <10% - REASSESS"
```

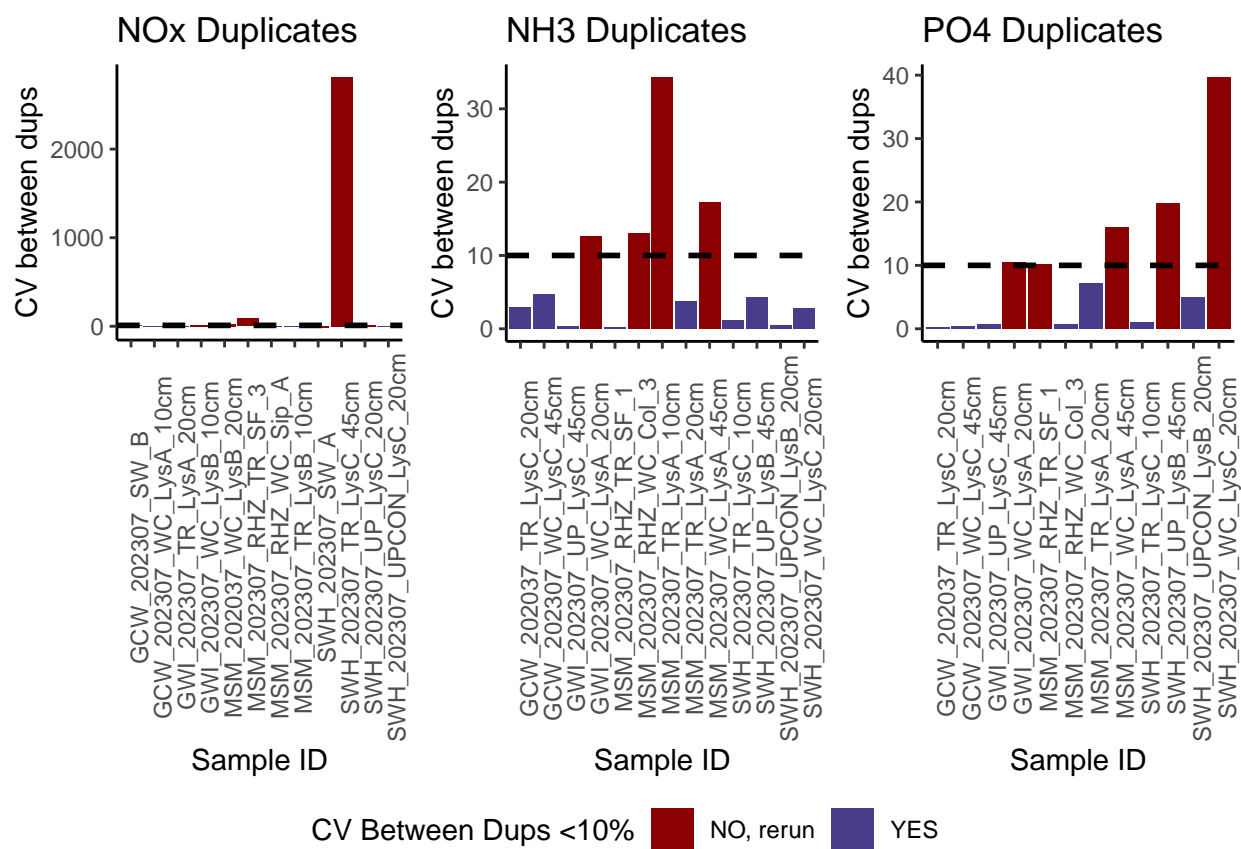
```
## Warning: Using 'size' aesthetic for lines was deprecated in ggplot2 3.4.0.
```

```
## 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.
```

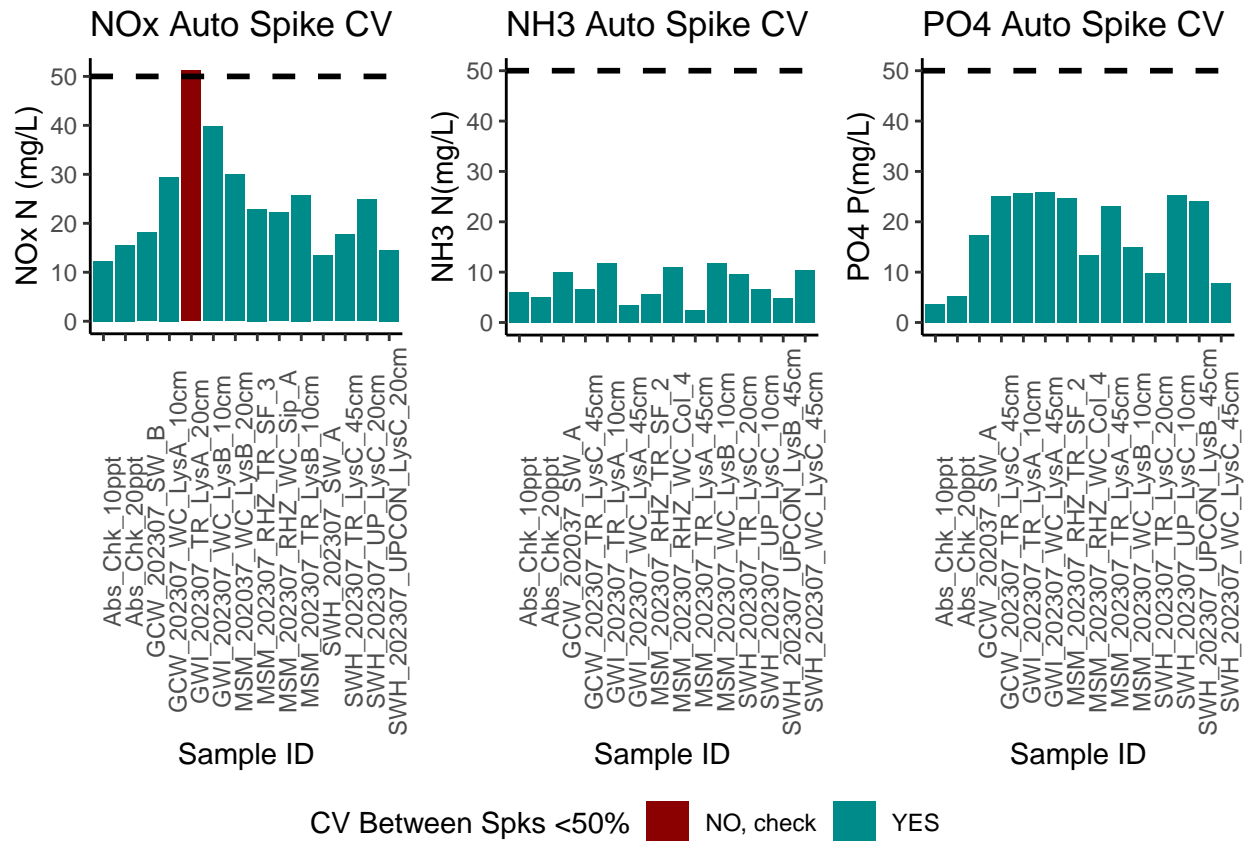


## 0.7 Spikes

## [1] ">60% of Spikes have a CV <50% - PROCEED"

## [1] ">60% of Spikes have a CV <50% - PROCEED"

## [1] ">60% of Spikes have a CV <50% - PROCEED"



## 0.8 Matrix Effects

```
## [1] "NO NOx Matrix Effect, PROCEED"
```

```
## [1] "NO NH3 Matrix Effect, PROCEED"
```

```
## [1] "NO PO4 Matrix Effect, PROCEED"
```

## 0.9 Unit Converted Data Column Added (mg/L to uM )

## 0.10 Sample Flagging - Within range of standard curve

```
## Sample Flagging
```

## 0.11 Pull out sample id information

```
## Sample Processing
```

```
## Warning: Expected 5 pieces. Missing pieces filled with 'NA' in 36 rows [19, 20, 21, 44,
## 45, 46, 83, 84, 85, 110, 111, 112, 131, 132, 133, 167, 168, 169, 199, 200,
## ...].
```

```
## Warning: There was 1 warning in 'mutate()'.
## i In argument: 'Samp_Time = ym(Samp_Time)'.
## Caused by warning:
## ! 9 failed to parse.
```

## 0.12 Pulling Rhizon Samples

## 0.13 Check to see if samples run match metadata & merge info

```
## Check Sample IDs with Metadata
```

```
## Some sample IDs are missing from metadata.
```

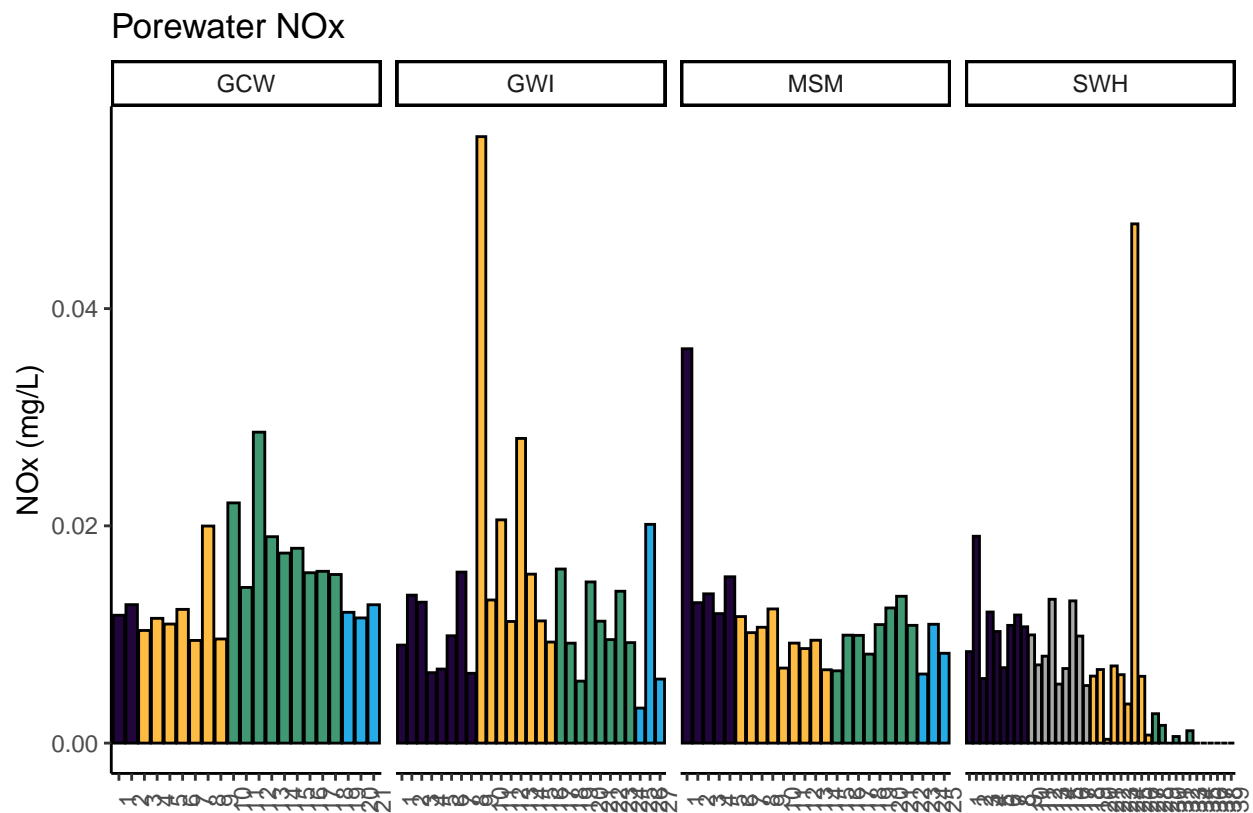
```
## [1] "GCW_202307_UP_LysA_20cm" "GCW_202307_UP_LysC_20cm"
## [3] "GCW_202307_TR_LysA_20cm" "GCW_202307_TR_LysA_45cm"
## [5] "GCW_202307_TR_LysB_45cm" "GCW_202307_TR_LysC_10cm"
## [7] "GCW_202307_TR_LysC_20cm" "GCW_202307_TR_LysC_45cm"
## [9] "GCW_202037_WC_LysB_45cm" "MSM_202037_WC_LysB_20cm"
## [11] "SWH_202307_UPCON_LysA_10cm" "SWH_202307_UPCON_LysA_20cm"
## [13] "SWH_202307_UPCON_LysA_45cm" "SWH_202307_UPCON_LysB_10cm"
## [15] "SWH_202307_UPCON_LysB_20cm" "SWH_202307_UPCON_LysB_45cm"
## [17] "SWH_202307_UPCON_LysC_10cm" "SWH_202307_UPCON_LysC_20cm"
```

```
## [19] "SWH_202307_UPCON_LysC_45cm" "SWH_202307_WC_LysA_10cm"
## [21] "SWH_202307_WC_LysA_20cm"      "SWH_202307_WC_LysA_45cm"
## [23] "SWH_202307_WC_LysB_10cm"      "SWH_202307_WC_LysB_20cm"
## [25] "SWH_202307_WC_LysB_45cm"      "SWH_202307_WC_LysC_10cm"
## [27] "SWH_202307_WC_LysC_20cm"      "SWH_202307_WC_LysC_45cm"
## [29] "GWI_202307_UP_LysA_10cm"      "GWI_202307_UP_LysB_20cm"
## [31] "GCW_202037_TR_LysC_20cm"      "GCW_202037_SW_A"
## [33] "MSM_202037_WC_LysC_10cm"
```

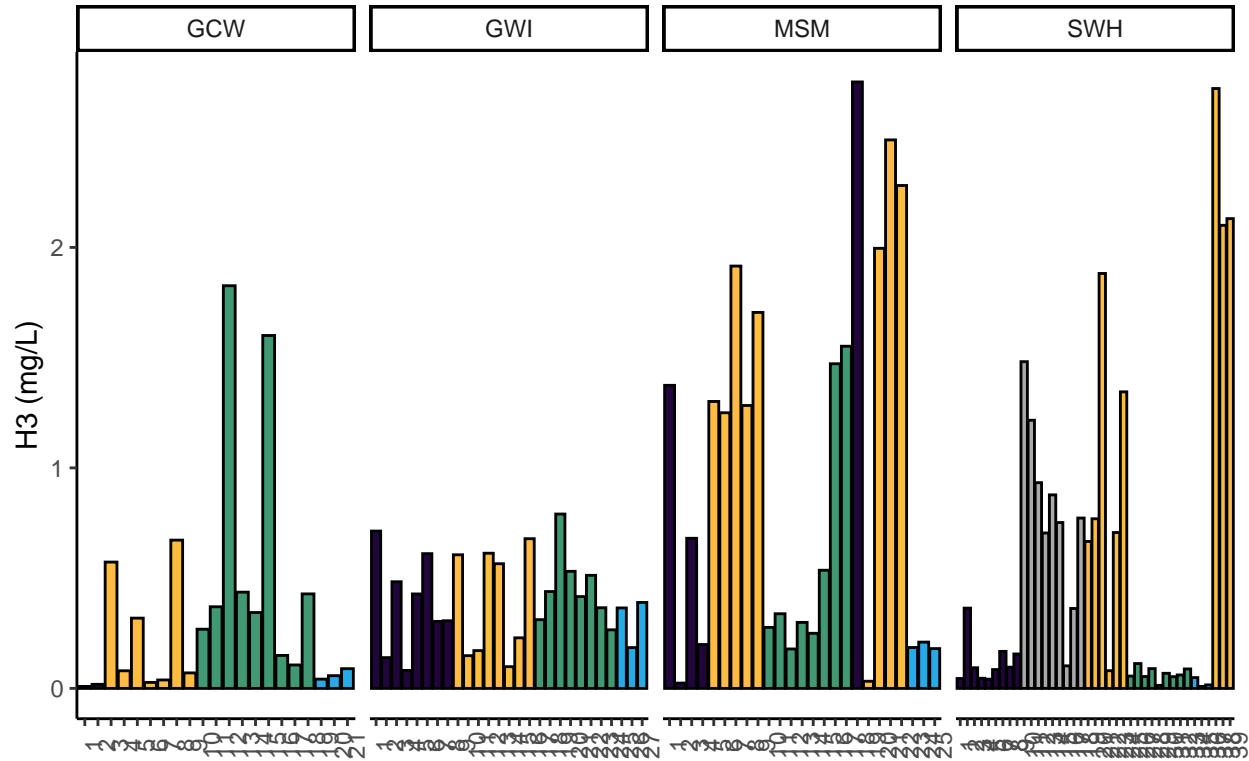
```
## Warning: Expected 5 pieces. Missing pieces filled with 'NA' in 36 rows [19, 20, 21, 44,
## 45, 46, 83, 84, 85, 110, 111, 112, 131, 132, 133, 167, 168, 169, 199, 200,
## ...].
```

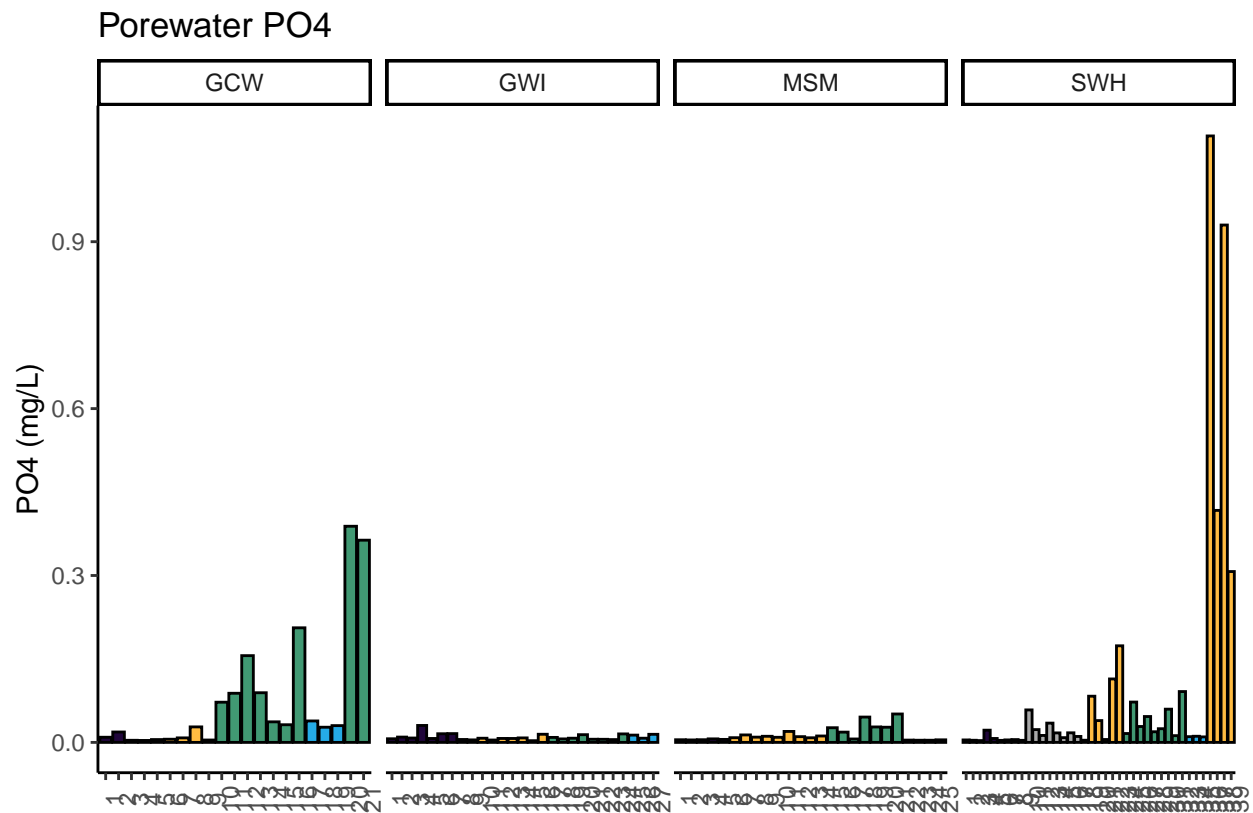
```
## Warning: There was 1 warning in 'mutate()'.
## i In argument: 'Samp_Time = ym(Samp_Time)'.
## Caused by warning:
## ! 9 failed to parse.
```

## ## Visualize Data



Porewater NH3





## 0.15 Export Processed Data

#end