

viruses_database

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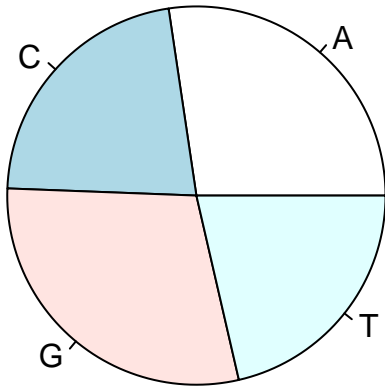
2024-04-24

```
genomes<-c('Zika virus', 'SARS coronavirus', 'Wuhan-Hu-1', 'coronavirus', 'Dengue virus 1', 'H1N185', 'H1N186', 'H1N187', 'H1N188', 'H1N189', 'H1N190', 'H1N191', 'H1N192')
size<-c(sizeZIKA, sizeSARS, sizeWUHAN, sizeMIDDLE, sizeDENGUE, sizeH1N185, sizeH1N186, sizeH1N187, sizeH1N188, sizeH1N189, sizeH1N190, sizeH1N191, sizeH1N192)
a<-c(aInZIKA, aInSARS, aInWUHAN, aInMIDDLE, aInDENGUE, aInH1N185, aInH1N186, aInH1N187, aInH1N188, aInH1N189, aInH1N190, aInH1N191, aInH1N192)
c<-c(cInZIKA, cInSARS, cInWUHAN, cInMIDDLE, cInDENGUE, cInH1N185, cInH1N186, cInH1N187, cInH1N188, cInH1N189, cInH1N190, cInH1N191, cInH1N192)
g<-c(gInZIKA, gInSARS, gInWUHAN, gInMIDDLE, gInDENGUE, gInH1N185, gInH1N186, gInH1N187, gInH1N188, gInH1N189, gInH1N190, gInH1N191, gInH1N192)
t<-c(tInZIKA, tInSARS, tInWUHAN, tInMIDDLE, tInDENGUE, tInH1N185, tInH1N186, tInH1N187, tInH1N188, tInH1N189, tInH1N190, tInH1N191, tInH1N192)
gc <- c(gcInZIKA, gcInSARS, gcInWUHAN, gcInMIDDLE, gcInDENGUE, gcInH1N185, gcInH1N186, gcInH1N187, gcInH1N188, gcInH1N189, gcInH1N190, gcInH1N191, gcInH1N192)
secuencias <- c(secZIKA, secSARS, secWUHAN, secMIDDLE, secDENGUE, secH1N185, secH1N186, secH1N187, secH1N188, secH1N189, secH1N190, secH1N191, secH1N192)
df <- data.frame(genomes,size,a,c,g,t,gc,secuencias)
print(df)
```

```
##          genomes  size      a      c      g      t      gc
## 1      Zika virus 10808 27.35011 22.04848 29.20984 21.39156 51.25833
## 2 SARS coronavirus 29739 28.46431 20.00740 20.85813 30.67016 40.86553
## 3      Wuhan-Hu-1 29903 29.94348 18.36605 19.60673 32.08374 37.97278
## 4      coronavirus 30110 26.21720 20.20591 20.92660 32.65028 41.13251
## 5      Dengue virus 1   445 30.11236 22.24719 25.39326 22.24719 47.64045
## 6          H1N185   2280 33.72807 18.94737 25.78947 21.53509 44.73684
## 7          H1N186   2274 35.75198 19.30519 22.64732 22.29551 41.95251
## 8          H1N187   2151 32.72896 19.66527 24.59321 23.01255 44.25848
## 9          H1N188   1701 35.27337 18.51852 22.28101 23.92710 40.79953
## 10         H1N189   1497 32.93253 19.57248 26.58651 20.90848 46.15898
## 11         H1N190   1410 31.77305 18.79433 23.47518 25.95745 42.26950
## 12         H1N191    982 28.92057 21.18126 25.96741 23.93075 47.14868
## 13         H1N192    844 31.63507 19.90521 23.81517 24.64455 43.72038
##                                     secuencias
## 1 agttgttgat ... catgggtctt \n tcaacaacta ... gtacccagaa
## 2 agggaaagcc ... atgacaaaaa \n tccttttcgg ... tactgttttt
## 3 attaaagggtt ... aaaaaaaaaa \n taatttccaa ... tttttttttt
## 4 gatttaagtg ... atttgcaaaa \n ctaaattcac ... taaacgtttt
## 5 ttcaatatgc ... ttgtgtgagg \n aagttatacg ... aacacactcc
## 6 atggagagaa ... catcaattag \n tacctctctt ... gtagttaatc
## 7 atggatgtca ... gcaaaaataa \n tacctacagt ... cgttttttatt
## 8 atggaagact ... actgaagtag \n taccttctga ... tgacttcatc
## 9 atgaaggcaa ... atgtatttaa \n tacttccgtt ... tacataaatt
## 10 atggcgtctc ... tgacagttag \n taccgcagag ... actgtcaact
## 11 atgaatccaa ... tgacaagtaa \n tacttaggtt ... actgttcatt
## 12 atgagtcttc ... gctagagtaa \n tactcagaag ... cgatctcatt
## 13 atggactcca ... ttaatgataa \n tacctgaggt ... aattactatt
```

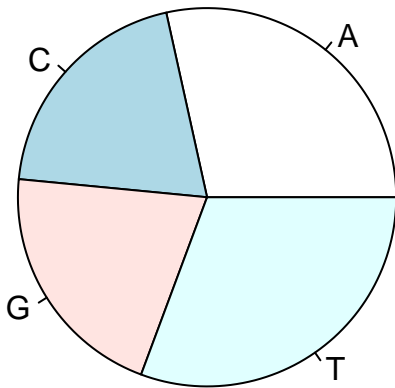
```
pie(c(aInZIKA, cInZIKA, gInZIKA, tInZIKA), labels = c("A", "C", "G", "T"), main = "Zika virus")
```

Zika virus



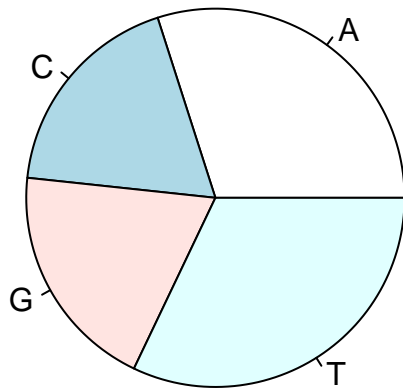
```
pie(c(aInSARS, cInSARS, gInSARS, tInSARS), labels = c("A", "C", "G", "T"), main = "SARS coronavirus")
```

SARS coronavirus



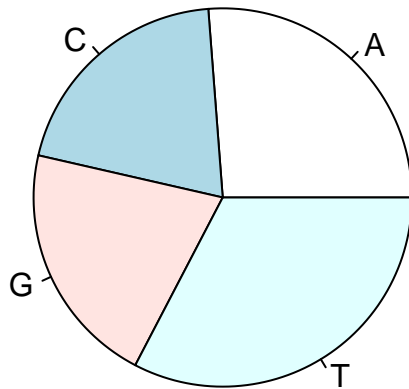
```
pie(c(aInWUHAN, cInWUHAN, gInWUHAN, tInWUHAN), labels = c("A", "C", "G", "T"), main = "Wuhan-Hu-1")
```

Wuhan-Hu-1



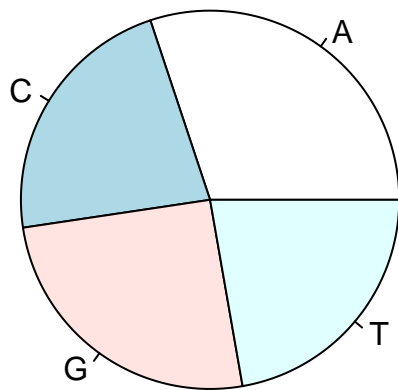
```
pie(c(aInMIDDLE, cInMIDDLE, gInMIDDLE, tInMIDDLE), labels = c("A", "C", "G", "T"), main = "Middle East respiratory syndrome coronavirus")
```

Middle East respiratory syndrome coronavirus



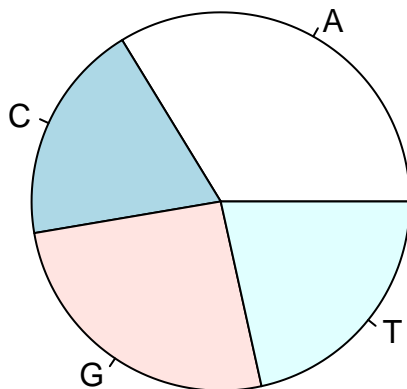
```
pie(c(aInDENGUE, cInDENGUE, gInDENGUE, tInDENGUE), labels = c("A", "C", "G", "T"), main = "Dengue virus")
```

Dengue virus 1



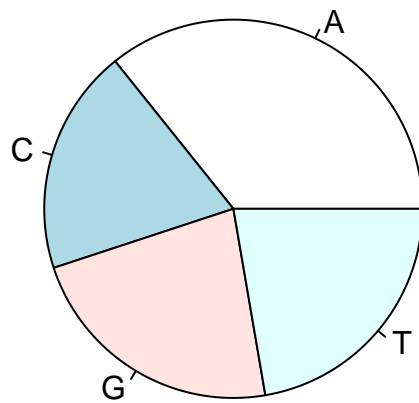
```
pie(c(aInH1N185, cInH1N185, gInH1N185, tInH1N185), labels = c("A", "C", "G", "T"), main = "H1N1_85")
```

H1N1_85



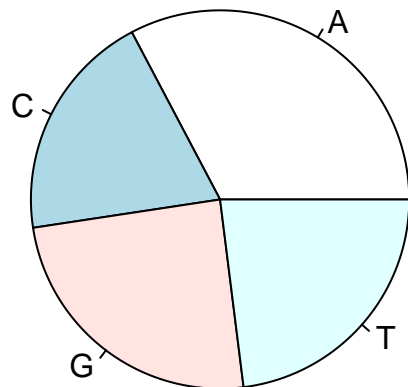
```
pie(c(aInH1N186, cInH1N186, gInH1N186, tInH1N186), labels = c("A", "C", "G", "T"), main = "H1N1_86")
```

H1N1_86



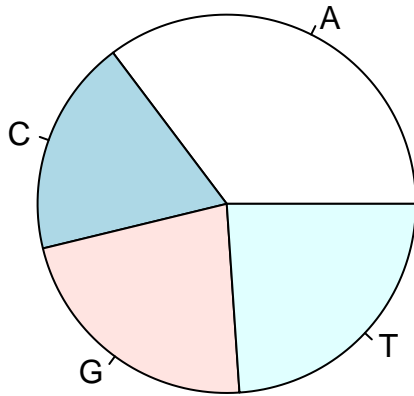
```
pie(c(aInH1N187, cInH1N187, gInH1N187, tInH1N187), labels = c("A", "C", "G", "T"), main = "H1N1_87")
```

H1N1_87



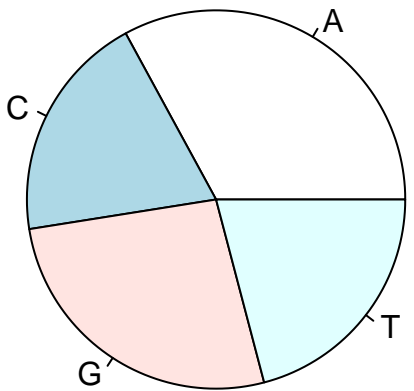
```
pie(c(aInH1N188, cInH1N188, gInH1N188, tInH1N188), labels = c("A", "C", "G", "T"), main = "H1N1_88")
```

H1N1_88



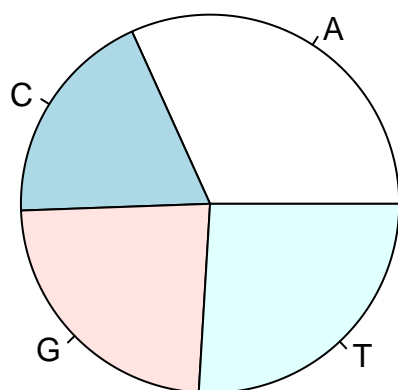
```
pie(c(aInH1N189, cInH1N189, gInH1N189, tInH1N189), labels = c("A", "C", "G", "T"), main = "H1N1_89")
```

H1N1_89



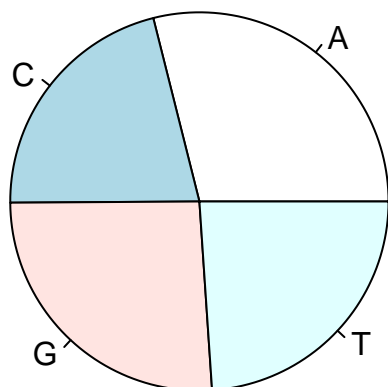
```
pie(c(aInH1N190, cInH1N190, gInH1N190, tInH1N190), labels = c("A", "C", "G", "T"), main = "H1N1_90")
```

H1N1_90



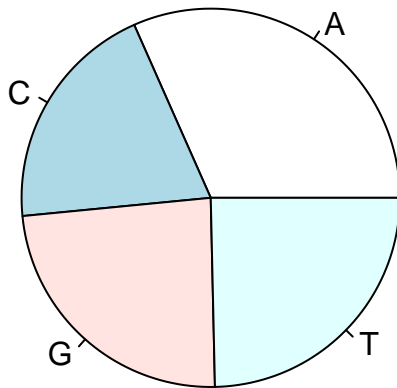
```
pie(c(aInH1N191, cInH1N191, gInH1N191, tInH1N191), labels = c("A", "C", "G", "T"), main = "H1N1_91")
```

H1N1_91



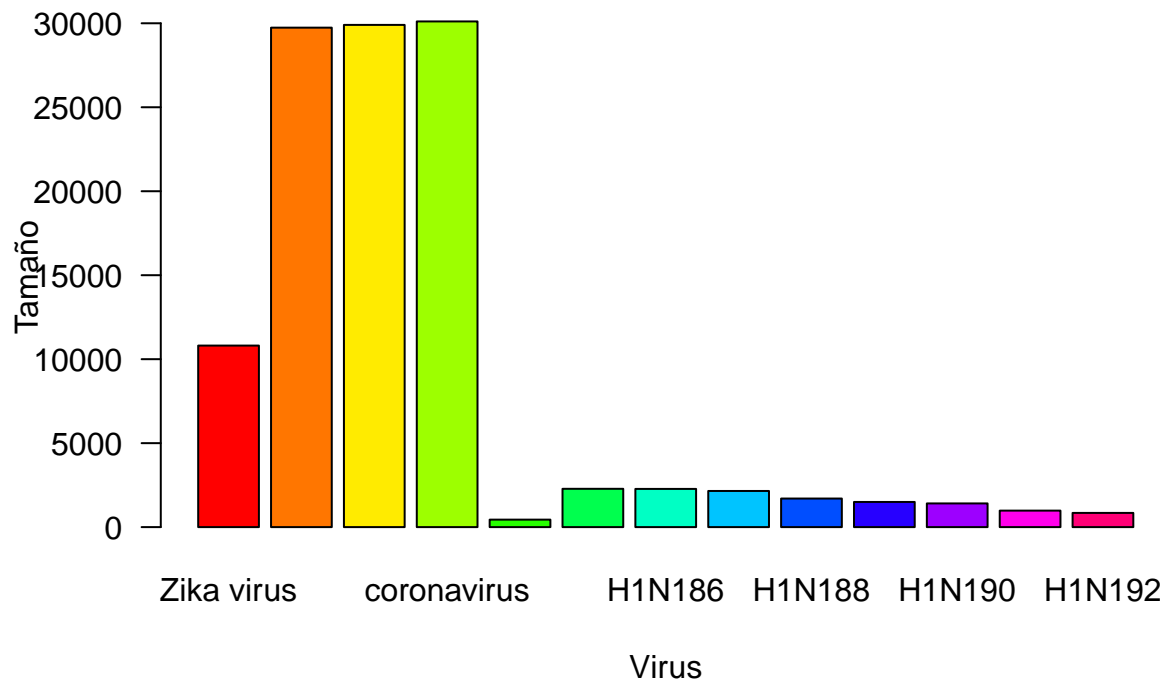
```
pie(c(aInH1N192, cInH1N192, gInH1N192, tInH1N192), labels = c("A", "C", "G", "T"), main = "H1N1_92")
```

H1N1_92



```
barplot(size, names.arg = genomes, las = 1, col = rainbow(13), main = "Tamaño de cada secuencia", ylab = "Tamaño")
```

Tamaño de cada secuencia



```
color_fuerte <- "#FF4500"
color_intermedio1 <- "#FF7F50"
color_intermedio2 <- "#FFA07A"
color_tenue <- "#FFE4B5"

heatmap(t(data.frame(a, c, g, t)), Rowv = NA, Colv = NA,
        xlab = "Nucleótidos", ylab = "Virus",
        main = "Composición de Nucleótidos en los Virus",
        col = colorRampPalette(c(color_tenue, color_intermedio1, color_intermedio2, color_fuerte))(100))
```


Composición de Nucleótidos en los Virus

