jhucovid19_code

COVID-19: Tidy the time series (tidyr + dplyr)

Use the two JHU CSVs (confirmed + deaths). Work at the country/region level.

```
library(dplyr)
library(gt)
library(ggplot2)
library(tidyr)
library(gtsummary)
library(arsenal)
library(lubridate)
library(stringr)
library(zoo)
library(scales)
library(countrycode)

covidconfirm <-read.csv("/Users/apple/Desktop/me/WCM/semester/fall1/datasci1/week3/cla
coviddeath <-read.csv("/Users/apple/Desktop/me/WCM/semester/fall1/datasci1/week3/class
#head(covidconfirm)
```

Import & reshape

Pivot both wide time series to long over date columns. Convert date columns (strings) to Date. Standardize country names (trim spaces; treat “Korea, South” vs “South Korea”).

```
############################## confirm ####################################
#Pivot both wide time series to long over date columns.
covidconfirm_long <- covidconfirm %>%
  pivot_longer(
    cols = starts_with("X"),              #choose cols
    names_to = "date",                    #name col to store the date
    values_to = "number_confirmed"        #name col to store the values
  )
head(covidconfirm_long)
```

```
# A tibble: 6 × 6
  Province.State Country.Region   Lat  Long date     number_confirmed
  <chr>          <chr>          <dbl> <dbl> <chr>               <dbl>
1 <NA>           Afghanistan     33.9  67.7 X1.22.20                0
2 <NA>           Afghanistan     33.9  67.7 X1.23.20                0
3 <NA>           Afghanistan     33.9  67.7 X1.24.20                0
4 <NA>           Afghanistan     33.9  67.7 X1.25.20                0
5 <NA>           Afghanistan     33.9  67.7 X1.26.20                0
6 <NA>           Afghanistan     33.9  67.7 X1.27.20                0
```

```
#Convert date columns (strings) to Date.
#remove X at the start
covidconfirm_clean<-covidconfirm_long %>%
```

```
  mutate(date = stringr::str_remove(date, "^X")) %>%
  #separate y\m\d into different cols
  #create new cols
  separate(date, into = c("mm","dd","yy"), sep = "\\.", #need \\ to use .
           #convert into numeric
           convert = TRUE, extra = "merge") %>%
  mutate(year = 2000 + yy,
         date = make_date(year, mm, dd))%>%


  # select the cols
  select(Province.State, Country.Region, Lat, Long, date, number_confirmed) %>%
#Standardize country names (trim spaces; treat “Korea, South” vs “South Korea” if pres
  #change the name
  mutate(
    Country_Region = str_trim(Country.Region),  #remove space
    #modify country colname
    Country_Region = case_when(
      Country_Region %in% c("Korea, South", "South Korea") ~ "South Korea",
      Country_Region %in% c("Korea, North", "North Korea") ~ "North Korea",
      TRUE ~ Country_Region
    )
  ) %>%
  select(-Country.Region)
#covidconfirm_clean
```

```
############################# death #####################################

coviddeath_long <- coviddeath %>%
  pivot_longer(
    cols = starts_with("X"),             #choose cols
    names_to = "date",                   #name col to store the date
    values_to = "number_death"       #name col to store the values
  )

#remove X at the start
covideath_clean<-coviddeath_long %>%
  mutate(date = stringr::str_remove(date, "^X")) %>%
  #separate y\m\d into different cols
  #create new cols
  separate(date, into = c("mm","dd","yy"), sep = "\\.", #need \\ to use .
           #convert into numeric
           convert = TRUE, extra = "merge") %>%
  mutate(year = 2000 + yy,
         date = make_date(year, mm, dd))%>%


  # select tghe cols
  select(Province.State, Country.Region, Lat, Long, date, number_death) %>%
  #change the name
  mutate(
    Country_Region = str_trim(Country.Region),  #remove space
    #modify country colname
```

```
    Country_Region = case_when(
      Country_Region %in% c("Korea, South", "South Korea") ~ "South Korea",
      Country_Region %in% c("Korea, North", "North Korea") ~ "North Korea",
      TRUE ~ Country_Region
    )
  ) %>%
  select(-Country.Region)
#covideath_clean
```

Aggregate

Aggregate to country-date (sum across provinces). Verify no double-counting

```
############################# confirm ################################
#Aggregate to country-date (sum across provinces). Verify no double-counting.
#aggregate
covid_confirm_country_date <- covidconfirm_clean %>%
  group_by(Country_Region, date) %>%  #group by country and region
  summarise(
    total_confirmed = sum(number_confirmed, na.rm = TRUE),  #sum
    province_count = n()  #This number is for further validation
  ) %>%
  ungroup()

#filter(covid_confirm_country_date,Country_Region=="China")
############################# death ####################################
covid_death_country_date <- covideath_clean %>%
  group_by(Country_Region, date) %>%  #group by country and region
  summarise(
    total_death = sum(number_death, na.rm = TRUE),  #sum
    province_count = n()  #This number is for further validation
  ) %>%
  ungroup()
```

Daily increments

Compute new cases and new deaths by countries Replace small negative blips with NA (data rectifications)

```
############################# confirm ################################
covid_confirm_country_date_new <- covid_confirm_country_date %>%
  arrange(Country_Region, date) %>%
  group_by(Country_Region) %>%
  mutate(
    new_confirmed = total_confirmed - lag(total_confirmed),  # daily increment
    new_confirmed = ifelse(new_confirmed < 0, NA, new_confirmed) # replace negatives w
  ) %>%
  ungroup()
#covid_confirm_country_date_new
#head(filter(covid_confirm_country_date_new,Country_Region=="China"))
############################# death ################################
covid_death_country_date_new <-  covid_death_country_date %>%
  arrange(Country_Region, date) %>%
```

```
  group_by(Country_Region) %>%
  mutate(
    new_death = total_death - lag(total_death),  # daily increment
    new_death = ifelse(new_death < 0, NA, new_death) # replace negatives with NA
  ) %>%
  ungroup()
```

7-day average

#####Compute 7-day average new cases and new death

```
#Compute 7-day average new cases and new death
############################## confirm ################################
covid_confirm_country_date_avg <- covid_confirm_country_date_new %>%
  group_by(Country_Region) %>%
  arrange(date) %>%
  mutate(
    new_confirmed_7day = rollmean(new_confirmed, k = 7, fill = NA, align = "right")#7
  ) %>%
  ungroup()
#head(filter(covid_death_country_date_avg,Country_Region=="China"),15)

############################## death ################################
covid_death_country_date_avg <- covid_death_country_date_new %>%
  group_by(Country_Region) %>%
  arrange(date) %>%
  mutate(
    new_death_7day = rollmean(new_death, k = 7, fill = NA, align = "right")
  ) %>%
  ungroup()
covid_confirm_country_date_avg
```

```
# A tibble: 229,743 × 6
   Country_Region      date       total_confirmed province_count new_confirmed
   <chr>               <date>               <dbl>          <int>         <dbl>
 1 Afghanistan         2020-01-22               0              1            NA
 2 Albania             2020-01-22               0              1            NA
 3 Algeria             2020-01-22               0              1            NA
 4 Andorra             2020-01-22               0              1            NA
 5 Angola              2020-01-22               0              1            NA
 6 Antarctica          2020-01-22               0              1            NA
 7 Antigua and Barbuda 2020-01-22               0              1            NA
 8 Argentina           2020-01-22               0              1            NA
 9 Armenia             2020-01-22               0              1            NA
10 Australia           2020-01-22               0              8            NA
# ℹ 229,733 more rows
# ℹ 1 more variable: new_confirmed_7day <dbl>
```

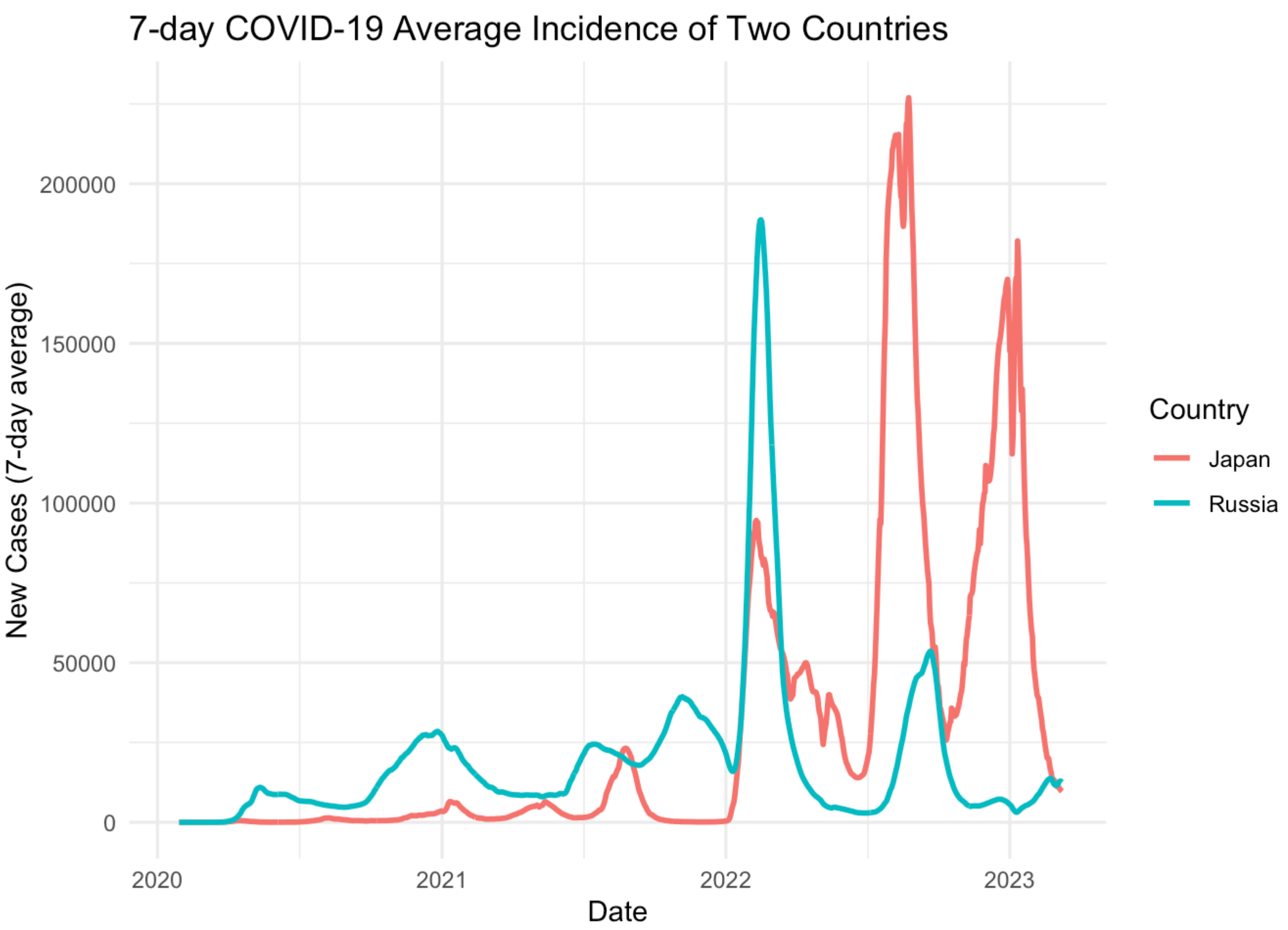
Peaks

For each country, find the top 2 peaks (dates and values) separately for new cases and new deaths, using the variables names: new_cases_ma7 and new_deaths_ma7 .

Return a table showing the top 10 countries ranked by maximum incidence. Pick two countries from the top-10 list and plot new_cases_ma7 over time (lines, diferent colors, labeled legend, sensible date breaks).

```
#name new variables
covid_confirm_country_date_avg <- covid_confirm_country_date_avg %>%
  rename(new_cases_ma7 = new_confirmed_7day)
covid_death_country_date_avg <- covid_death_country_date_avg %>%
  rename(new_deaths_ma7 = new_death_7day)

covid_country_date <- covid_confirm_country_date_avg %>%
  left_join(
    covid_death_country_date_avg %>%
      select(Country_Region, date, new_deaths_ma7),
    by = c("Country_Region", "date")
  )
#top2 peaks of the incidence of each country
peaks_cases <- covid_country_date %>%
  group_by(Country_Region) %>%
  arrange(desc(new_cases_ma7)) %>%
  slice_head(n = 2) %>%
  mutate(type = "cases")

#top2 peaks of the death cases of each country
peaks_deaths <- covid_country_date %>%
  group_by(Country_Region) %>%
  arrange(desc(new_deaths_ma7)) %>%
  slice_head(n = 2) %>%
  mutate(type = "deaths")

#bind
peaks_all <- bind_rows(peaks_cases, peaks_deaths) %>%
  ungroup()

top10_countries <- covid_country_date %>%
  group_by(Country_Region) %>%
  summarise(max_incidence = max(new_cases_ma7, na.rm = TRUE)) %>%
  arrange(desc(max_incidence)) %>%
  slice_head(n = 10)

#top10_countries



plot_data <- covid_country_date %>%
  filter(Country_Region %in% c("Japan", "Russia"))

ggplot(plot_data, aes(x = date, y = new_cases_ma7, color = Country_Region)) +
  geom_line(size = 1) +
  labs(
    title = "7-day COVID-19 Average Incidence of Two Countries ",
    x = "Date",
    y = "New Cases (7-day average)",
    color = "Country"
```

```
  ) +
  theme_minimal()
```



Japan and Russia show very different epidemic patterns over time. Russia experienced earlier and more frequent peaks in 2020–2021, with a large surge in late 2021, followed by a sharp decline. Japan, by contrast, had relatively low incidence until mid-2022, when it saw very large and prolonged waves, peaking much higher than Russia. This suggests that the timing and scale of COVID-19 waves varied substantially between the two countries, likely reflecting differences in outbreak timing, interventions, and variant spread.

COVID-19: Summary tables (gtsummary)

Pick a snapshot date. Create continent labels with countrycode.

gtsummary Table 1

Build a summary table using tbl_summary stratified by continent for new_cases_ma7 and new_deaths_ma7 (continuous) and a high-incidence flag (categorical).

The high-incidence is defined as above overall qunatile level 0.75. (Hint: use countrycode package to extract continent)

Use type = “continuous2” for two-line stats (mean (SD) + median [IQR]); add overall counts, p-values, and clearly labeled units.

```
#choose a date
coviddate<-as.Date("2021-01-06")
covid_data<-covid_country_date %>%
  filter(date ==coviddate)
# use countrycode package to extract continent
covid_data_code<-covid_data%>%
  mutate(
    continent=countrycode(sourcevar=Country_Region,
                          origin="country.name",
                          destination="continent")
  )

q75<-quantile(covid_data_code$new_cases_ma7, 0.75, na.rm = TRUE)
#above overall quantile level 0.75.
covid_snapshot<-covid_data_code%>%
  mutate(
    high_incidence=ifelse(new_cases_ma7>q75,"High","Low/Medium")
  )

library(gtsummary)
#summary(covid_snapshot)
ex1 <-covid_snapshot %>%
  dplyr::select(continent, new_cases_ma7, new_deaths_ma7, high_incidence) %>%
  tbl_summary(by =continent)
```

```
6 missing rows in the "continent" column have been removed.
```

```
ex2<-covid_snapshot%>%
  dplyr::select(continent, new_cases_ma7, new_deaths_ma7, high_incidence) %>%
  tbl_summary(
    by=continent,
    type=list(new_cases_ma7~"continuous2",new_deaths_ma7~"continuous2"),
    statistic=list(
      all_continuous() ~ c("{mean} ({sd})",
                           "{median} [{p25}, {p75}]"),
      all_categorical() ~ "{n} / {N} ({p}%)"
    ),
    label=list(
      new_cases_ma7~"New Cases",
      new_deaths_ma7~"New Deaths",
      high_incidence ~ "High Incidence"
    ),
    digits = list(all_continuous() ~ 1  )

  )  %>%
  add_overall() %>%
  add_p() %>%
  modify_caption("**COVID-19 Snapshot on 2021-01-06 by Continent**")
```

```
6 missing rows in the "continent" column have been removed.
```

```
#packageVersion("gtsummary")
```

```
#ex2
```

Efect sizes

Add a difference column comparing Europe vs Americas using add_difference. For continuous variables, set 2 significant figures, for categorical variables, set 1 decimal. (Hint: use style_sigfig and style_percent).

Hint: Pay attention to NAs. Ensure the by column (here continent) has exactly two levels afer filtering. Use droplevels() (or forcats::fct_drop) to remove lefover factor level

```
#Europe vs Americas
ex3 <- covid_snapshot %>%
  filter(continent %in% c("Europe", "Americas")) %>%
  droplevels() %>%
  select(continent, new_cases_ma7, new_deaths_ma7, high_incidence) %>%

  tbl_summary(
    by = continent,
    type = list(
      new_cases_ma7 ~ "continuous2",
      new_deaths_ma7 ~ "continuous2"
    ),
    statistic = list(
      all_continuous() ~ c("{mean} ({sd})", "{median} [{p25}, {p75}]"),
      all_categorical() ~ "{n} / {N} ({p}%)"
    ),
    label = list(
      new_cases_ma7 ~ "New Cases (7-day avg)",
      new_deaths_ma7 ~ "New Deaths (7-day avg)",
      high_incidence ~ "High Incidence"
    ),
    missing = "no"
  ) %>%

  #difference(Europe vs Americas)
  add_difference(
    test = list(
      all_continuous() ~ "t.test",
      all_categorical() ~ "chisq.test"
    ),
    estimate_fun = list(
      all_continuous()  ~ function(x) style_sigfig(x, digits = 2),
      all_categorical() ~ function(x) style_percent(x, digits = 1)
    )
  ) %>%

  modify_caption("**COVID-19 Europe vs Americas: Effect Sizes**")

ex3
```

COVID-19 Europe vs Americas: Effect Sizes

Characteristic	Americas N = 35[1]	Europe N = 44[1]	Difference[2]	95% CI[2]	p-value[2]
New Cases (7-day avg)			4,121	-9,854, 18,097	0.6
Mean (SD)	9,314 (39,858)	5,192 (9,873)			
Median [Q1, Q3]	255 [13, 1,646]	1,729 [389, 6,297]			
New Deaths (7-day avg)			39	-133, 211	0.7
Mean (SD)	144 (478)	105 (185)			
Median [Q1, Q3]	3 [0, 44]	37 [5, 99]			
High Incidence					
High	10 / 35 (29%)	24 / 44 (55%)			
Low/Medium	25 / 35 (71%)	20 / 44 (45%)			

[1] n / N (%)

[2] Welch Two Sample t-test

Abbreviation: CI = Confidence Interval

##Join with OWID metadata: per-capita analysis and plot

From OWID, keep: iso_code`, location (country), continent, and population. Remove duplicates. Show glimpse() of these 4 columns.

```
#read csv
owid_covid_url <- "https://raw.githubusercontent.com/owid/covid-19-data/master/public/
owid_covid <- read.csv(owid_covid_url, stringsAsFactors = FALSE, check.names = FALSE)

owid_covid_clean<-owid_covid%>%
  select(iso_code, location, continent,population)%>%
  distinct()             #remove duplicates
glimpse(owid_covid_clean)
```

```
Rows: 255
Columns: 4
$ iso_code   <chr> "AFG", "OWID_AFR", "ALB", "DZA", "ASM", "AND", "AGO", "AIA"…
$ location   <chr> "Afghanistan", "Africa", "Albania", "Algeria", "American Sa…
$ continent  <chr> "Asia", "", "Europe", "Africa", "Oceania", "Europe", "Afric…
$ population <dbl> 41128772, 1426736614, 2842318, 44903228, 44295, 79843, 3558…
```

Check unmatched countries the tidy JHU dataset has country names.

Use anti_join() both ways to find unmatched names between JHU and OWID. Show the first 5 rows of each. Write 1 bullet. Hint: use anti_join

```
jhu_not_in_owid <- covid_country_date %>%
  anti_join(owid_covid_clean,  c("Country_Region" = "location"))
#different col names need c()
owid_not_in_jhu <- owid_covid_clean %>%
  anti_join(covid_country_date, by = c( "location"="Country_Region"))

head(jhu_not_in_owid, 5)
```

```
# A tibble: 5 × 7
  Country_Region      date       total_confirmed province_count new_confirmed
  <chr>               <date>               <dbl>          <int>         <dbl>
1 Antarctica          2020-01-22               0              1            NA
2 Burma               2020-01-22               0              1            NA
3 Cabo Verde          2020-01-22               0              1            NA
4 Congo (Brazzaville) 2020-01-22               0              1            NA
5 Congo (Kinshasa)    2020-01-22               0              1            NA
# ℹ 2 more variables: new_cases_ma7 <dbl>, new_deaths_ma7 <dbl>
```

```
head(owid_not_in_jhu, 5)
```

```
  iso_code       location     continent population
1 OWID_AFR         Africa               1426736614
2      ASM American Samoa       Oceania      44295
3      AIA       Anguilla North America      15877
4      ABW          Aruba North America     106459
5 OWID_ASI           Asia               4721383370
```

The unmatched country names are mainly due to naming differences.For example, “Burma” (JHU) vs “Myanmar” (OWID), “Cabo Verde” (JHU) vs “Cape Verde” (OWID), “Congo (Brazzaville)” (JHU) vs “Republic of Congo” (OWID), and “Congo (Kinshasa)” (JHU) vs “Democratic Republic of Congo” (OWID).

c. Join + compute per-capita rates (8 pts) lef_join() JHU tidy data with OWID metadata. Compute: cases_per100k : cumulative confirmed cases per 100,000 population. new_cases_ma7_per100k : 7-day average of new cases per 100,000 population. Show the first 3 rows (country, date, population, confirmed, new_cases_ma7_per100k).

```
summary(owid_covid_clean)
```

```
   iso_code           location          continent           population       
 Length:255         Length:255         Length:255         Min.   :4.700e+01  
 Class :character   Class :character   Class :character   1st Qu.:4.864e+05  
 Mode  :character   Mode  :character   Mode  :character   Median :5.643e+06  
                                                          Mean   :1.270e+08  
                                                          3rd Qu.:2.823e+07  
                                                          Max.   :7.975e+09  
```

```r
covid_joined<-covid_country_date %>%
  left_join(owid_covid_clean,by =c("Country_Region"="location")) %>%
  mutate(
    cases_per100k=total_confirmed/population*100000,
    new_cases_ma7_per100k=new_cases_ma7/population*100000
  )

covid_joined_show<-select(covid_joined,Country_Region, date, population, total_confirm

#summary(covid_joined)
head(covid_joined_show, 3)
```

```
# A tibble: 3 × 5
  Country_Region date       population total_confirmed new_cases_ma7_per100k
  <chr>          <date>          <dbl>           <dbl>                 <dbl>
1 Afghanistan    2020-01-22   41128772               0                    NA
2 Albania        2020-01-22    2842318               0                    NA
3 Algeria        2020-01-22   44903228               0                    NA
```

```r
#summary(covid_joined$date)
#summary(covid_snapshot$date)
```

Snapshot ranking

Pick snapshot_date <- as.Date("2021-01-15") . Find the top 15 countries by new_cases_ma7_per100k . - Show that 15-row table (country, continent, population, new_cases_ma7_per100k rounded to 1 decimal).

```r
str(covid_joined$date)
```

```
 Date[1:229743], format: "2020-01-22" "2020-01-22" "2020-01-22" "2020-01-22" "2020-01-
22" ...
```

```r
unique(head(covid_joined$date, 10))#validate the same date type
```

```
[1] "2020-01-22"
```

```r
snapshot_date <- as.Date("2021-01-15")

top15_snapshot <- covid_joined %>%
  filter(date == snapshot_date) %>%
  arrange(desc(new_cases_ma7_per100k)) %>%
  select(Country_Region, continent, population, new_cases_ma7_per100k) %>%
  # rounded to 1 decimal
  mutate(new_cases_ma7_per100k = round(new_cases_ma7_per100k, 1)) %>%
  slice_head(n = 15)

top15_snapshot
```

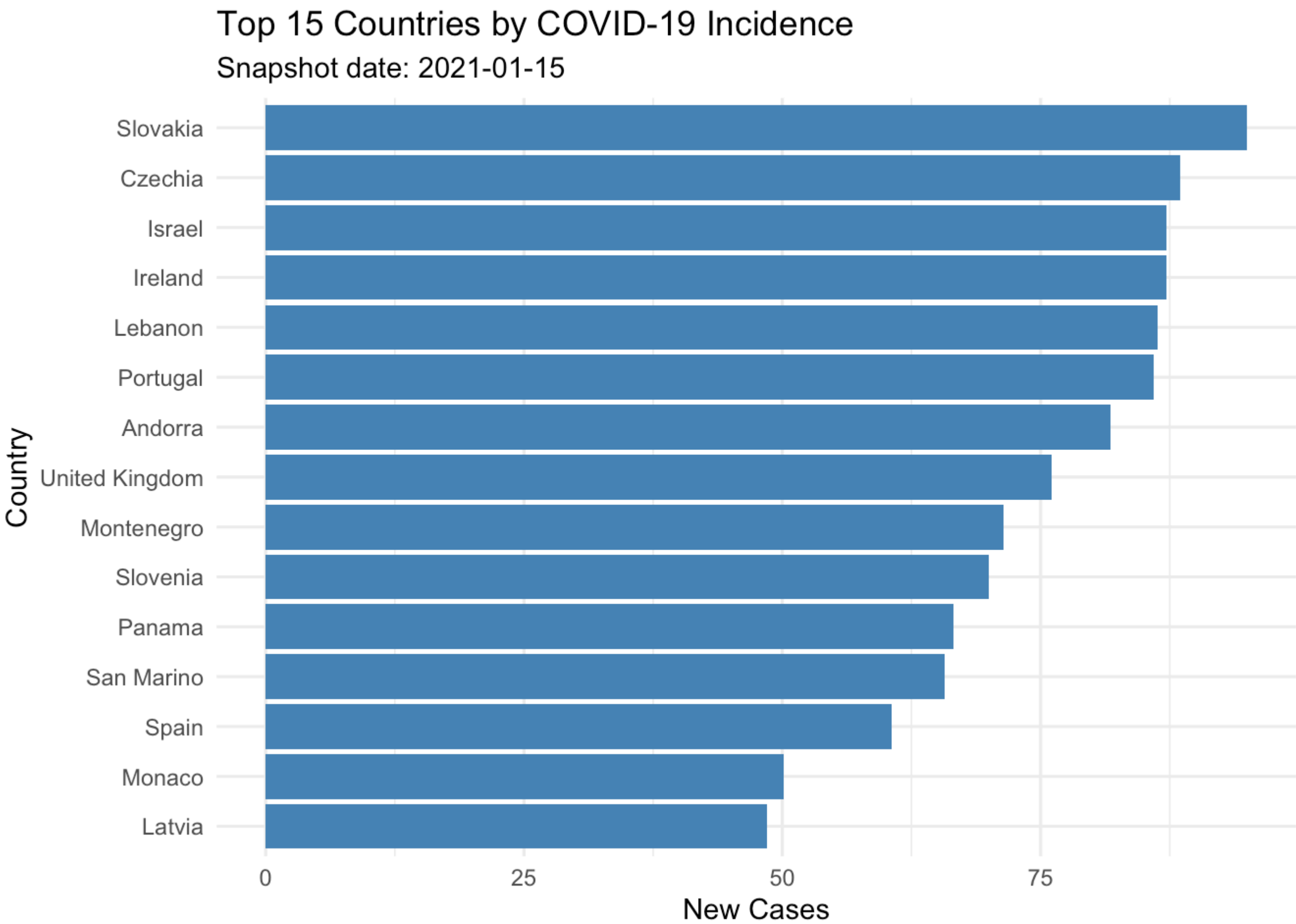
```
# A tibble: 15 × 4
   Country_Region continent     population new_cases_ma7_per100k
```

```
   <chr>          <chr>              <dbl>                     <dbl>
 1 Slovakia       Europe           5643455                      95
 2 Czechia        Europe          10493990                      88.5
 3 Israel         Asia             9449000                      87.2
 4 Ireland        Europe           5023108                      87.2
 5 Lebanon        Asia             5489744                      86.3
 6 Portugal       Europe          10270857                      85.9
 7 Andorra        Europe             79843                      81.8
 8 United Kingdom Europe          67508936                      76.1
 9 Montenegro     Europe            627082                      71.4
10 Slovenia       Europe           2119843                      70
11 Panama         North America    4408582                      66.6
12 San Marino     Europe             33690                      65.7
13 Spain          Europe          47558632                      60.6
14 Monaco         Europe             36491                      50.1
15 Latvia         Europe           1850654                      48.5
```

Plot

Bar chart of these top 15 countries sorted descending by new_cases_ma7_per100k . Rotate x-axis labels for readability; subtitle should include the date

```
g<-ggplot(top15_snapshot,aes(x=reorder(Country_Region,new_cases_ma7_per100k), y =new_c
  geom_col(fill = "steelblue") +
  coord_flip() +   #Rotate x-axis labels
  labs(
    title = "Top 15 Countries by COVID-19 Incidence",
    #subtitle should include the date.
    subtitle = paste("Snapshot date:", snapshot_date),
    x = "Country",
    y = "New Cases"
  ) +
  theme_minimal()
g
```


Top 15 Countries by COVID-19 Incidence
Snapshot date: 2021-01-15
Slovakia
Czechia
Israel
Ireland
Lebanon
Portugal
Andorra
United Kingdom
Montenegro
Slovenia
Panama
San Marino
Spain
Monaco
Latvia
Country
0
25
50
75
New Cases