

N-Mixture/CMR Exploratory - Pennsylvania

Load Packages

```
if (!require(librarian)){
  install.packages("librarian")
  library(librarian)
}

librarian::shelf(tidyverse, RPostgres, DBI, unmarked, here, lubridate, kableExtra)
```

Connect to survey_data schema in ribbitr database

```
tryCatch({
  drv <- dbDriver("Postgres")
  print("Connecting to Database...")
  connection <- dbConnect(drv,
    dbname = Sys.getenv("aws_dbname"),
    host = Sys.getenv("aws_host"),
    port = Sys.getenv("aws_port"),
    user = Sys.getenv("aws_user"),
    password = Sys.getenv("aws_password"),
    timezone=NULL)
  print("Database Connected!")
},
error=function(cond) {
  print("Unable to connect to Database.")
})

#search path
dbExecute(connection, "set search_path to survey_data")
```

Query 2022 CMR Penn data

```
# Data
cmr_q <- "select r.region, s.site, v.date, v.survey_time, s2.duration_minutes,
  c.species_capture, c.capture_type
  from region r
  join site s on r.region_id = s.region_id
  full join visit v on s.site_id = v.site_id
  join survey s2 on v.visit_id = s2.visit_id
  join capture c on s2.survey_id = c.survey_id
  where r.region = 'pennsylvania'
  and v.date > '2022-01-01';"

raw_data <- dbGetQuery(connection, cmr_q) %>%
  select(!c(region, survey_time, duration_minutes)) %>%
  arrange(date)

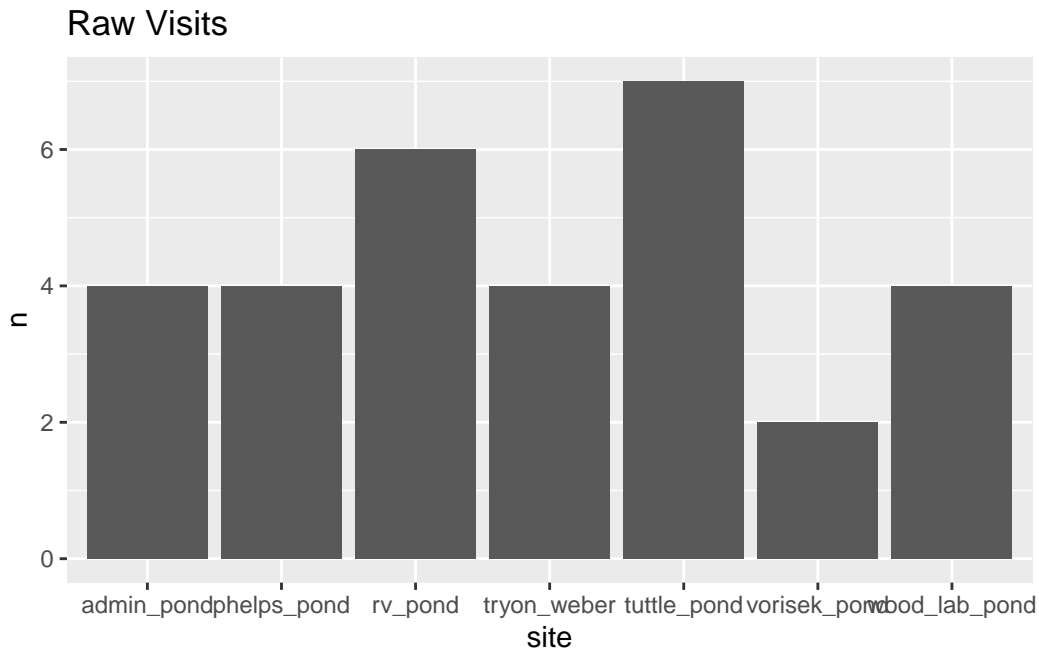
# find all visits
visit_cmr_q <- "select r.region, s.site, v.date, v.survey_time
  from region r
  join site s on r.region_id = s.region_id
  join visit v on s.site_id = v.site_id
  where r.region = 'pennsylvania'
  and v.date > '2022-01-01';"

raw_visits <-dbGetQuery(connection, visit_cmr_q) %>%
  arrange(date) %>%
  select(site, date)
```

Visualize all Visits

```
viz <- raw_visits %>%
  group_by(site) %>%
  summarise(n = n())

ggplot(data = viz) +
  geom_col(aes(x=site, y = n)) +
  ggtitle("Raw Visits")
```



Clean up species list with counts

Filter for CMR focal species and summarize species counts. Then populate zeros for 3 focal species into the data set for visits when captures did not occur.

```
# filter for CMR focal species and summarize counts
mid_clean_up <- raw_data %>%
  filter(species_capture %in% c("pseudacris_crucifer", "rana_catesbeiana",
                                "rana_clamitans")) %>%
  mutate(capture_type = if_else(is.na(capture_type), "new", capture_type)) %>%
  group_by(date, site, species_capture) %>%
  summarise(n = n()) %>%
  ungroup()
```

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

```
# populate zeros
clean_up <- raw_visits %>%
  left_join(mid_clean_up) %>%
  complete(nesting(date, site),
           species_capture = unique(mid_clean_up$species_capture),
```

```
fill = list(n = 0))
```

Joining with `by = join_by(site, date)`

Warning in left_join(., mid_clean_up): Detected an unexpected many-to-many relationship between variables `site` and `date`.

- i Row 1 of `x` matches multiple rows in `y`.
- i Row 34 of `y` matches multiple rows in `x`.
- i If a many-to-many relationship is expected, set `relationship = "many-to-many"` to silence this warning.

rana_catesbeiana

Table formatting

Filter data for rana_catesbeiana, tally the number of visits, pivot data frame into correct matrix form, and finally populate zeros into the NAs if sites were visited.

```
bull_frog_visits <- clean_up %>%
  select(site, date, species_capture, n) %>%
  filter(species_capture == "rana_catesbeiana") %>%
  select(!species_capture) %>%
  group_by(site) %>%
  mutate(n_visit = match(date, unique(date)),
         n_visit = paste0("visit_", n_visit, sep = "")) %>%
  select(!date) %>%
  ungroup() %>%
  pivot_wider(names_from = c("n_visit"), values_from = c("n")) %>%
  group_by(site) %>%
  mutate(across(contains("visit"),
                ~ifelse(is.na(.) &
                        !is.na(lag(.)), 0, .)))
```

```
kableExtra::kable(bull_frog_visits)
```

site	visit_1	visit_2	visit_3	visit_4	visit_5	visit_6	visit_7
wood_lab_pond	2	4	3	0	NA	NA	NA
phelps_pond	4	3	6	0	NA	NA	NA
admin_pond	9	15	20	0	NA	NA	NA
rv_pond	1	7	5	13	29	11	NA
tuttle_pond	15	22	0	39	31	29	20
tryon_weber	0	0	0	NA	NA	NA	NA
vorisek_pond	14	13	NA	NA	NA	NA	NA

static n-mixture unmarked models no covariates

```
bull_frog_unmarked_nmixture <- bull_frog_visits %>%
  ungroup() %>%
  select(!c(site))

umf <- unmarkedFramePCount(y = bull_frog_unmarked_nmixture)

summary(umf)
```

unmarkedFrame Object

7 sites

Maximum number of observations per site: 7

Mean number of observations per site: 4.29

Sites with at least one detection: 6

Tabulation of y observations:

0	1	2	3	4	5	6	7	9	11	13	14	15	20	22	29
7	1	1	2	2	1	1	1	1	1	2	1	2	2	1	2
31	39	<NA>													
1	1	19													

```
fm1 <- pcount(~1 ~1, data = umf)
```

Warning in pcount(~1 ~ 1, data = umf): K was not specified and was set to 139.

```
# Get estimates on link scale
backTransform(fm1, "state")
```

Backtransformed linear combination(s) of Abundance estimate(s)

Estimate	SE	LinComb	(Intercept)
40.7	7.97	3.71	1

Transformation: exp

```
# Get estimates on natural scale  
backTransform(fm1, "det")
```

Backtransformed linear combination(s) of Detection estimate(s)

Estimate	SE	LinComb	(Intercept)
0.232	0.0421	-1.2	1

Transformation: logistic

Assuming the sites and enviro variables are exactly the same we can say there is 40.7 \pm 7.9 frogs at these sites and we are only detecting 23% of the frogs.

pseudacris_crucifer

Table formatting

Filter data for pseudacris_crucifer, tally the numbner of visits, pivot data frame into correct matrix form, and finally populate zeros into the NAs if sites were visited.

```
peep_frog_visits <- clean_up %>%  
  select(site, date, species_capture, n) %>%  
  filter(species_capture == "pseudacris_crucifer") %>%  
  select(!species_capture) %>%  
  group_by(site) %>%  
  mutate(n_visit = match(date, unique(date)),  
         n_visit = paste0("visit_", n_visit, sep = "")) %>%  
  select(!date) %>%  
  ungroup() %>%  
  pivot_wider(names_from = c("n_visit"), values_from = c("n")) %>%  
  group_by(site) %>%  
  mutate(across(contains("visit"),  
               ~ifelse(is.na(.)) &
```

```
!is.na(lag(.)), 0, .)))
```

```
kable(peep_frog_visits)
```

site	visit_1	visit_2	visit_3	visit_4	visit_5	visit_6	visit_7
wood_lab_pond	2	0	0	0	NA	NA	NA
phelps_pond	4	0	0	0	NA	NA	NA
admin_pond	4	2	3	1	NA	NA	NA
rv_pond	16	0	0	0	0	0	NA
tuttle_pond	0	0	0	0	0	0	0
tryon_weber	0	0	0	NA	NA	NA	NA
vorisek_pond	0	0	NA	NA	NA	NA	NA

static n-mixture unmarked models no covariates

```
peep_unmarked_nmixture <- peep_frog_visits %>%
  ungroup() %>%
  #filter(capture_type == "new") %>%
  select(!c(site))

umf <- unmarkedFramePCount(y = peep_unmarked_nmixture)

summary(umf)
```

unmarkedFrame Object

7 sites

Maximum number of observations per site: 7

Mean number of observations per site: 4.29

Sites with at least one detection: 4

Tabulation of y observations:

```
  0   1   2   3   4  16 <NA>
23   1   2   1   2   1   19
```

```
fm1 <- pcount(~1 ~1, data = umf)
```

Warning in pcount(~1 ~ 1, data = umf): K was not specified and was set to 116.

```
backTransform(fm1, "state")
```

Backtransformed linear combination(s) of Abundance estimate(s)

Estimate	SE	LinComb	(Intercept)
85.8	24.4	4.45	1

Transformation: exp

```
backTransform(fm1, "det")
```

Backtransformed linear combination(s) of Detection estimate(s)

Estimate	SE	LinComb	(Intercept)
0.0124	0.00411	-4.38	1

Transformation: logistic

Assuming the sites and enviro variables are exactly the same we can estimate there is 85.7 ±24.4 frogs at these sites and we are only detecting 1.2% of the frogs.

rana_clamitans

Table formatting

Filter data for rana_clamitans, tally the numbner of visits, pivot data frame into correct matrix form, and finally populate zeros into the NAs if sites were visited.

```
green_frog_visits <- clean_up %>%
  select(site, date, species_capture, n) %>%
  filter(species_capture == "rana_clamitans") %>%
  #select(!species_capture) %>%
  group_by(site) %>%
  mutate(n_visit = match(date, unique(date)),
         n_visit = paste0("visit_", n_visit, sep = "")) %>%
  select(!date) %>%
```



```

ungroup() %>%
group_by(site, n_visit, ) %>%
summarise(n = sum(n)) %>%
ungroup() %>%
pivot_wider(names_from = c("n_visit"), values_from = c("n")) %>%
#add_row(site = "phelps_pond", capture_type = "recapture") %>%
group_by(site) %>%
mutate(across(contains("visit"),
              ~ifelse(is.na(.) &
                      !is.na(lag(.)), 0, .)))

```

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

static n-mixture with no co-variates

```

green_frog_unmarked_nmixture <- green_frog_visits %>%
  ungroup() %>%
  select(!c(site))

umf <- unmarkedFramePCount(y = green_frog_unmarked_nmixture)

summary(umf)

```

unmarkedFrame Object

7 sites

Maximum number of observations per site: 7

Mean number of observations per site: 4.29

Sites with at least one detection: 7

Tabulation of y observations:

0	1	2	3	5	7	8	10	16	19	22	<NA>
8	4	5	5	1	2	1	1	1	1	1	19

```
fm1 <- pcount(~1 ~1, data = umf)
```

Warning in pcount(~1 ~ 1, data = umf): K was not specified and was set to 122.

```
backTransform(fm1, "state")
```

Backtransformed linear combination(s) of Abundance estimate(s)

Estimate	SE	LinComb	(Intercept)
94.8	13.1	4.55	1

Transformation: exp

```
backTransform(fm1, "det")
```

Backtransformed linear combination(s) of Detection estimate(s)

Estimate	SE	LinComb	(Intercept)
0.0434	0.00693	-3.09	1

Transformation: logistic

Assuming the sites and enviro variables are exactly the same we estimate there is 94.8 ±13.1 frogs at these sites and we are only detecting 4.3% of the frogs.

Table forming capture-recapture

```
# mid_clean_up <- raw_data %>%
#   filter(species_capture %in% c("pseudacris_crucifer", "rana_catesbeiana",
#                                 "rana_clamitans")) %>%
#   mutate(capture_type = if_else(is.na(capture_type), "new", capture_type)) %>%
#   group_by(date, site, capture_type, species_capture) %>%
#   summarise(n = n()) %>%
#   ungroup()
#
# # populate zeros
# clean_up <- raw_visits %>%
#   left_join(mid_clean_up) %>%
#   complete(nesting(date, site),
#             species_capture = unique(mid_clean_up$species_capture),
#             fill = list(n = 0)) %>%
#   mutate(capture_type = if_else(is.na(capture_type), "new", capture_type))
```

```
#
```

Bullfrog CMR data

```
# bull_frog_cmr <- clean_up %>%
#   select(site, date, capture_type, species_capture, n) %>%
#   filter(species_capture == "rana_catesbeiana") %>%
#   select(!species_capture) %>%
#   group_by(site) %>%
#   mutate(n_visit = match(date, unique(date)),
#          n_visit = paste0("visit_", n_visit, sep = "")) %>%
#   select(!date) %>%
#   ungroup() %>%
#   pivot_wider(names_from = c("n_visit"), values_from = c("n")) %>%
#   add_row(site = "phelps_pond", capture_type = "recapture") %>%
#   add_row(site = "tryon_weber", capture_type = "recapture", visit_1 = 0, visit_2 = 0, vi
#   group_by(site) %>%
#   mutate(across(contains("visit"),
#                  ~ifelse(is.na(.) &
#                           !is.na(lag(.)), 0, .)))

# t <- clean_up %>%
#   select(site, date, species_capture, n) %>%
#   filter(species_capture == "rana_catesbeiana") %>%
#   select(!species_capture) %>%
#   group_by(site) %>%
#   mutate(n_visit = match(date, unique(date)),
#          n_visit = paste0("visit_", n_visit, sep = "")) %>%
#   select(!date) %>%
#   ungroup() %>%
#   pivot_wider(names_from = c("n_visit"), values_from = c("n")) %>%
#   group_by(site) %>%
#   mutate(across(contains("visit"),
#                  ~ifelse(is.na(.) &
#                           !is.na(lag(.)), 0, .)))
```