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

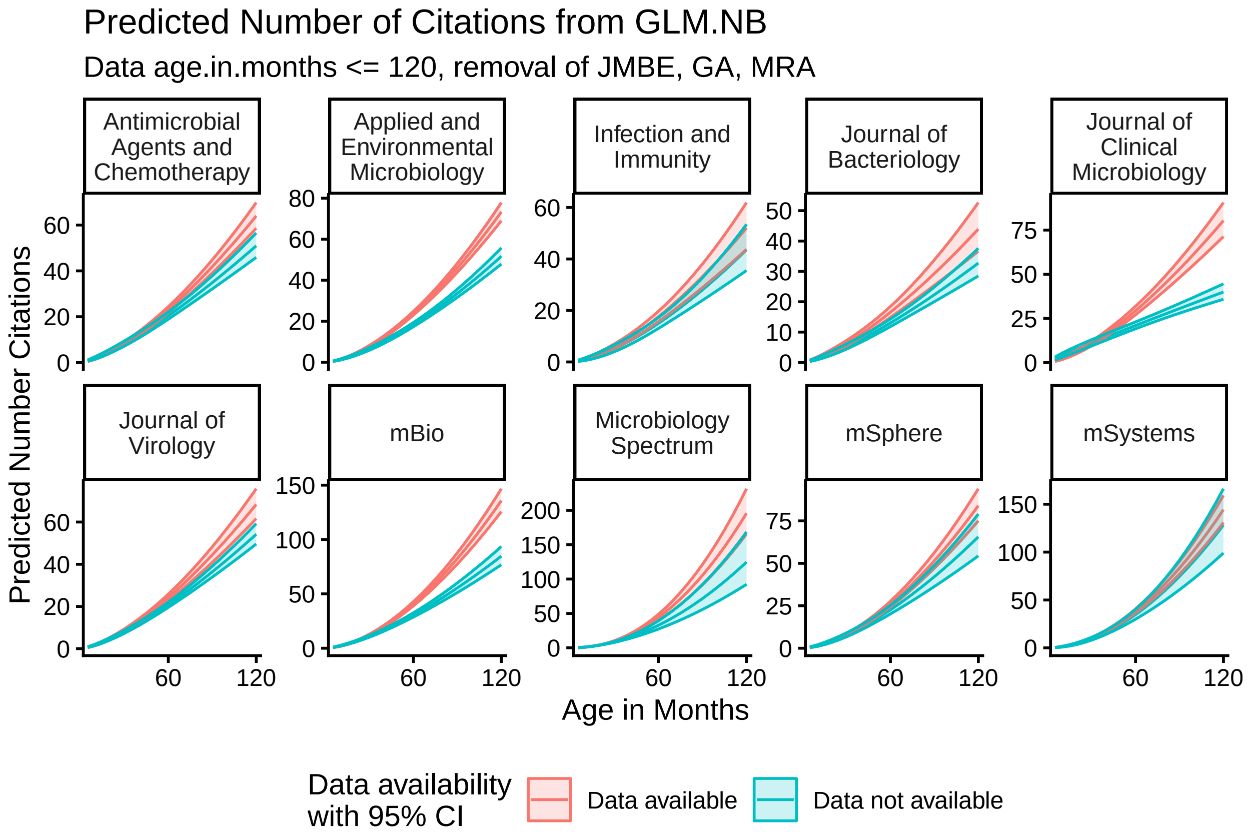
```
#filter to remove jmbe, mra, ga and for age.in.months <= 120
ten_metadata <-
  nsd_yes_metadata %>%
  filter(journal_abrev != "jmbe" & journal_abrev != "mra" & journal_abrev != "genomea" & age.in.months


#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
```

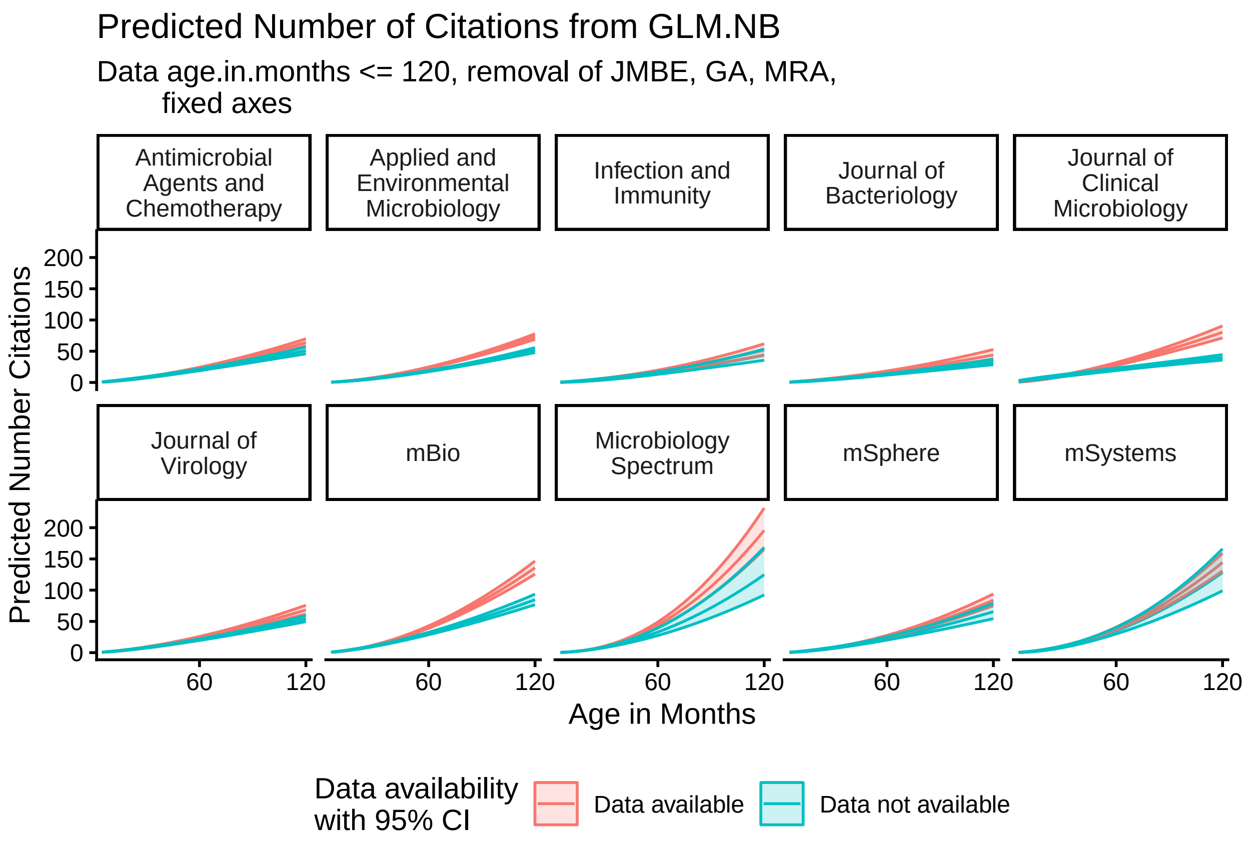
```
ten_metadata %>%
  count(age.in.months) %>%
  tail()
```

```
## # 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
```

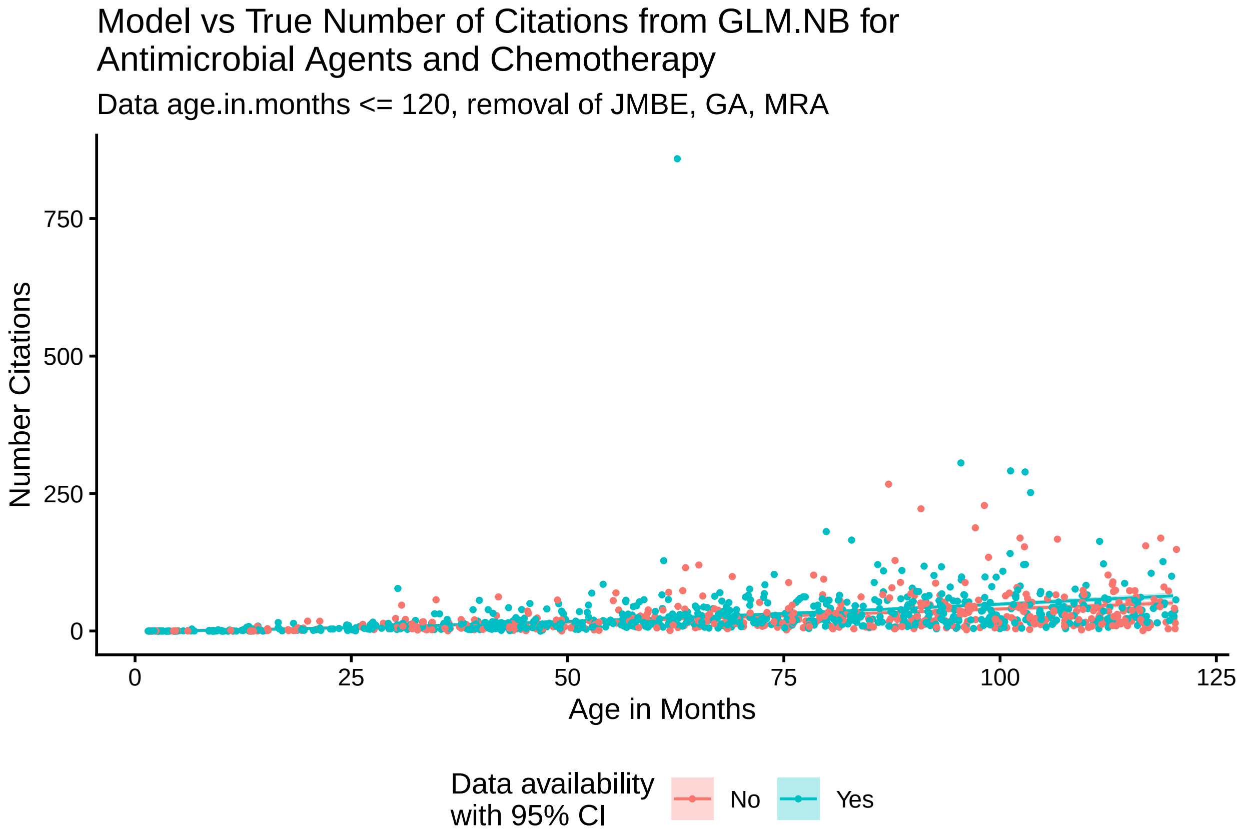


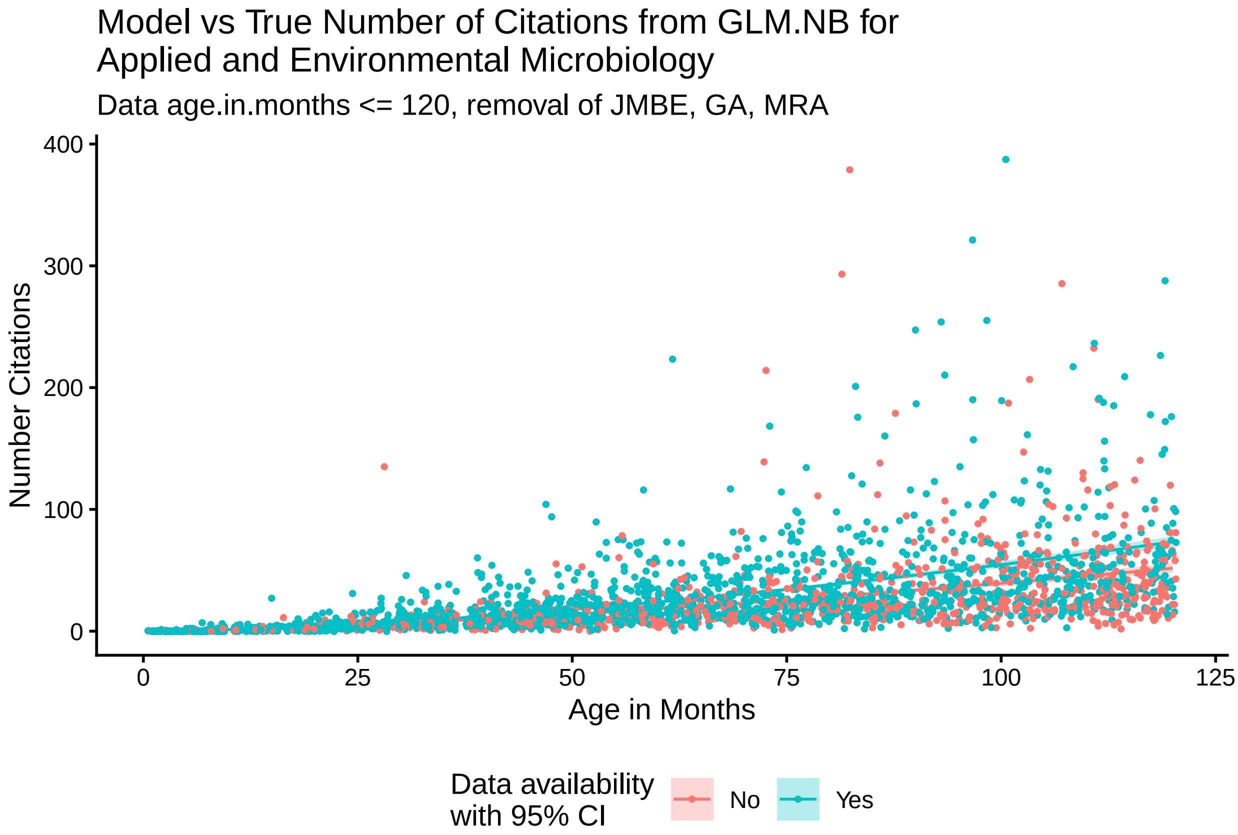
```
predicted_plot_fixed
```

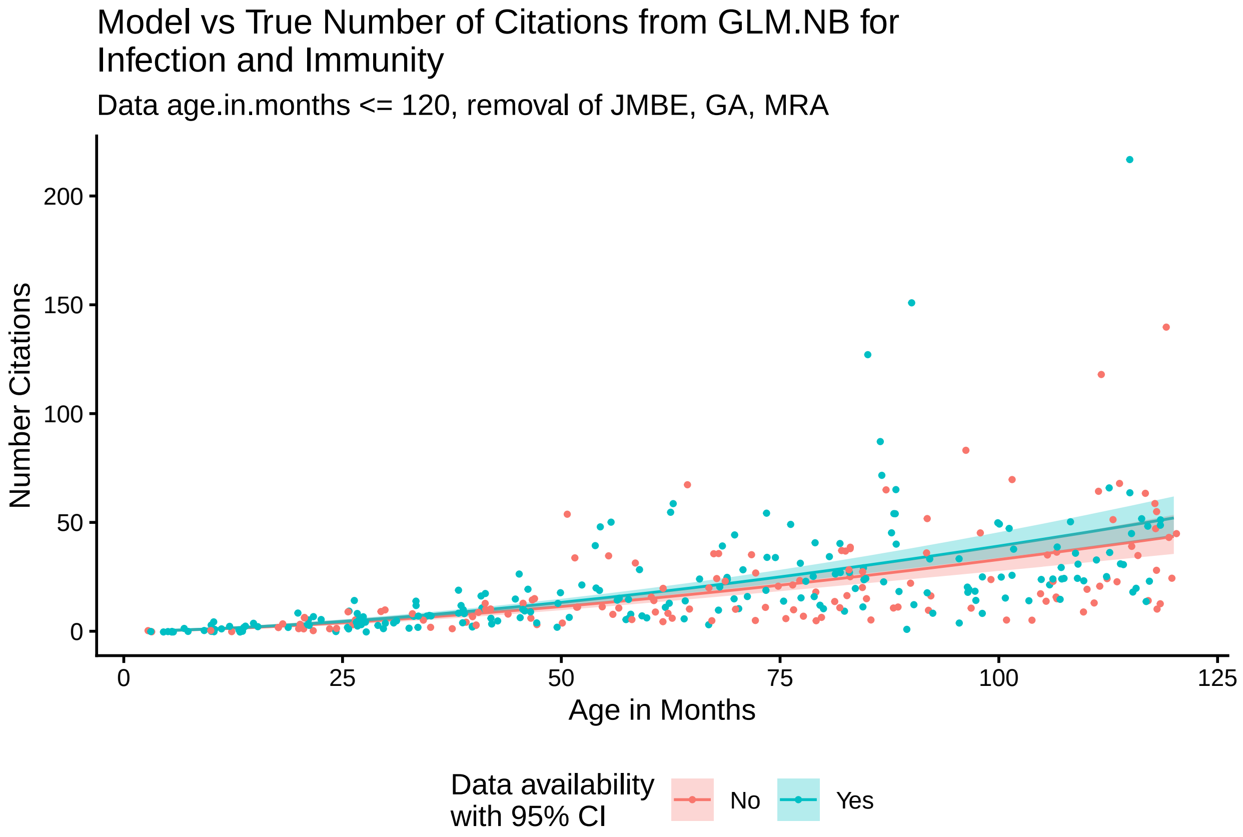


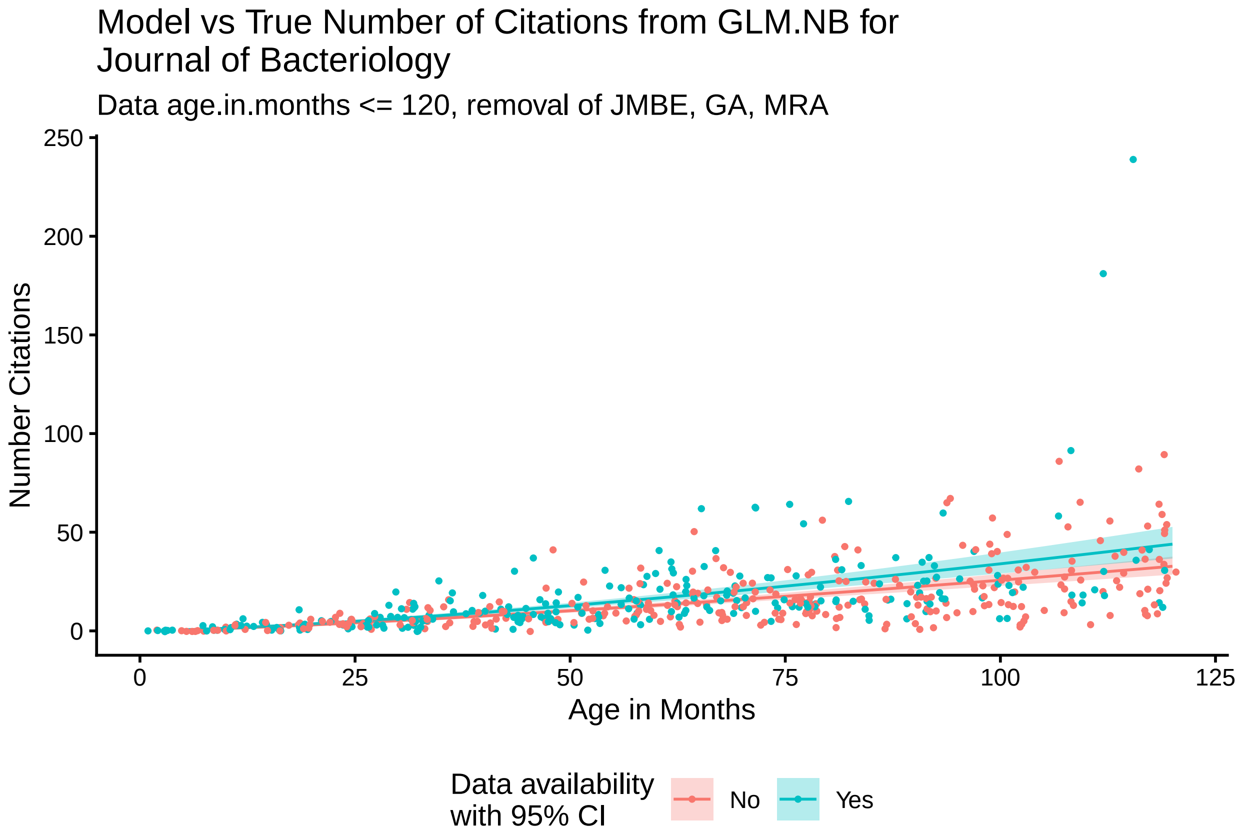
For each journal separately, overlay citations by paper on model output for DA yes and DA no

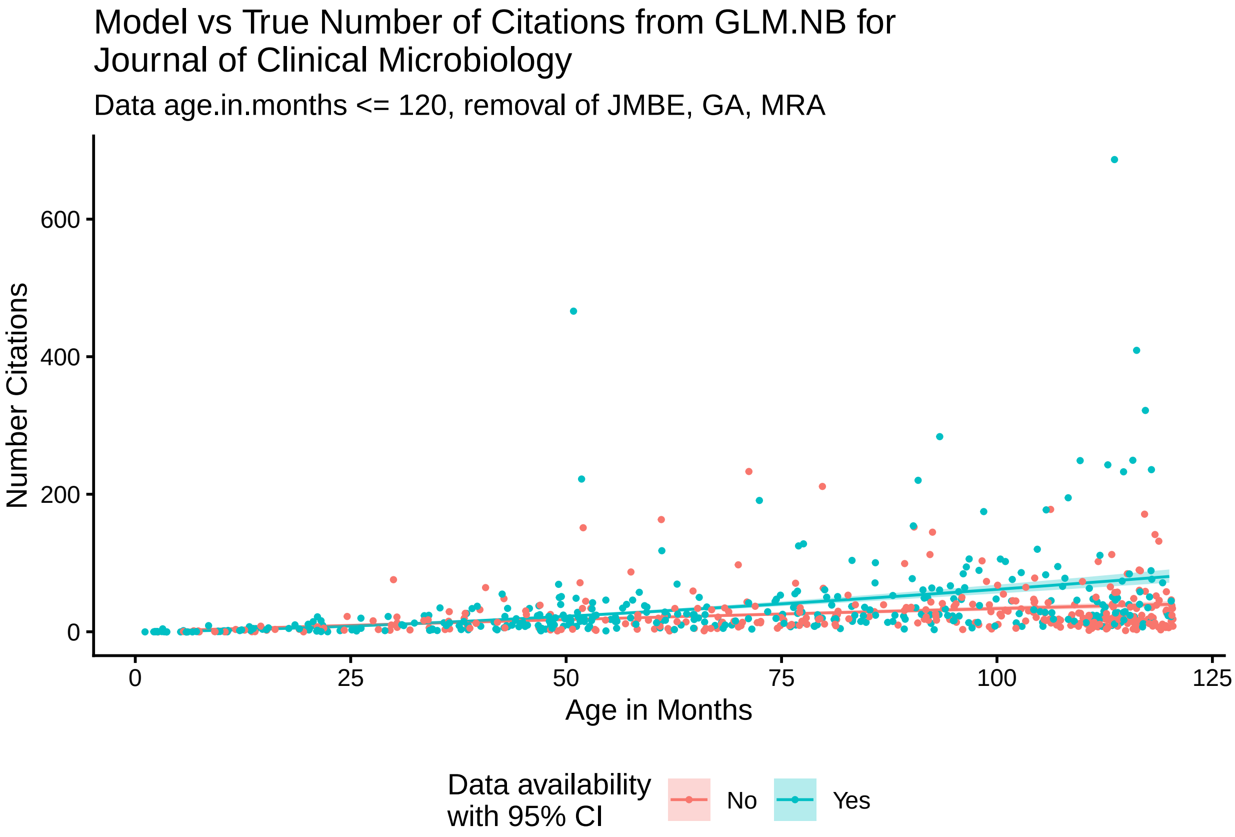
```
#lol i just add the data in each geom
journals <- ten_metadata %>%
  count(container.title) %>%
  mutate(container.title = as.character(container.title)) %>%
  dplyr::select(container.title)

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

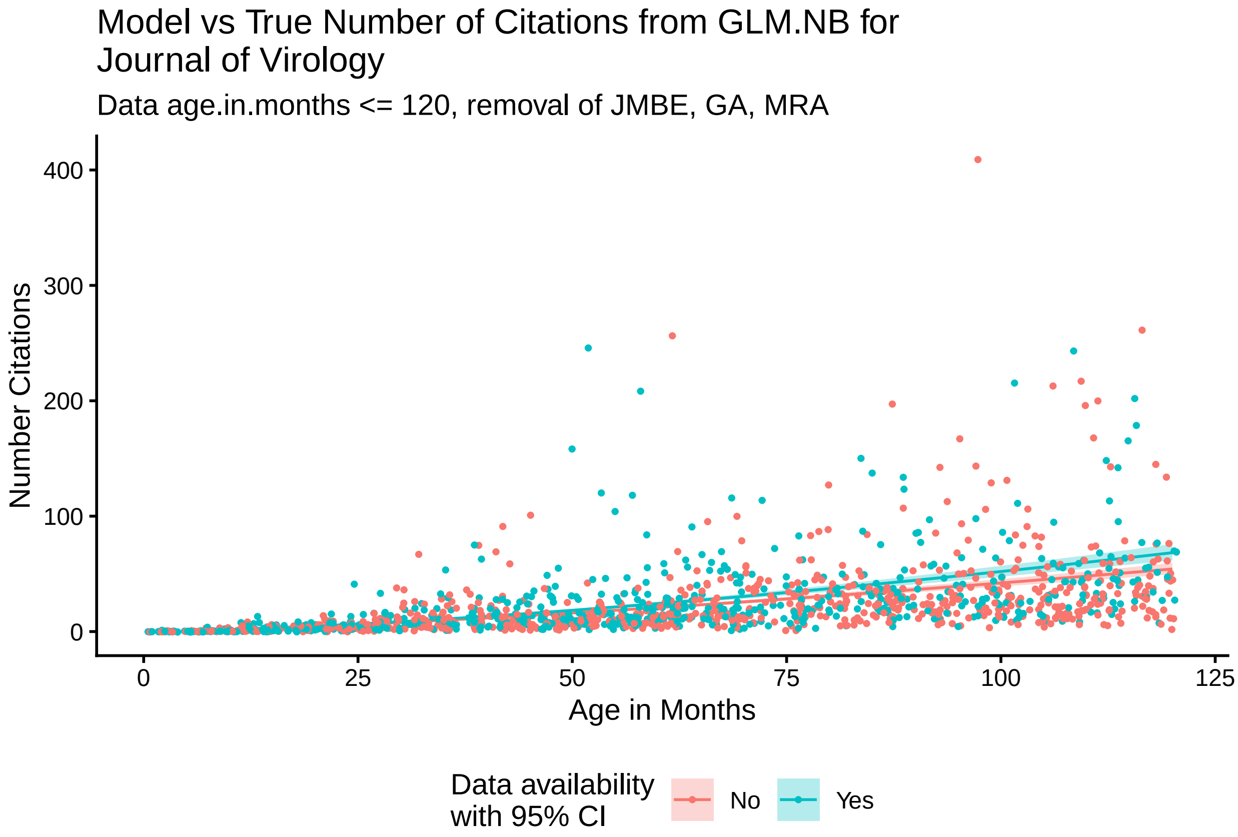

Model vs True Number of Citations from GLM.NB for
Infection and Immunity
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
200
150
100
50
0
0
25
50
75
100
125
Age in Months
Data availability
with 95% CI
No
Yes


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



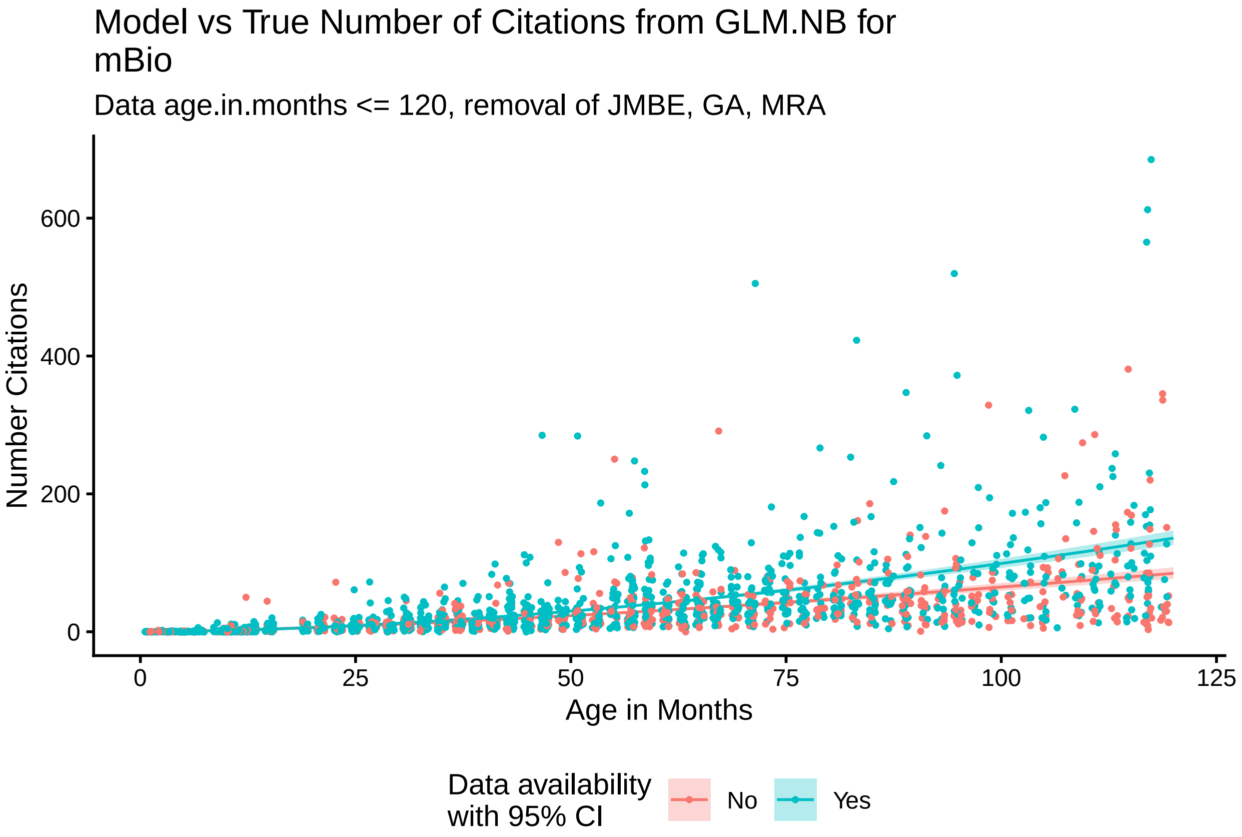
Model vs True Number of Citations from GLM.NB for
Journal of Clinical Microbiology

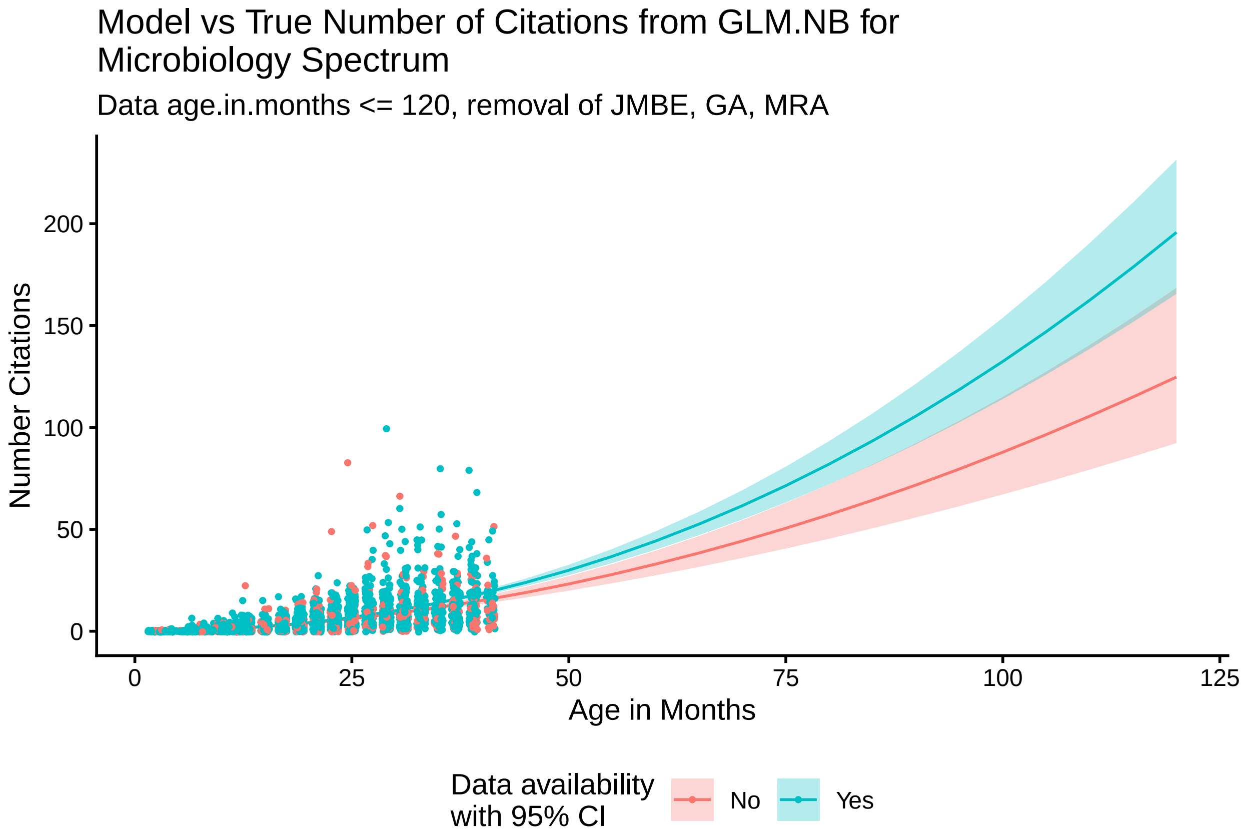
Data age.in.months <= 120, removal of JMBE, GA, MRA

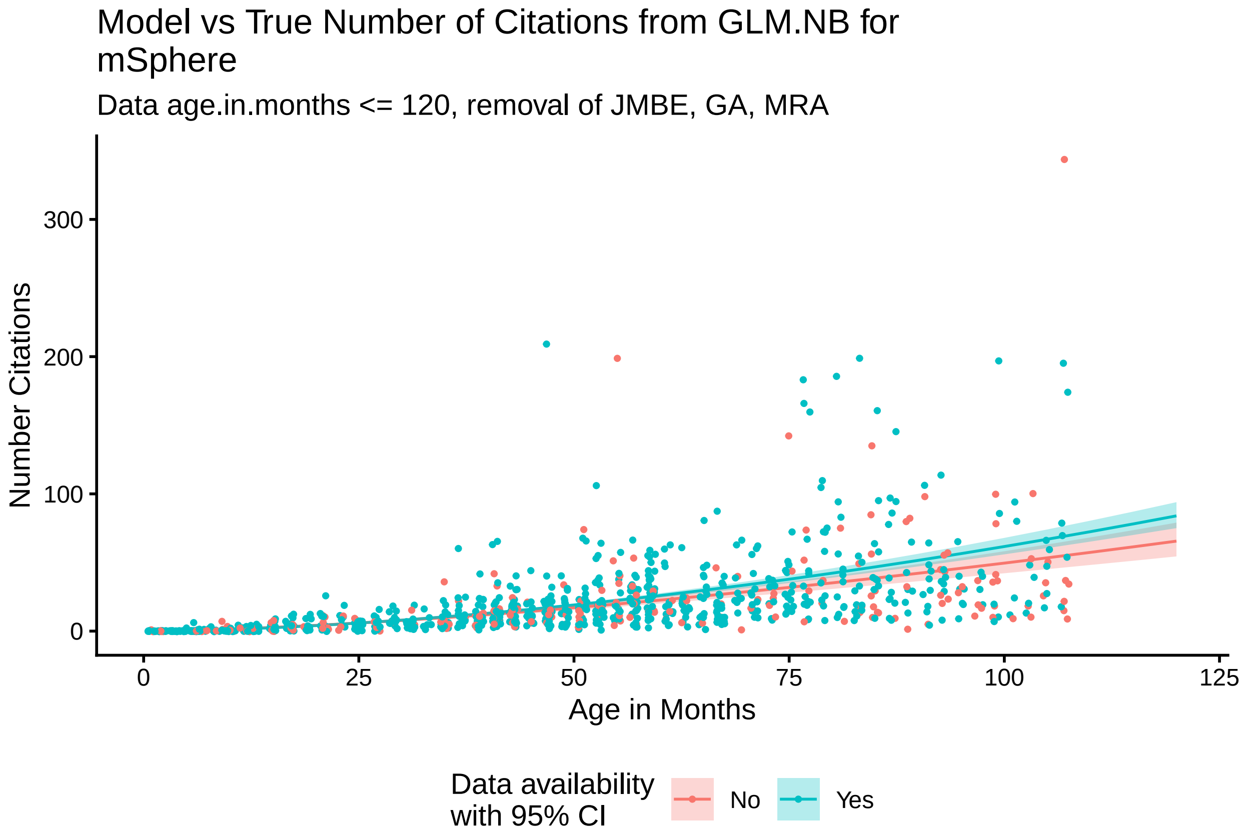


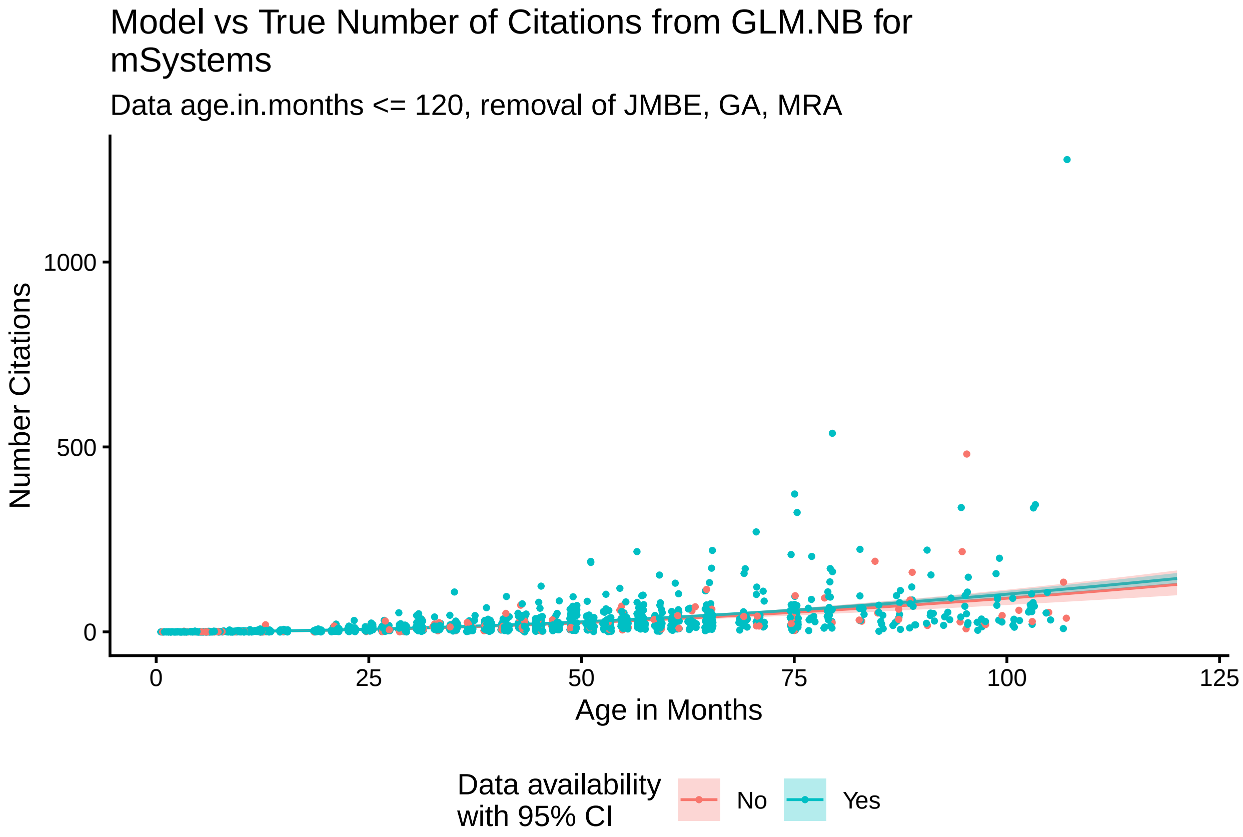
Model vs True Number of Citations from GLM.NB for Journal of Virology

Data age.in.months <= 120, removal of JMBE, GA, MRA


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

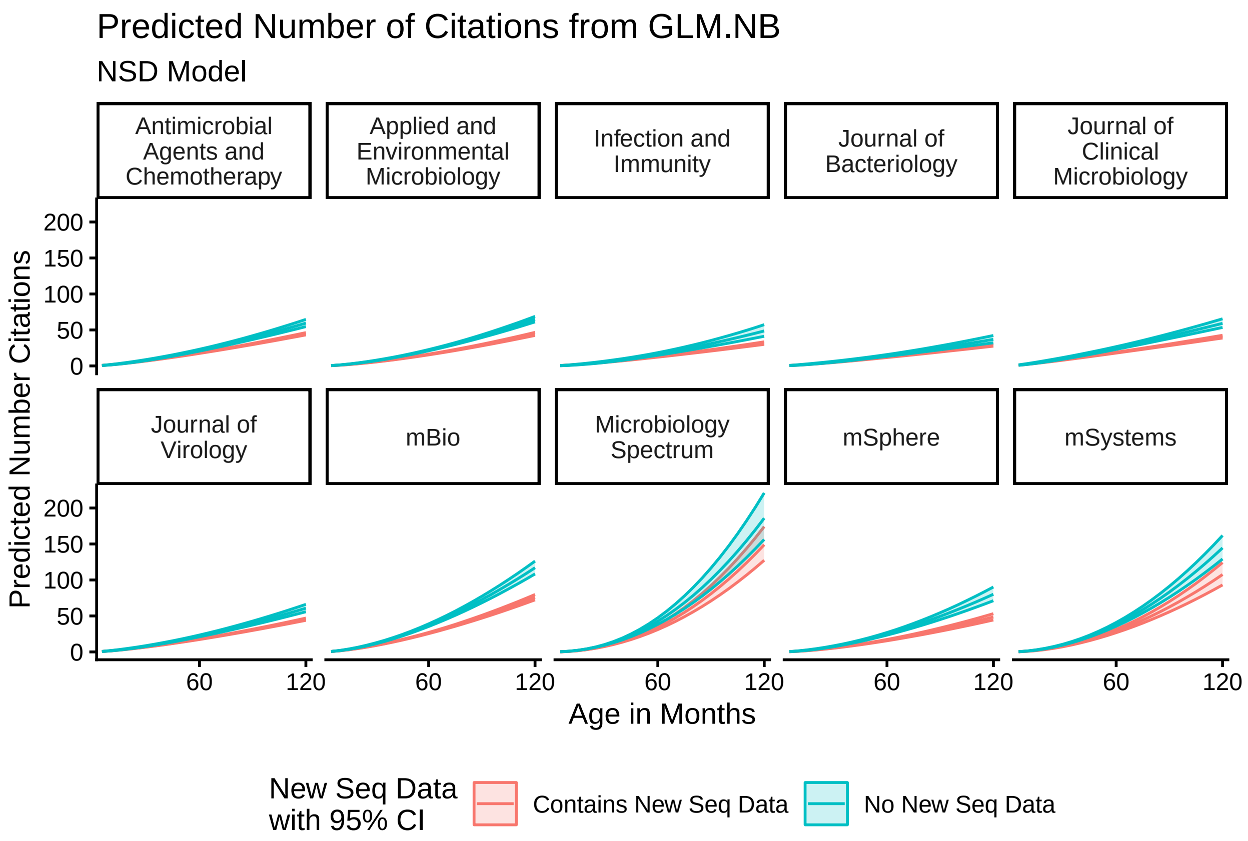

Model vs True Number of Citations from GLM.NB for
Microbiology Spectrum
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
200
150
100
50
0
0
25
50
75
100
125
Age in Months
Data availability
with 95% CI
No
Yes


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(.$x == 1, "Contains New Seq Data", "No New Seq Data"), predicted_citat
          age.in.months = .$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
```



## Grab top 6 papers in spectrum for Pat (manually)

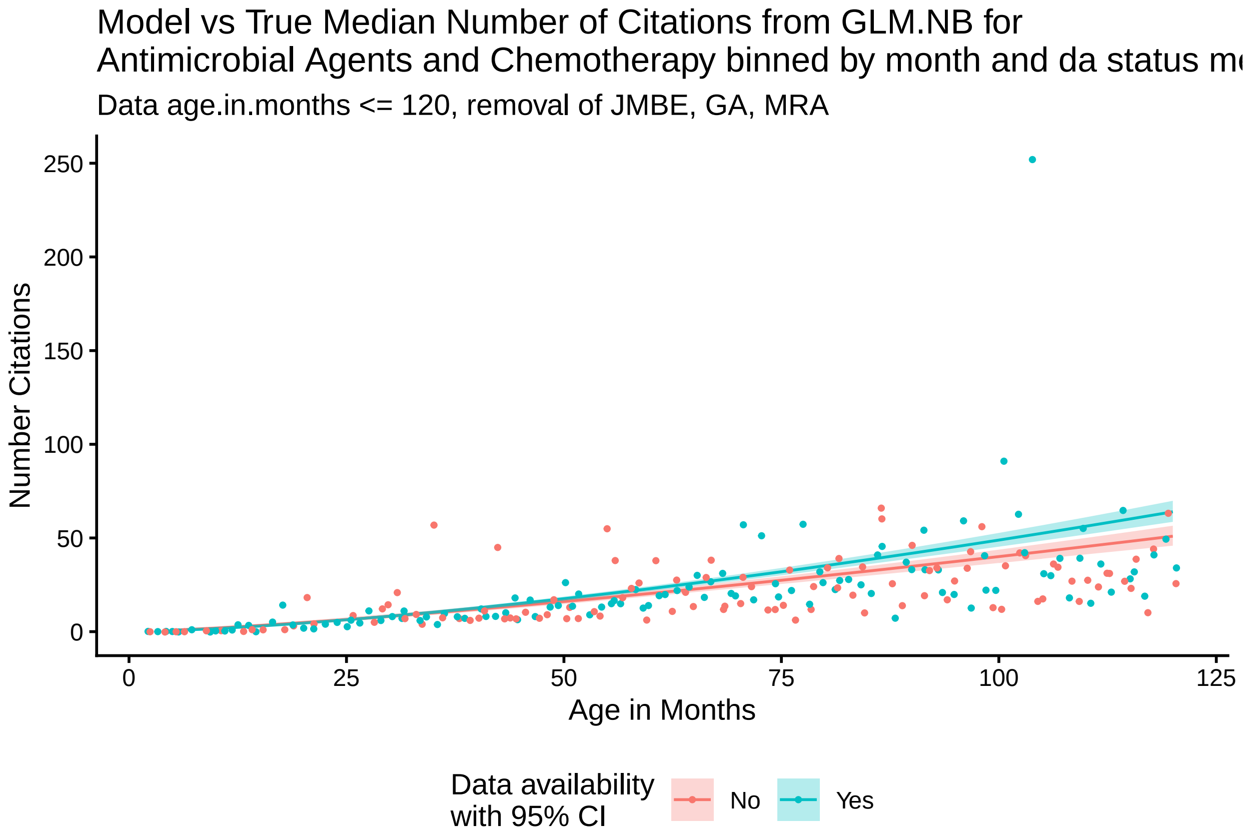
```
#get spectrum data

#i did this by hand - filtered and then viewed and sorted by citations

 # j_metadata <-
  ten_metadata %>%
      filter(container.title == "Microbiology Spectrum")
```

```
## # A tibble: 2,736 x 80
##    file                 da    nsd   paper.x doi   doi_no_underscore journal_abrev
##    <chr>                <chr> <chr> <chr>   <chr> <chr>             <chr>
##  1 Data/html/10.1128_~ No    Yes   https:~ 10.1~ 10.1128/spectrum~ spectrum
##  2 Data/html/10.1128_~ Yes   Yes   https:~ 10.1~ 10.1128/spectrum~ spectrum
##  3 Data/html/10.1128_~ Yes   Yes   https:~ 10.1~ 10.1128/spectrum~ spectrum
##  4 Data/html/10.1128_~ Yes   Yes   https:~ 10.1~ 10.1128/spectrum~ spectrum
##  5 Data/html/10.1128_~ Yes   Yes   https:~ 10.1~ 10.1128/spectrum~ spectrum
##  6 Data/html/10.1128_~ Yes   Yes   https:~ 10.1~ 10.1128/spectrum~ spectrum
##  7 Data/html/10.1128_~ Yes   Yes   https:~ 10.1~ 10.1128/spectrum~ spectrum
##  8 Data/html/10.1128_~ No    Yes   https:~ 10.1~ 10.1128/spectrum~ spectrum
##  9 Data/html/10.1128_~ Yes   Yes   https:~ 10.1~ 10.1128/spectrum~ spectrum
## 10 Data/html/10.1128_~ Yes   Yes   https:~ 10.1~ 10.1128/spectrum~ spectrum
## # i 2,726 more rows
## # i 73 more variables: container.title <fct>, predicted <chr>,
## #   alternative.id <chr>, created <date>, deposited <date>,
## #   published.print <chr>, indexed <date>, issn <chr>, issue <dbl>,
## #   issued <chr>, member <dbl>, page <chr>, prefix <dbl>, publisher <chr>,
## #   score <dbl>, source <chr>, reference.count <dbl>, references.count <dbl>,
## #   is.referenced.by.count <dbl>, title <chr>, type <chr>, ...
```

```
# %>%
#   view()
```

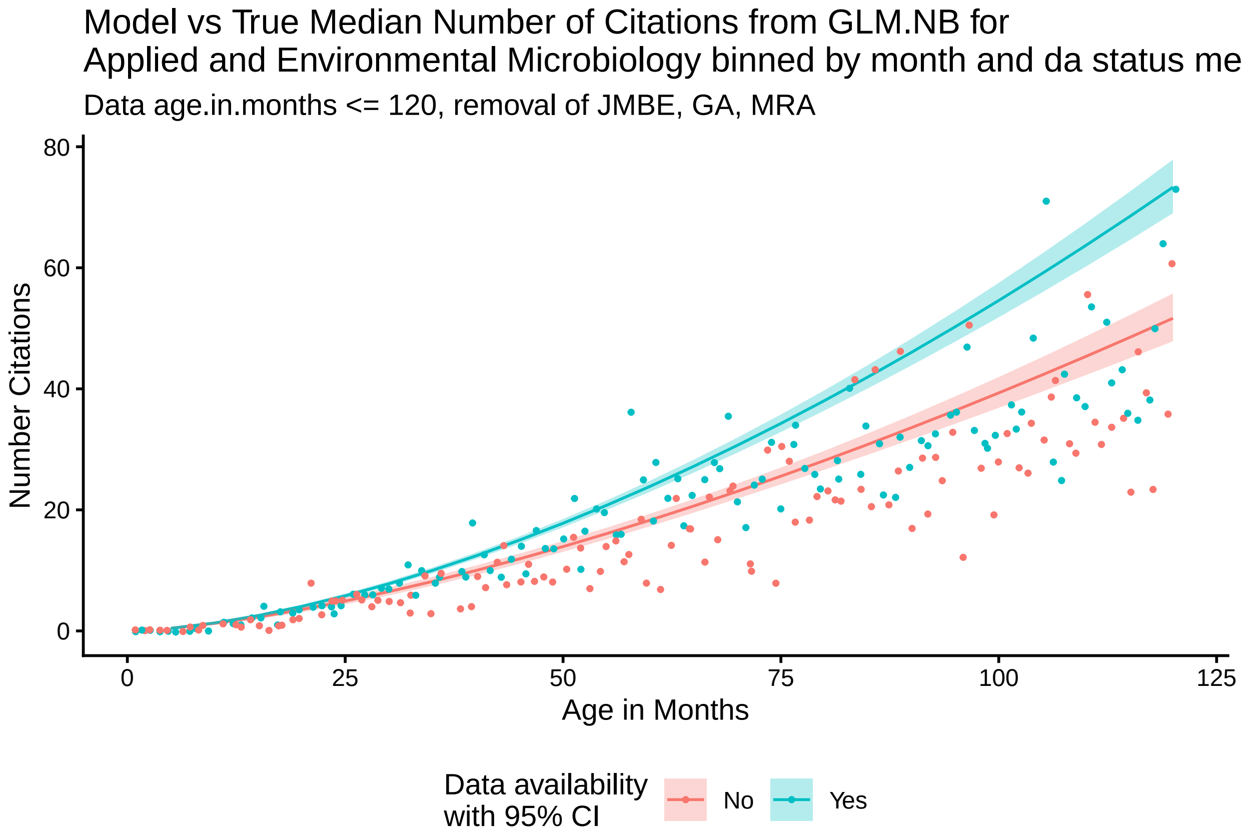
Trying binned data by month to evaluate model fit

```
#let's try this for one month and then for the rest of them

# j<- 6

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

  j_monthly <-
    j_metadata %>%
      summarize(monthly_median = median(is.referenced.by.count),
             .by = c("da_factor", "age.in.months"))


  #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() +
   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_monthly, aes(x = age.in.months,
                                      y = monthly_median, color = da_factor),
                                      position = position_jitter(width =0.5), size = 0.6) +
   labs(title = paste0("Model vs True Median Number of Citations from GLM.NB for\n", journals$container
        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)
}
```



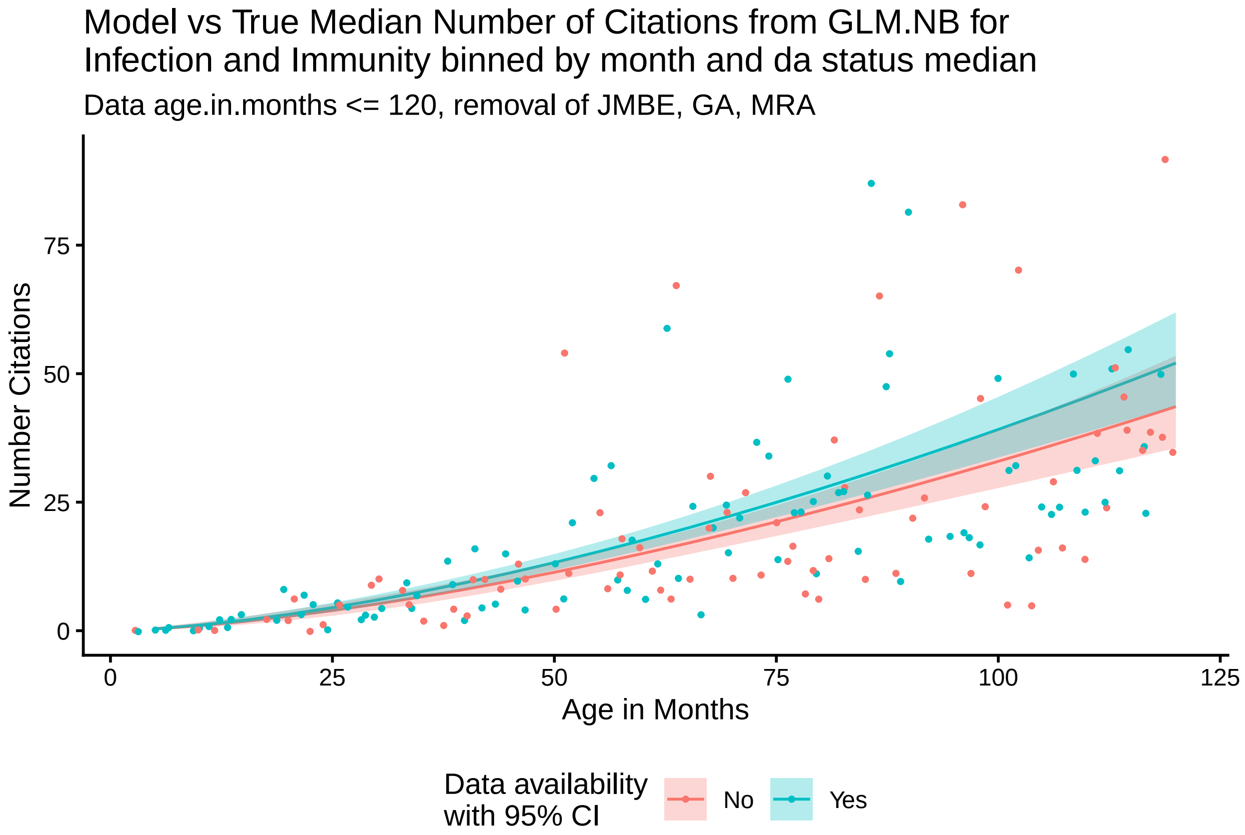
Model vs True Median Number of Citations from GLM.NB for
Antimicrobial Agents and Chemotherapy binned by month and da status m

Data age.in.months <= 120, removal of JMBE, GA, MRA



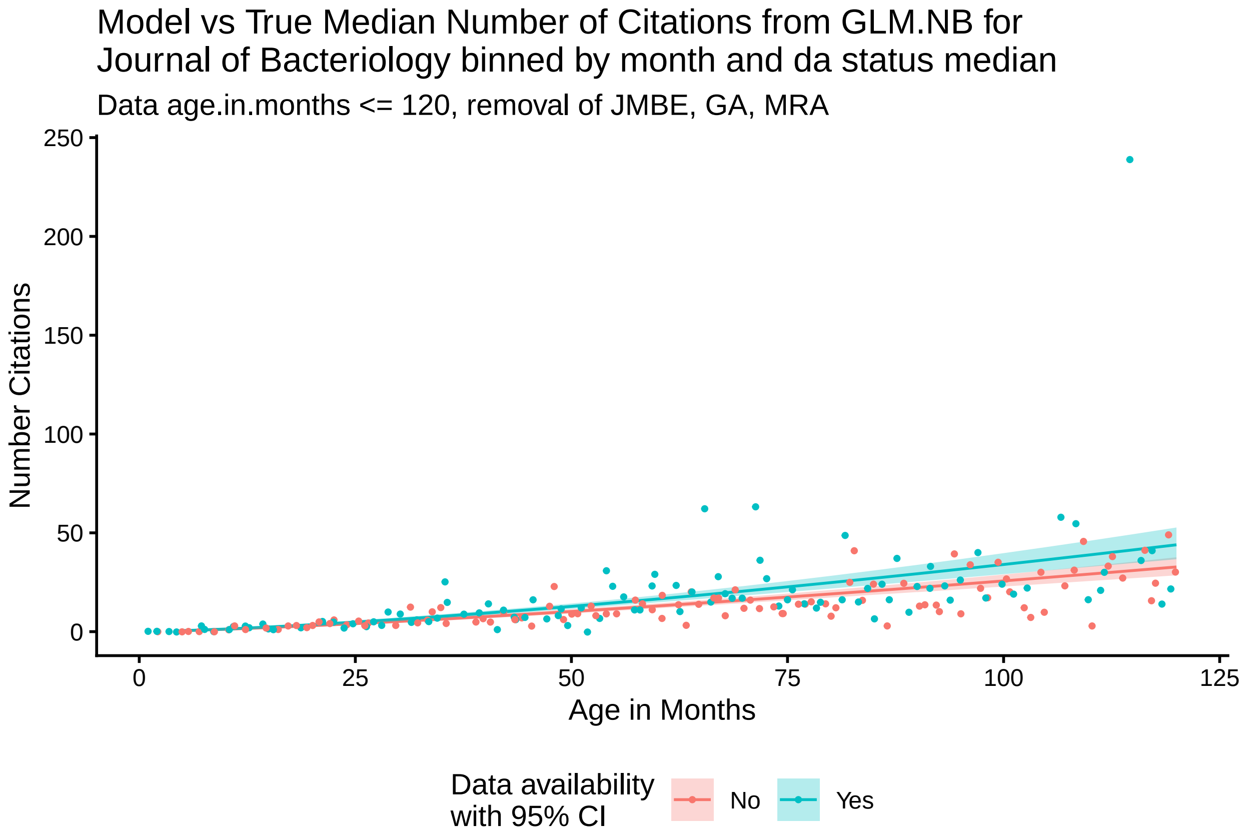
Model vs True Median Number of Citations from GLM.NB for
Applied and Environmental Microbiology binned by month and da status me

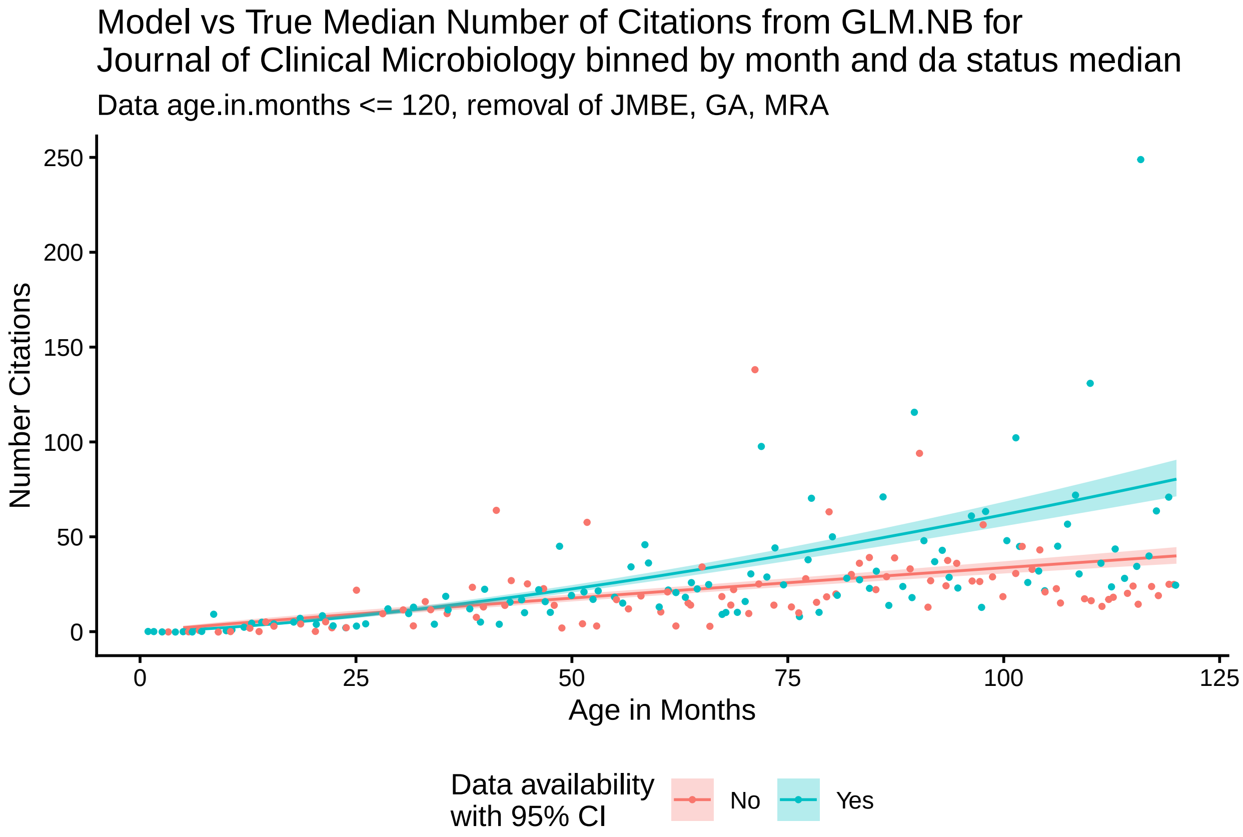
Data age.in.months <= 120, removal of JMBE, GA, MRA



Model vs True Median Number of Citations from GLM.NB for Infection and Immunity binned by month and da status median

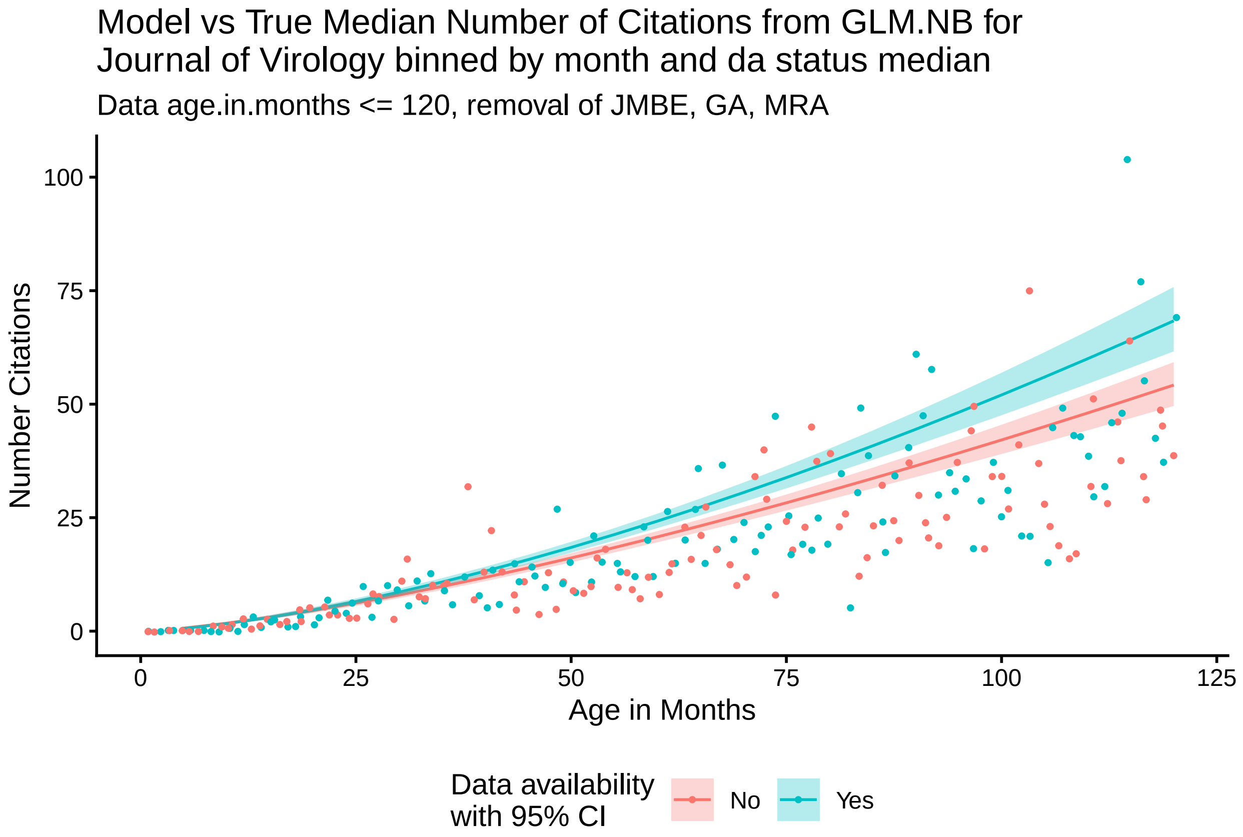
Data age.in.months <= 120, removal of JMBE, GA, MRA

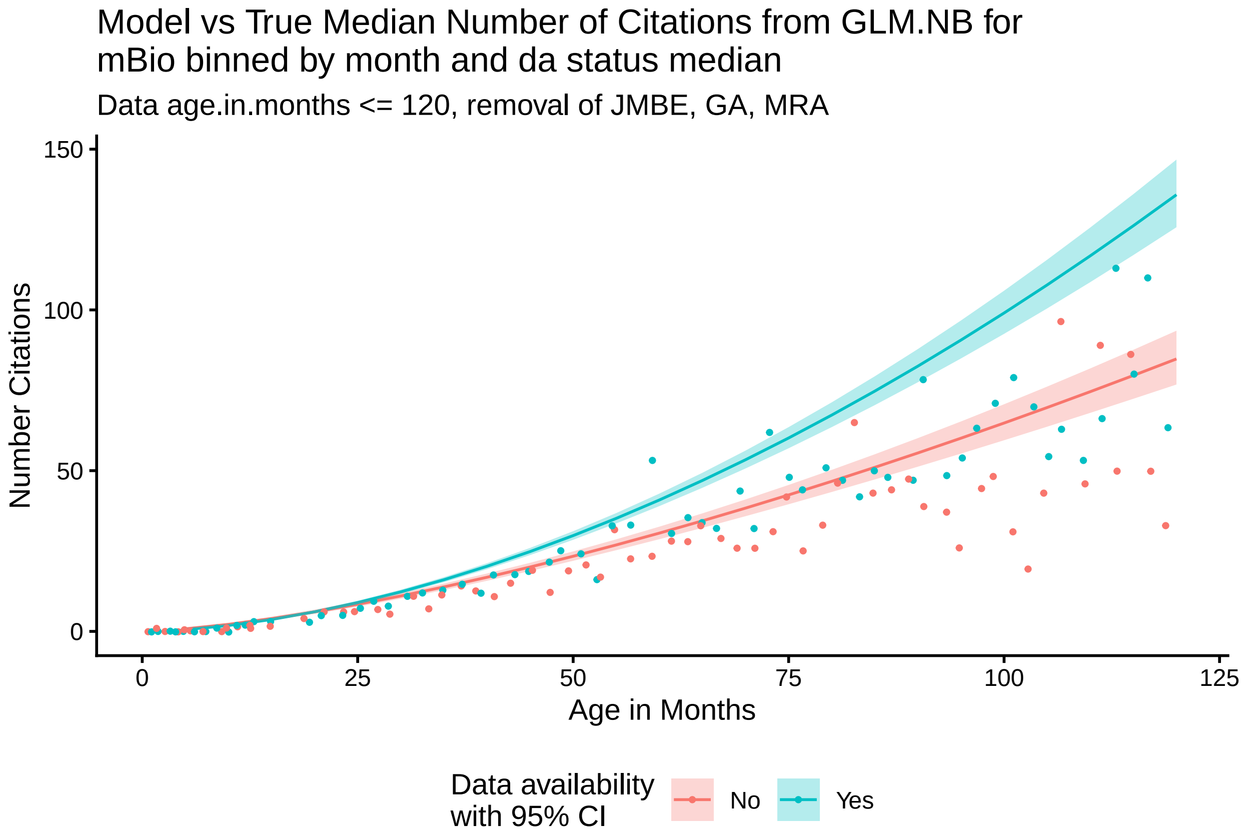

Model vs True Median Number of Citations from GLM.NB for
Journal of Bacteriology binned by month and da status median
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
250
200
150
100
50
0
0
25
50
75
100
125
Age in Months
Data availability
with 95% CI
No
Yes

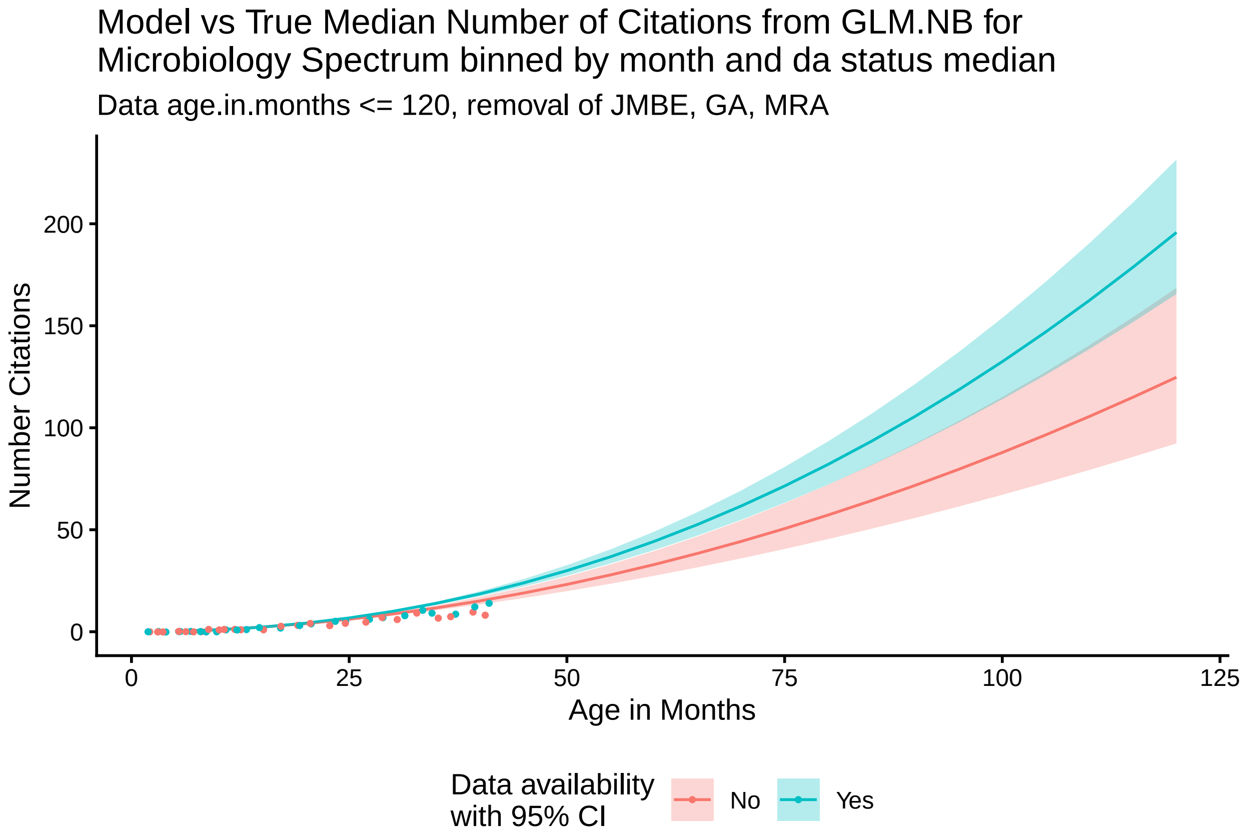


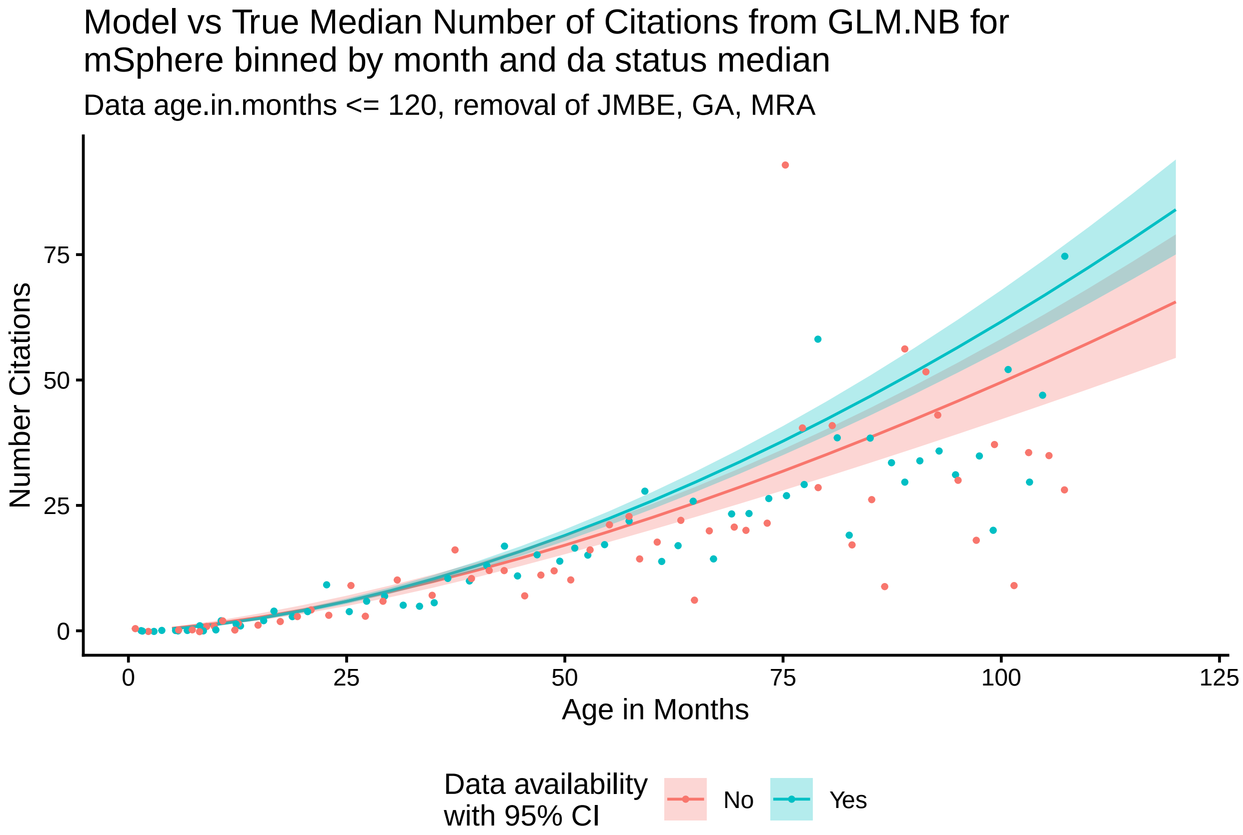
Model vs True Median Number of Citations from GLM.NB for
Journal of Clinical Microbiology binned by month and da status median

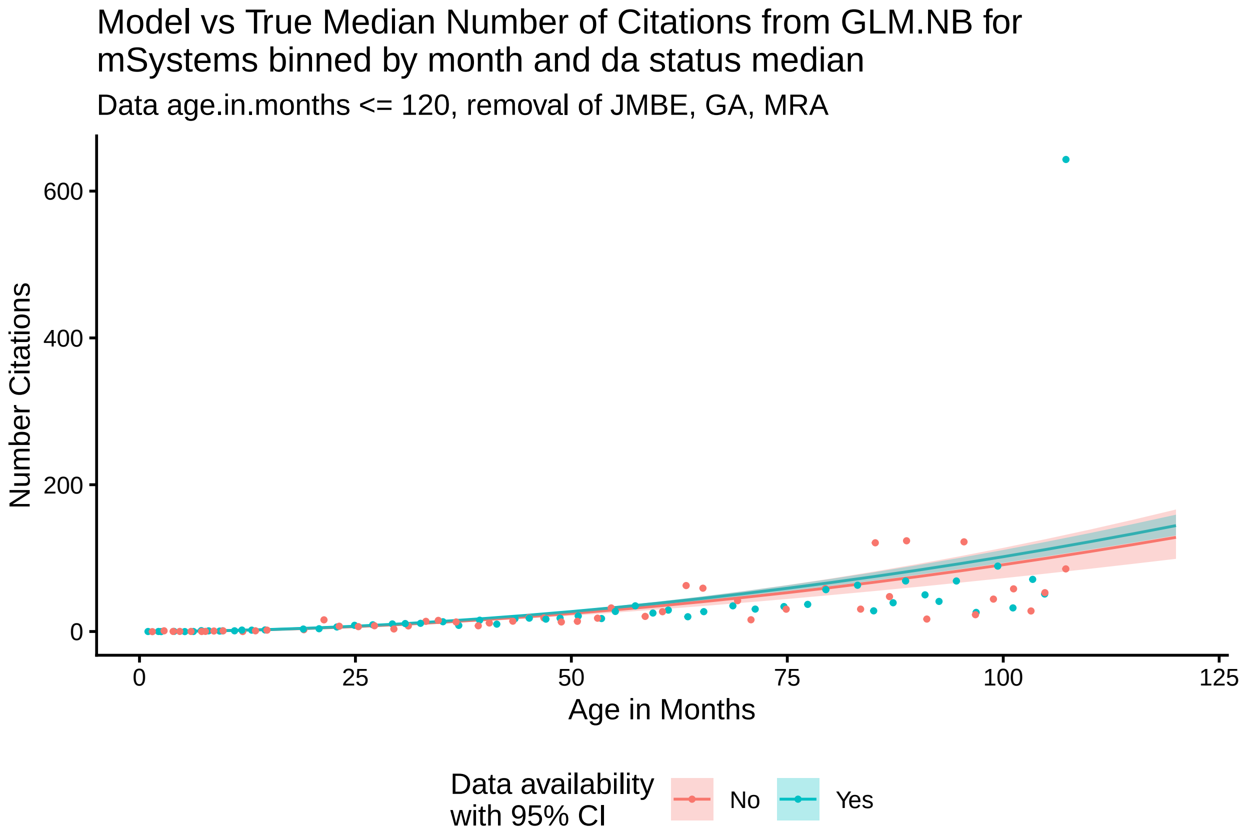
Data age.in.months <= 120, removal of JMBE, GA, MRA


Model vs True Median Number of Citations from GLM.NB for
Journal of Virology binned by month and da status median
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
0
25
50
75
100
Age in Months
0
25
50
75
100
125
Data availability
with 95% CI
No
Yes


Model vs True Median Number of Citations from GLM.NB for
mBio binned by month and da status median
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
150
100
50
0
0
25
50
75
100
125
Age in Months
Data availability
with 95% CI
No
Yes


Model vs True Median Number of Citations from GLM.NB for
Microbiology Spectrum binned by month and da status median
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 Median Number of Citations from GLM.NB for
mSphere binned by month and da status median
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
0
25
50
75
0
25
50
75
100
125
Age in Months
Data availability
with 95% CI
No
Yes

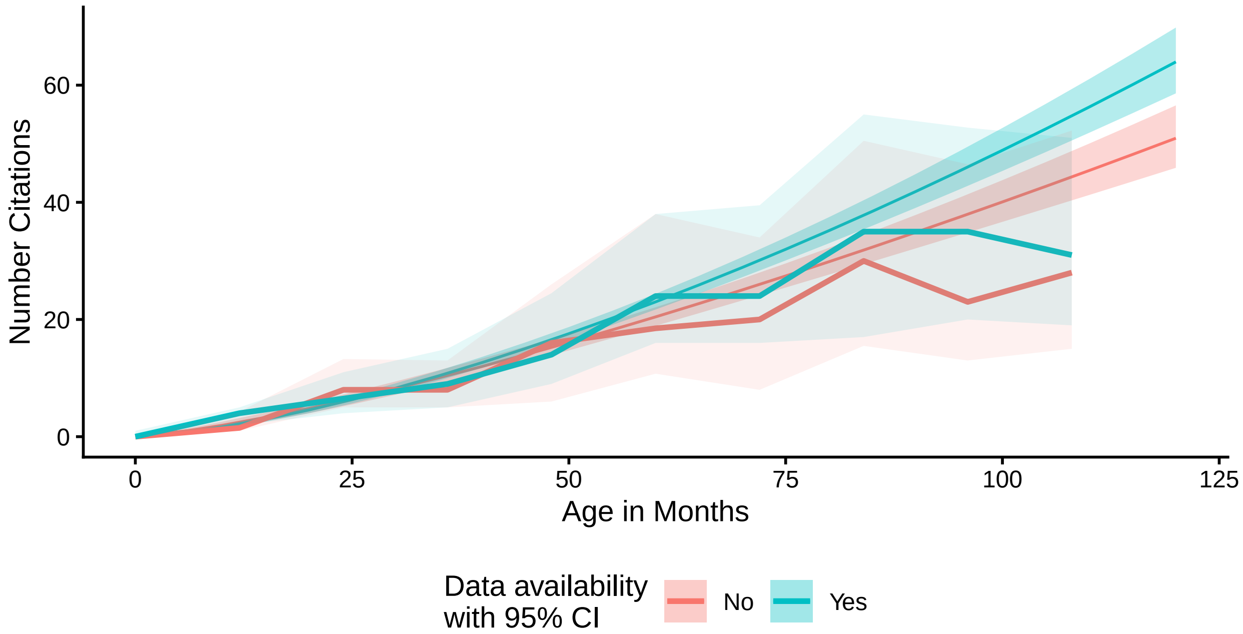


## Bin the data by the month and whether the data are available. Then calculate the median and the 25th and 75th quantile. Plot the median as a line plot and the 25th and 75th percentiles as the boundary as a ribbon. Might do it by the year if the viz looks too clunky because there aren't enough points to get a smooth curve.

```
#let's try this for one month and then for the rest of them

j<- 6

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

  j_yearly <-
    j_metadata %>%
      summarize(yearly_median = median(is.referenced.by.count),
                yearly_25 = quantile(is.referenced.by.count, probs = 0.25),
                yearly_75 = quantile(is.referenced.by.count, probs = 0.75),
                age.in.months = (2024-year.published)*12,
             .by = c("da_factor", "year.published"))


  #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() +
   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_line(data = j_yearly, aes(x = age.in.months,
                                   y = yearly_median,
                                   color = da_factor,
                                   ), size = 1.0) +
    geom_ribbon(data = j_yearly, mapping = aes(x = age.in.months, y = yearly_median,
                                               ymin = yearly_25, ymax = yearly_75,
                             group = da_factor, fill = da_factor), alpha = 0.1) +

   labs(title = paste0("Model vs True Median Number of Citations from GLM.NB for\n", journals$container
        subtitle = "Data age.in.months <= 120, removal of JMBE, GA, MRA\nLighter values = median and qua
        x = "Age in Months",
        y = "Number Citations",
        color = "Data availability\nwith 95% CI",
        fill = "Data availability\nwith 95% CI") +
    theme_classic() +
    theme(legend.position = "bottom")

print(plot)
}
```

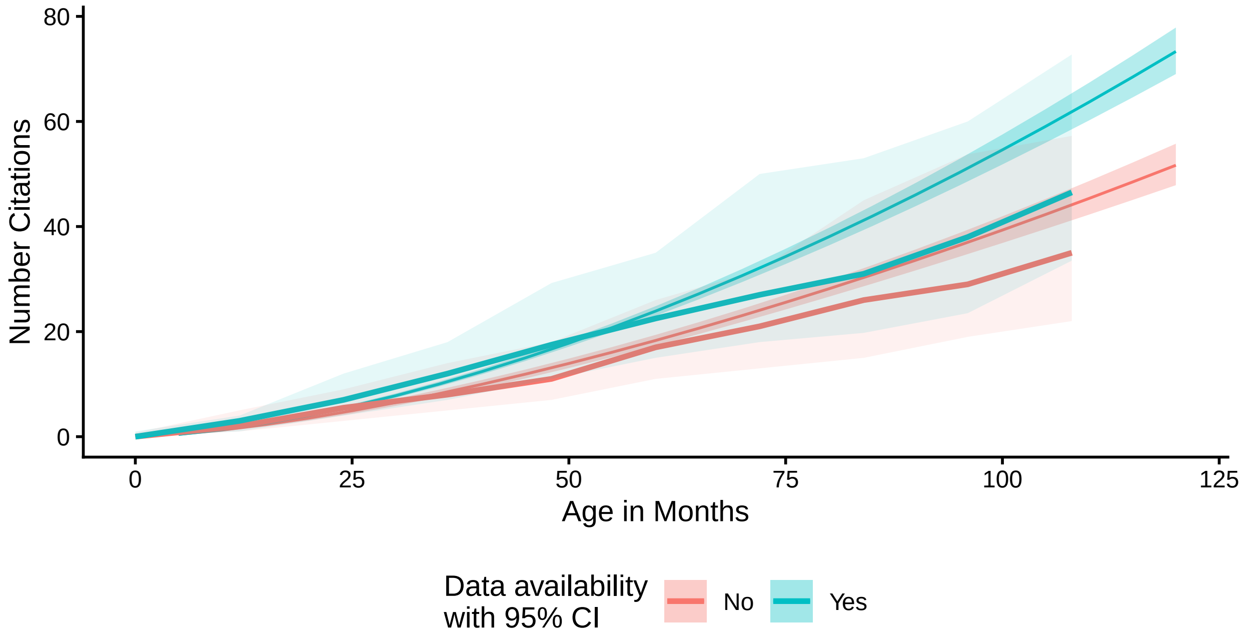
Model vs True Median Number of Citations from GLM.NB for Antimicrobial Agents and Chemotherapy binned by year, da status median, 25% & 75%

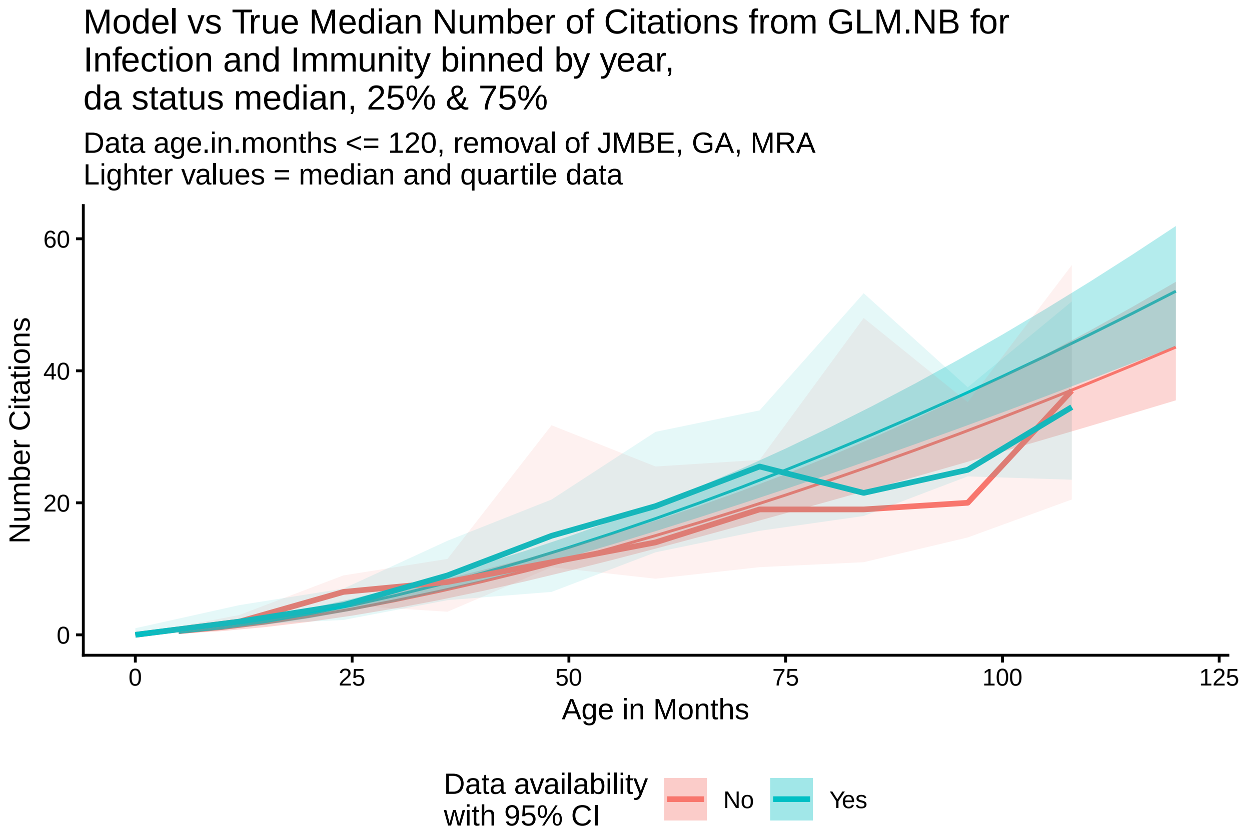
Data age.in.months <= 120, removal of JMBE, GA, MRA
Lighter values = median and quartile data



Model vs True Median Number of Citations from GLM.NB for
Applied and Environmental Microbiology binned by year,
da status median, 25% & 75%

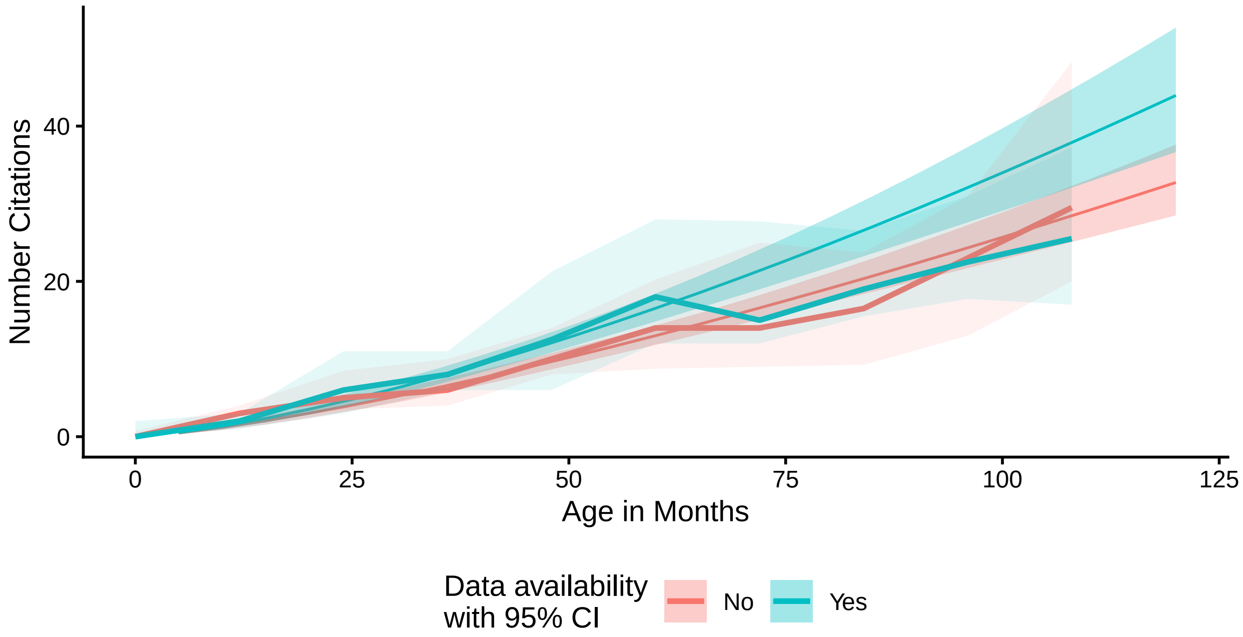
Data age.in.months <= 120, removal of JMBE, GA, MRA
Lighter values = median and quartile data

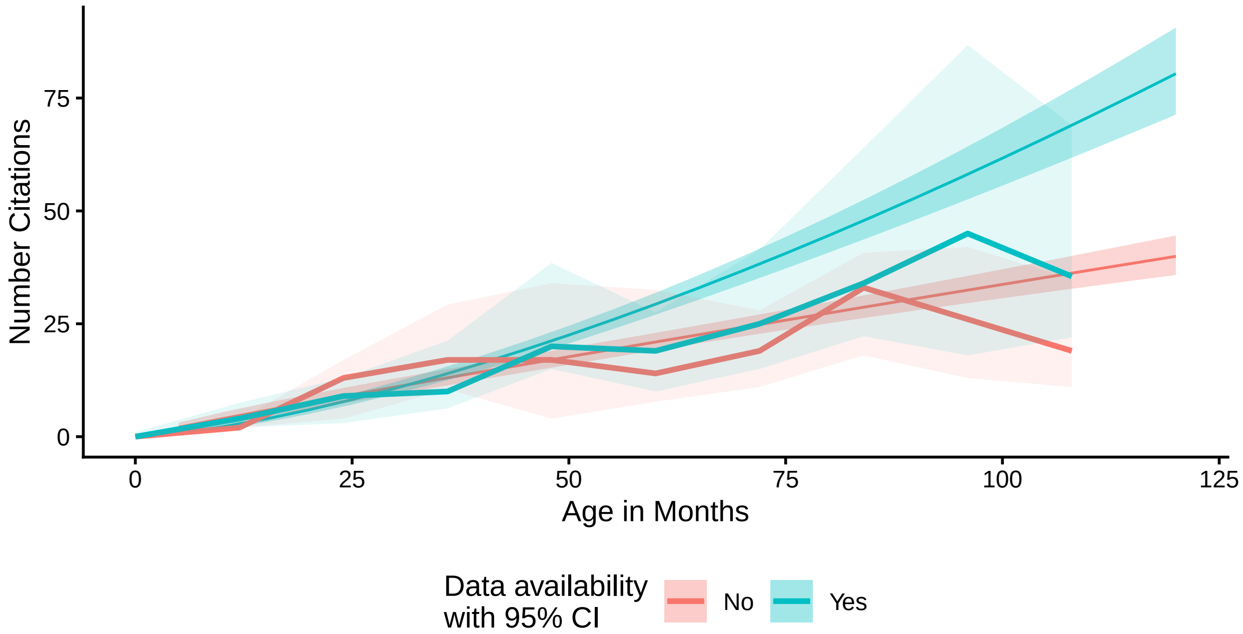



Model vs True Median Number of Citations from GLM.NB for
Infection and Immunity binned by year,
da status median, 25% & 75%
Data age.in.months <= 120, removal of JMBE, GA, MRA
Lighter values = median and quartile data
Number Citations
0
20
40
60
0
25
50
75
100
125
Age in Months
Data availability
with 95% CI
No
Yes

Model vs True Median Number of Citations from GLM.NB for
Journal of Bacteriology binned by year,
da status median, 25% & 75%

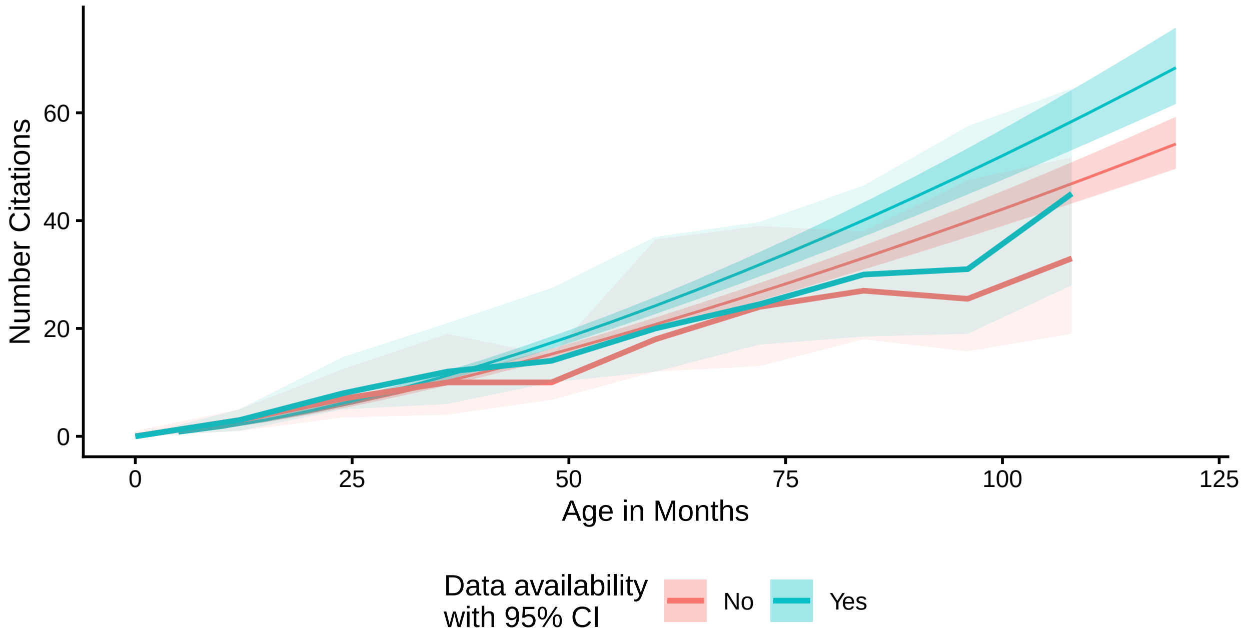
Data age.in.months <= 120, removal of JMBE, GA, MRA
Lighter values = median and quartile data





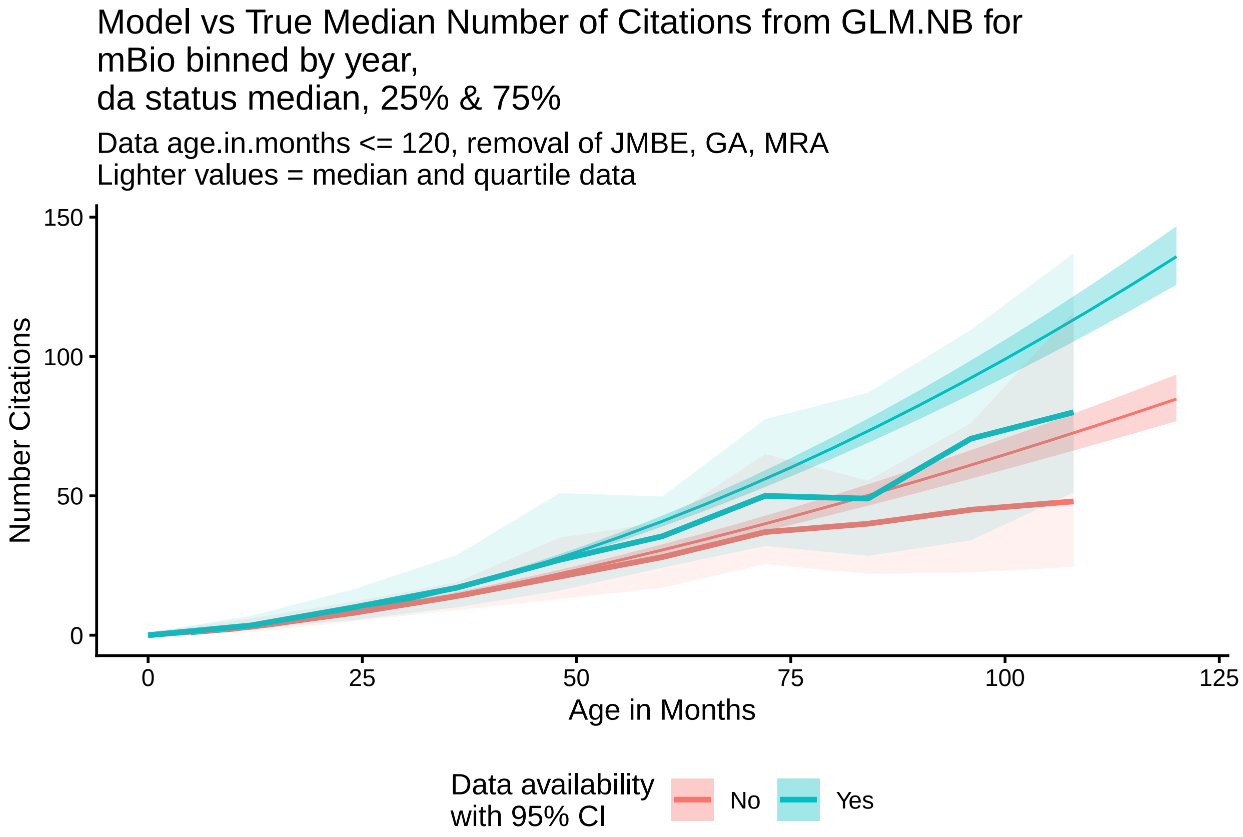
Model vs True Median Number of Citations from GLM.NB for
Journal of Clinical Microbiology binned by year,
da status median, 25% & 75%

Data age.in.months <= 120, removal of JMBE, GA, MRA
Lighter values = median and quartile data



Model vs True Median Number of Citations from GLM.NB for
Journal of Virology binned by year,
da status median, 25% & 75%

Data age.in.months <= 120, removal of JMBE, GA, MRA
Lighter values = median and quartile data

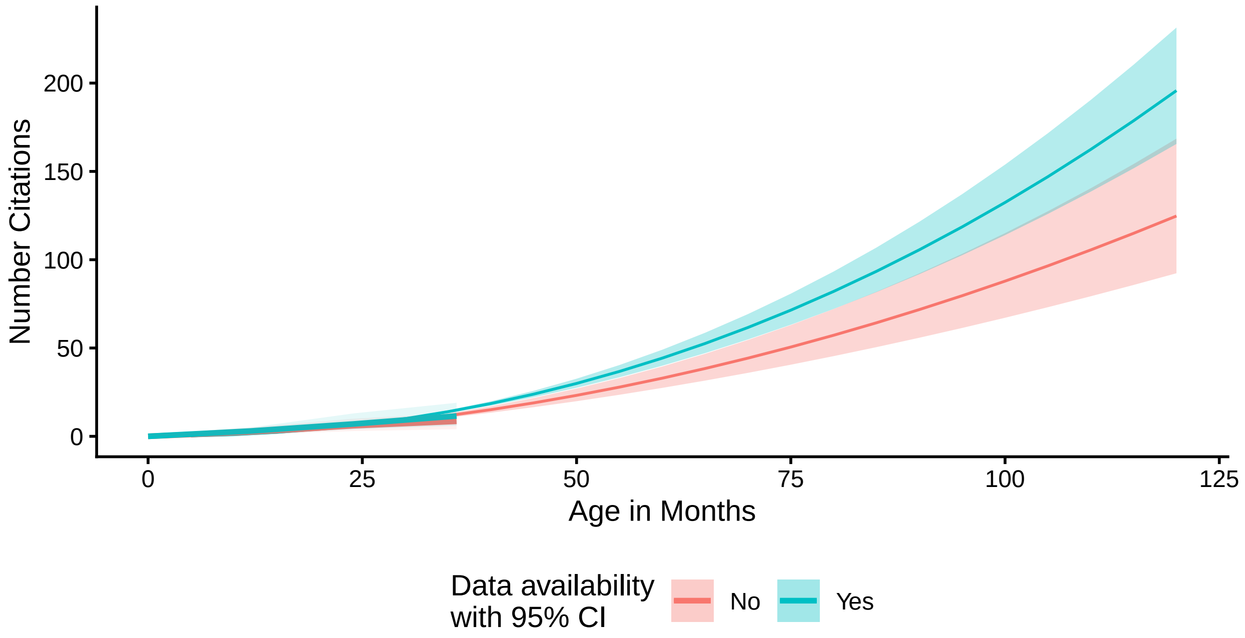


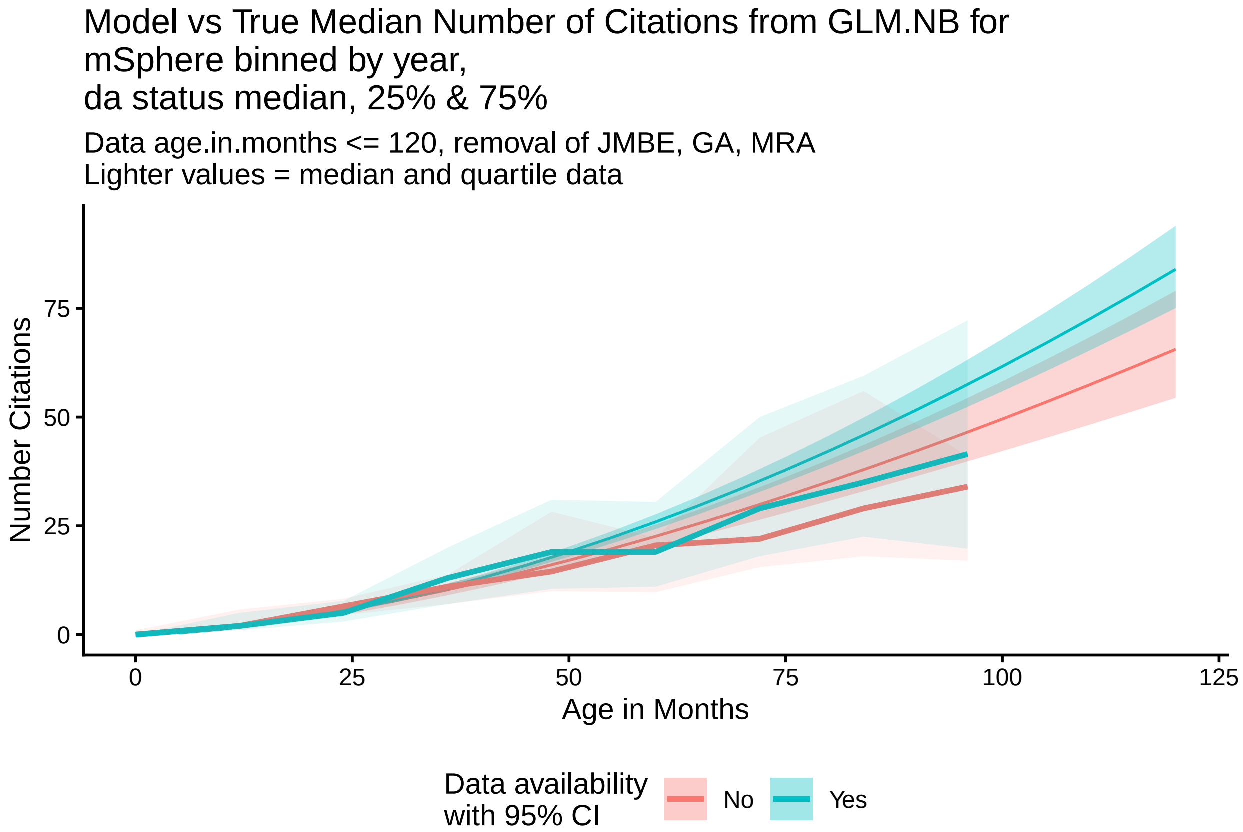
Model vs True Median Number of Citations from GLM.NB for
mBio binned by year,
da status median, 25% & 75%

Data age.in.months <= 120, removal of JMBE, GA, MRA
Lighter values = median and quartile data

Model vs True Median Number of Citations from GLM.NB for Microbiology Spectrum binned by year,
da status median, 25% & 75%

Data age.in.months <= 120, removal of JMBE, GA, MRA
Lighter values = median and quartile data



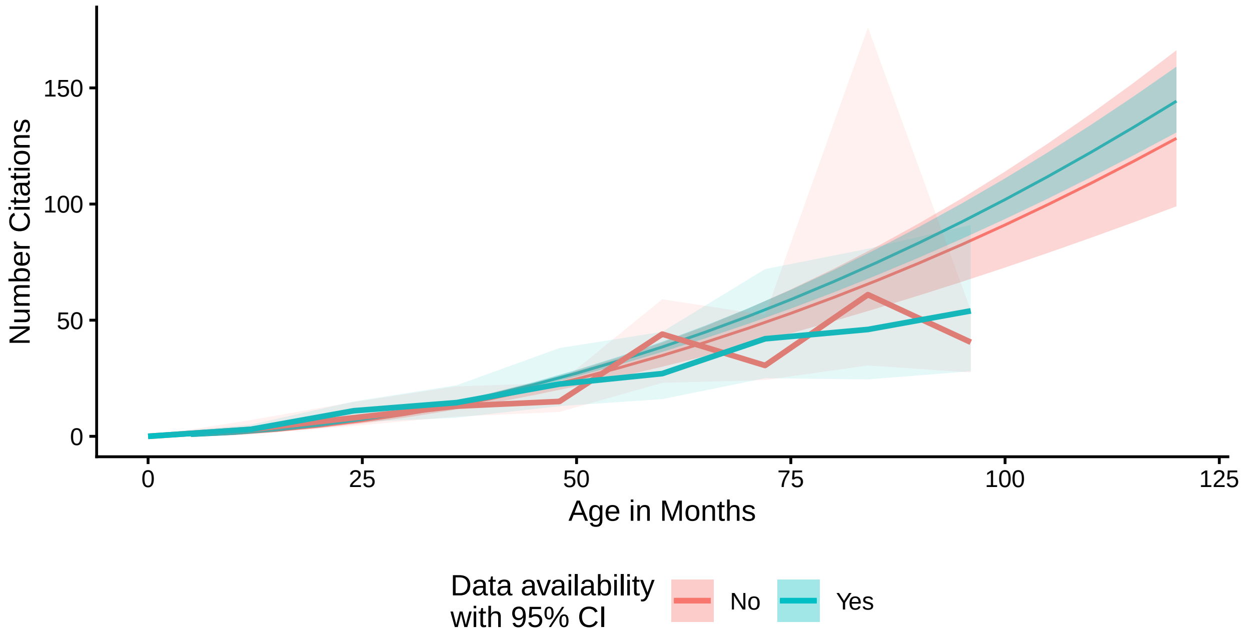


Model vs True Median Number of Citations from GLM.NB for mSphere binned by year,
da status median, 25% & 75%

Data age.in.months <= 120, removal of JMBE, GA, MRA
Lighter values = median and quartile data

Model vs True Median Number of Citations from GLM.NB for mSystems binned by year,
da status median, 25% & 75%

Data age.in.months <= 120, removal of JMBE, GA, MRA
Lighter values = median and quartile data


Number Citations
Age in Months
Data availability
with 95% CI
No
Yes