

# 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 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 %>%
  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.

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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)
)

```

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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",
    "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())
)

```

Amphibian Visual Encounter Survey and

Site	RACA Adult	RACA Juvenile	RADR Adult	RADR Juvenile	RAXX	BUBO Adult
CABIN	0	4	0	0	19	
GRAMPS	0	0	0	0	0	
GDPND006	0	0	0	0	0	
GDPND005	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	

### 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 = {
)

```

Amphibians were caught at 88.9% of SFEB sites in May 2022, and Bd was detected on frogs with

```

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 = {
)

```

Amphibians were found at 100% of SFEB sites in May 2022, and Bd was detected on frogs with a

```

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)

```