Daily_measurements

PutnamLab

7/19/2022

This script plots daily measurements from the CBLS Wet lab for the Putnam lab. Run this script daily after daily measurements are taken and inputted into the datasheet.

Script updated 11/14/23 by ZD. Script updated 11/16/23 by JA - added upper and lower threshold lines on plots.

Load packages

Load data

```
daily <- read.csv("Data/2023_Daily_measurements_tracking.csv")
head(daily)
```

```
##       Date Time Date.Time Observer.Initials     Tank_ID Temperature_C pH_mv
## 1 20230101             NA                       BT 1/2         26.24 -59.4
## 2 20230102             NA                       BT 1/2         26.32 -61.3
## 3 20230105             NA                   header_tank         26.23 -51.5
## 4 20230105             NA                       BT 1/2         26.27 -52.3
## 5 20230105             NA                       BT 3/4         26.26 -52.6
## 6 20230106             NA                   header_tank         26.26 -51.9
##   Salinity_psu Orion_Temp tris.date Probe.Set notes
## 1        34.37         NA  20221019    Probe1
## 2        34.44         NA  20221019    Probe1
## 3        34.48         NA  20221019    Probe1
## 4        34.45         NA  20221019    Probe1
## 5        34.41         NA  20221019    Probe1
## 6        34.58         NA  20221019    Probe1
```

```
tail(daily) # check to make sure data from today is there
```

```
##         Date  Time Date.Time Observer.Initials     Tank_ID Temperature_C pH_mv
## 718 20231222 16:45        NA                HP      BT 1/2         26.60 -59.2
## 719 20231222 16:45        NA                HP      BT 3/4         26.60 -59.7
## 720 20231222 16:45        NA                HP header_tank         26.52 -59.2
## 721 20231224 12:05        NA                HP      BT 1/2         26.58 -57.6
## 722 20231224 12:05        NA                HP      BT 3/4         26.60 -57.7
## 723 20231224 12:05        NA                HP header_tank         26.55 -57.7
##     Salinity_psu Orion_Temp tris.date Probe.Set notes
## 718        34.61         NA  20231220    Probe1
## 719        34.61         NA  20231220    Probe1
## 720        34.60         NA  20231220    Probe1
## 721        34.63         NA  20231220    Probe1
```

```
## 722        34.65         NA  20231220    Probe1
## 723        34.68         NA  20231220    Probe1
```

Set dates as characters (needs to be done for merging with the tris calibration file)

```
daily$Date <- as.character(daily$Date)
daily$tris.date <- as.character(daily$tris.date)
```

Probe Set 1 (for the header, all corals, and for the non-quarantine tank) e.g., BT 3/4 and header tank and salt mixing tank

```
daily.probe1 <- daily %>%
  filter(Probe.Set == "Probe1")

range(na.omit(daily.probe1$Temperature_C))
```

```
## [1] 22.220 26.906
```

```
range(na.omit(daily.probe1$pH_mv))
```

```
## [1] -69.6 -38.0
```

```
range(na.omit(daily.probe1$Salinity_psu))
```

```
## [1] 33.40 41.36
```

```
daily.probe2 <- daily %>%
  filter(Probe.Set == "Probe2")

range(na.omit(daily.probe2$Temperature_C))
```

```
## [1] 22.25 26.48
```

```
range(na.omit(daily.probe2$pH_mv))
```

```
## [1] -76.0 -43.7
```

```
range(na.omit(daily.probe2$Salinity_psu))
```

```
## [1] 34.23 36.13
```

Calculate total pH from Probe Set 1

Calculate the calibration curve from the Tris calibration and calculate pH on the total scale from pH.mV.

```
pHcalib<-read_csv("Data/Tris_Calibration.csv")
```

```
## Rows: 240 Columns: 3
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## dbl (3): tris.date, mVTris, TTris
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
pHcalib$tris.date<-as.character(pHcalib$tris.date)

pHSlope.probe1 <- pHcalib %>%
  group_by(tris.date) %>%
  nest() %>%
```

```
  mutate(fitpH = map(data, ~ lm(mVTris ~ TTris, data = .x))) %>%
  mutate(tidy_fit = map(fitpH, broom::tidy)) %>%
  unnest(tidy_fit) %>%
  select(tris.date, term, estimate) %>%
  pivot_wider(names_from = term, values_from = estimate) %>%
  left_join(daily.probe1, ., by = "tris.date") %>%
  mutate(mVTris = Temperature_C * TTris + `(Intercept)`)

range(pHSlope.probe1$Temperature_C)
```

```
## [1] NA NA
```

```
pHSlope.probe1 <- pHSlope.probe1 %>% filter(!is.na(Temperature_C))
range(pHSlope.probe1$Temperature_C)
```

```
## [1] 22.220 26.906
```

```
range(pHSlope.probe1$pH_mv)
```

```
## [1] NA NA
```

```
pHSlope.probe1 <- pHSlope.probe1 %>% filter(!is.na(pH_mv))
range(pHSlope.probe1$pH_mv)
```

```
## [1] -69.6 -38.0
```

```
range(pHSlope.probe1$Salinity_psu)
```

```
## [1] 33.40 40.51
```

```
pHSlope.probe1 <- pHSlope.probe1 %>% filter(!is.na(Salinity_psu))
range(pHSlope.probe1$Salinity_psu)
```

```
## [1] 33.40 40.51
```

```
range(pHSlope.probe1$pH_mv)
```

```
## [1] -69.6 -38.0
```

```
pHSlope.probe1 <- pHSlope.probe1 %>% filter(!is.na(pH_mv))
range(pHSlope.probe1$pH_mv)
```

```
## [1] -69.6 -38.0
```

```
range(pHSlope.probe1$mVTris)
```

```
## [1] -63.89333 -55.28032
```

```
pHSlope.probe1 <- pHSlope.probe1 %>% filter(!is.na(mVTris))
range(pHSlope.probe1$mVTris)
```

```
## [1] -63.89333 -55.28032
```

```
pHSlope.probe1 <- pHSlope.probe1 %>%
  mutate(pH.total = seacarb::pH(Ex = pH_mv, Etris = mVTris, S=Salinity_psu, T=Temperature_C))
```

```
## Warning: There was 1 warning in `mutate()`.
## i In argument: `pH.total = seacarb::pH(Ex = pH_mv, Etris = mVTris, S =
##   Salinity_psu, T = Temperature_C)`.
## Caused by warning in `tris()`:
## ! S, T, and/or b is outside the range of validity for the TRIS buffer pH formulation by DelValls and
```

Calculate total pH from Probe Set 2

Probe Set 2 (for the header, all corals, and for the non-quarantine tank) e.g., BT 1/2 while HI corals were islotaed and quarantine tank

Calculate the calibration curve from the Tris calibration and calculate pH on the total scale from pH.mV.

```
pHcalib2<-read_csv("Data/Tris_Calibration_BT1_2.csv")
```

```
## Rows: 47 Columns: 3
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## dbl (3): tris.date, mVTris, TTris
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
pHcalib2$tris.date<-as.character(pHcalib2$tris.date)

pHSlope.probe2 <- pHcalib2 %>%
  group_by(tris.date) %>%
  nest() %>%
  mutate(fitpH = map(data, ~ lm(mVTris ~ TTris, data = .x))) %>%
  mutate(tidy_fit = map(fitpH, broom::tidy)) %>%
  unnest(tidy_fit) %>%
  select(tris.date, term, estimate) %>%
  pivot_wider(names_from = term, values_from = estimate) %>%
  left_join(daily.probe2, ., by = "tris.date") %>%
  mutate(mVTris = Temperature_C * TTris + `(Intercept)`)

range(pHSlope.probe2$Temperature_C)
```

```
## [1] NA NA
```

```
pHSlope.probe2 <- pHSlope.probe2 %>% filter(!is.na(Temperature_C))
range(pHSlope.probe2$Temperature_C)
```

```
## [1] 22.25 26.48
```

```
range(pHSlope.probe2$pH_mv)
```

```
## [1] -76.0 -43.7
```

```
pHSlope.probe2 <- pHSlope.probe2 %>% filter(!is.na(pH_mv))
range(pHSlope.probe2$pH_mv)
```

```
## [1] -76.0 -43.7
```

```
range(pHSlope.probe2$Salinity_psu)
```

```
## [1] 34.23 36.05
```

```
pHSlope.probe2 <- pHSlope.probe2 %>% filter(!is.na(Salinity_psu))
range(pHSlope.probe2$Salinity_psu)
```

```
## [1] 34.23 36.05
```

```
range(pHSlope.probe2$pH_mv)
```

```
## [1] -76.0 -43.7
```

```
pHSlope.probe2 <- pHSlope.probe2 %>% filter(!is.na(pH_mv))
range(pHSlope.probe2$pH_mv)
```

```
## [1] -76.0 -43.7
```

```
range(pHSlope.probe2$mVTris)
```

```
## [1] NA NA
```

```
pHSlope.probe2 <- pHSlope.probe2 %>% filter(!is.na(mVTris))
range(pHSlope.probe2$mVTris)
```

```
## [1] -70.93191 -66.57079
```

```
pHSlope.probe2 <- pHSlope.probe2 %>%
  mutate(pH.total = seacarb::pH(Ex = pH_mv, Etris = mVTris, S=Salinity_psu, T=Temperature_C))
```

Join Probe 1 and Probe 2 Sets

```
pHSlope <- rbind(pHSlope.probe1, pHSlope.probe2)
```

Convert date to ymd for plotting

```
pHSlope <- pHSlope %>%
  filter(!Tank_ID == "quarantine_tank")

pHSlope$Date <- ymd(pHSlope$Date) # convert 8 digit date into datetime format

pHSlope <- pHSlope %>% relocate("pH.total", .after = Salinity_psu) %>%
  relocate(pH_mv, .after = pH.total)
```

Change to long format

Change data format to long format

```
pHSlope.long <-pHSlope %>% pivot_longer(cols=Temperature_C:pH.total,
  names_to = "metric",
  values_to = "value")
```

Filter by relevant dates if needed

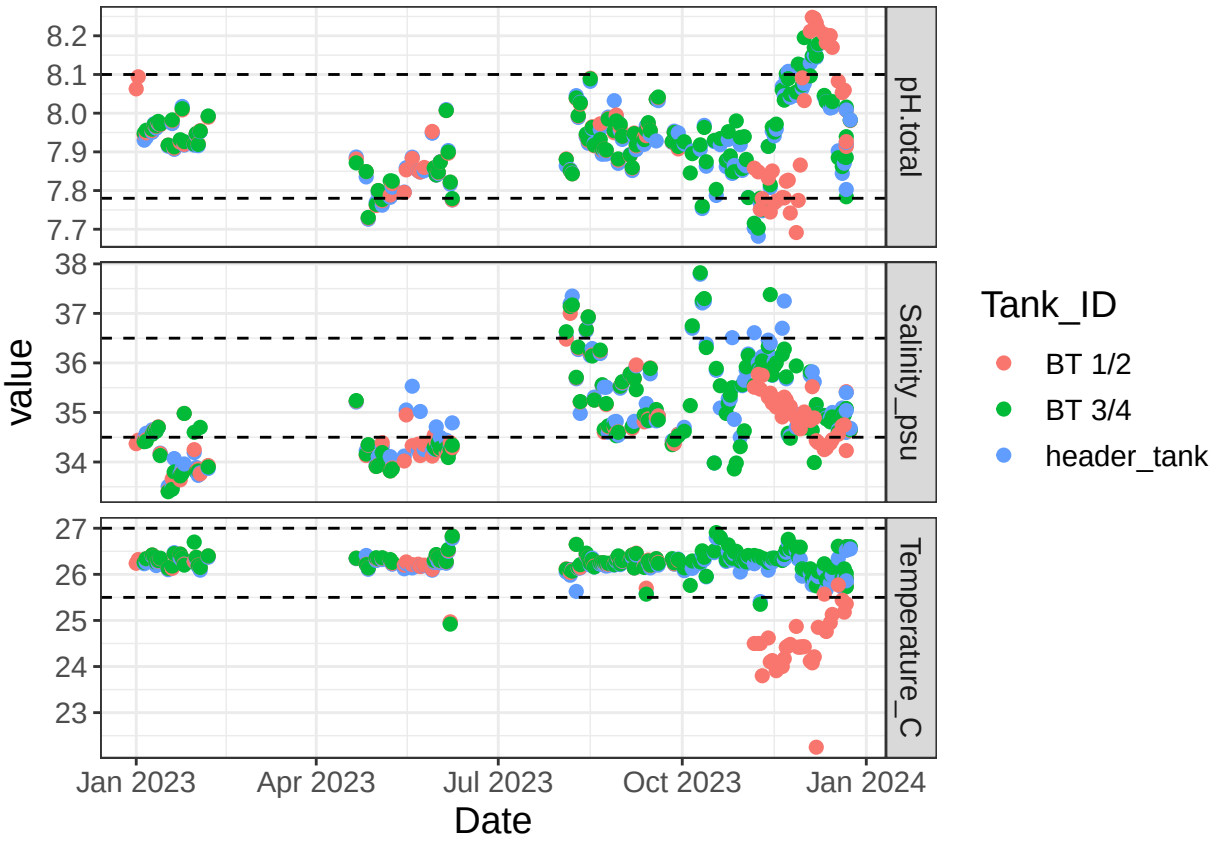
Plot

Make a list of dataframes, each containing a horizontal line that will correspond to the upper and lower threshold of each parameter (temperature, salinity, pH total)

```
hlines_data <- list(
  data.frame(yintercept = 25.5, metric = "Temperature_C"), # lower threshold for temperature in C°
  data.frame(yintercept = 27, metric = "Temperature_C"), # upper threshold for temperature in C°
  data.frame(yintercept = 34.5, metric = "Salinity_psu"), # lower threshold for salinity in psu
  data.frame(yintercept = 36.5, metric = "Salinity_psu"), # upper threshold for salinity in psu
  data.frame(yintercept = 7.78, metric = "pH.total"), # lower threshold for total pH
  data.frame(yintercept = 8.1, metric = "pH.total") # upper threshold for total pH
    )
```

Plot all dates

```
daily_tank<-pHSlope.long %>%
  ggplot(aes(x=Date, y=value, colour=Tank_ID))+
  geom_point(size=2)+
  xlab("Date")+
  facet_grid(metric ~ ., scales = "free")+
  geom_hline(data = hlines_data[[1]], aes(yintercept = yintercept), linetype = "dashed") +
  geom_hline(data = hlines_data[[2]], aes(yintercept = yintercept), linetype = "dashed") +
  geom_hline(data = hlines_data[[3]], aes(yintercept = yintercept), linetype = "dashed") +
  geom_hline(data = hlines_data[[4]], aes(yintercept = yintercept), linetype = "dashed") +
  geom_hline(data = hlines_data[[5]], aes(yintercept = yintercept), linetype = "dashed") +
  geom_hline(data = hlines_data[[6]], aes(yintercept = yintercept), linetype = "dashed") +
  theme_bw() +
  theme(text = element_text(size = 14)); daily_tank
```




```
# Save plot
ggsave("Output/Daily_Measurements.pdf", daily_tank, width = 20, height = 15, units = c("in"))
```

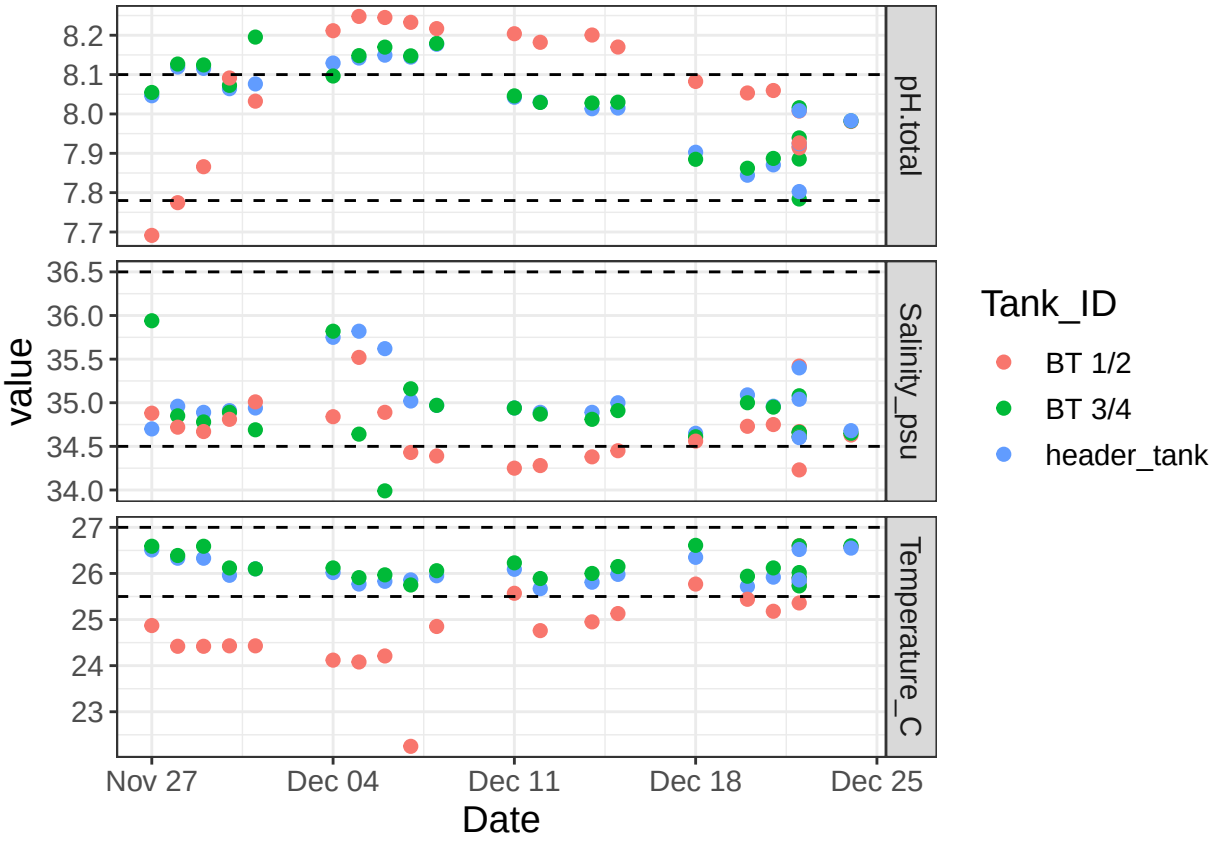
It isn't super informative to look at multiple years in one plot.

Filter and plot by the past month

```
# Filter to the past 30 days
daily_month <- pHSlope.long %>%
  filter(Date >= Sys.Date() - 30)  # Adjust 30 to the number of days you want to consider

# Plot data from the past month
daily_month_plot <-daily_month %>%
  ggplot(aes(x=Date, y=value, colour=Tank_ID))+
```

```
  geom_point(size=2)+
  xlab("Date")+
  facet_grid(metric ~ ., scales = "free")+
  geom_hline(data = hlines_data[[1]], aes(yintercept = yintercept), linetype = "dashed") +
  geom_hline(data = hlines_data[[2]], aes(yintercept = yintercept), linetype = "dashed") +
  geom_hline(data = hlines_data[[3]], aes(yintercept = yintercept), linetype = "dashed") +
  geom_hline(data = hlines_data[[4]], aes(yintercept = yintercept), linetype = "dashed") +
  geom_hline(data = hlines_data[[5]], aes(yintercept = yintercept), linetype = "dashed") +
  geom_hline(data = hlines_data[[6]], aes(yintercept = yintercept), linetype = "dashed") +
  theme_bw() +
  theme(text = element_text(size = 14))
daily_month_plot
```




```
# Save plot
ggsave("Output/Daily_Measurements_Past_Month.pdf", daily_month_plot, width = 20, height = 15, units = c
```

Summarize daily measurements over the past month (this will use the `daily` df from above instead of the the `daily.long` df)

```
daily_month <- pHSlope %>%
  filter(Date >= Sys.Date() - 30)  # Adjust 30 to the number of days you want to consider

summary<-daily_month%>%
  group_by(Tank_ID)%>%
  #select(!tank)%>%
  select(Temperature_C:pH.total) %>%
  summarise(across(everything(), list(mean = mean, sd = sd), na.rm = TRUE)); summary
```

```
## Adding missing grouping variables: `Tank_ID`
```

```
## Warning: There was 1 warning in `summarise()`.
## i In argument: `across(everything(), list(mean = mean, sd = sd), na.rm =
##   TRUE)`.
## i In group 1: `Tank_ID = "BT 1/2"`.
## Caused by warning:
## ! The `...` argument of `across()` is deprecated as of dplyr 1.1.0.
## Supply arguments directly to `.fns` through an anonymous function instead.
##
##   # Previously
##   across(a:b, mean, na.rm = TRUE)
##
##   # Now
##   across(a:b, \(x) mean(x, na.rm = TRUE))
```

```
## # A tibble: 3 x 7
##   Tank_ID  Temperature_C_mean Temperature_C_sd Salinity_psu_mean Salinity_psu_sd
##   <chr>                 <dbl>            <dbl>             <dbl>           <dbl>
## 1 BT 1/2                 25.0            0.949              34.7           0.335
## 2 BT 3/4                 26.2            0.286              34.9           0.400
## 3 header_~               26.0            0.278              35.0           0.339
## # i 2 more variables: pH.total_mean <dbl>, pH.total_sd <dbl>
```