Results of PangoVis

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2021-03-12

Load Packages and Data

```
# Packages that Art hates
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(tidyr)
library(ggplot2)
library(stringr)
library(here)
```

```
## here() starts at /home/devan/OneDriveUWO/0postdoc/sup
```

```
dirich <- params$dirich

# Read in CSV files
csvs <- list.files("../data/pangolineages",
    pattern = ifelse(dirich, "*_d.csv", "*.csv"),
    full.names = TRUE)

# Remove any copies
csvs <- csvs[!grepl("-1", csvs)]
# Proper names
#csvs <- paste0("../data/pangolineages/", csvs)

# Bring them into one data frame
lins <- bind_rows(lapply(csvs, read.csv))

# Taxon is encoded as _ACCSESSIONNUMBER.ID, split into ACCESSIONNUMBER and ID
lins <- lins %>%
    separate(col = "taxon", sep = "\\.",
        into = c("taxon", "sample")) %>%
    mutate(taxon = str_replace(taxon, "\\_", ""))
```

```
#### Visualize the uncertainty in the base calls ----
taxons <- unique(lins$taxon)
length(taxons)
```

```
## [1] 35
```

Abstract Info

```
summs <- lins %>%
    group_by(taxon) %>%
    summarise(maxperc = mean(lineage == names(sort(table(lineage),
        decreasing = TRUE))[1]),
        uniques = length(unique(lineage)),
        minpango = min(probability),
        maxpango = max(probability),
        menpango = mean(probability),
        max = names(sort(table(lineage), decreasing = TRUE))[1])
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
print("summary info")
```

```
## [1] "summary info"
```

```
print(summs)
```

```
## # A tibble: 35 x 7
##    taxon      maxperc uniques minpango maxpango menpango max
##    <chr>        <dbl>   <int>    <dbl>    <dbl>    <dbl> <chr>
##  1 ERR4085809   0.356      86        1        1        1 A
##  2 ERR4204823   0.701       9        1        1        1 A
##  3 ERR4363387   0.939      11        1        1        1 B.1.222
##  4 ERR4364007   0.838      48        1        1        1 B.1.1.29
##  5 ERR4664555   0.968      15        1        1        1 B.1.1.253
##  6 ERR4667618   0.990       7        1        1        1 B.1.1.315
##  7 ERR4692364   0.932      25        1        1        1 B.1
##  8 ERR4693034   0.901      34        1        1        1 B.1.1.310
##  9 ERR4693061   0.958      11        1        1        1 B.23
## 10 ERR4693079   0.864      45        1        1        1 B.1.1.310
## # ... with 25 more rows
```

```
1 - mean(summs$maxperc); 1 - mean(summs$menpango)
```

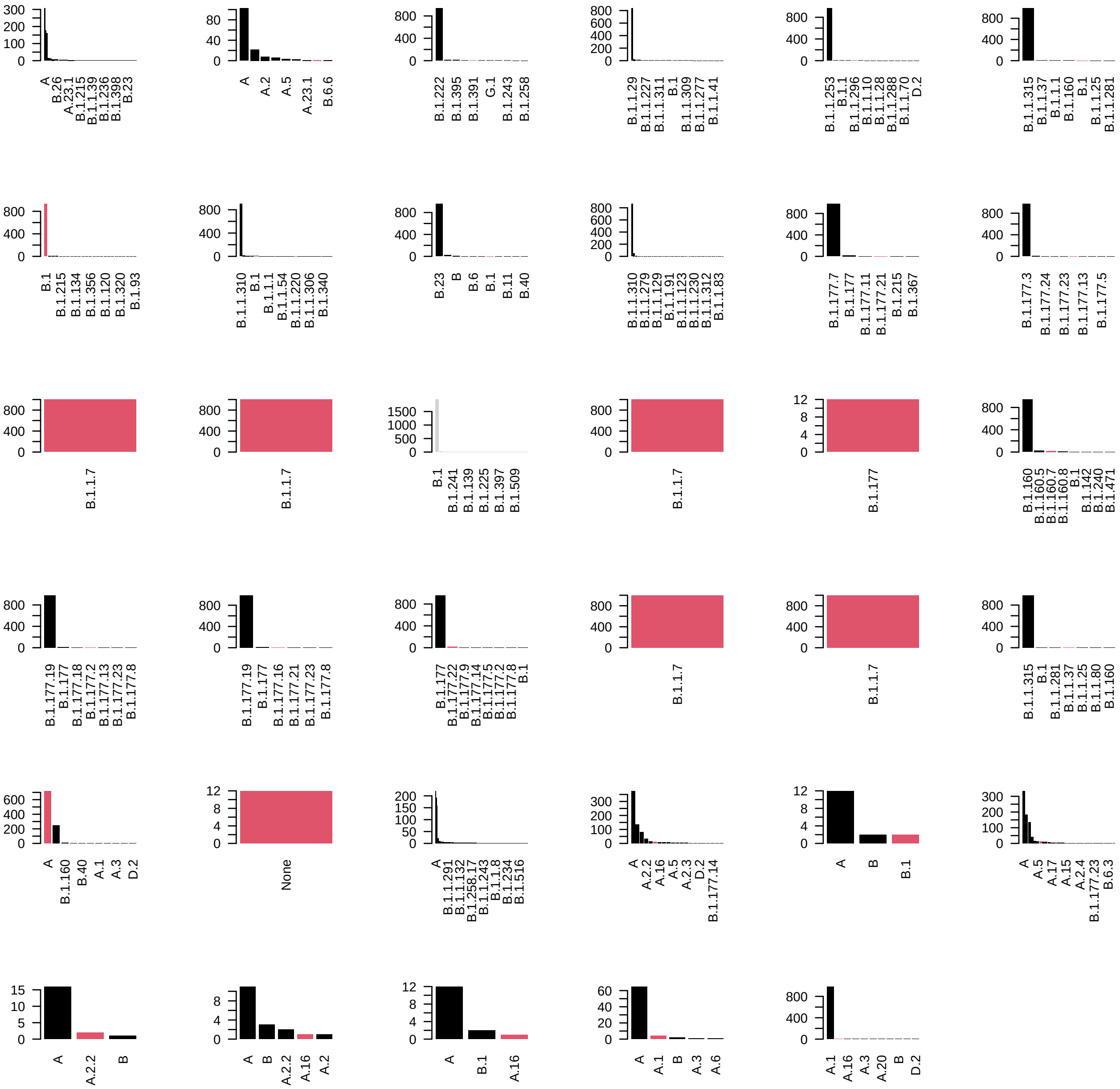
```
## [1] 0.1421196
```

```
## [1] 0.02857143
```

As a Pareto plot

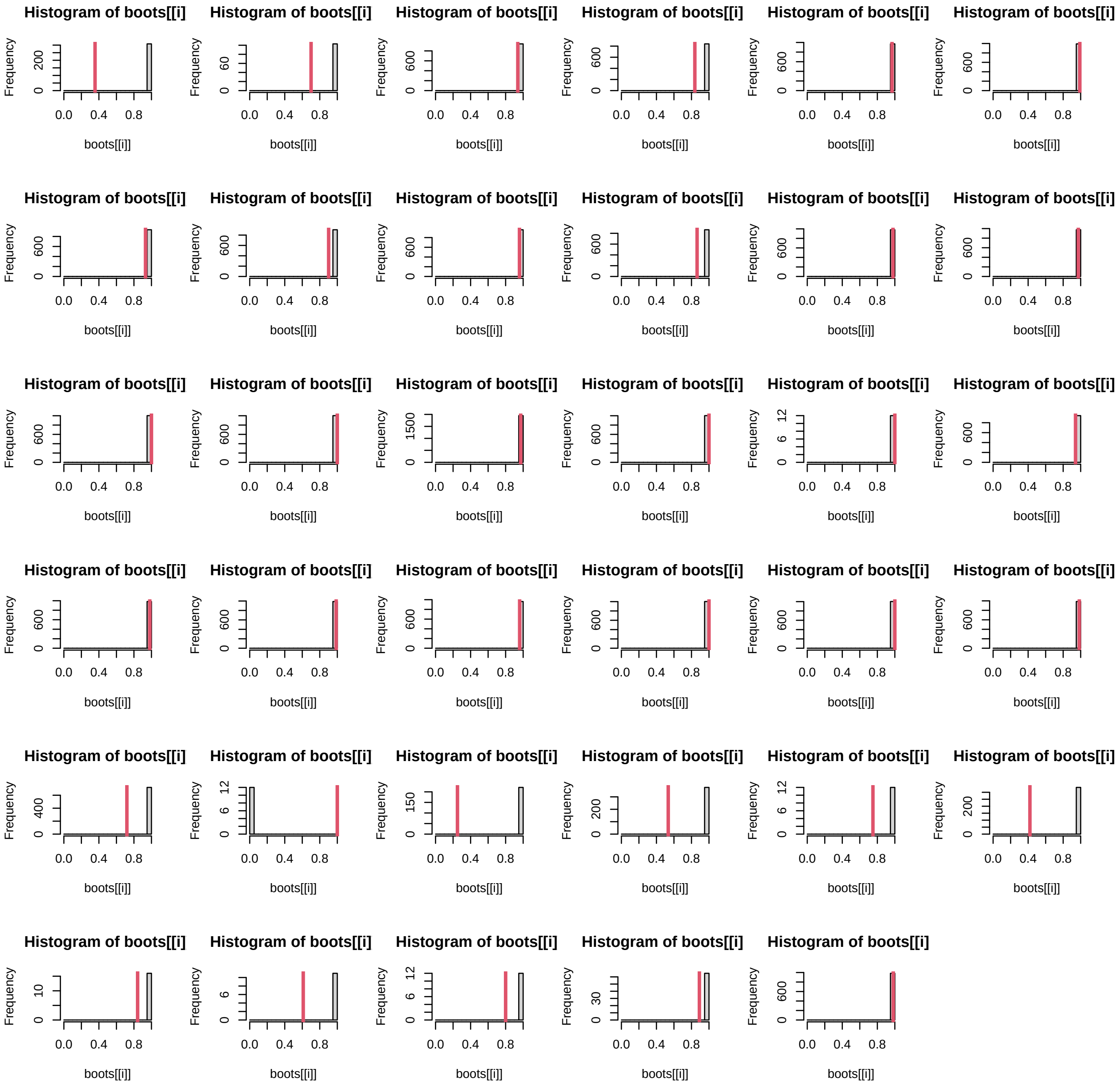
```
par(mfrow = c(6, 6))
for(i in 1:length(unique(lins$taxon))){
    thistab <- table(lins$lineage[lins$taxon == taxons[i]])
    called <- lins$lineage[lins$taxon == taxons[i] &
        lins$sample == 0]
    print(called)

    if(length(called) == 1) {
        colours <- rep(1, length(thistab))
        colours[names(thistab) == called] <- 2
    } else {
        colours <- "lightgrey"
    }

    barplot(sort(thistab, decreasing = TRUE),
        las = 2, col = colours, border = NA)
}
```

```
## [1] "B.1"
## [1] "B.40"
## [1] "B.1.222"
## [1] "B.1.1.29"
## [1] "B.1.1.253"
## [1] "B.1.1.315"
## [1] "B.1"
## [1] "B.1.1.310"
## [1] "B.23"
## [1] "B.1.1.310"
## [1] "B.1.177.7"
## [1] "B.1.177.3"
## [1] "B.1.1.7"
## [1] "B.1.1.7"
## [1] "B.1" "B.1"
## [1] "B.1.1.7"
## [1] "B.1.177"
## [1] "B.1.160"
## [1] "B.1.177.19"
## [1] "B.1.177.19"
## [1] "B.1.177"
## [1] "B.1.1.7"
## [1] "B.1.1.7"
## [1] "B.1.1.315"
## [1] "A"
## [1] "None"
## [1] "B.1.1.241"
## [1] "A.2.2"

## [1] "B.1"

## [1] "A.2.2"

## [1] "A.2.2"

## [1] "A.2.2"

## [1] "B.1"

## [1] "A.1"

## [1] "A.1"
```



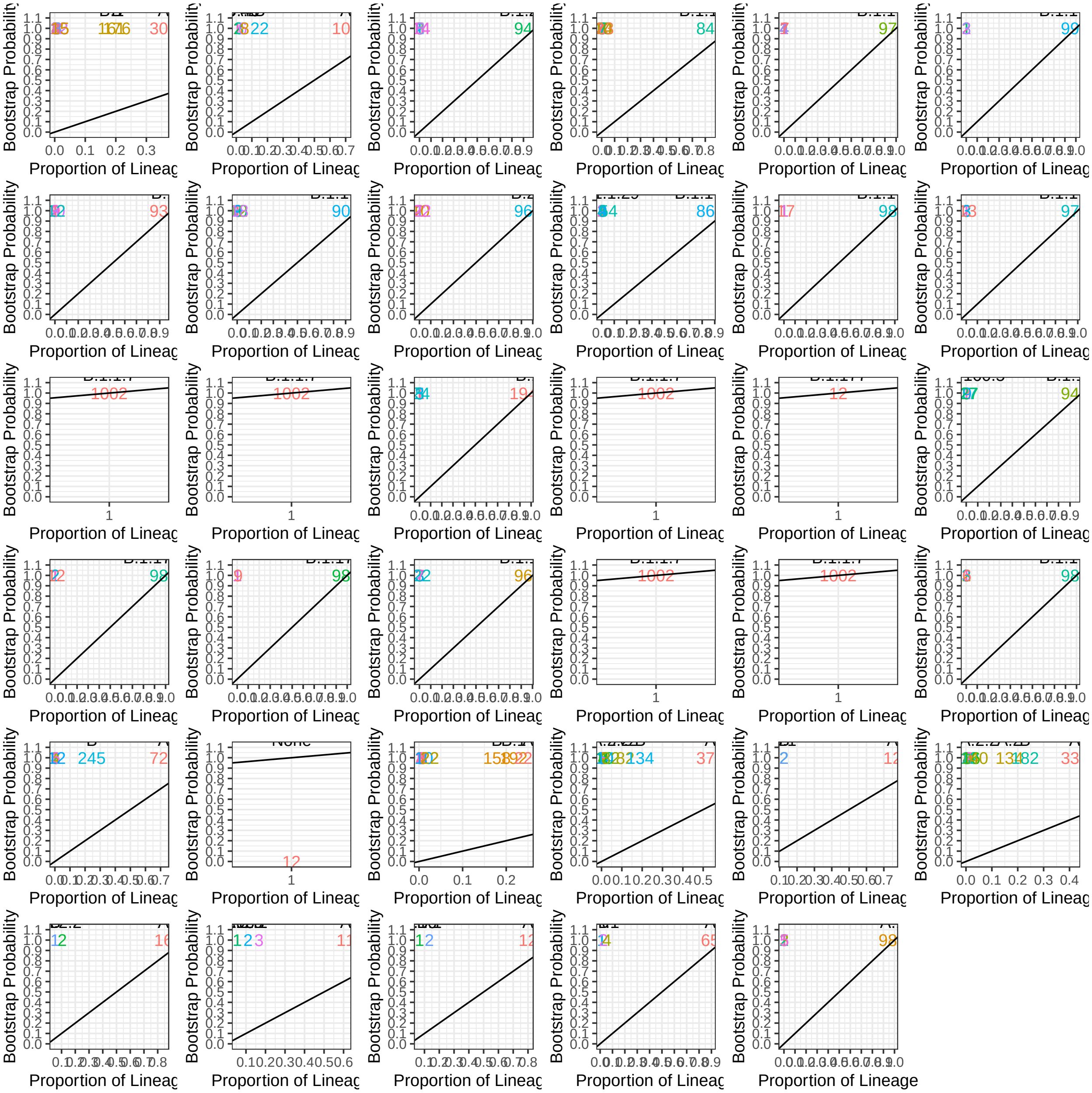
Probability Bars

```r
boots <- vector(mode = "list", length = length(taxons))
par(mfrow = c(6,6))
for(i in 1:length(taxons)){
    # Find modal lineage
    thistab <- table(lins$lineage[lins$taxon == taxons[i]])
    maxtab <- names(thistab)[which.max(thistab)]
    # Record "probability" for all sequences labelled with this lineage
    boots[[i]] <- lins$probability[lins$taxon == taxons[i] &
            lins$lineage == maxtab]

    # histogram of probabilities of that lineage
    hist(boots[[i]], breaks = seq(0, 1, 0.05),
        xlim = c(0, 1))
    # Add a line for the number of genomes that actually had that lineage
    abline(v = mean(lins$lineage[lins$taxon == taxons[i]] == maxtab),
        col = 2, lwd = 3)
}
```



Scatterplot

```
gglist <- list()
for(i in 1:length(taxons)){
    pang <- lins[lins$taxon == taxons[i], ]
    pang2 <- lapply(unique(pang$lineage), function(x) {
        data.frame(lineage = x,
            prop = mean(pang$lineage == x))
    }) %>%
        bind_rows() %>%
        right_join(pang, by = "lineage")
    #pang2
    ggplot(pang2) +
        aes(x = prop, y = probability,
            colour = lineage, label = lineage) +
        geom_point() +
        #geom_text_repel() +
        theme(legend.position = "none")

    pangtab <- pang2 %>%
        group_by(prop, lineage) %>%
        summarise(y = 1, count = n(), .groups = "drop") %>%
        filter(prop > 0.025)

    gglist[[i]] <- pang2 %>%
        # round to nearest 0.5
        #mutate(prop = round(prop*2, 1)/2,
        #    probability = round(probability*2, 1)/2) %>%
        group_by(prop, probability, lineage) %>%
        summarise(count = n(), .groups = "drop") %>%
        ggplot() + theme_bw() +
        aes(x = prop, y = probability, colour = lineage,
            label = count) +
        geom_text() +
        theme(legend.position = "none") +
        annotate("text", x = pangtab$prop, y = 1,
            label = pangtab$lineage,
            hjust = 0.5, vjust = -1) +
        labs(x = "Proportion of Lineage",
            y = "Bootstrap Probability",
            title = NULL) +
        scale_x_continuous(breaks = seq(0,1,0.1)) +
        scale_y_continuous(breaks = seq(0,1.1,0.1)) +
        coord_cartesian(ylim = c(0, 1.1)) +
        geom_abline(slope = 1, intercept = 0)
}
cowplot::plot_grid(plotlist = gglist)
```


Bootstrap Probability
Proportion of Lineag
Proportion of Lineage
B.1.1.7
1002
None
12
245
72
30
22
94
84
97
93
90
96
86
98
19
134
37
65