```r
#choropleth map


#load ggplot, maps, already installed maps
#install.packages(c("ggplot2", "maps"))
library(ggplot2)
library(maps)

#sample data
us_states <- map_data("state")
unique_states <- unique(us_states$region)
set.seed(123)
data <- data.frame(region = unique_states,
                   value = rnorm(length(unique_states)))

#choropleth with map & sample data
choropleth_data <- merge(us_states, data, by = "region", all.x = TRUE)


#map info
#add +
ggplot(data = choropleth_data, aes(x = long, y = lat, group = group, fill = value)) +
  geom_polygon(color = "white") +
  coord_fixed(1.3) +
  scale_fill_gradient(low = "pink", high = "maroon") +
  labs(title = "choropleth map of US states",
       fill = "value")
```