Explore FMD data

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Description: This script uses some popular R libraries to explore and visualise a Foot and Mouth disease dataset

Begin by importing the relevant packages

```
library(readxl)
library(dplyr)
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##
       filter, lag
## The following objects are masked from 'package:base':
##
##
       intersect, setdiff, setequal, union
library(ggplot2)
library(gridExtra)
##
## Attaching package: 'gridExtra'
## The following object is masked from 'package:dplyr':
##
##
       combine
library(scales)
```

Load and explore dataset

```
#Load data
df <- read_excel("C:/Users/colum/Desktop/For me/Data projects/WOAH/clean_data.xlsx")
## New names:
## * '' -> '...1'
```

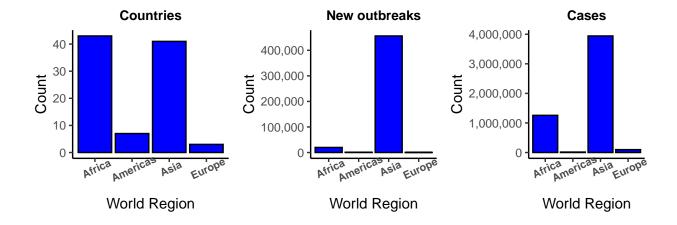
head(df)

```
## # A tibble: 6 x 16
                              'World region' Country 'Administrative Division'
##
      ...1 Year Semester
##
     <dbl> <dbl> <chr>
                              <chr>
                                             <chr>
                                                     <chr>
## 1
        0 2005 Jul-Dec 2005 Africa
                                             Benin
                                                     Abomev
        1 2005 Jul-Dec 2005 Africa
                                                     Banikoara
## 2
                                             Benin
## 3
        2 2005 Jul-Dec 2005 Africa
                                             Benin
                                                     Come
## 4
        3 2005 Jul-Dec 2005 Africa
                                             Benin
                                                     Djougou
        4 2005 Jul-Dec 2005 Africa
                                             Benin
                                                     Gogounou
        5 2005 Jul-Dec 2005 Africa
## 6
                                             Benin
                                                     Kandi
## # i 10 more variables: 'Animal Category' <chr>, Species <chr>,
      'New outbreaks' <dbl>, Susceptible <dbl>, 'Measuring units' <chr>,
      Cases <dbl>, 'Killed and disposed of' <dbl>, Slaughtered <dbl>,
      Deaths <dbl>, Vaccinated <dbl>
## #
```

Group data by region for descriptive figures

Create Barchart subplots

```
bar_vars <- c('Countries','New outbreaks','Cases')</pre>
plt_cnt <-1</pre>
subplots <- list()</pre>
for (ivar in bar_vars){
 plt <- ggplot(df_region_descriptives, aes(`World region`, .data[[ivar]]),</pre>
                  height = 0.5, width = 1) +
  geom bar(stat = "identity", colour = "black", fill = "Blue") +
  labs(x = "World Region", y = "Count", title = ivar)+
  scale_y_continuous(labels = comma)+
  theme classic()
 plt <- plt + theme(plot.title = element_text(hjust = 0.5, size = 10, face = "bold"),</pre>
                          axis.text.x = element_text(face = "bold", size = 8,angle = 25))
  subplots[[plt_cnt]] <- plt</pre>
  plt_cnt<-plt_cnt+1
  }
# Arrange plots into a grid. Note that the extra row is simply for height aesthetics
grid.arrange(grobs = subplots, nrow =2, ncol = 3)
```



Group by variables of interest and year for time-series plots

Create time-series plots

