Advanced Network Analysis

Intro to Spatial Statistics

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Dependence in Observational Data

- Individuals are nested in social networks
  - Individual decisions are influenced by their friends.
- Provinces are surrounded by other provinces
  - Provinces mimic one another's policies
- Country-level outcomes are often a result of negotiations with other countries:
  - Economic or environmental policies

Three Mechanisms for Spatial Dependence

- Common exposure---similarity in outcomes is driven by an exogenous factor that affects nearby units (the effect of earthquakes on housing prices)
- Homophily---similarity in outcomes is endogenous, units are similar because they self-select into the same outcome (e.g., partisan geo-sorting)
- Diffusion---nearby units affect each other through learning, imitation, etc (e.g., policy diffusion)

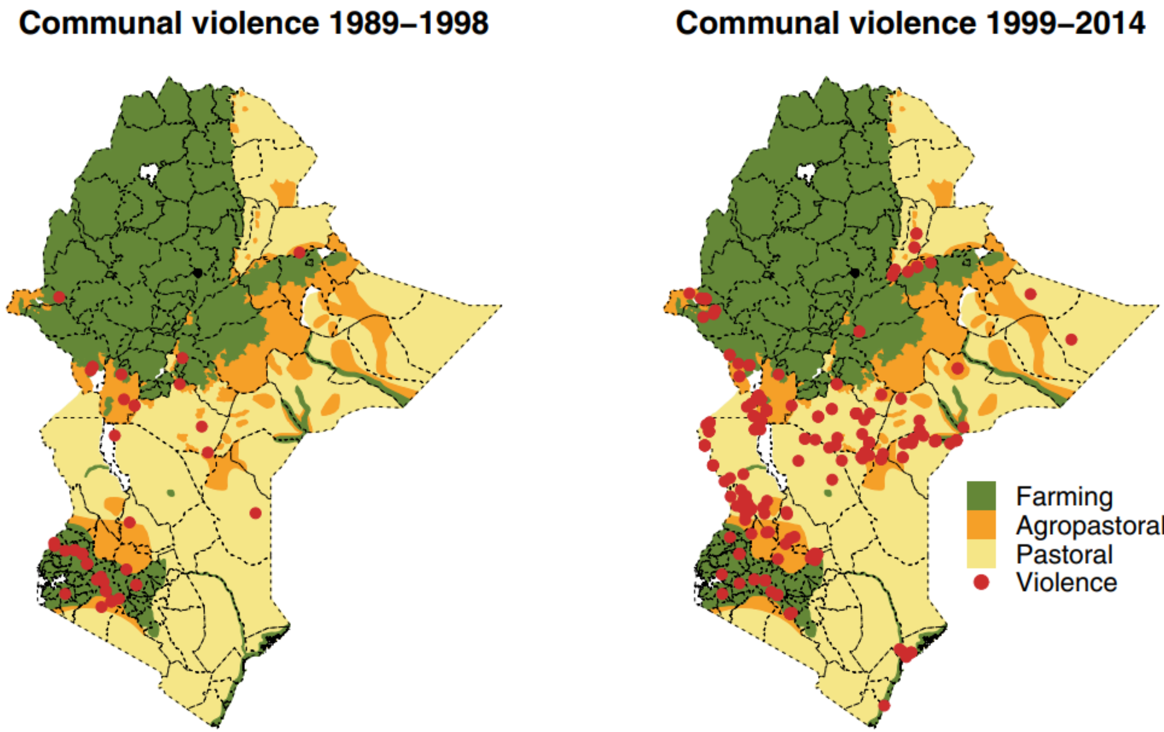


Figure 3. Location of individual communal violence events in Ethiopia and Kenya between 1989/98 and 1999/2014
Livelihood zones capture the dominant livelihood strategy within area. Data from UCDP, FEWS Net.

Source: van Weezel S. "On climate and conflict: Precipitation decline and communal conflict in Ethiopia and Kenya." *Journal of Peace Research*. 2019;56(4):514--528.

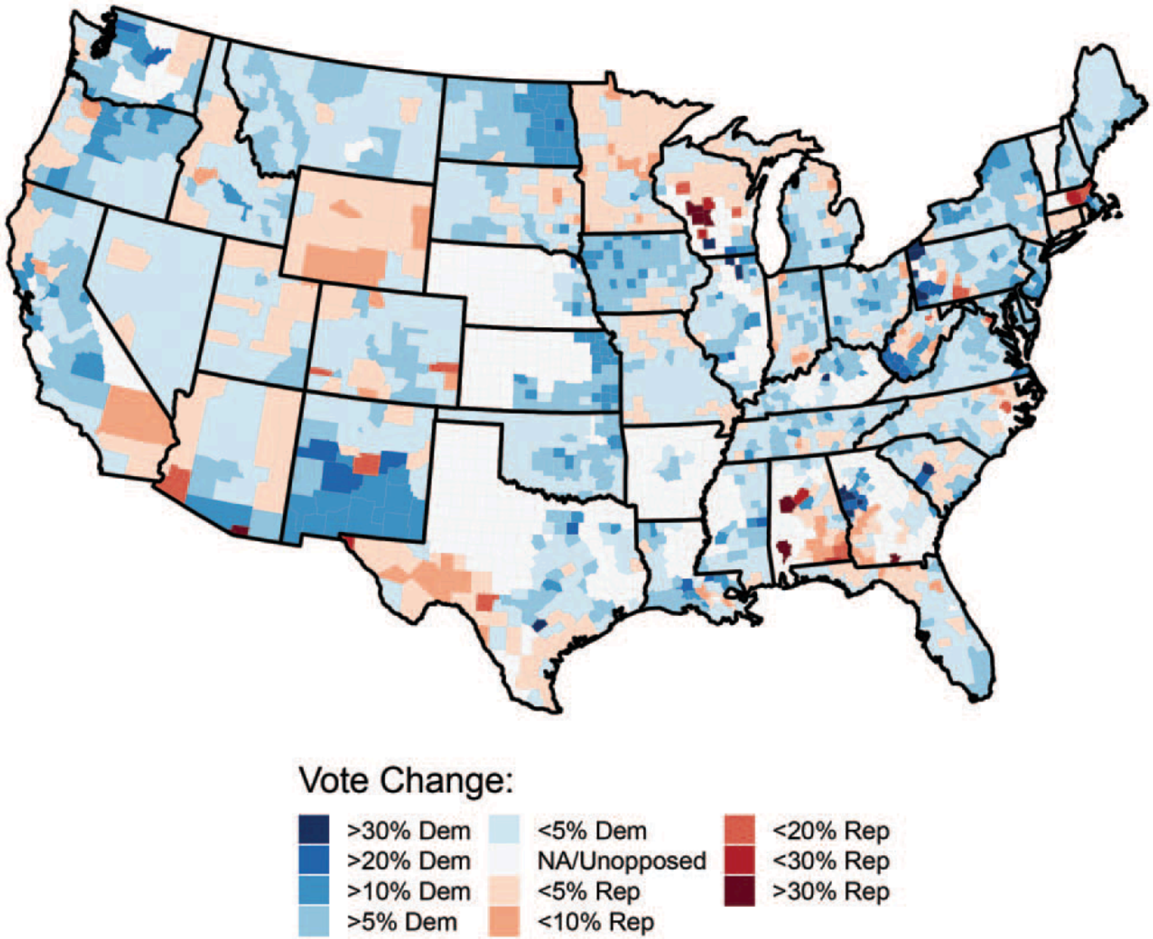
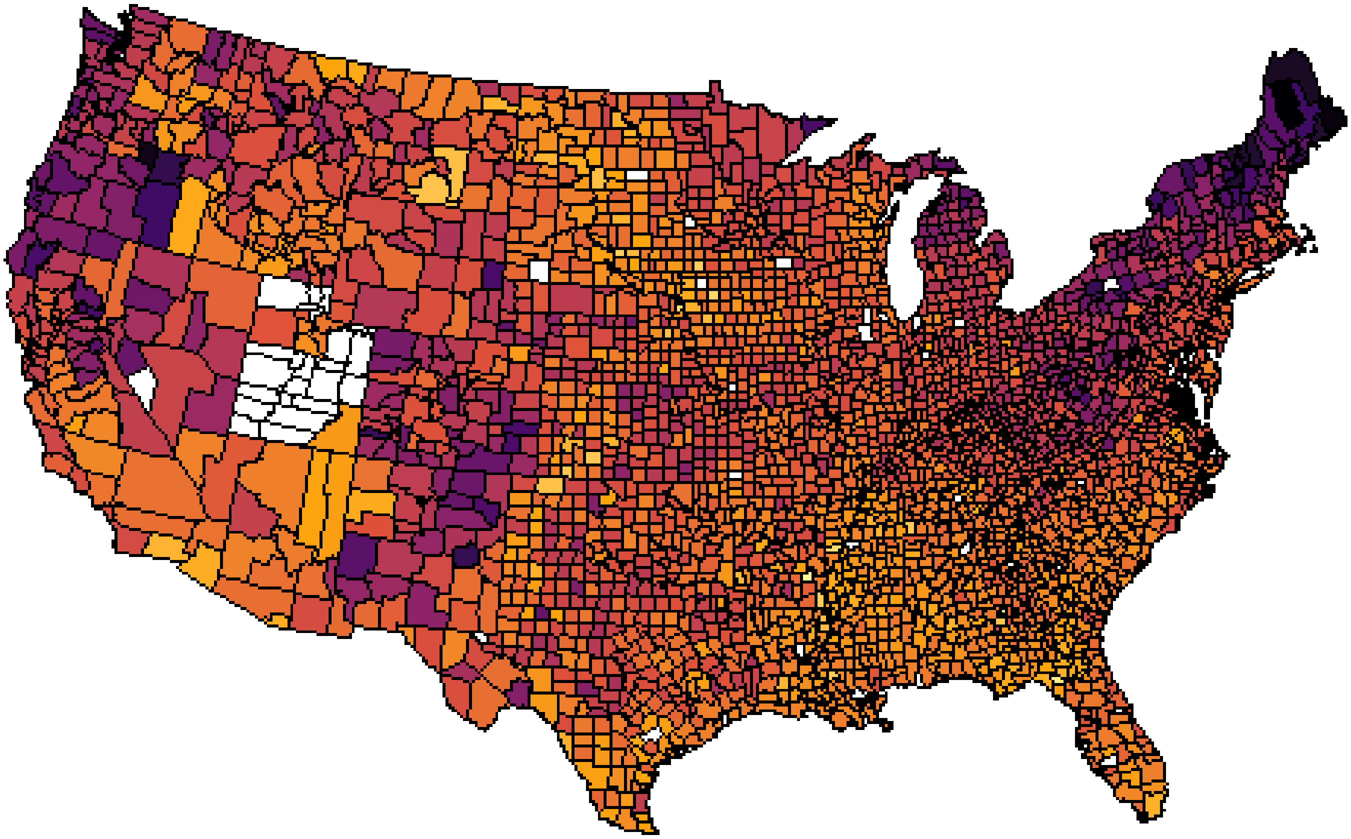


Figure 1. Change in vote share between the 2016 and 2018 congressional elections

Source: Chyzh, Olga V. and R. Urbatsch. 2021. "Bean Counters: The Effect of Soy Tariffs on Change in Republican Vote Share Between the 2016 and 2018 Elections."*Journal of Politics* 83 (1): 415--419.

What Explains Variation in Covid-19 Cases?



Common Exposure

Neighboring counties have similar Covid-19 rates because of their underlying similarities, e.g. demographics, political ideology (anti-mask sentiment), etc.

$$Covid19\ cases/cap_i = \beta_0 + \beta_1 Urban_i + \beta_2 Trump16_i + \beta_3 medinc_i + u_i,$$

Homophily: Spatial X

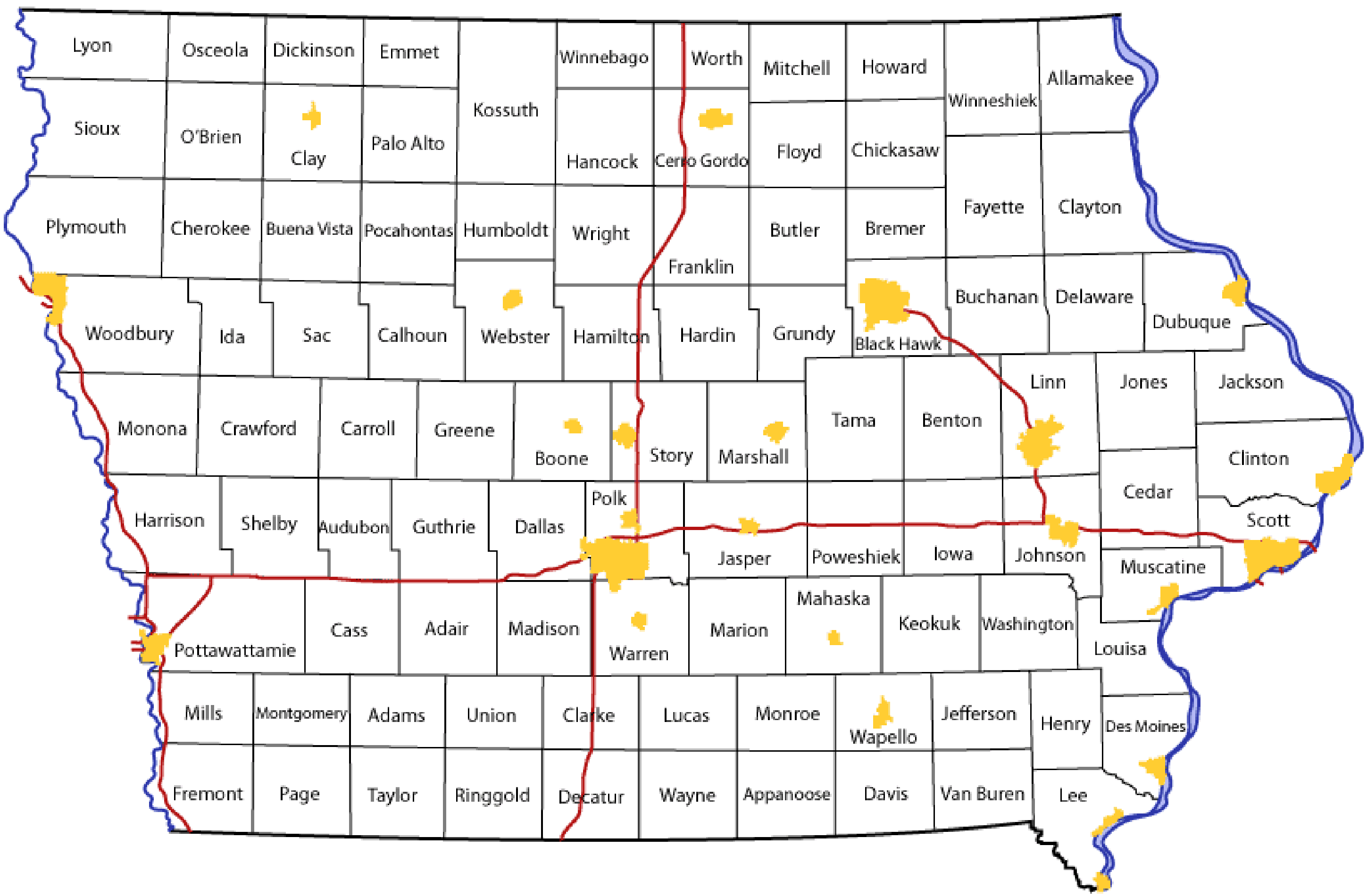
Neighboring units tend to converge on outcomes because the causal variables (anti-vaccine sentiments) cluster by neighborhood locations (partisan geo-sorting).

$$
\begin{aligned}
Covid19\ cases/cap_i = \beta_0 + \beta_1 Urban_i + \beta_2 Trump16_i + \\
\beta_3 medinc_i + \rho \sum_{j \neq i}^{N} w_{ij}\ Trump16_j + u_i,
\end{aligned}
$$

where ρ is the estimation parameter for spatial dependence, and w_{ij} measures whether i and j are neighbors.

- This is a spatial-X regression.
- $\sum_{j \neq i}^{N} w_{ij}\ Trump16_j$ is a spatially lagged independent variable measuring the average Trump support in neighboring counties.
- The coefficient ρ is a measure of spatial homophily.

Contiguity Matrix W



Contiguity Matrix W

```
##         Benton Linn Jones Iowa Johnson Cedar
## Benton       0    1     0    1       0     0
## Linn         1    0     1    0       1     1
## Jones        0    1     0    0       0     1
## Iowa         1    0     0    0       1     0
## Johnson      0    1     0    1       0     1
## Cedar        0    1     1    0       1     0
```

Row Standardized W

Divide by the row sum, so that each neighbor's influence decreases with the total number of neighbors.

```
##         Benton Linn Jones Iowa Johnson Cedar
## Benton    0.00 0.50  0.00 0.50    0.00  0.00
## Linn      0.25 0.00  0.25 0.00    0.25  0.25
## Jones     0.00 0.50  0.00 0.00    0.00  0.50
## Iowa      0.50 0.00  0.00 0.00    0.50  0.00
## Johnson   0.00 0.33  0.00 0.33    0.00  0.33
## Cedar     0.00 0.33  0.33 0.00    0.33  0.00
```

Diffusion: Spatial Y

$$Covid19\ cases/cap_i = \beta_0 + \beta_1 Urban_i + \beta_2 Trump16_i + \beta_3 medinc_i + \rho \sum_{j \neq i}^{N} w_{ij}\ Covid19\ cases/cap_j + u_i,$$

where ρ is the estimation parameter for spatial dependence, and w_{ij} measures whether i and j are neighbors.

- This is a spatial-Y regression.
- $\sum_{j \neq i}^{N} w_{ij}\ Covid19\ cases/cap_j$ is a spatially lagged dependent variable measuring the average number of Covid-19 cases in neighboring counties.
- The coefficient ρ is a measure of spatial dependence.

Spatial Y Model

$$\mathbf{y} = \rho \mathbf{W} \mathbf{y} + \mathbf{X} \boldsymbol{\beta} + \boldsymbol{\epsilon},$$

- $\mathbf{y}$ the dependent variable, is an N x 1 vector of cross sections stacked by period;
- ρ is the spatial coefficient;
- $\mathbf{W}$ is an N x N spatial-weighting matrix;
- $\mathbf{X}$ contains N observations on k independent variables
- $\boldsymbol{\beta}$ is a k x 1 vector of coefficients;
- $\boldsymbol{\epsilon}$ is an N by 1 vector of stochastic components.

Spatial Y Model

$$\begin{bmatrix} y_1 \\ y_2 \\ y_3 \\ \vdots \\ y_N \end{bmatrix} = \rho \begin{bmatrix} 0 & W_{12} & W_{13} & \cdots & W_{1N} \\ W_{21} & 0 & W_{23} & \cdots & W_{2N} \\ W_{31} & W_{32} & 0 & \cdots & W_{3N} \\ \vdots & \ddots & \vdots & \ddots & \vdots \\ W_{N1} & W_{N2} & W_{N3} & \cdots & 0 \end{bmatrix} +$$

$$\begin{bmatrix} x_{11} & x_{12} & \cdots & x_{1k} \\ x_{21} & x_{22} & \cdots & x_{2k} \\ \vdots & \vdots & \ddots & \vdots \\ x_{N1} & x_{N2} & \cdots & x_{Nk} \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \\ \vdots \\ \beta_k \end{bmatrix} + \begin{bmatrix} \epsilon_1 \\ \epsilon_2 \\ \vdots \\ \epsilon_N \end{bmatrix}$$

Spatial Lag Model

$$\mathbf{y} = \rho \mathbf{W} \mathbf{y} + \mathbf{X} \boldsymbol{\beta} + \boldsymbol{\epsilon},$$

By re-arranging, can isolate $\mathbf{y}$ on the left-hand side:

$$\mathbf{y} = [\boldsymbol{I_N} - \rho \mathbf{W}_N]^{-1} \{\mathbf{X} \boldsymbol{\beta} + \boldsymbol{\epsilon}\}$$

Likelihood

$$\mathbf{y} = \rho\mathbf{W}\mathbf{y} + \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\varepsilon} \Rightarrow \boldsymbol{\varepsilon} = (\mathbf{I} - \rho\mathbf{W})\mathbf{y} - \mathbf{X}\boldsymbol{\beta} \equiv \mathbf{A}\mathbf{y} - \mathbf{X}\boldsymbol{\beta}. \tag{10}$$

Assuming i.i.d. normality, the likelihood function for $\boldsymbol{\varepsilon}$ is then just the typical linear one:

$$L(\boldsymbol{\varepsilon}) = \left(\frac{1}{\sigma^2 2\pi}\right)^{\frac{NT}{2}} \exp\left(-\frac{\boldsymbol{\varepsilon}'\boldsymbol{\varepsilon}}{2\sigma^2}\right), \tag{11}$$

which, in this case, will produce a likelihood in terms of $\mathbf{y}$ as follows:

$$L(\mathbf{y}) = |\,\mathbf{A}\,| \left(\frac{1}{\sigma^2 2\pi}\right)^{\frac{NT}{2}} \exp\left[-\frac{1}{2\sigma^2}(\mathbf{A}\mathbf{y} - \mathbf{X}\boldsymbol{\beta})'(\mathbf{A}\mathbf{y} - \mathbf{X}\boldsymbol{\beta})\right]. \tag{12}$$

Other Types of Space

- Ideology
- International trade
- Alliances
- Other examples?

Lab

Example: Spatial X

```
mydata<-read.csv("./data/covid_data.csv", header=TRUE)
mydata$trumpmarg[is.na(mydata$trumpmarg)]<-0
contigmat<-read.table("data/contigmat.txt") |> as.matrix()
contigmat1<-contigmat/apply(contigmat,1,sum) #row-standardize

mydata$W_trumpmarg<-contigmat1%*%mydata$trumpmarg

m1<-lm(data=mydata, cases_pc~urb2010+trumpmarg+medinc1317)
m2<-lm(data=mydata, cases_pc~urb2010+trumpmarg+medinc1317+W_trumpmarg
```

Spatial Regression

```
library(spdep)
library(spatialreg)

contigmat<-read.table("./data/contigmat.txt")
contigmat<-as.matrix(contigmat)
W1<-mat2listw(contigmat, row.names = NULL, style="W", zero.policy = T
summary(W1$neighbours)

W2<-nb2listw(W1$neighbours, glist=NULL, style="W", zero.policy=TRUE)

m3 <- lagsarlm(data=mydata, cases_pc~log(totpop1317)+urb2010+trumpmar
summary(m3)

saveRDS(m3,"m3.RDS")
```

Interpretation

Set up a hypothetical scenario:

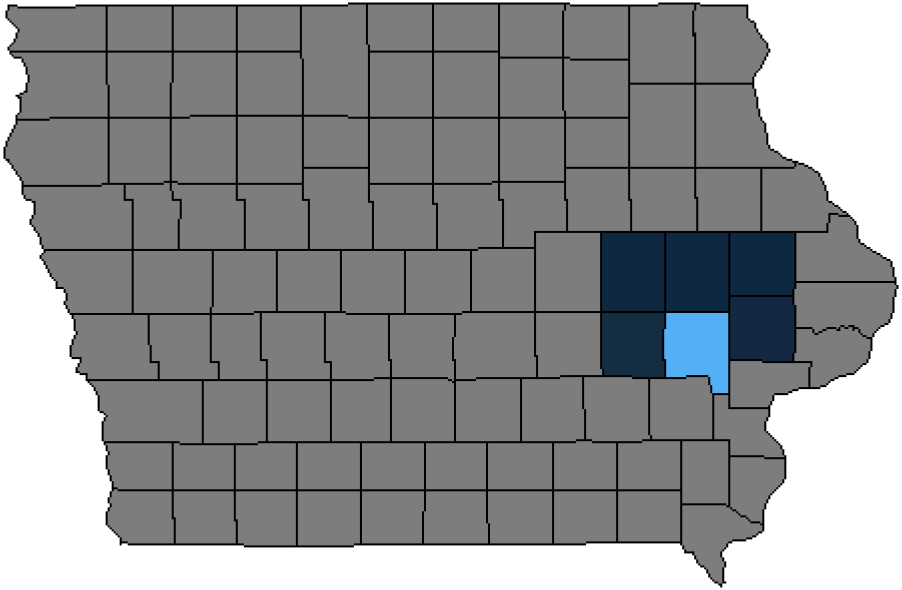
- Expected change in Covid-19 cases that would result from increasing urbanization in Johnson county, IA

```
names<-c("benton","cedar","iowa","johnson","jones","linn")
mymat<-matrix(c(0,0,1,0,0,1,
                0,0,0,1,1,1,
                1,0,0,1,0,0,
                0,1,1,0,0,1,
                0,1,0,0,0,1,
                1,1,0,1,1,0),nrow=6,ncol=6)
dimnames(mymat)<-list(names,names)
mymat<-round(mymat/apply(mymat,1,sum),2)
d<-dplyr::filter(mydata, state=="IA" & county %in% names)
```

Set up A Comparison by Shocking One of the Units on X

```
m3<- readRDS("m3.RDS")

I<- diag(6)
X0<-as.matrix(cbind(1,log(d$totpop1317), d$urb2010, d$trumpmarg, d$me

urb<-d$urb2010
urb[4]<-1
X1<-as.matrix(cbind(1,log(d$totpop1317), urb, d$trumpmarg, d$medinc13
A<-solve(I-coef(m3)[1]*mymat)

mycoef<-as.matrix(coef(m3))

Yhat0<- A%*%(X0%*%mycoef)
Yhat1<- A%*%(X1%*%mycoef)

Y_ch<-Yhat1-Yhat0
sim<- cbind.data.frame(names,Y_ch)
```

Visualize the Effect



Your Turn 1

Suppose you want to test whether variable *urb2010* is spatially clustered.

1. Calculate a measure of the average urbanization in neighboring states.
2. Estimate a model that accounts for clustering in urbanization.
3. Is the effect of neighbor's urbanization positive or negative?
4. Is this effect statistically significant?

Your Turn 2

Suppose you want to test whether variable *votech* (the change in Republican vote share between the 2016 and 2018 Congressional election) is spatially clustered.

1. Calculate a measure of the average change in Republican vote share in neighboring states.
2. Estimate a model of *votech* as a function of *urb2010*, *medinc1317*, *perc_HS_GED*, *perclatino1317* and *trumpmarg*.
3. Estimate the same model plus a the average change in Republican vote share in neighboring states.

Making Maps

```r
library(tidyverse)
library(mapproj)
library(maps)
library(mapdata)
states <- map_data("state")

head(states)
```

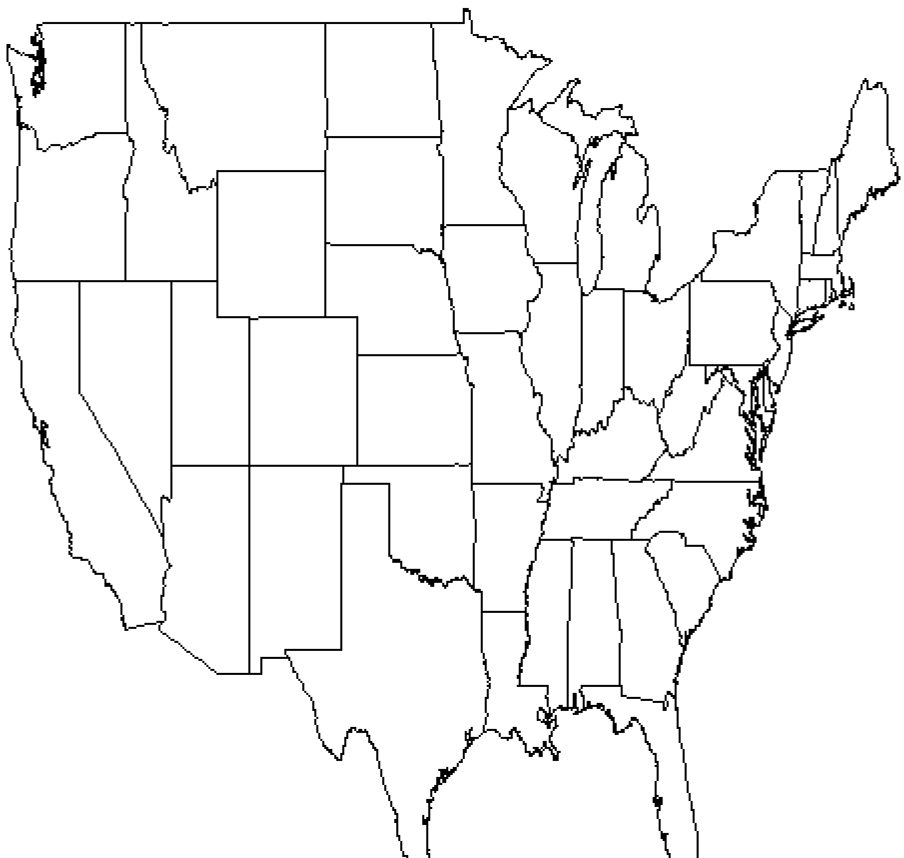
```
##        long      lat group order  region subregion
## 1 -87.46201 30.38968     1     1 alabama      <NA>
## 2 -87.48493 30.37249     1     2 alabama      <NA>
## 3 -87.52503 30.37249     1     3 alabama      <NA>
## 4 -87.53076 30.33239     1     4 alabama      <NA>
## 5 -87.57087 30.32665     1     5 alabama      <NA>
## 6 -87.58806 30.32665     1     6 alabama      <NA>
```

What You Need

- Latitude/longitude points for all map boundaries
- Need to know to which boundary/state lat/long points belong
- Need to know the order to connect points within each group

A Basin (Rather Hideous) Map

```
library(ggplot2)
ggplot() +  geom_path(data=states, aes(x=long, y=lat, group=group),co
```

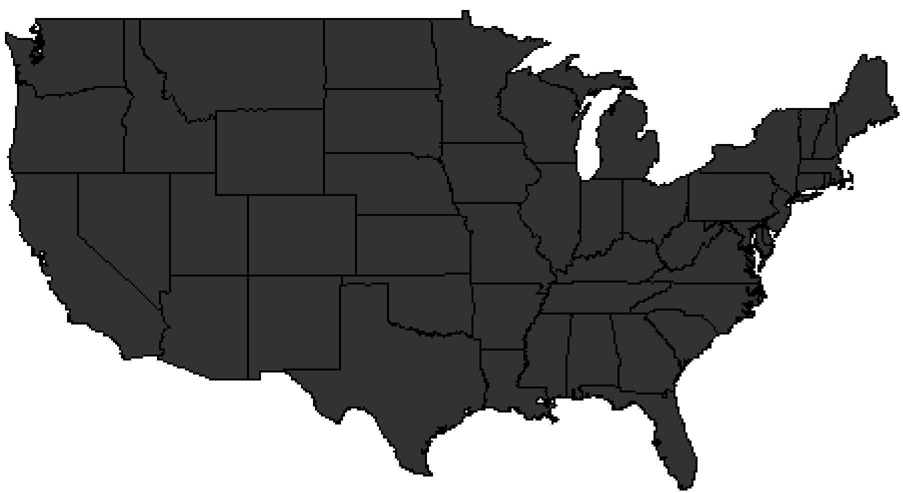


A Bit Nicer of a Map

```
#Set theme options:
theme_set(theme_grey() + theme(axis.text=element_blank(),
                               axis.ticks=element_blank(),
                               axis.title.x=element_blank(),
                               axis.title.y=element_blank(),
                               panel.grid.major = element_blank(),
                               panel.grid.minor = element_blank(),
                               panel.border = element_blank(),
                               panel.background = element_blank(),
                               legend.position="none"))
ggplot() +  geom_path(data=states, aes(x=long, y=lat, group=group),co
```

Polygon instead of Path

```
ggplot() +  geom_polygon(data=states, aes(x=long, y=lat, group=group)
```



Incorporate Information About States

- Add other geographic information (e.g., counties) by adding geometric layers to the plot
- Add non-geographic information by altering the fill color for each state
  - Use geom = "polygon" to treat states as solid shapes to add color
  - Incorporate numeric information using color shade or intensity
  - Incorporate categorical informaion using color hue

Categorical Information Using Hue

If a categorical variable is assigned as the fill color then ggplot will assign different hues for each category.

Let's load in a state regions dataset:

```
statereg<- read.csv("./data/statereg.csv")

head(statereg)
```

```
##         State StateGroups
## 1 california        West
## 2     nevada        West
## 3     oregon        West
## 4 washington        West
## 5      idaho        West
## 6    montana        West
```

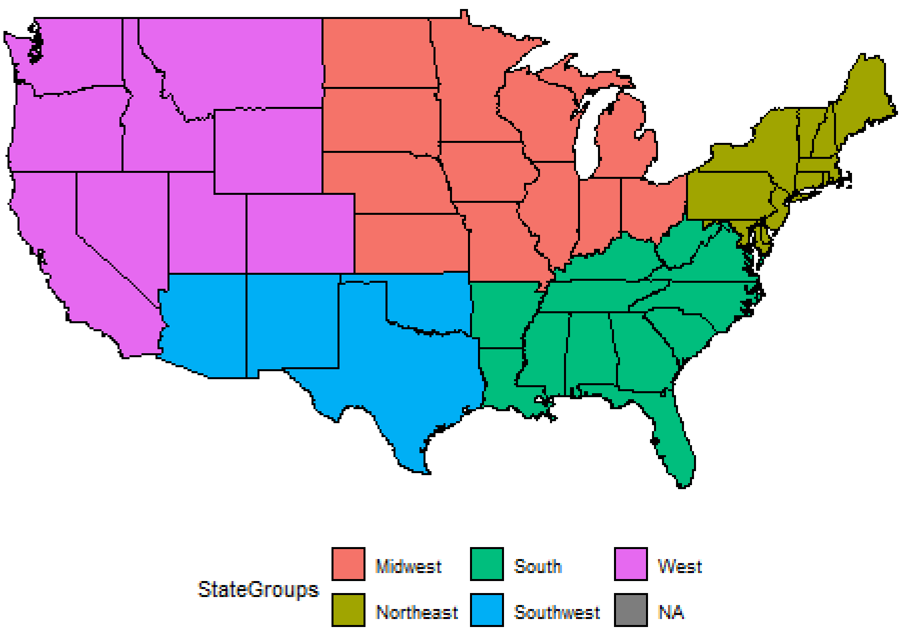
Join the Data

```
states.class.map <- left_join(states, statereg, by = c("region" = "St
head(states.class.map)
```

```
##        long      lat group order  region subregion StateGroups
## 1 -87.46201 30.38968     1     1 alabama      <NA>       South
## 2 -87.48493 30.37249     1     2 alabama      <NA>       South
## 3 -87.52503 30.37249     1     3 alabama      <NA>       South
## 4 -87.53076 30.33239     1     4 alabama      <NA>       South
## 5 -87.57087 30.32665     1     5 alabama      <NA>       South
## 6 -87.58806 30.32665     1     6 alabama      <NA>       South
```

Plot the Regions

```
ggplot() +  geom_polygon(data=states.class.map, aes(x=long, y=lat, gr
```



Your Turn

Use color to show the expected change in Covid-19 cases that result from increasing urbanization in Johnson county, IA on a map.

Your Turn (Advanced)

1. Read in the animal.csv data:

```
animal <- read.csv("./data/animal.csv")
```

1. Plot the location of animal sightings on a map of the region
2. On this plot, try to color points by class of animal and/or status of animal
3. **Advanced**: Could we indicate time somehow?