

# 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 <= 120)

#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" )

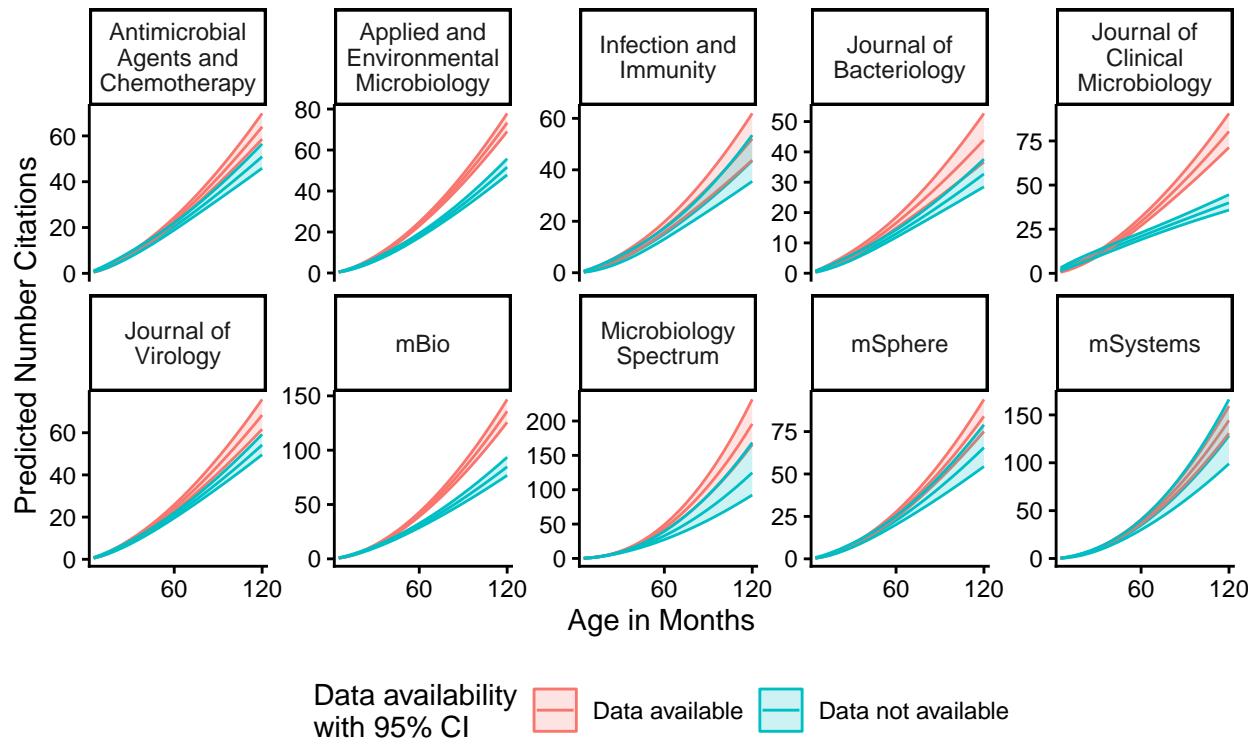
predicted_plot_fixed <-
  ggplot(data = p_10, mapping = aes(x = as.numeric(age.in.months), y = predicted_citations,
                                      color = da_factor)) +
  geom_line(aes(x = age.in.months, y = predicted_citations, group = da_factor)) +
  geom_ribbon(mapping = aes(ymin = conf.low, 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 Number of Citations from GLM.NB

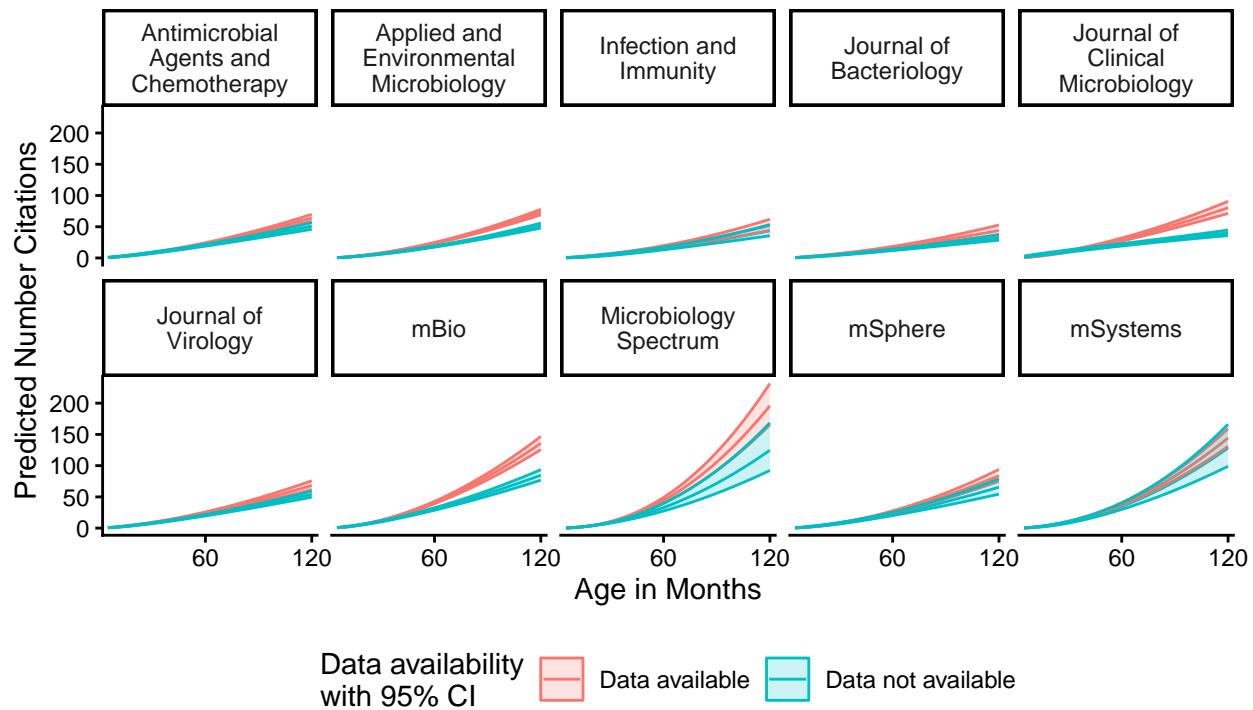
Data age.in.months <= 120, removal of JMBE, GA, MRA



predicted\_plot\_fixed

## Predicted Number of Citations from GLM.NB

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



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 <-
```

```

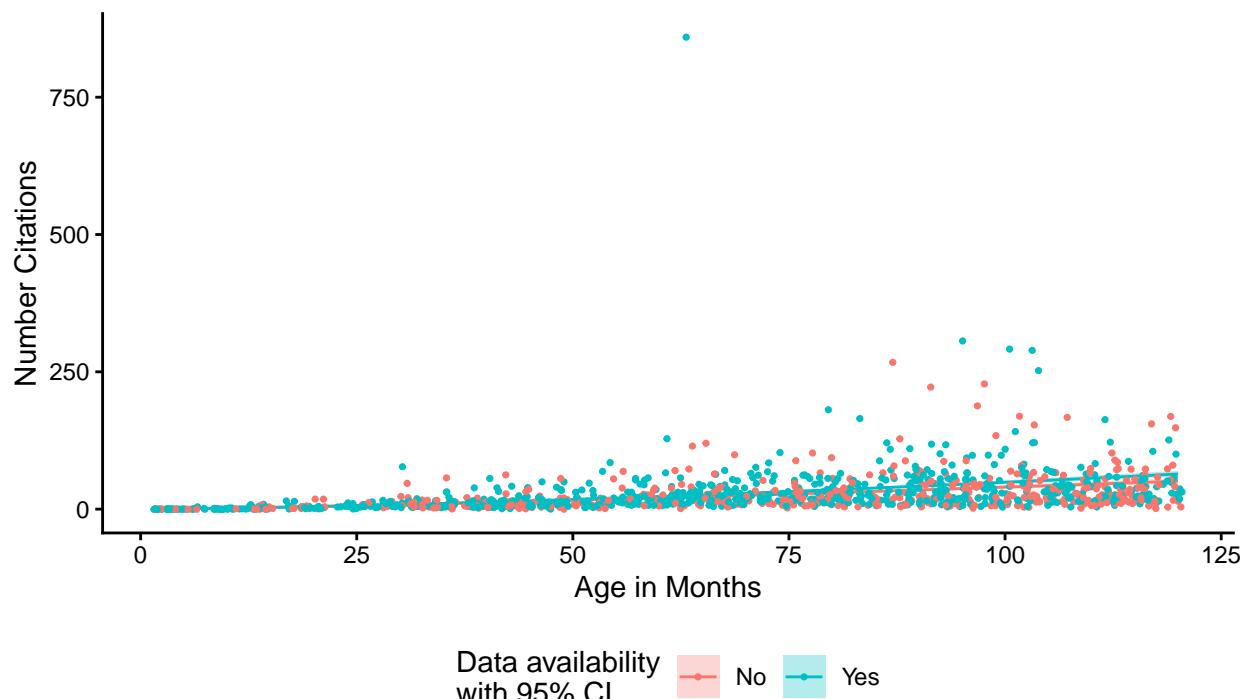
ggplot() +
  # mapping = aes(x = age.in.months, y = predicted_citations,
  #                 color = da_factor)) +
  geom_line(data = model_data, aes(x = age.in.months, y = predicted_citations, group = da_factor, color = da_factor),
  geom_ribbon(data = model_data, mapping = aes(x = age.in.months, y = predicted_citations, 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[1]),
  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)
}

```

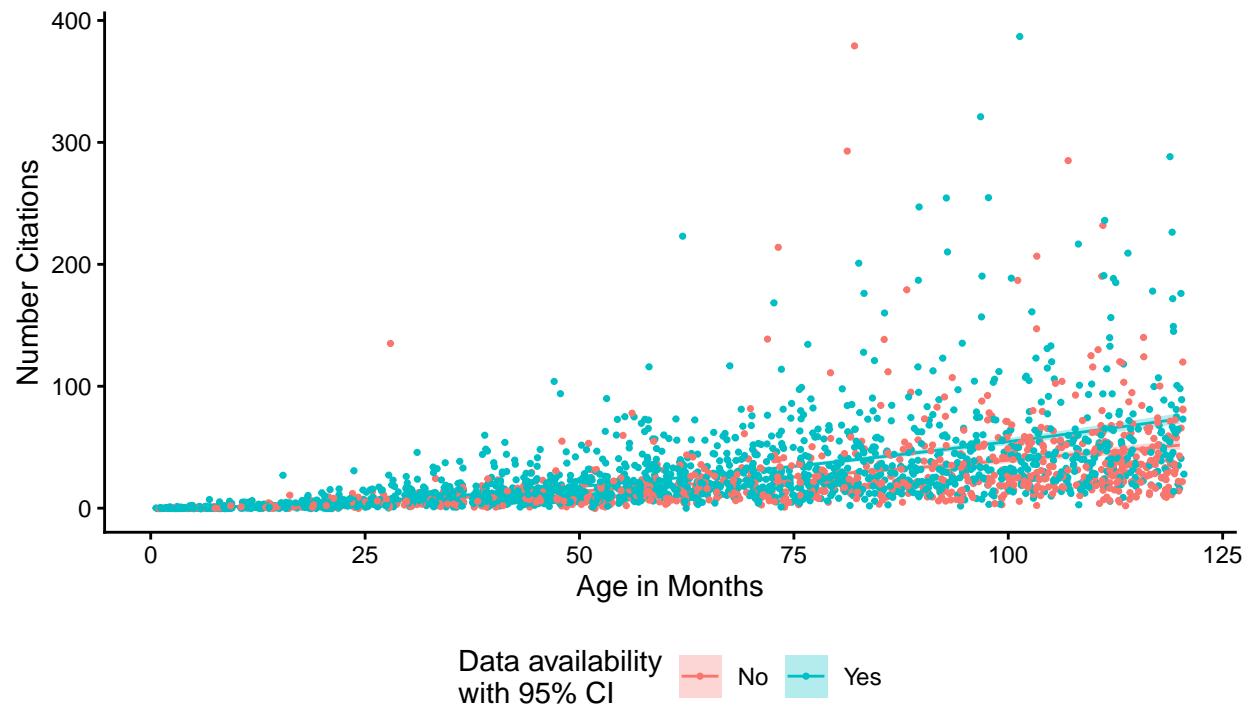
## Model vs True Number of Citations from GLM.NB for Antimicrobial Agents and Chemotherapy

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



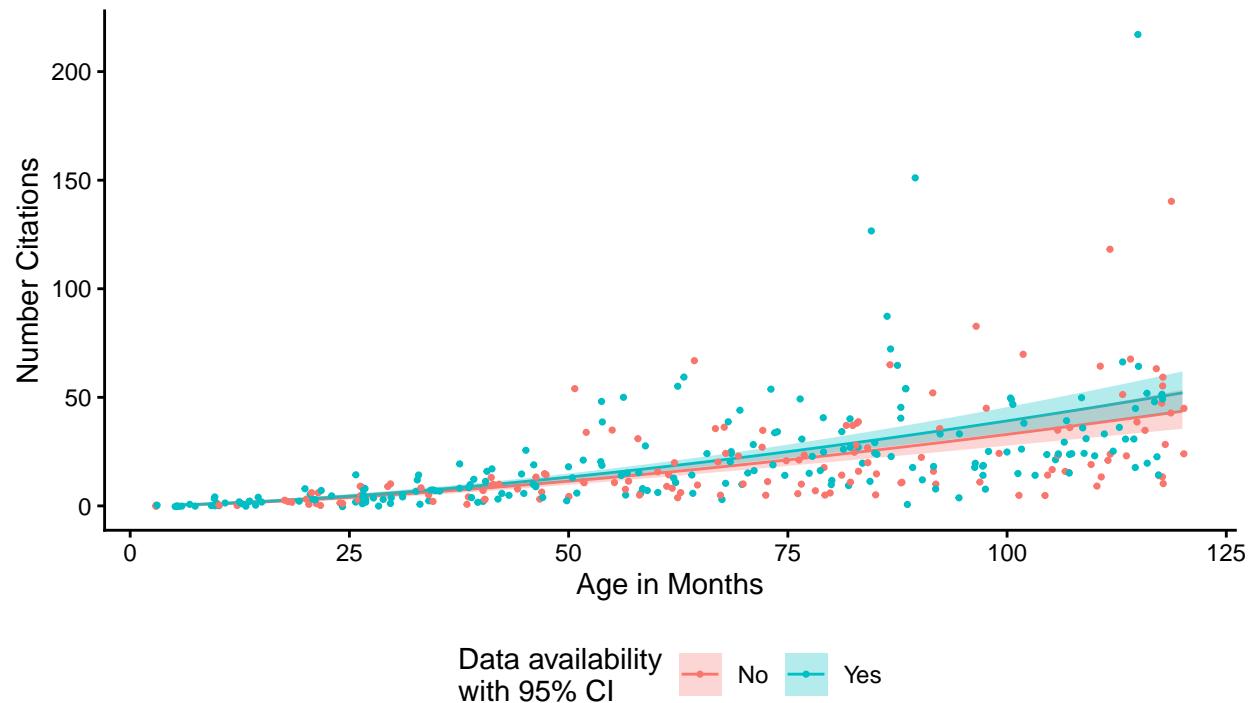
## Model vs True Number of Citations from GLM.NB for Applied and Environmental Microbiology

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



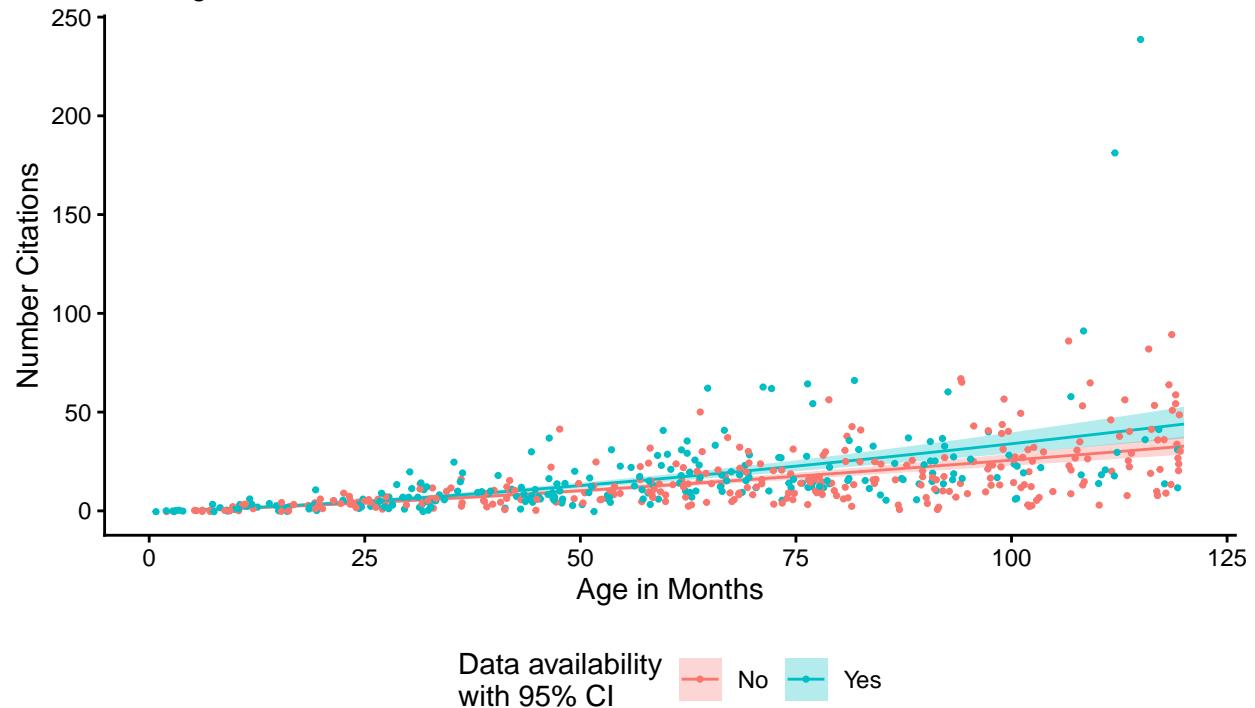
## Model vs True Number of Citations from GLM.NB for Infection and Immunity

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



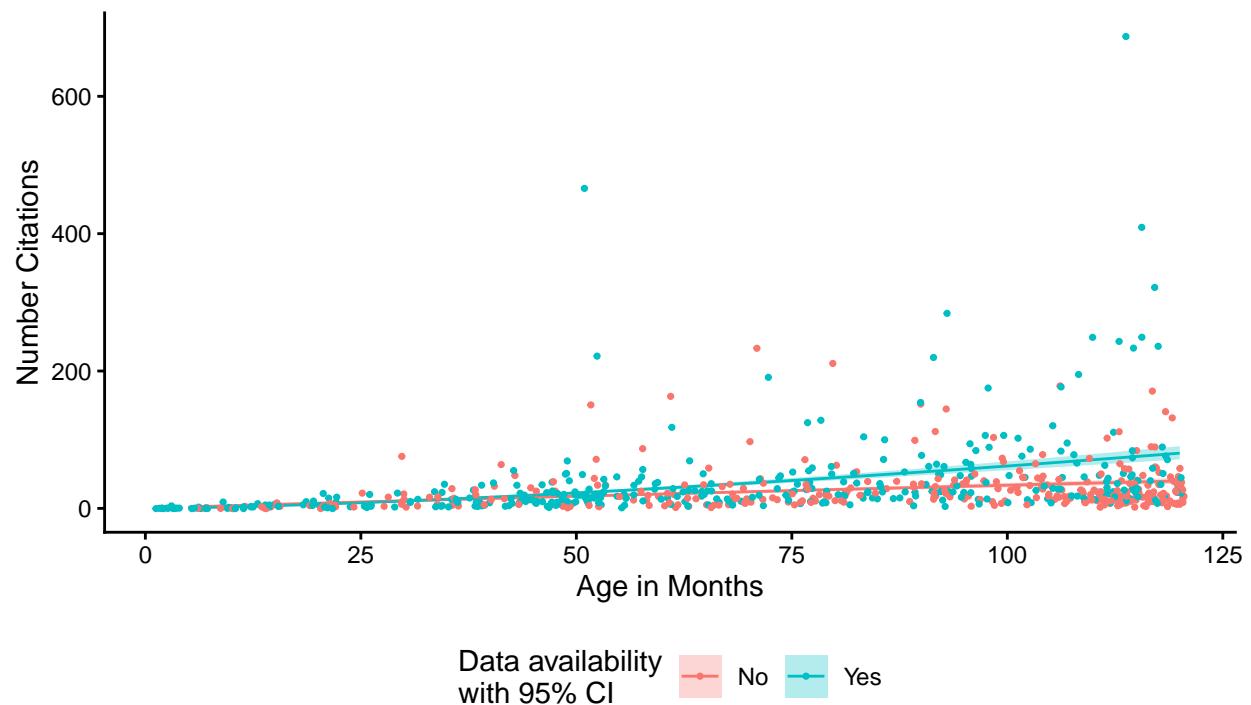
## Model vs True Number of Citations from GLM.NB for Journal of Bacteriology

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



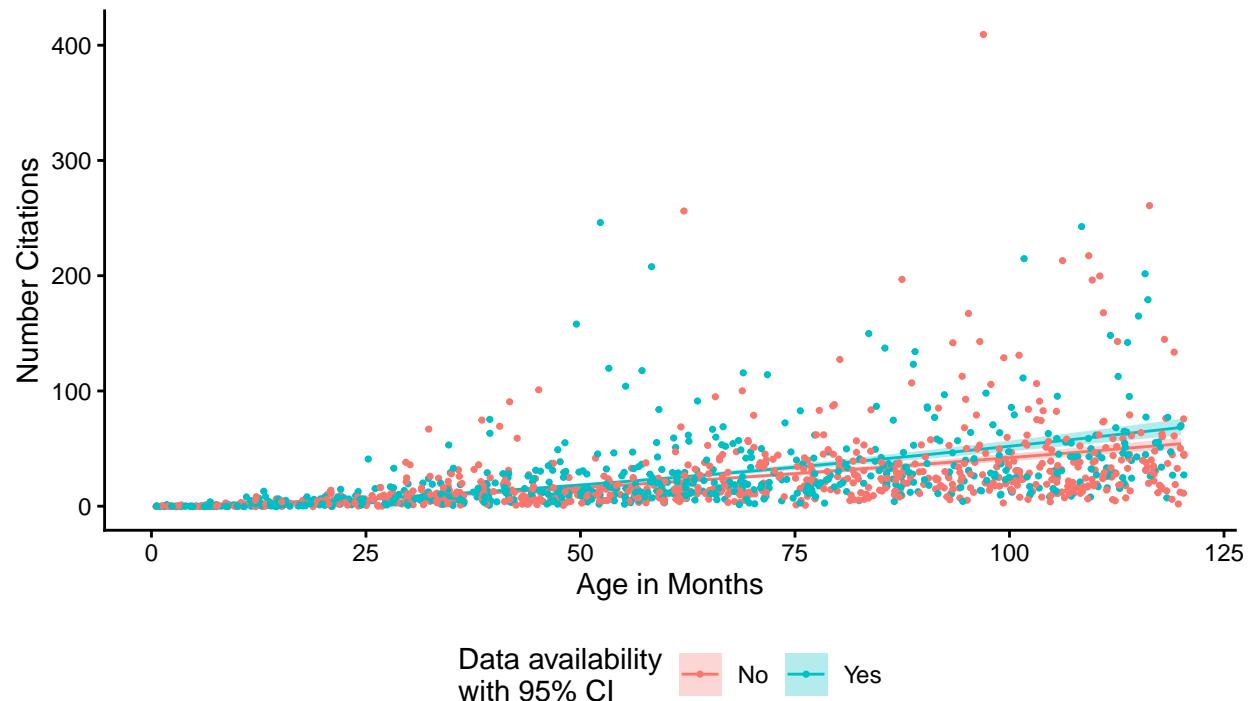
Model vs True Number of Citations from GLM.NB for  
Journal of Clinical Microbiology

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



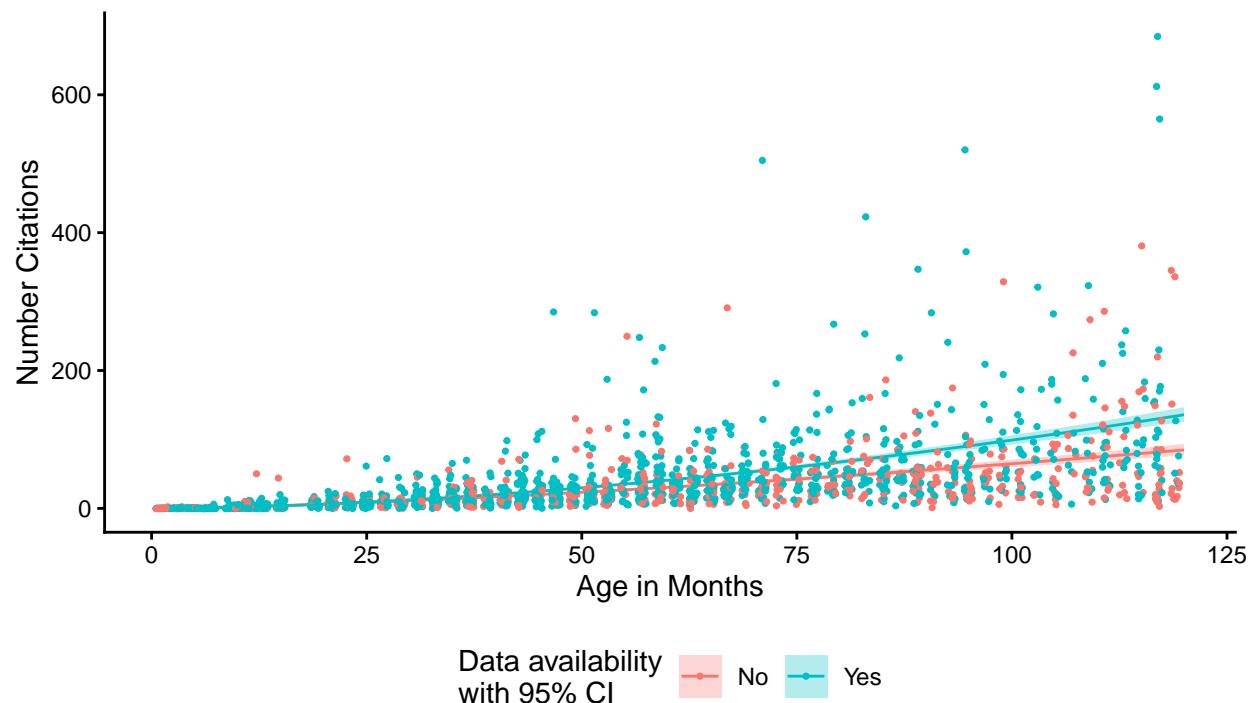
## Model vs True Number of Citations from GLM.NB for Journal of Virology

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



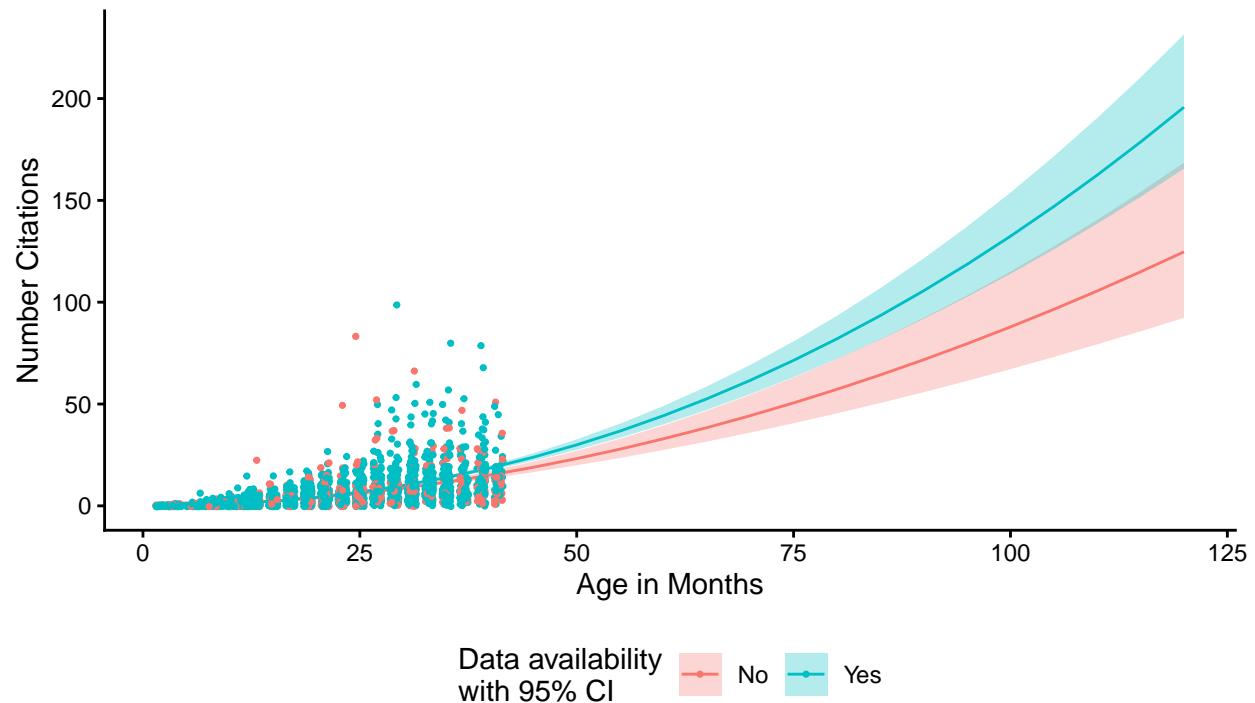
## Model vs True Number of Citations from GLM.NB for mBio

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



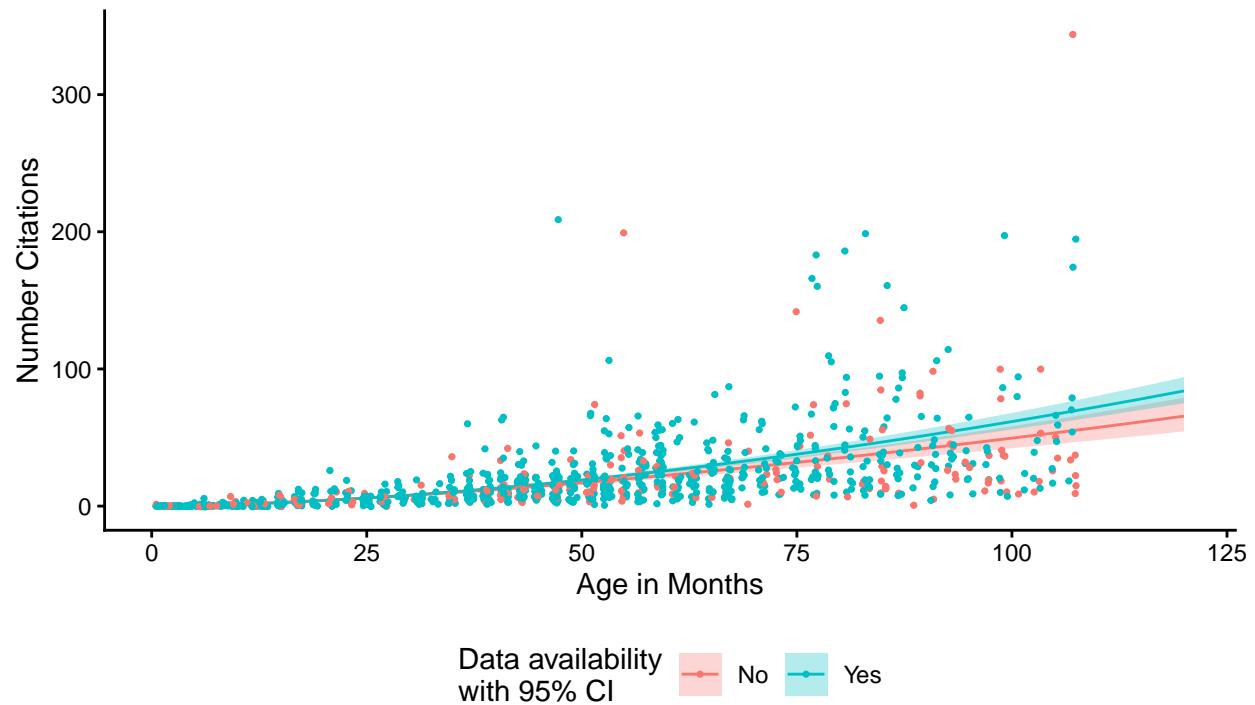
## Model vs True Number of Citations from GLM.NB for Microbiology Spectrum

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



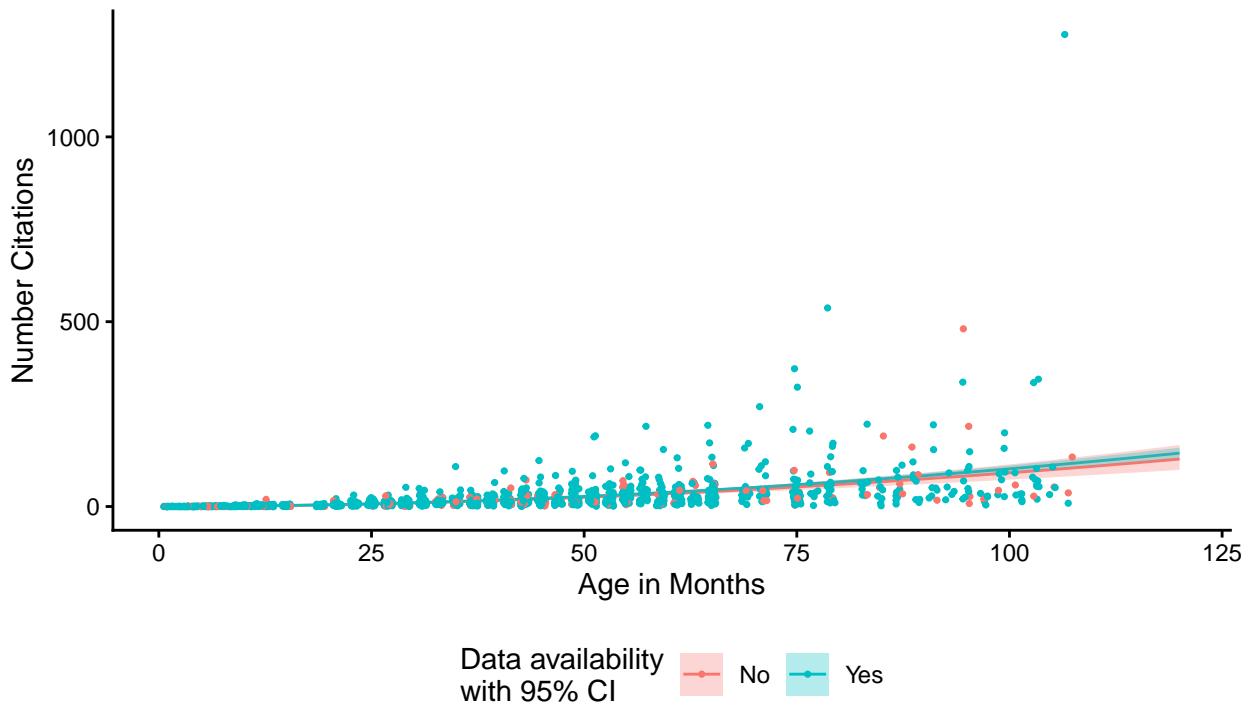
## Model vs True Number of Citations from GLM.NB for mSphere

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



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

Data age.in.months <= 120, removal of JMME, 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 <= 120) %>%
  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_citation
age.in.months = .\$group, container.title = .\$facet)

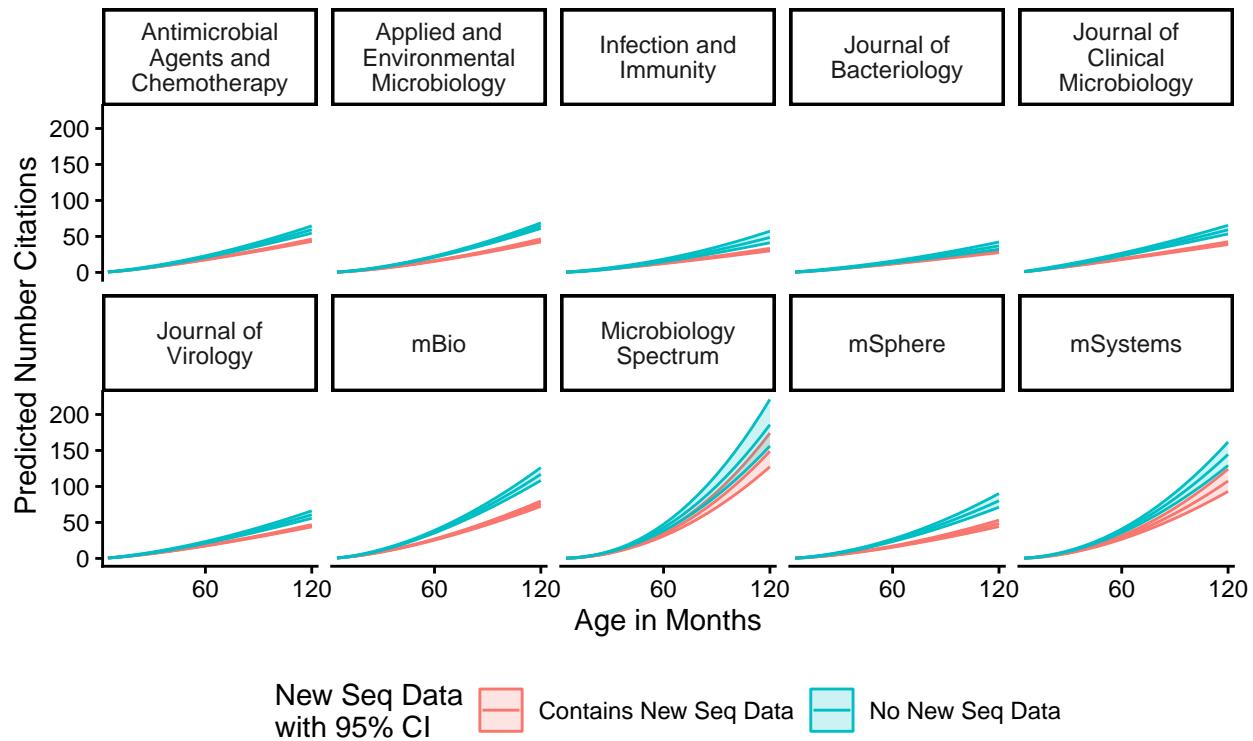
predicted_plot_nsd <-
  ggplot(data = p_nsd, mapping = aes(x = as.numeric(age.in.months), y = predicted_citations,
                                      color = nsd_factor)) +
  geom_line(aes(x = age.in.months, y = predicted_citations, group = nsd_factor)) +
  geom_ribbon(mapping = aes(ymin = conf.low, 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



```
## 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://doi.org/10.1128/spectrum~ spectrum
## 2 Data/html/10.1128/~ Yes  Yes  https://doi.org/10.1128/spectrum~ spectrum
## 3 Data/html/10.1128/~ Yes  Yes  https://doi.org/10.1128/spectrum~ spectrum
## 4 Data/html/10.1128/~ Yes  Yes  https://doi.org/10.1128/spectrum~ spectrum
## 5 Data/html/10.1128/~ Yes  Yes  https://doi.org/10.1128/spectrum~ spectrum
## 6 Data/html/10.1128/~ Yes  Yes  https://doi.org/10.1128/spectrum~ spectrum
## 7 Data/html/10.1128/~ Yes  Yes  https://doi.org/10.1128/spectrum~ spectrum
## 8 Data/html/10.1128/~ No   Yes  https://doi.org/10.1128/spectrum~ spectrum
## 9 Data/html/10.1128/~ Yes  Yes  https://doi.org/10.1128/spectrum~ spectrum
## 10 Data/html/10.1128/~ Yes  Yes  https://doi.org/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"))

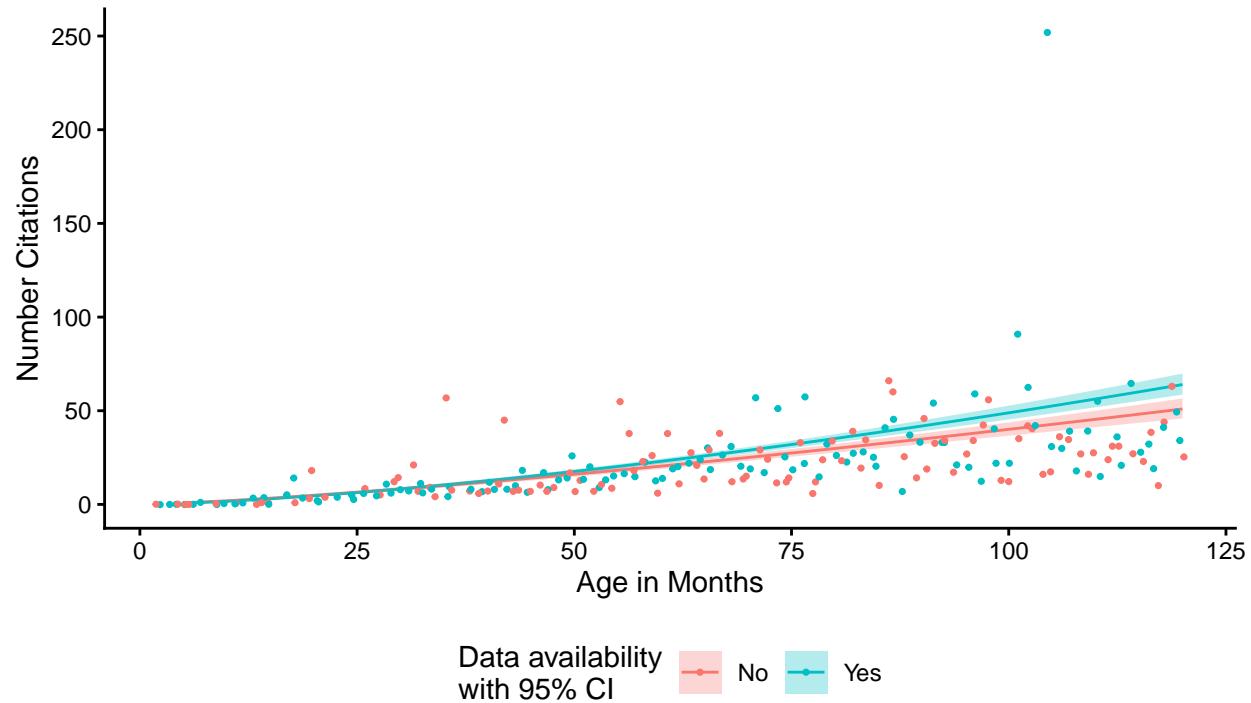
  #filter p_10
  model_data <- p_10 %>%
    filter(container.title == journals$container.title[[j]]) %>%
    mutate(da_factor = ifelse(da_factor == "Data available", "Yes", "No"),
          age.in.months = as.numeric(as.character(age.in.months)))

  #make plot
  plot <-
  ggplot() +
    geom_line(data = model_data, aes(x = age.in.months, y = predicted_citations, group = da_factor, color = da_factor),
              geom_ribbon(data = model_data, mapping = aes(x = age.in.months, y = predicted_citations, 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.title[j]),
         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" )

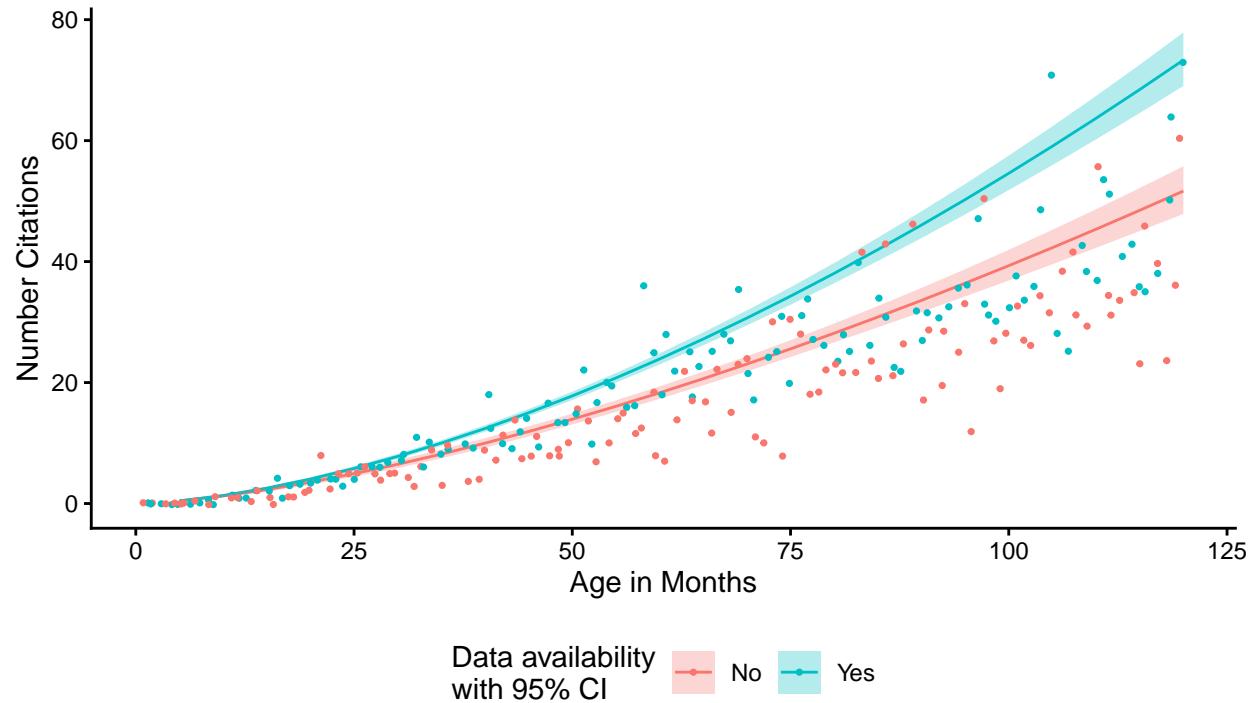
  print(plot)
}

```

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

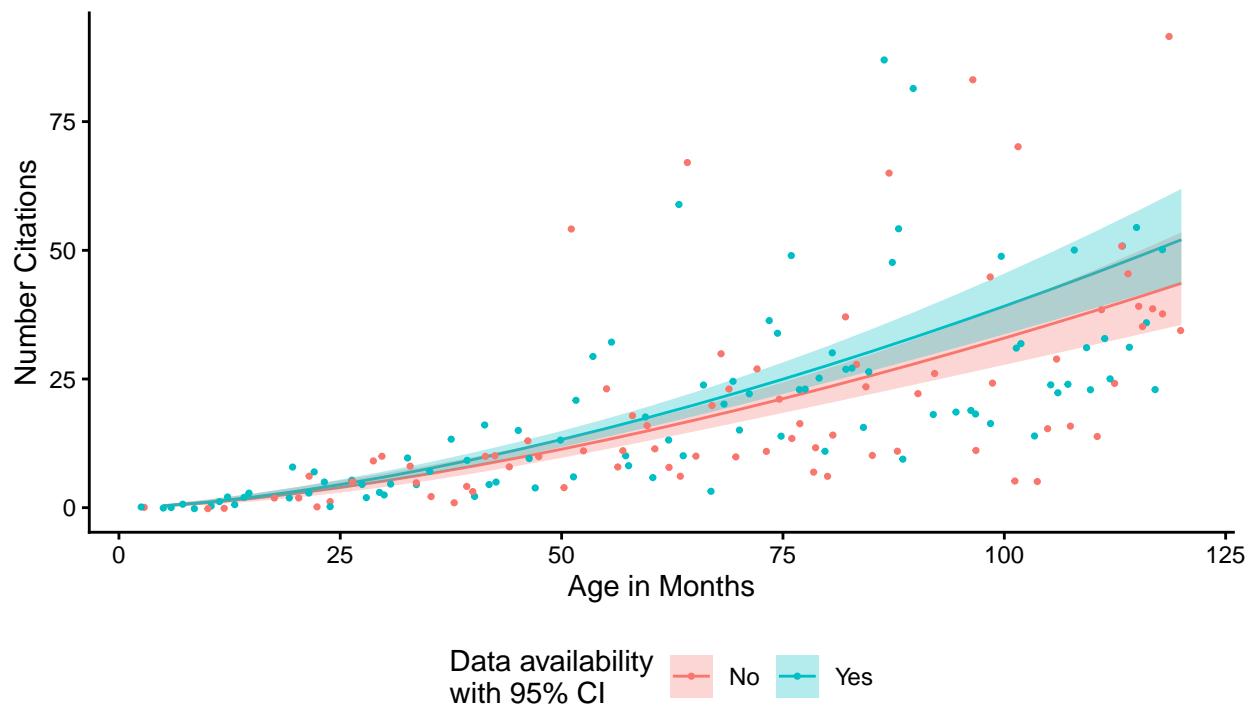


Model vs True Median Number of Citations from GLM.NB for Applied and Environmental Microbiology binned by month and da status me  
 Data age.in.months <= 120, removal of JMBE, GA, MRA

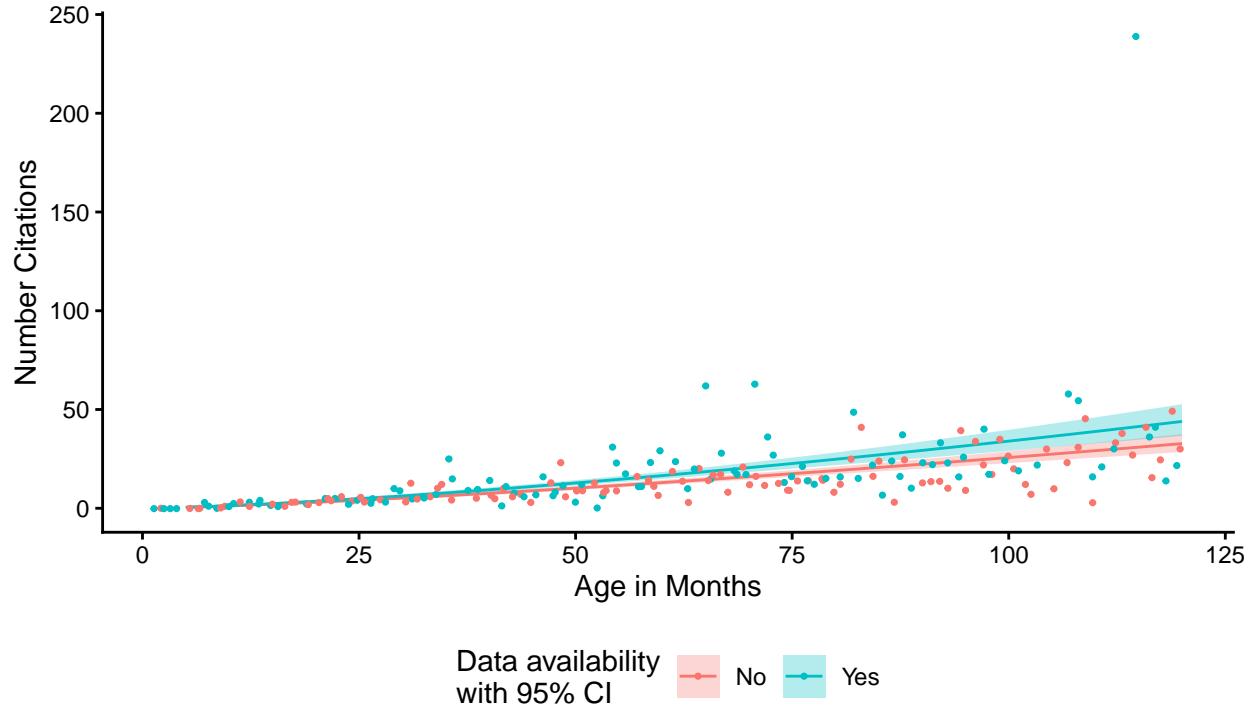


Model vs True Median Number of Citations from GLM.NB for Infection and Immunity binned by month and da status median

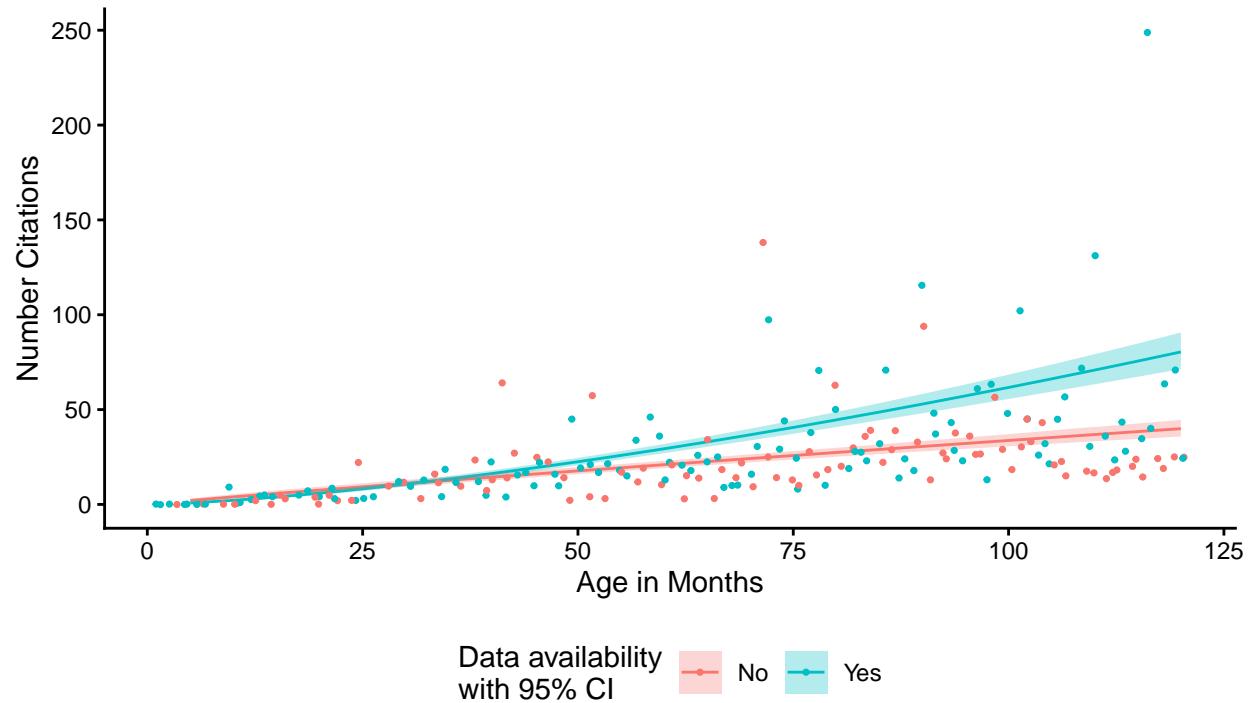
Data age.in.months <= 120, removal of JMBE, GA, MRA



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

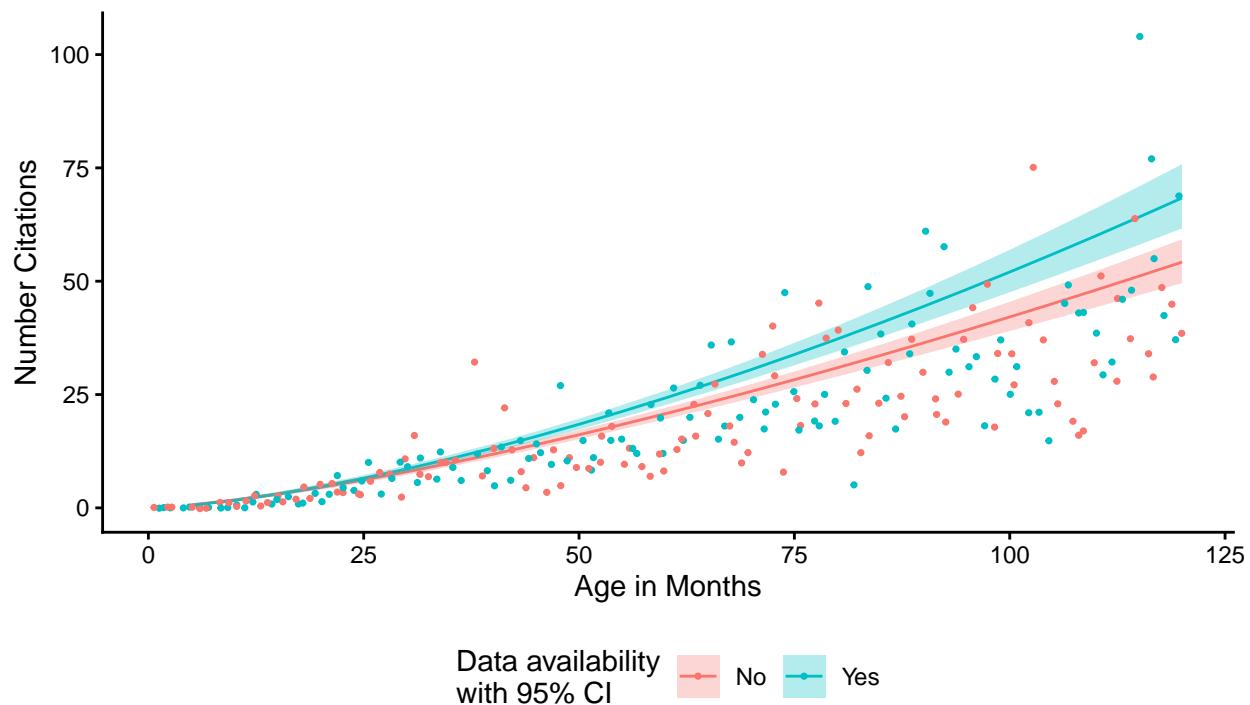


Model vs True Median Number of Citations from GLM.NB for  
 Journal of Clinical Microbiology binned by month and da status median  
 Data age.in.months <= 120, removal of JMBE, GA, MRA



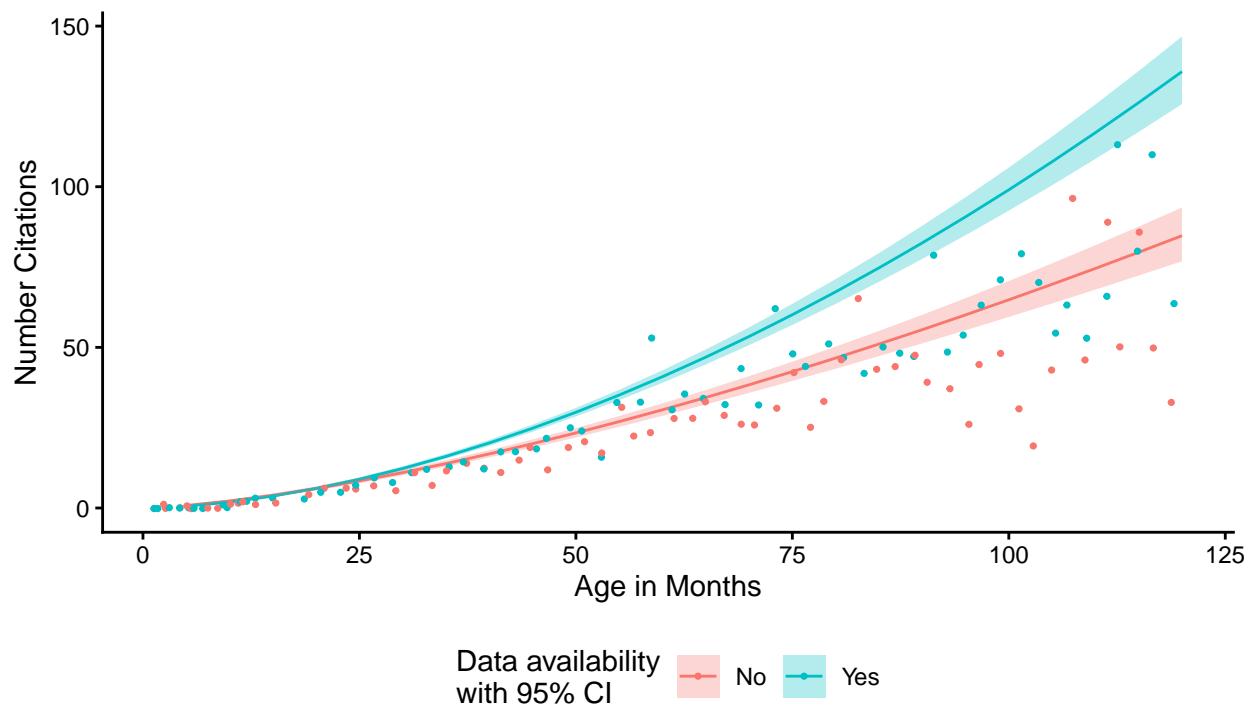
Model vs True Median Number of Citations from GLM.NB for  
Journal of Virology binned by month and da status median

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

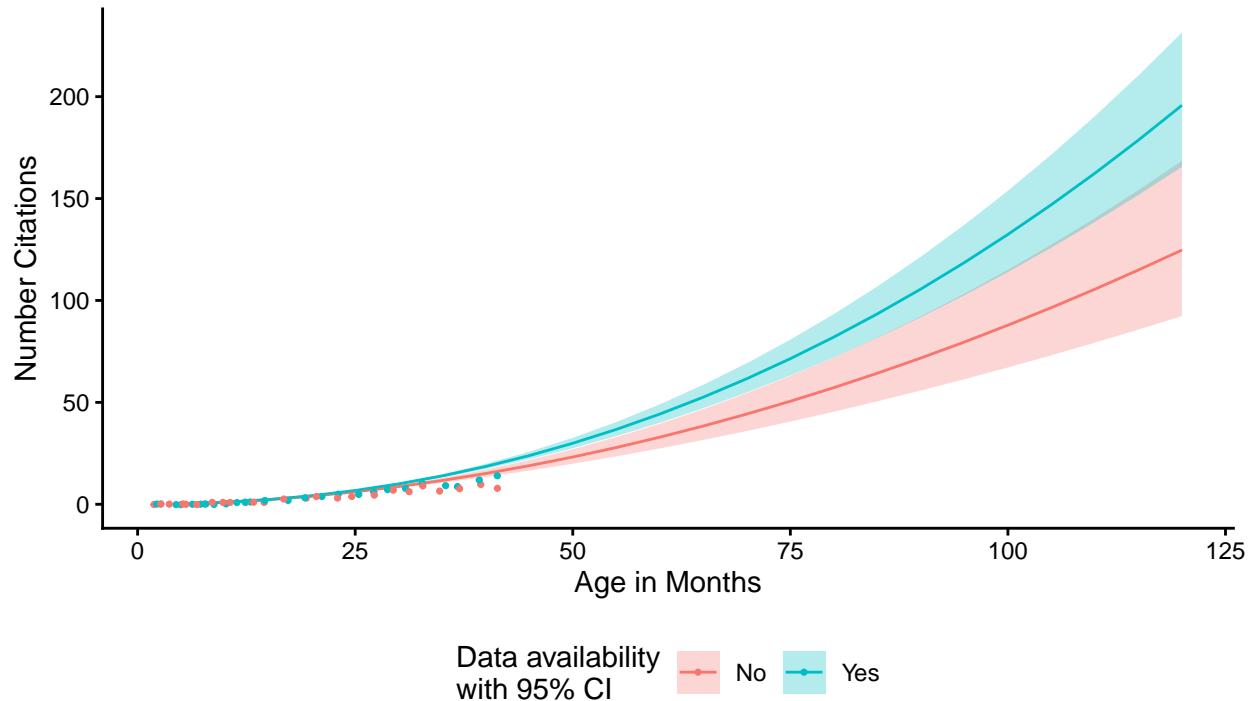


Model vs True Median Number of Citations from GLM.NB for  
mBio binned by month and da status median

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

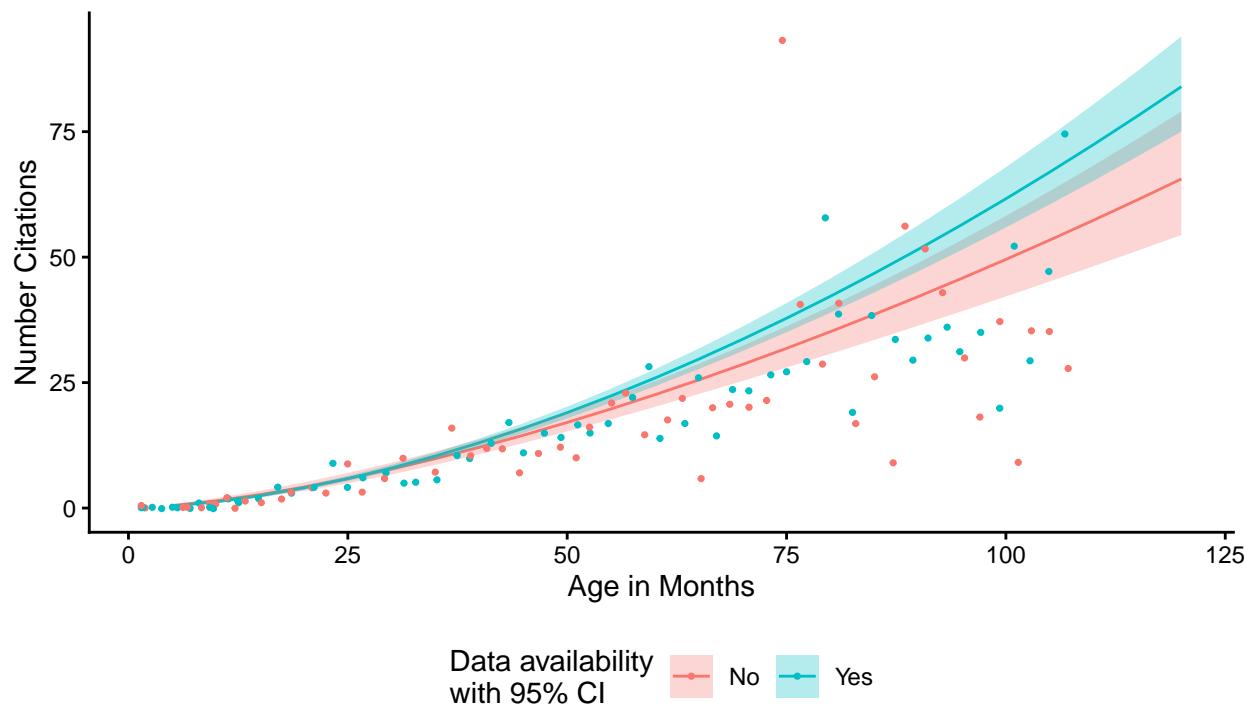


Model vs True Median Number of Citations from GLM.NB for Microbiology Spectrum binned by month and da status median  
Data age.in.months <= 120, removal of JMBE, GA, MRA



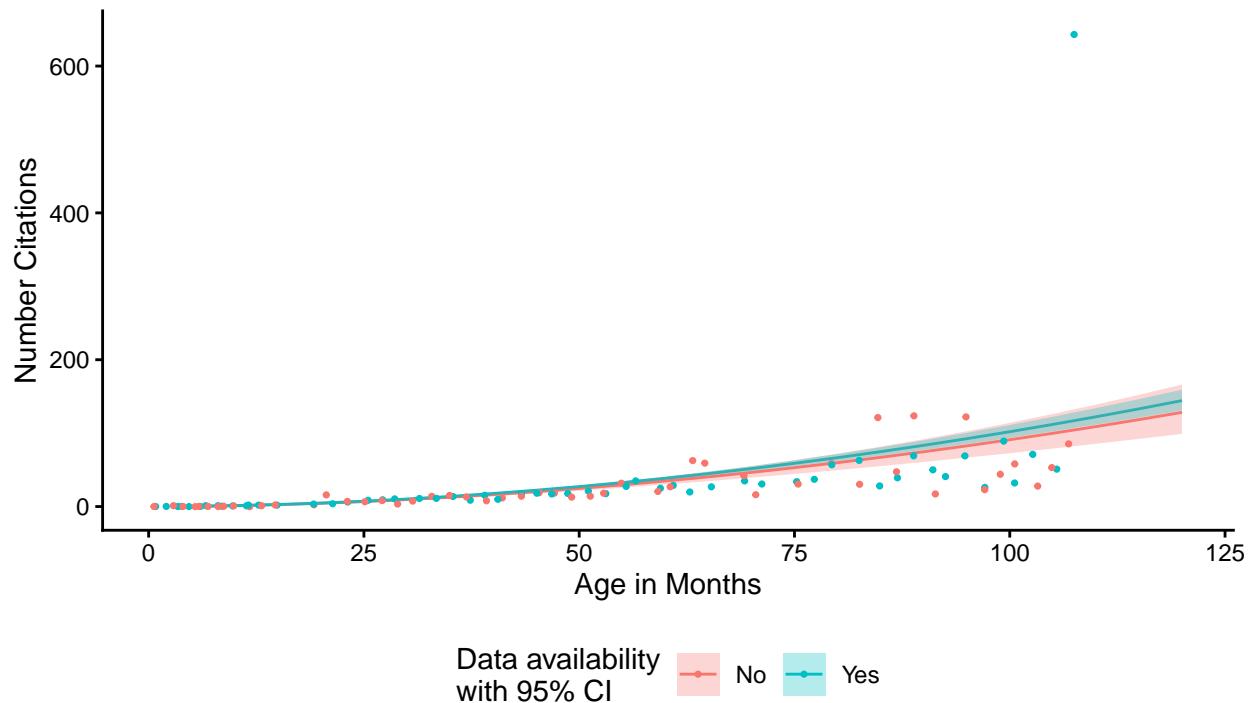
Model vs True Median Number of Citations from GLM.NB for  
mSphere binned by month and da status median

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



## 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



```
## 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))

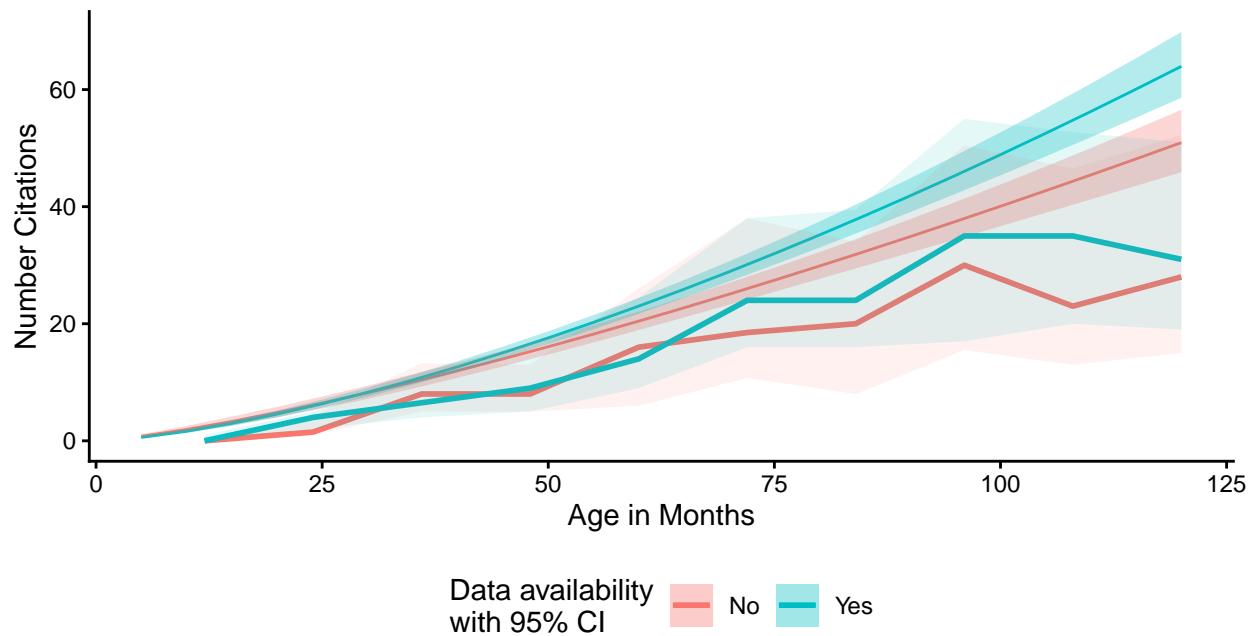
#make plot
plot <-
ggplot() +
  geom_line(data = model_data, aes(x = age.in.months, y = predicted_citations, group = da_factor, color = da_factor)) +
  geom_ribbon(data = model_data, mapping = aes(x = age.in.months, y = predicted_citations, group = da_factor, fill = da_factor), alpha = 0.3) +
  geom_line(data = 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 quantiles",
       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)
}

```

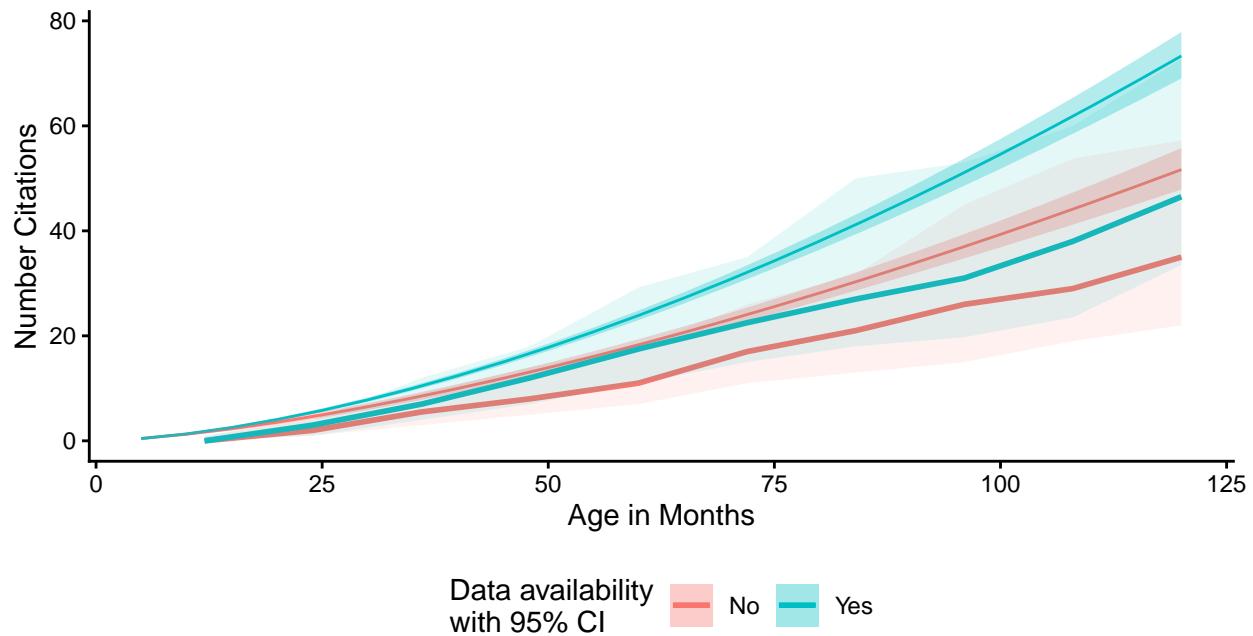
Model vs True Median Number of Citations from GLM.NB for  
Antimicrobial Agents and Chemotherapy binned by year,  
da status median, 25% & 75%

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



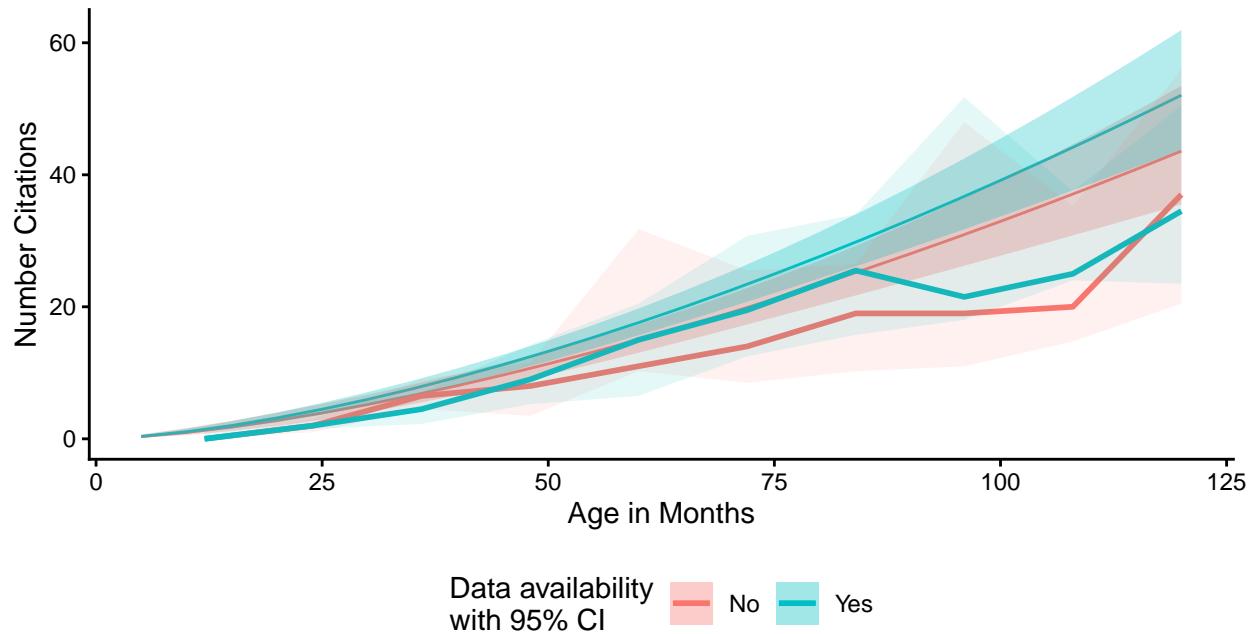
Model vs True Median Number of Citations from GLM.NB for Applied and Environmental Microbiology binned by year, da status median, 25% & 75%

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



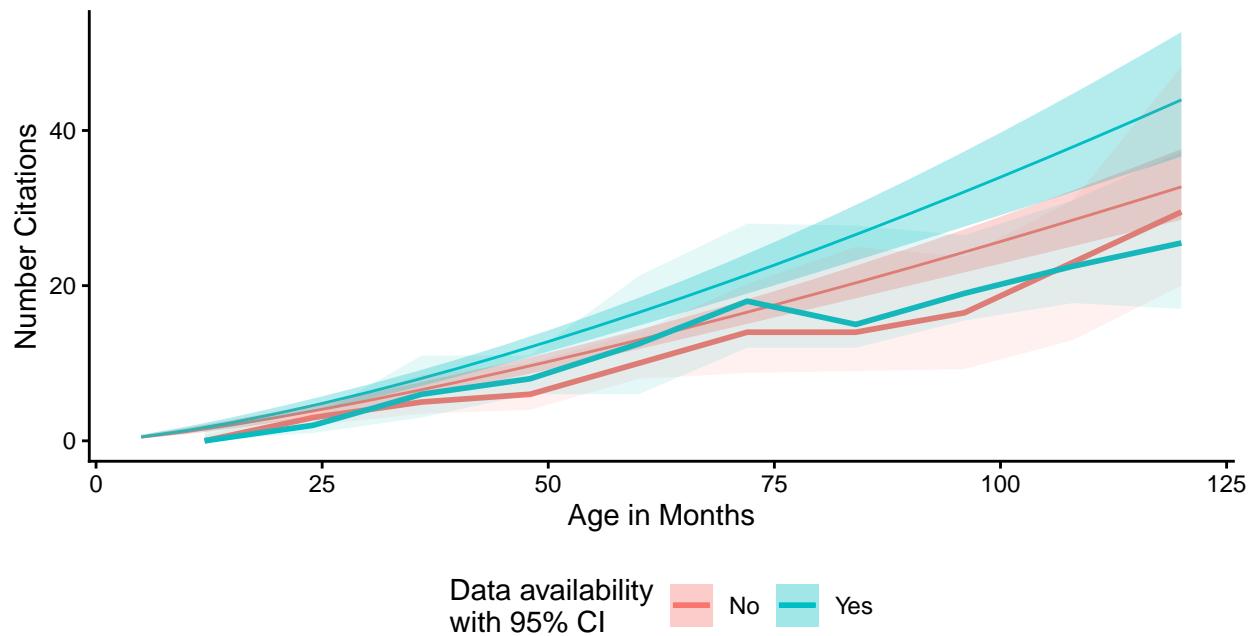
Model vs True Median Number of Citations from GLM.NB for  
Infection and Immunity binned by year,  
da status median, 25% & 75%

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



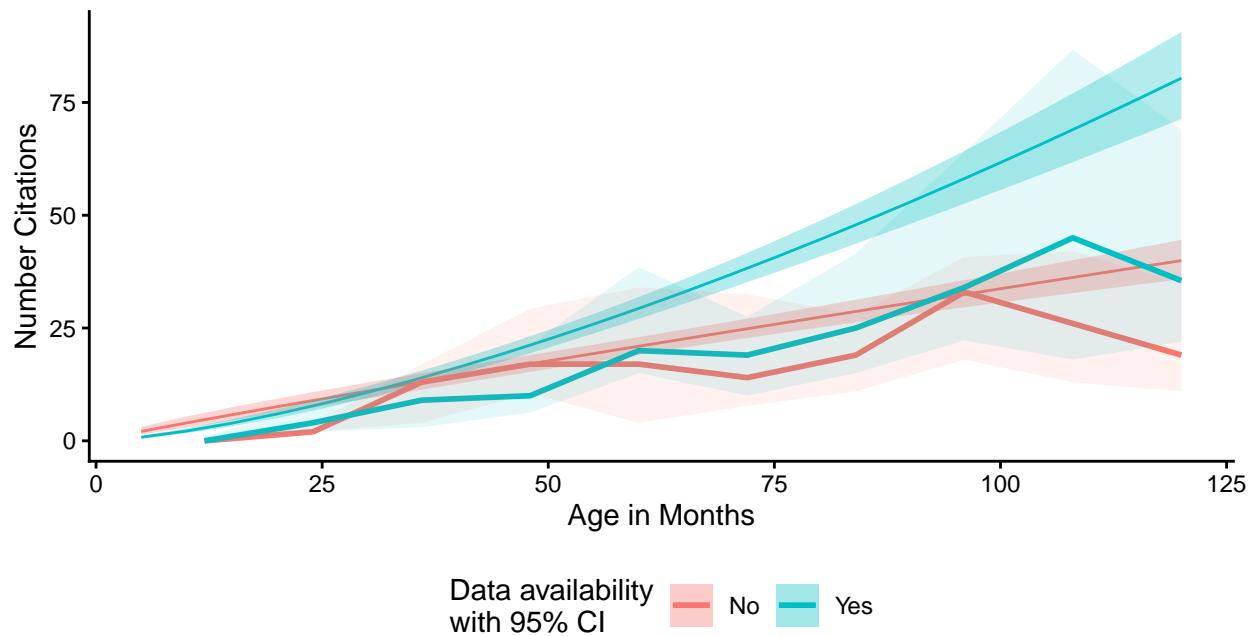
Model vs True Median Number of Citations from GLM.NB for  
Journal of Bacteriology binned by year,  
da status median, 25% & 75%

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



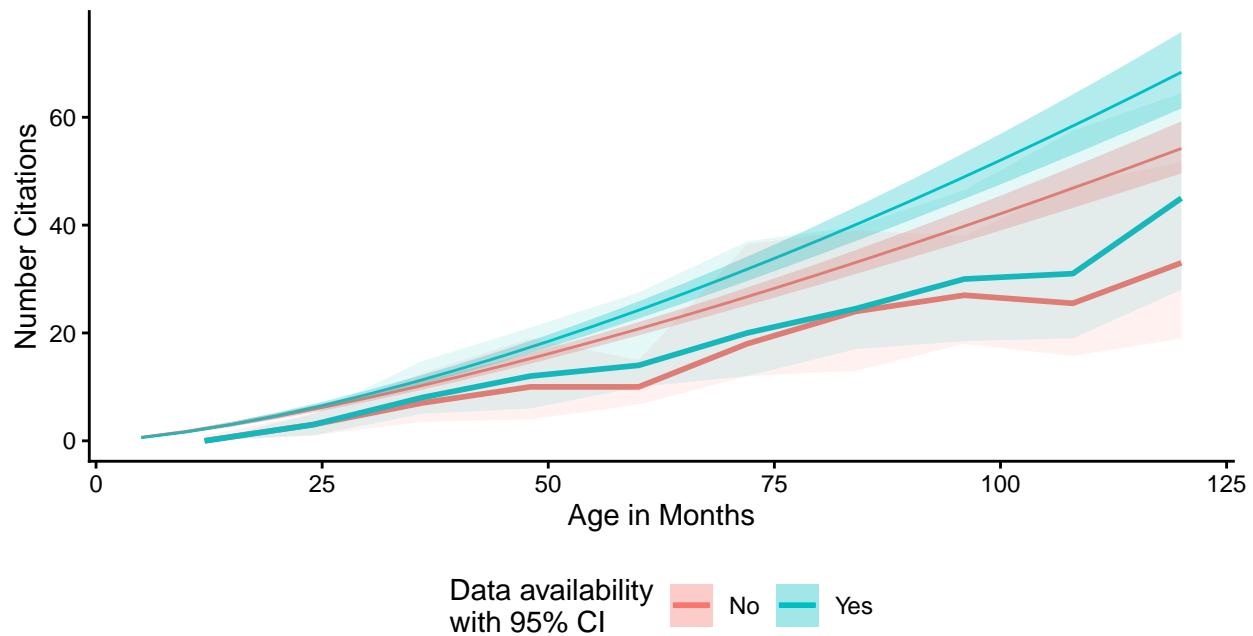
Model vs True Median Number of Citations from GLM.NB for  
Journal of Clinical Microbiology binned by year,  
da status median, 25% & 75%

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



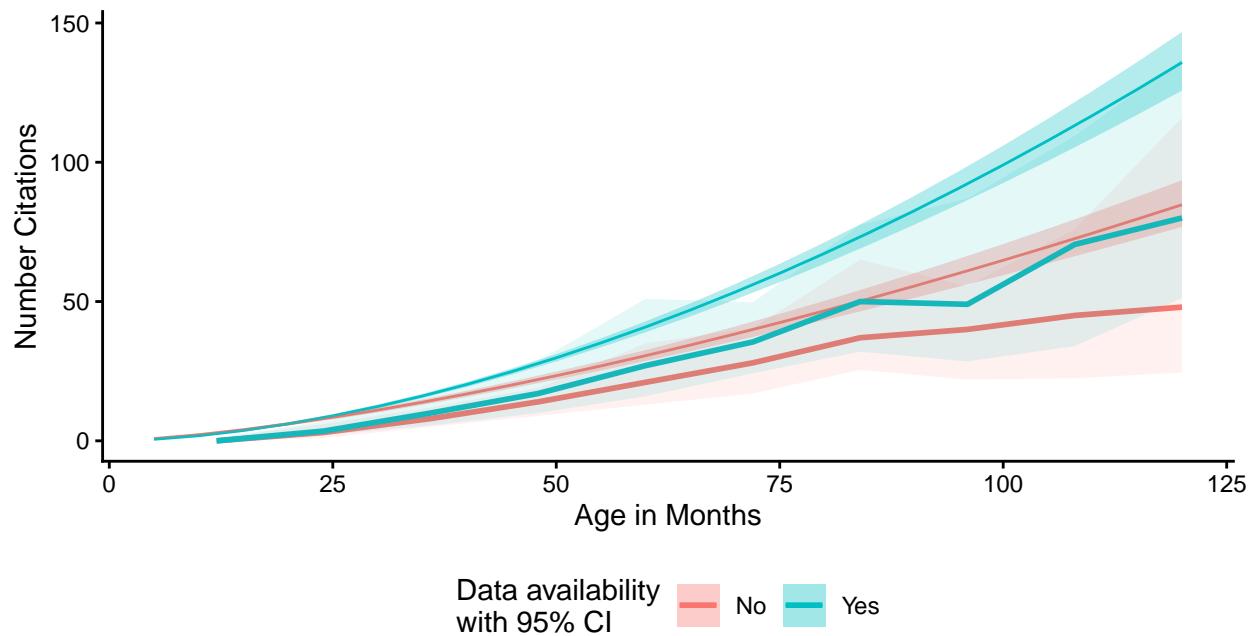
Model vs True Median Number of Citations from GLM.NB for  
Journal of Virology binned by year,  
da status median, 25% & 75%

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



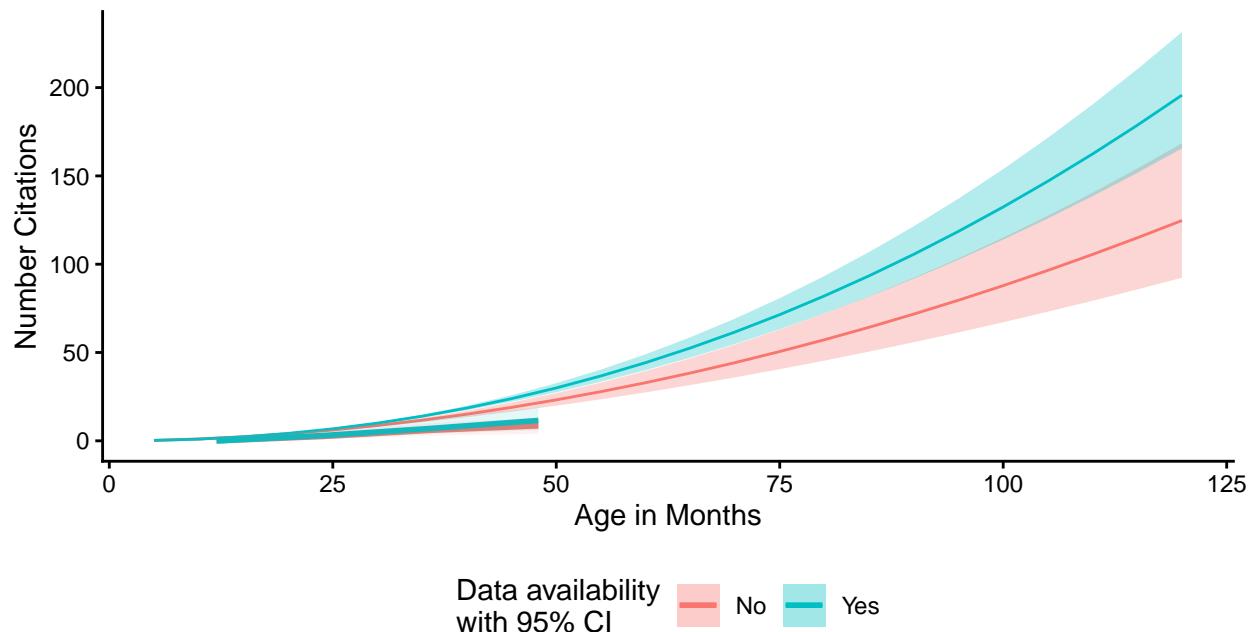
Model vs True Median Number of Citations from GLM.NB for  
mBio binned by year,  
da status median, 25% & 75%

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



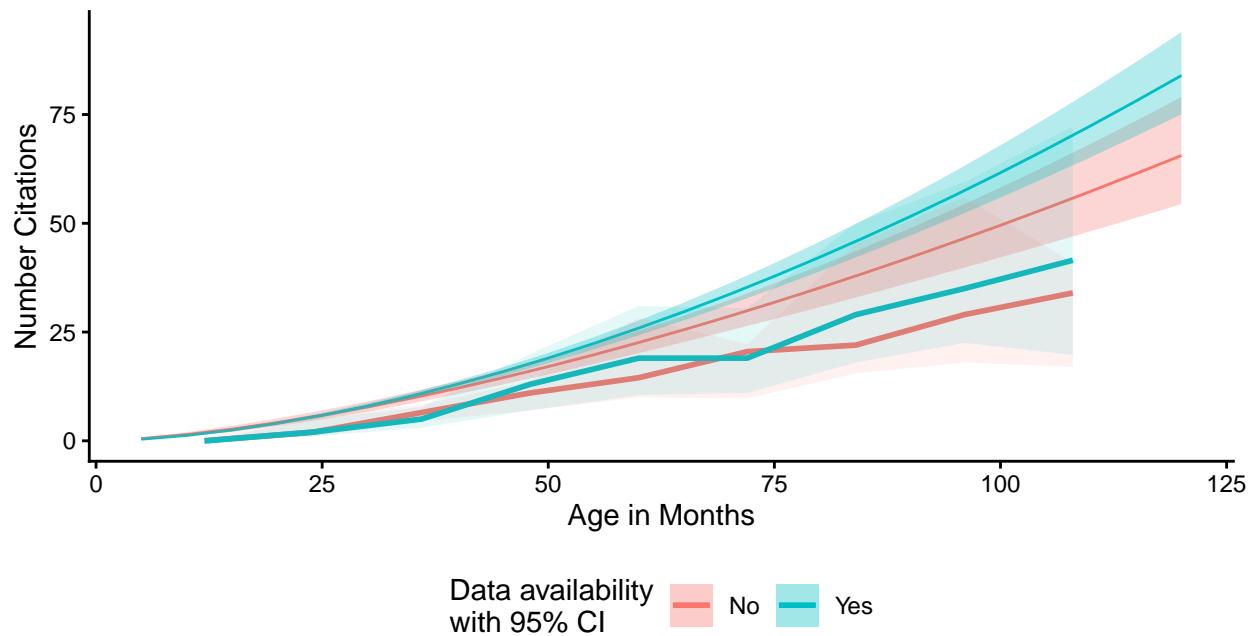
Model vs True Median Number of Citations from GLM.NB for Microbiology Spectrum binned by year,  
da status median, 25% & 75%

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



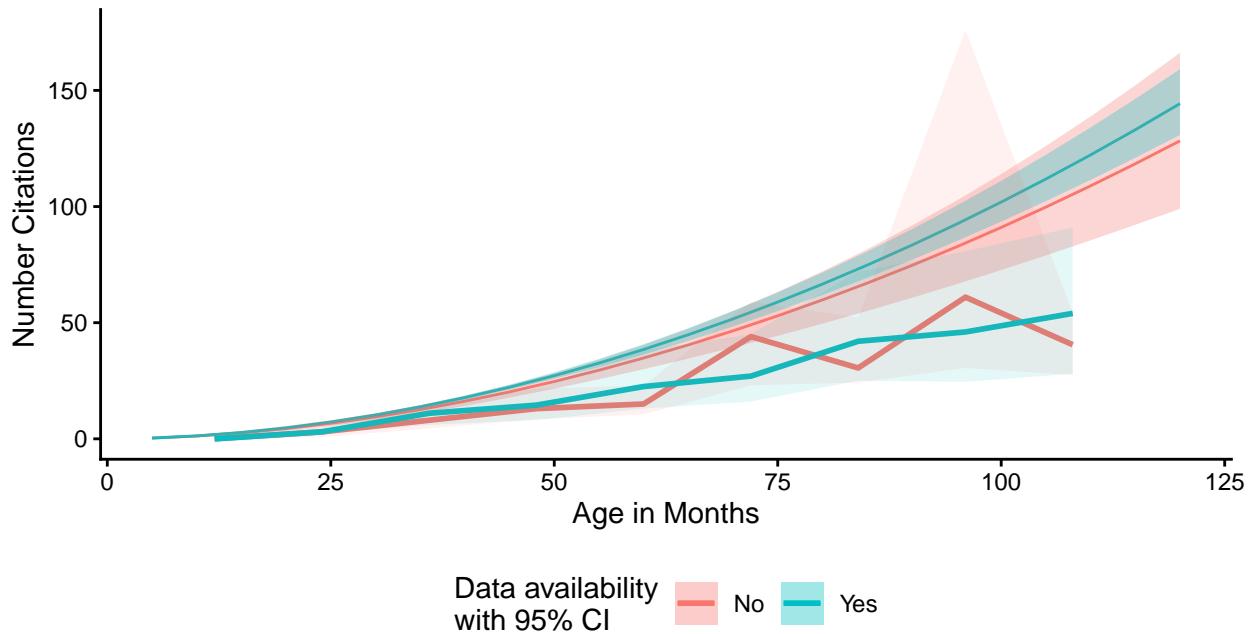
Model vs True Median Number of Citations from GLM.NB for  
mSphere binned by year,  
da status median, 25% & 75%

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



```
## 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, color = da_factor),
geom_ribbon(data = model_data, mapping = aes(x = age.in.months, y = predicted_citations, 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 median",
       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")

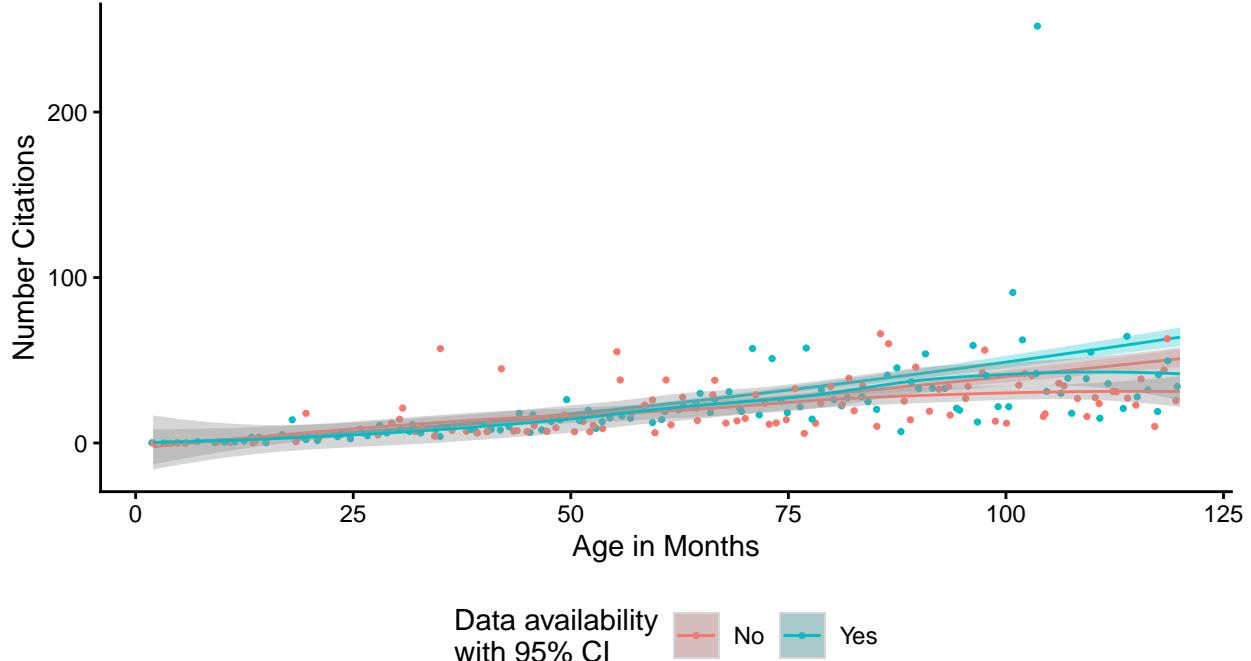
print(plot)
}

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

```

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

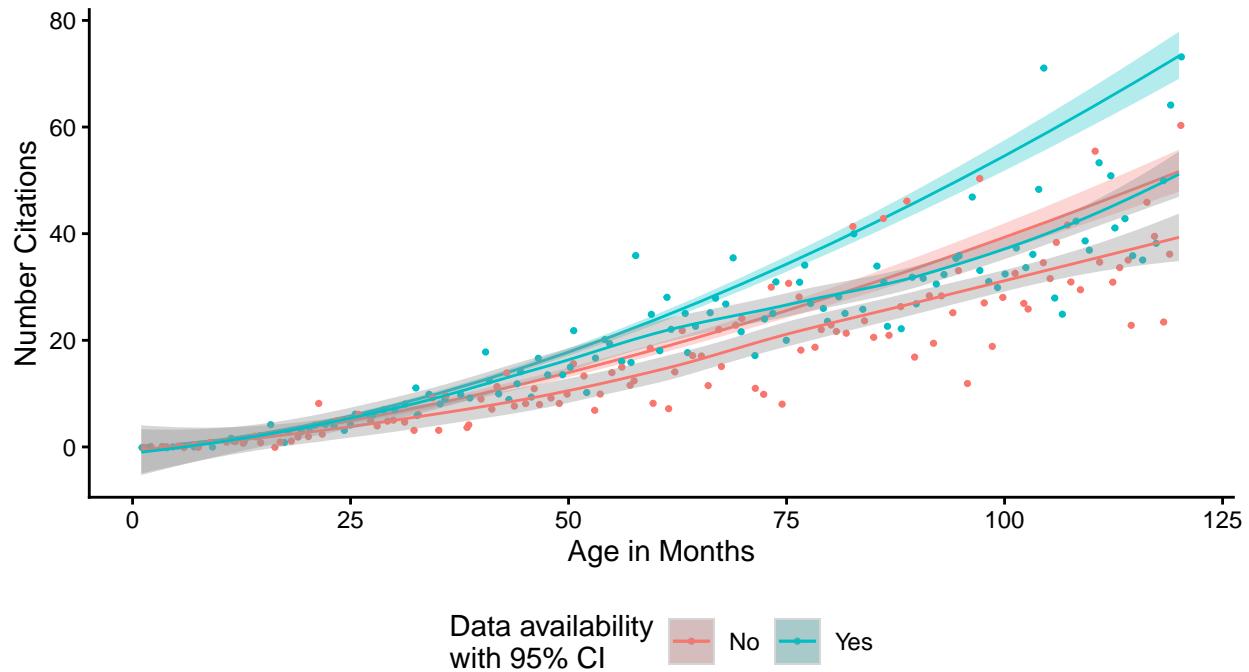
Data age.in.months <= 120, removal of JMBE, GA, MRA  
grey geom\_smooth through the median



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

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

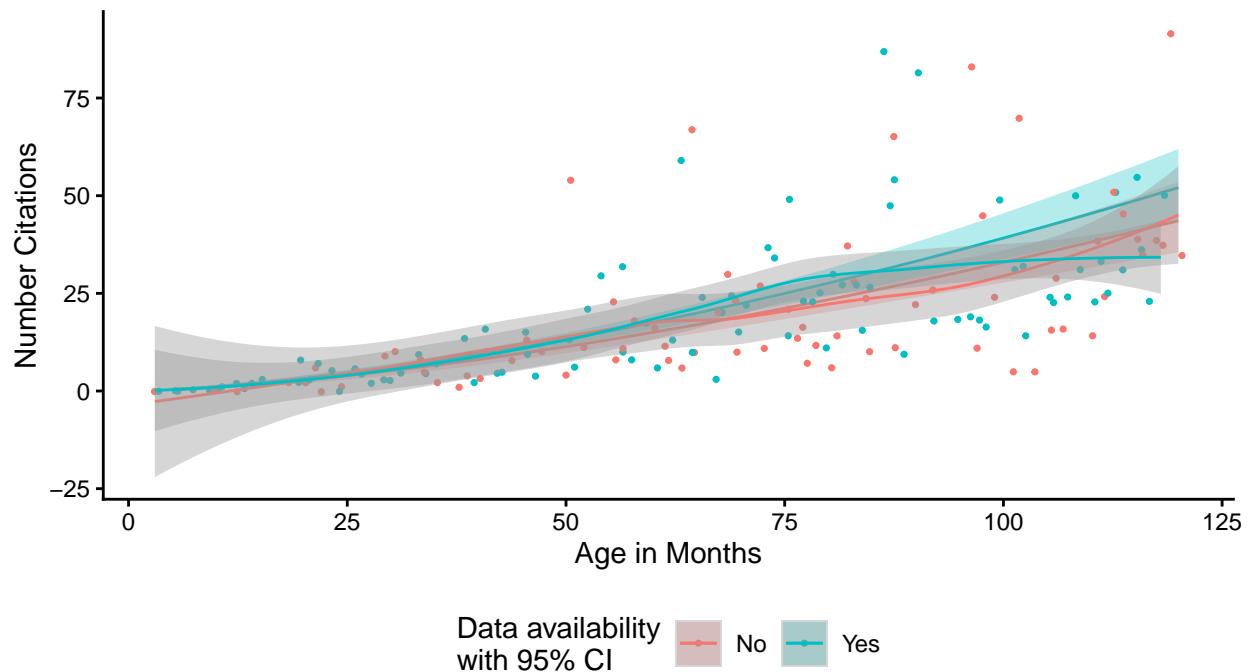
Data age.in.months <= 120, removal of JMBE, GA, MRA  
grey geom\_smooth through the median



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

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

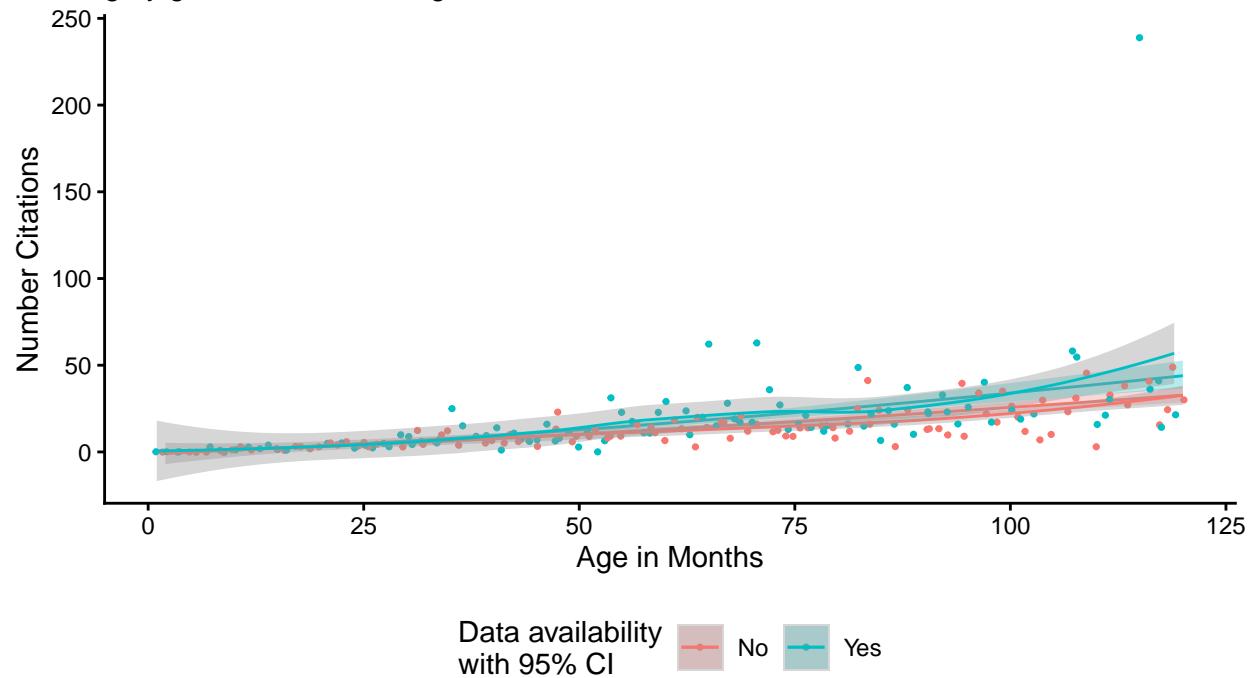
Data age.in.months <= 120, removal of JMME, GA, MRA  
grey geom\_smooth through the median



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

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

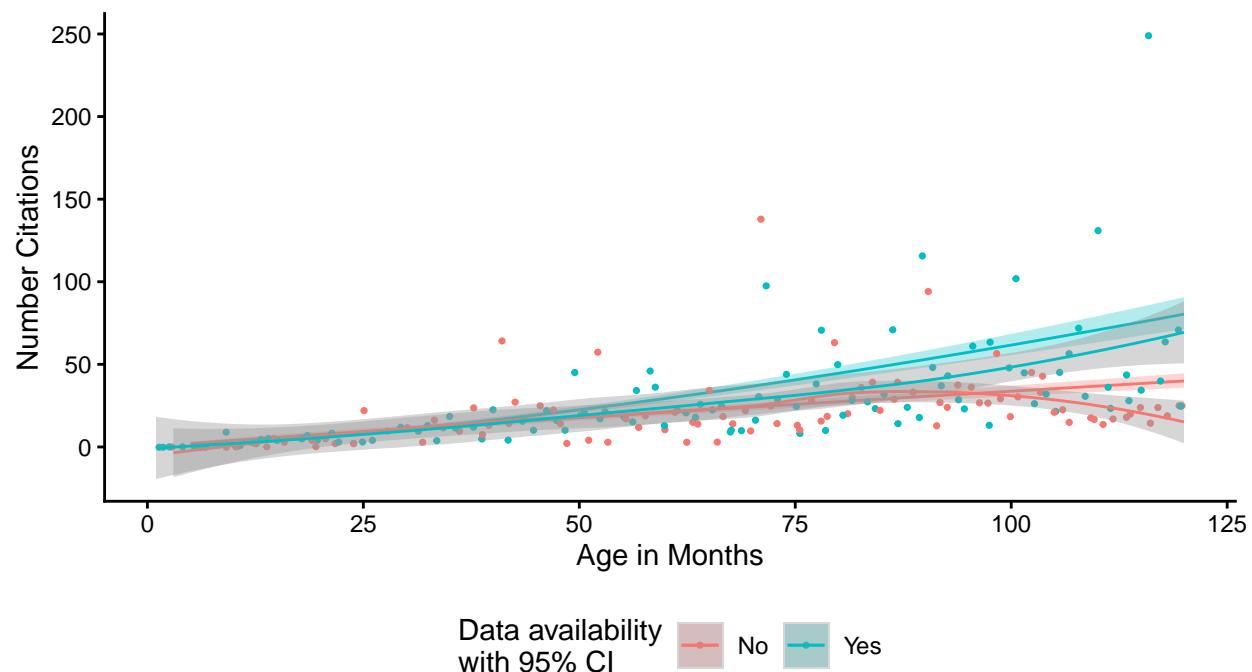
Data age.in.months <= 120, removal of JMME, GA, MRA  
grey geom\_smooth through the median



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

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

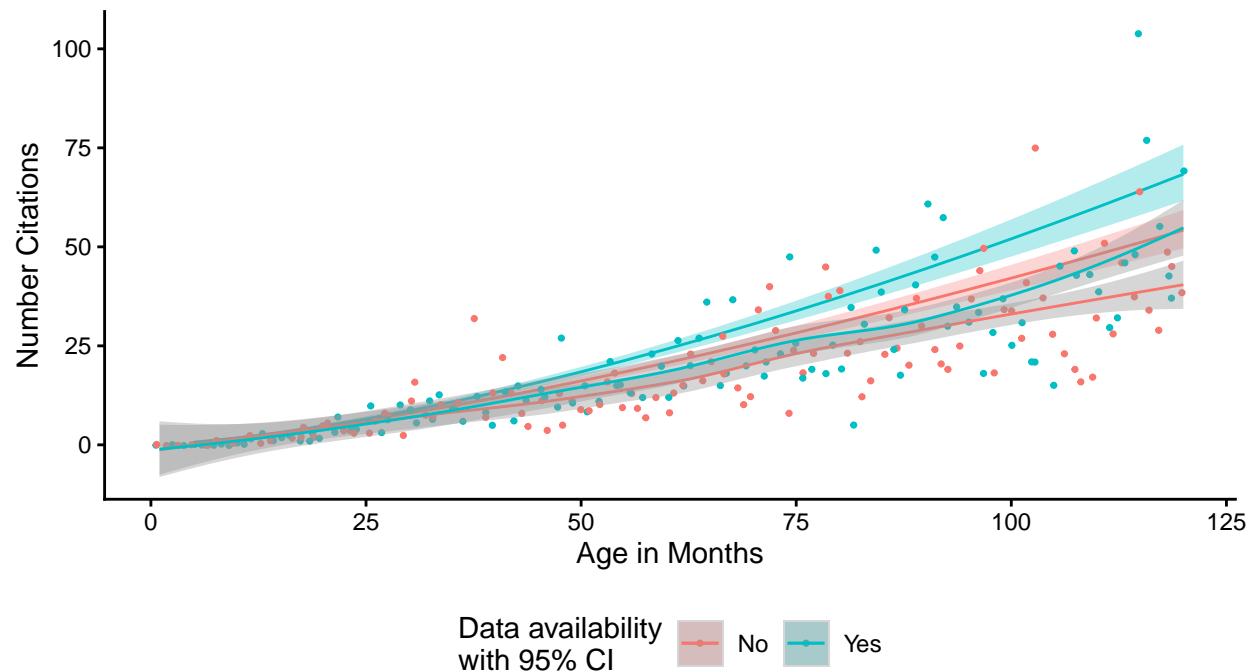
Data age.in.months <= 120, removal of JMME, GA, MRA  
grey geom\_smooth through the median



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

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

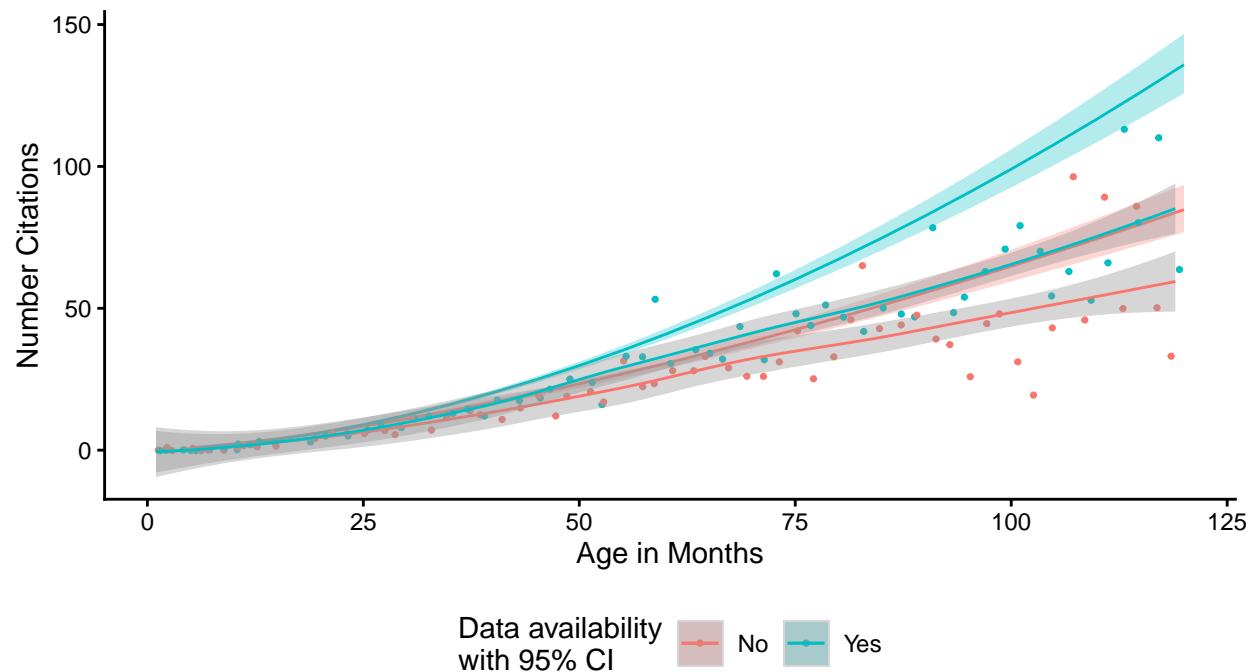
Data age.in.months <= 120, removal of JMME, GA, MRA  
grey geom\_smooth through the median



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

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

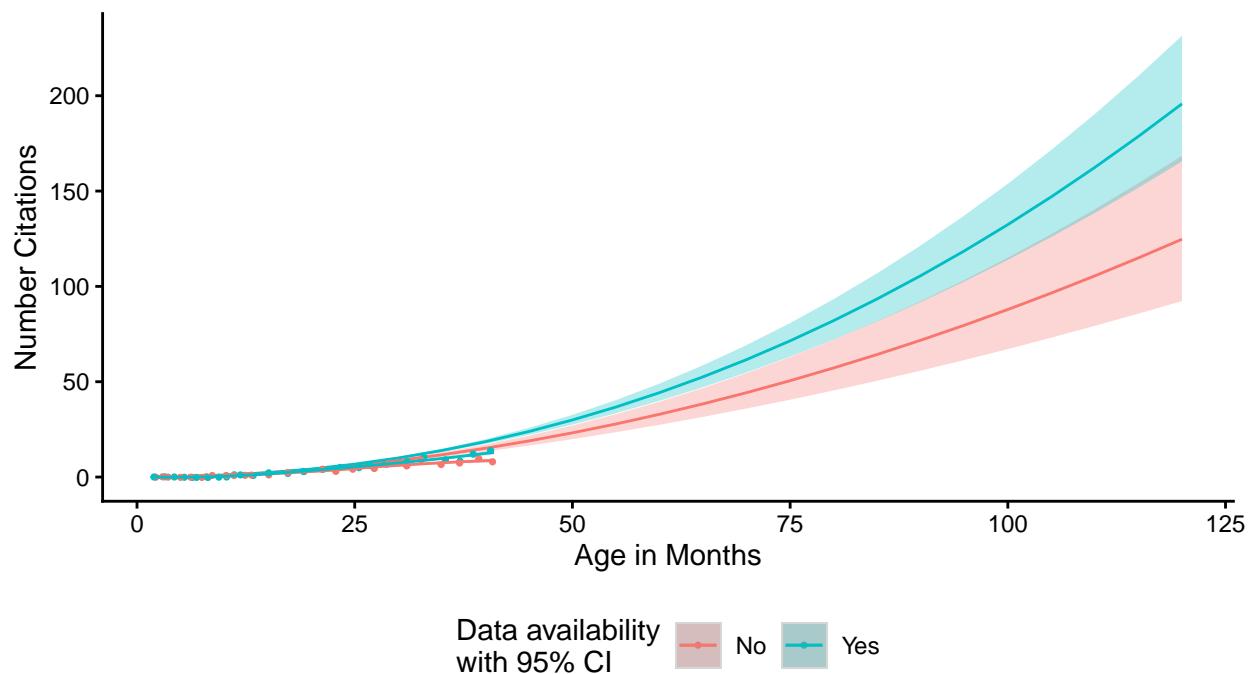
Data age.in.months <= 120, removal of JMME, GA, MRA  
grey geom\_smooth through the median



```
## `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

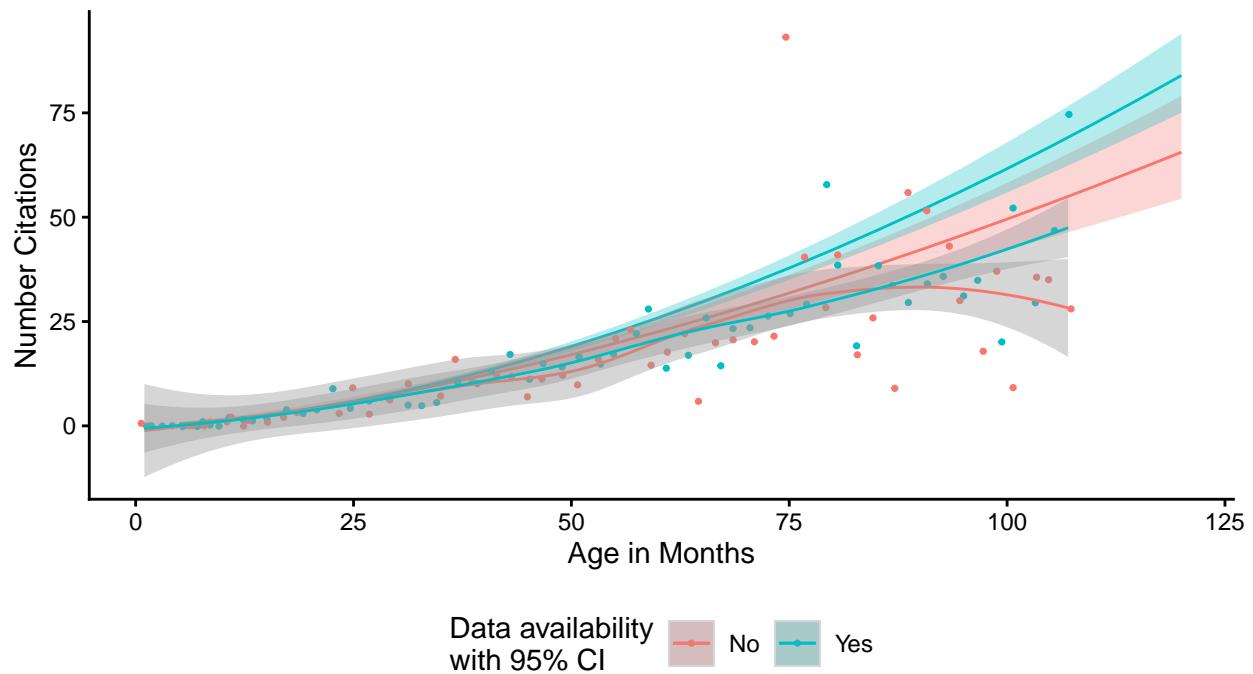
Data age.in.months <= 120, removal of JMBE, GA, MRA  
grey geom\_smooth through the median



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

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

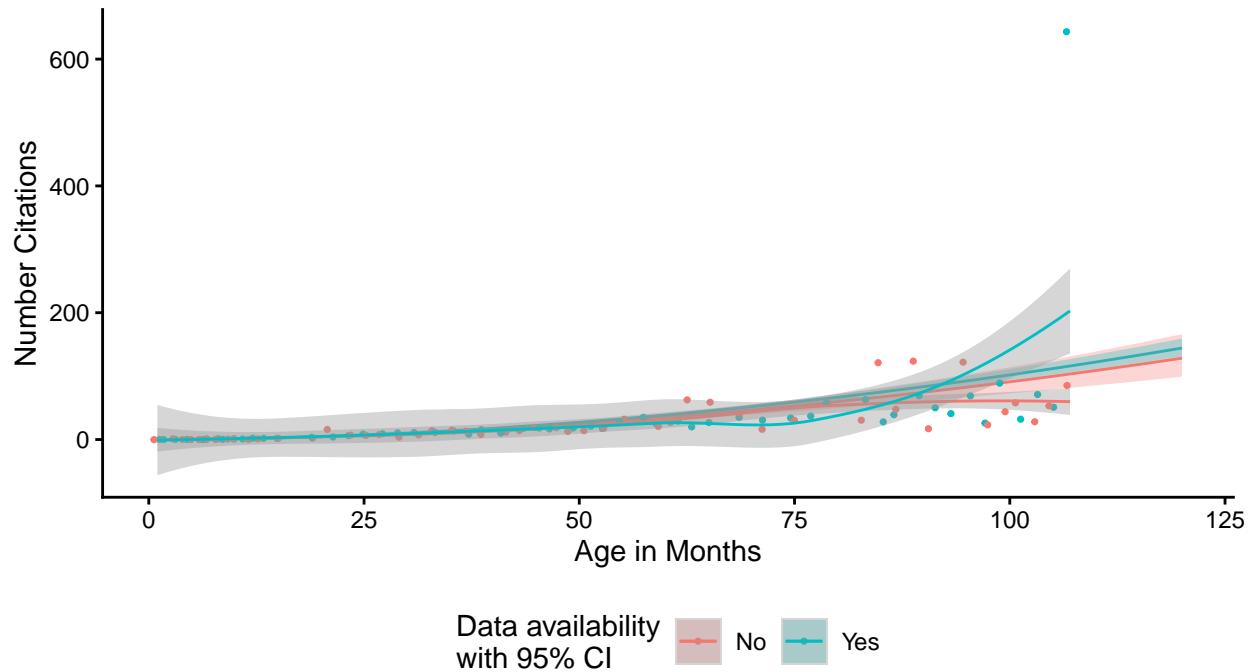
Data age.in.months <= 120, removal of JMBE, GA, MRA  
grey geom\_smooth through the median



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

## Model vs True Median Number of Citations from GLM.NB for 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 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]])

  #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, color = da_factor))
    geom_ribbon(data = model_data, mapping = aes(x = age.in.months, y = predicted_citations, ymin = predicted_citations - 1.96 * std.error, ymax = predicted_citations + 1.96 * std.error), fill = NA)
```

```

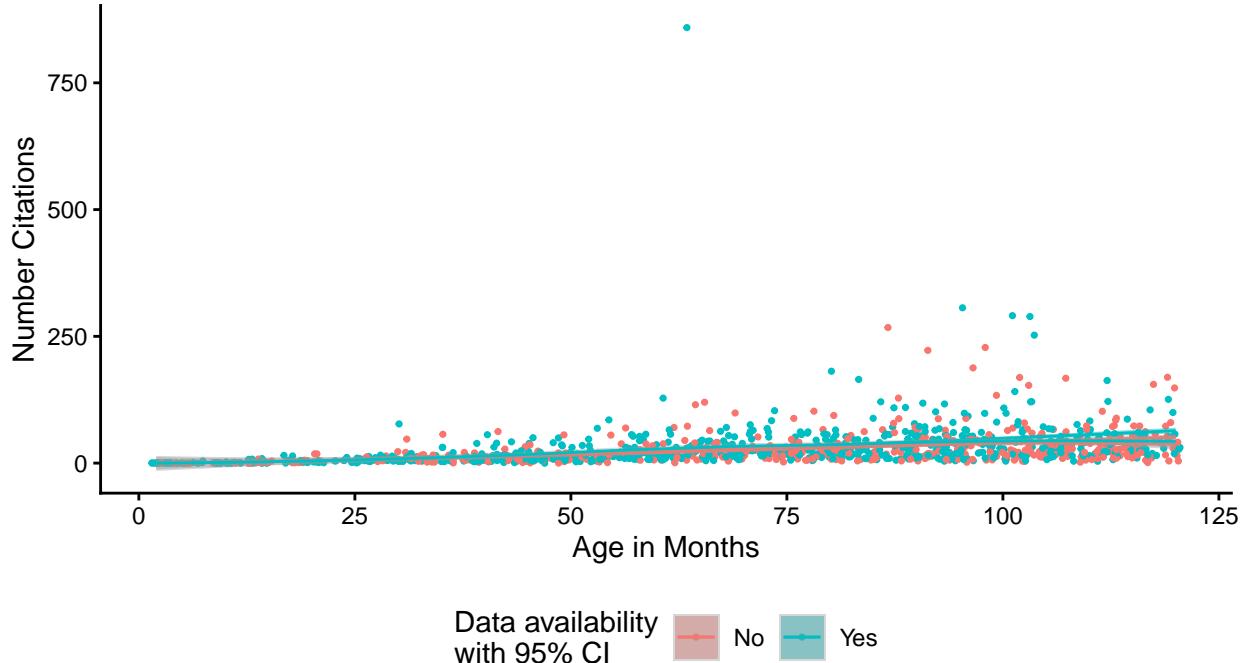
group = da_factor, fill = da_factor), alpha = 0.5) +
  geom_smooth(data = j_metadata, aes(x = age.in.months,
                                     y = is.referenced.by.count, color = da_factor), size = 0.5, alpha =
  labs(title = paste0("Model vs True Median Number of Citations from GLM.NB for\n", journals$container
  subtitle = "Data age.in.months <= 120, removal of JMBE, GA, MRA\ngrey geom_smooth through the da
  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'

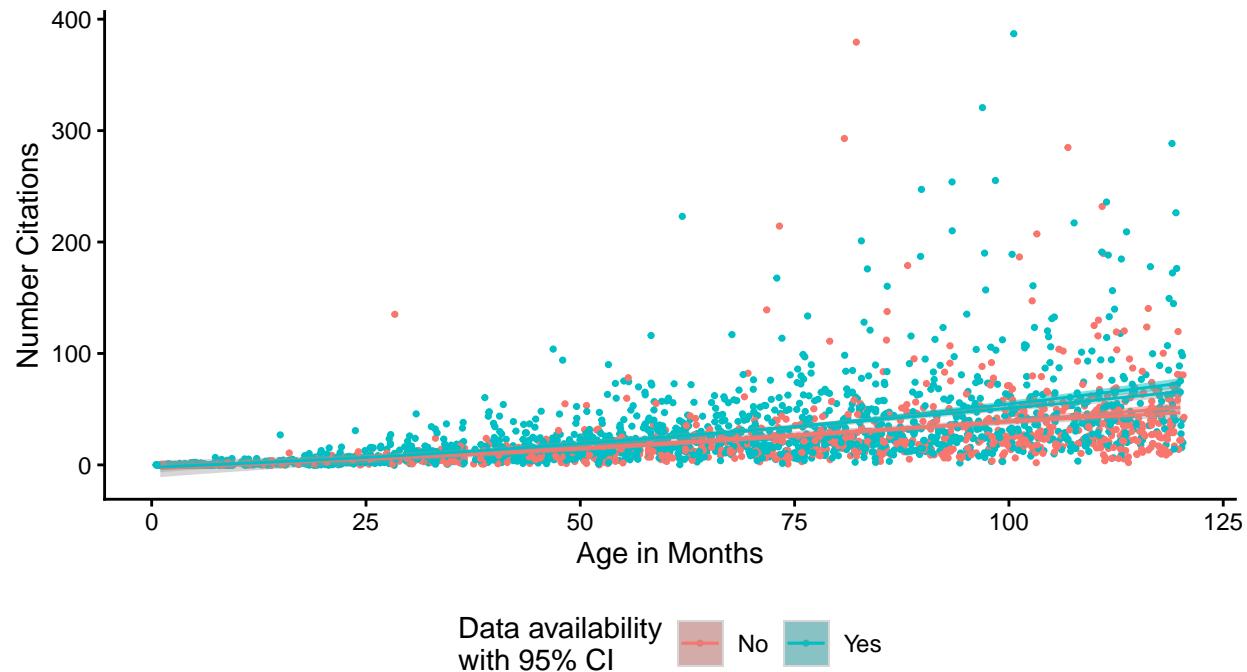
Model vs True Median Number of Citations from GLM.NB for  
 Antimicrobial Agents and Chemotherapy binned by month and da status  
 Data age.in.months <= 120, removal of JMBE, GA, MRA  
 grey geom\_smooth through the data



## 'geom\_smooth()' using method = 'gam' and formula = 'y ~ s(x, bs = "cs")'

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

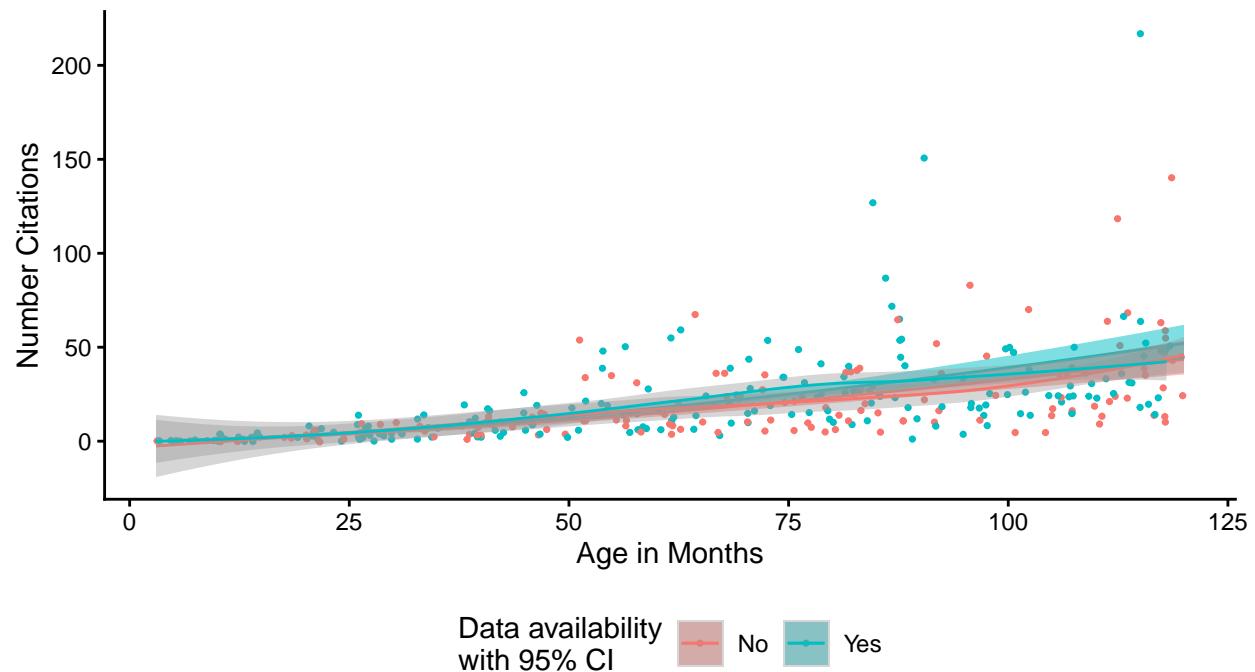
Data age.in.months <= 120, removal of JMBE, GA, MRA  
grey geom\_smooth through the data



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

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

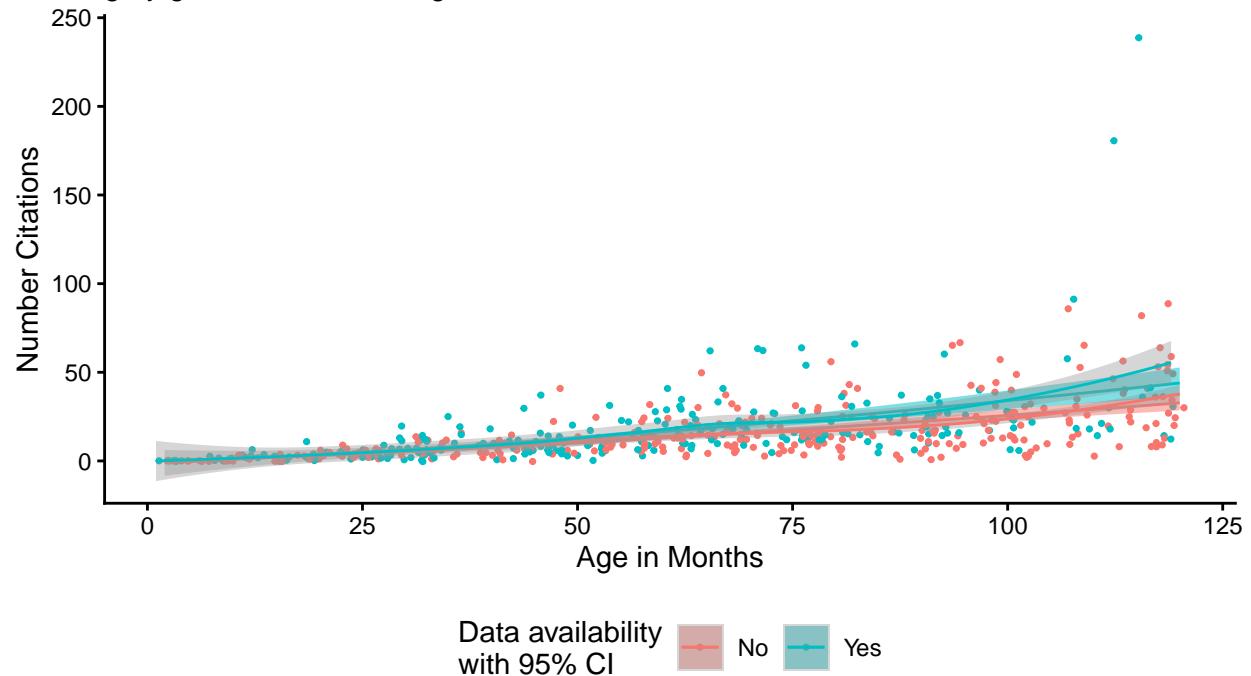
Data age.in.months <= 120, removal of JMBE, GA, MRA  
grey geom\_smooth through the data



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

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

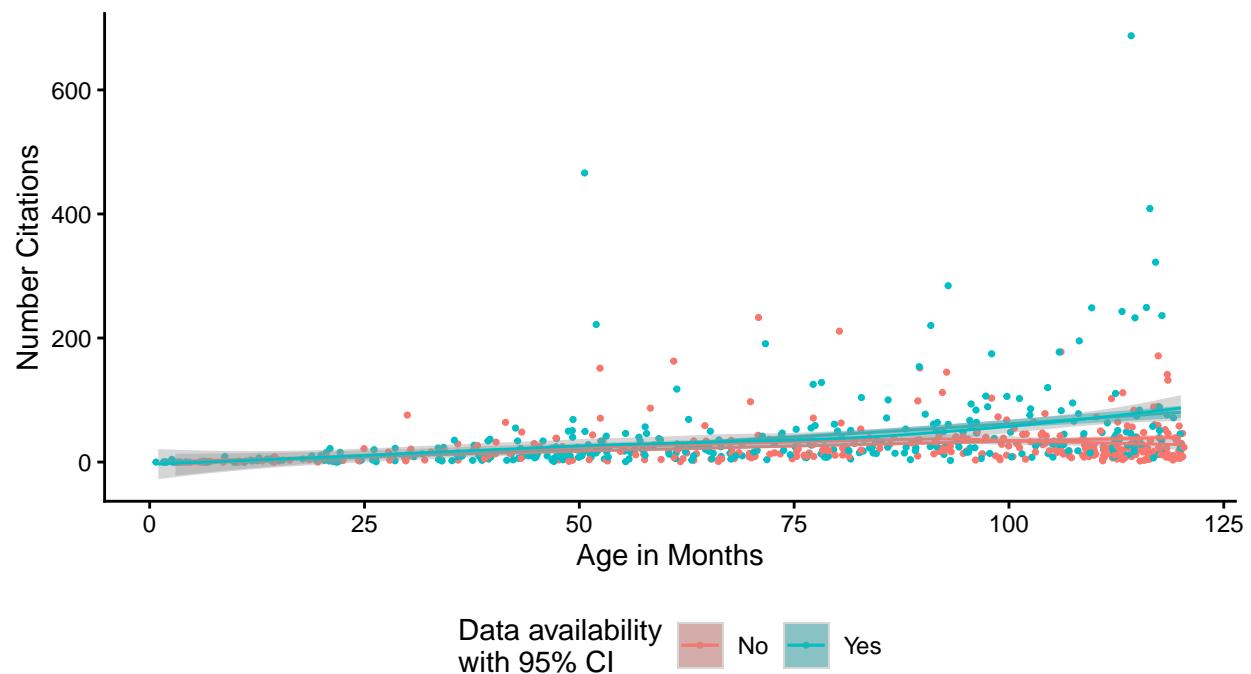
Data age.in.months <= 120, removal of JMBE, GA, MRA  
grey geom\_smooth through the data



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

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

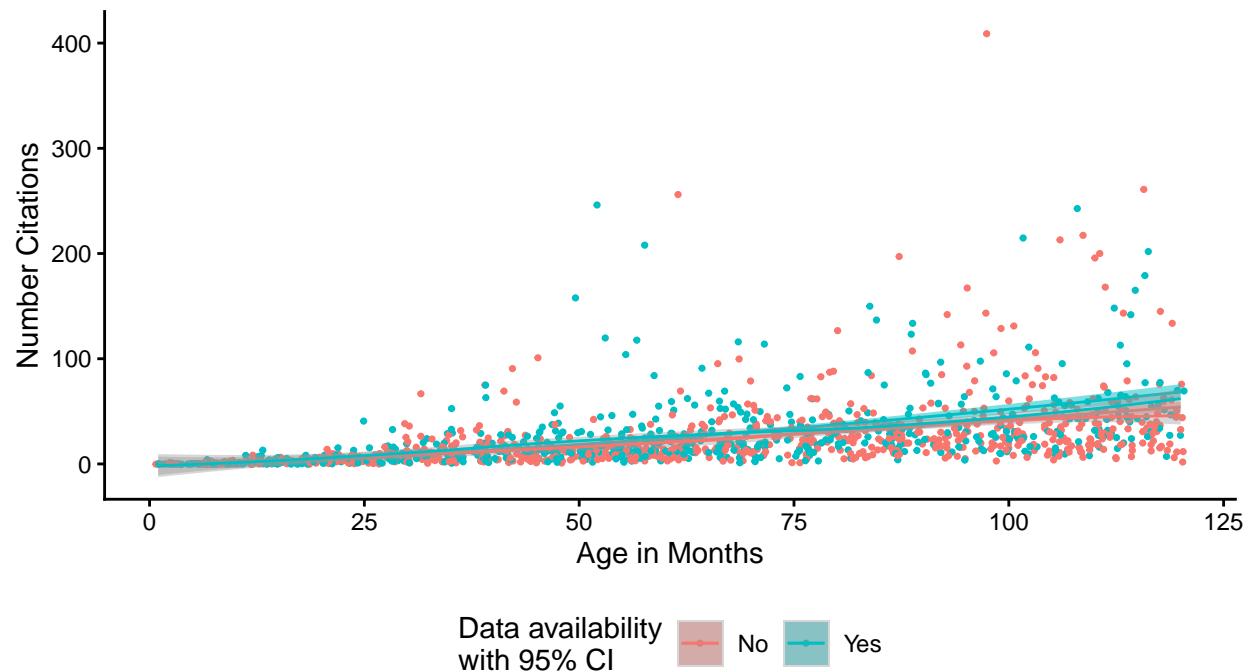
Data age.in.months <= 120, removal of JMME, GA, MRA  
grey geom\_smooth through the data



```
## `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

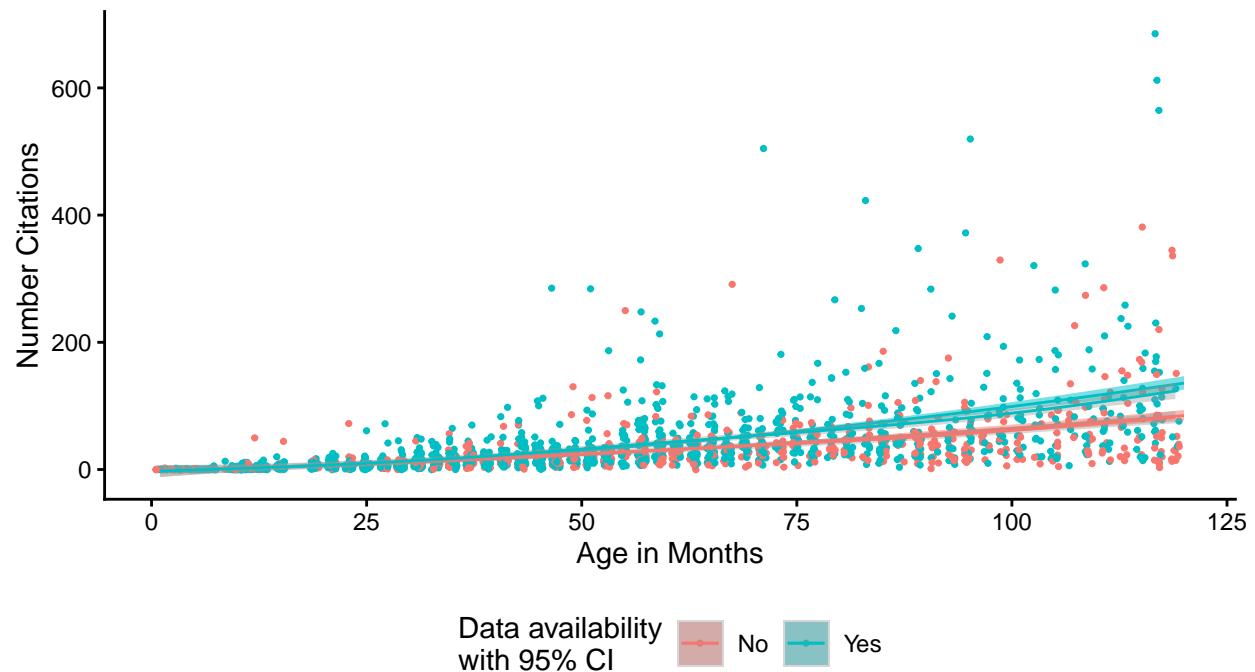
Data age.in.months <= 120, removal of JMBE, GA, MRA  
grey geom\_smooth through the data



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

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

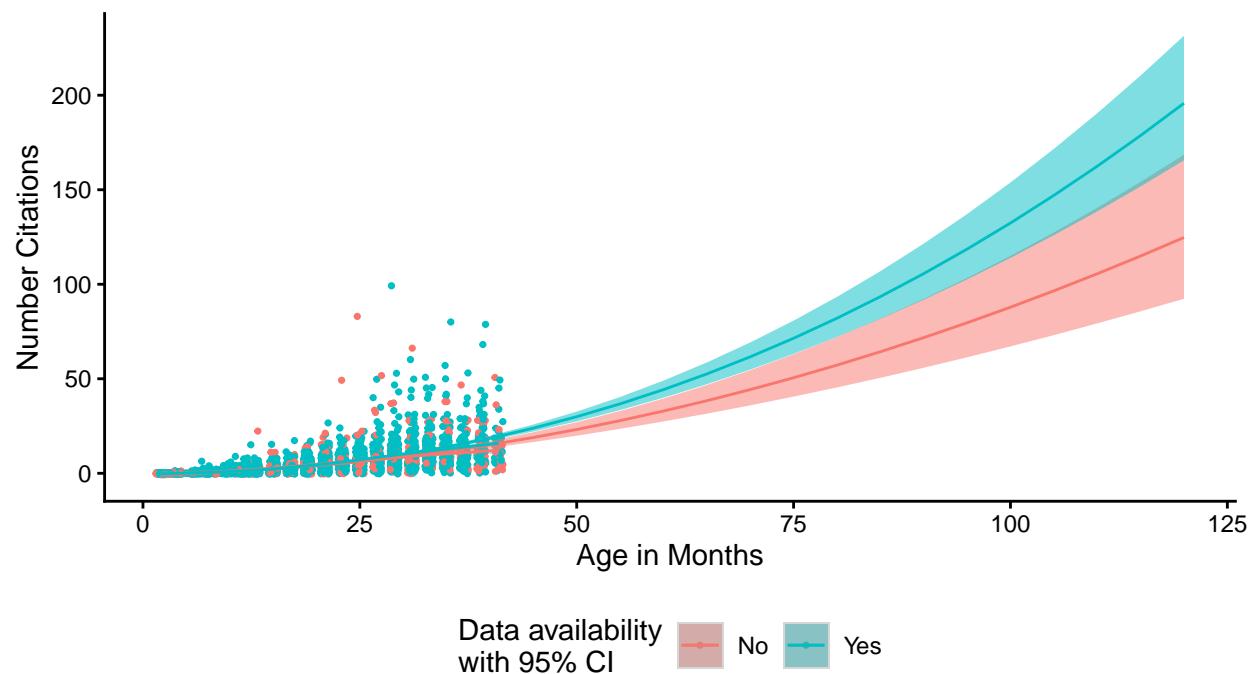
Data age.in.months <= 120, removal of JMBE, GA, MRA  
grey geom\_smooth through the data



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

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

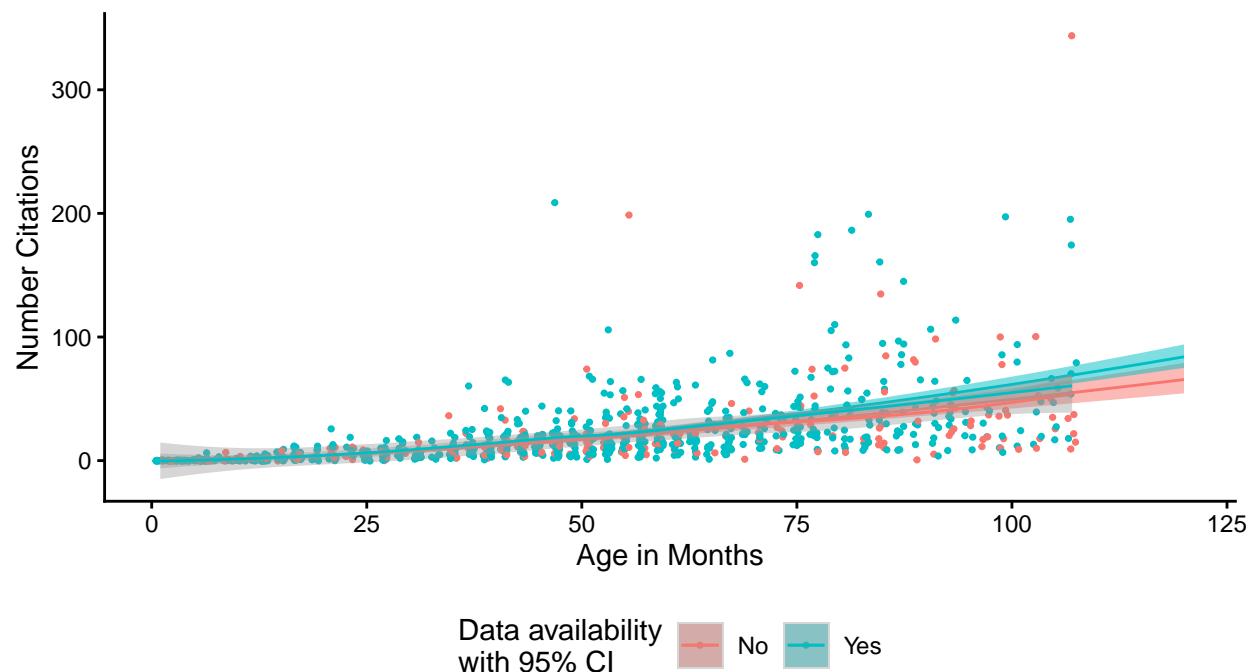
Data age.in.months <= 120, removal of JMBE, GA, MRA  
grey geom\_smooth through the data



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

Model vs True Median Number of Citations from GLM.NB for  
mSphere 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")'
```

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

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

