Results Section: Public Metadata

```
library(staphopia)
library(dplyr)

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':

##
## filter, lag

## The following objects are masked from 'package:base':

##
## intersect, setdiff, setequal, union

library(ggplot2)
library(reshape2)
USE_DEV = TRUE
```

Aggregating Data For Public Samples

First we'll get all publicly available S. aureus samples.

```
ps <- get_public_samples()</pre>
```

We now have 42949 samples to work with. Next we will acquire metadata associated with each sample.

We will also get information pertaining to submissions by year and how any publication links were made.

```
submissions <- get_submission_by_year()
publication_links <- get_publication_links()</pre>
```

Next we are going to pull down any metadata associated with the public samples.

```
metrics <- merge(
   ps,
   get_metadata(ps$sample_id),
   by='sample_id'
)</pre>
```

We are now going to add two columns rank_name and year.

```
metrics$year <- sapply(
    metrics$first_public,
    function(x) {
        strsplit(x, "-")[[1]][1]
    }
)

metrics$rank_name <- ifelse(
    metrics$rank.x == 3,
    'Gold',
    ifelse(
        metrics$rank.x == 2,
        'Silver',</pre>
```

```
'Bronze'
)
```

Publication Information

Summary

Here are details looking at total submissions and their publication status.

```
t(submissions[submissions$year == max(submissions$year),])
```

```
## year 2017
## published 17
## unpublished 6698
## count 6715
## overall_published 11921
## overall_unpublished 31028
## overall 42949
```

Here is information on how publication links were made.

t(publication_links)

```
## 1
## elink 6712
## text 5656
## elink_pmid 48
## text_pmid 30
## total 11921
## total_pmid 78
```

There are 6 rows and their names are as follows:

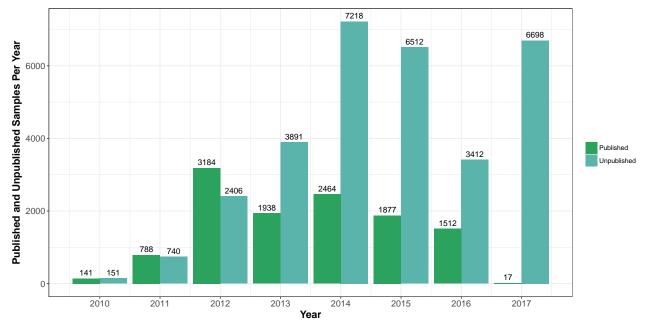
- 1. elink: Number samples linked to a PubMed ID identified from eLink
- 2. text: Number samples linked to a PubMed ID identified from text mining (not through eLink)
- 3. elink_pmid: Number of PubMed IDs identified from eLink
- 4. text_pmid: Number of PubMed IDs identified from text mining (not through eLink)
- 5. total: Total number of samples associated with a PubMed ID
- 6. total_pmid: Total number of PubMed IDs associated with published samples

Percent of Samples Published

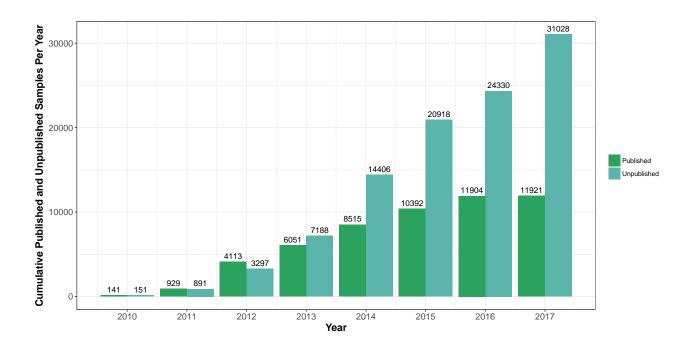
```
stats <- submissions[submissions$year == max(submissions$year),]
stats$overall_published / stats$overall * 100</pre>
```

```
## [1] 27.75618
```

Published vs Unpublished Submissions Per Year



Overall Published vs Unpublished Submissions



Metadata Information

Number of Samples With A Collection Date

```
has_collection_date <- nrow(metrics[metrics$collection_date != "",])
pasteO(has_collection_date," (", has_collection_date / nrow(metrics) * 100, " %)")
## [1] "17034 (39.660993271089 %)"
```

Number of Samples With A Location Information

```
has_location <- nrow(metrics[metrics$location != "unknown/missing",])
pasteO(has_location," (", has_location / nrow(metrics) * 100, " %)")
```

[1] "14983 (34.8855619455633 %)"

Number of Locations

```
nrow(as.data.frame(table(metrics[metrics$location != "unknown/missing",]$location)))
```

[1] 123

Countries

```
country_data <- as.data.frame(table(metrics[(metrics$country != "unknown/missing" ) & (metrics$country
colnames(country_data) <- c("Country", "total")
country_data <- arrange(country_data, desc(total))
country_data</pre>
```

```
## Country total
## 1 United States of America (USA) 5823
## 2 United Kingdom (UK) 5177
## 3 Germany 966
## 4 Denmark 480
```

```
## 5
                              Thailand
                                          277
## 6
                             Singapore
                                          247
## 7
                              Tanzania
                                          153
## 8
                           Netherlands
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## 39
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```

Number of Countries

```
pasteO(nrow(country_data), " countries, represented by ", sum(country_data$total), " samples")
## [1] "40 countries, represented by 14528 samples"
```

Number of Samples With Isolation Source

```
has_source <- nrow(metrics[metrics$isolation_source != "",])
pasteO(has_source," (", has_source / nrow(metrics) * 100, " %)")

## [1] "14768 (34.3849682181192 %)"
```

Isolation Sources

```
as.data.frame(table(metrics[metrics$isolation_source != "",]$isolation_source))
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```

Number of Isolation Sources

```
nrow(as.data.frame(table(metrics[metrics$isolation_source != "",]$isolation_source)))
## [1] 396
```