

Benthic percent cover and biomass

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2023-02-01

0. set up

```
# libraries
library(tidyverse)
library(janitor)
library(lubridate)

# function to clean up variables for use
benthic_cleaning_fxn <- function(df) {
  df %>%
    clean_names() %>%
    # change to lower case
    mutate_at(c("group", "mobility", "growth_morph", "site"), str_to_lower) %>%
    # # create a sample_ID for each sampling date at each site
    unite("sample_ID", site, year, remove = FALSE) %>%
    # only include algae
    filter(group == "algae") %>%
    # make sure that sp_code for Nienburgia andersoniana isn't NA
    mutate(sp_code = case_when(
      scientific_name == "Nienburgia andersoniana" ~ "Nandersoniana",
      TRUE ~ as.character(as.character(sp_code))
    ))
}

# percent cover data
percov_2021 <- read_csv(here::here("data", "SBC-LTER-benthics",
                                   "Annual_Cover_All_Years_20211020.csv")) %>%
  benthic_cleaning_fxn()

percov_2022 <- read_csv(here::here("data", "SBC-LTER-benthics",
                                   "Annual_Cover_All_Years_20220809.csv")) %>%
  benthic_cleaning_fxn()

# biomass data
biomass_2021 <- read_csv(here::here("data", "SBC-LTER-benthics",
                                   "Annual_All_Species_Biomass_at_transect_20211020.csv")) %>%
  benthic_cleaning_fxn() %>%
  # replace all -99999 values with NA
  mutate(dry_gm2 = replace(dry_gm2, dry_gm2 < 0, NA),
         wm_gm2 = replace(wm_gm2, wm_gm2 < 0, NA),
         density = replace(density, density < 0, NA)) %>%
  mutate(date = ymd(date))
```

```

biomass_2022 <- read_csv(here::here("data", "SBC-LTER-benthics",
                                   "Annual_All_Species_Biomass_at_transect_20220809.csv")) %>%
  benthic_cleaning_fxn() %>%
  # replace all -99999 values with NA
  mutate(dry_gm2 = replace(dry_gm2, dry_gm2 < 0, NA),
         wm_gm2 = replace(wm_gm2, wm_gm2 < 0, NA),
         density = replace(density, density < 0, NA)) %>%
  mutate(date = ymd(date))

```

Taonia lennebackerae example

2021

```

aque_tale_percov_2021 <- percov_2021 %>%
  filter(site == "aque" & sp_code == "TALE" & year == 2021) %>%
  group_by(transect) %>%
  summarize(mean_percov = mean(percent_cover))

```

```

aque_tale_biomass_2021 <- biomass_2021 %>%
  filter(site == "aque" & sp_code == "TALE" & year == 2021)

```

```
aque_tale_percov_2021
```

```

## # A tibble: 6 x 2
##   transect mean_percov
##   <dbl>      <dbl>
## 1     1         1.25
## 2     2          0
## 3     3          0
## 4     4          0
## 5     5          0
## 6     6          0

```

```
aque_tale_biomass_2021
```

```

## # A tibble: 6 x 25
##   sample_ID year month date      site transect sp_code perce-1 density wm_gm2
##   <chr>      <dbl> <dbl> <date>   <chr>   <dbl> <chr>      <dbl>   <dbl> <dbl>
## 1 aque_2021 2021     7 2021-07-22 aque     1 TALE      1.25     NA    15
## 2 aque_2021 2021     7 2021-07-22 aque     2 TALE       0      NA     0
## 3 aque_2021 2021     7 2021-07-22 aque     3 TALE       0      NA     0
## 4 aque_2021 2021     7 2021-07-22 aque     4 TALE       0      NA     0
## 5 aque_2021 2021     7 2021-07-22 aque     5 TALE       0      NA     0
## 6 aque_2021 2021     7 2021-07-22 aque     6 TALE       0      NA     0
## # ... with 15 more variables: dry_gm2 <dbl>, sfdm <dbl>, afdm <dbl>,
## #   scientific_name <chr>, common_name <chr>, taxon_kingdom <chr>,
## #   taxon_phylum <chr>, taxon_class <chr>, taxon_order <chr>,
## #   taxon_family <chr>, taxon_genus <chr>, group <chr>, mobility <chr>,
## #   growth_morph <chr>, coarse_grouping <chr>, and abbreviated variable name
## #   1: percent_cover

```

2022

```
aque_tale_percov_2022 <- percov_2022 %>%  
  filter(site == "aque" & sp_code == "TALE" & year == 2022) %>%  
  group_by(transect) %>%  
  summarize(mean_percov = mean(percent_cover))
```

```
aque_tale_biomass_2022 <- biomass_2022 %>%  
  filter(site == "aque" & sp_code == "TALE" & year == 2022)
```

aque_tale_percov_2022

```
## # A tibble: 6 x 2  
##   transect mean_percov  
##   <dbl>      <dbl>  
## 1      1      1.25  
## 2      2      0  
## 3      3      0  
## 4      4      0  
## 5      5      0  
## 6      6      0
```

aque_tale_biomass_2022

```
## # A tibble: 0 x 26  
## # ... with 26 variables: sample_ID <chr>, year <dbl>, month <dbl>, date <date>,  
## #   site <chr>, transect <dbl>, vis <dbl>, sp_code <chr>, percent_cover <dbl>,  
## #   density <dbl>, wm_gm2 <dbl>, dry_gm2 <dbl>, sfdm <dbl>, afdm <dbl>,  
## #   scientific_name <chr>, common_name <chr>, taxon_kingdom <chr>,  
## #   taxon_phylum <chr>, taxon_class <chr>, taxon_order <chr>,  
## #   taxon_family <chr>, taxon_genus <chr>, group <chr>, mobility <chr>,  
## #   growth_morph <chr>, coarse_grouping <chr>
```