Berkeley Analysis of Human Schisto Data

Background

Longitudinal data analysis of human parasitological data among communities in Senegal with prawn interventions, vegetation removal, and net addition. Three parasitological sampling events in February of 2016, 2017, and 2018 attempted to measure *S. haematobium* eggs/10mL urine and *S. mansoni* EPG among school children in 16 communities. Praziquantel administration occurred in April 2016 and in June of 2017. Vegetation removal and prawn introduction interventions were initiated following PZQ administration in June 2017. Nets were added in 4 villages following PZQ administration in Feb 2016 to assess if there is a net effect independent of prawn addition.

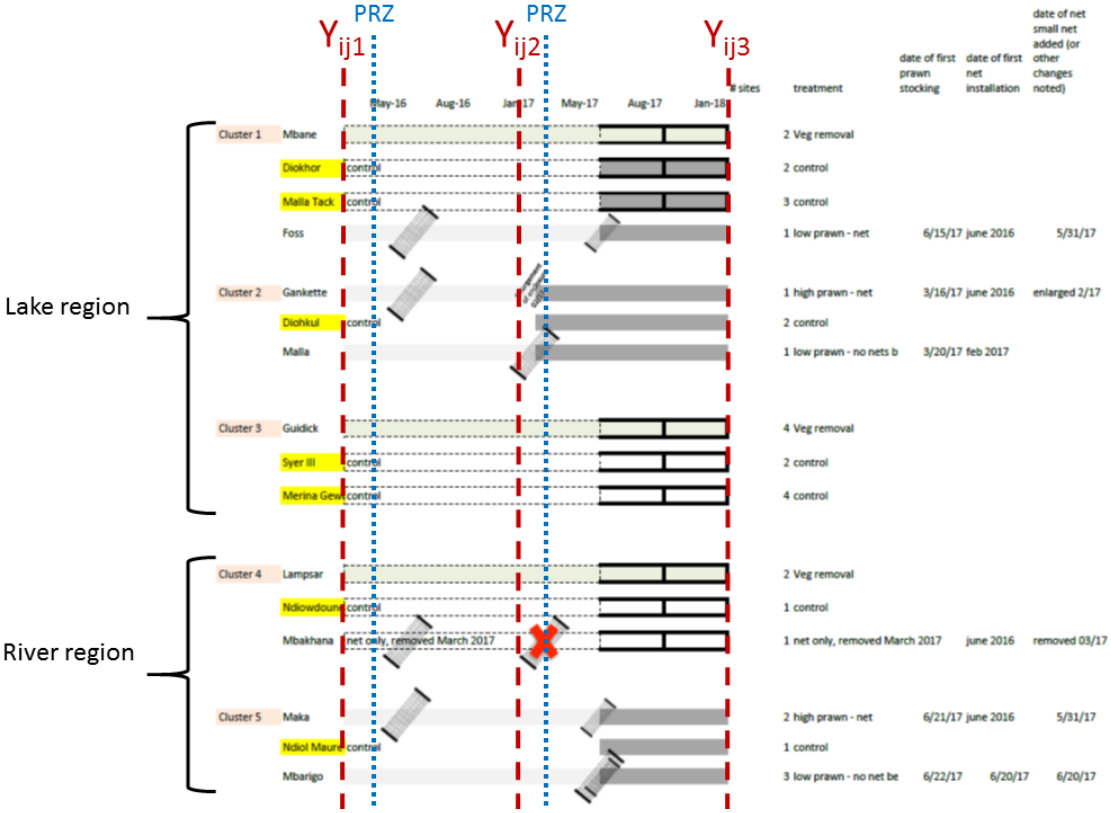


Figure 1: Study design

Our main question is: how do the interventions affect transmission? The interventions were implemented in June/July 2017 following the 2017 PZQ administration and therefore only affect the 2018 survey data. An ideal analysis should therefore leverage the earlier surveys to account for individual, community, and regional variability while relying on the 2018 survey to identify the effects of each intervention. More formally, our statistical question may be framed as:

$$\mathbb{E}[Y_{ij3}|Y_{ij2}, Y_{ij1}] = \mathbb{E}[Y_{ij3}|I_{j3}, Y_{ij2}, Y_{ij1}]$$

where Y_{ijt} is the egg burden of individual i in community j in year t and I_{j3} is the intervention that community j receives in year 3 (2018). We would hope:

$$\mathbb{E}[Y_{ij3}|Y_{ij2}, Y_{ij1}] > \mathbb{E}[Y_{ij3}|I_{j3}, Y_{ij2}, Y_{ij1}]$$

but what we want to be sure of is that the intervention is not harmful or:

$$\mathbb{E}[Y_{ij3}|Y_{ij2}, Y_{ij1}] < \mathbb{E}[Y_{ij3}|I_{j3}, Y_{ij2}, Y_{ij1}]$$

Clarifying Questions:

Safe to assume all children with egg burden measures were treated with PZQ?
+ Yes

What is the source/point of clusters?
+ From Giulio: "the 5 groups were derived through a rigorous cluster analysis that accounted for location (lake/river), population size and distance (to simply logistic and homogenized microclimate differences through the geographical reason)"
+ From Sanna: "There was a protocol to assign clusters based on matching of several variables for each site: latitude, longitude, water point # and cattle presence (qualitative). Once clusters were assigned, they were used to stratify the randomization of treatment. With such a small sample size (16 sites), randomization might otherwise have failed — ie. all prawn treatments may have ended up on the Lake, or at high cattle use sites, or at places with many water points. Thus, we intended to assign one high prawn and one low prawn village in each cluster randomly and ensure control sites of comparable ecology were also being tracked. Somewhere in the middle of the experiment (at the end of the first follow up year) because we lacked prawns, [difficult] executive decisions were made by Giulio, so he can explain more why one high and one low prawn treatment were applied in each of 3 clusters (rather than one single density (or several densities) of prawns were assigned in each of the 5 clusters). Whether"cluster" remains in the analysis doesn't matter as much to me as having used the clusters in the first place to ensure a wide stratification of treatments and controls in space and across other influential ecological variables. Note that "high prawn" and "low prawn" should probably be referred to as "very low prawn" and "extremely low prawn" when we look at the actual realized densities across the transmission periods in the prawn sites."
Better to use mean of multiple data points or single data point for less missingness?
+ Giulio says using a single stool sample for *S. mansoni* underestimates prevalence on the village level, but that for four communities, only 1 stool sample was collaected. In our analyses to follow average individual egg burden is estimated for each individual and for each species (mansoni and haematobium) and an additional weight variable is constructed which indicates the number of egg burden estimates that contribute to that mean (max of 2 for haematobium, max of 4 for mansoni)

Data loading, cleaning, and merging

```
#My interventions data generated form interpretation of spreadsheets shared by Giulio
interventions <- read_csv("~/RemaisWork/Schisto/Stanford/Human_Parasitology_data/Village_interventions.csv") %
  mutate(Intervention = factor(Intervention, levels = c("control", "net", "prawn", "veg_removal")),
         Region = factor(Region),
         Prawn_cat = factor(Prawn_cat, levels = c("No", "low", "high")))
```

```
## Parsed with column specification:
## cols(
##   Intervention_2018 = col_character(),
##   Intervention = col_character(),
##   Village = col_character(),
##   School = col_character(),
##   Region = col_character(),
##   year = col_integer(),
##   Veg = col_integer(),
##   Veg_tons = col_double(),
##   Net = col_integer(),
##   Net_months = col_integer(),
##   Prawn_cat = col_character(),
##   Prawns = col_integer(),
##   Prawn_density = col_double(),
##   Prawn_biomass = col_double()
## )
```

```
dat1 <- read_csv("~/RemaisWork/Schisto/Stanford/Human_Parasitology_data/First_round_human_subject_analysis_APL
#data munging
  #sort(unique(dat1$P2_omega_total))

# Get means from different samples, rename variables, and reorder
  dat1 <- dat1 %>%
    group_by(Child_ID) %>%
    mutate(year = 2016, School = as.character(School),
           # Replace >200 with 200 then coerce to numeric
            P2_omega_total = as.numeric(ifelse(P2_omega_total == ">200", 200, P2_omega_total)),
```

```
          #Mean haematobium eggs/10mL
           s_haem_mean2016 = mean(c(P1_omega_total, P2_omega_total)),
          #Mean haematobium eggs/10mL NAs removed
           s_haem_mean2016_narm = mean(c(P1_omega_total, P2_omega_total), na.rm = TRUE),
          #Number of samples contributing to mean
           s_haem_mean2016_w = length(which(!is.na(c(P1_omega_total, P2_omega_total)))),
          #WHO infection intensity labels
           s_haem_mean_cat2016 = cut(s_haem_mean2016_narm,
                                     breaks = c(0, 1, 50, Inf),
                                     labels = c("No", "Lo", "Hi"), right = FALSE),
          #Mean mansoni epg from 1st kato katz
           s_mans_mean1 = mean(c(P1_kk1, P1_kk2)),
          ##Mean mansoni epg from 2nd kato katz
           s_mans_mean2 = mean(c(P2_kk1, P2_kk2)),
          #Mean mansoni epg from 1st/2nd kato katz
           s_mans_mean2016 = mean(c(P1_kk1, P1_kk2, P2_kk1, P2_kk2)),
          #Mean mansoni EPG NAs removed
           s_mans_mean2016_narm = mean(c(P1_kk1, P1_kk2, P2_kk1, P2_kk2), na.rm = TRUE),
          #Number of non-NA measurements
           s_mans_mean2016_w = length(which(!is.na(c(P1_kk1, P1_kk2, P2_kk1, P2_kk2)))),
          #WHO infection levels
           s_mans_mean_cat2016 = cut(s_mans_mean2016_narm,
                                     breaks = c(0,1,100,400,Inf),
                                     labels = c("No", "Lo", "Md", "Hi"), right = FALSE),
           pzq = 0,
           extra_pzq = 0) %>%
    select(Child_ID, year, School, pzq, extra_pzq,
           s_haem1 = P1_omega_total,
           s_haem2 = P2_omega_total,
           s_haem_mean = s_haem_mean2016,
           s_haem_mean_narm = s_haem_mean2016_narm,
           s_haem_mean_w = s_haem_mean2016_w,
           s_haem_mean_cat = s_haem_mean_cat2016,
           s_mans1_1 = P1_kk1,
           s_mans1_2 = P1_kk2,
           s_mans2_1 = P2_kk1,
           s_mans2_2 = P2_kk2,
           s_mans_mean1,
           s_mans_mean2,
           s_mans_mean12 = s_mans_mean2016,
           s_mans_mean_narm = s_mans_mean2016_narm,
           s_mans_mean_w = s_mans_mean2016_w,
           s_mans_mean_cat = s_mans_mean_cat2016) %>% ungroup()

#Data check
  #make sure each subject only has one record:
    bad_id_dat1 <- dat1 %>%
      group_by(Child_ID) %>%
      summarise(nobs = n()) %>%
      filter(nobs > 1) %>%
      pull(Child_ID)

    length(bad_id_dat1)
```

```
## [1] 0
```

```
dat2 <- read_csv("~/RemaisWork/Schisto/Stanford/Human_Parasitology_data/Second_round_human_subject_analysis_API

# Get means from different samples, rename variables, and reorder
```

```r
  dat2 <- dat2 %>%
    group_by(Child_ID) %>%
    mutate(year = 2017, School = as.character(School),
           # Replace >200 with 200 then coerce to numeric
           P4_omega_total = as.numeric(ifelse(P4_omega_total == ">200", 200, P4_omega_total)),
           #Mean haematobium eggs/10mL
           s_haem_mean2017 = mean(c(P3_omega_total, P4_omega_total)),
           #Mean haematobium eggs/10mL NAs removed
           s_haem_mean2017_narm = mean(c(P3_omega_total, P4_omega_total), na.rm = TRUE),
           #Number of samples contributing to mean
           s_haem_mean2017_w = length(which(!is.na(c(P3_omega_total, P4_omega_total)))),
          #WHO infection intensity labels
           s_haem_mean_cat2017 = cut(s_haem_mean2017_narm,
                                     breaks = c(0, 1, 50, Inf),
                                     labels = c("No", "Lo", "Hi"), right = FALSE),
          #Mean mansoni epg from 1st kato katz
           s_mans_mean1 = mean(c(P3_kk1, P3_kk2)),
          #Mean mansoni epg from 2nd kato katz
           s_mans_mean2 = mean(c(P4_kk1, P4_kk2)),
          #Mean mansoni epg from 1st/2nd kato katz
           s_mans_mean2017 = mean(c(P3_kk1, P3_kk2, P4_kk1, P4_kk2)),
          #Mean mansoni epg NAs removed
           s_mans_mean2017_narm = mean(c(P3_kk1, P3_kk2, P4_kk1, P4_kk2), na.rm = TRUE),
          #Number of non-NA measurements
           s_mans_mean2017_w = length(which(!is.na(c(P3_kk1, P3_kk2, P4_kk1, P4_kk2)))),
          #Number of samples contributing to mean
           s_mans_mean_cat2017 = cut(s_mans_mean2017_narm,
                                     breaks = c(0,1,100,400, Inf),
                                     labels = c("No", "Lo", "Md", "Hi"), right = FALSE),
           pzq = 1,
           extra_pzq = as.numeric(!is.na(PZQ_date_before_analyses)))  %>%
    select(Child_ID, year, School, pzq, extra_pzq,
           s_haem1 = P3_omega_total,
           s_haem2 = P4_omega_total,
           s_haem_mean = s_haem_mean2017,
           s_haem_mean_narm = s_haem_mean2017_narm,
           s_haem_mean_w = s_haem_mean2017_w,
           s_haem_mean_cat = s_haem_mean_cat2017,
           s_mans1_1 = P3_kk1,
           s_mans1_2 = P3_kk2,
           s_mans2_1 = P4_kk1,
           s_mans2_2 = P4_kk2,
           s_mans_mean1,
           s_mans_mean2,
           s_mans_mean12 = s_mans_mean2017,
           s_mans_mean_narm = s_mans_mean2017_narm,
           s_mans_mean_w = s_mans_mean2017_w,
           s_mans_mean_cat = s_mans_mean_cat2017) %>% ungroup()

#Data check
  #make sure each subject only has one record:
    bad_id_dat2 <- dat2 %>%
      group_by(Child_ID) %>%
      summarise(nobs = n()) %>%
      filter(nobs > 1) %>%
      pull(Child_ID)

    length(bad_id_dat2)
```

```
## [1] 0
```

```
dat3 <- read_csv("~/RemaisWork/Schisto/Stanford/Human_Parasitology_data/Third_round_human_subject_analysis_APL
# Replace **_ numbers with just number and coerce to numeric
  dat3$P5_omega_total <- as.numeric(sub("**", "", dat3$P5_omega_total, fixed = TRUE))
  dat3$P6_omega_total <- sub("**", "*", dat3$P6_omega_total, fixed = TRUE)
  dat3$P6_omega_total <- as.numeric(sub("*", "", dat3$P6_omega_total, fixed = TRUE))

# Get means from different samples, rename variables, and reorder
  dat3 <- dat3 %>%
    group_by(Child_ID) %>%
    mutate(year = 2018,
           School = strsplit(Child_ID, "/")[[1]][1],
           #Mean haematobium eggs/10mL
           s_haem_mean2018 = mean(c(P5_omega_total, P6_omega_total)),
           #Mean haematobium eggs/10mL, NAs removed
           s_haem_mean2018_narm = mean(c(P5_omega_total, P6_omega_total), na.rm = TRUE),
           #Number of samples contributing to mean
           s_haem_mean2018_w = length(which(!is.na(c(P5_omega_total, P6_omega_total)))),
           #WHO infection intensity labels
           s_haem_mean_cat2018 = cut(s_haem_mean2018_narm,
                                     breaks = c(0, 1, 50, Inf),
                                     labels = c("No", "Lo", "Hi"), right = FALSE),
           #Mean mansoni epg from 1st kato katz
           s_mans_mean1 = mean(c(P5_kk1_epg, P5_kk2_epg)),
           ##Mean mansoni epg from 2nd kato katz
           s_mans_mean2 = mean(c(P6_kk1_epg, P6_kk2_epg)),
           #Mean mansoni epg from 1st/2nd kato katz
           s_mans_mean2018 = mean(c(P5_kk1_epg, P5_kk2_epg, P6_kk1_epg, P6_kk2_epg)),
           #Mean mansoni epg from 1st/2nd kato katz, NAs removed
           s_mans_mean2018_narm = mean(c(P5_kk1_epg, P5_kk2_epg, P6_kk1_epg, P6_kk2_epg), na.rm = TRUE),
           #Number of samples contributing to mean
           s_mans_mean2018_w = length(which(!is.na(c(P5_kk1_epg, P5_kk2_epg, P6_kk1_epg, P6_kk2_epg)))),
           #WHO infection categories
           s_mans_mean_cat2018 = cut(s_mans_mean2018_narm,
                                     breaks = c(0,1,100,400, Inf),
                                     labels = c("No", "Lo", "Md", "Hi"), right = FALSE),
           pzq = 1,
           extra_pzq = 0)  %>%
    select(Child_ID, year, School, pzq, extra_pzq,
           s_haem1 = P5_omega_total,
           s_haem2 = P6_omega_total,
           s_haem_mean = s_haem_mean2018,
           s_haem_mean_narm = s_haem_mean2018_narm,
           s_haem_mean_w = s_haem_mean2018_w,
           s_haem_mean_cat = s_haem_mean_cat2018,
           s_mans1_1 = P5_kk1_epg,
           s_mans1_2 = P5_kk2_epg,
           s_mans2_1 = P6_kk1_epg,
           s_mans2_2 = P6_kk2_epg,
           s_mans_mean1,
           s_mans_mean2,
           s_mans_mean12 = s_mans_mean2018,
           s_mans_mean_narm = s_mans_mean2018_narm,
           s_mans_mean_w = s_mans_mean2018_w,
           s_mans_mean_cat = s_mans_mean_cat2018) %>% ungroup()

#Data check
  #make sure each subject only has one record:
    bad_id_dat3 <- dat3 %>%
```

```
      group_by(Child_ID) %>%
      summarise(nobs = n()) %>%
      filter(nobs > 1) %>%
      pull(Child_ID)

      bad_id_dat3
```

```
## [1] "LR/1/053"
```

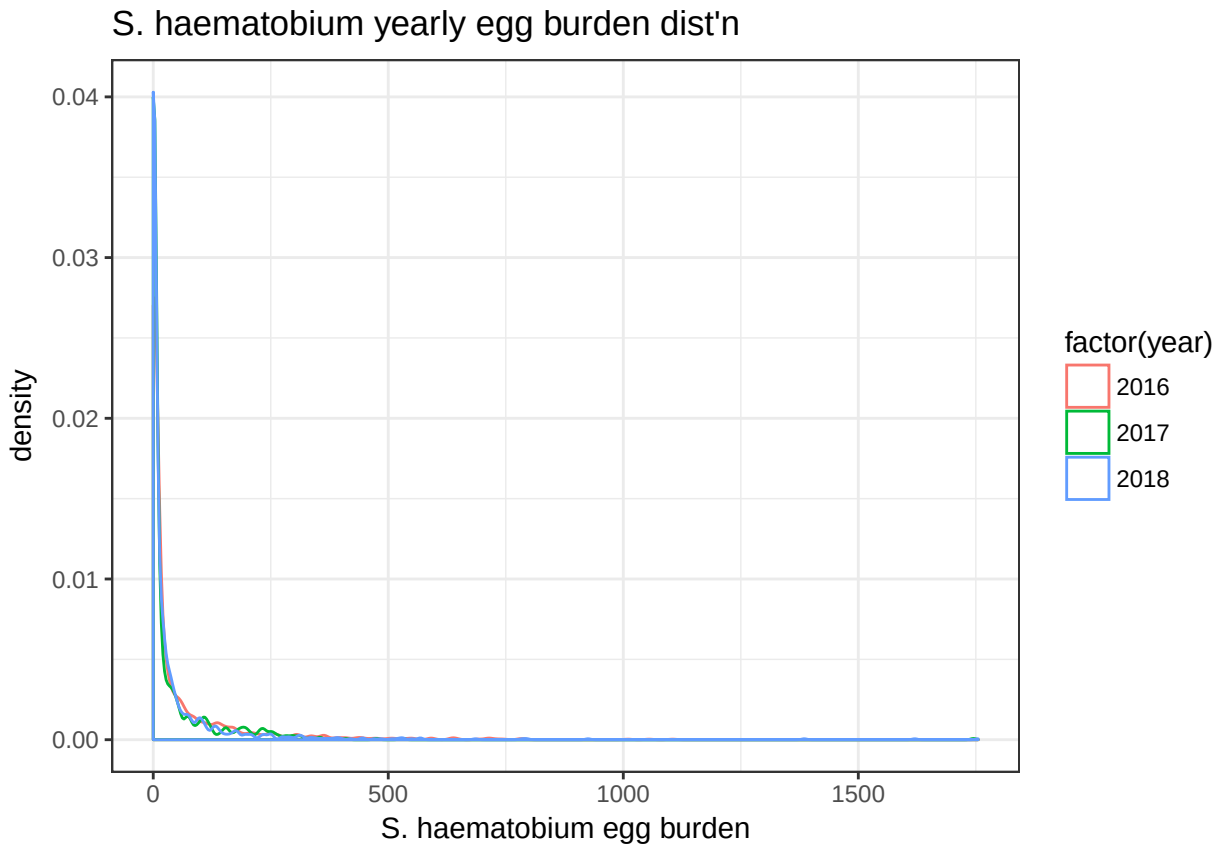
```
  #This person ended up with two records somehow, going to take the safe route: remove both records
    dat3 <- dat3 %>% filter(Child_ID != enquo(bad_id_dat3)[[2]])
```

```
#Full dataset (in long format) shared by Stanford, constructed by Isabel
stanford <- read_csv("~/RemaisWork/Schisto/Stanford/Human_Parasitology_data/human_data_2018Mat1518.csv") %>%
  mutate(ID = factor(ID),    #Convert some variables to factors
         School = factor(School),
         Village = factor(Village),
         year_fac = factor(year),
         cluster = factor(cluster),
         Intervention.type = factor(Intervention.type),
         pzq = ifelse(year %in% c(2017, 2018), 1, 0))

#same code as above to remove individual with multiple observation in the same year
    stanford <- stanford %>% filter(ID != enquo(bad_id_dat3)[[2]])

#Jason's full dataset
jason_dat <- read_csv("~/RemaisWork/Schisto/Stanford/Human_Parasitology_data/Jason_human_data_2018.csv") %>%
    mutate(ID = factor(ID),    #Convert some variables to factors
           School = factor(School),
           Village = factor(Village),
           year_fac = factor(year),
           sex = factor(sex),
           cluster = factor(cluster),
           Intervention.type = factor(Intervention.type),
           pzq = ifelse(year %in% c(2017, 2018), 1, 0))


#Full dataset in long format from data reads/manipulations above
full_long <- rbind(dat1, dat2, dat3) %>%
  full_join(interventions, by = c("School", "year")) %>%
  #Join with stanford dataset to get cluster and sex
  full_join(stanford %>% select(ID, year, sex, cluster),
            by = c("Child_ID" = "ID", "year" = "year")) %>%
  mutate(School = factor(School),
         Child_ID = factor(Child_ID),
         year_fac = factor(year),
         pzq = factor(pzq))

#Full dataset in wide format
full_wide <- dat1 %>%
  full_join(dat2 %>% filter(extra_pzq != 1),
            by = c("Child_ID", "School"),
            suffix = c("_2016", "_2017")) %>%
  full_join(dat3, by = c("Child_ID", "School")) %>%
  full_join(interventions %>% filter(year == 2018), by = c("School"))
```

Exploratory

Check egg burden distribution

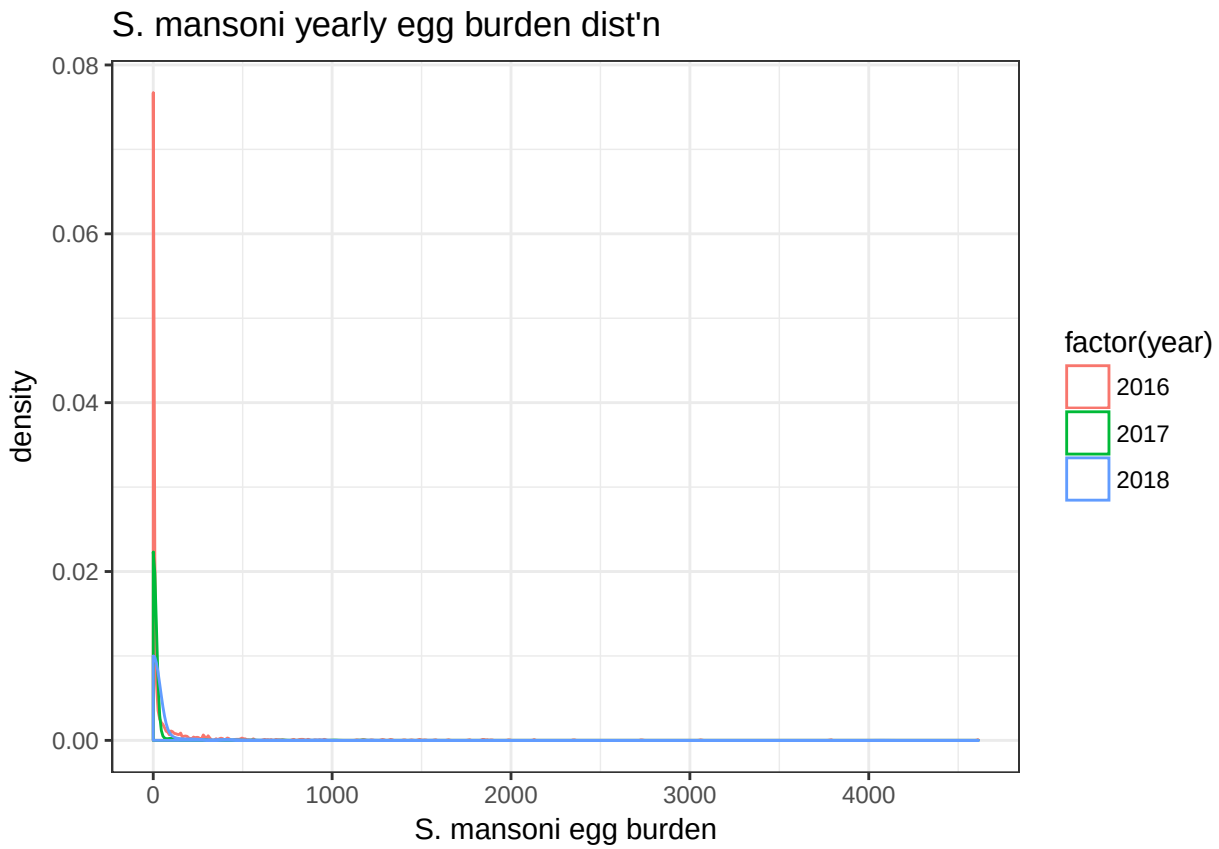
```
full_long %>% filter(extra_pzq != 1) %>%
  ggplot(aes(x = s_haem_mean_narm, col = factor(year))) + geom_density() +
  theme_bw() + xlab("S. haematobium egg burden") + ggtitle("S. haematobium yearly egg burden dist'n")
```




```
full_long %>% filter(extra_pzq != 1) %>%
  group_by(year, School) %>%
  summarise(mean_haem = mean(s_haem_mean_narm),
            var_haem = var(s_haem_mean_narm),
            mean_haem_rmv0 = mean(s_haem_mean_narm[which(s_haem_mean_narm != 0)]),
            var_haem_rmv0 = var(s_haem_mean_narm[which(s_haem_mean_narm != 0)]))
```

```
## # A tibble: 44 x 6
## # Groups:   year [?]
##     year School mean_haem var_haem mean_haem_rmv0 var_haem_rmv0
##    <dbl> <fct>      <dbl>    <dbl>          <dbl>         <dbl>
##  1 2016. DF          7.38     289.           10.4          379.
##  2 2016. DT         66.1    17172.           73.3        18529.
##  3 2016. FS         38.4     6952.           42.5         7544.
##  4 2016. GG         45.0     4629.           53.7         5063.
##  5 2016. GK         52.2    10327.           63.9        11915.
##  6 2016. LR        NaN        NaN            78.3        15122.
##  7 2016. MA        111.     28788.          112.         28991.
##  8 2016. MB          9.29     577.           18.1          971.
##  9 2016. MD         84.1    17075.           95.0        18266.
## 10 2016. ME         91.0    31524.          107.         35288.
## # ... with 34 more rows
```

```
full_long %>% filter(extra_pzq != 1) %>%
  ggplot(aes(x = s_mans_mean12, col = factor(year))) + geom_density() + theme_bw() +
  xlab("S. mansoni egg burden") + ggtitle("S. mansoni yearly egg burden dist'n")
```



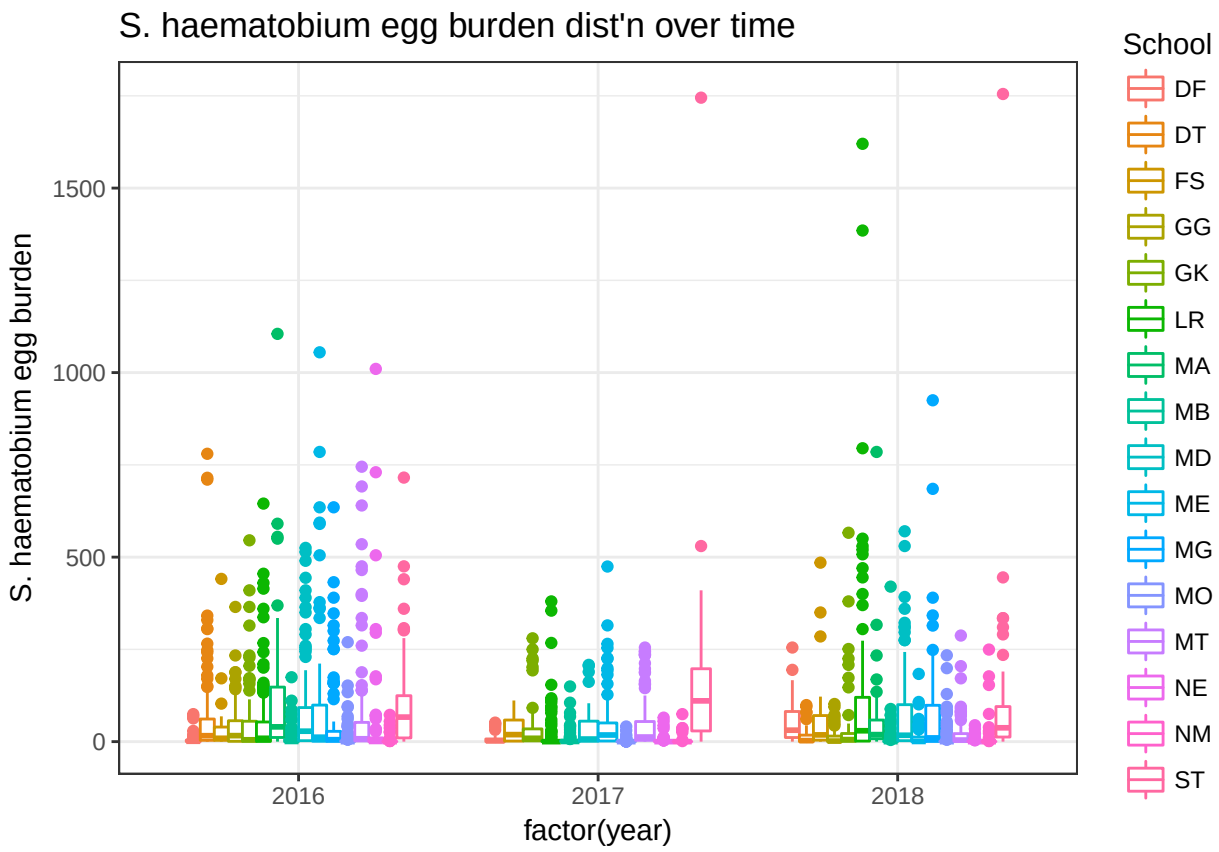

```
full_long %>% filter(extra_pzq != 1) %>%
  group_by(year, School) %>%
  summarise(mean_mans = mean(s_mans_mean_narm),
            var_mans = var(s_mans_mean_narm),
            mean_mans_rmv0 = mean(s_mans_mean_narm[which(s_mans_mean_narm != 0)]),
            var_mans_rmv0 = var(s_mans_mean_narm[which(s_mans_mean_narm != 0)]))
```

```
## # A tibble: 44 x 6
## # Groups:   year [?]
##     year School mean_mans  var_mans mean_mans_rmv0 var_mans_rmv0
##    <dbl> <fct>      <dbl>     <dbl>          <dbl>         <dbl>
##  1 2016. DF         8.25     718.            56.6          2437.
##  2 2016. DT       NaN        NaN             18.0           104.
##  3 2016. FS         0.266      2.20           8.25           NA
##  4 2016. GG       557.    448243.          602.         457359.
##  5 2016. GK         0.         0.           NaN             NA
##  6 2016. LR       130.    274885.          334.         647577.
##  7 2016. MA       NaN        NaN             307.         256249.
##  8 2016. MB        39.1    14983.           103.          33401.
##  9 2016. MD       NaN        NaN             51.6          9415.
## 10 2016. ME         6.49    1504.            37.1          7817.
## # ... with 34 more rows
```

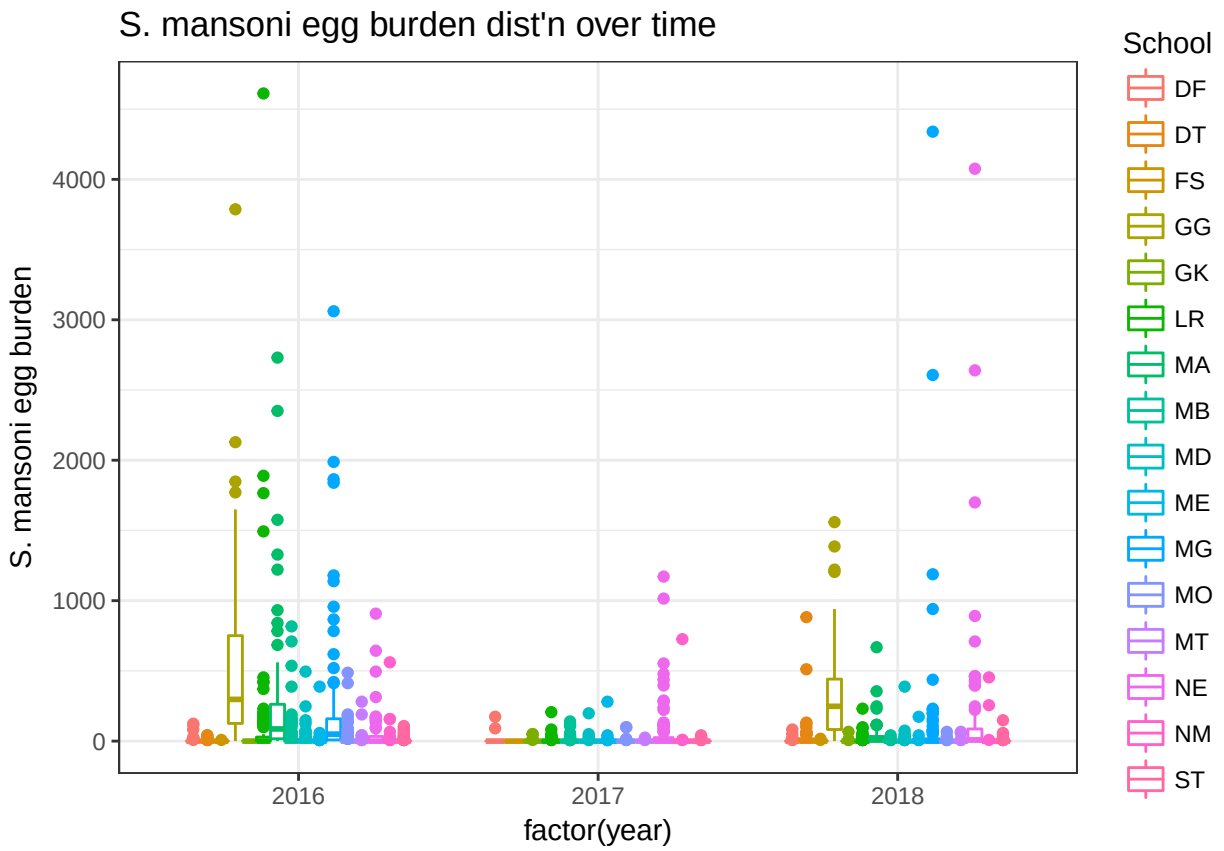
Data is clearly overdispersed. Negative binomial distribution, maybe 0-inflated model will be necessary

Community level egg burden over time

```
full_long %>% filter(extra_pzq != 1) %>%
  ggplot(aes(x = factor(year), y = s_haem_mean_narm, col = School)) + theme_bw() + geom_boxplot() +
    ylab("S. haematobium egg burden") + ggtitle("S. haematobium egg burden dist'n over time")
```

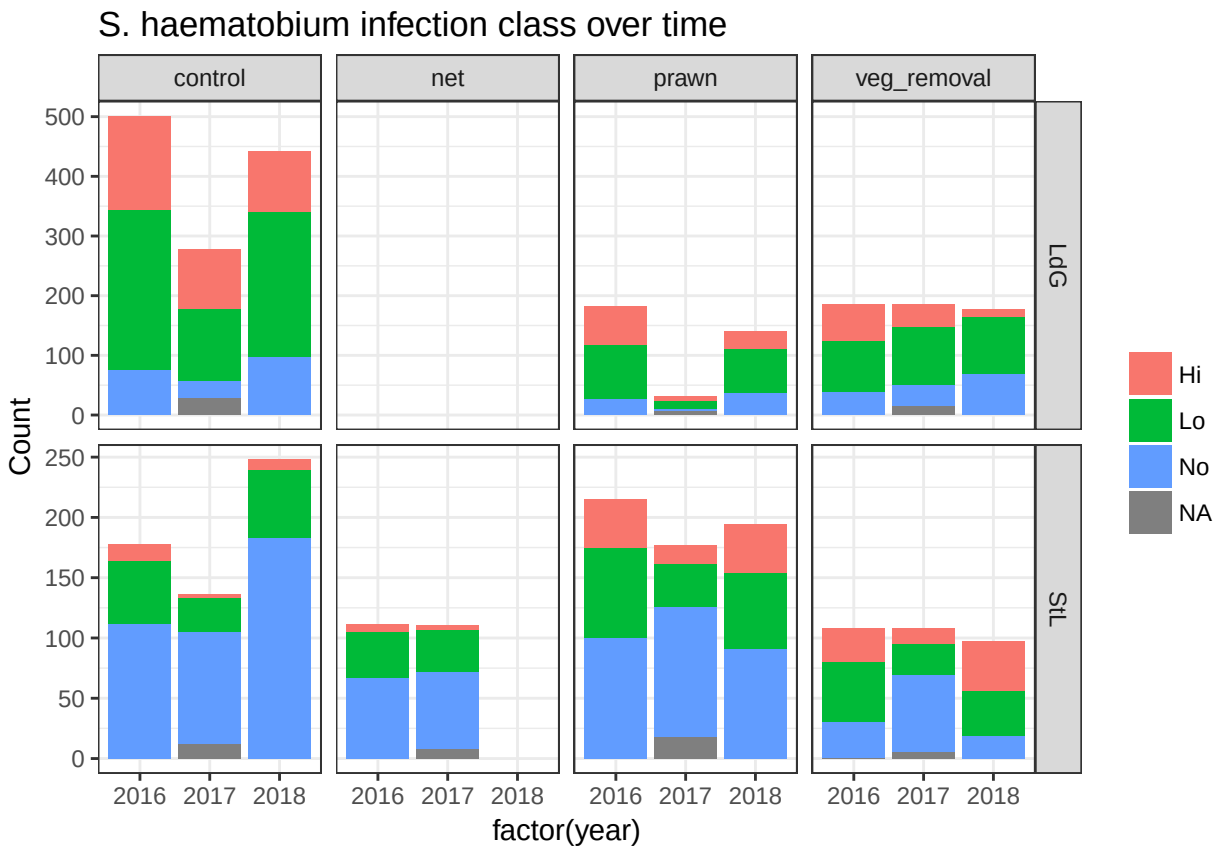



```
full_long %>% filter(extra_pzq != 1) %>%
  ggplot(aes(x = factor(year), y = s_mans_mean_narm, col = School)) + theme_bw() + geom_boxplot() +
  ylab("S. mansoni egg burden") + ggtitle("S. mansoni egg burden dist'n over time")
```



Intervention grouped infection level (WHO categories) over time

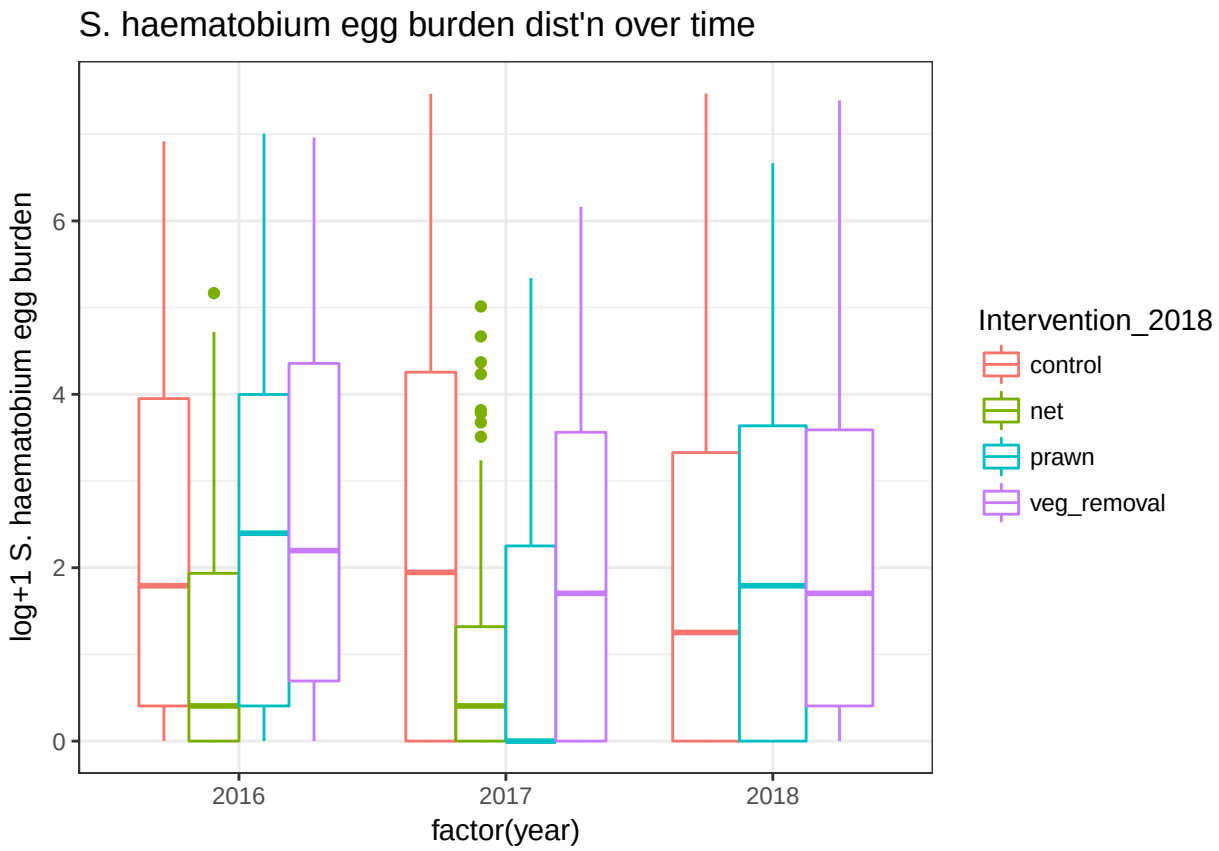
```
full_long %>% filter(extra_pzq != 1) %>%
  ggplot(aes(x = factor(year), fill = factor(s_haem_mean_cat, levels = c("Hi", "Lo", "No")))) +
    geom_bar() +
    theme_bw() + theme(legend.title = element_blank()) +
    ylab("Count") + ggtitle("S. haematobium infection class over time") +
    facet_grid(Region~Intervention_2018, scales = "free_y")
```



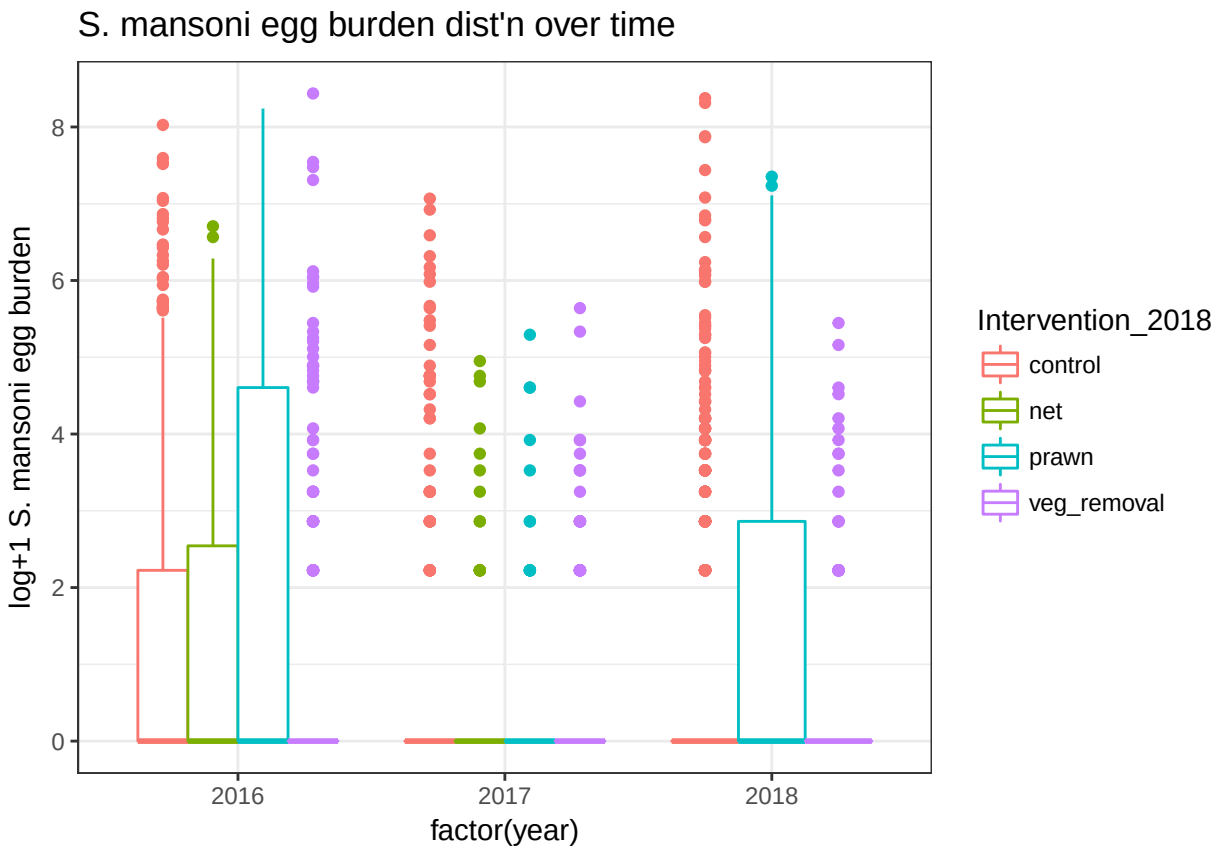

```
full_long %>% filter(extra_pzq != 1) %>%
  ggplot(aes(x = factor(year), fill = factor(s_mans_mean_cat, levels = c("Hi", "Md", "Lo", "No")))) +
    geom_bar() +
    theme_bw() + theme(legend.title = element_blank()) +
    ylab("Count") + ggtitle("S. mansoni infection class over time") +
    facet_grid(Region~Intervention_2018, scales = "free_y")
```

Intervention status log+1 egg burden over time

```
full_long %>% filter(extra_pzq != 1) %>%
  ggplot(aes(x = factor(year), y = log(s_haem_mean_narm+1), col = Intervention_2018)) +
    theme_bw() + geom_boxplot() +
    ylab("log+1 S. haematobium egg burden") +
    ggtitle("S. haematobium egg burden dist'n over time")
```

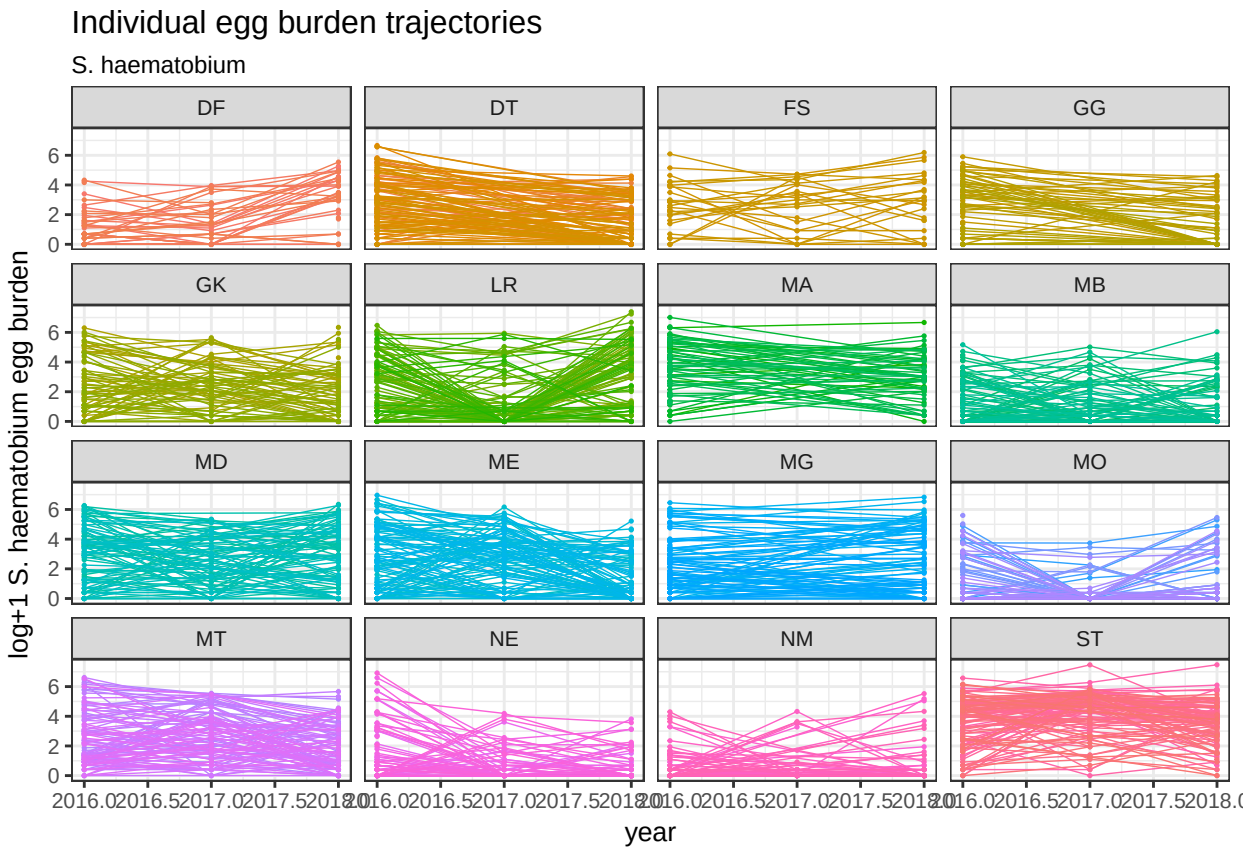



```
full_long %>% filter(extra_pzq != 1) %>%
  ggplot(aes(x = factor(year), y = log(s_mans_mean_narm+1), col = Intervention_2018)) +
    theme_bw() + geom_boxplot() +
    ylab("log+1 S. mansoni egg burden") +
    ggtitle("S. mansoni egg burden dist'n over time")
```

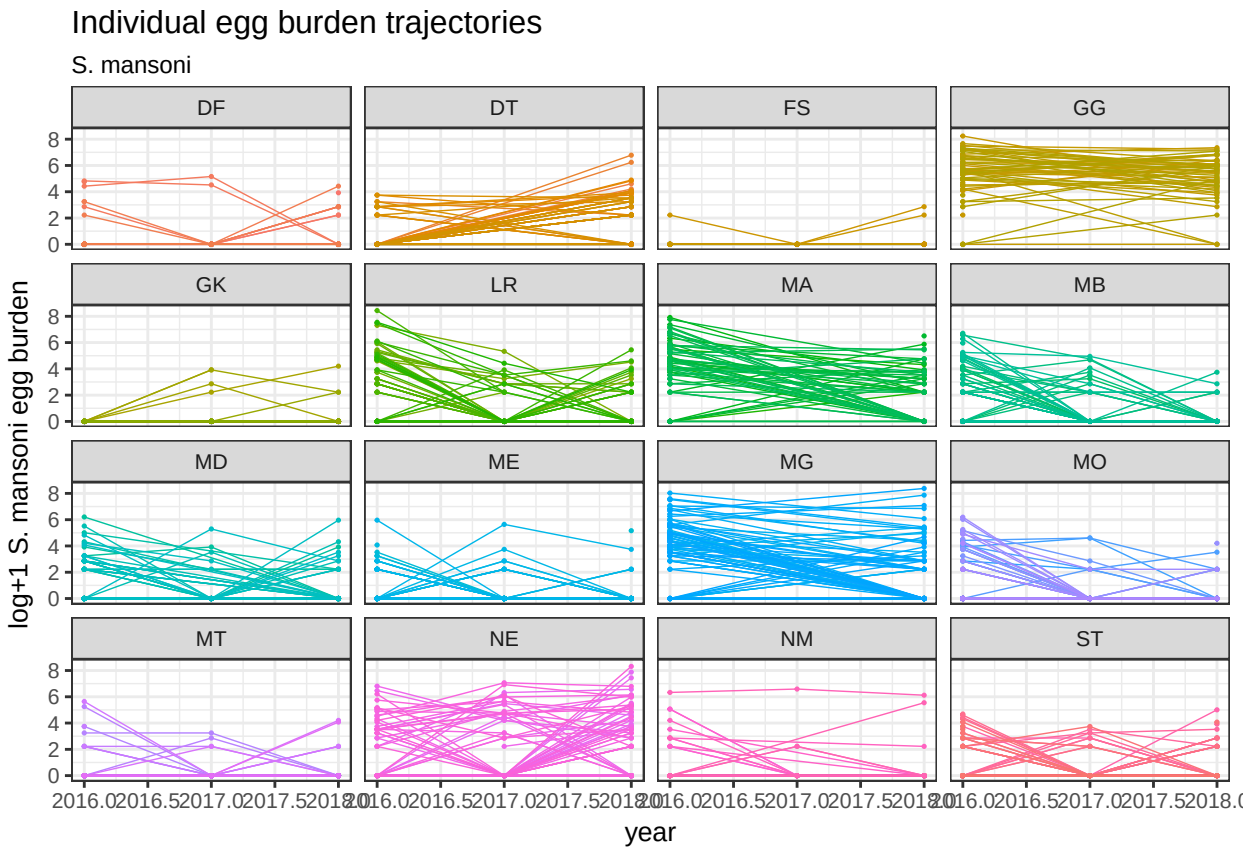


Individual level mean egg burden over time (spaghetti plots)

```
full_long %>% filter(extra_pzq != 1) %>%
  ggplot(aes(x = year, y = log(s_haem_mean_narm+1), col = Child_ID)) +
    geom_line(size = 0.25) + geom_point(size = 0.25) +
    theme_bw(base_size = 10) + theme(legend.position = "none") +
    facet_wrap(~School, ncol = 4) +
    ylab("log+1 S. haematobium egg burden") +
    ggtitle("Individual egg burden trajectories", subtitle = "S. haematobium")
```

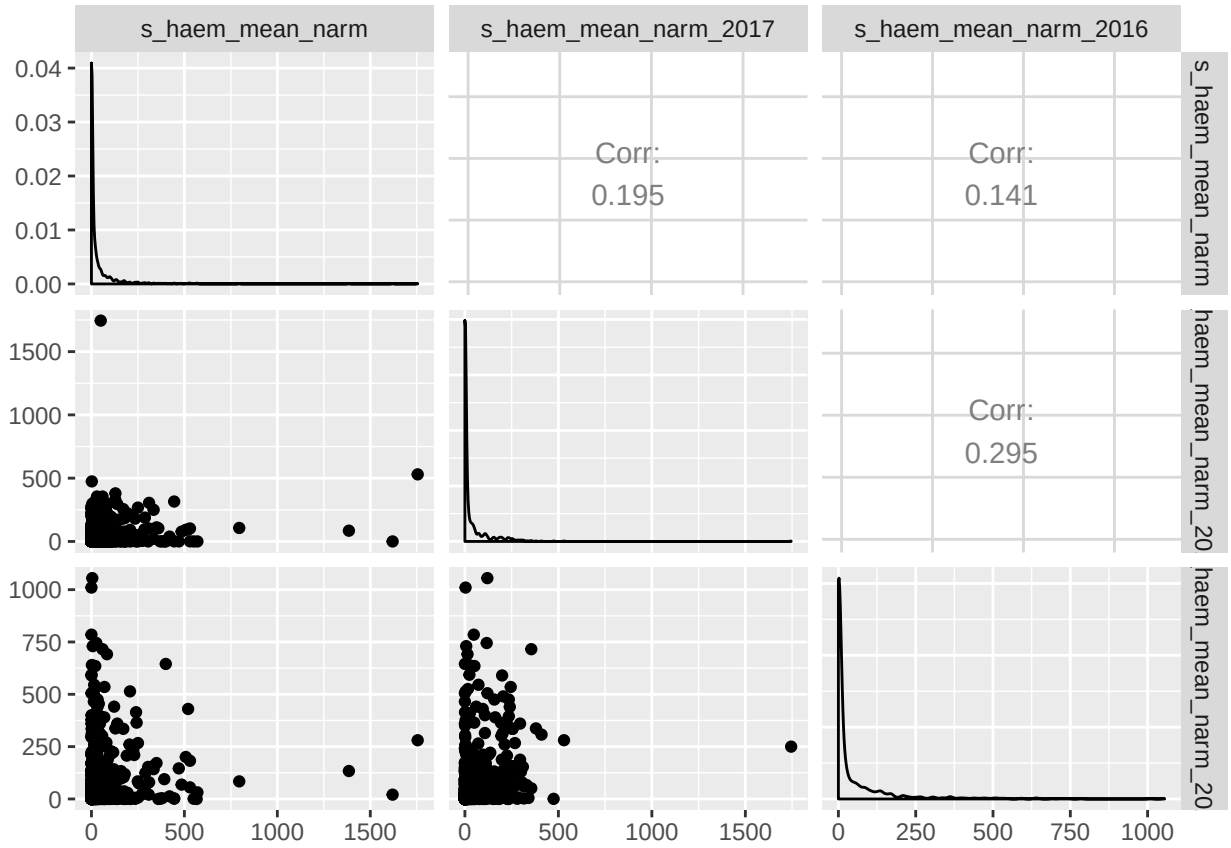



```
full_long %>% filter(extra_pzq != 1) %>%
  ggplot(aes(x = year, y = log(s_mans_mean_narm+1), col = Child_ID)) +
    geom_line(size = 0.25) + geom_point(size = 0.25) +
    theme_bw(base_size = 10) + theme(legend.position = "none") +
    facet_wrap(~School, ncol = 4) +
    ylab("log+1 S. mansoni egg burden") +
    ggtitle("Individual egg burden trajectories", subtitle = "S. mansoni")
```

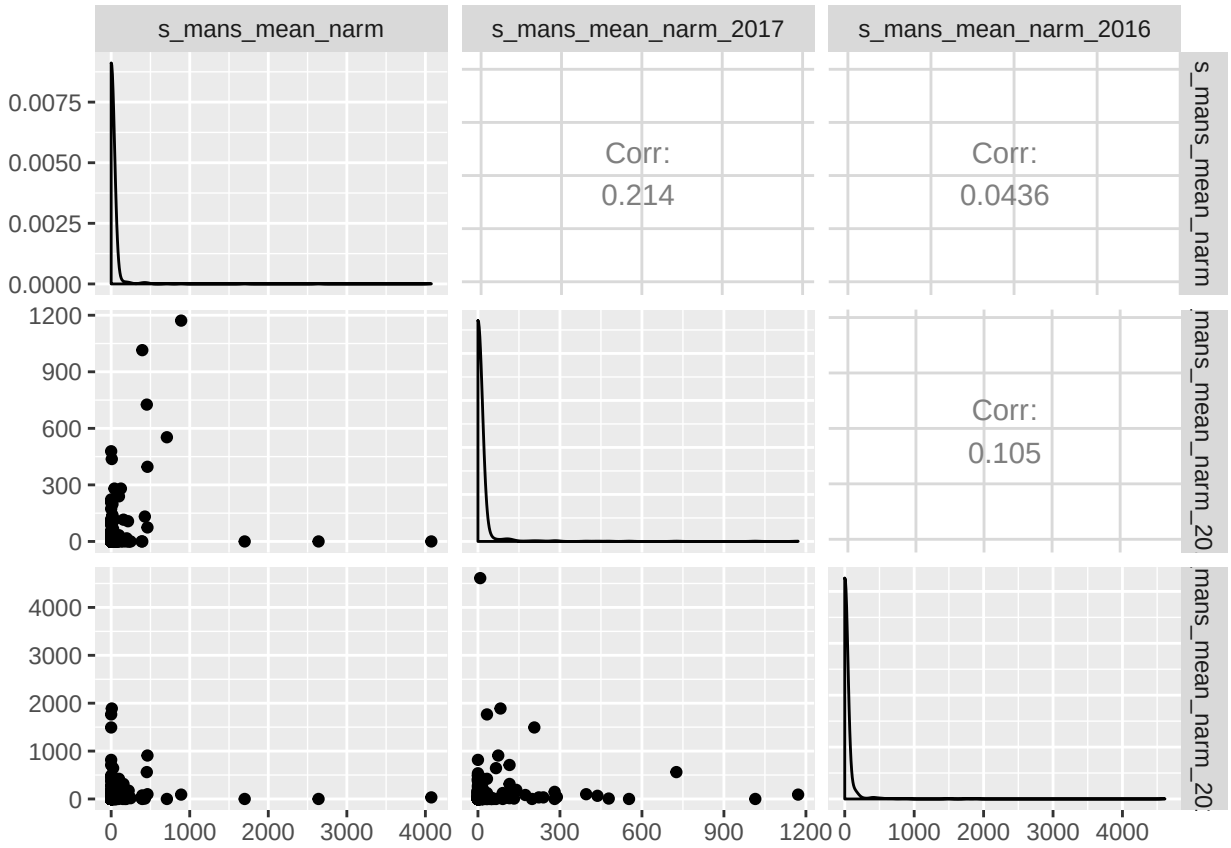


Correlation between past infection and infection in 2018

```
full_wide %>%
  filter(extra_pzq_2017 != 1) %>%
  select(s_haem_mean_narm, s_haem_mean_narm_2017, s_haem_mean_narm_2016) %>%
  ggpairs()
```

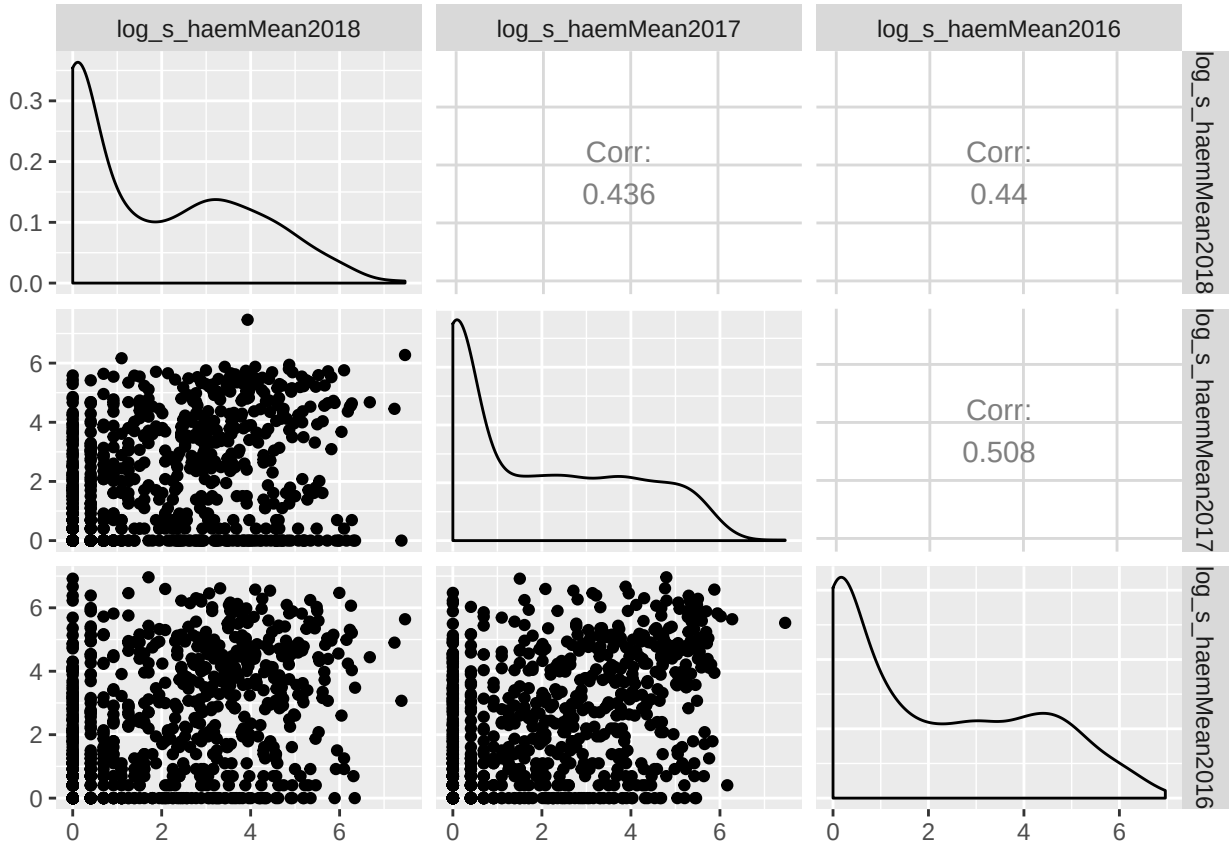



```
full_wide %>%
  filter(extra_pzq_2017 != 1) %>%
  select(s_mans_mean_narm, s_mans_mean_narm_2017, s_mans_mean_narm_2016) %>%
  ggpairs()
```

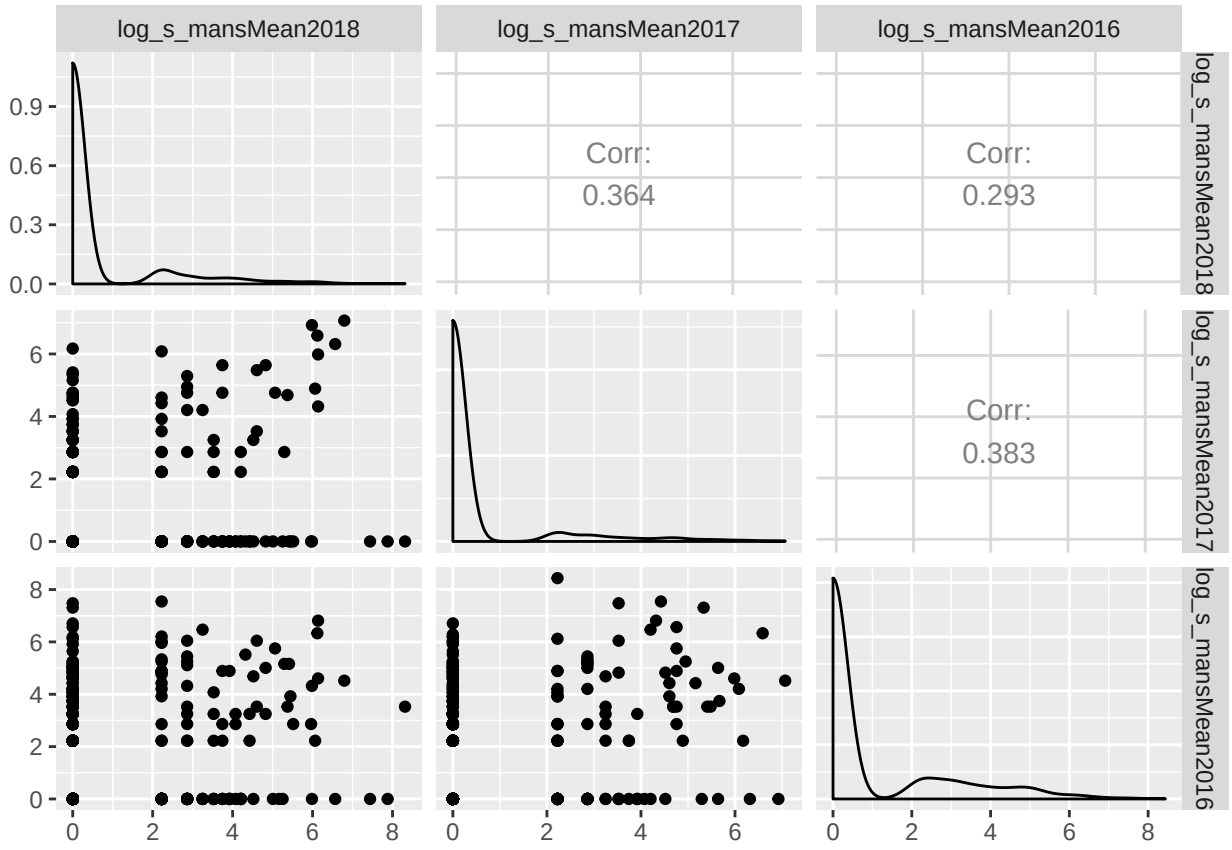


Correlation between past infection and infection in 2018, log+1 transformed

```
full_wide %>% filter(extra_pzq_2017 != 1) %>%
  mutate(log_s_haemMean2018 = log(s_haem_mean_narm+1),
         log_s_haemMean2017 = log(s_haem_mean_narm_2017+1),
         log_s_haemMean2016 = log(s_haem_mean_narm_2016+1)) %>%
  select(log_s_haemMean2018, log_s_haemMean2017, log_s_haemMean2016) %>%
  ggpairs()
```

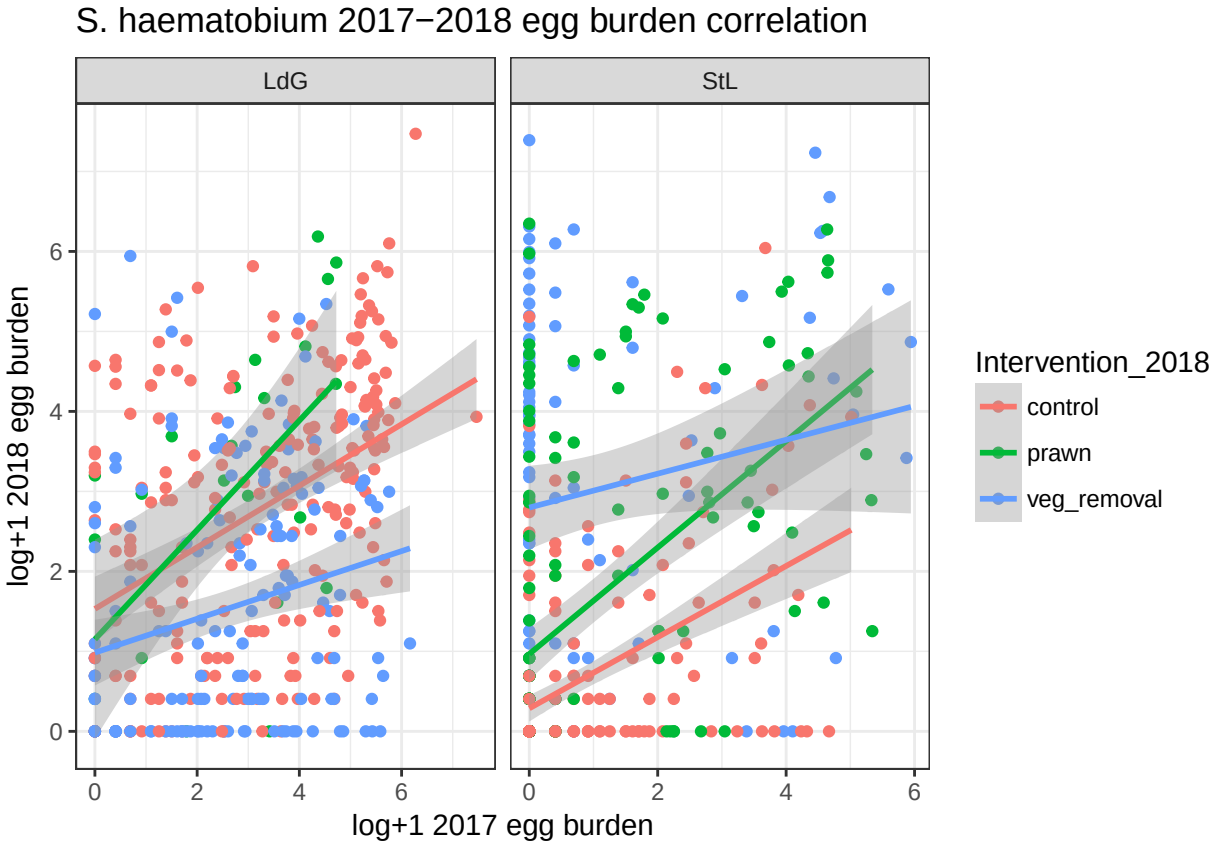



```
full_wide %>% filter(extra_pzq_2017 != 1) %>%
  mutate(log_s_mansMean2018 = log(s_mans_mean_narm+1),
         log_s_mansMean2017 = log(s_mans_mean_narm_2017+1),
         log_s_mansMean2016 = log(s_mans_mean_narm_2016+1)) %>%
  select(log_s_mansMean2018,
         log_s_mansMean2017,
         log_s_mansMean2016) %>%
  ggpairs()
```

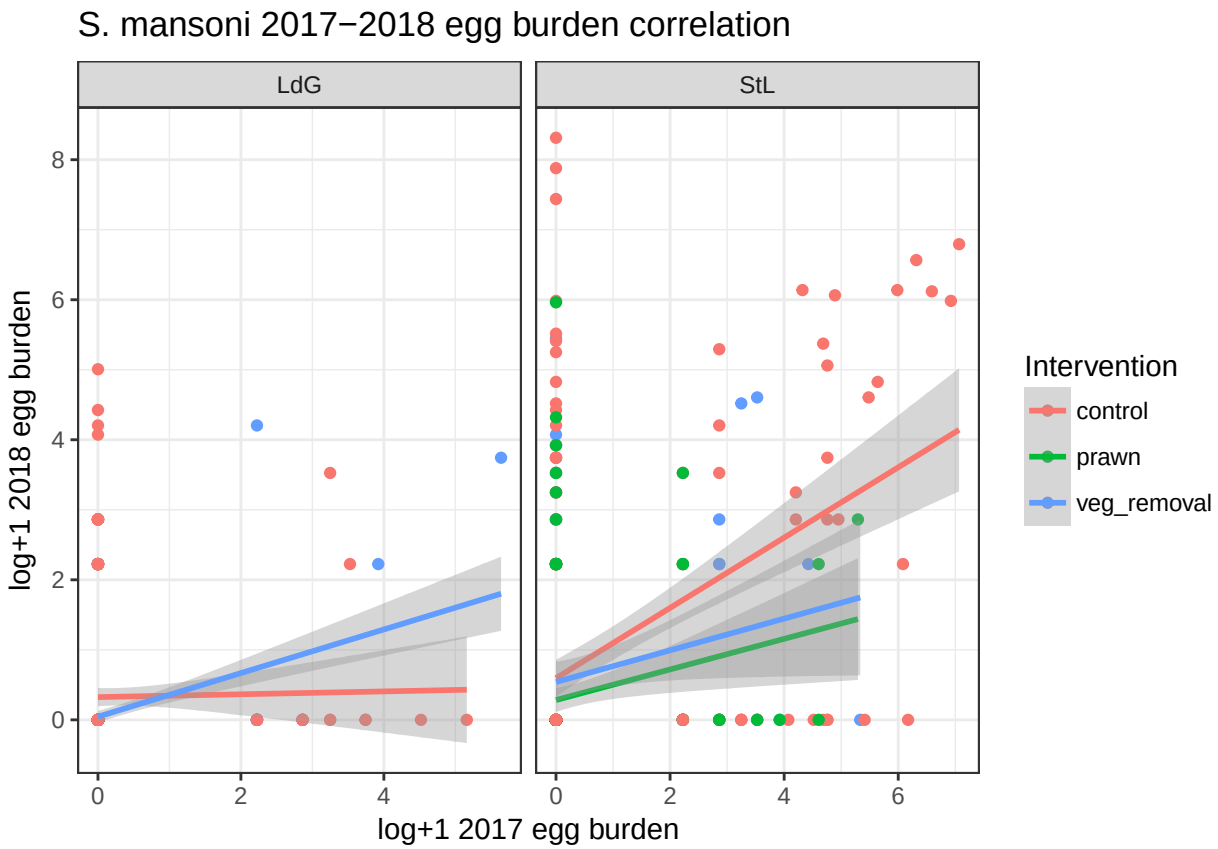


Correlations between egg burden in 2017 and egg burden in 2018, stratified by intervention

```
full_wide %>% filter(extra_pzq_2017 != 1) %>%
  ggplot(aes(x = log(s_haem_mean_narm_2017+1), y = log(s_haem_mean_narm+1), col = Intervention_2018)) +
    geom_point() + stat_smooth(method = "lm") +
    facet_grid(.~Region, scales = "free") +
    theme_bw() + xlab("log+1 2017 egg burden") + ylab("log+1 2018 egg burden") +
    ggtitle("S. haematobium 2017-2018 egg burden correlation")
```

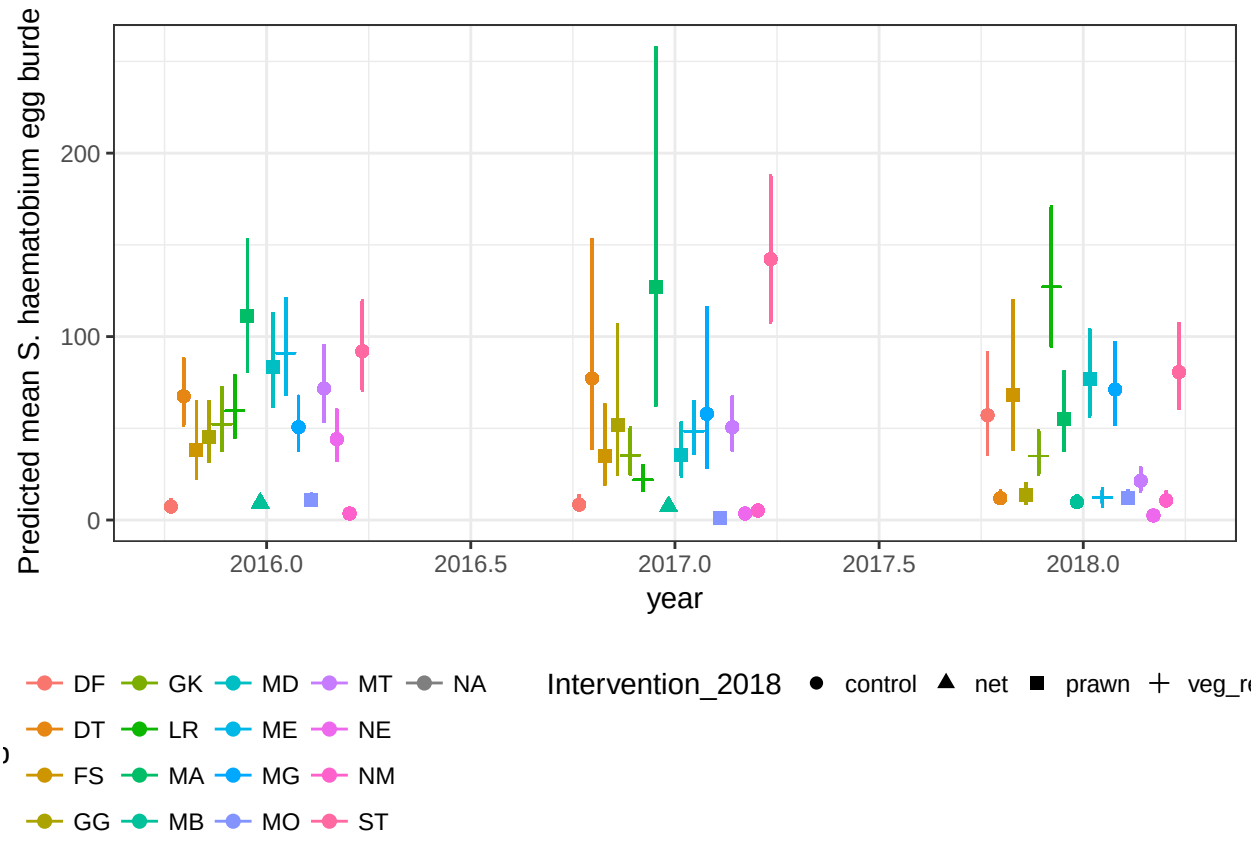



```
full_wide %>% filter(extra_pzq_2017 != 1) %>%
  ggplot(aes(x = log(s_mans_mean_narm_2017+1), y = log(s_mans_mean_narm+1), col = Intervention)) +
    geom_point() + stat_smooth(method = "lm") +
    facet_grid(.~Region, scales = "free") +
    theme_bw() + xlab("log+1 2017 egg burden") + ylab("log+1 2018 egg burden") +
    ggtitle("S. mansoni 2017-2018 egg burden correlation")
```

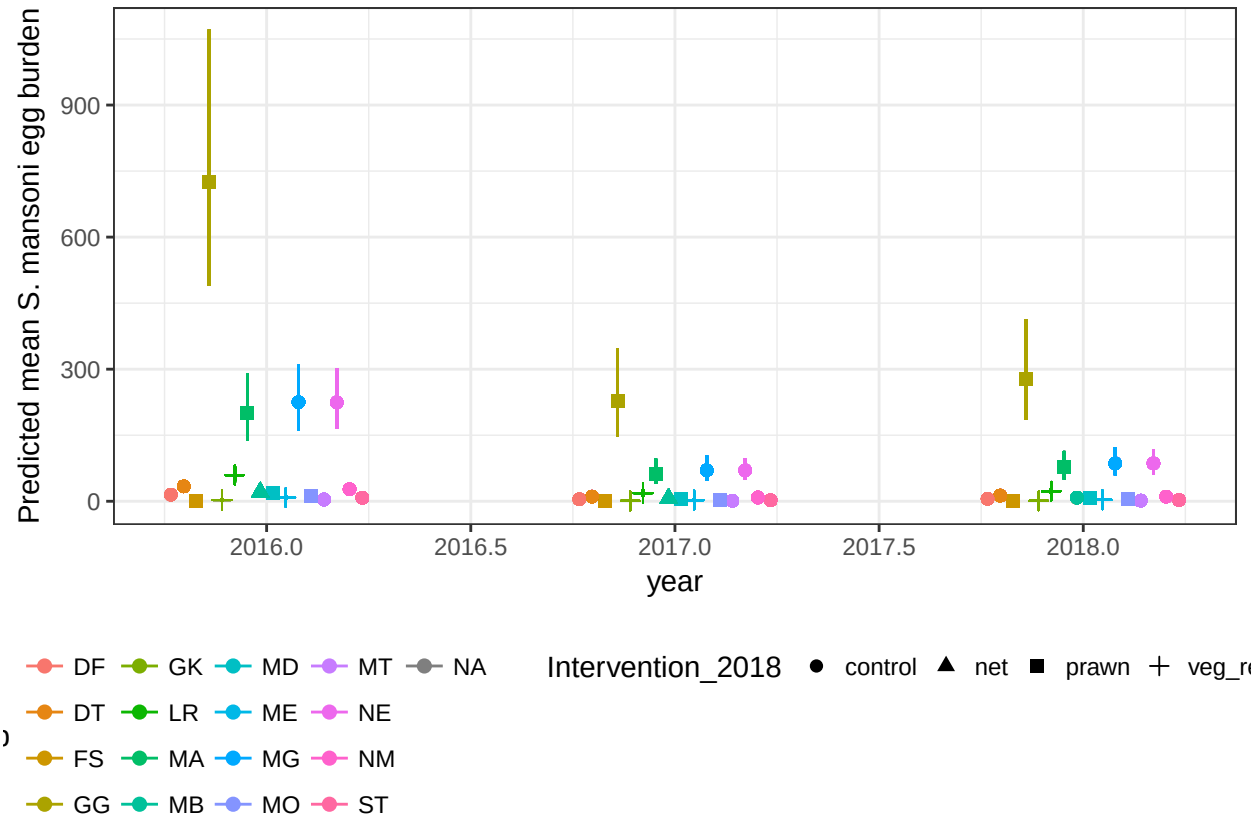


Community level mean egg burden across years and communities

```
haem_int_yr <- glm.nb(round(s_haem_mean_narm) ~ year_fac*School,
                      weights = s_haem_mean_w,
                      data = full_long %>% filter(extra_pzq != 1))

  ggpredict(haem_int_yr, c("year_fac", "School")) %>%
    mutate(year = factor(x)) %>%
    full_join(full_long %>% select(year_fac, School, Intervention_2018),
              by = c("year" = "year_fac", "group" = "School")) %>%
    ggplot(aes(x = x, y = predicted, col = group, shape = Intervention_2018)) +
      geom_point(position = position_dodge(width = 0.5), size = 2) +
      geom_errorbar(aes(ymin = conf.low, ymax = conf.high, x = x),
                    position = position_dodge(width = 0.5),
                    width = 0.1) +
      theme_bw() + theme(legend.position = "bottom") +
      xlab("year") + ylab("Predicted mean S. haematobium egg burden")
```




```
mans_int_yr <- glm.nb(round(s_mans_mean_narm) ~ year_fac+School,
                      weights = s_mans_mean_w,
                      data = full_long %>% filter(extra_pzq != 1))

    ggpredict(mans_int_yr, c("year_fac", "School")) %>%
    mutate(year = factor(x)) %>%
    full_join(full_long %>% select(year_fac, School, Intervention_2018),
              by = c("year" = "year_fac", "group" = "School")) %>%
    ggplot(aes(x = x, y = predicted, col = group, shape = Intervention_2018)) +
      geom_point(position = position_dodge(width = 0.5), size = 2) +
      geom_errorbar(aes(ymin = conf.low, ymax = conf.high, x = x),
                    position = position_dodge(width = 0.5),
                    width = 0.1) +
      theme_bw() + theme(legend.position = "bottom") +
      xlab("year") + ylab("Predicted mean S. mansoni egg burden")
```



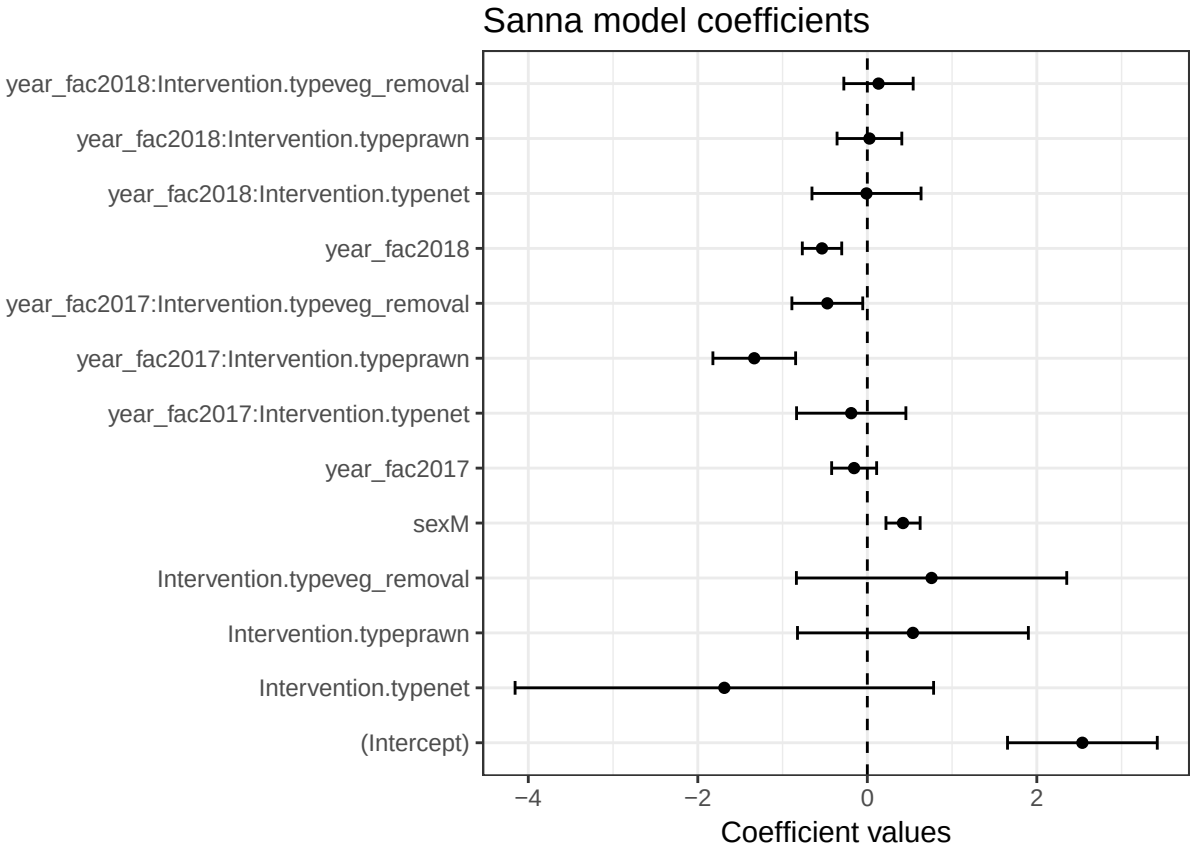
Others' models

Sanna: neg binomial egg output w/ individual and community (`school`) random effects

$$Y_{ijt} = \beta_0 + \epsilon_{0i} + \epsilon_{0j} + \beta_1 year_t + \beta_2 Intervention_{jt} + \beta_3 year_t \times Intervention_{jt} + \beta_4 sex_i$$

where β_{0i} and β_{0j} are individual and community level random effects

```
#Original code from Sanna's script:
#nbinom.SH<-glmmadmb(Data~(1|ID)+(1|Village)+Label*treatment+sex, data = SH.df, family="nbinom")

#glmmadmb throws an error for me, use updated version, glmmTMB
#Run original model with stanford data:
mods_haem_stan <- glmmTMB(ShW~year_fac*Intervention.type+sex + (1|ID) + (1|School),
                          data = stanford %>% filter(Tx_early != 1),
                          family="nbinom2")

  as.data.frame(round(cbind(summary(mods_haem_stan)$coef[[1]],
                            confint(mods_haem_stan)[1:13,]), 3)[,c(1,2,5,6,3,4)]) %>%
    rename("lower" = !!names(.[3]),
           "upper" = !!names(.[4])) %>%
    mutate(coefficient = rownames(summary(mods_haem_stan)$coef[[1]])) %>%
  ggplot(aes(x = Estimate, y = coefficient)) + theme_bw() +
    geom_point() + geom_errorbarh(aes(xmin = lower, xmax = upper, y = coefficient), height = 0.25) +
    geom_vline(xintercept = 0, lty = 2) +
    ylab("") + xlab("Coefficient values") +
    ggtitle("Sanna model coefficients")
```




```
#Stanford summary of interventions in villages
stanford %>% group_by(School, year) %>%
  summarise(net01 = mean(net),
            prawn01 = mean(prawn),
            veg01 = mean(veg_removal),
            Intervention = unique(Intervention.type))
```

```
## # A tibble: 48 x 6
## # Groups:   School [?]
##    School  year net01 prawn01 veg01 Intervention
##    <fct>  <int> <dbl>   <dbl> <dbl> <fct>
##  1 DF      2016    0.      0.    0. control
##  2 DF      2017    0.      0.    0. control
##  3 DF      2018    0.      0.    0. control
##  4 DT      2016    0.      0.    0. control
##  5 DT      2017    0.      0.    0. control
##  6 DT      2018    0.      0.    0. control
##  7 FS      2016    1.      1.    0. prawn
##  8 FS      2017    1.      1.    0. prawn
##  9 FS      2018    1.      1.    0. prawn
## 10 GG      2016    1.      1.    0. prawn
## # ... with 38 more rows
```

I think there's an issue with how the dataset is formatted here: since the intervention is assigned to the community and doesn't vary across years in the dataset, this model is trying to estimate the effect of intervention across all three years, when it was only acting on the third (2018) data point in reality

Jason: BACI analysis with individual and year random effects nested within community (`village`) random effects

$$Y_{ijt} = \beta_0 + \epsilon_{0j} + \epsilon_{0ij} + \epsilon_{0jt} + \beta_1 year_t + \beta_2 Intervention_{jt} + \beta_3 year_t \times Intervention_{jt} + \beta_4 sex_i + \beta_5 lake_j$$

```
jas_mod <- glmer(Sh ~ Intervention.type*year + sex + lake + (1|Village/ID) + (1|Village/year), family="binomia
###NOT CONVERGING###
```

I can't get this model to converge. I'm also not sure it's getting the most out of our data: surely 2016 holds valuable information for us. We're also parsing egg burden down to a binary presence-absence variable and using a logistic model which causes us to lose quite a lot of information on infection intensity.

I also think we need to think critically about our use of random effects model. After all, a random effect is an assumption placed on the distribution of the variable for which we are estimating a random effect. Here we're assuming that communities' mean egg burden is normally distributed around some global mean and within that community, each individual's egg burden is normally distributed around the village level mean, and each year

Berkeley approach

We propose a sequence of analyses with increasingly *fewer* assumptions in order to estimate the effect of interventions on egg burden. We assume individual egg burden follows a negative binomial distribution $Y_{ijt} \sim NB(\mu, \theta)$

Model 1: Individual egg burden, Y_{ijt} is determined by a common transmission intensity shared by all communities, T, praziquantel administration, P_t, and intervention in a given year, I_{jt}

Proposed DAG:

Graphical representation of the data-generating mechanism corresponding to assumptions of Model 1. Y_{ijt} is the measured egg burden at each time point, T is the transmission intensity that produces Y_{ijt} at each time point, I_{jt} is the intervention in each community at time t, and P_t is praziquantel administration

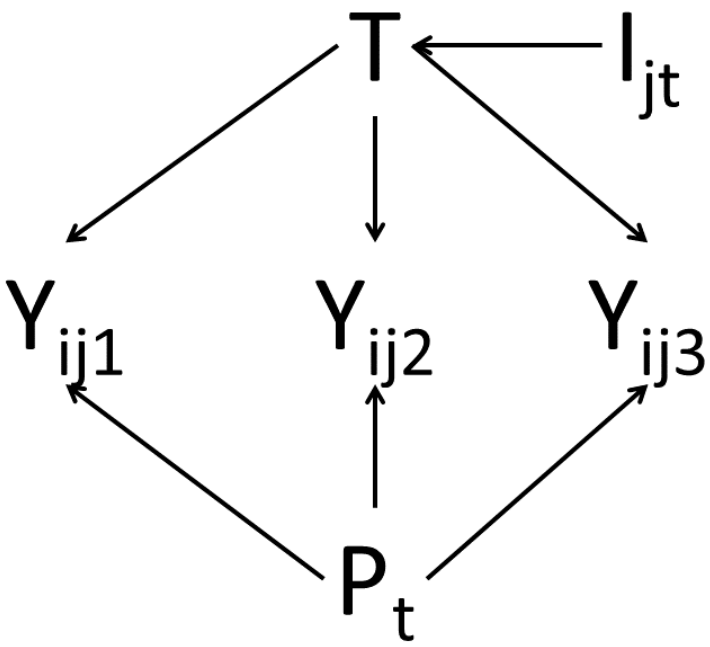


Figure 2: Proposed DAG for model 1

Proposed Model:

$$Y_{ijt} = \beta_0 + \beta_1 I_{jt} + \beta_2 P_t$$

Therefore in year 1 with no Praziquantel and no intervention:

$$Y_{ij1} = \beta_0$$

In year 2 with praziquantel, but no intervention:

$$Y_{ij2} = \beta_0 + \beta_2$$

And in year 3 with both praziquantel and intervention:

$$Y_{ij3} = \beta_0 + \beta_1 I_{jt} + \beta_2$$

This model will be fit by stratifying on intervention groups and comapring them to control communities, making I_{jt} a simple binary variable defined at the community level with control communities as the reference group and estimate β_1 as our parameter of interest using a negative binomial GLM

Since this model fails to account for variability in transmission between communities other than that which is presumed to be caused by the intervention, associations may be confounded by baseline variability in community-level transmission: e.g. intervention communities have inherently higher transmission intensity than control communities. Model 2 addresses this by including main effects of communities.

Model 2: Individual egg burden, Y_{ijt} is determined by each community's unique transmission intensity, T_j, praziquantel administration, P_t, and interventions, I_{jt}

Proposed DAG:

Graphical representation of the data-generating mechanism corresponding to assumptions of Model 2. Y_{ijt} is the measured egg burden at each time point, T_j is the transmission intensity unique to each community that produces Y_{ijt} at each time point, I_{jt} is the intervention in each community, and P_t is praziquantel administration

Proposed Model:

$$Y_{ijt} = \beta_0 + \beta_1 I_{jt} + \beta_2 P_t + \beta_3 T_j$$

Therefore in year 1 with no Praziquantel and no intervention:

$$Y_{ij1} = \beta_0 + \beta_3 T_j$$

In year 2 with praziquantel, but no intervention:

$$Y_{ij2} = \beta_0 + \beta_2 + \beta_3 T_j$$

And in year 3 with both praziquantel and intervention:

$$Y_{ij3} = \beta_0 + \beta_1 I_{jt} + \beta_2 + \beta_3 T_j$$

We'll again fit this model with I_{jt} as a simple binary variable defined at the community-year level with control communities as the reference group and estimate β_1 as our parameter of interest using a negative binomial GLM. $\beta_0 + \beta_3$ can be interpreted as the community-level transmission intensity, T_j

This is better since we're treating communities as their own entities and therefore controlling for inter-community variability in transmission, but we're still treating *individual* egg burdens as independent when we know that individuals are likely correlated. Model 3 will address this concern by controlling for individuals' previous egg burden. In addition to controlling for confounding by inter-community and inter-individual variability, conditioning on prior outcome is also a good way to control for potential unmeasured confounding from other sources

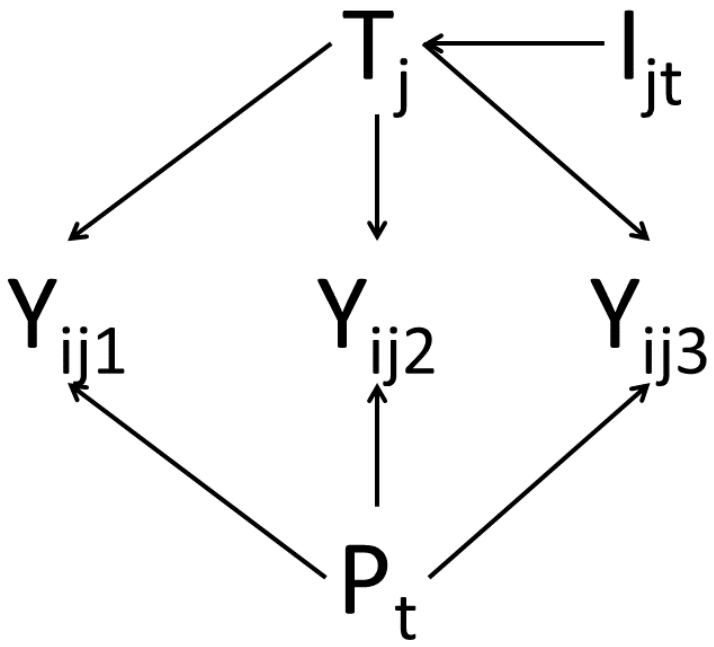


Figure 3: Proposed DAG for model 2

Model 3: Individual egg burden, Y_{ijt} is determined by each community's unique transmission intensity that varies by year, T_{jt}, praziquantel administration, P_t, and interventions, I_{jt}

Proposed DAG:

Graphical representation of the data-generating mechanism corresponding to assumptions of Model 3. Y_{ijt} is the measured egg burden at each time point, T_j is the transmission intensity unique to each community that produces Y_{ijt} at each time point, I_{jt} is the intervention in each community, and P_t is praziquantel administration

Proposed Model:

$$Y_{ijt} = \beta_0 + \beta_1 I_{jt} + \beta_2 P_t + \beta_3 T_j + \beta_4 Year_t + \beta_5 T_j \times Year_t$$

Therefore in year 1 with no Praziquantel and no intervention:

$$Y_{ij1} = \beta_0 + \beta_3 T_j$$

In year 2 with praziquantel, but no intervention:

$$Y_{ij2} = \beta_0 + \beta_2 + \beta_3 T_j + \beta_4 Year_2 + \beta_5 T_j \times Year_2$$

And in year 3 with both praziquantel and intervention:

$$Y_{ij3} = \beta_0 + \beta_1 I_{jt} + \beta_2 + \beta_3 T_j + \beta_4 Year_3 + \beta_5 T_j \times Year_3$$

We'll again fit this model with I_{jt} as a simple binary variable defined at the community-year level with control communities as the reference group and estimate β_1 as our parameter of interest using a negative binomial GLM. $\beta_0 + \beta_3 + \beta_4 + \beta_5$ can be interpreted as the community-level transmission intensity in year t, T_{jt}

This model is still not accounting for potential correlation between individuals that is not explained at the community level, which is what models 4 and 5 will account for

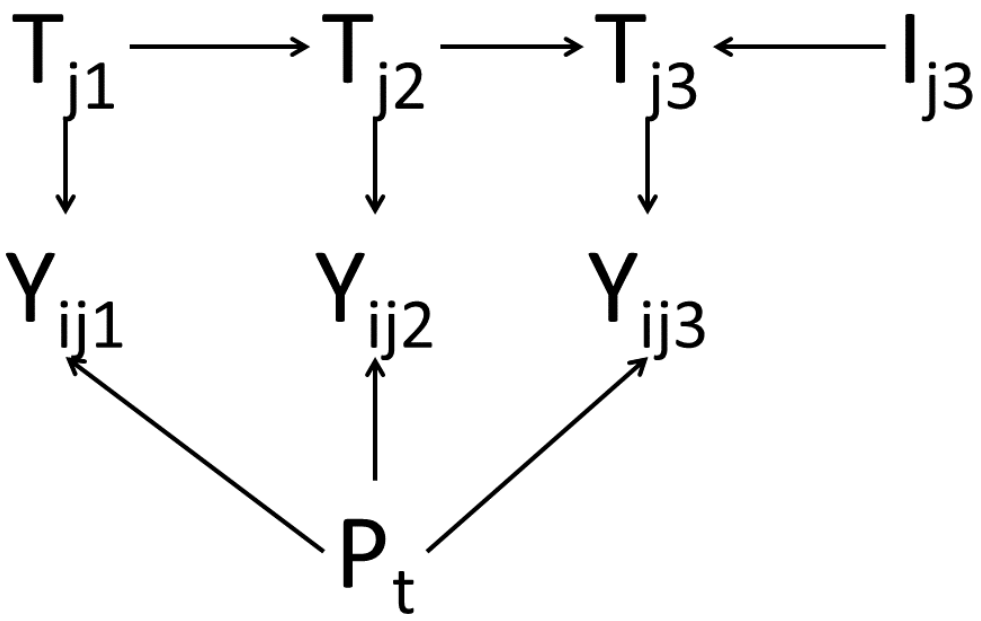


Figure 4: Proposed DAG for model 3

Model 4: Transition model in which individual egg burden, Y_{ijt} is associated with previous infection, Y_{ijt-1}, and determined by each community's transmission intensity, T_j and interventions, I_{jt}

Proposed DAG:

Graphical representation of the data-generating mechanism corresponding to assumptions of Model 4. Y_{ijt} is the measured egg burden at each time point, T_j is the transmission intensity unique to each community that produces Y_{ijt} at each time point, and I_{jt} is the intervention in each community. Including Y_{ijt-1} controls for confounding by T_j regardless of whether dummy variables on communities serve as a good proxy for T_j.

Proposed Model:

$$Y_{ijt} = \beta_0 + \beta_1 I_{jt} + \beta_2 \log(Y_{ijt-1} + 1) + \beta_3 T_j$$

Therefore in year 2 with no intervention:

$$Y_{ij2} = \beta_0 + \beta_2 \log(Y_{ij1} + 1) + \beta_3 T_j$$

And in year 3 with intervention:

$$Y_{ij3} = \beta_0 + \beta_1 I_{jt} + \beta_2 \log(Y_{ij2} + 1) + \beta_3 T_j$$

We'll again fit this model with I_{jt} as a simple binary variable defined at the community level with control communities as the reference group and estimate β_1 as our parameter of interest using a negative binomial GLM. Since the outcome is only defined in 2017 and 2018, no need to control for praziquantel administration which occurred in both years.

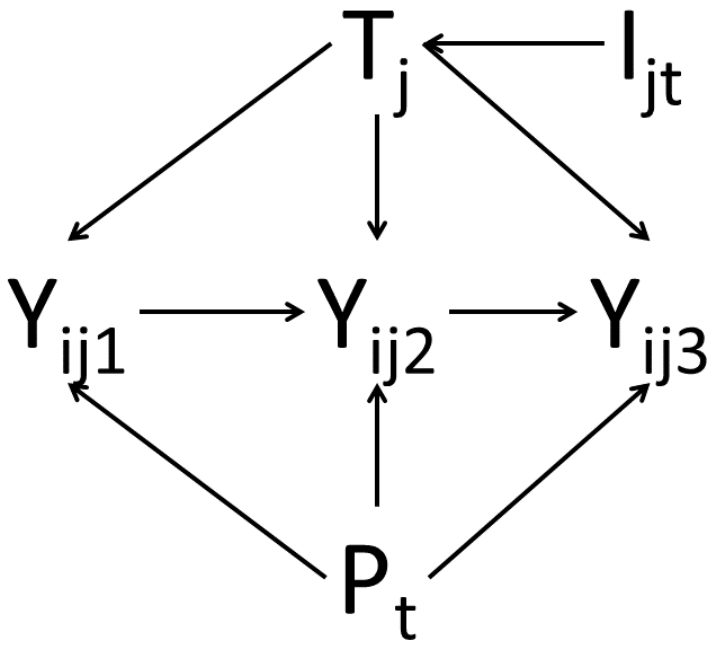


Figure 5: Proposed DAG for model 4

Model 5: Transition model in which individual egg burden, Y_{ijt} is associated with previous infection, Y_{ijt-1}, and determined by each community's transmission intensity that varies with year, $T_j t$, and interventions, I_{jt}

Proposed DAG:

Graphical representation of the data-generating mechanism corresponding to assumptions of Model 5. Y_{ijt} is the measured egg burden at each time point, $T_j t$ is the transmission intensity unique to each community in each year that produces Y_{ijt} at each time point, and I_{jt} is the intervention in each community. Including Y_{ijt-1} controls for confounding by T_j regardless of whether dummy variables on communities serve as a good proxy for T_j.

Proposed Model:

$$Y_{ijt} = \beta_0 + \beta_1 I_{jt} + \beta_2 \log(Y_{ijt-1} + 1) + \beta_3 T_j + \beta_4 Year_t + \beta_5 T_j \times Year_t$$

Therefore in year 2 with no intervention (and year 2 as reference for the $Year_t$ variable):

$$Y_{ij2} = \beta_0 + \beta_2 \log(Y_{ij1} + 1) + \beta_3 T_j$$

And in year 3 with intervention:

$$Y_{ij3} = \beta_0 + \beta_1 I_{jt} + \beta_2 \log(Y_{ij2} + 1) + \beta_3 T_j + \beta_4 Year_t + \beta_5 T_j \times Year_t$$

We'll again fit this model with I_{jt} as a simple binary variable defined at the community level with control communities as the reference group and estimate β_1 as our parameter of interest using a negative binomial GLM. Since the outcome is only defined in 2017 and 2018, no need to control for praziquantel administration which occurred in both years.

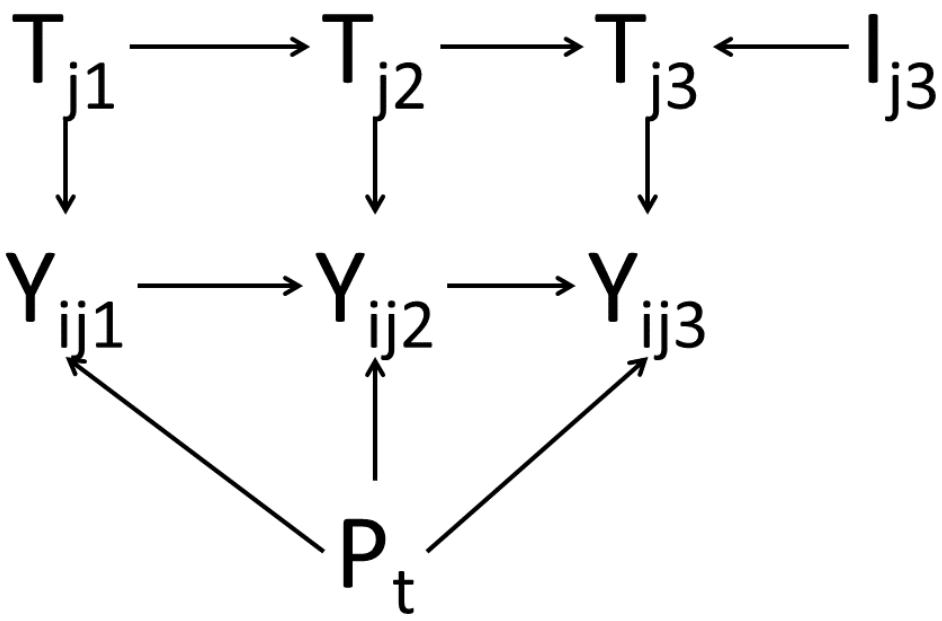


Figure 6: Proposed DAG for model 5

Implementation

Models 4 and 5 actually require a bit more data wrangling to add the lag variables:

```
mod4_dat <- full_long %>% arrange(Child_ID, year) %>% group_by(Child_ID) %>%
  mutate(s_haem_mean_l1 = lag(s_haem_mean),
         log_s_haem_mean_l1 = lag(log(s_haem_mean+1)),
         s_haem_mean_narm_l1 = lag(s_haem_mean_narm),
         log_s_haem_mean_narm_l1 = lag(log(s_haem_mean_narm+1)),
         s_mans_mean1_l1 = lag(s_mans_mean1),
         log_s_mans_mean1_l1 = lag(log(s_mans_mean1+1)),
         s_mans_mean2_l1 = lag(s_mans_mean2),
         log_s_mans_mean2_l1 = lag(log(s_mans_mean2+1)),
         s_mans_mean12_l1 = lag(s_mans_mean12),
         log_s_mans_mean12_l1 = lag(log(s_mans_mean12+1)),
         s_mans_mean_narm_l1 = lag(s_mans_mean_narm),
         log_s_mans_mean_narm_l1 = lag(log(s_mans_mean_narm+1)))
```

Schistosoma haematobium

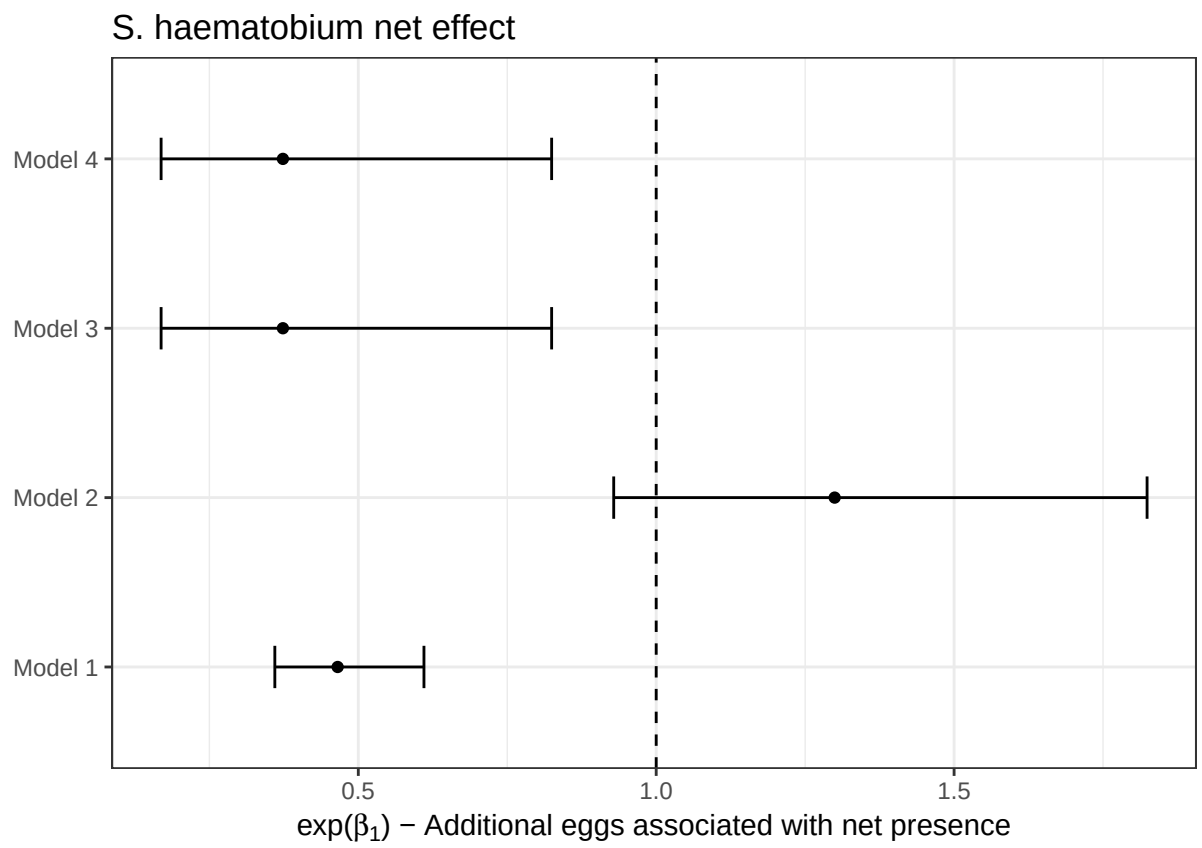
Net effect

To test for a net effect, we'll compare communities which had a net installed in 2016 (therefore influencing egg burden in 2017) to control communities which had no net leading up to 2017

```
#Model 1
mod1_haem_mean_narm_net <- glm.nb(round(s_haem_mean_narm) ~ Net + pzq,
                                  weights = s_haem_mean_w,
                                  data = full_long %>% filter(extra_pzq != 1 &
```

```
                                                    Intervention %in% c("control", "net") &
                                                    year != 2018))

  mod1_haem_narm_net_res <- as.data.frame(round(cbind(summary(mod1_haem_mean_narm_net)$coef,
                                      confint(mod1_haem_mean_narm_net)), 3)[,c(1,2,5,6,3,4)])
    mod1_haem_narm_net_res$model <- "Model 1"

#Model 2
mod2_haem_mean_narm_net <- glm.nb(round(s_haem_mean_narm) ~ Net + pzq + School,
                                  weights = s_haem_mean_w,
                                  data = full_long %>% filter(extra_pzq != 1 &
                                                    Intervention %in% c("control", "net") &
                                                    year != 2018))

  mod2_haem_narm_net_res <- as.data.frame(round(cbind(summary(mod2_haem_mean_narm_net)$coef,
                                      confint(mod2_haem_mean_narm_net)), 3)[,c(1,2,5,6,3,4)])
    mod2_haem_narm_net_res$model <- "Model 2"

#Model 3
mod3_haem_mean_narm_net <- glm.nb(round(s_haem_mean_narm) ~ Net + pzq + School*year_fac,
                                  weights = s_haem_mean_w,
                                  data = full_long %>% filter(extra_pzq != 1 &
                                                    Intervention %in% c("control", "net") &
                                                    year != 2018))

  mod3_haem_narm_net_res <- as.data.frame(round(cbind(summary(mod3_haem_mean_narm_net)$coef,
                                    na.omit(confint(mod3_haem_mean_narm_net))), 3)[,c(1,2,5,6,3,4)])
    mod3_haem_narm_net_res$model <- "Model 3"

#Model 4
mod4_haem_mean_narm_net <- glm.nb(round(s_haem_mean_narm) ~ Net + School + log_s_haem_mean_narm_l1,
                                  weights = s_haem_mean_w,
                                  data = mod4_dat %>% filter(extra_pzq != 1 &
                                                    Intervention %in% c("control", "net") &
                                                    year != 2018))

  mod4_haem_narm_net_res <- as.data.frame(round(cbind(summary(mod3_haem_mean_narm_net)$coef,
                                     na.omit(confint(mod3_haem_mean_narm_net))), 3)[,c(1,2,5,6,3,4)])
    mod4_haem_narm_net_res$model <- "Model 4"

## Model 5 not run since can't exclude 2018 ##
#mod5_haem_mean_narm_net <- glm.nb(round(s_haem_mean_narm) ~ Net + School*year_fac + log_s_haem_mean_narm_l1,
#                                  weights = s_haem_mean_w,
#                                  data = mod4_dat %>% filter(extra_pzq != 1 &
#                                                    Intervention %in% c("control", "net")))

#  mod5_haem_narm_net_res <- as.data.frame(round(cbind(summary(mod5_haem_mean_narm_net)$coef,
#                                     na.omit(confint(mod5_haem_mean_narm_net))), 3)[,c(1,2,5,6,3,4)])
#    mod5_haem_narm_net_res$model <- "Model 5"

#Plot net effect estimate
rbind(mod1_haem_narm_net_res["Net",], mod2_haem_narm_net_res["Net",], mod3_haem_narm_net_res["Net",],
      mod4_haem_narm_net_res["Net",]) %>%
  rename("lower" = !!names(.[3]),
         "upper" = !!names(.[4])) %>%
  ggplot(aes(x = exp(Estimate), y = model)) + theme_bw() +
    geom_point() + geom_errorbarh(aes(xmin = exp(lower), xmax = exp(upper), y = model), height = 0.25) +
    geom_vline(xintercept = 1, lty = 2) +
    ylab("") + xlab(expression(paste("exp(",beta[1], ") - Additional eggs associated with net presence"))) +
```

```
    ggtitle("S. haematobium net effect")
```

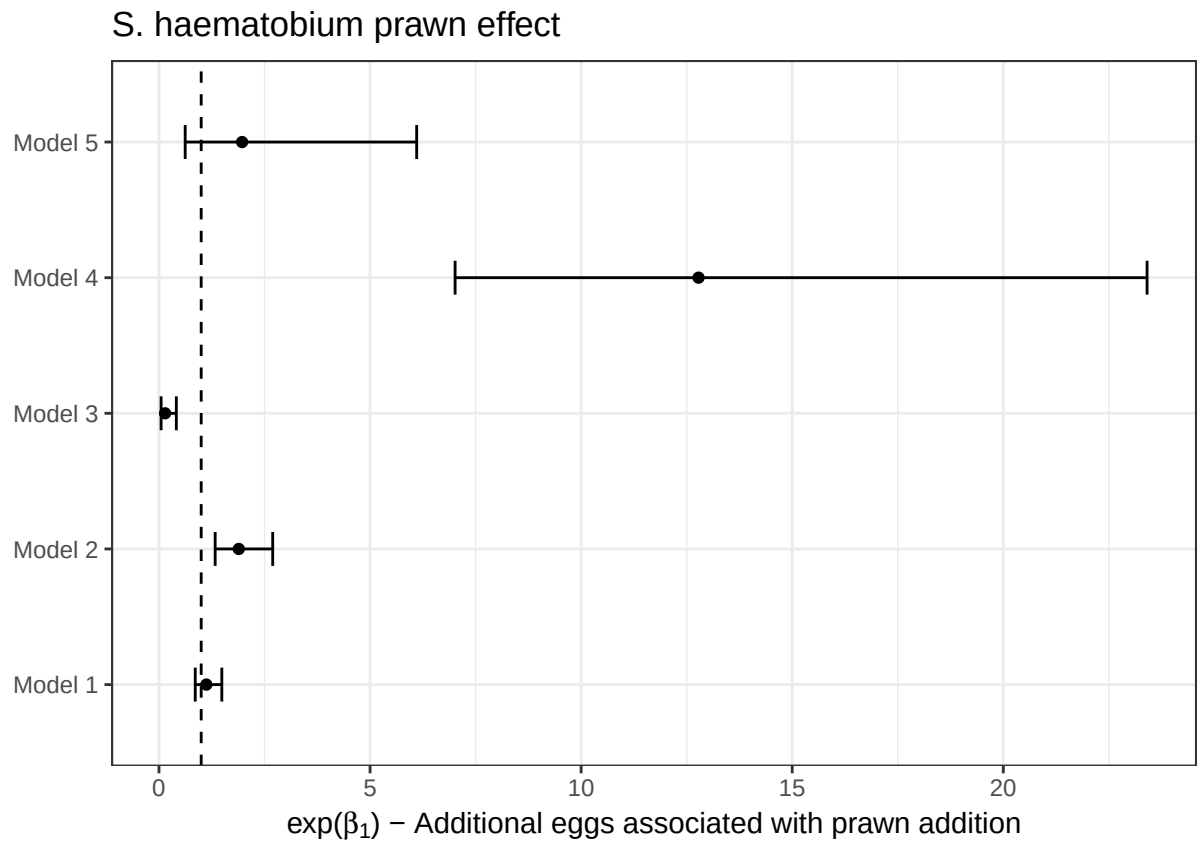


Prawn effect

To test for a prawn effect, we'll compare communities which had prawns introduced in 2017 to control communities which had no net in 2016

```
#Model 1
mod1_haem_mean_narm_prawn <- glm.nb(round(s_haem_mean_narm) ~ Prawns + pzq,
                                data = full_long %>% filter(extra_pzq != 1 &
                                                              Intervention %in% c("control", "prawn")))

  mod1_haem_narm_prawn_res <- as.data.frame(round(cbind(summary(mod1_haem_mean_narm_prawn)$coef,
                                                        confint(mod1_haem_mean_narm_prawn)), 3)[,c(1,2,5,6,3,4)])
    mod1_haem_narm_prawn_res$model <- "Model 1"


#Model 2
mod2_haem_mean_narm_prawn <- glm.nb(round(s_haem_mean_narm) ~ Prawns + pzq + School,
                                data = full_long %>% filter(extra_pzq != 1 &
                                                              Intervention %in% c("control", "prawn")))

  mod2_haem_narm_prawn_res <- as.data.frame(round(cbind(summary(mod2_haem_mean_narm_prawn)$coef,
                                                        confint(mod2_haem_mean_narm_prawn)), 3)[,c(1,2,5,6,3,4)])
    mod2_haem_narm_prawn_res$model <- "Model 2"

#Model 3
mod3_haem_mean_narm_prawn <- glm.nb(round(s_haem_mean_narm) ~ Prawns + pzq + School*year_fac,
                                data = full_long %>% filter(extra_pzq != 1 &
                                                              Intervention %in% c("control", "prawn")))
```

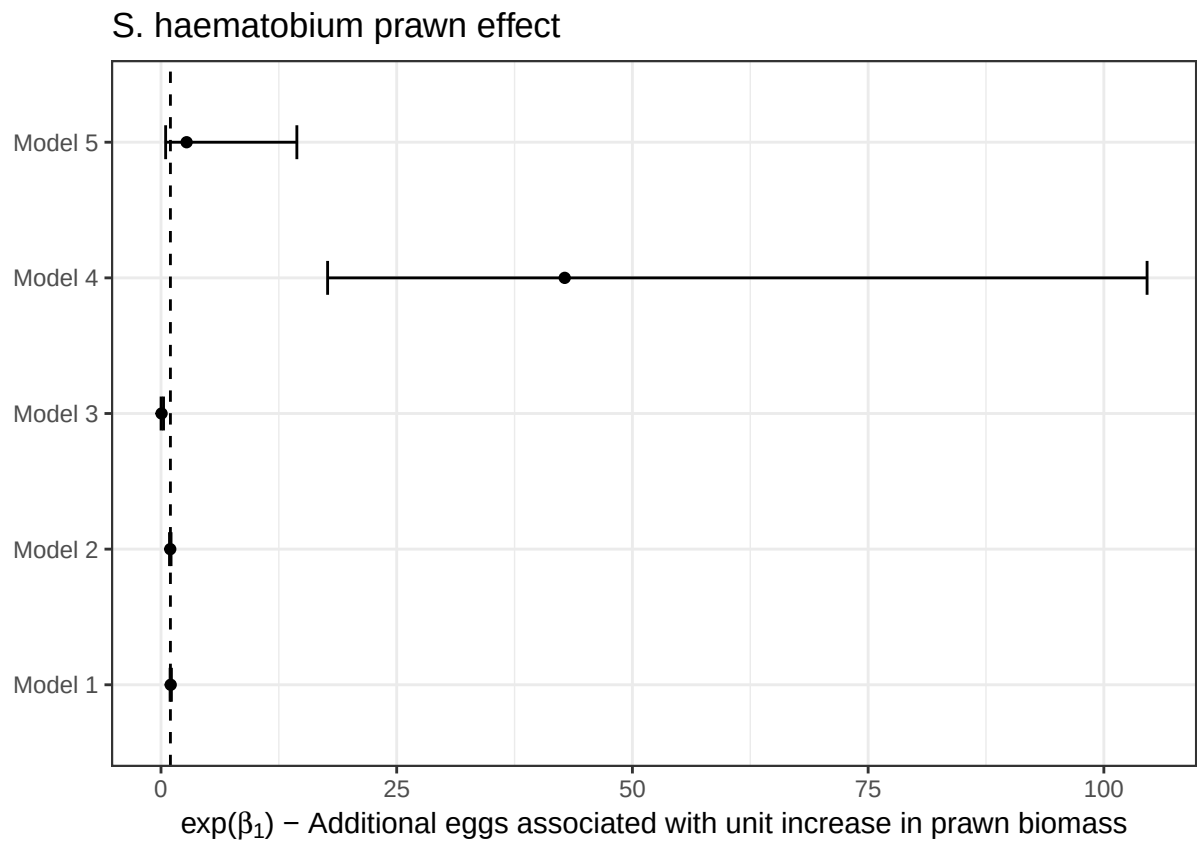
```
  mod3_haem_narm_prawn_res <- as.data.frame(round(cbind(summary(mod3_haem_mean_narm_prawn)$coef,
                                                        na.omit(confint(mod3_haem_mean_narm_prawn))), 3)[,c(1,2,5,6,
    mod3_haem_narm_prawn_res$model <- "Model 3"

#Model 4
mod4_haem_mean_narm_prawn <- glm.nb(round(s_haem_mean_narm) ~ Prawns + School + log_s_haem_mean_narm_l1,
                                    data = mod4_dat %>% filter(extra_pzq != 1 &
                                                               Intervention %in% c("control", "prawn")))

  mod4_haem_narm_prawn_res <- as.data.frame(round(cbind(summary(mod4_haem_mean_narm_prawn)$coef,
                                                        confint(mod4_haem_mean_narm_prawn)), 3)[,c(1,2,5,6,3,4)])
    mod4_haem_narm_prawn_res$model <- "Model 4"

#Model 5
mod5_haem_mean_narm_prawn <- glm.nb(round(s_haem_mean_narm) ~ Prawns + School*year_fac + log_s_haem_mean_narm_
                                    data = mod4_dat %>% filter(extra_pzq != 1 &
                                                               Intervention %in% c("control", "prawn")))

  mod5_haem_narm_prawn_res <- as.data.frame(round(cbind(summary(mod5_haem_mean_narm_prawn)$coef,
                                                        na.omit(confint(mod5_haem_mean_narm_prawn))), 3)[,c(1,2,5,6,
    mod5_haem_narm_prawn_res$model <- "Model 5"

#Plot prawn effect estimate
rbind(mod1_haem_narm_prawn_res["Prawns",],
      mod2_haem_narm_prawn_res["Prawns",],
      mod3_haem_narm_prawn_res["Prawns",],
      mod4_haem_narm_prawn_res["Prawns",],
      mod5_haem_narm_prawn_res["Prawns",]) %>%
  rename("lower" = !!names(.[3]),
         "upper" = !!names(.[4])) %>%
  ggplot(aes(x = exp(Estimate), y = model)) + theme_bw() +
    geom_point() + geom_errorbarh(aes(xmin = exp(lower), xmax = exp(upper), y = model), height = 0.25) +
    geom_vline(xintercept = 1, lty = 2) +
    ylab("") +
    xlab(expression(paste("exp(",beta[1], ") - Additional eggs associated with prawn addition"))) +
    ggtitle("S. haematobium prawn effect")
```



In addition to a binary prawn intervention variable, we'll also investigate the continuous effect of prawn biomass measured as kg prawn/m^2/month

```
#Model 1
mod1_haem_mean_narm_prawn_c <- glm.nb(round(s_haem_mean_narm) ~ Prawn_biomass + pzq,
                                data = full_long %>% filter(extra_pzq != 1 &
                                                              Intervention %in% c("control", "prawn")))

  mod1_haem_narm_prawn_res_c <- as.data.frame(round(cbind(summary(mod1_haem_mean_narm_prawn_c)$coef,
                                                          confint(mod1_haem_mean_narm_prawn_c)), 3)[,c(1,2,5,6,3,4)])
    mod1_haem_narm_prawn_res_c$model <- "Model 1"


#Model 2
mod2_haem_mean_narm_prawn_c <- glm.nb(round(s_haem_mean_narm) ~ Prawn_biomass + pzq + School,
                                data = full_long %>% filter(extra_pzq != 1 &
                                                              Intervention %in% c("control", "prawn")))

  mod2_haem_narm_prawn_res_c <- as.data.frame(round(cbind(summary(mod2_haem_mean_narm_prawn_c)$coef,
                                                          confint(mod2_haem_mean_narm_prawn_c)), 3)[,c(1,2,5,6,3,4)])
    mod2_haem_narm_prawn_res_c$model <- "Model 2"

#Model 3
mod3_haem_mean_narm_prawn_c <- glm.nb(round(s_haem_mean_narm) ~ Prawn_biomass + pzq + School*year_fac,
                                data = full_long %>% filter(extra_pzq != 1 &
                                                              Intervention %in% c("control", "prawn")))

  mod3_haem_narm_prawn_res_c <- as.data.frame(round(cbind(summary(mod3_haem_mean_narm_prawn_c)$coef,
                                                           na.omit(confint(mod3_haem_mean_narm_prawn_c))), 3)[,c(1,2,
    mod3_haem_narm_prawn_res_c$model <- "Model 3"

#Model 4
```

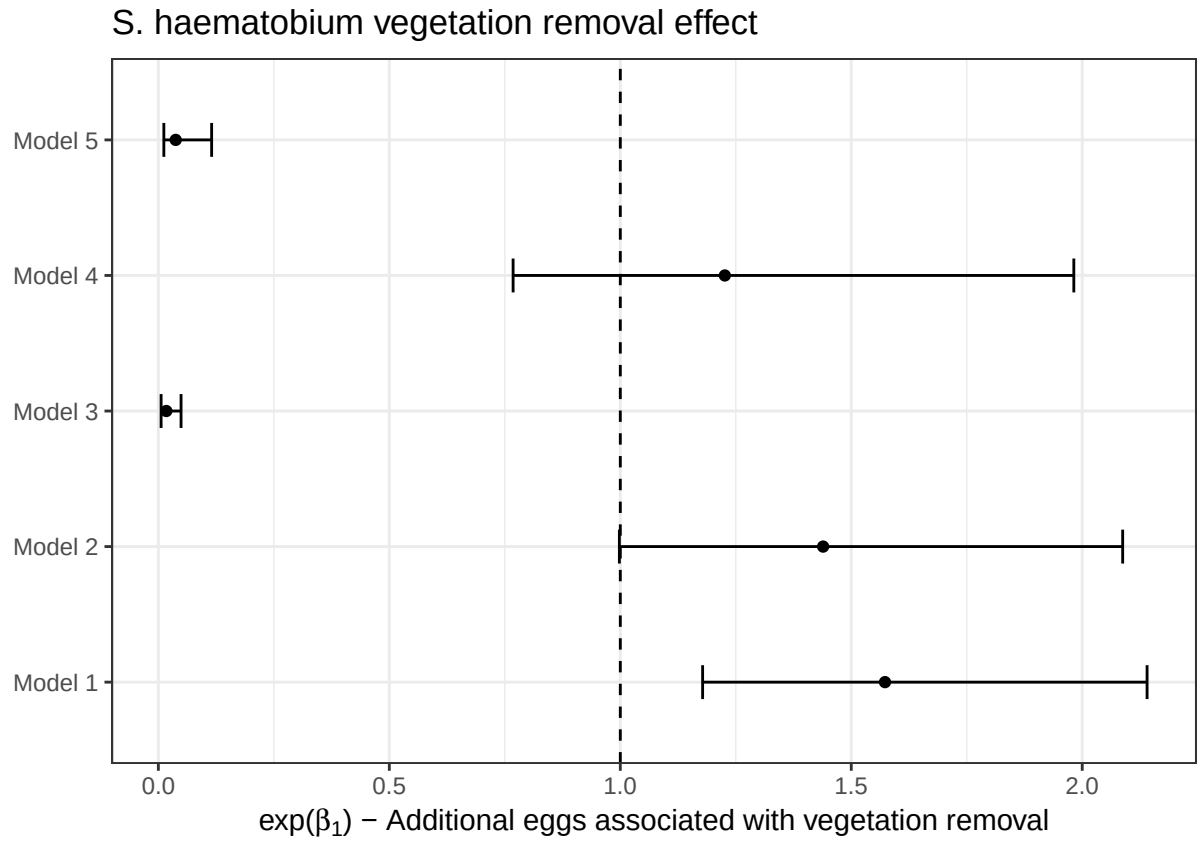
```r
mod4_haem_mean_narm_prawn_c <- glm.nb(round(s_haem_mean_narm) ~ Prawn_biomass + School + log_s_haem_mean_narm_
                               data = mod4_dat %>% filter(extra_pzq != 1 &
                                                          Intervention %in% c("control", "prawn")))

  mod4_haem_narm_prawn_res_c <- as.data.frame(round(cbind(summary(mod4_haem_mean_narm_prawn_c)$coef,
                                                confint(mod4_haem_mean_narm_prawn_c)), 3)[,c(1,2,5,6,3,4)]
    mod4_haem_narm_prawn_res_c$model <- "Model 4"

#Model 5
mod5_haem_mean_narm_prawn_c <- glm.nb(round(s_haem_mean_narm) ~ Prawn_biomass + School*year_fac + log_s_haem_m
                               data = mod4_dat %>% filter(extra_pzq != 1 &
                                                          Intervention %in% c("control", "prawn")))

  mod5_haem_narm_prawn_res_c <- as.data.frame(round(cbind(summary(mod5_haem_mean_narm_prawn_c)$coef,
                                                na.omit(confint(mod5_haem_mean_narm_prawn_c))), 3)[,c(1,2,
    mod5_haem_narm_prawn_res_c$model <- "Model 5"

#Plot prawn effect estimate
rbind(mod1_haem_narm_prawn_res_c["Prawn_biomass",],
      mod2_haem_narm_prawn_res_c["Prawn_biomass",],
      mod3_haem_narm_prawn_res_c["Prawn_biomass",],
      mod4_haem_narm_prawn_res_c["Prawn_biomass",],
      mod5_haem_narm_prawn_res_c["Prawn_biomass",]) %>%
  rename("lower" = !!names(.[3]),
         "upper" = !!names(.[4])) %>%
  ggplot(aes(x = exp(Estimate), y = model)) + theme_bw() +
    geom_point() + geom_errorbarh(aes(xmin = exp(lower), xmax = exp(upper), y = model), height = 0.25) +
    geom_vline(xintercept = 1, lty = 2) +
    ylab("") +
  xlab(expression(paste("exp(",beta[1], ") - Additional eggs associated with unit increase in prawn biomass"))
    ggtitle("S. haematobium prawn effect")
```



Vegetation removal effect

```
#Model 1
mod1_haem_mean_narm_veg <- glm.nb(round(s_haem_mean_narm) ~ Veg + pzq,
                              data = full_long %>% filter(extra_pzq != 1 &
                                                            Intervention %in% c("control", "veg_removal")))

  mod1_haem_narm_veg_res <- as.data.frame(round(cbind(summary(mod1_haem_mean_narm_veg)$coef,
                                          confint(mod1_haem_mean_narm_veg)), 3)[,c(1,2,5,6,3,4)])
    mod1_haem_narm_veg_res$model <- "Model 1"

#Model 2
mod2_haem_mean_narm_veg <- glm.nb(round(s_haem_mean_narm) ~ Veg + pzq + School,
                              data = full_long %>% filter(extra_pzq != 1 &
                                                            Intervention %in% c("control", "veg_removal")))

  mod2_haem_narm_veg_res <- as.data.frame(round(cbind(summary(mod2_haem_mean_narm_veg)$coef,
                                          confint(mod2_haem_mean_narm_veg)), 3)[,c(1,2,5,6,3,4)])
    mod2_haem_narm_veg_res$model <- "Model 2"

#Model 3
mod3_haem_mean_narm_veg <- glm.nb(round(s_haem_mean_narm) ~ Veg + pzq + School*year_fac,
                              data = full_long %>% filter(extra_pzq != 1 &
                                                            Intervention %in% c("control", "veg_removal")))

  mod3_haem_narm_veg_res <- as.data.frame(round(cbind(summary(mod3_haem_mean_narm_veg)$coef,
                                        na.omit(confint(mod3_haem_mean_narm_veg))), 3)[,c(1,2,5,6,3,4)])
    mod3_haem_narm_veg_res$model <- "Model 3"

#Model 4
mod4_haem_mean_narm_veg <- glm.nb(round(s_haem_mean_narm) ~ Veg + School + log_s_haem_mean_narm_l1,
                              data = mod4_dat %>% filter(extra_pzq != 1 &
                                                           Intervention %in% c("control", "veg_removal")))

  mod4_haem_narm_veg_res <- as.data.frame(round(cbind(summary(mod4_haem_mean_narm_veg)$coef,
                                        na.omit(confint(mod4_haem_mean_narm_veg))), 3)[,c(1,2,5,6,3,4)])
    mod4_haem_narm_veg_res$model <- "Model 4"

#Model 5
mod5_haem_mean_narm_veg <- glm.nb(round(s_haem_mean_narm) ~ Veg + School*year_fac + log_s_haem_mean_narm_l1,
                              data = mod4_dat %>% filter(extra_pzq != 1 &
                                                           Intervention %in% c("control", "veg_removal")))

  mod5_haem_narm_veg_res <- as.data.frame(round(cbind(summary(mod5_haem_mean_narm_veg)$coef,
                                        na.omit(confint(mod5_haem_mean_narm_veg))), 3)[,c(1,2,5,6,3,4)])
    mod5_haem_narm_veg_res$model <- "Model 5"

#Plot net effect estimate
rbind(mod1_haem_narm_veg_res["Veg",],
      mod2_haem_narm_veg_res["Veg",],
      mod3_haem_narm_veg_res["Veg",],
      mod4_haem_narm_veg_res["Veg",],
      mod5_haem_narm_veg_res["Veg",]) %>%
  rename("lower" = !!names(.[3]),
         "upper" = !!names(.[4])) %>%
  ggplot(aes(x = exp(Estimate), y = model)) + theme_bw() +
    geom_point() + geom_errorbarh(aes(xmin = exp(lower), xmax = exp(upper), y = model), height = 0.25) +
    geom_vline(xintercept = 1, lty = 2) +
    ylab("") +
```

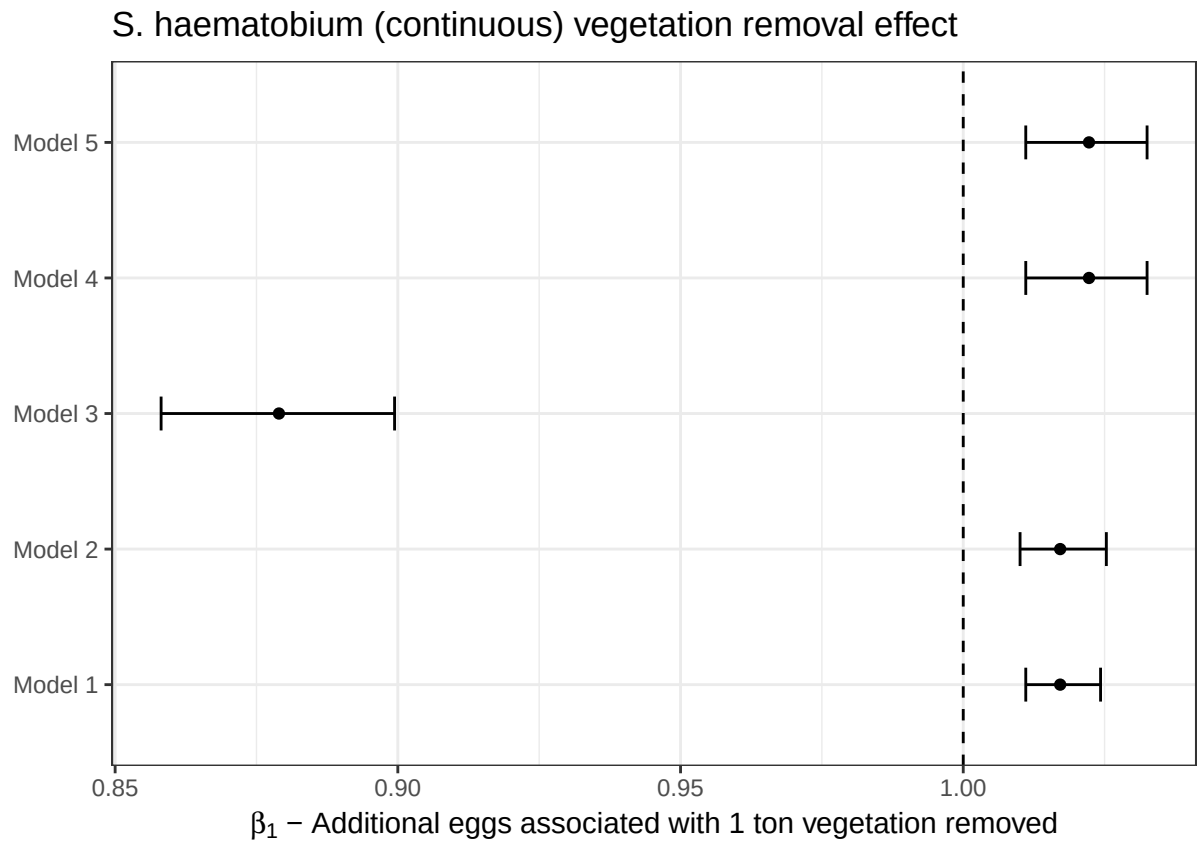
```
    xlab(expression(paste("exp(",beta[1], ") - Additional eggs associated with vegetation removal"))) +
    ggtitle("S. haematobium vegetation removal effect")
```



Also investigate veg removal as a continuous variable: tons of vegetation removed

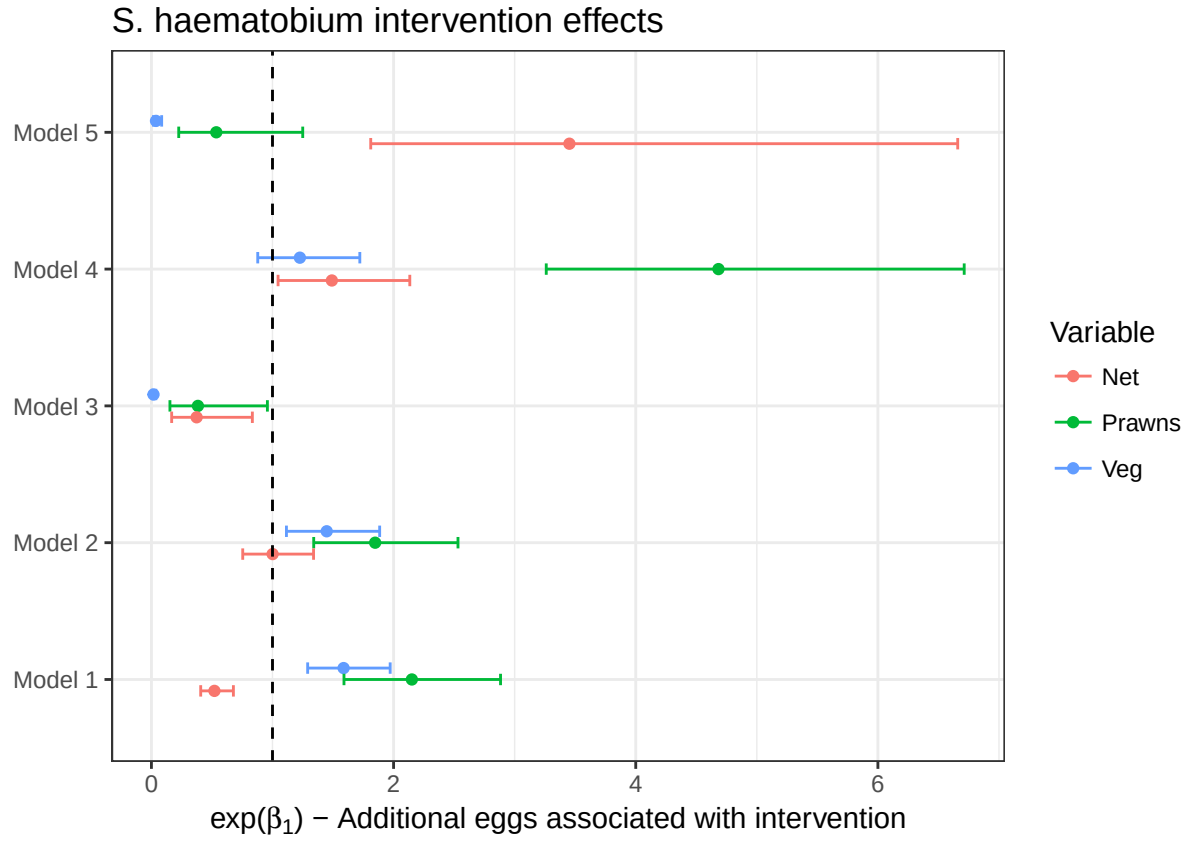
```
#Model 1
mod1_haem_mean_narm_veg_c <- glm.nb(round(s_haem_mean_narm) ~ Veg_tons + pzq,
                                    weights = s_haem_mean_w,
                                    data = full_long %>% filter(extra_pzq != 1 &
                                                                Intervention %in% c("control", "veg_removal"))

  mod1_haem_narm_veg_res_c <- as.data.frame(round(cbind(summary(mod1_haem_mean_narm_veg_c)$coef,
                                    confint(mod1_haem_mean_narm_veg_c)), 3)[,c(1,2,5,6,3,4)])
    mod1_haem_narm_veg_res_c$model <- "Model 1"

#Model 2
mod2_haem_mean_narm_veg_c <- glm.nb(round(s_haem_mean_narm) ~ Veg_tons + pzq + School,
                                    weights = s_haem_mean_w,
                                    data = full_long %>% filter(extra_pzq != 1 &
                                                                Intervention %in% c("control", "veg_removal"))

  mod2_haem_narm_veg_res_c <- as.data.frame(round(cbind(summary(mod2_haem_mean_narm_veg_c)$coef,
                                    confint(mod2_haem_mean_narm_veg_c)), 3)[,c(1,2,5,6,3,4)])
    mod2_haem_narm_veg_res_c$model <- "Model 2"

#Model 3
mod3_haem_mean_narm_veg_c <- glm.nb(round(s_haem_mean_narm) ~ Veg_tons + pzq + School*year_fac,
                                    weights = s_haem_mean_w,
                                    data = full_long %>% filter(extra_pzq != 1 &
                                                                Intervention %in% c("control", "veg_removal"))

  mod3_haem_narm_veg_res_c <- as.data.frame(round(cbind(summary(mod3_haem_mean_narm_veg_c)$coef,
```

```
                                        na.omit(confint(mod3_haem_mean_narm_veg_c))), 3)[,c(1,2,5,6,3,4)])
    mod3_haem_narm_veg_res_c$model <- "Model 3"

#Model 4
mod4_haem_mean_narm_veg_c <- glm.nb(round(s_haem_mean_narm) ~ Veg_tons + School + log_s_haem_mean_narm_l1,
                                    weights = s_haem_mean_w,
                                    data = mod4_dat %>% filter(extra_pzq != 1 &
                                                               Intervention %in% c("control", "veg_removal")))

  mod4_haem_narm_veg_res_c <- as.data.frame(round(cbind(summary(mod4_haem_mean_narm_veg_c)$coef,
                                        na.omit(confint(mod4_haem_mean_narm_veg_c))), 3)[,c(1,2,5,6,3,4)])
    mod4_haem_narm_veg_res_c$model <- "Model 4"

#Model 5
mod5_haem_mean_narm_veg_c <- glm.nb(round(s_haem_mean_narm) ~ Veg_tons + School + log_s_haem_mean_narm_l1,
                                    weights = s_haem_mean_w,
                                    data = mod4_dat %>% filter(extra_pzq != 1 &
                                                               Intervention %in% c("control", "veg_removal")))

  mod5_haem_narm_veg_res_c <- as.data.frame(round(cbind(summary(mod5_haem_mean_narm_veg_c)$coef,
                                        na.omit(confint(mod5_haem_mean_narm_veg_c))), 3)[,c(1,2,5,6,3,4)])
    mod5_haem_narm_veg_res_c$model <- "Model 5"

#Plot net effect estimate
rbind(mod1_haem_narm_veg_res_c["Veg_tons",],
      mod2_haem_narm_veg_res_c["Veg_tons",],
      mod3_haem_narm_veg_res_c["Veg_tons",],
      mod4_haem_narm_veg_res_c["Veg_tons",],
      mod5_haem_narm_veg_res_c["Veg_tons",]) %>%
  rename("lower" = !!names(.[3]),
         "upper" = !!names(.[4])) %>%
  ggplot(aes(x = exp(Estimate), y = model)) + theme_bw() +
    geom_point() + geom_errorbarh(aes(xmin = exp(lower), xmax = exp(upper), y = model), height = 0.25) +
    geom_vline(xintercept = 1, lty = 2) +
    ylab("") +
    xlab(expression(paste(beta[1], " - Additional eggs associated with 1 ton vegetation removed"))) +
    ggtitle("S. haematobium (continuous) vegetation removal effect")
```




```
#Model 1
mod1_haem_mean_narm_all <- glm.nb(round(s_haem_mean_narm) ~ Net + Veg + Prawns + pzq,
                                  weights = s_haem_mean_w,
                                  data = full_long %>% filter(extra_pzq != 1))

  mod1_haem_narm_all_res <- as.data.frame(round(cbind(summary(mod1_haem_mean_narm_all)$coef,
                                        confint(mod1_haem_mean_narm_all)), 3)[,c(1,2,5,6,3,4)])
    mod1_haem_narm_all_res$model <- "Model 1"

#Model 2
mod2_haem_mean_narm_all <- glm.nb(round(s_haem_mean_narm) ~ Net + Veg + Prawns + pzq + School,
                                  weights = s_haem_mean_w,
                                  data = full_long %>% filter(extra_pzq != 1))

  mod2_haem_narm_all_res <- as.data.frame(round(cbind(summary(mod2_haem_mean_narm_all)$coef,
                                        confint(mod2_haem_mean_narm_all)), 3)[,c(1,2,5,6,3,4)])
    mod2_haem_narm_all_res$model <- "Model 2"

#Model 3
mod3_haem_mean_narm_all <- glm.nb(round(s_haem_mean_narm) ~ Net + Veg + Prawns + pzq + School*year_fac,
                                  weights = s_haem_mean_w,
                                  data = full_long %>% filter(extra_pzq != 1))

  mod3_haem_narm_all_res <- as.data.frame(round(cbind(summary(mod3_haem_mean_narm_all)$coef,
                                      na.omit(confint(mod3_haem_mean_narm_all))), 3)[,c(1,2,5,6,3,4)])
    mod3_haem_narm_all_res$model <- "Model 3"


#Model 4
mod4_haem_mean_narm_all <- glm.nb(round(s_haem_mean_narm) ~ Net + Veg + Prawns + School + log_s_haem_mean_narm
                                  weights = s_haem_mean_w,
                                  data = mod4_dat %>% filter(extra_pzq != 1))
```

```
  mod4_haem_narm_all_res <- as.data.frame(round(cbind(summary(mod4_haem_mean_narm_all)$coef,
                                        na.omit(confint(mod4_haem_mean_narm_all))), 3)[,c(1,2,5,6,3,4)])
    mod4_haem_narm_all_res$model <- "Model 4"

#Model 5
mod5_haem_mean_narm_all <- glm.nb(round(s_haem_mean_narm) ~ Net + Veg + Prawns + School*year_fac + log_s_haem_
                                  weights = s_haem_mean_w,
                                  data = mod4_dat %>% filter(extra_pzq != 1))

  mod5_haem_narm_all_res <- as.data.frame(round(cbind(summary(mod5_haem_mean_narm_all)$coef,
                                        na.omit(confint(mod5_haem_mean_narm_all))), 3)[,c(1,2,5,6,3,4)])
    mod5_haem_narm_all_res$model <- "Model 5"

#Plot intervention effect estimates
rbind(mod1_haem_narm_all_res[c("Net", "Veg", "Prawns"),],
      mod2_haem_narm_all_res[c("Net", "Veg", "Prawns"),],
      mod3_haem_narm_all_res[c("Net", "Veg", "Prawns"),],
      mod4_haem_narm_all_res[c("Net", "Veg", "Prawns"),],
      mod5_haem_narm_all_res[c("Net", "Veg", "Prawns"),]) %>%
  rename("lower" = !!names(.[3]),
         "upper" = !!names(.[4])) %>%
  mutate(Variable = rep(c("Net", "Veg", "Prawns"), 5)) %>%
  ggplot(aes(y = exp(Estimate), x = model, col = Variable)) + theme_bw() +
    geom_point(position = position_dodge(width = 0.25)) +
    geom_errorbar(aes(ymin = exp(lower), ymax = exp(upper), x = model),
                  width = 0.25, position = position_dodge(width = 0.25)) +
    geom_hline(yintercept = 1, lty = 2) + coord_flip() +
    xlab("") +
    ylab(expression(paste("exp(", beta[1], ") - Additional eggs associated with intervention"))) +
    ggtitle("S. haematobium intervention effects")
```



```r
summary(mod5_haem_mean_narm_all)
```

```
##
## Call:
## glm.nb(formula = round(s_haem_mean_narm) ~ Net + Veg + Prawns +
##     School * year_fac + log_s_haem_mean_narm_l1, data = mod4_dat %>%
##     filter(extra_pzq != 1), weights = s_haem_mean_w, init.theta = 0.2400641919,
##     link = log)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.6202  -1.7345  -1.0703  -0.1228   5.2513
##
## Coefficients: (7 not defined because of singularities)
##                          Estimate Std. Error z value Pr(>|z|)
## (Intercept)               1.66166    0.23762   6.993 2.69e-12 ***
## Net                       1.23878    0.33368   3.712 0.000205 ***
## Veg                      -3.26934    0.40925  -7.989 1.36e-15 ***
## Prawns                   -0.62364    0.43444  -1.436 0.151138
## SchoolDT                 -1.75746    0.30894  -5.689 1.28e-08 ***
## SchoolFS                 -0.13500    0.50471  -0.267 0.789102
## SchoolGG                 -2.55619    0.38385  -6.659 2.75e-11 ***
## SchoolGK                  1.23148    0.29521   4.171 3.03e-05 ***
## SchoolLR                  0.31850    0.27938   1.140 0.254279
## SchoolMA                 -0.82001    0.37589  -2.182 0.029143 *
## SchoolMB                 -1.47383    0.43430  -3.394 0.000690 ***
## SchoolMD                 -0.29503    0.35728  -0.826 0.408929
## SchoolME                  1.41064    0.27900   5.056 4.28e-07 ***
## SchoolMG                  0.18172    0.30654   0.593 0.553302
## SchoolMO                 -2.01478    0.28608  -7.043 1.88e-12 ***
## SchoolMT                  1.27249    0.27856   4.568 4.92e-06 ***
## SchoolNE                 -0.77259    0.28844  -2.679 0.007395 **
## SchoolNM                 -0.12177    0.33028  -0.369 0.712360
## SchoolST                  2.16116    0.27840   7.763 8.31e-15 ***
## year_fac2018              1.88773    0.35294   5.349 8.86e-08 ***
## log_s_haem_mean_narm_l1   0.29641    0.01948  15.218  < 2e-16 ***
## SchoolDT:year_fac2018         NA         NA      NA       NA
## SchoolFS:year_fac2018    -0.87922    0.48831  -1.801 0.071779 .
## SchoolGG:year_fac2018         NA         NA      NA       NA
## SchoolGK:year_fac2018     1.11676    0.32503   3.436 0.000591 ***
## SchoolLR:year_fac2018     3.90735    0.29526  13.234  < 2e-16 ***
## SchoolMA:year_fac2018         NA         NA      NA       NA
## SchoolMB:year_fac2018    -0.57682    0.52913  -1.090 0.275656
## SchoolMD:year_fac2018         NA         NA      NA       NA
## SchoolME:year_fac2018         NA         NA      NA       NA
## SchoolMG:year_fac2018         NA         NA      NA       NA
## SchoolMO:year_fac2018         NA         NA      NA       NA
## SchoolMT:year_fac2018    -2.72486    0.40901  -6.662 2.70e-11 ***
## SchoolNE:year_fac2018    -2.25139    0.42847  -5.254 1.48e-07 ***
## SchoolNM:year_fac2018    -1.17239    0.45500  -2.577 0.009976 **
## SchoolST:year_fac2018    -2.75940    0.40665  -6.786 1.15e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(0.2401) family taken to be 1)
##
##     Null deviance: 5826.7  on 2147  degrees of freedom
## Residual deviance: 4340.6  on 2119  degrees of freedom
##   (1657 observations deleted due to missingness)
```

```
## AIC: 29335
##
## Number of Fisher Scoring iterations: 1
##
##
##               Theta:  0.24006
##           Std. Err.:  0.00582
##
##  2 x log-likelihood:  -29274.84900
```

Schistosoma mansoni

Net effect

```
#Model 1
mod1_mans_mean_narm_net <- glm.nb(round(s_mans_mean_narm) ~ Net + pzq,
                                  weights = s_mans_mean_w,
                                  data = full_long %>% filter(extra_pzq != 1 &
                                                              Intervention %in% c("control", "net") &
                                                              year != 2018))

  mod1_mans_narm_net_res <- as.data.frame(round(cbind(summary(mod1_mans_mean_narm_net)$coef,
                                        confint(mod1_mans_mean_narm_net)), 3)[,c(1,2,5,6,3,4)])
    mod1_mans_narm_net_res$model <- "Model 1"

#Model 2
mod2_mans_mean_narm_net <- glm.nb(round(s_mans_mean_narm) ~ Net + pzq + School,
                                  weights = s_mans_mean_w,
                                  data = full_long %>% filter(extra_pzq != 1 &
                                                              Intervention %in% c("control", "net") &
                                                              year != 2018))

  mod2_mans_narm_net_res <- as.data.frame(round(cbind(summary(mod2_mans_mean_narm_net)$coef,
                                        confint(mod2_mans_mean_narm_net)), 3)[,c(1,2,5,6,3,4)])
    mod2_mans_narm_net_res$model <- "Model 2"

#Model 3
mod3_mans_mean_narm_net <- glm.nb(round(s_mans_mean_narm) ~ Net + School + log_s_mans_mean12_l1,
                                  weights = s_mans_mean_w,
                                  data = mod4_dat %>% filter(extra_pzq != 1 &
                                                             Intervention %in% c("control", "net") &
                                                             year != 2018),
                                  control = glm.control(maxit = 300))

  mod3_mans_narm_net_res <- as.data.frame(round(cbind(summary(mod3_mans_mean_narm_net)$coef,
                                          na.omit(confint(mod3_mans_mean_narm_net))), 3)[,c(1,2,5,
    mod3_mans_narm_net_res$model <- "Model 3"

#Plot net effect estimate
rbind(mod1_mans_narm_net_res["Net",], mod2_mans_narm_net_res["Net",], mod3_mans_narm_net_res["Net",]) %>%
  rename("lower" = !!names(.[3]),
         "upper" = !!names(.[4])) %>%
  ggplot(aes(x = exp(Estimate), y = model)) + theme_bw() +
    geom_point() + geom_errorbarh(aes(xmin = exp(lower), xmax = exp(upper), y = model), height = 0.25) +
    geom_vline(xintercept = 1, lty = 2) +
    ylab("") + xlab(expression(paste(beta[1], " - Additional eggs associated with net presence"))) +
    ggtitle("S. mansoni net effect")
```

Prawn effect

```
#Model 1
mod1_mans_mean_narm_prawn <- glm.nb(round(s_mans_mean_narm) ~ Prawns + pzq,
                                    weights = s_mans_mean_w,
                                    data = full_long %>% filter(extra_pzq != 1 &
                                                                  Intervention %in% c("control", "prawn")))

  mod1_mans_narm_prawn_res <- as.data.frame(round(cbind(summary(mod1_mans_mean_prawn)$coef,
                                                        confint(mod1_mans_mean_prawn)), 3)[,c(1,2,5,6,3,4)])
    mod1_mans_narm_prawn_res$model <- "Model 1"


#Model 2
mod2_mans_mean_narm_prawn <- glm.nb(round(s_mans_mean_narm) ~ Prawns + pzq + School,
                                    weights = s_mans_mean_w,
                                    data = full_long %>% filter(extra_pzq != 1 &
                                                                  Intervention %in% c("control", "prawn")))

  mod2_mans_narm_prawn_res <- as.data.frame(round(cbind(summary(mod2_mans_mean_narm_prawn)$coef,
                                                        confint(mod2_mans_mean_narm_prawn)), 3)[,c(1,2,5,6,3,4)])
    mod2_mans_narm_prawn_res$model <- "Model 2"

#Model 3
mod3_mans_mean_narm_prawn <- glm.nb(round(s_mans_mean_narm) ~ Prawns + School + log_s_mans_mean_narm_l1,
                                    weights = s_mans_mean_w,
                                    data = mod4_dat %>% filter(extra_pzq != 1 &
                                                                 Intervention %in% c("control", "prawn")),
                                    control = glm.control(maxit = 200))

  mod3_mans_narm_prawn_res <- as.data.frame(round(cbind(summary(mod3_mans_mean_narm_prawn)$coef,
                                                        confint(mod3_mans_mean_narm_prawn)), 3)[,c(1,2,5,6,3,4)])
    mod3_mans_narm_prawn_res$model <- "Model 3"

#Plot prawn effect estimate
rbind(mod1_mans_narm_prawn_res["Prawns",],
      mod2_mans_narm_prawn_res["Prawns",],
      mod3_mans_narm_prawn_res["Prawns",]) %>%
  rename("lower" = !!names(.[3]),
         "upper" = !!names(.[4])) %>%
  ggplot(aes(x = exp(Estimate), y = model)) + theme_bw() +
    geom_point() + geom_errorbarh(aes(xmin = exp(lower), xmax = exp(upper), y = model), height = 0.25) +
    geom_vline(xintercept = 1, lty = 2) +
    ylab("") + xlab(expression(paste(beta[1], " - Additional eggs associated with prawn addition"))) +
    ggtitle("S. mansoni prawn effect")
```

```
#Model 1
mod1_mans_mean_prawn_c <- glm.nb(round(s_mans_mean12) ~ Prawn_biomass + pzq + sex,
                                 data = full_long %>% filter(extra_pzq != 1 & Intervention %in% c("control", "pr

  mod1_mans_prawn_res_c <- as.data.frame(round(cbind(summary(mod1_mans_mean_prawn_c)$coef,
                                                     confint(mod1_mans_mean_prawn_c)), 3)[,c(1,2,5,6,3,4)])
    mod1_mans_prawn_res_c$model <- "Model 1"


#Model 2
mod2_mans_mean_prawn_c <- glm.nb(round(s_mans_mean12) ~ Prawn_biomass + pzq + sex + School,
                                 data = full_long %>% filter(extra_pzq != 1 & Intervention %in% c("control", "pr
```

```
  mod2_mans_prawn_res_c <- as.data.frame(round(cbind(summary(mod2_mans_mean_prawn_c)$coef,
                                                     confint(mod2_mans_mean_prawn_c)), 3)[,c(1,2,5,6,3,4)])
    mod2_mans_prawn_res_c$model <- "Model 2"

#Model 3
mod3_mans_mean_prawn_c <- glm.nb(round(s_mans_mean12) ~ Prawn_biomass + sex + School + log_s_mans_mean12_l1,
                                 data = mod4_dat %>% filter(extra_pzq != 1 & Intervention %in% c("control", "pra

  mod3_mans_prawn_res_c <- as.data.frame(round(cbind(summary(mod3_mans_mean_prawn_c)$coef,
                                                     confint(mod3_mans_mean_prawn_c)), 3)[,c(1,2,5,6,3,4)])
    mod3_mans_prawn_res_c$model <- "Model 3"

#Plot prawn effect estimate
rbind(mod1_mans_prawn_res_c["Prawn_biomass",], mod2_mans_prawn_res_c["Prawn_biomass",], mod3_mans_prawn_res_c[
  rename("lower" = !!names(.[3]),
         "upper" = !!names(.[4])) %>%
  ggplot(aes(x = exp(Estimate), y = model)) + theme_bw() +
    geom_point() + geom_errorbarh(aes(xmin = exp(lower), xmax = exp(upper), y = model), height = 0.25) +
    geom_vline(xintercept = 1, lty = 2) +
    ylab("") + xlab(expression(paste(beta[1], " - Additional eggs associated with unit increase in prawn bioma
    ggtitle("S. mansoni prawn effect")
```

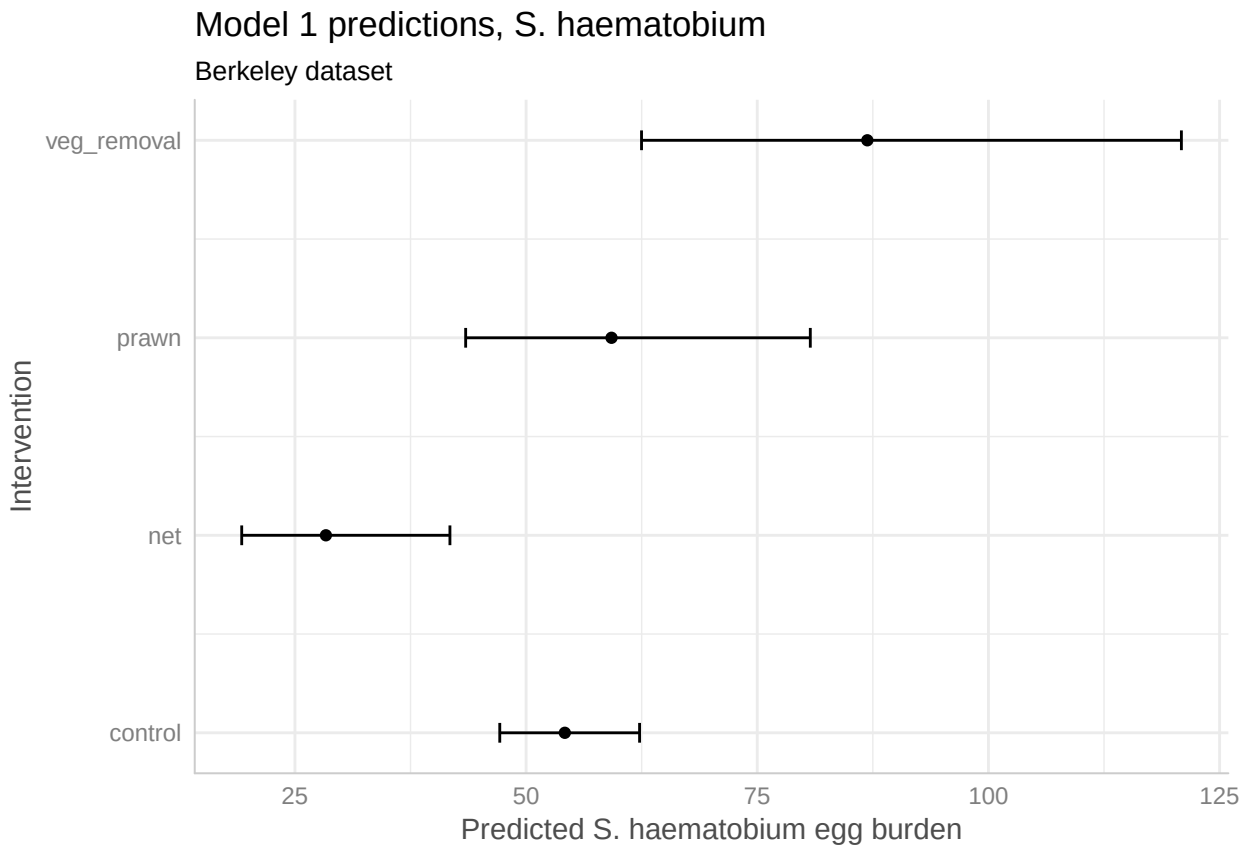
Scratch

```
#Global model
mod1_haem_mean <- glm.nb(round(s_haem_mean) ~ Intervention + pzq + sex,
                         data = full_long %>% filter(extra_pzq != 1))

  round(cbind(summary(mod1_haem_mean)$coef, confint(mod1_haem_mean)), 3)[,c(1,2,5,6,3,4)]
```

```
## Waiting for profiling to be done...
```

```
##                          Estimate Std. Error  2.5 % 97.5 % z value Pr(>|z|)
## (Intercept)                 4.012      0.072  3.872  4.157  55.493    0.000
## Interventionnet            -0.648      0.184 -0.993 -0.269  -3.520    0.000
## Interventionprawn           0.089      0.141 -0.180  0.374   0.632    0.527
## Interventionveg_removal     0.472      0.153  0.180  0.785   3.078    0.002
## pzq1                       -0.382      0.086 -0.551 -0.213  -4.426    0.000
## sexM                       -0.019      0.077 -0.170  0.131  -0.252    0.801
```

```
  plot(ggpredict(mod1_haem_mean, c("Intervention"))) + coord_flip() +
    ylab("Predicted S. haematobium egg burden") + ggtitle("Model 1 predictions, S. haematobium", subtitle = "B
```




```
#Compare prawn biomass to only controls
mod1_haem_mean_prawn_bm <- glm.nb(round(s_haem_mean) ~ Prawn_biomass + year_fac + sex,
                                  data = full_long %>% filter(extra_pzq != 1 & Intervention %in% c("control",

  round(cbind(summary(mod1_haem_mean_prawn_bm)$coef, confint(mod1_haem_mean_prawn_bm)), 3)[,c(1,2,5,6,3,4)]
```

```
## Waiting for profiling to be done...
```

```
##               Estimate Std. Error  2.5 % 97.5 % z value Pr(>|z|)
## (Intercept)      4.023      0.074  3.880  4.171  54.658    0.000
## Prawn_biomass    0.038      0.036 -0.029  0.115   1.077    0.282
## year_fac2017    -0.270      0.104 -0.473 -0.064  -2.595    0.009
## year_fac2018    -0.480      0.100 -0.675 -0.281  -4.793    0.000
## sexM            -0.040      0.082 -0.200  0.120  -0.489    0.625
```

```
#Compare prawn biomass to only controls with net effect
mod1_haem_mean_prawn_bm_net <- glm.nb(round(s_haem_mean) ~ Prawn_biomass + Net + year_fac + sex,
                                  data = full_long %>% filter(extra_pzq != 1 & Intervention %in% c("control",

  round(cbind(summary(mod1_haem_mean_prawn_bm_net)$coef, confint(mod1_haem_mean_prawn_bm_net)), 3)[,c(1,2,5,6,
```

```
## Waiting for profiling to be done...
```

```
##               Estimate Std. Error  2.5 % 97.5 % z value Pr(>|z|)
## (Intercept)      4.024      0.073  3.882  4.172  54.946    0.000
## Prawn_biomass    0.076      0.041 -0.007  0.169   1.824    0.068
## Net             -0.242      0.140 -0.522  0.051  -1.723    0.085
## year_fac2017    -0.353      0.101 -0.546 -0.156  -3.479    0.001
## year_fac2018    -0.424      0.104 -0.633 -0.211  -4.076    0.000
## sexM            -0.042      0.080 -0.199  0.114  -0.534    0.594
```

```r
#Compare veg removal to controls
mod1_haem_mean_veg <- glm.nb(round(s_haem_mean) ~ Veg + year_fac + sex,
                             data = full_long %>% filter(extra_pzq != 1 & Intervention %in% c("control", "veg_

  round(cbind(summary(mod1_haem_mean_veg)$coef, confint(mod1_haem_mean_veg)), 3)[,c(1,2,5,6,3,4)]
```

```
## Waiting for profiling to be done...
```

```
##              Estimate Std. Error  2.5 % 97.5 % z value Pr(>|z|)
## (Intercept)     3.997      0.074  3.855  4.145  54.237    0.000
## Veg             0.609      0.166  0.291  0.942   3.677    0.000
## year_fac2017   -0.268      0.104 -0.470 -0.061  -2.574    0.010
## year_fac2018   -0.522      0.107 -0.729 -0.308  -4.864    0.000
## sexM            0.008      0.082 -0.153  0.170   0.102    0.919
```

```r
#Rerun with stanford variables
mod1_haem_mean_stan <- glm.nb(round(ShW) ~ pzq + net + prawn + veg_removal + sex,
                              data = stanford %>% filter(Tx_early != 1))

  round(cbind(summary(mod1_haem_mean_stan)$coef, confint(mod1_haem_mean_stan)), 3)[,c(1,2,5,6,3,4)]
```

```
## Waiting for profiling to be done...
```

```
##             Estimate Std. Error  2.5 % 97.5 % z value Pr(>|z|)
## (Intercept)    3.960      0.082  3.802  4.123  48.535    0.000
## pzq           -0.323      0.078 -0.478 -0.170  -4.154    0.000
## net           -0.367      0.105 -0.644 -0.090  -3.499    0.000
## prawn          0.208      0.099 -0.051  0.475   2.100    0.036
## veg_removal    0.241      0.097  0.055  0.432   2.478    0.013
## sexM          -0.020      0.076 -0.171  0.130  -0.264    0.792
```

For *S. haematobium*, these results show a significant effect of praziquantel administration, as we'd expect, but show no significant effect of the prawn or vegetation removal interventions. A protective effect of prawns and a harmful effect of vegetation removal are borderline insignificant. Individuals in the single community that had a net intervention (e.g. net but no prawns) is driving the significant net effect, but this community is a low transmission environment in general, so this is not surprising

Schistosoma mansoni

```r
mod1_mans_mean <- glm.nb(round(s_mans_mean12) ~ pzq + Intervention + sex,
                         data = full_long %>% filter(extra_pzq != 1))

  round(cbind(summary(mod1_mans_mean)$coef, confint(mod1_mans_mean)), 3)[,c(1,2,5,6,3,4)]

  plot(ggpredict(mod1_mans_mean, c("Intervention"))) +
    ylab("Predicted S. mansoni egg burden") + ggtitle("Model 1 predictions, S. mansoni")
```

For *S. mansoni*, these results again show a significant protective effect of praziquantel administration, as we'd expect. They also show the same net effect, that should not be interpreted too strongly. However, these results do imply a significant protective effect of vegetation removal and significant harmful effect of prawn addition.

Schistosoma haematobium

```
mod2_haem_mean <- glm.nb(round(s_haem_mean) ~ pzq + Intervention + School + sex,
                         data = full_long %>% filter(extra_pzq != 1))

  round(cbind(summary(mod2_haem_mean)$coef, na.omit(confint(mod2_haem_mean))), 3)[,c(1,2,5,6,3,4)]

  plot(ggpredict(mod2_haem_mean, c("Intervention"))) +
    ylab("Predicted S. haematobium egg burden") + ggtitle("Model 2 predictions, S. haematobium")



#Compare prawn biomass to only controls
mod2_haem_mean_prawn_bm <- glm.nb(round(s_haem_mean) ~ Prawn_biomass + year_fac + sex + School,
                                  data = full_long %>% filter(extra_pzq != 1 & Intervention %in% c("control",

  round(cbind(summary(mod2_haem_mean_prawn_bm)$coef, confint(mod2_haem_mean_prawn_bm)), 3)[,c(1,2,5,6,3,4)]

#Compare prawn biomass to only controls with net effect
mod2_haem_mean_prawn_bm_net <- glm.nb(round(s_haem_mean) ~ Prawn_biomass + Net + year_fac + sex + School,
                                  data = full_long %>% filter(extra_pzq != 1 & Intervention %in% c("control",

  round(cbind(summary(mod2_haem_mean_prawn_bm_net)$coef, confint(mod2_haem_mean_prawn_bm_net)), 3)[,c(1,2,5,6,

#Compare veg removal to controls
mod2_haem_mean_veg <- glm.nb(round(s_haem_mean) ~ Veg + year_fac + sex + School,
                             data = full_long %>% filter(extra_pzq != 1 & Intervention %in% c("control", "veg_

  round(cbind(summary(mod2_haem_mean_veg)$coef, confint(mod2_haem_mean_veg)), 3)[,c(1,2,5,6,3,4)]
```

For *S. haematobium* these results show that there is a large degree of inter-community variability in transmission that influences estimates of β_1 our target parameter. Adding the term on communities accounts for baseline differences in transmission intensity that may obscure our ability to detect an effect of a particular intervention. Accounting for this variability leads to a significantly protective prawn effect and signficicantly harmful vegetation effect. The net effect also remains, implying there may actually be a protective net effect that is not exaplained by that community's low egg burden alone. This may also imply that the prawn effect is actually driven by a net effect. To dig into this a bit deeper, we'll add another model that considers prawn density as a continuous variable (model 2.1 below). This is better since we're treating villages as their own entities, but we're still treating individual egg burdens as independent when we know that individuals are likely correlated. Model 3 will address this concern.

```
mod2_mans_mean <- glm.nb(round(s_mans_mean12) ~ pzq + Intervention + School + sex,
                         data = full_long %>% filter(extra_pzq != 1))

  round(cbind(summary(mod2_mans_mean)$coef, na.omit(confint(mod2_mans_mean))), 3)[,c(1,2,5,6,3,4)]

  plot(ggpredict(mod2_mans_mean, c("Intervention"))) +
    ylab("Predicted S. mansoni egg burden") + ggtitle("Model 2 predictions, S. mansoni")
```

For *S. mansoni*, the protective effect of vegetation removal and harmful effect of prawn addition are both eliminated when includeing community effects, implying that variability in transmission intensity between communities may explain these effects.

This is better since we're treating villages as their own entities, but we're still treating individual egg burdens as independent when we know that individuals are likely correlated. Model 3 will address this concern.

Model 2.1: Further exploration of effect of interventions on egg burden controlling for inter-village variability

```r
#Note: observations from 2016 should automatically be omitted since the lag variable will be NA, but let's che
mod4_dat %>% group_by(year) %>% summarise(sum(!is.na(log_s_haem_mean_l1)))

#Confirmed, no non-NA observations in 2016
mod3_haem_mean <- glm.nb(round(s_haem_mean) ~ Intervention + School + log_s_haem_mean_l1, data = mod4_dat)
  round(cbind(summary(mod3_haem_mean)$coef, na.omit(confint(mod3_haem_mean))), 3)[,c(1,2,5,6,3,4)]
  plot(ggpredict(mod3_haem_mean, c("Intervention"))) +
    ylab("Predicted S. haematobium egg burden") + ggtitle("Model 3 predictions, S. haematobium")
  plot(ggpredict(mod3_haem_mean, c("log_s_haem_mean_l1", "Intervention"))) +
    ylab("Predicted S. haematobium egg burden") + ggtitle("Model 3 predictions, S. haematobium")
```

```r
mod3_haem_mean <- glm.nb(round(s_haem_mean) ~ Veg + Net + Prawn_biomass + School + log_s_haem_mean_l1, data = m
  round(cbind(summary(mod3_haem_mean)$coef, na.omit(confint(mod3_haem_mean))), 3)[,c(1,2,5,6,3,4)]
  plot(ggpredict(mod3_haem_mean, c("Prawn_biomass"))) +
    ylab("Predicted S. haematobium egg burden") + ggtitle("Model 3 predictions, S. haematobium")


#Compare prawn biomass to only controls
mod3_haem_mean_prawn_bm <- glm.nb(round(s_haem_mean) ~ Prawn_biomass + sex + School + log_s_haem_mean_l1,
                                  data = mod4_dat %>% filter(extra_pzq != 1 & Intervention %in% c("control", "

  round(cbind(summary(mod3_haem_mean_prawn_bm)$coef, confint(mod3_haem_mean_prawn_bm)), 3)[,c(1,2,5,6,3,4)]

#Compare prawn biomass to only controls with net effect
mod3_haem_mean_prawn_bm_net <- glm.nb(round(s_haem_mean) ~ Prawn_biomass + Net + sex + School + log_s_haem_mea
                                  data = mod4_dat %>% filter(extra_pzq != 1 & Intervention %in% c("control", "

  round(cbind(summary(mod3_haem_mean_prawn_bm_net)$coef, confint(mod3_haem_mean_prawn_bm_net)), 3)[,c(1,2,5,6,

#Compare veg removal to controls
mod3_haem_mean_veg <- glm.nb(round(s_haem_mean) ~ Veg + sex + School + log_s_haem_mean_l1,
                             data = mod4_dat %>% filter(extra_pzq != 1 & Intervention %in% c("control", "veg_r

  round(cbind(summary(mod3_haem_mean_veg)$coef, confint(mod3_haem_mean_veg)), 3)[,c(1,2,5,6,3,4)]
```

```r
#see if using only first haematobium urine sample makes a difference since using mean introduces some missingn
mod3_haem1 <- glm.nb(s_haem1 ~ Intervention + School + log_s_haem1_l1, data = mod4_dat)
  round(cbind(summary(mod3_haem1)$coef, na.omit(confint(mod3_haem1))), 3)[,c(1,2,5,6,3,4)]
#Doesn't qualitatively change results
```

```r
mod3_mans_mean <- glm.nb(s_mans_mean12 ~ Intervention + School + log_s_mans_mean12_l1, data = mod4_dat)
  round(cbind(summary(mod3_mans_mean)$coef, na.omit(confint(mod3_mans_mean))), 3)[,c(1,2,5,6,3,4)]
  plot(ggpredict(mod3_mans_mean, c("log_s_mans_mean12_l1", "Intervention"))) +
    ylab("Predicted S. mansoni egg burden") + ggtitle("Model 3 predictions, S. mansoni")
```

For each independent variable of interest (e.g. interventions) there are a couple of measurements of interest we might consider:

Net addition

- Binary (net installed or no)
- Continuous-ish (months with net installed over reinfection period)
- Continuous (area enclosed by net)

I think binary makes the most sense here as I'm not sure how different n

Prawn stocking

- Binary (prawns stocked or no)
- Categorical (no prawns, low or high stocking density)
- Continuous (mean monthly prawn density over reinfection period)

I think it's worth exploring each of these sequentially

Vegetation removal

- Binary (Vegetation removal or no)
- Continuous (tons of vegetation removed over reinfection period)

I think binary makes sense here since I believe all vegetation possible was removed at each site

We'll treat egg burden of each Schistosome species as our dependent variable in separate analyses

Old Models

Appendix

A litany of data cleaning/aggregating/integrating notes:
+ Months during reinfection with net added were calculated as inclusive of the month the net was added, but excluded the month when infection was estimated
+ Mean monthly prawn density was estimated as the mean monthly density over the number of months in the reinfection period
+ Mean monthly prawn density for communities with more than one water access point were estimated as an average of all water access points
+ Vegetation removal in communities with multiple water contact sites was estimated as the mean total tons of vegetation removed per site