Bayesian SAE using Complex Survey Data

Lecture 2: Introduction to R

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Outline

R and R studio

Example: simple Bayesian data analysis in R

Example: estimating population mean

Example: working with data and map together

Example: King county data

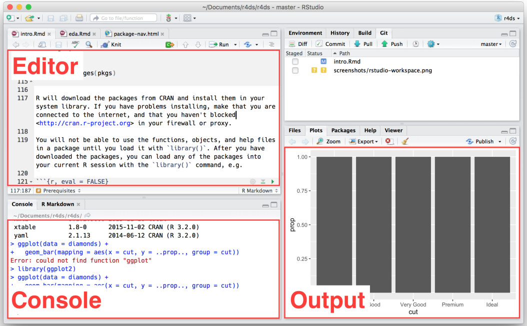
R and R studio

R

- R is a free software environment for statistical computing and graphics.
- To download R, go to the comprehensive R archive network (CRAN)
- A new major version of R comes out once a year
- 2-3 minor releases every year
- An active community and ecosystem
  - packages on CRAN
  - one of the top languages on stackoverflow
  - #rstat on twitter

RStudio

- Unfortunately the default R app is not very user friendly
- RStudio is a good integrated development environment (IDE)
- It is also free and runs on multiple platforms with similar interface



Get started

- Check if R/RStudio is installed on your computer
- Find the version of R
  - R 3.5.0 released on 4/23
  - R 3.4.4 released on 3/15
  - R 3.4.3 is the one I'm using locally
  - If your R version is older than 3.4.2, consider reinstall a new version!
- Version of RStudio does not matter much in this course, but newer versions are better more stable.

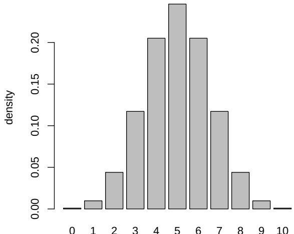
Script and workspace

- An **R script** contains the codes to perform analysis. It is always better to save an R script than directly typing into R console.
- As we run through codes, many objects (loaded data, intermediate values, results, ...) are stored in your R session.
- The multiple objects (e.g., x, y, and z above) are accumulated in your **workspace**.
- When quitting R, you need to decide if you want to save your workspace (into a .RData file)
  - Pro: if saved, next time you can reload and pick up all the objects you have created this time.
  - Con: if you accidentally modified something, there's no easy way to spot the change from looking at the .RData file
- Good practice for reproducibility: take your script as where the analysis 'live' instead of the workspace.

Simple R examples

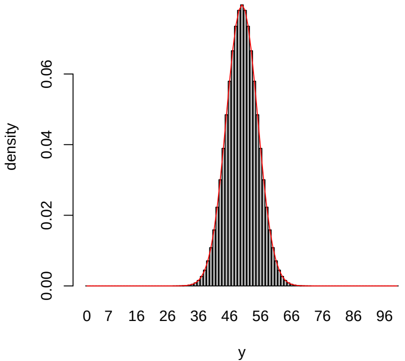
- In R, either "$=$" or "$<-$" can be used to assign values to an object.
- Object names cannot start with a digit and cannot contain certain special characters (e.g., comma or space)
- R has many built-in functions to perform common tasks.

```
n <- 10
p <- 0.5
y <- 0:n
bar <- barplot(dbinom(x = y, size = n, prob = p), xlab = "y",
    ylab = "density", names.arg = y)
```



Simple R examples

```
n <- 100
y <- 0:n
bar <- barplot(dbinom(x = y, size = n, prob = p), xlab = "y",
    ylab = "density", names.arg = y)
lines(bar[, 1], dbinom(x = y, size = n, prob = p),
    col = "red")
```



Data types

Some common types

- **vector**: a set of values (ordered) of the same mode. We create vectors by using the `c` function (short for combine or concatenate)
- **matrix**: a 2-dimensional version of vector (internally saved as vector)
- **array**: a k-dimensional version of vector
- **data.frame**: a list of vectors where each vector is a column. The vectors may be of different modes. This is typically what we have in mind as ‘data’
- **list**: an ordered collection of any objects

Some common modes

- numeric: `c(1, 2/5, -2.10)`
- character: `c("red", "blue", "Seattle")`
- factor: `factor(c("red", "blue", "Seattle"))`
- logical: `c("TRUE", "FALSE", "FALSE")`

vectorization

- One of the most efficient way to deal with data in R is the vectorization
- i.e., functions can be written to perform operations on vectors element-wise
- e.g., instead of

```
x <- 1:1000
for (i in 1:1000) {
    x[i] <- x[i]^2 + 1
}
```

  we may write

```
x <- x^2 + 1
```

- Similarly for matrices and arrays.

vectorization

- More example:

```
x <- matrix(1:12, nrow = 3, ncol = 4)
y <- x^2
z <- y + x
```

- Warning: vectorized operations of different length

```
x <- c(1, 2, 3)
y <- c(1, 2, 3, 4, 5)
z <- x + y
```

- Warning: operation on objects with different dimensions

```
x <- matrix(1:12, nrow = 3, ncol = 4)
y <- x + c(100, 1000)
```

factors and characters

- Factors are used to represent ordinal data.
- They are internally saved as integer values.
- Sometimes R automatically make your data vectors, which can be troubling, e.g., you cannot assign values to a `factor` vector outside its `levels`.
  - e.g., common data input functions like `read.csv`, `read.table`, ...
- Especially when you think you have a character variable, check they are not factors!
- There are some new packages that deals with undesired factors better, e.g. `readr`, `tibble`, `forcats`, but we'll stick to R's default behaviors in this course.

factors and characters

Reassign levels to factors

```
x <- factor(c("r", "g", "b"))
levels(x)

## [1] "b" "g" "r"

levels(x) <- c("blue", "green", "red")
```

Turn factors into characters

```
as.character(x)

## [1] "red"   "green" "blue"
```

factors and characters

Change orders of factors

```r
x <- factor(c("r", "g", "b"))
as.numeric(x)

## [1] 3 2 1

x <- factor(x, levels = c("r", "g", "b", "o"))
as.numeric(x)

## [1] 1 2 3
```

More examples

Missing values

```
x <- c(1, 2, NA, 4, 5, 6)
mean(x)
which(is.na(x))
mean(x, na.rm = TRUE)
```

Subsetting data

```
x[c(1, 2)]
x[-c(1, 2)]
x[x != "r"]
x[x %in% c("r", "g")]
```

Combine data

```
x <- c(1, 2, 3, 4)
y <- x^2
cbind(x, y)
rbind(x, y)
data.frame(x = x, y = y)
```

Functions and R packages

```r
getsuminv <- function(x, y, z) {
    return(1/x + 1/y + 1/z)
}
suminv <- getsuminv(c(1, 2), c(2, 3), c(3, 4))
```

- A function has a name, a list of arguments/inputs, and a returned object (to return multiple objects, combine them into a list)
- Variables defined in functions are local. Variables outside of the function can be used within functions without being passed in (but sometimes dangerous!)
- **Packages** are the fundamental unit of shareable codes, data, and document. Many packages are hosted on CRAN.
- Use `install.packages("pkgname")` to download and install from CRAN.
- Use `library("pkgname")` to load them

List of packages we will use in this course

```
install.packages("ggplot2", dep=TRUE)
install.packages("INLA", repos=c(getOption("repos"),
  INLA="https://inla.r-inla-download.org/R/stable"), dep=TRUE)
install.packages("maptools", dep=TRUE)
install.packages("spdep", dep=TRUE)
install.packages("survey", dep=TRUE)
```

And some optional ones:

```
install.packages("ggrepel", dep=TRUE)
install.packages("RColorBrewer", dep=TRUE)
install.packages("gridExtra", dep=TRUE)
install.packages("rgdal", dep=TRUE)
install.packages("SUMMER", dep=TRUE)
```

R programming resources

- R for Data science book (online):
  `http://r4ds.had.co.nz/introduction.html`
  - A more modern tutorial in dealing with data efficiently in R
- Some other popular R courses:
  - DataCamp's free R tutorial:
    `https://www.datacamp.com/courses/free-introduction-to-r`
  - Jenny Bryan's course materials at UBC:
    `http://stat545.com/index.html`
  - R Programming on Coursera (from Johns Hopkins University)
- (for Advanced R user) The R Inferno
  `http://www.burns-stat.com/pages/Tutor/R_inferno.pdf`
  - many many miscellaneous R weird things that may trip you up

Example: simple Bayesian data analysis in R

Bayesian statistics: recap

Three step process

- Prior: Setup up a full probability model.
- Data: Condition on observed data.
- Posterior: evaluate the fit of the model and posterior distribution's implications.

Inference

- Estimate unknown quantities (parameters) of interest.
- Estimate uncertainty of the unknown quantities.
  - "There is a 95% probability that the unknown parameter is in the interval ..."

A simple binomial example

- p is the infection rate of a virus in a community.
- y is the number of infected people in screening n randomly selected people.
- p and y and unknown before screening.
- p should be less uncertain after observing y.
- p should be less uncertain after observing y with a large n.

A simple binomial example

- Data likelihood: $y|p \sim \text{Binomial}(n, p)$
- Prior: $p \sim \text{Beta}(a, b)$
- Posterior: distribution of $p|y$
- Bayes rule:

$$p(p|y) = \frac{p(p)p(y|p)}{p(y)} \propto p^{a+y-1}(1-p)^{b+n-y-1}$$

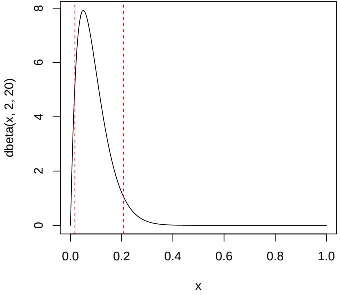
- We have an analytical representation of the posterior

$$p|y \sim \text{Beta}(a+y, b+n-y)$$

Choosing a and b

- Choice of a and b reflects the "prior" belief of the infection rate.
- e.g., for $a = 2$, $b = 20$, 90% of the mass lies between 0.02 and 0.21

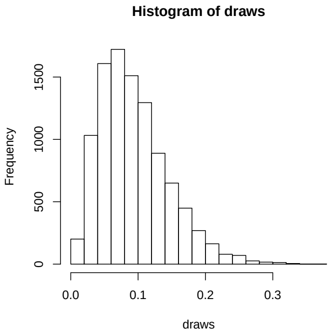
```
x <- seq(0, 1, len = 200)
plot(x, dbeta(x, 2, 20), type = "l")
abline(v = qbeta(0.05, 2, 20), lty = 2, col = "red")
abline(v = qbeta(0.95, 2, 20), lty = 2, col = "red")
```



A simple binomial example

- Assume we observe $n = 10$, $y = 1$
- Sample from the posterior

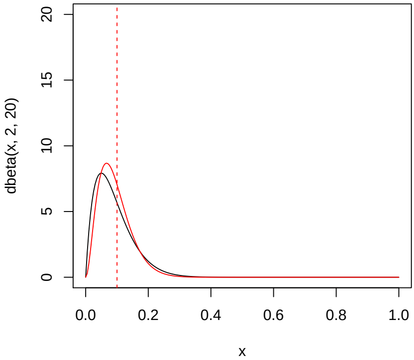
```r
Nsim <- 10000
y <- 1
n <- 10
draws <- rbeta(Nsim, 2 + y, 20 + n - y)
hist(draws)
```



A simple binomial example

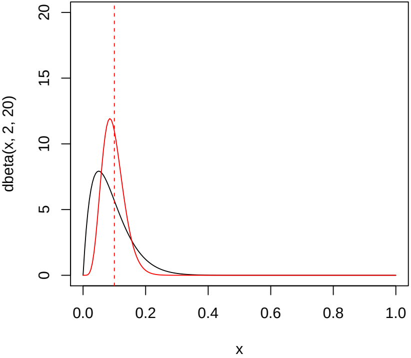
- The posterior distribution is available analytically

```
plot(x, dbeta(x, 2, 20), type = "l", ylim = c(0, 20))
lines(x, dbeta(x, 2 + y, 20 + n - y), col = "red")
abline(v = y/n, lty = 2, col = "red")
```



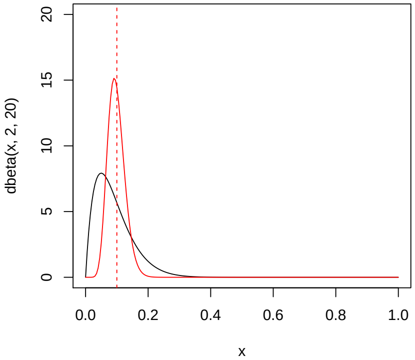
A simple binomial example

```r
n <- 50
y <- 5
plot(x, dbeta(x, 2, 20), type = "l", ylim = c(0, 20))
lines(x, dbeta(x, 2 + y, 20 + n - y), col = "red")
abline(v = y/n, lty = 2, col = "red")
```



A simple binomial example

```r
n <- 100
y <- 10
plot(x, dbeta(x, 2, 20), type = "l", ylim = c(0, 20))
lines(x, dbeta(x, 2 + y, 20 + n - y), col = "red")
abline(v = y/n, lty = 2, col = "red")
```



Example: estimating population mean

Bayesian inference for the normal distribution: recap

- Data: $y_1, ...y_n|\mu \sim \text{Normal}(\mu, \sigma^2)$.
- Prior: $\mu \sim \text{Normal}(\mu_0, \sigma_0^2)$.
- Assume σ, μ_0, and σ_0 are known
- Posterior: $\mu|y_1, ..., y_n \sim \text{Normal}(\mu_n, \sigma_n^2)$,

$$\mu_n = \mu_0(1 - w) + \bar{y}w, \quad \sigma_n^2 = w\frac{\sigma^2}{n}$$

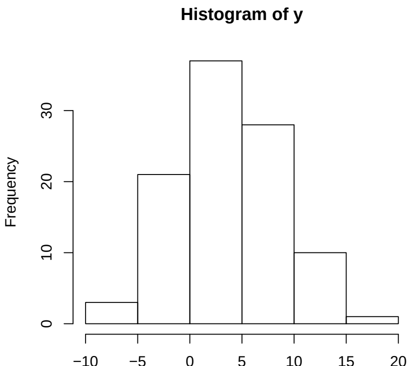
- The weight

$$w = \frac{\sigma_0^2}{\sigma_0^2 + \sigma^2/n}$$

A simple normal example

- Simulate a dataset

```r
sigma <- 5
mu <- 4
n <- 100
y <- rnorm(n, mu, sigma)
hist(y)
```



A simple normal example

- MLE and variance of MLE

```
mean(y)  # MLE of sample mean

## [1] 3.804005

var(y)/n  # variance of sample mean

## [1] 0.2379144
```

A simple normal example

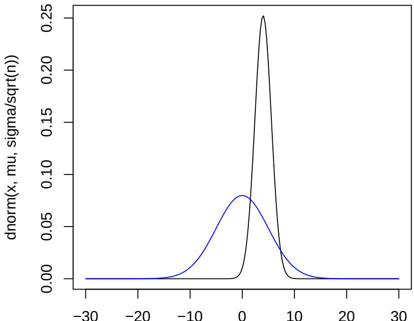
- What if sample size is smaller

```r
set.seed(1)
n <- 10
yy <- rnorm(n, mu, sigma)
mean(yy)  # MLE of sample mean

## [1] 4.661014

var(yy)/n  # variance of sample mean

## [1] 1.523286
```

A simple normal example

- A wide prior on μ: $\mu \sim \text{Normal}(0, 20)$

```
mu0 <- 0
sigma0 <- 5
x <- seq(-30, 30, len = 200)
plot(x, dnorm(x, mu, sigma/sqrt(n)), type = "l")
lines(x, dnorm(x, mu0, sigma0), col = "blue")
```



A simple normal example: the posterior

- Posterior: $\mu | y_1, ..., y_n \sim \text{Normal}(\mu_n, \sigma_n^2)$,

$$\mu_n = \mu_0(1 - w) + \bar{y}w, \quad \sigma_n^2 = w\frac{\sigma^2}{n}$$

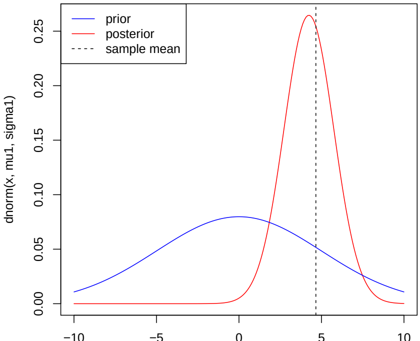
- The weight

$$w = \frac{\sigma_0^2}{\sigma_0^2 + \sigma^2/n}$$

```
w <- sigma0^2/(sigma0^2 + sigma^2/length(yy))
mu1 <- mu0 * (1 - w) + mean(yy) * w
sigma1 <- sqrt(w * sigma^2/length(yy))
```

A simple normal example: the posterior

```
x <- seq(-10, 10, len = 200)
plot(x, dnorm(x, mu1, sigma1), type = "l", col = "red")
lines(x, dnorm(x, mu0, sigma0), col = "blue")
abline(v = mean(yy), lty = 2)
legend("topleft", c("prior", "posterior", "sample mean"),
    col = c("blue", "red", "black"), lty = c(1, 1,
        2))
```



A simple normal example: the posterior

- Prior mean: 0, prior variance: 25.
- MLE mean: 4.66, MLE variance: 2.5.
- Posterior mean: 4.24, posterior variance: 2.27.

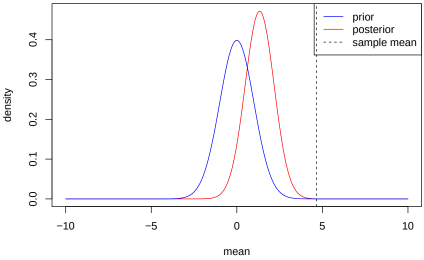
A simple normal example: a more informative prior

- It's usually easier to write functions in R to perform tasks with varying parameters.

```
getpost <- function(y, sigma, mu0, sigma0) {
    w <- sigma0^2/(sigma0^2 + sigma^2/length(yy))
    mu1 <- mu0 * (1 - w) + mean(yy) * w
    sigma1 <- sqrt(w * sigma^2/length(yy))
    return(list(mu1 = mu1, sigma1 = sigma1))
}

plotpost <- function(y, sigma, mu0, sigma0) {
    post <- getpost(y, sigma, mu0, sigma0)
    x <- seq(-10, 10, len = 200)
    plot(x, dnorm(x, post$mu, post$sigma1), type = "l",
        col = "red", xlab = "mean", ylab = "density")
    lines(x, dnorm(x, mu0, sigma0), col = "blue")
    abline(v = mean(yy), lty = 2)
    legend("topright", c("prior", "posterior", "sample mean"),
        col = c("blue", "red", "black"), lty = c(1,
            1, 2))
}
```

A simple normal example: a more informative prior

```
mu0 <- 0
sigma0 <- 1
posterior <- getpost(yy, sigma, mu0, sigma0)
plotpost(yy, sigma, mu0, sigma0)
```



- Prior mean: 0, prior variance: 1.
- MLE mean: 4.66, MLE variance: 2.5.
- Posterior mean: 1.33, posterior variance: 0.71.

Example: working with data and map together

Simulated dataset: King country example

- Read the simulated dataset, `simKing`, from `http://faculty.washington.edu/jonno/PAA-SAE.html`.
- .rda is the extension for saved R datasets
- In R, you can either load data directly from an URL, or download the file first and read from local directory

```
load(url("http://faculty.washington.edu/jonno/PAA-SAE/simKing.rda"))
```

Or

```
load("../data/simKing.rda")
```

Simulated dataset: King country example

The data contains 172,406 observations of simulated "population" data.

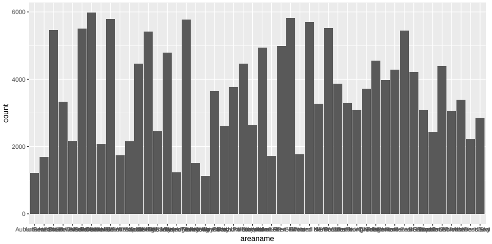
- **areas**: numerical indicator of areas, 1, ..., 49.
- **weight**: numerical value of weight in pounds.
- **diabetes**: binary indicator of diabetes.
- **areaname**: name of the areas.

```
dim(pop)

## [1] 172406      4

head(pop)

##   area   weight diabetes  areaname
## 1    1 188.5412        0 Sammamish
## 2    1 166.1342        0 Sammamish
## 3    1 186.1471        0 Sammamish
## 4    1 183.1891        0 Sammamish
## 5    1 171.5022        0 Sammamish
## 6    1 177.1157        0 Sammamish
```

Getting to know the data

- It's usually helpful to first get to know your data by visually checking to
- ggplot2 package makes exploratory analysis easier most of the time

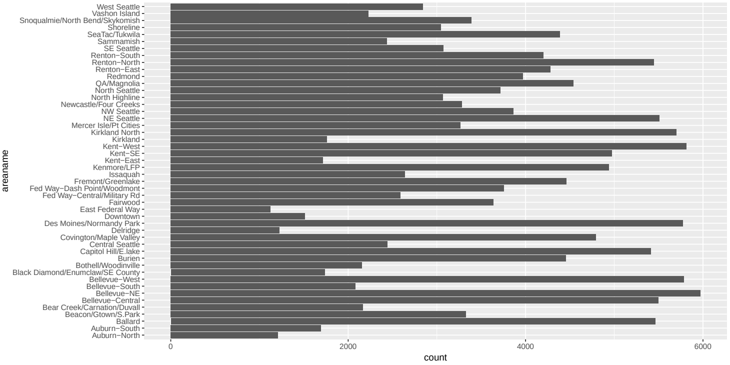
```
library(ggplot2)
ggplot(data = pop) + geom_bar(aes(x = areaname))
```



Not very pretty at first!

Getting to know the data

```
ggplot(data = pop) + geom_bar(aes(x = areaname)) +
    coord_flip()
```



Getting to know the data

```r
pop$diabetes2 <- factor(pop$diabetes, levels = c(0,
    1))
ggplot(data = pop) + geom_bar(aes(x = areaname, fill = diabetes2)) +
    coord_flip()
```

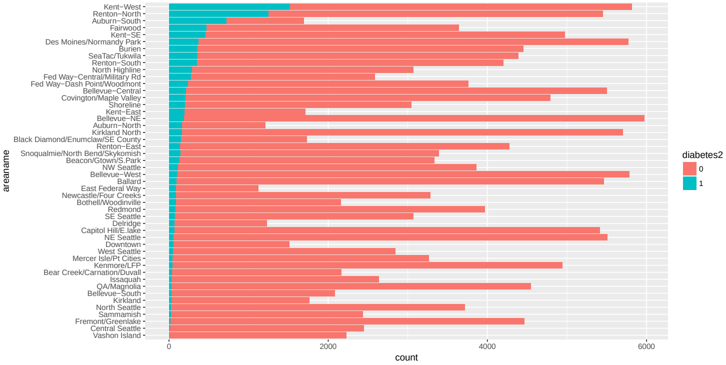
Getting to know the data

```
n.d <- aggregate(diabetes ~ areaname, pop, sum)
head(n.d)

##                          areaname diabetes
## 1                    Auburn-North      166
## 2                    Auburn-South      724
## 3                         Ballard       92
## 4             Beacon/Gtown/S.Park      132
## 5 Bear Creek/Carnation/Duvall           40
## 6                 Bellevue-Central      212
```

Getting to know the data

Count the number of diabetes cases by region.

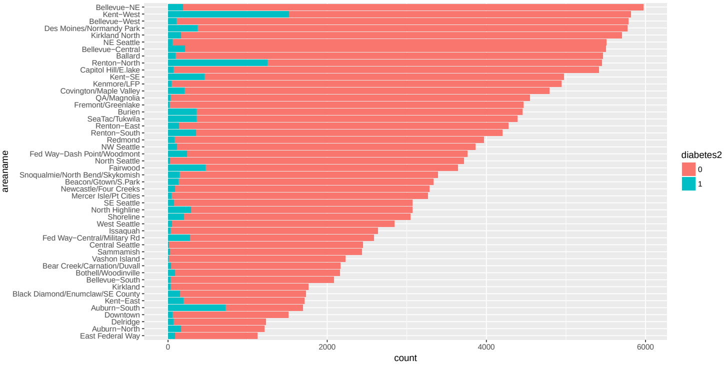
```
names.ordered <- n.d[order(n.d[, 2]), 1]
pop$areaname <- factor(pop$areaname, levels = names.ordered)
ggplot(data = pop) + geom_bar(aes(x = areaname, fill = diabetes2)) +
    coord_flip()
```



Getting to know the data

Count the number of total observations by region.

```
n.t <- aggregate(cbind(total = diabetes) ~ areaname,
    pop, length)
names.ordered <- n.t[order(n.t[, 2]), 1]
pop$areaname <- factor(pop$areaname, levels = names.ordered)
ggplot(data = pop) + geom_bar(aes(x = areaname, fill = diabetes2)) +
    coord_flip()
```



Shapefiles

- ESRI (a company one of whose products is ArcGIS) shapefiles consist of three files, and this is a common form.
- The first file (*.shp) contains the geography of each shape.
- The second file (*.shx) is an index file which contains record offsets.
- The third file (*.dbf) contains feature attributes with one record per feature.

We will briefly discuss the basics of using geographic data in R, for more detailed tutorials, see
`https://geocompr.robinlovelace.net/index.html`

Read map files into R

Download the shapefiles from
http://faculty.washington.edu/jonno/PAA-SAE/HRA_ShapFiles/

maptools package provide the easiest way to read in shapefile. However, it does not load in the spatial referencing information.

```
# install.packages('maptools')
library(maptools)
f <- "../data/HRA_ShapeFiles/HRA_2010Block_Clip.shp"
kingshape <- readShapePoly(f)
```

rgdal package provides more powerful ways to read in geographical data. But, additional steps to install GDAL is required.

```
# install.packages('rgdal')
library(rgdal)
kingshape <- readOGR("../data/HRA_ShapeFiles", layer = "HRA_2010Block_C

## OGR data source with driver: ESRI Shapefile
## Source: "../data/HRA_ShapeFiles", layer: "HRA_2010Block_Clip"
## with 48 features
## It has 9 fields
```

Read map files into R

- Installing GDAL can be tricky for some operating systems.
- There are many packages to manipulate and plot geographical data. In this course, we will mostly use `ggplot2`
- A more complete spatial visualization tutorial: `https://github.com/Robinlovelace/Creating-maps-in-R`

Combine map and data

Turn the map into a 'data.frame' in R

```
geo <- fortify(kingshape, region = "HRA2010v2_")
```

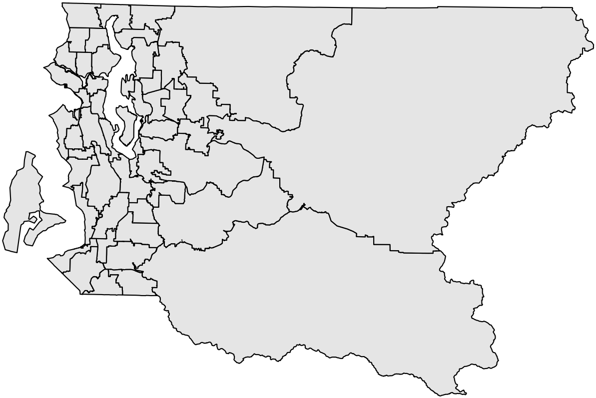
Merge the dataset with the map

```
geo <- merge(geo, n.t, by = "id", by.y = "areaname")
```

Visualize maps

Count the number of total observations by region.

```
g <- ggplot(geo) + geom_polygon(aes(x = long, y = lat,
    group = group), color = "black", fill = "gray90")
g <- g + theme_void()
g
```

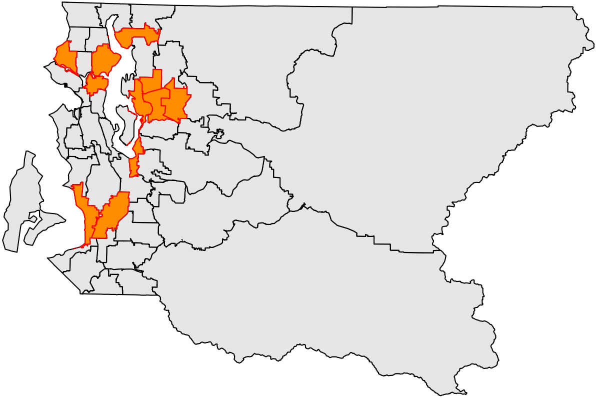


Visualize maps: highlight a region

```
g <- ggplot(geo, aes(x = long, y = lat, group = group)) +
    geom_polygon(color = "black", fill = "gray90")
g <- g + geom_polygon(data = subset(geo, id == "Kirkland"),
    fill = "darkorange", color = "red")
g <- g + theme_void()
g
```

Visualize maps: highlight a region

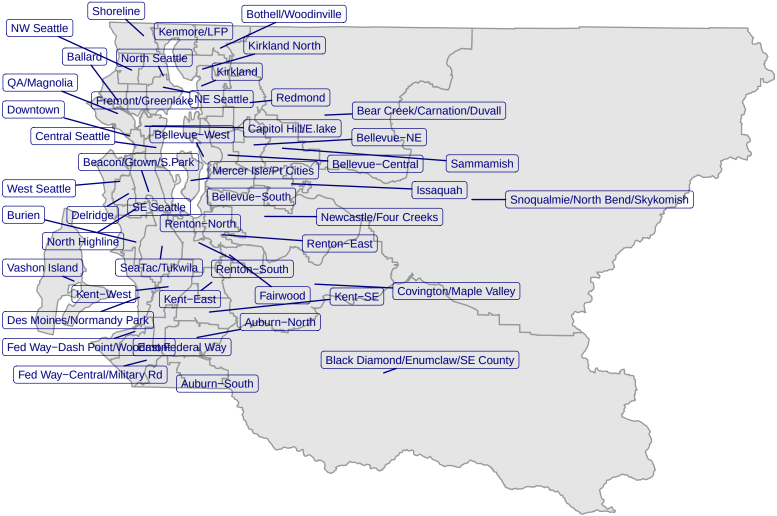
```
g <- ggplot(geo, aes(x = long, y = lat, group = group)) +
    geom_polygon(color = "black", fill = "gray90")
g <- g + geom_polygon(data = subset(geo, total > 5000),
    fill = "darkorange", color = "red")
g <- g + theme_void()
g
```



Visualize maps: label regions

```r
library(ggrepel)
cnames <- aggregate(cbind(long, lat) ~ id, data = geo,
    function(x) {
        mean(x)
    })
g <- ggplot(geo) + geom_polygon(aes(x = long, y = lat,
    group = group), color = "gray60", fill = "gray90")
g <- g + geom_label_repel(aes(x = long, y = lat, label = id),
    data = cnames, size = 3, color = "navy", fill = NA)
g <- g + theme_void()
g
```

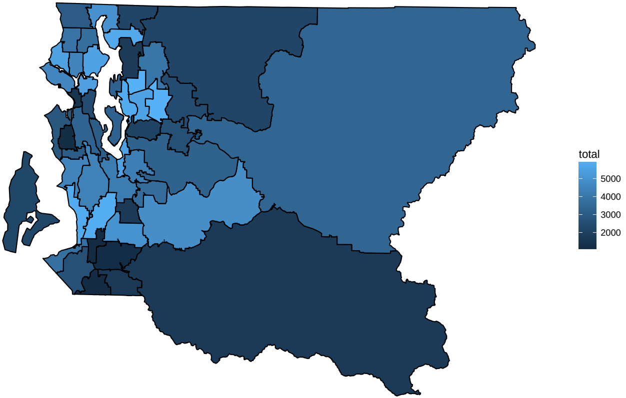
Visualize maps: label regions



Visualize maps: color by variable

Visualize the total population size

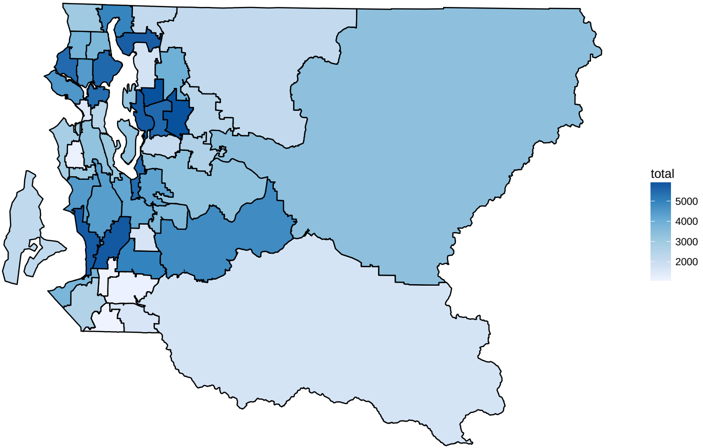
```
g <- ggplot(geo) + geom_polygon(aes(x = long, y = lat,
    group = group, fill = total), color = "black")
g <- g + theme_void()
g
```



Visualize maps: change color scales

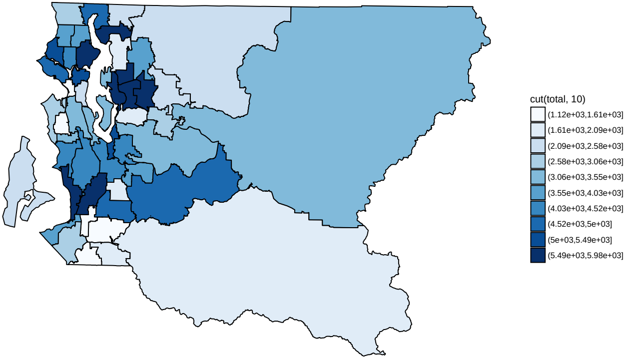
Reverse the scale so that lighter color represent smaller number

```
g <- g + scale_fill_distiller(direction = 1)
g
```



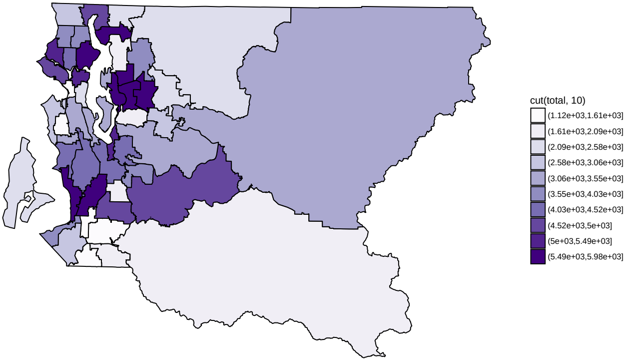
Visualize maps: bin continuous variables

```
library(RColorBrewer)
g <- ggplot(geo) + geom_polygon(aes(x = long, y = lat,
    group = group, fill = cut(total, 10)), color = "black") +
    theme_void()
g <- g + scale_fill_manual(values = colorRampPalette(brewer.pal(9,
    "Blues"))(10))
g
```



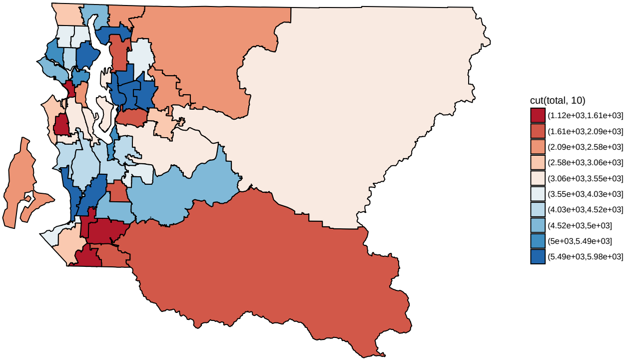
Visualize maps: change color scheme

```
g <- g + scale_fill_manual(values = colorRampPalette(brewer.pal(9,
    "Purples"))(10))
g
```



Visualize maps: change color scheme

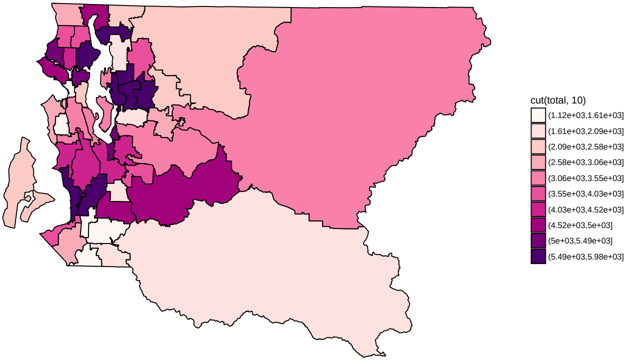
```r
g <- g + scale_fill_manual(values = colorRampPalette(brewer.pal(9,
    "RdBu"))(10))
g
```



Visualize maps: change color scheme

An useful website to choose color palette: `http://colorbrewer2.org/`

```
g <- g + scale_fill_manual(values = colorRampPalette(c("#fff7f3",
    "#fde0dd", "#fcc5c0", "#fa9fb5", "#f768a1", "#dd3497",
    "#ae017e", "#7a0177", "#49006a"))(10))
g
```



More about visualization

- ggplot2 allows many more customization
- Check out `theme_bw()`, `theme_dark()`, `theme_linedraw()`, `coord_map()`, ...

Some useful ggplot2 tutorials:

- Introductory tutorial: http://tutorials.iq.harvard.edu/R/Rgraphics/Rgraphics.html
- Gallery: https://www.r-graph-gallery.com/portfolio/ggplot2-package/
- Geocomputation with R book: https://geocompr.robinlovelace.net/index.html

Example: King county data

Simple random sampling

- Perform a simple random sampling of $2,000$ observations in the simulated population.
- Calculate the average weight and observed fraction of diabetes in this sample.
- `set.seed()` is usually a good idea to improve reproducibility.

```
set.seed(123)
n <- 2000
is.sample <- sample(1:dim(pop)[1], n)
sample <- pop[is.sample, ]
w.hat <- aggregate(weight ~ areaname, sample, mean)
d.hat <- aggregate(diabetes ~ areaname, sample, mean)
```

Simple random sampling: MLE

Recall the formulas for the MLE before

```
# simple MLE
size <- aggregate(weight ~ areaname, sample, length)[,
    2]
d.sum <- aggregate(diabetes ~ areaname, sample, sum)[,
    2]
w.sd <- aggregate(weight ~ areaname, sample, sd)[,
    2]/sqrt(size)
d.sd <- sqrt(d.hat[, 2] * (1 - d.hat[, 2])/size)
```

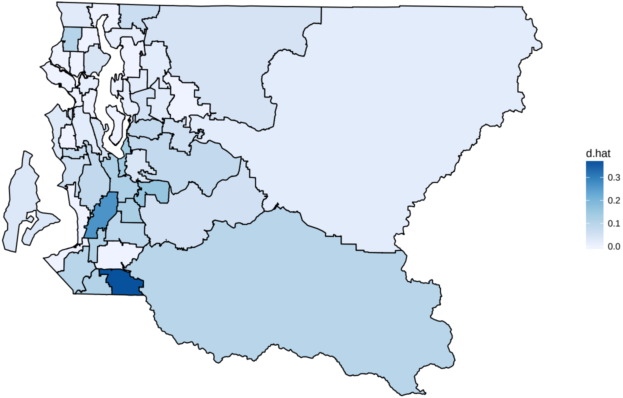
Change the 0 into NA for more informative visualization

```
d.sd[d.hat[, 2] == 0] <- NA
d.sum[d.sum == 0] <- NA
mle <- data.frame(areaname = w.hat[, 1], size = size,
    w.hat = w.hat[, 2], w.sd = w.sd, d.sum = d.sum,
    d.hat = d.hat[, 2], d.sd = d.sd)
```

Simple random sampling: MLE

Visualize the observed fraction of diabetes

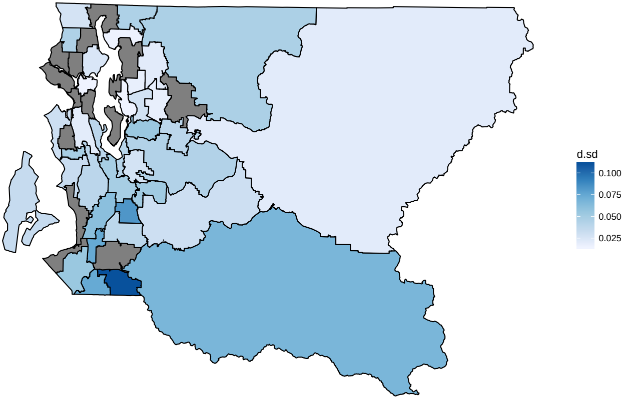
```
geo <- merge(geo, mle, by = "id", by.y = "areaname")
g <- ggplot(geo) + geom_polygon(aes(x = long, y = lat,
    group = group, fill = d.hat), color = "black")
g <- g + theme_void() + scale_fill_distiller(direction = 1)
g
```



Simple random sampling: MLE

Visualize the standard error of the observed fraction of diabetes

```
g <- ggplot(geo) + geom_polygon(aes(x = long, y = lat,
    group = group, fill = d.sd), color = "black")
g <- g + theme_void() + scale_fill_distiller(direction = 1)
g
```



Simple random sampling: Bayesian calculation

Similar to before, write a function for posterior mean and standard deviation for normal and binomial distribution respectively.

```
getpost <- function(y, sigma, mu0, sigma0) {
    w <- sigma0^2/(sigma0^2 + sigma^2/length(y))
    mu1 <- mu0 * (1 - w) + mean(y) * w
    sigma1 <- sqrt(w * sigma^2/length(y))
    return(c(mu1, sigma1))
}
getpost.bin <- function(y, a, b) {
    a1 <- a + sum(y == 1)
    b1 <- b + length(y) - sum(y == 1)
    mu1 <- a1/(a1 + b1)
    sd1 <- sqrt(a1 * b1/(a1 + b1)^2/(a1 + b1 + 1))
    return(c(mu1, sd1))
}
```

Simple random sampling: Bayesian calculation

- Let y_i and n_i denote the number of individuals having type II diabetes and the number of samples in the i-th area.
- Let w_{ij} denote the weight of the j-th individual in the i-th area.
- To start, here we estimate the most basic independent model assuming for $i = 1, ..., n$

$$y_i | p_i \sim \text{Binomial}(n_i, p_i), \quad p_i \sim \text{Beta}(a, b)$$

  and

$$w_{ij} | \mu \sim \text{Normal}(\mu_i, \sigma^2), \quad \mu_i \sim \text{Normal}(\mu_0, \sigma_0^2)$$

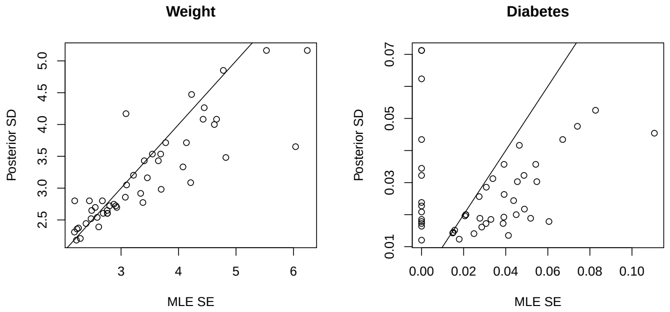
- Assume we know σ^2 and fix a, b, μ_0, and σ_0^2.
- For now, we model each area independently. We'll revisit and relax this in the next lecture.

Simple random sampling: Bayesian calculation

```r
post.est <- matrix(NA, 48, 4)
sigma = 20
mu0 = 180
sigma0 = 10
a0 = 1
b0 = 1
rownames(post.est) <- unique(sample$areaname)
for (area in rownames(post.est)) {
    sub <- sample[sample$areaname == area, ]
    w.post <- getpost(sub$weight, sigma, mu0, sigma0)
    d.post <- getpost.bin(sub$weight, a0, b0)
    post.est[area, ] <- c(w.post, d.post)
}
colnames(post.est) <- c("w.hat2", "w.sd2", "d.hat2",
    "d.sd2")
post.est <- data.frame(post.est)
post.est$areaname <- rownames(post.est)
```

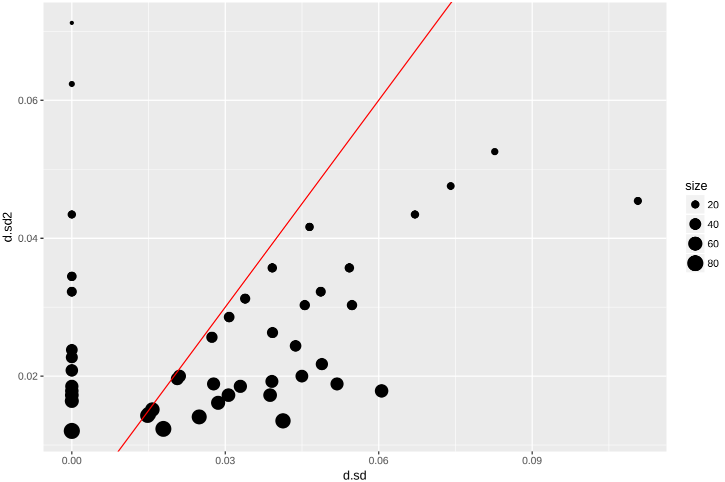
Compare standard errors

```r
post.est <- merge(post.est, mle)
post.est$d.sd[is.na(post.est$d.sd)] <- 0
par(mfrow = c(1, 2))
plot(post.est$w.sd, post.est$w.sd2, xlab = "MLE SE",
    ylab = "Posterior SD", main = "Weight")
abline(c(0, 1))
plot(post.est$d.sd, post.est$d.sd2, xlab = "MLE SE",
    ylab = "Posterior SD", main = "Diabetes")
abline(c(0, 1))
```



Compare standard errors

```
g <- ggplot(post.est, aes(x = d.sd, y = d.sd2, size = size))
g <- g + geom_point() + geom_abline(color = "red")
g
```



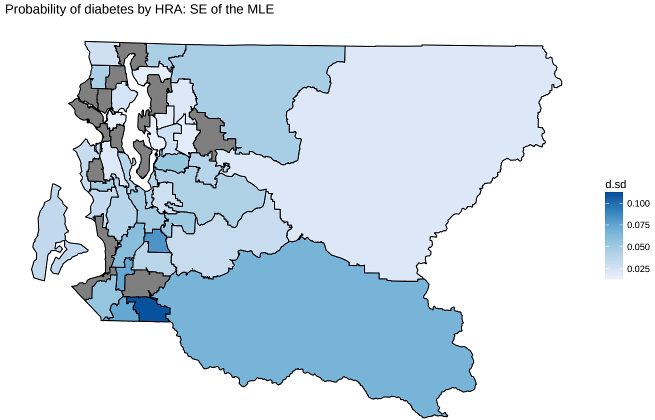
Visualize results with map

Merge the posterior estimates into the spatial data frame

```
post.est$d.sd[post.est$d.sd == 0] <- NA
geo <- fortify(kingshape, region = "HRA2010v2_")
geo <- merge(geo, post.est, by = "id", by.y = "areaname")
lim <- range(c(post.est$d.sd, post.est$d.sd2), na.rm = TRUE)
```

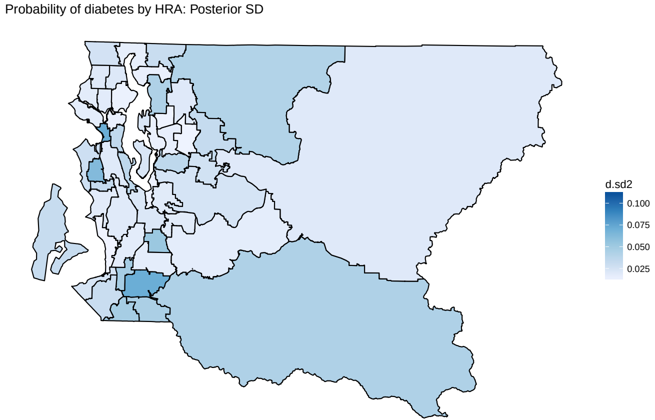
Visualize results with map: MLE SE

```r
g <- ggplot(geo) + geom_polygon(aes(x = long, y = lat,
    group = group, fill = d.sd), color = "black")
g <- g + theme_void() + scale_fill_distiller(limits = lim,
    direction = 1)
g <- g + ggtitle("Probability of diabetes by HRA: SE of the MLE")
g
```



Visualize results with map: Posterior SD

```r
g <- ggplot(geo) + geom_polygon(aes(x = long, y = lat,
    group = group, fill = d.sd2), color = "black")
g <- g + theme_void() + scale_fill_distiller(limits = lim,
    direction = 1)
g <- g + ggtitle("Probability of diabetes by HRA: Posterior SD")
g
```



Visualize multiple metrics with map

Transform data from 'wide' to 'long' format

```
library(reshape2)
library(plyr)
post.est.wide <- melt(post.est[, c(1, 5, 11)])
head(post.est.wide)

##                          areaname variable      value
## 1                     Auburn-North    d.sd2 0.07121693
## 2                     Auburn-South    d.sd2 0.04540298
## 3                          Ballard    d.sd2 0.01785419
## 4              Beacon/Gtown/S.Park    d.sd2 0.01960392
## 5 Bear Creek/Carnation/Duvall    d.sd2 0.04162727
## 6                 Bellevue-Central    d.sd2 0.01612686

post.est.wide$variable <- revalue(post.est.wide$variable,
    c(d.sd = "MLE SE", d.sd2 = "Posterior SE"))
```

Visualize multiple metrics with map

```r
geo <- merge(geo, post.est.wide, by = "id", by.y = "areaname")
g <- ggplot(geo) + geom_polygon(aes(x = long, y = lat,
    group = group, fill = value), color = "black")
g <- g + theme_void() + facet_wrap(~variable)
g <- g + scale_fill_distiller(direction = 1)
g
```