SARS-CoV-2 State introductions

Transmission Lineage Summary for Hamburg

Last modified: 27 Jun 2021

Contents

1 Summary

This notebook plots summary statistics and figures of the German transmission lineages extracted from the GISAID tree and Sankoff algorithm analyses.

2 Transmission lineage statistics

2.1 Input data

- Transmission lineages and singletons, on the dataset, n = 178672 sequences (n = Germany : 111283, Germany : 62% from the Germany').

```
## Warning in if (class(try(col2rgb(palette), silent = TRUE)) == "try-error")
## stop("color palette is not correct"): the condition has length > 1 and only the
## first element will be used
```
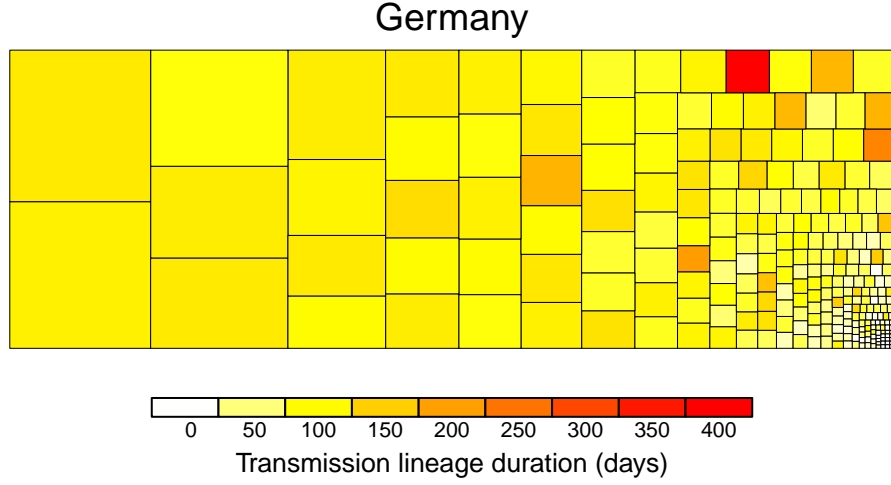
Figure 1: Partition of `r nrow(metadata)` `r states` genomes into `r states` transmission lineages and singletons, coloured by duration of lineage detection (time between the lineage's oldest and most recent genomes). (Transmission lineages from the MCC trees).
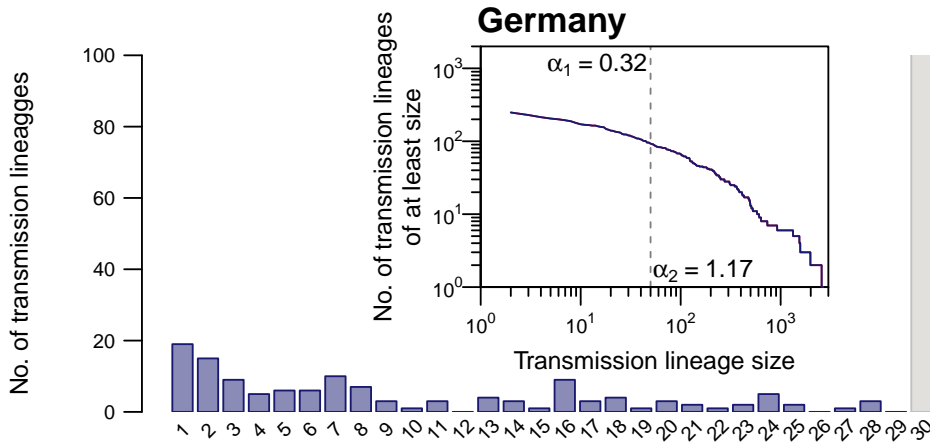

Figure 2: Distribution of `r states` transmission lineage sizes (MCC trees). Blue bars show the number of transmission lineages of each size (red bars=95% HPD of these sizes across the posterior tree distribution). Inset: the corresponding complementary cumulative frequency distribution of lineage size (blue line), on double logarithmic axes (red shading=95% HPD of this distribution across the posterior tree distribution). Values either side of vertical dashed line show coefficients of power-law distributions (P[X >= x] ~ x^alpha)) fitted to lineages containing <=50 (alpha1) and >50 (alpha2) virus genomes, respectively.

3 Transmission lineage TMRCA distribution

```
## Error in seq.int(0, to0 - from, by): 'to' must be a finite number
```
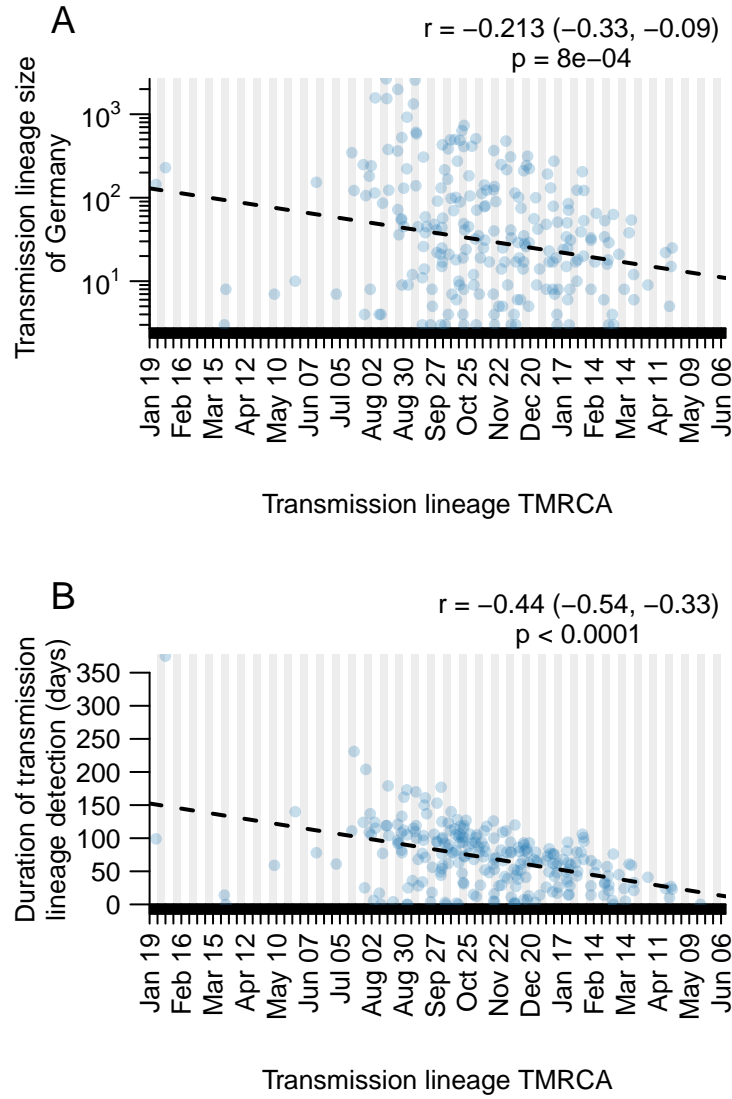
4 Size and duration vs. TMRCA

A

r = −0.213 (−0.33, −0.09)
p = 8e−04

Transmission lineage size of Germany

Transmission lineage TMRCA

B

r = −0.44 (−0.54, −0.33)
p < 0.0001

Duration of transmission lineage detection (days)

Transmission lineage TMRCA

Figure 3: Scatterplots showing the relationship between (A) `r states` transmission lineage size and lineage TMRCA and between (B) `r states` transmission lineage sampling duration and lineage TMRCA. Pearson correlation coefficients, 95% CIs and p-values are shown in the top-right corners.
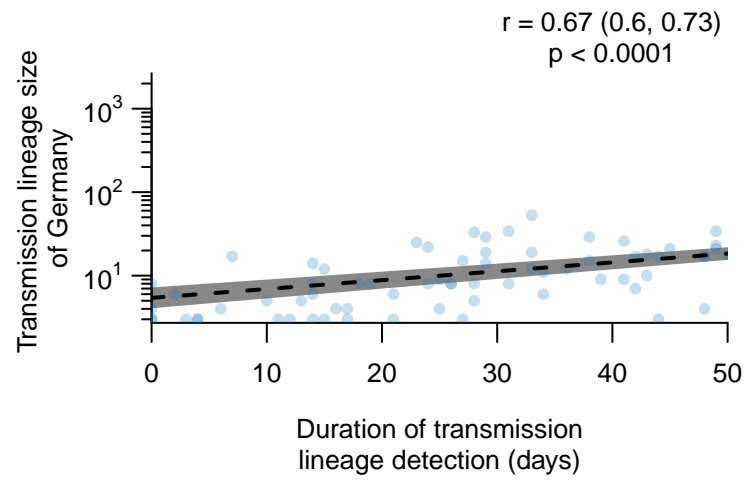
Figure 4: Scatterplot showing the strong relationship between `r states` transmission lineage size and sampling duration. The Pearson correlation coefficient, 95% CI and p-value are shown.

5 Time since lineage last sampled
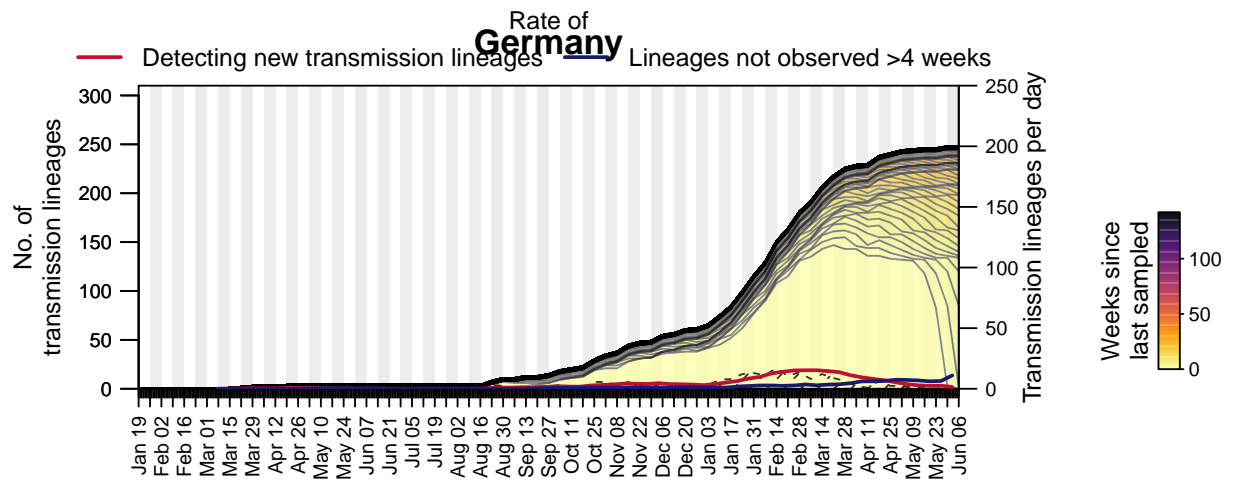
`## 2.181 sec elapsed`

Figure 5: Trends through time in the detection of `r states` transmission lineages (absolute values). For each day, all lineages detected up to that day are coloured by the time since the transmission lineage was last sampled. Isoclines correspond to weeks. Shaded area=transmission lineages that were first sampled <1 week ago.

6 Session info

```
## R version 4.1.0 (2021-05-18)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 20.04.2 LTS
##
## Matrix products: default
## BLAS:   /usr/lib/x86_64-linux-gnu/atlas/libblas.so.3.10.3
## LAPACK: /usr/lib/x86_64-linux-gnu/atlas/liblapack.so.3.10.3
##
## 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] tictoc_1.0.1      beastio_0.3.3     viridis_0.6.1     viridisLite_0.4.0
## [5] coda_0.19-4       treemap_2.4-2     gplots_3.1.1      lubridate_1.7.10
## [9] stringr_1.4.0
##
## loaded via a namespace (and not attached):
##  [1] gtools_3.8.2      tidyselect_1.1.1  xfun_0.23         purrr_0.3.4
##  [5] lattice_0.20-44   colorspace_2.0-1  generics_0.1.0    vctrs_0.3.8
##  [9] htmltools_0.5.1.1 yaml_2.2.1        utf8_1.2.1        rlang_0.4.11
## [13] later_1.2.0       pillar_1.6.1      glue_1.4.2        RColorBrewer_1.1-2
## [17] lifecycle_1.0.0   munsell_0.5.0     gtable_0.3.0      caTools_1.18.2
## [21] codetools_0.2-18  evaluate_0.14     knitr_1.33        fastmap_1.1.0
## [25] httpuv_1.6.1      fansi_0.5.0       highr_0.9         Rcpp_1.0.6
## [29] KernSmooth_2.23-20 xtable_1.8-4     promises_1.2.0.1  scales_1.1.1
## [33] mime_0.10         gridExtra_2.3     ggplot2_3.3.3     digest_0.6.27
## [37] stringi_1.6.2     dplyr_1.0.6       shiny_1.6.0       grid_4.1.0
## [41] tools_4.1.0       bitops_1.0-7      magrittr_2.0.1    tibble_3.1.2
## [45] crayon_1.4.1      pkgconfig_2.0.3   ellipsis_0.3.2    gridBase_0.4-7
## [49] data.table_1.14.0 rmarkdown_2.8    R6_2.5.0          igraph_1.2.6
## [53] compiler_4.1.0
```