

# Circulación de virus respiratorios por período epidemiológico

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## R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
# Cargamos las funciones
source("scripts/utils/load_libraries.R")
source("scripts/loading/get_all_tables.R")
source("scripts/loading/print_all_tables.R")
source("scripts/loading/get_selected_table.R")
source("scripts/cleaning/fill_down_year.R")

##
## 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

source("scripts/cleaning/clean_colnames_suffixes.R")
source("scripts/cleaning/clean_colnames_spaces.R")

#Declaramos variables constantes
PACKAGES <- c("dplyr", "readxl", "ggplot2")
FILE_NAME <- "data/VIRUS RESPIRATORIO 2022 A 2024.xlsx"
SHEET_NAME <- "POR PERIODO"
INDICADOR <- 2 #Sleccionar el numero de la tabla que se desea utilizar.

# LOADING
install_and_load_packages(PACKAGES)

## [1] TRUE
```

```
tables <- get_all_tables(FILE_NAME, SHEET_NAME)
```

```
## New names:
## * 'PERIODO EPIDEMIOLOGICO' -> 'PERIODO EPIDEMIOLOGICO...2'
## * 'A(H1N1)pdm09' -> 'A(H1N1)pdm09...4'
## * 'A no subtipificado' -> 'A no subtipificado...5'
## * 'A(H3)' -> 'A(H3)...6'
## * 'Influenza B' -> 'Influenza B...7'
## * 'Parainfluenza' -> 'Parainfluenza...8'
## * 'VSR' -> 'VSR...9'
## * 'Adenovirus' -> 'Adenovirus...10'
## * 'Metapneumovirus' -> 'Metapneumovirus...11'
## * 'Rinovirus' -> 'Rinovirus...12'
## * 'Bocavirus' -> 'Bocavirus...13'
## * 'Otros Virus' -> 'Otros Virus...14'
## * '' -> '...17'
## * '' -> '...18'
## * '' -> '...19'
## * 'PERIODO EPIDEMIOLOGICO' -> 'PERIODO EPIDEMIOLOGICO...21'
## * 'A(H1N1)pdm09' -> 'A(H1N1)pdm09...22'
## * 'A no subtipificado' -> 'A no subtipificado...23'
## * 'A(H3)' -> 'A(H3)...24'
## * 'Influenza B' -> 'Influenza B...25'
## * 'Parainfluenza' -> 'Parainfluenza...26'
## * 'VSR' -> 'VSR...27'
## * 'Adenovirus' -> 'Adenovirus...28'
## * 'Metapneumovirus' -> 'Metapneumovirus...29'
## * 'Rinovirus' -> 'Rinovirus...30'
## * 'Bocavirus' -> 'Bocavirus...31'
## * 'Otros Virus' -> 'Otros Virus...32'
```

```
tabla <- get_selected_table(tables, INDICADOR)
```

#### # CLEANING

```
tabla <- tabla %>%
  clean_colnames_suffixes() %>%
  clean_colnames_spaces() %>%
  fill_down_year("AÑO") %>%
  slice(1:32)
```

#### #PREPROCESSING

```
data <- tabla
```

```
stacked_data <- data %>%
  pivot_longer(cols = `A(H1N1)pdm09`:`Otros_Virus`,
    names_to = "Virus_Type",
    values_to = "Cases") %>%
  mutate(YearWeek = paste(AÑO, sprintf("%02d", PERIODO_EPIDEMIOLOGICO), sep = "-"))
# Prepare line data for the line chart, ensuring YearWeek is created consistently
line_data <- data %>%
  mutate(YearWeek = paste(AÑO, sprintf("%02d", PERIODO_EPIDEMIOLOGICO), sep = "-")) %>%
```

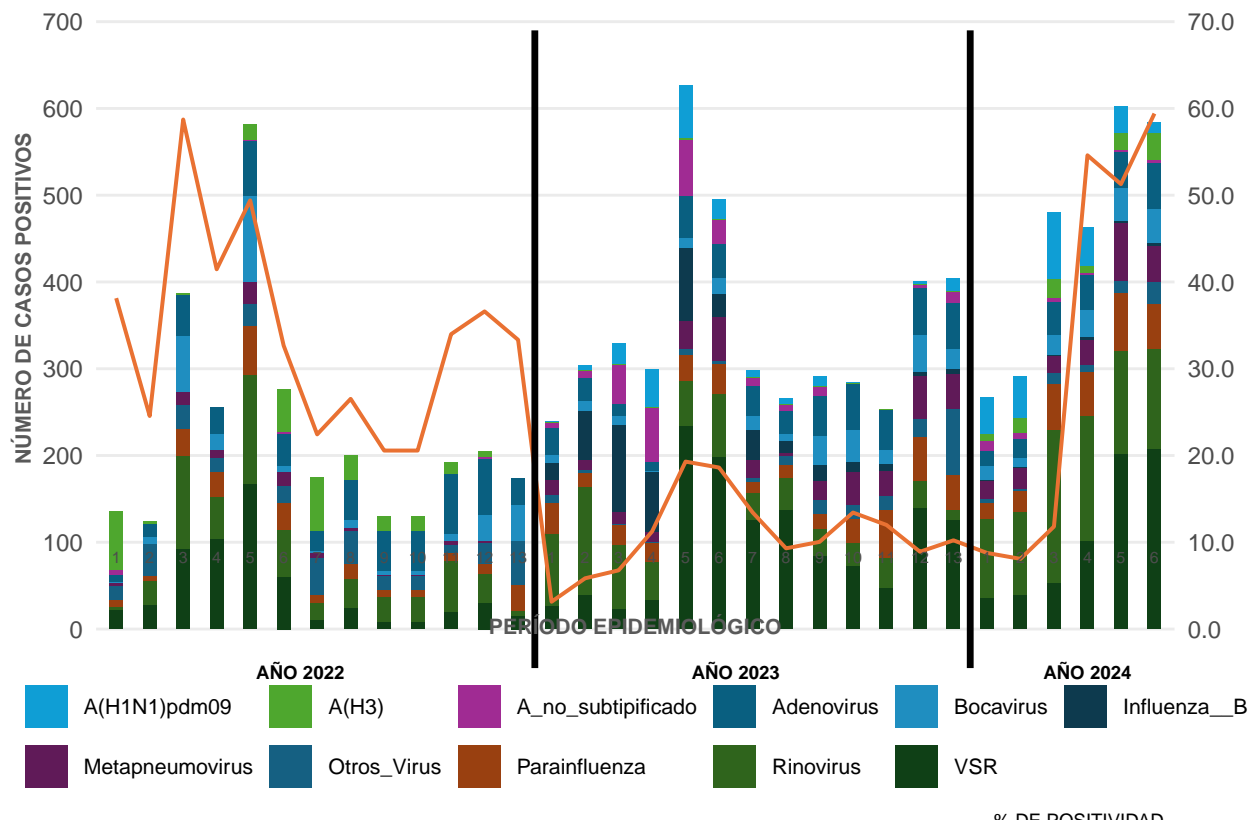
```
select(YearWeek, Percent_Positivity = `_%DE_POSITIVIDAD`) %>%
drop_na(Percent_Positivity) # Remove any NA values in Percent_Positivity

# VISUALIZING

# Calculate the scaling factor for dual y-axes
scaling_factor <- 700 / 70 # Scale Cases to match a max of 700 on the left and 70% on the right
```

## Including Plots

You can also embed plots, for example:



Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.