The main reason for me sharing this code is that I did not find code that merges standardized country level identifiers to to the data in a semi-automatic way. These identifiers are important whenever you want to merge additional country level data for additional analyses, like, e.g. population data to calculate per capita measures. Also, I thought that the steps presented below are nice small case on how to obtain, tidy and merge country-level data from public sources.

Pulling and tidying the Johns Hopkins Covid-19 data to long format

So, without much ado, here is the code for pulling and tidying the data.

```
library(tidyverse)
library(lubridate)
library(rvest)
library(stringdist)
# Function to read the raw CSV files. The files are aggregated to the country
# level and then converted to long format
clean_jhd_to_long <- function(df) {</pre>
 df str <- deparse(substitute(df))</pre>
  var str <- substr(df str, 1, str length(df str) - 4)</pre>
  df %>% group_by(`Country/Region`) %>%
    filter(`Country/Region` != "Cruise Ship") %>%
    select(-`Province/State`, -Lat, -Long) %>%
    mutate at(vars(-group cols()), sum) %>%
    distinct() %>%
    ungroup() %>%
    rename(country = `Country/Region`) %>%
    pivot_longer(
      -country,
      names to = "date str",
      values to = var str
    ) 응>응
    mutate(date = mdy(date str)) %>%
    select(country, date, !! sym(var str))
}
confirmed raw <- read csv ("https://raw.githubusercontent.com/CSSEGISandData/COVID-19/
master/csse_covid_19_data/csse_covid_19_time_series/time_series_covid19_confirmed_global.csv")
deaths raw <- read csv("https://raw.githubusercontent.com/CSSEGISandData/COVID-19/
master/csse_covid_19_data/csse_covid_19_time_series/time_series_covid19_deaths_global.csv")
jh covid19 data <- clean jhd to long(confirmed raw) %>%
  full_join(clean_jhd_to_long(deaths_raw))
# Next, I pull official country level indicators from the UN Statstics Division
# to get country level identifiers.
jhd countries <- tibble(country = unique(jh covid19 data$country)) %>%
arrange(country)
ctry ids <- read html("https://unstats.un.org/unsd/methodology/m49/") %>%
 html_table()
```

```
un m49 <- ctry ids[[1]]
colnames(un m49) <- c("country", "un m49", "iso3c")</pre>
# Merging by country name is messy. I start with a fuzzy matching approach
# using the {stringdist} package
ctry names dist <- matrix(NA, nrow = nrow(jhd countries), ncol = nrow(un m49))
for(i in 1:length(jhd countries$country)) {
  for(j in 1:length(un m49$country)) {
    ctry names dist[i,j] <- stringdist(tolower(jhd countries$country[i]),</pre>
                                 tolower(un_m49$country[j]))
  }
}
min ctry name dist <- apply(ctry names dist, 1, min)</pre>
matched ctry names <- NULL
for(i in 1:nrow(jhd countries)) {
  un m49 row <- match(min ctry name dist[i], ctry names dist[i,])
  if (length(which(ctry_names_dist[i,] %in% min_ctry_name_dist[i])) > 1)
un m49 row <- NA
  matched ctry names <- rbind(matched ctry names,
                         tibble(
                            jhd_countries_row = i,
                           un m49 row = un m49 row,
                           jhd ctry name = jhd countries$country[i],
                           un m49 name = ifelse(is.na(un m49 row), NA,
                                                 un m49$country[un m49 row])
                         ))
}
# This matches most cases well but some cases need to be adjusted by hand.
# In addition there are two jurisdictions (Kosovo, Taiwan)
# that cannot be matched as they are no 'country' as far as the U.N.
# Statistics Devision is concerned.
# WATCH OUT: The data from JHU is subject to change without notice.
# New countries are being added and names/spelling might change.
# Also, in the long run, the data provided by the UNSD might change.
# Inspect 'matched ctry names' before using the data.
matched ctry names$un m49 row[matched ctry names$jhd ctry name == "Bolivia"] <-</pre>
matched ctry names$un m49 row[matched ctry names$jhd ctry name == "Brunei"] <-</pre>
matched ctry names$un m49 row[matched ctry names$jhd ctry name == "Congo
(Brazzaville)"] <- 54
matched ctry names$un m49 row[matched ctry names$jhd ctry name == "Congo
(Kinshasa)"] <- 64
matched ctry names$un m49 row[matched ctry names$jhd ctry name == "East Timor"]
matched ctry names$un m49 row[matched ctry names$jhd ctry name == "Iran"] <- 109
matched ctry names$un m49 row[matched ctry names$jhd ctry name == "Korea,
South"] <- 180
matched ctry names$un m49 row[matched ctry names$jhd ctry name == "Kosovo"] <-</pre>
```

```
NΑ
matched ctry names$un m49 row[matched ctry names$jhd ctry name == "Moldova"] <-</pre>
matched ctry names$un m49 row[matched ctry names$jhd ctry name == "Russia"] <-</pre>
184
matched ctry names$un m49 row[matched ctry names$jhd ctry name == "Taiwan*"] <-</pre>
matched ctry names$un m49 row[matched ctry names$jhd ctry name == "Tanzania"] <-</pre>
matched ctry names$un m49 row[matched ctry names$jhd ctry name == "United
Kingdom"] <- 235
matched ctry names$un m49 row[matched ctry names$jhd ctry name == "US"] <- 238</pre>
matched ctry names$un m49 row[matched ctry names$jhd ctry name == "Venezuela"]
# Last Step: Match country identifier data and save file (commented out here)
jhd countries %>%
  left join(matched ctry names %>%
              select(jhd ctry name, un m49 row),
            by = c(country = "jhd ctry name")) %>%
  left join(un m49 %>% mutate(un m49 row = row number()), by = "un m49 row") %>%
  rename(country = country.x) %>%
  select(country, iso3c) -> jhd countries
jh covid19 data <- jh covid19 data %>% left join(jhd countries) %>%
  select(country, iso3c, date, confirmed, deaths)
# write csv(jh covid19 data, sprintf("jh covid19 data %s.csv", Sys.Date()))
```

The code essentially follows the following steps

- Read the relevant CSV files for confirmed cases, casualties and recovered patients from the Github repository
- Aggregate the data at country level and discard data that is not required
- Scrape official country identifiers from the U.N. Statistics Division
- Fuzzy match these to the countries present in the JH data. Apply manual corrections that were correct based on the data pulled March 23, 2020 (check the match when you use this code later)
- Merge the identifiers with the longitudinal data and save the result as a tidy CSV file.

Merging some World Bank data

The next code snippet pulls some World Bank data using the {wbstats} package.

```
rename (year = date,
           iso2c = iso2c.y,
           country = country.y) %>%
    select(iso3c, iso2c, country, region, income, everything()) %>%
    select(-iso2c.x, -country.x) %>%
    filter(!is.na(NY.GDP.PCAP.KD),
           region != "Aggregates") -> wb data
  wb data$year <- as.numeric(wb data$year)</pre>
  wb data def<- left join(data.frame(var name = names(wb data),</pre>
                                      stringsAsFactors = FALSE),
                           wb data def, by = "var name")
  wb data def$var def[1:6] <- c(</pre>
    "Three letter ISO country code as used by World Bank",
    "Two letter ISO country code as used by World Bank",
    "Country name as used by World Bank",
    "World Bank regional country classification",
    "World Bank income group classification",
    "Calendar year of observation"
  wb data def$type = c("cs id", rep("factor", 4), "ts id",
                        rep("numeric", ncol(wb_data) - 6))
 return(list(wb data, wb data_def))
}
vars <- c("SP.POP.TOTL", "AG.LND.TOTL.K2", "EN.POP.DNST", "EN.URB.LCTY",
"SP.DYN.LEOO.IN", "NY.GDP.PCAP.KD")
wb list <- pull worldbank data(vars)</pre>
wb data <- wb list[[1]]</pre>
wb_data_def <- wb_list[[2]]</pre>
wb data %>%
  group by(iso3c) %>%
  arrange(iso3c, year) %>%
  summarise(
    population = last(na.omit(SP.POP.TOTL)),
    land_area_skm = last(na.omit(AG.LND.TOTL.K2)),
    pop density = last(na.omit(EN.POP.DNST)),
    pop largest city = last(na.omit(EN.URB.LCTY)),
    gdp_capita = last(na.omit(NY.GDP.PCAP.KD)),
    life expectancy = last(na.omit(SP.DYN.LE00.IN))
  ) %>% left join(wb data %>% select(iso3c, region, income) %>% distinct()) ->
wb cs
# write_csv(wb_cs, "jh_add_wbank_data.csv")
```

Use the data

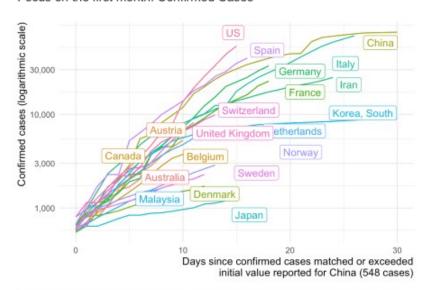
And finally, some code to use the data for typical event time visualizations.

```
suppressPackageStartupMessages({
    library(tidyverse)
    library(lubridate)
    library(gghighlight)
    library(ggrepel)
})

dta <- read_csv(
    "https://joachim-gassen.github.io/data/jh_covid19_data_2020-03-24.csv",</pre>
```

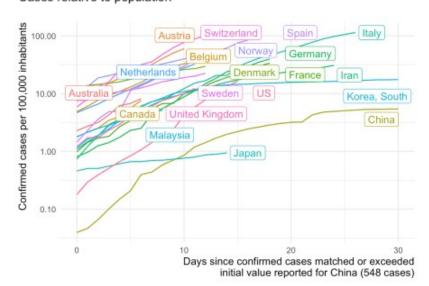
```
col types = cols()
) 응>응
  mutate(date = ymd(date))
wb cs <- read csv(
  "https://joachim-gassen.github.io/data/jh_add_wbank_data.csv",
  col types = cols()
# I define event time zero where, for a given country, the confirmed
# cases match or exceed the Chinese case number at the beginning of the
# data so that all countries can be compared across event time.
# Also a require each country to have at least 7 days post event day 0
dta %>%
 group by (country) %>%
  filter(confirmed >= min(dta$confirmed[dta$country == "China"])) %>%
  summarise(edate confirmed = min(date)) -> edates confirmed
dta %>%
  left_join(edates_confirmed, by = "country") %>%
   edate confirmed = as.numeric(date - edate confirmed)
  ) 응>응
  filter(edate confirmed >= 0) %>%
  group by (country) %>%
  filter (n() >= 7) %>%
 ungroup() %>%
  left join(wb cs, by = "iso3c") %>%
 mutate(
   confirmed le5pop = le5*confirmed/population
  ) -> df
lab notes <- paste0(</pre>
  "Data as provided by Johns Hopkins University Center for Systems Science ",
  "and Engineering (JHU CSSE)\nand obtained on March 23, 2020. ",
  "The sample is limited to countries with at least seven days of positive\n",
  "event days data. Code and walk-through: https://joachim-gassen.github.io."
lab x axis confirmed <- sprintf(paste(</pre>
  "Days since confirmed cases matched or exceeded\n",
  "initial value reported for China (%d cases) \n"
), min(dta$confirmed[dta$country == "China"]))
gg my blob <- list(
  scale y continuous(trans='log10', labels = scales::comma),
  theme minimal(),
  theme (
    plot.title.position = "plot",
    plot.caption.position = "plot",
    plot.caption = element text(hjust = 0),
    axis.title.x = element text(hjust = 1),
    axis.title.y = element text(hjust = 1),
  ),
  labs(caption = lab notes,
       x = lab x axis confirmed,
```

Focus on the first month: Confirmed Cases



Data as provided by Johns Hopkins University Center for Systems Science and Engineering (JHU CSSE) and obtained on March 23, 2020. The sample is limited to countries with at least seven days of positive event days data. Code and walk-through: https://joachim-gassen.github.io.

Cases relative to population



Data as provided by Johns Hopkins University Center for Systems Science and Engineering (JHU CSSE) and obtained on March 23, 2020. The sample is limited to countries with at least seven days of positive event days data. Code and walk-through: https://joachim-gassen.github.io.

Wrap-Up

This is it. I hope that somebody might fight this useful. In any case, help #FlattenTheCurve and stay healthy, everybody!