

# Summary Stats for DA Project

2025-08-20

```
#library statements
library(tidyverse)

## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v ggplot2   3.5.2     v tibble    3.3.0
## v lubridate 1.9.4     v tidyr    1.3.1
## v purrr    1.0.4

## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()   masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors

#import data
data <- read_csv("~/Documents/Schloss/Colovas_Data_Accessibility/Data/final/predictions_with_metadata.csv")

## New names:
## * 'NA...9' -> 'NA...55'
## * 'NA...10' -> 'NA...56'

## Warning: One or more parsing issues, call 'problems()' on your data frame for details,
## e.g.:
##   dat <- vroom(...)
##   problems(dat)

## Rows: 154720 Columns: 77
## -- Column specification -----
## Delimiter: ","
## chr (32): file, da, nsd, paper.x, doi, doi_no_underscore, journal_abrev, co...
## dbl (12): issue, member, prefix, score, reference.count, references.count, ...
## lgl (28): assertion, author, link, license, reference, update_to, subtitle, ...
## date (5): created, deposited, indexed, published.online, pub_date
##
## i Use 'spec()' to retrieve the full column specification for this data.
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
```

How many papers are nsd papers by journal?

```

nsd_yes <- data %>%
  count(container.title,
        nsd) %>%
  filter(!is.na(nsd)) %>%
  group_by(container.title) %>%
  mutate(nsd,
        total = sum(`n`),
        nsd_fract = `n`/total) %>%
  filter(nsd == "Yes")

knitr::kable(nsd_yes)

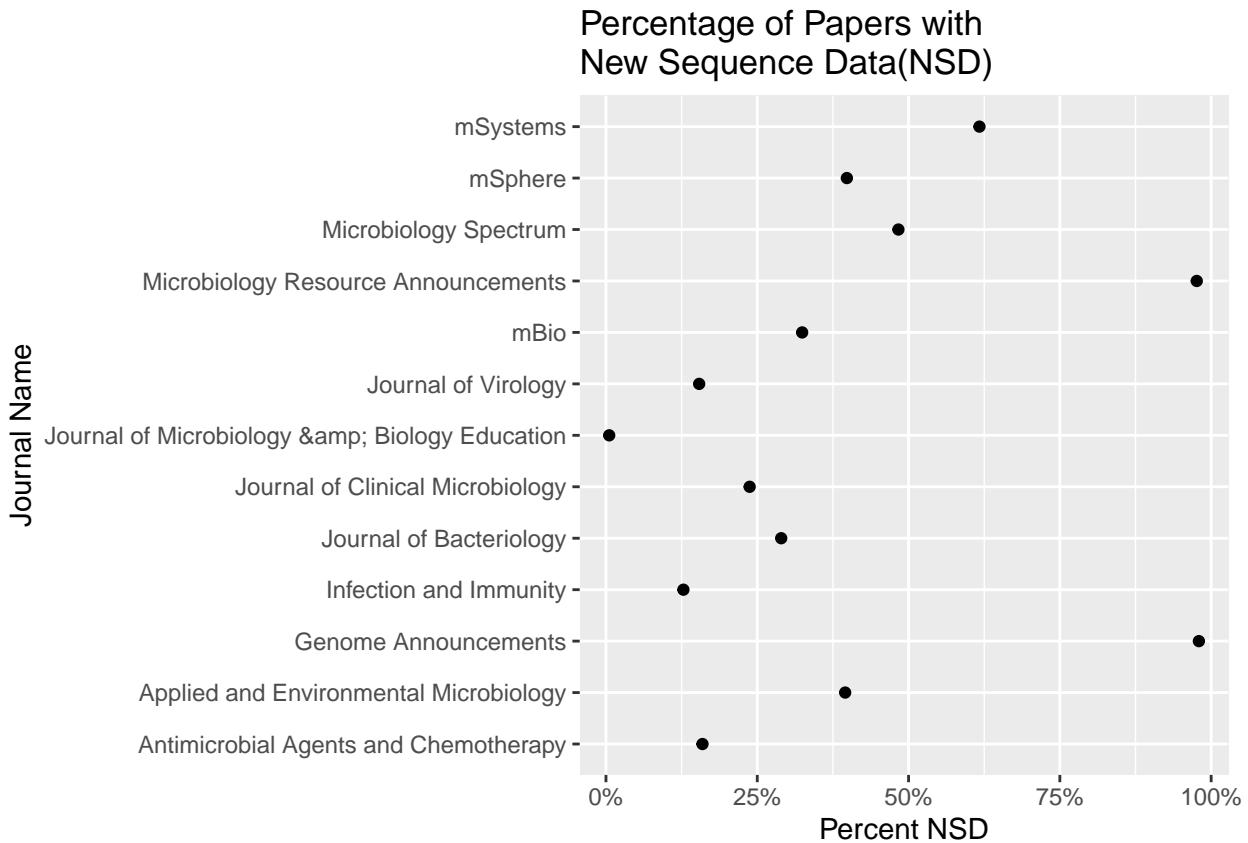
```

| container.title                             | nsd | n    | total | nsd_fract |
|---|-----|------|-------|-----------|
| Antimicrobial Agents and Chemotherapy       | Yes | 3237 | 20297 | 0.1594817 |
| Applied and Environmental Microbiology      | Yes | 8638 | 21853 | 0.3952775 |
| Genome Announcements                        | Yes | 6578 | 6714  | 0.9797438 |
| Infection and Immunity                      | Yes | 1854 | 14490 | 0.1279503 |
| Journal of Bacteriology                     | Yes | 4867 | 16806 | 0.2895990 |
| Journal of Clinical Microbiology            | Yes | 4374 | 18422 | 0.2374335 |
| Journal of Microbiology & Biology Education | Yes | 7    | 1305  | 0.0053640 |
| Journal of Virology                         | Yes | 4583 | 29761 | 0.1539935 |
| Microbiology Resource Announcements         | Yes | 5738 | 5878  | 0.9761824 |
| Microbiology Spectrum                       | Yes | 2957 | 6119  | 0.4832489 |
| mBio  | Yes | 2498 | 7705  | 0.3242051 |
| mSphere                                     | Yes | 1041 | 2615  | 0.3980880 |
| mSystems                                    | Yes | 1436 | 2327  | 0.6171036 |

```

ggplot(data = nsd_yes, aes(y = container.title, x = nsd_fract)) +
  geom_point() +
  scale_x_continuous(labels = scales::label_percent()) +
  labs(title = "Percentage of Papers with\nNew Sequence Data(NSD)",
       y = "Journal Name",
       x = "Percent NSD")

```



How many papers are nsd papers by journal?

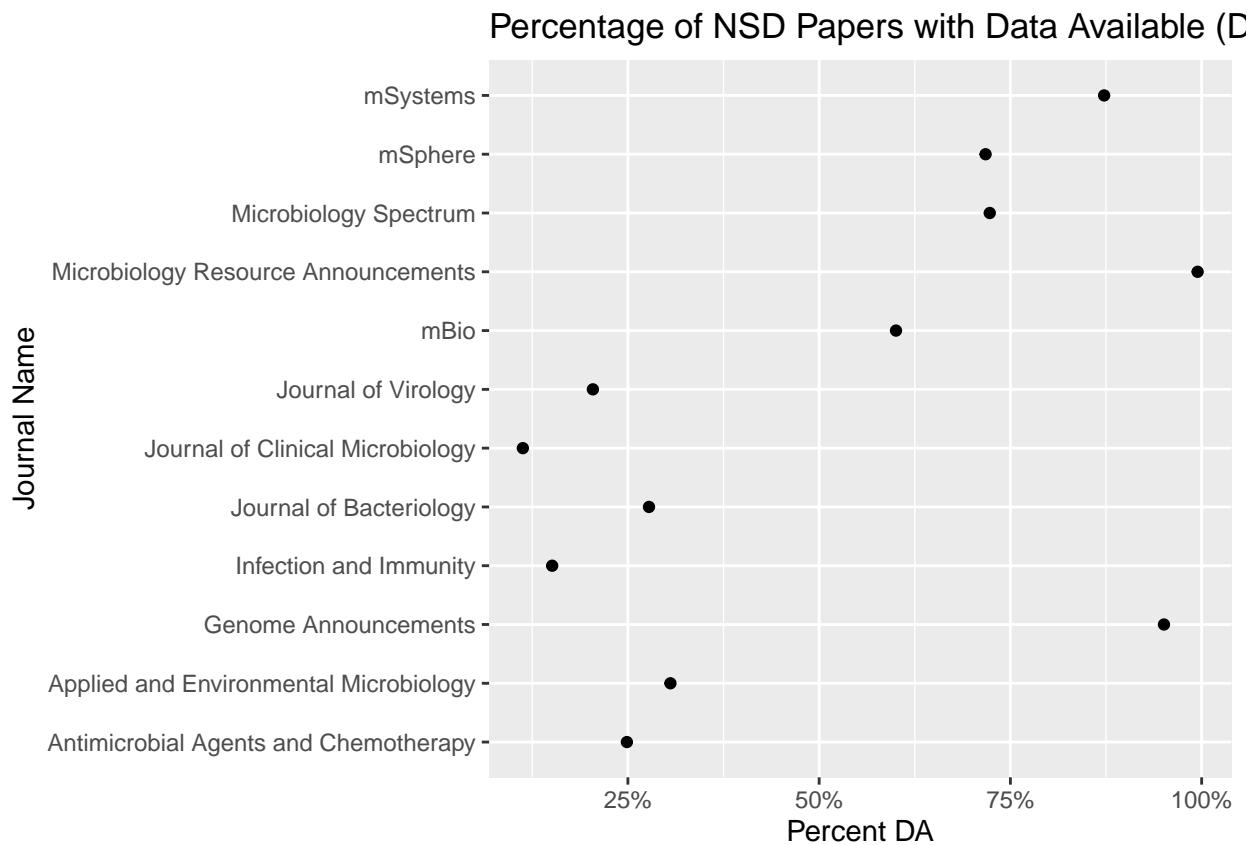
```
da_yes <- data %>%
  filter(nsd == "Yes") %>%
  count(container.title,
        da) %>%
  filter(!is.na(da)) %>%
  group_by(container.title) %>%
  mutate(da,
        total = sum(`n`),
        da_fract = `n`/total) %>%
  filter(da == "Yes")

knitr::kable(da_yes)
```

| container.title                        | da  | n    | total | da_fract  |
|--|-----|------|-------|-----------|
| Antimicrobial Agents and Chemotherapy  | Yes | 805  | 3237  | 0.2486871 |
| Applied and Environmental Microbiology | Yes | 2640 | 8638  | 0.3056263 |
| Genome Announcements                   | Yes | 6254 | 6578  | 0.9507449 |
| Infection and Immunity                 | Yes | 280  | 1854  | 0.1510248 |
| Journal of Bacteriology                | Yes | 1351 | 4867  | 0.2775837 |
| Journal of Clinical Microbiology       | Yes | 493  | 4374  | 0.1127115 |

| container.title                     | da  | n    | total | da_fract  |
|-------------------------------------|-----|------|-------|-----------|
| Journal of Virology                 | Yes | 936  | 4583  | 0.2042330 |
| Microbiology Resource Announcements | Yes | 5708 | 5738  | 0.9947717 |
| Microbiology Spectrum               | Yes | 2138 | 2957  | 0.7230301 |
| mBio                                | Yes | 1500 | 2498  | 0.6004804 |
| mSphere                             | Yes | 747  | 1041  | 0.7175793 |
| mSystems                            | Yes | 1253 | 1436  | 0.8725627 |

```
ggplot(data = da_yes, aes(y = container.title, x = da_fract)) +
  geom_point() +
  scale_x_continuous(labels = scales::label_percent()) +
  labs(title = "Percentage of NSD Papers with Data Available (DA)",
       y = "Journal Name",
       x = "Percent DA")
```



```
#i think this needs to be of nsd yes papers
```