Amphibian data for biofilm MS

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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

# 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",  
# "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",  
# "GDPND005", "GDPND009", "GDPND006",  
# "PRPND004", "PRPND009", "PRPND010"  
# )) %>%  
# filter(sampling\_id %in% c(  
# "Mar\_22", "May\_22", "Jun\_22"  
# ))  
# write.csv(swab\_mj, "swab\_mar-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 × 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())  
 )

Table 1: 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 %>%  
 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())  
)

Table 1: 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) %>% # remove code, reorder  
 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)  
 )

Table 1: 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())  
 )

Table 1: 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",  
 "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  
 ) %>%   
 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",  
 "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),  
 .groups = "drop"  
 )

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())  
 )

Table 1: Amphibian Visual Encounter Survey and Water Temperature (May 2022)

| Site | RACA Adult | RACA Juvenile | RADR Adult | RADR Juvenile | RAXX | BUBO Adult | BUBO Juvenile | PSRE Adult | PSRE Juvenile | TAXX Adult | TAXX Juvenile | Temp (°C) |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| CABIN | 0 | 4 | 0 | 0 | 19 | 1 | 0 | 2 | 0 | 0 | 0 | 20 |
| GRAMPS | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 4 | 0 | 0 | 21 |
| GDPND006 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 2 | 0 | 0 | 24 |
| GDPND005 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 21 |
| GDPND009 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 25 |
| PRPND010 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 4 | 9 | 0 | 0 | 18 |
| PRPND009 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 5 | 0 | 0 | 20 |
| PRPND004 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 18 |
| WEST | 0 | 0 | 0 | 0 | 6 | 0 | 0 | 2 | 28 | 0 | 0 | 24 |

### summary sentence

Note - no frogs caught at P4, but I guess we saw a toad in the VES

n\_total\_sites <- ves\_may %>%  
 distinct(site\_code) %>%  
 nrow()  
  
n\_sites\_with\_swabs <- swab\_summary2 %>%  
 distinct(code) %>%  
 nrow()  
  
percent\_sites\_with\_swabs <- round(100 \* n\_sites\_with\_swabs / n\_total\_sites, 1)  
  
total\_frogs <- sum(swab\_summary2$n\_frogs, na.rm = TRUE)  
total\_bd\_pos <- sum(swab\_summary2$bd\_positive, na.rm = TRUE)  
overall\_prevalence <- round(100 \* total\_bd\_pos / total\_frogs, 1)  
  
glue::glue(  
 "Amphibians were caught at {percent\_sites\_with\_swabs}% of SFEB sites in May 2022, ",  
 "and Bd was detected on frogs with an overall prevalence of {overall\_prevalence}% (n = {total\_frogs} amphibians)."  
)

Amphibians were caught at 88.9% of SFEB sites in May 2022, and Bd was detected on frogs with an overall prevalence of 25% (n = 40 amphibians).

glue::glue(  
 "Amphibians were found at 100% of SFEB sites in May 2022, ",  
 "and Bd was detected on frogs with an overall prevalence of {overall\_prevalence}% (n = {total\_frogs} amphibians)."  
)

Amphibians were found at 100% of SFEB sites in May 2022, and Bd was detected on frogs with an overall prevalence of 25% (n = 40 amphibians).

n\_total\_sites <- ves\_may %>%  
 distinct(site\_code) %>%  
 nrow()  
  
  
n\_sites\_with\_frogs <- ves\_may %>%  
 mutate(taxx\_juvenile = as.numeric(taxx\_juvenile)) %>%  
 rowwise() %>%  
 mutate(total\_frogs = sum(c\_across(raca\_adult:taxx\_juvenile), na.rm = TRUE)) %>%  
 ungroup() %>%  
 filter(total\_frogs > 0) %>%  
 nrow()  
  
  
percent\_sites\_with\_frogs <- round(100 \* n\_sites\_with\_frogs / n\_total\_sites, 1)