

# Synoptic CB: Porewater Nutrients

JULY 2024 Samples

2025-08-11

## Contents

```

##Run Information

cat("Run Information: NAME ") #lets you know what section you're in

## Run Information: NAME

#set the run date & user name
run_date <- "05/20/2025"
sample_year <- "2024"
sample_month <- "JULY"
user <- "Isabelle Van Benschoten"

#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/COMPASS_Synoptic_CB_202407_VNOx_1.csv",
              "Raw Data/COMPASS_Synoptic_CB_202407_VNOx_2.csv",
              "Raw Data/COMPASS_Synoptic_CB_202407_VNOx_3.csv")
NH3_P04_files <- c("Raw Data/COMPASS_Synoptic_CB_202407_NH3_P04_1.csv",
                   "Raw Data/COMPASS_Synoptic_CB_202407_NH3_P04_2.csv",
                   "Raw Data/COMPASS_Synoptic_CB_202407_NH3_P04_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_2024.csv"
final_path <- "Processed Data/COMPASS_Synoptic_Nutrients_202407.csv"

#record any notes about the run or anything other info here:
run_notes <- "Reduction Effieciency was not ran for all of the runs included within this month.
               One NH3 check standard was ut of range but CV was within.
               One P04 blank was out of range but CV was within.
               P04 duplicates out of range.
               Metadata is missing:
               MSM_202407_TR_LysC_45cm, SWH_202407_UP_LysC_10cm, and SWH_202407_WC_LysA_45cm"

#Set up file path for metadata
#downloaded metadata csv - downloaded from Google drive as csv for this year
Raw_Metadata = "Raw Data/COMPASS_SynopticCB_PW_SampleLog_2024.csv"

cat(run_notes)

## Reduction Effieciency was not ran for all of the runs included within this month.
## One NH3 check standard was ut of range but CV was within.
## One P04 blank was out of range but CV was within.
## P04 duplicates out of range.
## Metadata is missing:
## MSM_202407_TR_LysC_45cm, SWH_202407_UP_LysC_10cm, and SWH_202407_WC_LysA_45cm

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

```

## 0.1 Import Data & Clean

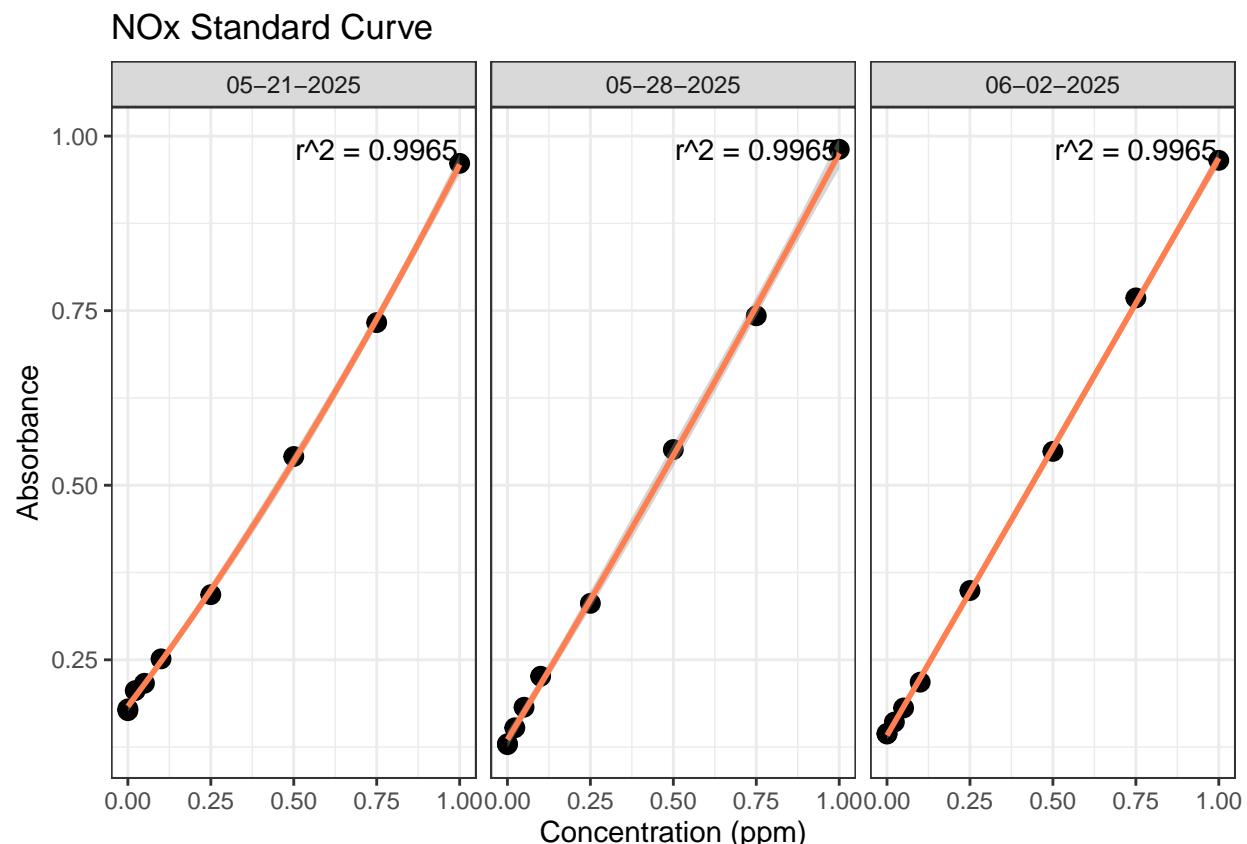
## 0.2 Assessing standard Curves

```
#Pull out standards data
```

```
## Assess Standard Curves
```

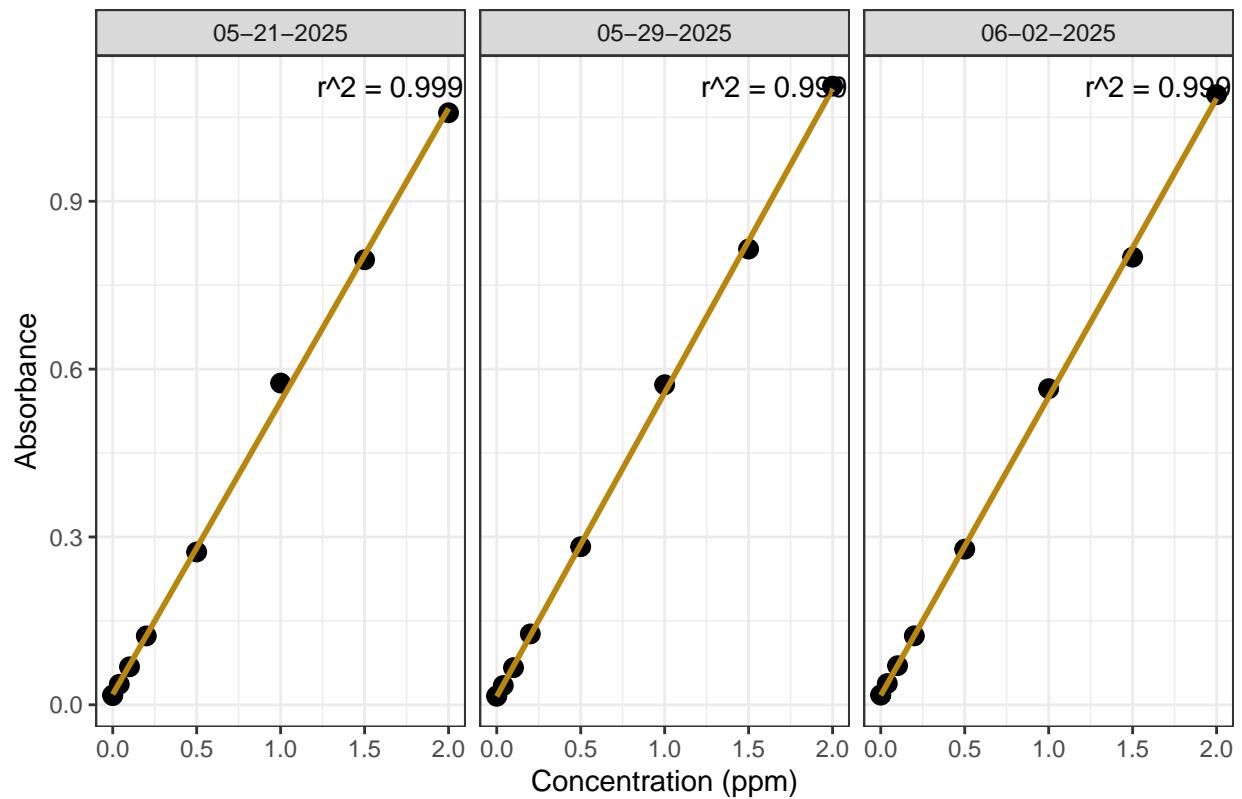
```
#Plot standards data
```

```
## Assess Standard Curves
```



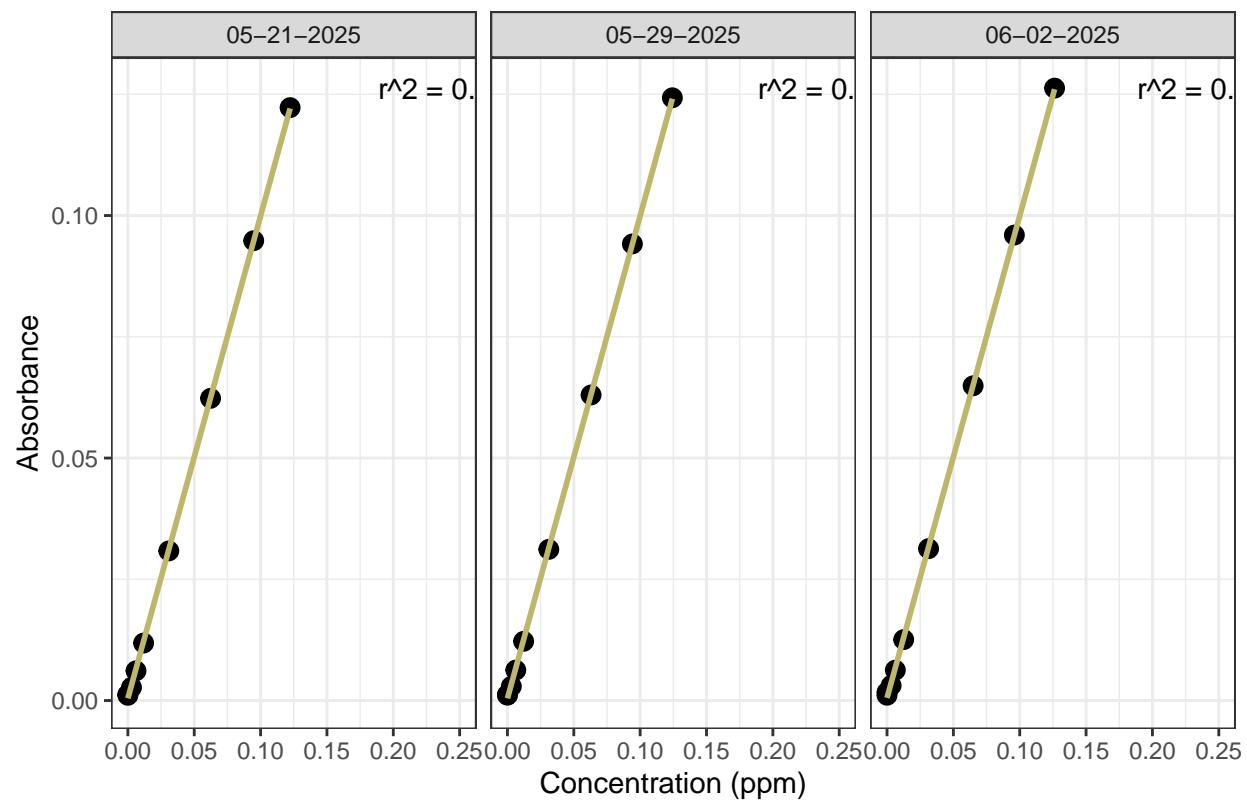
```
## `geom_smooth()` using formula = 'y ~ x'
```

### 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."
```

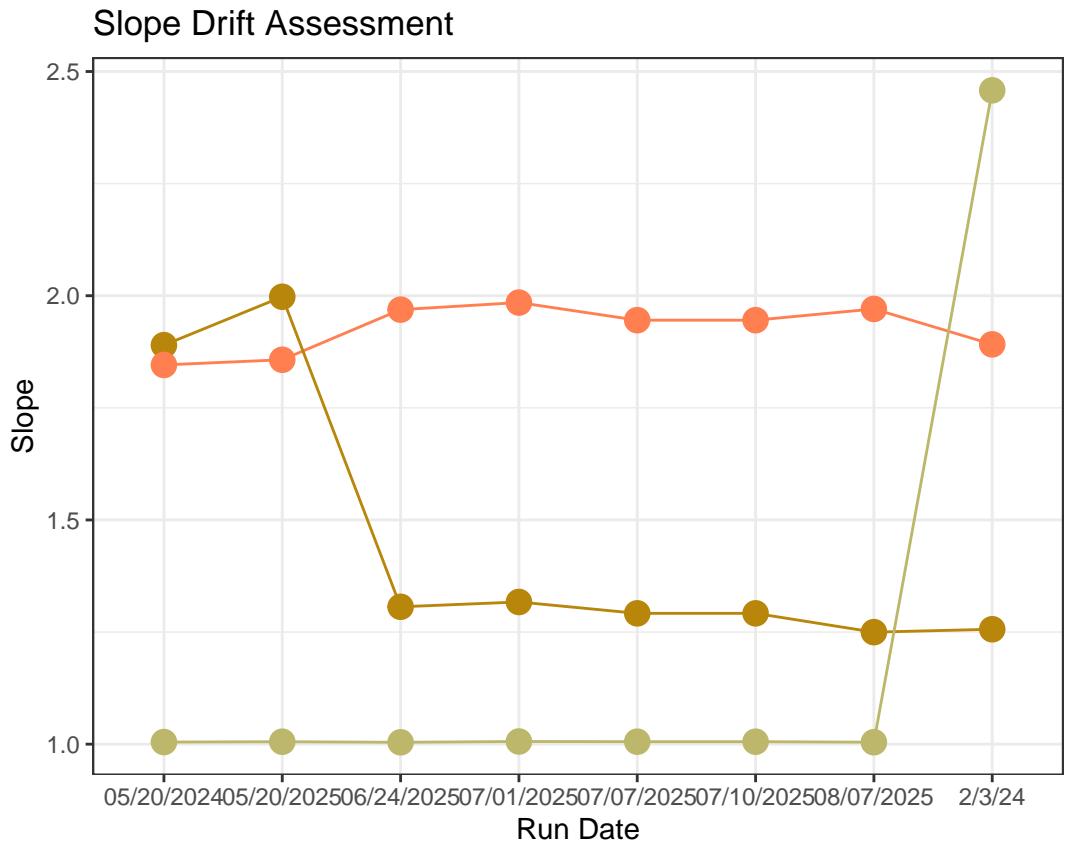


Table 1: Average Slope by Analyte

Test	avg_slope
NH3	1.926
NOx	1.450
PO4	1.187