Bayesian Spatial Analysis on Global Suicide Rates

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Introduction

Mental health has become an increasingly important topic and suicide remains a significant public health concern worldwide, with rates varying across regions due to complex social, economic, and cultural factors. Therefore, understanding the geographic distribution of suicide rates may be important for the development of targeted mental health policies and preventative measures. Although place of habitation clearly affect mental and physical lifestyles, there have few studies conducted on the geographical relationship between suicide rates and mental well-being.

In this study, we apply a Bayesian hierarchical model with a conditionally autoregressive (CAR) prior to investigate spatial patterns in suicide rates across countries. We model the suicide rate as a continuous outcome using a Gaussian likelihood, with a global intercept, a temporal effect comparing 2019 and 2021, and spatial random effects that capture regional deviations.

Our analysis focuses specifically on the years 2019 and 2021, to investigate any observable changes in suicide patterns potentially influenced by global events like the COVID-19 pandemic. Inference is performed using MCMC sampling in Stan. Our main research question is: Are there identifiable spatial patterns that persist after taking global and temporal effects into account, and did suicide rates change significantly between 2019 and 2021 at a global level?

This approach allows us to identify high-risk regions, quantify uncertainty, and better understand how suicide rates are spatially structure, with similarities among neighboring countries. Valuable insights from this analysis may provide the opportunity to create more data-informed mental health interventions.

The GitHub repository can be found at the following link:
https://github.com/minhVu03/Bayesian-Data-Analysis-Project

Literature Review

In a recent press release, the CDC stated that suicide rates in the US decreased from 2019 to 2020, but then increased from 2020 to 2021 (Centers for Disease Control and Prevention, 2022). Additionally, another paper stated that factors such as domestic violence, financial strain, and mental health conditions were prominent issues during the pandemic, and "the social restriction practices and policies imposed by different countries secondary to the COVID-19 pandemic might have negatively influenced the fore-said risk factors that has been indirectly led increased

rates of suicidal attempts and deaths" (Pathirathna et al., 2022). This information leads us to believe that it would be worthwhile to study the difference in suicide rates in 2019 and 2021.

A similar study on the relationship between location and suicide has been conducted, but the data was limited to regions in London and with the rise of social media and the global pandemic, the information may now be outdated (Congdon, P., 1997). In comparison, our dataset contains over 150 countries and the analysis focuses on 2019 and 2021, which may show the impact of the COVID-19 pandemic on suicide rates.

Dataset

Dataset Name: Crude Suicide Rate (Per 100,000 Population)
Source: https://www.who.int/data/gho/data/themes/mental-health/suicide-rates
Description: The raw dataset has notable features like country, age group, sex, and suicide rate (per 100,000 people) that can be extracted.

Variables:
Location: Country name
Period: Year (2019, 2021)
Dim1: Sex ("Female, "Both Sexes," "Male")
FactValueNumeric: Number of suicide deaths in a year, divided by the population and multiplied by 100,000 (as indicated in the original data source)
FactValueNumericLow: Low estimate
FactValueNumericHigh: High estimate

Note: The FactValueNumeric data are estimates of the number of suicides. The data was obtained from the WHO Global Health Estimates (GHE), but some countries may not have an accurate way of recording the exact number of deaths, potentially leading to inaccurate estimations. Hence, there is a high and a low in the death rates. The source states, "for countries without high-quality death registration data, cause of death estimates are calculated using other data, including household surveys with verbal autopsy, sample or sentinel registration systems, special studies" (World Health Organization, n.d.).

Data Cleaning

We filter out observations where sex is "Both Sexes" to remove duplicates, as this level accounts for observations that are already labeled either as "Female" or "Male." See (A2) for the R code. The first six rows of the dataset are shown below:

Description: df [6 × 6]

	Location <chr>	Period <int>	Dim1 <chr>	FactValueNumeric <dbl>	FactValueNumericLow <dbl>	FactValueNumericHigh <dbl>
1	Saint Vincent and the Grenadines	2021	Female	0.00	0.00	0.00
2	Oman	2021	Female	0.21	0.12	0.34
3	occupied Palestinian territory, including east Jerusalem	2021	Female	0.23	0.14	0.36
4	Jordan	2021	Female	0.29	0.18	0.43
5	Kuwait	2021	Female	0.34	0.25	0.39
6	Syrian Arab Republic	2021	Female	0.26	0.16	0.42

6 rows

Data Analysis

As we have obtained the data for suicide rates in 2019 and 2021, we can now declare a prior model based on information obtained from previous studies.

Model

In 2020, the global average suicide rate was 9.2 people per 100,000 people (World Health Organization, n.d.). Therefore, we've chosen this as the mean for our prior on the estimate of the global suicide rate μ. Additionally, a standard deviation of 3 allows for reasonable uncertainty around the average without being overly tight.

The β parameter represents the effect of time. In the US, the suicide rate in 2019 was 13.9 people per 100,000, then decreased to 13.5 people per 100,000 in 2020. It increased to 14 people per 100,000 in 2021, so we've used the overall change in suicide rate, 0.1, from 2019 to 2021 as the mean parameter.

The prior on both the standard deviation of spatial effects σ_ϕ and the observation noise σ is Exp(1), which allows for smaller, more reasonable standard deviations. We've chosen to use weakly informative parameters here. Put together, we have the following model.

Priors:

$\mu \sim N(9.2,\ 3)$

$\beta \sim N(0.1, 0.05)$

$\sigma_\phi \sim Exp(1)$

$\sigma \sim Exp(1)$

$\phi_{node1[i]} - \phi_{node2[i]} \sim N(0,\ \sigma_\phi)\ for\ i = 1,\ldots, N_{edges}$

$\sum_{r=1}^{R} \phi_r^2 \sim N(0,\ R * \sigma_\phi^2)$

Likelihood:

$y_n \sim (\mu + \beta\ * t_n + \phi_{r_n}, \sigma)\ for\ n = 1,\ldots, N$

Get Adjacency Pairs and Convert Neighbor List to Adjacency Pairs

Our dataset does not include information on the neighbors of each country, so we've used an additional dataset *rnaturalearthdata* to inform the conditional autoregressive aspect of the model. We renamed the country names in our dataset to match that of *rnaturalearthdata*'s. See (A3) for the R code. Then, we can join the two datasets so our original dataset will have adjacency parameters from the *world_sf* dataset. We also convert the country-level spatial polygons into adjacency pairs to represent neighboring countries, which we will use to build the CAR prior structure in our model. See (A4) and (A5) for the R code.

Note: After discussing with the TA during office hours, we made the decision to remove countries without neighbors (e.g. islands) from the dataset for the sake of simplicity.

Stan Data List

Now we can build our list of data inputs formatted for our Stan model. See (A11) for the Stan file and A(6) for the R code.

Note: We've chosen to use *iter=4000* and *warmup=2000* to improve MCMC mixing. Initially, we attempted using *iter=2000* and found that the chains did not mix well for μ, and increasing the number of iterations provided a slight improvement.

Posterior

Now, we can estimate the posterior. See (A7) for the R code. The estimates for the first 7 parameters are given below:

```
Inference for Stan model: anon_model.
4 chains, each with iter=4000; warmup=2000; thin=1;
post-warmup draws per chain=2000, total post-warmup draws=8000.

              mean se_mean    sd     2.5%      25%      50%      75%    97.5% n_eff Rhat
mu            9.21    0.41  3.23     3.50     6.81     9.15    11.40    15.76    62 1.07
beta          0.10    0.00  0.05     0.00     0.06     0.10     0.13     0.19  6745 1.00
phi[1]       -5.35    0.42  4.54   -14.34    -8.49    -5.31    -2.19     3.35   116 1.04
phi[2]       -5.64    0.42  4.62   -14.61    -8.79    -5.68    -2.41     3.42   122 1.04
phi[3]       -6.99    0.40  4.52   -16.09   -10.04    -6.90    -3.82     1.58   125 1.04
phi[4]       -1.40    0.42  4.58   -10.65    -4.43    -1.36     1.66     7.47   120 1.04
phi[5]       -8.50    0.42  4.68   -17.84   -11.63    -8.42    -5.30     0.48   127 1.03
```

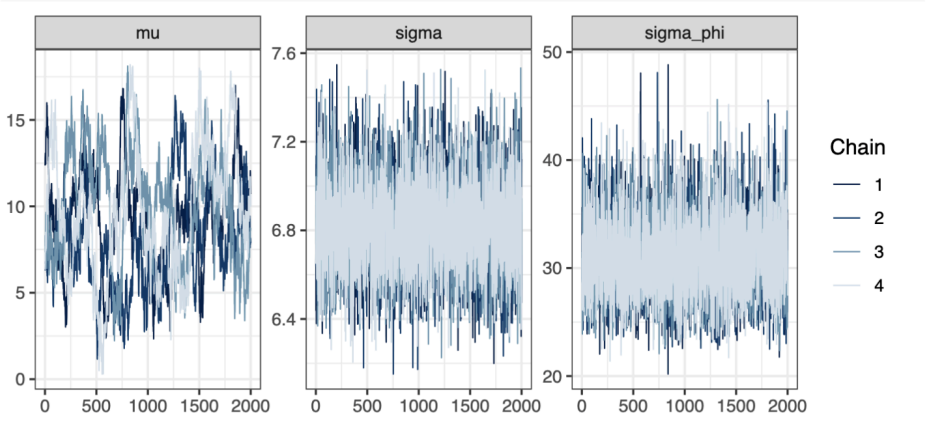
We see that the temporal effect β has a mean of 0.10, which suggests a slight increase in suicide rates in 2021 compared to 2019. However, zero is barely included in the 95% credible interval, which suggests that there is weak evidence of a time effect. Therefore, we conclude that there may be a small increased in suicide rates from 2019 to 2021, but the evidence is weak.

The *phi[r]* values represent the country-level deviations from the global suicide rate after adjusting for time. These come from a CAR prior, so they reflect spatial smoothing. We see that many of the values are non-zero (e.g. *phi[5]* = -8.50, indicating that this country has a suicide rate that is much lower than expected). This supports our assumption that spatial effects are strong and certain regions differ notably from the global mean, even after controlling for year. Additionally, some of the 95% credible intervals exclude 0, which provides strong evidence of spatial variation. See A(8) for a longer output of the estimates.

Our current model also requires that we estimate a parameter for every country, which has led to a very complex model. In further studies, it would be helpful to use Rao Blackwellization or similar methods to reduce the complexity of the model.

Model Diagnostics

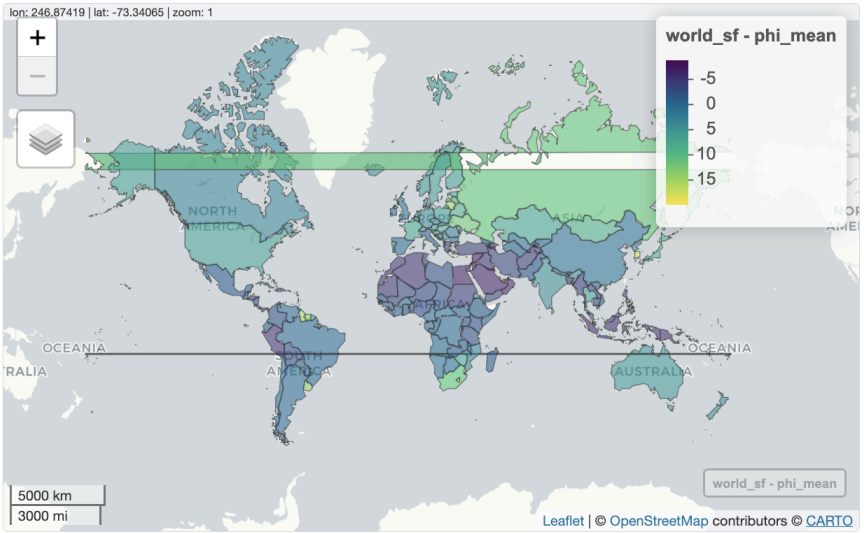
Now we can assess how well MCMC is mixing by using trace plots. See (A9) for the R code.



We observe that the trace plots for σ and σ_ϕ seem to be mixing well and converging. This indicates that σ is reliably estimated and the CAR prior is sampling effectively. However, we note that the trace plot for μ shows that the chains do not overlap well and may not converge. We've run the program multiple times to rule out "bad luck" as the cause and increased the number of iterations from 2000 to 4000, which helped minimally. The next steps would be to try a different proposal distribution, a different MCMC algorithm, or simplify the model.

Posterior Visualization

Now we can use the *mapview* library to visualize the posterior mean of the spatial effects on a map. See (A10) for the R code.



This visualization tells us how much each country deviates from the global average suicide rate, after adjusting for time. Countries that are darker in color indicate a lower-than-expected suicide rate, while countries that are lighter in color indicate a higher-than-expected suicide rate.

We see that cluster of high and low *phi_mean* are clearly visible (e.g. Eastern Europe countries are lighter in color and Sub-Saharan Africa countries are darker in color). Since the colorings are not random, they form geographically contiguous regions and strongly suggest spatial structure.

Discussion

Results

This analysis provides strong evidence that there is a spatial pattern in suicide rates. Our model identified strong regional deviations in suicide rates, even after adjusting for time, and many countries shower posterior mean spatial effects that were significantly above or below the global average. Since these deviations form geographic clusters rather than being randomly distributed, the analysis suggests that suicide rates are spatially dependent.

The time effect parameter β had a posterior mean of 0.1 and a 95% credible interval that barely excluded zero. This suggests that there may be a slight increase in suicide rates from 2019 to 2021, which could be linked to the COVID-19 pandemic. However, the magnitude is small and not strongly supported by the posterior.

Based on these results, it may be beneficial to focus on employing more mental health resources in countries like Russia and South Africa, where the suicide rates are higher than expected. Looking further into countries with suicide rates that are lower than expected may also be helpful, as they may offer protective factors worth studying (e.g. cultural or social influences).

Limitations

The spatial prior assumes that nearby countries have similar suicide rates, so if there are sharp differences between neighboring regions, the model may over-smooth and underrepresent the true variation. Additionally, the focus of this analysis is whether or not there is a spatial relationship between location and suicide rate, but it does not consider underlying factors, such as culture, mental health resources, and economic state. For example, the topic of mental health is considered to be taboo in many countries, resulting in limited access to mental health resources.

A next step would be to incorporate Rao Blackwellization or another form of model reduction to reduce the number of parameters and provide easier interpretability. It may also be helpful to look further into these underlying factors and determine whether or not there is a relationship between the factor and suicide rate (e.g. is there a relationship between suicide rate and lower income households in the United States and Canada?). This can be combined with information about distribution of suicide rates across sex and age to give more insight into which subset of groups should be targeted for suicide prevention methods in certain countries.

Member Contributions

Minh worked on the introduction, finding the dataset, model formulation, and data analysis. Jana worked on the literature review, model formulation, model diagnostics and posterior visualization, and discussion.

Appendix

(A1) Loading the Libraries

```
options(repos = c(CRAN = "https://cloud.r-project.org"))
knitr::opts_chunk$set(warning = FALSE, message = FALSE, error = TRUE)
library(tidyverse)
theme_set(theme_bw())
require(extraDistr) #need for rdunif
library(dplyr)
install.packages("webshot")
webshot::install_phantomjs()
suppressPackageStartupMessages(require(rstan))

required_packages <- c("sf", "spdep", "terra", "dplyr", "readr", "rnaturalearth",
"rnaturalearthdata")
installed_packages <- rownames(installed.packages())

for (pkg in required_packages) {
  if (!(pkg %in% installed_packages)) {
    install.packages(pkg)
  }
}

library(sf)
library(spdep)
library(terra)
library(dplyr)
library(readr)
library(rnaturalearth)
library(rnaturalearthdata)
library(ggplot2)
library(bayesplot)
library(mapview)
library(webshot)
library(htmlwidgets)

install.packages("fuzzyjoin")
library(fuzzyjoin)
```

(A2) Loading the Data

```
data_raw = read.csv("suicide_rate_raw.csv", header = TRUE)

#filter out "both sexes" to avoid duplication
data = as.data.frame(data_raw |> select(Location, Period, Dim1, FactValueNumeric,
FactValueNumericLow, FactValueNumericHigh) |> filter(Dim1 %in% c("Female", "Male")) |> filter
(Period %in% c(2019,2021)))
unique(data$Period)

max(data$FactValueNumeric)
min(data$FactValueNumeric)

nrow(data)
head(data)
```

(A3) Get Adjacency Pairs

```
data_cleaned <- data %>%
  mutate(Location = case_when(
    Location == "Viet Nam" ~ "Vietnam",
    Location == "Türkiye" ~ "Turkey",
    Location == "Iran (Islamic Republic of)" ~ "Iran",
    Location == "Russian Federation" ~ "Russia",
    Location == "Republic of Korea" ~ "South Korea",
    Location == "Syrian Arab Republic" ~ "Syria",
    Location == "Brunei Darussalam" ~ "Brunei",
    Location == "Netherlands (Kingdom of the)" ~ "Netherlands",
    Location == "Republic of Moldova" ~ "Moldova",
    Location == "Lao People's Democratic Republic" ~ "Laos",
    Location == "United Kingdom of Great Britain and Northern Ireland" ~ "United Kingdom",
    Location == "Venezuela (Bolivarian Republic of)" ~ "Venezuela",
    Location == "Bolivia (Plurinational State of)" ~ "Bolivia",
    Location == "Democratic People's Republic of Korea" ~ "North Korea",
    Location == "Micronesia (Federated States of)" ~ "Federated States of Micronesia",
    Location == "Cote d'Ivoire" ~ "Ivory Coast",
    Location == "Eswatini" ~ "eSwatini",
    Location == "Timor-Leste" ~ "East Timor",
    Location == "occupied Palestinian territory, including east Jerusalem" ~ "Palestine",
    Location == "Sao Tome and Principe" ~ "São Tomé and Principe",
    Location == "Bahamas" ~ "The Bahamas",
    Location == "Congo" ~ "Republic of the Congo",
    Location == "Serbia" ~ "Republic of Serbia",
    TRUE ~ Location  # keep all other names unchanged
  ))
```

(A4) Joining the Dataset

```
# From rnaturalearth dataset
world_sf <- ne_countries(scale = "medium", returnclass = "sf") %>%
  st_make_valid() %>%
  filter(admin %in% data_cleaned$Location) %>%
  arrange(admin)  # ensure a consistent order

world_sf$region_id <- 1:nrow(world_sf)

data_matched <- data_cleaned %>%
  filter(Location %in% world_sf$admin) %>%
  left_join(world_sf %>% st_drop_geometry() %>% select(admin, region_id),
            by = c("Location" = "admin"))

stopifnot(all(!is.na(data_matched$region_id)))

any(world_sf$region_id == 0)
```

(A5) Convert Neighbor List to Adjacency Pairs

```
world_sp <- as(world_sf, "Spatial")

neighbors <- poly2nb(world_sp, row.names = world_sf$region_id)

num_neighbors <- sapply(neighbors, length)
R <- length(neighbors)

#regions with at least one neighbor -> we want to leave out countries with no neighbors
valid_indices <- which(num_neighbors > 0)

node1 <- c()
node2 <- c()

for (i in valid_indices) { #only make nodes for countries with neighbors
  for (j in neighbors[[i]]) {
    if (j != 0 && world_sf$region_id[j] != 0) { #purposefully excluded zeros so node2 doesnt
                                                # have 0 "indexing" from region_id in world_sf
      node1 <- c(node1, world_sf$region_id[i])
      node2 <- c(node2, world_sf$region_id[j])
    }
  }
}

stopifnot(!any(node2 == 0))
length(node1)
length(node2)
any(node2==0)
```

(A6) Stan Data List

```
nrow(data_matched)
stan_data <- list(
  N = nrow(data_matched),
  y = data_matched$FactValueNumeric,
  time = as.integer(data_matched$Period == 2021),
  R = R,
  region = data_matched$region_id,
  N_edges = length(node1),
  node1 = node1,
  node2 = node2,
  num_neighbors = num_neighbors
)
```

(A7) Posterior

```
model <- stan_model(file = "model.stan")
fit <- sampling(model, data = stan_data, iter = 4000, warmup = 2000, chains = 4, seed = 123)
print(fit)
```

(A8) Posterior Output

	mean	se_mean	sd	2.5%	25%	50%	75%	97.5%	n_eff	Rhat
mu	9.21	0.41	3.23	3.50	6.81	9.15	11.40	15.76	62	1.07
beta	0.10	0.00	0.05	0.00	0.06	0.10	0.13	0.19	6745	1.00
phi[1]	-5.35	0.42	4.54	-14.34	-8.49	-5.31	-2.19	3.35	116	1.04
phi[2]	-5.64	0.42	4.62	-14.61	-8.79	-5.68	-2.41	3.42	122	1.04
phi[3]	-6.99	0.40	4.52	-16.09	-10.04	-6.90	-3.82	1.58	125	1.04
phi[4]	-1.40	0.42	4.58	-10.65	-4.43	-1.36	1.66	7.47	120	1.04
phi[5]	-8.50	0.42	4.68	-17.84	-11.63	-8.42	-5.30	0.48	127	1.03
phi[6]	-0.37	0.42	4.56	-9.44	-3.47	-0.29	2.84	8.11	117	1.04
phi[7]	-6.40	0.43	4.62	-15.39	-9.57	-6.31	-3.29	2.83	117	1.04
phi[8]	4.39	0.42	4.71	-4.80	1.12	4.45	7.65	13.24	123	1.04
phi[9]	5.24	0.42	4.53	-3.59	2.12	5.23	8.40	13.90	117	1.04
phi[10]	-6.90	0.42	4.54	-16.04	-9.96	-6.83	-3.73	1.66	118	1.04
phi[11]	-4.91	0.42	4.69	-14.23	-8.14	-4.84	-1.61	4.07	124	1.04
phi[12]	-6.11	0.42	4.57	-15.27	-9.17	-5.98	-2.98	2.52	121	1.04
phi[13]	-4.98	0.42	4.79	-14.25	-8.31	-4.96	-1.72	4.33	128	1.04
phi[14]	8.38	0.42	4.60	-0.69	5.28	8.42	11.64	17.16	122	1.03
phi[15]	8.50	0.42	4.67	-0.67	5.26	8.51	11.69	17.58	126	1.03
phi[16]	-4.61	0.42	4.56	-13.72	-7.75	-4.56	-1.55	4.16	120	1.04
phi[17]	-2.14	0.42	4.57	-11.28	-5.23	-2.01	0.95	6.66	121	1.04
phi[18]	-4.20	0.41	4.62	-13.54	-7.34	-4.14	-0.97	4.46	125	1.03
phi[19]	-4.23	0.42	4.54	-13.17	-7.30	-4.18	-1.05	4.46	115	1.04
phi[20]	1.22	0.41	4.66	-7.96	-1.88	1.22	4.45	9.98	129	1.03
phi[21]	-0.18	0.43	4.58	-9.09	-3.40	-0.11	3.03	8.71	113	1.04
phi[22]	-0.99	0.42	4.48	-10.03	-3.97	-0.93	2.05	7.56	114	1.04
phi[23]	-6.54	0.41	4.62	-15.62	-9.62	-6.49	-3.37	2.39	125	1.03
phi[24]	0.01	0.42	4.57	-9.02	-3.08	0.06	3.21	8.73	120	1.04
phi[25]	-1.08	0.42	4.52	-10.07	-4.16	-1.03	2.02	7.64	118	1.03
phi[26]	-1.94	0.41	4.55	-10.71	-5.03	-1.91	1.29	6.51	120	1.04
phi[27]	5.28	0.42	4.68	-4.13	2.10	5.37	8.48	14.27	123	1.04
phi[28]	-4.46	0.41	4.70	-13.79	-7.65	-4.33	-1.24	4.46	130	1.04
phi[29]	-1.08	0.42	4.52	-10.07	-4.12	-1.02	2.08	7.41	114	1.04
phi[30]	1.91	0.42	4.72	-7.33	-1.31	1.93	5.19	10.93	124	1.03
phi[31]	-0.15	0.42	4.52	-9.13	-3.16	-0.09	2.96	8.51	117	1.04
phi[32]	-3.95	0.42	4.54	-13.15	-7.10	-3.90	-0.75	4.82	118	1.04
phi[33]	-0.73	0.41	4.56	-9.91	-3.81	-0.64	2.46	8.00	125	1.04
phi[34]	-0.32	0.42	4.40	-8.91	-3.34	-0.35	2.80	8.16	110	1.04
phi[35]	-4.10	0.41	4.48	-12.92	-7.23	-4.07	-1.01	4.33	117	1.04
phi[36]	-3.16	0.42	4.67	-12.26	-6.33	-3.12	0.05	5.82	125	1.03
phi[37]	-1.83	0.42	4.71	-11.21	-4.94	-1.82	1.36	7.33	128	1.03
phi[38]	6.28	0.41	4.54	-2.69	3.18	6.34	9.43	14.88	123	1.03

```
phi[39]       4.62    0.42  4.75    -4.66     1.43     4.63     7.85    13.92   130 1.03
phi[40]      -5.50    0.41  4.68   -14.81    -8.67    -5.46    -2.16     3.13   132 1.04
phi[41]       3.67    0.42  4.59    -5.40     0.58     3.70     6.78    12.73   120 1.04
phi[42]      -0.94    0.41  4.44    -9.88    -3.98    -0.86     2.12     7.49   116 1.04
phi[43]       1.73    0.42  4.63    -7.44    -1.44     1.80     4.94    10.55   123 1.04
phi[44]      -1.19    0.42  4.66   -10.45    -4.25    -1.08     2.02     7.70   124 1.04
phi[45]      -4.24    0.42  4.65   -13.71    -7.36    -4.14    -1.02     4.73   121 1.04
phi[46]      -5.61    0.41  4.61   -14.68    -8.76    -5.50    -2.50     3.37   126 1.03
phi[47]      -1.44    0.42  4.65   -10.52    -4.58    -1.35     1.77     7.61   126 1.03
phi[48]      -8.27    0.41  4.52   -17.14   -11.37    -8.20    -5.11     0.54   123 1.03
phi[49]      -1.45    0.42  4.66   -10.75    -4.58    -1.33     1.70     7.40   126 1.03
phi[50]      -1.99    0.42  4.61   -11.08    -5.05    -1.91     1.21     6.79   122 1.04
phi[51]       3.45    0.42  4.60    -5.49     0.35     3.43     6.65    12.27   122 1.04
phi[52]       6.71    0.42  4.62    -2.61     3.66     6.71     9.85    15.64   123 1.04
phi[53]      -3.16    0.42  4.55   -12.18    -6.19    -3.10    -0.10     5.65   117 1.04
phi[54]      10.88    0.41  4.68     1.47     7.74    10.87    14.06    19.87   128 1.03
phi[55]      -0.43    0.42  4.77    -9.72    -3.64    -0.49     2.83     8.89   128 1.03
phi[56]       5.39    0.42  4.62    -3.84     2.29     5.48     8.64    14.03   122 1.04
phi[57]       6.24    0.41  4.52    -2.74     3.23     6.25     9.34    14.93   120 1.03
phi[58]      -1.32    0.41  4.66   -10.55    -4.50    -1.29     1.82     7.73   127 1.03
phi[59]      -4.29    0.41  4.65   -13.36    -7.45    -4.25    -1.14     4.54   132 1.03
phi[60]      -2.63    0.42  4.60   -11.53    -5.75    -2.58     0.50     6.39   123 1.04
phi[61]       3.61    0.42  4.47    -5.41     0.60     3.73     6.62    12.24   113 1.04
phi[62]      -3.74    0.43  4.64   -12.92    -6.80    -3.70    -0.57     5.10   118 1.04
phi[63]      -4.21    0.41  4.57   -13.30    -7.27    -4.15    -1.06     4.60   122 1.03
phi[64]      -8.10    0.41  4.69   -17.49   -11.32    -7.99    -4.82     0.85   130 1.03
phi[65]      -3.86    0.42  4.60   -13.07    -6.94    -3.72    -0.65     4.76   120 1.04
phi[66]      -4.13    0.42  4.53   -13.19    -7.16    -4.05    -1.01     4.41   117 1.04
phi[67]      -1.80    0.41  4.56   -10.74    -4.86    -1.80     1.29     7.12   125 1.03
phi[68]      16.36    0.41  4.57     7.20    13.32    16.38    19.47    25.38   122 1.04
phi[69]      -1.11    0.42  4.69   -10.58    -4.25    -1.04     2.17     7.74   124 1.03
phi[70]      -6.04    0.42  4.59   -15.16    -9.08    -6.01    -2.88     2.76   121 1.04
phi[71]       7.44    0.42  4.50    -1.53     4.43     7.45    10.51    16.12   117 1.04
phi[72]       2.54    0.40  4.69    -6.96    -0.63     2.63     5.75    11.47   136 1.03
phi[73]       3.05    0.42  4.56    -5.90    -0.04     3.13     6.23    11.80   116 1.04
phi[74]      -7.68    0.42  4.61   -16.88   -10.82    -7.61    -4.53     1.03   121 1.04
phi[75]      -5.11    0.42  4.47   -13.95    -8.11    -5.05    -2.03     3.36   113 1.04
phi[76]      -6.33    0.42  4.50   -15.25    -9.37    -6.27    -3.24     2.31   116 1.04
phi[77]      -0.87    0.42  4.69   -10.21    -4.11    -0.78     2.42     8.00   125 1.03
phi[78]      -5.01    0.42  4.53   -14.03    -8.10    -4.95    -1.83     3.52   118 1.03
phi[79]      -1.54    0.42  4.60   -10.45    -4.73    -1.46     1.73     7.24   123 1.04

phi[80]      -1.98    0.43  4.61   -10.87    -5.14    -1.91     1.27     6.82   114 1.04
phi[81]      -7.57    0.41  4.70   -16.78   -10.81    -7.54    -4.27     1.53   132 1.03
phi[82]       7.88    0.42  4.72    -1.43     4.70     7.92    11.13    16.87   127 1.04
phi[83]      -8.43    0.41  4.56   -17.45   -11.51    -8.38    -5.29     0.34   121 1.04
phi[84]       7.10    0.42  4.64    -2.22     4.00     7.16    10.36    15.81   124 1.04
phi[85]      -3.65    0.42  4.53   -12.49    -6.71    -3.64    -0.56     5.11   115 1.04
phi[86]       9.86    0.42  4.75     0.39     6.71     9.97    13.04    19.07   130 1.04
phi[87]      -7.42    0.42  4.67   -16.80   -10.52    -7.32    -4.18     1.45   124 1.03
phi[88]      -1.38    0.42  4.58   -10.36    -4.46    -1.38     1.75     7.54   120 1.04
phi[89]      -4.30    0.42  4.60   -13.57    -7.35    -4.22    -1.14     4.37   120 1.04
phi[90]       8.03    0.42  4.61    -1.19     5.03     8.07    11.17    16.80   118 1.04
phi[91]      -8.46    0.41  4.66   -17.79   -11.57    -8.40    -5.30     0.60   128 1.04
phi[92]      19.55    0.41  4.66    10.70    16.29    19.60    22.78    28.54   127 1.03
phi[93]      -3.31    0.42  4.60   -12.19    -6.46    -3.24    -0.16     5.60   121 1.03
phi[94]      -4.14    0.42  4.55   -13.06    -7.31    -4.03    -0.94     4.51   120 1.04
phi[95]      15.32    0.42  4.63     6.17    12.16    15.37    18.53    24.20   123 1.03
phi[96]       0.78    0.41  4.57    -8.24    -2.39     0.78     3.95     9.54   125 1.04
phi[97]      -3.26    0.42  4.66   -12.36    -6.40    -3.20    -0.13     5.84   124 1.03
phi[98]      -1.67    0.41  4.59   -10.80    -4.80    -1.56     1.50     7.03   124 1.04
 [ reached getOption("max.print") -- omitted 90 rows ]

Samples were drawn using NUTS(diag_e) at Sat Apr 19 22:14:10 2025.
For each parameter, n_eff is a crude measure of effective sample size,
and Rhat is the potential scale reduction factor on split chains (at
convergence, Rhat=1).
```

(A9) Model Diagnostics/Trace Plot

```
head(summary(fit)$summary)
mcmc_trace(as.array(fit), pars = c("mu", "sigma", "sigma_phi"))
```

(A10) Posterior Visualization

```
# posterior samples for phi
phi_samples <- rstan::extract(fit)$phi

# posterior mean of phi for each region
phi_mean <- apply(phi_samples, 2, mean)

world_sf$phi_mean <- phi_mean

m <- mapview(world_sf, zcol = "phi_mean")
m

# uncomment the following lines to convert to png
#mapshot(m, file = "phi_map.png")
#knitr::include_graphics("phi_map.png")
```

(A11) Stan file

```
data {
  int<lower=1> N;   // #of observations
  vector[N] y;//suicide rate (continuous)
  int<lower=0, upper=1> time[N];// Time indicator: 0 = 2019, 1 = 2021
  int<lower=1> R; // # regions (countries)
  int<lower=1, upper=R> region[N];//Region index per obs

  // CAR prior-specific inputs
  int<lower=0> N_edges; // # edges (adjacency links)
  int<lower=1, upper=R> node1[N_edges];
  int<lower=1, upper=R> node2[N_edges];
  int<lower=0> num_neighbors[R];// Number of neighbors per region
}

parameters {
  real mu; // global mean suicide rate
  real beta; // time effect
  vector[R] phi;  //spatial random effect (for CAR)
  real<lower=0> sigma_phi; //SD for spatial effect
  real<lower=0> sigma;// Observation noise
}

model {
  // priors
  mu ~ normal(9.2, 3); //lit reviewed global average
  beta ~ normal(0.1, 0.05);  //time effect prior
  sigma_phi ~ exponential(1);
  sigma ~ exponential(1);

  for (i in 1:N_edges) {
    target += -0.5 * square((phi[node1[i]] - phi[node2[i]]) / sigma_phi);
  }

  //soft sum-to-zero constraint for identifiability
  target += -0.5 * dot_self(phi) / (R * sigma_phi^2);

  //likelihood
  for (n in 1:N) {
    y[n] ~ normal(mu + beta * time[n] + phi[region[n]], sigma);
  }
}
```

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