

geospatial_HCV

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R Markdown

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

```
## -- 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 lubridate  1.9.4      v tibble     3.2.1
```

```
## v purrr      1.0.4      v tidyr      1.3.1
```

```
## -- Conflicts ----- tidyverse_conflicts() --
```

```
## 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
```

```
##
```

```
## Attaching package: 'rnatrualearthdata'
```

```
##
```

```
##
```

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

```
##
```

```
##      countries110
```

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

```
##
```

```
## Attaching package: 'cowplot'
```

```
##
```

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

```
##
```

```
##      get_legend
```

```
##
```

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

```
##
```

```
##      align_plots
```

```
##
```

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

```
##
```

```
##      stamp
```

```
# Get the list of all states
```

```
all_states <- states()
```

```
# Define a color for each state: light yellow for Kaduna, grey for others
state_colors <- ifelse(all_states == "Kaduna", "lightyellow", "grey")

# Plot the map with specified state colors
map_ng(region = all_states, col = state_colors, show.text = TRUE, title = "Map of Nigeria Highlighting Kaduna State")
```

Map of Nigeria Highlighting Kaduna State



```
library(readxl)
```

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

```
hiv_data<- read_excel("C:/Users/Usman Ola/Documents/Spatial_abs_present/data for geospatial distribution of HIV")
# hcv_data<- read_excel("data for geospatial distribution of HCV.xlsx",sheet = "HCV RNA")
# hcv_data<- hcv_data %>% rename(
#   "name"="Local Government of",
#   "present"="POSITIVE FOR HCV RNA"
# ) %>%group_by(name) %>%
#   count(present) %>% mutate(name=str_replace(name,"soba","Soba"))

names(hiv_data)<-c("name","hcv_ab")
hiv_data<- hiv_data %>%
  mutate(name=recode(name,"soba"="Soba")) %>%
  group_by(name) %>%
  count(hcv_ab)
```

```

# Download Natural Earth data for administrative level 1 (states/provinces)
nigeria_states <- ne_states(country = "Nigeria", returnclass = "sf")
#nigeria<-ne_countries(country = "Nigeria")
# Filter the data to include only Kaduna State
kaduna_state <- nigeria_states[nigeria_states$name == "Kaduna", ]

# Merge the spatial data with the HIV data
data <- nigeria_states %>%
  left_join(hiv_data, by = c("name"))
# Plot Nigeria state boundaries

# Replace with the path to your extracted shapefile
nigeria_lga_shapefile <- "C:/Users/Usman Ola/Documents/Spatial_abs_present/NGA_adm2.shp"

# Read the shapefile
nigeria_lgas <- st_read(nigeria_lga_shapefile)

```

```

## Reading layer 'NGA_adm2' from data source
## 'C:\Users\Usman Ola\Documents\Spatial_abs_present\NGA_adm2.shp'
## using driver 'ESRI Shapefile'
## Simple feature collection with 775 features and 11 fields
## Geometry type: MULTIPOLYGON
## Dimension: XY
## Bounding box: xmin: 2.668431 ymin: 4.270418 xmax: 14.67642 ymax: 13.89201
## Geodetic CRS: WGS 84

```

```

kaduna_state <- nigeria_lgas %>% filter(NAME_1 == "Kaduna")

```

```

# Merge the spatial data with the HIV data
data <- nigeria_states %>%
  left_join(hiv_data, by = "name")
# Plot Nigeria's state boundaries
p3<-ggplot() +
  geom_sf(data = nigeria_states, fill = "white", color = "black") + # Other states
  geom_sf(data = kaduna_state, fill = "yellow", color = "black") + # Kaduna State
  #labs(title = "Map of Nigeria Highlighting Kaduna State") +
  theme_minimal() +
  theme(
    panel.grid.major = element_blank(), # Remove major grid lines
    panel.grid.minor = element_blank(), # Remove minor grid lines
    axis.title = element_blank(), # Remove axis titles
    axis.text = element_blank(), # Remove axis text
    axis.ticks = element_blank(), # Remove axis ticks
    panel.background = element_blank(), # Remove background
    legend.position = "right" # Position legend on the right
  )

# Replace with the path to your extracted shapefile
nigeria_lga_shapefile <- "C:/Users/Usman Ola/Documents/Spatial_abs_present/NGA_adm2.shp"

```

```

# Read the shapefile
nigeria_lgas <- st_read(nigeria_lga_shapefile)

## Reading layer 'NGA_adm2' from data source
## 'C:\Users\Usman Ola\Documents\Spatial_abs_present\NGA_adm2.shp'
## using driver 'ESRI Shapefile'
## Simple feature collection with 775 features and 11 fields
## Geometry type: MULTIPOLYGON
## Dimension: XY
## Bounding box: xmin: 2.668431 ymin: 4.270418 xmax: 14.67642 ymax: 13.89201
## Geodetic CRS: WGS 84

kaduna_state <- nigeria_lgas %>% filter(NAME_1 == "Kaduna")

# Plot Nigeria's LGAs
ggplot(data = filter(nigeria_lgas, NAME_1 == "Kaduna")) +
  geom_sf(fill = "lightyellow", color = "black") +
  geom_sf_text(aes(label = NAME_2), size = 2) + # Adjust 'NAME_2' based on your shapefile's column name
  labs(title = "Map of Nigeria with Local Government Areas") +
  theme_minimal() +
  theme(
    panel.grid.major = element_blank(), # Remove major grid lines
    panel.grid.minor = element_blank(), # Remove minor grid lines
    axis.title = element_blank(), # Remove axis titles
    axis.text = element_blank(), # Remove axis text
    axis.ticks = element_blank(), # Remove axis ticks
    panel.background = element_blank(), # Remove background
    legend.position = "right" # Position legend on the right
  )

## Warning in st_point_on_surface.sfc(sf::st_zm(x)): st_point_on_surface may not
## give correct results for longitude/latitude data

```

Map of Nigeria with Local Government Areas



```
# Merge the spatial data with the HIV data
data <- nigeria_lgas[nigeria_lgas$NAME_1=="Kaduna",] %>%
  left_join(hiv_data, by = c( "NAME_2"="name"))

### hcv data result from kaduna
p1<-ggplot(data = data) +
  geom_sf(aes(fill = n), color = "black") +
  geom_sf_text(aes(label = NAME_2), size = 2) +
  scale_fill_viridis_c(name = "HCV AB Prevalence (%)", na.value = "white") +
  labs(title = "HCV AB Prevalence Rates in Kaduna") +
  theme_minimal() +
  theme(
    panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(),
    axis.title = element_blank(),
    axis.text = element_blank(),
    axis.ticks = element_blank(),
    panel.background = element_blank(),
    legend.position = "right"
  ) + annotation_scale(location = "bl", width_hint = 0.4) +
  annotation_north_arrow(location = "bl", which_north = "true",
    pad_x = unit(.2, "in"), pad_y = unit(4, "in"),
    style = north_arrow_fancy_orienteering)

#### HCV RNA prevalence data
```

```

data2 <- nigeria_lgas[nigeria_lgas$NAME_1=="Kaduna",] %>%
  left_join(hiv_data, by = c( "NAME_2"="name"))

p2<-ggplot(data = data2) +
  geom_sf(aes(fill = n), color = "black") +
  geom_sf_text(aes(label = NAME_2), size = 2) +
  scale_fill_viridis_c(name = "HCV AB Prevalence (%)", na.value = "white") +
  labs(title = "HCV AB Prevalence Rates in Kaduna") +
  theme_minimal() +
  theme(
    panel.grid.major = element_blank(),
    panel.grid.minor = element_blank(),
    axis.title = element_blank(),
    axis.text = element_blank(),
    axis.ticks = element_blank(),
    panel.background = element_blank(),
    legend.position = "right"
  ) + annotation_scale(location = "bl", width_hint = 0.4) +
  annotation_north_arrow(location = "bl", which_north = "true",
    pad_x = unit(.2, "in"), pad_y = unit(4, "in"),
    style = north_arrow_fancy_orienteering)

# Arrange plots in a single column
combined_plot <- p1 / p2

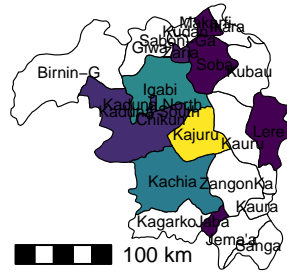
# Combine plots with a shared legend
combined_plot <- ggarrange(p1, p2,
  ncol = 1, nrow = 2,
  common.legend = TRUE, legend = "bottom")

## Warning in st_point_on_surface.sfc(sf::st_zm(x)): st_point_on_surface may not
## give correct results for longitude/latitude data
## Warning in st_point_on_surface.sfc(sf::st_zm(x)): st_point_on_surface may not
## give correct results for longitude/latitude data
## Warning in st_point_on_surface.sfc(sf::st_zm(x)): st_point_on_surface may not
## give correct results for longitude/latitude data

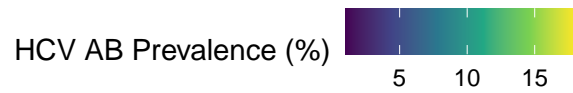
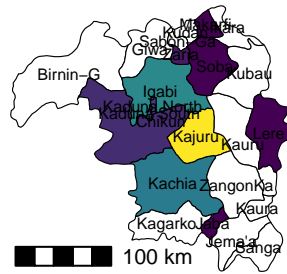
# Display the combined plot
print(combined_plot)

```

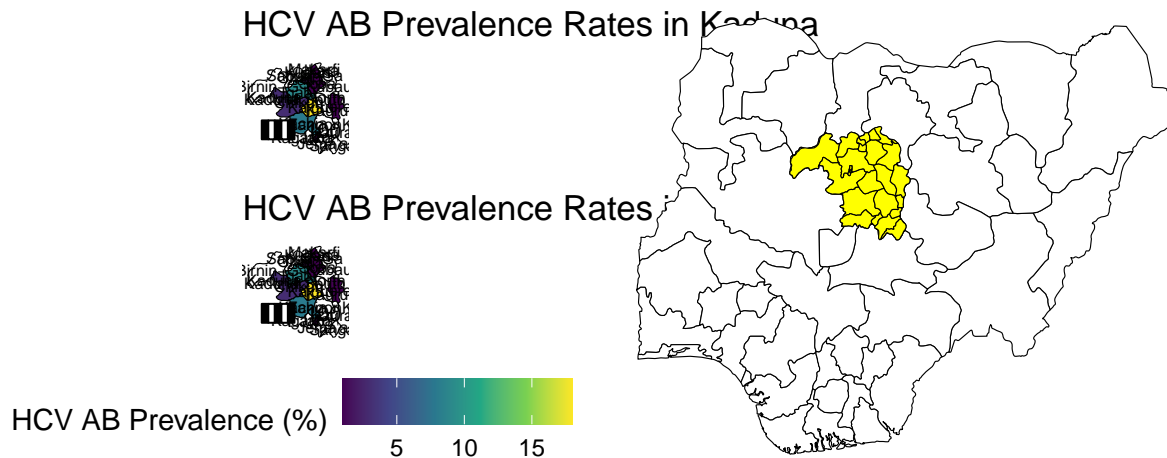
HCV AB Prevalence Rates in Kaduna



HCV AB Prevalence Rates in Kaduna



combined_plot+p3



```
# Define the bounding box of the inset map
bbox <- st_bbox(kaduna_state)

# Create the main map with a rectangle indicating the inset area
main_map_with_inset <- p3 +
  geom_rect(aes(xmin = bbox["xmin"], xmax = bbox["xmax"], ymin = bbox["ymin"], ymax = bbox["ymax"]),
    color = "red", fill = NA, size = 1)
```

```
## 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.
```

```
# Combine the main map and the inset map
combined_map <- ggdraw() +
  draw_plot(main_map_with_inset,width = 0.5,height = 1) +
  draw_plot(p1, x = 0.4, y = 0.15, width = 0.8, height = 0.95) +
  draw_line(x = c(0.26, 0.6), y = c(0.6, 0.8), color = "red", size = 1, arrow = arrow())
```

```
## Warning in st_point_on_surface.sfc(sf::st_zm(x)): st_point_on_surface may not
## give correct results for longitude/latitude data
```



```
#draw_line(x = c(0.26, 0.6), y = c(0.6, 0.4), color = "red", size = 1, arrow = arrow())
# Display the combined map
print(combined_map)
```

HCV AB Prevalence Rates in Kaduna

