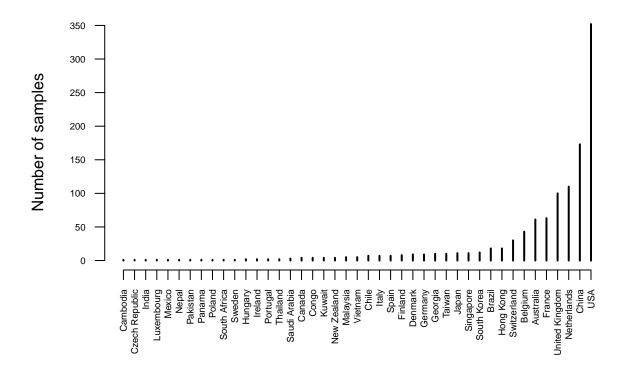
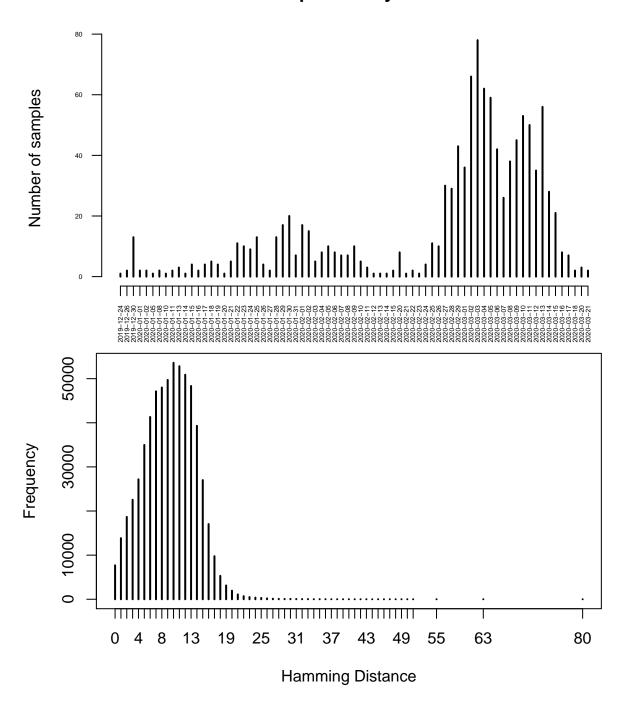
Preliminary Molecular Clock Check and Summary Statistics

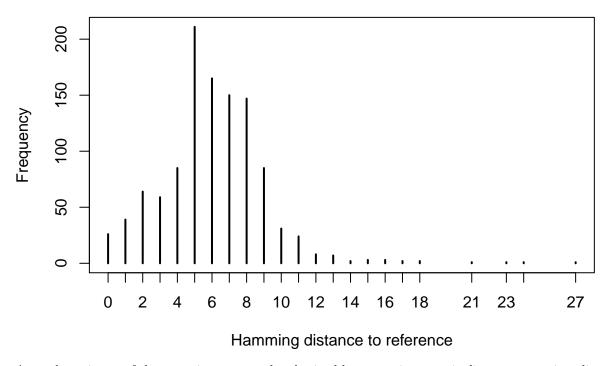
```
##
## Attaching package: 'lubridate'
## The following object is masked from 'package:base':
##
## date
```

A total of 1117 from 43 countries -- Fri Mar 27 11:46:45 2020



Sequences by date

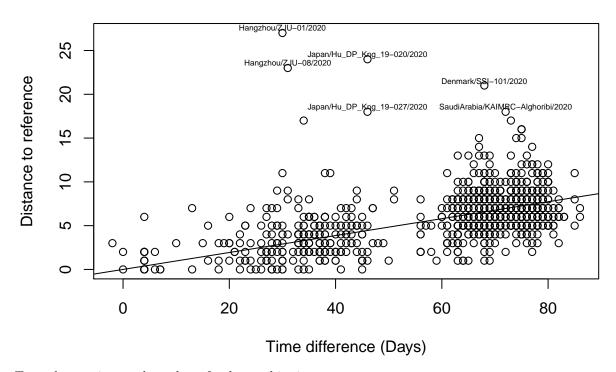




A rought estimate of the mutation rate can be obtained by regressing genetic divergence on time divergence. This estimate ignores correlation among samples, population structure and pairwise information. A more reliable estimate can be found in the mutation section.

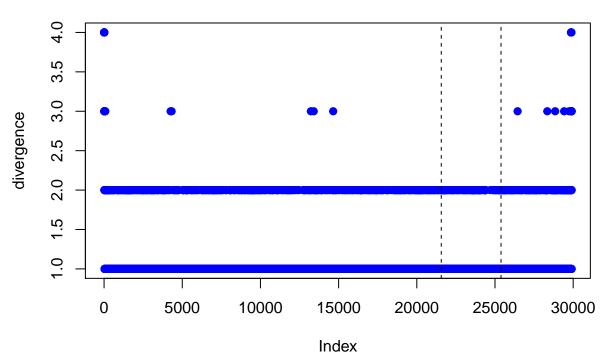
```
##
## Call:
## lm(formula = hamming[ref, ] ~ -1 + x)
##
## Residuals:
##
       Min
                1Q Median
                                 3Q
                                        Max
  -5.6678 -1.5419 -0.3443
##
                            1.4245 24.1009
##
## Coefficients:
##
     Estimate Std. Error t value Pr(>|t|)
## x 0.096635
                0.001197
                            80.7
                                    <2e-16 ***
##
                  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Signif. codes:
##
## Residual standard error: 2.578 on 1116 degrees of freedom
## Multiple R-squared: 0.8537, Adjusted R-squared: 0.8536
## F-statistic: 6513 on 1 and 1116 DF, p-value: < 2.2e-16
                Denmark/SSI-101/2020|2020-03-03
##
##
                                             158
##
                Hangzhou/ZJU-01/2020|2020-01-25
##
                                             371
                Hangzhou/ZJU-08/2020|2020-01-26
##
##
                                             378
##
         Japan/Hu_DP_Kng_19-020/2020|2020-02-10
##
                                             410
##
         Japan/Hu_DP_Kng_19-027/2020|2020-02-10
##
                                             411
```

A total of 2.71 of mutations per month



To explore regions and number of polymorphic sites

[1] 29903



Reference:

Rambaut, Andrew, Tommy T. Lam, Luiz Max Carvalho, and Oliver G. Pybus. "Exploring the temporal structure of heterochronous sequences using TempEst (formerly Path-O-Gen)." Virus evolution 2, no. 1 (2016).