20251021_predicted_nb_updated

2025-10-21

```
#setup dataset and model
nsd_yes_metadata <-
  metadata %>%
  filter(nsd == "Yes") %>%
  filter(., age.in.months != "NA" & da != "NA" & container.title != "NA") %>%
  mutate(da_factor = factor(da),
         container.title = factor(container.title))


nsd_yes_model <-
  glm.nb(is.referenced.by.count~ da_factor + log(age.in.months) + container.title +
  + container.title*da_factor + log(age.in.months)*da_factor + container.title*log(age.in.months) +
  log(age.in.months)*da_factor*container.title, data = nsd_yes_metadata, link = log)
```

Validation of fit

- How many citations did a paper published in 2021 receive in each journal?

```
nsd_yes_metadata %>%
  filter(year.published == 2021) %>%
  summarize(mean_cites_2021 = mean(is.referenced.by.count),
            median_cites_2021 = median(is.referenced.by.count),
            .by = container.title)
```

```
## # A tibble: 11 x 3
##    container.title                          mean_cites_2021 median_cites_2021
##    <fct>                                              <dbl>             <dbl>
##  1 Antimicrobial Agents and Chemotherapy              12.3                  8
##  2 Applied and Environmental Microbiology             13.9                 11
##  3 Infection and Immunity                              9.19                 9
##  4 Journal of Bacteriology                             9.40                 7
##  5 Journal of Clinical Microbiology                   16.5                 12
##  6 Journal of Virology                                16.3                 11
##  7 mBio                                               21.4                 16
##  8 Microbiology Resource Announcements                 2.31                 1
##  9 mSphere                                            15.6                 12
## 10 mSystems                                           18.1                 14
## 11 Microbiology Spectrum                              13.3                 10
```

Using the existing model

- Remove JMBE, MRA, GA from modeling

- Train on papers <= 10 years old (age.in.months <= 120)
- Re-create figure with and without a common axis
- Previously N = 41,271, now N = 13,911

```
#filter to remove jmbe, mra, ga and for age.in.months <= 120
ten_metadata <-
  nsd_yes_metadata %>%
  filter(journal_abrev != "jmbe" & journal_abrev != "mra" & journal_abrev != "genomea" & age.in.months
```

```
#sanity check
ten_metadata %>%
  count(journal_abrev)
```

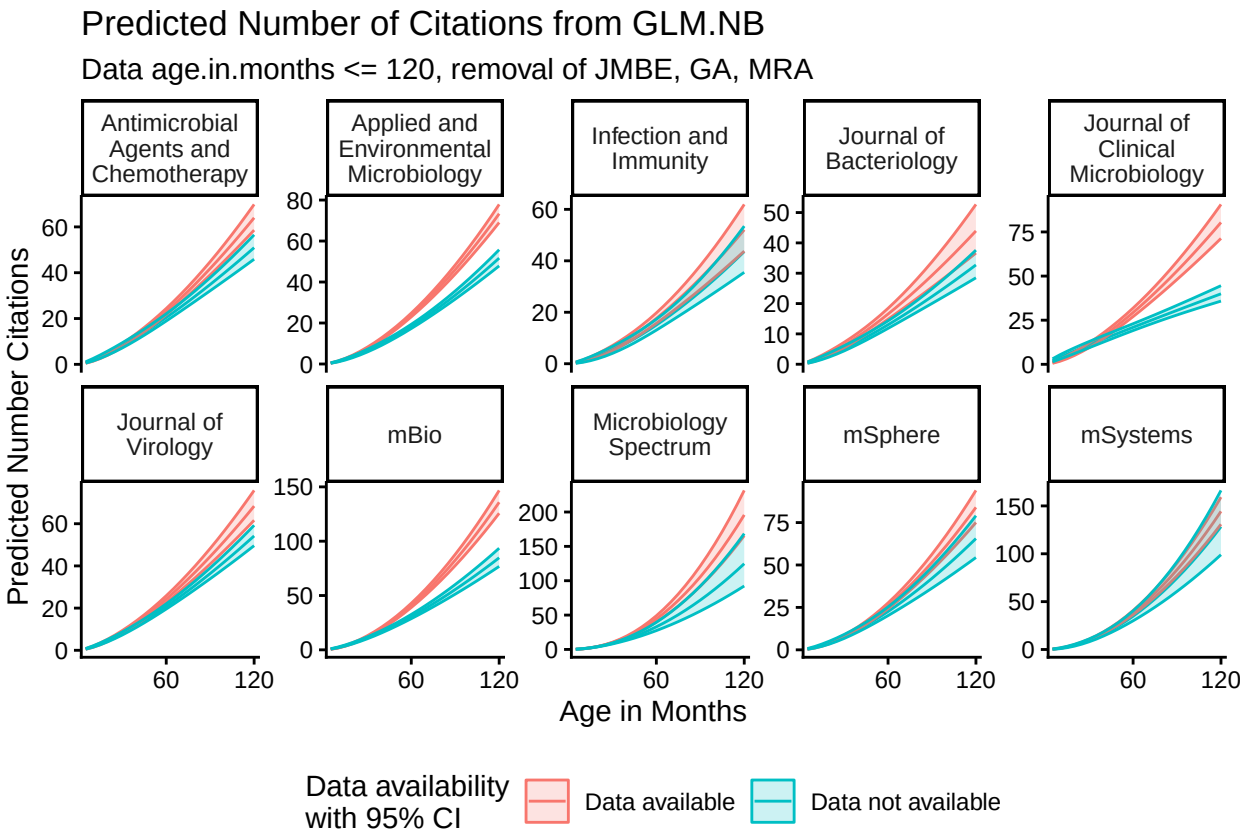
```
## # A tibble: 10 x 2
##    journal_abrev     n
##    <chr>         <int>
##  1 aac            1197
##  2 aem            2695
##  3 iai             342
##  4 jb              536
##  5 jcm             699
##  6 jvi            1353
##  7 mbio           1982
##  8 msphere         971
##  9 msystems       1400
## 10 spectrum       2736
```

```
ten_metadata %>%
  count(age.in.months) %>%
  tail()
```

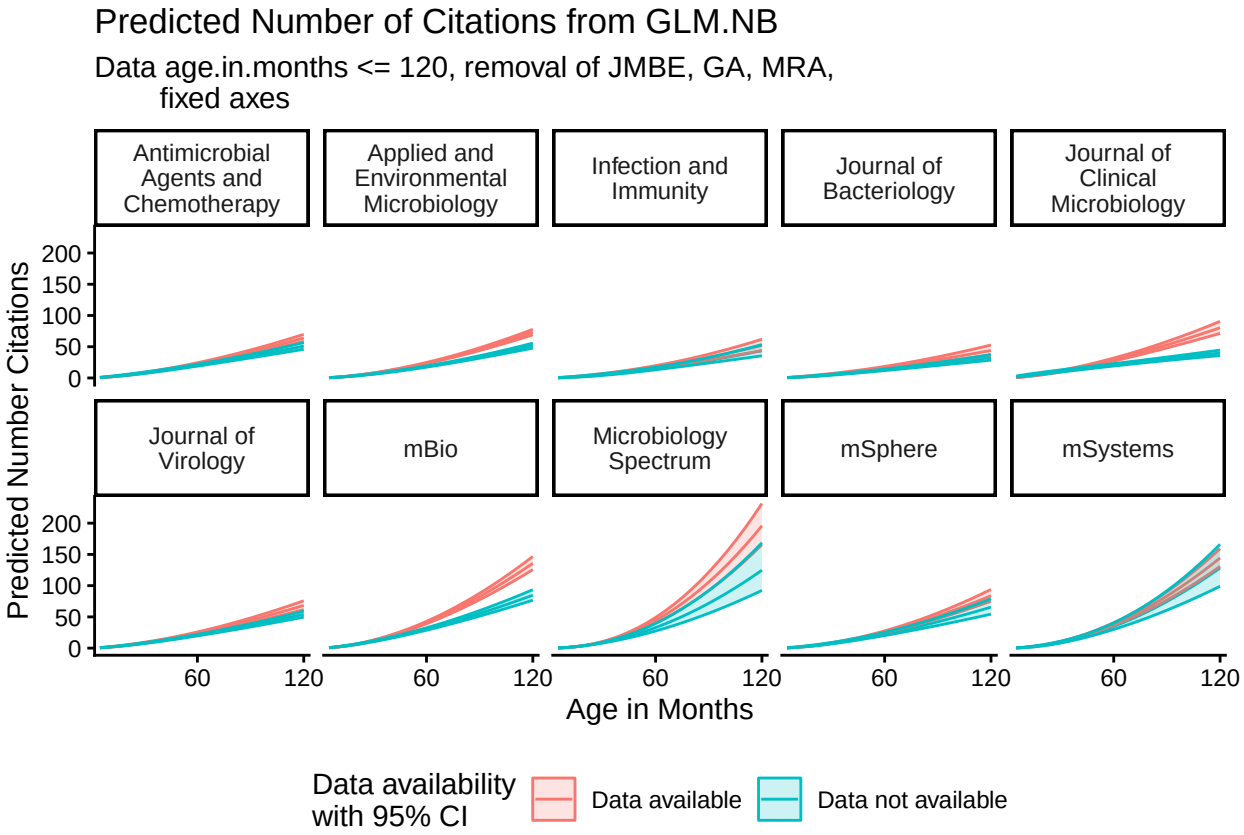
```
## # A tibble: 6 x 2
##   age.in.months     n
##           <dbl> <int>
## 1           115    77
## 2           116    68
## 3           117   110
## 4           118    74
## 5           119    83
## 6           120    68
```

```
#retrain model
ten_model <-
  glm.nb(is.referenced.by.count~ da_factor + log(age.in.months) + container.title +
  + container.title*da_factor + log(age.in.months)*da_factor + container.title*log(age.in.months) +
  log(age.in.months)*da_factor*container.title, data = ten_metadata, link = log)

#get data out of model

age_values <- seq(5, 120, 5)
  p_10 <-  get_model_data(model = ten_model, type = "pred",
```

```
                    terms = c("da_factor", "age.in.months[age_values]", "container.title"),
                    colors = "bw") %>%
      tibble(da_factor = ifelse(.$x == 1, "Data not available", "Data available"), predicted_citations =
          age.in.months = .$group, container.title = .$facet)


#re-create figure with free axes

predicted_plot <-
    ggplot(data = p_10, mapping = aes(x = as.numeric(age.in.months), y = predicted_citations,
                                color = da_factor)) +
   geom_line(aes(x = age.in.months, y = predicted_citations, group = da_factor)) +
   geom_ribbon(mapping = aes(ymin = conf.low, ymax = conf.high,
                             group = da_factor, fill = da_factor), alpha = 0.2) +
  facet_wrap(~ container.title, nrow = 2,
               labeller = label_wrap_gen(width = 18),
               scale = "free_y") +
   labs(title = "Predicted Number of Citations from GLM.NB",
        subtitle = "Data age.in.months <= 120, removal of JMBE, GA, MRA",
        x = "Age in Months",
        y = "Predicted Number Citations",
        color = "Data availability\nwith 95% CI",
        fill = "Data availability\nwith 95% CI") +
    scale_x_discrete(breaks = seq(12, 120, 12)) +
    theme_classic() +
    theme(legend.position = "bottom" )


predicted_plot_fixed <-
    ggplot(data = p_10, mapping = aes(x = as.numeric(age.in.months), y = predicted_citations,
                                color = da_factor)) +
   geom_line(aes(x = age.in.months, y = predicted_citations, group = da_factor)) +
   geom_ribbon(mapping = aes(ymin = conf.low, ymax = conf.high,
                             group = da_factor, fill = da_factor), alpha = 0.2) +
  facet_wrap(~ container.title, nrow = 2,
               labeller = label_wrap_gen(width = 18)) +
   labs(title = "Predicted Number of Citations from GLM.NB",
        subtitle = "Data age.in.months <= 120, removal of JMBE, GA, MRA,
        fixed axes",
        x = "Age in Months",
        y = "Predicted Number Citations",
        color = "Data availability\nwith 95% CI",
        fill = "Data availability\nwith 95% CI") +
    scale_x_discrete(breaks = seq(12, 120, 12)) +
    theme_classic() +
    theme(legend.position = "bottom" )

predicted_plot
```



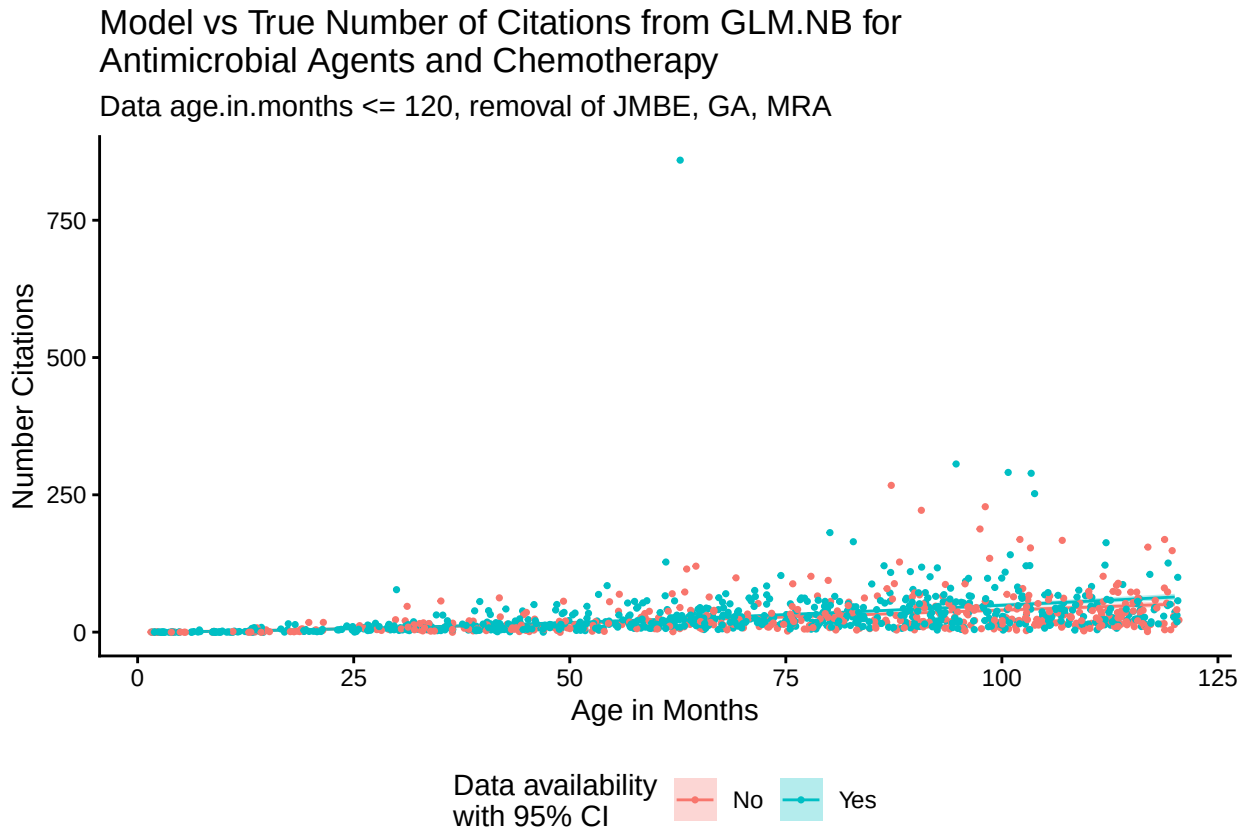

```
predicted_plot_fixed
```

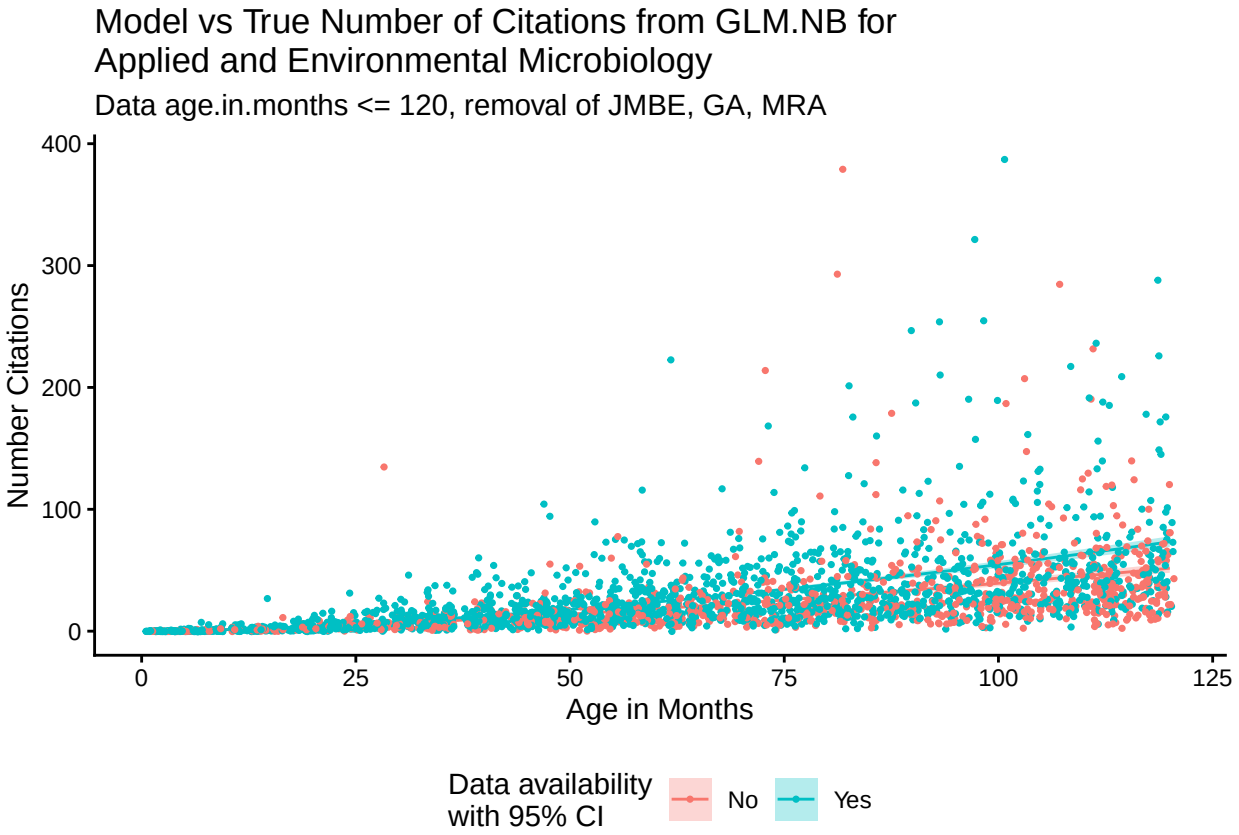


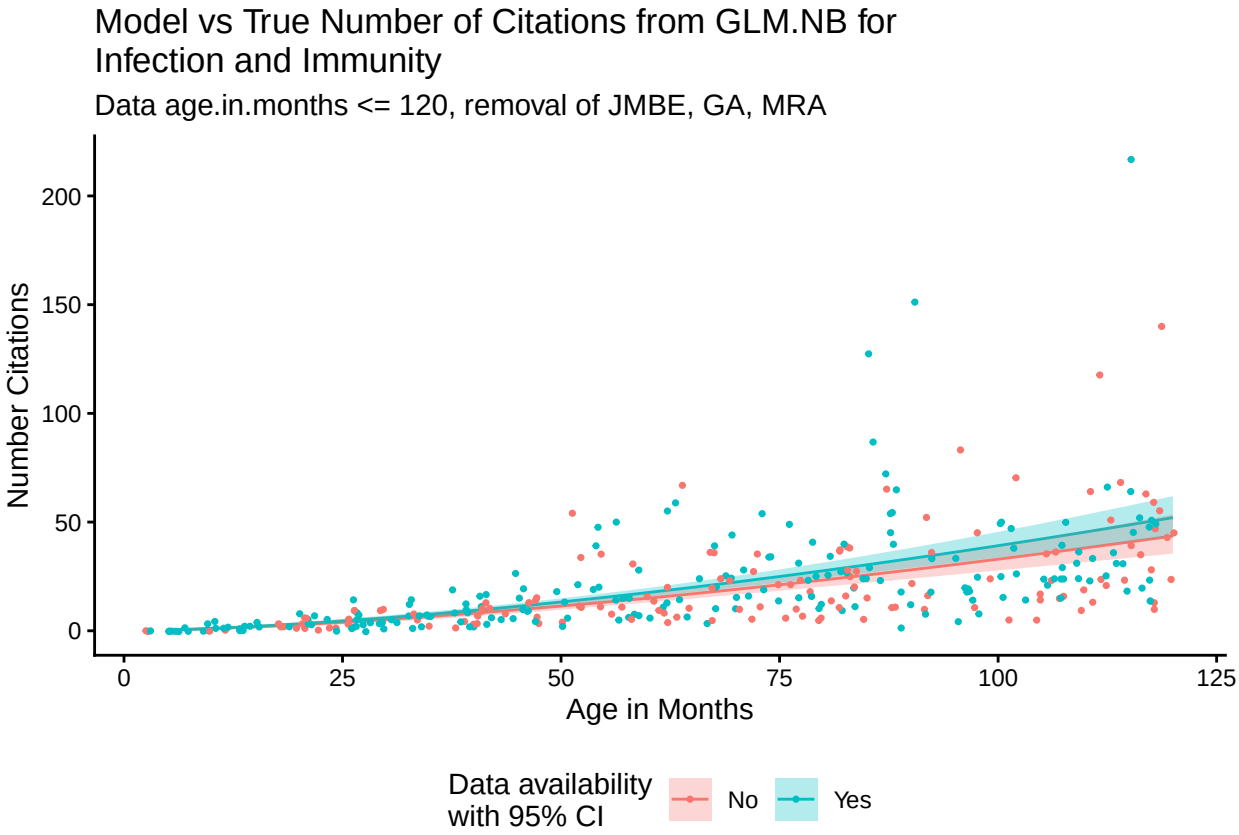
For each journal separately, overlay citations by paper on model output for DA yes and DA no

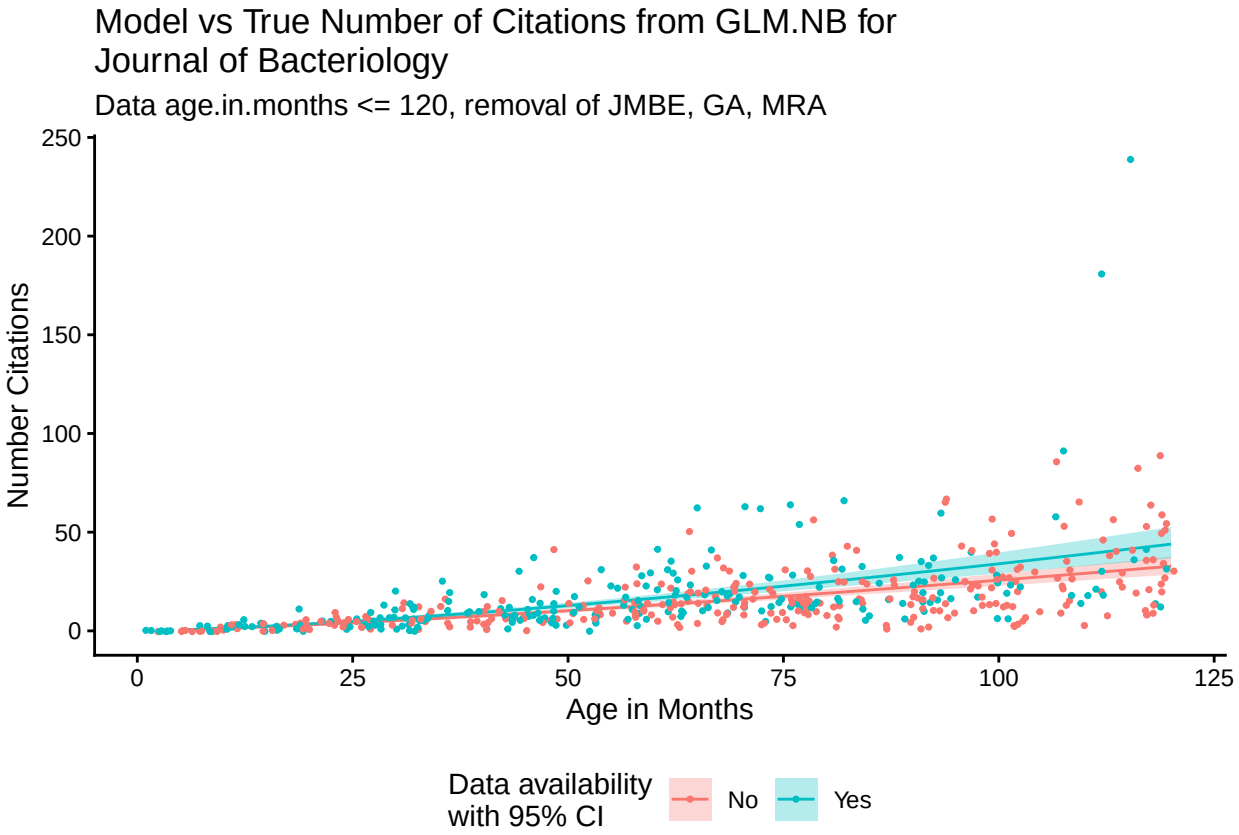
```
#lol i just add the data in each geom
journals <- ten_metadata %>%
  count(container.title) %>%
  mutate(container.title = as.character(container.title)) %>%
  dplyr::select(container.title)

j<- 6

for(j in 1:nrow(journals)) {
  #filter metadata for that journal
  j_metadata <- ten_metadata %>%
      filter(container.title == journals$container.title[[j]])

  #filter p_10
  model_data <- p_10 %>%
    filter(container.title == journals$container.title[[j]]) %>%
    mutate(da_factor = ifelse(da_factor == "Data available", "Yes", "No"),
           age.in.months = as.numeric(as.character(age.in.months)))

  #make plot
  plot <-
```

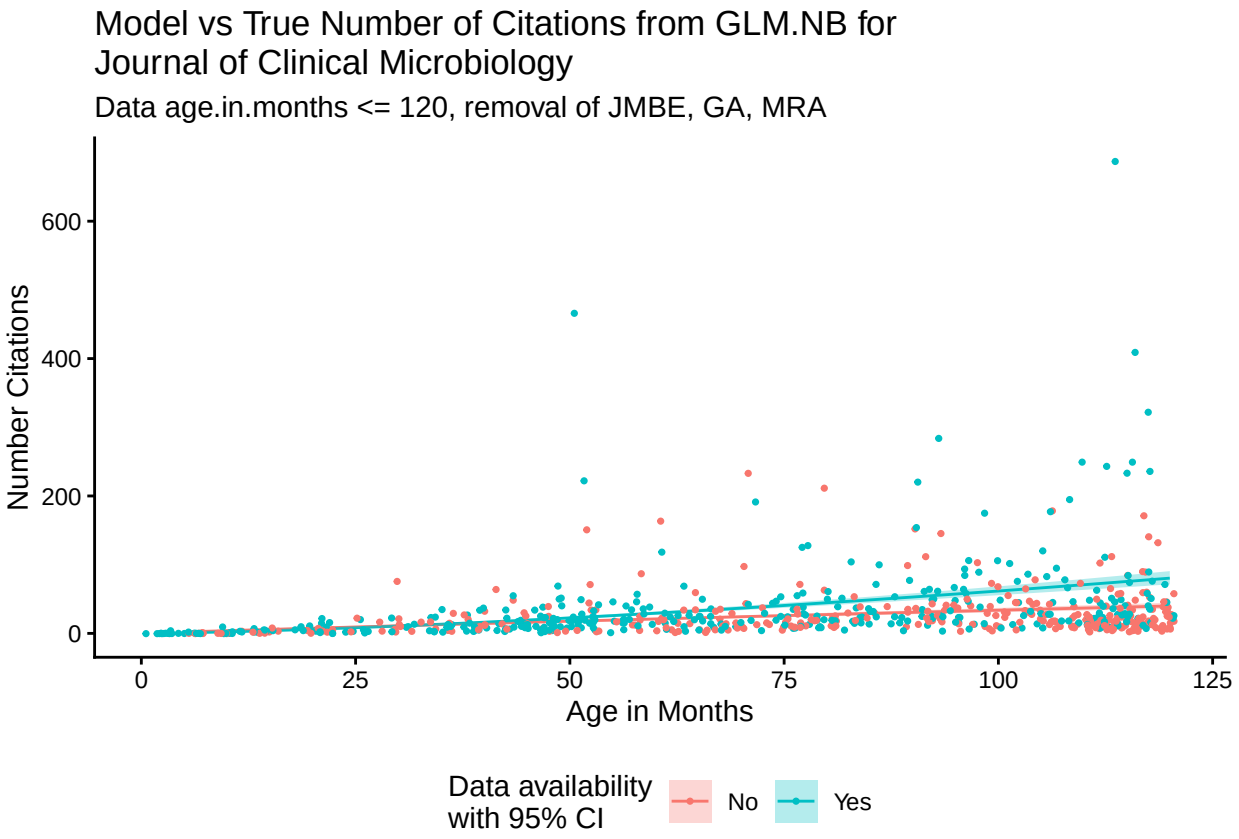
```
  ggplot() +
    # mapping = aes(x = age.in.months, y = predicted_citations,
    #                                color = da_factor)) +
   geom_line(data = model_data, aes(x = age.in.months, y = predicted_citations, group = da_factor, colo
   geom_ribbon(data = model_data, mapping = aes(x = age.in.months, y = predicted_citations,    ymin = c
                              group = da_factor, fill = da_factor), alpha = 0.3) +
    geom_point(data = j_metadata, aes(x = age.in.months,
                                      y = is.referenced.by.count, color = da_factor),
                                      position = position_jitter(width =0.5), size = 0.6) +
   labs(title = paste0("Model vs True Number of Citations from GLM.NB for\n", journals$container.title[
        subtitle = "Data age.in.months <= 120, removal of JMBE, GA, MRA",
        x = "Age in Months",
        y = "Number Citations",
        color = "Data availability\nwith 95% CI",
        fill = "Data availability\nwith 95% CI") +
   # scale_x_discrete(breaks = seq(12, 120, 12)) +
    theme_classic() +
    theme(legend.position = "bottom" )

print(plot)
}
```

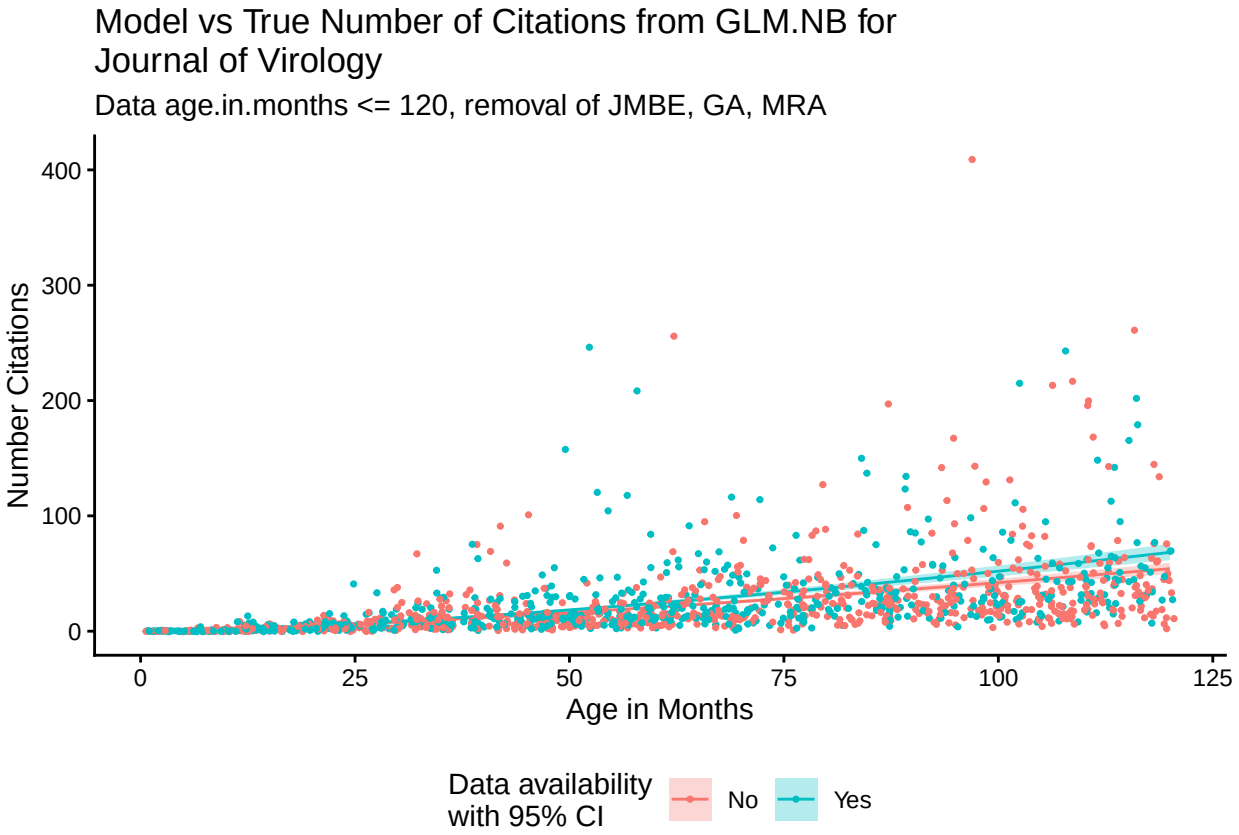


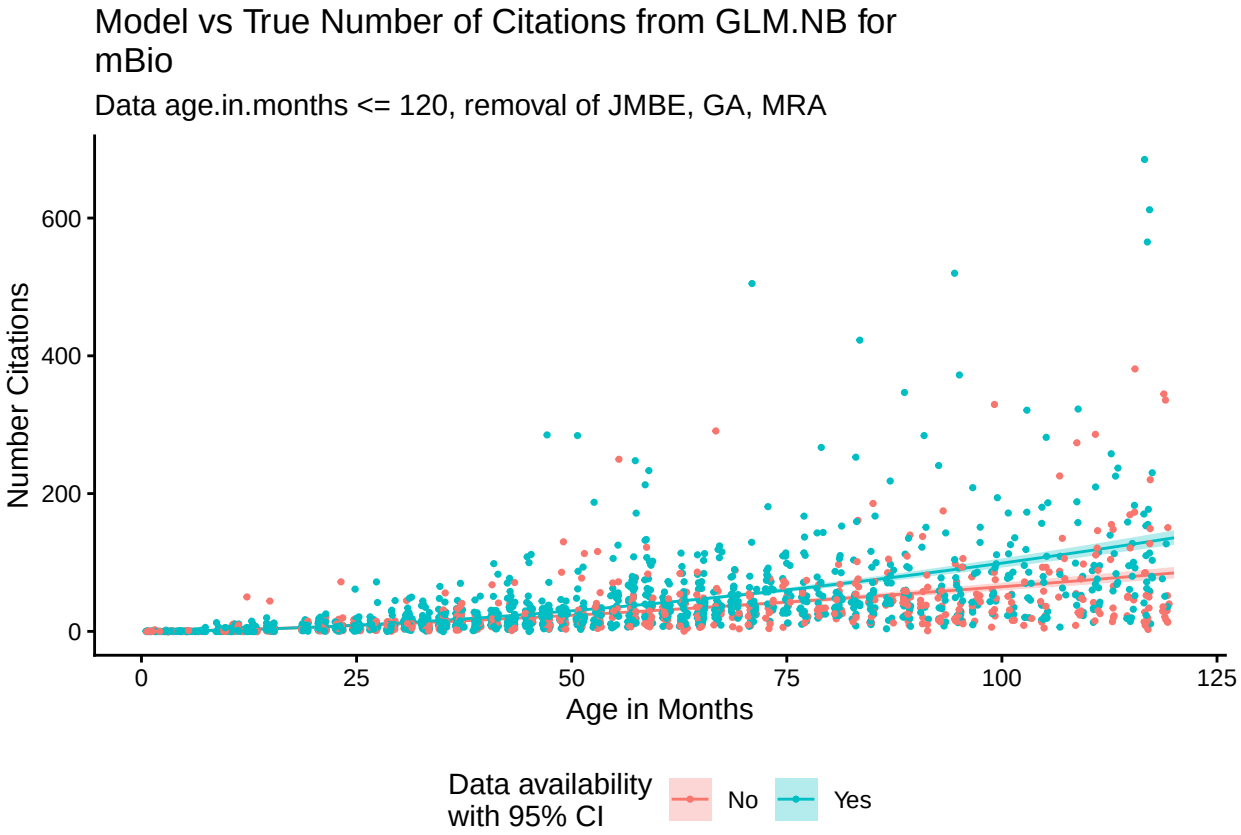

Model vs True Number of Citations from GLM.NB for
Applied and Environmental Microbiology
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
400
300
200
100
0
0
25
50
75
100
125
Age in Months
Data availability
with 95% CI
No
Yes

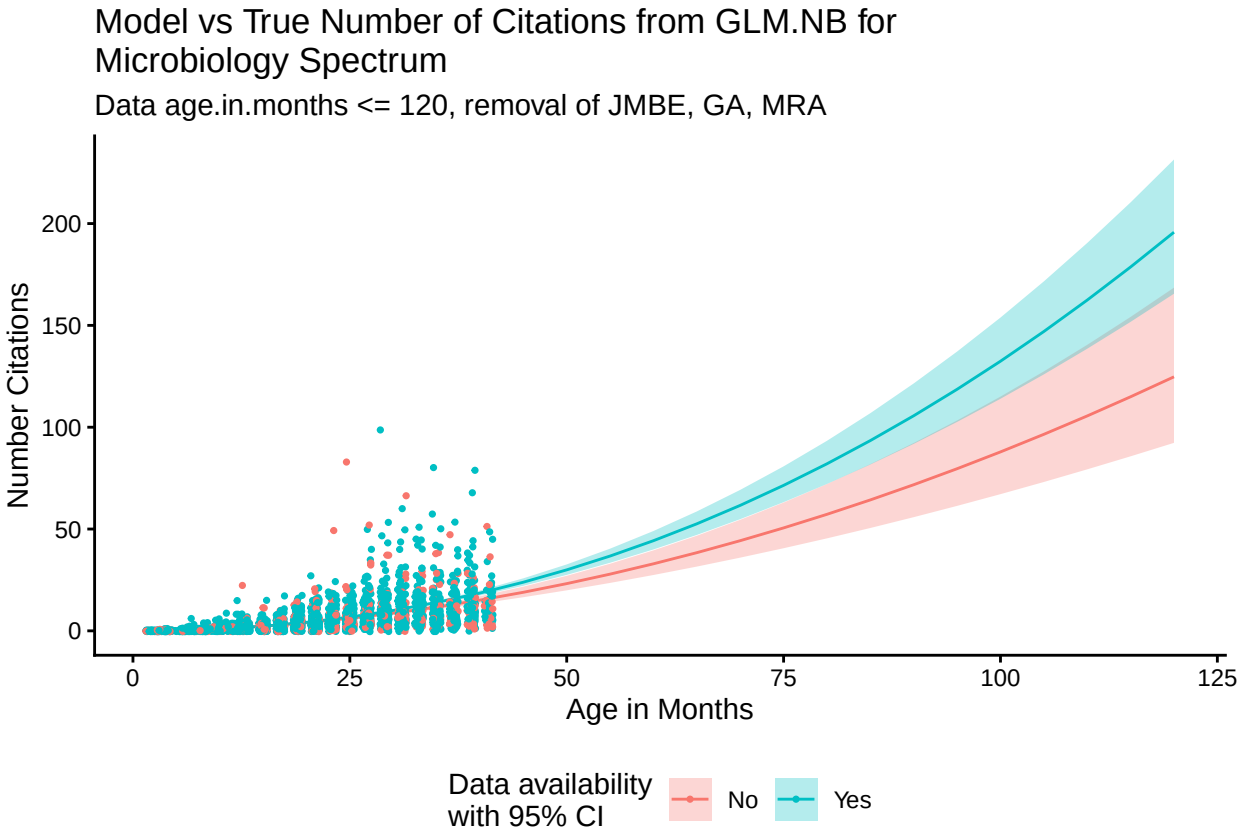

Model vs True Number of Citations from GLM.NB for Infection and Immunity
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
200
150
100
50
0
0
25
50
75
100
125
Age in Months
Data availability with 95% CI
No
Yes

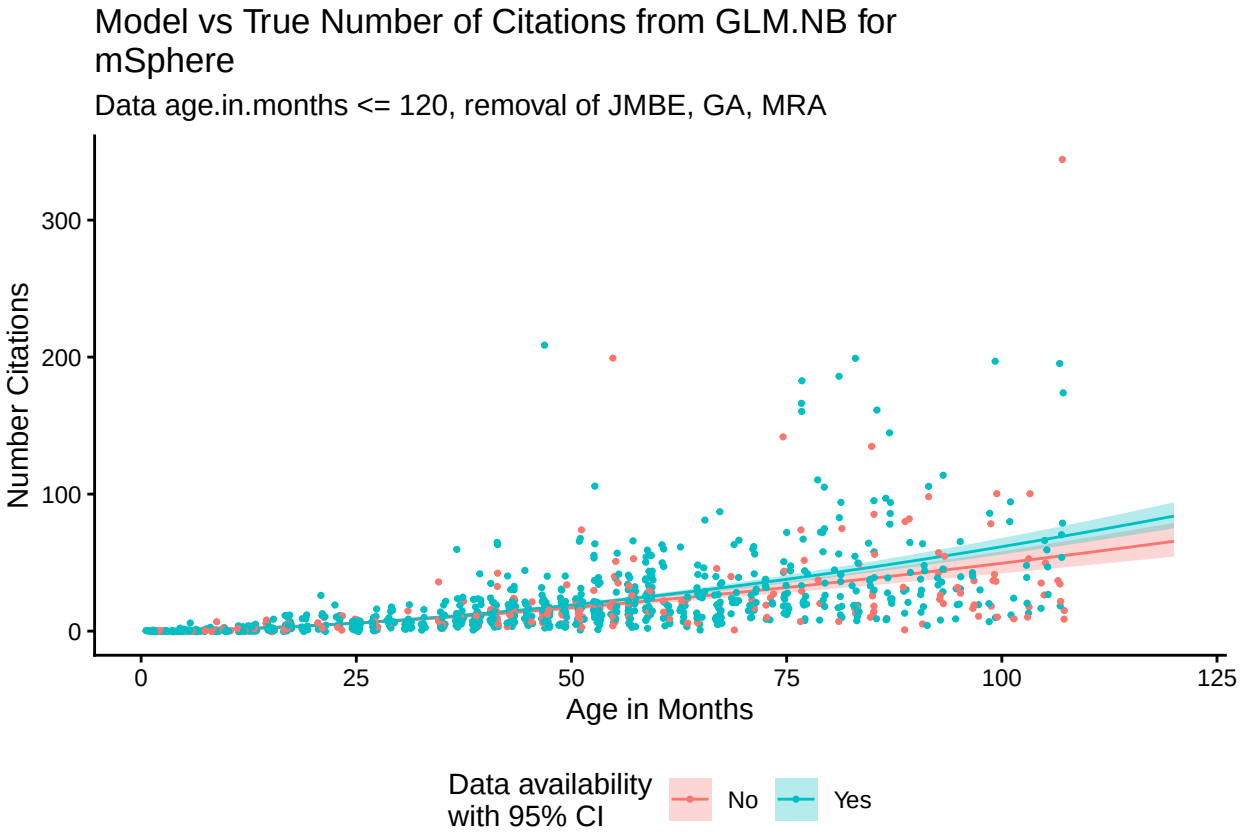

Model vs True Number of Citations from GLM.NB for Journal of Bacteriology
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
250
200
150
100
50
0
0
25
50
75
100
125
Age in Months
Data availability with 95% CI
No
Yes

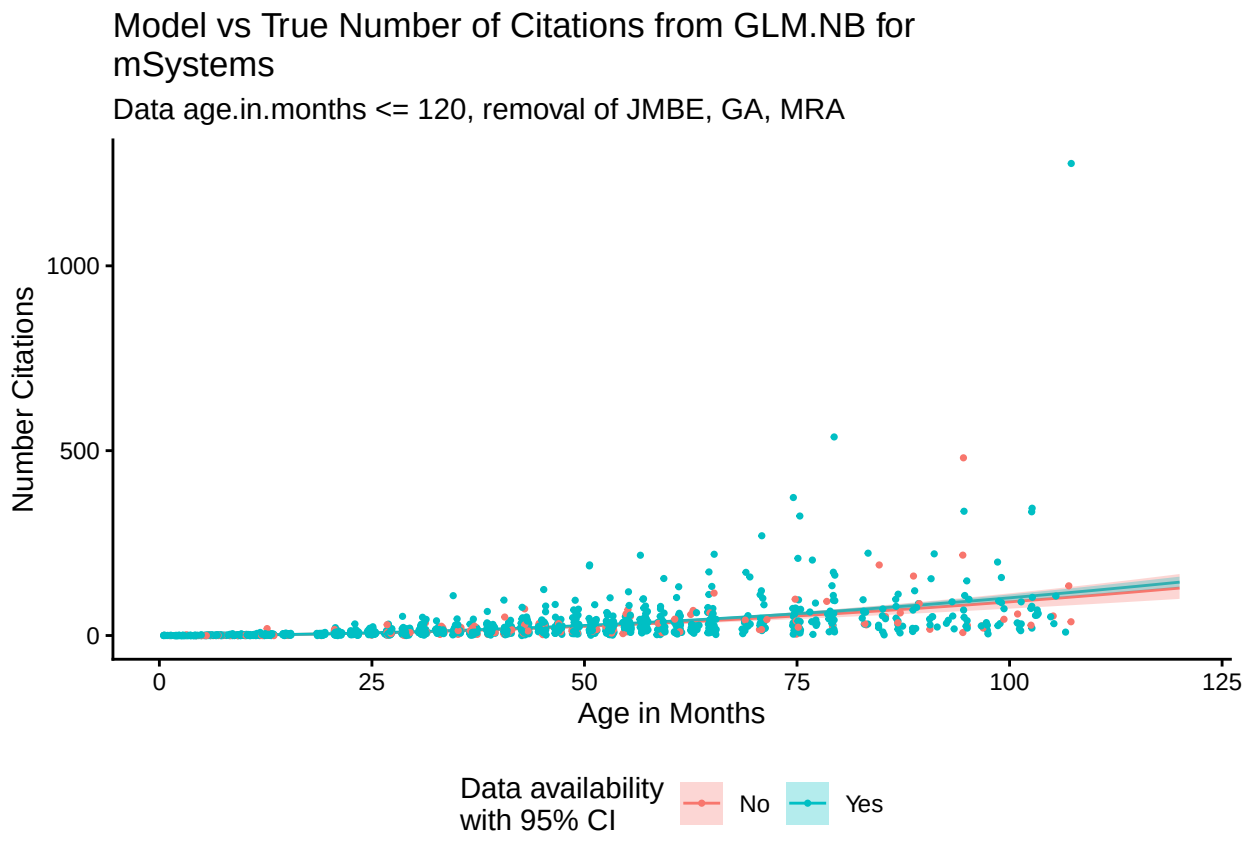

Model vs True Number of Citations from GLM.NB for
Journal of Clinical Microbiology
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
600
400
200
0
0
25
50
75
100
125
Age in Months
Data availability
with 95% CI
No
Yes


Model vs True Number of Citations from GLM.NB for Journal of Virology
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
400
300
200
100
0
0
25
50
75
100
125
Age in Months
Data availability with 95% CI
No
Yes


Model vs True Number of Citations from GLM.NB for mBio
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
600
400
200
0
0
25
50
75
100
125
Age in Months
Data availability with 95% CI
No
Yes


Model vs True Number of Citations from GLM.NB for Microbiology Spectrum
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
200
150
100
50
0
0
25
50
75
100
125
Age in Months
Data availability with 95% CI
No
Yes

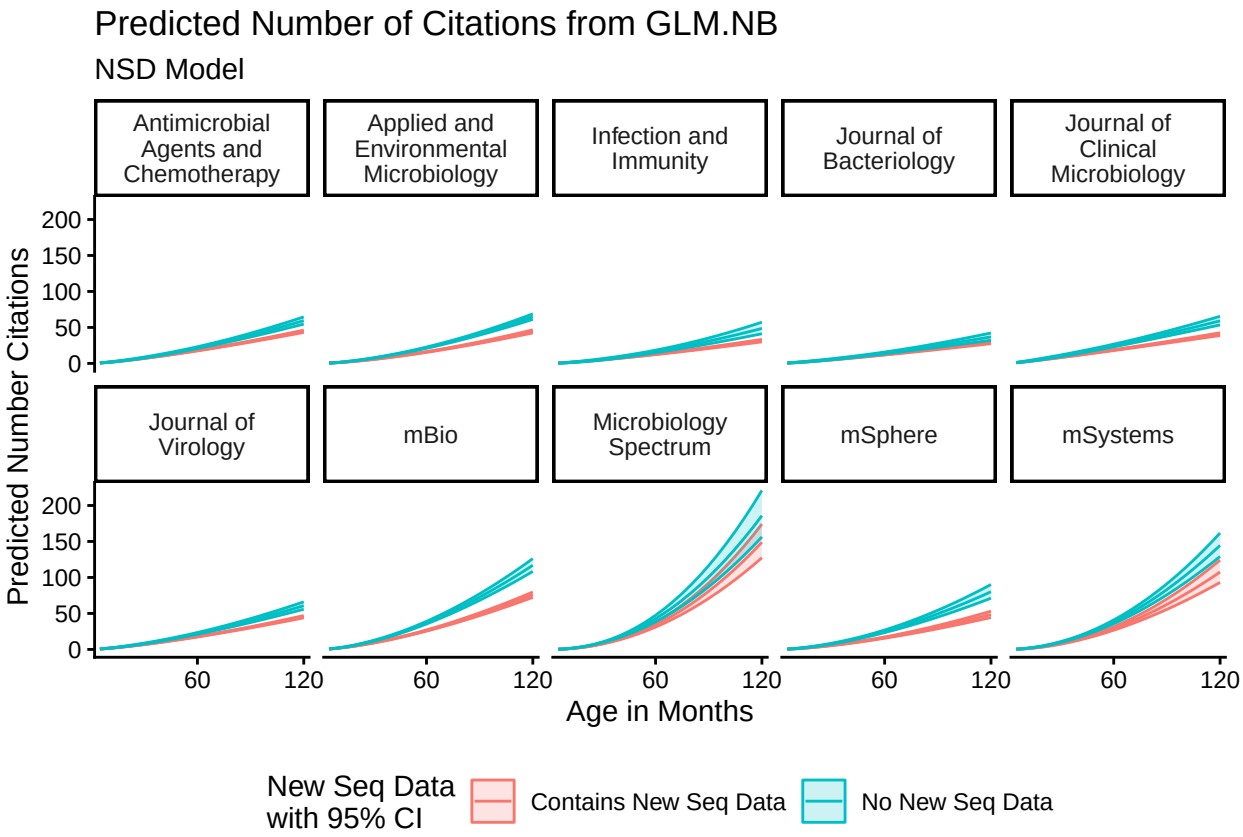

Model vs True Number of Citations from GLM.NB for mSphere
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
300
200
100
0
0
25
50
75
100
125
Age in Months
Data availability with 95% CI
No
Yes



Create a new model for sequence data vs no new sequence data

```
#setup dataset and model

#filter dataset for no nas, filter out jmbe, mra, ga, age in months <= 120
nsd_model_metadata <-
  metadata %>%
  filter(., age.in.months != "NA" & nsd != "NA" & container.title != "NA") %>%
  filter(journal_abrev != "jmbe" & journal_abrev != "mra" & journal_abrev != "genomea" & age.in.months <
  mutate(nsd_factor = factor(nsd),
         container.title = factor(container.title))


nsd_model <-
  glm.nb(is.referenced.by.count~ nsd_factor + log(age.in.months) + container.title +
  + container.title*nsd_factor + log(age.in.months)*nsd_factor + container.title*log(age.in.months) +
  log(age.in.months)*nsd_factor*container.title, data = nsd_model_metadata, link = log)


# make plots for each journal

  p_nsd <-  get_model_data(model = nsd_model, type = "pred",
                    terms = c("nsd_factor", "age.in.months[age_values]", "container.title"),
                    colors = "bw") %>%
```

```
      tibble(nsd_factor = ifelse(.$x == 1, "Contains New Seq Data", "No New Seq Data"), predicted_citati
          age.in.months = .$group, container.title = .$facet)



  predicted_plot_nsd <-
    ggplot(data = p_nsd, mapping = aes(x = as.numeric(age.in.months), y = predicted_citations,
                                color = nsd_factor)) +
   geom_line(aes(x = age.in.months, y = predicted_citations, group = nsd_factor)) +
   geom_ribbon(mapping = aes(ymin = conf.low, ymax = conf.high,
                             group = nsd_factor, fill = nsd_factor), alpha = 0.2) +
  facet_wrap(~ container.title, nrow = 2,
               labeller = label_wrap_gen(width = 18),
               scale = "free_y") +
   labs(title = "Predicted Number of Citations from GLM.NB",
        subtitle = "NSD Model",
        x = "Age in Months",
        y = "Predicted Number Citations",
        color = "New Seq Data\nwith 95% CI",
        fill = "New Seq Data\nwith 95% CI") +
    scale_x_discrete(breaks = seq(12, 120, 12)) +
    theme_classic() +
    theme(legend.position = "bottom" )


  predicted_plot_nsd <-
    ggplot(data = p_nsd, mapping = aes(x = as.numeric(age.in.months), y = predicted_citations,
                                color = nsd_factor)) +
   geom_line(aes(x = age.in.months, y = predicted_citations, group = nsd_factor)) +
   geom_ribbon(mapping = aes(ymin = conf.low, ymax = conf.high,
                             group = nsd_factor, fill = nsd_factor), alpha = 0.2) +
  facet_wrap(~ container.title, nrow = 2,
               labeller = label_wrap_gen(width = 18),
              ) +
   labs(title = "Predicted Number of Citations from GLM.NB",
        subtitle = "NSD Model",
        x = "Age in Months",
        y = "Predicted Number Citations",
        color = "New Seq Data\nwith 95% CI",
        fill = "New Seq Data\nwith 95% CI") +
    scale_x_discrete(breaks = seq(12, 120, 12)) +
    theme_classic() +
    theme(legend.position = "bottom" )
predicted_plot_nsd
```


Predicted Number of Citations from GLM.NB
NSD Model
Antimicrobial Agents and Chemotherapy
Applied and Environmental Microbiology
Infection and Immunity
Journal of Bacteriology
Journal of Clinical Microbiology
Journal of Virology
mBio
Microbiology Spectrum
mSphere
mSystems
Predicted Number Citations
0
50
100
150
200
60
120
Age in Months
New Seq Data with 95% CI
Contains New Seq Data
No New Seq Data