20251021_predicted_nb_updated

2025-10-21

```r
#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?

```r
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)
```

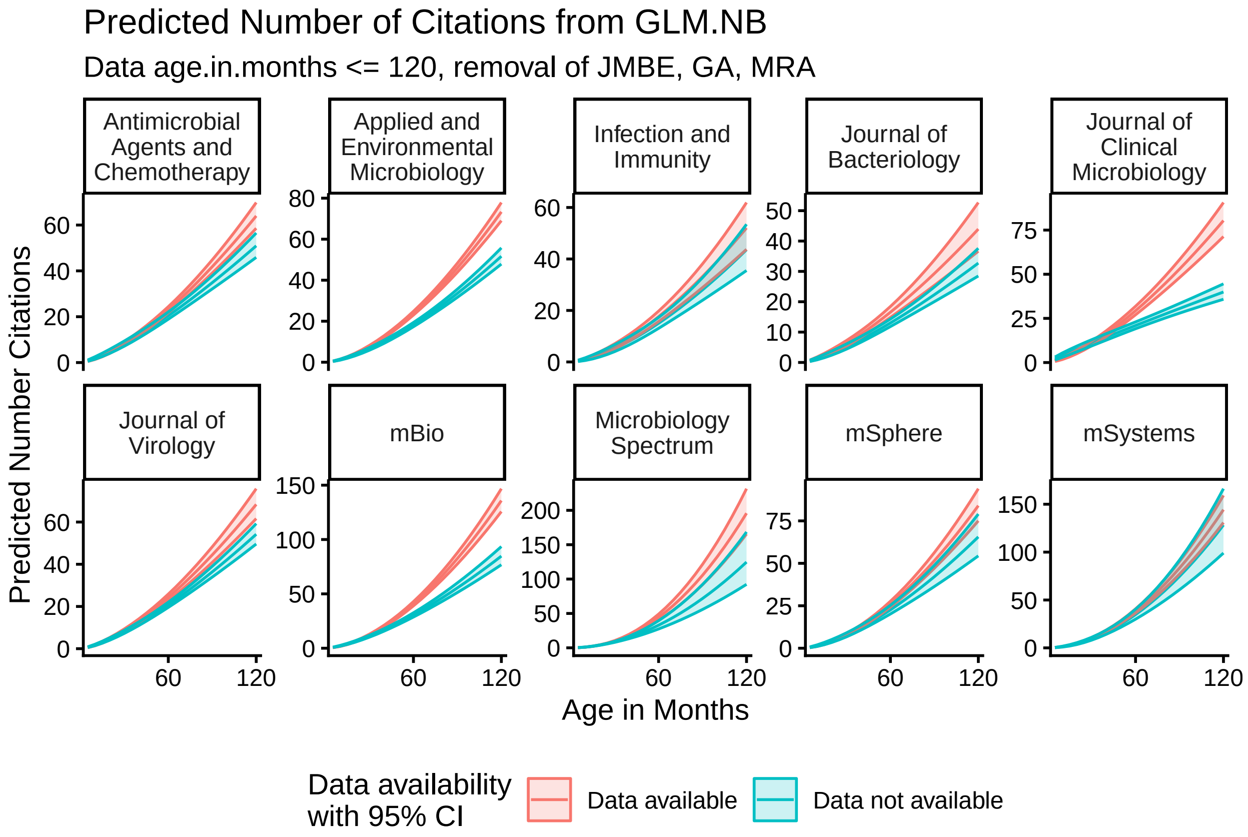
```
## # A tibble: 10 x 2
##    journal_abrev     n
##    <chr>         <int>
##  1 aac            1197
##  2 aem            2695
##  3 iai             342
##  4 jb              536
##  5 jcm             699
##  6 jvi            1353
##  7 mbio           1982
##  8 msphere         971
##  9 msystems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

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

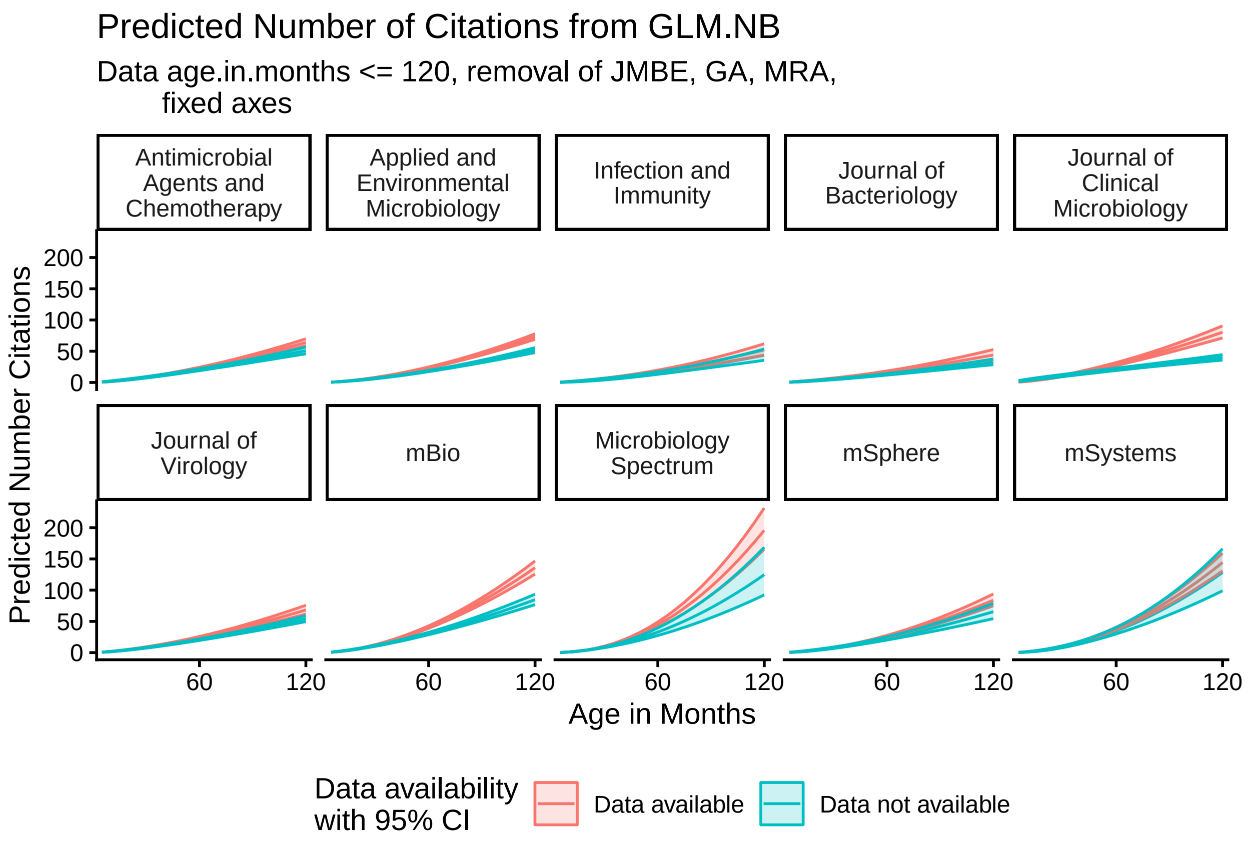
```
## # A tibble: 6 x 2
##   age.in.months     n
##           <dbl> <int>
## 1           115    77
## 2           116    68
## 3           117   110
## 4           118    74
## 5           119    83
## 6           120    68
```

```
#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",
```

```r
                    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
```

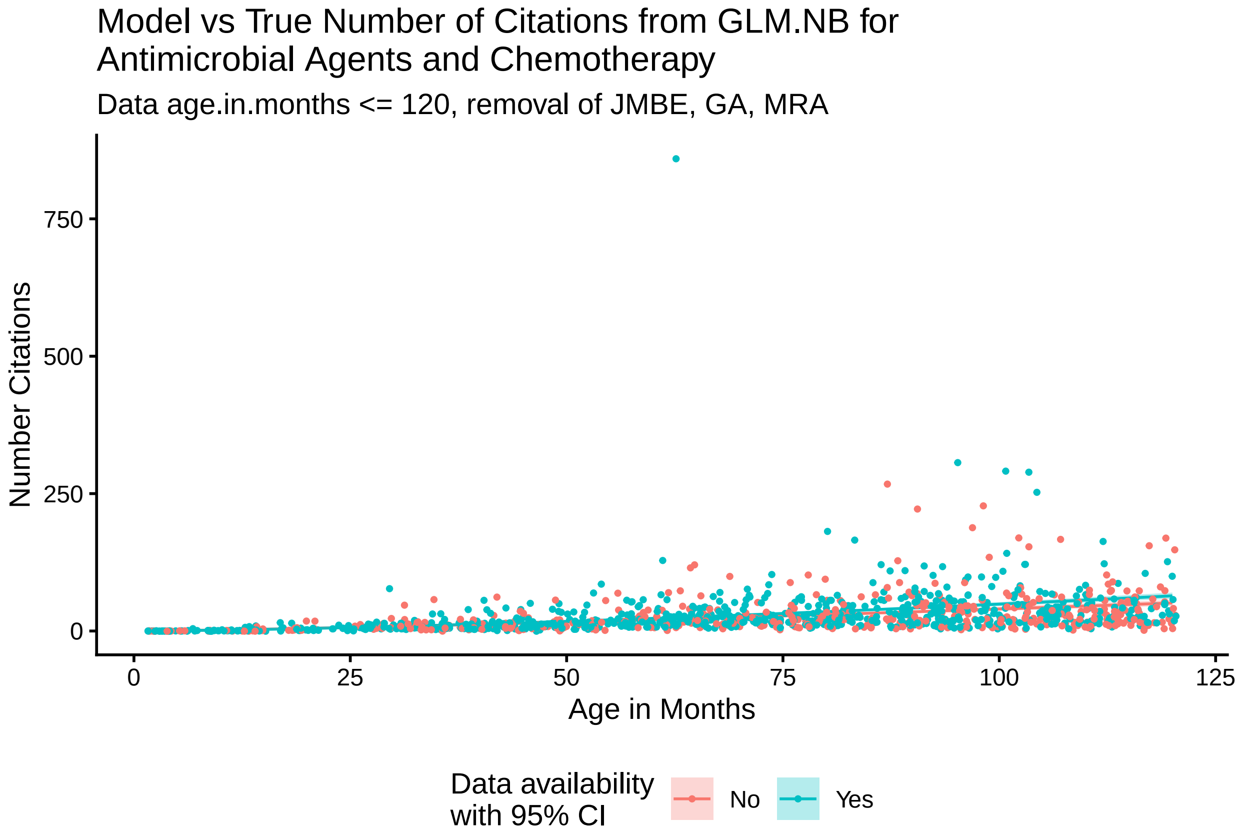


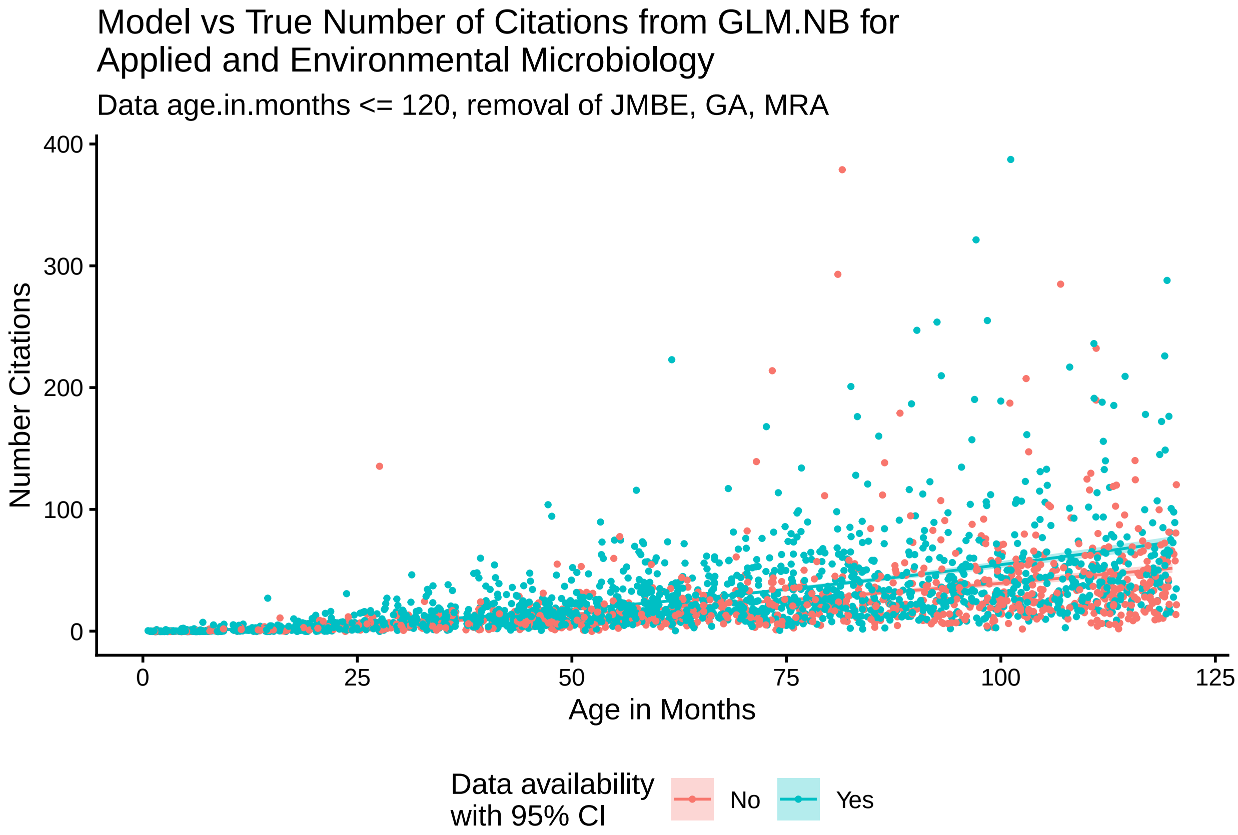
```
predicted_plot_fixed
```



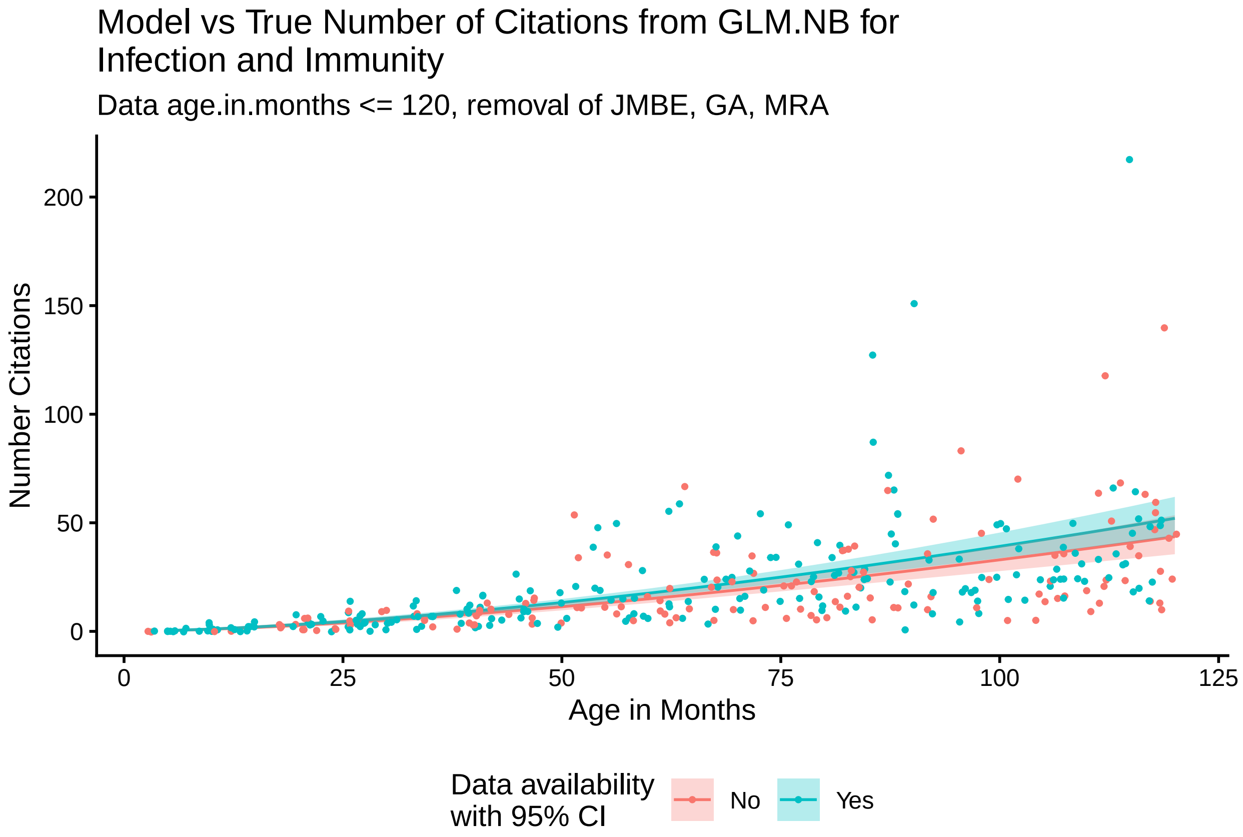
For each journal separately, overlay citations by paper on model output for DA yes and DA no

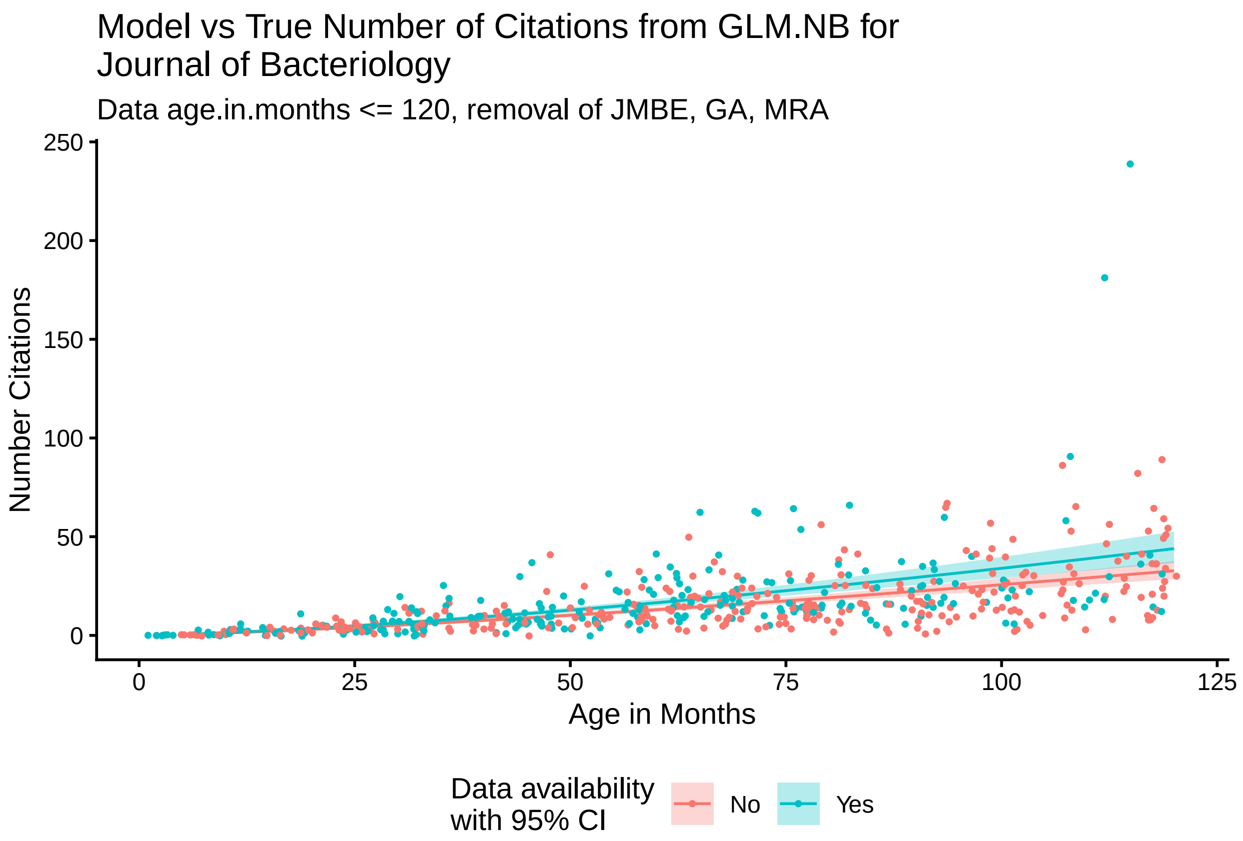
```
#lol i just add the data in each geom
journals <- ten_metadata %>%
  count(container.title) %>%
  mutate(container.title = as.character(container.title)) %>%
  dplyr::select(container.title)

# 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

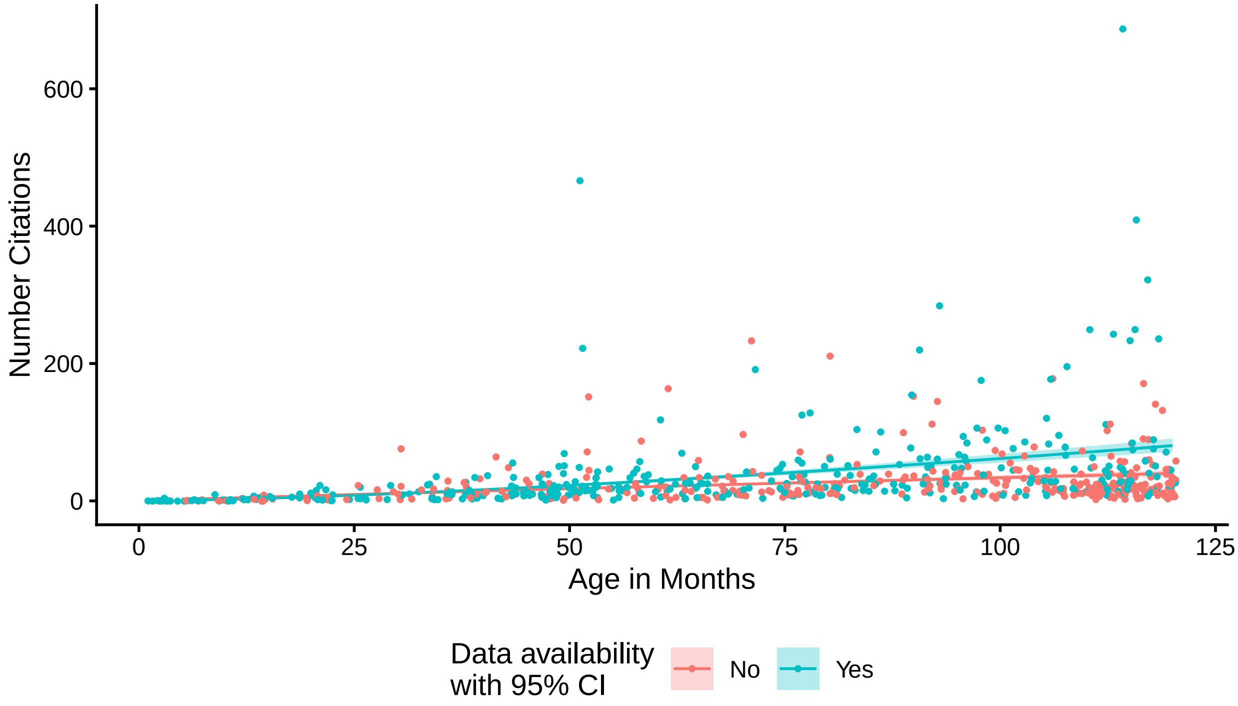
Data age.in.months <= 120, removal of JMBE, GA, MRA

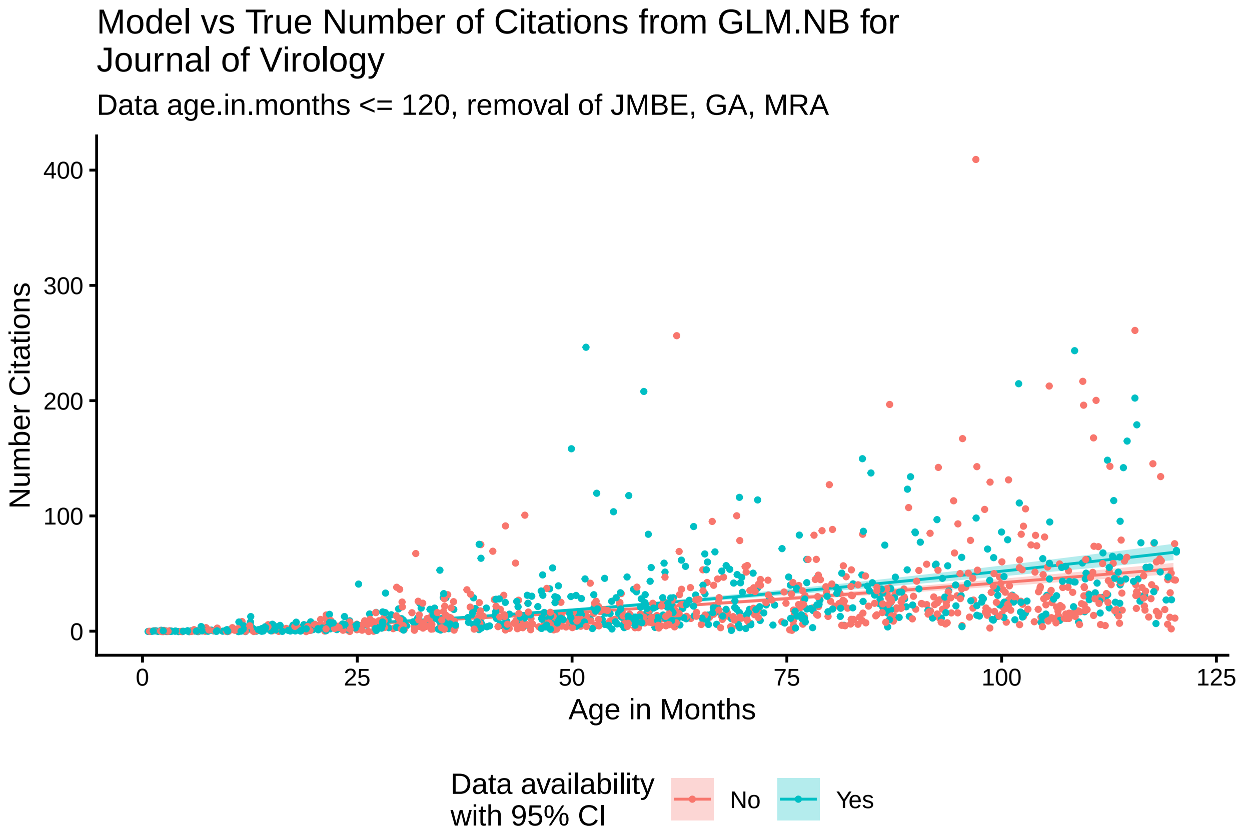

Model vs True Number of Citations from GLM.NB for
Infection and Immunity
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
200
150
100
50
0
0
25
50
75
100
125
Age in Months
Data availability
with 95% CI
No
Yes

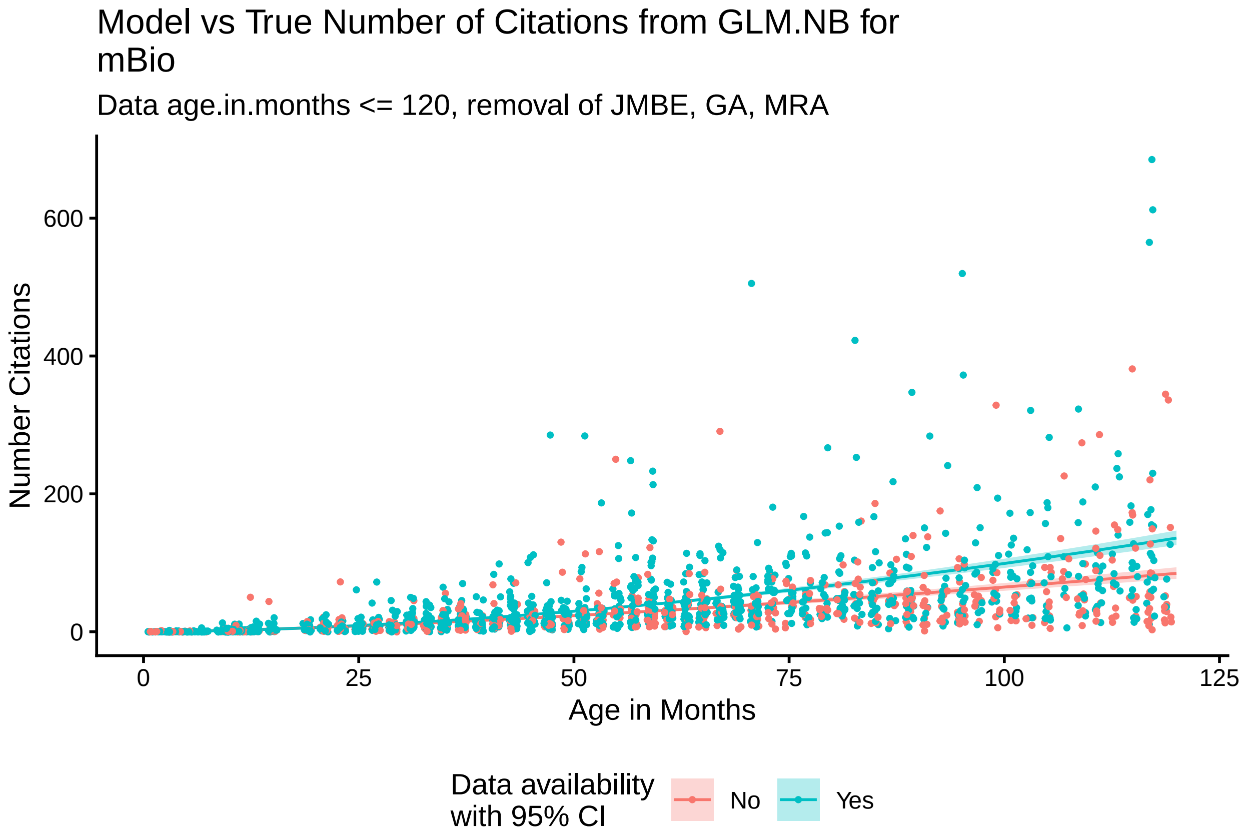

Model vs True Number of Citations from GLM.NB for
Journal of Bacteriology
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
250
200
150
100
50
0
0
25
50
75
100
125
Age in Months
Data availability
with 95% CI
No
Yes

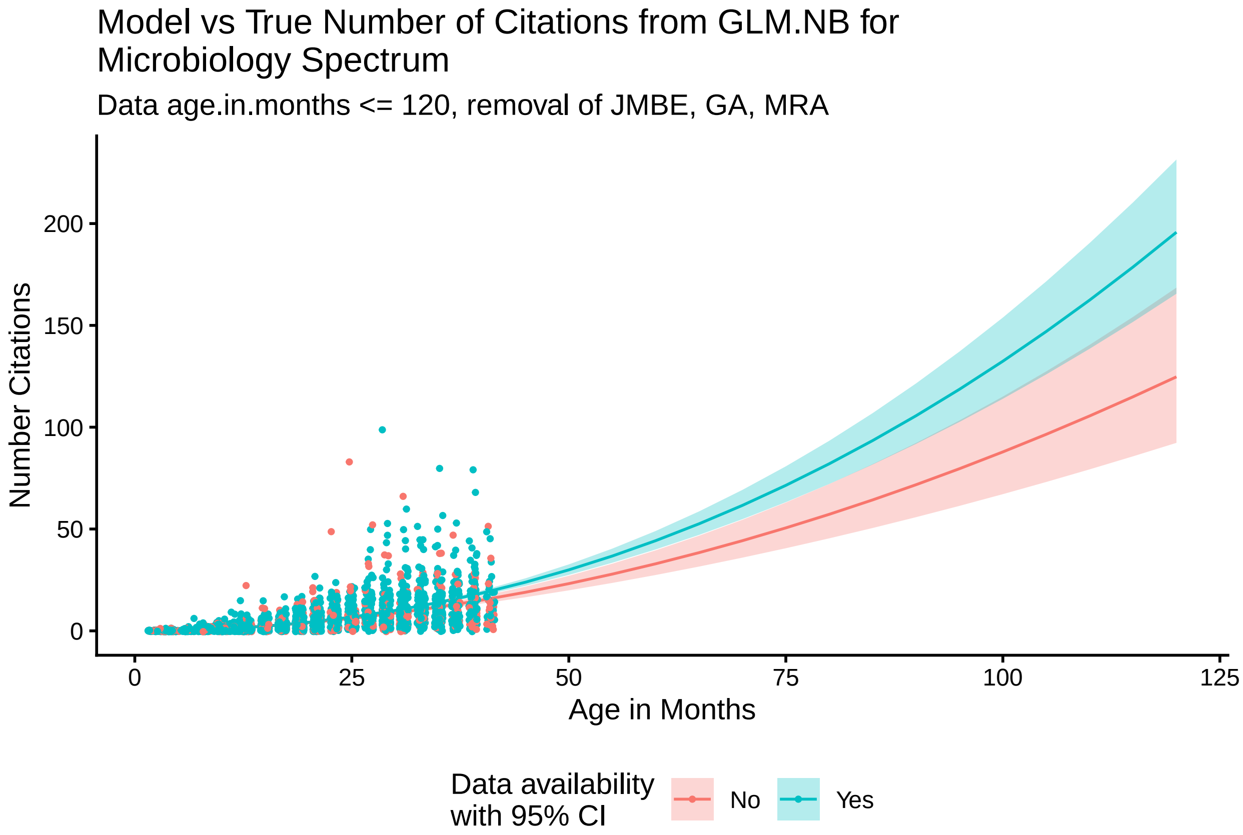
Model vs True Number of Citations from GLM.NB for Journal of Clinical Microbiology

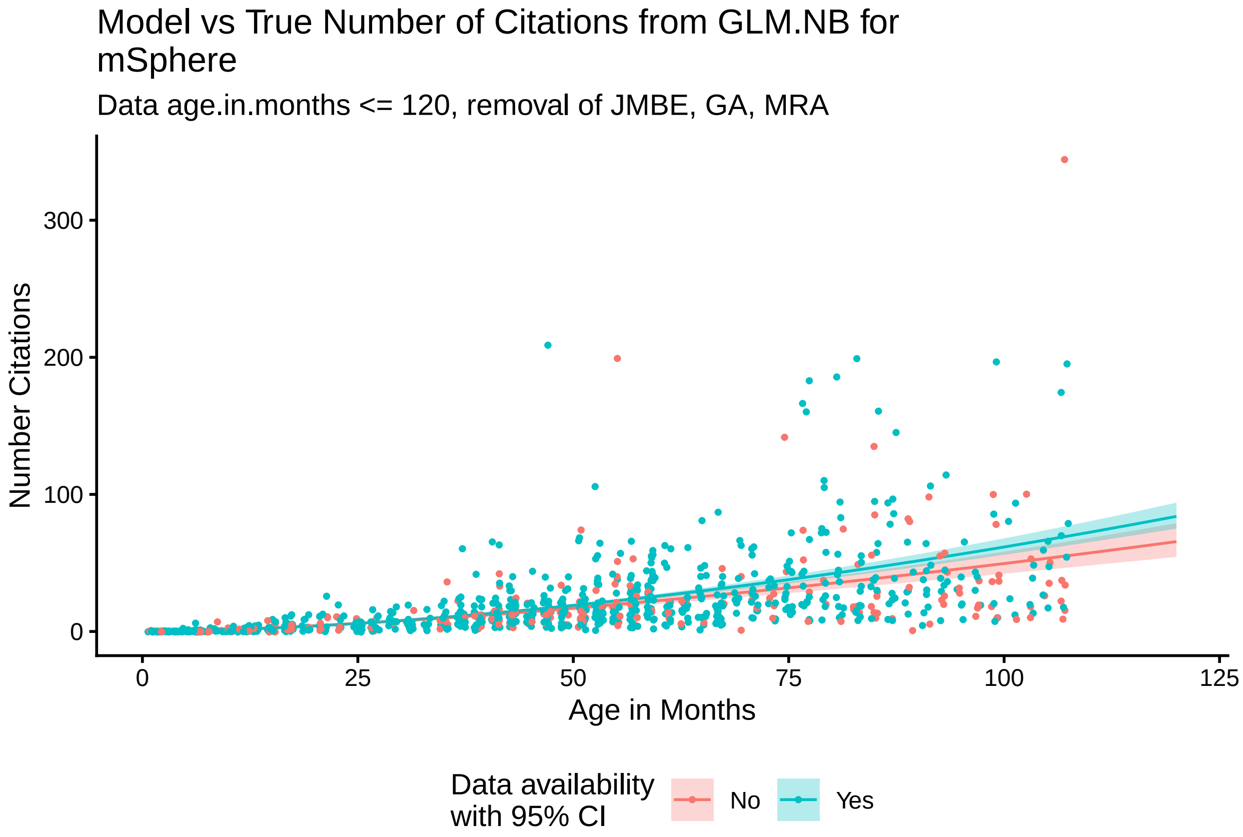
Data age.in.months <= 120, removal of JMBE, GA, MRA

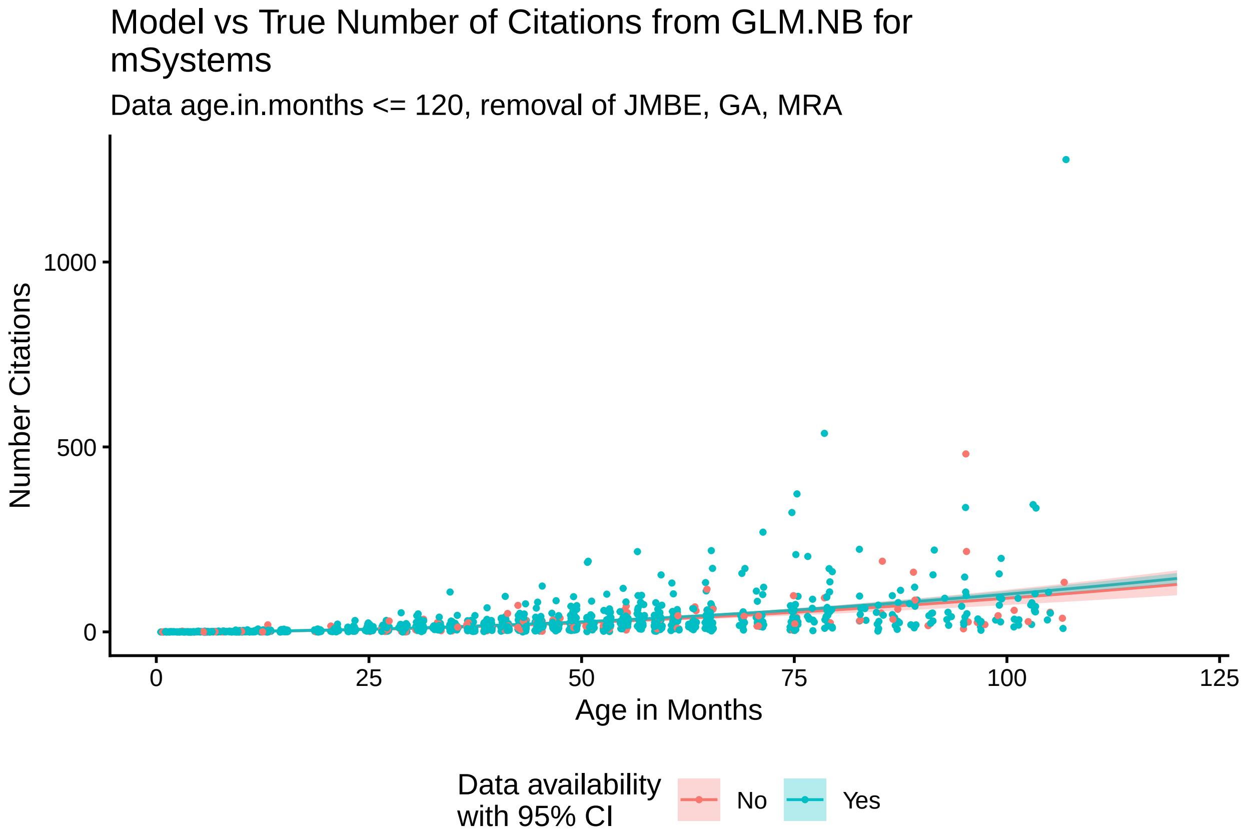



Model vs True Number of Citations from GLM.NB for
Journal of Virology
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
400
300
200
100
0
0
25
50
75
100
125
Age in Months
Data availability
with 95% CI
No
Yes


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

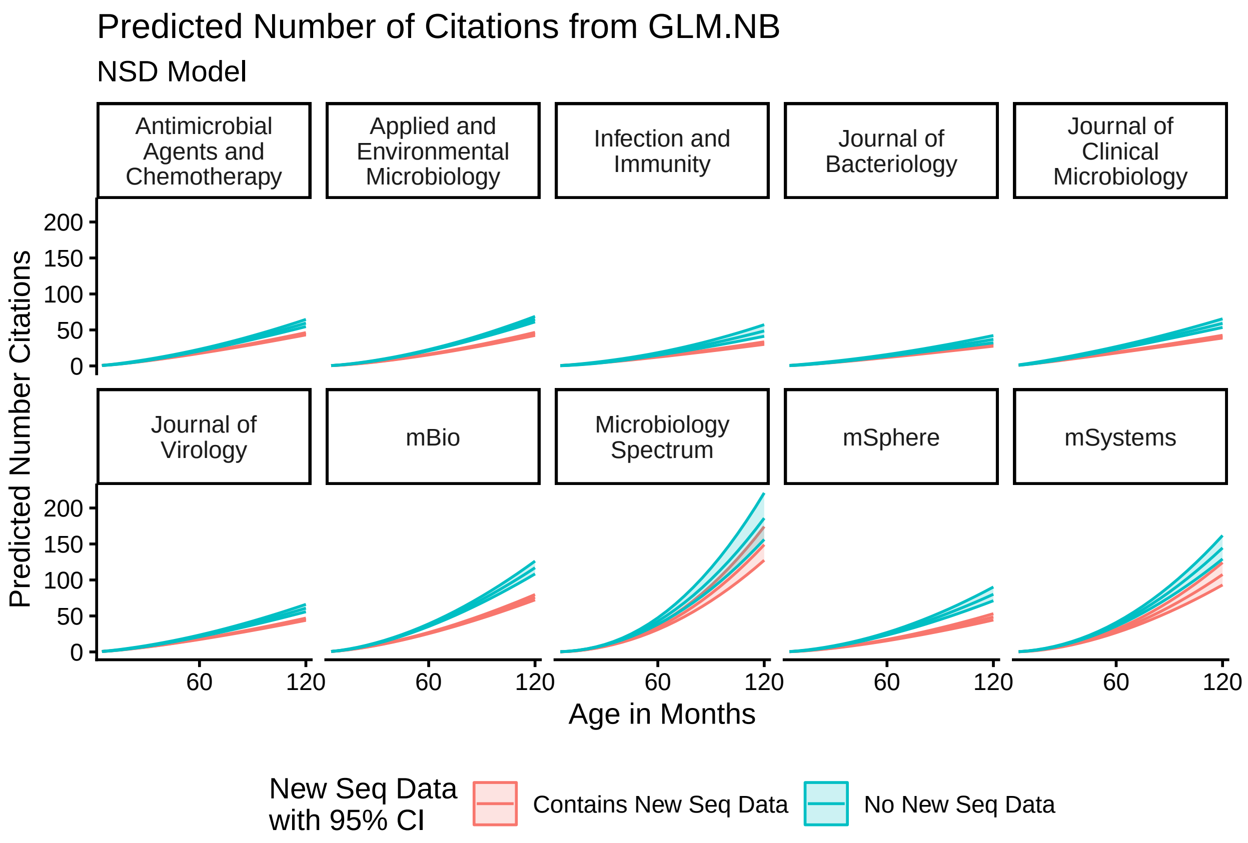

Model vs True Number of Citations from GLM.NB for mSphere
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
300
200
100
0
0
25
50
75
100
125
Age in Months
Data availability with 95% CI
No
Yes


Model vs True Number of Citations from GLM.NB for mSystems

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

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)

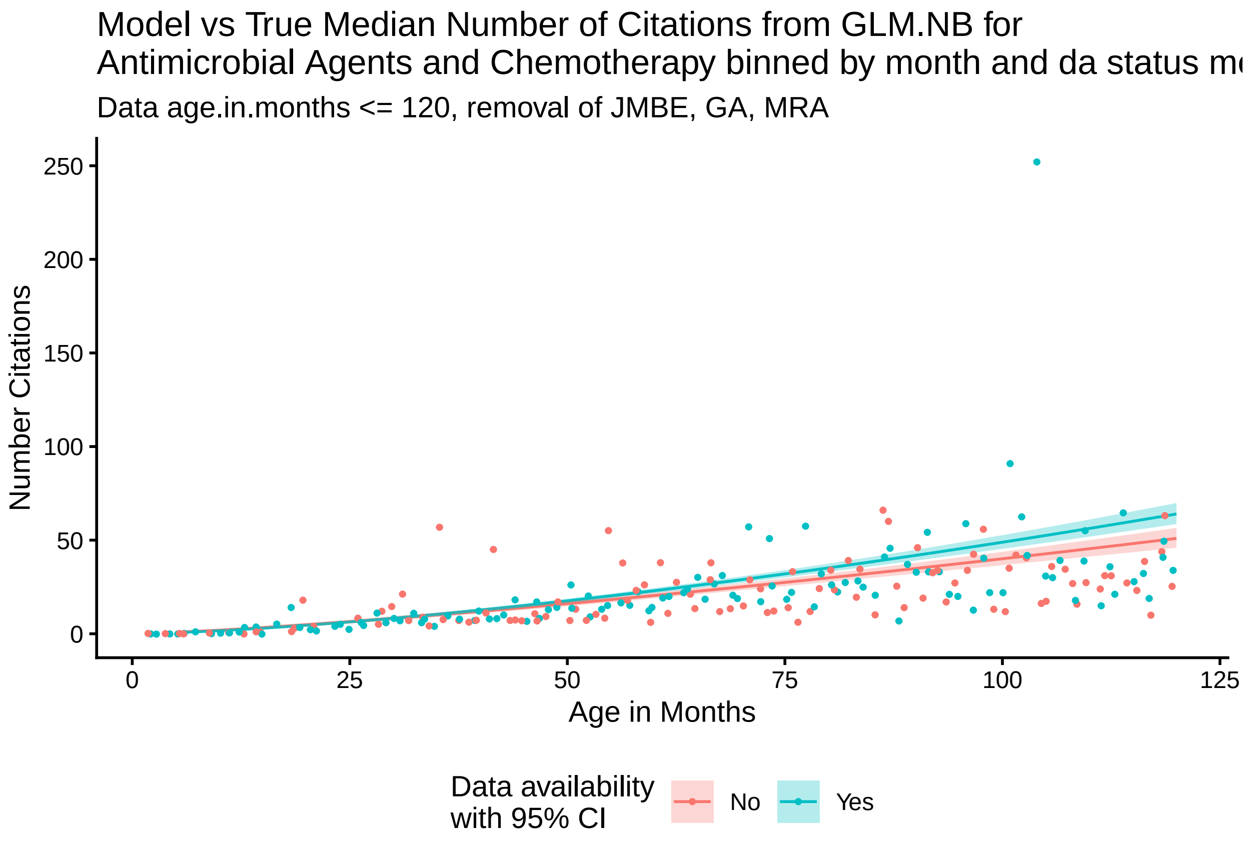
```
#get spectrum data

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

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

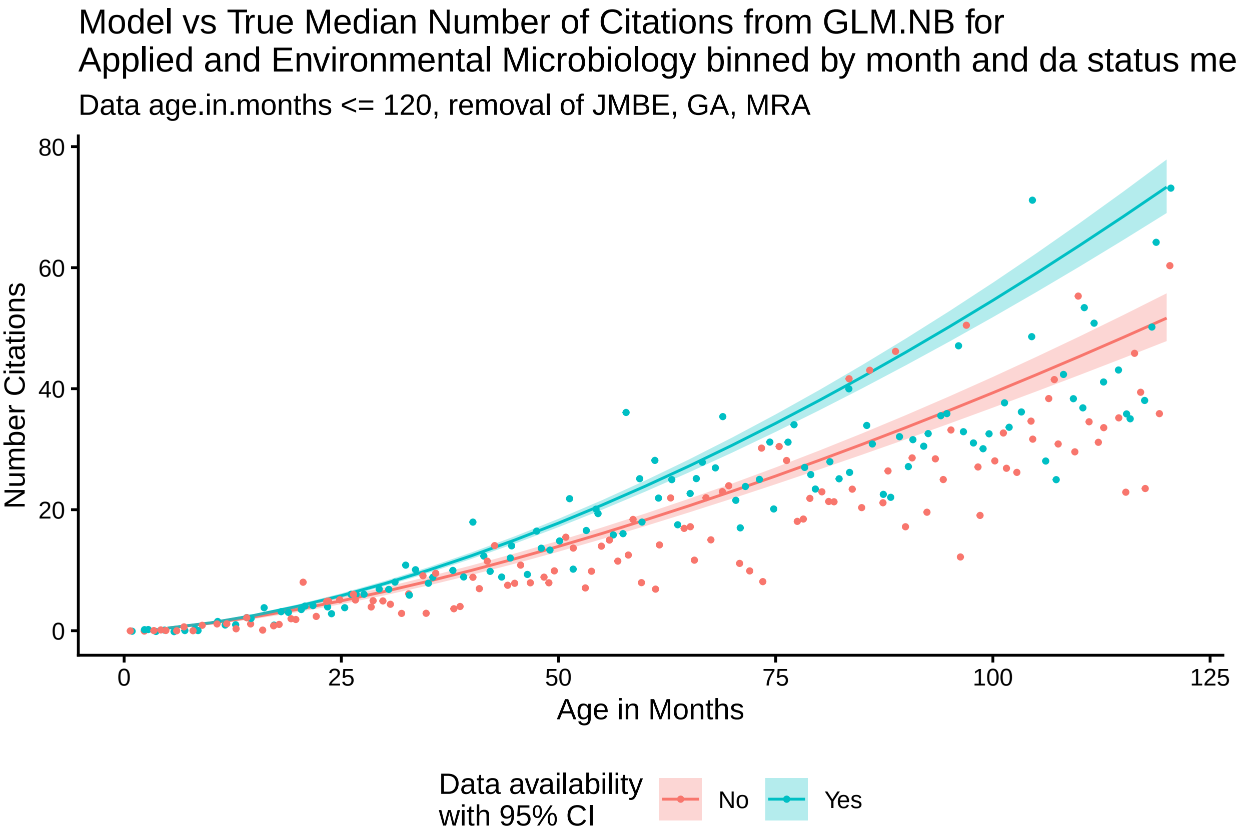
```
## # A tibble: 2,736 x 80
##    file                 da    nsd   paper.x doi   doi_no_underscore journal_abrev
##    <chr>                <chr> <chr> <chr>   <chr> <chr>             <chr>
##  1 Data/html/10.1128_~ No    Yes   https:~ 10.1~ 10.1128/spectrum~ spectrum
##  2 Data/html/10.1128_~ Yes   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>, ...
```

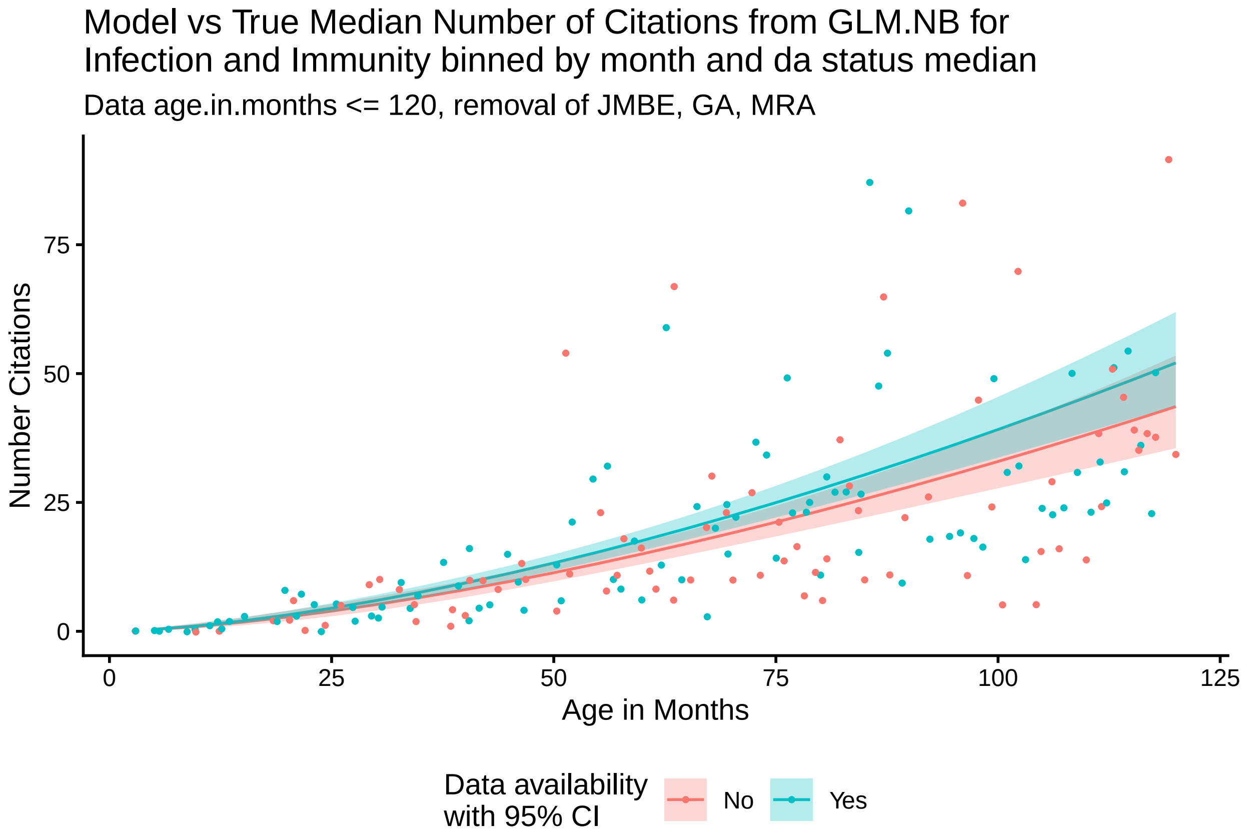
```
# %>%
#   view()
```

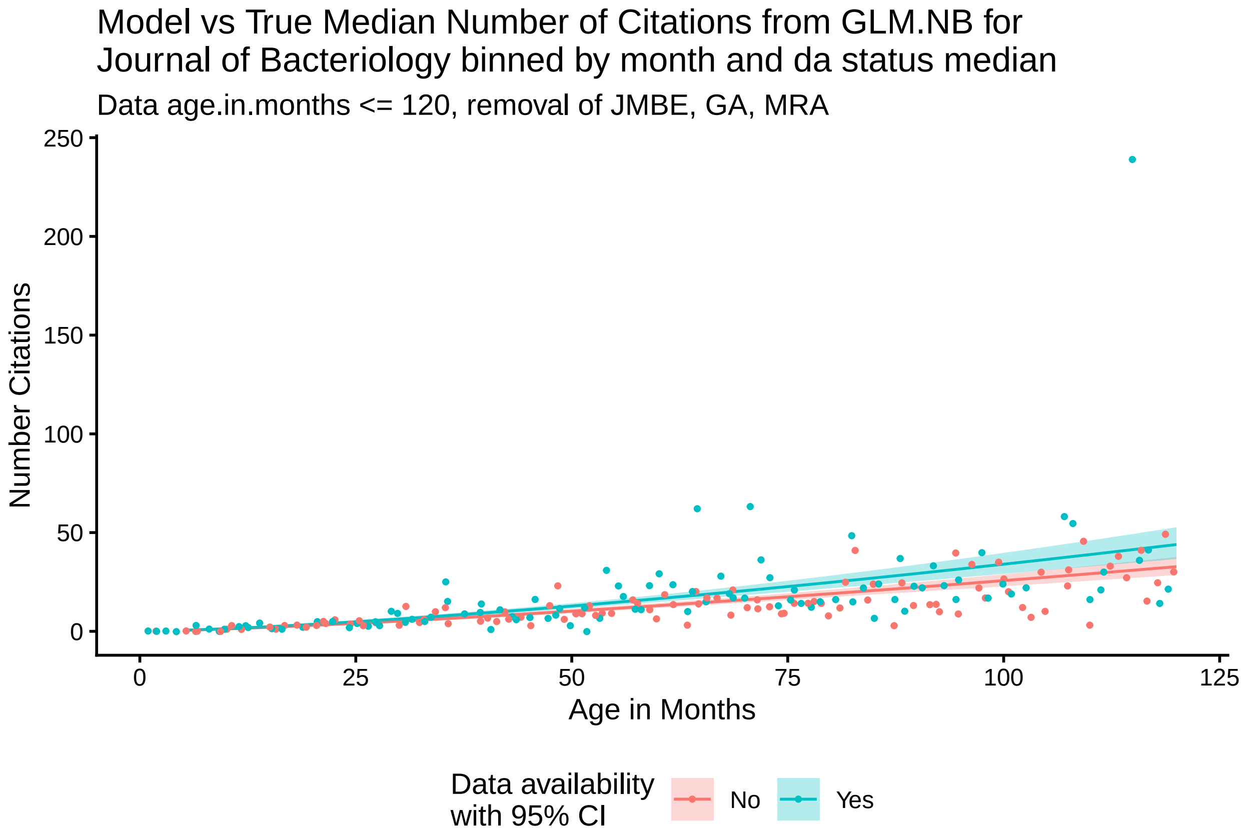
Trying binned data by month to evaluate model fit

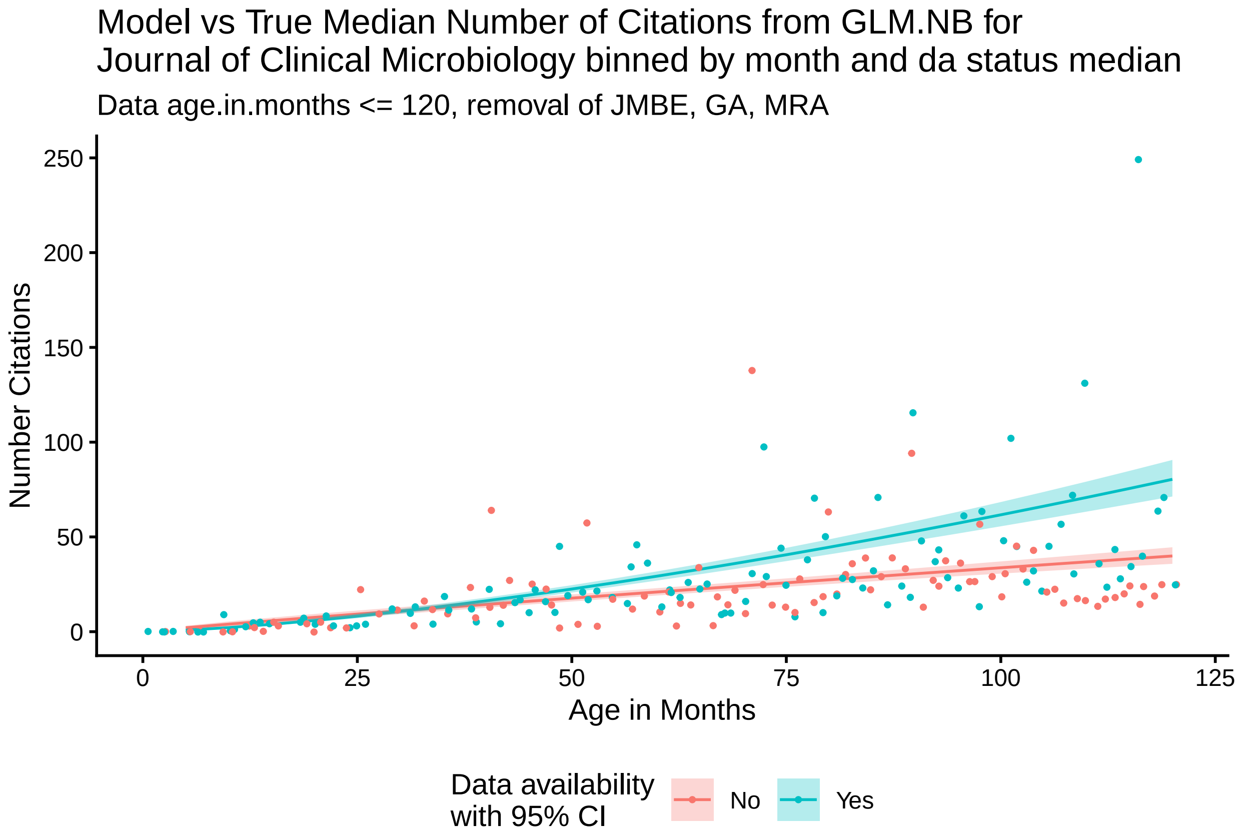
```
#let's try this for one month and then for the rest of them

# 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)
}
```

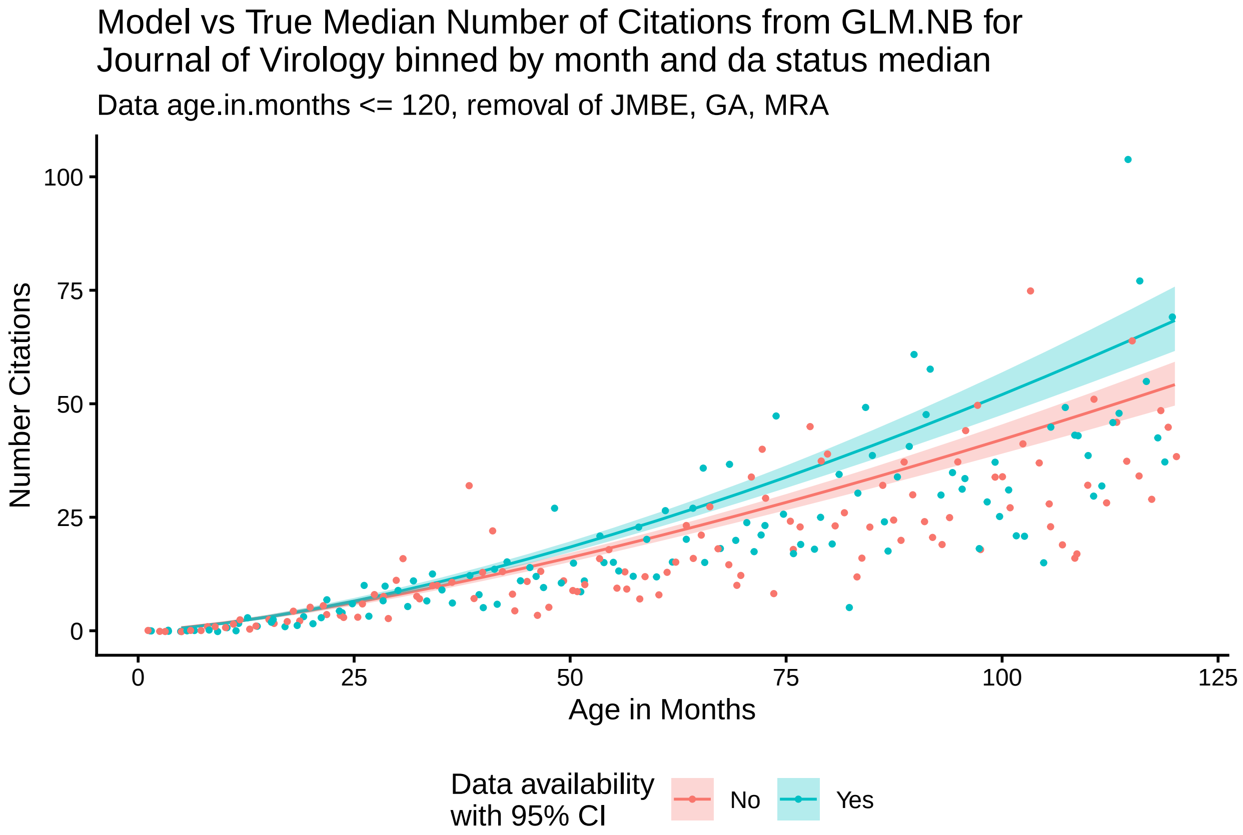

Model vs True Median Number of Citations from GLM.NB for
Antimicrobial Agents and Chemotherapy binned by month and da status m
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
0
50
100
150
200
250
Age in Months
0
25
50
75
100
125
Data availability
with 95% CI
No
Yes

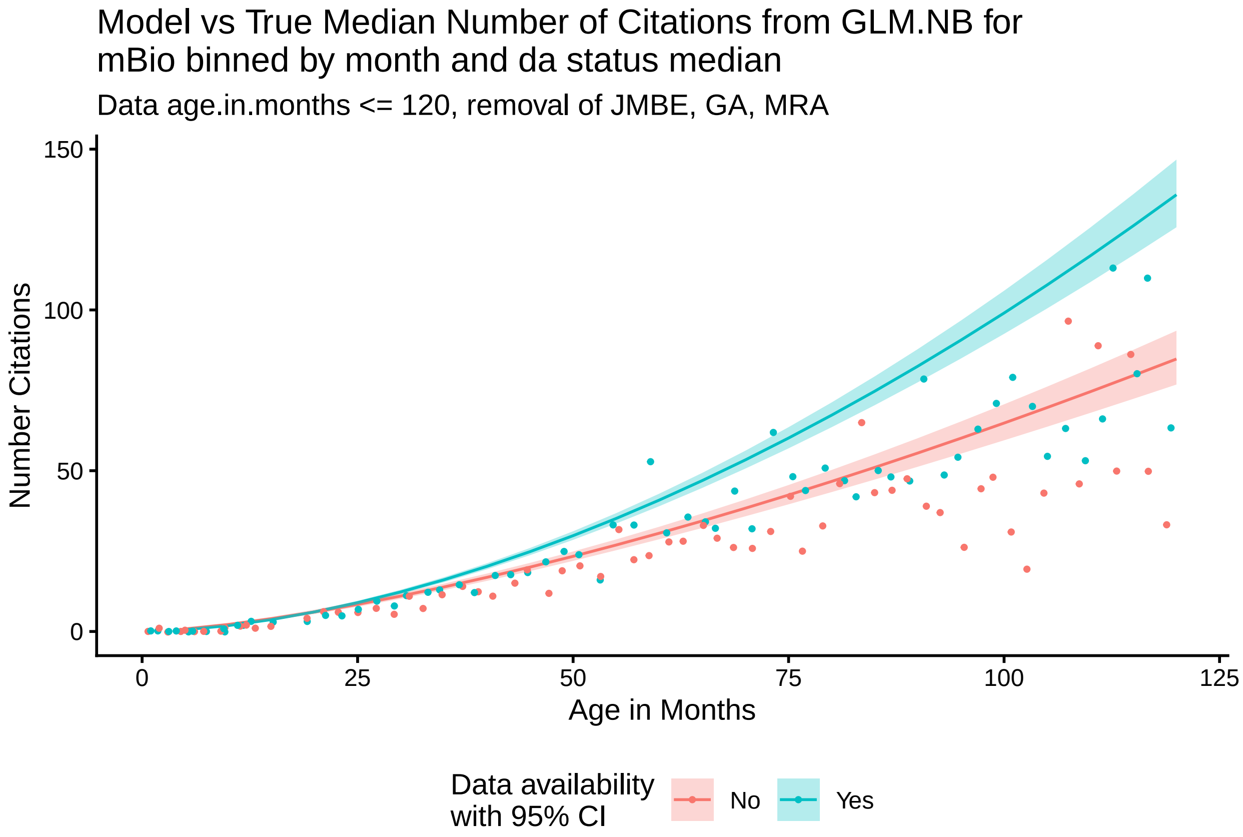

Model vs True Median Number of Citations from GLM.NB for
Applied and Environmental Microbiology binned by month and da status me
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
0
20
40
60
80
0
25
50
75
100
125
Age in Months
Data availability
with 95% CI
No
Yes

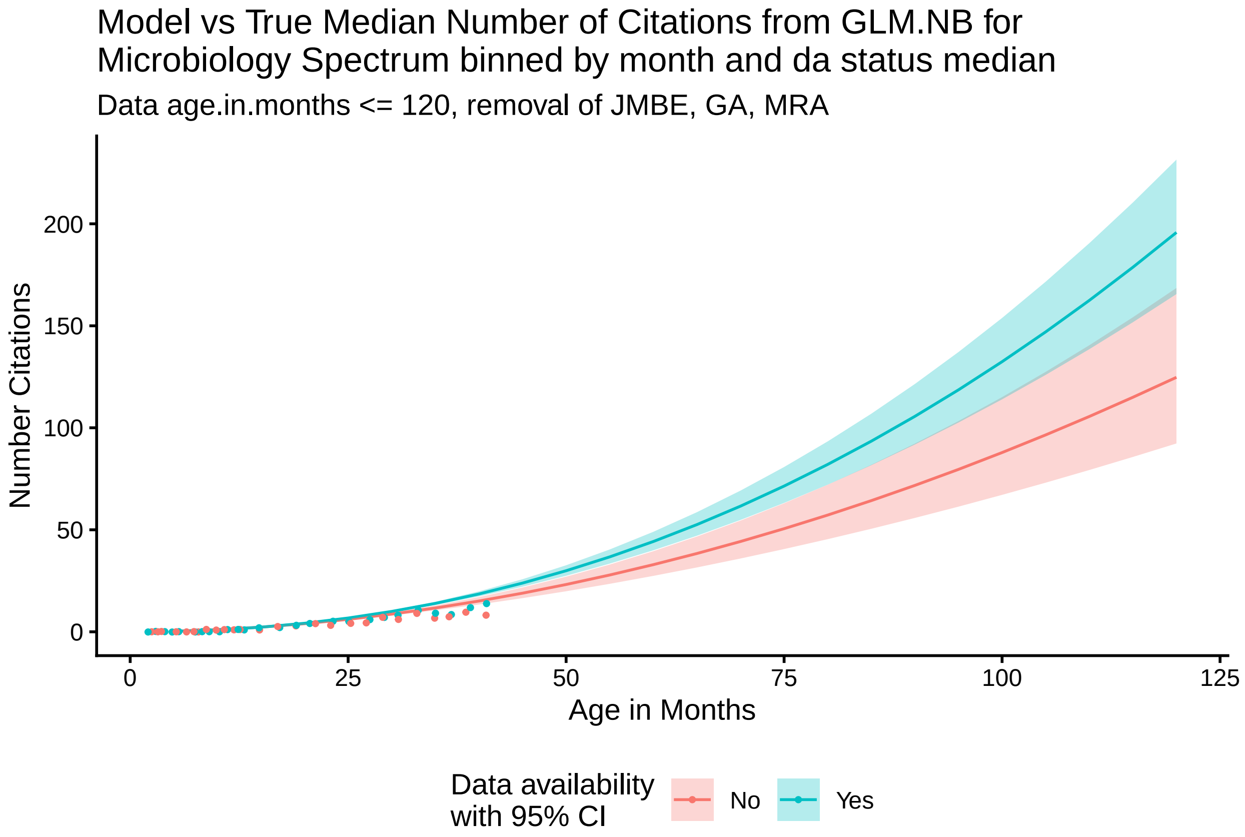

Model vs True Median Number of Citations from GLM.NB for
Infection and Immunity binned by month and da status median
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
0
25
50
75
Age in Months
0
25
50
75
100
125
Data availability
with 95% CI
No
Yes

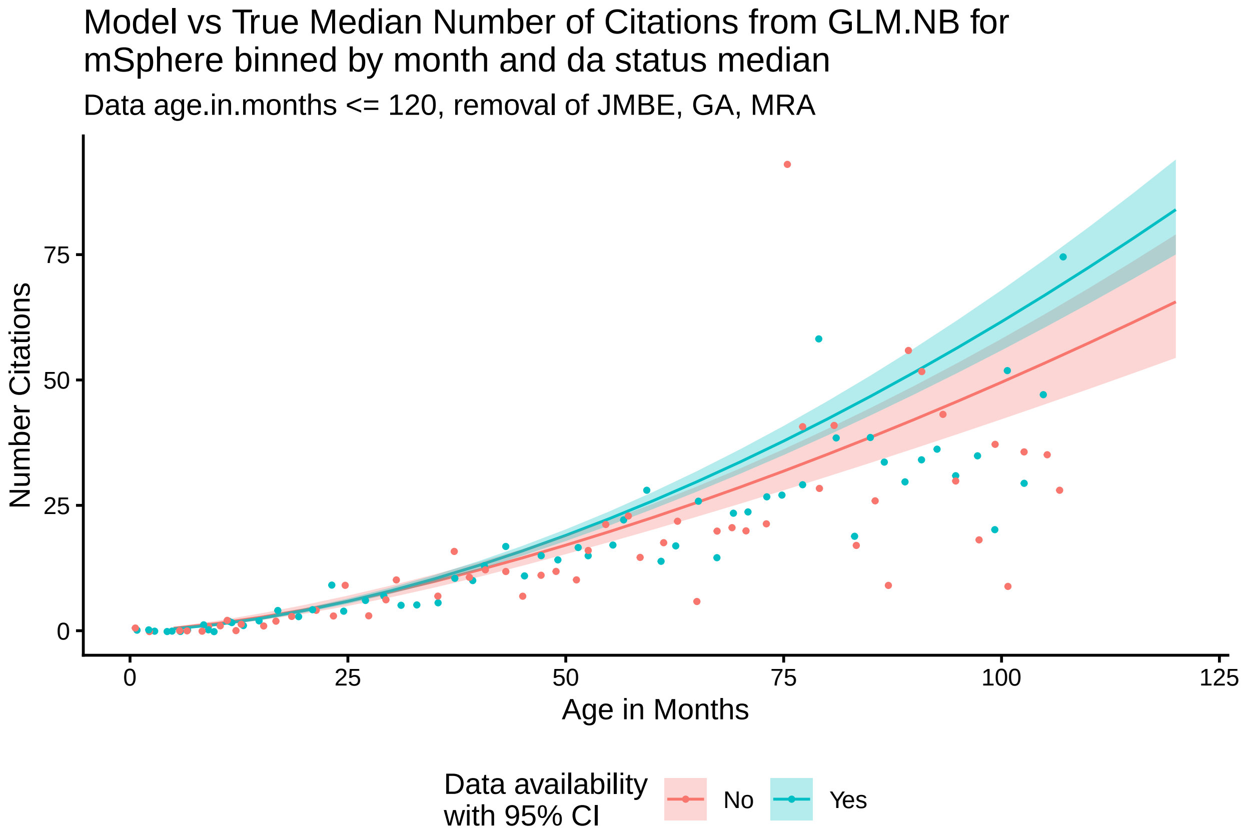

Model vs True Median Number of Citations from GLM.NB for
Journal of Bacteriology binned by month and da status median
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
250
200
150
100
50
0
0
25
50
75
100
125
Age in Months
Data availability
with 95% CI
No
Yes


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
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 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

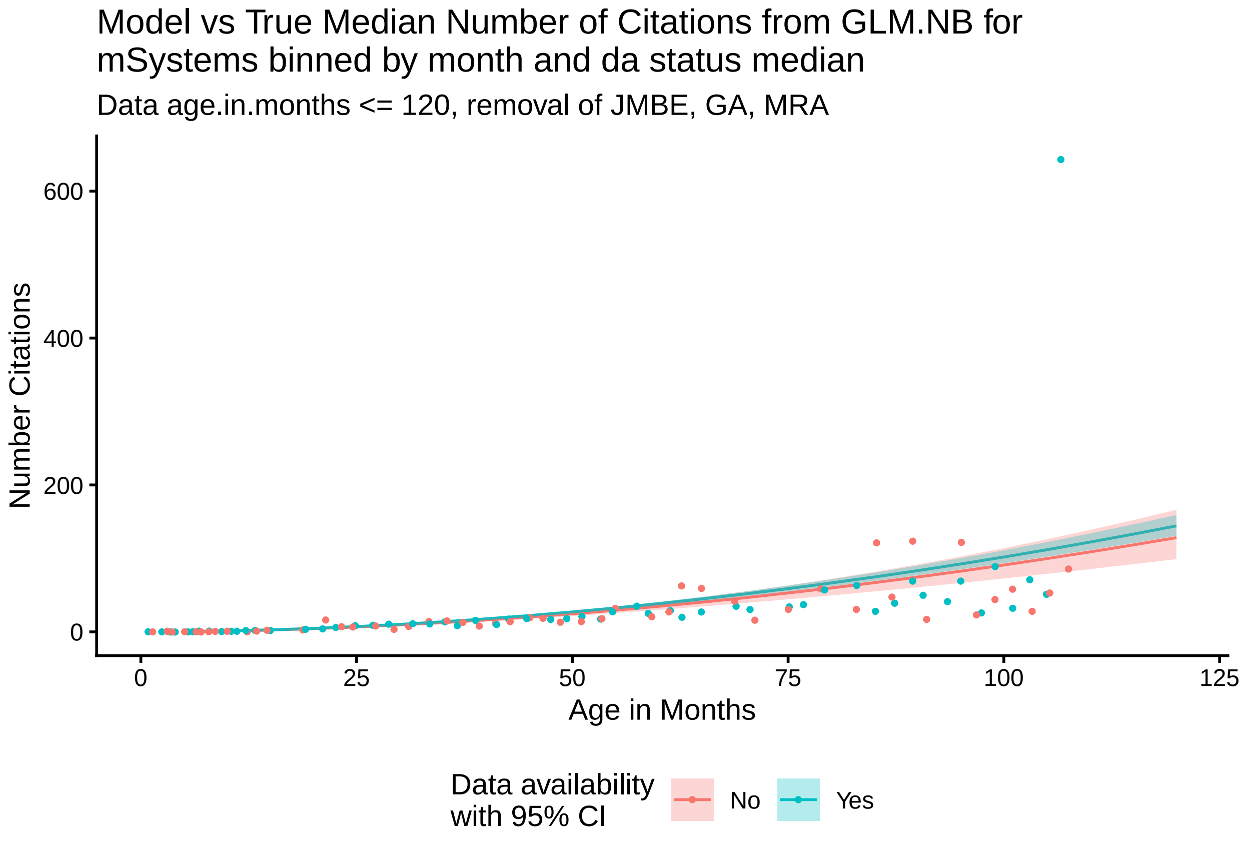

Model vs True Median Number of Citations from GLM.NB for
mBio binned by month and da status median
Data age.in.months <= 120, removal of JMBE, GA, MRA
Number Citations
150
100
50
0
0
25
50
75
100
125
Age in Months
Data availability
with 95% CI
No
Yes


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

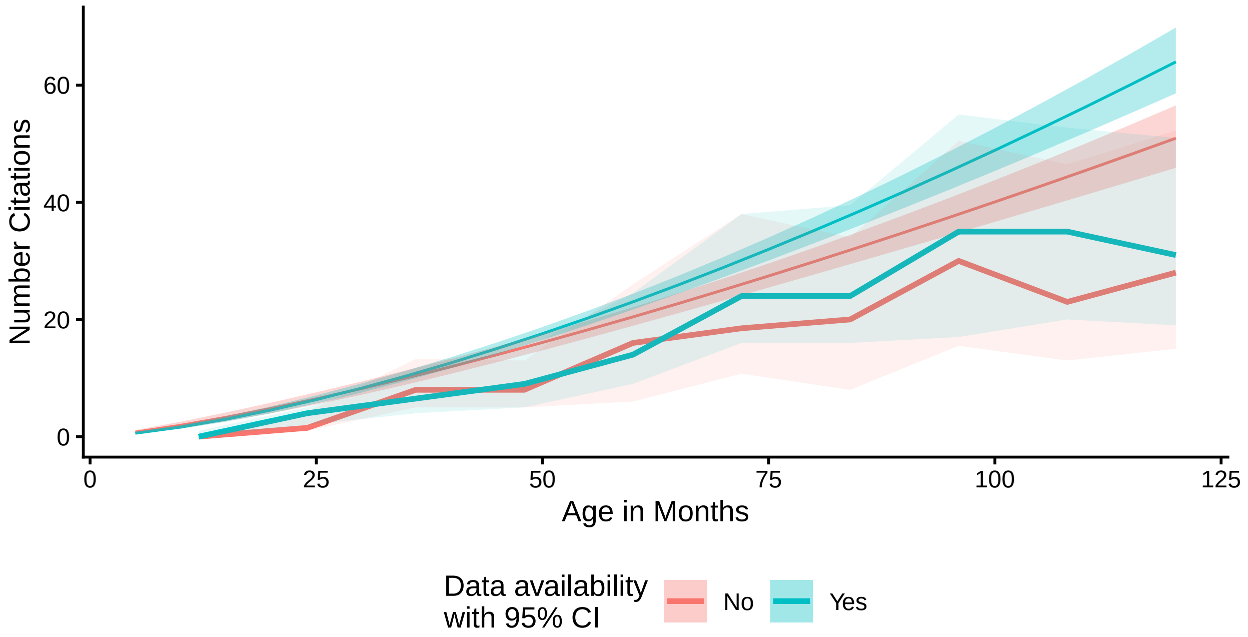


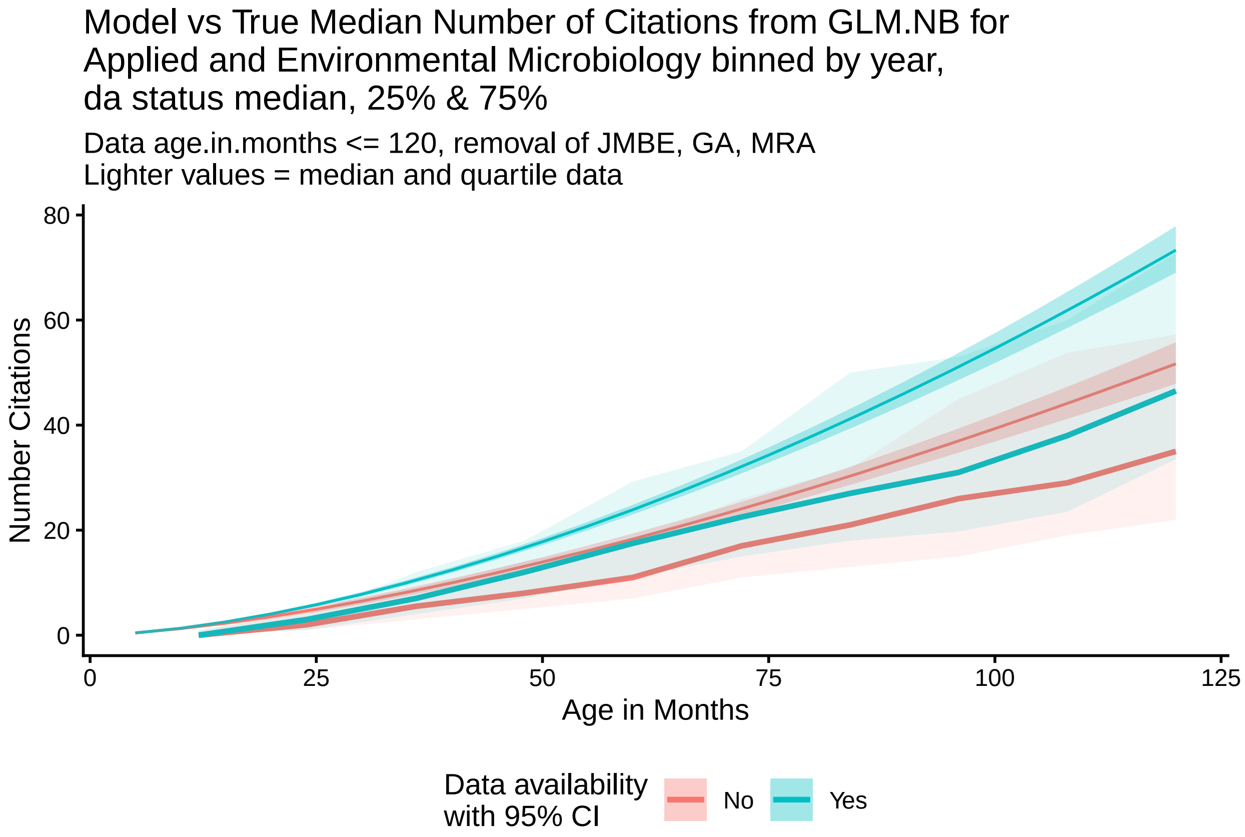
Bin the data by the month and whether the data are available. Then calculate the median and the 25th and 75th quantile. Plot the median as a line plot and the 25th and 75th percentiles as the boundary as a ribbon. Might do it by the year if the viz looks too clunky because there aren't enough points 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 = (2025-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



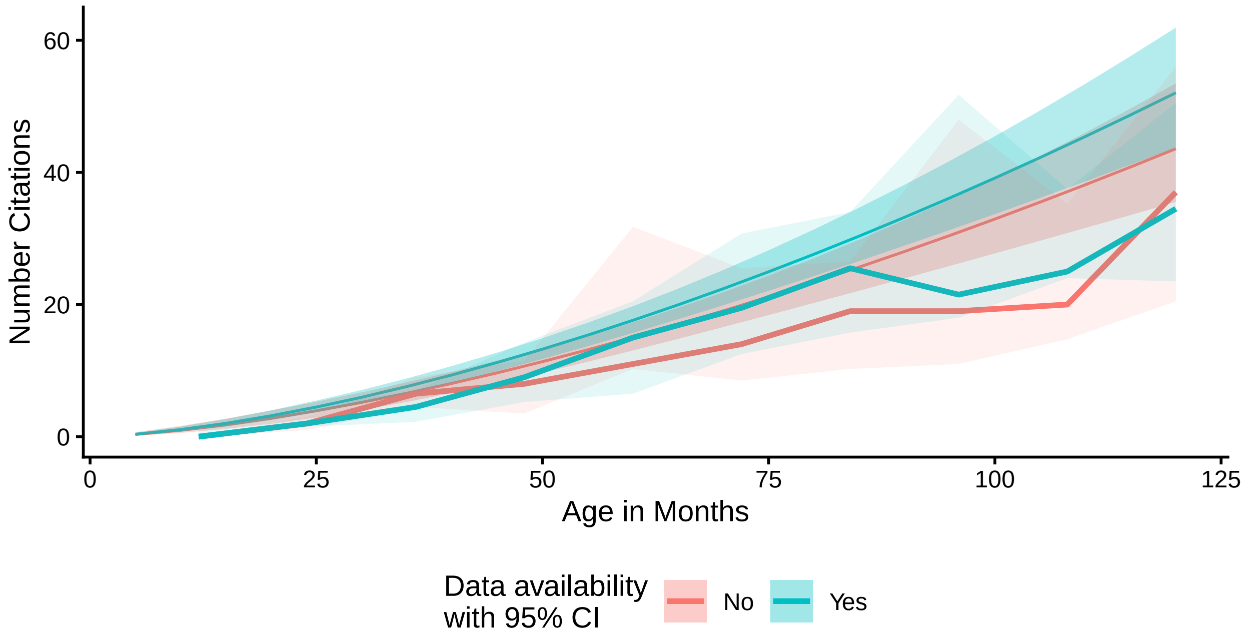


Model vs True Median Number of Citations from GLM.NB for Applied and Environmental Microbiology binned by year, da status median, 25% & 75%

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

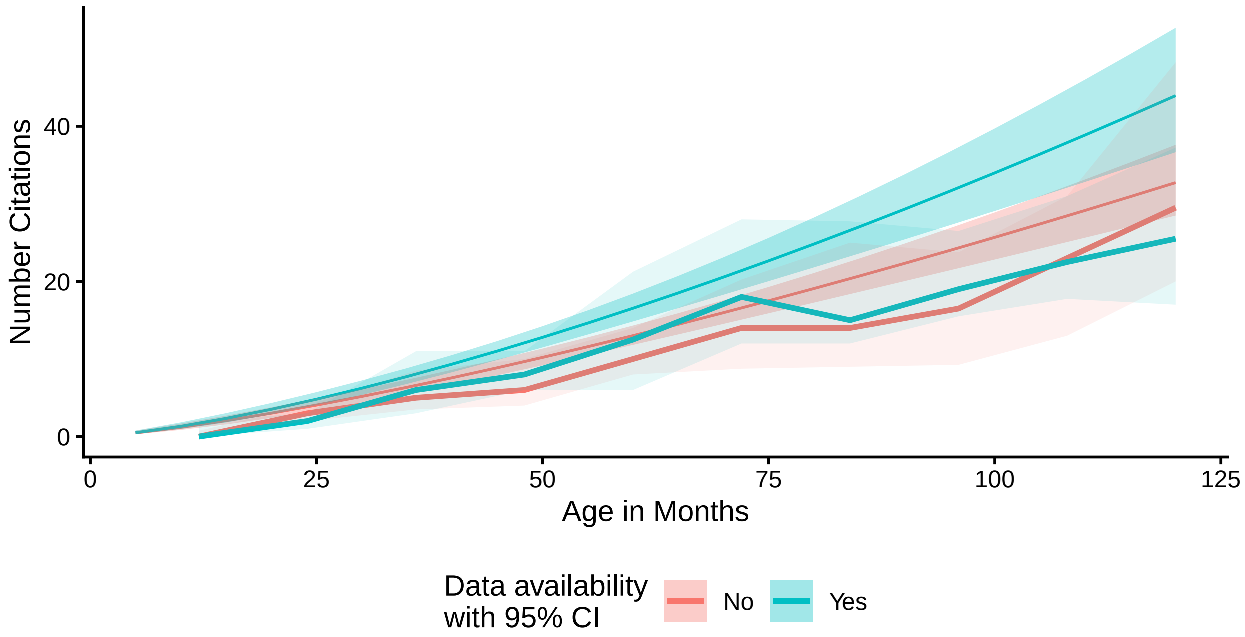
Model vs True Median Number of Citations from GLM.NB for Infection and Immunity binned by year, da status median, 25% & 75%

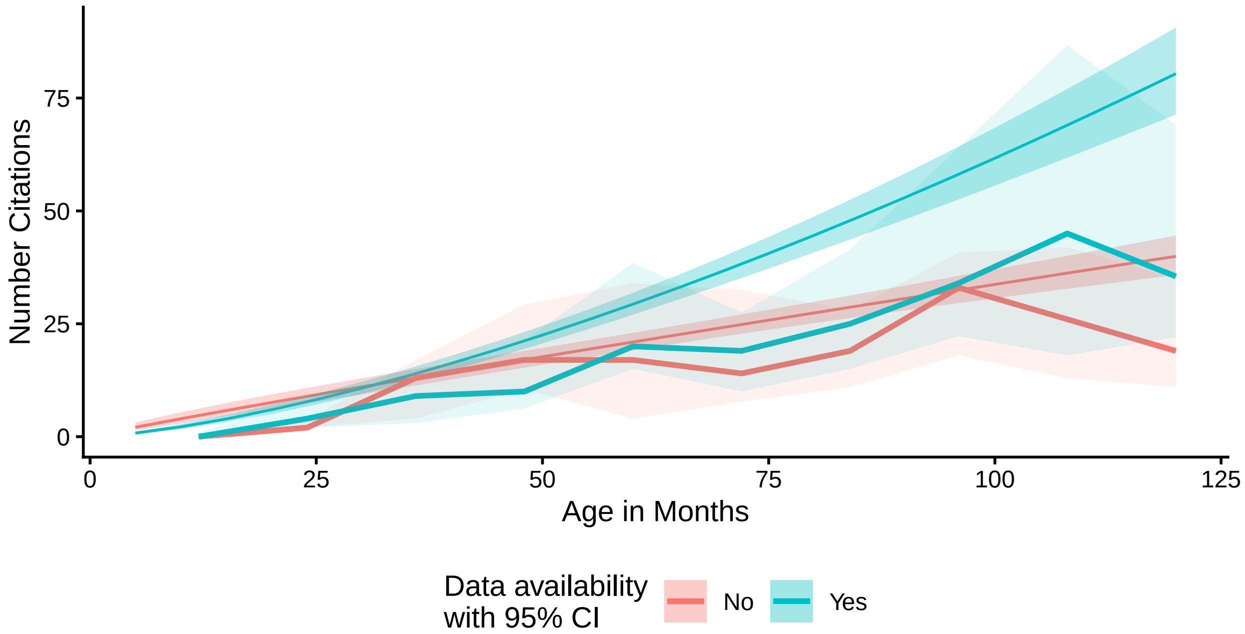
Data age.in.months <= 120, removal of JMBE, GA, MRA
Lighter values = median and quartile data



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

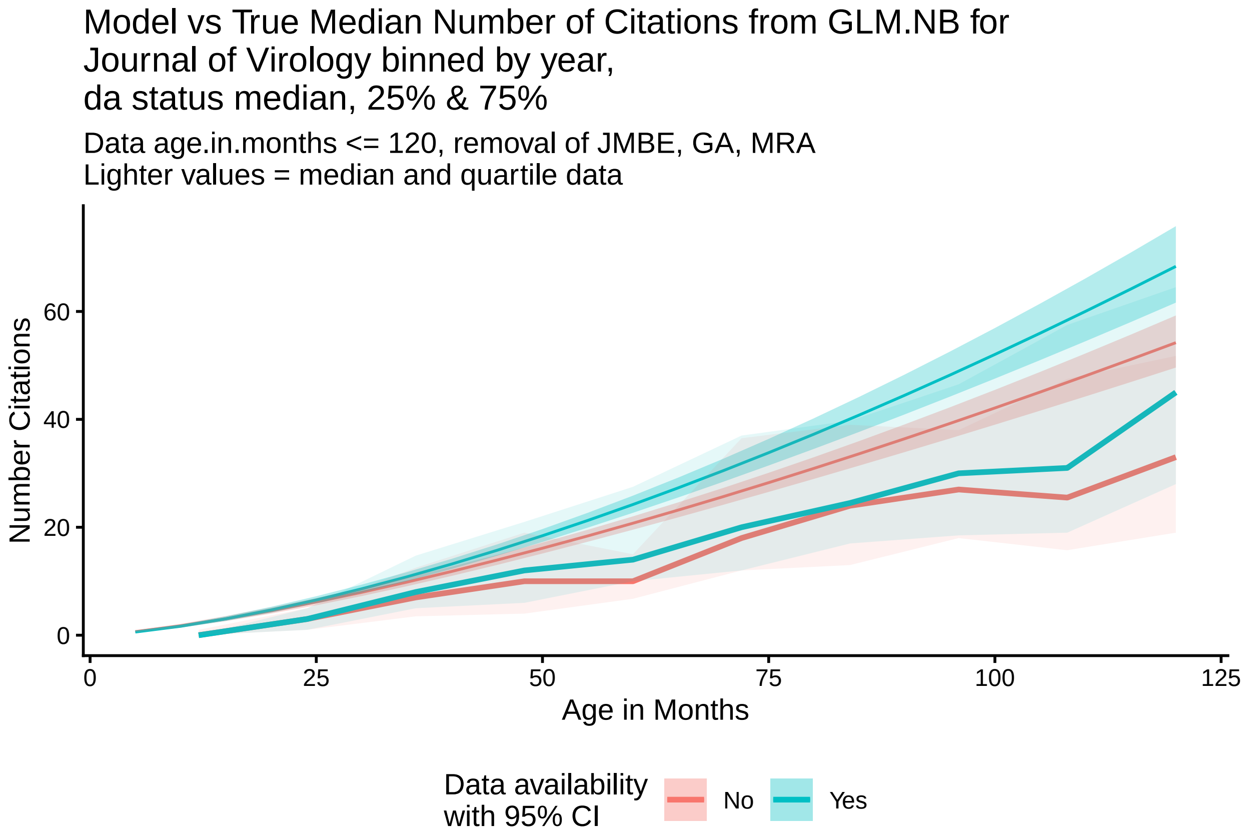
Data age.in.months <= 120, removal of JMBE, GA, MRA
Lighter values = median and quartile data

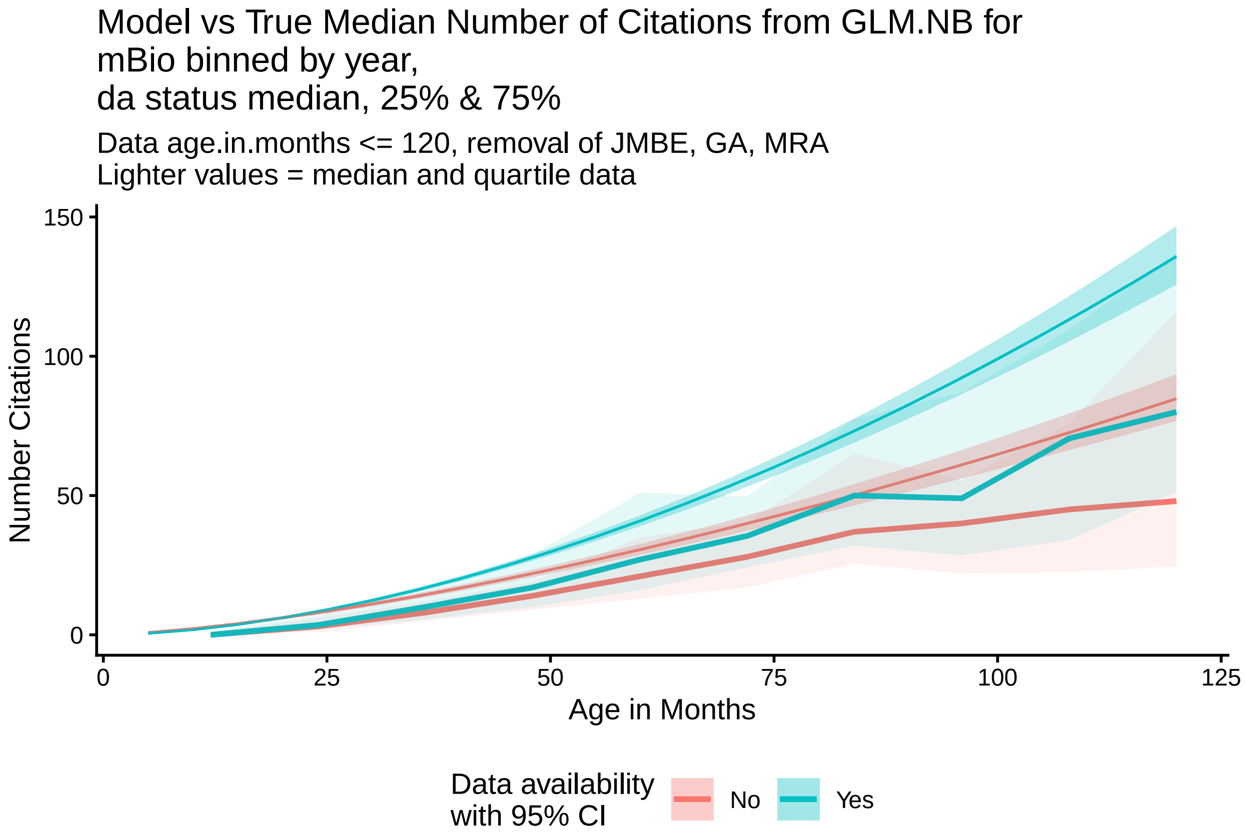


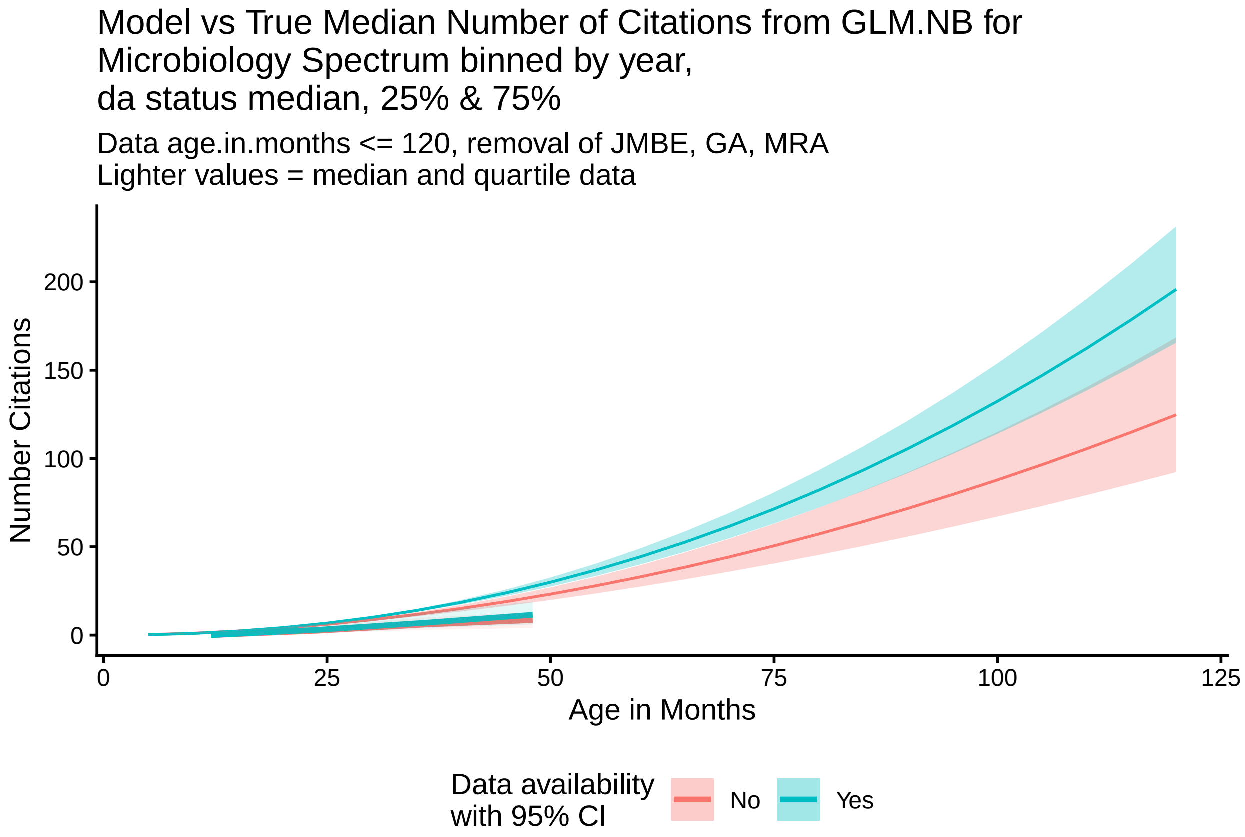


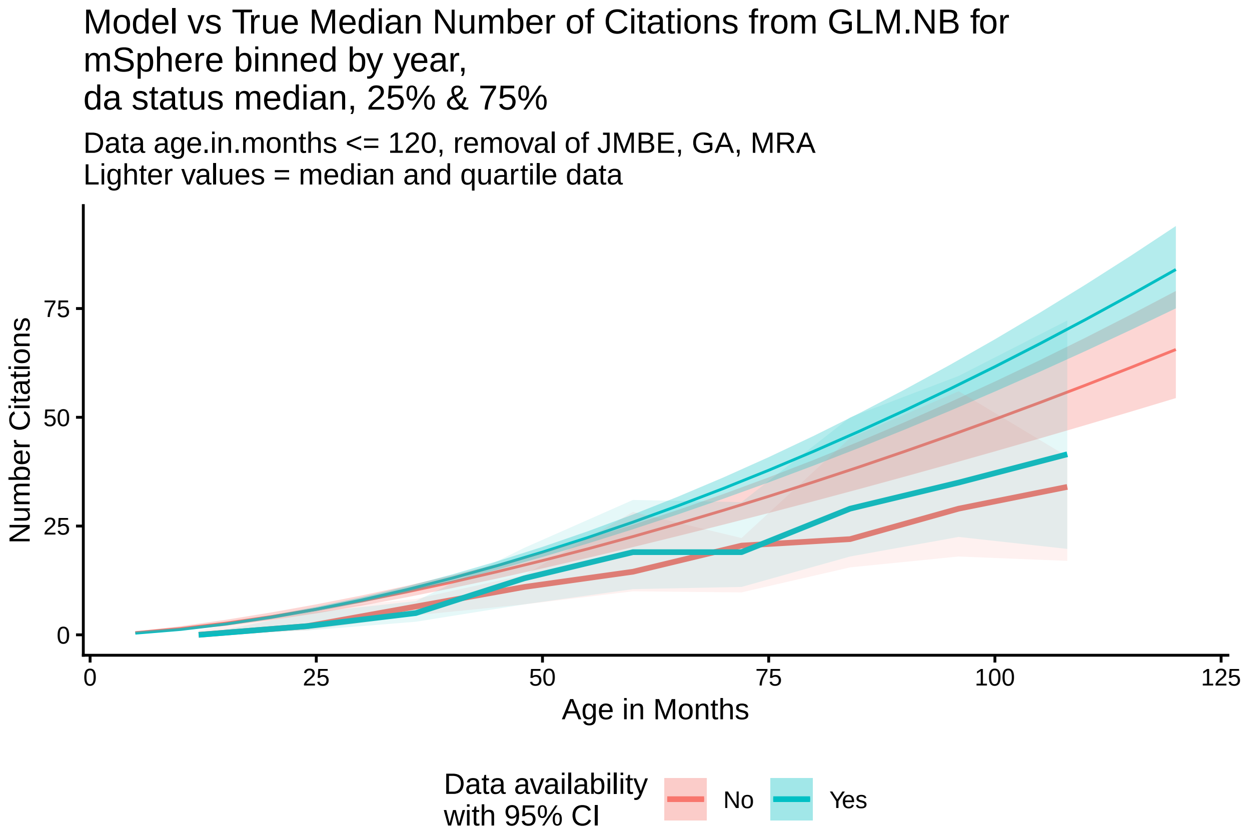
Model vs True Median Number of Citations from GLM.NB for
Journal of Clinical Microbiology binned by year,
da status median, 25% & 75%

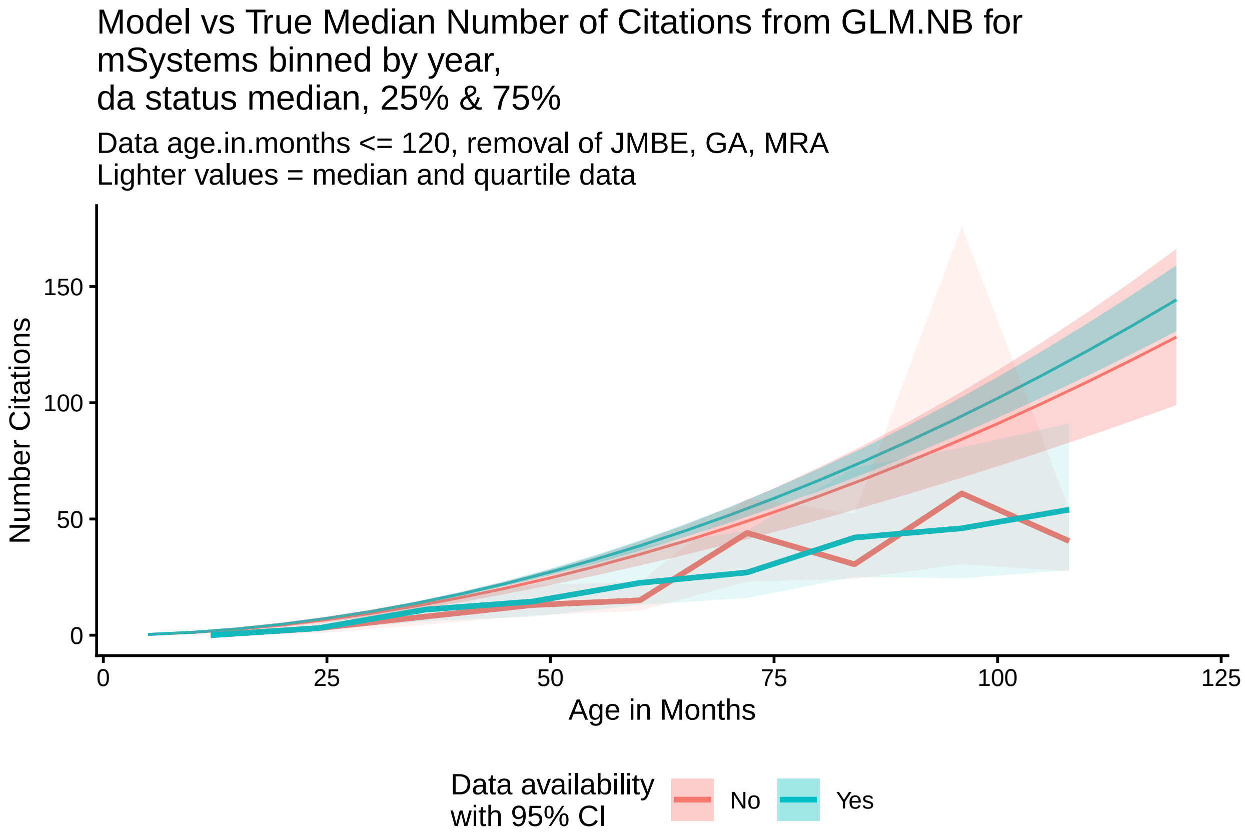
Data age.in.months <= 120, removal of JMBE, GA, MRA
Lighter values = median and quartile data


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
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
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
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 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
50
100
150
200
0
25
50
75
100
125
Age in Months
Data availability
with 95% CI
No
Yes

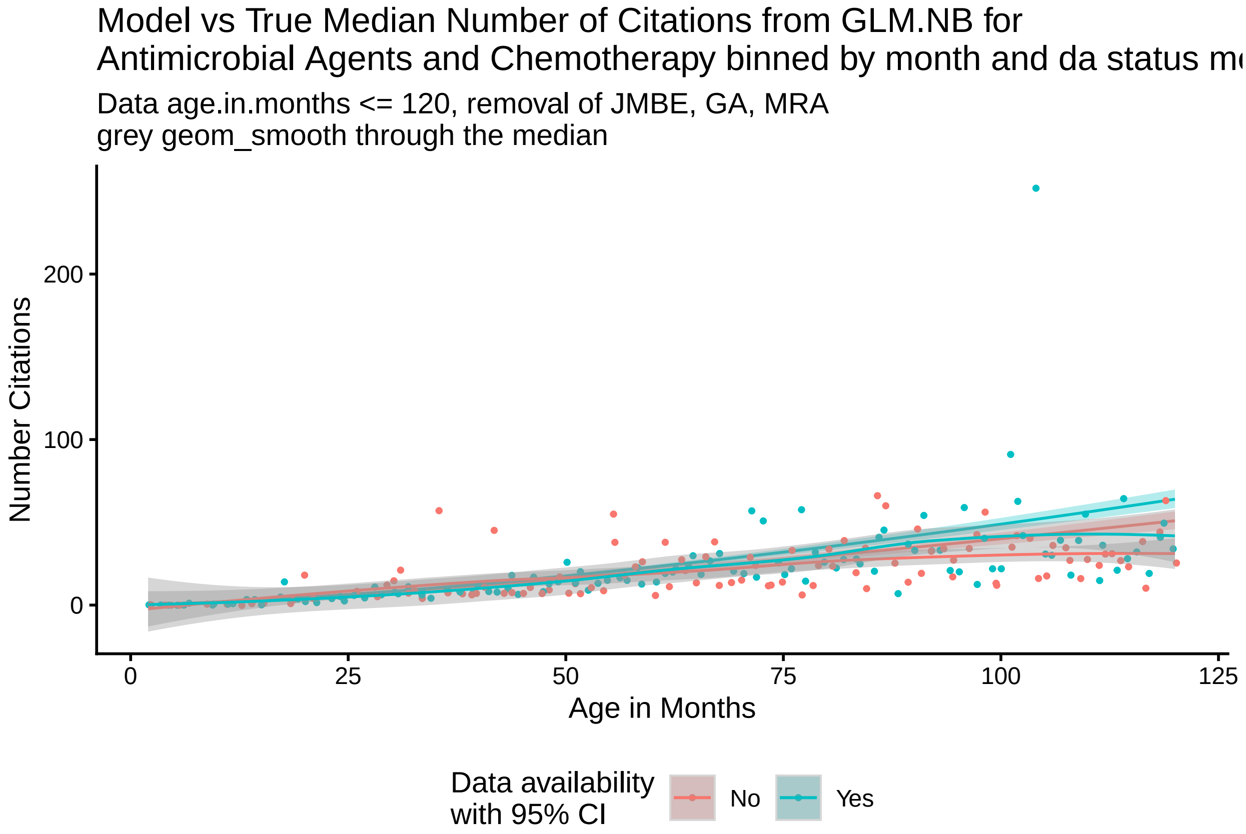

Model vs True Median Number of Citations from GLM.NB for
mSphere binned by year,
da status median, 25% & 75%
Data age.in.months <= 120, removal of JMBE, GA, MRA
Lighter values = median and quartile data
Number Citations
0
25
50
75
0
25
50
75
100
125
Age in Months
Data availability
with 95% CI
No
Yes



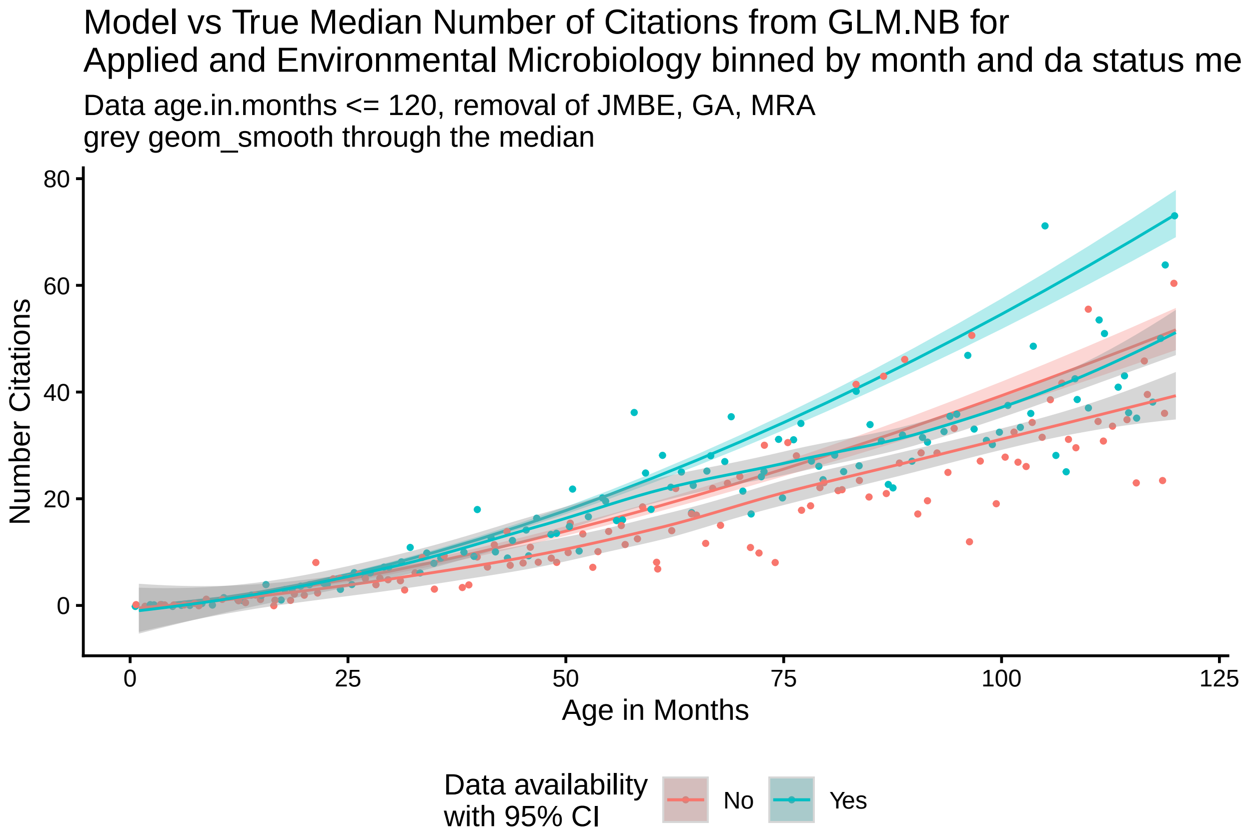
Using geom_smooth to fit a smoothed curve through the monthly data after taking the median on the data

```
#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$container.title[[j]]) %>%
    mutate(da_factor = ifelse(da_factor == "Data available", "Yes", "No"),
           age.in.months = as.numeric(as.character(age.in.months)))
  #make plot
  plot <-
  ggplot() +
   geom_line(data = model_data, aes(x = age.in.months, y = predicted_citations, group = da_factor, colo
   geom_ribbon(data = model_data, mapping = aes(x = age.in.months, y = predicted_citations,    ymin = c
                             group = da_factor, fill = da_factor), alpha = 0.3) +
    geom_point(data = j_monthly, aes(x = age.in.months,
                                      y = monthly_median, color = da_factor),
                                      position = position_jitter(width =0.5), size = 0.6) +
    geom_smooth(data = j_monthly, aes(x = age.in.months,
                                      y = monthly_median, color = da_factor), size = 0.5)+
   labs(title = paste0("Model vs True Median Number of Citations from GLM.NB for\n", journals$container
        subtitle = "Data age.in.months <= 120, removal of JMBE, GA, MRA\ngrey geom_smooth through the m
        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)
}
```

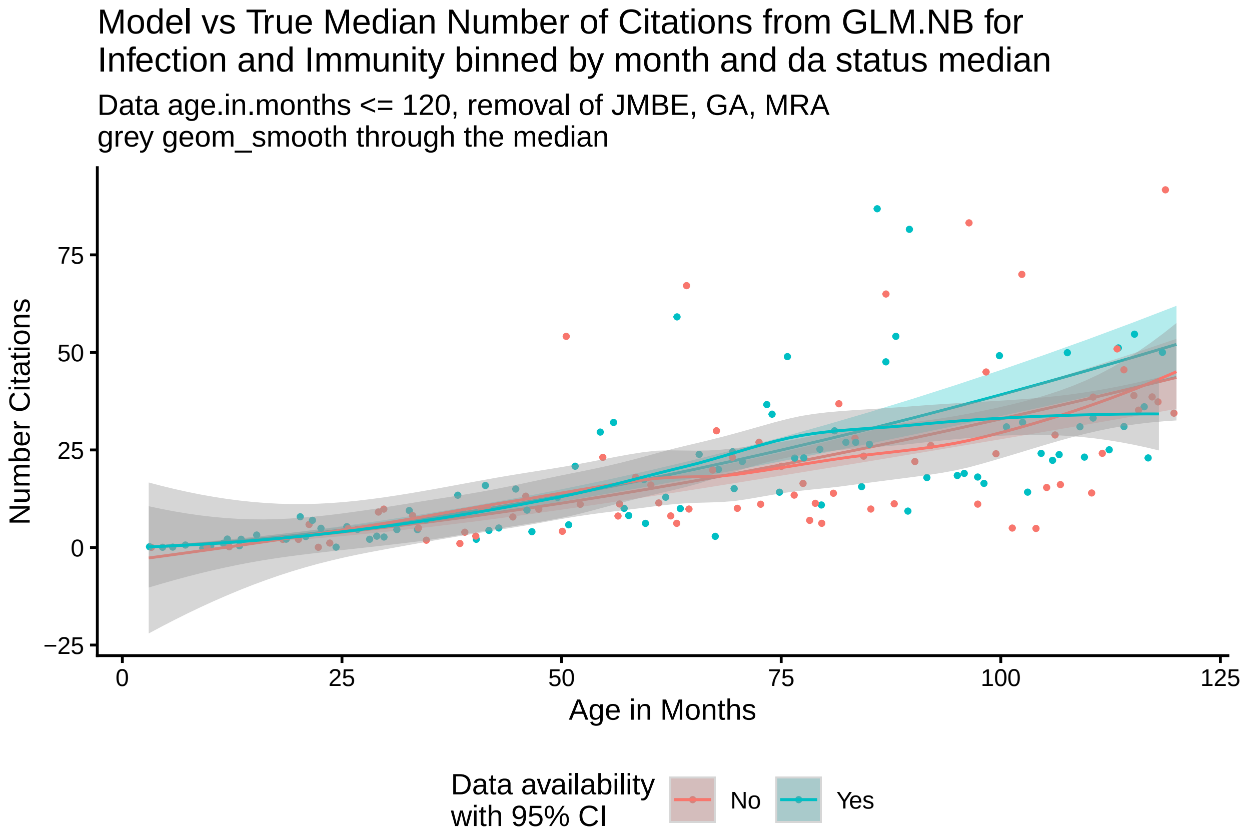
```
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



```
## ‘geom_smooth()‘ using method = ’loess’ and formula = ’y ~ x’
```



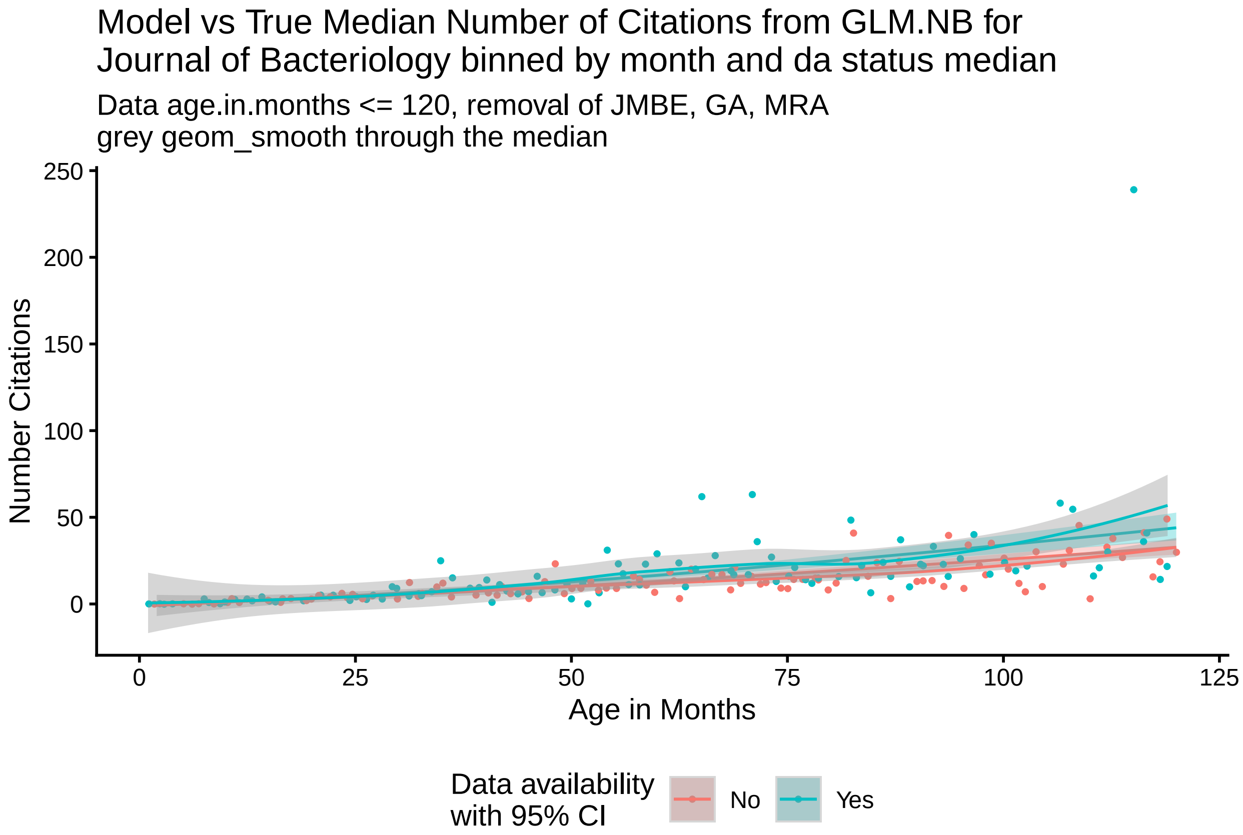
```
## ‘geom_smooth()‘ using method = ’loess’ and formula = ’y ~ x’
```



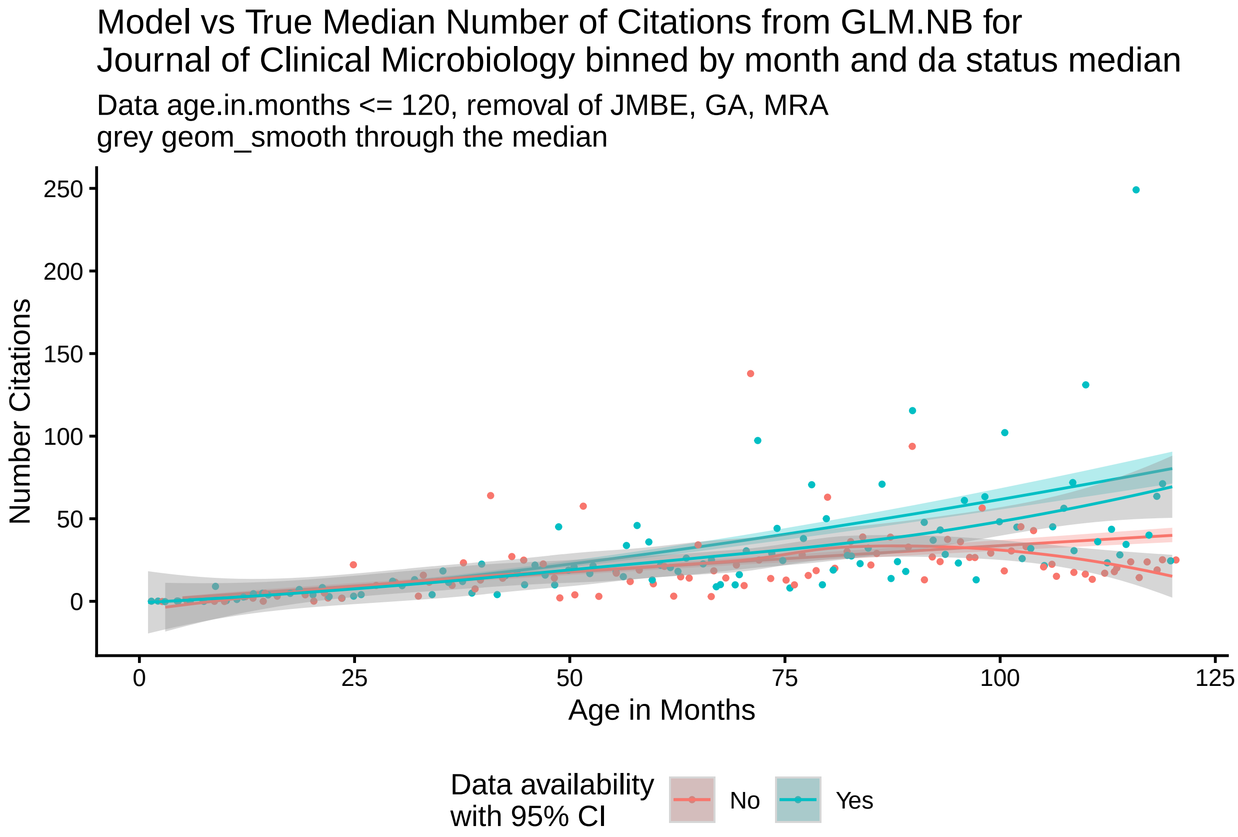
Model vs True Median Number of Citations from GLM.NB for Infection and Immunity binned by month and da status median

Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the median

```
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



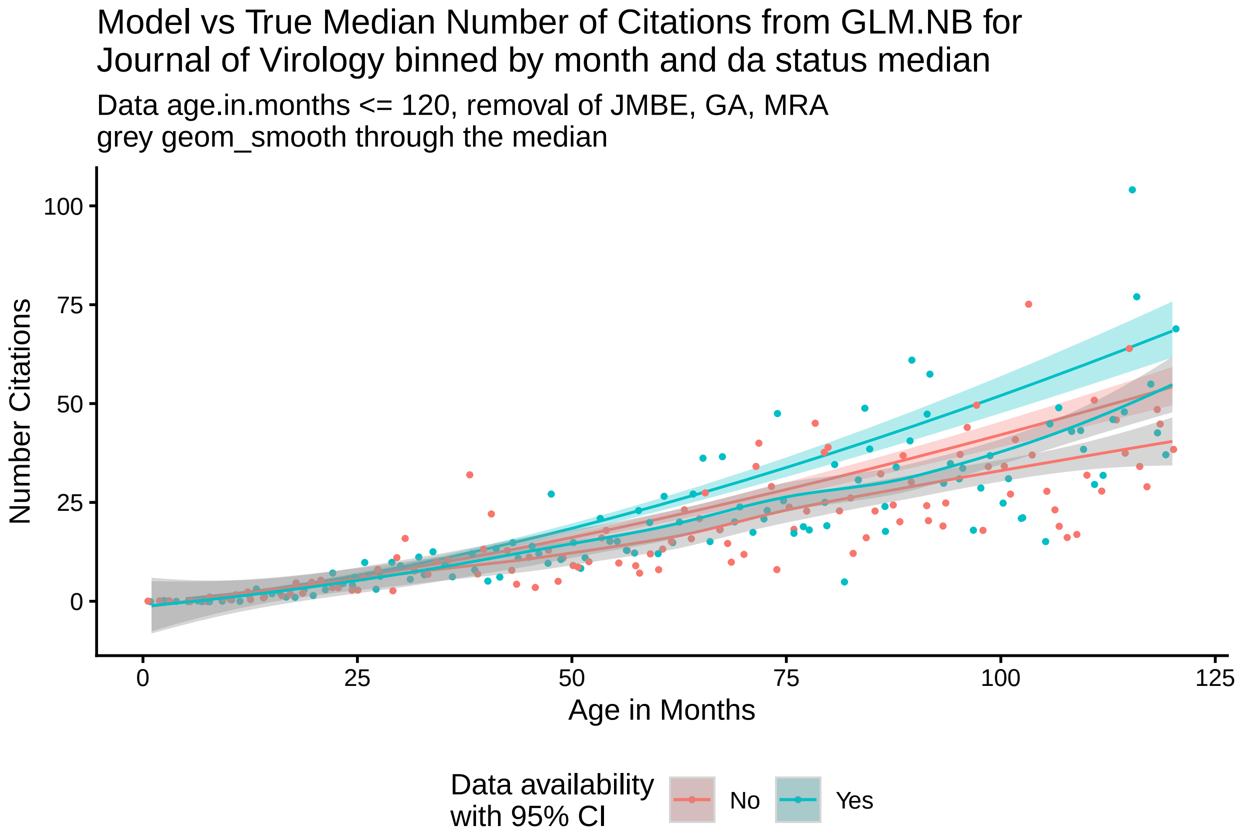
```
## ‘geom_smooth()‘ using method = ’loess’ and formula = ’y ~ x’
```



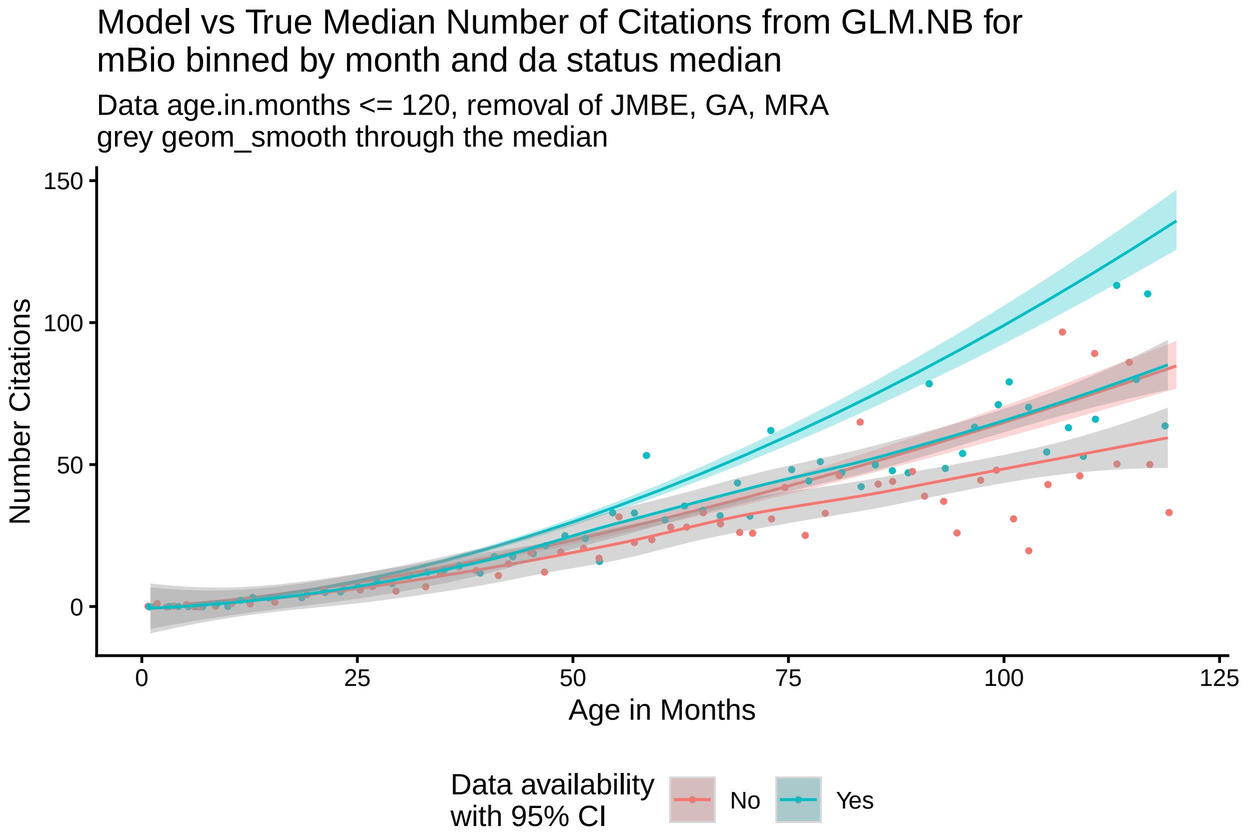
Model vs True Median Number of Citations from GLM.NB for
Journal of Clinical Microbiology binned by month and da status median

Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the median

```
## ‘geom_smooth()‘ using method = ’loess’ and formula = ’y ~ x’
```



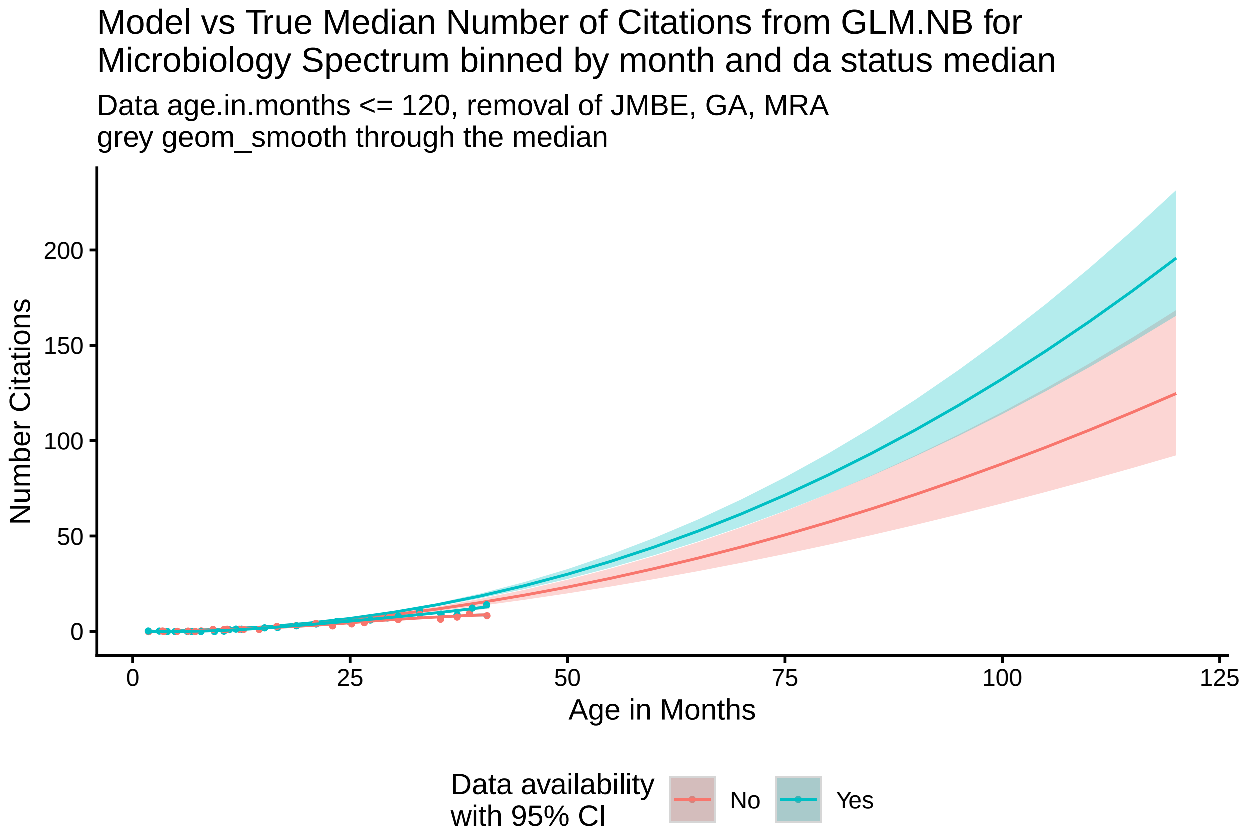
```
## 'geom_smooth()' using method = 'loess' and formula = 'y ~ x'
```



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
grey geom_smooth through the median

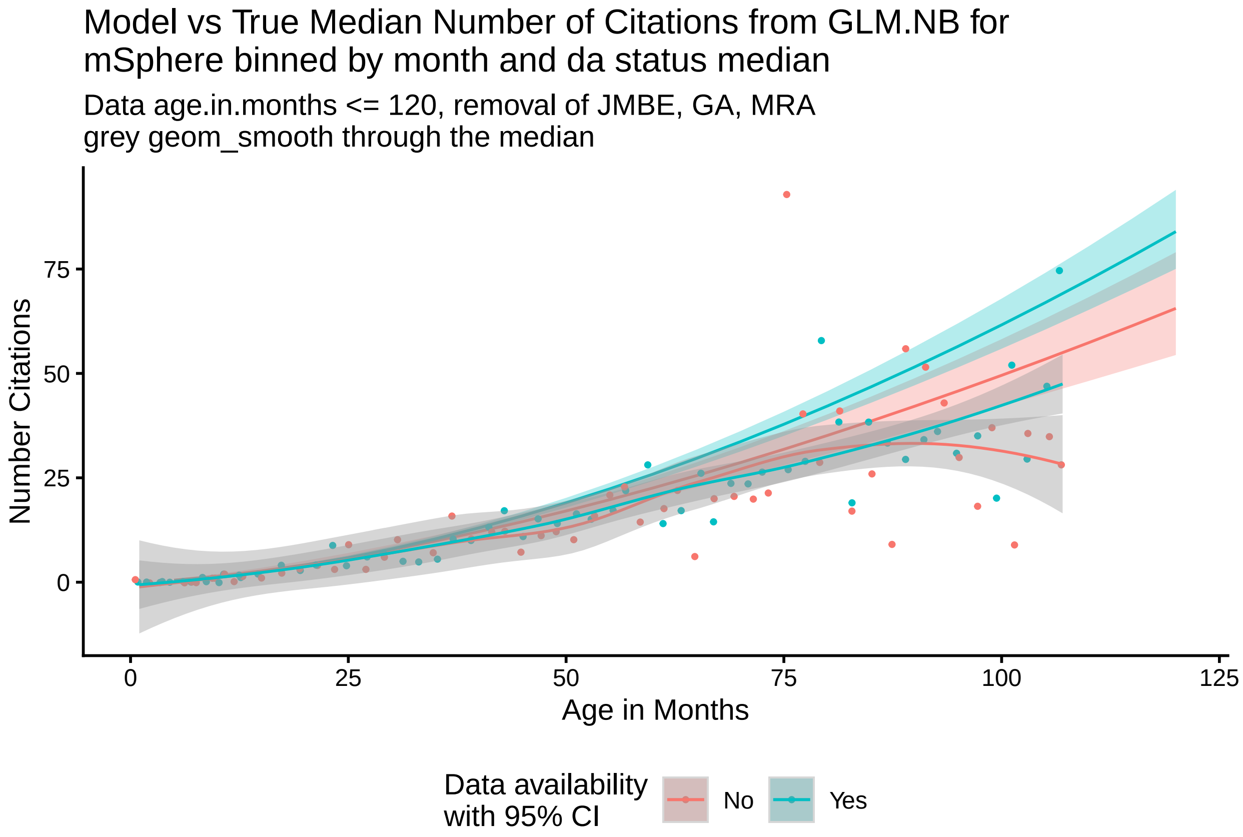
```
## 'geom_smooth()' using method = 'loess' and formula = 'y ~ x'
```



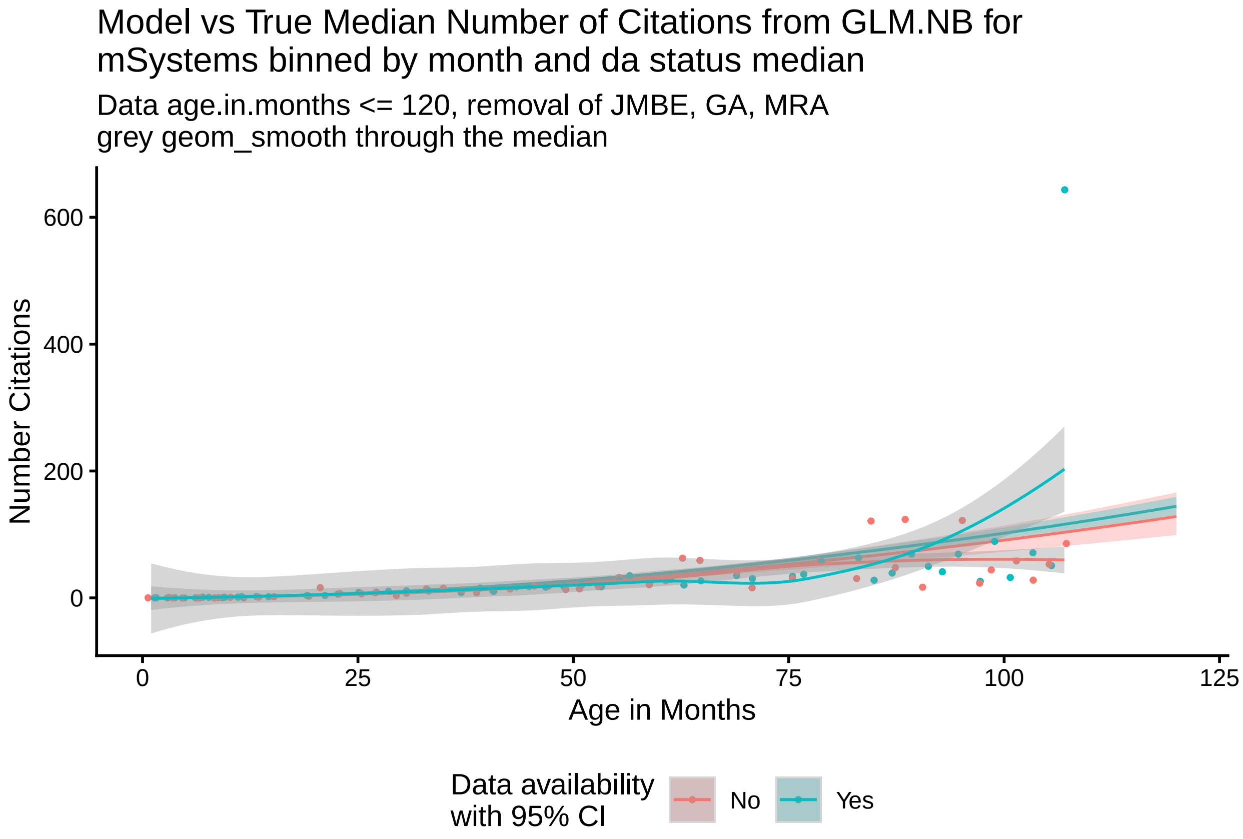
Model vs True Median Number of Citations from GLM.NB for Microbiology Spectrum binned by month and da status median

Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the median

```
## ‘geom_smooth()‘ using method = ’loess’ and formula = ’y ~ x’
```



```
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

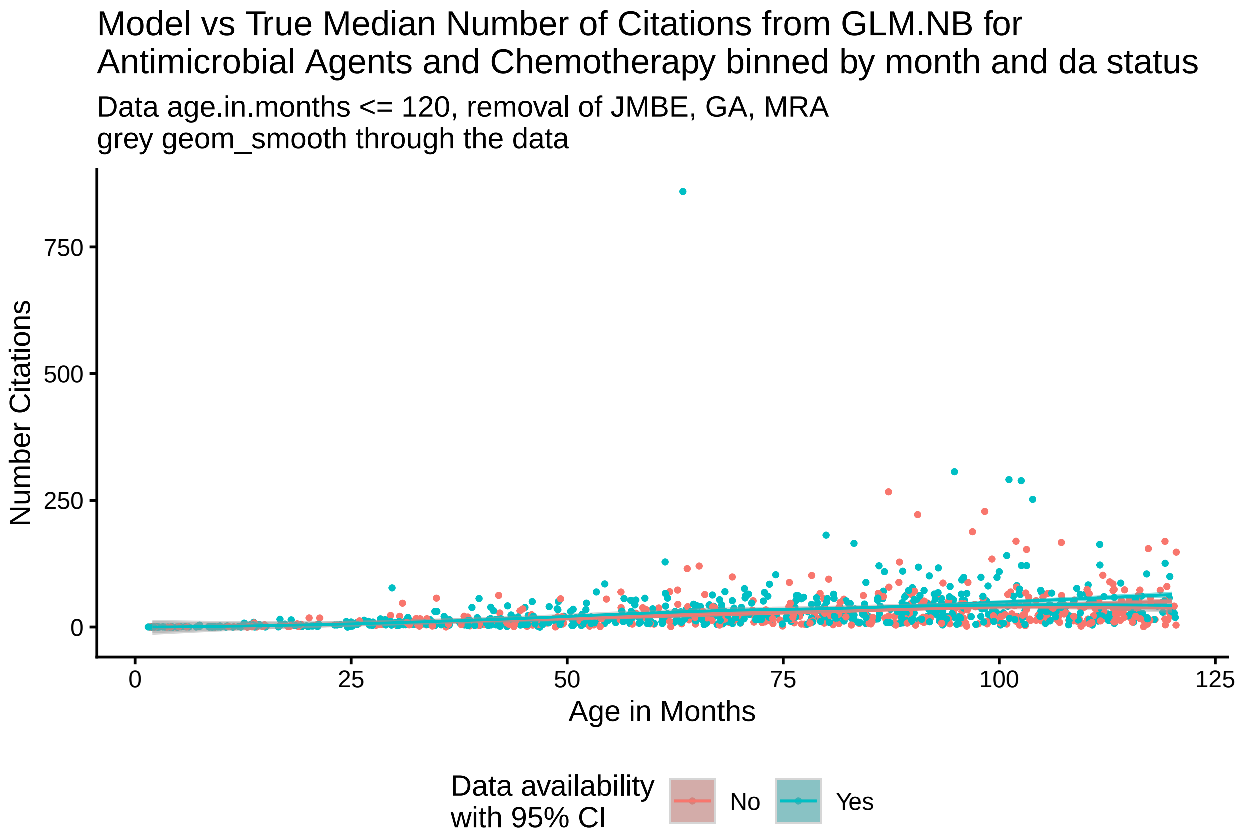

Model vs True Median Number of Citations from GLM.NB for mSystems binned by month and da status median

Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the median

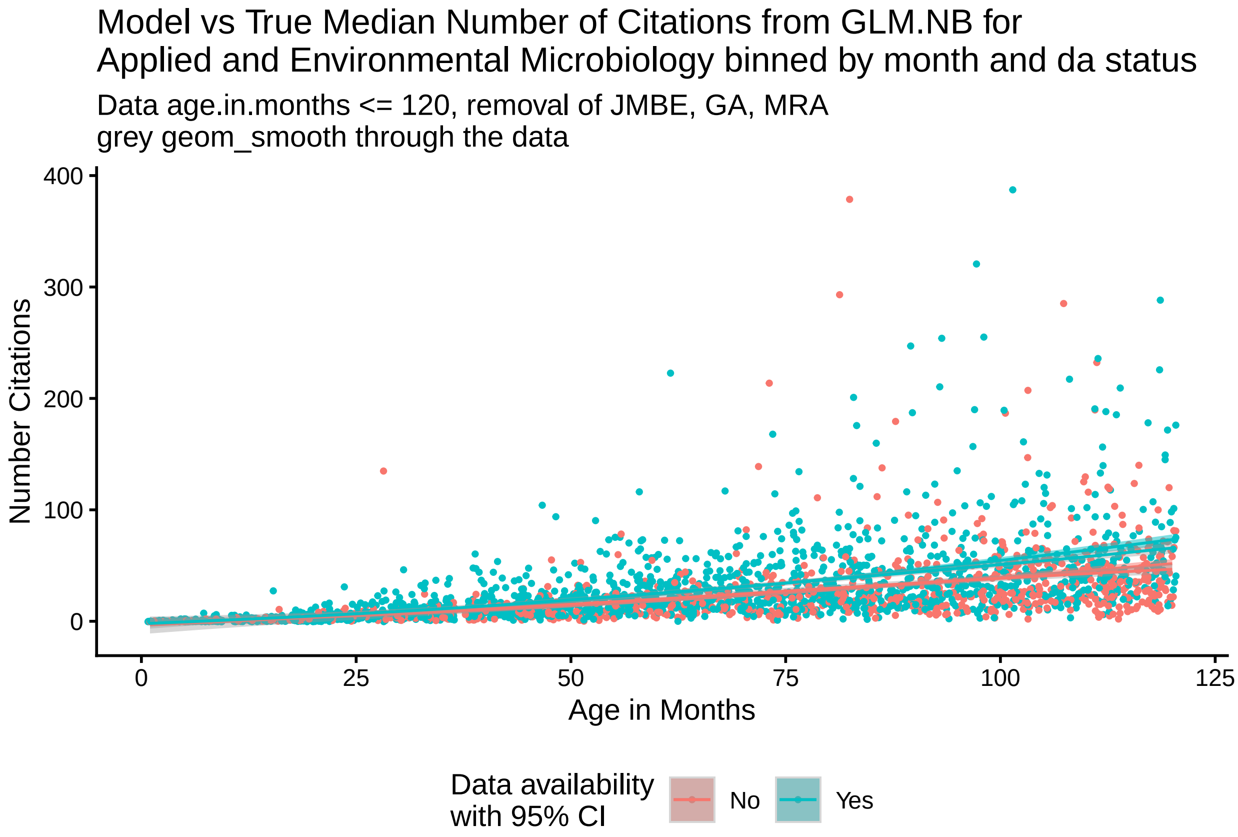
Using geom_smooth to fit a smoothed curve through the monthly data without taking the median on the dat

```
#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]])


  #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_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) +
   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 = 0.5) +

    geom_smooth(data = j_metadata, aes(x = age.in.months,
                                      y = is.referenced.by.count, color = da_factor), size = 0.5, alpha
   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\ngrey geom_smooth through the d
        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)
}
```

```
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```



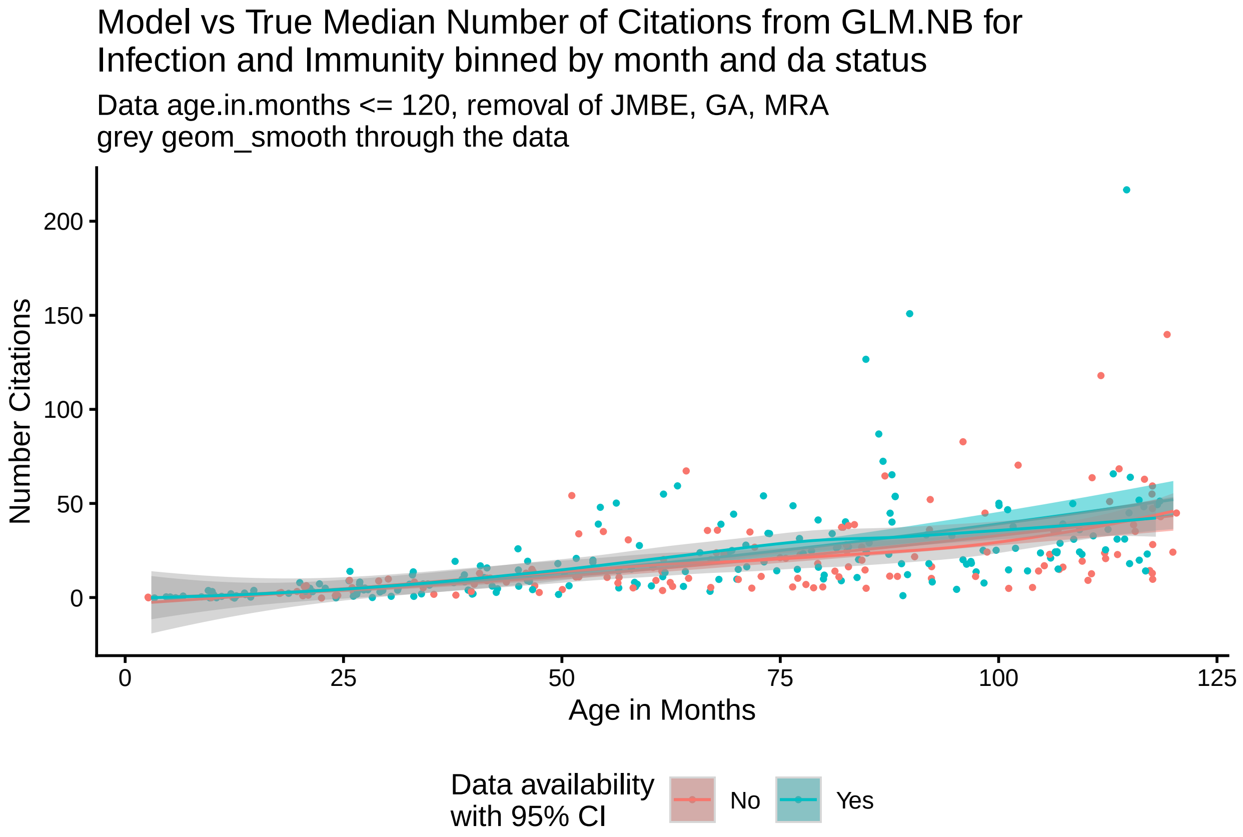
```
## `geom_smooth()` using method = 'gam' and formula = 'y ~ s(x, bs = "cs")'
```



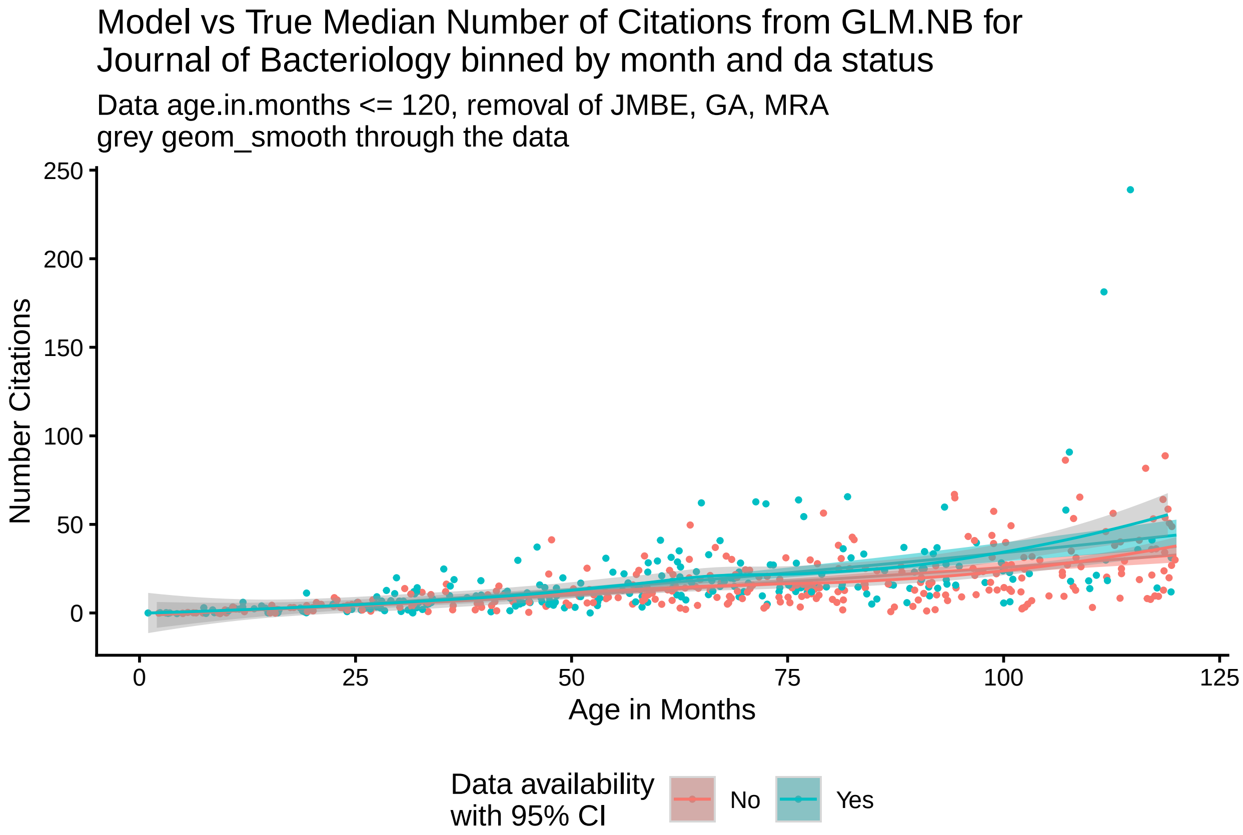
Model vs True Median Number of Citations from GLM.NB for
Applied and Environmental Microbiology binned by month and da status

Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the data

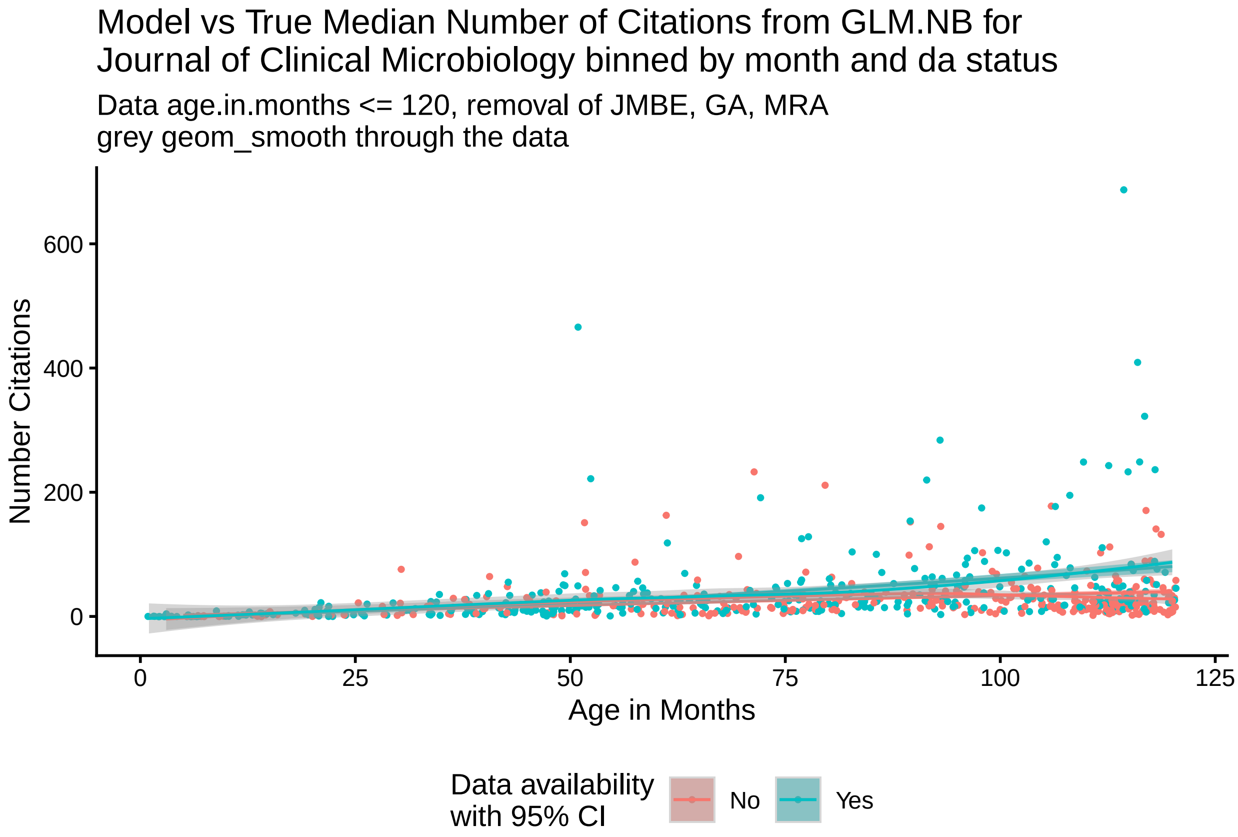
```
## 'geom_smooth()' using method = 'loess' and formula = 'y ~ x'
```



```
## ‘geom_smooth()‘ using method = ’loess’ and formula = ’y ~ x’
```



```
## 'geom_smooth()' using method = 'loess' and formula = 'y ~ x'
```

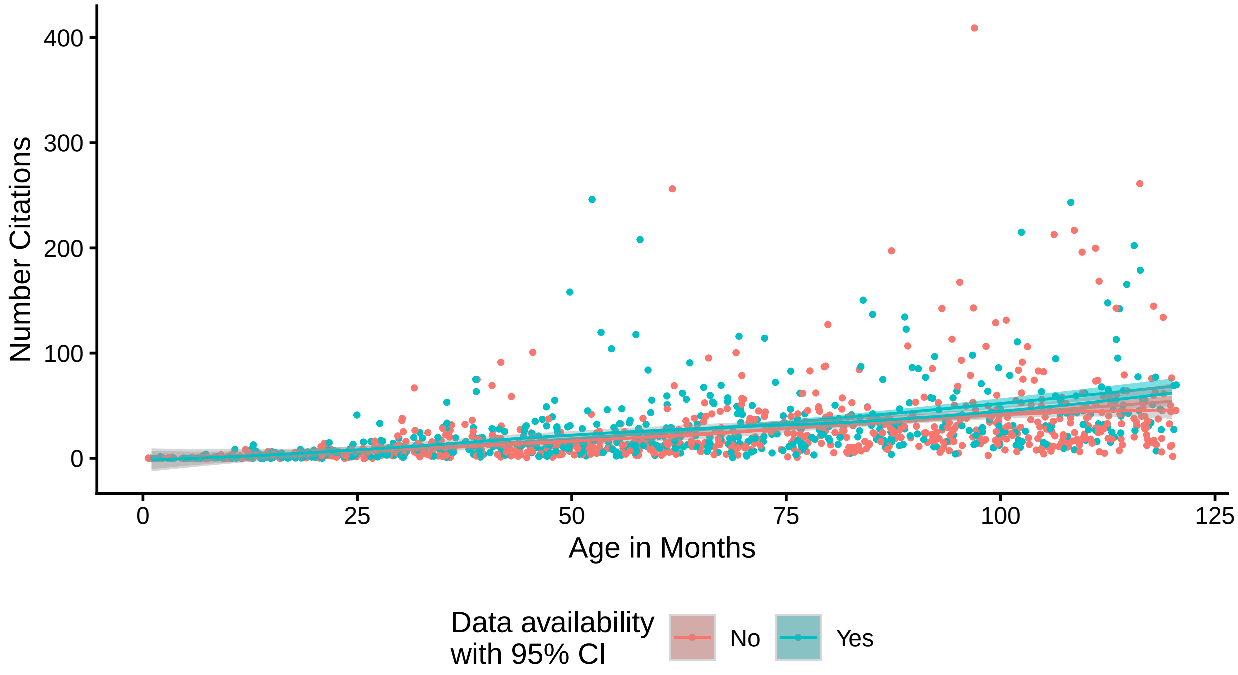

Model vs True Median Number of Citations from GLM.NB for Journal of Clinical Microbiology binned by month and da status

Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the data

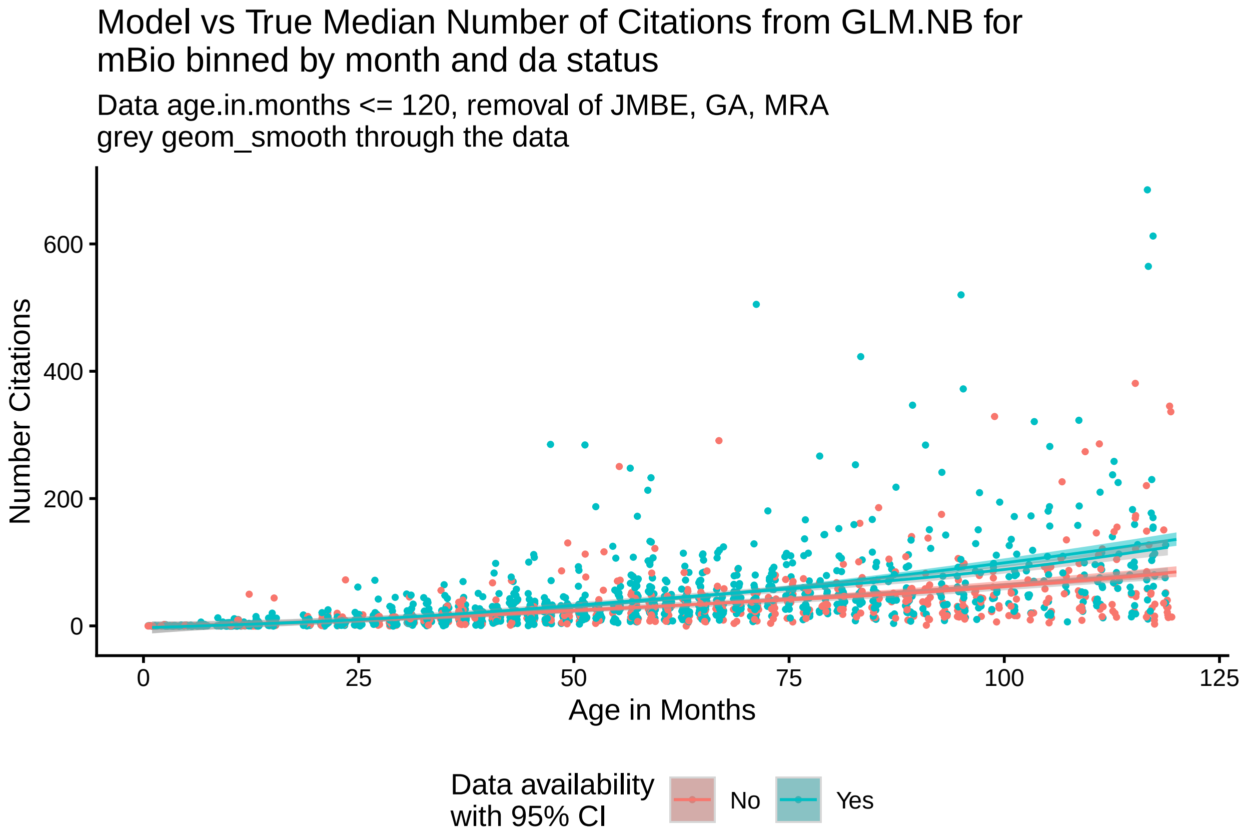
```
## 'geom_smooth()' using method = 'loess' and formula = 'y ~ x'
```

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

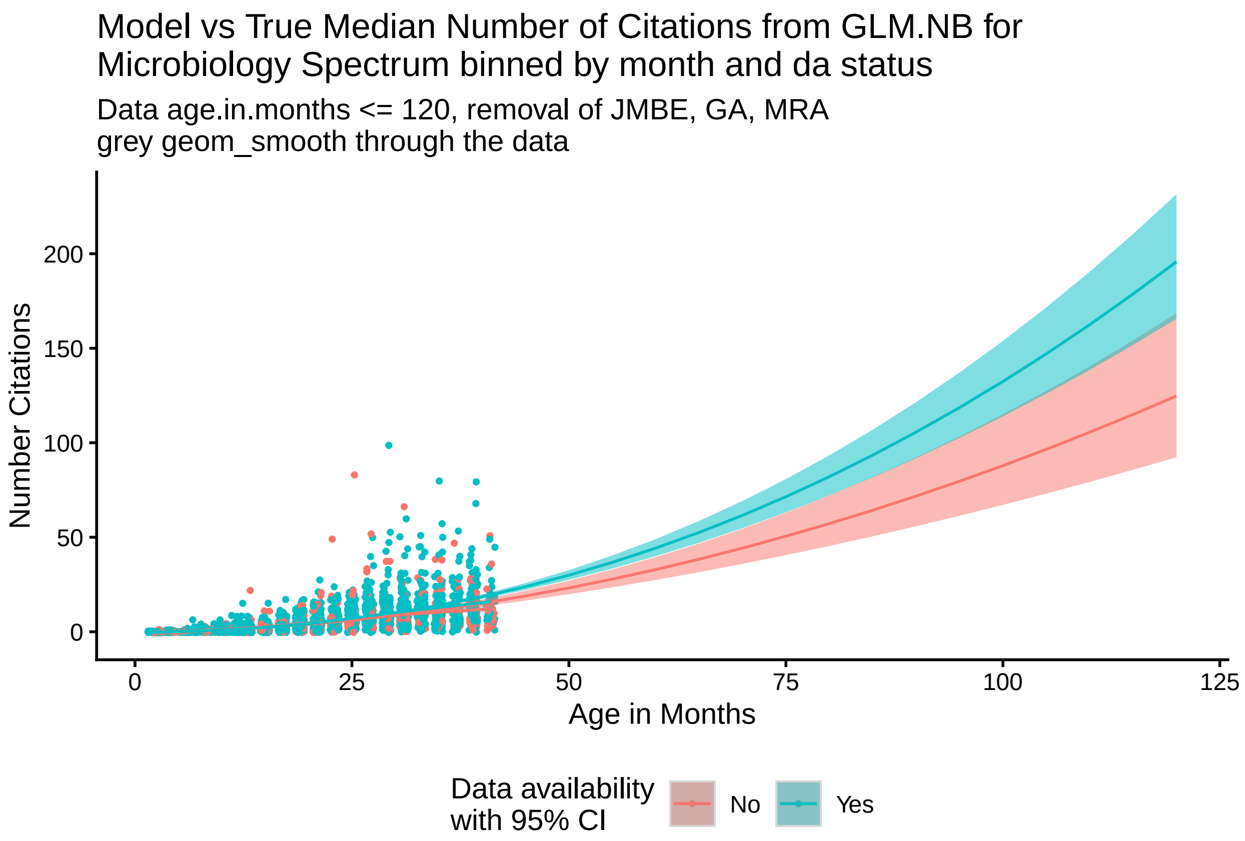
Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the data



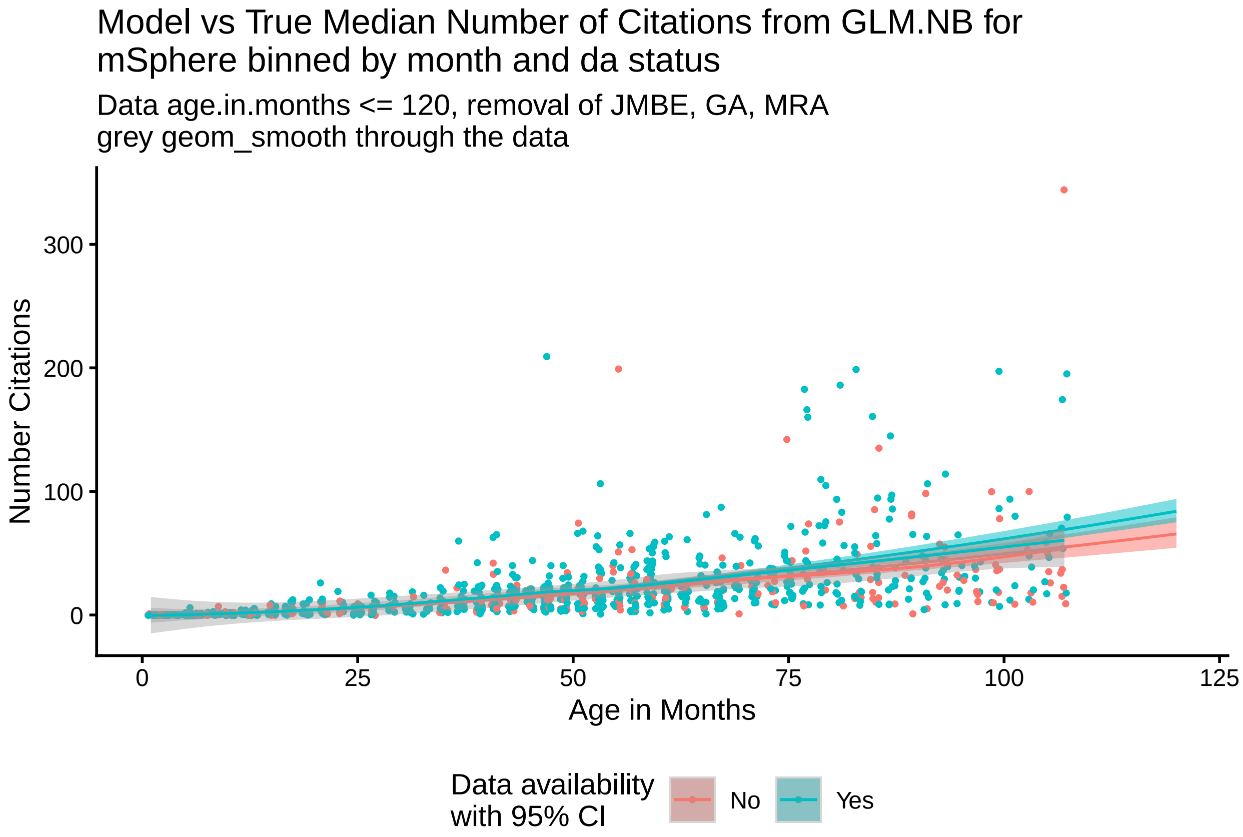
```
## `geom_smooth()` using method = 'gam' and formula = 'y ~ s(x, bs = "cs")'
```



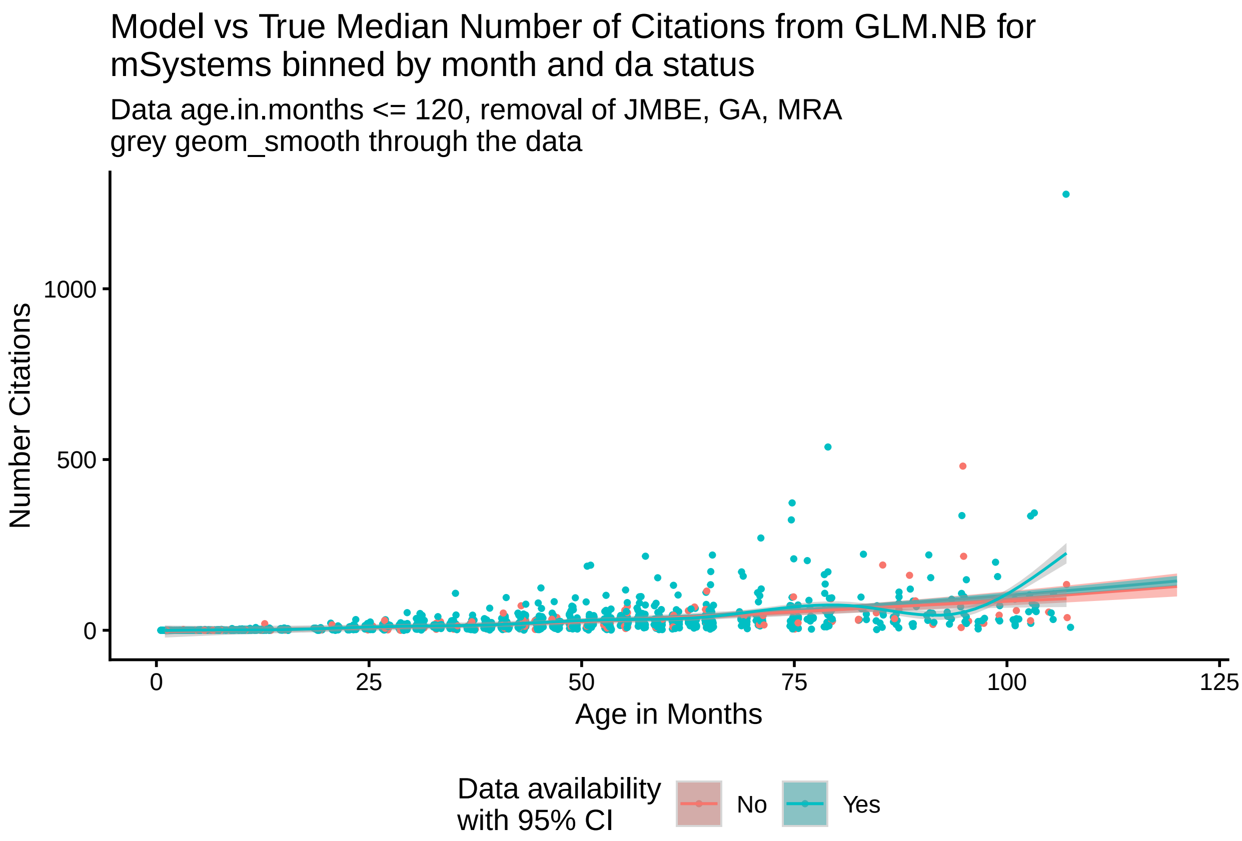
```
## ‘geom_smooth()‘ using method = ’gam’ and formula = ’y ~ s(x, bs = "cs")’
```



```
## ‘geom_smooth()‘ using method = ’loess’ and formula = ’y ~ x’
```



```
## ‘geom_smooth()‘ using method = ’gam’ and formula = ’y ~ s(x, bs = "cs")’
```



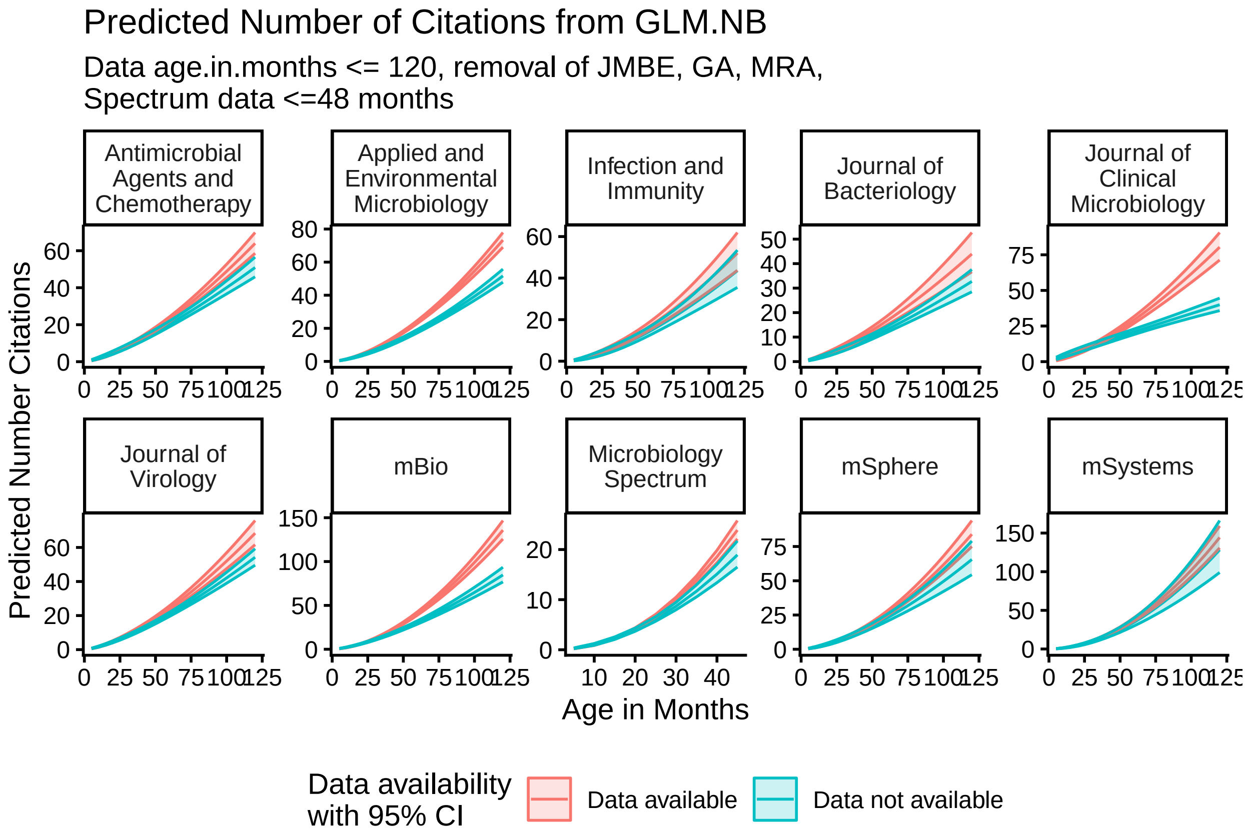
Updating the NB prediction for Microbiology Spectrum to only show predictions for 4 years

- I used free_x and free_y axes so that Spectrum more closely resembled the graphs for the others, but let me know if you want them fixed instead.

```
#get data from 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)  %>%
     mutate(age.in.months = as.numeric(as.character(age.in.months)))

#filter data from model to spectrum for 4 years (age.in.months <= 48)
 spec_remove <-
   p_10 %>%
    mutate(age.in.months = as.numeric(as.character(age.in.months))) %>%
    filter(container.title == "Microbiology Spectrum" & age.in.months >= 48)

 p_10_spec_trunc <- anti_join(p_10, spec_remove)
```

```
## Joining with `by = join_by(x, predicted, std.error, conf.low, conf.high, group,
## facet, group_col, da_factor, predicted_citations, age.in.months,
## container.title)`
```

```
#re-create figure with free axes

predicted_plot_spec <-
    ggplot(data =  p_10_spec_trunc ,
           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" ) +
   labs(title = "Predicted Number of Citations from GLM.NB",
        subtitle = "Data age.in.months <= 120, removal of JMBE, GA, MRA,\nSpectrum data <=48 months",
        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_spec
```


Predicted Number of Citations from GLM.NB
Data age.in.months <= 120, removal of JMBE, GA, MRA,
Spectrum data <=48 months
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
0
20
40
60
80
10
30
50
25
75
100
150
0 25 50 75 100 125
10 20 30 40
Predicted Number Citations
Age in Months
Data availability with 95% CI
Data available
Data not available