# Results Section: Public Genetic Diversity

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

In this section we will look into genetic diversity that has been sequenced in *Staphylococcus aureus*. In order to do so, we'll use variant counts, cgMLST and MLST as measures of diversity.

### Aggregating Data For Public Samples

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

```
ps <- get_public_samples()
```

### MLST

Next we will will use the MLST information has a measure of genitic diversity. In this case we are interested in the total number of unique sequence types sequenced. We'll use *get_st_by_year()* to get some basic stats about how many STs have been sequenced. We will also use *get_top_sequence_types()* to get each ST represented in the database and the total number of samples with each ST. (*Note: 5000 is just an arbitrarly large number to retreive all STs*)

```
sequence_types <- get_st_by_year()
top_st <- get_top_sequence_types(5000)
colnames(sequence_types)
```

```
##  [1] "year"                       "unique"
##  [3] "novel"                      "assigned"
##  [5] "assigned_agree"             "assigned_disagree"
##  [7] "unassigned"                 "unassigned_agree"
##  [9] "unassigned_disagree"        "predicted_novel"
## [11] "all"                        "partial"
## [13] "ariba_blast"                "mentalist_blast"
## [15] "mentalist_ariba"            "single"
## [17] "ariba"                      "mentalist"
## [19] "blast"                      "count"
## [21] "overall_novel"              "overall_assigned"
## [23] "overall_assigned_agree"     "overall_assigned_disagree"
## [25] "overall_unassigned"         "overall_unassigned_agree"
## [27] "overall_unassigned_disagree" "overall_predicted_novel"
## [29] "overall_all"                "overall_partial"
## [31] "overall_ariba_blast"        "overall_mentalist_blast"
## [33] "overall_mentalist_ariba"    "overall_single"
## [35] "overall_ariba"              "overall_mentalist"
## [37] "overall_blast"              "overall"
```

This gives us 38 columns for each year. These columns are:

1. year: The year.
2. unique: The Number of unique STs for a given year.

3. novel: Number of STs not sequenced previously.
4. assigned: Samples which a ST was determined.
5. assigned_agree: Samples in which each program that called an ST agreed in ST.
6. assigned_disagree: Samples in which programs did not each call the same ST.
7. unassigned: Samples which a ST was not determined.
8. unassigned_agree: Each program was unable to assign an ST.
9. unassigned_disagree: Samples in which no ST was determined, but each program does not agree
10. predicted_novel: Samples with a match to each Loci, but allele pattern does not exist.
11. all: Samples with an ST determined with agreement between each program.
12. partial: Samples with an ST determined with agreement between two programs. 13: ariba_blast: Samples with an ST determined with agreement between Ariba and BLAST.
13. mentalist_blast: Samples with an ST determined with agreement between MentaLiST and BLAST.
14. mentalist_ariba: Samples with an ST determined with agreement between MentaLiST and Ariba.
15. single: Samples with an ST determined by only a single program.
16. ariba: Samples with an ST determined by only Ariba.
17. mentalist: Samples with an ST determined by only MentaLiST.
18. blast: Samples with an ST determined by only BLAST.
19. count: Total number of samples in a given year. 21-38: overall_$X$: The cumulative totals of previous years for column $x$

### Summary of MLST Diversity

#### Assignment Breakdown

```
t(sequence_types[sequence_types$year == max(sequence_types$year),21:38])
```

```
##                                   8
## overall_novel                  1098
## overall_assigned              42337
## overall_assigned_agree        42243
## overall_assigned_disagree        94
## overall_unassigned              612
## overall_unassigned_agree        612
## overall_unassigned_disagree       0
## overall_predicted_novel         306
## overall_all                   41226
## overall_partial                 922
## overall_ariba_blast              81
## overall_mentalist_blast         669
## overall_mentalist_ariba         172
## overall_single                  189
## overall_ariba                    29
## overall_mentalist               111
## overall_blast                    49
## overall                       42949
```

#### Top STs

```
top_st[1:10,]
```

```
##      st count percent overall
## 1    22  7189   16.74   16.74
## 2     8  6184   14.40   31.14
## 3     5  4664   10.86   42.00
```

```
## 4   239  3123    7.27   49.27
## 5   398  2326    5.42   54.68
## 6    30  1872    4.36   59.04
## 7    45  1663    3.87   62.91
## 8    15  1172    2.73   65.64
## 9    36   857    2.00   67.64
## 10  105   857    2.00   69.63
```

This gives us 4 columns for each ST, in descending order based on the *count* column. In other words the most represented STs are seen first. These columns are:

1. st: The sequence type.
2. count: The number of samples with given ST.
3. percent: The percent of samples represented by given ST.
4. overall: The percent of samples represented by given ST and previous STs.

### How many unique STs represented?

```r
nrow(top_st[top_st$st > 0,])
```

```
## [1] 1098
```

### How many STs represented by a single sample?

```r
nrow(top_st[top_st$count == 1, ])
```

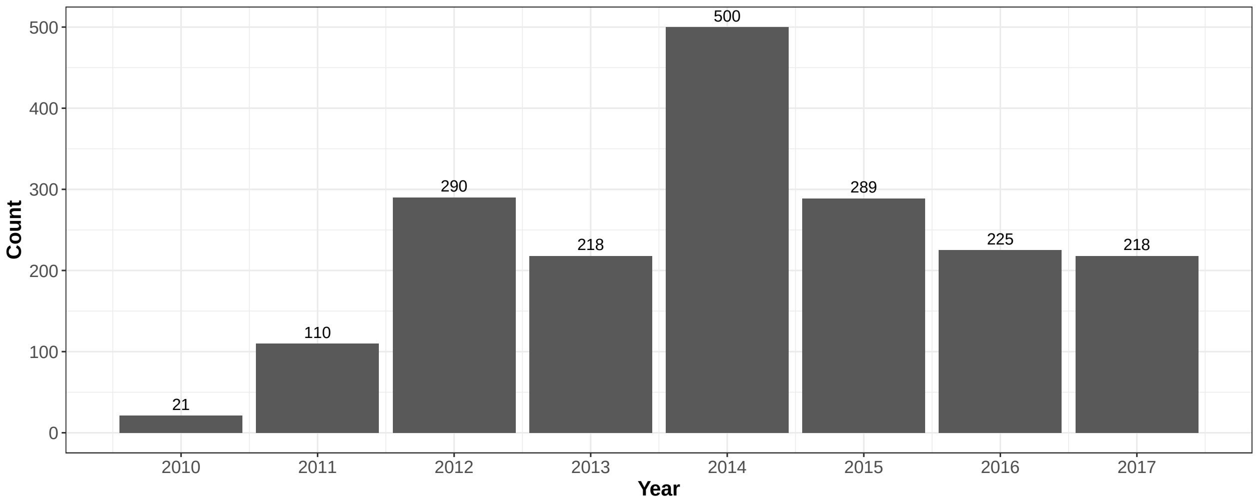
```
## [1] 588
```

### Visualizing MLST Diversity

The following sections will be plots to visualize relationships in the data.

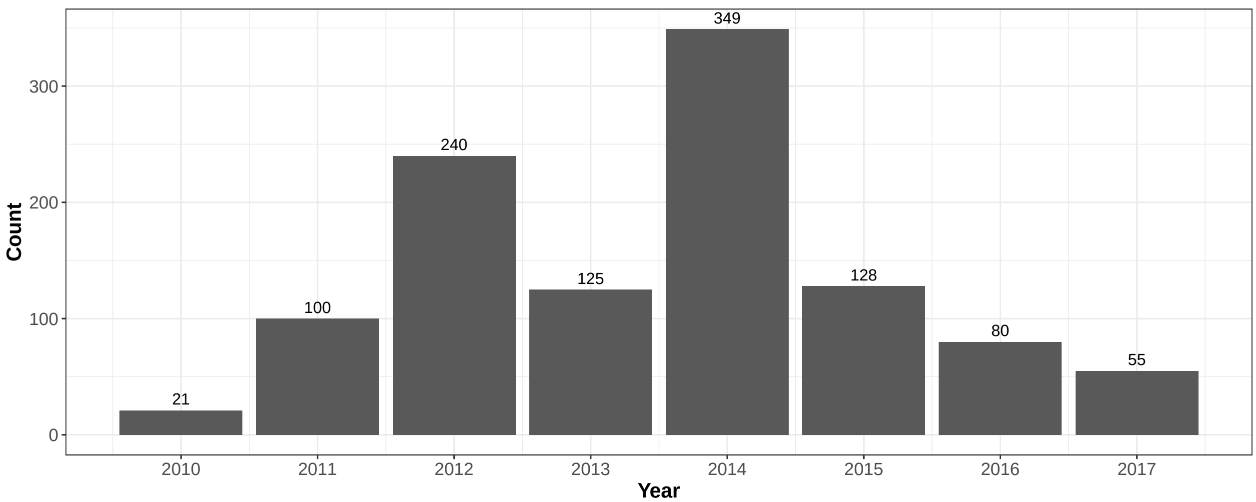
### Unique Sequence Types By Year

```r
p <- ggplot(data=sequence_types, aes(x=year, y=unique)) +
    xlab("Year") +
    ylab("Count") +
    geom_bar(stat='identity') +
    geom_text(aes(label=unique), vjust = -0.5) +
    scale_x_continuous(breaks = round(seq(min(sequence_types$year), max(sequence_types$year), by = 1),1
    theme_bw() +
    theme(axis.text=element_text(size=12),
          axis.title=element_text(size=14,face="bold"))
p
```




### Novel Sequence Types By Year

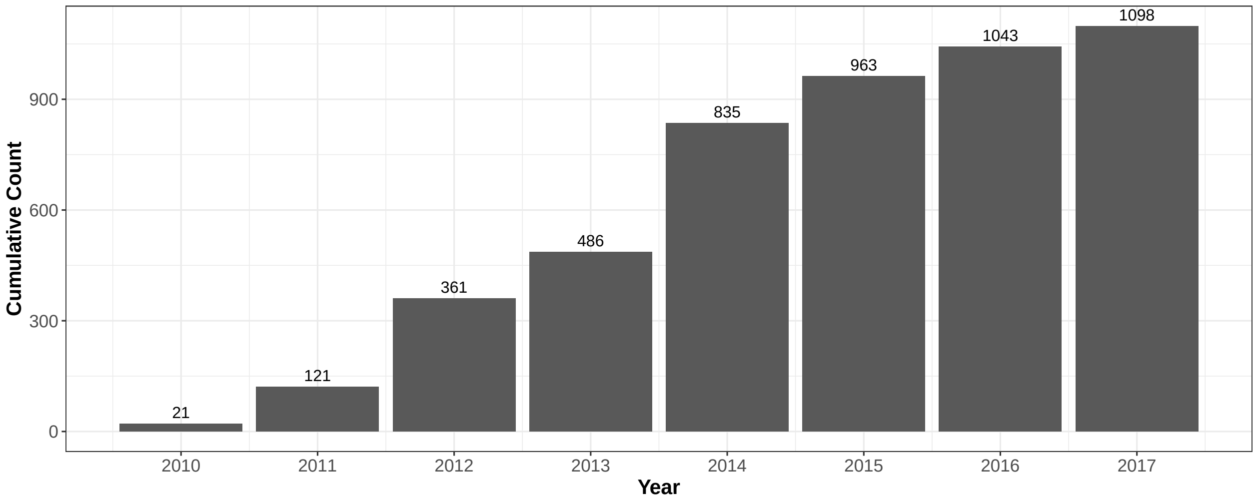
```
p <- ggplot(data=sequence_types, aes(x=year, y=novel)) +
    xlab("Year") +
    ylab("Count") +
    geom_bar(stat='identity') +
    geom_text(aes(label=novel), vjust = -0.5) +
    scale_x_continuous(breaks = round(seq(min(sequence_types$year), max(sequence_types$year), by = 1),1
    theme_bw() +
    theme(axis.text=element_text(size=12),
          axis.title=element_text(size=14,face="bold"))
p
```




### Overall Novel Sequence Types By Year

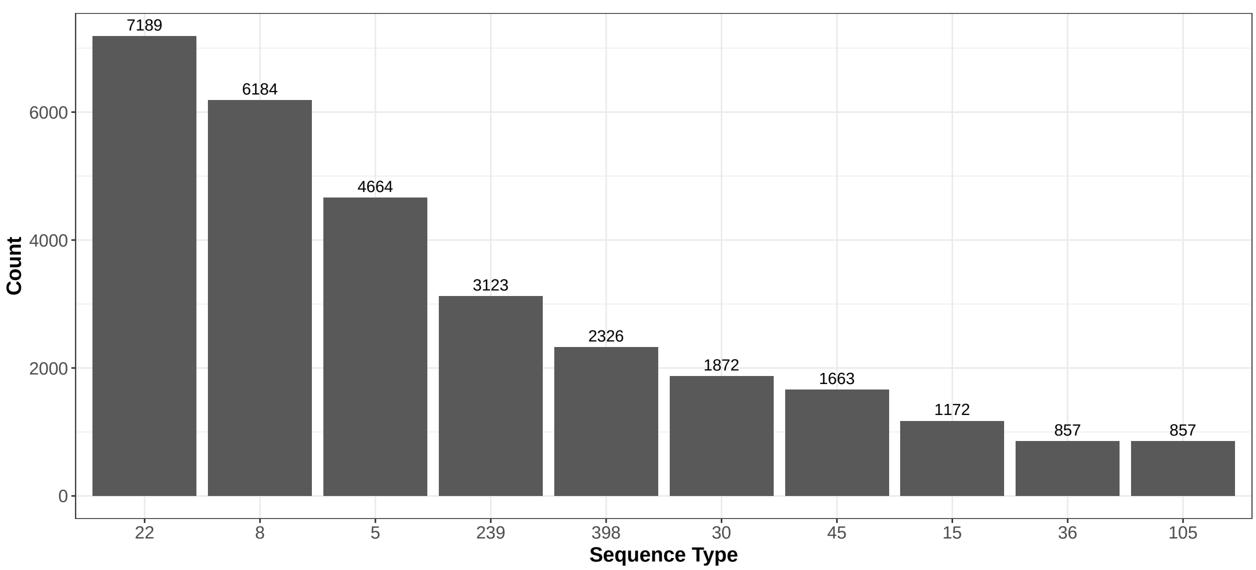
```
p <- ggplot(data=sequence_types, aes(x=year, y=overall_novel)) +
    xlab("Year") +
    ylab("Cumulative Count") +
    geom_bar(stat='identity') +
    geom_text(aes(label=overall_novel), vjust = -0.5) +
    scale_x_continuous(breaks = round(seq(min(sequence_types$year), max(sequence_types$year), by = 1),1
```

```r
    theme_bw() +
    theme(axis.text=element_text(size=12),
          axis.title=element_text(size=14,face="bold"))
p
```




## Top 10 Sequence Types

```r
p <- ggplot(data=top_st[1:10,], aes(x=reorder(st, -count), y=count)) +
    xlab("Sequence Type") +
    ylab("Count") +
    geom_bar(stat="identity") +
    geom_text(aes(label=count), vjust = -0.5) +
    theme_bw() +
    theme(axis.text=element_text(size=12),
          axis.title=element_text(size=14,face="bold"))
p
```

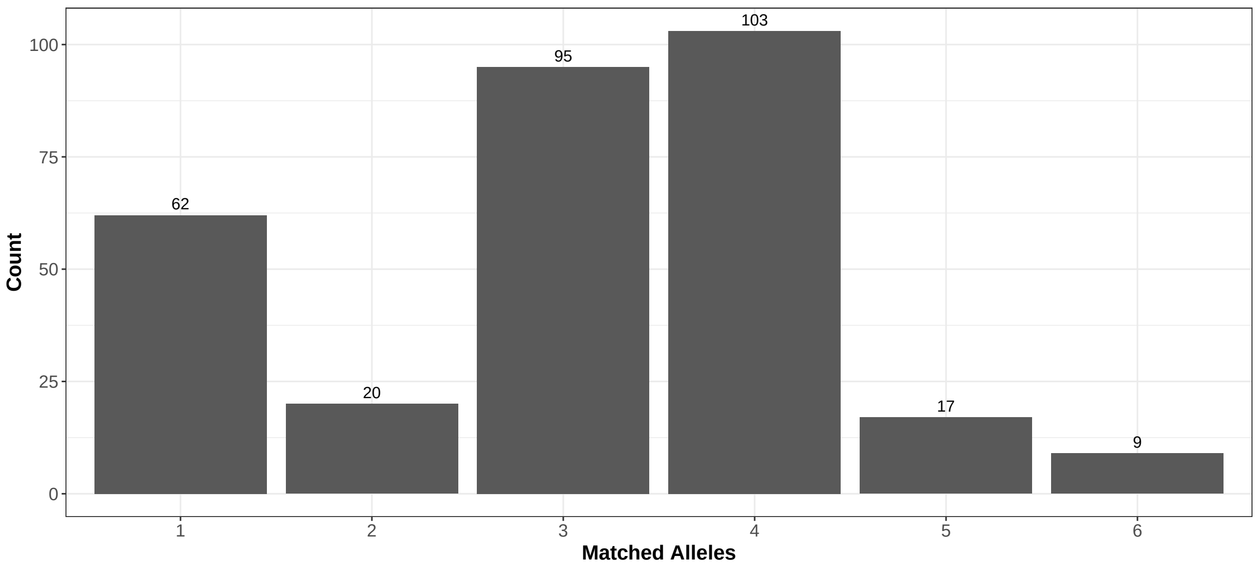



```r
# Output plot to PDF and PNG
staphopia::write_plot(p, paste0(getwd(), '/images/figure-x-top-10-sequence-types'))
```

### Total Allele Matches For Unassigned Samples

```
allele_matches <- get_mlst_allele_matches(ps[ps$st == 0,]$sample_id)
df <- as.data.frame(table(allele_matches[allele_matches$matches < 7,]$matches))
colnames(df) <- c("matches", "count")

p <- ggplot(data=df, aes(x=matches, y=count)) +
    xlab("Matched Alleles") +
    ylab("Count") +
    geom_bar(stat="identity") +
    geom_text(aes(label=count), vjust = -0.5) +
    theme_bw() +
    theme(axis.text=element_text(size=12),
          axis.title=element_text(size=14,face="bold"))
p
```




## cgMLST Patterns

Finally, we'll look at cgMLST as a measure of genetic diversity. We will use the *get_cgmlst()* function to get the cgMLST results for each Sample. This function might take a little while to retrieve all teh results.

```
cgmlst <- get_public_cgmlst_patterns()
cgmlst$percent <- cgmlst$count / sum(cgmlst$total_samples)
cgmlst
```

```
##    samples_in_pattern count total_samples      percent
## 1                 170     1           170 2.328343e-05
## 2                 133     1           133 2.328343e-05
## 3                  99     1            99 2.328343e-05
## 4                  83     1            83 2.328343e-05
## 5                  79     1            79 2.328343e-05
## 6                  61     1            61 2.328343e-05
## 7                  59     1            59 2.328343e-05
## 8                  52     1            52 2.328343e-05
## 9                  39     1            39 2.328343e-05
## 10                 36     1            36 2.328343e-05
```

```
## 11                     34     1              34 2.328343e-05
## 12                     33     1              33 2.328343e-05
## 13                     30     3              90 6.985029e-05
## 14                     29     1              29 2.328343e-05
## 15                     28     1              28 2.328343e-05
## 16                     26     1              26 2.328343e-05
## 17                     24     3              72 6.985029e-05
## 18                     22     1              22 2.328343e-05
## 19                     21     4              84 9.313372e-05
## 20                     19     2              38 4.656686e-05
## 21                     18     2              36 4.656686e-05
## 22                     15     3              45 6.985029e-05
## 23                     14     4              56 9.313372e-05
## 24                     13     3              39 6.985029e-05
## 25                     12     4              48 9.313372e-05
## 26                     11     8              88 1.862674e-04
## 27                     10     5              50 1.164171e-04
## 28                      9     5              45 1.164171e-04
## 29                      8    16             128 3.725349e-04
## 30                      7    28             196 6.519360e-04
## 31                      6    25             150 5.820857e-04
## 32                      5    47             235 1.094321e-03
## 33                      4    86             344 2.002375e-03
## 34                      3   223             669 5.192205e-03
## 35                      2  1363            2726 3.173531e-02
## 36                      1 36827           36827 8.574588e-01
```

This gives us two columns:

1. samples_in_pattern: The number of samples with a given cgMLST pattern.
2. count: The number patterns with a given number of samples.
3. total_samples: Number of samples represented by a row (samples_in_pattern * count)
4. percent: Percent of samples represented

For example, if samples_in_pattern is 100 and the count is 2. That means there are **2** (count=2) cgMLST patterns that are shared by **100 samples** (samples_in_count=100) each, representing a total of **200 samples** (count * samples_in_count).

### Total Number of Distinct cgMLST Patterns

```r
sum(cgmlst$count)
```

```
## [1] 38677
```

### How many shared cgMLST patterns?

```r
sum(cgmlst[cgmlst$samples_in_pattern > 1, ]$count)
```

```
## [1] 1850
```

#### How many samples share a cgMLST pattern?

```
sum(cgmlst[cgmlst$samples_in_pattern > 1, ]$total_samples)
```

```
## [1] 6122
```

#### How many samples have a unique cgMLST pattern?

```
cgmlst$percent <- cgmlst$count / sum(cgmlst$total_samples)
cgmlst[cgmlst$samples_in_pattern == 1, ]
```

```
##    samples_in_pattern count total_samples   percent
## 36                  1 36827         36827 0.8574588
```

## Session Info

```
sessionInfo()
```

```
## R version 3.4.3 (2017-11-30)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 16.04.2 LTS
##
## Matrix products: default
## BLAS: /usr/lib/libblas/libblas.so.3.6.0
## LAPACK: /usr/lib/lapack/liblapack.so.3.6.0
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] scales_0.5.0    reshape2_1.4.3  ggplot2_2.2.1   staphopia_0.1.9
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_0.12.15        knitr_1.20          magrittr_1.5
##  [4] munsell_0.4.3       colorspace_1.3-2    R6_2.2.2
##  [7] rlang_0.1.6         stringr_1.2.0       httr_1.3.1
## [10] plyr_1.8.4          tools_3.4.3         grid_3.4.3
## [13] data.table_1.10.4-3 gtable_0.2.0        htmltools_0.3.6
## [16] yaml_2.1.18         lazyeval_0.2.1      rprojroot_1.3-2
## [19] digest_0.6.15       tibble_1.4.2        curl_3.1
## [22] evaluate_0.10.1     rmarkdown_1.9       labeling_0.3
## [25] stringi_1.1.6       compiler_3.4.3      pillar_1.1.0
## [28] backports_1.1.2     jsonlite_1.5
```