

Synoptic_CB_Nutrients_2023_AnalysisTemplate

Month of Data Being Analyzed

2025-07-03

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##Run Information

```
cat("Run Information: 2023/11 - I. Van Benschoten") #lets you know what section you're in
```

Run Information: 2023/11 - I. Van Benschoten

```
#set the run date & user name
```

```
run_date <- "02/03/24"  
sample_year <- 2023  
sample_month <- "November"  
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_Nov2023_1.csv",  
              "Raw Data/SEAL_COMPASS_Synoptic_NOx_Nov2023_2.csv",  
              "Raw Data/SEAL_COMPASS_Synoptic_NOx_Nov2023_3.csv")  
NH3_PO4_files <- c("Raw Data/SEAL_COMPASS_Synoptic_NH3_PO4_Nov2023_1.csv",  
                  "Raw Data/SEAL_COMPASS_Synoptic_NH3_PO4_Nov2023_2.csv",  
                  "Raw Data/SEAL_COMPASS_Synoptic_NH3_PO4_Nov2023_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_Nov2023.xlsx"
```

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

```
run_notes <- ""
```

```
#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

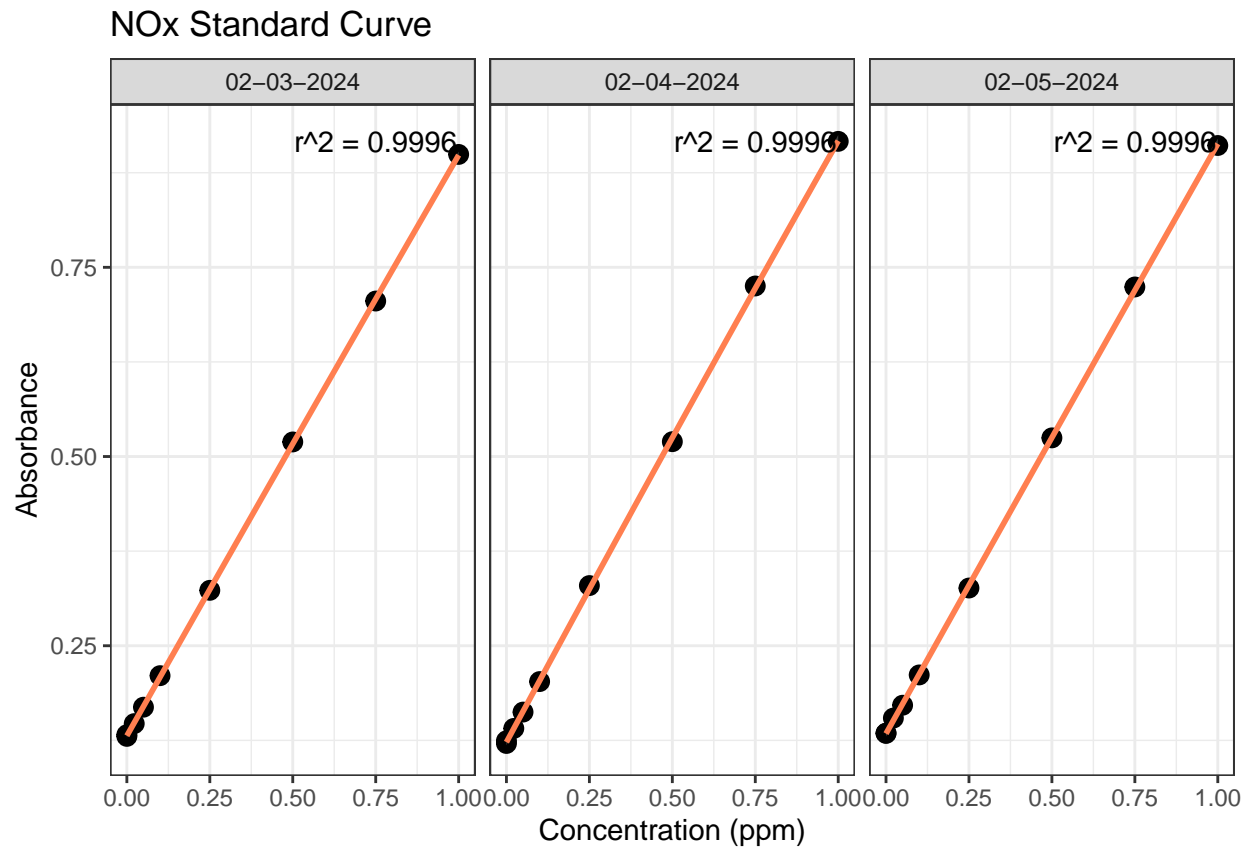
0.2 Assessing standard Curves

```
#Pull out standards data
```

```
## Assess Standard Curves
```

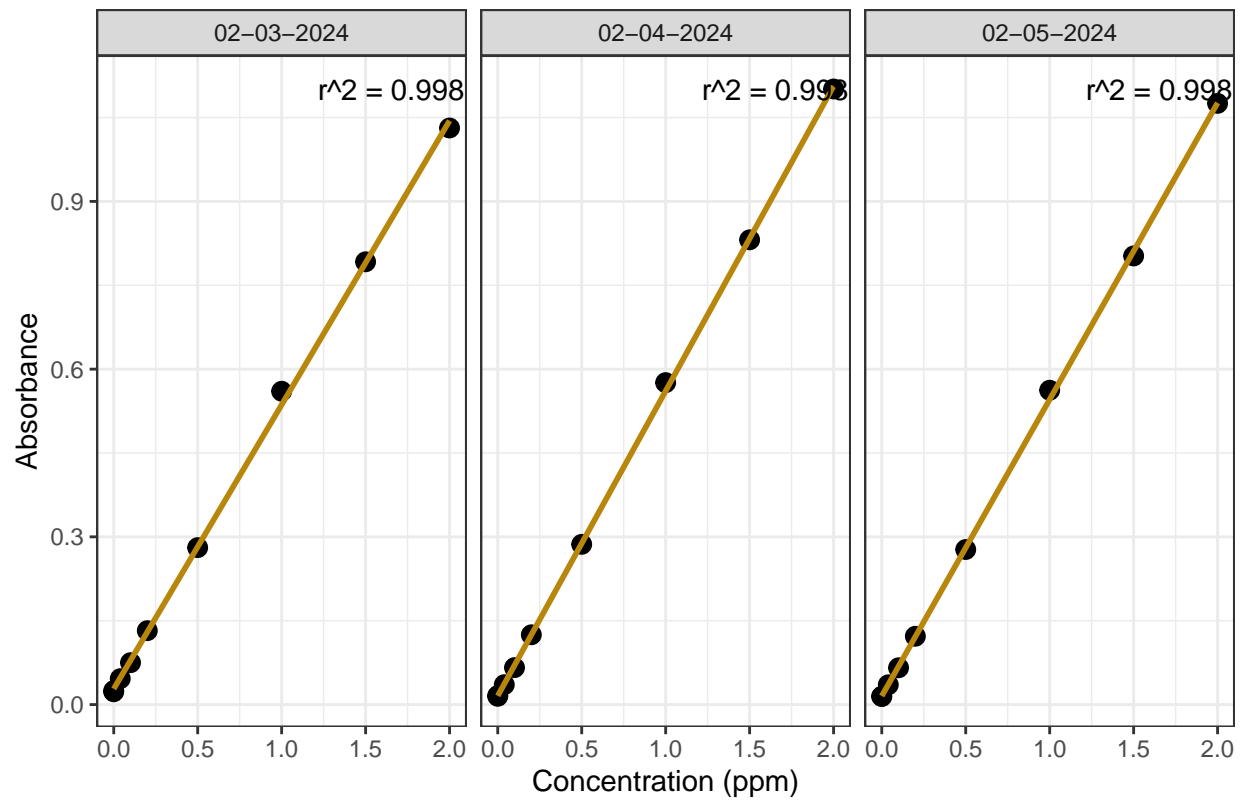
```
#Plot standards data
```

```
## Assess Standard Curves
```



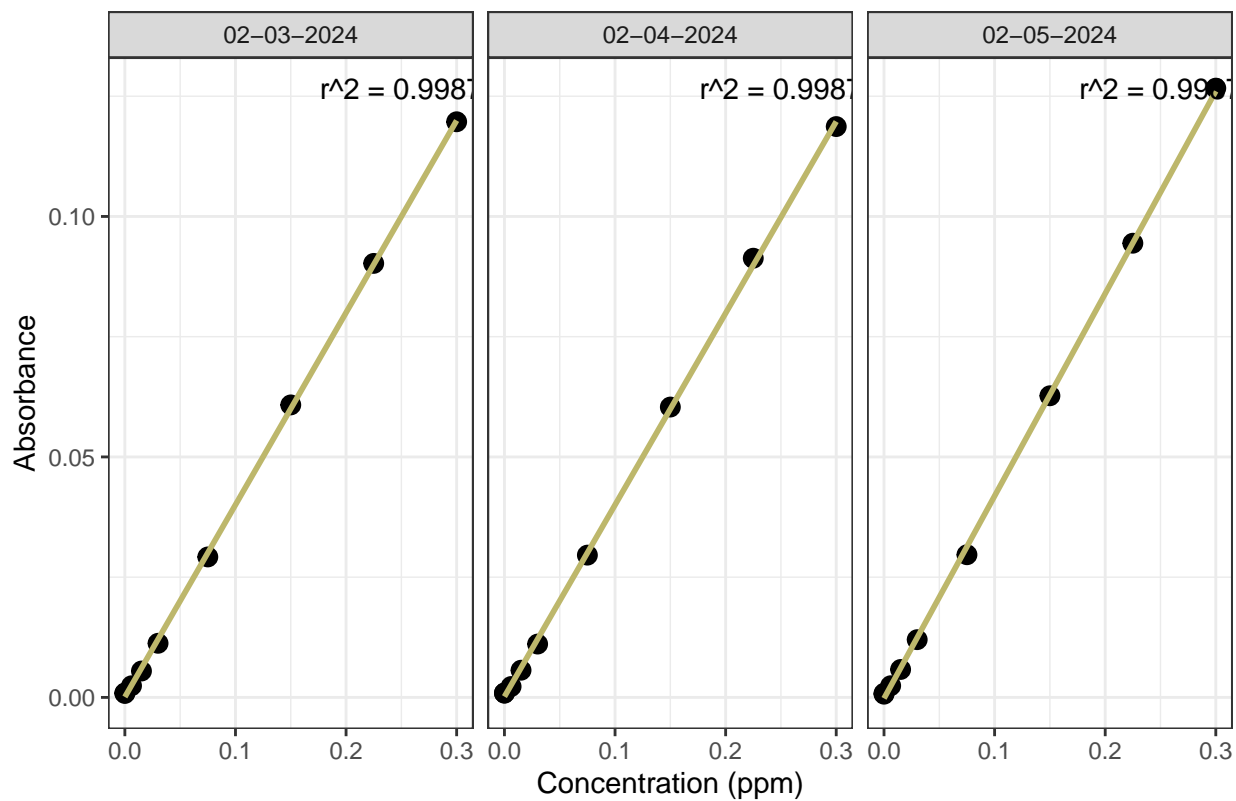
```
## 'geom_smooth()' using formula = 'y ~ x'
```

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."
```

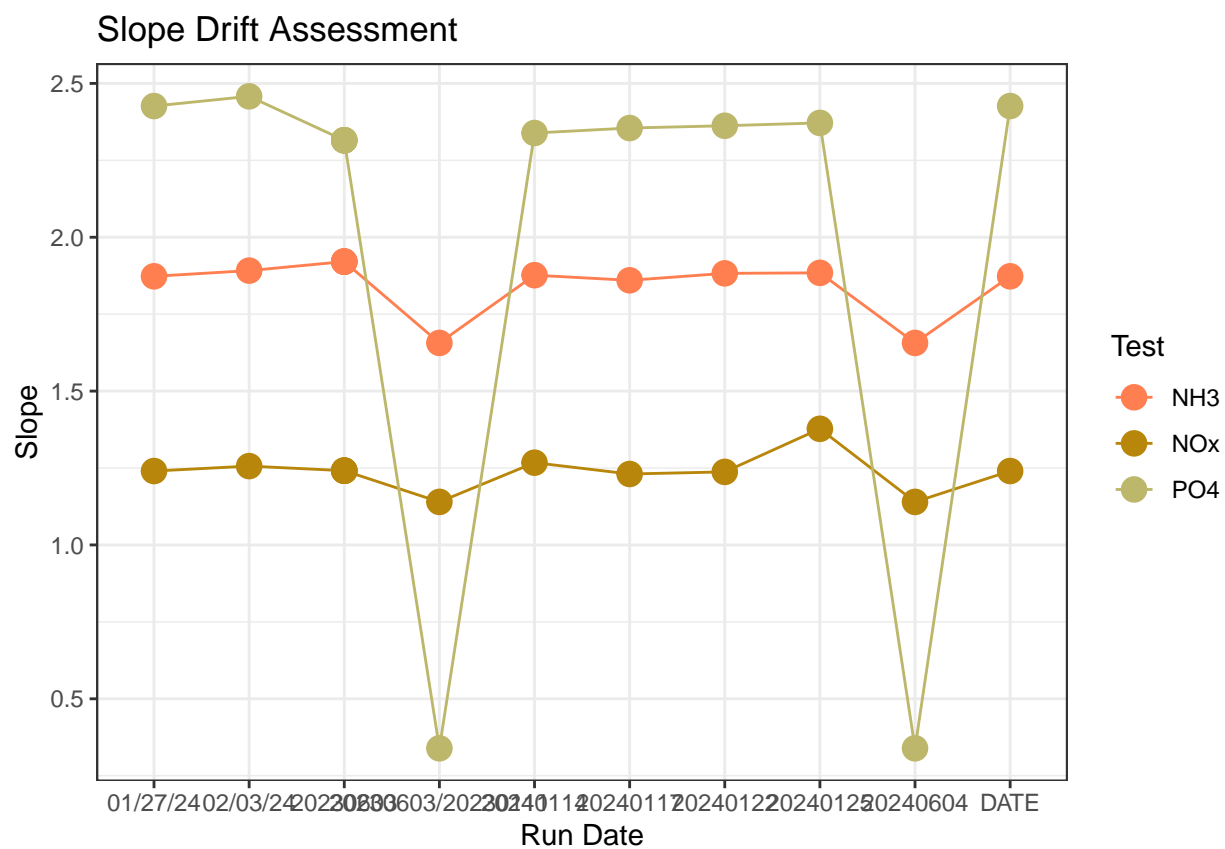


Table 1: Average Slope by Analyte

Test	avg_slope
NH3	1.857
NOx	1.238
PO4	2.052

0.3 Dilution Corrections - ensure the latest dilution is kept

```
## Dilution Corrections
```

```
## Duplicated samples: GCW_202311_WC_LysA_45cm, GCW_202311_WC_LysB_45cm, MSM_202311_TR_LysA_20cm, MSM_202311_TR_LysB_20cm
```

```
## All duplicated samples have valid dilutions. No naming issues detected.
```

0.4 Performance Check

```
## [1] "NOx pe Check has a % Difference <10% - PROCEED"
```

```
## Run mean = 0.7103023
```

```
## Expected = 0.706
```

```
## [1] "NH3 pe Check has a % Difference >10% - REASSESS"
```

```
## Run mean = 1.588525
```

```
## Expected = 0.948
```

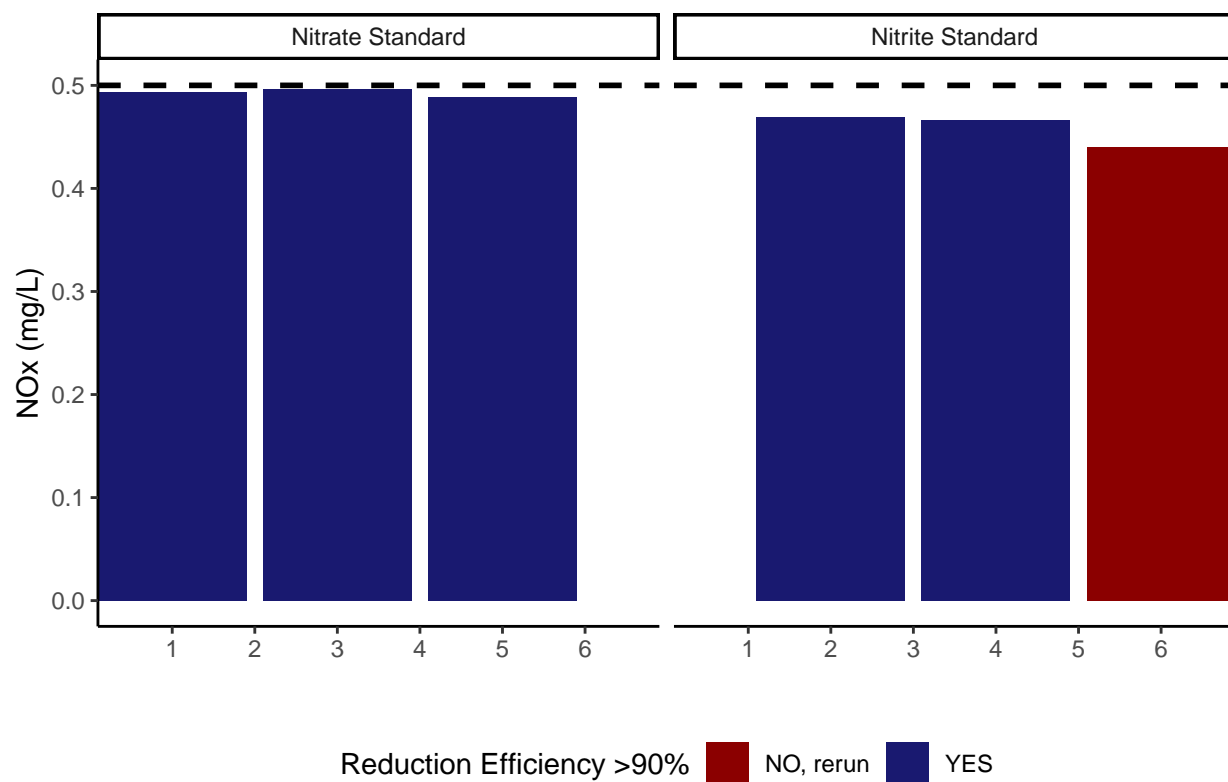
```
## [1] "PO4 pe Check has a % Difference >10% - REASSESS"
```

```
## Run mean = 0.900952
```

```
## Expected = 0.818
```

```
#Check NOx Reduction Efficiency
```

```
## Assess Reduction Efficiency
```



```
## [1] "Mean NOx Reduction Efficiency >95% - PROCEED"
```

```
## [1] 95.15817
```

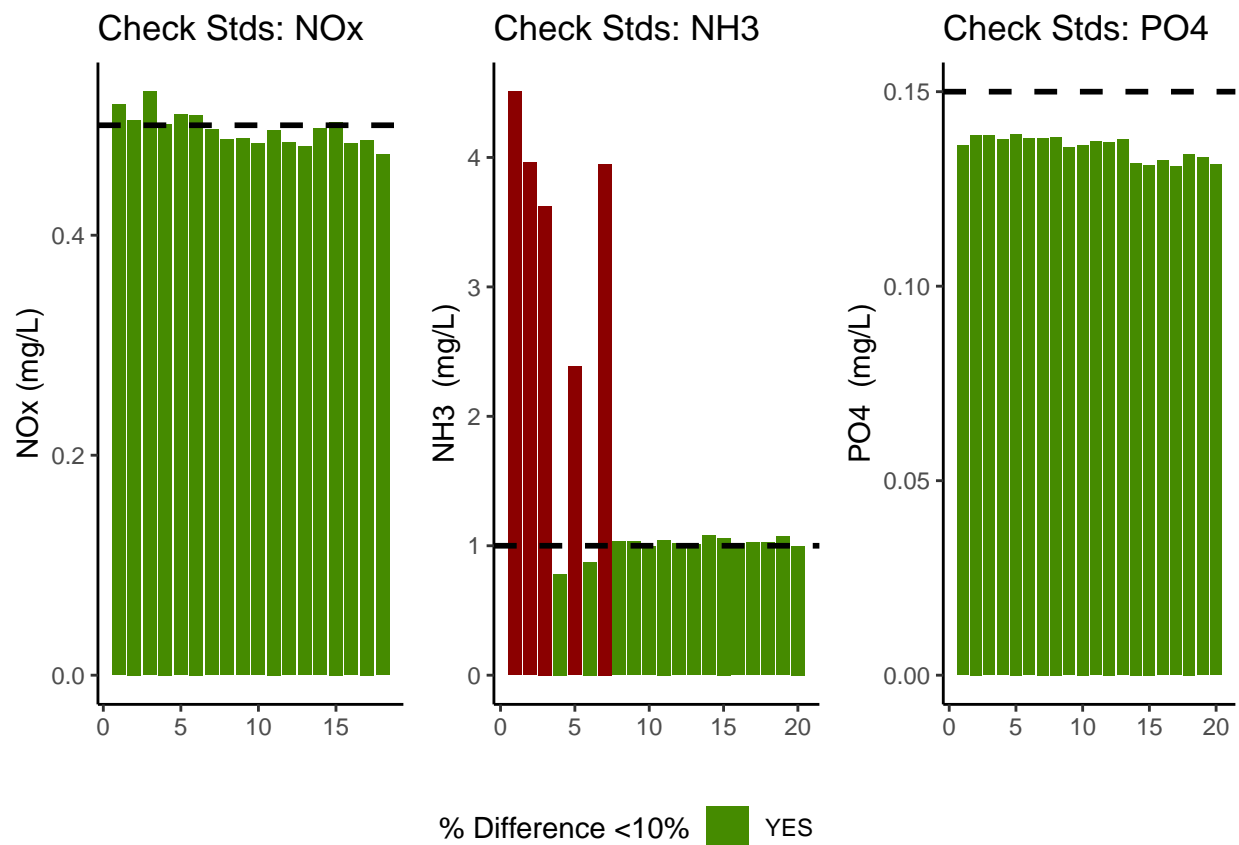

0.5 Analyze the Check Standards

```
## Analyze Check Standards
```

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

```
## [1] "NH3 CHECK STANDARD RSD TOO HIGH - REASSESS"
```

```
## [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"
```

0.6 Analyze Blanks

```
## Assess Blanks
```

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

```
## [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"
```

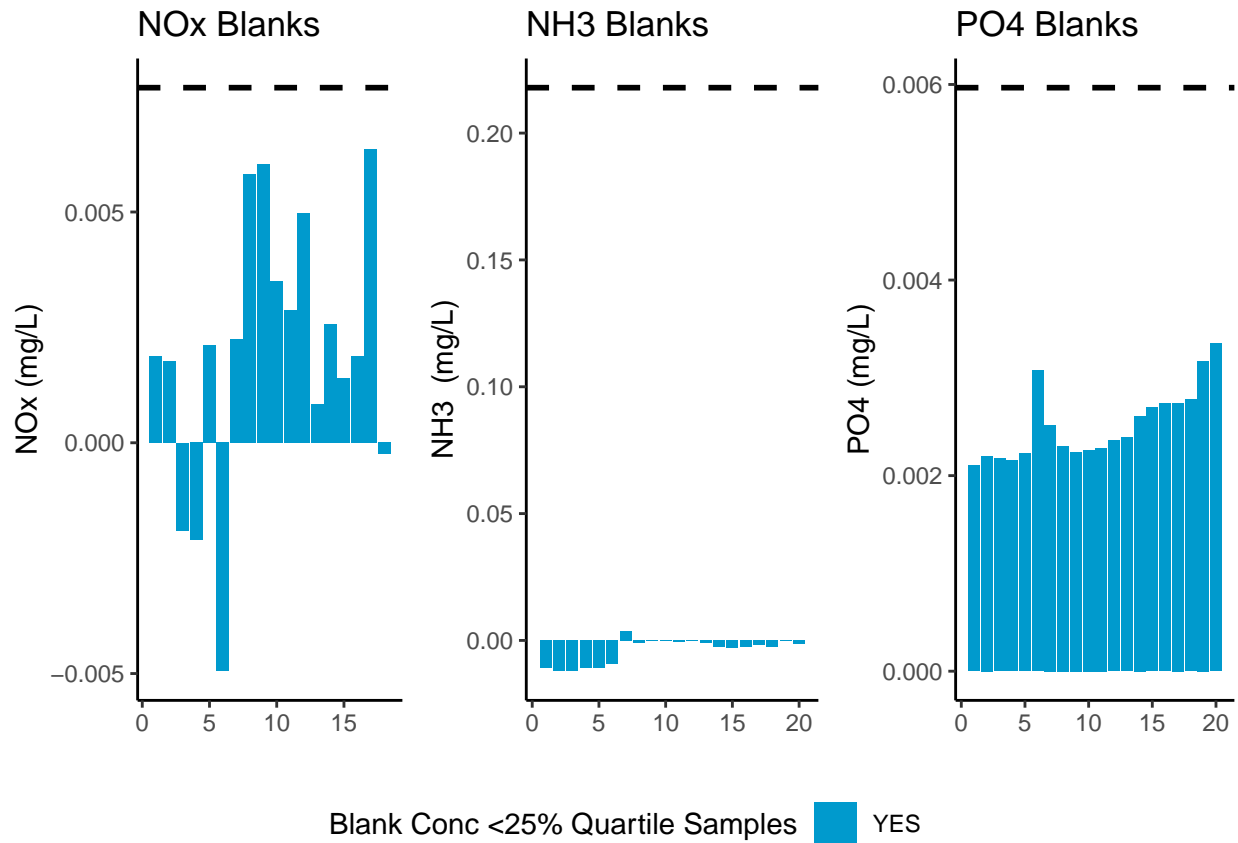


Table 2: Mean Concentration of Blanks

Test	Blank_Mean_Conc
NOx	0.0019
NH3	-0.0040
PO4	0.0025

0.7 Analyze Duplicates

```
## Analyze Duplicates
```

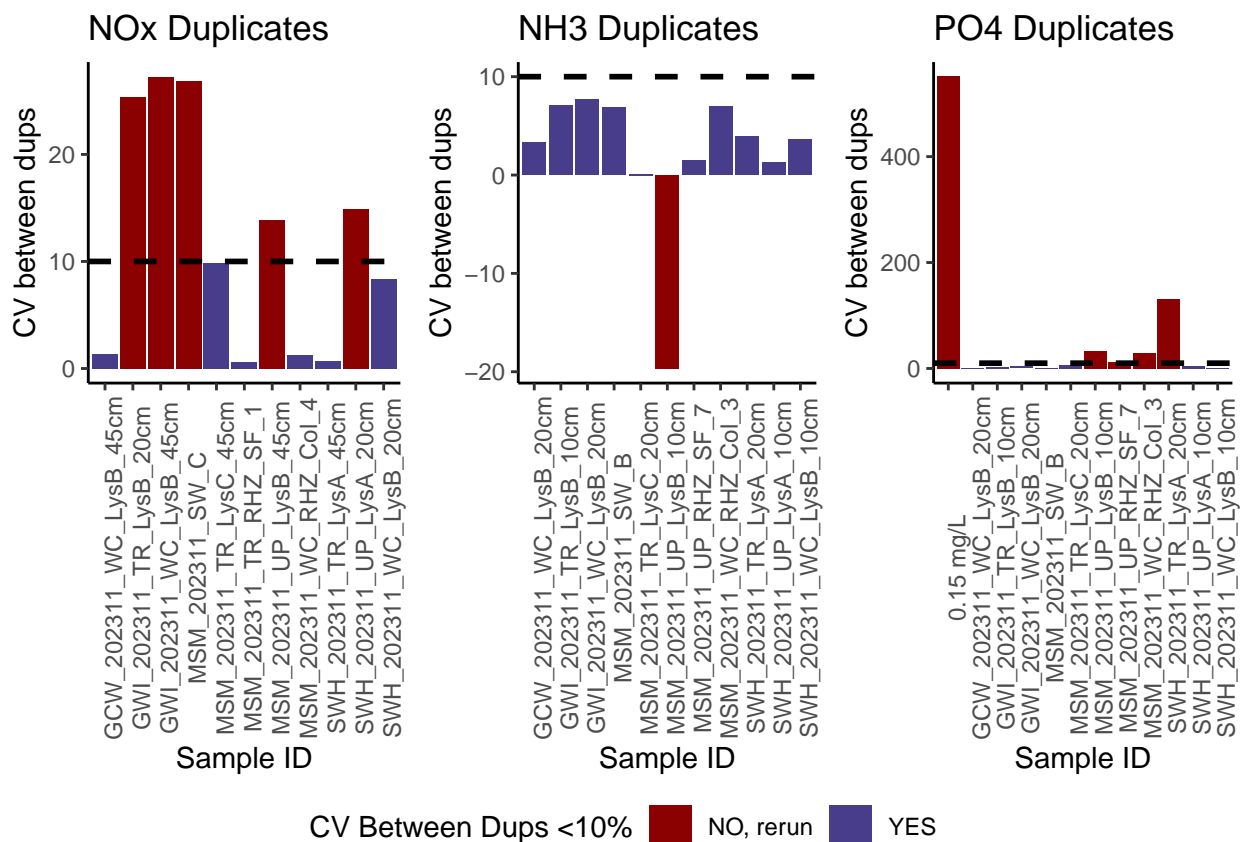
```
## Warning: Returning more (or less) than 1 row per 'summarise()' group was deprecated in
## dplyr 1.1.0.
## i Please use 'reframe()' instead.
## i When switching from 'summarise()' to 'reframe()', remember that 'reframe()'
## always returns an ungrouped data frame and adjust accordingly.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.
```

```
## [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.
```

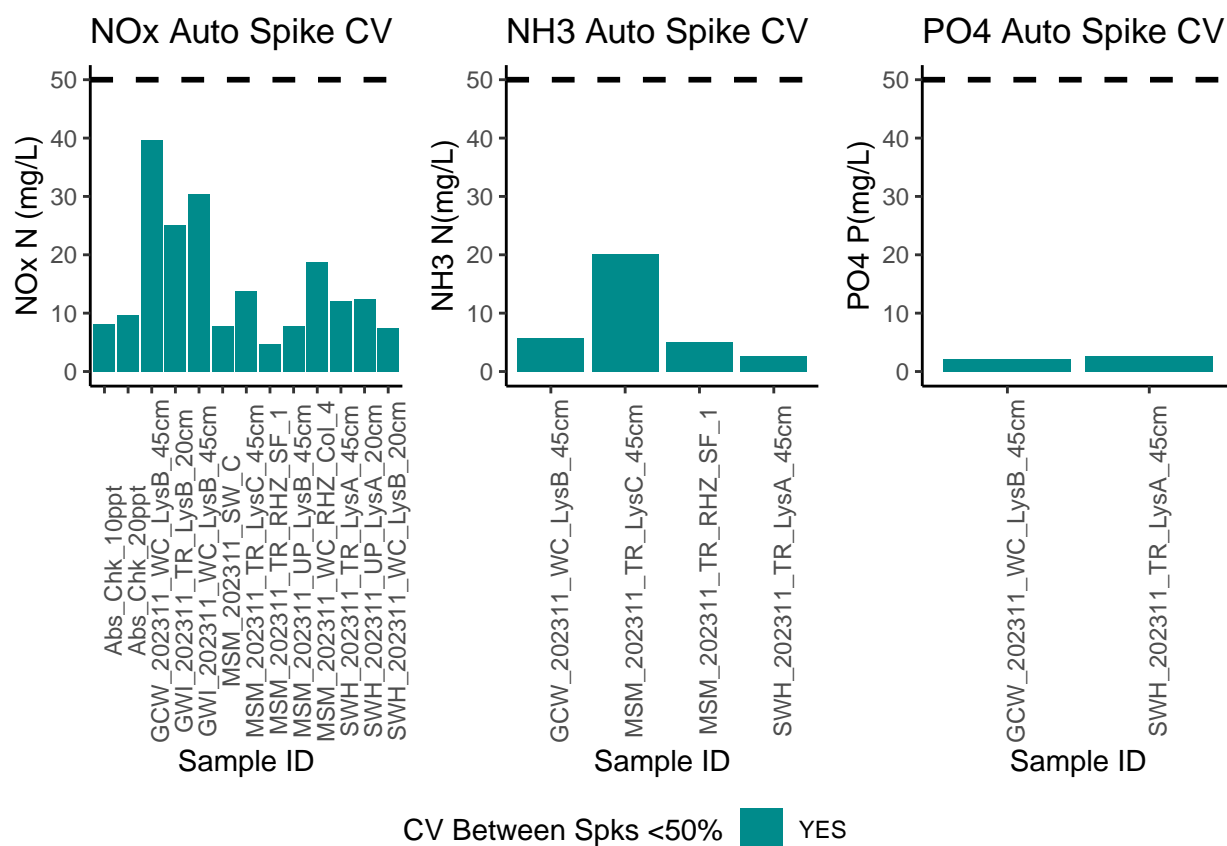


0.8 Spikes

```
## [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"
```



0.9 Matrix Effects

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

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

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

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

0.11 Sample Flagging - Within range of standard curve

```
## Sample Flagging
```

0.12 Pull out sample id information

```
## Sample Processing
```

```
## Warning: Expected 5 pieces. Missing pieces filled with 'NA' in 36 rows [14, 15, 16, 38,  
## 39, 40, 75, 76, 77, 100, 101, 102, 114, 115, 116, 132, 133, 134, 146, 147,  
## ...].
```

0.13 Pulling Rhizon Samples

```
# Filter rhizon and peeper samples  
df_rhizon <- df_all %>%  
  filter(str_detect(Sample_Name, "RHZ"))  
df_peep <- df_all %>%  
  filter(str_detect(Sample_Name, "PPR"))  
  
# Timestamp for backups  
timestamp <- format(Sys.time(), "%Y-%m-%d_%H%M")  
  
# Paths  
folder_path <- file.path("Raw Data", "Rhizon+Peeper")  
dir.create(folder_path, recursive = TRUE, showWarnings = FALSE)  
  
rhizon_main <- file.path(folder_path, "rhizon_data.csv")  
peeper_main <- file.path(folder_path, "peeper_data.csv")  
  
rhizon_backup <- file.path(folder_path, paste0("rhizon_data_", timestamp, ".csv"))  
peeper_backup <- file.path(folder_path, paste0("peeper_data_", timestamp, ".csv"))  
  
# Write timestamped backups  
write.csv(df_rhizon, rhizon_backup, row.names = FALSE)  
write.csv(df_peep, peeper_backup, row.names = FALSE)  
  
# Overwrite the main files with latest data  
write.csv(df_rhizon, rhizon_main, row.names = FALSE)
```

```
write.csv(df_peep, peeper_main, row.names = FALSE)
```

```
## ^^ I think there is a cleaner way to write this out, but this should work for now ^^
```

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

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

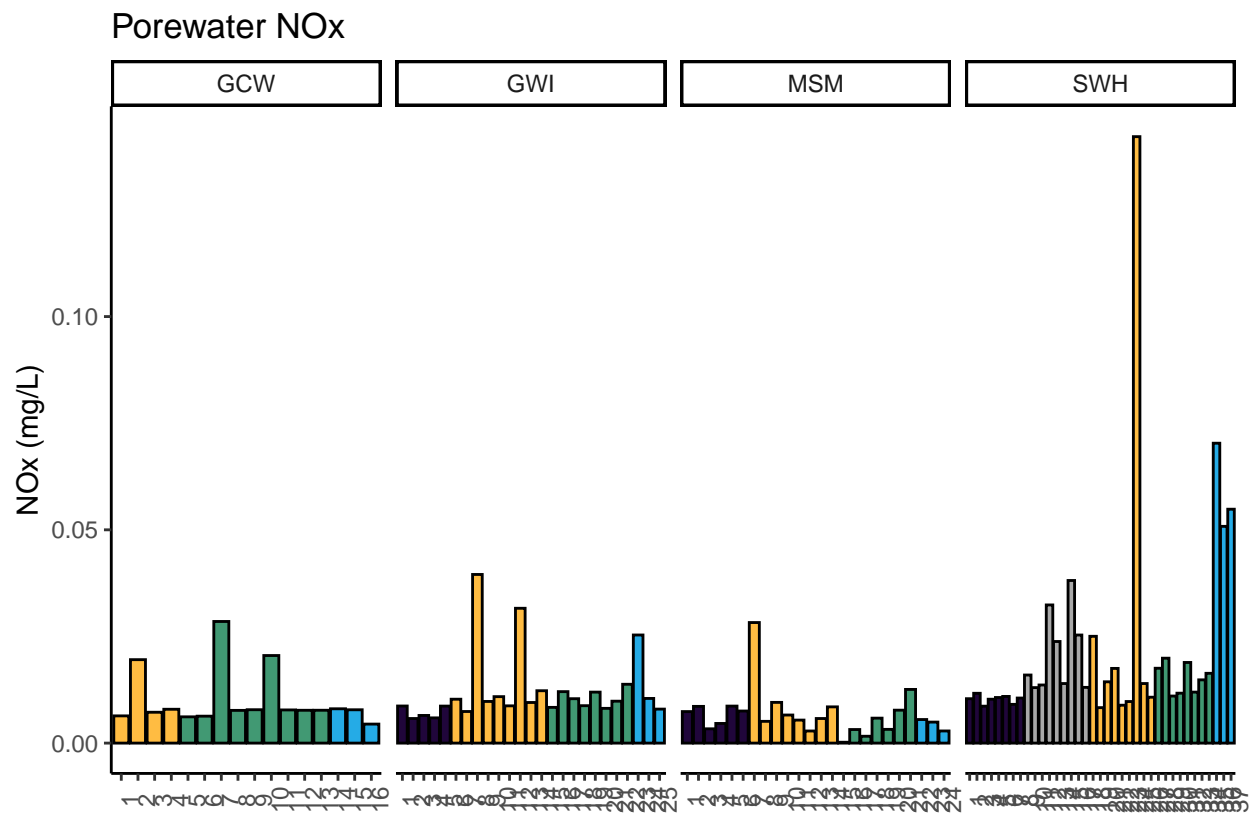
```
## Some sample IDs are missing from metadata.
```

```
## [1] "MSM_202311_TR_LysC_10cm"      "MSM_202311_WC_LysC_45cm"  
## [3] "SWH_202311_UPCON_LysA_10cm"   "SWH_202311_UPCON_LysA_20cm"  
## [5] "SWH_202311_UPCON_LysA_45cm"   "SWH_202311_UPCON_LysB_10cm"  
## [7] "SWH_202311_UPCON_LysB_20cm"   "SWH_202311_UPCON_LysB_45cm"  
## [9] "SWH_202311_UPCON_LysC_20cm"   "SWH_202311_UPCON_LysC_45cm"  
## [11] "GWI_202311_TR_LysA_45cm"
```

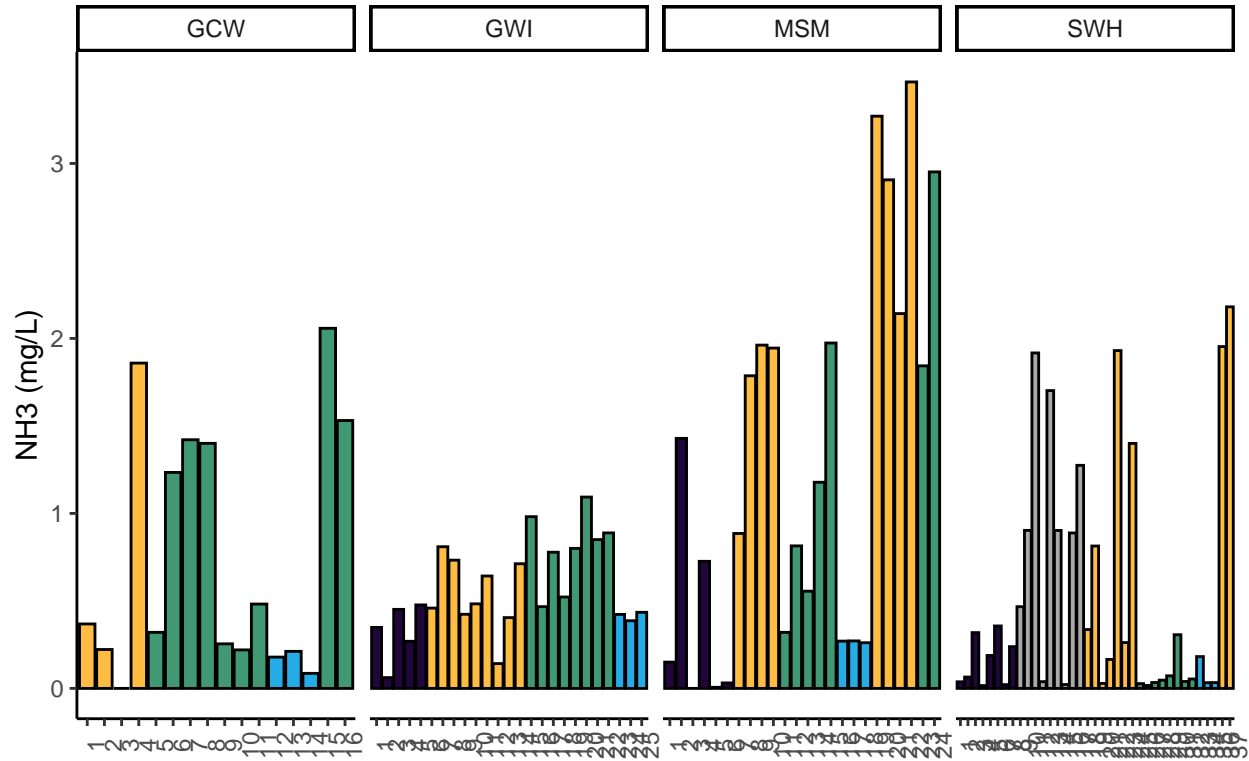
```
## Warning: Expected 5 pieces. Missing pieces filled with 'NA' in 36 rows [14, 15, 16, 38,  
## 39, 40, 75, 76, 77, 100, 101, 102, 114, 115, 116, 132, 133, 134, 146, 147,  
## ...].
```

0.15 Visualize Data

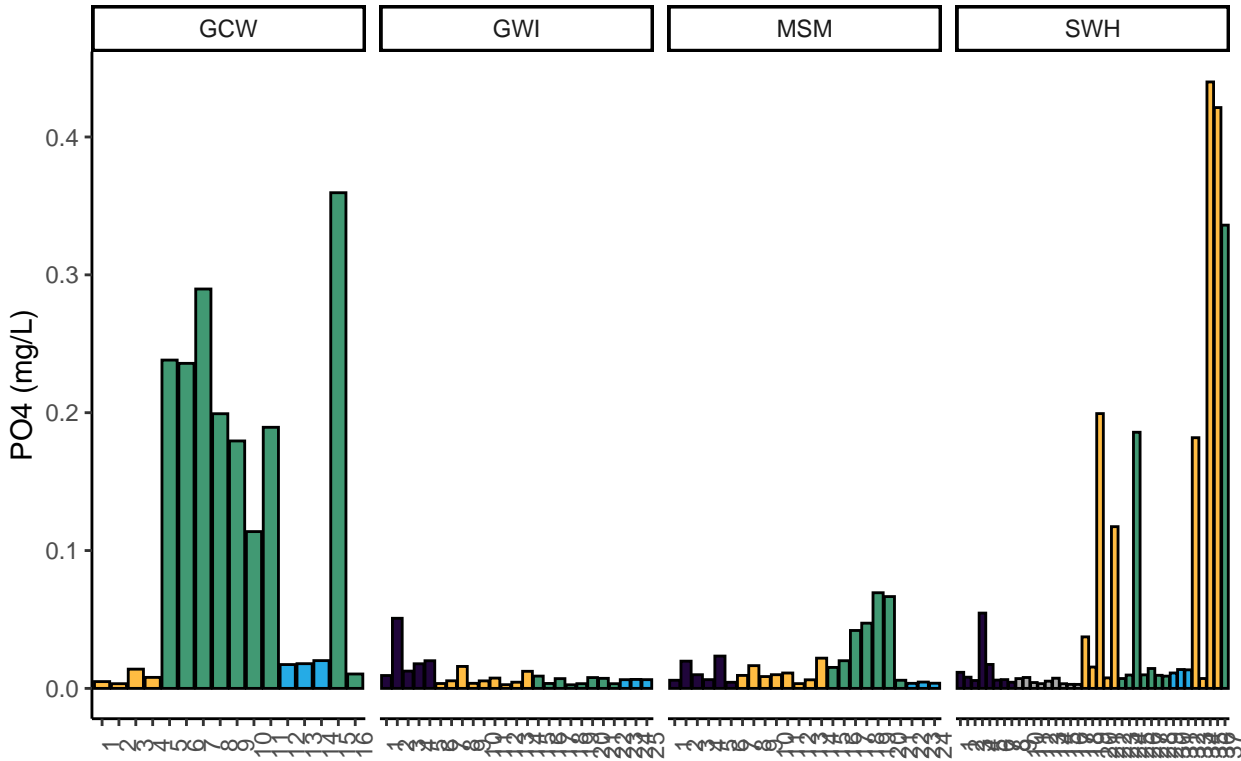
Visualize Data



Porewater NH3



Porewater PO₄



0.16 Export Processed Data

#end