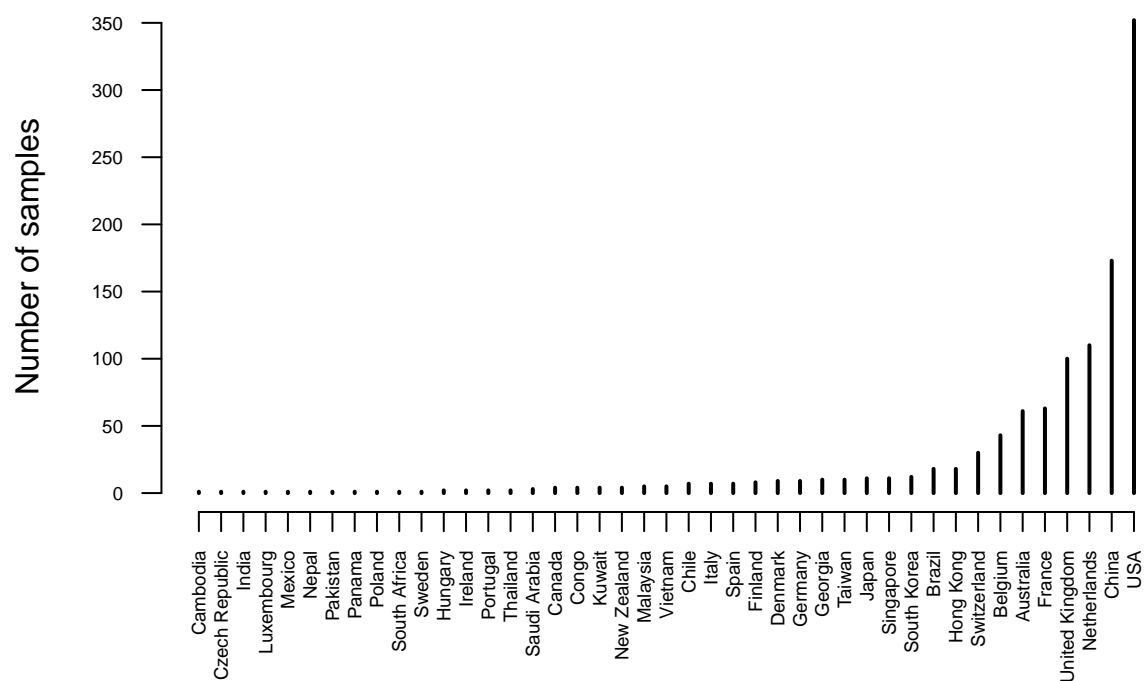


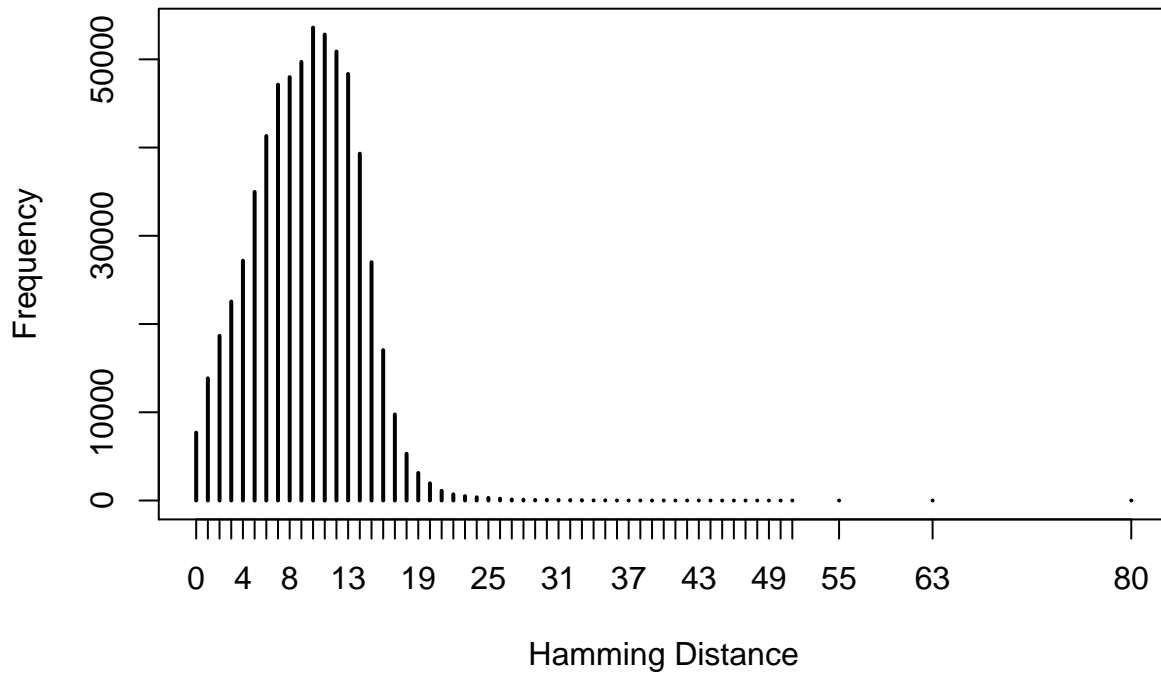
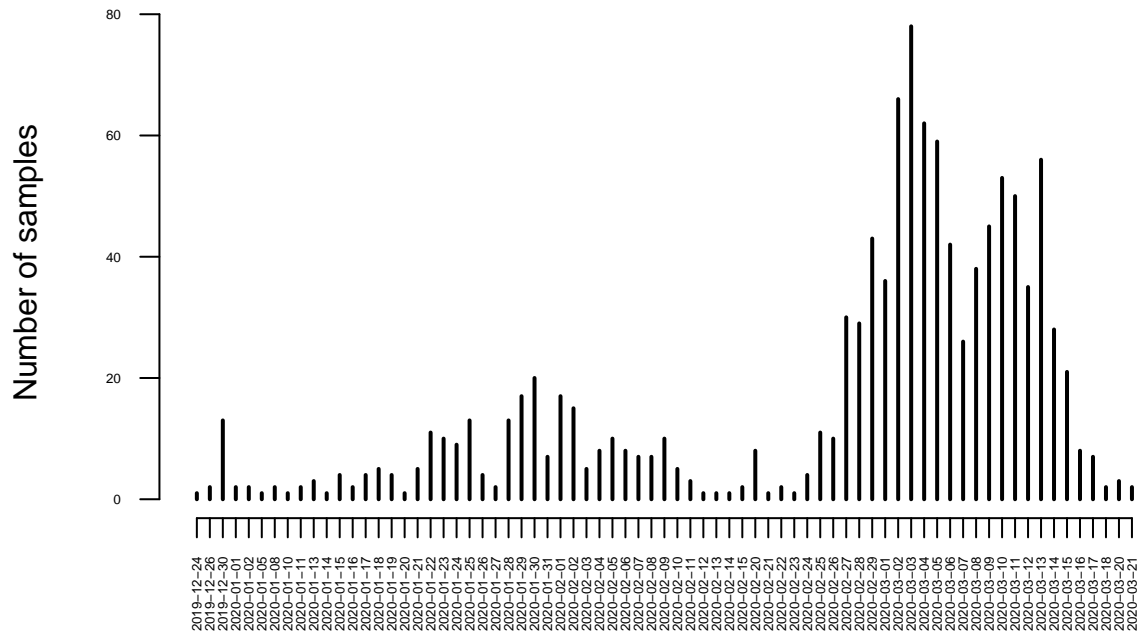
# Preliminary Molecular Clock Check and Summary Statistics

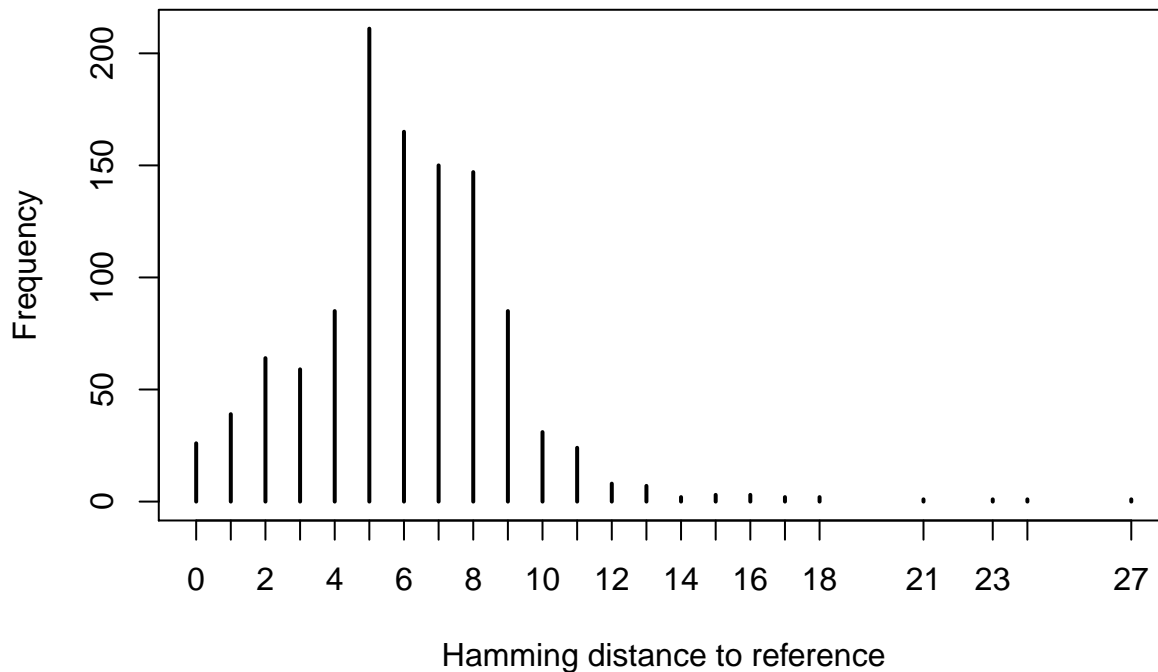
```
##  
## Attaching package: 'lubridate'  
  
## The following object is masked from 'package:base':  
##  
##     date
```

**A total of 1117 from 43 countries -- Fri Mar 27 12:00:04 2020**



## Sequences by date





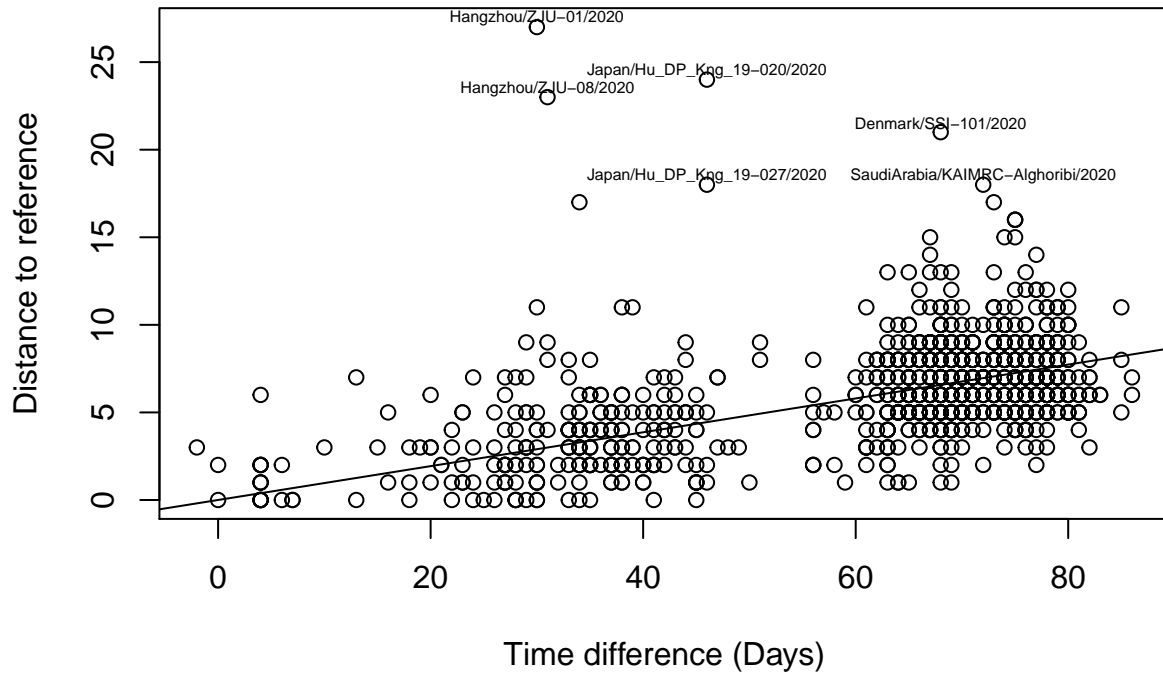
A rough estimate of the mutation rate can be obtained by regressing genetic divergence on time divergence. This estimate ignores correlation among samples, population structure and pairwise information. A more reliable estimate can be found in the mutation section.

```
##
## 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 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## 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
```

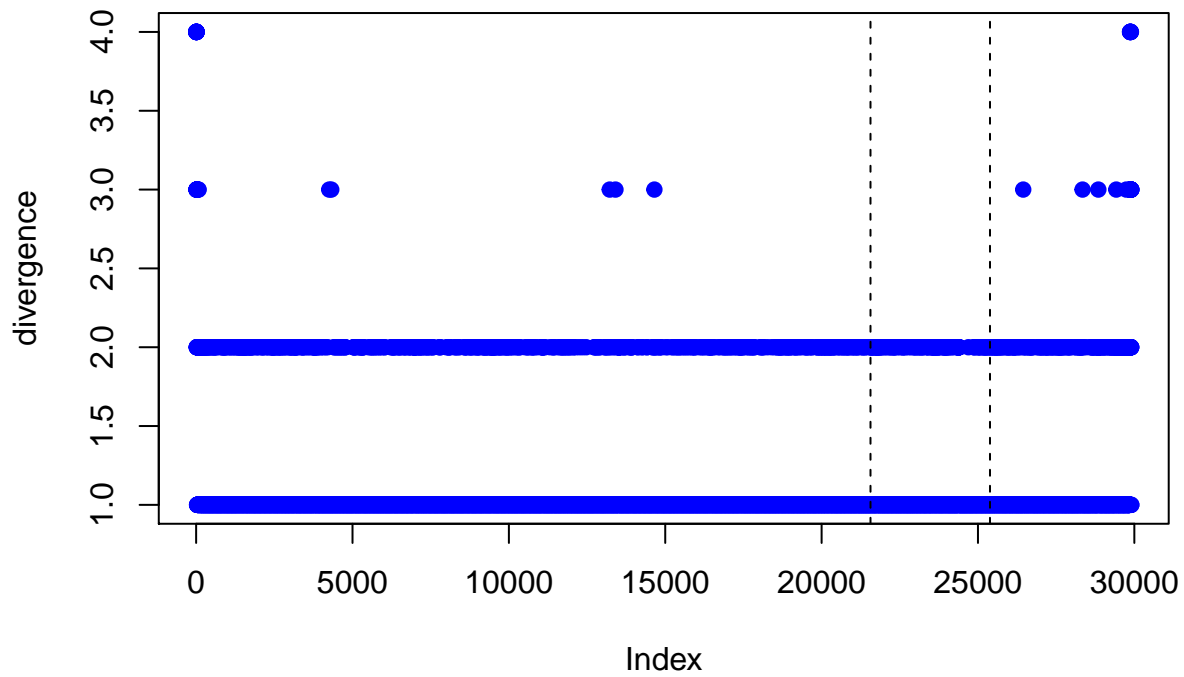
```
## SaudiArabia/KAIMRC-Alghoribi/2020|2020-03-07
##                                     560
```

**A total of 2.71 of mutations per month**



To explore regions and number of polymorphic sites

```
## [1] 29903
```



Of the total 29903 sites in the reference sequence, 28875 are monomorphic sites, 963 are binary, and only 65 have 3 or 4 types. Largest entropy is observed in the first 80 bases and the last 26447 bases.

## 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).