Results of PangoVis

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Load Packages and Data

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

dirich <- params$dirich

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

# Remove any copies
csvs <- csvs[!grepl("-1", 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, "\\_", ""))

badlins <- table(lins$taxon)
badlins <- names(badlins[which(badlins < 5000)])
cat(length(badlins), " runs were removed for having too few samples.")
```

```
## 11  runs were removed for having too few samples.
```

```
lins <- filter(lins, !taxon %in% badlins)

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

```
## [1] 80
```

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: 80 x 7
##    taxon      maxperc uniques minpango maxpango menpango max
##    <chr>        <dbl>   <int>    <dbl>    <dbl>    <dbl> <chr>
##  1 ERR4363387   0.950      19        1        1        1 B.1.222
##  2 ERR4364007   0.821      84        1        1        1 B.1.1.29
##  3 ERR4664555   0.963      27        1        1        1 B.1.1.253
##  4 ERR4667618   0.993       7        1        1        1 B.1.1.315
##  5 ERR4692364   0.914      55        1        1        1 B.1
##  6 ERR4693034   0.869      77        1        1        1 B.1.1.310
##  7 ERR4693061   0.954      19        1        1        1 B.23
##  8 ERR4693079   0.874      99        1        1        1 B.1.1.310
##  9 ERR4693537   0.973       9        1        1        1 B.1.177.7
## 10 ERR4693605   0.968      15        1        1        1 B.1.177.3
## # ... with 70 more rows
```

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

```
## [1] 0.09735665
```

```
## [1] 0.0249975
```

```
#print(summs, n = Inf)
```

Stacked Bar Plots

```
max_label <- 250
other_label <- 100

par(mfrow = c(17, 1), mar = c(0.05, 7.75, 0.05, 0.05))
if (exists("seq_info")) rm(seq_info)
for (i in seq_along(taxons)) {
    pang <- lins[lins$taxon == taxons[i], ]
    called <- pang$lineage[pang$sample == 0][1]
    pangtab <- sort(table(pang$lineage), decreasing = TRUE)
```

```
    seq_info_i <- data.frame(
        called = called,
        mode = names(pangtab)[1],
            mode_count = pangtab[1],
            perc = round(100*pangtab[1] / sum(pangtab), 2),
        runner_up = names(pangtab)[2],
            runner_up_count = pangtab[2],
        unique = length(pangtab), atoms = sum(pangtab == 1))
    seq_info_i$taxon <- taxons[i]

    if (!exists("seq_info")) {
        seq_info <- seq_info_i
    } else {
        seq_info <- bind_rows(seq_info, seq_info_i)
    }

    colvec <- rep("grey", length(pangtab))
    colvec[which(names(pangtab) == called)] <- "red"

    n <- sum(pangtab > max_label)
    if (n > 1) {
        add_other <- FALSE
        if (sum(pangtab < other_label) > 10) {
            add_other <- TRUE
            other_count <- sum(pangtab <= other_label)
            pangtab <- c(pangtab[pangtab > other_label],
                c("other" = sum(pangtab[pangtab <= other_label])))
            colvec[which(names(pangtab) == "other")] <- "black"
        }
        barlabx <- c(0, cumsum(pangtab[1:(n - 1)])) +
            pangtab[1:n] / 2
        barlabels <- names(pangtab)[1:n]
        barlens <- sapply(gregexpr("\\.", barlabels), length)
        for (j in seq_along(barlabels)) {
            if (pangtab[j] < 400 & barlens[j] >= 2) {
                barsplit <- strsplit(barlabels[j], split = "\\.")[[1]]
                barn <- length(barsplit)
                half <- floor(barn / 2)
                barlabels[j] <- paste0(
                    paste(barsplit[1:half], collapse = "."),
                    ".\n",
                    paste(barsplit[(half + 1):barn], collapse = ".")
                )
            }
        }

        barplot(as.matrix(pangtab),
            col = colvec, hori = TRUE, axes = FALSE)
        text(barlabx, 0.7, barlabels, cex = 1.5)
        if (add_other) {
            text(x = sum(pangtab) - pangtab["other"] / 2,
            y = 0.7, col = "white", cex = 1.5,
            label = paste0("Others:\n", other_count))
```

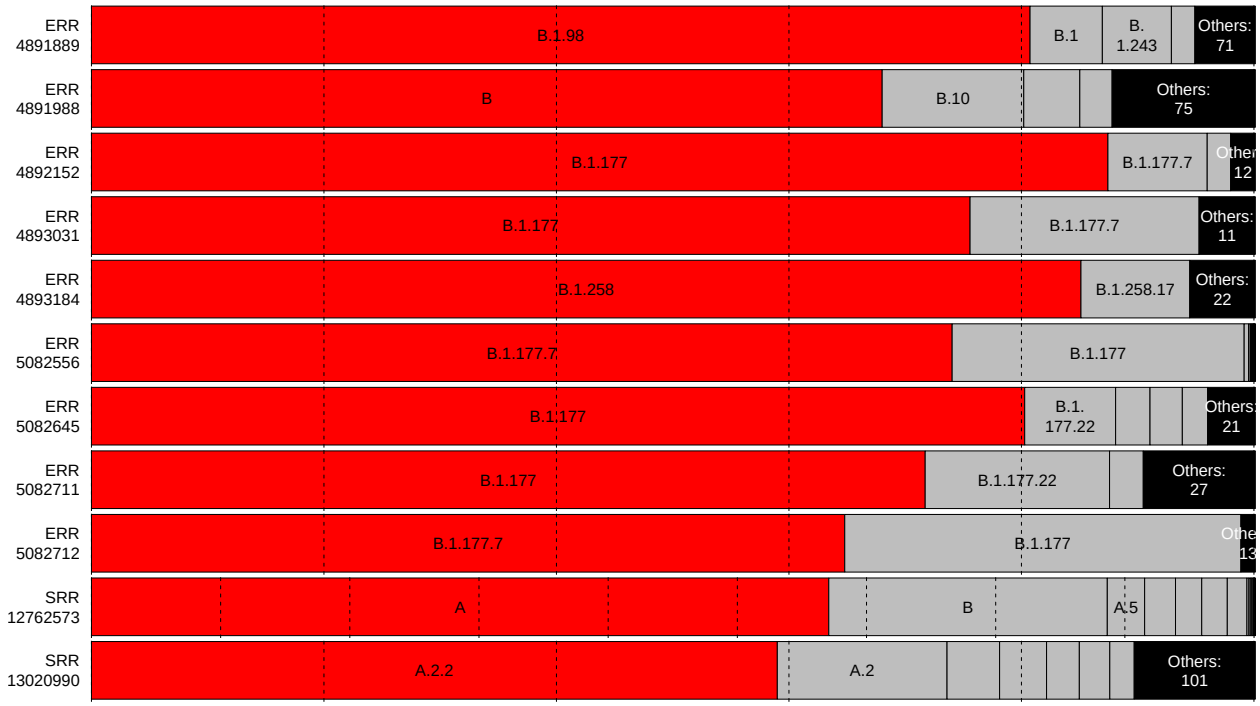
```
        }
        mtext(side = 2, cex = 1, las = 1,
            text = paste(substr(taxons[i], 1, 3),
                substr(taxons[i], 4, 20), sep = "\n"))
        abline(v = seq(0, 10000, 1000), lty = 2)
        "pretty_labels <- seq(0, sum(pangtab),
                by = ifelse(sum(pangtab) < 2000, 100, 1000))
        mtext(side = 1,
            at = pretty_labels,
            text = pretty_labels,
            line = 0,
            cex = 0.75
        )"
    }
}

seq_info$taxon <- taxons
seq_info <- arrange(seq_info, mode, mode_count)
knitr::kable(seq_info, row.names = FALSE)
```

called	mode	mode_count	perc	runner_up	runner_up_count	unique	atoms	taxon
A	A	5708	63.35	B	2156	16	0	SRR12762573
A.1	A.1	8879	98.55	B.40	57	20	6	SRR13092002
A.2.2	A.2.2	2950	58.93	A.2	730	108	47	SRR13020990
B	B	3401	67.94	B.10	609	79	32	ERR4891988
B	B	4408	88.05	B.23	189	30	7	ERR4891715
B.1	B.1	3736	74.63	B.1.243	91	216	49	ERR4891841
B.1	B.1	4378	87.46	B.1.88	140	50	16	ERR4893013
B.1	B.1	4577	91.43	B.1.400	92	55	12	ERR4692364
B.1	B.1	4829	96.46	B.1.247	75	43	14	ERR5069624
B.1.1.162	B.1.1.162	3001	59.95	B.1.1.209	112	198	66	ERR4892293
B.1.1.216	B.1.1.216	4179	83.48	B.1	135	132	48	ERR4891863
B.1.1.216	B.1.1.216	4441	88.71	B.1.1.208	52	100	43	ERR4893186
B.1.1.216	B.1.1.216	4528	90.45	B.1.1.29	38	76	18	ERR4892203
B.1.1.253	B.1.1.253	4819	96.26	B.1	52	27	9	ERR4664555
B.1.1.29	B.1.1.29	1384	27.65	B.1.1.59	239	213	41	ERR4892066
B.1.1.29	B.1.1.29	2445	48.84	B.1.1.39	101	231	29	ERR4893037
B.1.1.29	B.1.1.29	4112	82.14	B.1.1.44	130	84	27	ERR4364007
B.1.1.304	B.1.1.304	4856	97.00	B.1.1.4	16	34	11	ERR4891898
B.1.1.307	B.1.1.307	4885	97.58	B.1	46	40	22	ERR4893033
B.1.1.307	B.1.1.307	4957	99.02	B.1	20	15	10	ERR4893353
B.1.1.307	B.1.1.307	4975	99.38	B.1	10	14	8	ERR4892048
B.1.1.310	B.1.1.310	4352	86.94	B.1.1.59	185	77	31	ERR4693034
B.1.1.310	B.1.1.310	4375	87.40	B.1.1.29	212	99	40	ERR4693079
B.1.1.311	B.1.1.311	4876	97.40	B.1	54	14	8	ERR5080913
B.1.1.315	B.1.1.315	4403	87.95	B.1.1.281	244	39	18	ERR5082696
B.1.1.315	B.1.1.315	4853	96.94	B.1	61	15	6	ERR5082664
B.1.1.315	B.1.1.315	4969	99.26	B.1	22	7	2	ERR4667618
B.1.1.7	B.1.1.7	5006	100.00	NA	NA	1	0	ERR5069584
B.1.1.7	B.1.1.7	5006	100.00	NA	NA	1	0	ERR5069616
B.1.1.7	B.1.1.7	5006	100.00	NA	NA	1	0	ERR5069871
B.1.1.7	B.1.1.7	5006	100.00	NA	NA	1	0	ERR5070294
B.1.1.7	B.1.1.7	5006	100.00	NA	NA	1	0	ERR5077411

called	mode	mode_count	perc	runner_up	runner_up_count	unique	atoms	taxon
B.1.1.7	B.1.1.7	5006	100.00	NA	NA	1	0	ERR5077618
B.1.1.7	B.1.1.7	5006	100.00	NA	NA	1	0	ERR5082610
B.1.160	B.1.160	4663	93.15	B.1.160.8	184	17	7	ERR5074314
B.1.160	B.1.160	4857	97.02	B.1.160.5	61	15	5	ERR5082569
B.1.177	B.1.177	3586	71.63	B.1.177.22	793	30	7	ERR5082711
B.1.177	B.1.177	3779	75.49	B.1.177.7	985	13	0	ERR4893031
B.1.177	B.1.177	4014	80.18	B.1.177.22	391	26	9	ERR5082645
B.1.177	B.1.177	4372	87.34	B.1.177.7	427	15	3	ERR4892152
B.1.177	B.1.177	4463	89.15	B.1.177.22	227	19	2	ERR5082695
B.1.177	B.1.177	4529	90.47	B.1.177.23	181	17	0	ERR4892339
B.1.177	B.1.177	4620	92.29	B.1.177.22	240	21	2	ERR5082580
B.1.177	B.1.177	4667	93.23	B.1.177.22	182	20	5	ERR5081301
B.1.177	B.1.177	4710	94.09	B.1.177.22	130	22	4	ERR5080918
B.1.177	B.1.177	4724	94.37	B.1.177.22	131	13	3	ERR4893242
B.1.177	B.1.177	4779	95.47	B.1.177.22	133	21	7	ERR5062571
B.1.177	B.1.177	4783	95.55	B.1.177.22	115	18	3	ERR5064166
B.1.177	B.1.177	4802	95.92	B.1.177.22	114	19	4	ERR5077151
B.1.177	B.1.177	4819	96.26	B.1.177.22	98	12	4	ERR4893080
B.1.177	B.1.177	4830	96.48	B.1.177.22	81	17	1	ERR4892392
B.1.177	B.1.177	4841	96.70	B.1.177.22	115	14	2	ERR5070060
B.1.177	B.1.177	4844	96.76	B.1.177.23	68	17	6	ERR4893197
B.1.177.15	B.1.177.15	4845	96.78	B.1.177	130	11	3	ERR5081316
B.1.177.16	B.1.177.16	4964	99.16	B.1.177	29	4	1	ERR4893138
B.1.177.17	B.1.177.17	4967	99.22	B.1.177	39	2	0	ERR4892200
B.1.177.19	B.1.177.19	4852	96.92	B.1.177	113	12	6	ERR5076748
B.1.177.19	B.1.177.19	4875	97.38	B.1.177	74	13	2	ERR5076163
B.1.177.19	B.1.177.19	4914	98.16	B.1.177	64	8	1	ERR5063165
B.1.177.3	B.1.177.3	4847	96.82	B.1.177	62	15	1	ERR4693605
B.1.177.4	B.1.177.4	4980	99.48	B.1.177.2	15	8	5	ERR5082590
B.1.177.4	B.1.177.4	4983	99.54	B.1.177.2	11	13	10	ERR5081304
B.1.177.6	B.1.177.6	4875	97.38	B.1.177	80	11	2	ERR5082674
B.1.177.6	B.1.177.6	4944	98.76	B.1.177.9	31	8	1	ERR4891805
B.1.177.7	B.1.177.7	3240	64.72	B.1.177	1704	15	1	ERR5082712
B.1.177.7	B.1.177.7	3702	73.95	B.1.177	1256	12	1	ERR5082556
B.1.177.7	B.1.177.7	4871	97.30	B.1.177	125	9	4	ERR4693537
B.1.177.7	B.1.177.7	4879	97.46	B.1.177	113	10	4	ERR5082630
B.1.222	B.1.222	4756	95.01	B.1	108	19	3	ERR4363387
B.1.258	B.1.258	4256	85.02	B.1.258.17	468	24	6	ERR4893184
B.1.36	B.1.36	4724	94.37	B.1.36.9	71	26	8	ERR4891711
B.1.36.17	B.1.36.17	4785	95.59	B.1	125	15	5	ERR5080897
B.1.523	B.1.523	4501	89.91	B.1	228	30	6	ERR4892423
B.1.523	B.1.523	4598	91.85	B.1	122	32	7	ERR4893393
B.1.98	B.1.98	4037	80.64	B.1	311	75	36	ERR4891889
B.23	B.23	4776	95.41	B.48	112	19	6	ERR4693061
B.39	B.39	4817	96.22	B	113	22	8	ERR4892112
B.40	B.40	4974	99.36	B	13	7	1	ERR4892386
None	None	5002	99.98	B.1	1	2	1	ERR4891916
None	None	5006	100.00	NA	NA	1	0	SRR12639958

```
rm(seq_info)
```


ERR 4891889
B.1.98
B.1
B. 1.243
Others: 71
ERR 4891988
B
B.10
Others: 75
ERR 4892152
B.1.177
B.1.177.7
Other 12
ERR 4893031
B.1.177
B.1.177.7
Others: 11
ERR 4893184
B.1.258
B.1.258.17
Others: 22
ERR 5082556
B.1.177.7
B.1.177
ERR 5082645
B.1.177
B.1. 177.22
Others: 21
ERR 5082711
B.1.177
B.1.177.22
Others: 27
ERR 5082712
B.1.177.7
B.1.177
Othe 13
SRR 12762573
A
B
A.5
SRR 13020990
A.2.2
A.2
Others: 101