

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" )

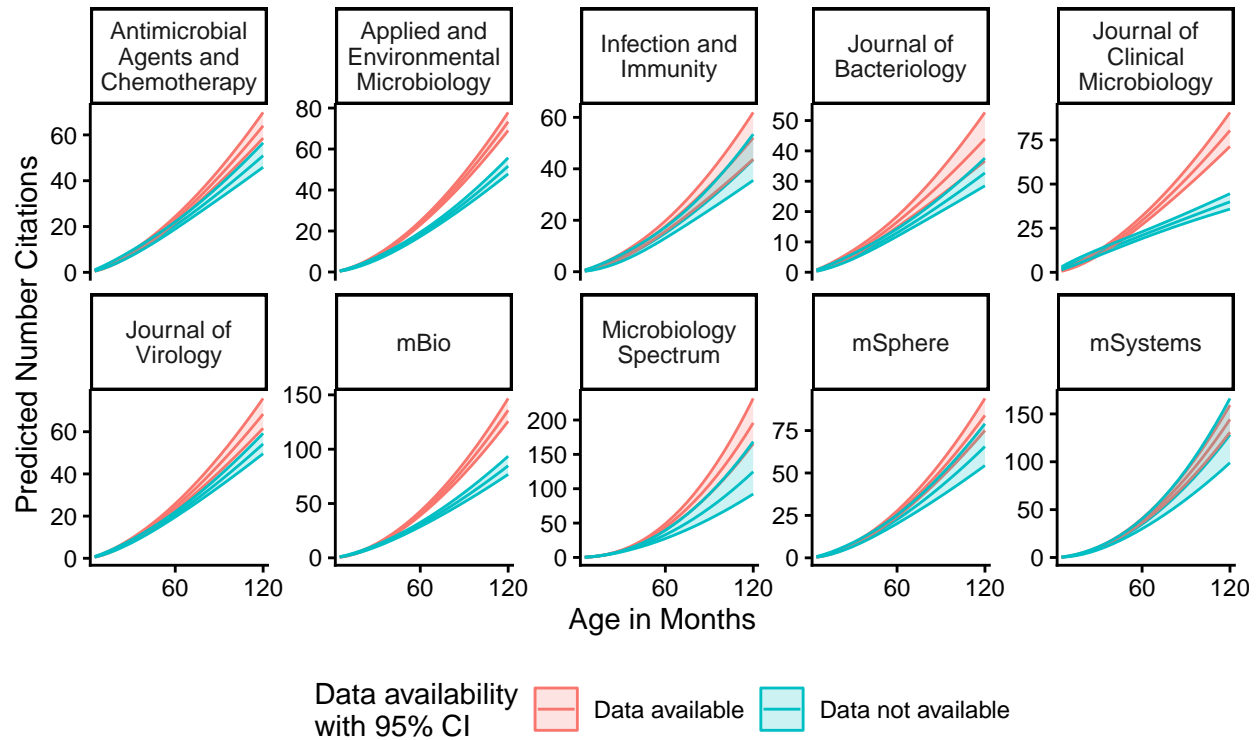
predicted_plot_fixed <-
  ggplot(data = p_10, mapping = aes(x = as.numeric(age.in.months), y = predicted_citations,
    color = da_factor)) +
  geom_line(aes(x = age.in.months, y = predicted_citations, group = da_factor)) +
  geom_ribbon(mapping = aes(ymin = conf.low, ymax = conf.high,
    group = da_factor, 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

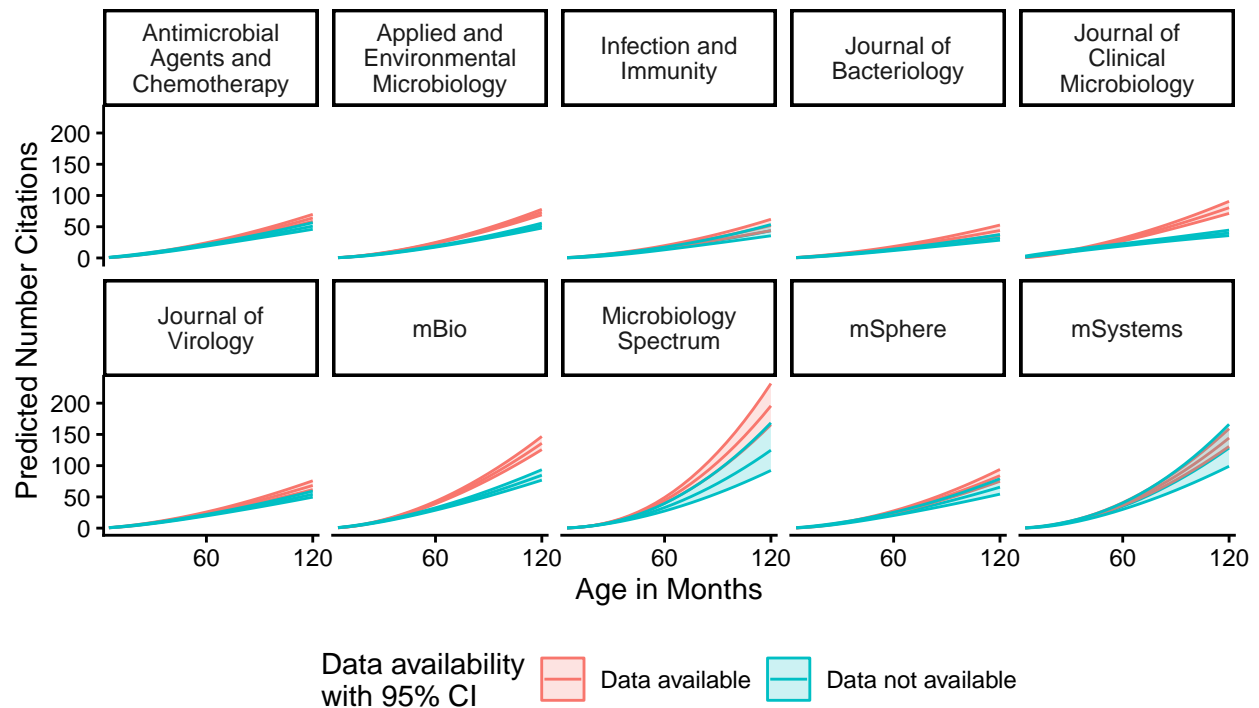
Data age.in.months <= 120, removal of JMBE, GA, MRA



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 <-
```

```

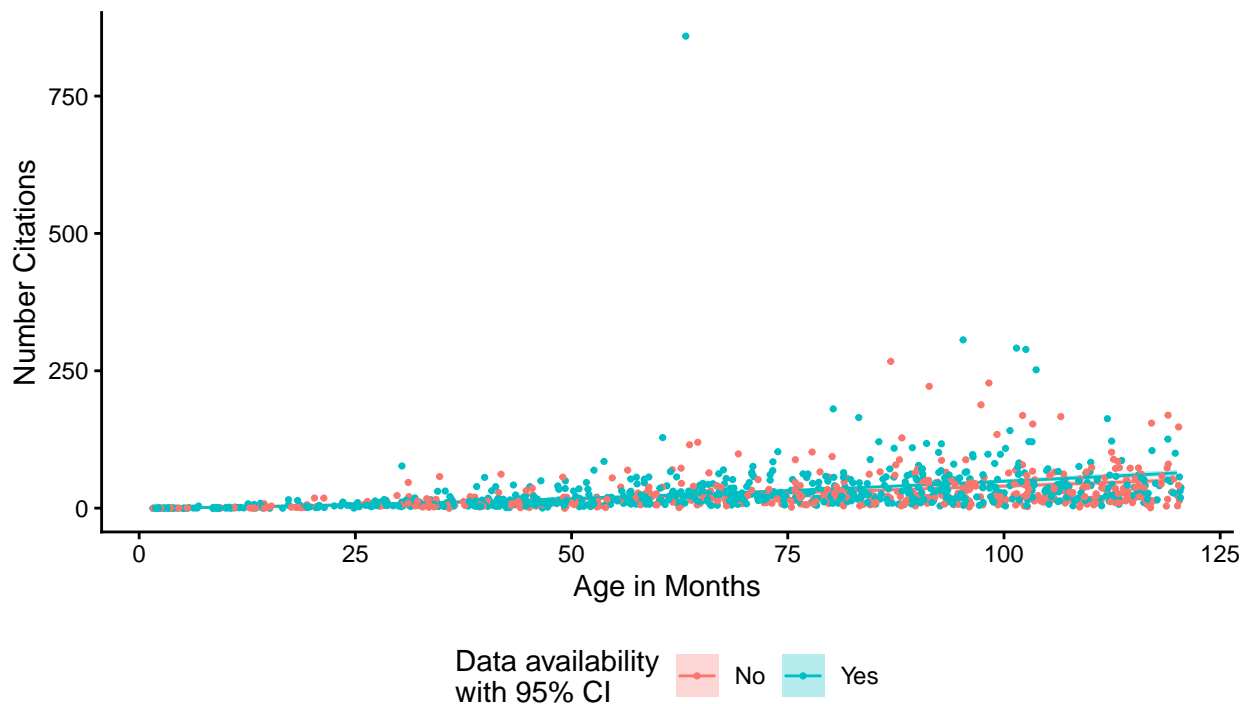
ggplot() +
  # mapping = aes(x = age.in.months, y = predicted_citations,
  #               color = da_factor)) +
  geom_line(data = model_data, aes(x = age.in.months, y = predicted_citations, group = da_factor, color = da_factor)) +
  geom_ribbon(data = model_data, mapping = aes(x = age.in.months, y = predicted_citations, ymin = lower_95, ymax = upper_95,
  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", 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)
}

```

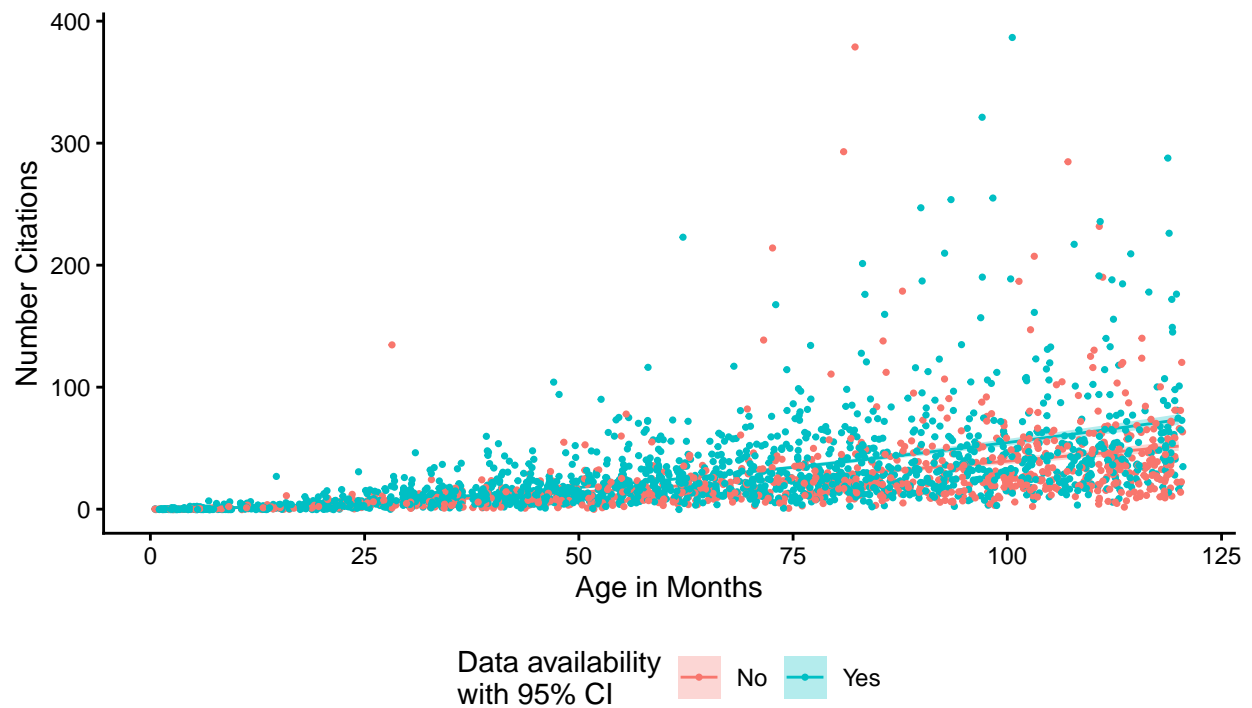
Model vs True Number of Citations from GLM.NB for Antimicrobial Agents and Chemotherapy

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



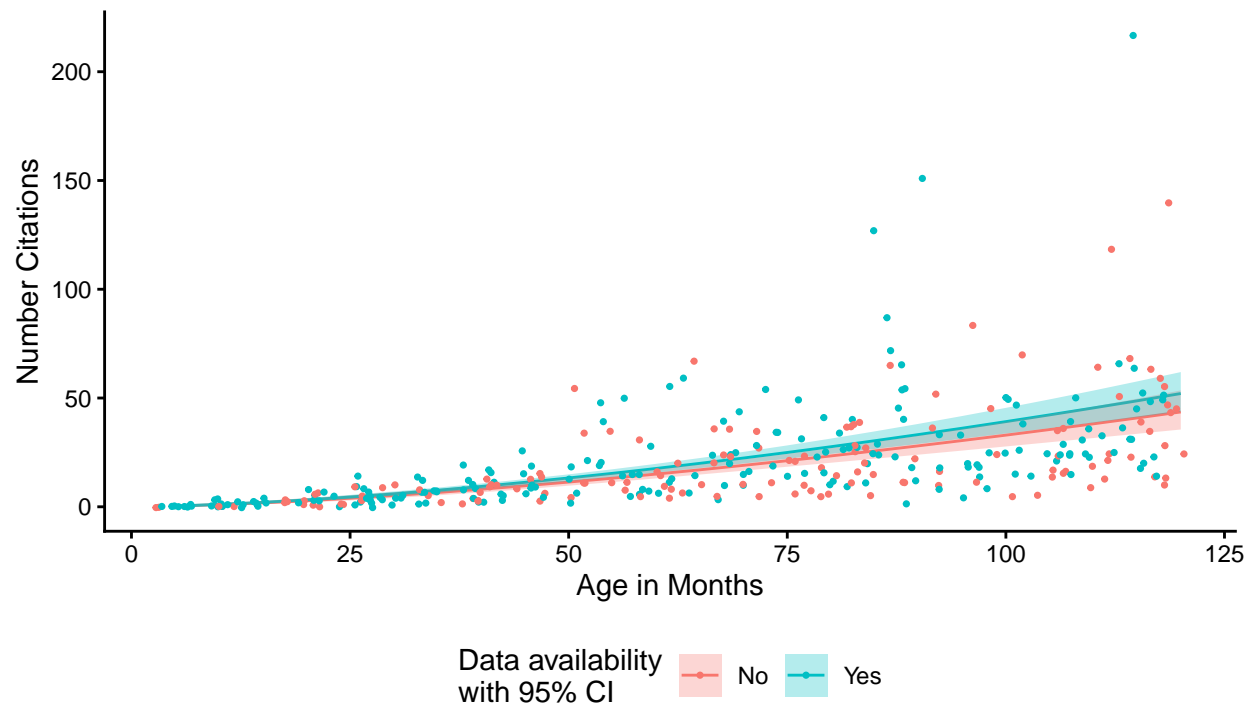
Model vs True Number of Citations from GLM.NB for Applied and Environmental Microbiology

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



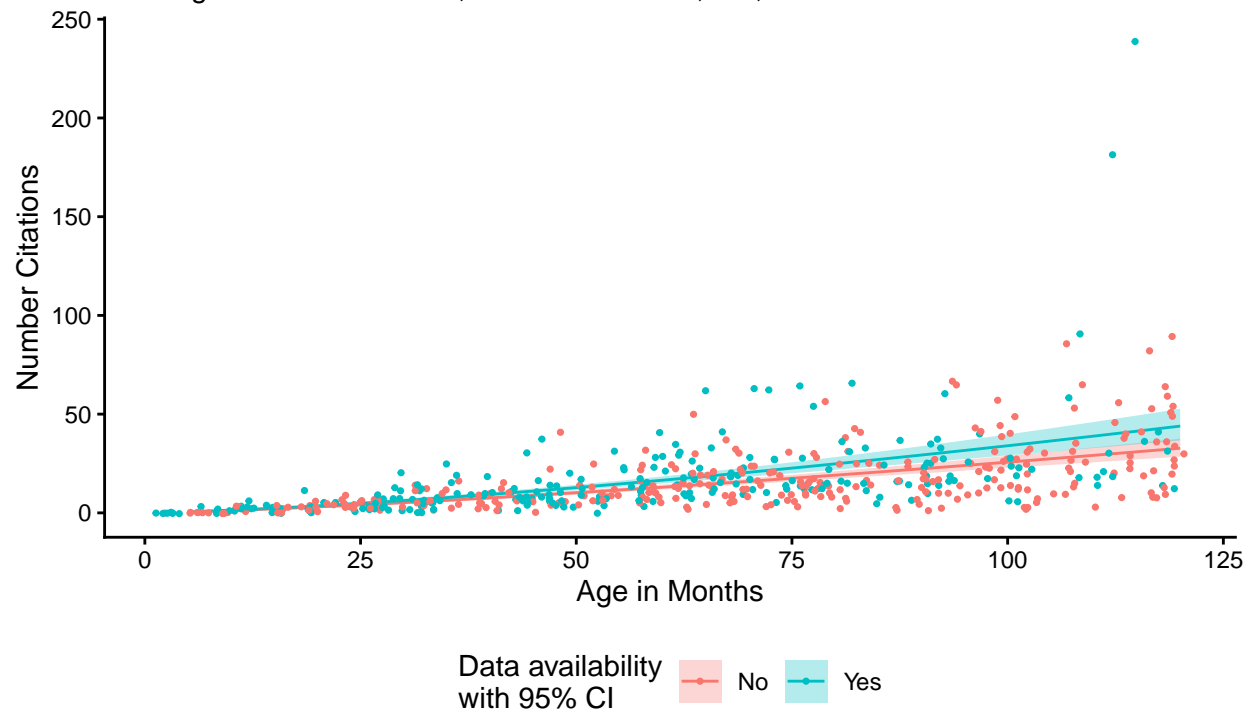
Model vs True Number of Citations from GLM.NB for Infection and Immunity

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



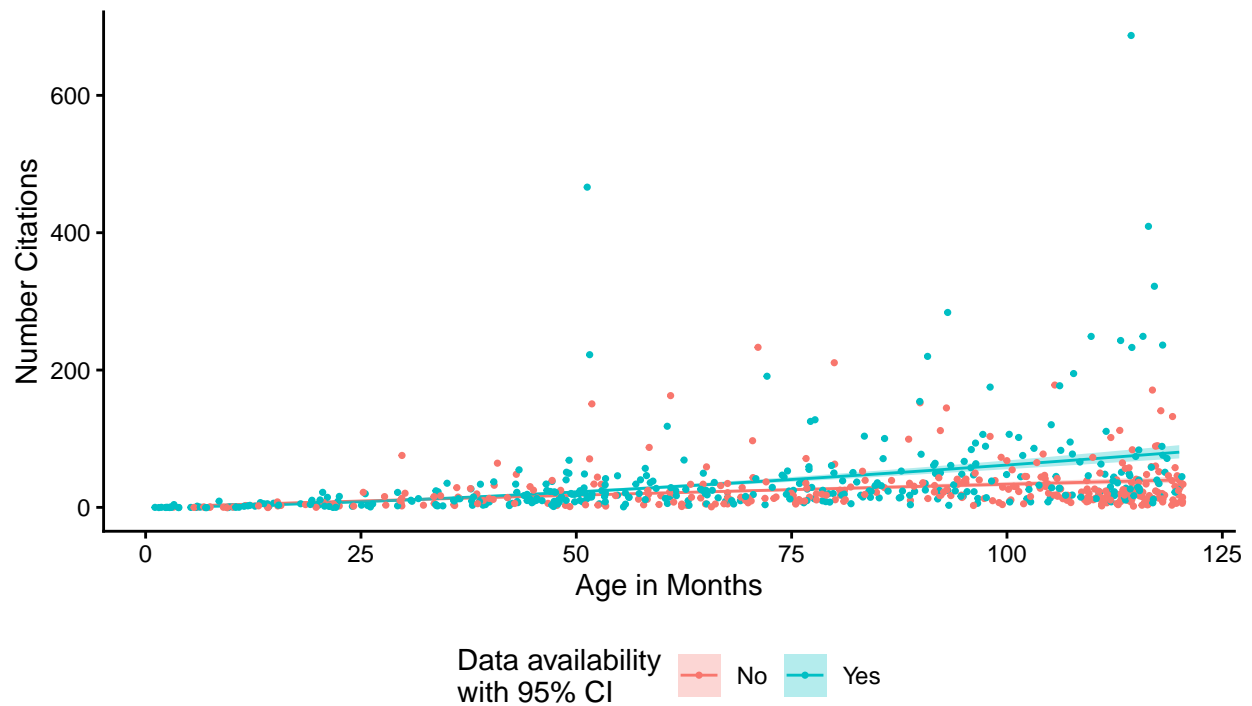
Model vs True Number of Citations from GLM.NB for Journal of Bacteriology

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



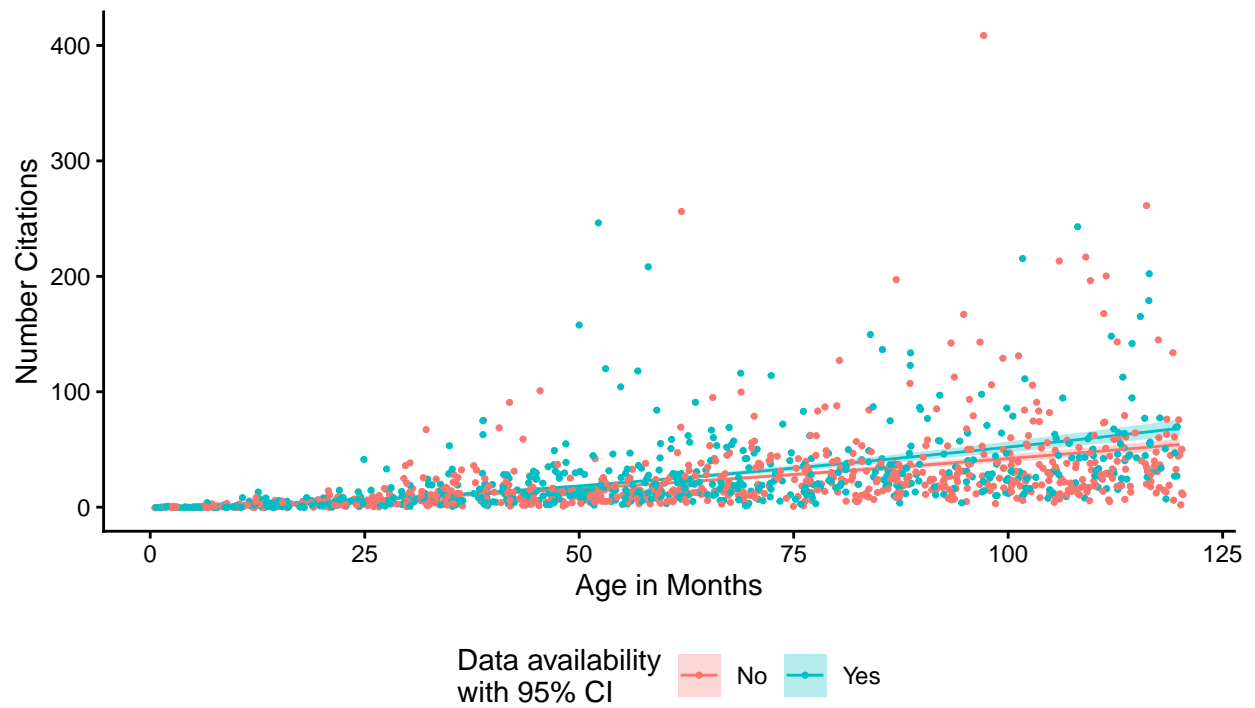
Model vs True Number of Citations from GLM.NB for Journal of Clinical Microbiology

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



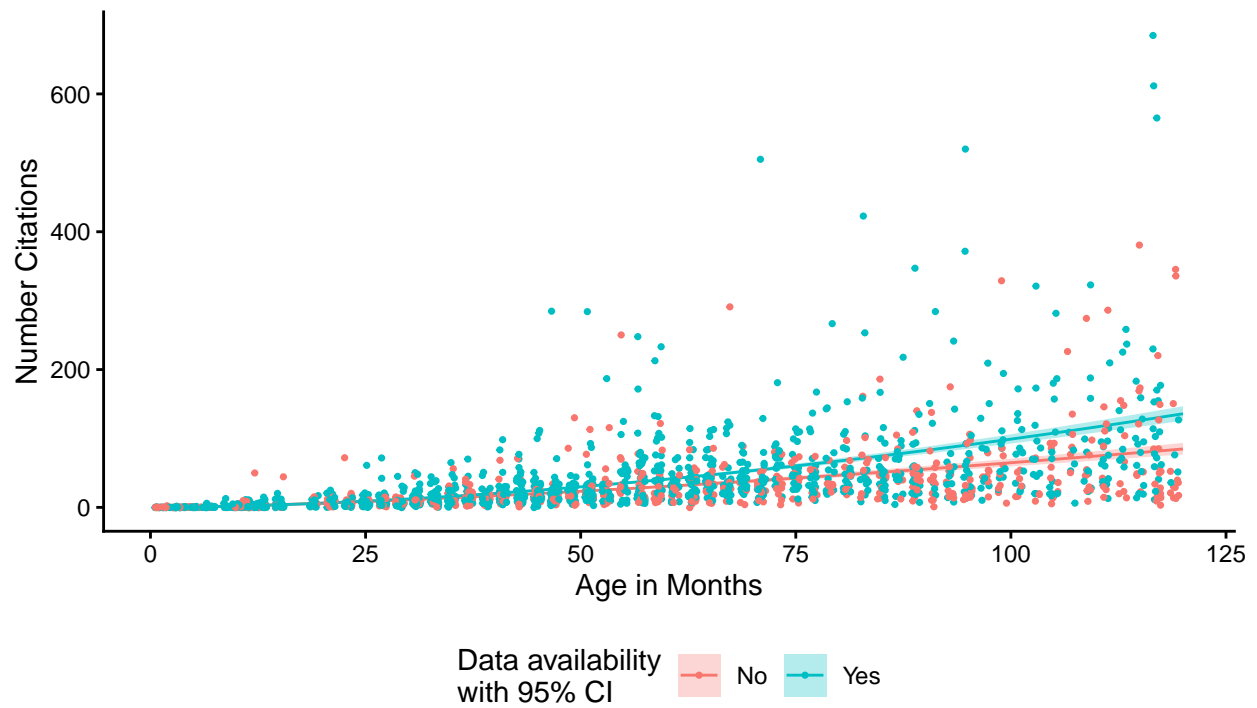
Model vs True Number of Citations from GLM.NB for Journal of Virology

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



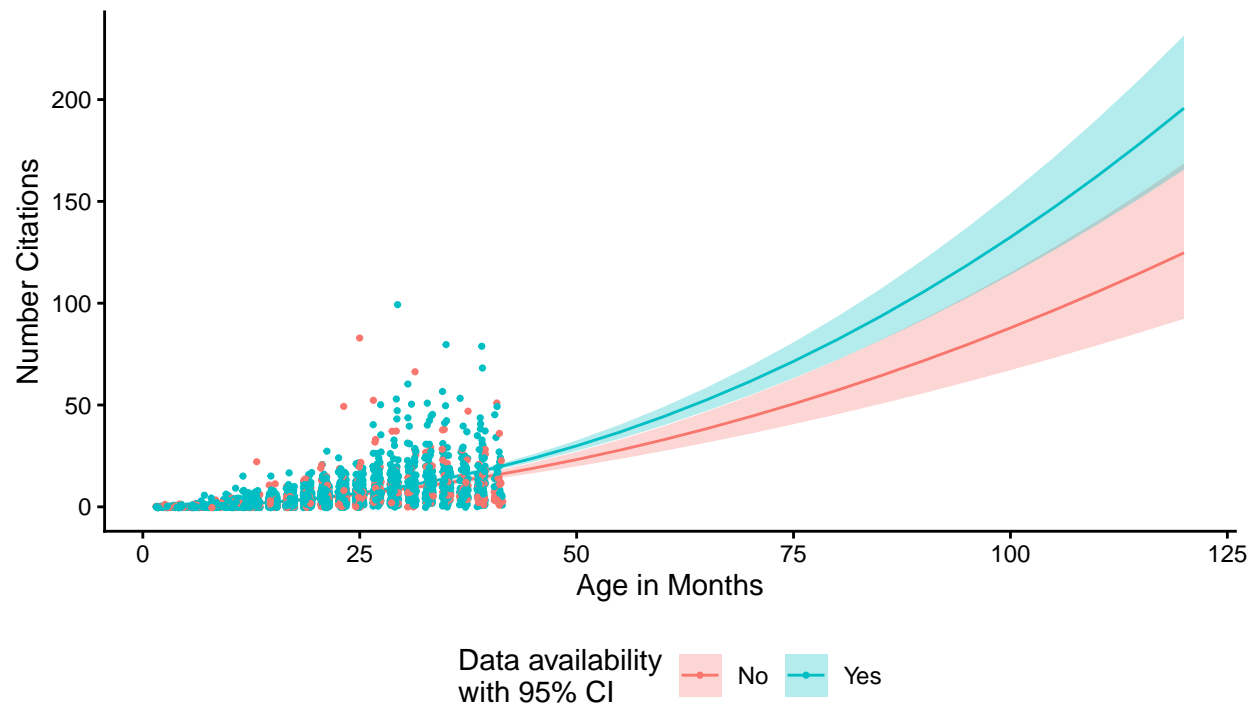
Model vs True Number of Citations from GLM.NB for mBio

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



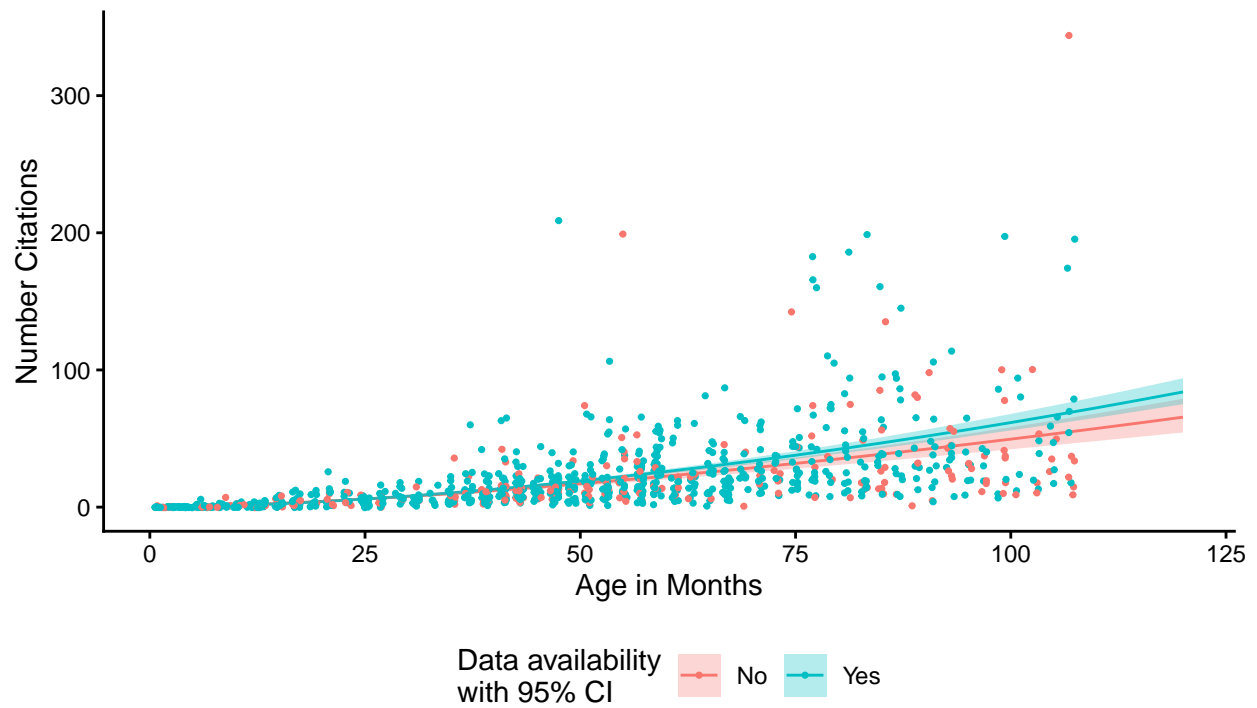
Model vs True Number of Citations from GLM.NB for Microbiology Spectrum

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



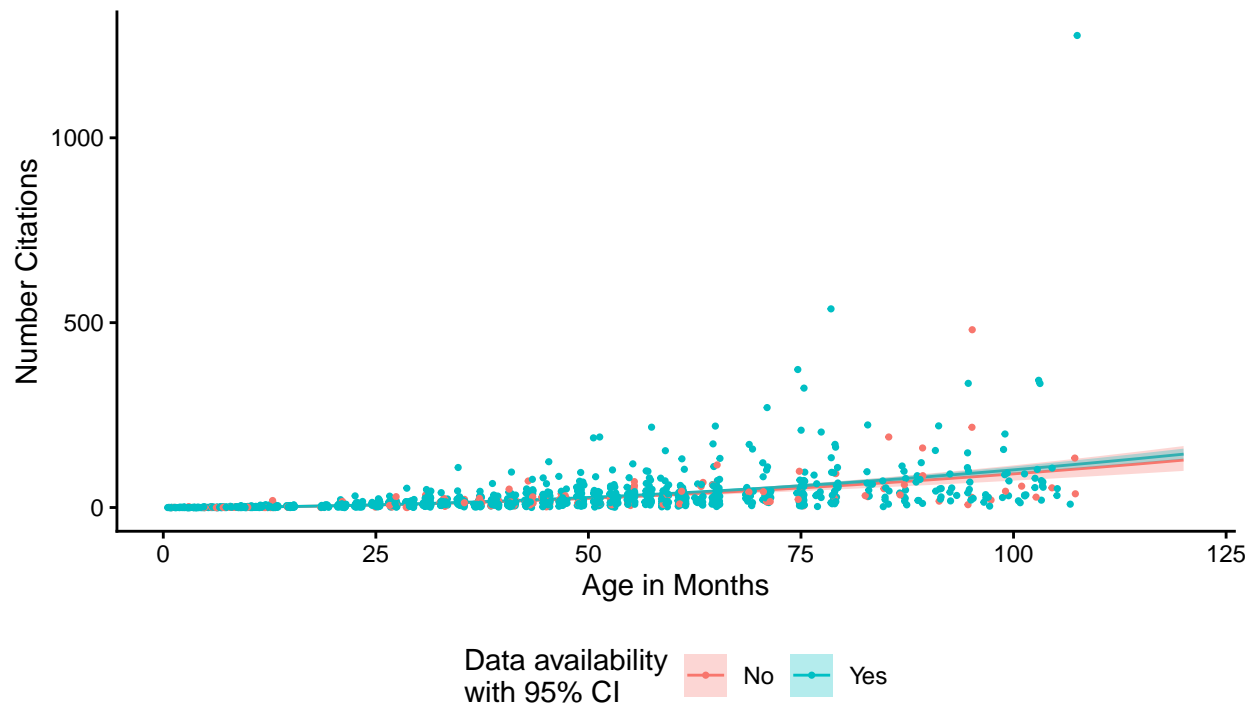
Model vs True Number of Citations from GLM.NB for mSphere

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 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)

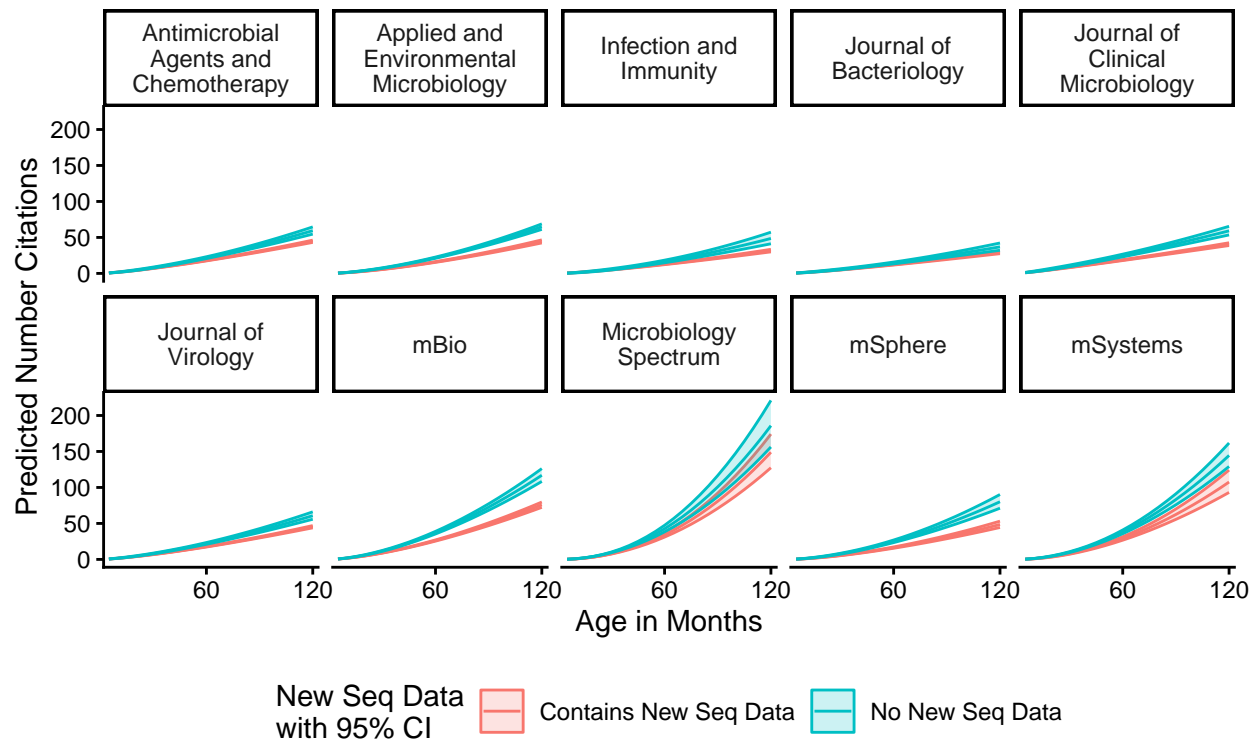
predicted_plot_nsd <-
  ggplot(data = p_nsd, mapping = aes(x = as.numeric(age.in.months), y = predicted_citations,
    color = nsd_factor)) +
  geom_line(aes(x = age.in.months, y = predicted_citations, group = nsd_factor)) +
  geom_ribbon(mapping = aes(ymin = conf.low, ymax = conf.high,
    group = nsd_factor,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

```


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:~ 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]])

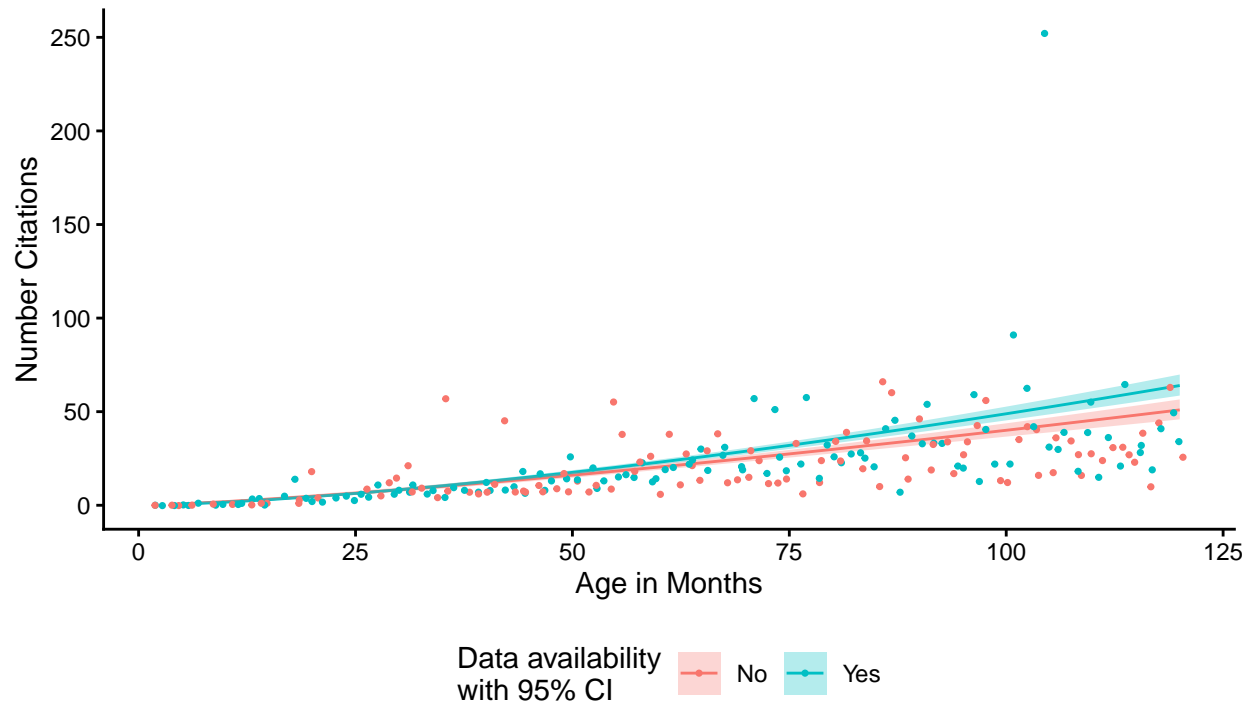
  j_monthly <-
    j_metadata %>%
      summarize(monthly_median = median(is.referenced.by.count),
                .by = c("da_factor", "age.in.months"))

  #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)))

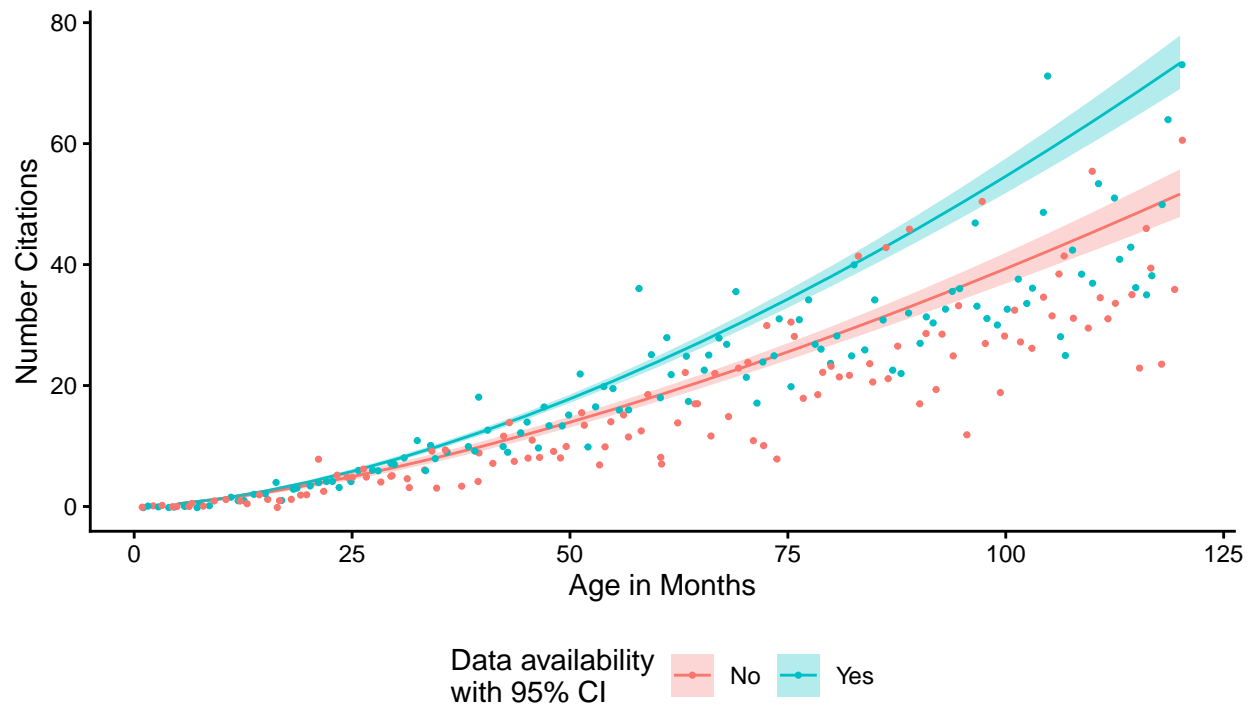
  #make plot
  plot <-
  ggplot() +
    geom_line(data = model_data, aes(x = age.in.months, y = predicted_citations, group = da_factor, color = da_factor),
              alpha = 0.3) +
    geom_ribbon(data = model_data, mapping = aes(x = age.in.months, y = predicted_citations, group = da_factor, fill = da_factor),
               ymin = 0, ymax = predicted_citations, 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", 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

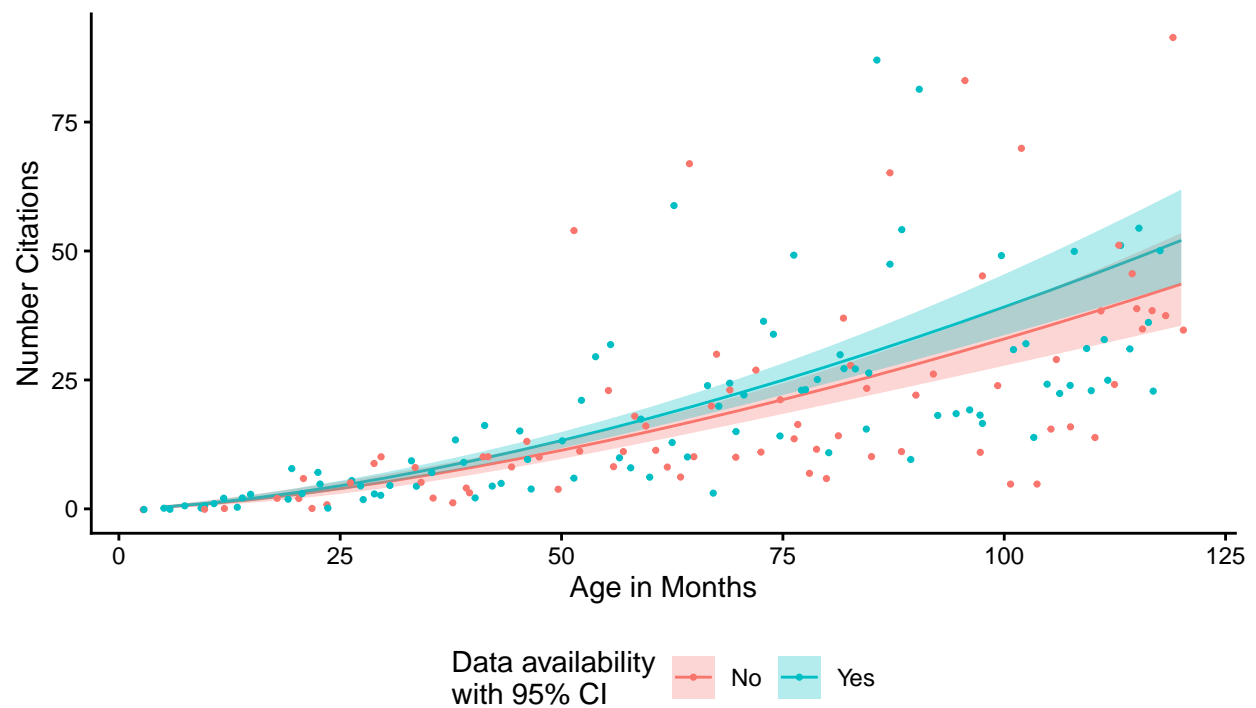


Model vs True Median Number of Citations from GLM.NB for
Applied and Environmental Microbiology binned by month and da status me
Data age.in.months <= 120, removal of JMBE, GA, MRA



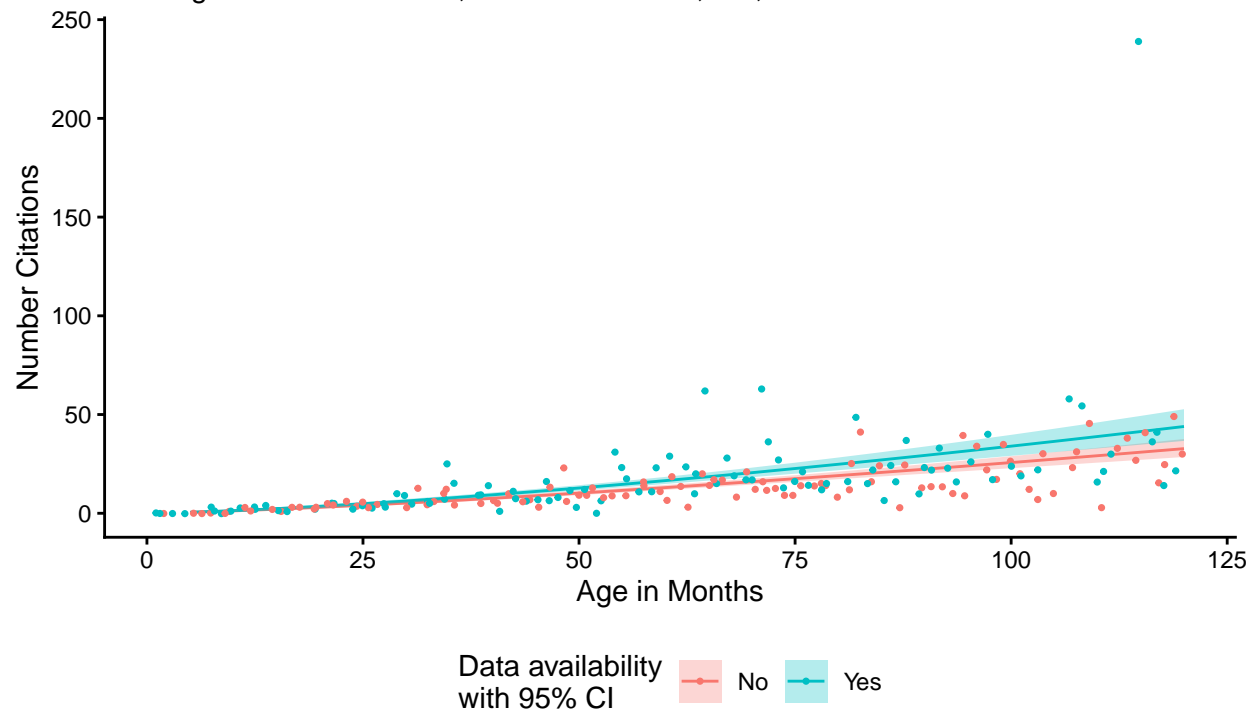
Model vs True Median Number of Citations from GLM.NB for Infection and Immunity binned by month and da status median

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

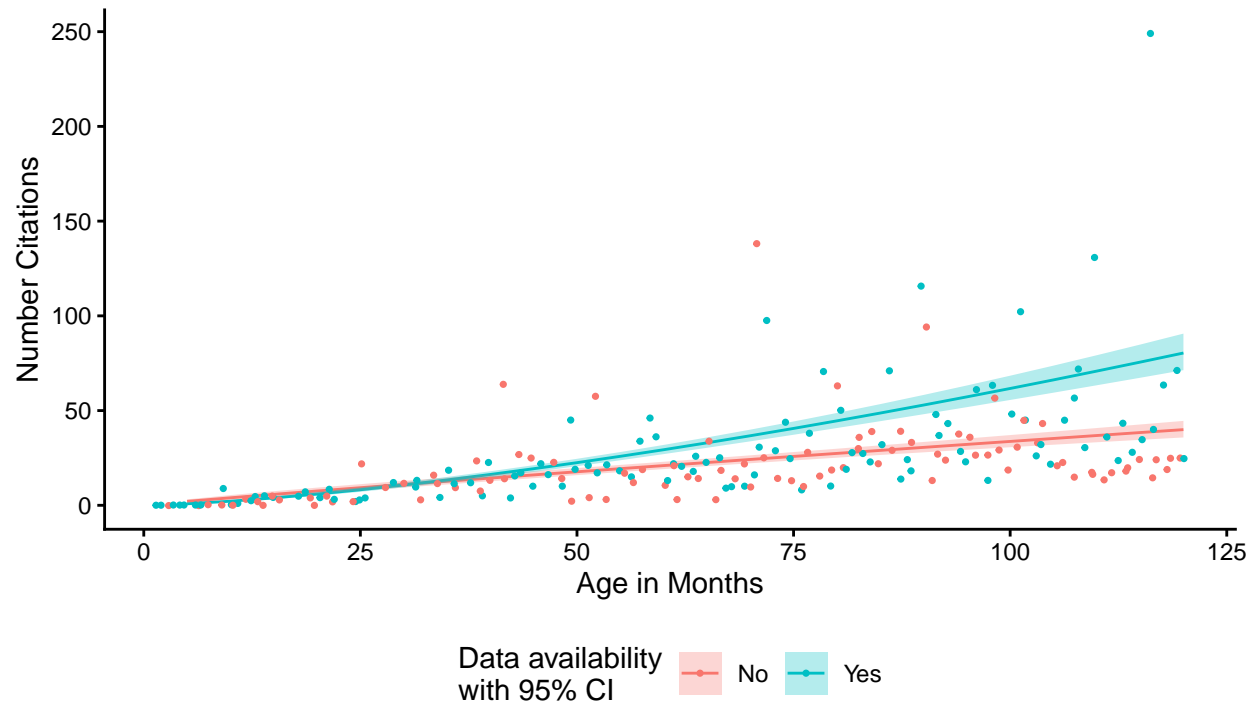


Model vs True Median Number of Citations from GLM.NB for
Journal of Bacteriology binned by month and da status median

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

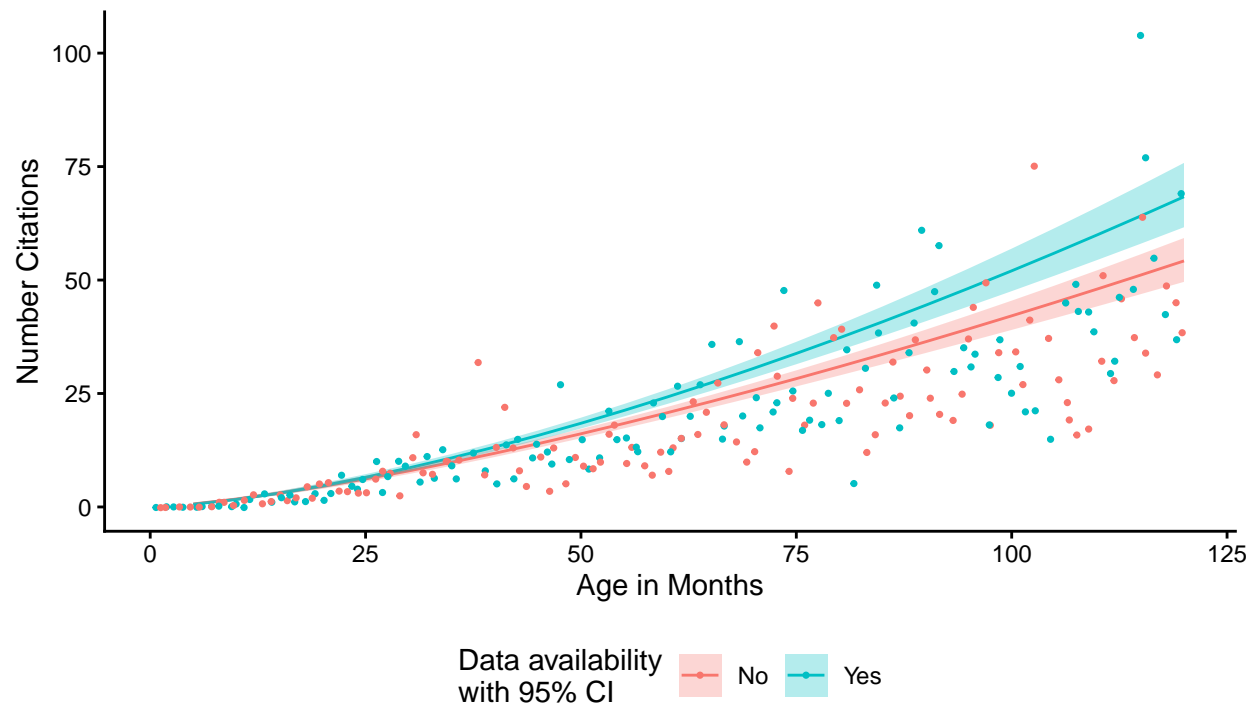


Model vs True Median Number of Citations from GLM.NB for
Journal of Clinical Microbiology binned by month and da status median
Data age.in.months <= 120, removal of JMBE, GA, MRA



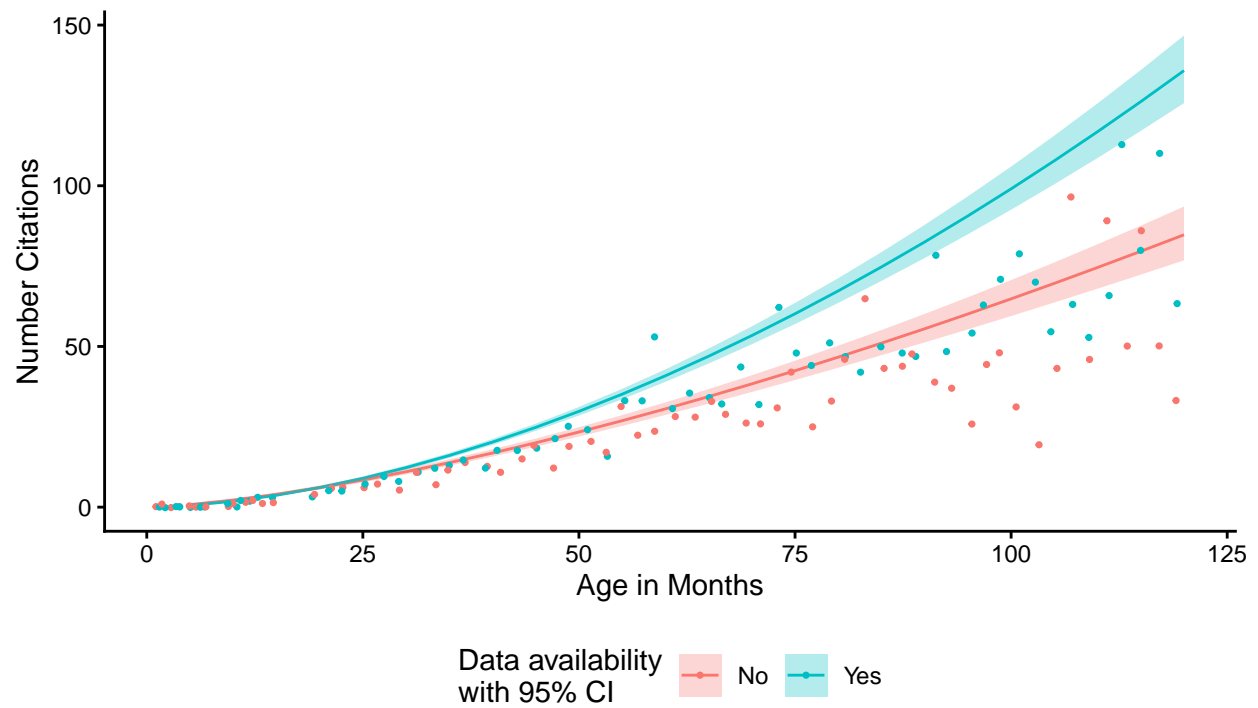
Model vs True Median Number of Citations from GLM.NB for
Journal of Virology binned by month and da status median

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

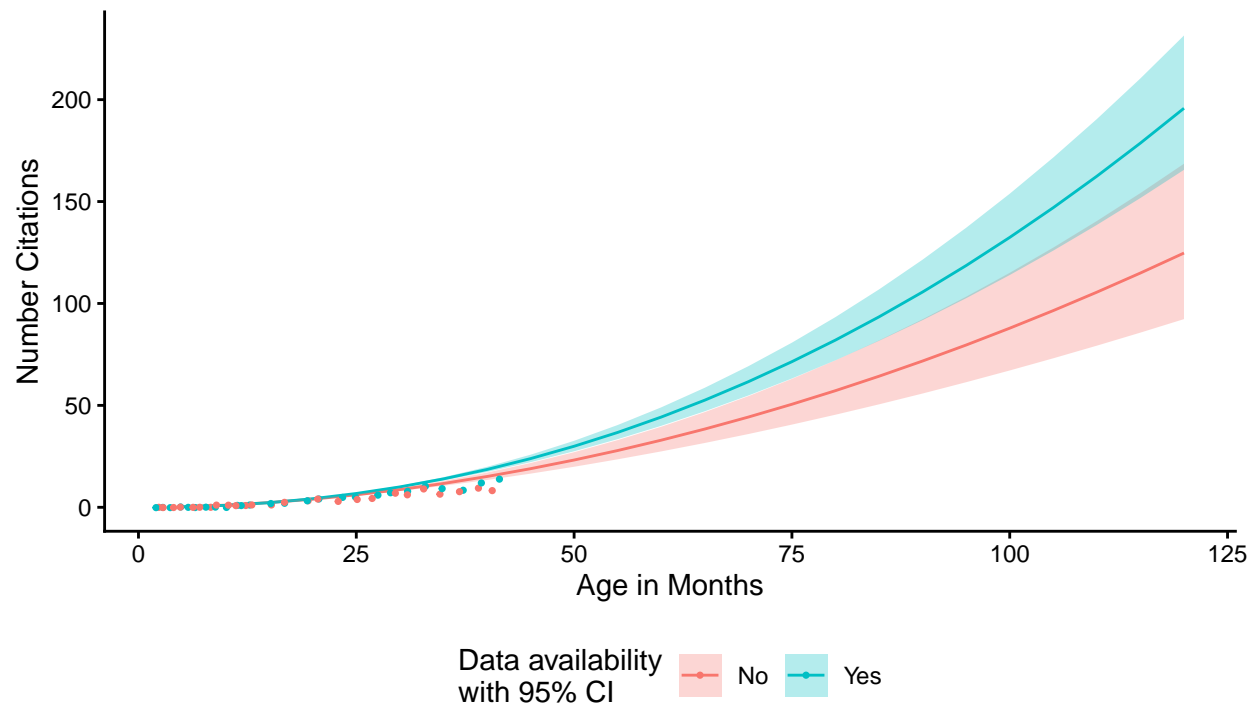


Model vs True Median Number of Citations from GLM.NB for mBio binned by month and da status median

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

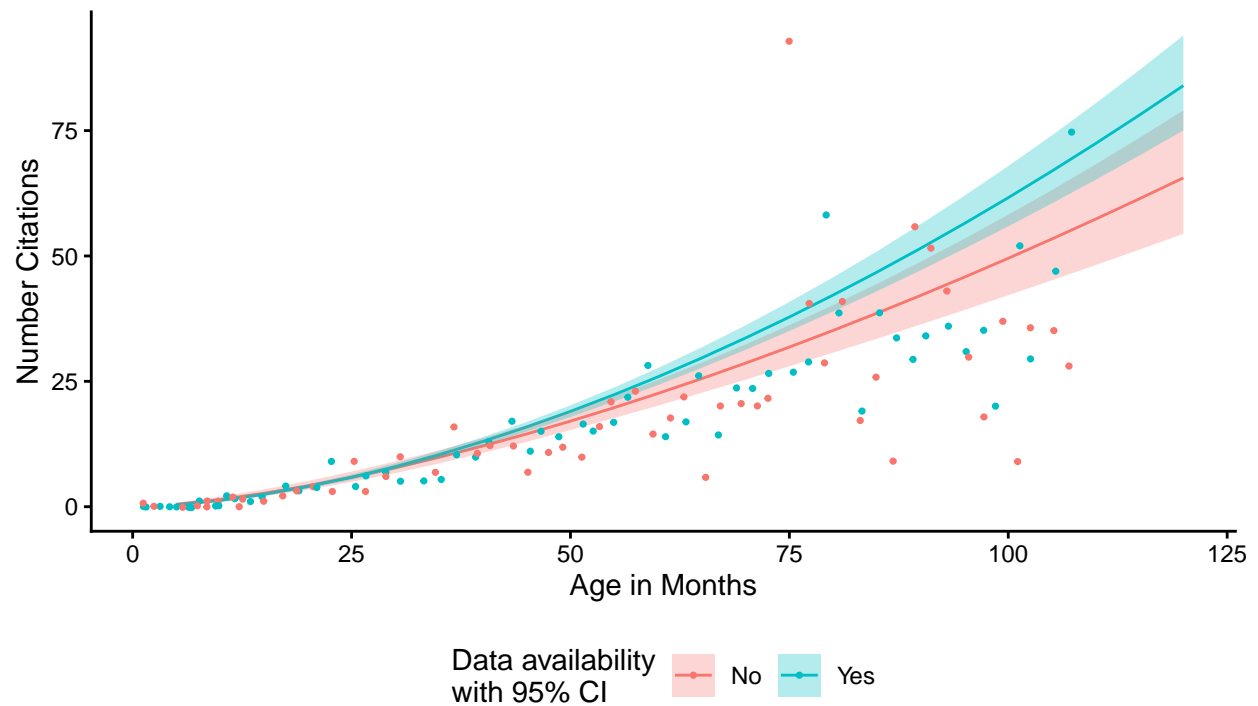


Model vs True Median Number of Citations from GLM.NB for
Microbiology Spectrum binned by month and da status median
Data age.in.months <= 120, removal of JMBE, GA, MRA



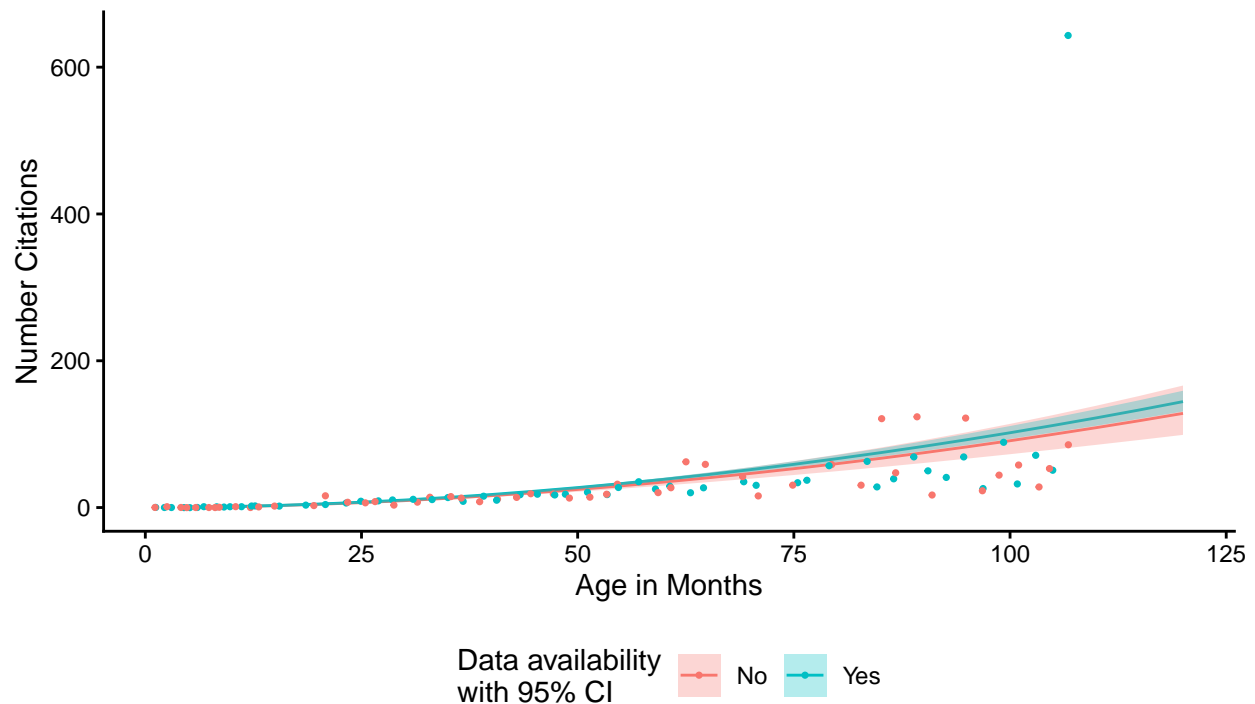
Model vs True Median Number of Citations from GLM.NB for mSphere binned by month and da status median

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),
            alpha = 0.3) +
  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) +
            , 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) +

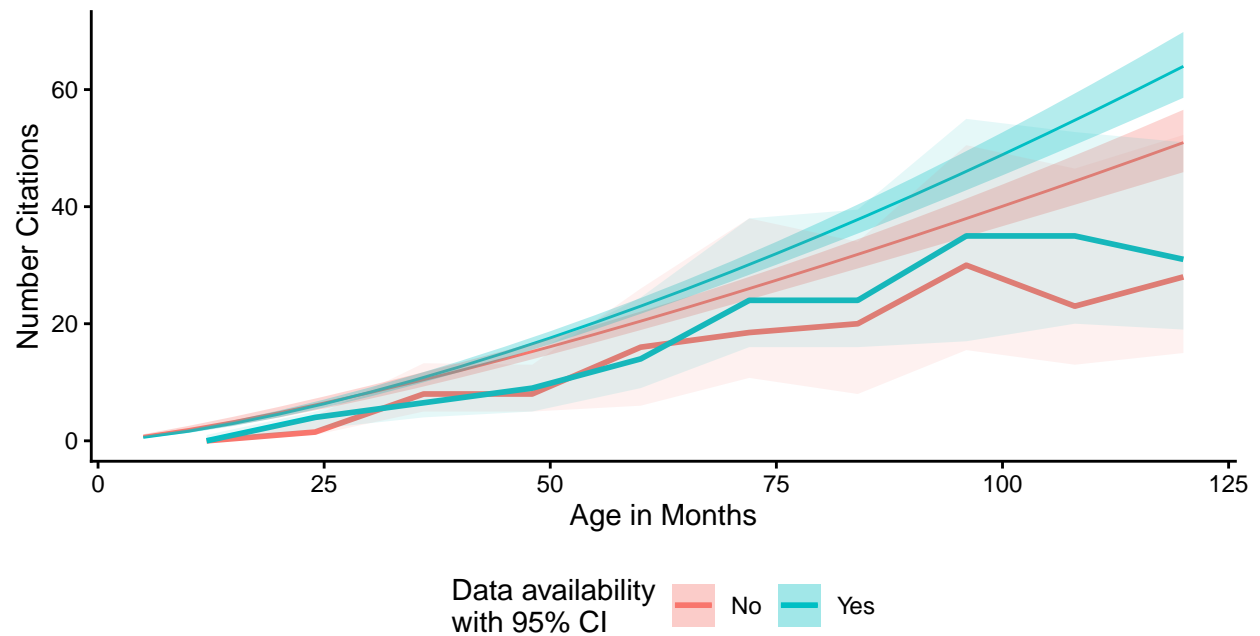
  labs(title = paste0("Model vs True Median Number of Citations from GLM.NB for\n", journals$container.title[j]),
        subtitle = "Data age.in.months <= 120, removal of JMBE, GA, MRA\nLighter values = median and 95% CI",
        x = "Age in Months",
        y = "Number Citations",
        color = "Data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

print(plot)
}

```

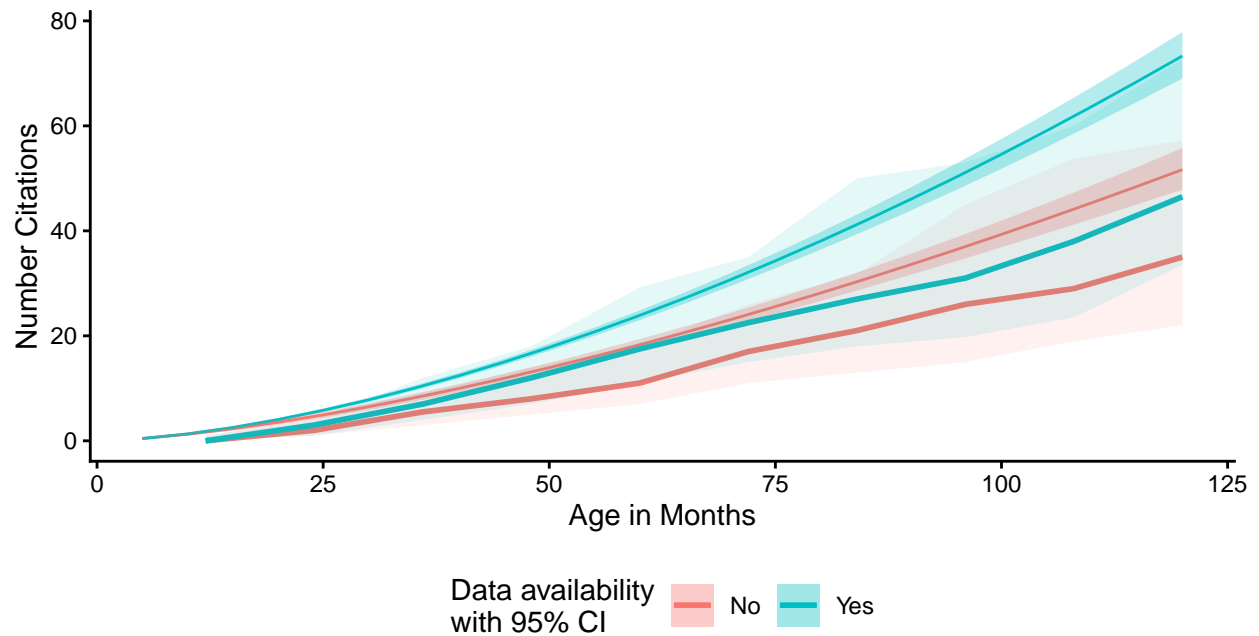
Model vs True Median Number of Citations from GLM.NB for
Antimicrobial Agents and Chemotherapy binned by year,
da status median, 25% & 75%

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



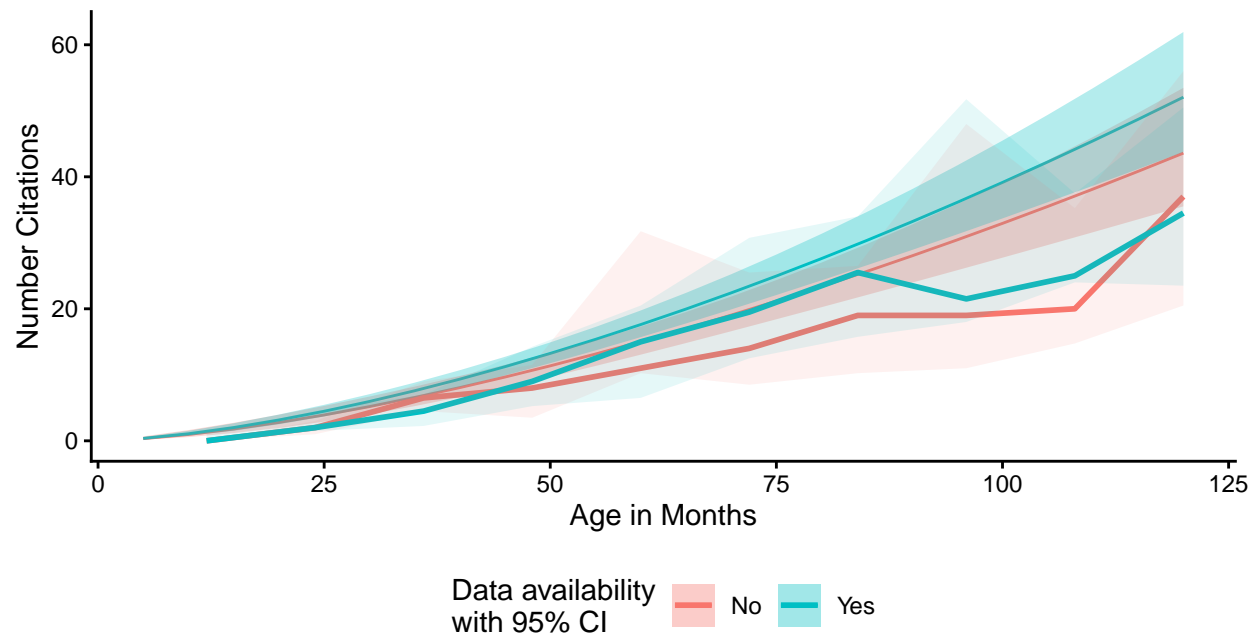
Model vs True Median Number of Citations from GLM.NB for
Applied and Environmental Microbiology binned by year,
da status median, 25% & 75%

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



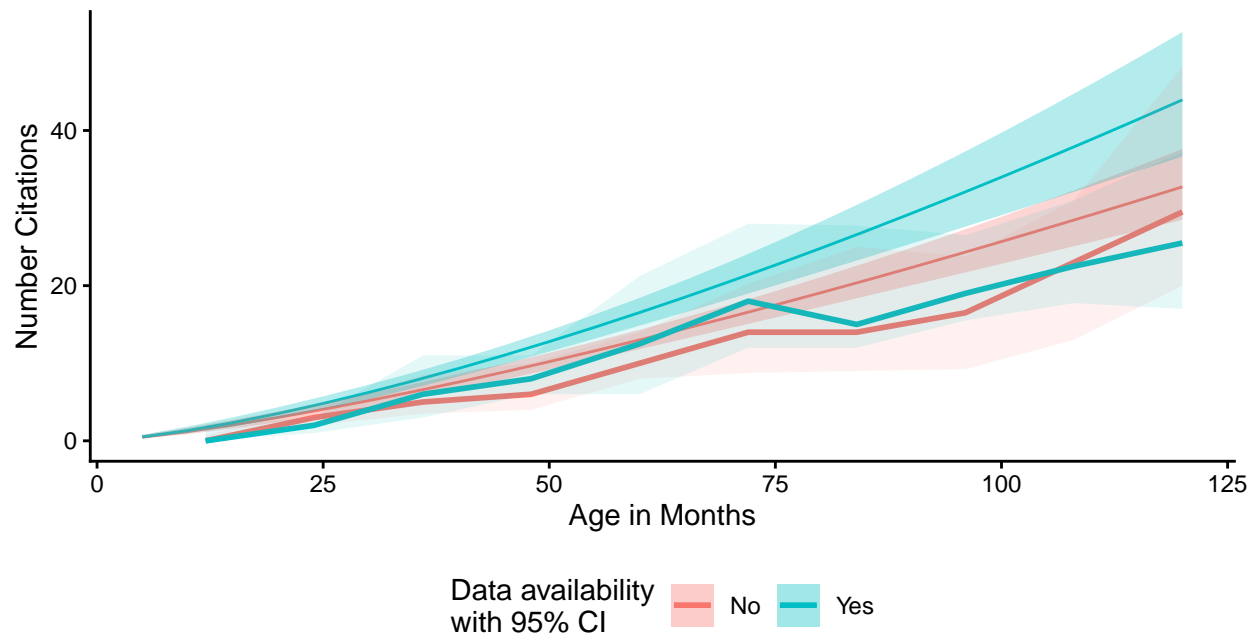
Model vs True Median Number of Citations from GLM.NB for
Infection and Immunity binned by year,
da status median, 25% & 75%

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



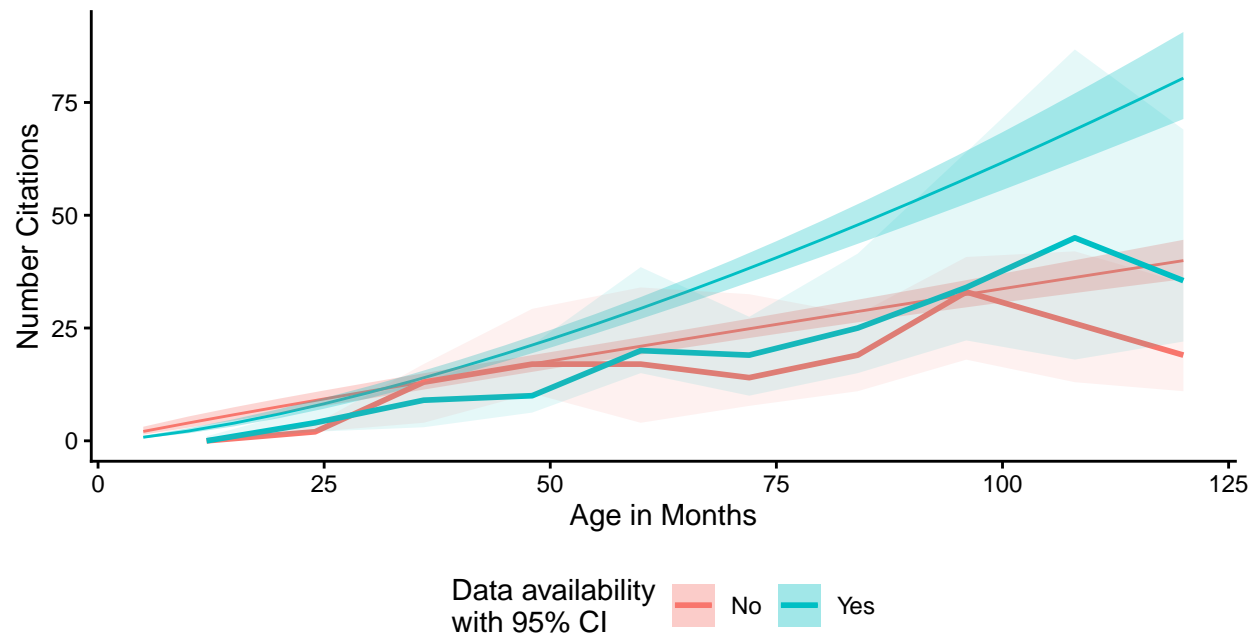
Model vs True Median Number of Citations from GLM.NB for
Journal of Bacteriology binned by year,
da status median, 25% & 75%

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



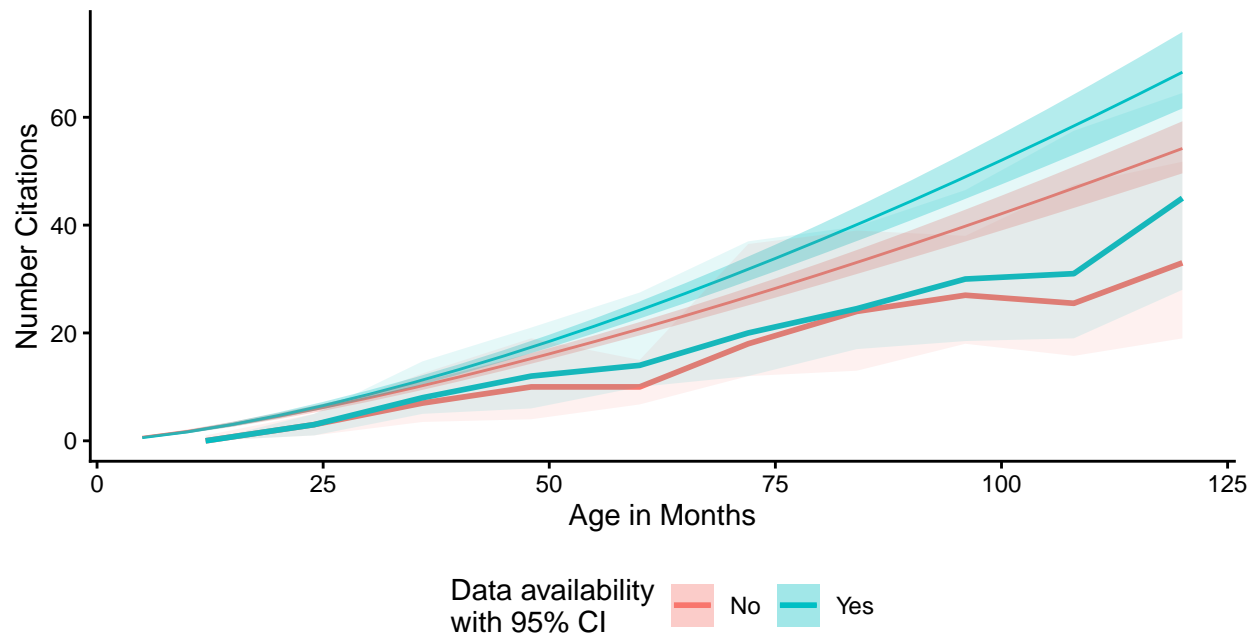
Model vs True Median Number of Citations from GLM.NB for
Journal of Clinical Microbiology binned by year,
da status median, 25% & 75%

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



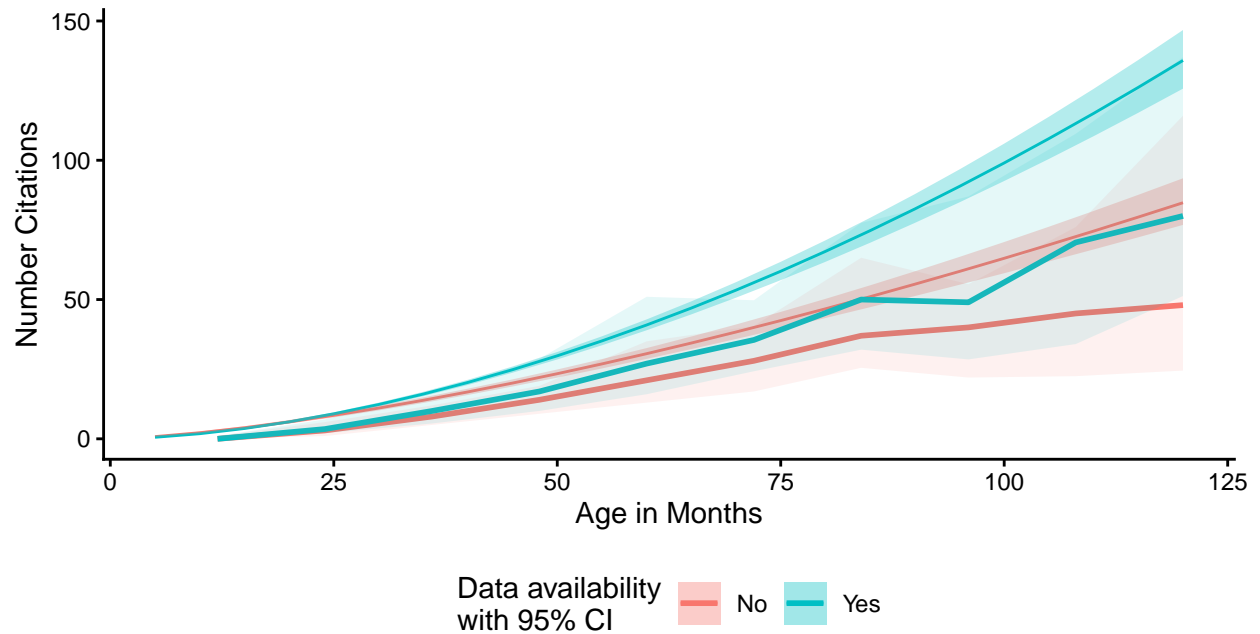
Model vs True Median Number of Citations from GLM.NB for
Journal of Virology binned by year,
da status median, 25% & 75%

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



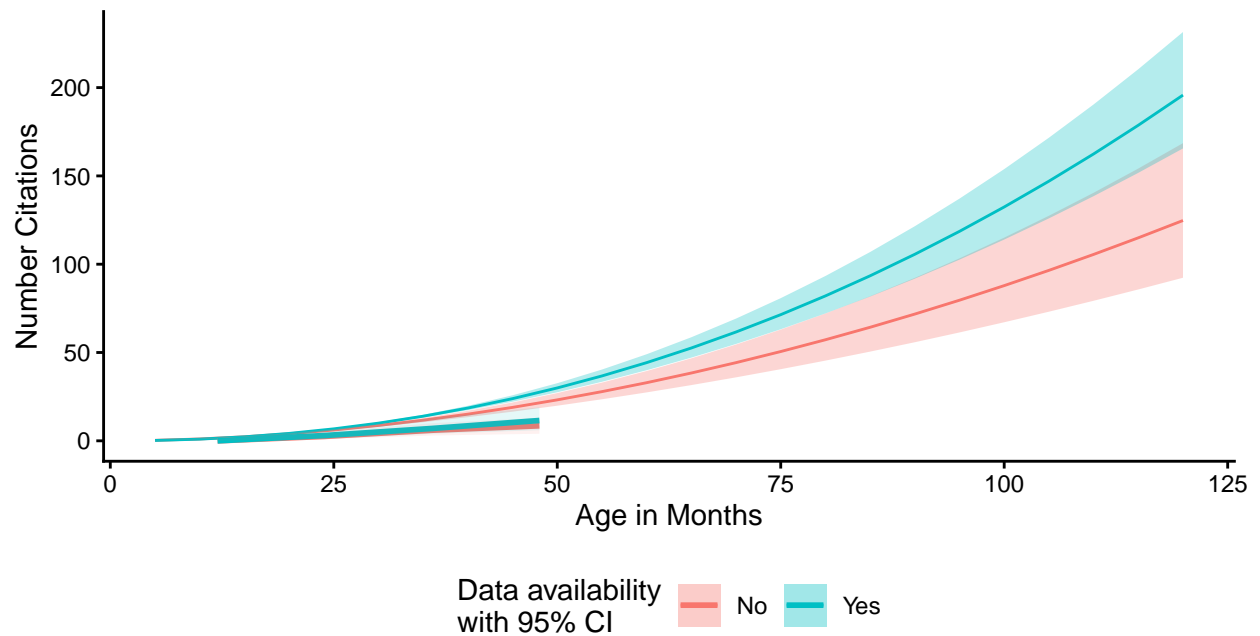
Model vs True Median Number of Citations from GLM.NB for
mBio binned by year,
da status median, 25% & 75%

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



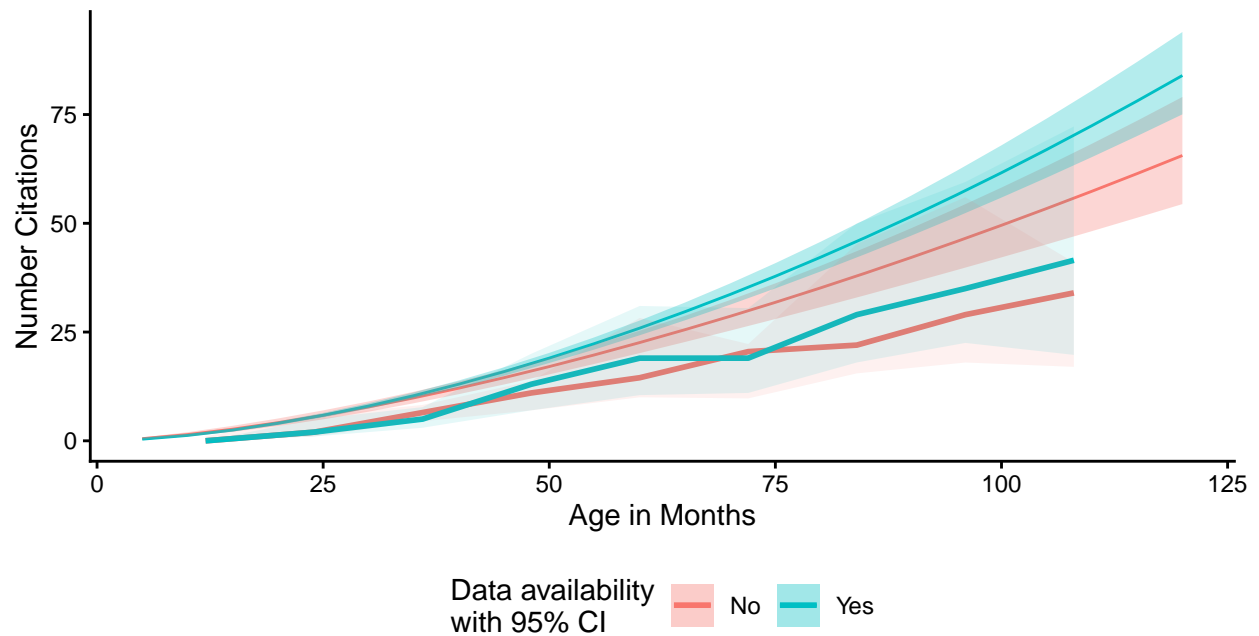
Model vs True Median Number of Citations from GLM.NB for
Microbiology Spectrum binned by year,
da status median, 25% & 75%

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



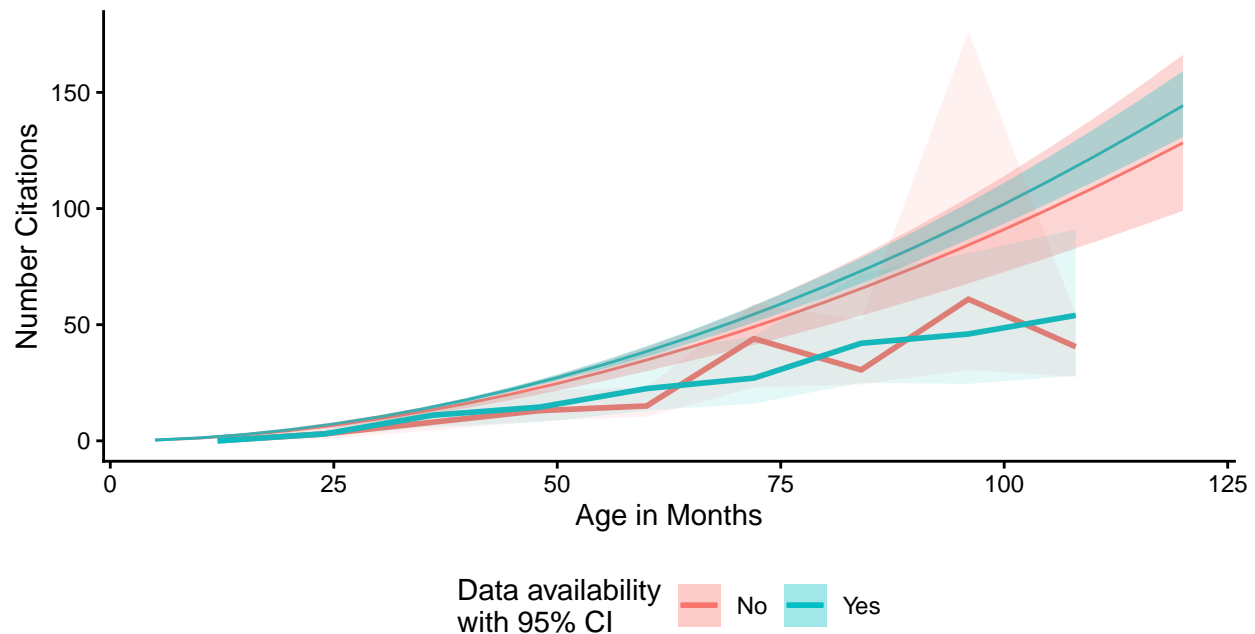
Model vs True Median Number of Citations from GLM.NB for
mSphere binned by year,
da status median, 25% & 75%

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)))
}
```

```

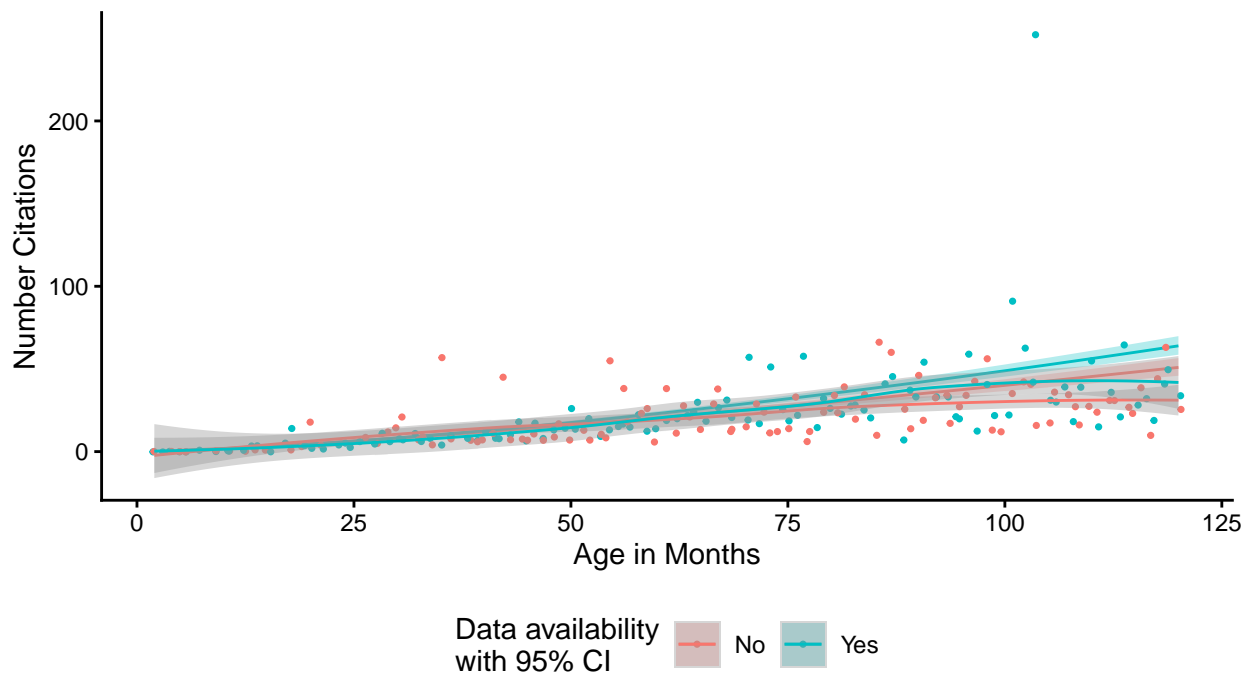
#make plot
plot <-
ggplot() +
  geom_line(data = model_data, aes(x = age.in.months, y = predicted_citations, group = da_factor, color = da_factor),
  geom_ribbon(data = model_data, mapping = aes(x = age.in.months, y = predicted_citations, y_min = c
    group = da_factor, fill = da_factor), alpha = 0.3) +
  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\n", grey 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'
```

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
grey geom_smooth through the median

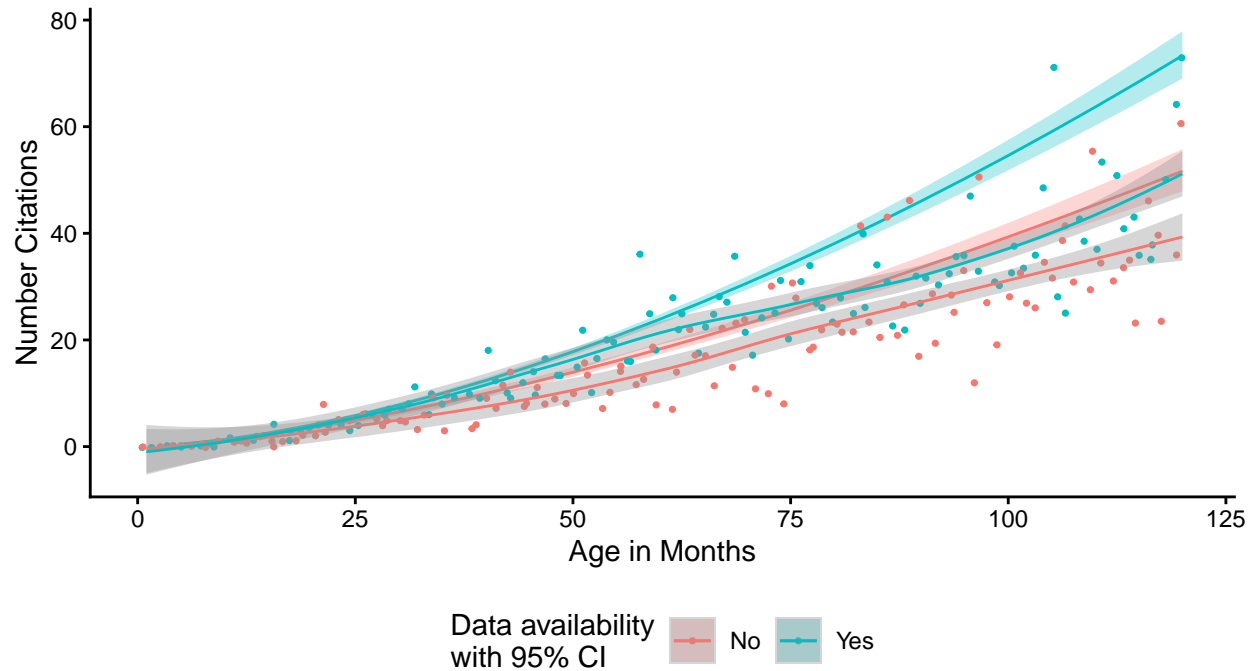



```
## 'geom_smooth()' using method = 'loess' and formula = 'y ~ x'
```

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

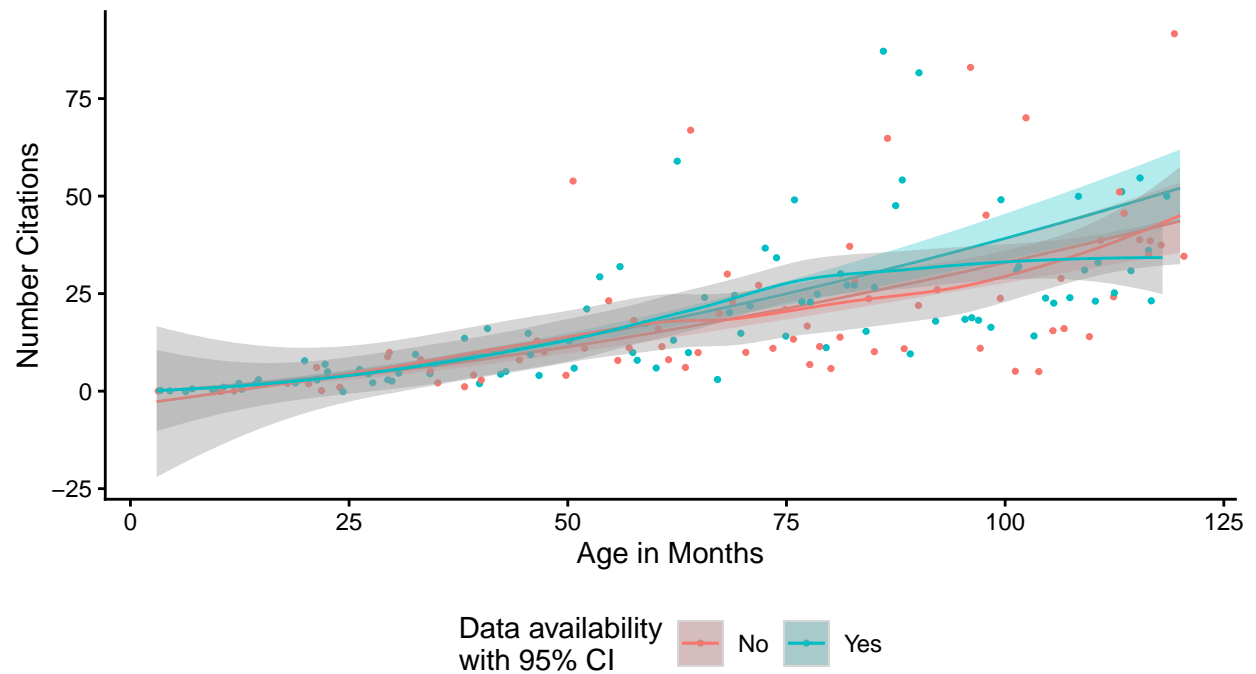
grey geom_smooth through the median



```
## '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

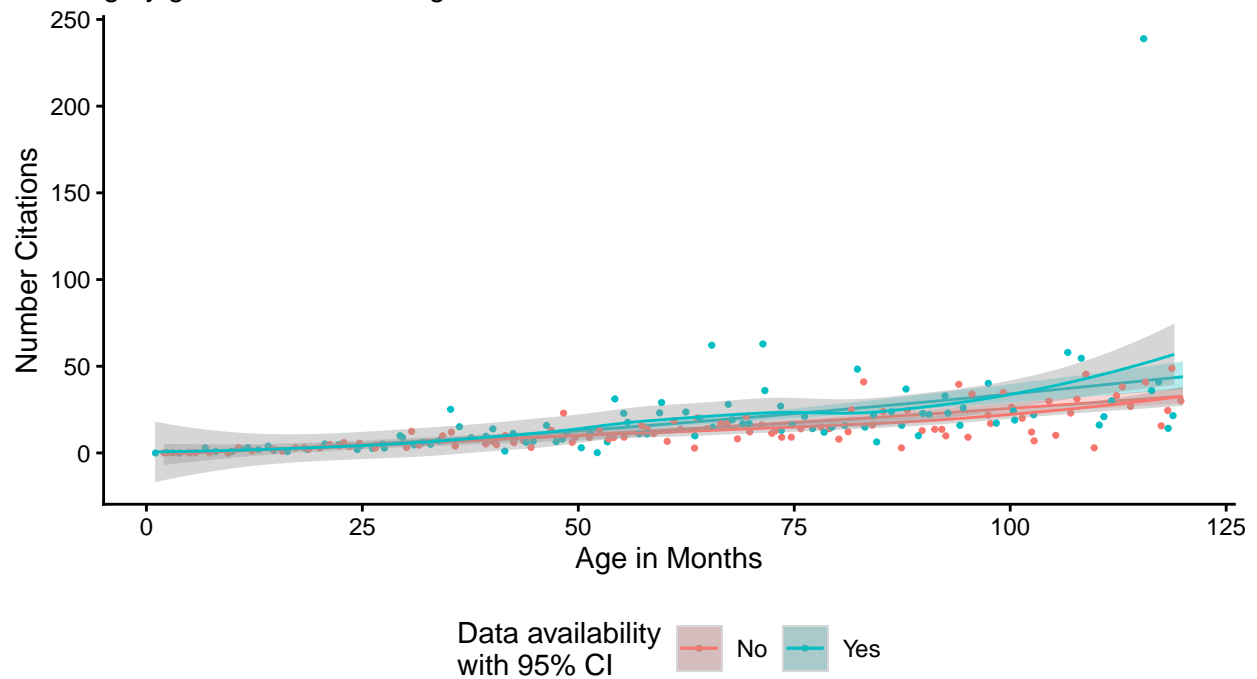
Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the median



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

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

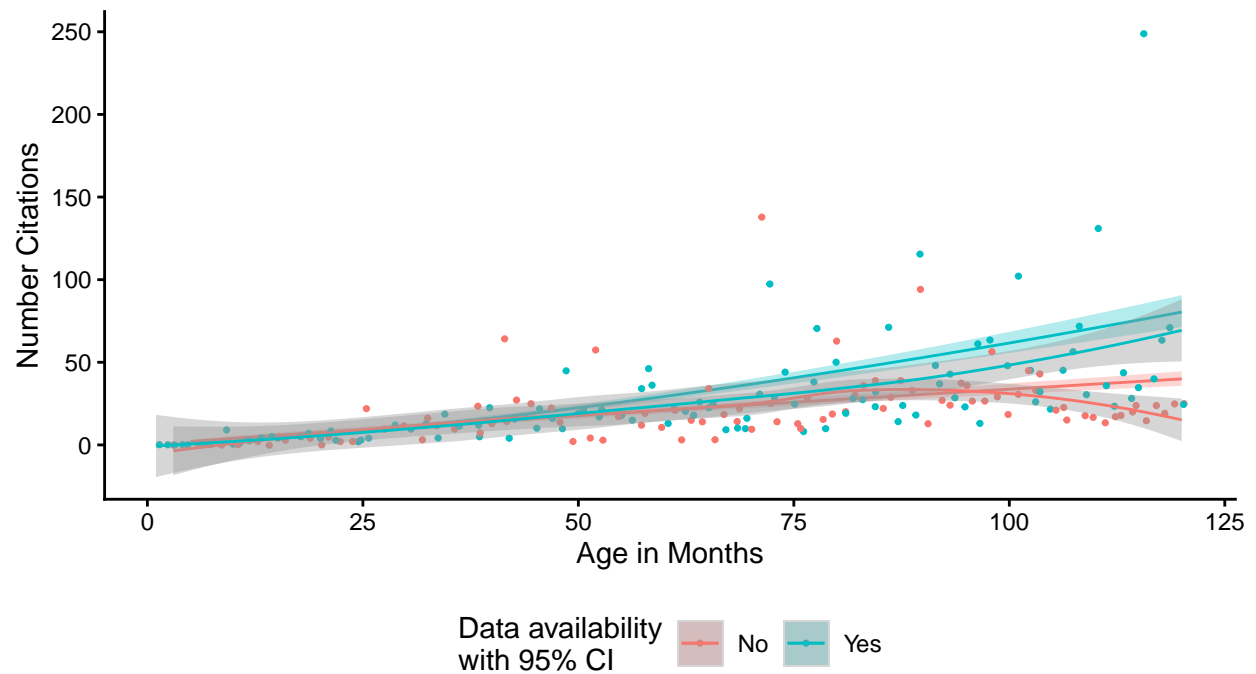
Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the median



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

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

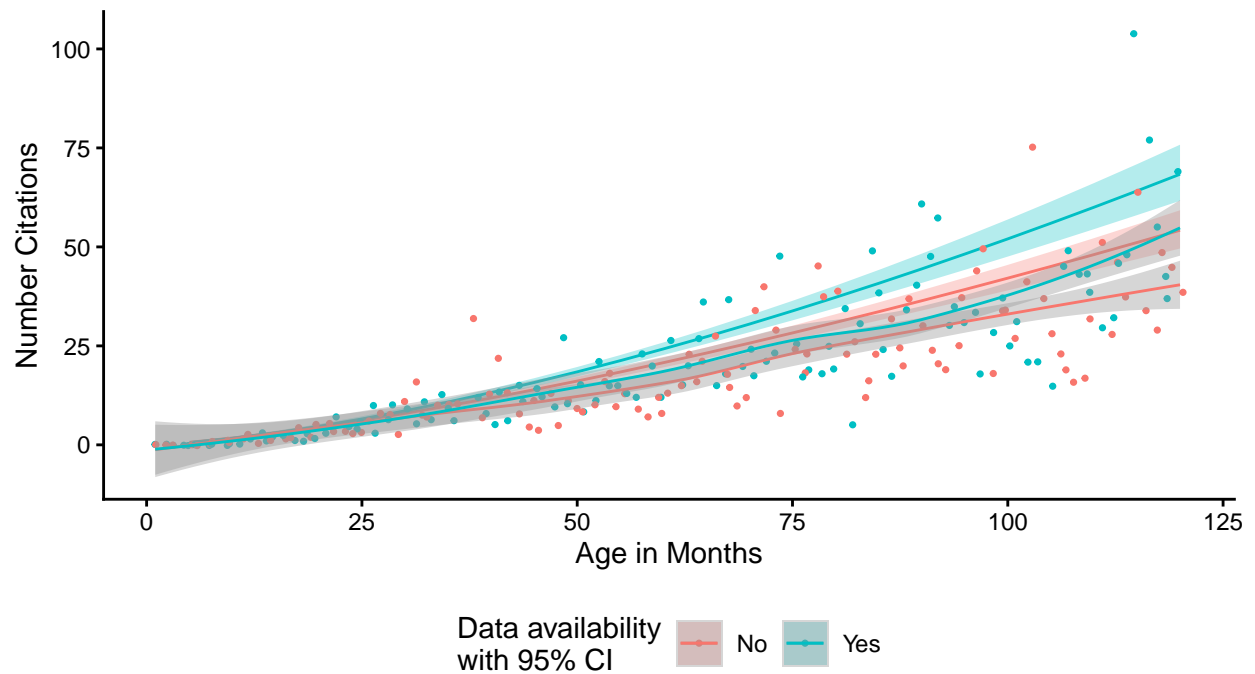
Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the median



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

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

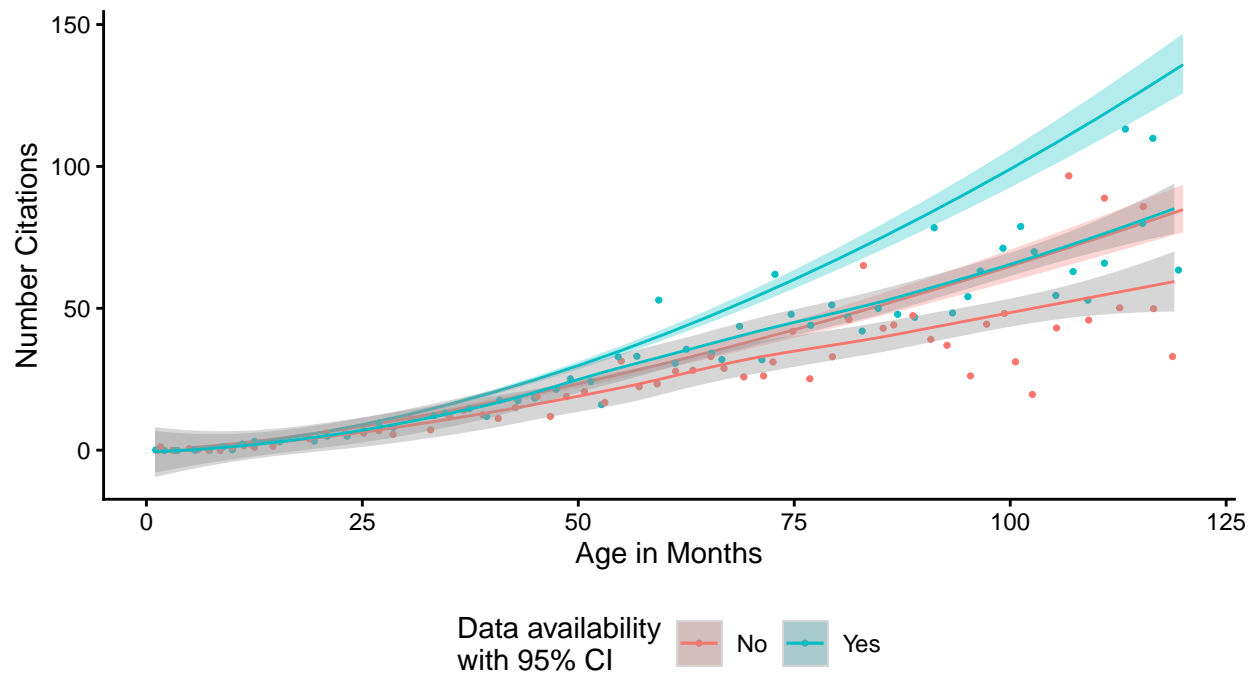
Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the median



```
## '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

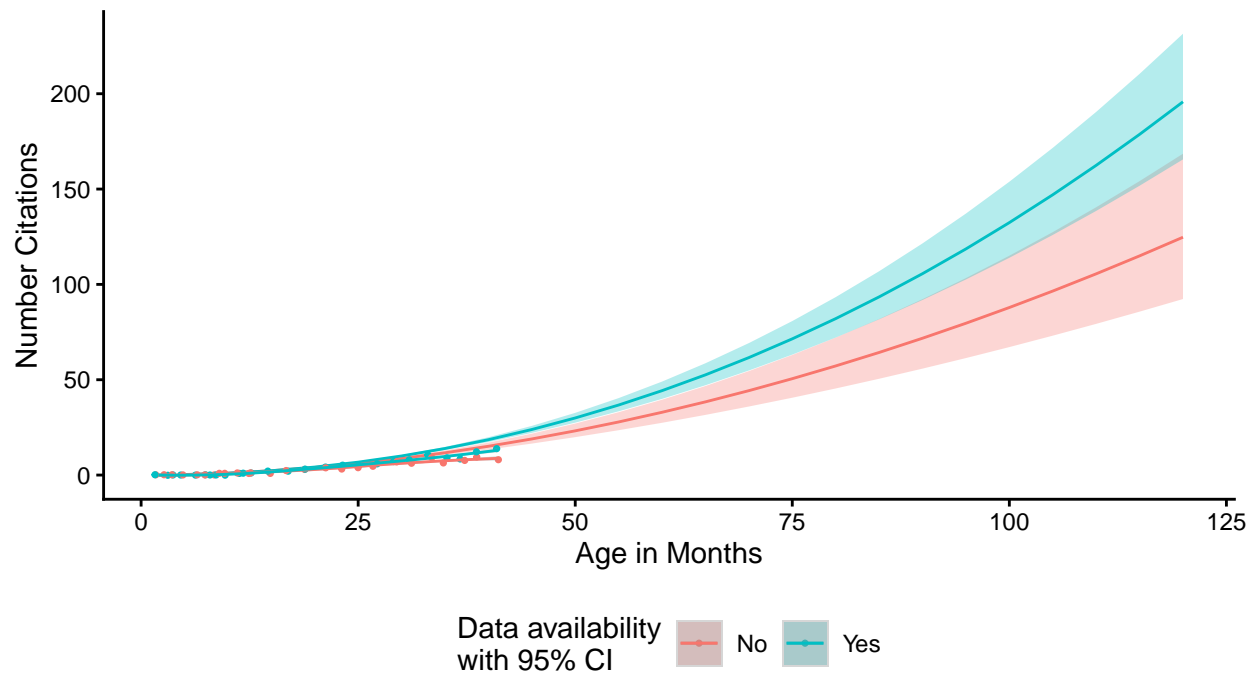
Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the median



```
## '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

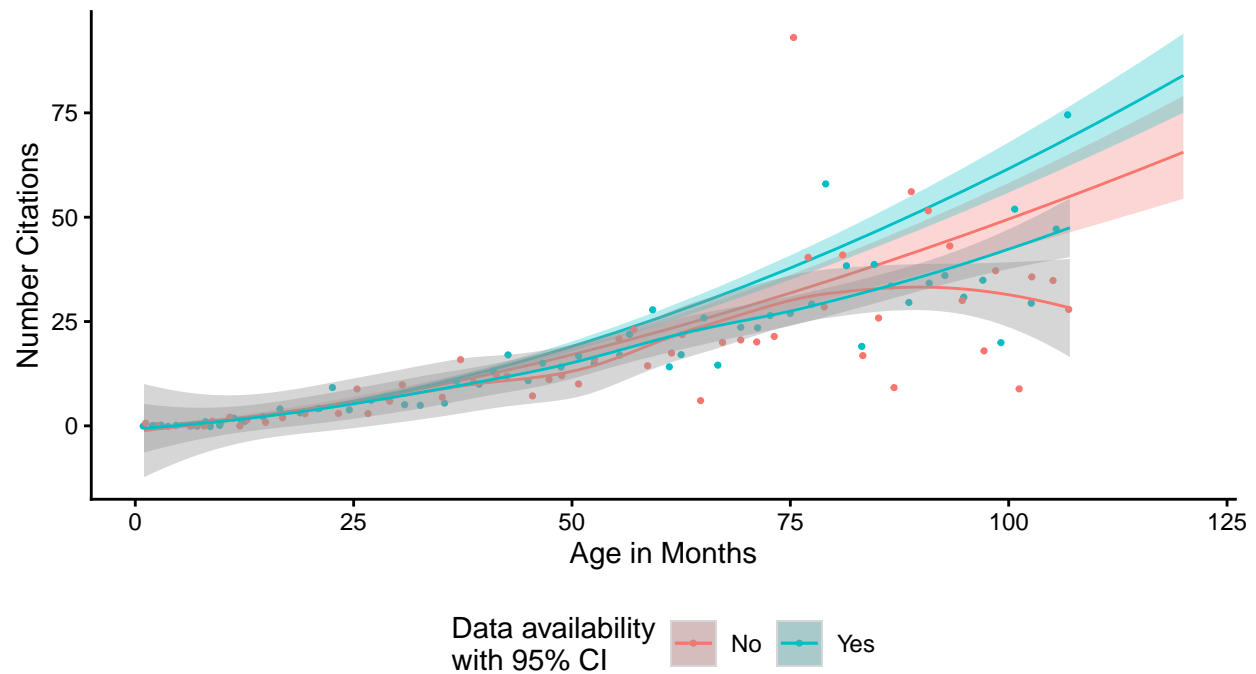
Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the median



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

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

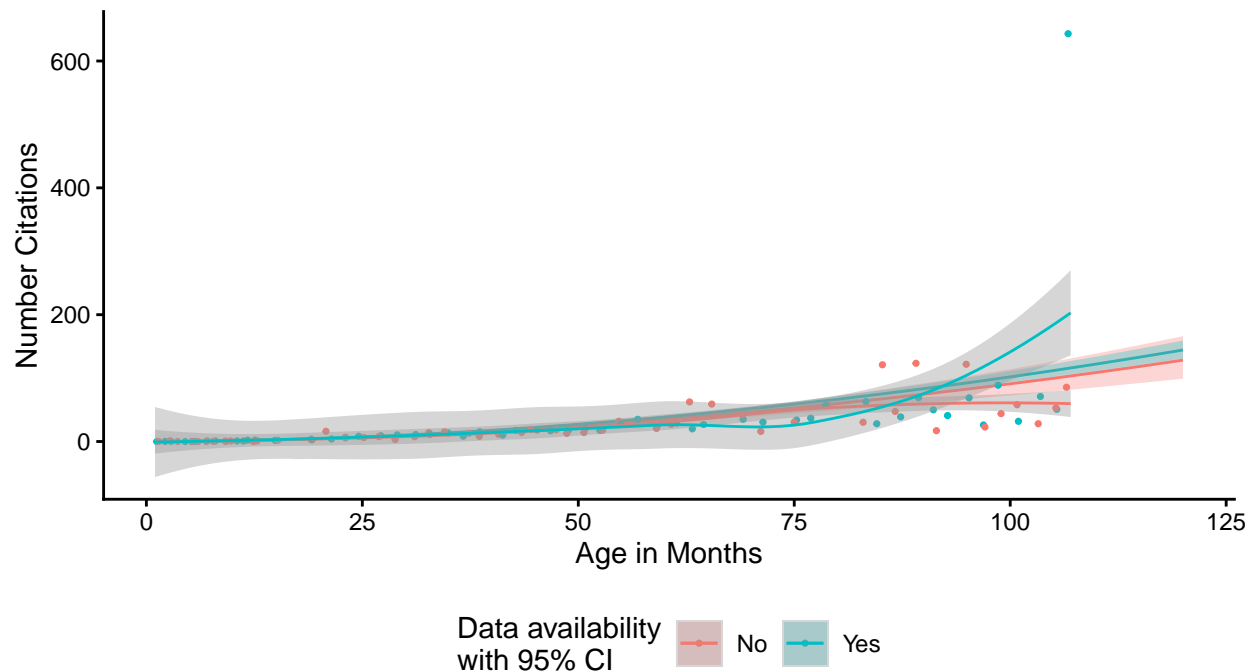
Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the median



```
## '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 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, color = da_factor), size = 1) +
geom_ribbon(data = model_data, mapping = aes(x = age.in.months, y = predicted_citations, ymin = ci_lower, ymax = ci_upper,
                                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 = 0.5)

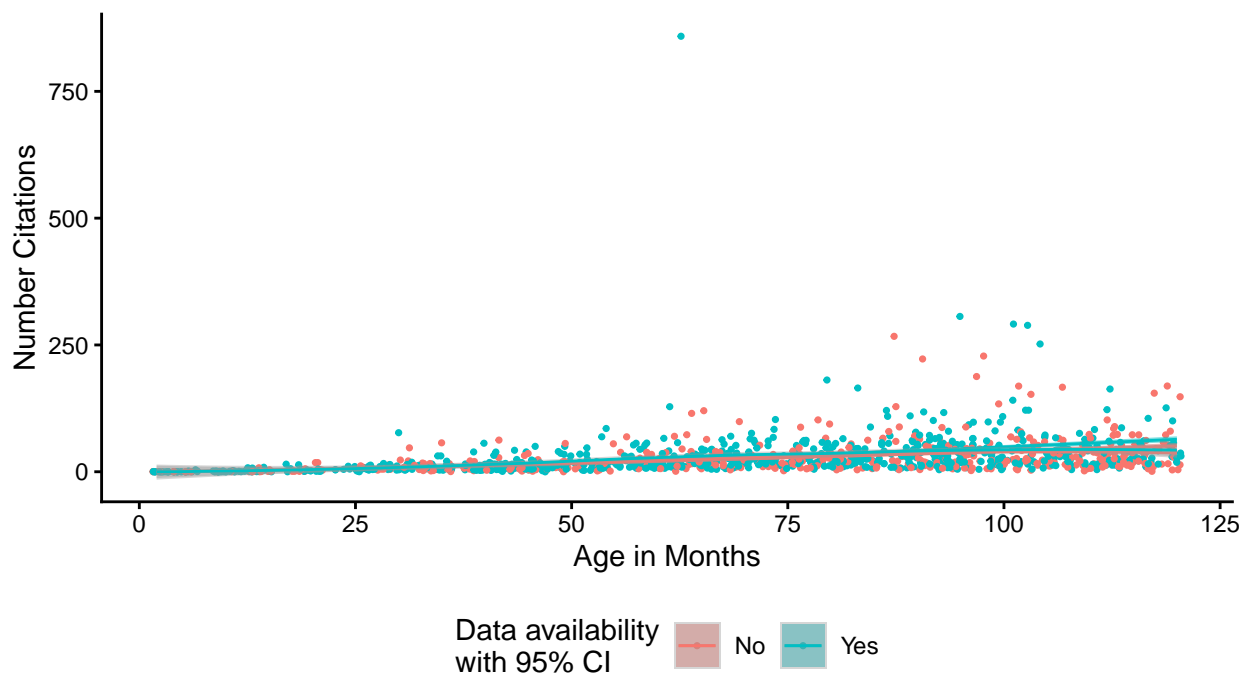
labs(title = paste0("Model vs True Median Number of Citations from GLM.NB for", journals$container),
     subtitle = "Data age.in.months <= 120, removal of JMBE, GA, MRA", grey geom_smooth through the data",
     x = "Age in Months",
     y = "Number Citations",
     color = "Data availability\nwith 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'

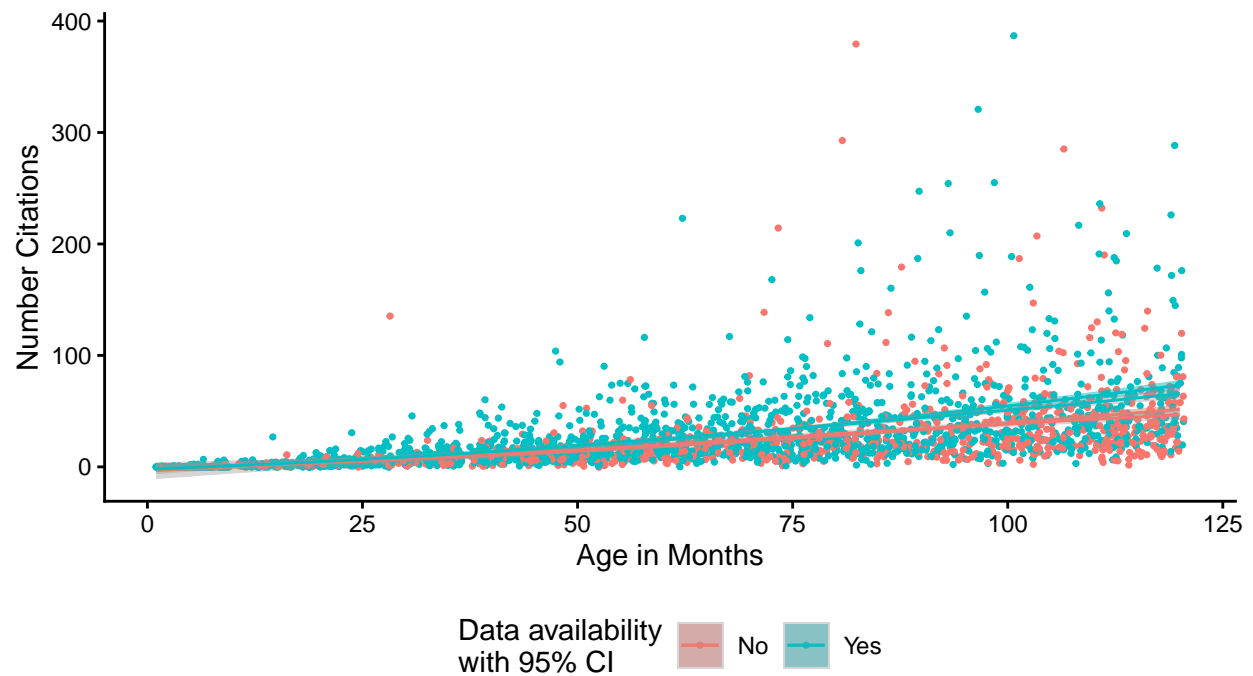
Model vs True Median Number of Citations from GLM.NB for
Antimicrobial Agents and Chemotherapy binned by month and da status
Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the data



'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

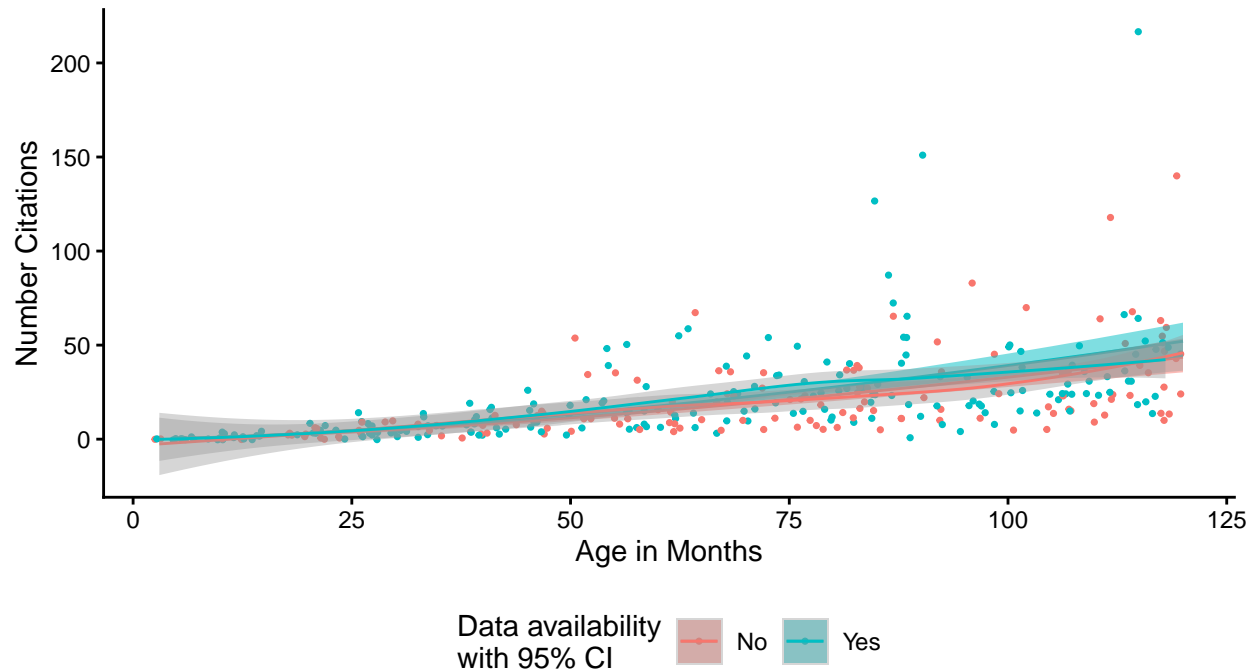
Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the data



```
## '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

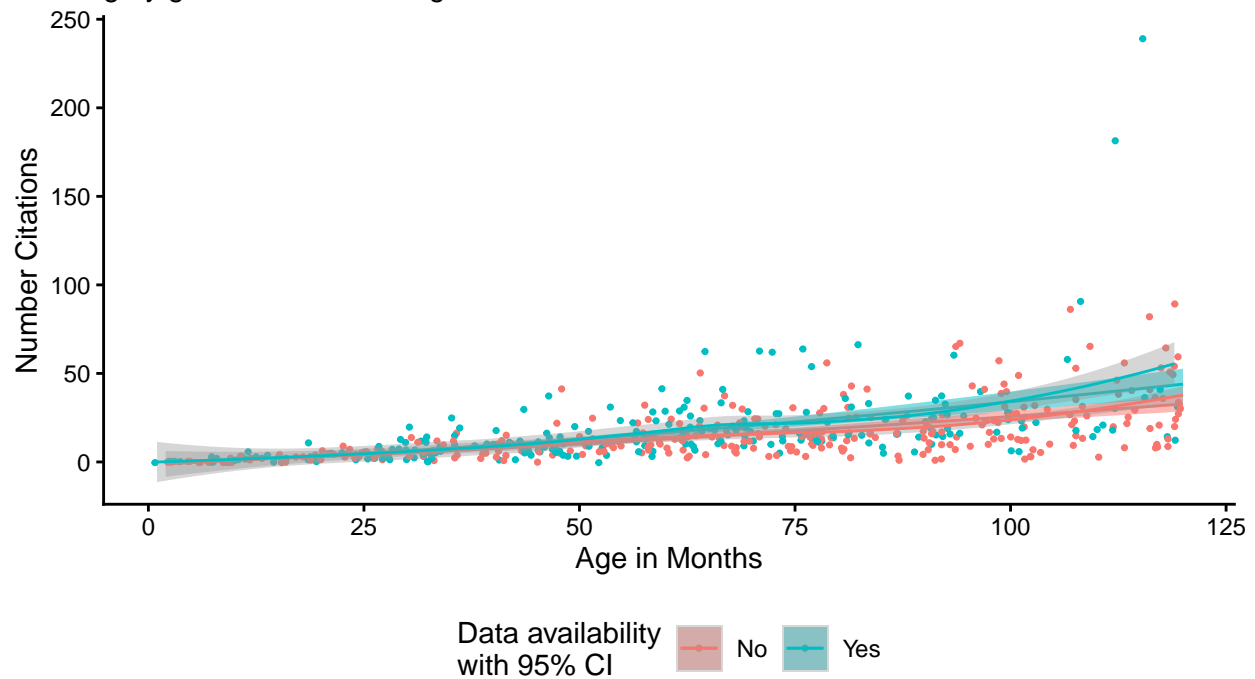
Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the data



```
## '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

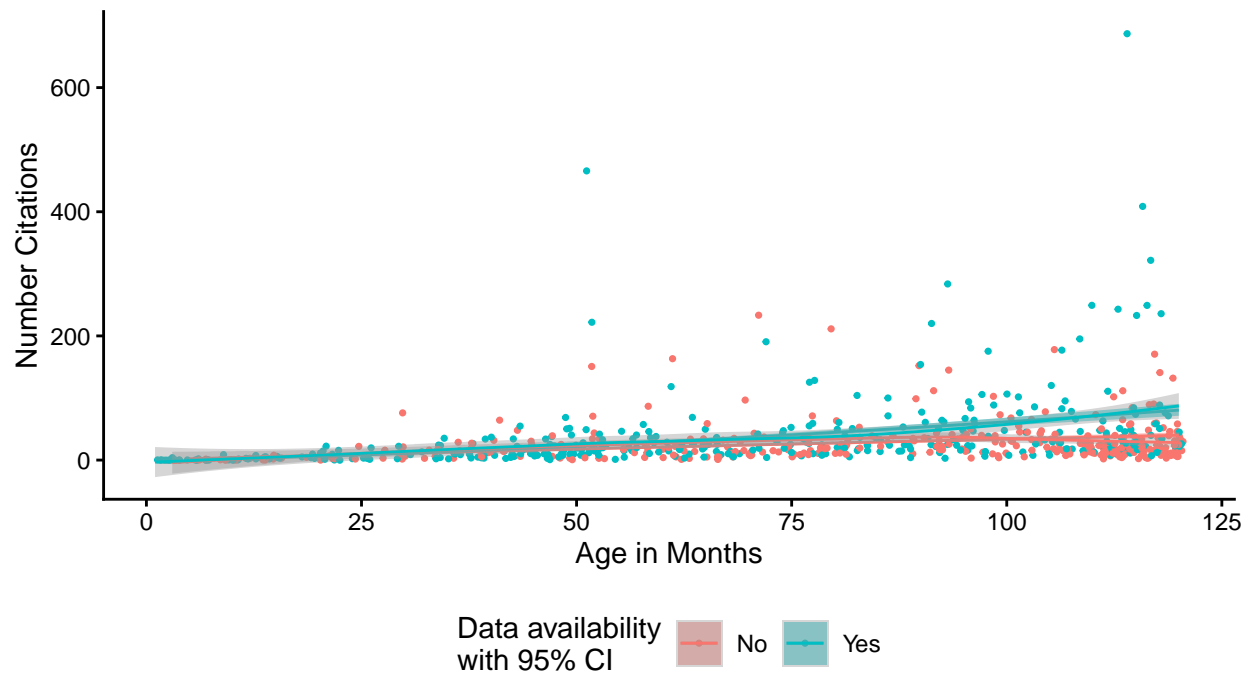
Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the data



```
## '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

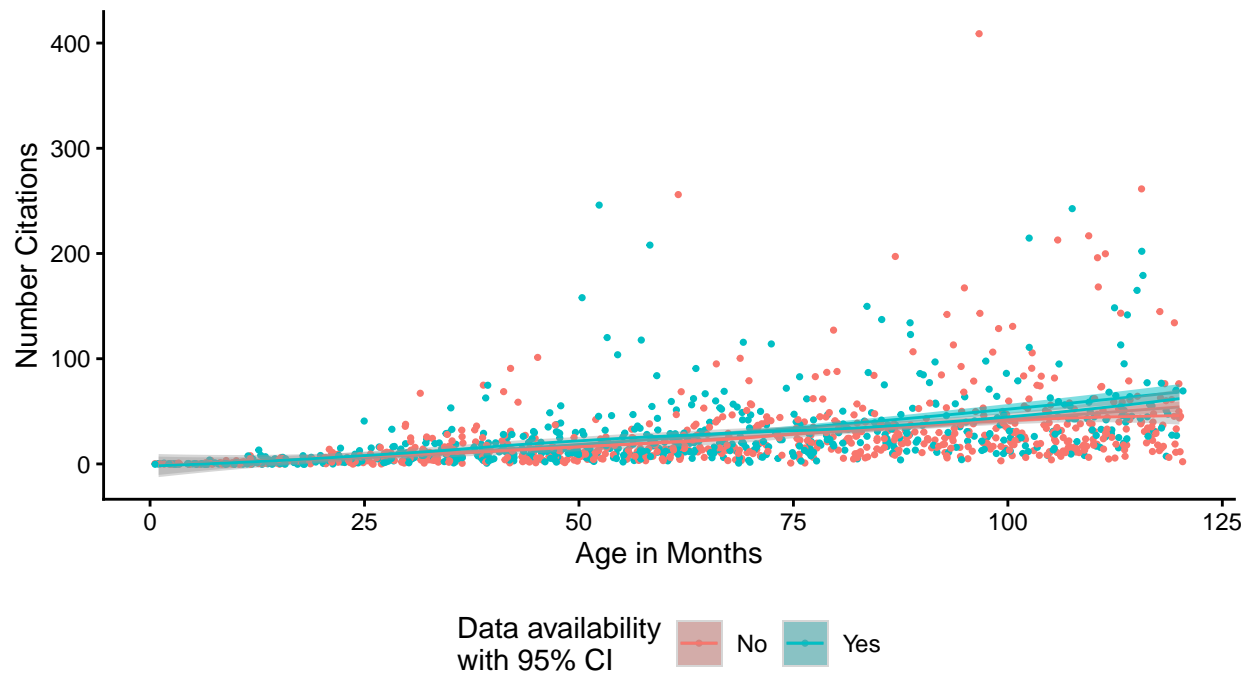
Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the data



```
## '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

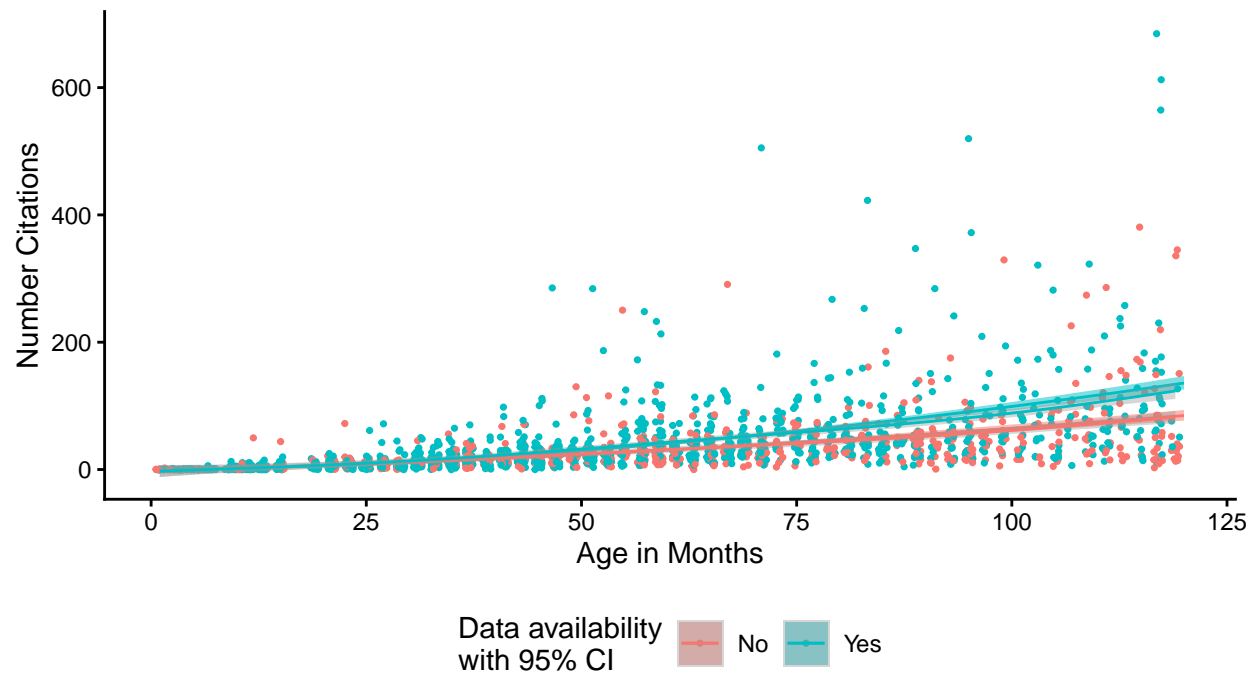
Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the data



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

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

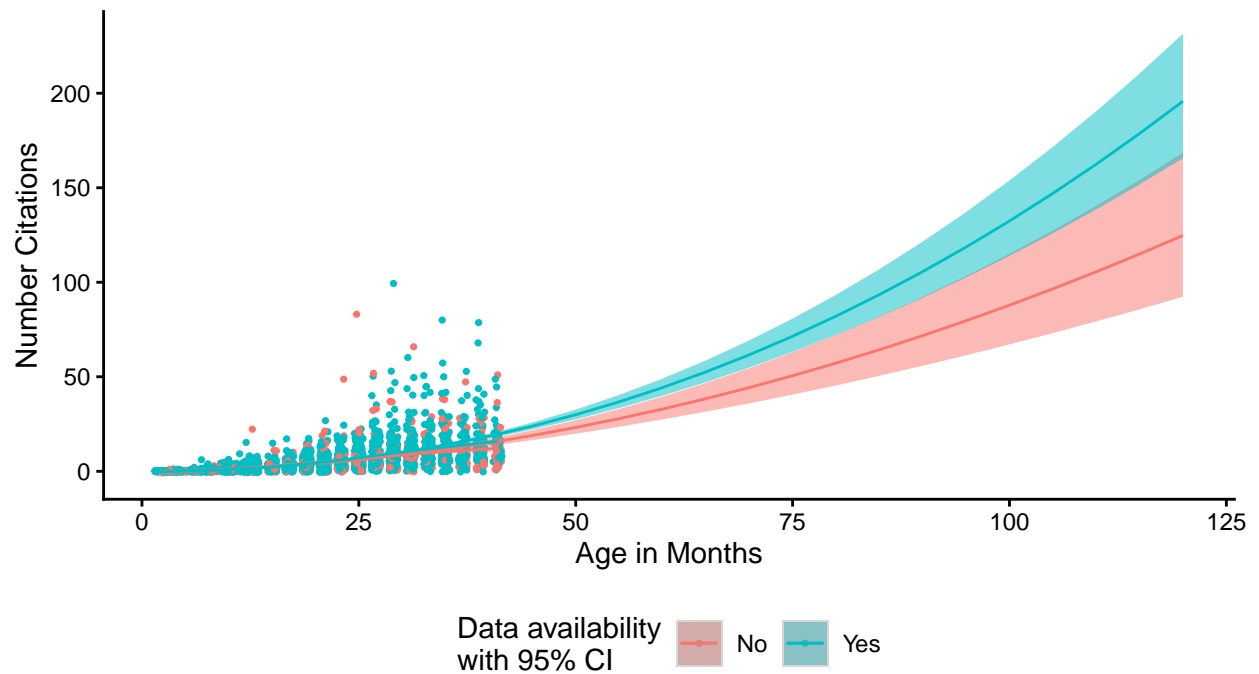
Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the data



```
## '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

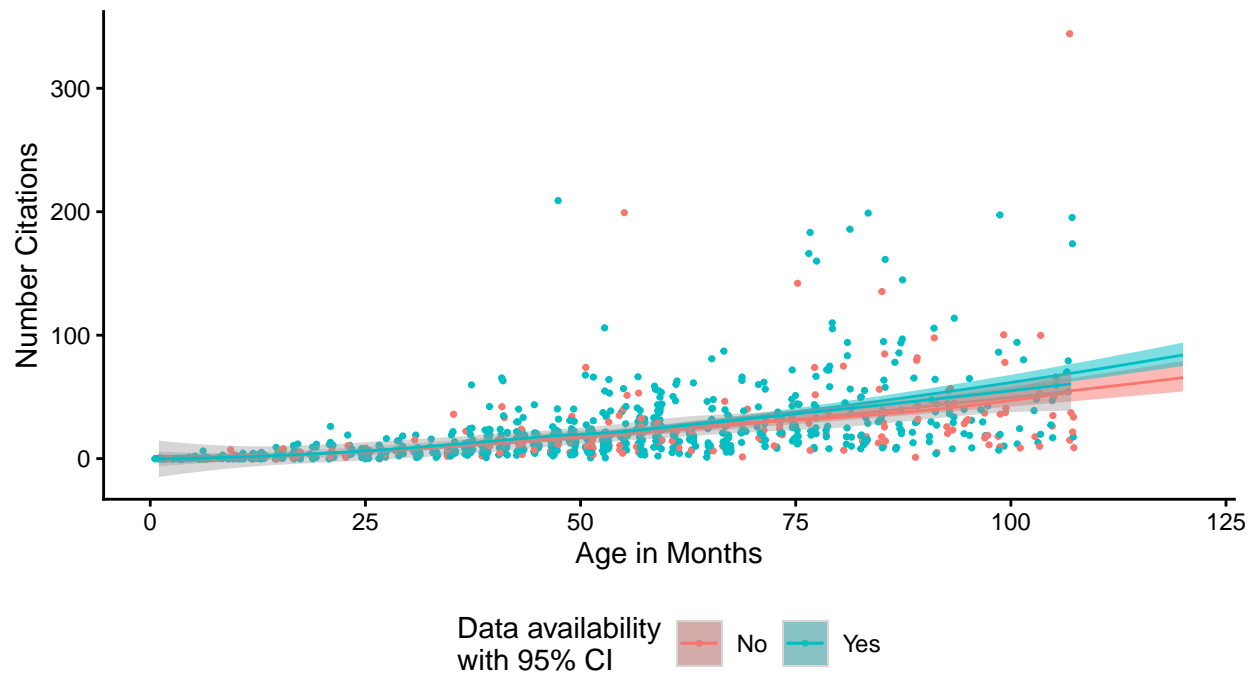
Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the data



```
## '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

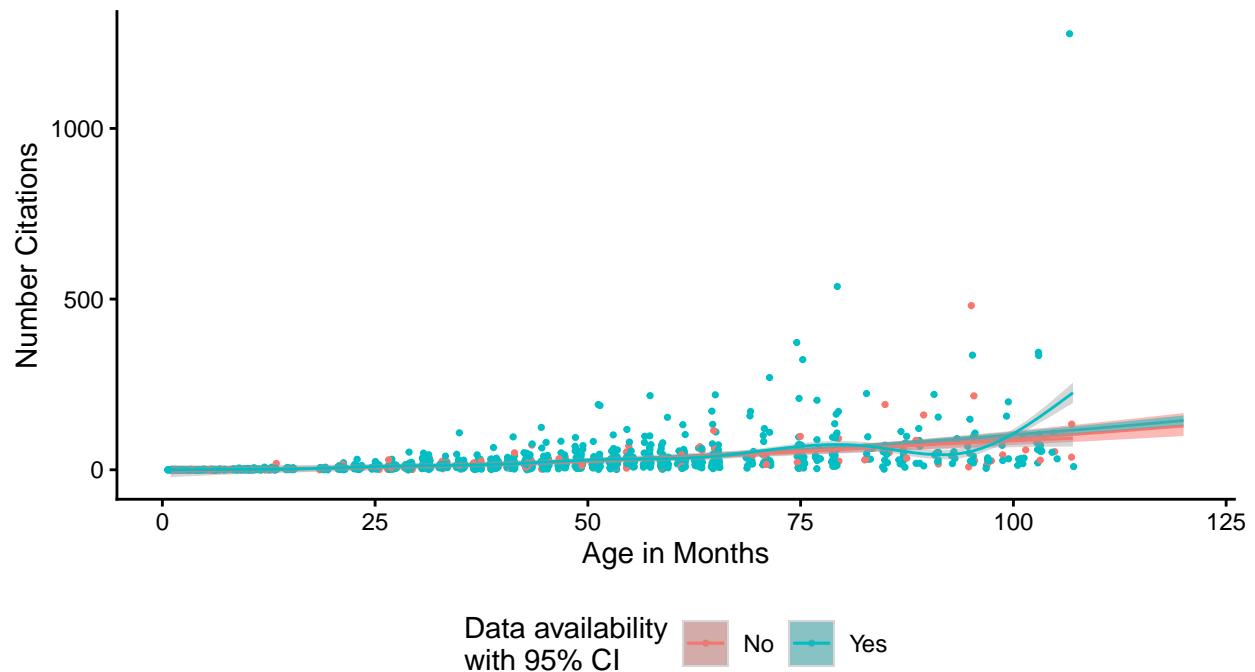
Data age.in.months <= 120, removal of JMBE, GA, MRA
grey geom_smooth through the data



```
## '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



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)'
```

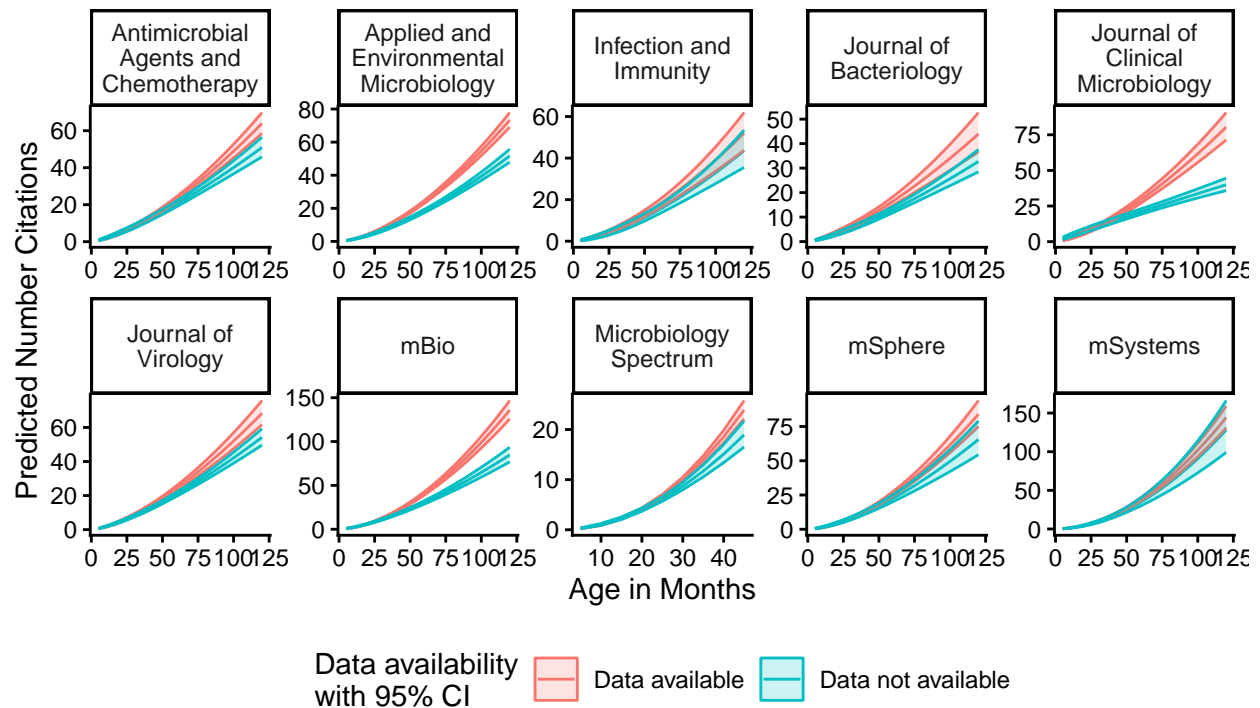
```
#re-create figure with free axes
```

```
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



Checking on how much data we have from other journals to make sure we truncate all of them correctly

- msphere and msystems we have data from 2016
 - $(2025-2016)*12 = 108$ months
- spectrum we have data from 2021
 - $(2025-2021)*12 = 48$ months

Truncating msystems, msphere, and spectrum to 9, 9, and 4 years respectively

```
#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 = . $y,
    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)

#filter data from model to msystems and msphere to 9 years (age.in.months <=108)
m_remove <-
p_10 %>%
  mutate(age.in.months = as.numeric(as.character(age.in.months))) %>%
  filter((container.title == "mSystems" | container.title == "mSphere") & age.in.months >= 108)

to_remove <- full_join(spec_remove, m_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)'

```

```

p_10_trunc <- anti_join(p_10, to_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

```

```

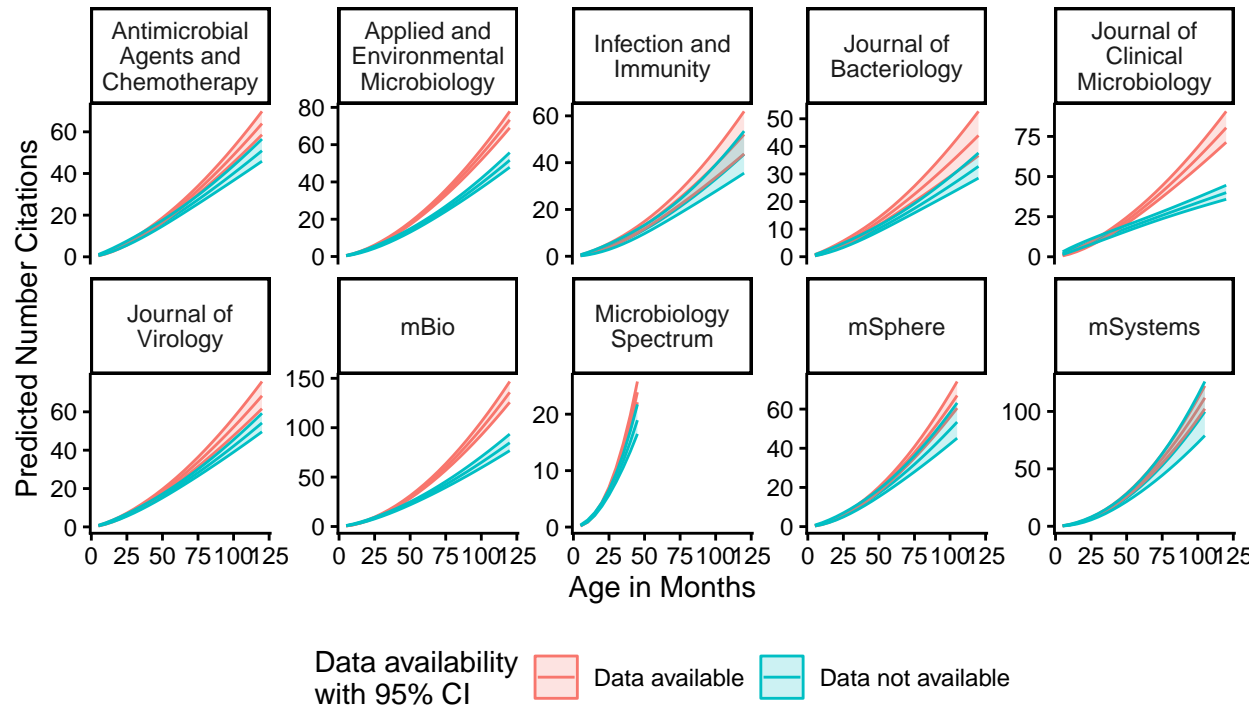
predicted_plot_spec <-
  ggplot(data = p_10_trunc ,
    mapping = aes(x = as.numeric(age.in.months),
      y = predicted_citations,
      color = da_factor)) +
  geom_line(aes(x = age.in.months, y = predicted_citations, group = da_factor)) +
  geom_ribbon(mapping = aes(ymin = conf.low, ymax = conf.high,
    group = da_factor, fill = da_factor), alpha = 0.2) +
  facet_wrap(~ container.title, nrow = 2,
    labeller = label_wrap_gen(width = 18),
    scale = "free_y" ) +
  labs(title = "Predicted Number of Citations from GLM.NB",
    subtitle = "Data age.in.months <= 120, removal of JMBE, GA, MRA, \nSpectrum data <=48 months, mS",
    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, mSystems and mSphere <= 108 months



Truncating for ratio plot

```
# Define the age values you want to examine (in months)
age_values <- seq(5, 120, 5)

# Get emmeans on the link scale for all combinations
emm <- emmeans(ten_model, ~ da_factor + age.in.months | container.title,
  at = list(age.in.months = age_values), CIs = TRUE,
  type = "response")

# Get pairwise comparisons (differences) between da_factor levels
differences <- contrast(
  emm, by = c("age.in.months", "container.title"),
  method = "revpairwise",
  ratios = TRUE, CIs = TRUE
)

# See the contrasts
# summary(differences)
# Plot the contrasts
# plot(differences, ratios = TRUE)

# Plot the contrasts
ratios_df <- as.data.frame(plot(differences, ratios = TRUE)$data) %>%
  mutate(age.in.months = as.numeric(as.character(age.in.months))) %>%
  filter(container.title != "Journal of Microbiology & Biology Education" &
    container.title != "Genome Announcements" &
    container.title != "Microbiology Resource Announcements")
```

```
## Warning: 'aes_()' was deprecated in ggplot2 3.0.0.
## i Please use tidy evaluation idioms with 'aes()'
## i The deprecated feature was likely used in the emmeans package.
## Please report the issue at <https://github.com/rvlenth/emmeans/issues>.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.
```

```
m_remove <-
ratios_df %>%
  filter((container.title == "mSystems" | container.title == "mSphere") & age.in.months >= 108)

spec_remove <-
ratios_df %>%
  filter((container.title == "Microbiology Spectrum" & age.in.months >= 48))

to_remove <-
  full_join(m_remove, spec_remove)
```

```
## Joining with 'by = join_by(contrast, age.in.months, container.title,
## the.emmean, SE, df, asymp.LCL, asymp.UCL, pri.fac, lcl, ucl)'
```

```
ratios_df_trunc <-
  anti_join(ratios_df, to_remove)
```

```
## Joining with 'by = join_by(contrast, age.in.months, container.title,
## the.emmean, SE, df, asymp.LCL, asymp.UCL, pri.fac, lcl, ucl)'
```

```
contrast_plot <-
ggplot(
  data = ratios_df_trunc,
  mapping = aes(x = age.in.months, y = the.emmean)
) +
  geom_hline(yintercept = 1.0, linetype = 2, linewidth = 0.25) +
  geom_line() +
  geom_ribbon(
    mapping = aes(ymin = lcl, ymax = ucl),
    alpha = 0.3 # transparency of confidence intervals
  ) +
  facet_wrap(~ container.title, nrow = 2,
    labeller = label_wrap_gen(width = 20)) +
  labs(x = 'Age in months', y = 'Ratio of daYes/daNo') +
  coord_cartesian(ylim = c(0.25, 2.5)) +
  theme_classic() +
  scale_x_continuous(breaks = seq(12, 120, 24))

contrast_plot
```