20250716_Abner

2025-07-16

Project Summary

- We are using data from the American Society of Microbiology's (ASM) 12 published journals to investigate the relationship between the number of citations (variable 'is.referenced.by.count') a published scientific article receives and if the authors have included access to their raw sequencing data (variable 'da', data availability) in the manuscript.
- We are trying to understand if publishing raw data helps to improve citation metrics. We have data from 2000-2024, and will also adjust for time published (variable 'age.in.months'), as older papers have had the opportunity to accumulate more citations over time.

Model Format

- Use model format for data from each journal:
  - MASS::glm.nb(is.referenced.by.count~ da_factor + log(age.in.months) + log(age.in.months)*da_factor, data = <each journal>, link = log)
  - Data with N > 10 to create model
  - is.referenced.by.count = Number of citations received as of 2/1/25
  - age.in.months = age of paper in months
  - da_factor = Is raw sequencing data available? Yes/No as a factor.

Journal Case Study: mBio

- mBio is an ASM family journal that has been around ~15 years (2015-2025)
- See below for the plot of the model, the simulated residuals from DHARMa, and the residual plots.

```
#smaller model with 2 terms
two_term_glmnb <-function(model_data, model_name) {

  total_model <-MASS::glm.nb(is.referenced.by.count~ da_factor + log(age.in.months) +
       + log(age.in.months)*da_factor + log(age.in.months)*da_factor, data = model_data, link = log)

  return(total_model)

}

journals <-
  nsd_yes_metadata %>%
  count(journal_abrev) %>%
  filter(journal_abrev != "jmbe")
```

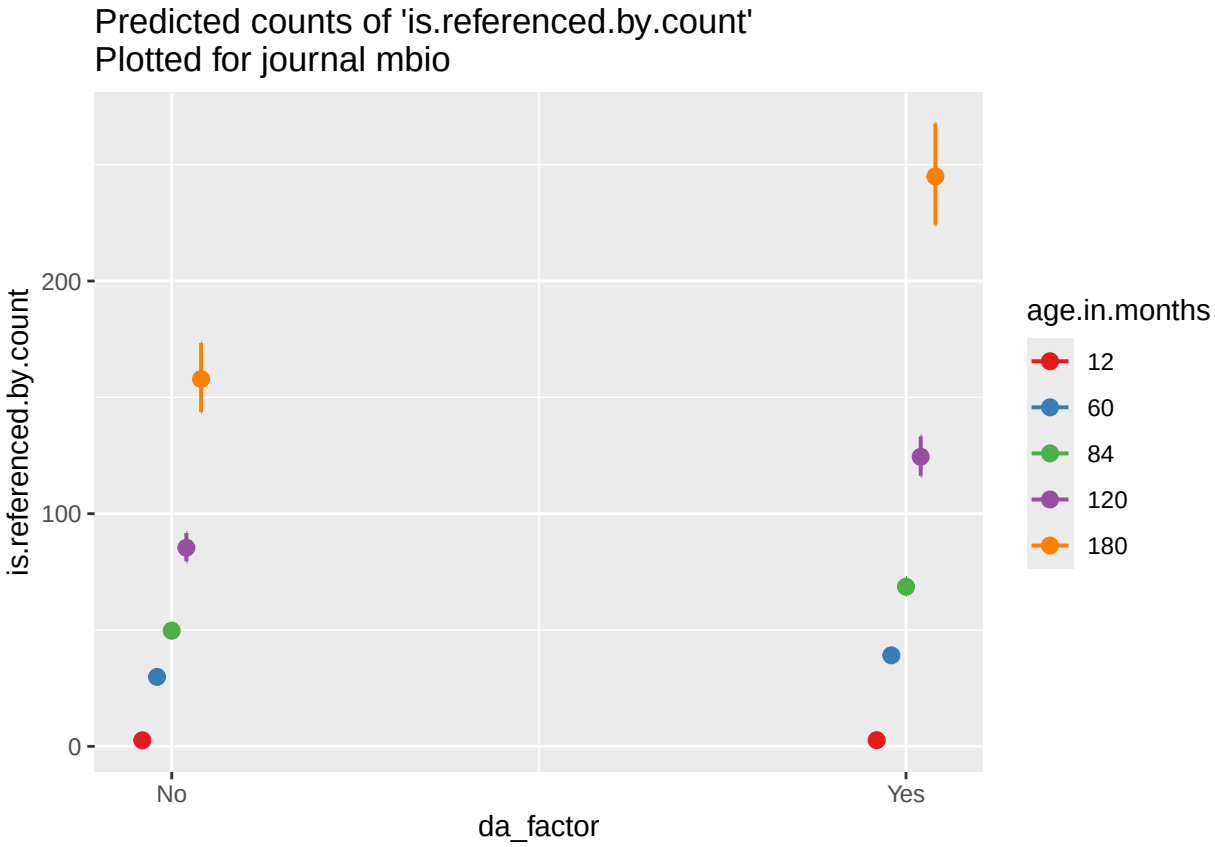
```r
j <- 8 #mbio


 journal_data <-
 nsd_yes_metadata %>%
   filter(journal_abrev == journals[[j,1]]) %>%
   mutate(da_factor = factor(da))


 model <- two_term_glmnb(journal_data, journals[[j,1]])


 plot_model <- plot_model(model, type = "pred", terms = c("da_factor", "age.in.months[12,60,84,120,180]

print(plot_model)
```

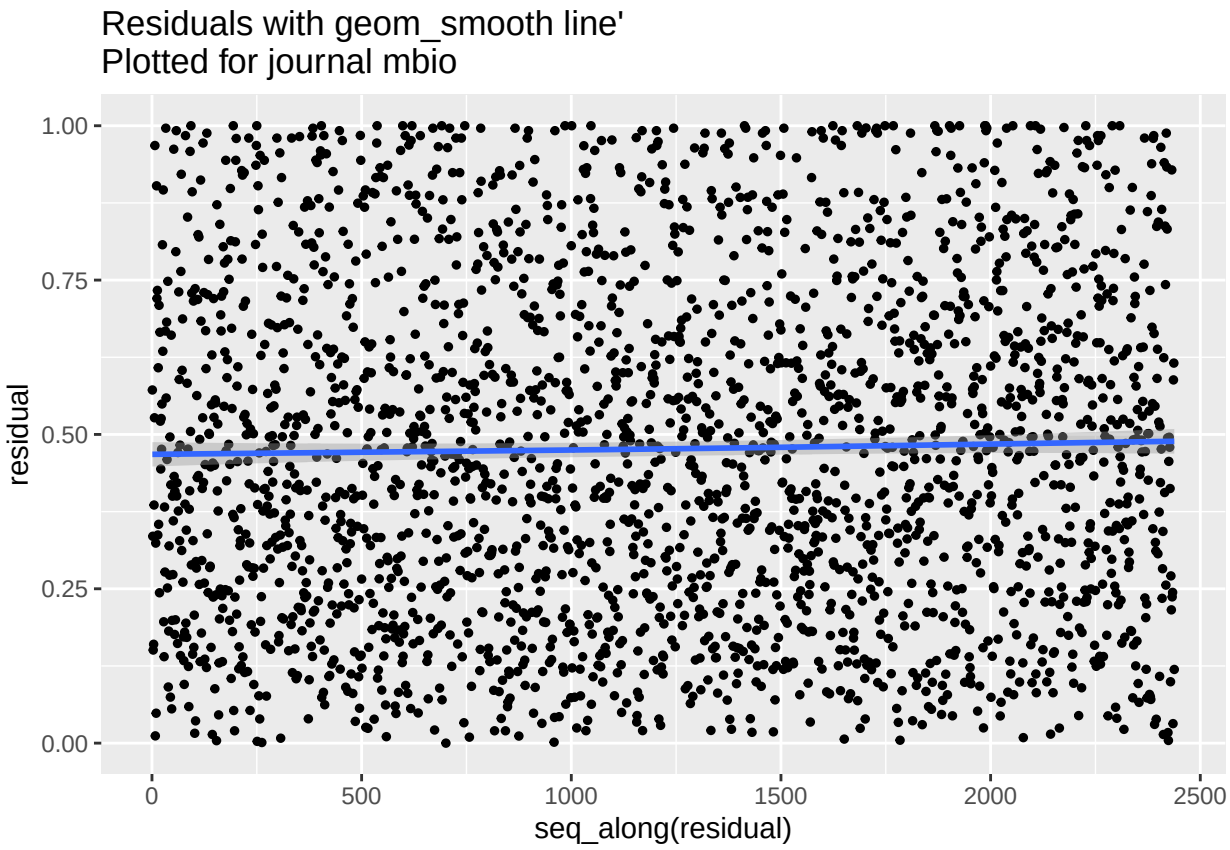



```r
simulation <- simulateResiduals(fittedModel = model, plot = F)

# residuals(simulation)  %>%
# plot(main = paste0("Residuals plotted for journal ", journals[[j,1]]), pch = ".")
residuals <-
 residuals(simulation) %>%  tibble(residual = .) %>%
   ggplot(aes(y = residual, x = seq_along(residual) )) +
   geom_point(size = 1) +
   geom_smooth() +
```

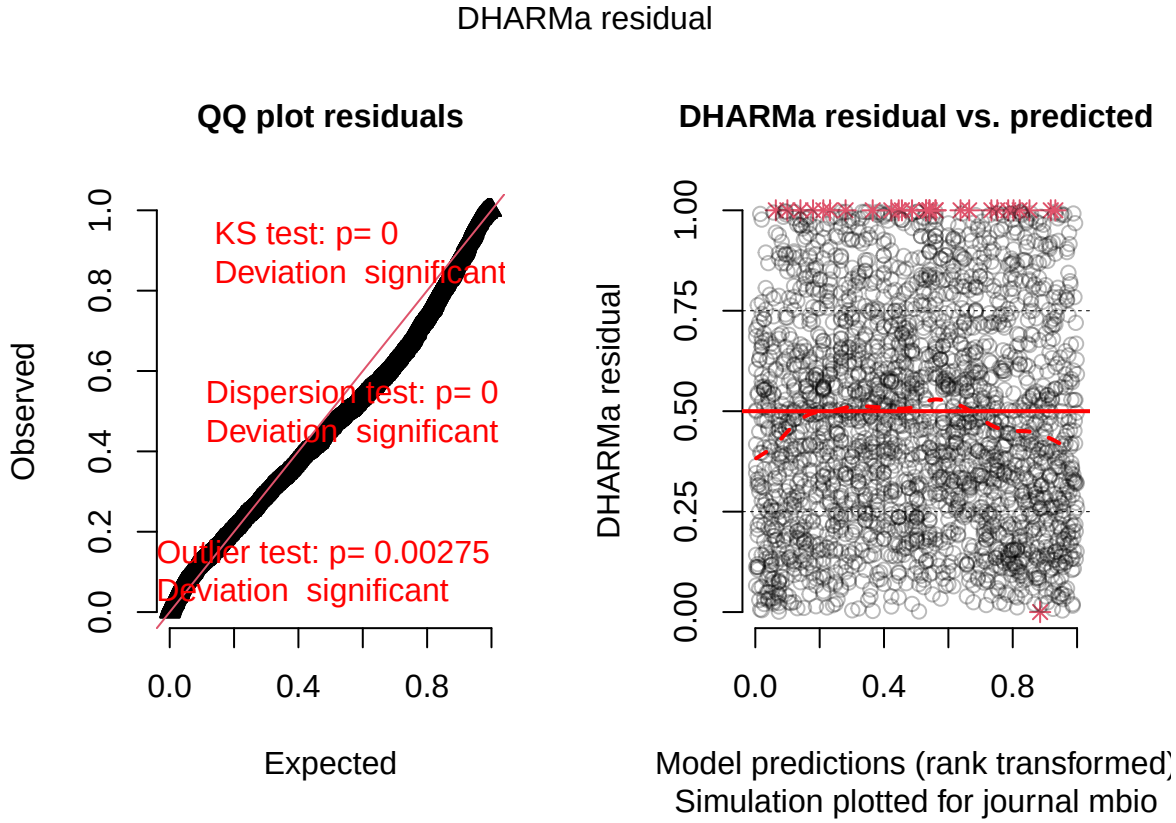
```
    ggtitle(paste0("Residuals with geom_smooth line' \nPlotted for journal ", journals[[j,1]]))
  print(residuals)
```

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




```
  plot(simulation, sub = paste0("Simulation plotted for journal ", journals[[j,1]]))
```

```
## DHARMa:testOutliers with type = binomial may have inflated Type I error rates for integer-valued dis
```



Questions

- This is one example from our 12 journal set, if all of the plots look roughly like this, we are assuming the models fit well and can proceed with using them.
- We've looked at the residuals 3 ways using DHARMa.
  - When using the QQ plot, should we be worried about the significance of the three tests?
  - Does this occur because there are a large number of observations in the dataset (N = 2438)?
  - Should we be interpreting this differently?
- In the plotted model data, we see that the slope increases with time, and there are confidence intervals on these estimates.
  - Is this enough to say that these data are different?
  - Should we perform more hypothesis testing such as a T test?
  - Could we get a p-value to satisfy reviewers? How might we do that?