France on GISAID

FD

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Initializations

```
# Colors definitions
library(RColorBrewer)
colsV <- rep(c(brewer.pal(12, "Paired"), brewer.pal(12, "Set3"), brewer.pal(9, "Set1")), 20)
colsP <- brewer.pal(5, "Set1")
names(colsP) <- c("autre", "HCL", "HMN", "IHU", "IPP")
colsC <- c(brewer.pal(9, "Set1"), brewer.pal(6, "Set2"), brewer.pal(12, "Set3"))
colsV2 <- brewer.pal(9, "Set3")

colGISAID <- "#106b63"
colECDC <- "#69b023"
colSPF <- "#e30155"

cols <- c(colGISAID, colECDC, colSPF, "#FE6100", "#785EF0")
names(cols) <- c("GISAID", "TESSy", "Flash", "criblage", "option")

pchs <- c(16, 15, 2, 17, 1)
names(pchs) <- c(names(cols)[1:3], "Flash2", "TESSyGISAID")
```

```
# Function to identify entries that are NA or empty
is.NAempty <- function(x){
  is.na(x) | x == ""
}
```

Load and clean data

Data source: `metadata.tsv` file, downloaded from GISAID.

Then, in console

`grep "hCoV-19/France" metadata.tsv`

to extract sequences from France (as country) only. The resulting file is stored in the `data/` folder.

Note: Oversea territories are referenced as independent on GISAID

Extracted data for Martinique and Guadeloupe as well (`grep Martinique` and `grep Guadeloupe`).

Load data

```
thedate <- "2021-10-18"
# Load France data
```

```
dat <- read.csv(paste0("data/", thedate, "_France.tsv"), sep = "\t", stringsAsFactors = FALSE, header =

# Load data DROM
dat2 <- read.csv(paste0("data/", thedate, "_Martinique.tsv"), sep = "\t", stringsAsFactors = FALSE, head
dat3 <- read.csv(paste0("data/", thedate, "_Guadeloupe.tsv"), sep = "\t", stringsAsFactors = FALSE, head

# Add column to distinguish metro from DROM
dat$metropole <- TRUE
dat2$metropole <- FALSE
dat3$metropole <- FALSE

# Join the datasets
dat <- rbind(dat, dat2, dat3)

head(dat)
# Add names
# (names are not in the datafiles because "grep" was used to extract data)
names(dat) <- c("Virus.name", "Type", "Accession.ID", "Collection.date", "Location", "Additional.locati
```

There are 113573 lines in the dataset; 112465 for mainland France, 527 for Martinique and 581 for Guadeloupe.

Clean data

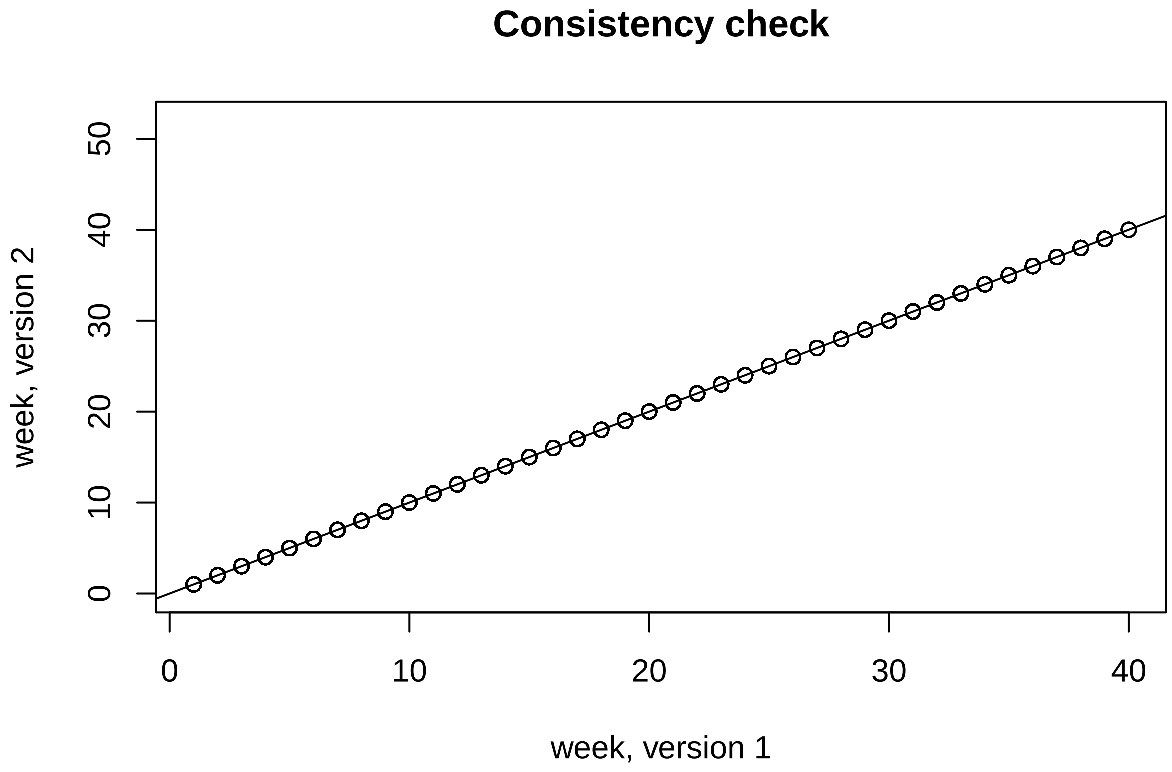
Extract dates: full date, year-month and year

```
# Reformat dates

# Table of the lengths of the different dates
table(nchar(dat$Collection.date)) # There are incomplete dates
table(nchar(dat$Submission.date))

# Turn dates into date format, and put NA for incomplete dates
getDate <- function(v){
  out <- v
  # Remove lines with incomplete date information
  out[nchar(out) < 10] <- NA
  base::as.Date(out)
}

dat$Collection.date.YMD <- getDate(dat$Collection.date)
dat$Submission.date.YMD <- getDate(dat$Submission.date)

# Extract month
getYM <- function(v){
  out <- v
  # Remove lines with incomplete date information
  out[nchar(out) < 7] <- NA
  substr(out, 1, 7)
}

dat$Collection.date.YM <- getYM(dat$Collection.date)
dat$Submission.date.YM <- getYM(dat$Submission.date)

# Extract year
```

```r
getY <- function(v){
  out <- v
  # Remove lines with incomplete date information
  out[nchar(out) < 4] <- NA
  substr(out, 1, 4)
}

dat$Collection.date.Y <- getY(dat$Collection.date)
dat$Submission.date.Y <- getY(dat$Submission.date)
```

Dates: get week numbers
(currently only done for 2021)

```r
# Version 1, only for 2021 (hard-coded)

endDay <- max(dat$Submission.date.YMD)
beginDay <- seq(base::as.Date("2021-01-04"), base::as.Date("2021-12-27"), by = 7)
endDay <- seq(base::as.Date("2021-01-10"), base::as.Date("2022-01-02"), by = 7)
weeks <- as.data.frame(cbind(weekBegin = beginDay, weekEnd = endDay, week = 1:52))

# Assign weeks
  # Initialize week numbers
dat$Collection.week <- NA
dat$Submission.week <- NA

for(iw in weeks$week){
  # Collection week
  dat[which(base::as.Date(dat$Collection.date.YMD) >= base::as.Date(weeks[iw, "weekBegin"], origin = "19

  # Submission week
  dat[which(base::as.Date(dat$Submission.date.YMD) >= base::as.Date(weeks[iw, "weekBegin"], origin = "19
}

#--------------------------------------
# Version 2, using `format`

dat$Collection.date.wk <- format(as.Date(dat$Collection.date.YMD), "%W")
dat$Submission.date.wk <- format(as.Date(dat$Submission.date.YMD), "%W")

dat$Collection.Ywk <- paste0(dat$Collection.date.Y, "-", dat$Collection.date.wk)
dat$Submission.Ywk <- paste0(dat$Submission.date.Y, "-", dat$Submission.date.wk)

sort(unique(dat$Collection.Ywk))

# A sequence with an odd date
dat[dat$Collection.Ywk == "2020-00", ]

# Check weeks in the two versions
plot(dat$Collection.week, dat$Collection.date.wk,
     xlab = "week, version 1", ylab = "week, version 2", main = "Consistency check")
abline(a = 0, b = 1)
```



Difference between submission and collection dates

```
dat$diffSubCol <- as.numeric(dat$Submission.date.YMD - dat$Collection.date.YMD)
```

Locations:

Try to get some uniformity automatically because some spellings differ

```
# Split locations

# Locations are presented as a single string, which we split
locs <- strsplit(dat$Location, " / ")
# The strings are of different lengths / precision; get length (number of geographic divisions)
lenlocs <- sapply(locs, length)
table(lenlocs)

# Turn into matrix, filling with NAs
# Source: https://stackoverflow.com/a/15201690
mat <- as.data.frame(t(sapply(locs, "[", i = 1:max(lenlocs))))
names(mat) <- c("continent", "country", "region", "div4", "div5")
# Add the dataset
dat <- cbind(dat, mat)
# Also add information about location precision
dat <- cbind(dat, locationLength = lenlocs)

# Load dictionary to convert region names
infoRegion <- read.csv("data_public/correspondance_regions.csv")

# Check that we have all names -- focusing on Metropole
rr <- unique(dat[dat$metropole, "region"])
rr <- rr[!is.na(rr)]
```

```r
all(is.element(rr, infoRegion$Region_on_GISAID))

# If FALSE, which ones are we missing?
if(!all(is.element(rr, infoRegion$Region_on_GISAID))){
  rr[which(!is.element(rr, infoRegion$Region_on_GISAID))]
}

# Stop if we are missing names
stopifnot(is.element(rr, infoRegion$Region_on_GISAID))

# Convert into dictionary
dic.regnames <- c(infoRegion$region)
names(dic.regnames) <- infoRegion$Region_on_GISAID

# Save old region names
dat$oldRegion <- dat$region

# Convert names into the proper region names
dat$region <- dic.regnames[dat$oldRegion]

regions <- sort(unique(dat$region))

# Note: For DROM, information is in Country instead
```

Hosts

```r
# Uniformize notation
dat[dat$Host == "human", "Host"] <- "Human"
```

Variants

Use short names
Needs to be manually checked from time to time

```r
# Initialize new column
dat$VariantShort <- dat$Variant

# Current variants in GISAID
variants <- sort(unique(dat$Variant))

# Short versions of the names
variantsShort <- c("", "Alpha", "Beta", "Delta", "Gamma", "Lambda", "Mu")

# Check consistency
cbind(variants, variantsShort)
```

```
##      variants
## [1,] ""
## [2,] "VOC Alpha 202012/01 GRY (B.1.1.7+Q.x) first detected in the UK"
## [3,] "VOC Beta GH/501Y.V2 (B.1.351+B.1.351.2+B.1.351.3) first detected in South Africa"
## [4,] "VOC Delta GK/478K.V1 (B.1.617.2+AY.x) first detected in India"
## [5,] "VOC Gamma GR/501Y.V3 (P.1+P.1.x) first detected in Brazil/Japan"
## [6,] "VOI Lambda GR/452Q.V1 (C.37+C.37.1) first detected in Peru"
## [7,] "VOI Mu GH (B.1.621+B.1.621.1) first detected in Colombia"
##      variantsShort
## [1,] ""
## [2,] "Alpha"
## [3,] "Beta"
## [4,] "Delta"
## [5,] "Gamma"
## [6,] "Lambda"
## [7,] "Mu"
```

```
# Assign shorter name
for(i in seq_along(variants)){
  dat[which(dat$Variant == variants[i]), "VariantShort"] <- variantsShort[i]
}
```

Submitters

Get submitter information from Virus name

```
# Find lines with the 3-letter code of each platform
ipp <- grep(dat$Virus.name, pattern = "IPP")
hcl <- grep(dat$Virus.name, pattern = "HCL")
ihu <- grep(dat$Virus.name, pattern = "IHU")
hmn <- grep(dat$Virus.name, pattern = "HMN")

# Assign submitter names
dat$submitter <- rep("autre", nrow(dat))
dat[ipp, "submitter"] <- "IPP"
dat[hcl, "submitter"] <- "HCL"
dat[ihu, "submitter"] <- "IHU"
dat[hmn, "submitter"] <- "HMN"

# Show total number of sequences per submitter
table(dat$submitter, useNA = "ifany")
```

```
##
## autre   HCL   HMN   IHU   IPP
## 24628 32304 14238 24274 18129
```

```
# Just the list of submitter names
submitters <- sort(unique(dat$submitter))
```

Countries

```
# Check countries
table(country = dat$country)
```

```
dat[dat$country == "Switzerland", ]
# Seems to have been sequenced in France but to come from Switzerland
# -> Remove it
dat <- dat[which(dat$country != "Switzerland"), ]
```

Enquêtes Flash

Load Flash dates Available on https://www.santepubliquefrance.fr/etudes-et-enquetes/enquetes-flash-evaluation-de-la-circulation-des-variants-du-sars-cov-2-en-france

```
datesFlash <- read.csv("data_public/datesFlash.csv", stringsAsFactors = FALSE)
datesFlash.all <- datesFlash
# Remove Flash 1 and 2, which were not on a random sample
datesFlash <- datesFlash[datesFlash$FlashNb >=3 , ]
```

Flash data Typed from pdfs available on https://www.santepubliquefrance.fr/etudes-et-enquetes/enquetes-flash-evaluation-de-la-circulation-des-variants-du-sars-cov-2-en-france#block-337272, accessed 2021-07-21

```
dat.Flash <- read.csv("data_public/2021-07-21_Flash.csv")
head(dat.Flash)

# Add confidence interval for Delta
dat.Flash$deltaCI <- 1.96 * sqrt(dat.Flash$Proportion * (1 - dat.Flash$Proportion) / dat.Flash$NbPrelev
```

Specific Flash data (for Beta) – extracted by hand from the pdfs

```
# Load Flash 11 data
flash11 <- read.csv("data_public/Flash11_Beta.csv")
flash11 <- flash11[flash11$Region != "Total", ]
flash11$nBeta <- round(flash11$pBeta * flash11$Prelevements)

# Load Flash 10 data
flash10 <- read.csv("data_public/Flash10_Beta.csv")
flash10 <- flash10[flash10$Region != "Total", ]
flash10$nBeta <- round(flash10$pBeta * flash10$Prelevements)

# Load Flash 09 data
flash09 <- read.csv("data_public/Flash09_Beta.csv")
flash09 <- flash09[flash09$Region != "Total", ]
flash09$nBeta <- round(flash09$pBeta * flash09$Prelevements)

# Get codes of Outre-Mer regions
unique(c(flash09$Region, flash10$Region, flash11$Region))
reg_OM <- c("GUA", "REU", "MAR", "MAY")

# Remove Outre-Mer
flash11.noOM <- flash11[which(!is.element(flash11$Region, reg_OM)), ]
flash10.noOM <- flash10[which(!is.element(flash10$Region, reg_OM)), ]
flash09.noOM <- flash09[which(!is.element(flash09$Region, reg_OM)), ]

# Compute total numbers of sequences, and Beta sequences
tot11 <- apply(flash11.noOM[, c("Prelevements", "nBeta")], 2, sum)
tot10 <- apply(flash10.noOM[, c("Prelevements", "nBeta")], 2, sum)
tot09 <- apply(flash09.noOM[, c("Prelevements", "nBeta")], 2, sum)

# Construct final dataset with the results
totFlash.noOM <- data.frame(week = c(19, 21, 23))
totFlash.noOM$nTot <- c(tot09[1], tot10[1], tot11[1])
totFlash.noOM$pBeta <- c(tot09[2]/tot09[1], tot10[2]/tot10[1], tot11[2]/tot11[1])
totFlash.noOM$deltaCI <- 1.96 * sqrt(totFlash.noOM$pBeta * (1-totFlash.noOM$pBeta) / totFlash.noOM$nTot
totFlash.noOM
```

Sequence metadata

Check completeness of the different fields

Dates and locations

Dates

- The fraction of samples with missing full day of collection is 0.13

Distribution of samples with incomplete collection date information, by submitter

```
totSeq <- table(dat$submitter)
tt <- table(dat[which(is.na(dat$Collection.date.YMD)), "submitter"])

tmp <- rbind(incomplete_collectionDate = tt, tot_seq = totSeq[names(tt)])
rbind(tmp, prop_incomplete_collectionDate = round(tmp[1, ]/tmp[2, ], 4))
```

```
##                                     autre        IHU        IPP
## incomplete_collectionDate       5283.0000  9373.0000   630.0000
## tot_seq                        24627.0000 24274.0000 18129.0000
## prop_incomplete_collectionDate     0.2145     0.3861     0.0348
```

Location

- The fraction of samples with missing regional information is 0.06

Distribution of entries with incomplete location, by submitter

```
tt <- table(dat[which(is.na(dat$region)), "submitter"])

tmp <- rbind(missing_region = tt, tot_seq = totSeq[names(tt)])
rbind(tmp, prop_missing_region = round(tmp[1, ]/tmp[2, ], 4))
```

```
##                         autre       HCL        HMN        IHU        IPP
## missing_region       1257.000   679.000   773.0000  2654.0000  1038.0000
## tot_seq             24627.000 32304.000 14238.0000 24274.0000 18129.0000
## prop_missing_region     0.051     0.021     0.0543     0.1093     0.0573
```

Metadata on hosts

Type of host

```
# Hosts
table(dat$Host)
```

```
## 
##  Human 
## 113572
```

Age

```
# Age
dat[which(is.element(dat$Patient.age, c("unknown", "Unknown"))), "Patient.age"] <- NA

# Convert to numeric values
# if contains characters -> NA
dat$Patient.age <- suppressWarnings(as.numeric(dat$Patient.age))
```

The fraction of samples with missing or incorrect age information is 0.29.

Missing age by submitter

```
tt <- table(dat[which(is.na(dat$Patient.age)), "submitter"])
tmp <- rbind(missing_age = tt, tot_seq = totSeq[names(tt)])
rbind(tmp, prop_missing_age = round(tmp[1, ]/tmp[2, ], 4))
```

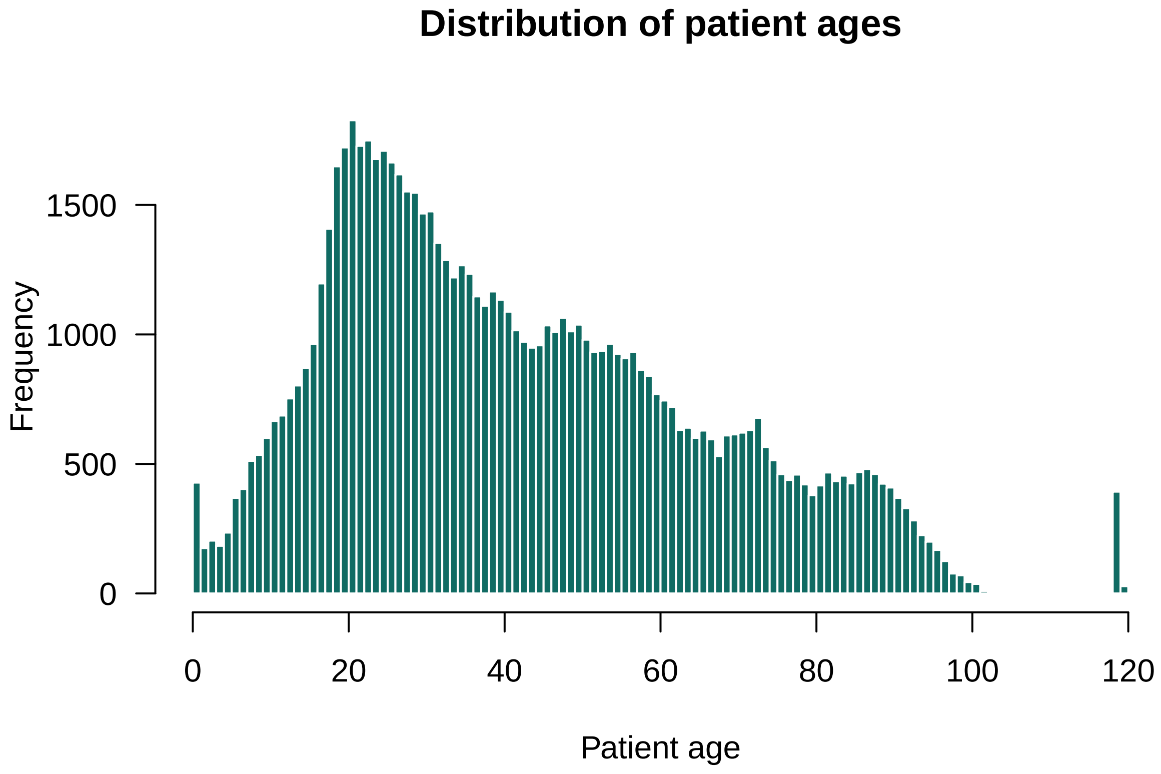
```
##                       autre        HCL        HMN   IHU        IPP
## missing_age       6237.0000   982.0000   147.0000 24273  1116.0000
## tot_seq          24627.0000 32304.0000 14238.0000 24274 18129.0000
## prop_missing_age     0.2533     0.0304     0.0103     1     0.0616
```

Distribution of ages

```
par(las = 1)
range(dat$Patient.age, na.rm = TRUE)
```

```
## [1]    0 2021
```

```
dat[which(dat$Patient.age >120), "Patient.age"] <- NA
hist(dat$Patient.age, xlab = "Patient age", main = "Distribution of patient ages", breaks = seq(0, max(
```



Odd ages

- 119 yo

Who submitted data with this age?

```
table(dat[which(dat$Patient.age == 119), "submitter"])
```

```
##
## autre   HCL   HMN
##     3   389     1
```

When were they submitted?

```r
table(dat[which(dat$Patient.age == 119), "Submission.date"])
```

```
## 
## 2021-01-29 2021-03-26 2021-04-02 2021-05-04 2021-06-25 2021-07-09 2021-07-11 
##          3          1         25          7          3          1          4 
## 2021-07-14 2021-07-29 2021-08-03 2021-08-13 2021-08-18 2021-08-24 2021-09-18 
##          2         17         18          1          3          2         99 
## 2021-09-20 2021-09-30 2021-10-04 
##        111         93          3
```

- 0 yo

Who submitted data with this age?

```r
table(dat[which(dat$Patient.age == 0), "submitter"])
```

```
## 
## autre   HCL   HMN   IPP 
##   136     6    57    13
```

When were they submitted?

```r
table(dat[which(dat$Patient.age == 0), "Submission.date"])
```

```
## 
## 2020-04-01 2020-05-12 2020-08-04 2020-11-04 2020-12-10 2020-12-29 2021-02-02 
##          1          2          1          1          1          1          1 
## 2021-02-26 2021-03-01 2021-03-09 2021-03-20 2021-03-23 2021-03-26 2021-03-30 
##          4          2          1          2          1          4          2 
## 2021-03-31 2021-04-13 2021-04-14 2021-04-21 2021-04-22 2021-04-23 2021-04-27 
##          1          1          1          2          1          9          5 
## 2021-04-28 2021-04-30 2021-05-05 2021-05-06 2021-05-10 2021-05-12 2021-05-18 
##         15          1          2          2          1          1          2 
## 2021-05-19 2021-05-20 2021-05-22 2021-05-26 2021-05-27 2021-05-29 2021-05-31 
##          5          2          3          2         17          1          8 
## 2021-06-08 2021-06-09 2021-06-12 2021-06-14 2021-06-18 2021-06-22 2021-07-01 
##          2          1          4          4          2          2          1 
## 2021-07-13 2021-07-16 2021-07-28 2021-08-06 2021-08-09 2021-08-13 2021-08-15 
##          2          2          1          2          1          6          6 
## 2021-08-17 2021-08-18 2021-08-19 2021-08-20 2021-08-23 2021-08-27 2021-09-01 
##          3          5          1          5          1         12          2 
## 2021-09-02 2021-09-14 2021-09-16 2021-09-27 2021-09-30 2021-10-12 2021-10-14 
##          1          5          1          8          2         19          5
```

Sex

“Gender” information

```r
unique(dat$Gender)
# Clean
dat[which(is.element(dat$Gender, c("unknown", "Unknown", "Femal", "Maleale"))), "Gender"] <- NA

table(dat$Gender, useNA = "ifany")
```

```r
# Distribution by submitter
tt <- table(dat[which(is.na(dat$Gender)), "submitter"])
```

```
tmp <- rbind(missing_sex = tt, tot_seq = totSeq[names(tt)])
rbind(tmp, prop_missing_sex = round(tmp[1, ]/tmp[2, ], 4))
```

```
##                       autre       HCL        HMN        IHU        IPP
## missing_sex       4657.0000   389.000   478.0000 24271.0000  2369.0000
## tot_seq          24627.0000 32304.000 14238.0000 24274.0000 18129.0000
## prop_missing_sex     0.1891     0.012     0.0336     0.9999     0.1307
```

Virus

GISAID Clades

```
table(dat$Clade, useNA = "ifany")
```

```
##
##             G    GH    GK    GR   GRY    GV     L     O     S     V
##     3 11453 14190 47028  7211 29066  2483    40  1419   634    45
```

Pango lineage info is missing in a fraction 0 of items.

Pangolin version

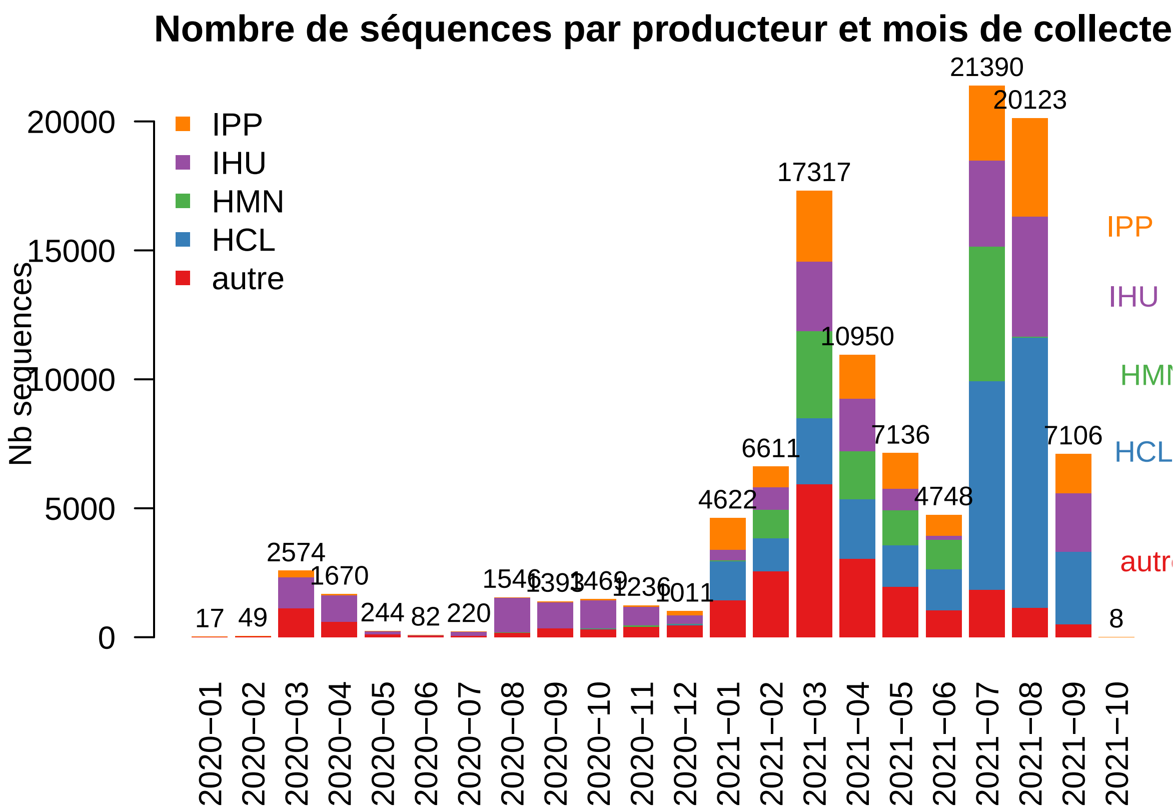
```
table(dat$Pangolin.version)
```

```
##
## 2021-06-15 2021-09-16 2021-09-28
##          1       1958     111613
```

Submissions

By Platform

```
tabFRsub <- aggregate(dat$Virus.name, by = list(subID = dat$submitter, subM = dat$Collection.date.YM), 

tabFRsub.month <- aggregate(dat$Virus.name, by = list(subM = dat$Collection.date.YM), FUN = length)


par(mgp = c(3, 1, 0))
par(mar = c(5, 5, 3, 1))
x <- barplot(tabFRsub$x ~ tabFRsub$subID + tabFRsub$subM, col = colsP[1:(length(unique(tabFRsub$subID))
             xlab = "", ylab = "Nb sequences", las = 2,
             main = "Nombre de séquences par producteur et mois de collecte")

z <- tabFRsub[tabFRsub$subM == "2021-03", ]
text(x = rep(x[length(x)-1], 5), y = cumsum(z$x) - z$x/2, labels = z$subID, adj = c(-0.7, 0.5), col = c
par(xpd = TRUE)
text(x = x, y = tabFRsub.month$x, labels = tabFRsub.month$x, cex = 0.8, adj = c(0.5, -0.5))
legend("topleft", col = rev(colsP), legend = rev(names(colsP)), pch = 15, bty = "n")
```

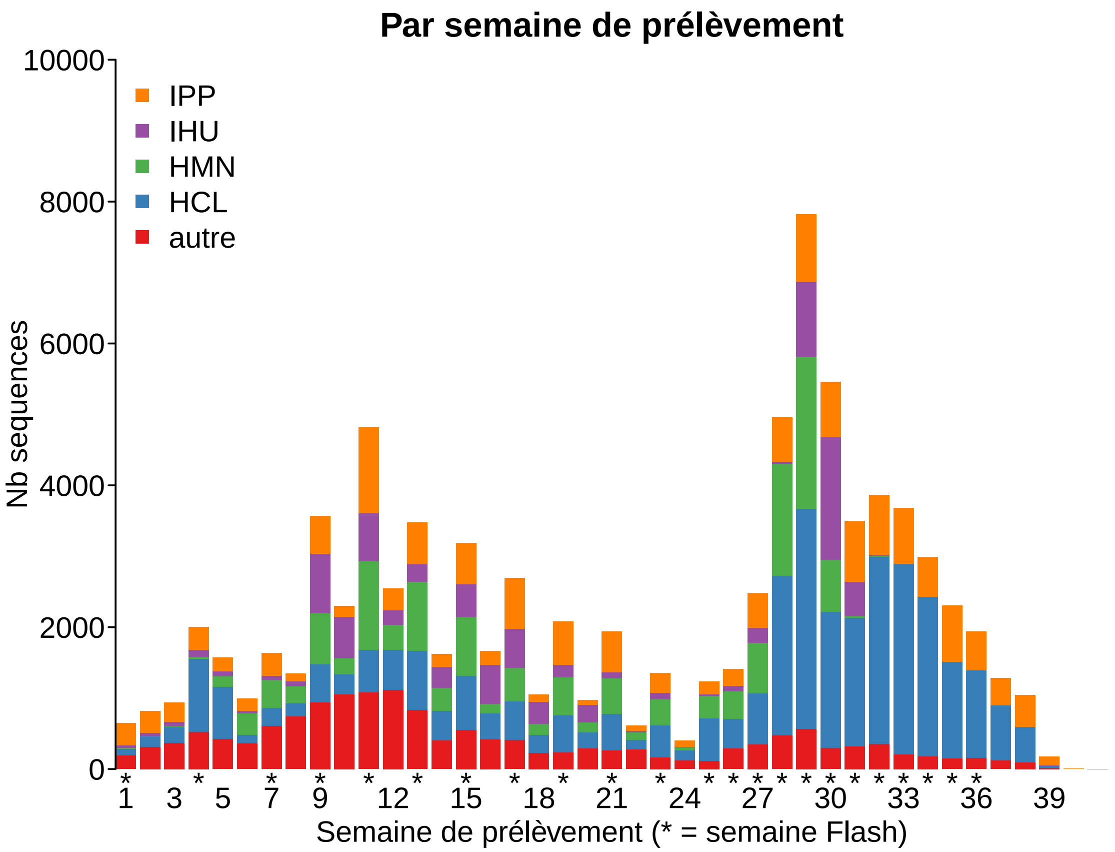


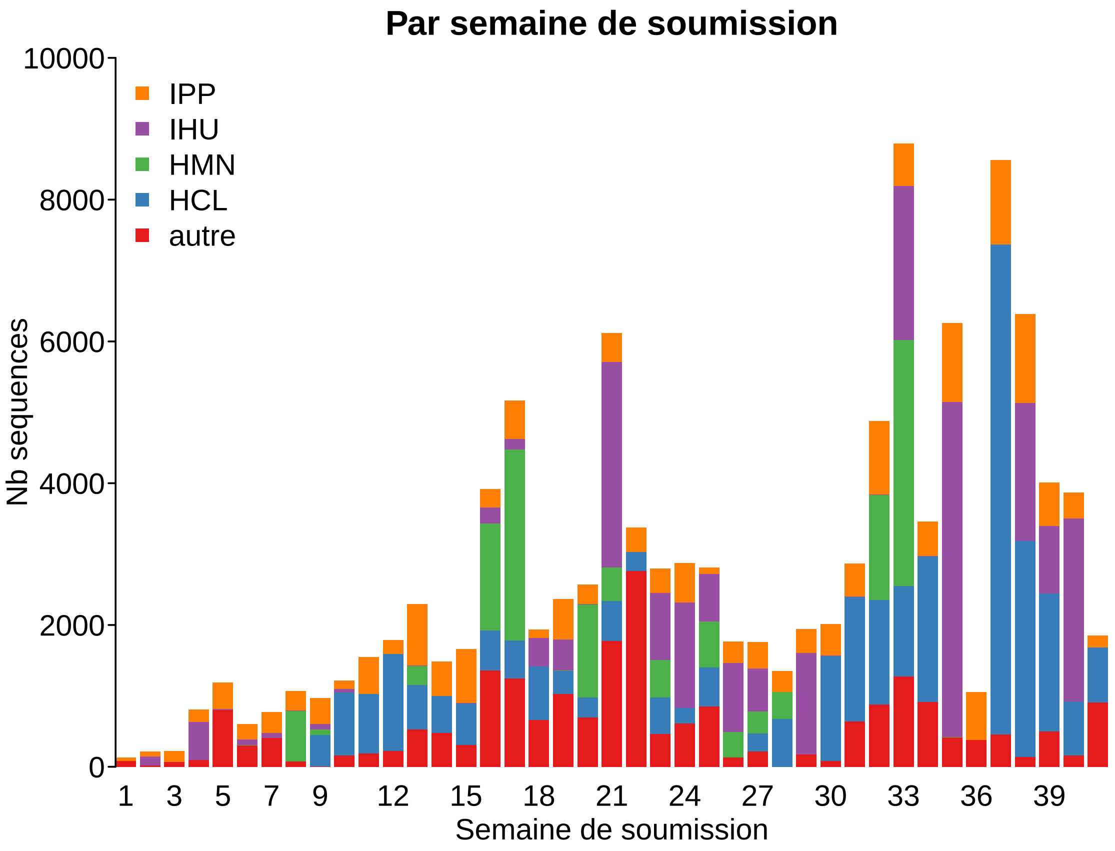
```
par(xpd = FALSE)
```

By platform, by week

```
# By collection week
tabFRsub.byweek <- aggregate(dat$Virus.name, by = list(subID = dat$submitter, subweek = dat$Collection.w
names(tabFRsub.byweek)[3] <- "byCollectionDate"

tabFRsubS.byweek <- aggregate(dat$Virus.name, by = list(subID = dat$submitter, subweek = dat$Submission
names(tabFRsubS.byweek)[3] <- "bySubmissionDate"

seq.byWeek <- merge(tabFRsub.byweek, tabFRsubS.byweek, all = TRUE)
ymax <- 10000

seq.byWeek[is.na(seq.byWeek$byCollectionDate), "byCollectionDate"] <- 0
seq.byWeek[is.na(seq.byWeek$bySubmissionDate), "bySubmissionDate"] <- 0

par(mfrow = c(2, 1))
themar <- c(3, 3.5, 2, 1)
thetck <- -0.01
themgp <- c(2.3, 0.3, 0)
par(mar = themar, mgp = themgp, tck = thetck)

x <- barplot(seq.byWeek$byCollectionDate ~ seq.byWeek$subID + seq.byWeek$subweek, col = colsP[1:(length
             xlab = "", ylab = "Nb sequences", las = 1,
             main = "Par semaine de prélèvement", xaxs = "i", yaxs = "i", ylim = c(0, ymax))
legend("topleft", col = rev(colsP), legend = rev(names(colsP)), pch = 15, bty = "n")

stopifnot(length(x) == length(unique(seq.byWeek$subweek))) # Make sure that lengths match
```

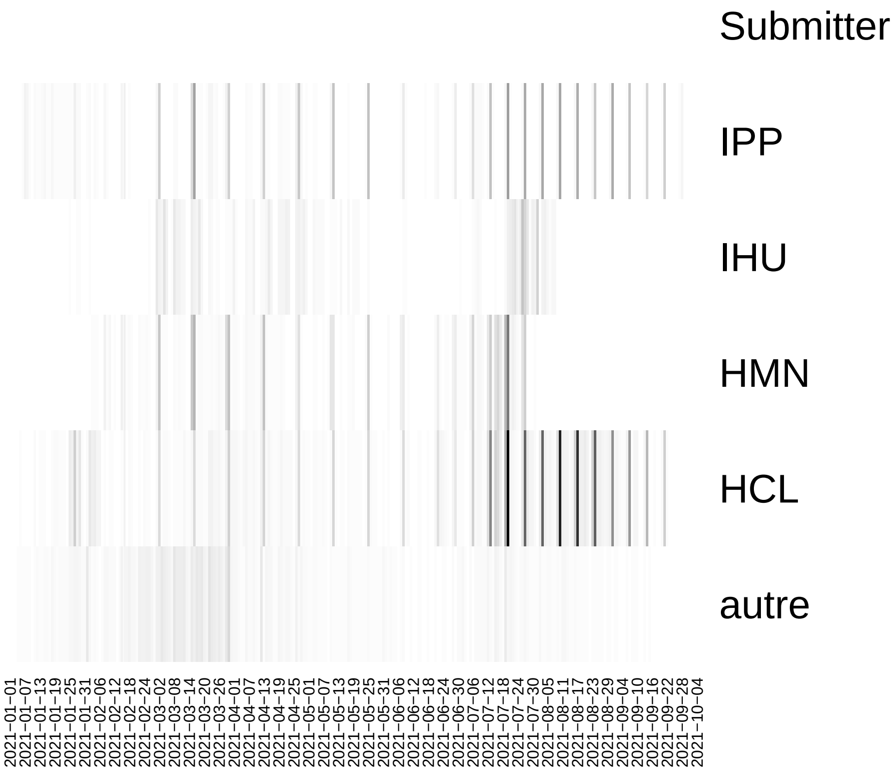
```
xw <- data.frame(cbind(x = x, week = unique(seq.byWeek$subweek)))
ii <- is.element(xw$week, datesFlash.all$week)
par(xpd = TRUE)
text(labels = "*", x = xw[ii, "x"], y = rep(-100, length(xw[ii, "x"])))
par(xpd = FALSE)
mtext("Semaine de prélèvement (* = semaine Flash)", side = 1, line = 1.25)


par(mar = themar, mgp = themgp, tck = thetck)
x2 <- barplot(seq.byWeek$bySubmissionDate ~ seq.byWeek$subID + seq.byWeek$subweek, col = colsP[1:(lengt
             xlab = "", ylab = "Nb sequences", las = 1,
             main = "Par semaine de soumission", xaxs = "i", yaxs = "i", ylim = c(0, ymax))
legend("topleft", col = rev(colsP), legend = rev(names(colsP)), pch = 15, bty = "n")
mtext("Semaine de soumission", side = 1, line = 1.25)
```


Par semaine de prélèvement


Par semaine de soumission

Submitters x Collection dates

```
dat2 <- dat[order(dat$Collection.date.YMD), ]
dat2 <- dat2[dat2$Collection.date.Y == 2021,]

# Add phantom lab with all days
alldates <- seq(as.Date("2021-01-01"), as.Date(max(dat2$Collection.date.YMD, na.rm = TRUE)), by = "day"

phantom <- data.frame(matrix(rep(NA, length(alldates)*ncol(dat)), byrow = TRUE, nrow = length(alldates)
names(phantom) <- names(dat)
phantom$Collection.date.YMD <- alldates
phantom$submitter <- "Submitter"
dat3 <- rbind(dat2, phantom)
xx <- table(dat3$submitter, as.Date(dat3$Collection.date.YMD))

# diff(as.Date(unique(as.data.frame(xx)$Var2)))
heatmap(table(dat3$submitter, as.Date(dat3$Collection.date.YMD)), Rowv = NA, Colv = NA, scale = "none",
```



Focus IHU

```
# All sequences
subIHU <- dat[dat$submitter == "IHU", ]
```

```
is.short <- (subIHU$Sequence.length < 5000)
missing.day <- (is.na(subIHU$Collection.date.YMD))
missing.month <- (is.na(subIHU$Collection.date.YM))

aggregate(subIHU$Virus.name, by = list(Sanger = is.short, missingDay = missing.day, missingMonth = miss
```

```
##   Sanger missingDay missingMonth     x
## 1  FALSE      FALSE        FALSE 13325
## 2   TRUE      FALSE        FALSE  1576
## 3  FALSE       TRUE        FALSE  9088
## 4   TRUE       TRUE        FALSE   285
```

```
# Subset of data with full seqs and missing days
subIHU.NGS.missingday <- subIHU[!is.short & missing.day, ]

# Export data with missing day
write.csv(subIHU.NGS.missingday[, c("Virus.name", "Accession.ID", "Collection.date", "Submission.date")]
```

Submission dates of the data with missing full dates

```
table(subIHU.NGS.missingday$Submission.date.YMD)
```

```
##
## 2021-04-20 2021-05-26 2021-06-08 2021-06-17 2021-06-23 2021-06-24 2021-06-30
##          1         25          3          4          1          2          4
## 2021-07-08 2021-07-23 2021-08-16 2021-08-31 2021-09-03 2021-09-22 2021-10-01
##         60         92         64       2014       1371       1949        950
## 2021-10-07
##       2548
```

```
# IHU submission dates
table(subIHU$Submission.date.YMD)

subIHU.mostrecent <- subIHU[which(subIHU$Submission.date.YMD == max(subIHU$Submission.date.YMD)),]
```

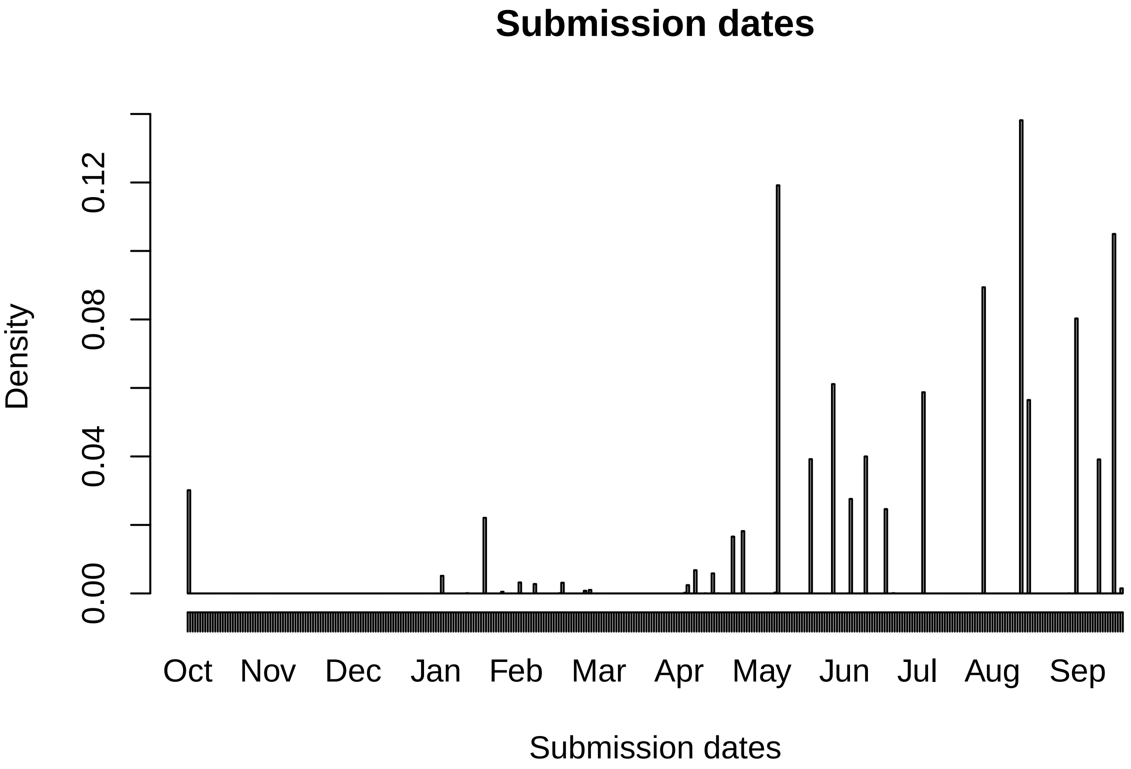
Locations in the IHU dataset

```
table(subIHU$Location)
```

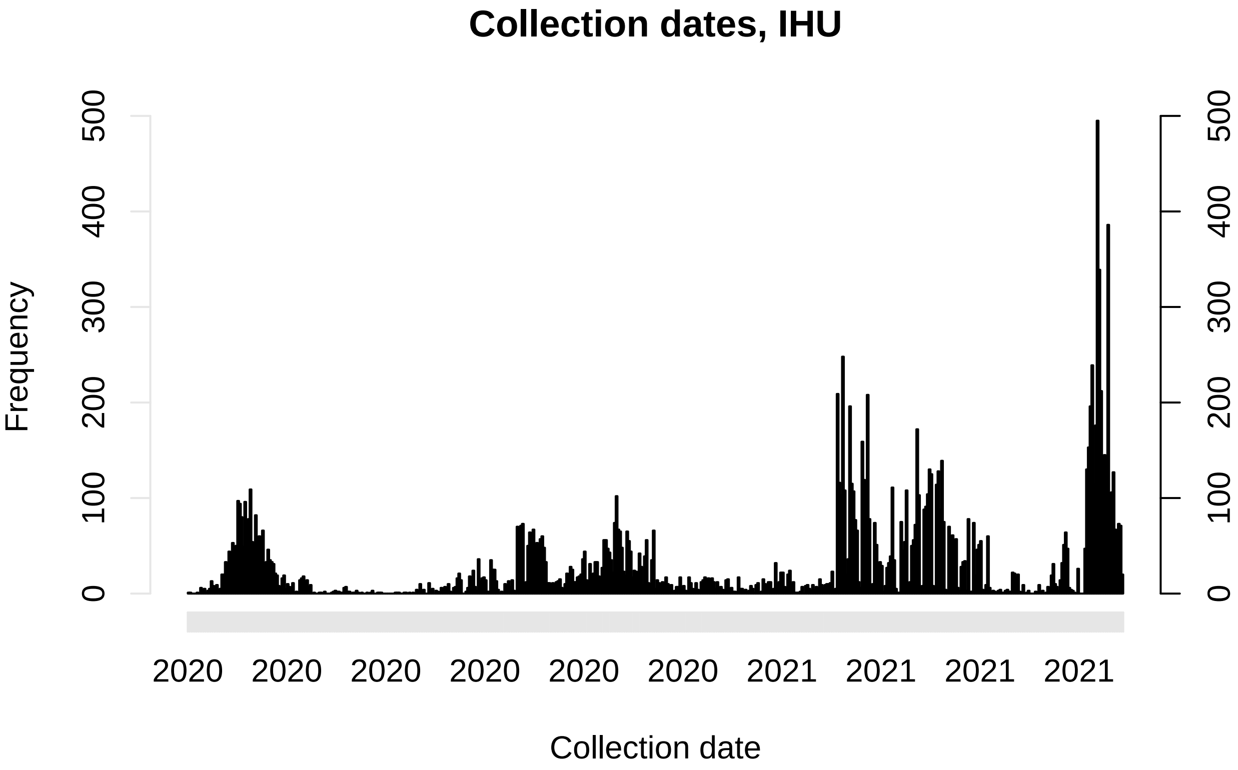
```
##
##                              Europe / France / Marseille
##                                                     4427
##                  Europe / France / Occitanie / Marseille
##                                                        2
## Europe / France / Provence Alpes Cote d’Azur / Marseille
##                                                     1371
##             Europe / France / Provence-Alpes-Cote d'Azur
##                                                       40
## Europe / France / Provence-Alpes-Cote d'Azur / Marseille
##                                                    13555
## Europe / France / Provence-Alpes-Cote-d'Azur / Marseille
##                                                     3596
## Europe / France / Provence-Alpes-Cote-d’Azur / Marseille
##                                                     1281
##              Europe / France / Provence-Alpes-Cote-dAzur
##                                                        2
```

```
# Focus on recent submissions
dataset <- subIHU[subIHU$Collection.date.YMD > "2021-04-01", ]


table(dataset$Submission.date.YMD)

table(dataset$Collection.date.YMD)
```

```r
hist(as.Date(subIHU$Submission.date.YMD), breaks = 500, main = "Submission dates", xlab = "Submission da
```

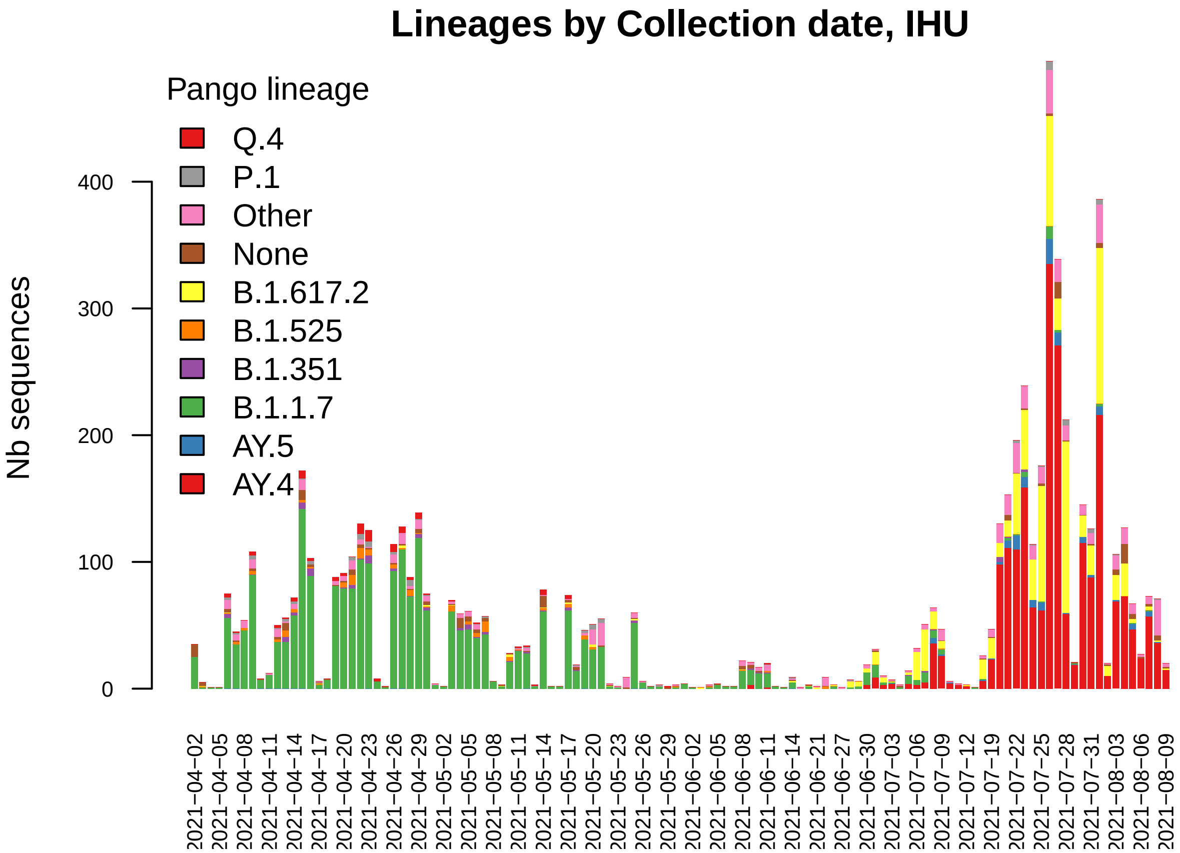


```r
hist(as.Date(subIHU$Collection.date.YMD), breaks = 500, freq = TRUE, xlab = "Collection date", main = "
axis(4)
```

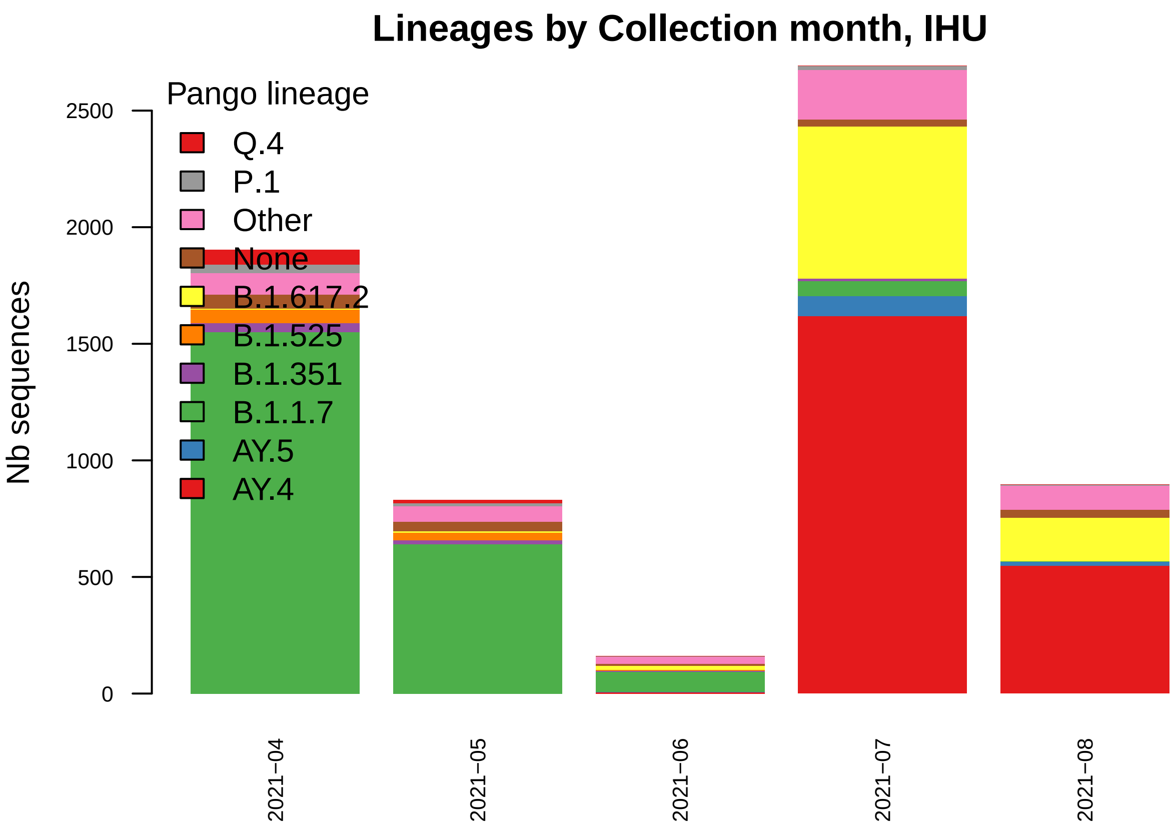


```
table(subIHU$Collection.date.YM)

# Rewrite lineage to only plot the most frequent ones
thr <- 0.01 # Threshold for number of sequences: percentage of all sequences
tb <- table(dataset$Pango.lineage) # Number of seqs associated to each lineage
isFreq <- (tb/sum(tb) > thr) # Identify lineages above the abundance threshold
cbind(tb, isFreq) # Check
dataset$newlineage <- dataset$Pango.lineage # Create new column with new lineage
dataset[!is.element(dataset$newlineage, names(tb[isFreq])), "newlineage"] <- "Other" # Write unfrequent

byLin <- aggregate(dataset$newlineage, by = list(Lineage = dataset$newlineage, Collection.date = dataset
totdate <- aggregate(dataset$newlineage, by = list(Collection.date = dataset$Collection.date.YMD), FUN =
names(totdate)[2] <- "tot"

byL <- merge(byLin, totdate, by = "Collection.date")
byL$p <- byL$x / byL$tot

# By month instead of just full collection date
byLinMonth <- aggregate(dataset$newlineage, by = list(Lineage = dataset$newlineage, Collection.date = da
totdate <- aggregate(dataset$newlineage, by = list(Collection.date = dataset$Collection.date.YM), FUN =
names(totdate)[2] <- "tot"

byLM <- merge(byLinMonth, totdate, by = "Collection.date")
byLM$p <- byLM$x / byLM$tot



byVar <- aggregate(dataset$VariantShort, by = list(Variant = dataset$VariantShort, Collection.date = dat
totdate <- aggregate(dataset$VariantShort, by = list(Collection.date = dataset$Collection.date.YMD), FUN
names(totdate)[2] <- "tot"

byV <- merge(byVar, totdate, by = "Collection.date")
byV$p <- byV$x / byV$tot


byL[order(byL$p), ]
```

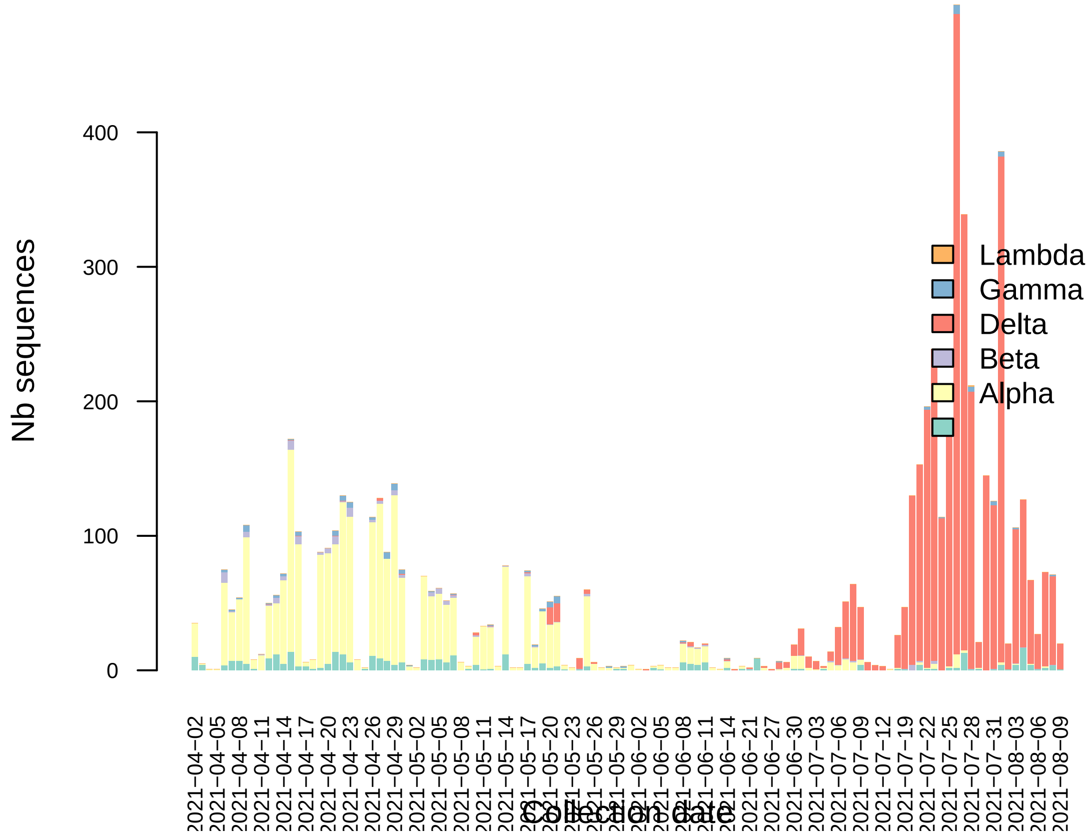
```
# By full collection date
par(mfrow = c(1, 1), las = 2, cex.axis = 0.7,
    mar = c(4, 4, 2, 1))
bL <- barplot(byL$x ~ byL$Lineage + byL$Collection.date, border = gray(0, 0),
              xlab = "", ylab = "Nb sequences",
              legend = TRUE, args.legend = list(x = "topleft", title = "Pango lineage", cex = 1, pt.cex
```



```
bLM <- barplot(byLM$x ~ byLM$Lineage + byLM$Collection.date, border = gray(0, 0),
               xlab = "", ylab = "Nb sequences",
               legend = TRUE, args.legend = list(x = "topleft", title = "Pango lineage", cex = 1, pt.cex =
```



```
par(mar = c(4, 4, 1, 4), las = 2)
barplot(byV$x ~ byV$Variant + byV$Collection.date, border = gray(0, 0),
             xlab = "Collection date", ylab = "Nb sequences",
             legend = TRUE, args.legend = list(x = "right", cex = 0.9, pt.cex = 0.9, bty = "n"), col =
```



What about recent submissions

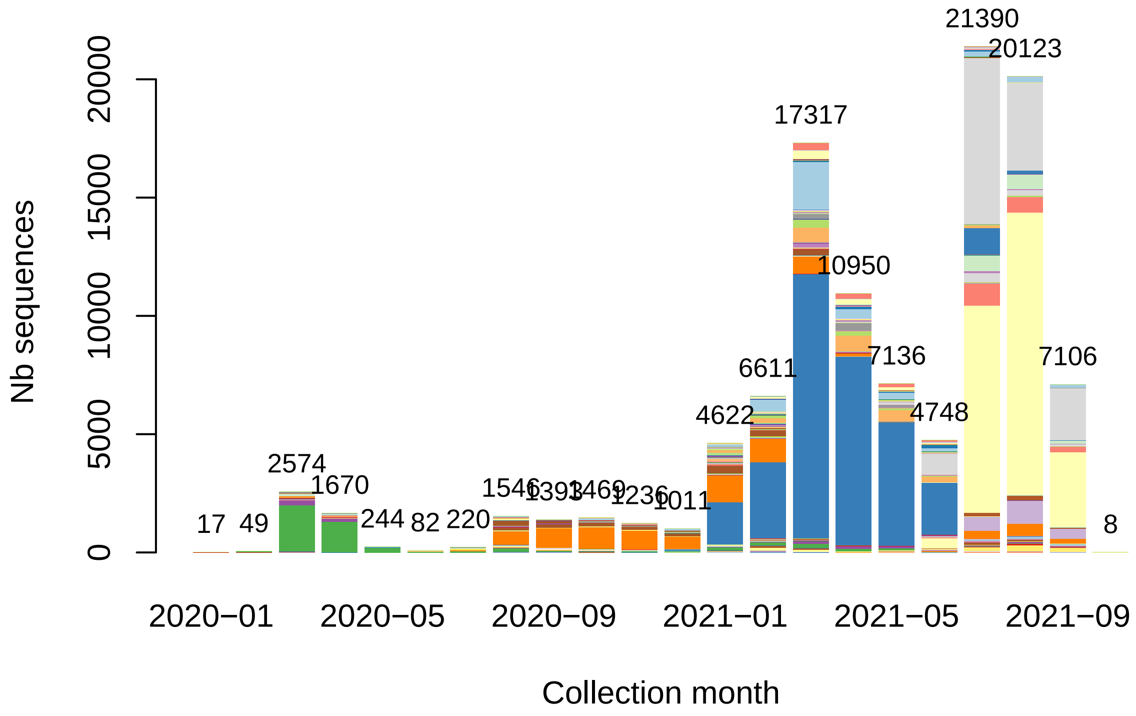
```
tmp <- subIHU[subIHU$Submission.date.YM >= "2021-10", ]
dim(tmp)

table(tmp$Submission.date)

table(tmp$Collection.date)

table(subIHU$Collection.date)
```

Lineages over time

All lineages, histograms

Pango clades

```
tabFR <- aggregate(dat$Virus.name, by = list(pango = dat$Pango.lineage, subM = dat$Collection.date.YM),

tabFR.month <- aggregate(dat$Virus.name, by = list(subM = dat$Collection.date.YM), FUN = length)

x <- barplot(tabFR$x ~ tabFR$pango + tabFR$subM, col = colsV[1:(length(unique(tabFR$pango)))], border =
             xlab = "Collection month", ylab = "Nb sequences")

nV <- 6
par(xpd = TRUE)
text(rep(x[length(x)] + (x[2]-x[1])/2, nV), tmp[1:nV, "cumx"] - tmp[1:nV, "x"]/2, labels = tmp[1:nV, "pa
     adj = 0)

text(x, y = tabFR.month$x, tabFR.month$x, adj = c(0.5, -1), cex = 0.8)
```



```
par(xpd = FALSE)
```

With threshold to plot lineage

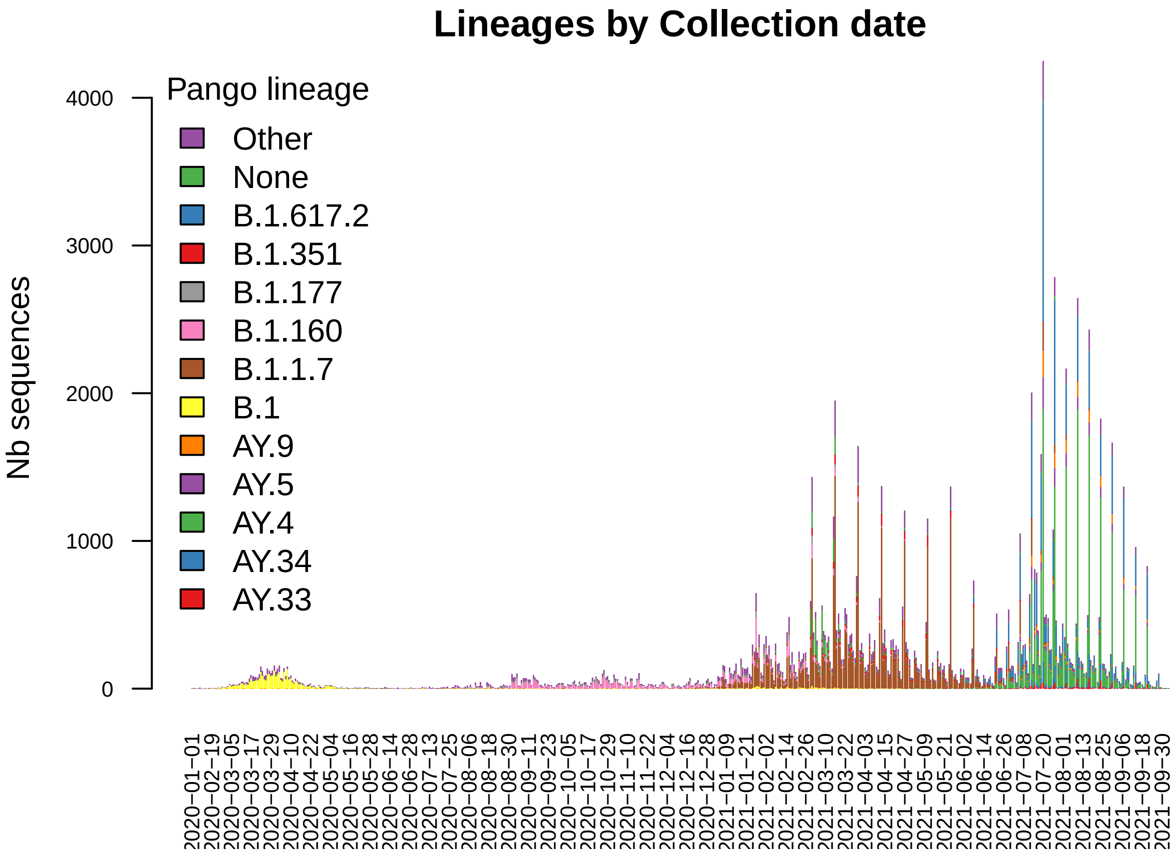
```
# Rewrite lineage to only plot the most frequent ones
thr <- 0.01 # Threshold for number of sequences: percentage of all sequences
tb <- table(dat$Pango.lineage) # Number of seqs associated to each lineage
isFreq <- (tb/sum(tb) > thr) # Identify lineages above the abundance threshold
cbind(tb, isFreq) # Check
dat$newlineage <- dat$Pango.lineage # Create new column with new lineage
dat[!is.element(dat$newlineage, names(tb[isFreq])), "newlineage"] <- "Other" # Write unfrequent lineage
```

```
byLin <- aggregate(dat$newlineage, by = list(Lineage = dat$newlineage, Collection.date = dat$Collection
totdate <- aggregate(dat$newlineage, by = list(Collection.date = dat$Collection.date.YMD), FUN = length
names(totdate)[2] <- "tot"

byL <- merge(byLin, totdate, by = "Collection.date")
byL$p <- byL$x / byL$tot

# By week
byWeek <- aggregate(dat$newlineage, by = list(Lineage = dat$newlineage, Collection.Ywk = dat$Collection
totdate <- aggregate(dat$newlineage, by = list(Collection.Ywk = dat$Collection.Ywk), FUN = length)
names(totdate)[2] <- "tot"

byW <- merge(byWeek, totdate, by = "Collection.Ywk")
byW$p <- byW$x / byW$tot

# By month instead of just full collection date
```

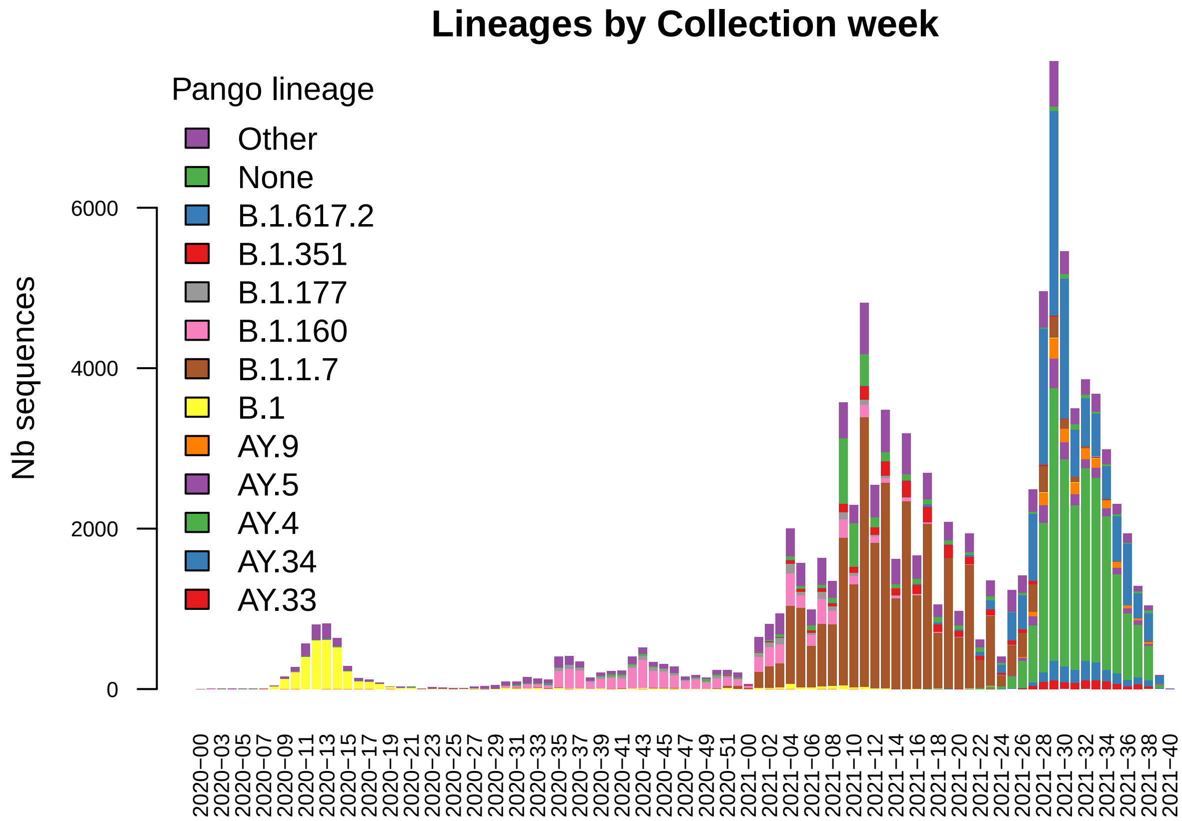
```
byLinMonth <- aggregate(dat$newlineage, by = list(Lineage = dat$newlineage, Collection.date = dat$Colle
totdate <- aggregate(dat$newlineage, by = list(Collection.date = dat$Collection.date.YM), FUN = length)
names(totdate)[2] <- "tot"

byLM <- merge(byLinMonth, totdate, by = "Collection.date")
byLM$p <- byLM$x / byLM$tot



byVar <- aggregate(dat$VariantShort, by = list(Variant = dat$VariantShort, Collection.date = dat$Collec
totdate <- aggregate(dat$VariantShort, by = list(Collection.date = dat$Collection.date.YMD), FUN = leng
names(totdate)[2] <- "tot"

byV <- merge(byVar, totdate, by = "Collection.date")
byV$p <- byV$x / byV$tot

length(unique(byV$Variant))
```

```
## [1] 7
```

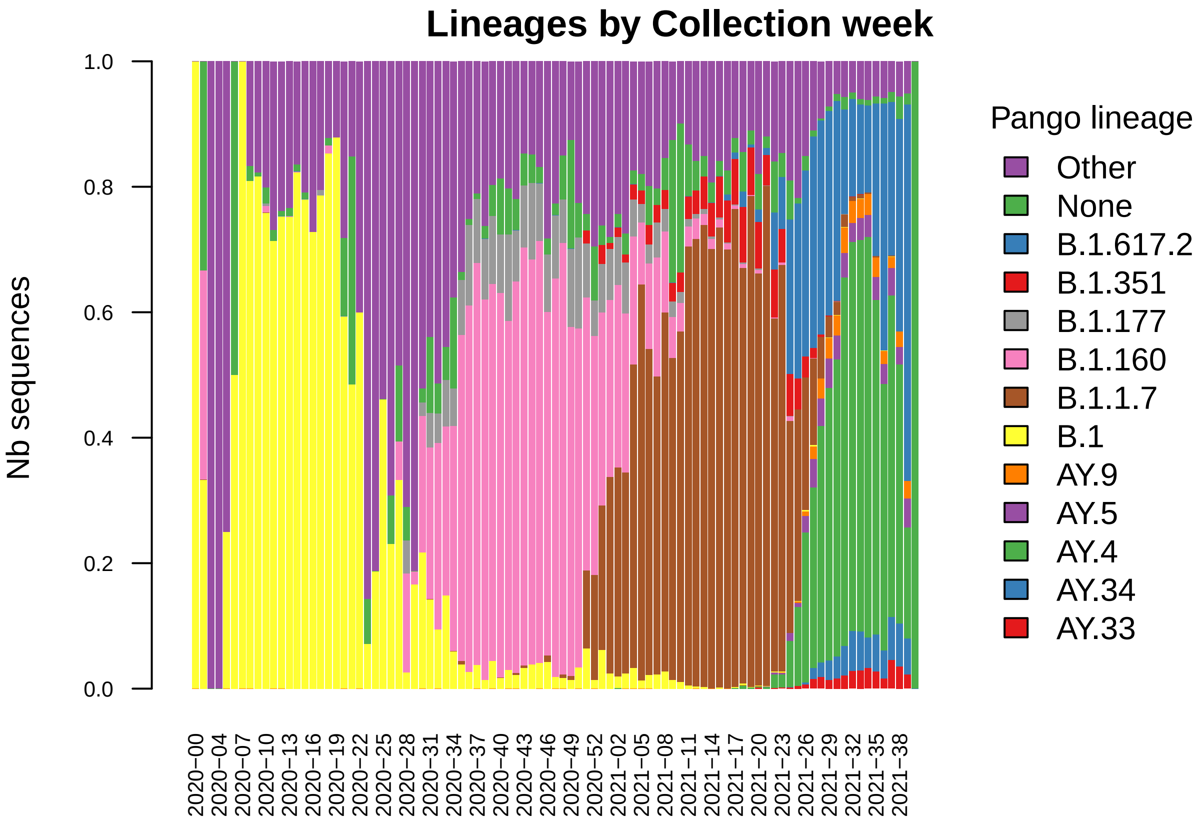
```
#byL[order(byL$p), ]

# By full collection date
par(mfrow = c(1, 1), las = 2, cex.axis = 0.7,
    mar = c(4, 4, 2, 1))
bL <- barplot(byL$x ~ byL$Lineage + byL$Collection.date, border = gray(0, 0),
             xlab = "", ylab = "Nb sequences",
             legend = TRUE, args.legend = list(x = "topleft", title = "Pango lineage", cex = 1, pt.cex =
```



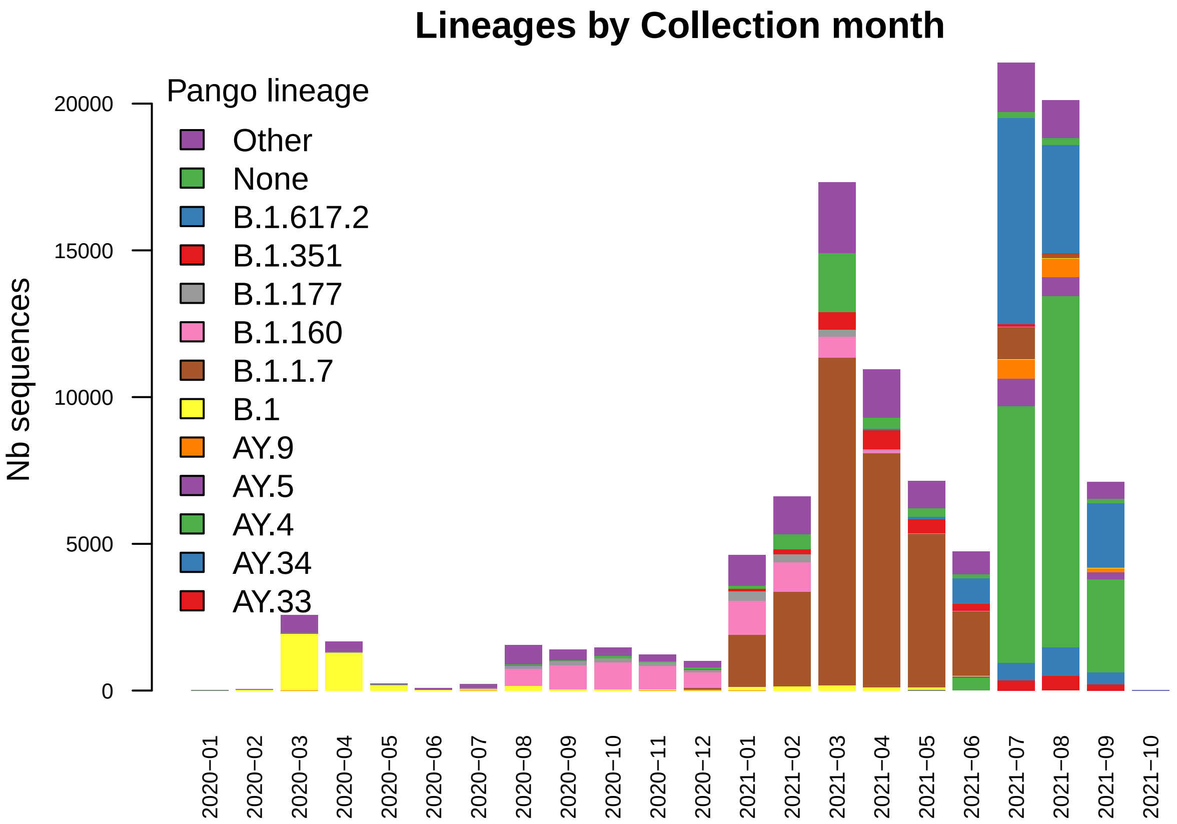
```
# By week
# Remove "2021-NA"
byW <- byW[!is.element(byW$Collection.Ywk, c("2020-NA", "2021-NA")),]

bW <- barplot(byW$x ~ byW$Lineage + byW$Collection.Ywk, border = gray(0, 0),
             xlab = "", ylab = "Nb sequences",
             legend = TRUE, args.legend = list(x = "topleft", title = "Pango lineage", cex = 1, pt.cex =
```



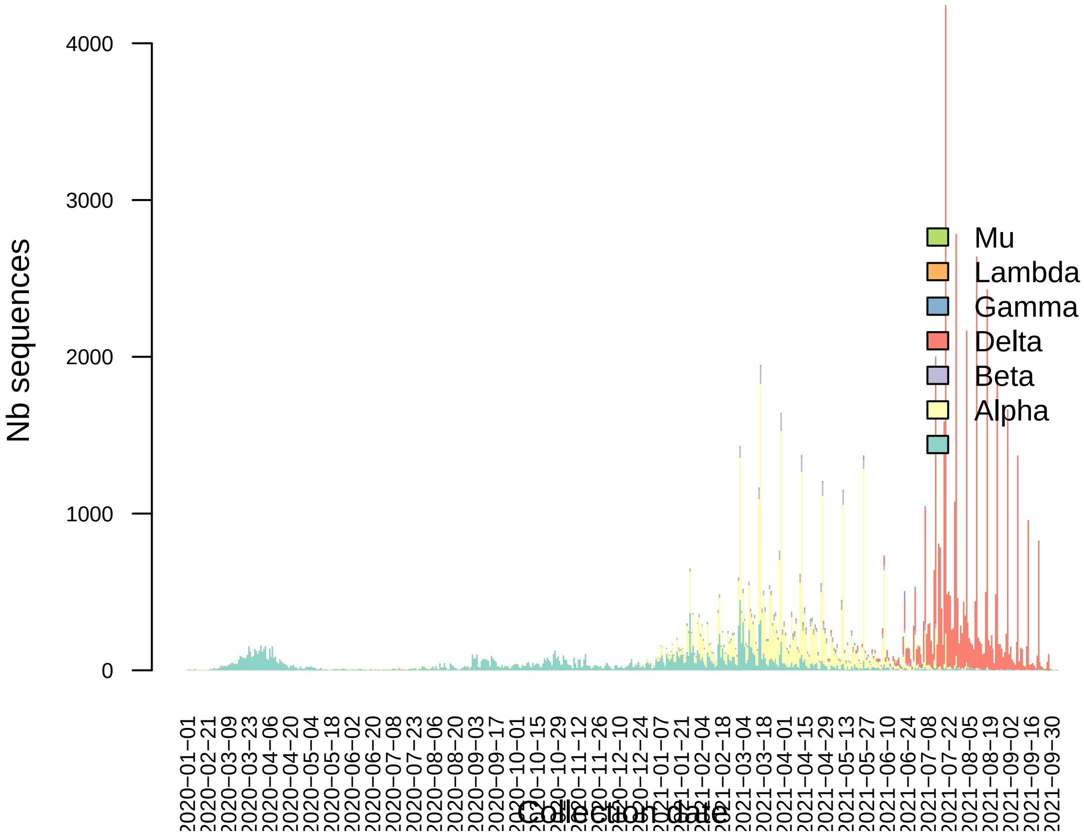
```
# As proportions
barplot(byW$p ~ byW$Lineage + byW$Collection.Ywk, border = gray(0, 0), xlim = c(0, 150),
             xlab = "", ylab = "Nb sequences",
             legend = TRUE, args.legend = list(x = "right", title = "Pango lineage", cex = 1, pt.cex = 
```



```
# By month
bLM <- barplot(byLM$x ~ byLM$Lineage + byLM$Collection.date, border = gray(0, 0),
               xlab = "", ylab = "Nb sequences",
               legend = TRUE, args.legend = list(x = "topleft", title = "Pango lineage", cex = 1, pt.cex =
```

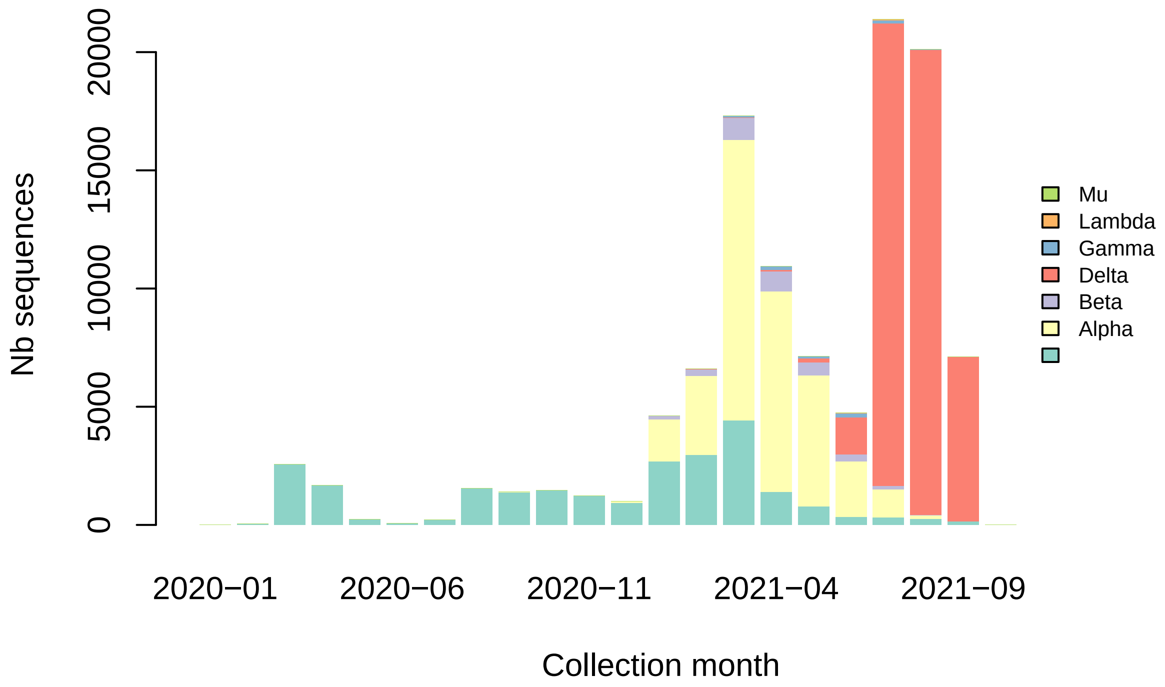


```
par(mar = c(4, 4, 1, 4), las = 2)
barplot(byV$x ~ byV$Variant + byV$Collection.date, border = gray(0, 0),
             xlab = "Collection date", ylab = "Nb sequences",
             legend = TRUE, args.legend = list(x = "right", cex = 0.9, pt.cex = 0.9, bty = "n"), col =
```



Variants

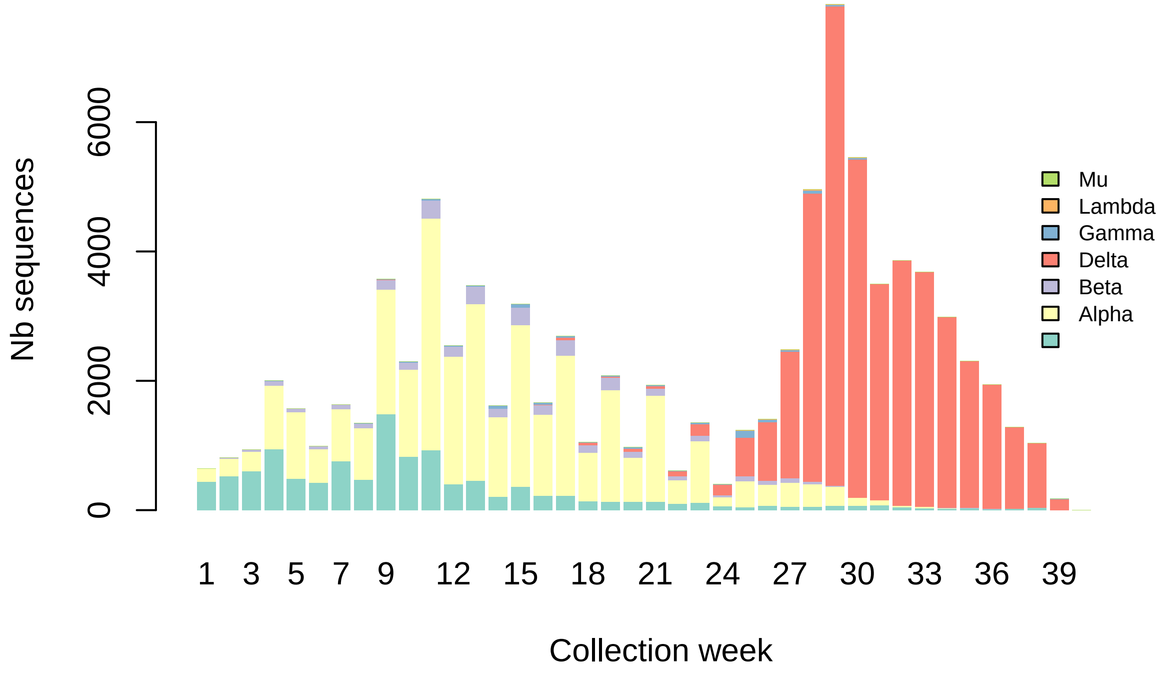
```
subFRVar <- aggregate(dat$Virus.name, by = list(month = dat$Collection.date.YM, variant = dat$VariantSho
subFRVar.month <- aggregate(dat$Virus.name, by = list(month = dat$Collection.date.YM), FUN = length)

x <- barplot(subFRVar$x ~ subFRVar$variant + subFRVar$month, col = colsV2[1:(length(unique(subFRVar$vari
             xlab = "Collection month", ylab = "Nb sequences", legend = TRUE, xlim= c(0, 30), args.legen
```



```
#legend(x = "topleft", legend = rev(unique(subFRVar$variant)), col = rev(colsV2[1:(length(unique(subFRV
```

2021

```
subFRVar <- aggregate(dat$Virus.name, by = list(week = dat$Collection.week, variant = dat$VariantShort)
subFRVar.week <- aggregate(dat$Virus.name, by = list(week = dat$Collection.week), FUN = length)

subFRVar2 <- merge(subFRVar, subFRVar.week, by = "week")
names(subFRVar2)[c(3,4)] <- c("x", "nbSeq")
subFRVar2$prop <- subFRVar2$x / subFRVar2$nbSeq

# Consistency check
# aggregate(subFRVar2[, 3], by = list(subFRVar2$week), FUN= sum) - subFRVar.week

x <- barplot(subFRVar$x ~ subFRVar$variant + subFRVar$week, col = colsV2[1:(length(unique(subFRVar$vari
             xlab = "Collection week", ylab = "Nb sequences",
             legend = TRUE, xlim= c(0, 50), args.legend = list(x = "right", cex = 0.7, pt.cex = 0.9, bty
```



```
#legend(x = "topleft", legend = rev(unique(subFRVar$variant)), col = rev(colsV2[1:(length(unique(subFRV
```

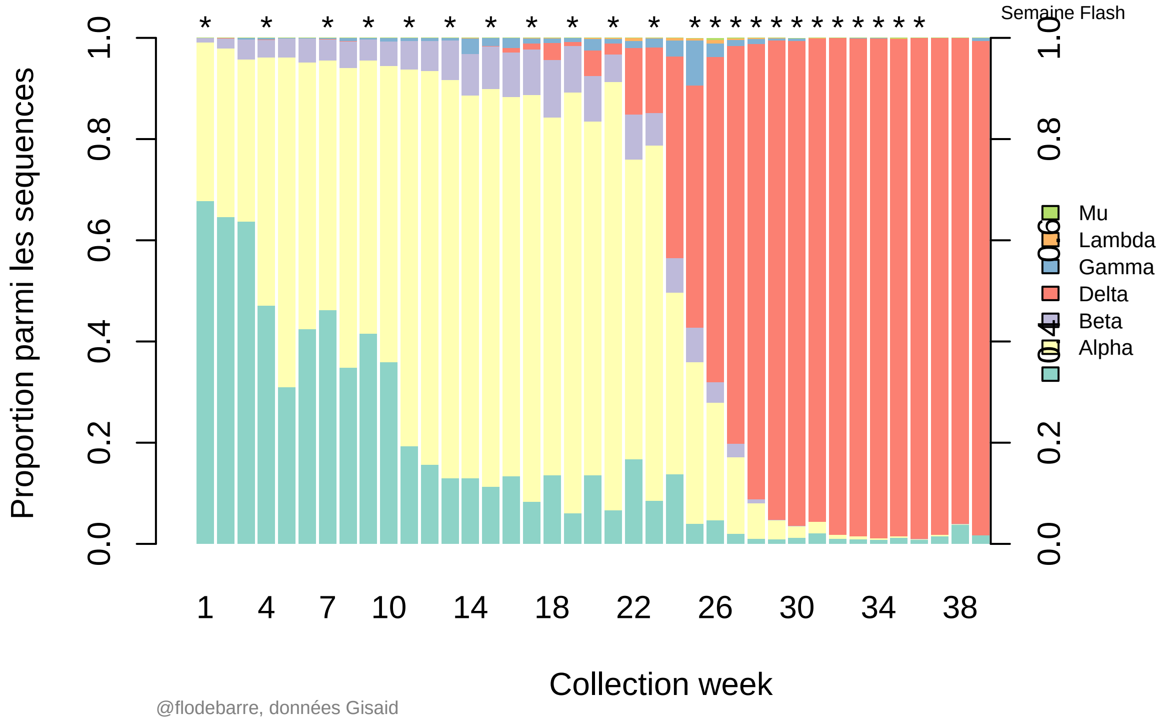
```
# Remove week if too few sequences
thrNbSeq <- 100
subFRVar2 <- subFRVar2[subFRVar2$nbSeq > thrNbSeq, ]

nbW <- length(unique(subFRVar2$week))
# Proportion
x <- barplot(subFRVar2$prop ~ subFRVar2$variant + subFRVar2$week, col = colsV2[1:(length(unique(subFRVa
             xlab = "Collection week", ylab = "Proportion parmi les sequences",
             legend = TRUE, xlim= c(0, 55), args.legend = list(x = "right", cex = 0.7, pt.cex = 0.9, bty

par(xpd = TRUE)
yy <- 1
adjy <- -0.5
cexx <- 0.6
# text(x, y = yy, labels = subFRVar.week$x, adj = c(0.5, adjy), cex = cexx)
# text(x = max(x) + x[2] - x[1], y = yy, adj = c(0, adjy), cex = cexx, labels = "Nb sequences")

posW <- as.data.frame(cbind(x = x, week = subFRVar.week$week))
```

Proportion

```
## Warning in cbind(x = x, week = subFRVar.week$week): number of rows of result is
## not a multiple of vector length (arg 1)
```

```
posWFlash <- posW[is.element(posW$week, datesFlash.all$week), ]
yFlash <- 1.09
text(x = c(posWFlash$x),
     y = yFlash, adj = c(0.5, 2),
     labels = "*")
text(x = max(x) + x[2] - x[1], y = yFlash, adj = c(0, 2), labels = "Semaine Flash", cex = cexx)
```

```
axis(4, pos = max(x) + (x[2] - x[1])/2)
par(xpd = FALSE)

mtext(side = 1, "@flodebarre, données Gisaid", line = 3.5, adj = 0, cex = 0.6, col = gray(0.5), las = 1
```



Load TESSy data

```
dlData <- FALSE # Whether to download the data again from the ECDC website
source("TESSy.R")
```

Beta

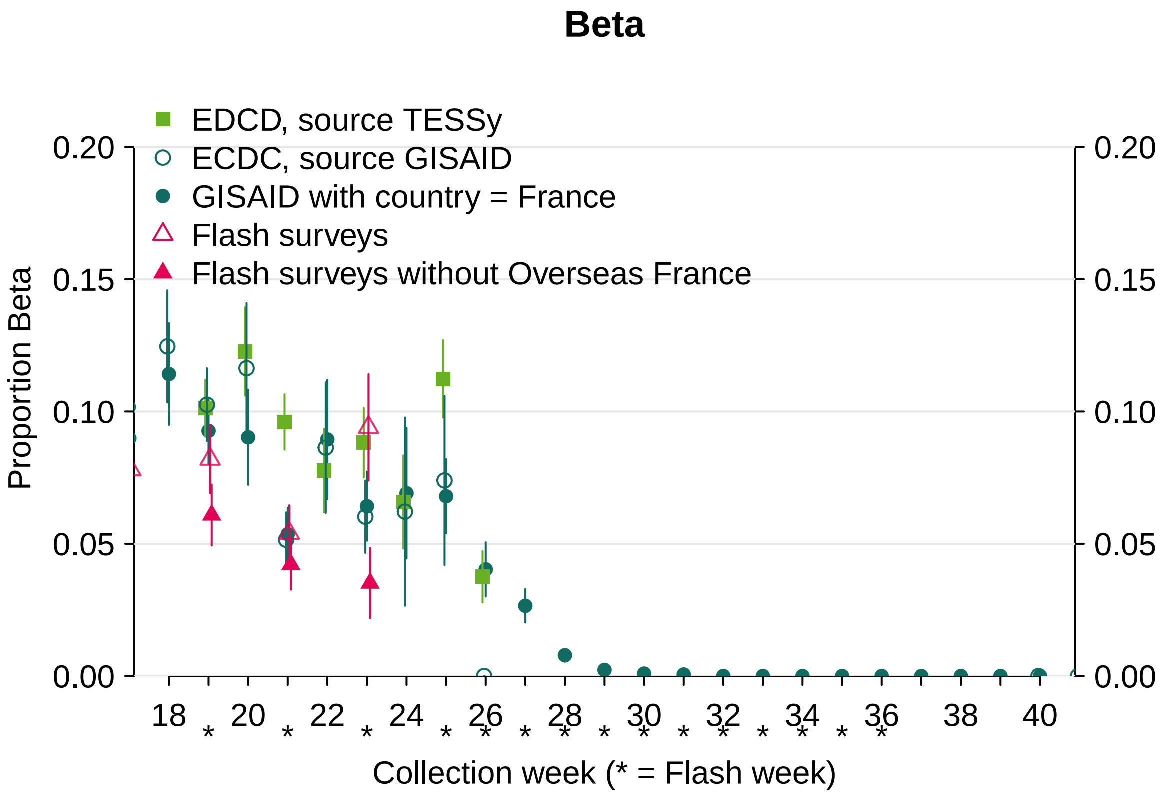
```
tessy.Beta <- (dat.tessy.FR$variant == "B.1.351")
tmp <- dat.tessy.FR[tessy.Beta, ]


# Aggregate the data by week of collection
tmp.nBeta <- aggregate(tmp$number_detections_variant, by = list(week = tmp$week), FUN = sum)
# Number of sequences that week
tmp.n <- aggregate(dat.tessy.FR$number_detections_variant, by = list(week = dat.tessy.FR$week), FUN = s
tmp.n2 <- aggregate(dat.tessy.FR$number_sequenced, by = list(week = dat.tessy.FR$week), FUN = unique, na
cbind(tmp.n, tmp.n2)

# Merge and name
tessyBeta.byweek <- merge(tmp.nBeta, tmp.n, by = "week")
names(tessyBeta.byweek) <- c("week", "nBeta", "n")
tessyBeta.byweek$p <- tessyBeta.byweek$nBeta / tessyBeta.byweek$n
# Confidence interval for proportion
```

```r
tessyBeta.byweek$deltaCI <- with(tessyBeta.byweek, 1.96 * sqrt(p * (1-p)/n))

tessyBeta.byweek
```

```r
# Same with GISAID data on TESSy
gisaidTESSy.Beta <- (dat.gisaid.FR$variant == "B.1.351")
gisaidTESSy.byweek <- dat.gisaid.FR[which(gisaidTESSy.Beta), ]

# Are there duplicate values
stopifnot(!any(duplicated(tmp$year_week)))

# Total number of detection
sum(gisaidTESSy.byweek$number_detections_variant)

gisaidTESSy.byweek$p <- gisaidTESSy.byweek$number_detections_variant / gisaidTESSy.byweek$number_sequen

# Confidence interval for proportion
gisaidTESSy.byweek$deltaCI <- with(gisaidTESSy.byweek, 1.96 * sqrt(p * (1-p)/number_sequenced))

gisaidTESSy.byweek
```

```r
par(mfrow = c(1,1))
# is.Beta <- dat$VariantShort == "Beta"

# Version 2 with sublineages
is.Beta <- (substr(dat$Pango.lineage, 1, 7) == "B.1.351")
#sum(is.Beta)
#mean(is.Beta)

# Aggregate the data by week of collection
tmp.mean <- aggregate(is.Beta, by = list(week = dat$Collection.week), FUN = mean)
# Number of sequences that week
tmp.n <- aggregate(is.Beta, by = list(week = dat$Collection.week), FUN = length)
# Merge and name
Beta.byweek <- merge(tmp.mean, tmp.n, by = "week")
names(Beta.byweek) <- c("week", "p", "n")
# Confidence interval for proportion
Beta.byweek$deltaCI <- with(Beta.byweek, 1.96 * sqrt(p * (1-p)/n))

par(las = 1, mar = c(4, 4, 3, 4),
    mgp = c(2.5, 0.5, 0), tck = -0.015,
    xpd = FALSE)
plot(Beta.byweek$week, Beta.byweek$p,
     xlim = c(19, max(Beta.byweek$week)) + c(-1, 0),
     xlab = "", ylab = "Proportion Beta", ylim = c(0, 0.225),
     frame.plot = FALSE, yaxs = "i", main = "Beta",
     type = "n",
     axes = FALSE)
axis(4)
axis(1, at =  seq(18, max(Beta.byweek$week), by = 1))
axis(2)
mtext(side = 1, text = "Collection week (* = Flash week)", line = 2)

deltaX <- 0.04 # Offset
```

```r
for(i in seq(0, 1, by = 0.05)) abline(h = i, col = gray(0.9))

points(Beta.byweek$week, Beta.byweek$p, col = cols["GISAID"], pch = pchs["GISAID"])

arrows(x0 = Beta.byweek$week, y0 = Beta.byweek$p + Beta.byweek$deltaCI,
       x1 = Beta.byweek$week, y1 = Beta.byweek$p - Beta.byweek$deltaCI,
       code = 3, angle = 90, length = 0.00, col = cols["GISAID"])

# Add TESSy data
points(as.numeric(tessyBeta.byweek$week) - 2*deltaX, tessyBeta.byweek$p, col = cols["TESSy"], pch = pchs

arrows(x0 = as.numeric(tessyBeta.byweek$week) - 2*deltaX, y0 = tessyBeta.byweek$p + tessyBeta.byweek$del
       x1 = as.numeric(tessyBeta.byweek$week) - 2*deltaX, y1 = tessyBeta.byweek$p - tessyBeta.byweek$del
       code = 3, angle = 90, length = 0.00, col = cols["TESSy"])

# Add TESSy GISAID data
points(as.numeric(gisaidTESSy.byweek$week) - deltaX, gisaidTESSy.byweek$p, col = cols["GISAID"], pch = p

arrows(x0 = as.numeric(gisaidTESSy.byweek$week) - deltaX, y0 = gisaidTESSy.byweek$p + gisaidTESSy.byweek
       x1 = as.numeric(gisaidTESSy.byweek$week) - deltaX, y1 = gisaidTESSy.byweek$p - gisaidTESSy.byweek
       code = 3, angle = 90, length = 0.00, col = cols["GISAID"])


# Add Flash data
dat.Flash.beta <- dat.Flash[dat.Flash$Variant_short == "Beta", ]

points(dat.Flash.beta$week + deltaX, dat.Flash.beta$Proportion, col = adjustcolor(cols["Flash"], 0.8), p
arrows(x0 = as.numeric(dat.Flash.beta$week) + deltaX, y0 = dat.Flash.beta$Proportion + dat.Flash.beta$d
       x1 = as.numeric(dat.Flash.beta$week) + deltaX, y1 = dat.Flash.beta$Proportion - dat.Flash.beta$d
       code = 3, angle = 90, length = 0.00, col = cols["Flash"])

# Add Flash data without Outre-Mer
points(totFlash.noOM$week + 2*deltaX, totFlash.noOM$pBeta, col = cols["Flash"], pch = pchs["Flash2"])
arrows(x0 = as.numeric(totFlash.noOM$week) + 2*deltaX, y0 = totFlash.noOM$pBeta + totFlash.noOM$deltaCI
       x1 = as.numeric(totFlash.noOM$week) + 2*deltaX, y1 = totFlash.noOM$pBeta - totFlash.noOM$deltaCI
       code = 3, angle = 90, length = 0.00, col = cols["Flash"])


par(xpd = TRUE)
text(datesFlash[datesFlash$week >=18, "week"], -0.02, "*")
par(xpd = FALSE)
legend("topleft", col = cols[c("TESSy", "GISAID", "GISAID", "Flash", "Flash")], legend = c("EDCD, sourc
```



There are 3272 Beta sequences.

This is 0.0288099 of all sequences.
This is 0.0260842 of sequences collected since April (included) This is 0.016559 of sequences collected since May (included) This is 0.0081499 of sequences collected since June (included)

```
tessyBeta.byweek

sum(tessyBeta.byweek$nBeta)
sum(tessyBeta.byweek$nBeta)/sum(tessyBeta.byweek$n)

sum(unique(dat.tessy.FR$number_sequenced))
```

Details on the Beta variant

```
dat.Beta <- dat[which(is.Beta), ]

table(dat.Beta$submitter)
#head(dat.Beta)

tt <- table(dat.Beta[which(is.na(dat.Beta$Collection.date.YMD)), "submitter"])
tt
sum(tt)

tt2 <- table(dat.Beta[which(is.na(dat.Beta$region)), "submitter"])
tt2

# -> dates and regions are OK
```

```
agg.Beta.region.month1 <- aggregate(is.Beta, by = list(region = dat$region, month = dat$Collection.date
names(agg.Beta.region.month1)[3] <- "nBeta"

agg.Beta.region.month2 <- aggregate(is.Beta, by = list(region = dat$region, month = dat$Collection.date
names(agg.Beta.region.month2)[3] <- "nSeq"

agg.Beta.region.month <- merge(agg.Beta.region.month1, agg.Beta.region.month2, all = TRUE)

agg.Beta.region.month$pBeta <- agg.Beta.region.month$nBeta / agg.Beta.region.month$nSeq
agg.Beta.region.month$deltaCI <- 1.96 * sqrt((agg.Beta.region.month$pBeta * (1-agg.Beta.region.month$pBe
```

```
max(agg.Beta.region.month$nSeq)
```

```
## [1] 4455
```

```
max(agg.Beta.region.month$nBeta)
```

```
## [1] 408
```

```
# Remove single sequence
agg.Beta.region.month <- agg.Beta.region.month[agg.Beta.region.month$nBeta != agg.Beta.region.month$nSe

# Consistency check
sum(agg.Beta.region.month$nBeta)
```

```
## [1] 3115
```

```
fname <- "beta_regions.pdf"
pdf(file = fname, width = 10, height = 12)
layout(matrix(c(0, 7, 14,
         9, 8, 6,
         3, 4, 2,
         12, 1, 13,
         10, 11, 5), byrow = TRUE, ncol = 3))
cexx <- 0.7
ln <- 2
for(reg in regions){

  sub <- agg.Beta.region.month[agg.Beta.region.month$region == reg, ]
  # Source trick https://stackoverflow.com/questions/6242955/converting-year-and-month-yyyy-mm-format-t

  xmin <- min(agg.Beta.region.month[agg.Beta.region.month$nBeta>0, "month"])
  xmax <- max(agg.Beta.region.month[agg.Beta.region.month$nBeta>0, "month"])
  xx <- seq(as.Date(paste(xmin, "-01", sep="")), as.Date(paste(xmax, "-01", sep="")), by = "month")


  coln <- "#2A7A6A"
  colp <- "#BF9142"#"#f18956"

  ymax <- max(agg.Beta.region.month$nBeta)
  xa <- pretty(seq(0, ymax, by = 50))
  ymax <- max(xa)

  par(mgp = c(2.75, 0.25, 0), tck = -0.01,
      mar = c(5, 4, 3, 4),
      las = 1)
  plot(as.Date(paste(sub$month, "-01", sep="")), sub$nBeta, xlim = range(xx), ylim = c(0, max(agg.Beta.
       xlab = "Collection month",
       ylab = "", yaxs = "i",
       type = "n")

  for(i in seq(0, ymax, by = 50)){
    abline(h = i, col = gray(0.9))
  }

  points(as.Date(paste(sub$month, "-01", sep="")), sub$nBeta, xlim = range(xx),
       col = coln, pch = 16,
       type = "h", lwd = 20, lend = "butt")

  axis(1, at = xx, labels = format.Date(xx, "%Y %b"), las = 3, cex.axis = 0.6)

  axis(2, col = coln, col.axis = coln, at = xa)
  mtext(side = 2, text = "Number of Beta", las = 3, line = ln, col = coln, cex = cexx)
  points(as.Date(paste(sub$month, "-01", sep="")), sub$pBeta * ymax, col = colp, pch = 17, type = "o", 
  arrows(x0 = as.Date(paste(sub$month, "-01", sep="")),
         y0 = (sub$pBeta - sub$deltaCI)* ymax,
         x1 = as.Date(paste(sub$month, "-01", sep="")),
         y1 = (sub$pBeta + sub$deltaCI)* ymax,
         code = 3, length = 0, lwd = 2, col = colp
  )

  axis(4, col = colp, col.axis = colp, at = xa, labels = xa /max(xa))
  mtext(side = 4, text = "Proportion of Beta", las = 3, line = ln, col = colp, cex = cexx)

  title(main = reg)

}

plot(0, type = "n", axes = FALSE, xlab = "", ylab = "", xlim = c(-1, 1), ylim = c(-1, 1))

legend(x = 0, y = 0, legend = paste0("Source: GISAID, ", thedate, ".\nDistribution across regions and m

dev.off()
```

```
## pdf
##   2
```

```
system(paste0("open ", fname))
```

IDF in May

```
sub <- dat[which(dat$region == "Île-de-France" & is.Beta), ]

table(sub$submitter, sub$Pango.lineage)

sub2 <- dat[which(dat$region == "Île-de-France" & dat$Collection.date.YM == "2021-05"), ]
table(sub2$submitter)

table(sub$div4, useNA = "ifany")
table(dat$region, dat$submitter)
```

AA changes

Load screening data (criblage)

```
source("publicData_criblage.R")
```

```
# Extract AA
tmp <- gsub('\\(', '', dat$AA.Substitutions)
tmp <- gsub('\\)', '', tmp)
aa <- strsplit(tmp, ",")
```

L452R

```
# Extract information on whether the S:L452R is present as aa substitution in the sequence
i.L452R <- sapply(aa, function(x){(is.element("Spike_L452R", x))})
```

Overall, fraction of all sequences with the L452R mutation: 0.4258268.

```
# Aggregate the data by week of collection
# Proportion of sequences with L452R that week
tmp.mean <- aggregate(i.L452R, by = list(week = dat$Collection.week), FUN = mean)
# Number of sequences that week
tmp.n <- aggregate(i.L452R, by = list(week = dat$Collection.week), FUN = length)
# Merge and name
L452R.byweek <- merge(tmp.mean, tmp.n, by = "week")
names(L452R.byweek) <- c("week", "p", "n")
# Confidence interval for proportion
L452R.byweek$deltaCI <- with(L452R.byweek, 1.96 * sqrt(p * (1-p)/n))
```

Which variants harbor the L452R mutation?

```
tV <- table(dat[which(dat$Collection.week >= 21 & i.L452R), "VariantShort"], useNA = "ifany")
tV/sum(tV)*100
```

```
##
##                     Alpha       Delta
##  0.88809947  0.03700414 99.07489639
```

Pango lineages with the L452R mutation

```
table(dat[which(dat$Collection.week >= 21 & i.L452R), "Pango.lineage"])
```

```
##
##         A      AY.1     AY.10     AY.11     AY.12     AY.13     AY.14     AY.15
##         1        22        34        14        34         3         4        10
##     AY.16     AY.17     AY.19      AY.2     AY.20     AY.21     AY.22     AY.23
##       208        76        13         1       155         5        34       179
##     AY.24     AY.25     AY.26     AY.27     AY.29      AY.3     AY.30     AY.32
##        80        54       147         2         8        20        23        14
##     AY.33     AY.34     AY.36     AY.37     AY.38      AY.4    AY.4.1      AY.5
##       890      1721        48       337        10     20635         1      1645
##    AY.5.1    AY.5.2      AY.6      AY.7    AY.7.1    AY.7.2      AY.9       B.1
##        25        13        78        12       390       123      1281         1
## B.1.1.528   B.1.1.7 B.1.617.1 B.1.617.2   B.1.629   B.1.630      C.16      C.36
##         1        15         1     11812         6         3         1         5
##    C.36.3      None
##        39       302
```

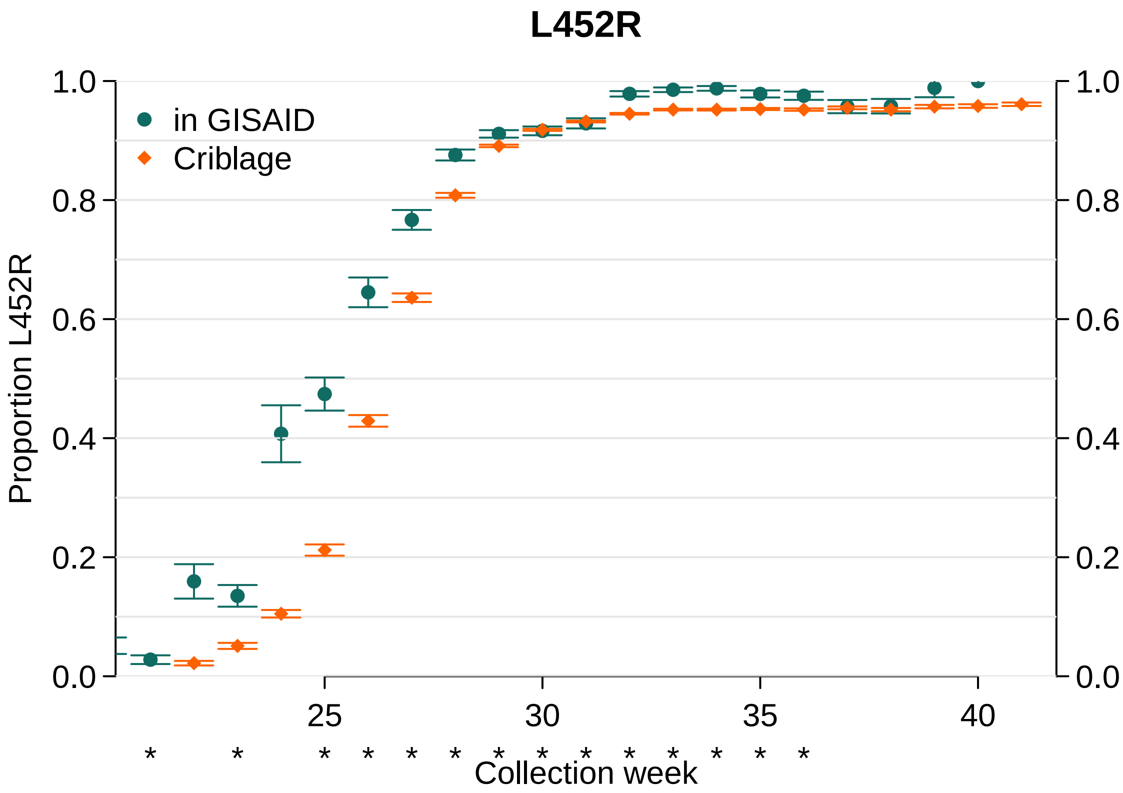
```
dat.France$deltaCI_C1 <- 1.96 * sqrt(dat.France$tx_C1/100 * (1-dat.France$tx_C1/100) / (dat.France$nb_C
```

Comparison of the frequency of L452R in GISAID vs criblage

```
par(las = 1, mar = c(4, 4, 3, 4),
    mgp = c(2., 0.5, 0), tck = -0.02,
    xpd = FALSE)
plot(L452R.byweek$week, L452R.byweek$p, xlim = range(dat.France$week, na.rm = TRUE) + c(-1, 0),
     xlab = "Collection week", ylab = "Proportion L452R", ylim = c(0, 1),
     frame.plot = FALSE, yaxs = "i", col = cols["GISAID"], pch = 16, main = "L452R")
axis(4)

for(i in seq(0, 1, by = 0.1)) abline(h = i, col = gray(0.9))

arrows(x0 = L452R.byweek$week, y0 = L452R.byweek$p + L452R.byweek$deltaCI,
       x1 = L452R.byweek$week, y1 = L452R.byweek$p - L452R.byweek$deltaCI,
       code = 3, angle = 90, length = 0.1, col = cols["GISAID"])
```

```
## Warning in arrows(x0 = L452R.byweek$week, y0 = L452R.byweek$p +
## L452R.byweek$deltaCI, : zero-length arrow is of indeterminate angle and so
## skipped
```

```
points(dat.France$week, dat.France$tx_C1/100, col = cols["criblage"], pch = 18)

arrows(x0 = dat.France$week, y0 = dat.France$tx_C1/100 + dat.France$deltaCI_C1,
       x1 = dat.France$week, y1 = dat.France$tx_C1/100 - dat.France$deltaCI_C1,
       code = 3, angle = 90, length = 0.1, col = cols["criblage"])

legend("topleft", col = cols[c("GISAID", "criblage")], legend = c("in GISAID", "Criblage"), pch = c(16,

par(xpd = TRUE)
text(datesFlash[which(datesFlash$week >= min(dat.France$week, na.rm = TRUE) -1), "week"], -0.125, "*")
```



Que se passe-t-il en semaine 24-25, pourquoi un tel écart ? Etait-ce un focus sur certaines regions ?

Nombres de sequences par regions

```
tmp25 <- dat[which(i.L452R & dat$Collection.week == 25), ]
table(tmp25$region)
```

```
##
##       Auvergne-Rhône-Alpes    Bourgogne-Franche-Comté
##                        201                         38
##                   Bretagne       Centre-Val de Loire
##                         14                         23
##                  Grand Est           Hauts-de-France
##                         39                          8
##              Île-de-France                 Normandie
##                        133                          5
##         Nouvelle-Aquitaine                 Occitanie
##                         72                         30
##           Pays de la Loire Provence-Alpes-Côte d'Azur
##                          4                         17
```

```
tmp24 <- dat[which(i.L452R & dat$Collection.week == 24), ]
table(tmp24$region)
```

```
##
##       Auvergne-Rhône-Alpes    Bourgogne-Franche-Comté
##                         35                          4
##                   Bretagne       Centre-Val de Loire
##                          2                          5
##                  Grand Est           Hauts-de-France
##                           6                          13
##               Île-de-France                   Normandie
##                          43                           1
##          Nouvelle-Aquitaine                   Occitanie
##                          33                           5
##            Pays de la Loire Provence-Alpes-Côte d'Azur
##                           5                           3
```

E484K

```
# Extract information on whether the S:E484K is present as aa substitution in the sequence
i.E484K <- sapply(aa, function(x){(is.element("Spike_E484K", x))})
mean(i.E484K)
```

```
## [1] 0.05059346
```

```
# Aggregate the data by week of collection
# Proportion of sequences with L452R that week
tmp.mean <- aggregate(i.E484K, by = list(week = dat$Collection.week), FUN = mean)
# Number of sequences that week
tmp.n <- aggregate(i.E484K, by = list(week = dat$Collection.week), FUN = length)
# Merge and name
E484K.byweek <- merge(tmp.mean, tmp.n, by = "week")
names(E484K.byweek) <- c("week", "p", "n")
# Confidence interval for proportion
E484K.byweek$deltaCI <- with(E484K.byweek, 1.96 * sqrt(p * (1-p)/n))
```

Variants with the mutation

```
table(dat[which(dat$Collection.week >= 21 & i.E484K), "VariantShort"])
```

```
##
##       Alpha  Beta Delta Gamma    Mu
##   268   324   441    14   317    21
```

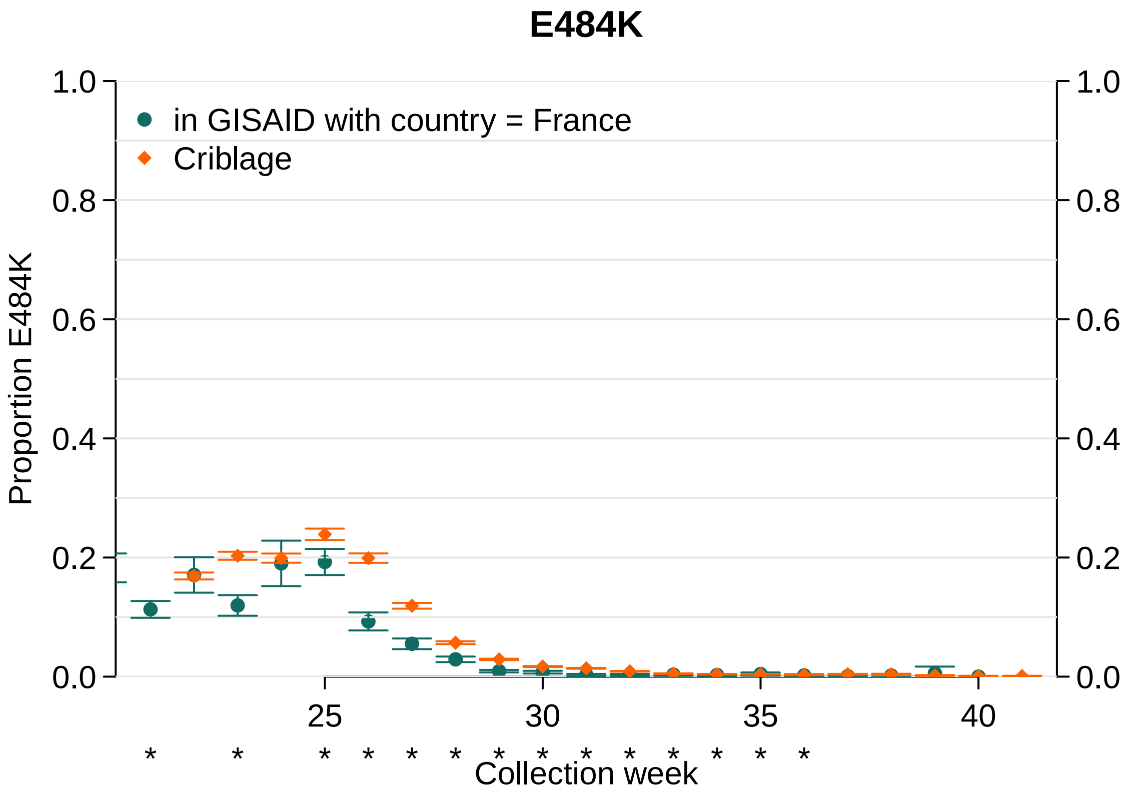
```
dat.France$deltaCI_A1 <- 1.96 * sqrt(dat.France$tx_A1/100 * (1-dat.France$tx_A1/100) / (dat.France$nb_A
```

```
par(las = 1, mar = c(4, 4, 3, 4),
    mgp = c(2., 0.5, 0), tck = -0.02,
    xpd = FALSE)
plot(E484K.byweek$week, E484K.byweek$p, xlim = range(dat.France$week, na.rm = TRUE) + c(-1, 0),
     xlab = "Collection week", ylab = "Proportion E484K", ylim = c(0, 1),
     frame.plot = FALSE, yaxs = "i", col = cols["GISAID"], pch = 16, main = "E484K")
axis(4)

for(i in seq(0, 1, by = 0.1)) abline(h = i, col = gray(0.9))

arrows(x0 = E484K.byweek$week, y0 = E484K.byweek$p + E484K.byweek$deltaCI,
       x1 = E484K.byweek$week, y1 = E484K.byweek$p - E484K.byweek$deltaCI,
       code = 3, angle = 90, length = 0.1, col = cols["GISAID"])
```

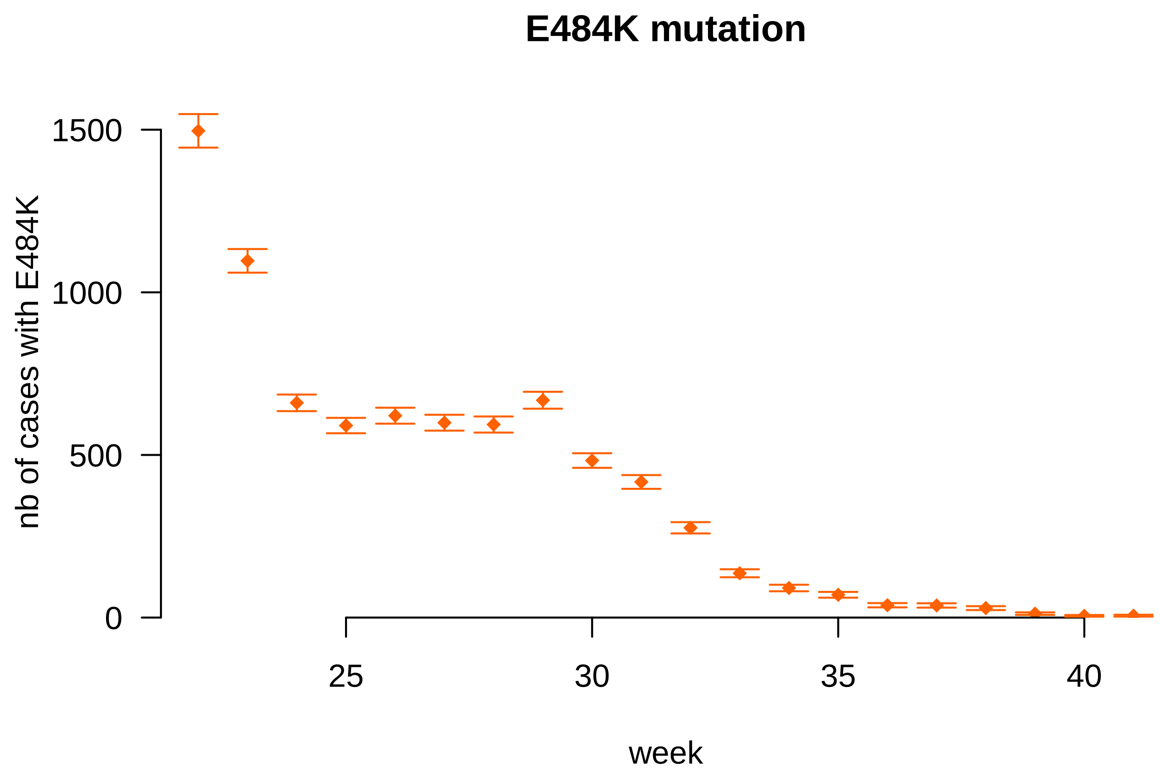
```
## Warning in arrows(x0 = E484K.byweek$week, y0 = E484K.byweek$p +
## E484K.byweek$deltaCI, : zero-length arrow is of indeterminate angle and so
## skipped
```

```
points(dat.France$week, dat.France$tx_A1/100, col = cols["criblage"], pch = 18)
```

```
arrows(x0 = dat.France$week, y0 = dat.France$tx_A1/100 + dat.France$deltaCI_A1,
       x1 = dat.France$week, y1 = dat.France$tx_A1/100 - dat.France$deltaCI_A1,
       code = 3, angle = 90, length = 0.1, col = cols["criblage"])

legend("topleft", col = cols[c("GISAID", "criblage")], legend = c("in GISAID with country = France", "C

par(xpd = TRUE)
text(datesFlash[which(datesFlash$week >= min(dat.France$week, na.rm = TRUE) -1), "week"], -0.125, "*")
```



```
par(las = 1)
plot(dat.France$week, dat.France$nb_pos/7 * dat.France$tx_A1/100, col = cols["criblage"], pch = 18,
     yaxs = "i",
     frame.plot = FALSE, ylim = c(0, 1.05*max(dat.France$nb_pos/7 * dat.France$tx_A1/100)),
     xlab = "week", ylab = "nb of cases with E484K", main = "E484K mutation")

arrows(x0 = dat.France$week, y0 = dat.France$nb_pos/7 * (dat.France$tx_A1/100 + dat.France$deltaCI_A1),
       x1 = dat.France$week, y1 = dat.France$nb_pos/7 * (dat.France$tx_A1/100 - dat.France$deltaCI_A1),
       code = 3, angle = 90, length = 0.1, col = cols["criblage"])
```



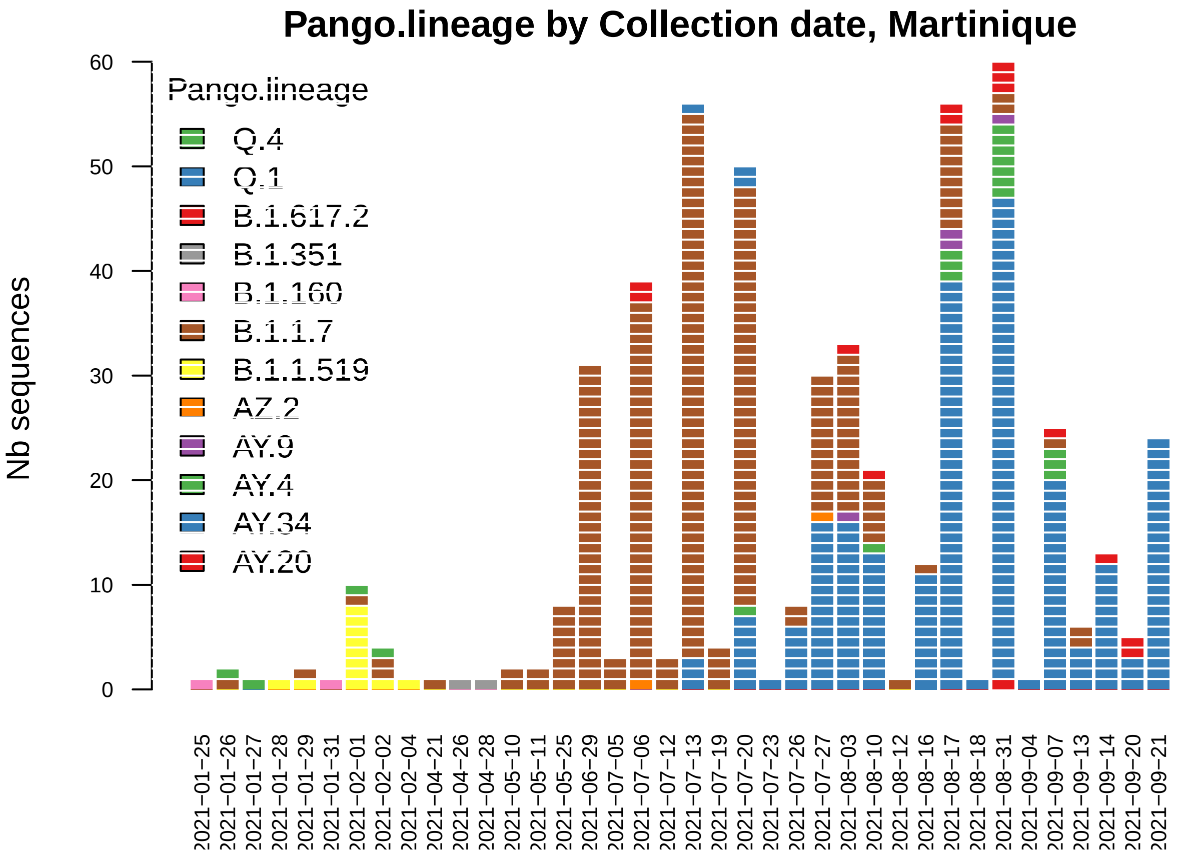
```
for(cw in 22:28){
  tmp <- dat[which(dat$Collection.week == cw & i.E484K), ]
  print(cw)
  tb <- table(tmp$VariantShort)
  print(tb)
  print(c(sum(tb), tb["Beta"], tb["Beta"]/sum(tb)))
}
table(dat[which(dat$Collection.week >= 21 & i.E484K), "VariantShort"])
```

DROM

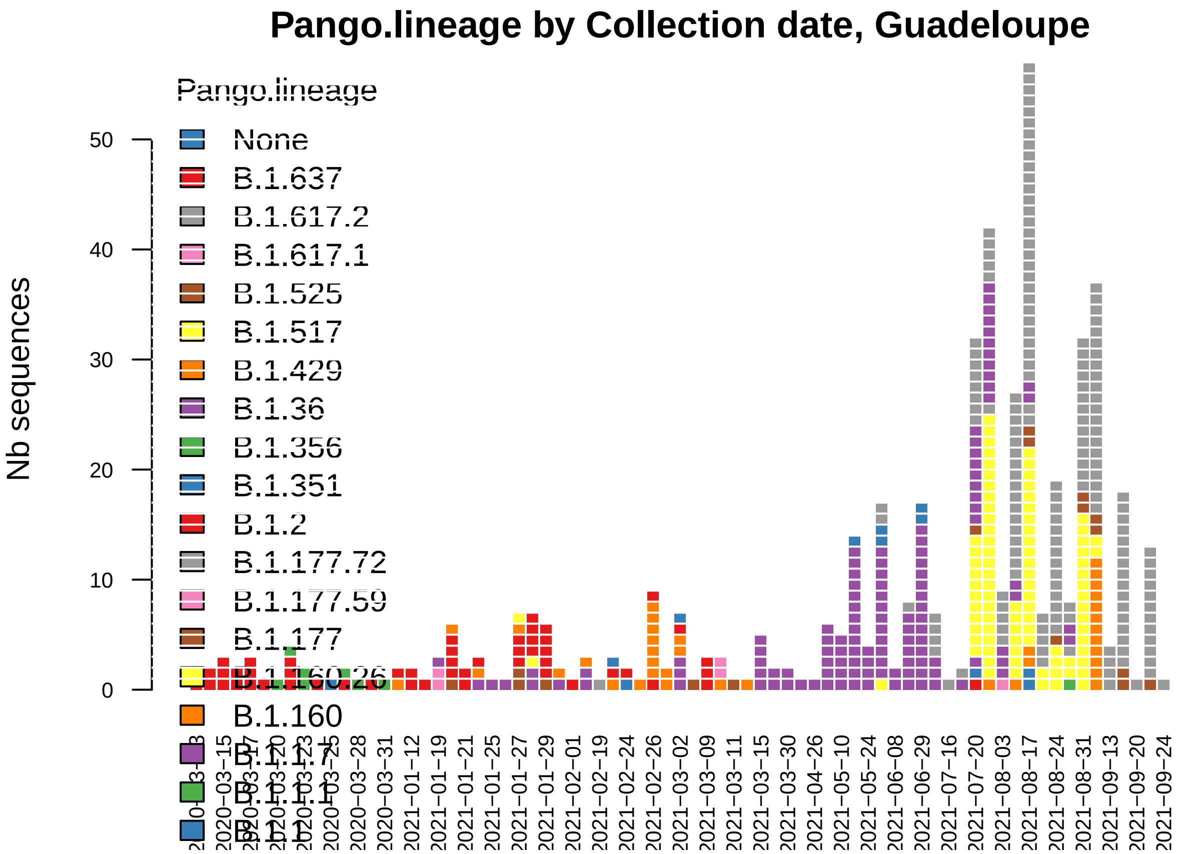
```
datM <- dat[dat$country == "Martinique", ]
datG <- dat[dat$country == "Guadeloupe", ]


for(col in c("Pango.lineage", "VariantShort")){
for(ctr in c("Martinique", "Guadeloupe")){
dataset <- dat[dat$country == ctr, ]

# Extract AA
tmp <- gsub('\\(', '', dataset$AA.Substitutions)
tmp <- gsub('\\)', '', tmp)
aaa <- strsplit(tmp, ",")

# Extract information on whether the S:L452R is present as aa substitution in the sequence
ii.L452R <- sapply(aaa, function(x){(is.element("Spike_L452R", x))})

cat(ctr, "\n")
```

```
print(table(dataset[which(ii.L452R), "Pango.lineage"]))

byLin <- aggregate(dataset[, col], by = list(Lineage = dataset[, col], Collection.date = dataset$Collec
totdate <- aggregate(dataset[, col], by = list(Collection.date = dataset$Collection.date.YMD), FUN = len
names(totdate)[2] <- "tot"
byL <- merge(byLin, totdate, by = "Collection.date")
byL$p <- byL$x / byL$tot
# byL[order(byL$p), ]

# By full collection date
par(mfrow = c(1, 1), las = 2, cex.axis = 0.7,
    mar = c(4, 4, 2, 1))
bL <- barplot(byL$x ~ byL$Lineage + byL$Collection.date, border = gray(0, 0),
              xlab = "", ylab = "Nb sequences",
              legend = TRUE, args.legend = list(x = "topleft", title = col, cex = 1, pt.cex = 2, bty = "
par(xpd = FALSE)
for(i in 1:100){
  abline(h = i, col = gray(1))
}
}
}
```

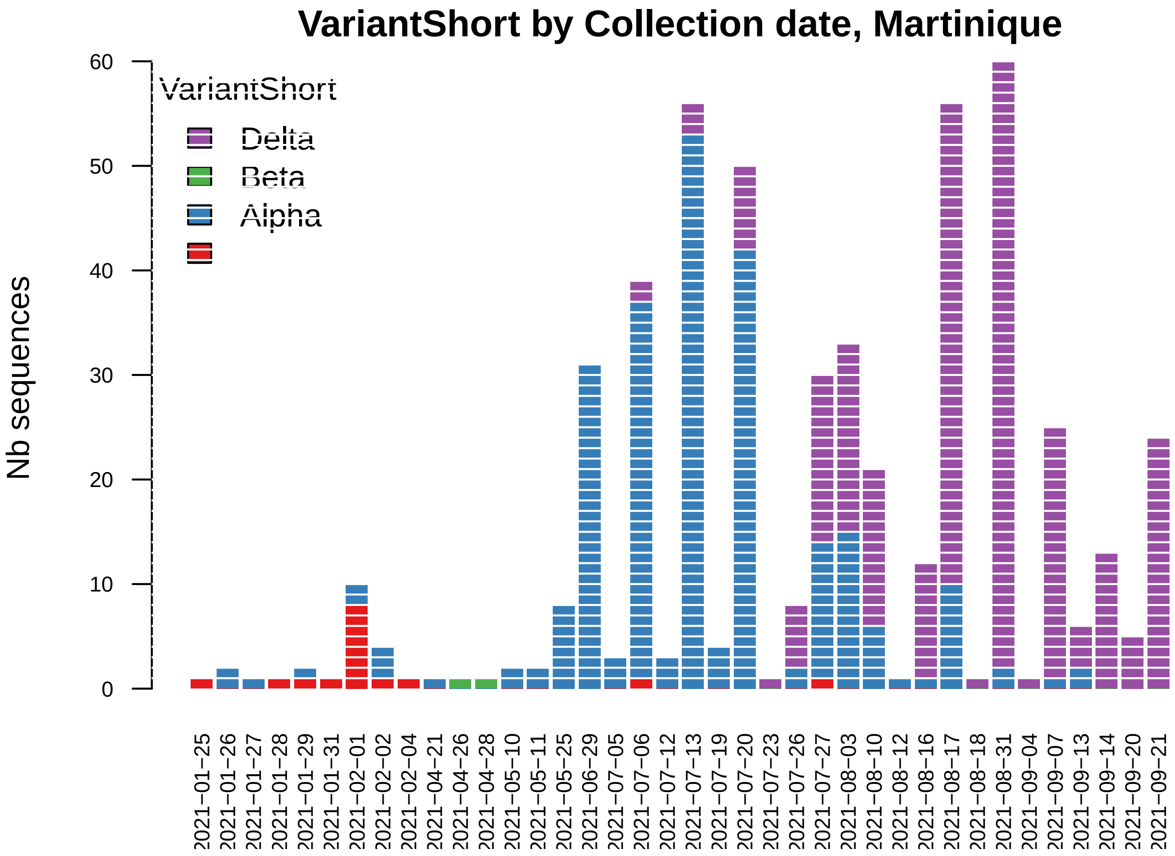
```
## Martinique
##
##     AY.20     AY.34      AY.4      AY.9 B.1.617.2
##         1       216        14         4        13
```



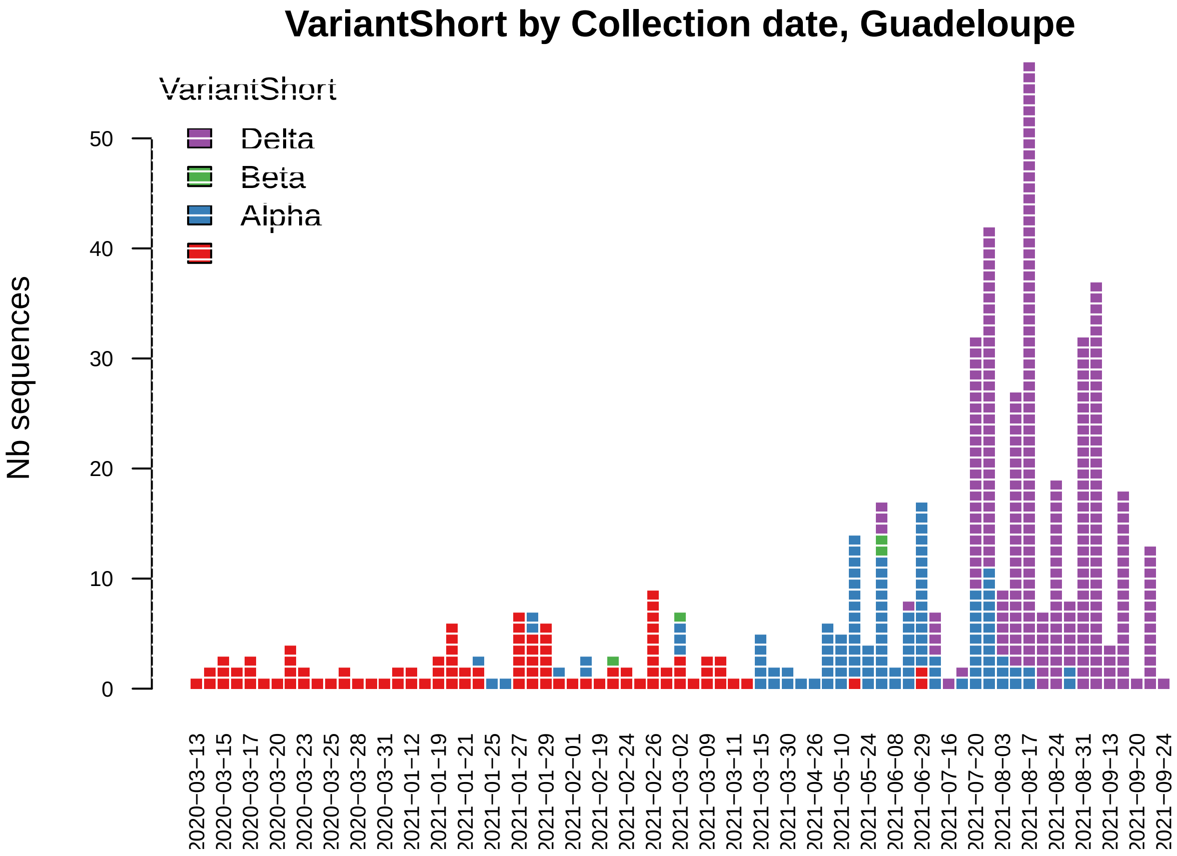
```
## Guadeloupe
##
##      AY.11      AY.25      AY.26      AY.34       AY.4       AY.5       AY.6       AY.9
##          1          1          1         17        113         11          1         15
##    B.1.429 B.1.617.1 B.1.617.2    B.1.637
##          4          2        178          3
```



```
## Martinique
##
##      AY.20      AY.34       AY.4       AY.9 B.1.617.2
##          1        216         14          4        13
```



```
## Guadeloupe
##
##      AY.11      AY.25      AY.26      AY.34       AY.4       AY.5       AY.6       AY.9
##          1          1          1         17        113         11          1         15
##    B.1.429 B.1.617.1 B.1.617.2    B.1.637
##          4          2        178          3
```


VariantShort by Collection date, Guadeloupe
VariantShort
🟪 Delta
🟩 Beta
🟦 Alpha
🟥
Nb sequences
0
10
20
30
40
50
2020−03−13
2020−03−15
2020−03−17
2020−03−20
2020−03−23
2020−03−25
2020−03−28
2020−03−31
2021−01−12
2021−01−19
2021−01−21
2021−01−25
2021−01−27
2021−01−29
2021−02−01
2021−02−19
2021−02−24
2021−02−26
2021−03−02
2021−03−09
2021−03−11
2021−03−15
2021−03−30
2021−04−26
2021−05−10
2021−05−24
2021−06−08
2021−06−29
2021−07−16
2021−07−20
2021−08−03
2021−08−17
2021−08−24
2021−08−31
2021−09−13
2021−09−20
2021−09−24