

Exploratory Data Analysis of COVID-19 Data

Your Name

The Date

Section 1: Exploratory Data Analysis (EDA)

Supplementary Dataset EDA to Select Transmission Rate Proxy

```
## This subsection is dedicated to performing an Exploratory Data Analysis (EDA)
# on the supplementary COVID-19 dataset.
## The rationale for this analysis is twofold:

## 1. Comparative Data Analysis:
##   - The supplementary dataset provides a broader, global context to the
#     COVID-19 pandemic.
##   - By exploring this data, we can compare and contrast different
#     regions/countries in terms of COVID-19 impact and response.
##   - This comparative analysis is crucial to understand regional variations
#     in pandemic progression and policy effectiveness.

# 2. Data Compatibility and Integrity Check:
#   - Conducting an EDA on this dataset is essential for verifying its
#     compatibility with our primary data source.
#   - We need to ensure that the metrics and trends in this dataset align with
#     those in our primary dataset, providing a cohesive analytical base.
#   - This step is also necessary to check for data integrity issues such as
#     missing values, outliers, or inconsistencies, which could affect our
#     overall analysis.

# The insights derived from this EDA will help in framing our analysis, guiding
# subsequent data processing steps,
# and ensuring that our conclusions are based on a comprehensive understanding
# of both datasets.

# Read COVID-19 data into 'cd' dataframe
cd <- read_csv("owid-covid-data.csv")
```

```

Rows: 358803 Columns: 67
-- Column specification -----
Delimiter: ","
chr   (4): iso_code, continent, location, tests_units
dbl   (62): total_cases, new_cases, new_cases_smoothed, total_deaths, new_dea...
date  (1): date

i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.

```

```
glimpse(cd)
```

```

Rows: 358,803
Columns: 67
$ iso_code           <chr> "AFG", "AFG", "AFG", "AFG", ~
$ continent          <chr> "Asia", "Asia", "Asia", "As~
$ location            <chr> "Afghanistan", "Afghanistan~
$ date               <date> 2020-01-03, 2020-01-04, 20~
$ total_cases         <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ new_cases           <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, ~
$ new_cases_smoothed <dbl> NA, NA, NA, NA, NA, 0, 0, 0~
$ total_deaths        <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ new_deaths          <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, ~
$ new_deaths_smoothed <dbl> NA, NA, NA, NA, NA, 0, 0, 0~
$ total_cases_per_million <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ new_cases_per_million <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, ~
$ new_cases_smoothed_per_million <dbl> NA, NA, NA, NA, NA, 0, 0, 0~
$ total_deaths_per_million <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ new_deaths_per_million <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, ~
$ new_deaths_smoothed_per_million <dbl> NA, NA, NA, NA, NA, 0, 0, 0~
$ reproduction_rate   <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ icu_patients        <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ icu_patients_per_million <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ hosp_patients       <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ hosp_patients_per_million <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ weekly_icu_admissions <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ weekly_icu_admissions_per_million <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ weekly_hosp_admissions <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ weekly_hosp_admissions_per_million <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ total_tests         <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ new_tests           <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ total_tests_per_thousand <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ new_tests_per_thousand <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ new_tests_smoothed <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ new_tests_smoothed_per_thousand <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ positive_rate       <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ tests_per_case      <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ tests_units         <chr> NA, NA, NA, NA, NA, NA, NA, ~
$ total_vaccinations  <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ people_vaccinated   <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ people_fully_vaccinated <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ total_boosters      <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ new_vaccinations    <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ new_vaccinations_smoothed <dbl> NA, NA, NA, NA, NA, NA, NA, ~
$ total_vaccinations_per_hundred <dbl> NA, NA, NA, NA, NA, NA, NA, ~

```

```

$ people_vaccinated_per_hundred      <dbl> NA, NA, NA, NA, NA, NA, NA,~
$ people_fully_vaccinated_per_hundred <dbl> NA, NA, NA, NA, NA, NA, NA,~
$ total_boosters_per_hundred         <dbl> NA, NA, NA, NA, NA, NA, NA,~
$ new_vaccinations_smoothed_per_million <dbl> NA, NA, NA, NA, NA, NA, NA,~
$ new_people_vaccinated_smoothed      <dbl> NA, NA, NA, NA, NA, NA, NA,~
$ new_people_vaccinated_smoothed_per_hundred <dbl> NA, NA, NA, NA, NA, NA, NA,~
$ stringency_index                   <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, ~
$ population_density                 <dbl> 54.422, 54.422, 54.422, 54.~
$ median_age                         <dbl> 18.6, 18.6, 18.6, 18.6, 18.~
$ aged_65_older                     <dbl> 2.581, 2.581, 2.581, 2.581,~
$ aged_70_older                     <dbl> 1.337, 1.337, 1.337, 1.337,~
$ gdp_per_capita                     <dbl> 1803.987, 1803.987, 1803.98~
$ extreme_poverty                   <dbl> NA, NA, NA, NA, NA, NA, NA,~
$ cardiovasc_death_rate              <dbl> 597.029, 597.029, 597.029, ~
$ diabetes_prevalence                <dbl> 9.59, 9.59, 9.59, 9.59, 9.5~
$ female_smokers                     <dbl> NA, NA, NA, NA, NA, NA, NA,~
$ male_smokers                       <dbl> NA, NA, NA, NA, NA, NA, NA,~
$ handwashing_facilities             <dbl> 37.746, 37.746, 37.746, 37.~
$ hospital_beds_per_thousand         <dbl> 0.5, 0.5, 0.5, 0.5, 0.5, 0.~
$ life_expectancy                    <dbl> 64.83, 64.83, 64.83, 64.83,~
$ human_development_index            <dbl> 0.511, 0.511, 0.511, 0.511,~
$ population                         <dbl> 41128772, 41128772, 4112877~
$ excess_mortality_cumulative_absolute <dbl> NA, NA, NA, NA, NA, NA, NA,~
$ excess_mortality_cumulative        <dbl> NA, NA, NA, NA, NA, NA, NA,~
$ excess_mortality                   <dbl> NA, NA, NA, NA, NA, NA, NA,~
$ excess_mortality_cumulative_per_million <dbl> NA, NA, NA, NA, NA, NA, NA,~

```

```
summary(cd)
```

iso_code	continent	location	date
Length:358803	Length:358803	Length:358803	Min. :2020-01-01
Class :character	Class :character	Class :character	1st Qu.:2020-12-25
Mode :character	Mode :character	Mode :character	Median :2021-12-13
			Mean :2021-12-13
			3rd Qu.:2022-12-01
			Max. :2023-11-30

total_cases	new_cases	new_cases_smoothed	total_deaths
Min. : 1	Min. : 0	Min. : 0	Min. : 1
1st Qu.: 8355	1st Qu.: 0	1st Qu.: 0	1st Qu.: 129
Median : 72719	Median : 1	Median : 23	Median : 1349
Mean : 6862419	Mean : 9376	Mean : 9409	Mean : 86954
3rd Qu.: 784483	3rd Qu.: 244	3rd Qu.: 474	3rd Qu.: 12019
Max. :772165753	Max. :8401963	Max. :6402036	Max. :6981250
NA's :38175	NA's :9771	NA's :11030	NA's :59717

new_deaths	new_deaths_smoothed	total_cases_per_million
Min. : 0.00	Min. : 0.000	Min. : 0
1st Qu.: 0.00	1st Qu.: 0.000	1st Qu.: 2693
Median : 0.00	Median : 0.143	Median : 29666
Mean : 83.52	Mean : 83.807	Mean :104442
3rd Qu.: 2.00	3rd Qu.: 4.857	3rd Qu.:138729
Max. :57889.00	Max. :14822.000	Max. :746008
NA's :9714	NA's :10944	NA's :38175

new_cases_per_million	new_cases_smoothed_per_million	total_deaths_per_million
Min. : 0.00	Min. : 0.00	Min. : 0.00

1st Qu.:	0.00	1st Qu.:	0.03	1st Qu.:	61.64
Median :	0.06	Median :	5.95	Median :	388.26
Mean :	141.89	Mean :	142.40	Mean :	883.47
3rd Qu.:	32.89	3rd Qu.:	78.60	3rd Qu.:	1382.95
Max. :	228872.02	Max. :	37241.78	Max. :	6511.88
NA's :	9771	NA's :	11030	NA's :	59717
new_deaths_per_million new_deaths_smoothed_per_million reproduction_rate					
Min. :	0.000	Min. :	0.000	Min. :	-0.07
1st Qu.:	0.000	1st Qu.:	0.000	1st Qu.:	0.72
Median :	0.000	Median :	0.008	Median :	0.95
Mean :	0.887	Mean :	0.890	Mean :	0.91
3rd Qu.:	0.156	3rd Qu.:	0.541	3rd Qu.:	1.14
Max. :	603.656	Max. :	148.641	Max. :	5.87
NA's :	9714	NA's :	10944	NA's :	173986
icu_patients icu_patients_per_million hosp_patients					
Min. :	0.0	Min. :	0.0	Min. :	0
1st Qu.:	22.0	1st Qu.:	2.5	1st Qu.:	197
Median :	96.0	Median :	6.9	Median :	784
Mean :	675.1	Mean :	16.2	Mean :	3936
3rd Qu.:	434.0	3rd Qu.:	19.9	3rd Qu.:	3056
Max. :	28891.0	Max. :	180.7	Max. :	154497
NA's :	320958	NA's :	320958	NA's :	319562
hosp_patients_per_million weekly_icu_admissions					
Min. :	0.0	Min. :	0.0		
1st Qu.:	33.8	1st Qu.:	20.2		
Median :	76.9	Median :	105.0		
Mean :	129.4	Mean :	336.6		
3rd Qu.:	164.2	3rd Qu.:	408.0		
Max. :	1526.8	Max. :	4838.0		
NA's :	319562	NA's :	348489		
weekly_icu_admissions_per_million weekly_hosp_admissions					
Min. :	0.0	Min. :	0		
1st Qu.:	1.8	1st Qu.:	241		
Median :	5.1	Median :	887		
Mean :	10.2	Mean :	4325		
3rd Qu.:	13.4	3rd Qu.:	3996		
Max. :	225.0	Max. :	153977		
NA's :	348489	NA's :	335296		
weekly_hosp_admissions_per_million total_tests new_tests					
Min. :	0.0	Min. :	0.000e+00	Min. :	1
1st Qu.:	25.6	1st Qu.:	3.647e+05	1st Qu.:	2244
Median :	58.7	Median :	2.067e+06	Median :	8783
Mean :	85.4	Mean :	2.110e+07	Mean :	67285
3rd Qu.:	113.7	3rd Qu.:	1.025e+07	3rd Qu.:	37229
Max. :	712.1	Max. :	9.214e+09	Max. :	35855632
NA's :	335296	NA's :	279416	NA's :	283400
total_tests_per_thousand new_tests_per_thousand new_tests_smoothed					
Min. :	0.00	Min. :	0.00	Min. :	0
1st Qu.:	43.59	1st Qu.:	0.29	1st Qu.:	1486
Median :	234.14	Median :	0.97	Median :	6570
Mean :	924.25	Mean :	3.27	Mean :	142178
3rd Qu.:	894.37	3rd Qu.:	2.91	3rd Qu.:	32205
Max. :	32925.83	Max. :	531.06	Max. :	14769984
NA's :	279416	NA's :	283400	NA's :	254838

new_tests_smoothed_per_thousand	positive_rate	tests_per_case
Min. : 0.00	Min. :0.00	Min. : 1.0
1st Qu.: 0.20	1st Qu.:0.02	1st Qu.: 7.1
Median : 0.85	Median :0.06	Median : 17.5
Mean : 2.83	Mean :0.10	Mean : 2403.6
3rd Qu.: 2.58	3rd Qu.:0.14	3rd Qu.: 54.6
Max. :147.60	Max. :1.00	Max. :1023631.9
NA's :254838	NA's :262876	NA's :264455

tests_units	total_vaccinations	people_vaccinated
Length:358803	Min. :0.000e+00	Min. :0.000e+00
Class :character	1st Qu.:1.706e+06	1st Qu.:9.055e+05
Mode :character	Median :1.207e+07	Median :6.278e+06
	Mean :4.617e+08	Mean :2.049e+08
	3rd Qu.:9.857e+07	3rd Qu.:4.478e+07
	Max. :1.353e+10	Max. :5.630e+09
	NA's :278655	NA's :282092

people_fully_vaccinated	total_boosters	new_vaccinations
Min. :1.000e+00	Min. :1.000e+00	Min. : 0
1st Qu.:8.557e+05	1st Qu.:4.676e+05	1st Qu.: 2572
Median :5.747e+06	Median :4.674e+06	Median : 24383
Mean :1.870e+08	Mean :1.201e+08	Mean : 792131
3rd Qu.:4.272e+07	3rd Qu.:3.530e+07	3rd Qu.: 204079
Max. :5.178e+09	Max. :2.802e+09	Max. :49673299
NA's :285397	NA's :310461	NA's :292694

new_vaccinations_smoothed	total_vaccinations_per_hundred
Min. : 0	Min. : 0.00
1st Qu.: 311	1st Qu.: 39.66
Median : 4230	Median :120.74
Mean : 299839	Mean :119.07
3rd Qu.: 34106	3rd Qu.:191.56
Max. :43691637	Max. :406.90
NA's :174761	NA's :278655

people_vaccinated_per_hundred	people_fully_vaccinated_per_hundred
Min. : 0.00	Min. : 0.00
1st Qu.: 25.61	1st Qu.: 19.26
Median : 61.44	Median : 55.35
Mean : 52.21	Mean : 47.26
3rd Qu.: 77.46	3rd Qu.: 73.32
Max. :129.07	Max. :126.89
NA's :282092	NA's :285397

total_boosters_per_hundred	new_vaccinations_smoothed_per_million
Min. : 0.00	Min. : 0
1st Qu.: 4.76	1st Qu.: 129
Median : 33.74	Median : 681
Mean : 34.55	Mean : 1950
3rd Qu.: 56.64	3rd Qu.: 2565
Max. :150.47	Max. :117113
NA's :310461	NA's :174761

new_people_vaccinated_smoothed	new_people_vaccinated_smoothed_per_hundred
Min. : 0	Min. : 0.00
1st Qu.: 54	1st Qu.: 0.00
Median : 936	Median : 0.02
Mean : 110941	Mean : 0.08
3rd Qu.: 10456	3rd Qu.: 0.08

Max. :21071272		Max. :11.71	
NA's :175013		NA's :175013	
stringency_index	population_density	median_age	aged_65_older
Min. : 0.00	Min. : 0.14	Min. :15.1	Min. : 1.14
1st Qu.: 22.22	1st Qu.: 37.73	1st Qu.:22.2	1st Qu.: 3.53
Median : 42.59	Median : 90.67	Median :29.7	Median : 6.38
Mean : 42.71	Mean : 401.25	Mean :30.5	Mean : 8.70
3rd Qu.: 62.04	3rd Qu.: 222.87	3rd Qu.:38.7	3rd Qu.:13.93
Max. :100.00	Max. :20546.77	Max. :48.2	Max. :27.05
NA's :161152	NA's :54145	NA's :75516	NA's :85385
aged_70_older	gdp_per_capita	extreme_poverty	cardiovasc_death_rate
Min. : 0.53	Min. : 661.2	Min. : 0.10	Min. : 79.37
1st Qu.: 2.08	1st Qu.: 3823.2	1st Qu.: 0.60	1st Qu.:175.70
Median : 3.87	Median : 12294.9	Median : 2.50	Median :245.46
Mean : 5.50	Mean : 18968.4	Mean :13.84	Mean :264.30
3rd Qu.: 8.64	3rd Qu.: 27216.4	3rd Qu.:21.40	3rd Qu.:333.44
Max. :18.49	Max. :116935.6	Max. :77.60	Max. :724.42
NA's :78356	NA's :81125	NA's :179808	NA's :80468
diabetes_prevalence	female_smokers	male_smokers	handwashing_facilities
Min. : 0.99	Min. : 0.10	Min. : 7.70	Min. : 1.19
1st Qu.: 5.35	1st Qu.: 1.90	1st Qu.:22.60	1st Qu.: 20.86
Median : 7.20	Median : 6.30	Median :33.10	Median : 49.84
Mean : 8.56	Mean :10.79	Mean :32.91	Mean : 50.79
3rd Qu.:10.79	3rd Qu.:19.30	3rd Qu.:41.30	3rd Qu.: 82.50
Max. :30.53	Max. :44.00	Max. :78.10	Max. :100.00
NA's :66300	NA's :149976	NA's :152816	NA's :222460
hospital_beds_per_thousand	life_expectancy	human_development_index	
Min. : 0.1	Min. :53.28	Min. :0.39	
1st Qu.: 1.3	1st Qu.:69.59	1st Qu.:0.60	
Median : 2.5	Median :75.05	Median :0.74	
Mean : 3.1	Mean :73.71	Mean :0.72	
3rd Qu.: 4.2	3rd Qu.:79.46	3rd Qu.:0.83	
Max. :13.8	Max. :86.75	Max. :0.96	
NA's :113056	NA's :28656	NA's :89027	
population	excess_mortality_cumulative_absolute		
Min. :4.700e+01	Min. : -37726.1		
1st Qu.:4.490e+05	1st Qu.: 121.6		
Median :5.882e+06	Median : 5969.0		
Mean :1.286e+08	Mean : 53121.7		
3rd Qu.:2.830e+07	3rd Qu.: 37707.3		
Max. :7.975e+09	Max. :1289776.5		
	NA's :346592		
excess_mortality_cumulative	excess_mortality		
Min. : -44.2	Min. : -95.9		
1st Qu.: 1.4	1st Qu.: -1.6		
Median : 8.1	Median : 5.7		
Mean : 9.8	Mean : 11.3		
3rd Qu.: 15.4	3rd Qu.: 16.3		
Max. : 76.6	Max. :377.6		
NA's :346592	NA's :346592		
excess_mortality_cumulative_per_million			
Min. : -2752.9			
1st Qu.: 73.8			
Median : 1116.0			

```
Mean    : 1675.4
3rd Qu.: 2746.7
Max.    :10292.9
NA's    :346592
```

```
# The 'date' column contains temporal data ranging from 01-01-2020 to
# 30-11-2023, which is crucial for time series analysis.
# This allows us to track the progression of COVID-19 metrics over time and to
# examine trends, seasonality, and the impact of interventions.
# To facilitate this analysis, it's essential to ensure that the 'date' column
# is in the proper date format.
# Converting the 'date' column to R's Date type will enable accurate
# chronological ordering and time-based operations.
cd$date <- as.Date(cd$date, format="%Y-%m-%d") # Convert 'date' column to Date format.
```

```
# Check the range of dates
date_range <- range(cd$date, na.rm = TRUE)
```

```
# Format and print the date range in a more readable format
formatted_date_range <- format(date_range, "%Y-%m-%d")
cat("The date range in the dataset is from", formatted_date_range[1], "to", formatted_date_range[2], "\n")
```

The date range in the dataset is from 2020-01-01 to 2023-11-30

```
# To check for any missing dates, we can use the `seq` function to generate a complete
# sequence of dates and then identify which ones are not in the 'date' column of our dataset
all_dates <- seq(from = min(cd$date, na.rm = TRUE), to = max(cd$date, na.rm = TRUE), by = "day")
missing_dates <- setdiff(all_dates, cd$date)
```

```
# Display missing dates, if any
if (length(missing_dates) > 0) {
  cat("There are", length(missing_dates), "missing dates in the dataset:\n")
  print(missing_dates)
} else {
  cat("No missing dates in the dataset.\n")
}
```

No missing dates in the dataset.

```
unique_regions <- unique(cd$location)
print(unique_regions)
```

[1] "Afghanistan"	"Africa"
[3] "Albania"	"Algeria"
[5] "American Samoa"	"Andorra"
[7] "Angola"	"Anguilla"
[9] "Antigua and Barbuda"	"Argentina"
[11] "Armenia"	"Aruba"
[13] "Asia"	"Australia"
[15] "Austria"	"Azerbaijan"
[17] "Bahamas"	"Bahrain"
[19] "Bangladesh"	"Barbados"
[21] "Belarus"	"Belgium"
[23] "Belize"	"Benin"
[25] "Bermuda"	"Bhutan"
[27] "Bolivia"	"Bonaire Sint Eustatius and Saba"
[29] "Bosnia and Herzegovina"	"Botswana"

[31] "Brazil"	"British Virgin Islands"
[33] "Brunei"	"Bulgaria"
[35] "Burkina Faso"	"Burundi"
[37] "Cambodia"	"Cameroon"
[39] "Canada"	"Cape Verde"
[41] "Cayman Islands"	"Central African Republic"
[43] "Chad"	"Chile"
[45] "China"	"Colombia"
[47] "Comoros"	"Congo"
[49] "Cook Islands"	"Costa Rica"
[51] "Cote d'Ivoire"	"Croatia"
[53] "Cuba"	"Curacao"
[55] "Cyprus"	"Czechia"
[57] "Democratic Republic of Congo"	"Denmark"
[59] "Djibouti"	"Dominica"
[61] "Dominican Republic"	"Ecuador"
[63] "Egypt"	"El Salvador"
[65] "England"	"Equatorial Guinea"
[67] "Eritrea"	"Estonia"
[69] "Eswatini"	"Ethiopia"
[71] "Europe"	"European Union"
[73] "Faeroe Islands"	"Falkland Islands"
[75] "Fiji"	"Finland"
[77] "France"	"French Guiana"
[79] "French Polynesia"	"Gabon"
[81] "Gambia"	"Georgia"
[83] "Germany"	"Ghana"
[85] "Gibraltar"	"Greece"
[87] "Greenland"	"Grenada"
[89] "Guadeloupe"	"Guam"
[91] "Guatemala"	"Guernsey"
[93] "Guinea"	"Guinea-Bissau"
[95] "Guyana"	"Haiti"
[97] "High income"	"Honduras"
[99] "Hong Kong"	"Hungary"
[101] "Iceland"	"India"
[103] "Indonesia"	"Iran"
[105] "Iraq"	"Ireland"
[107] "Isle of Man"	"Israel"
[109] "Italy"	"Jamaica"
[111] "Japan"	"Jersey"
[113] "Jordan"	"Kazakhstan"
[115] "Kenya"	"Kiribati"
[117] "Kosovo"	"Kuwait"
[119] "Kyrgyzstan"	"Laos"
[121] "Latvia"	"Lebanon"
[123] "Lesotho"	"Liberia"
[125] "Libya"	"Liechtenstein"
[127] "Lithuania"	"Low income"
[129] "Lower middle income"	"Luxembourg"
[131] "Macao"	"Madagascar"
[133] "Malawi"	"Malaysia"
[135] "Maldives"	"Mali"
[137] "Malta"	"Marshall Islands"

[139]	"Martinique"	"Mauritania"
[141]	"Mauritius"	"Mayotte"
[143]	"Mexico"	"Micronesia (country)"
[145]	"Moldova"	"Monaco"
[147]	"Mongolia"	"Montenegro"
[149]	"Montserrat"	"Morocco"
[151]	"Mozambique"	"Myanmar"
[153]	"Namibia"	"Nauru"
[155]	"Nepal"	"Netherlands"
[157]	"New Caledonia"	"New Zealand"
[159]	"Nicaragua"	"Niger"
[161]	"Nigeria"	"Niue"
[163]	"North America"	"North Korea"
[165]	"North Macedonia"	"Northern Cyprus"
[167]	"Northern Ireland"	"Northern Mariana Islands"
[169]	"Norway"	"Oceania"
[171]	"Oman"	"Pakistan"
[173]	"Palau"	"Palestine"
[175]	"Panama"	"Papua New Guinea"
[177]	"Paraguay"	"Peru"
[179]	"Philippines"	"Pitcairn"
[181]	"Poland"	"Portugal"
[183]	"Puerto Rico"	"Qatar"
[185]	"Reunion"	"Romania"
[187]	"Russia"	"Rwanda"
[189]	"Saint Barthelemy"	"Saint Helena"
[191]	"Saint Kitts and Nevis"	"Saint Lucia"
[193]	"Saint Martin (French part)"	"Saint Pierre and Miquelon"
[195]	"Saint Vincent and the Grenadines"	"Samoa"
[197]	"San Marino"	"Sao Tome and Principe"
[199]	"Saudi Arabia"	"Scotland"
[201]	"Senegal"	"Serbia"
[203]	"Seychelles"	"Sierra Leone"
[205]	"Singapore"	"Sint Maarten (Dutch part)"
[207]	"Slovakia"	"Slovenia"
[209]	"Solomon Islands"	"Somalia"
[211]	"South Africa"	"South America"
[213]	"South Korea"	"South Sudan"
[215]	"Spain"	"Sri Lanka"
[217]	"Sudan"	"Suriname"
[219]	"Sweden"	"Switzerland"
[221]	"Syria"	"Taiwan"
[223]	"Tajikistan"	"Tanzania"
[225]	"Thailand"	"Timor"
[227]	"Togo"	"Tokelau"
[229]	"Tonga"	"Trinidad and Tobago"
[231]	"Tunisia"	"Turkey"
[233]	"Turkmenistan"	"Turks and Caicos Islands"
[235]	"Tuvalu"	"Uganda"
[237]	"Ukraine"	"United Arab Emirates"
[239]	"United Kingdom"	"United States"
[241]	"United States Virgin Islands"	"Upper middle income"
[243]	"Uruguay"	"Uzbekistan"
[245]	"Vanuatu"	"Vatican"

[247]	"Venezuela"	"Vietnam"
[249]	"Wales"	"Wallis and Futuna"
[251]	"Western Sahara"	"World"
[253]	"Yemen"	"Zambia"
[255]	"Zimbabwe"	

```
names(cd)
```

```
[1] "iso_code"
[2] "continent"
[3] "location"
[4] "date"
[5] "total_cases"
[6] "new_cases"
[7] "new_cases_smoothed"
[8] "total_deaths"
[9] "new_deaths"
[10] "new_deaths_smoothed"
[11] "total_cases_per_million"
[12] "new_cases_per_million"
[13] "new_cases_smoothed_per_million"
[14] "total_deaths_per_million"
[15] "new_deaths_per_million"
[16] "new_deaths_smoothed_per_million"
[17] "reproduction_rate"
[18] "icu_patients"
[19] "icu_patients_per_million"
[20] "hosp_patients"
[21] "hosp_patients_per_million"
[22] "weekly_icu_admissions"
[23] "weekly_icu_admissions_per_million"
[24] "weekly_hosp_admissions"
[25] "weekly_hosp_admissions_per_million"
[26] "total_tests"
[27] "new_tests"
[28] "total_tests_per_thousand"
[29] "new_tests_per_thousand"
[30] "new_tests_smoothed"
[31] "new_tests_smoothed_per_thousand"
[32] "positive_rate"
[33] "tests_per_case"
[34] "tests_units"
[35] "total_vaccinations"
[36] "people_vaccinated"
[37] "people_fully_vaccinated"
[38] "total_boosters"
[39] "new_vaccinations"
[40] "new_vaccinations_smoothed"
[41] "total_vaccinations_per_hundred"
[42] "people_vaccinated_per_hundred"
[43] "people_fully_vaccinated_per_hundred"
[44] "total_boosters_per_hundred"
[45] "new_vaccinations_smoothed_per_million"
[46] "new_people_vaccinated_smoothed"
[47] "new_people_vaccinated_smoothed_per_hundred"
```

```

[48] "stringency_index"
[49] "population_density"
[50] "median_age"
[51] "aged_65_older"
[52] "aged_70_older"
[53] "gdp_per_capita"
[54] "extreme_poverty"
[55] "cardiovasc_death_rate"
[56] "diabetes_prevalence"
[57] "female_smokers"
[58] "male_smokers"
[59] "handwashing_facilities"
[60] "hospital_beds_per_thousand"
[61] "life_expectancy"
[62] "human_development_index"
[63] "population"
[64] "excess_mortality_cumulative_absolute"
[65] "excess_mortality_cumulative"
[66] "excess_mortality"
[67] "excess_mortality_cumulative_per_million"

```

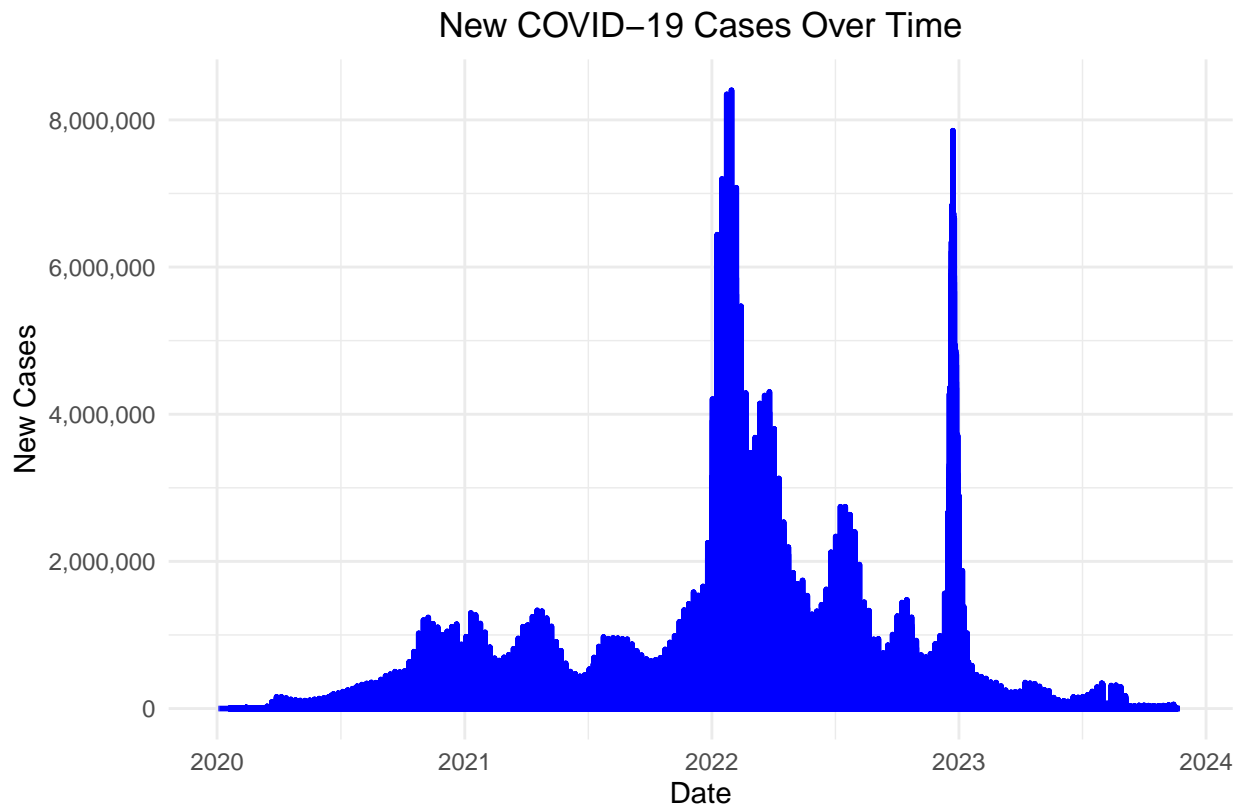
```

# Plotting new cases over time with formatted y-axis labels
ggplot(cd, aes(x = date, y = new_cases)) +
  geom_line(color = "blue", size = 1) +
  labs(title = "New COVID-19 Cases Over Time",
       x = "Date",
       y = "New Cases",
       caption = "Data Source: OWID") +
  scale_y_continuous(labels = scales::comma) + # Formats the y-axis labels with commas
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5)) # Centering the title

```

Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
 i Please use `linewidth` instead.
 This warning is displayed once every 8 hours.
 Call `lifecycle::last_lifecycle_warnings()` to see where this warning was generated.

Warning: Removed 147 rows containing missing values (`geom_line()`).



Data Source: OWID

*# 'new_cases' is considered a good proxy for transmission rates because it
directly reflects the number of new COVID-19
cases reported, offering insights into the current spread of the virus. This metric is timely
and typically available across different regions, providing a near-real-time
snapshot of the pandemic's progression.*

*# However, there are limitations to consider:
- The number of new cases can be influenced by the rate and criteria of testing.
Increased testing may lead to more cases being detected.
- Reporting delays and practices can vary, potentially leading to fluctuations
that don't necessarily represent actual changes in transmission.
- Asymptomatic or undetected cases mean that the actual number of new infections
could be higher than reported.
- Changes in testing protocols or public health policies can also impact the
number of cases detected over time.*

Behavioral Dataset Exploratory Data Analysis (EDA)

*# This subsection is dedicated to performing an Exploratory Data Analysis (EDA)
on the primary COVID-19 behaviors dataset.*

```
# Purpose:
# The following code conducts an initial assessment of the primary behaviors dataset ('bd').
# This EDA aims to uncover the dataset's basic structure, identify any immediate data quality issues,
# and prepare the data for more detailed analysis.
```

```
# Steps:
# 1. Preview the data to get a sense of the information contained in the first few rows.
# 2. Explore the structure of the dataset, including data types and the first few entries, to
#    understand how the data is organized.
# 3. Generate summary statistics for each column to capture central tendency, dispersion, and
#    the presence of NA values, which will be crucial for assessing data quality.
# 4. Check for missing values across the dataset to determine if any imputation or data cleaning
#    steps are necessary.
# 5. Identify and count duplicate rows to ensure the uniqueness of data points in the dataset.
```

```
# Code Execution:
# The results from these exploratory steps will inform how we handle data preprocessing and guide
# the analytical techniques applied in subsequent stages of the analysis.
```

```
# Read COVID-19 behaviors data into 'bd' dataframe
```

```
bd <- read_csv("covid_behaviors (1).csv")
```

```
Rows: 291 Columns: 32
```

```
-- Column specification -----
```

```
Delimiter: ","
```

```
chr (1): Country
```

```
dbl (31): Days since outbreak, Counts.Household contacts, Counts.Total conta...
```

```
i Use `spec()` to retrieve the full column specification for this data.
```

```
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
# Preview the first few rows of the dataset
```

```
head(bd)
```

```
# A tibble: 6 x 32
```

	Country	`Days since outbreak`	Counts.Household cont~1	Counts.Total contact~2
	<chr>	<dbl>	<dbl>	<dbl>
1	Australia	85	2	8.2
2	Australia	115	2.3	8
3	Australia	146	2.5	14.3
4	Australia	176	2.4	13
5	Australia	207	2.5	14.4
6	Australia	238	2.1	15.5

```
# i abbreviated names: 1: `Counts.Household contacts`,
```

```
# 2: `Counts.Total contacts`
```

```
# i 28 more variables: `Counts.Times left home` <dbl>, Counts.Handwashes <dbl>,
```

```
# `Scores.Isolate.Willingness if symptoms` <dbl>,
```

```
# `Scores.Isolate.Willingness if advised` <dbl>,
```

```
# Scores.Isolate.Difficulty <dbl>, `Scores.Masks.Outside home` <dbl>,
```

```
# `Scores.Masks.Grocery store` <dbl>, ...
```

```
# View the structure of the dataset: column names, data types, and the first
# few entries in each column
```

```
str(bd)
```

```
spc_tbl_ [291 x 32] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
```

```

$ Country : chr [1:291] "Australia" "Australia" "Australia" "Australia"
$ Days since outbreak : num [1:291] 85 115 146 176 207 238 268 299 329 360 ...
$ Counts.Household contacts : num [1:291] 2 2.3 2.5 2.4 2.5 2.1 2.2 3.2 2.3 2.2 ...
$ Counts.Total contacts : num [1:291] 8.2 8 14.3 13 14.4 15.5 17.7 19.9 19.5 20.5 .
$ Counts.Times left home : num [1:291] 1 1.1 1.3 1.4 1.3 1.4 1.4 1.5 1.4 1.4 ...
$ Counts.Handwashes : num [1:291] 11.5 10.3 9.6 10.5 10.2 9.6 10 9 10.3 10.8 .
$ Scores.Isolate.Willingness if symptoms : num [1:291] 85.8 83 80.8 83.7 84.2 83.2 81 78.5 78 80.2 .
$ Scores.Isolate.Willingness if advised : num [1:291] 14.3 13.6 13.9 14 13.8 15.7 14.7 16.3 16.6 16
$ Scores.Isolate.Difficulty : num [1:291] 91.9 90.3 89.3 90.5 90.7 88.8 89.4 88.5 89.4 8
$ Scores.Masks.Outside home : num [1:291] 23.9 24.1 22.2 24.9 49.5 48.1 43.2 45.2 41.7 5
$ Scores.Masks.Grocery store : num [1:291] 0 0 16.9 21.7 46.9 46 41.2 43.1 41.6 55.8 ...
$ Scores.Masks.Clothing store : num [1:291] 0 0 15.8 20.5 41.4 39.5 35.3 39.7 36.7 49.2 .
$ Scores.Masks.Work : num [1:291] 0 0 22 26.7 41.8 40.3 37.4 40.1 32.1 40.7 ...
$ Scores.Masks.Public transport : num [1:291] 0 0 19.1 24.3 43.3 42.4 38.5 42.3 39.5 50.1 .
$ Scores.Avoidance.Symptomatic people : num [1:291] 86.6 82.2 77.3 78.5 77 74.2 72.4 71.8 73.3 77
$ Scores.Avoidance.Going out : num [1:291] 77.6 67.9 51.6 51.3 55.7 49.1 42.2 39.7 37.9 4
$ Scores.Avoidance.Healthcare settings : num [1:291] 72.9 66.3 54.4 51.9 54.4 50.2 46.8 44.6 48.1 5
$ Scores.Avoidance.Public transport : num [1:291] 83.3 80.2 70.4 69.9 70 65.6 61.8 60.1 61.6 63
$ Scores.Avoidance.Working outside home : num [1:291] 59.4 54.6 43.3 41.2 42.1 40.9 30 40.9 35.5 40
$ Scores.Avoidance.Children going to school : num [1:291] 79.1 70 40.9 39.4 38.4 40.5 27.3 30.7 30.8 32
$ Scores.Avoidance.Having guests : num [1:291] 87.2 80.6 61.8 60.2 65.9 59.2 53.4 50.5 47.5 5
$ Scores.Avoidance.Gatherings.Small : num [1:291] 85.7 76.7 54.5 53 59.9 52.9 46.7 43.2 39.9 45
$ Scores.Avoidance.Gatherings.Medium : num [1:291] 90.9 84.3 63.8 64.4 67.3 60.9 55.2 52.2 47.4 5
$ Scores.Avoidance.Gatherings.Large : num [1:291] 92.7 89.2 76.1 76.4 76.7 72.6 66.9 63.3 58.7 6
$ Scores.Avoidance.Crowded areas : num [1:291] 89.8 84.7 75.7 77.5 77.5 72.5 68.7 66.6 64.5 6
$ Scores.Avoidance.Shops : num [1:291] 60.2 53.8 40.4 40.5 44.1 37.8 31 28.6 28.6 33
$ Scores.Precautions.Cleaned surfaces : num [1:291] 64.4 60.6 57.4 57.9 59.1 58.1 56.4 54.7 55 0
$ Scores.Precautions.Covered mouth sneeze : num [1:291] 91.8 90.3 90.6 91.2 92.8 90.2 92.1 91.3 89.7 9
$ Scores.Precautions.Used hand sanitiser : num [1:291] 72.9 75.1 77 81.2 80.9 78.8 79.1 80.3 78.8 81
$ Scores.Outlooks.Covid is dangerous : num [1:291] 0 0 49.2 55.7 54 52.9 49.1 47.6 52.5 49.9 ...
$ Scores.Outlooks.Likely to get covid : num [1:291] 0 0 18.9 24.6 20.7 19.6 18 19.8 19.4 17.8 ...
$ Scores.Outlooks.Life greatly impacted : num [1:291] 0 0 46.1 49.2 52.2 51.1 43.8 45.7 41.3 43.7 .
- attr(*, "spec")=
.. cols(
.. Country = col_character(),
.. `Days since outbreak` = col_double(),
.. `Counts.Household contacts` = col_double(),
.. `Counts.Total contacts` = col_double(),
.. `Counts.Times left home` = col_double(),
.. Counts.Handwashes = col_double(),
.. `Scores.Isolate.Willingness if symptoms` = col_double(),
.. `Scores.Isolate.Willingness if advised` = col_double(),
.. Scores.Isolate.Difficulty = col_double(),
.. `Scores.Masks.Outside home` = col_double(),
.. `Scores.Masks.Grocery store` = col_double(),
.. `Scores.Masks.Clothing store` = col_double(),
.. Scores.Masks.Work = col_double(),
.. `Scores.Masks.Public transport` = col_double(),
.. `Scores.Avoidance.Symptomatic people` = col_double(),
.. `Scores.Avoidance.Going out` = col_double(),
.. `Scores.Avoidance.Healthcare settings` = col_double(),
.. `Scores.Avoidance.Public transport` = col_double(),
.. `Scores.Avoidance.Working outside home` = col_double(),
.. `Scores.Avoidance.Children going to school` = col_double(),

```

```

.. `Scores.Avoidance.Having guests` = col_double(),
.. Scores.Avoidance.Gatherings.Small = col_double(),
.. Scores.Avoidance.Gatherings.Medium = col_double(),
.. Scores.Avoidance.Gatherings.Large = col_double(),
.. `Scores.Avoidance.Crowded areas` = col_double(),
.. Scores.Avoidance.Shops = col_double(),
.. `Scores.Precautions.Cleaned surfaces` = col_double(),
.. `Scores.Precautions.Covered mouth sneeze` = col_double(),
.. `Scores.Precautions.Used hand sanitiser` = col_double(),
.. `Scores.Outlooks.Covid is dangerous` = col_double(),
.. `Scores.Outlooks.Likely to get covid` = col_double(),
.. `Scores.Outlooks.Life greatly impacted` = col_double()
.. )
- attr(*, "problems")=<externalptr>
# Generate summary statistics for each column
summary(bd)

Country Days since outbreak Counts.Household contacts
Length:291 Min. : 85.0 Min. : 1.500
Class :character 1st Qu.:146.0 1st Qu.: 2.300
Mode :character Median :238.0 Median : 2.900
Mean :246.2 Mean : 3.064
3rd Qu.:329.0 3rd Qu.: 3.500
Max. :480.0 Max. :10.000
Counts.Total contacts Counts.Times left home Counts.Handwashes
Min. : 4.00 Min. :0.600 Min. : 4.00
1st Qu.: 8.20 1st Qu.:1.400 1st Qu.: 8.70
Median :11.60 Median :1.700 Median :10.40
Mean :13.27 Mean :1.711 Mean :10.38
3rd Qu.:16.90 3rd Qu.:2.000 3rd Qu.:11.95
Max. :36.70 Max. :3.500 Max. :19.20
Scores.Isolate.Willingness if symptoms Scores.Isolate.Willingness if advised
Min. :22.00 Min. : 5.10
1st Qu.:71.35 1st Qu.:14.75
Median :79.70 Median :17.70
Mean :76.65 Mean :19.01
3rd Qu.:85.45 3rd Qu.:21.55
Max. :93.30 Max. :43.80
Scores.Isolate.Difficulty Scores.Masks.Outside home Scores.Masks.Grocery store
Min. :65.30 Min. : 4.20 Min. : 0.00
1st Qu.:79.55 1st Qu.:66.40 1st Qu.: 7.30
Median :83.40 Median :87.80 Median :88.20
Mean :82.73 Mean :73.97 Mean :61.27
3rd Qu.:87.20 3rd Qu.:94.25 3rd Qu.:94.60
Max. :95.70 Max. :98.20 Max. :98.60
Scores.Masks.Clothing store Scores.Masks.Work Scores.Masks.Public transport
Min. : 0.00 Min. : 0.00 Min. : 0.00
1st Qu.: 6.40 1st Qu.:10.90 1st Qu.:12.70
Median :76.20 Median :62.90 Median :74.60
Mean :57.77 Mean :51.72 Mean :58.83
3rd Qu.:92.50 3rd Qu.:86.50 3rd Qu.:92.70
Max. :98.40 Max. :95.40 Max. :98.40
Scores.Avoidance.Symptomatic people Scores.Avoidance.Going out
Min. :58.70 Min. :14.70

```

1st Qu.:76.55	1st Qu.:40.35
Median :83.40	Median :52.10
Mean :81.95	Mean :53.44
3rd Qu.:88.05	3rd Qu.:68.35
Max. :95.10	Max. :90.70
Scores.Avoidance.Healthcare settings	Scores.Avoidance.Public transport
Min. :36.20	Min. :25.20
1st Qu.:56.65	1st Qu.:62.60
Median :66.60	Median :71.70
Mean :65.71	Mean :69.53
3rd Qu.:75.05	3rd Qu.:78.25
Max. :93.20	Max. :95.60
Scores.Avoidance.Working outside home	
Min. :15.00	
1st Qu.:32.85	
Median :39.90	
Mean :42.24	
3rd Qu.:49.55	
Max. :86.70	
Scores.Avoidance.Children going to school	Scores.Avoidance.Having guests
Min. : 5.50	Min. :32.00
1st Qu.:21.75	1st Qu.:54.75
Median :39.40	Median :68.40
Mean :44.17	Mean :67.15
3rd Qu.:67.15	3rd Qu.:80.00
Max. :93.40	Max. :96.70
Scores.Avoidance.Gatherings.Small	Scores.Avoidance.Gatherings.Medium
Min. :23.50	Min. :34.70
1st Qu.:48.80	1st Qu.:63.05
Median :60.70	Median :72.40
Mean :61.38	Mean :71.27
3rd Qu.:75.80	3rd Qu.:82.45
Max. :92.80	Max. :96.20
Scores.Avoidance.Gatherings.Large	Scores.Avoidance.Crowded areas
Min. :49.50	Min. :53.50
1st Qu.:75.25	1st Qu.:73.70
Median :82.70	Median :80.80
Mean :80.84	Mean :79.74
3rd Qu.:88.10	3rd Qu.:87.05
Max. :97.30	Max. :97.10
Scores.Avoidance.Shops	Scores.Precautions.Cleaned surfaces
Min. :15.20	Min. : 0.00
1st Qu.:34.15	1st Qu.:28.25
Median :46.90	Median :53.30
Mean :47.03	Mean :44.70
3rd Qu.:59.25	3rd Qu.:66.70
Max. :87.40	Max. :85.00
Scores.Precautions.Covered mouth sneeze	Scores.Precautions.Used hand sanitiser
Min. :79.80	Min. :31.50
1st Qu.:87.60	1st Qu.:69.00
Median :90.80	Median :79.30
Mean :90.31	Mean :76.42
3rd Qu.:93.20	3rd Qu.:85.40
Max. :97.80	Max. :94.40


```

Scores.Outlooks.Covid is dangerous Scores.Outlooks.Likely to get covid
Min.   : 0.00                      Min.   : 0.00
1st Qu.:33.20                      1st Qu.:13.65
Median :45.90                      Median :21.20
Mean   :42.08                      Mean   :19.59
3rd Qu.:58.50                      3rd Qu.:26.80
Max.   :87.30                      Max.   :47.70
Scores.Outlooks.Life greatly impacted
Min.   : 0.00
1st Qu.:31.00
Median :51.60
Mean   :42.54
3rd Qu.:59.20
Max.   :75.70

```

```

# Identify missing values in the dataset - no missing values
sum(is.na(bd))

```

```
[1] 0
```

```

# Check for duplicate rows - no duplicate rows
sum(duplicated(bd))

```

```
[1] 0
```

```

# Get the column names of the behaviors dataset
column_names <- names(bd)
print(column_names)

```

```

[1] "Country"
[2] "Days since outbreak"
[3] "Counts.Household contacts"
[4] "Counts.Total contacts"
[5] "Counts.Times left home"
[6] "Counts.Handwashes"
[7] "Scores.Isolate.Willingness if symptoms"
[8] "Scores.Isolate.Willingness if advised"
[9] "Scores.Isolate.Difficulty"
[10] "Scores.Masks.Outside home"
[11] "Scores.Masks.Grocery store"
[12] "Scores.Masks.Clothing store"
[13] "Scores.Masks.Work"
[14] "Scores.Masks.Public transport"
[15] "Scores.Avoidance.Symptomatic people"
[16] "Scores.Avoidance.Going out"
[17] "Scores.Avoidance.Healthcare settings"
[18] "Scores.Avoidance.Public transport"
[19] "Scores.Avoidance.Working outside home"
[20] "Scores.Avoidance.Children going to school"
[21] "Scores.Avoidance.Having guests"
[22] "Scores.Avoidance.Gatherings.Small"
[23] "Scores.Avoidance.Gatherings.Medium"
[24] "Scores.Avoidance.Gatherings.Large"
[25] "Scores.Avoidance.Crowded areas"
[26] "Scores.Avoidance.Shops"
[27] "Scores.Precautions.Cleaned surfaces"

```

```
[28] "Scores.Precautions.Covered mouth sneeze"
[29] "Scores.Precautions.Used hand sanitiser"
[30] "Scores.Outlooks.Covid is dangerous"
[31] "Scores.Outlooks.Likely to get covid"
[32] "Scores.Outlooks.Life greatly impacted"

# Find common countries that are present in both datasets
common_countries <- intersect(unique(cd$location), unique(bd$Country))
```

Section 2: Dataset Reconciliation and Country Clustering

```
# Given the size of the datasets and the limited time for this assignment this analysis will focus
# on ten randomly selected countries. The hope is that by randomly selecting countries that appear
# in both datasets the results will be manageable but the selection process will not introduce bias.

# Random sample from the list of common countries
set.seed(123) # Setting a seed for reproducibility
random_common_countries <- sample(common_countries, 10)

# Check the selected countries
print(random_common_countries)

[1] "Mexico"      "Saudi Arabia" "Malaysia"     "Canada"      "India"
[6] "Philippines" "Spain"        "Indonesia"    "Denmark"     "Singapore"

# Sub-setting the dataframes by randomly selected countries.
# Subset the COVID data for the selected countries
cd_subset <- cd[cd$location %in% random_common_countries, ]

# Subset the behavior data for the selected countries
# Make sure to replace 'Country' with the actual column name for countries in the bd dataframe
bd_subset <- bd[bd$Country %in% random_common_countries, ]
```

Manual Selection Based on Outbreak Start Dates

```
# Issue:
# The 'Days since outbreak' column in the behavior dataset (bd) presented a challenge for analysis
# due to inconsistent or non-standardized outbreak start dates across different countries. Directly
# comparing behavioral responses between countries became problematic because the relative timelines
# did not align, potentially skewing any comparative analysis.

# Resolution:
# To address this, a manual review of country-specific outbreak start dates was conducted. By
```

```
# consulting individual country data files hosted on the GitHub repository, accurate outbreak start
# dates were determined for each country. Countries were then selected for inclusion in the analysis
# based on whether their outbreak start dates fell within a similar timeframe (within one month of
# each other). This manual curation ensured a more accurate and meaningful comparison of behavioral
# responses during comparable stages of the pandemic response.
```

```
# The manual approach, while more time-consuming, provided a level of precision and customization
# in the selection process. It allowed for the identification of a subset of countries with
# closely aligned outbreak timelines, thereby facilitating a more robust and reliable comparative
# analysis of behavioral data.
```

Country Selection Based on Proximal Outbreak Start Dates

```
# After a manual review of country-specific start dates for the COVID-19 outbreak,
# countries were categorized into groups based on the similarity of their outbreak onset.
# This categorization ensures that behavioral responses are compared during equivalent
# stages of the pandemic, allowing for more accurate cross-country comparisons.
```

```
# The following groups were identified:
```

```
# - Group 1 (Start Dates: February to March): Canada, Spain, Mexico, Singapore
#   These countries experienced the start of their outbreaks within one month of each other,
#   providing a comparable time frame for early pandemic behaviors.
```

```
# - Group 2 (Start Dates: January to February): India, Canada, Spain
#   Although Canada and Spain appear in both Group 1 and Group 2, the inclusion criteria
#   for Group 2 is based on a slightly earlier phase, capturing the very onset of the pandemic.
```

```
# - Group 3 (Start Dates: August to September):
#   Indonesia, Saudi Arabia, Philippines, Denmark, Malaysia
#   This group represents countries where the outbreak was recognized later, which may reflect
#   different stages of public awareness and response.
```

```
# Analysis will proceed with these groups, examining behavioral data within each group to
# assess patterns and responses to the pandemic. This approach acknowledges the temporal
# context of behavioral data, ensuring that findings are not confounded by vastly different
# stages of pandemic progression.
```

```
# Check if there is a "World" or similar entry indicating global data
any(cd$location == "World")
```

```
[1] TRUE
```

```
# Extract global data
global_cases <- cd[cd$location == "World", ]
```

```
# Ensure that the 'date' and 'new_cases' columns are correctly named and formatted
global_cases$date <- as.Date(global_cases$date)
```

```

# Convert the outbreak start date of each group to Date format
group1_start <- as.Date("2020-02-15") # replace with actual group start date
group2_start <- as.Date("2020-01-10")
group3_start <- as.Date("2020-08-20")

# These are the 'Days since outbreak' for group 1 you've listed
group1_days_since_outbreak <- c(85, 115, 146, 176, 207, 238, 268, 299, 329, 360, 391, 419, 450, 480)

# Convert these days to actual dates by adding them to the group's start date
group1_dates <- group1_start + group1_days_since_outbreak
group2_dates <- group2_start + group1_days_since_outbreak
group3_dates <- group3_start + group1_days_since_outbreak

# Initialize the plot with global new cases
p <- ggplot(global_cases, aes(x = date, y = new_cases)) +
  geom_line() +
  labs(title = "Global New COVID-19 Cases Over Time", x = "Date", y = "New Cases") +
  theme(plot.title = element_text(hjust = 0.5))

# Add vertical lines for group 1
for(i in group1_dates) {
  p <- p + geom_vline(xintercept = as.numeric(i), color = "blue", linetype = "longdash")
}

# Add vertical lines for group 2
for(i in group2_dates) {
  p <- p + geom_vline(xintercept = as.numeric(i), color = "red", linetype = "longdash")
}

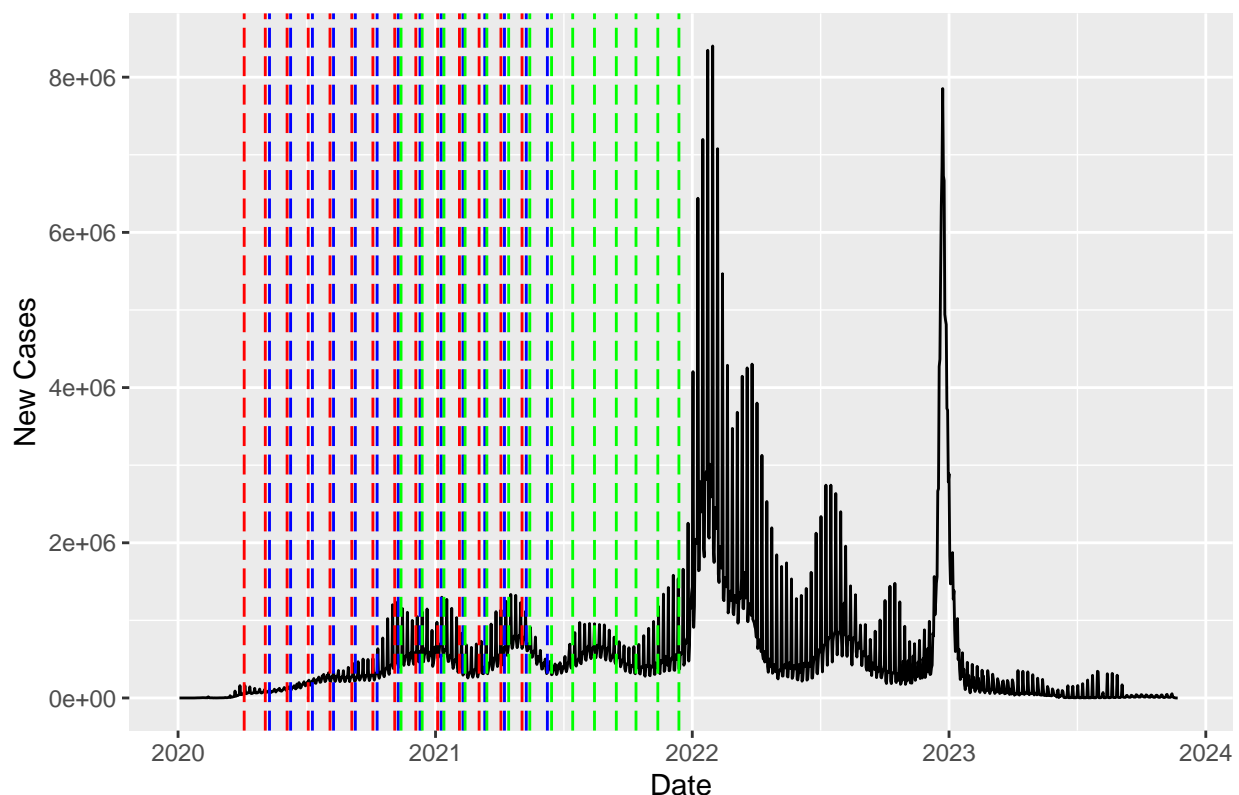
# Add vertical lines for group 3
for(i in group3_dates) {
  p <- p + geom_vline(xintercept = as.numeric(i), color = "green", linetype = "longdash")
}

# Print the plot
print(p)

```

Warning: Removed 7 rows containing missing values (`geom_line()`).

Global New COVID-19 Cases Over Time



```
cd$date <- as.Date(cd$date)

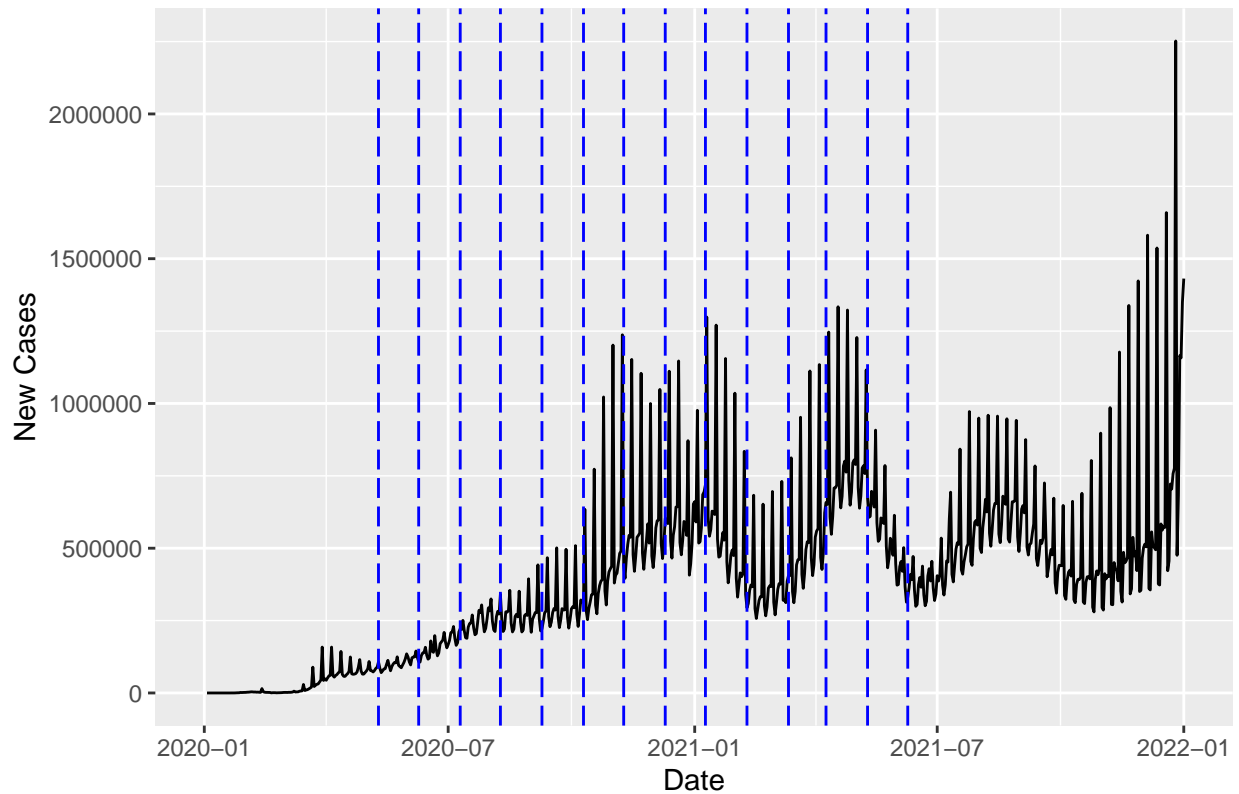
# Create subsets for each group based on the dates we've calculated
cd_group1 <- cd[cd$date %in% group1_dates, ]
cd_group2 <- cd[cd$date %in% group2_dates, ]
cd_group3 <- cd[cd$date %in% group3_dates, ]

# Filter global_cases to include dates up to January 2022
global_cases_filtered <- global_cases %>%
  filter(date <= as.Date("2022-01-01"))

# Plot for Group 1 with dates up to January 2022
p_group1 <- ggplot(global_cases_filtered, aes(x = date, y = new_cases)) +
  geom_line() +
  geom_vline(xintercept = as.numeric(group1_dates), color = "blue", linetype = "longdash") +
  labs(title = "Global New COVID-19 Cases Over Time (Group 1)", x = "Date", y = "New Cases") +
  xlim(as.Date("2020-01-01"), as.Date("2022-01-01")) # Set x-axis limits

print(p_group1)
```

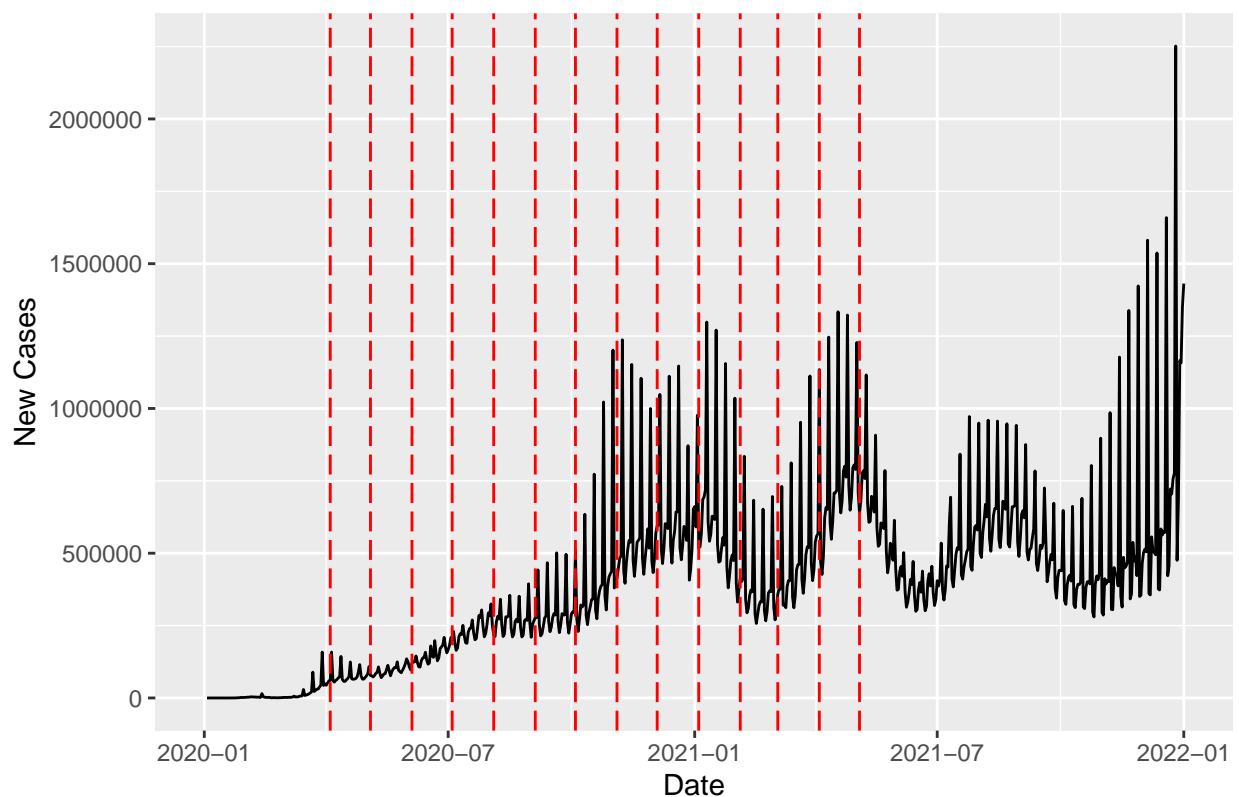
Global New COVID-19 Cases Over Time (Group 1)



```
# Plot for Group 2 with dates up to January 2022
p_group2 <- ggplot(global_cases_filtered, aes(x = date, y = new_cases)) +
  geom_line() +
  geom_vline(xintercept = as.numeric(group2_dates), color = "red", linetype = "longdash") +
  labs(title = "Global New COVID-19 Cases Over Time (Group 2)", x = "Date", y = "New Cases") +
  xlim(as.Date("2020-01-01"), as.Date("2022-01-01")) # Set x-axis limits

print(p_group2)
```

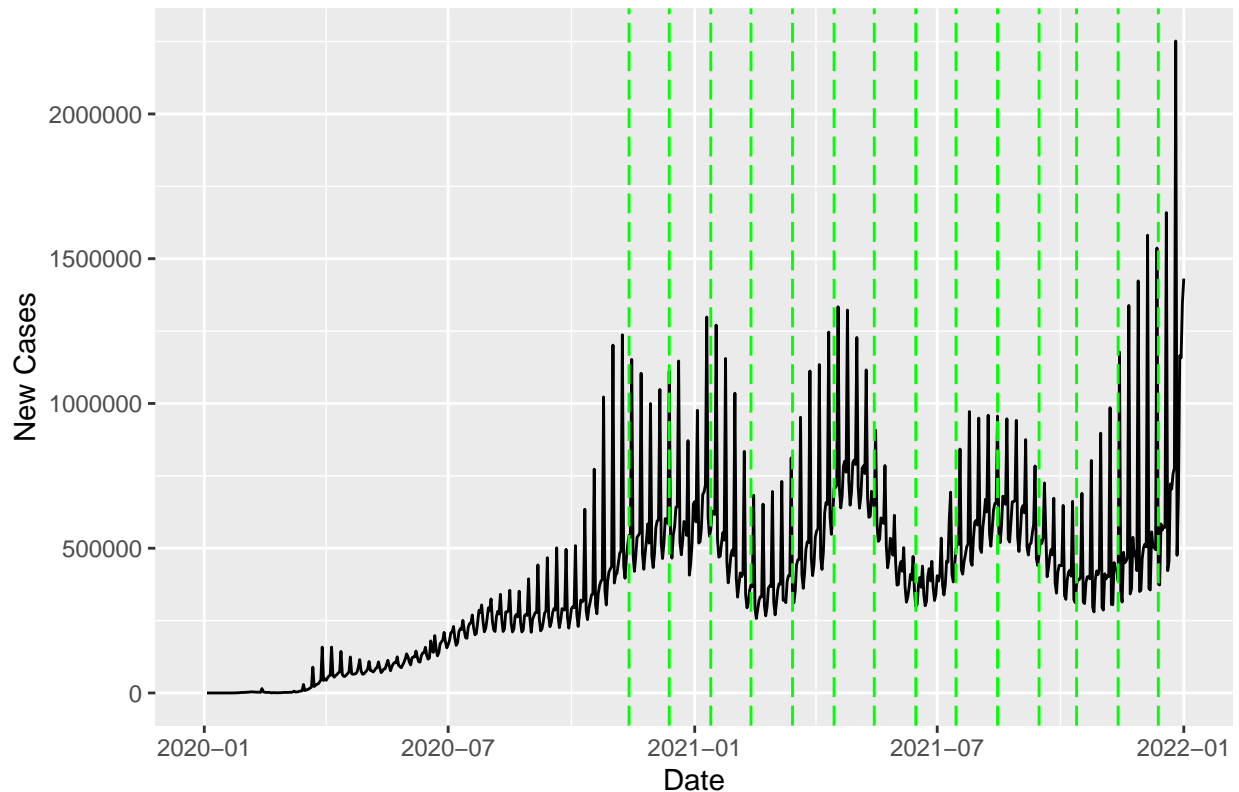
Global New COVID-19 Cases Over Time (Group 2)



```
# Plot for Group 3 with dates up to January 2022
p_group3 <- ggplot(global_cases_filtered, aes(x = date, y = new_cases)) +
  geom_line() +
  geom_vline(xintercept = as.numeric(group3_dates), color = "green", linetype = "longdash") +
  labs(title = "Global New COVID-19 Cases Over Time (Group 3)", x = "Date", y = "New Cases") +
  xlim(as.Date("2020-01-01"), as.Date("2022-01-01")) # Set x-axis limits

print(p_group3)
```

Global New COVID-19 Cases Over Time (Group 3)



Section 3: Dataset Analysis

```
# This section presents the analysis of the COVID-19 behaviors dataset, focusing
# on two specific research questions.
# The analyses leverage a cluster-based approach, where each cluster represents
# a group of countries with similar outbreak start dates, allowing for meaningful
# comparisons of behavioral responses within these clusters.

# The research questions addressed are:
# 1. How did the willingness to self-isolate change throughout the pandemic in different countries?
#   - This question is explored by analyzing self-isolation willingness scores
#     over time in a selected cluster of countries.
#   The analysis focuses on both the willingness to self-isolate if symptoms
#   are present and if advised, providing insights into public sentiment
#   evolution during the pandemic.

# 2. Which countries reported the highest levels of compliance with mask-wearing guidelines?
#   - This question is addressed by comparing mask-wearing compliance levels in
#     ten selected countries.
#   The analysis involves transforming raw mask-wearing scores into a Likert scale
#   and creating visualizations for various contexts of mask-wearing
```



```

# (outside home, grocery store, clothing store, work, public transport).

# The methodologies applied in these analyses aim to strike a balance between
# depth and practicality, considering the dataset size and project timeframe.
# The visualizations generated provide insights into how behavioral patterns
# in response to the pandemic evolved and varied across different countries and timeframes.

# Detailed comments are provided in each subsection to guide through the steps of data
# preparation, transformation, and visualization, ensuring clarity and reproducibility
# of the analysis.

# Willingness to Self-Isolate Analysis:
# - The analysis involves data preparation steps such as renaming columns,
# selecting relevant data, and transforming 'Days since outbreak' into actual dates.
# - Time series plots are created for each group, illustrating changes in willingness
# to self-isolate over time, accompanied by global transmission rates to provide context.

# Mask-Wearing Compliance Analysis:
# - The analysis begins with data preparation, including renaming columns and filtering
# for selected countries.
# - Scores are converted to a Likert scale, and average mask-wearing scores for
# different contexts are calculated.
# - Bar charts are created for each context of mask-wearing, displaying average
# scores in a Likert scale format
# across the selected countries.

# These analyses offer a comprehensive view of behavioral responses during the pandemic, highlighting
# the variations in public adherence to health guidelines and perceptions over time.

```

Q1 - Willingness to self-isolate

```

# Column renaming section using piping. The spaces in the original dataset column
# names were prevent analysis.
bd <- bd %>%
  rename(Days_since_outbreak = `Days since outbreak`)
bd <- bd %>%
  rename(Scores.Isolate.Willingness_if_symptoms = `Scores.Isolate.Willingness if symptoms`)
bd <- bd %>%
  rename(Scores.Isolate.Willingness_if_advised = `Scores.Isolate.Willingness if advised`)

# Data Preparation: Selecting relevant columns
isolation_data <- bd %>%
  select(Country, Days_since_outbreak, Scores.Isolate.Willingness_if_symptoms, Scores.Isolate.Willingness_if_advised)

# Time Series Analysis: Calculating average scores over time for each country
average_isolation_willingness <- isolation_data %>%
  group_by(Country, Days_since_outbreak) %>%
  summarise(Average_Willingness_if_symptoms = mean(Scores.Isolate.Willingness_if_symptoms, na.rm = TRUE),
    Average_Willingness_if_advised = mean(Scores.Isolate.Willingness_if_advised, na.rm = TRUE))

```

```
Average_Willingness_if_advised = mean(Scores.Isolate.Willingness_if_advised, na.rm = TRUE))
```

`summarise()` has grouped output by 'Country'. You can override using the
`.groups` argument.

```
# Check the structure of the summarised dataframe
```

```
str(average_isolation_willingness)
```

```
gropd_df [291 x 4] (S3: grouped_df/tbl_df/tbl/data.frame)
 $ Country          : chr [1:291] "Australia" "Australia" "Australia" "Australia" ...
 $ Days_since_outbreak : num [1:291] 85 115 146 176 207 238 268 299 329 360 ...
 $ Average_Willingness_if_symptoms: num [1:291] 85.8 83 80.8 83.7 84.2 83.2 81 78.5 78 80.2 ...
 $ Average_Willingness_if_advised : num [1:291] 14.3 13.6 13.9 14 13.8 15.7 14.7 16.3 16.6 16.1 ...
 - attr(*, "groups")= tibble [29 x 2] (S3: tbl_df/tbl/data.frame)
 ..$ Country: chr [1:29] "Australia" "Brazil" "Canada" "China" ...
 ..$ .rows : list<int> [1:29]
 .. ..$ : int [1:14] 1 2 3 4 5 6 7 8 9 10 ...
 .. ..$ : int [1:6] 15 16 17 18 19 20
 .. ..$ : int [1:14] 21 22 23 24 25 26 27 28 29 30 ...
 .. ..$ : int [1:6] 35 36 37 38 39 40
 .. ..$ : int [1:14] 41 42 43 44 45 46 47 48 49 50 ...
 .. ..$ : int [1:10] 55 56 57 58 59 60 61 62 63 64
 .. ..$ : int [1:14] 65 66 67 68 69 70 71 72 73 74 ...
 .. ..$ : int [1:14] 79 80 81 82 83 84 85 86 87 88 ...
 .. ..$ : int [1:6] 93 94 95 96 97 98
 .. ..$ : int [1:6] 99 100 101 102 103 104
 .. ..$ : int [1:6] 105 106 107 108 109 110
 .. ..$ : int [1:14] 111 112 113 114 115 116 117 118 119 120 ...
 .. ..$ : int [1:14] 125 126 127 128 129 130 131 132 133 134 ...
 .. ..$ : int [1:6] 139 140 141 142 143 144
 .. ..$ : int [1:6] 145 146 147 148 149 150
 .. ..$ : int [1:11] 151 152 153 154 155 156 157 158 159 160 ...
 .. ..$ : int [1:14] 162 163 164 165 166 167 168 169 170 171 ...
 .. ..$ : int [1:6] 176 177 178 179 180 181
 .. ..$ : int [1:6] 182 183 184 185 186 187
 .. ..$ : int [1:14] 188 189 190 191 192 193 194 195 196 197 ...
 .. ..$ : int [1:14] 202 203 204 205 206 207 208 209 210 211 ...
 .. ..$ : int [1:14] 216 217 218 219 220 221 222 223 224 225 ...
 .. ..$ : int [1:14] 230 231 232 233 234 235 236 237 238 239 ...
 .. ..$ : int [1:6] 244 245 246 247 248 249
 .. ..$ : int [1:6] 250 251 252 253 254 255
 .. ..$ : int [1:6] 256 257 258 259 260 261
 .. ..$ : int [1:14] 262 263 264 265 266 267 268 269 270 271 ...
 .. ..$ : int [1:10] 276 277 278 279 280 281 282 283 284 285
 .. ..$ : int [1:6] 286 287 288 289 290 291
 .. ..@ ptype: int(0)
 ..- attr(*, ".drop")= logi TRUE
```

```
# Make sure that 'Days_since_outbreak' is in the expected date or numeric format
```

```
str(bd$Days_since_outbreak)
```

```
num [1:291] 85 115 146 176 207 238 268 299 329 360 ...
```

```
# Make sure there are actual numeric values to plot and not just NA
```

```
summary(average_isolation_willingness$Average_Willingness_if_symptoms)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
22.00	71.35	79.70	76.65	85.45	93.30

```
summary(average_isolation_willingness$Average_Willingness_if_advised)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
5.10	14.75	17.70	19.01	21.55	43.80

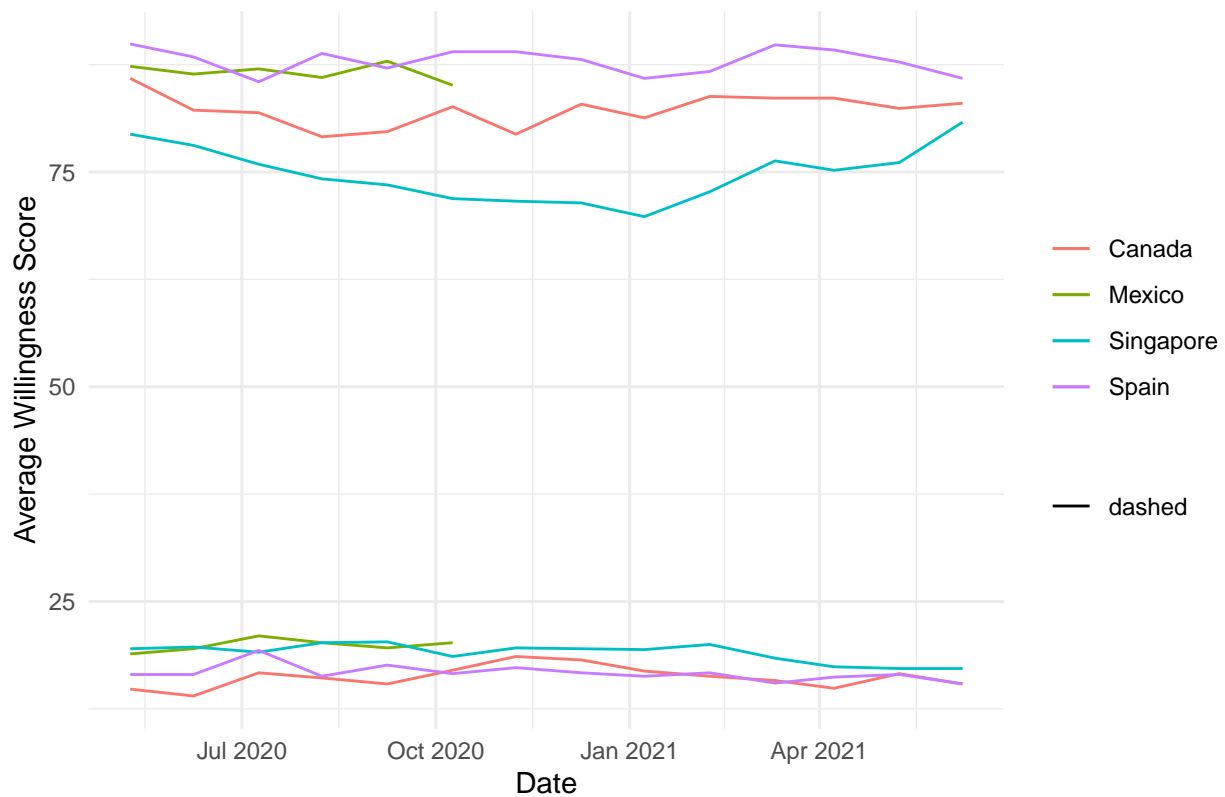
```
# Convert the 'Days_since_outbreak' to actual dates based on the group's start date
group1_start_date <- as.Date("2020-02-15") # Assuming this is the correct start date for Group 1
bd$Actual_Date <- group1_start_date + bd$Days_since_outbreak - 1 # Correcting for the start date
```

```
# Filtering for Group 1 countries and relevant dates
group1_isolation_data <- bd %>%
  filter(Country %in% c("Canada", "Spain", "Mexico", "Singapore"),
         Days_since_outbreak %in% c(85, 115, 146, 176, 207, 238, 268, 299,
                                     329, 360, 391, 419, 450, 480)) %>%
  select(Country, Actual_Date, Scores.Isolate.Willingness_if_symptoms,
         Scores.Isolate.Willingness_if_advised)
```

```
# Plotting the data for Group 1 with individual lines per country
group1_isolation_plot <- ggplot(group1_isolation_data, aes(x = Actual_Date, group = Country)) +
  geom_line(aes(y = Scores.Isolate.Willingness_if_symptoms, color = Country)) +
  geom_line(aes(y = Scores.Isolate.Willingness_if_advised, color = Country, linetype = "dashed")) +
  labs(title = "Average Willingness to Self-Isolate Over Time (Group 1)",
       x = "Date", y = "Average Willingness Score") +
  theme_minimal() +
  theme(legend.title = element_blank()) # Remove the legend title
```

```
# Print the plot
print(group1_isolation_plot)
```

Average Willingness to Self-Isolate Over Time (Group 1)



```
# Calculate the average transmission rate for each date for the global context
average_global_transmission <- global_cases %>%
  group_by(date) %>%
  summarise(Average_Transmission = mean(new_cases, na.rm = TRUE))
```

Country Cluster 1

```
# Merge the transmission data with the group 1 behavior data
# Ensure that 'Actual_Date' in your behavior data is converted to Date format
# and aligns with 'date' in transmission data
group1_data_combined <- group1_isolation_data %>%
  left_join(average_global_transmission, by = c("Actual_Date" = "date"))

# Check for the existence of 'Average_Transmission' in the combined dataset
# This step is to confirm that the data preparation steps were successful
# and that the Average_Transmission column is present for plotting
if("Average_Transmission" %in% names(group1_data_combined)) {
  print("Average_Transmission exists in the data frame.")
} else {
  print("Average_Transmission does not exist in the data frame. Check the data preparation steps.")
}
```

```
[1] "Average_Transmission exists in the data frame."
```

```
# View the structure of the combined data to confirm column names and data types  
# This function will give us an overview of the dataframe structure after the join  
str(group1_data_combined)
```

```
tibble [48 x 5] (S3: tbl_df/tbl/data.frame)
```

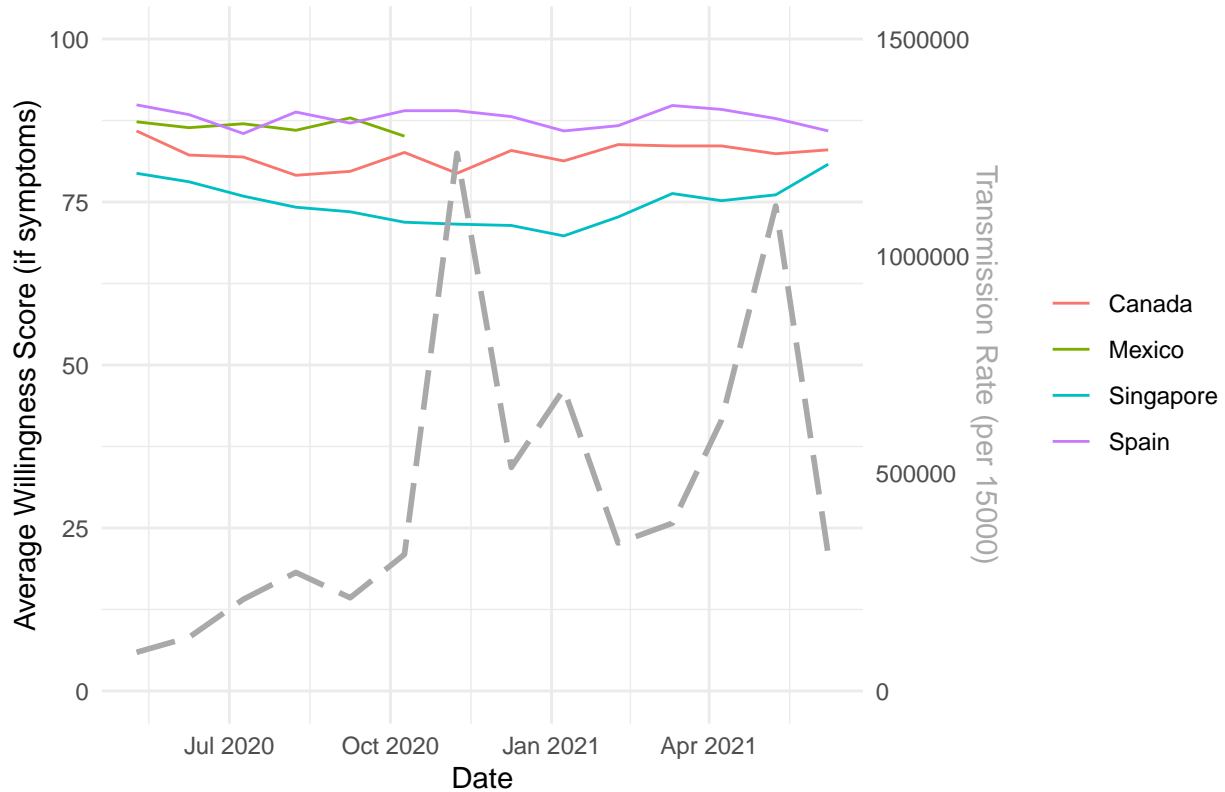
```
$ Country                : chr [1:48] "Canada" "Canada" "Canada" "Canada" ...  
$ Actual_Date            : Date[1:48], format: "2020-05-09" "2020-06-08" ...  
$ Scores.Isolate.Willingness_if_symptoms: num [1:48] 85.9 82.2 81.9 79.1 79.7 82.6 79.4 82.9 81.3 83.8  
$ Scores.Isolate.Willingness_if_advised : num [1:48] 14.8 14 16.7 16.1 15.4 17 18.6 18.2 16.9 16.3 ...  
$ Average_Transmission    : num [1:48] 89000 123431 211012 272733 214489 ...
```

```
# Merge the average global transmission data with the group 1 behavior data  
# This will append the transmission rate to the behavioral data, allowing for combined analysis  
group1_data_combined <- group1_data_combined %>%  
  left_join(average_global_transmission, by = c("Actual_Date" = "date"))
```

```
# First plot: Willingness to self-isolate if symptoms are present
```

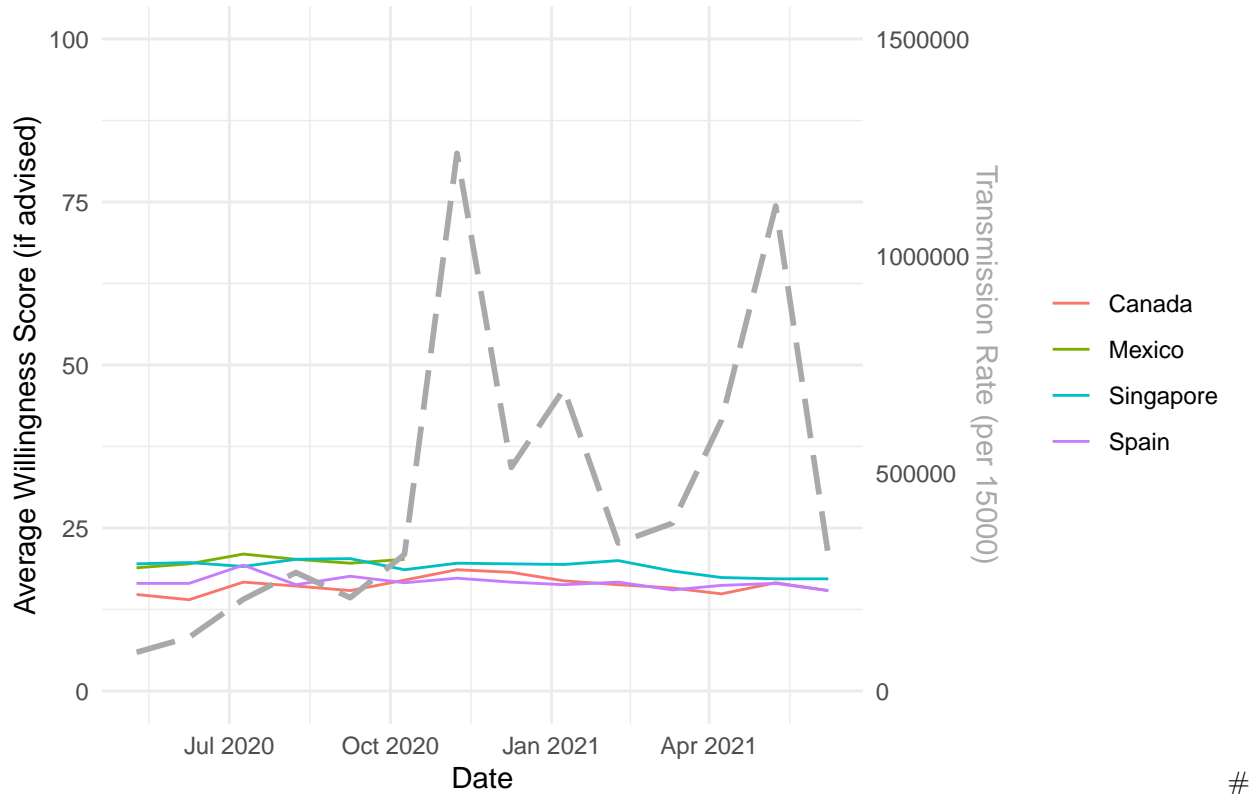
```
ggplot(group1_data_combined) +  
  geom_line(aes(x = Actual_Date, y = Scores.Isolate.Willingness_if_symptoms, color = Country)) +  
  geom_line(aes(x = Actual_Date, y = Average_Transmission.x/15000),  
            linetype = "longdash", color = "darkgrey", size = 1) +  
  scale_y_continuous(  
    name = "Average Willingness Score (if symptoms)",  
    limits = c(0, 100),  
    sec.axis = sec_axis(~ . * 15000, name = "Transmission Rate (per 15000)")  
  ) +  
  labs(  
    title = "Willingness to Self-Isolate If Symptoms Present Over Time (Group 1)",  
    x = "Date"  
  ) +  
  theme_minimal() +  
  theme(  
    legend.title = element_blank(),  
    axis.title.y.right = element_text(color = "darkgrey")  
  )
```

Willingness to Self-Isolate If Symptoms Present Over Time (Group 1)



```
# Second plot: Willingness to self-isolate if advised
ggplot(group1_data_combined) +
  geom_line(aes(x = Actual_Date, y = Scores.Isolate.Willingness_if_advised, color = Country)) +
  geom_line(aes(x = Actual_Date, y = Average_Transmission.x/15000),
            linetype = "longdash", color = "darkgrey", size = 1) +
  scale_y_continuous(
    name = "Average Willingness Score (if advised)",
    limits = c(0, 100),
    sec.axis = sec_axis(~ . * 15000, name = "Transmission Rate (per 15000)")
  ) +
  labs(
    title = "Willingness to Self-Isolate If Advised Over Time (Group 1)",
    x = "Date"
  ) +
  theme_minimal() +
  theme(
    legend.title = element_blank(),
    axis.title.y.right = element_text(color = "darkgrey")
  )
)
```

Willingness to Self-Isolate If Advised Over Time (Group 1)



```
# Convert the 'Days_since_outbreak' to actual dates based on the group's start date
group2_start_date <- as.Date("2020-01-10") # Assuming this is the correct start date for Group 1
bd$Actual_Date <- group2_start_date + bd$Days_since_outbreak - 1 # Correcting for the start date

group2_isolation_data <- bd %>%
  filter(Country %in% c("Canada", "Spain", "India"),
         Days_since_outbreak %in% c(85, 115, 146, 176, 207, 238, 268, 299, 329,
                                   360, 391, 419, 450, 480)) %>%
  select(Country, Actual_Date, Scores.Isolate.Willingness_if_symptoms,
         Scores.Isolate.Willingness_if_advised)

group2_data_combined <- group2_isolation_data %>%
  left_join(average_global_transmission, by = c("Actual_Date" = "date"))

# First plot: Willingness to self-isolate if symptoms are present
ggplot(group2_data_combined) +
  geom_line(aes(x = Actual_Date, y = Scores.Isolate.Willingness_if_symptoms, color = Country)) +
  geom_line(aes(x = Actual_Date, y = Average_Transmission/15000),
            linetype = "longdash", color = "darkgrey", size = 1) +
  scale_y_continuous(
    name = "Average Willingness Score (if symptoms)",
    limits = c(0, 100),
    sec.axis = sec_axis(~ . * 15000, name = "Transmission Rate (per 15000)")
  ) +
  labs(
    title = "Willingness to Self-Isolate If Symptoms Present Over Time (Group 2)",

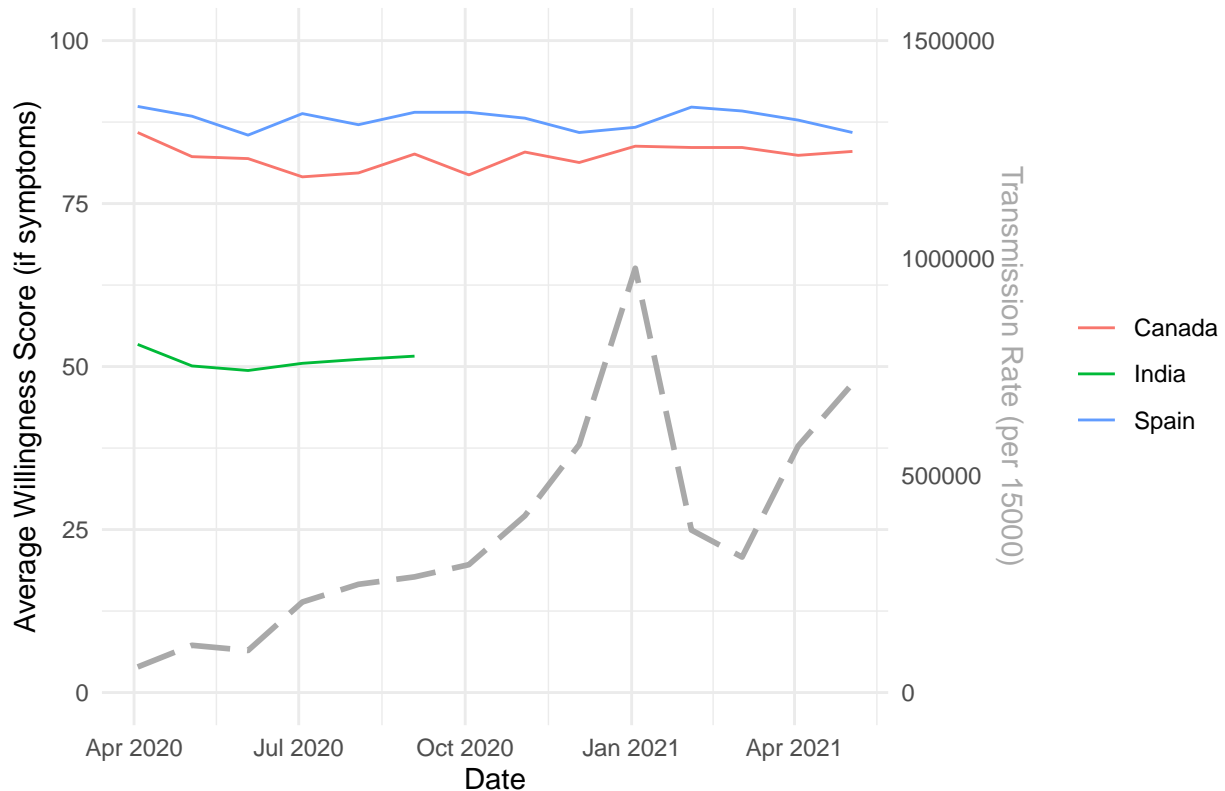
```

```

x = "Date"
) +
theme_minimal() +
theme(
  legend.title = element_blank(),
  axis.title.y.right = element_text(color = "darkgrey")
)

```

Willingness to Self-Isolate If Symptoms Present Over Time (Group 2)

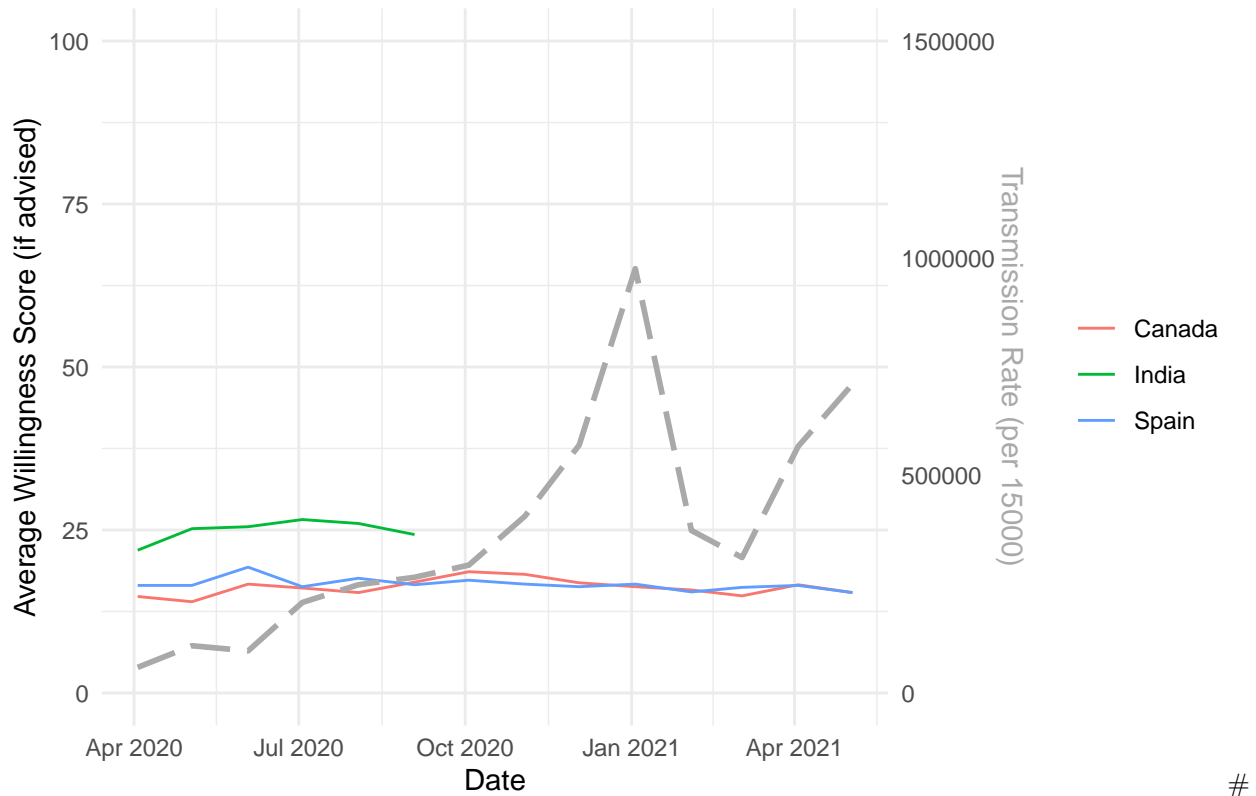


```

# Second plot: Willingness to self-isolate if advised
ggplot(group2_data_combined) +
  geom_line(aes(x = Actual_Date, y = Scores.Isolate.Willingness_if_advised, color = Country)) +
  geom_line(aes(x = Actual_Date, y = Average_Transmission/15000),
    linetype = "longdash", color = "darkgrey", size = 1) +
  scale_y_continuous(
    name = "Average Willingness Score (if advised)",
    limits = c(0, 100),
    sec.axis = sec_axis(~ . * 15000, name = "Transmission Rate (per 15000)")
  ) +
  labs(
    title = "Willingness to Self-Isolate If Advised Over Time (Group 2)",
    x = "Date"
  ) +
  theme_minimal() +
  theme(
    legend.title = element_blank(),
    axis.title.y.right = element_text(color = "darkgrey")
  )

```


Willingness to Self-Isolate If Advised Over Time (Group 2)



Country Cluster 3

```
# Convert the 'Days_since_outbreak' to actual dates based on the group's start date
group3_start_date <- as.Date("2020-08-20") # Assuming this is the correct start date for Group 1
bd$Actual_Date <- group3_start_date + bd$Days_since_outbreak - 1 # Correcting for the start date

group3_isolation_data <- bd %>%
  filter(Country %in% c("Indonesia", "Saudi Arabia", "Philippines", "Denmark", "Malaysia"),
         Days_since_outbreak %in% c(85, 115, 146, 176, 207, 238, 268, 299, 329,
                                   360, 391, 419, 450, 480)) %>%
  select(Country, Actual_Date, Scores.Isolate.Willingness_if_symptoms,
         Scores.Isolate.Willingness_if_advised)

group3_data_combined <- group3_isolation_data %>%
  left_join(average_global_transmission, by = c("Actual_Date" = "date"))

# First plot: Willingness to self-isolate if symptoms are present
ggplot(group3_data_combined) +
  geom_line(aes(x = Actual_Date, y = Scores.Isolate.Willingness_if_symptoms, color = Country)) +
  geom_line(aes(x = Actual_Date, y = Average_Transmission/15000),
            linetype = "longdash", color = "darkgrey", size = 1) +
  scale_y_continuous(
    name = "Average Willingness Score (if symptoms)",
    limits = c(0, 100),
    sec.axis = sec_axis(~ . * 15000, name = "Transmission Rate (per 15000)")
  ) +
  labs(
    title = "Willingness to Self-Isolate If Symptoms Present Over Time (Group 3)",
```

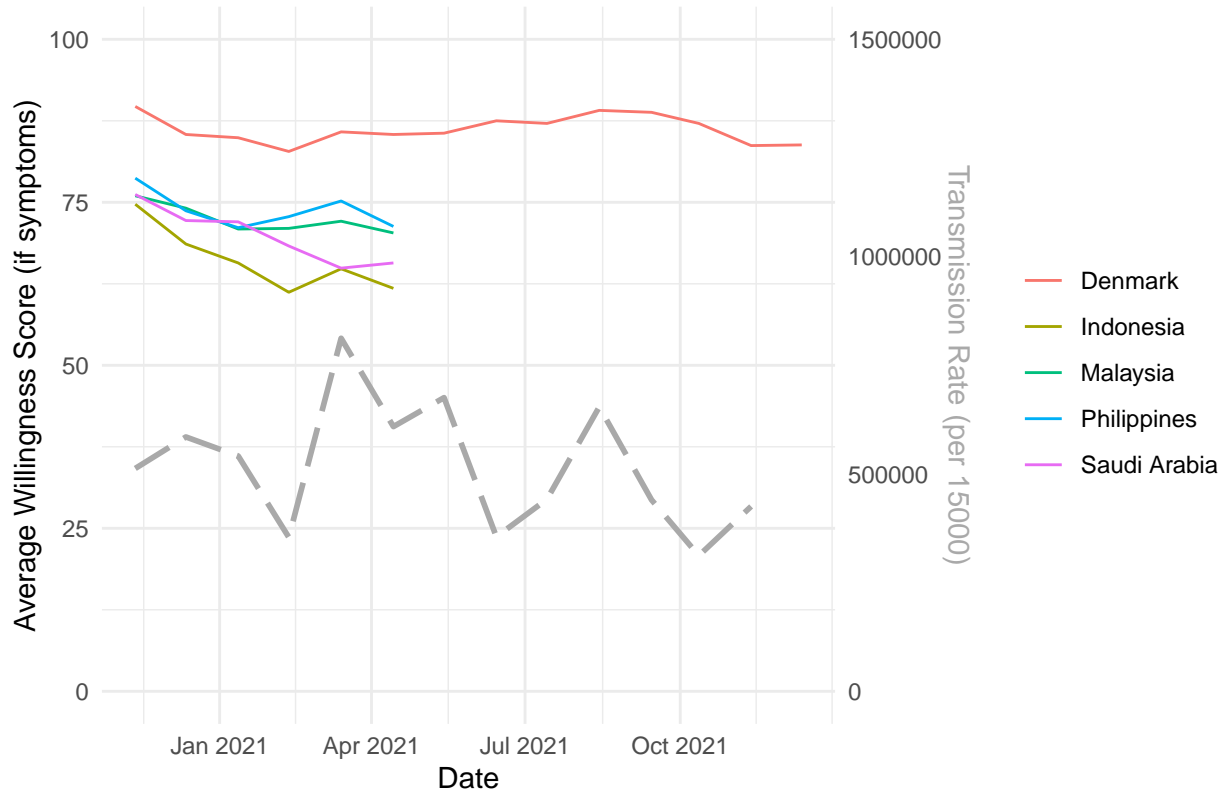
```

  x = "Date"
) +
theme_minimal() +
theme(
  legend.title = element_blank(),
  axis.title.y.right = element_text(color = "darkgrey")
)

```

Warning: Removed 1 row containing missing values (`geom_line()`).

Willingness to Self-Isolate If Symptoms Present Over Time (Group 3)



```

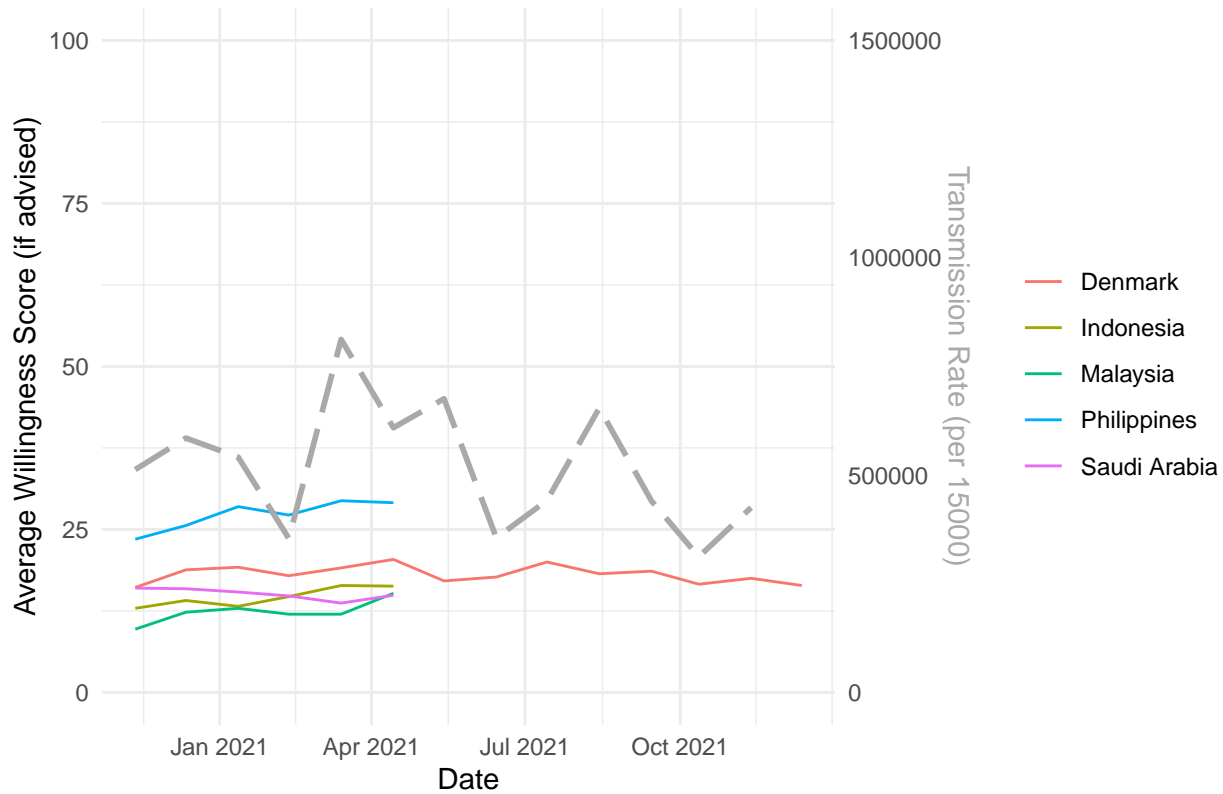
# Second plot: Willingness to self-isolate if advised
ggplot(group3_data_combined) +
  geom_line(aes(x = Actual_Date, y = Scores.Isolate.Willingness_if_advised, color = Country)) +
  geom_line(aes(x = Actual_Date, y = Average_Transmission/15000),
    linetype = "longdash", color = "darkgrey", size = 1) +
  scale_y_continuous(
    name = "Average Willingness Score (if advised)",
    limits = c(0, 100),
    sec.axis = sec_axis(~ . * 15000, name = "Transmission Rate (per 15000)")
  ) +
  labs(
    title = "Willingness to Self-Isolate If Advised Over Time (Group 3)",
    x = "Date"
  ) +
  theme_minimal() +
  theme(
    legend.title = element_blank(),

```

```
axis.title.y.right = element_text(color = "darkgrey")
)
```

Warning: Removed 1 row containing missing values (`geom_line()`).

Willingness to Self-Isolate If Advised Over Time (Group 3)



```
# Q2 - Masking Compliance #
# Renaming columns for consistency and to facilitate analysis
# The original dataset contains spaces in the column names which can cause issues during analysis
bd <- bd %>%
  rename(Scores.Masks.Outside_home = `Scores.Masks.Outside home`) %>%
  rename(Scores.Masks.Grocery_store = `Scores.Masks.Grocery store`) %>%
  rename(Scores.Masks.Clothing_store = `Scores.Masks.Clothing store`) %>%
  rename(Scores.Masks.Public_transport = `Scores.Masks.Public transport`)

# Defining a function to convert raw scores to a Likert scale
# This function will be applied to mask-wearing scores to normalize them on a scale of 1 to 5
convert_to_likert <- function(score, min_score, max_score, likert_min, likert_max) {
  # Perform a linear transformation to scale the raw score to the Likert scale
  likert_score <- likert_min + (score - min_score) * (likert_max - likert_min) / (max_score - min_score)
  return(round(likert_score))
}

# Filtering the dataset for the ten countries selected for analysis
selected_countries <- c("Canada", "Spain", "Mexico", "Singapore", "India", "Indonesia",
  "Saudi Arabia", "Philippines", "Denmark", "Malaysia")

bd_selected <- bd %>%
  filter(Country %in% selected_countries)
```

```

# Applying the Likert scale conversion to the mask-wearing scores
# The mutate function adds new columns to the dataframe with the transformed Likert scale values
bd_selected <- bd_selected %>%
  mutate(
    Likert_Masks_Outside_Home = convert_to_likert(Scores.Masks.Outside_home, 0, 100, 1, 5),
    Likert_Masks_Grocery_Store = convert_to_likert(Scores.Masks.Grocery_store, 0, 100, 1, 5),
    Likert_Masks_Clothing_Store = convert_to_likert(Scores.Masks.Clothing_store, 0, 100, 1, 5),
    Likert_Masks_Work = convert_to_likert(Scores.Masks.Work, 0, 100, 1, 5),
    Likert_Masks_Public_Transport = convert_to_likert(Scores.Masks.Public_transport, 0, 100, 1, 5)
  )

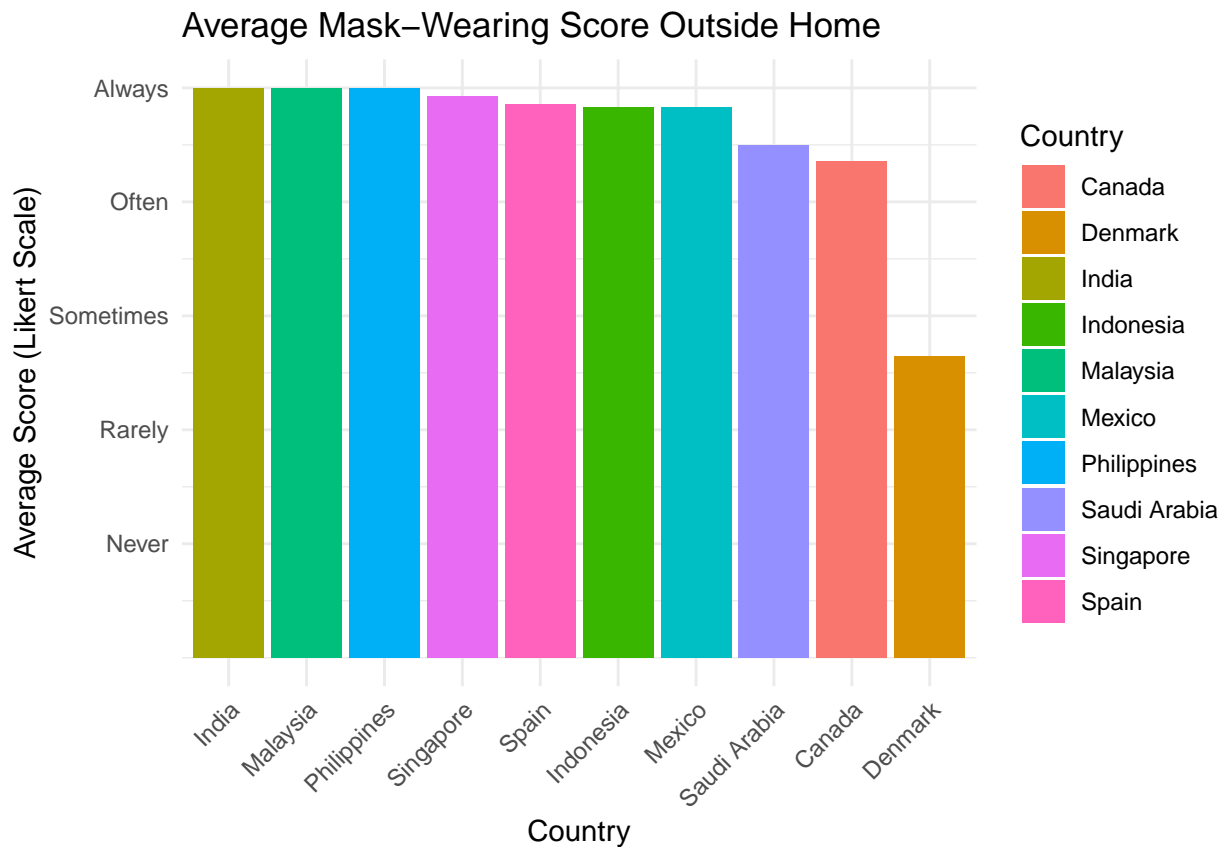
# Calculating the average Likert scale scores for each mask-wearing context by country
# This summary will be used to compare countries based on their mask-wearing compliance
mask_wearing_scores <- bd_selected %>%
  group_by(Country) %>%
  summarise(
    Average_Outside_Home = mean(Likert_Masks_Outside_Home, na.rm = TRUE),
    Average_Grocery_Store = mean(Likert_Masks_Grocery_Store, na.rm = TRUE),
    Average_Clothing_Store = mean(Likert_Masks_Clothing_Store, na.rm = TRUE),
    Average_Work = mean(Likert_Masks_Work, na.rm = TRUE),
    Average_Public_Transport = mean(Likert_Masks_Public_Transport, na.rm = TRUE)
  )

# Vector of labels for the Likert scale to be used on the y-axis of the bar charts
likert_labels <- c("Never", "Rarely", "Sometimes", "Often", "Always")

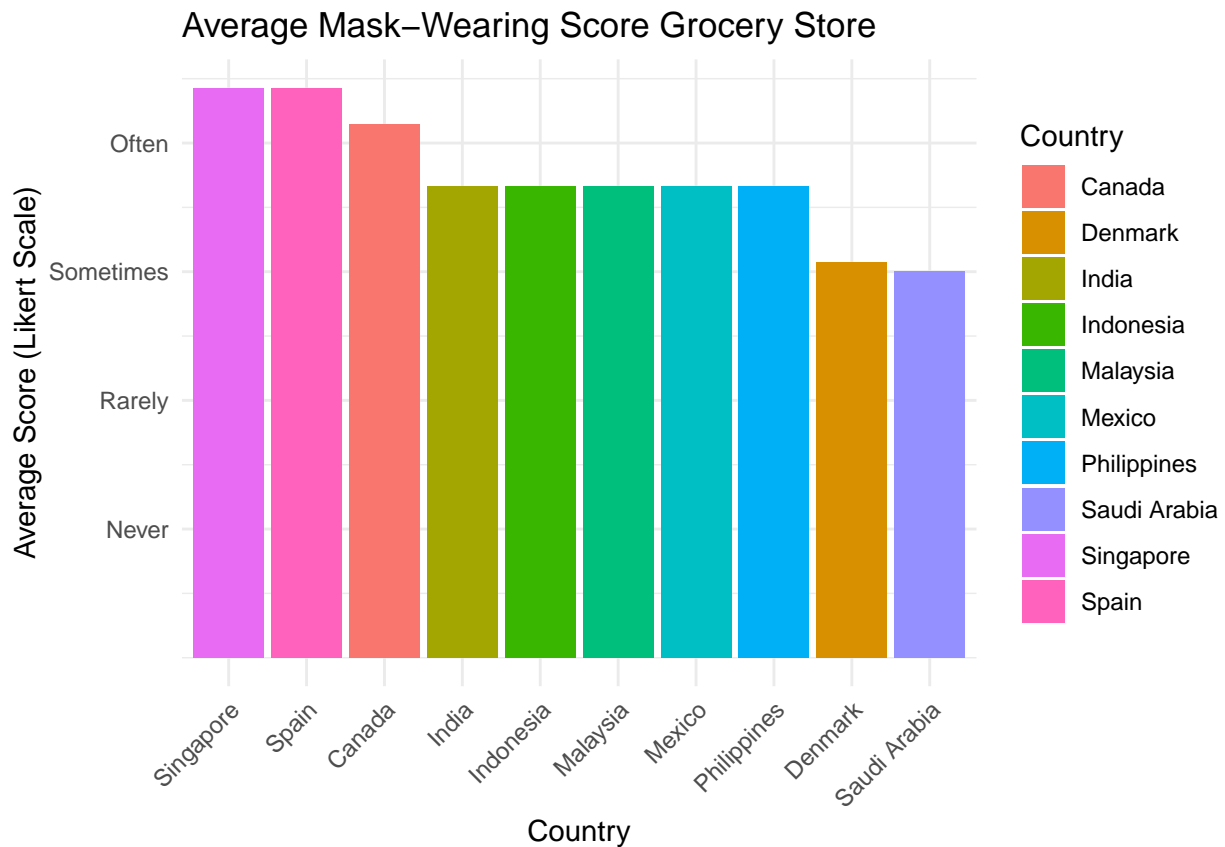
# Creating a series of bar charts for each mask-wearing context
# Each plot shows the average Likert scale score for mask-wearing in different contexts by country
# The reorder function arranges the countries on the x-axis based on their average score
# This allows for easier visual comparison of mask-wearing compliance across countries

# Plot the average mask-wearing score outside home with Likert scale labels
ggplot(mask_wearing_scores, aes(x = reorder(Country, -Average_Outside_Home),
                                y = Average_Outside_Home, fill = Country)) +
  geom_bar(stat = "identity") +
  scale_y_continuous(breaks = 1:5, labels = likert_labels) + # Apply Likert scale labels
  labs(title = "Average Mask-Wearing Score Outside Home",
       x = "Country",
       y = "Average Score (Likert Scale)") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))

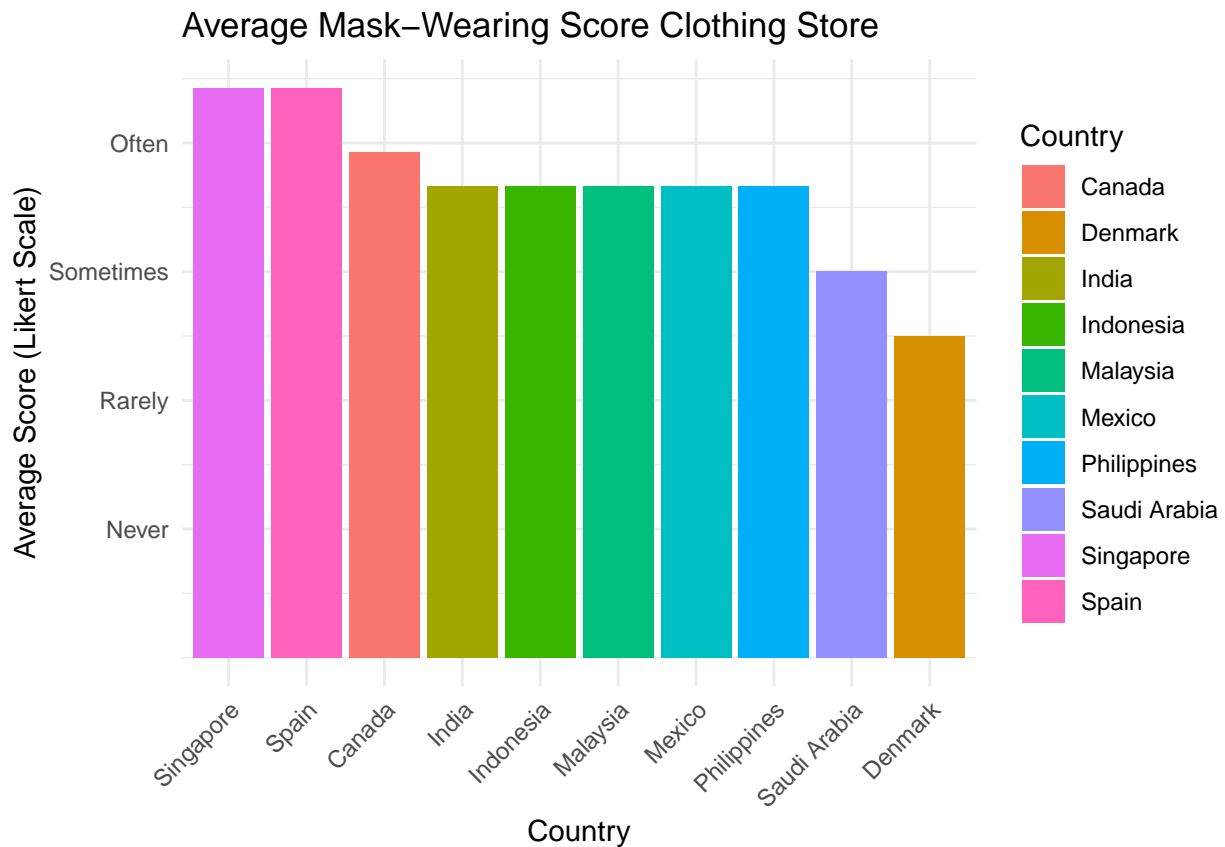
```



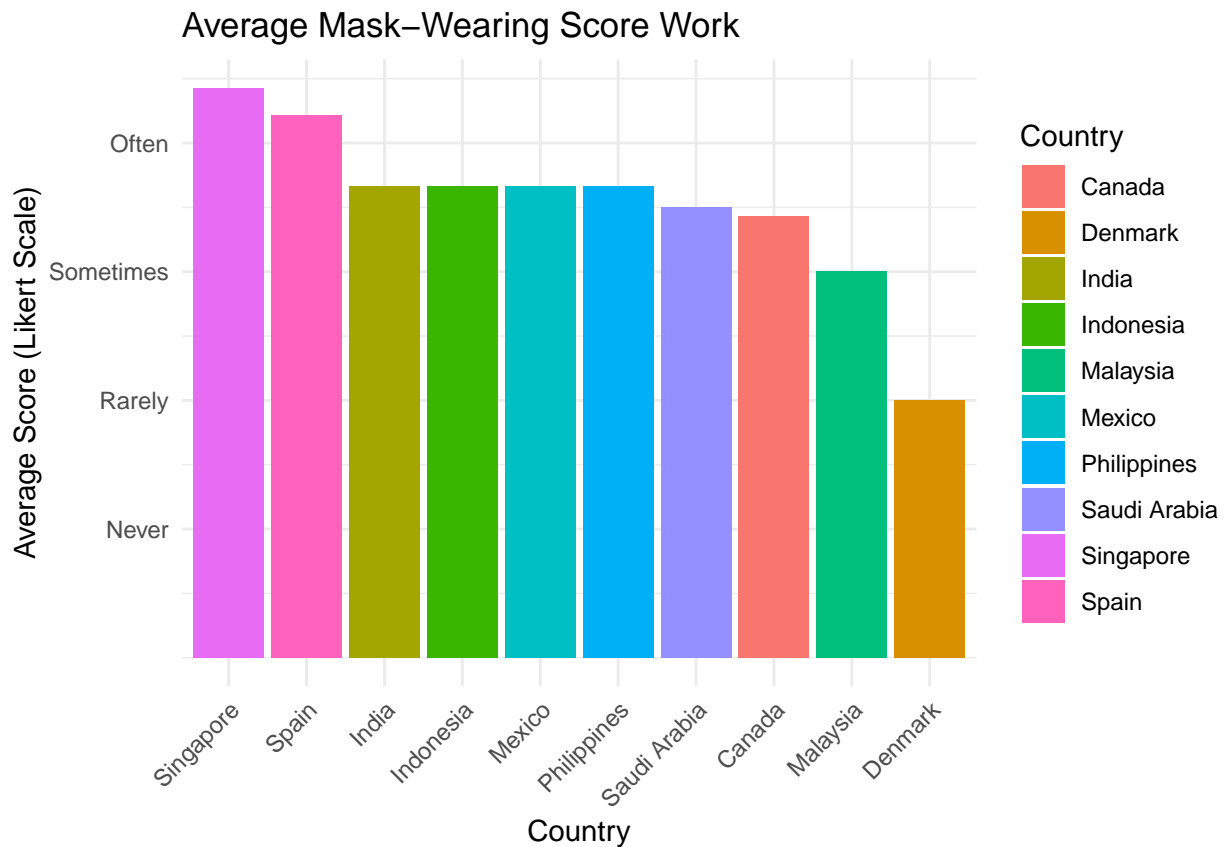
```
# Plot the average mask-wearing score outside home with Likert scale labels
ggplot(mask_wearing_scores, aes(x = reorder(Country, -Average_Grocery_Store),
                                   y = Average_Grocery_Store, fill = Country)) +
  geom_bar(stat = "identity") +
  scale_y_continuous(breaks = 1:5, labels = likert_labels) + # Apply Likert scale labels
  labs(title = "Average Mask-Wearing Score Grocery Store",
        x = "Country",
        y = "Average Score (Likert Scale)") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```



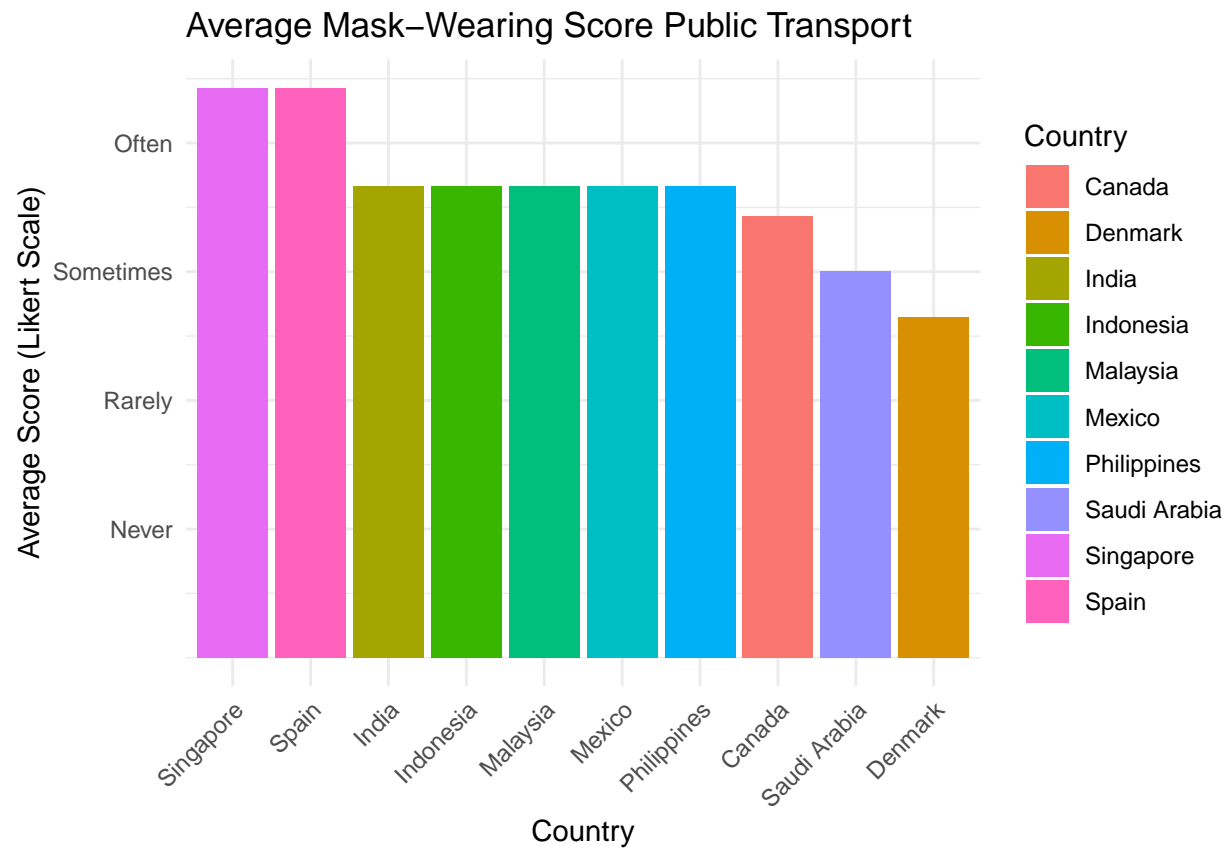
```
# Plot the average mask-wearing score outside home with Likert scale labels
ggplot(mask_wearing_scores, aes(x = reorder(Country, -Average_Clothing_Store),
                                   y = Average_Clothing_Store, fill = Country)) +
  geom_bar(stat = "identity") +
  scale_y_continuous(breaks = 1:5, labels = likert_labels) + # Apply Likert scale labels
  labs(title = "Average Mask-Wearing Score Clothing Store",
        x = "Country",
        y = "Average Score (Likert Scale)") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```



```
# Plot the average mask-wearing score outside home with Likert scale labels
ggplot(mask_wearing_scores, aes(x = reorder(Country, -Average_Work),
                                   y = Average_Work, fill = Country)) +
  geom_bar(stat = "identity") +
  scale_y_continuous(breaks = 1:5, labels = likert_labels) + # Apply Likert scale labels
  labs(title = "Average Mask-Wearing Score Work",
        x = "Country",
        y = "Average Score (Likert Scale)") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```



```
# Plot the average mask-wearing score outside home with Likert scale labels
ggplot(mask_wearing_scores, aes(x = reorder(Country, -Average_Public_Transport),
                                   y = Average_Public_Transport, fill = Country)) +
  geom_bar(stat = "identity") +
  scale_y_continuous(breaks = 1:5, labels = likert_labels) + # Apply Likert scale labels
  labs(title = "Average Mask-Wearing Score Public Transport",
        x = "Country",
        y = "Average Score (Likert Scale)") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```

These plots will be used to visually assess which countries had higher levels of compliance
 # with mask-wearing guidelines throughout the pandemic. The use of Likert scales facilitates
 # understanding the level of compliance in a standardized format.