Amphibian data for biofilm MS

Caitlin Nordheim-Maestas

```r
library(tidyverse) # for cleaning and viewing data
library(gt) # pretty stats tables
library(broom) # cleaning for gt
library(here) # for importing data
library(lubridate) # for date cleaning and use
```

Swabs

```r
# import wrangled data
swab_may22 <- read.csv(here("amphib-data", "swab_may2022_ninesites.csv"))
swab_mj <- read.csv(here("amphib-data", "swab_mar-jun22_filtered.csv"))

# #wrangle data that match our sampling

# swab_may22 <- read.csv(here("amphib-data", "allmonths_swabs_updated 2024-10-28.csv")) %>
#   filter(code %in% c(
#     "CABIN", "WEST", "GRAMPS",
#     "GDPND004", "GDPND005", "GDPND009", "GDPND006",
#     "PRPND004", "PRPND009", "PRPND010"
#   )) %>%
#     filter(sampling_id %in% c(
#     "May_22"
#   ))
# write.csv(swab_may22, "swab_may2022_ninesites.csv", row.names = FALSE)


# swab_mj <- read.csv(here("amphib-data", "allmonths_swabs_updated 2024-10-28.csv")) %>%
#   filter(code %in% c(
```

```
#       "CABIN", "WEST", "GRAMPS",
#       "GDPND004", "GDPND005", "GDPND009", "GDPND006",
#       "PRPND004", "PRPND009", "PRPND010"
#   )) %>%
#     filter(sampling_id %in% c(
#       "Mar_22", "May_22", "Jun_22"
#   ))
# write.csv(swab_mj, "swab_ma-jun22_filtered.csv", row.names = FALSE)
```

Calculate Bd prev per site

May 2022

```
swab_summary <- swab_may22 %>%
group_by(code) %>%
  summarise(
    n_frogs = n(),
    bd_positive = sum(infected == 1),
    prevalence = round(100 * bd_positive / n_frogs, 1),
    avg_load_bd_pos = round(mean(zsp_eq[infected == 1], na.rm = TRUE), 2)
  )
str(swab_summary)
```

```
tibble [8 x 5] (S3: tbl_df/tbl/data.frame)
 $ code           : chr [1:8] "CABIN" "GDPND005" "GDPND006" "GDPND009" ...
 $ n_frogs        : int [1:8] 6 1 2 2 5 5 9 10
 $ bd_positive    : int [1:8] 5 1 0 0 0 0 4 0
 $ prevalence     : num [1:8] 83.3 100 0 0 0 0 44.4 0
 $ avg_load_bd_pos: num [1:8] 502.76 1.13 NaN NaN NaN ...
```

```
swab_summary %>%
  gt() %>%
  cols_label(
    code = "Site",
    n_frogs = "Number Swabbed",
    bd_positive = "Bd Positive",
    prevalence = "Bd Prevalence (%)",
    avg_load_bd_pos = "Avg Bd Load (ZE)"
```

```
) %>%
tab_header(
  title = "Summary of Bd Infection by Site: May 2022"
) %>%
fmt_number(
  columns = c(prevalence, avg_load_bd_pos),
  decimals = 0
) %>%
tab_style(
  style = list(
    cell_text(weight = "bold")
  ),
  locations = cells_column_labels(everything())
)
```

Summary of Bd Infection by Site: May 2022

Site	Number Swabbed	Bd Positive	Bd Prevalence (%)	Avg Bd Load (ZE)
CABIN	6	5	83	503
GDPND005	1	1	100	1
GDPND006	2	0	0	NaN
GDPND009	2	0	0	NaN
GRAMPS	5	0	0	NaN
PRPND009	5	0	0	NaN
PRPND010	9	4	44	10,038
WEST	10	0	0	NaN

By species and site

```
swab_summary2 <- swab_may22 %>%
group_by(code, amphibian_spp) %>%
  summarise(
    n_frogs = n(),
    bd_positive = sum(infected == 1),
    prevalence = round(100 * bd_positive / n_frogs, 1),
    avg_load_bd_pos = round(mean(zsp_eq[infected == 1], na.rm = TRUE), 2)
  ) %>%
  mutate(
    avg_load_bd_pos = ifelse(is.nan(avg_load_bd_pos), NA, avg_load_bd_pos)
```

```
    )
```

`summarise()` has grouped output by 'code'. You can override using the
`.groups` argument.

```
  swab_summary2
```

```
# A tibble: 11 x 6
# Groups:    code [8]
   code       amphibian_spp n_frogs bd_positive prevalence avg_load_bd_pos
   <chr>      <chr>           <int>       <int>      <dbl>           <dbl>
 1 CABIN      BUBO                1           0          0              NA
 2 CABIN      PSRE                1           1        100           1320.
 3 CABIN      RACA                4           4        100            299.
 4 GDPND005   PSRE                1           1        100            1.13
 5 GDPND006   PSRE                2           0          0              NA
 6 GDPND009   PSRE                2           0          0              NA
 7 GRAMPS     BUBO                1           0          0              NA
 8 GRAMPS     PSRE                4           0          0              NA
 9 PRPND009   PSRE                5           0          0              NA
10 PRPND010   PSRE                9           4       44.4          10038.
11 WEST       PSRE               10           0          0              NA
```

```
  swab_summary2 %>%
    arrange(code, amphibian_spp) %>%
    mutate(site = code) %>%
    group_by(site) %>%
    mutate(site = ifelse(row_number() == 1, site, "")) %>%
    ungroup() %>%
    select(site, amphibian_spp, n_frogs, bd_positive, prevalence, avg_load_bd_pos) %>%
    gt() %>%
    cols_label(
      site = "Site",
      amphibian_spp = "Species",
      n_frogs = md("Count<br>Swabbed"),
      bd_positive = md("Count<br>Bd+"),
      prevalence = md("Bd<br>Prev (%)"),
      avg_load_bd_pos = md("Ave Bd<br>Load (ZE)")
    ) %>%
```

```
    fmt_number(
      columns = c(prevalence, avg_load_bd_pos),
      decimals = 0
    ) %>%
    tab_header(
      title = "Frog Bd Sampling and Bd Prevalence by Site and Species (May 2022)"
    ) %>%
    tab_style(
      style = cell_text(weight = "bold"),
      locations = cells_column_labels(everything())
    ) %>%
  tab_style(
    style = cell_text(align = "left"),
    locations = cells_column_labels(everything())
  )
```

Warning: HTML tags found, and they will be removed.
* Set `options(gt.html_tag_check = FALSE)` to disable this check.
HTML tags found, and they will be removed.
* Set `options(gt.html_tag_check = FALSE)` to disable this check.
HTML tags found, and they will be removed.
* Set `options(gt.html_tag_check = FALSE)` to disable this check.
HTML tags found, and they will be removed.
* Set `options(gt.html_tag_check = FALSE)` to disable this check.

Frog Bd Sampling and Bd Prevalence by Site and Species (May 2022)

Site	Species	CountSwabbed	CountBd+	BdPrev (%)	Ave BdLoad (ZE)
CABIN	BUBO	1	0	0	NA
	PSRE	1	1	100	1,320
	RACA	4	4	100	299
GDPND005	PSRE	1	1	100	1
GDPND006	PSRE	2	0	0	NA
GDPND009	PSRE	2	0	0	NA
GRAMPS	BUBO	1	0	0	NA
	PSRE	4	0	0	NA
PRPND009	PSRE	5	0	0	NA
PRPND010	PSRE	9	4	44	10,038
WEST	PSRE	10	0	0	NA

```
swab_summary2 %>%
  arrange(code, amphibian_spp) %>%
  mutate(site = code) %>%
  group_by(site) %>%
  mutate(site = ifelse(row_number() == 1, site, "")) %>%
  ungroup() %>%
  select(site, amphibian_spp, n_frogs, bd_positive, prevalence, avg_load_bd_pos) %>%  # re
  gt() %>%
  cols_label(
site = "Site",
  amphibian_spp = "Species",
  n_frogs = md("Count<br>Swabbed"),
  bd_positive = md("Count<br>Bd+"),
  prevalence = md("Bd<br>Prev (%)"),
  avg_load_bd_pos = md("Ave Bd<br>Load (ZE)")
  ) %>%
  fmt_number(
    columns = c(prevalence, avg_load_bd_pos),
    decimals = 0
  ) %>%
  tab_header(
    title = "Frog Bd Sampling and Bd Prevalence by Site (May 2022)"
  ) %>%
  tab_style(
    style = cell_text(weight = "bold"),
    locations = cells_column_labels(everything())
  ) %>%
  tab_style(
    style = cell_text(align = "center"),
    locations = cells_body(columns = site)
  )
```

```
Warning: HTML tags found, and they will be removed.
* Set `options(gt.html_tag_check = FALSE)` to disable this check.
HTML tags found, and they will be removed.
* Set `options(gt.html_tag_check = FALSE)` to disable this check.
HTML tags found, and they will be removed.
* Set `options(gt.html_tag_check = FALSE)` to disable this check.
HTML tags found, and they will be removed.
* Set `options(gt.html_tag_check = FALSE)` to disable this check.
```

Frog Bd Sampling and Bd Prevalence by Site (May 2022)

Site	Species	CountSwabbed	CountBd+	BdPrev (%)	Ave BdLoad (ZE)
CABIN	BUBO	1	0	0	NA
	PSRE	1	1	100	1,320
	RACA	4	4	100	299
GDPND005	PSRE	1	1	100	1
GDPND006	PSRE	2	0	0	NA
GDPND009	PSRE	2	0	0	NA
GRAMPS	BUBO	1	0	0	NA
	PSRE	4	0	0	NA
PRPND009	PSRE	5	0	0	NA
PRPND010	PSRE	9	4	44	10,038
WEST	PSRE	10	0	0	NA

Mar - **June 2022**

```
swab_summary_mj <- swab_mj %>%
group_by(code) %>%
  summarise(
    n_frogs = n(),
    bd_positive = sum(infected == 1),
    prevalence = round(100 * bd_positive / n_frogs, 1),
    avg_load_bd_pos = round(mean(zsp_eq[infected == 1], na.rm = TRUE), 2)
  )

swab_summary_mj %>%
   gt() %>%
  cols_label(
    code = "Site",
    n_frogs = "Number Swabbed",
    bd_positive = "Bd Positive",
    prevalence = "Bd Prevalence (%)",
    avg_load_bd_pos = "Avg Bd Load (ZE)"
  ) %>%
  tab_header(
    title = "Summary of Bd Infection by Site: Mar-Jun 2022"
  ) %>%
  fmt_number(
```

```
    columns = c(prevalence, avg_load_bd_pos),
    decimals = 0
  ) %>%
  tab_style(
    style = list(
      cell_text(weight = "bold")
    ),
    locations = cells_column_labels(everything())
  )
```

Summary of Bd Infection by Site: Mar-Jun 2022

Site	Number Swabbed	Bd Positive	Bd Prevalence (%)	Avg Bd Load (ZE)
CABIN	40	17	42	420
GDPND005	6	2	33	5
GDPND006	17	5	29	2,812
GDPND009	12	0	0	NaN
GRAMPS	23	4	17	24
PRPND004	54	4	7	181
PRPND009	29	1	3	17
PRPND010	40	7	18	5,745
WEST	51	7	14	88

Visual Encounter Survey

```
#wrangle data that match our sampling
ves_may <- read.csv(here("amphib-data", "cln_survey_data2025-04-21.csv")) %>%
  mutate(date = ymd(date)) %>%  # convert character to Date
  filter(month(date) == 5 & year(date) == 2022) %>%
  filter(site_code %in% c(
    "CABIN", "WEST", "GRAMPS",
    "GDPND004", "GDPND005", "GDPND009", "GDPND006",
    "PRPND004", "PRPND009", "PRPND010"
  )) %>%
  select(
    site_code, date,
    raca_adult, raca_juvenile,
    radr_adult, radr_juvenile,
```

```r
      raxx_adult_or_juvenile,
      bubo_adult, bubo_juvenile,
      psre_adult, psre_juvenile,
      taxx_adult, taxx_juvenile,
      temp
    ) %>%
    mutate(taxx_juvenile = as.numeric(taxx_juvenile))

#write.csv(ves_may, "ves_may22_filtered.csv", row.names = FALSE)

ves_mj <- read.csv(here("amphib-data", "cln_survey_data2025-04-21.csv")) %>%
    mutate(date = ymd(date)) %>%  # convert character to Date
    filter(month(date) %in% c(3, 5, 6) & year(date) == 2022) %>%
    filter(site_code %in% c(
      "CABIN", "WEST", "GRAMPS",
      "GDPND004", "GDPND005", "GDPND009", "GDPND006",
      "PRPND004", "PRPND009", "PRPND010"
    )) %>%
    select(
      site_code, date,
      raca_adult, raca_juvenile,
      radr_adult, radr_juvenile,
      raxx_adult_or_juvenile,
      bubo_adult, bubo_juvenile,
      psre_adult, psre_juvenile,
      taxx_adult, taxx_juvenile,
      temp
    )

ves_spring_2022_summary <- ves_mj %>%
    mutate(taxx_juvenile = as.numeric(taxx_juvenile)) %>%
    group_by(site_code) %>%
    summarise(
      across(
        c(raca_adult, raca_juvenile, radr_adult, radr_juvenile,
          raxx_adult_or_juvenile, bubo_adult, bubo_juvenile,
          psre_adult, psre_juvenile, taxx_adult, taxx_juvenile),
        ~sum(.x, na.rm = TRUE),
        .names = "{.col}_summed"
      ),
      avg_temp = mean(temp, na.rm = TRUE),
```

VES tables

```
ves_may %>%
  select(-date) %>%
  gt() %>%
  cols_label(
    site_code = "Site",
    raca_adult = "RACA Adult",
    raca_juvenile = "RACA Juvenile",
    radr_adult = "RADR Adult",
    radr_juvenile = "RADR Juvenile",
    raxx_adult_or_juvenile = "RAXX",
    bubo_adult = "BUBO Adult",
    bubo_juvenile = "BUBO Juvenile",
    psre_adult = "PSRE Adult",
    psre_juvenile = "PSRE Juvenile",
    taxx_adult = "TAXX Adult",
    taxx_juvenile = "TAXX Juvenile",
    temp = "Temp (°C)"
  ) %>%
  fmt_number(
    columns = -c(site_code),
    decimals = 0
  ) %>%
  tab_header(
    title = "Amphibian Visual Encounter Survey and Water Temperature (May 2022)"
  ) %>%
  tab_style(
    style = cell_text(weight = "bold"),
    locations = cells_column_labels(everything())
  )
```

Amphibian Visual Encounter Survey a

Site	RACA Adult	RACA Juvenile	RADR Adult	RADR Juvenile	RAXX	BUBO Adu
CABIN	0	4	0	0	19	
GRAMPS	0	0	0	0	0	
GDPND006	0	0	0	0	0	

GDPND005	0	0	0	0	0
GDPND004	0	0	0	0	0
GDPND009	0	0	0	0	0
PRPND010	0	0	0	0	1
PRPND009	0	0	0	0	0
PRPND004	0	0	0	0	0
WEST	0	0	0	0	6