

Bayesian Data Analysis Project

Members: Minh and Jana

```
options(repos = c(CRAN = "https://cloud.r-project.org"))
knitr::opts_chunk$set(warning = FALSE, message = FALSE, error = TRUE)
library(tidyverse)

## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr      1.1.4      v readr      2.1.5
## v forcats    1.0.0      v stringr   1.5.1
## v ggplot2    3.5.1      v tibble    3.2.1
## v lubridate  1.9.3      v tidyr     1.3.1
## v purrr      1.0.2
## -- Conflicts ----- tidyverse_conflicts() --
## x purrr::%||%() masks base::%||%()
## x dplyr::filter() masks stats::filter()
## x dplyr::lag() masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors

theme_set(theme_bw())
require(extraDistr) #need for rdunif

## Loading required package: extraDistr
##
## Attaching package: 'extraDistr'
##
## The following object is masked from 'package:purrr':
##
##      rdunif

library(dplyr)
suppressPackageStartupMessages(require(rstan))

#libraries for spatial data objects
#install these packages if they're not already installed :)
# install.packages(c("sf", "spdep", "rgdal")) #sf for vector datam-> shapefile
# install.packages("terra") # for raster data
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)
```

```
## Warning: package 'sf' was built under R version 4.4.3
```

```
## Linking to GEOS 3.13.0, GDAL 3.10.1, PROJ 9.5.1; sf_use_s2() is TRUE
```

```
library(spdep)
```

```
## Warning: package 'spdep' was built under R version 4.4.3
```

```
## Loading required package: spData
```

```
## Warning: package 'spData' was built under R version 4.4.3
```

```
## To access larger datasets in this package, install the spDataLarge  
## package with: 'install.packages('spDataLarge',  
## repos='https://nowosad.github.io/drat/', type='source')'
```

```
library(terra)
```

```
## Warning: package 'terra' was built under R version 4.4.3
```

```
## terra 1.8.42
```

```
##
```

```
## Attaching package: 'terra'
```

```
##
```

```
## The following object is masked from 'package:rstan':
```

```
##
```

```
##     extract
```

```
##
```

```
## The following object is masked from 'package:tidyr':
```

```
##
```

```
##     extract
```

```
library(dplyr)
```

```
library(readr)
```

```
library(rnaturalearth)
```

```
## Warning: package 'rnaturalearth' was built under R version 4.4.3
```

```
library(rnaturalearthdata)
```

```
## Warning: package 'rnaturalearthdata' was built under R version 4.4.3
```

```
##
```

```
## Attaching package: 'rnaturalearthdata'
```

```
##
```

```
## The following object is masked from 'package:rnaturalearth':
```

```
##
```

```
##     countries110
```

```
#For fuzzy matching rnaturalearthdata country names to our dataset's country names  
install.packages("fuzzyjoin")
```

```
## Installing package into 'C:/Users/Minh/AppData/Local/R/win-library/4.4'  
## (as 'lib' is unspecified)
```

```
## package 'fuzzyjoin' successfully unpacked and MD5 sums checked  
##  
## The downloaded binary packages are in  
## C:\Users\Minh\AppData\Local\Temp\Rtmpe4w70B\downloaded_packages
```

```
library(fuzzyjoin)
```

```
## Warning: package 'fuzzyjoin' was built under R version 4.4.3
```

Introduction

In our world today, mental health has become more crucial 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 is important for the development of targeted mental health policies and preventative measures. Although where we live in the world largely affects our mental and physical lifestyles, there has not been many studies done on the geographical characteristics of 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, stratified by sex groups. We will be using a Poisson likelihood to obtain a prior distribution. After which, inferential analysis will be done using Monte Carlo Markov Chain (MCMC) done in Stan.

This research specifically focuses on two recent years, 2019 and 2021, to investigate any observable changes in suicide patterns potentially influenced by global events like the COVID-19 pandemic. Our main research question is: Are there identifiable spatial clusters of high suicide rates, and do these rates differ between 2019 and 2021?

This approach allows us to identify high-risk regions, quantify uncertainty, and better understand how neighboring countries may influence each other's suicide rates, providing valuable insights for data-informed mental health interventions.

Literature Review

TO DO

Dataset and Data Cleaning

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.

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 estimates are derived from the WHO Global Health Estimates (GHE)” [data source]. However, 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 low in the death rates. “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” [data source].

```
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))
unique(data$Period)
```

```
## [1] 2021 2019
```

```
# unique(data$Location)
max(data$FactValueNumeric)
```

```
## [1] 48
```

```
min(data$FactValueNumeric)
```

```
## [1] 0
```

```
nrow(data)
```

```
## [1] 740
```

The dataset after filtering consists of 740 observations.

Data Analysis

As we have obtained the cleaned data for suicide rates in 2019 and 2021, we can now declare a prior model from information obtained historically.

Explanation of priors

... Numbers in the parameters list in stan code

Get adjacency pairs

Firstly we need to know which countries are neighbours of each other <https://cran.r-project.org/web/packages/rnaturalearth/vignettes/rnaturalearth.html>

During the data analysis process we realized that the country names in our dataset did not match with the country names of the rnaturalearthdata dataset that we are using to model the spatial data. This led to the model mistaking the countries as having no neighbours and producing nodes with values 0. To solve this, we renamed the country names in our dataset to match that of rnaturalworld's

```

# unique(data$Location)
# unique(world_sf$admin)

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 Príncipe",
    Location == "Bahamas" ~ "The Bahamas",
    Location == "Congo" ~ "Republic of the Congo",
    Location == "Serbia" ~ "Republic of Serbia",
    TRUE ~ Location # keep all other names unchanged
  ))

# Search for country names in both datasets for debugging and filtering names
# subset(data_cleaned, grepl("Singapore", Location, ignore.case = TRUE))
# unique(subset(world_sf, grepl("Singapore", admin, ignore.case = TRUE)))

```

Now we can join the two datasets so our original dataset will have adjacency parameters from world_sf

```

# From rnatuarearth 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)

```

```
## [1] FALSE
```

Convert Neighbor List to Adjacency Pairs

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

#### making neighbors!!
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$region_id[j] != 0) { #i purposely excluded zeros so node2 doesnt have 0 "ind
      node1 <- c(node1, world_sf$region_id[i])
      node2 <- c(node2, world_sf$region_id[j])
    }
  }
}

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

```
## [1] 610
```

```
length(node2)
```

```
## [1] 610
```

```
any(node2==0) #a lot of debugging led to this being false
```

```
## [1] FALSE
```

STAN Data List

```
nrow(data_matched)
```

```
## [1] 740
```

```
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
)

```

Extract posterior data from STAN code file Code reference: https://ubc-stat-ml.github.io/web447/w08_mcmc1/topic06_hands_on.html Why use iter = 2000 and chains = 4:

```

#setwd("C:/Users/Minh/OneDrive/Documents/Bayesian-Data-Analysis-Project")
model <- stan_model(file = "model.stan")
fit <- sampling(model, data = stan_data, iter = 2000, chains = 4, seed = 123)

```

```

##
## SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 1).
## Chain 1:
## Chain 1: Gradient evaluation took 0.00042 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 4.2 seconds.
## Chain 1: Adjust your expectations accordingly!
## Chain 1:
## Chain 1:
## Chain 1: Iteration:    1 / 2000 [  0%] (Warmup)
## Chain 1: Iteration:   200 / 2000 [ 10%] (Warmup)
## Chain 1: Iteration:   400 / 2000 [ 20%] (Warmup)
## Chain 1: Iteration:   600 / 2000 [ 30%] (Warmup)
## Chain 1: Iteration:   800 / 2000 [ 40%] (Warmup)
## Chain 1: Iteration:  1000 / 2000 [ 50%] (Warmup)
## Chain 1: Iteration:  1001 / 2000 [ 50%] (Sampling)
## Chain 1: Iteration:  1200 / 2000 [ 60%] (Sampling)
## Chain 1: Iteration:  1400 / 2000 [ 70%] (Sampling)
## Chain 1: Iteration:  1600 / 2000 [ 80%] (Sampling)
## Chain 1: Iteration:  1800 / 2000 [ 90%] (Sampling)
## Chain 1: Iteration:  2000 / 2000 [100%] (Sampling)
## Chain 1:
## Chain 1: Elapsed Time: 9.944 seconds (Warm-up)
## Chain 1:                7.555 seconds (Sampling)
## Chain 1:                17.499 seconds (Total)
## Chain 1:
##
## SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 2).
## Chain 2:
## Chain 2: Gradient evaluation took 0.000147 seconds
## Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 1.47 seconds.
## Chain 2: Adjust your expectations accordingly!
## Chain 2:
## Chain 2:
## Chain 2: Iteration:    1 / 2000 [  0%] (Warmup)
## Chain 2: Iteration:   200 / 2000 [ 10%] (Warmup)
## Chain 2: Iteration:   400 / 2000 [ 20%] (Warmup)
## Chain 2: Iteration:   600 / 2000 [ 30%] (Warmup)
## Chain 2: Iteration:   800 / 2000 [ 40%] (Warmup)

```

```

## Chain 2: Iteration: 1000 / 2000 [ 50%] (Warmup)
## Chain 2: Iteration: 1001 / 2000 [ 50%] (Sampling)
## Chain 2: Iteration: 1200 / 2000 [ 60%] (Sampling)
## Chain 2: Iteration: 1400 / 2000 [ 70%] (Sampling)
## Chain 2: Iteration: 1600 / 2000 [ 80%] (Sampling)
## Chain 2: Iteration: 1800 / 2000 [ 90%] (Sampling)
## Chain 2: Iteration: 2000 / 2000 [100%] (Sampling)
## Chain 2:
## Chain 2: Elapsed Time: 10.665 seconds (Warm-up)
## Chain 2: 4.279 seconds (Sampling)
## Chain 2: 14.944 seconds (Total)
## Chain 2:
##
## SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 3).
## Chain 3:
## Chain 3: Gradient evaluation took 0.000148 seconds
## Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 1.48 seconds.
## Chain 3: Adjust your expectations accordingly!
## Chain 3:
## Chain 3:
## Chain 3: Iteration: 1 / 2000 [ 0%] (Warmup)
## Chain 3: Iteration: 200 / 2000 [ 10%] (Warmup)
## Chain 3: Iteration: 400 / 2000 [ 20%] (Warmup)
## Chain 3: Iteration: 600 / 2000 [ 30%] (Warmup)
## Chain 3: Iteration: 800 / 2000 [ 40%] (Warmup)
## Chain 3: Iteration: 1000 / 2000 [ 50%] (Warmup)
## Chain 3: Iteration: 1001 / 2000 [ 50%] (Sampling)
## Chain 3: Iteration: 1200 / 2000 [ 60%] (Sampling)
## Chain 3: Iteration: 1400 / 2000 [ 70%] (Sampling)
## Chain 3: Iteration: 1600 / 2000 [ 80%] (Sampling)
## Chain 3: Iteration: 1800 / 2000 [ 90%] (Sampling)
## Chain 3: Iteration: 2000 / 2000 [100%] (Sampling)
## Chain 3:
## Chain 3: Elapsed Time: 10.886 seconds (Warm-up)
## Chain 3: 4.421 seconds (Sampling)
## Chain 3: 15.307 seconds (Total)
## Chain 3:
##
## SAMPLING FOR MODEL 'anon_model' NOW (CHAIN 4).
## Chain 4:
## Chain 4: Gradient evaluation took 0.00015 seconds
## Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 1.5 seconds.
## Chain 4: Adjust your expectations accordingly!
## Chain 4:
## Chain 4:
## Chain 4: Iteration: 1 / 2000 [ 0%] (Warmup)
## Chain 4: Iteration: 200 / 2000 [ 10%] (Warmup)
## Chain 4: Iteration: 400 / 2000 [ 20%] (Warmup)
## Chain 4: Iteration: 600 / 2000 [ 30%] (Warmup)
## Chain 4: Iteration: 800 / 2000 [ 40%] (Warmup)
## Chain 4: Iteration: 1000 / 2000 [ 50%] (Warmup)
## Chain 4: Iteration: 1001 / 2000 [ 50%] (Sampling)
## Chain 4: Iteration: 1200 / 2000 [ 60%] (Sampling)
## Chain 4: Iteration: 1400 / 2000 [ 70%] (Sampling)

```



```
## Chain 4: Iteration: 1600 / 2000 [ 80%] (Sampling)
## Chain 4: Iteration: 1800 / 2000 [ 90%] (Sampling)
## Chain 4: Iteration: 2000 / 2000 [100%] (Sampling)
## Chain 4:
## Chain 4: Elapsed Time: 9.939 seconds (Warm-up)
## Chain 4: 4.415 seconds (Sampling)
## Chain 4: 14.354 seconds (Total)
## Chain 4:
```

```
print(fit)
```

```
## Inference for Stan model: anon_model.
## 4 chains, each with iter=2000; warmup=1000; thin=1;
## post-warmup draws per chain=1000, total post-warmup draws=4000.
##
##               mean se_mean   sd    2.5%    25%    50%    75%    97.5%
## mu             9.59    0.55  3.00     3.33     7.78     9.57    11.52    15.33
## beta          -0.28    0.01  0.44    -1.15    -0.58    -0.27     0.03     0.59
## phi[1]         -5.55    0.55  4.38    -14.06    -8.59    -5.60    -2.65     3.39
## phi[2]         -5.86    0.56  4.46    -14.42    -8.89    -5.87    -2.88     3.13
## phi[3]         -7.19    0.54  4.42    -15.92   -10.25    -7.23    -4.15     1.38
## phi[4]         -1.56    0.57  4.43    -10.15    -4.53    -1.56     1.39     7.04
## phi[5]         -8.79    0.56  4.53    -17.66   -11.81    -8.78    -5.72     0.22
## phi[6]         -0.65    0.56  4.38     -8.93    -3.62    -0.69     2.20     8.27
## phi[7]         -6.61    0.55  4.45    -15.08    -9.67    -6.70    -3.65     2.26
## phi[8]           4.13    0.55  4.55     -4.61     1.11     4.14     7.24    13.01
## phi[9]           4.98    0.56  4.32     -3.51     2.03     4.91     7.86    13.48
## phi[10]        -7.16    0.57  4.38    -15.92   -10.13    -7.21    -4.21     1.35
## phi[11]        -5.21    0.56  4.54    -14.14    -8.22    -5.29    -2.26     3.90
## phi[12]        -6.25    0.55  4.45    -14.71    -9.29    -6.39    -3.17     2.65
## phi[13]        -5.16    0.53  4.53    -14.15    -8.21    -5.26    -1.95     3.88
## phi[14]          8.23    0.57  4.41     -0.33     5.22     8.24    11.25    16.90
## phi[15]          8.38    0.56  4.39      0.02     5.44     8.40    11.36    17.13
## phi[16]        -4.74    0.57  4.51    -13.27    -7.84    -4.77    -1.65     3.97
## phi[17]        -2.37    0.56  4.39    -10.89    -5.39    -2.38     0.52     6.36
## phi[18]        -4.43    0.56  4.52    -13.10    -7.55    -4.41    -1.53     5.01
## phi[19]        -4.41    0.57  4.43    -12.91    -7.46    -4.38    -1.38     4.23
## phi[20]          1.01    0.56  4.51     -7.94    -1.91     1.06     3.95     9.74
## phi[21]        -0.38    0.57  4.50     -9.03    -3.39    -0.43     2.53     8.58
## phi[22]        -1.16    0.55  4.32     -9.49    -4.13    -1.19     1.68     7.36
## phi[23]        -6.73    0.55  4.51    -15.50    -9.77    -6.68    -3.77     2.09
## phi[24]        -0.23    0.55  4.39     -8.83    -3.16    -0.31     2.65     8.52
## phi[25]        -1.18    0.56  4.48    -10.00    -4.18    -1.19     1.82     7.63
## phi[26]        -2.07    0.56  4.50    -10.78    -5.21    -2.13     0.94     6.48
## phi[27]          5.08    0.55  4.50     -3.87     2.09     5.09     8.14    13.91
## phi[28]        -4.63    0.55  4.44    -13.46    -7.60    -4.61    -1.62     4.13
## phi[29]        -1.25    0.55  4.43     -9.86    -4.25    -1.31     1.77     7.52
## phi[30]          1.77    0.54  4.46     -6.87    -1.30     1.72     4.79    10.28
## phi[31]        -0.26    0.56  4.35     -8.89    -3.25    -0.24     2.76     8.13
## phi[32]        -4.08    0.56  4.40    -12.83    -7.10    -4.04    -1.03     4.71
## phi[33]        -0.88    0.55  4.45     -9.47    -3.91    -0.87     2.15     7.96
## phi[34]        -0.48    0.55  4.15     -8.54    -3.26    -0.59     2.37     7.67
## phi[35]        -4.25    0.55  4.38    -13.10    -7.15    -4.21    -1.30     4.19
## phi[36]        -3.37    0.54  4.53    -11.94    -6.50    -3.38    -0.31     5.61
```

## phi[37]	-2.00	0.56	4.41	-10.78	-5.02	-1.93	1.07	6.38
## phi[38]	6.16	0.56	4.44	-2.61	3.18	6.08	9.18	14.91
## phi[39]	4.40	0.55	4.53	-4.67	1.35	4.40	7.47	13.17
## phi[40]	-5.63	0.54	4.51	-14.54	-8.62	-5.61	-2.58	3.05
## phi[41]	3.43	0.56	4.51	-5.29	0.36	3.39	6.47	12.36
## phi[42]	-1.19	0.57	4.35	-9.60	-4.19	-1.16	1.78	7.47
## phi[43]	1.56	0.56	4.52	-7.34	-1.50	1.55	4.55	10.28
## phi[44]	-1.43	0.55	4.52	-10.21	-4.42	-1.46	1.65	7.65
## phi[45]	-4.35	0.54	4.52	-13.09	-7.37	-4.34	-1.39	4.60
## phi[46]	-5.82	0.55	4.53	-14.81	-8.78	-5.79	-2.88	3.13
## phi[47]	-1.59	0.53	4.40	-10.04	-4.58	-1.61	1.31	7.15
## phi[48]	-8.46	0.57	4.45	-17.05	-11.46	-8.52	-5.38	0.24
## phi[49]	-1.68	0.54	4.46	-10.52	-4.64	-1.63	1.47	7.02
## phi[50]	-2.24	0.55	4.40	-10.71	-5.23	-2.17	0.75	6.18
## phi[51]	3.23	0.53	4.46	-5.63	0.28	3.14	6.11	11.84
## phi[52]	6.50	0.55	4.48	-2.42	3.51	6.50	9.54	15.12
## phi[53]	-3.30	0.55	4.37	-11.76	-6.24	-3.25	-0.33	5.18
## phi[54]	10.76	0.54	4.55	2.07	7.63	10.70	13.81	19.85
## phi[55]	-0.62	0.54	4.58	-9.74	-3.65	-0.60	2.48	8.25
## phi[56]	5.20	0.55	4.53	-3.86	2.20	5.22	8.20	14.19
## phi[57]	6.04	0.55	4.30	-2.30	3.06	5.94	8.94	14.42
## phi[58]	-1.48	0.54	4.36	-10.11	-4.43	-1.44	1.36	7.10
## phi[59]	-4.38	0.55	4.54	-13.38	-7.43	-4.43	-1.31	4.43
## phi[60]	-2.91	0.55	4.45	-11.83	-5.83	-2.89	0.15	5.97
## phi[61]	3.44	0.54	4.27	-4.78	0.55	3.37	6.28	11.91
## phi[62]	-3.91	0.55	4.43	-12.64	-6.86	-3.84	-0.96	4.75
## phi[63]	-4.37	0.54	4.38	-13.07	-7.27	-4.38	-1.43	4.50
## phi[64]	-8.34	0.56	4.60	-17.42	-11.52	-8.32	-5.24	0.93
## phi[65]	-3.89	0.56	4.46	-12.75	-6.81	-3.91	-1.06	5.19
## phi[66]	-4.33	0.56	4.42	-12.85	-7.18	-4.31	-1.41	4.52
## phi[67]	-2.04	0.56	4.57	-10.80	-5.17	-1.98	1.01	7.00
## phi[68]	16.23	0.55	4.50	7.29	13.20	16.20	19.25	25.21
## phi[69]	-1.28	0.55	4.59	-10.21	-4.44	-1.31	1.88	7.79
## phi[70]	-6.24	0.55	4.45	-14.98	-9.23	-6.32	-3.28	2.80
## phi[71]	7.26	0.57	4.42	-1.21	4.27	7.23	10.17	15.97
## phi[72]	2.40	0.56	4.56	-6.83	-0.49	2.43	5.52	11.11
## phi[73]	2.87	0.59	4.42	-5.83	-0.12	2.83	5.78	11.95
## phi[74]	-7.88	0.56	4.50	-16.46	-11.11	-7.86	-4.83	1.02
## phi[75]	-5.26	0.54	4.28	-13.64	-8.14	-5.25	-2.46	3.25
## phi[76]	-6.50	0.55	4.51	-15.13	-9.61	-6.58	-3.41	2.43
## phi[77]	-1.02	0.56	4.55	-9.78	-4.10	-0.94	1.99	8.12
## phi[78]	-5.15	0.55	4.42	-13.97	-8.03	-5.09	-2.17	3.43
## phi[79]	-1.73	0.54	4.41	-10.38	-4.70	-1.68	1.20	6.79
## phi[80]	-2.20	0.57	4.40	-10.70	-5.22	-2.12	0.85	6.16
## phi[81]	-7.81	0.55	4.61	-16.97	-10.91	-7.78	-4.81	1.45
## phi[82]	7.69	0.57	4.59	-1.19	4.55	7.63	10.84	16.84
## phi[83]	-8.69	0.56	4.40	-17.31	-11.58	-8.69	-5.76	-0.20
## phi[84]	6.90	0.56	4.45	-1.73	3.92	6.75	9.96	15.72
## phi[85]	-3.77	0.55	4.33	-12.12	-6.80	-3.83	-0.83	4.92
## phi[86]	9.72	0.57	4.52	0.75	6.53	9.73	12.87	18.48
## phi[87]	-7.69	0.54	4.55	-16.23	-10.86	-7.68	-4.56	1.37
## phi[88]	-1.60	0.56	4.41	-10.23	-4.56	-1.60	1.34	7.18
## phi[89]	-4.48	0.53	4.41	-13.03	-7.47	-4.54	-1.54	4.15
## phi[90]	7.94	0.55	4.52	-0.79	4.96	7.91	11.01	16.68

## phi[91]	-8.64	0.56	4.52	-17.40	-11.71	-8.73	-5.50	0.12
## phi[92]	19.41	0.57	4.63	10.45	16.25	19.46	22.59	28.85
## phi[93]	-3.50	0.56	4.53	-12.48	-6.47	-3.35	-0.55	5.26
## phi[94]	-4.27	0.56	4.37	-12.72	-7.23	-4.43	-1.28	4.43
## phi[95]	15.14	0.54	4.36	6.37	12.31	15.08	17.97	23.80
## phi[96]	0.71	0.57	4.55	-7.89	-2.44	0.69	3.72	9.56
## phi[97]	-3.47	0.56	4.54	-12.37	-6.58	-3.50	-0.37	5.61
## phi[98]	-1.84	0.56	4.46	-10.44	-4.95	-1.89	1.12	7.28
## phi[99]	-4.03	0.55	4.47	-12.81	-6.99	-4.06	-0.96	4.70
## phi[100]	-7.68	0.56	4.55	-16.19	-10.88	-7.65	-4.55	1.41
## phi[101]	-5.16	0.55	4.34	-13.84	-8.05	-5.19	-2.27	3.34
## phi[102]	-3.27	0.54	4.45	-12.06	-6.32	-3.21	-0.28	5.18
## phi[103]	-6.54	0.53	4.41	-15.00	-9.58	-6.56	-3.47	2.15
## phi[104]	0.70	0.54	4.49	-8.17	-2.39	0.66	3.70	9.33
## phi[105]	-2.70	0.54	4.49	-11.34	-5.70	-2.73	0.27	6.26
## phi[106]	4.85	0.56	4.49	-3.96	1.73	4.87	7.89	13.52
## phi[107]	8.33	0.54	4.45	-0.27	5.30	8.18	11.30	17.30
## phi[108]	3.38	0.56	4.43	-5.36	0.40	3.41	6.33	12.12
## phi[109]	-6.34	0.55	4.54	-15.35	-9.33	-6.25	-3.33	2.53
## phi[110]	2.17	0.56	4.37	-6.46	-0.84	2.35	5.11	10.71
## phi[111]	-5.85	0.56	4.36	-14.36	-8.83	-5.87	-2.89	3.10
## phi[112]	-0.49	0.54	4.40	-9.13	-3.46	-0.46	2.43	8.18
## phi[113]	1.02	0.57	4.50	-7.62	-2.05	1.02	3.98	9.99
## phi[114]	2.04	0.55	4.47	-6.73	-0.94	1.98	5.00	10.79
## phi[115]	2.43	0.56	4.66	-6.47	-0.69	2.38	5.55	11.55
## phi[116]	-4.96	0.56	4.45	-13.71	-7.96	-4.92	-1.88	3.92
## phi[117]	-4.79	0.56	4.39	-13.32	-7.76	-4.78	-1.84	3.86
## phi[118]	-4.67	0.54	4.34	-13.27	-7.60	-4.73	-1.86	4.14
## phi[119]	0.95	0.56	4.48	-7.75	-2.14	0.85	4.00	9.85
## phi[120]	-3.81	0.56	4.45	-12.46	-6.93	-3.75	-0.75	4.85
## phi[121]	3.67	0.57	4.47	-4.97	0.59	3.57	6.71	12.32
## phi[122]	-8.13	0.53	4.39	-16.57	-11.09	-8.24	-5.22	0.71
## phi[123]	-3.54	0.58	4.49	-12.27	-6.60	-3.51	-0.54	5.13
## phi[124]	-8.78	0.55	4.46	-17.60	-11.79	-8.78	-5.71	-0.14
## phi[125]	-6.40	0.55	4.49	-15.18	-9.43	-6.49	-3.43	2.47
## phi[126]	-7.53	0.57	4.45	-16.06	-10.57	-7.51	-4.62	1.19
## phi[127]	-2.34	0.57	4.45	-11.21	-5.34	-2.35	0.70	6.35
## phi[128]	-7.04	0.57	4.40	-15.54	-10.06	-7.17	-4.00	1.67
## phi[129]	-6.15	0.55	4.51	-15.18	-9.20	-6.09	-2.99	2.39
## phi[130]	5.06	0.53	4.29	-3.06	2.15	4.95	7.94	13.63
## phi[131]	2.88	0.54	4.49	-5.76	-0.19	2.89	6.06	11.60
## phi[132]	-3.63	0.54	4.52	-12.45	-6.72	-3.66	-0.68	5.56
## phi[133]	-5.27	0.56	4.58	-13.99	-8.40	-5.28	-2.16	4.00
## phi[134]	5.79	0.55	4.33	-2.80	2.77	5.84	8.76	14.35
## phi[135]	-2.42	0.55	4.37	-10.66	-5.49	-2.50	0.49	6.53
## phi[136]	0.81	0.57	4.45	-8.00	-2.12	0.80	3.79	9.60
## phi[137]	12.15	0.56	4.33	3.98	9.11	12.06	15.08	20.74
## phi[138]	-1.09	0.55	4.41	-9.48	-4.17	-1.06	1.93	7.63
## phi[139]	-3.13	0.55	4.59	-12.07	-6.24	-3.14	-0.06	5.97
## phi[140]	-9.04	0.56	4.51	-17.91	-12.04	-9.01	-6.11	-0.29
## phi[141]	2.95	0.54	4.67	-6.12	-0.23	3.03	6.13	11.93
## phi[142]	-8.34	0.56	4.33	-16.51	-11.29	-8.35	-5.45	0.39
## phi[143]	-2.74	0.55	4.44	-11.43	-5.72	-2.75	0.20	6.02
## phi[144]	-3.63	0.55	4.51	-12.29	-6.68	-3.71	-0.54	5.29

```

## phi[145]    -3.36    0.58    4.53   -12.25   -6.43   -3.34   -0.30    5.45
## phi[146]    -1.37    0.53    4.45   -10.30   -4.36   -1.28    1.55    7.46
## phi[147]     0.91    0.56    4.34    -7.61   -2.02    0.85    3.95    9.31
## phi[148]     9.08    0.54    4.46     0.49    6.02    9.00   12.17   18.03
## phi[149]    10.32    0.56    4.70     0.84    7.18   10.31   13.49   19.35
## phi[150]    -1.61    0.55    4.41   -10.22   -4.57   -1.69    1.34    7.00
## phi[151]    11.53    0.56    4.41     2.83    8.71   11.53   14.46   20.30
## phi[152]    18.12    0.58    4.52     9.33   15.05   18.14   21.13   26.83
## phi[153]    -1.95    0.54    4.33   -10.38   -4.91   -1.95    0.89    6.75
## phi[154]    -0.69    0.55    4.48    -9.24   -3.82   -0.67    2.28    8.36
## phi[155]     6.25    0.57    4.56    -2.75    3.09    6.32    9.30   15.30
## phi[156]    -5.69    0.56    4.41   -14.11   -8.70   -5.60   -2.75    2.95
## phi[157]    14.25    0.57    4.47     5.69   11.15   14.21   17.26   23.09
## phi[158]     4.73    0.57    4.53    -4.30    1.72    4.65    7.76   13.63
## phi[159]     4.48    0.54    4.41    -4.17    1.54    4.42    7.51   13.30
## phi[160]    -8.71    0.57    4.36   -17.26  -11.68   -8.68   -5.75   -0.24
## phi[161]    -8.56    0.55    4.62   -17.27  -11.75   -8.62   -5.48    0.63
## phi[162]    -6.49    0.54    4.41   -14.83   -9.55   -6.60   -3.48    2.16
## phi[163]     4.92    0.57    4.47    -3.90    1.91    4.93    7.91   13.84
## phi[164]    -5.82    0.55    4.47   -14.55   -8.78   -5.78   -2.84    3.01
## phi[165]    -0.10    0.56    4.46    -8.75   -3.09   -0.13    2.85    8.89
## phi[166]    -4.80    0.55    4.52   -13.64   -7.76   -4.84   -1.90    4.26
## phi[167]     4.25    0.53    4.52    -4.56    1.24    4.14    7.23   13.38
## phi[168]    -7.16    0.56    4.56   -16.15  -10.32   -7.13   -4.08    1.79
## phi[169]    -6.13    0.55    4.28   -14.37   -9.05   -6.13   -3.30    2.28
## phi[170]    -2.39    0.54    4.41   -11.15   -5.31   -2.35    0.60    6.13
## phi[171]    -3.90    0.56    4.49   -12.83   -6.90   -3.85   -0.91    4.89
## phi[172]    12.73    0.54    4.34     4.26    9.81   12.72   15.67   21.25
## phi[173]    -7.79    0.56    4.49   -16.46  -10.85   -7.80   -4.88    1.22
## phi[174]     0.01    0.56    4.54    -9.13   -2.99    0.06    3.03    8.99
## phi[175]    -4.12    0.54    4.32   -12.40   -7.09   -4.20   -1.20    4.48
## phi[176]     5.60    0.55    4.54    -2.89    2.50    5.62    8.56   14.57
## phi[177]    14.31    0.56    4.41     5.61   11.37   14.17   17.23   23.22
## phi[178]    -0.43    0.55    4.39    -8.75   -3.36   -0.47    2.44    8.35
## phi[179]     6.34    0.57    4.60    -2.67    3.20    6.28    9.38   15.38
## phi[180]    -1.14    0.55    4.45    -9.57   -4.17   -1.17    1.82    7.51
## phi[181]    -2.06    0.55    4.50   -10.86   -5.09   -2.08    0.96    6.75
## phi[182]    -5.33    0.57    4.47   -13.96   -8.40   -5.41   -2.42    3.48
## phi[183]    -2.53    0.56    4.36   -10.97   -5.52   -2.48    0.40    5.95
## phi[184]     6.81    0.54    4.43    -1.85    3.75    6.82    9.78   15.48
## phi[185]    18.06    0.54    4.50     9.32   14.96   17.95   20.99   27.16
## sigma_phi    31.23    0.07    3.47    24.96   28.87   30.99   33.39   38.77
## sigma        6.83    0.00    0.20     6.46    6.69    6.82    6.95    7.23
## lp__         -1841.86    0.30  11.10 -1865.53 -1849.27 -1841.36 -1834.09 -1821.73
##
##          n_eff Rhat
## mu          30 1.12
## beta       2149 1.00
## phi[1]       63 1.05
## phi[2]       64 1.05
## phi[3]       66 1.05
## phi[4]       60 1.05
## phi[5]       66 1.05
## phi[6]       62 1.05
## phi[7]       65 1.05

```

## phi[8]	68 1.05
## phi[9]	59 1.05
## phi[10]	60 1.05
## phi[11]	67 1.05
## phi[12]	65 1.05
## phi[13]	72 1.04
## phi[14]	60 1.06
## phi[15]	61 1.06
## phi[16]	63 1.05
## phi[17]	62 1.05
## phi[18]	65 1.05
## phi[19]	60 1.05
## phi[20]	65 1.05
## phi[21]	63 1.05
## phi[22]	61 1.05
## phi[23]	67 1.05
## phi[24]	64 1.05
## phi[25]	65 1.05
## phi[26]	65 1.05
## phi[27]	66 1.05
## phi[28]	65 1.05
## phi[29]	65 1.05
## phi[30]	69 1.05
## phi[31]	60 1.06
## phi[32]	62 1.05
## phi[33]	64 1.05
## phi[34]	58 1.06
## phi[35]	63 1.05
## phi[36]	71 1.05
## phi[37]	62 1.05
## phi[38]	63 1.05
## phi[39]	67 1.05
## phi[40]	69 1.05
## phi[41]	65 1.05
## phi[42]	57 1.06
## phi[43]	65 1.05
## phi[44]	69 1.05
## phi[45]	71 1.05
## phi[46]	67 1.05
## phi[47]	68 1.05
## phi[48]	62 1.05
## phi[49]	70 1.05
## phi[50]	64 1.05
## phi[51]	72 1.04
## phi[52]	67 1.05
## phi[53]	63 1.05
## phi[54]	70 1.05
## phi[55]	71 1.06
## phi[56]	68 1.05
## phi[57]	61 1.06
## phi[58]	66 1.05
## phi[59]	68 1.05
## phi[60]	66 1.05
## phi[61]	63 1.05

## phi[62]	65	1.05
## phi[63]	65	1.05
## phi[64]	67	1.05
## phi[65]	63	1.05
## phi[66]	61	1.06
## phi[67]	67	1.05
## phi[68]	68	1.05
## phi[69]	69	1.05
## phi[70]	65	1.05
## phi[71]	60	1.06
## phi[72]	65	1.05
## phi[73]	57	1.06
## phi[74]	64	1.05
## phi[75]	64	1.05
## phi[76]	66	1.05
## phi[77]	66	1.05
## phi[78]	64	1.05
## phi[79]	66	1.05
## phi[80]	61	1.06
## phi[81]	70	1.04
## phi[82]	64	1.05
## phi[83]	63	1.05
## phi[84]	62	1.05
## phi[85]	61	1.05
## phi[86]	63	1.05
## phi[87]	70	1.05
## phi[88]	62	1.05
## phi[89]	68	1.05
## phi[90]	68	1.05
## phi[91]	66	1.05
## phi[92]	67	1.05
## phi[93]	66	1.05
## phi[94]	61	1.05
## phi[95]	65	1.05
## phi[96]	65	1.05
## phi[97]	67	1.05
## phi[98]	65	1.05
## phi[99]	65	1.05
## phi[100]	65	1.05
## phi[101]	63	1.05
## phi[102]	67	1.05
## phi[103]	69	1.05
## phi[104]	70	1.05
## phi[105]	69	1.05
## phi[106]	65	1.05
## phi[107]	69	1.05
## phi[108]	62	1.05
## phi[109]	67	1.05
## phi[110]	61	1.05
## phi[111]	60	1.06
## phi[112]	65	1.05
## phi[113]	61	1.05
## phi[114]	65	1.05
## phi[115]	68	1.05

## phi[116]	64	1.05
## phi[117]	62	1.05
## phi[118]	65	1.05
## phi[119]	65	1.05
## phi[120]	62	1.05
## phi[121]	62	1.05
## phi[122]	69	1.05
## phi[123]	60	1.06
## phi[124]	66	1.05
## phi[125]	68	1.05
## phi[126]	60	1.06
## phi[127]	62	1.05
## phi[128]	59	1.06
## phi[129]	66	1.05
## phi[130]	66	1.05
## phi[131]	69	1.05
## phi[132]	69	1.05
## phi[133]	67	1.05
## phi[134]	62	1.05
## phi[135]	62	1.05
## phi[136]	62	1.06
## phi[137]	59	1.06
## phi[138]	65	1.05
## phi[139]	69	1.05
## phi[140]	64	1.06
## phi[141]	74	1.04
## phi[142]	60	1.05
## phi[143]	66	1.05
## phi[144]	66	1.05
## phi[145]	62	1.06
## phi[146]	70	1.04
## phi[147]	60	1.06
## phi[148]	67	1.05
## phi[149]	70	1.05
## phi[150]	63	1.05
## phi[151]	63	1.05
## phi[152]	62	1.05
## phi[153]	65	1.05
## phi[154]	67	1.05
## phi[155]	64	1.05
## phi[156]	62	1.05
## phi[157]	63	1.05
## phi[158]	64	1.05
## phi[159]	66	1.05
## phi[160]	58	1.06
## phi[161]	71	1.05
## phi[162]	68	1.05
## phi[163]	62	1.05
## phi[164]	66	1.05
## phi[165]	63	1.05
## phi[166]	68	1.05
## phi[167]	74	1.04
## phi[168]	66	1.05
## phi[169]	60	1.05

```

## phi[170]      66 1.05
## phi[171]      65 1.05
## phi[172]      64 1.05
## phi[173]      65 1.05
## phi[174]      65 1.05
## phi[175]      64 1.05
## phi[176]      68 1.05
## phi[177]      62 1.05
## phi[178]      64 1.05
## phi[179]      64 1.05
## phi[180]      66 1.05
## phi[181]      68 1.05
## phi[182]      62 1.05
## phi[183]      61 1.05
## phi[184]      66 1.04
## phi[185]      69 1.05
## sigma_phi    2828 1.00
## sigma        2300 1.00
## lp__         1380 1.00
##
## Samples were drawn using NUTS(diag_e) at Sat Apr 19 05:17:12 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).

```