Analysis of the 2016 US Presidential Election

he data for this analysis come from Tony McGovern. The response variable, Y_i , is the percentage change in Republican (GOP) support from 2012 to 2016, i.e.,

$$100\left(\frac{\%\text{ in }2016}{\%\text{ in }2012}-1\right),$$

in county $i = 1, \ldots, n$.

The $p = 10$ covariates X_{ij} are county-level census variables obtained from Kaggle are:

Population, percent change - April 1, 2010 to July 1, 2014

Persons 65 years and over, percent, 2014

Black or African American alone, percent, 2014

Hispanic or Latino, percent, 2014

High school graduate or higher, percent of persons age 25+, 2009-2013

Bachelor's degree or higher, percent of persons age 25+, 2009-2013

Homeownership rate, 2009-2013

Median value of owner-occupied housing units, 2009-2013

Median household income, 2009-2013

Persons below poverty level, percent, 2009-2013

For a county in state s, we assume the linear model

$$Y_i = \beta_{0s} + \sum_{j=1}^{p} X_i\beta_{sj} + \varepsilon_i,$$

where β_{js} is the effect of covariate j in state s. We compare three models for the β_{js}.

1. Constant slopes: $\beta_{js} = \beta_j$ for all counties.
2. Varying slopes with uninformative priors: $\beta_{js} \sim \text{Normal}(0, 100)$
3. Varying slopes with informative priors: $\beta_{js} \sim \text{Normal}(\mu_j, \sigma_j^2)$.

In the third model, the means μ_j and variances σ_j^2 are given prior and estimated from the data, therefore information is pooled across states via the prior. The three methods are compared using DIC, and final results are compared across models.

```
library(choroplethr)
```

```
## Loading required package: acs
```

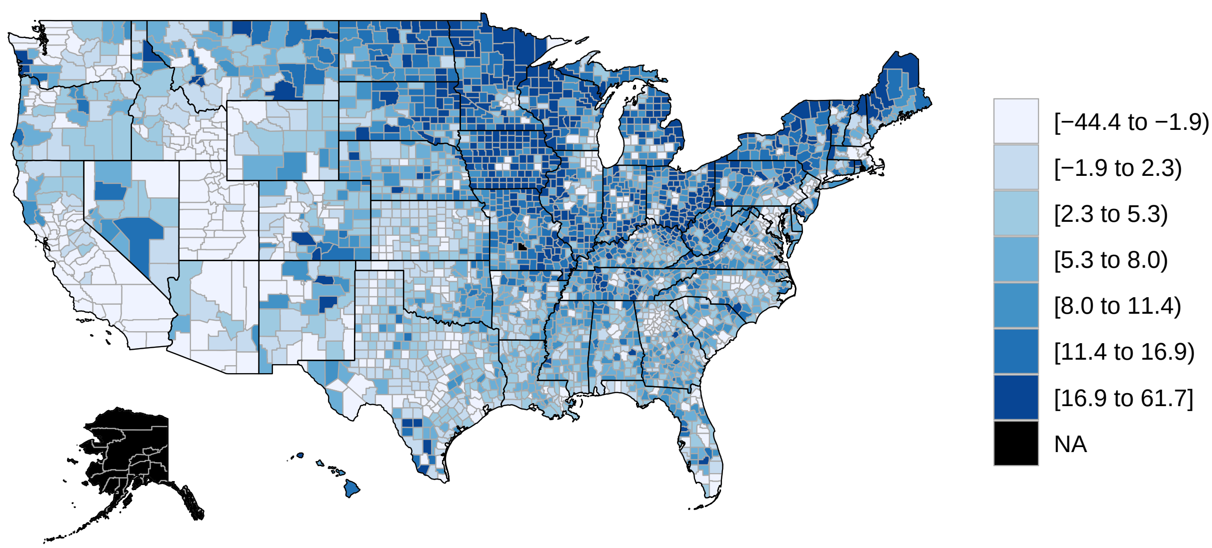
```
## Loading required package: stringr
```

```
## Loading required package: XML
```

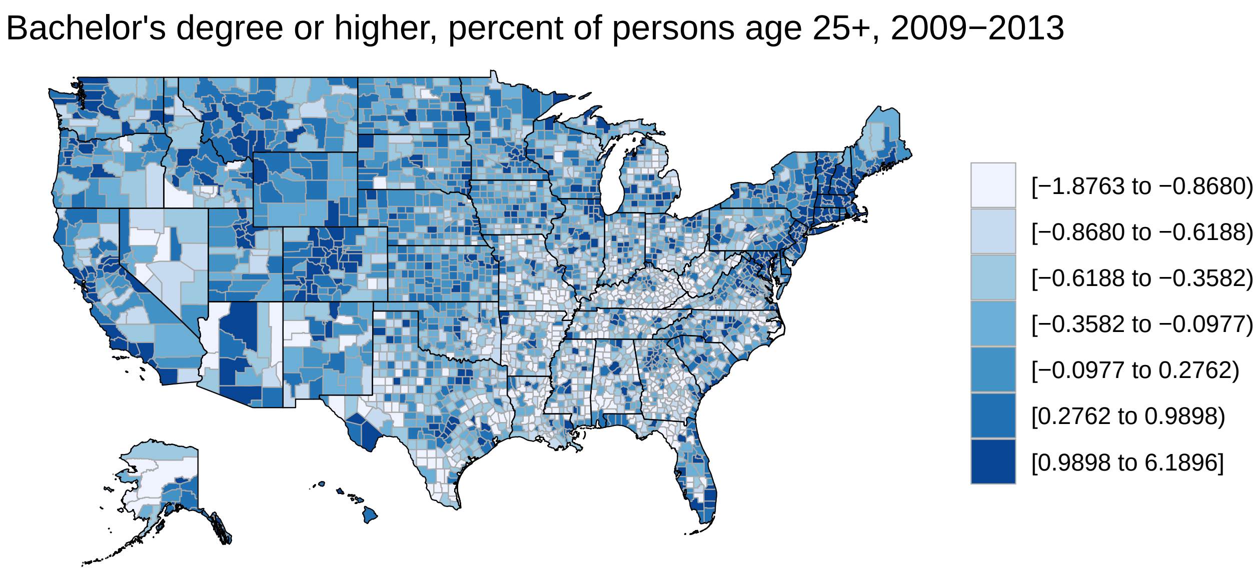
```
##
## Attaching package: 'acs'

## The following object is masked from 'package:base':
##
##     apply
```

```r
load("/Users/kamaladadashova/Documents/DoctoralCourses/Applied Bayesian Statistics/Lecture Notes with A
X      <- scale(X)     # Standardize the covariates
 X      <- cbind(1,X)
 short <- c("Intercept", "Pop change", "65+","African American",
            "Hispanic","HS grad","Bachelor's",
            "Homeownership rate","Home value",
            "Median income", "Poverty")
 names <- c("Intercept", as.character(names[1:11,2]))
 colnames(X) <- short

 # Define a function to make county maps
 county_plot <- function(fips,Y,main="",units=""){
   library(choroplethr)
   temp  <- as.data.frame(list(region=fips,value=Y))
   suppressWarnings(county_choropleth(temp,title=main,legend=units))
 }
 county_plot(fips,Y,main="Percent increase in GOP support",units="")
```

Percent increase in GOP support



```r
county_plot(fips,X[,7],main=names[7],units="")
```




```r
# Remove AK, HI and DC due to missing data
 state <- as.character(all_dat[,3])
 AKHI  <- state=="AK" | state=="HI" | state=="DC"
 fips  <- fips[!AKHI]
 Y     <- Y[!AKHI]
 X     <- X[!AKHI,]
 state <- state[!AKHI]

 # Assign a numeric id to the counties in each state
 st    <- unique(state)
 id    <- rep(NA,length(Y))
 for(j in 1:48){
   id[state==st[j]]<-j
 }

 n <- length(Y) # number of counties
 N <- 48        # number of states
 p <- ncol(X)   # number of covariates

 set.seed(0820)
 iters <- 50000
 burn  <- 10000
```

Constant slopes

```
model1_string <- "model{

   # Likelihood
   for(i in 1:n){
      Y[i]    ~ dnorm(mu[i],taue)
      mu[i] <- inprod(X[i,],beta[])
   }
   # Priors
   for(j in 1:p){beta[j] ~ dnorm(0,0.01)}
   taue ~ dgamma(0.1,0.1)
   sig <- 1/sqrt(taue)

   # WAIC calculations
   for(i in 1:n){
     like[i]    <- dnorm(Y[i],mu[i],taue)
   }
 }"

 library(rjags)
```

```
## Loading required package: coda

## Linked to JAGS 4.3.1

## Loaded modules: basemod,bugs
```

```
 # Load the model
 dat    <- list(Y=Y,n=n,X=X,p=p)
 init   <- list(beta=rep(0,p))
 model1 <- jags.model(textConnection(model1_string),n.chains=2,
                      inits=init,data = dat,quiet=TRUE)
 # Generate samples
 update(model1, burn, progress.bar="none")
 samp1   <- coda.samples(model1,
            variable.names="beta",
            n.iter=iters, progress.bar="none")

 # Compile results
 ESS1    <- effectiveSize(samp1)
 out1    <- summary(samp1)$quantiles
 rownames(out1)<-short

 # Compute DIC
 dic1    <- dic.samples(model1,n.iter=iters,progress.bar="none")

 # Compute WAIC
 waic1   <- coda.samples(model1,
            variable.names=c("like"),
            n.iter=iters, progress.bar="none")
 like1   <- waic1[[1]]
```

```
fbar1   <- colMeans(like1)
P1      <- sum(base::apply(log(like1),2,var))
WAIC1   <- -2*sum(log(fbar1))+2*P1
```

Slopes as fixed effects

```
model2_string <- "model{

   # Likelihood
   for(i in 1:n){
      Y[i]    ~ dnorm(mnY[i],taue)
      mnY[i] <- inprod(X[i,],beta[id[i],])
   }

   # Slopes
   for(j in 1:p){for(i in 1:N){
       beta[i,j] ~ dnorm(0,0.01)
   }}

   # Priors
   taue ~ dgamma(0.1,0.1)


   # WAIC calculations
   for(i in 1:n){
     like[i]    <- dnorm(Y[i],mnY[i],taue)
   }
  }"


  library(rjags)

  # Load the model
  dat    <- list(Y=Y,n=n,N=N,X=X,p=p,id=id)
  init   <- list(beta=matrix(0,N,p))
  model2 <- jags.model(textConnection(model2_string),n.chains=2,
                       inits=init,data = dat,quiet=TRUE)

  # Generate samples
  update(model2, burn, progress.bar="none")
  samp2  <- coda.samples(model2,
            variable.names="beta",
            n.iter=iters, progress.bar="none")

  # Compile results
  ESS2     <- effectiveSize(samp2)
  sum      <- summary(samp2)$stat
  post_mn2 <- matrix(sum[,1],N,p)
  post_sd2 <- matrix(sum[,2],N,p)

  # Compute DIC
```

```r
dic2   <- dic.samples(model2,n.iter=iters,progress.bar="none")

# Compute WAIC
waic2   <- coda.samples(model2,
           variable.names=c("like"),
           n.iter=iters, progress.bar="none")
like2   <- waic2[[1]]
fbar2   <- colMeans(like2)
P2      <- sum(base::apply(log(like2),2,var))
WAIC2   <- -2*sum(log(fbar2))+2*P2
```

Slopes as random effects

```r
model3_string <- "model{

  # Likelihood
  for(i in 1:n){
     Y[i]    ~ dnorm(mnY[i],taue)
     mnY[i] <- inprod(X[i,],beta[id[i],])
  }

  # Random slopes
  for(j in 1:p){
    for(i in 1:N){
      beta[i,j] ~ dnorm(mu[j],taub[j])
    }
    mu[j]    ~ dnorm(0,0.01)
    taub[j]  ~ dgamma(0.1,0.1)
  }

  # Priors
  taue ~ dgamma(0.1,0.1)


  # WAIC calculations
  for(i in 1:n){
    like[i]    <- dnorm(Y[i],mnY[i],taue)
  }
 }"


 library(rjags)

 # Load the model
 dat    <- list(Y=Y,n=n,N=N,X=X,p=p,id=id)
 init   <- list(beta=matrix(0,N,p))
 model3 <- jags.model(textConnection(model3_string),n.chains=2,
                      inits=init,data = dat,quiet=TRUE)

 # Generate samples
 update(model3, burn, progress.bar="none")
```

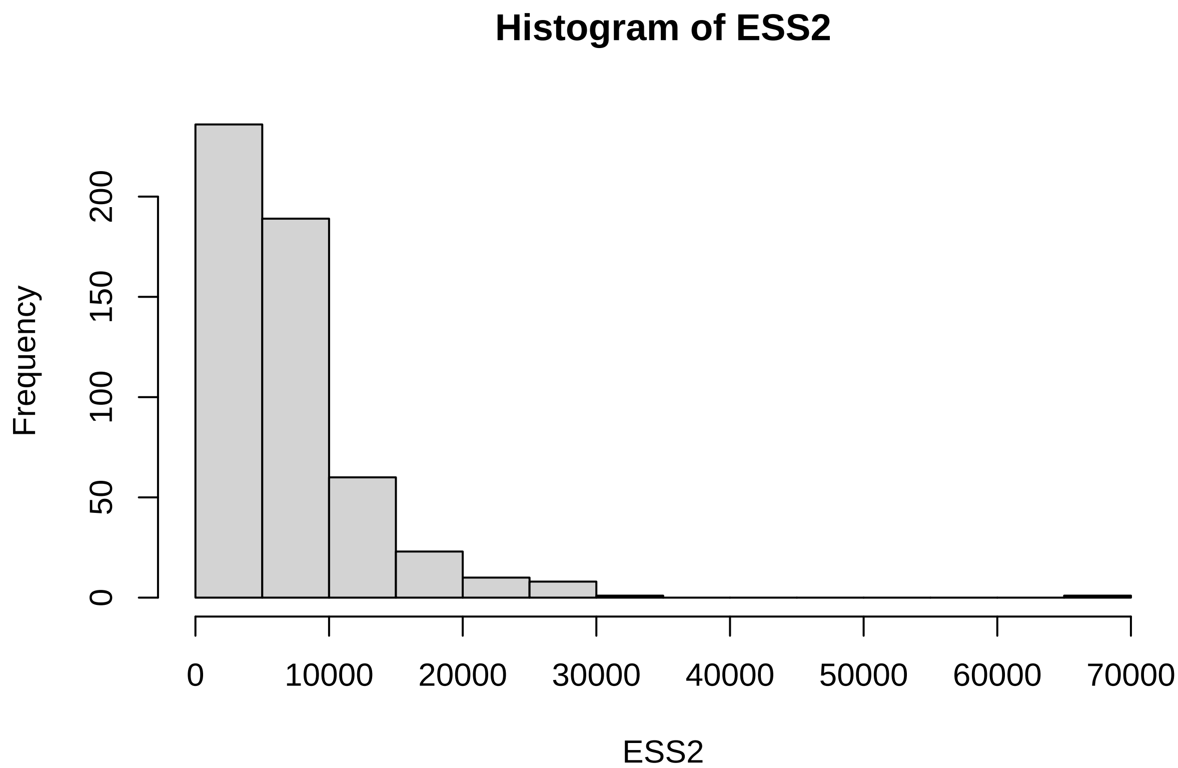
```r
samp3  <- coda.samples(model3,
          variable.names="beta",
          n.iter=iters, progress.bar="none")

# Compile results
ESS3     <- effectiveSize(samp3)
sum      <- summary(samp3)$stat
post_mn3 <- matrix(sum[,1],N,p)
post_sd3 <- matrix(sum[,2],N,p)

# Compute DIC
dic3    <- dic.samples(model3,n.iter=iters,progress.bar="none")

# Compute WAIC
waic3   <- coda.samples(model3,
           variable.names=c("like"),
           n.iter=iters, progress.bar="none")
like3   <- waic3[[1]]
fbar3   <- colMeans(like3)
P3      <- sum(base::apply(log(like3),2,var))
WAIC3   <- -2*sum(log(fbar3))+2*P3
```

Check convergence

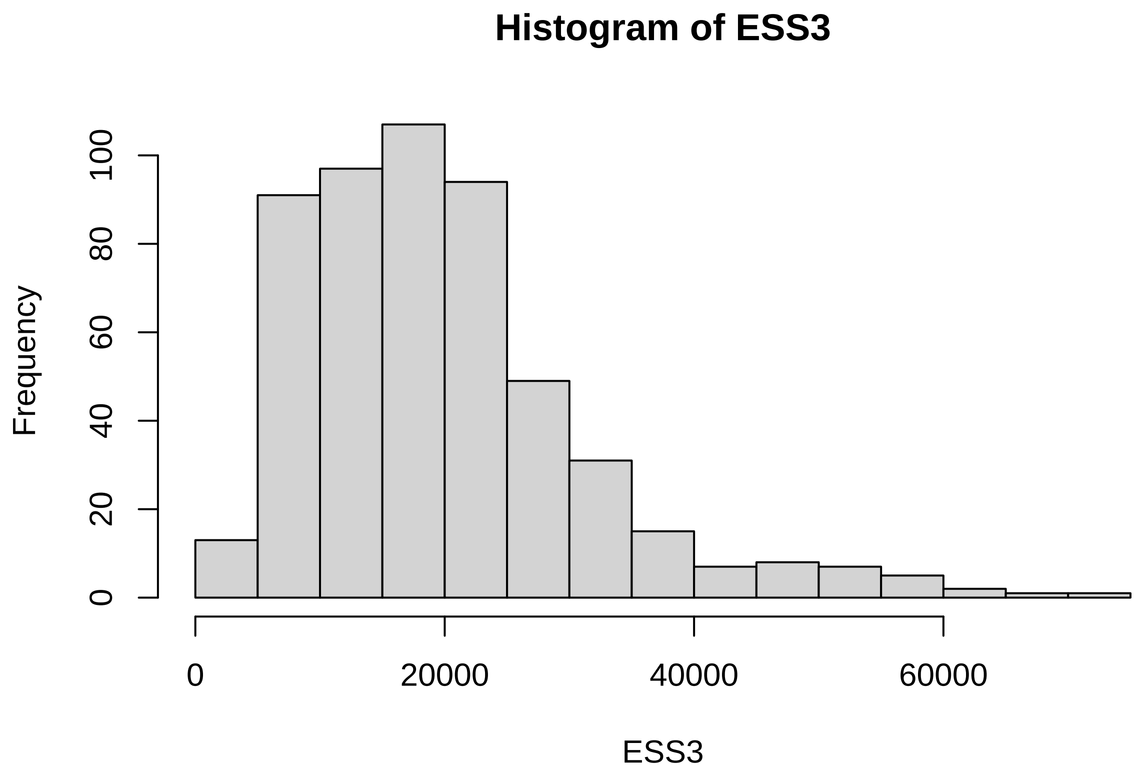
```r
ESS1
```

```
##    beta[1]    beta[2]    beta[3]    beta[4]    beta[5]    beta[6]    beta[7]
## 100000.000  54783.888  18098.126  41377.224  29620.781  16623.860  16510.458
##    beta[8]    beta[9]   beta[10]   beta[11]
##  23658.552  17431.601   8569.037  11775.625
```

```r
hist(ESS2)
```


Histogram of ESS2
Frequency
0
50
100
150
200
0
10000
20000
30000
40000
50000
60000
70000
ESS2

```r
hist(ESS3)
```



Summary: The effective sample size is large for all parameters and all models, therefore it seems the MCMC algorithm has converged.

Summarize the non-spatial model

```r
library(kableExtra)
 kbl(round(out1,2))
```

	2.5%	25%	50%	75%	97.5%
Intercept	6.41	6.58	6.67	6.76	6.93
Pop change	-1.45	-1.25	-1.14	-1.03	-0.82
65+	0.53	0.79	0.93	1.06	1.32
African American	-1.89	-1.67	-1.56	-1.45	-1.23
Hispanic	-2.40	-2.18	-2.06	-1.95	-1.73
HS grad	1.25	1.58	1.75	1.92	2.25
Bachelor's	-6.72	-6.37	-6.19	-6.01	-5.67
Homeownership rate	-0.38	-0.12	0.01	0.15	0.40
Home value	-1.98	-1.68	-1.52	-1.36	-1.05
Median income	1.13	1.62	1.87	2.13	2.61
Poverty	0.91	1.28	1.47	1.67	2.04

Summary: All but one (home ownership rate) of the covariates have 95% interval that excludes zero. GOP support tended to increase in counties with decreasing population high proportion of seniors and high school graduates low proportions of African Americans and Hispanics High income but low home value High poverty rate

Compare models with DIC

```
dic1
```

```
## Mean deviance:  21300
## penalty 11.99
## Penalized deviance: 21312
```

```
dic2
```

```
## Mean deviance:  18484
## penalty 455.6
## Penalized deviance: 18939
```

```
dic3
```

```
## Mean deviance:  18604
## penalty 238.1
## Penalized deviance: 18842
```

Summary: The first model with constant slopes is the simplest but fits the data poorly and thus has highest DIC. The second model with different slopes in each state has the best fit (smallest mean deviance), but is too complicated and has large p_D The final model has fairly small mean deviance and p_D, and thus balances fit and complexity to give the smallest DIC.

Compare models with WAIC

```
WAIC1; P1
```

```
## [1] 21334.81

## [1] 20.00944
```

```
WAIC2; P2
```

```
## [1] 18969.98

## [1] 405.1366
```

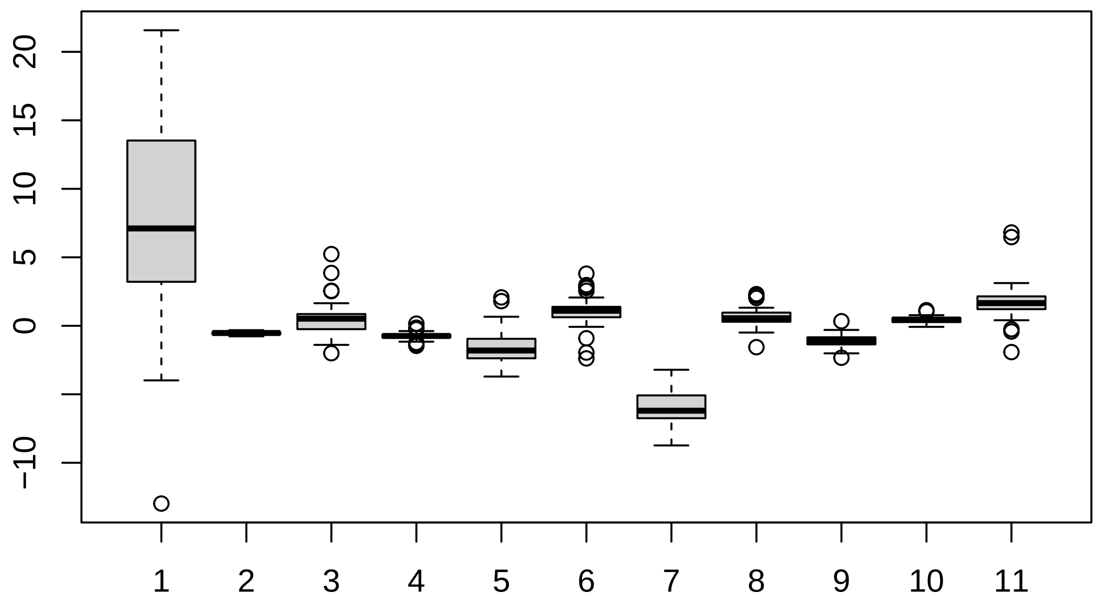
```
WAIC3; P3
```

```
## [1] 18909.09

## [1] 259.9894
```

Summary: WAIC agrees with DIC. Both prefer Model 3 with the regression coefficients treated as random effects.

Explore the results of the final model

```
boxplot(post_mn3)
```

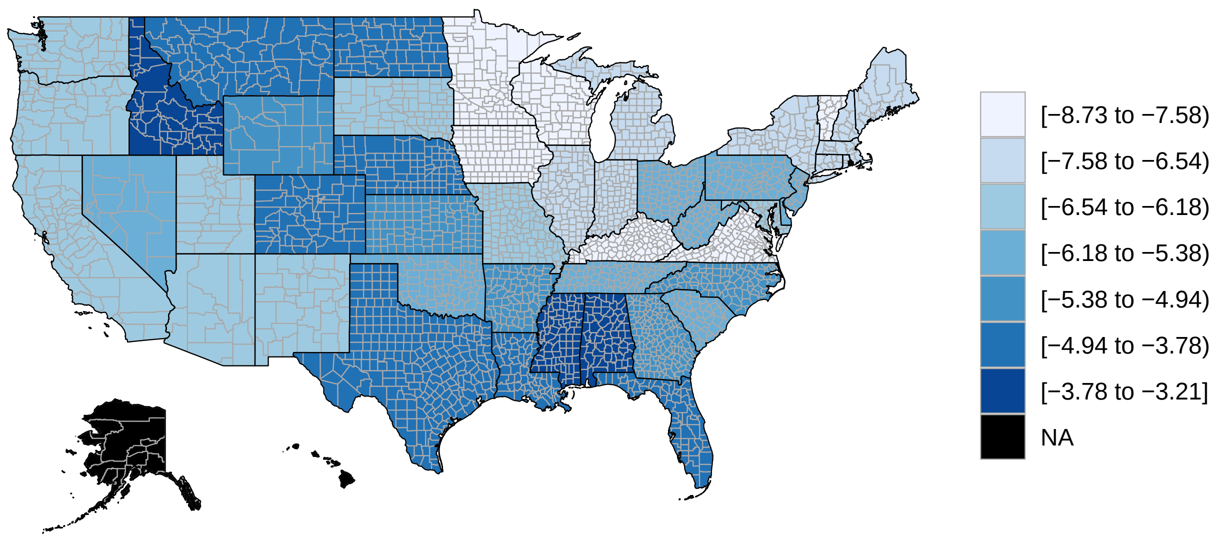


Summary: The effect of the proportion of college graduates varies the most across states

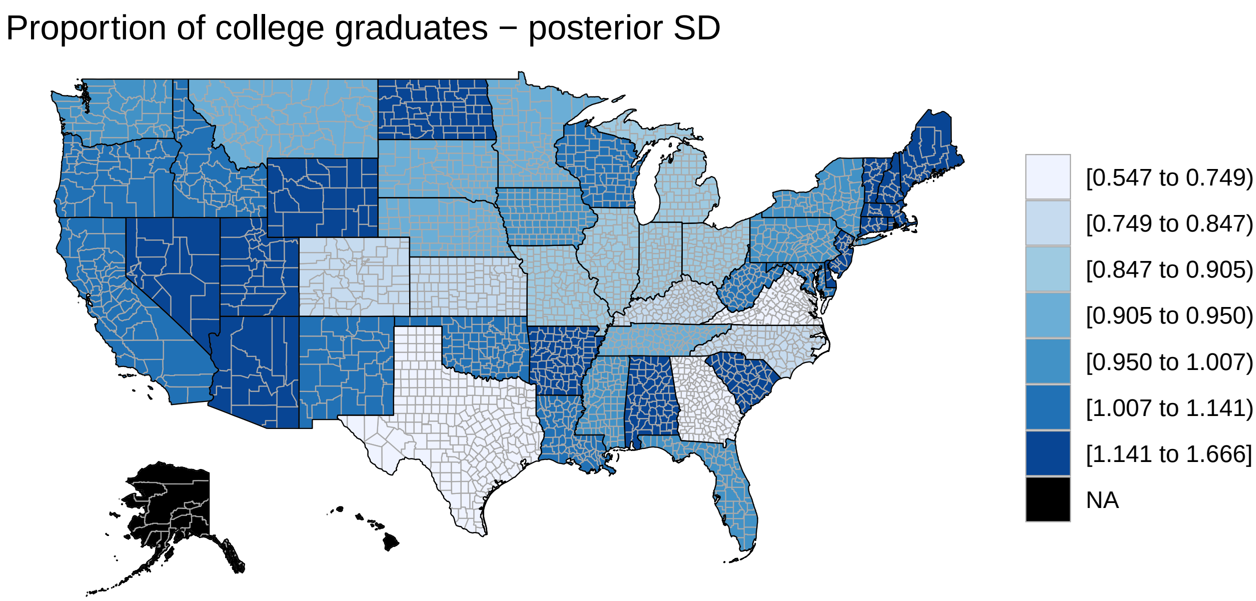
Explore the three estimate of the effects of college graduates

```
# Posterior mean
 county_plot(fips,post_mn3[id,7],
             main="Proportion of college graduates - posterior mean")
```

Proportion of college graduates − posterior mean




```
# Posterior sd
county_plot(fips,post_sd3[id,7],
main="Proportion of college graduates - posterior SD")
```



Summary: The effect of the proportion of college graduates is the strongest (most negative) in the midwest.