

# hw9.R

joebrew

Mon Nov 3 09:54:35 2014

```
library(rgdal)
```

```
## Loading required package: sp
## rgdal: version: 0.9-1, (SVN revision 518)
## Geospatial Data Abstraction Library extensions to R successfully loaded
## Loaded GDAL runtime: GDAL 1.10.1, released 2013/08/26
## Path to GDAL shared files: /usr/share/gdal/1.10
## Loaded PROJ.4 runtime: Rel. 4.8.0, 6 March 2012, [PJ_VERSION: 480]
## Path to PROJ.4 shared files: (autodetected)
```

```
#####
```

```
# BACKGROUND AND INSTRUCTIONS
```

```
#####
```

```
# Name2_: name of county in FL;
# CWF7094: number of breast cancer deaths in White females in FL;
# CBF7094: number of breast cancer deaths in Black females in FL;
# POPWF7094: Total number of population of White females in FL;
# POPBF7094: Total number of population of Black females in FL;
```

```
#####
```

```
# BEFORE STARTING, WRITE A FULL USEFUL PLOTTING FUNCTIONS
```

```
#####
```

```
#####
```

```
# Compass Rose
```

```
#####
```

```
 #(from http://r-sig-geo.2731867.n2.nabble.com/How-to-diplasy-a-compass-rose-on-a-map-td4509034.html)
```

```
compass_rose <-function(x,y,rot=0,cex=1) {
  oldcex<-par(cex=cex)
  mheight<-strheight("M")
  xylim<-par("usr")
  plotdim<-par("pin")
  xmult<-(xylim[2]-xylim[1])/(xylim[4]-xylim[3])*plotdim[2]/plotdim[1]
  point.angles<-seq(0,7*pi/4,by=pi/4)+pi*rot/180
  crspans<-rep(c(mheight*3,mheight/2),4)
  xpoints<-cos(point.angles)*crspans*xmult+x
  ypoints<-sin(point.angles)*crspans+y
  polygon(xpoints,ypoints)
  txtxpoints<-cos(point.angles[c(1,3,5,7)])*1.33*crspans[1]*xmult+x
  txtypoints<-sin(point.angles[c(1,3,5,7)])*1.33*crspans[1]+y
  text(txtxpoints,txtypoints,c("E","N","W","S"))
  par(oldcex)
}
```

```
#####
```

```
# COLLAPSE MAP INTO ONLY OUTER BOUNDARY
```

```
#####
collapse_map <- function(x){
  require(mapttools)
  boundary <- unionSpatialPolygons(x, rep(1, length(x@polygons)))
}

library(RColorBrewer)
library(classInt)

#####
# CHOROPLETH MAP
#####
choro <- function(
  shape = NULL,
  boundary = NULL,
  main = NULL,
  var = NULL,
  color1 = "lightblue",
  color2 = "darkorange",
  legend_round = 2,
  legend_pos = "bottomleft",
  long_legend = TRUE,
  fixed_scale = NULL,
  lwd = 0.2,
  border = TRUE){
  my_colors <- colorRampPalette(c(color1, "white", color2))(10)
  if(!is.null(fixed_scale)){
    if(length(fixed_scale) != 10){stop("Fixed scale must be of length 10")}
    my_quantiles <- fixed_scale
  } else{
    my_quantiles <- quantile(var, na.rm = TRUE, probs = seq(0,1, length = 10))
  }
  my_values <- vector(mode = "numeric", length = length(var))
  for (i in 1:length(var)){
    diffs <- (var[i] - as.numeric(my_quantiles))^2
    best <- which.min(diffs)[1]
    my_values[i] <- best
  }
  map_colors <- my_colors[my_values]
  plot(shape, col = map_colors, border = border, lwd = lwd,
       main = main)
  plot(boundary, add = TRUE)
  if(long_legend){
    legend_colors <- colorRampPalette(my_colors)(25)
    legend(legend_pos, # position
          legend = c(min(round(my_quantiles, digits = legend_round)),
                     rep(NA, 11),
                     median(round(my_quantiles, digits = legend_round)),
                     rep(NA, 11),
                     max(round(my_quantiles, digits = legend_round))),
          fill = legend_colors,
          cex = 0.75,
          y.intersp = 0.5,
```

```

        border=NA,
        bty = "n")
} else{
  legend_colors <- colorRampPalette(my_colors)(11)
  legend(legend_pos, # position
        legend = c(min(round(my_quantiles, digits = legend_round)),
                    rep(NA, 4),
                    median(round(my_quantiles, digits = legend_round)),
                    rep(NA, 4),
                    max(round(my_quantiles, digits = legend_round))),
        fill = legend_colors,
        cex = 0.75,
        y.intersp = 0.5,
        border=NA,
        bty = "n")
}

compass_rose(x = -80.5 ,y = 30,rot=0,cex=0.25)
}

#####
# 1. Open the shapefile of "Florida_breat_cancer" into OpenGeoda ;
#####

# set local working directory
setwd("/home/joebrew/Documents/uf/phc6194/hw9")

# read in shape file
fl <- readOGR(".", "Florida_breat_cancer")

## OGR data source with driver: ESRI Shapefile
## Source: ".", layer: "Florida_breat_cancer"
## with 67 features and 12 fields
## Feature type: wkbPolygon with 2 dimensions

# make easier to understand column names
names(fl@data)[c(2, 9:12)] <-
  c("county", "white_female_deaths", "black_female_deaths",
    "white_female_population", "black_female_population")

# # There are some errors in the data! How is it that there are more deaths
# # than females in some counties?
# fl$county[which(fl$white_female_deaths > fl$white_female_population)]
# fl$county[which(fl$black_female_deaths > fl$black_female_population)]
# fl$county[which((fl$white_female_deaths / fl$white_female_population) > 0.2)]
# fl$county[which((fl$black_female_deaths / fl$black_female_population) > 0.2)]
#
# # I'm going to remove those
# fl <- fl[which(!fl$county %in% c("CALHOUN", "DE SOTO", "HOLMES",
#                                "FLAGLER", "GILCHRIST", "LAFAYETTE", "WAKULLA")),]
#
# plot to confirm that there are no problems
boundary <- collapse_map(fl)

```

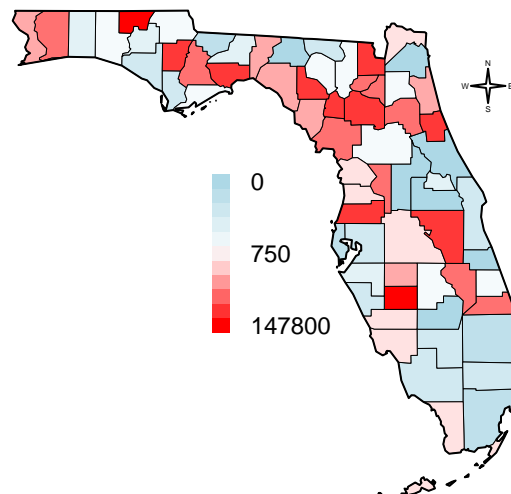
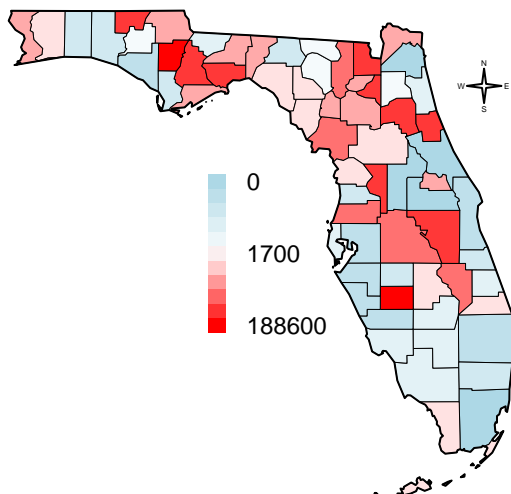
```
## Loading required package: maptools
## Checking rgeos availability: TRUE
## Loading required package: rgeos
## rgeos version: 0.3-8, (SVN revision 460)
## GEOS runtime version: 3.4.2-CAPI-1.8.2 r3921
## Polygon checking: TRUE
```

```
# plot
par(mfrow = c(1,2))
par(mar=c(1,1,1,1))
par(oma = c(0,0,0,0))
choro(shape = fl,
      boundary = boundary,
      var = fl$white_female_deaths / fl$white_female_population * 100000,
      long_legend = FALSE,
      legend_pos = "center",
      legend_round = -2,
      color1 = "lightblue",
      color2 = "red")
title(main = "White female breast cancer deaths per 100,000",
      cex.main = 0.5)

choro(shape = fl,
      boundary = boundary,
      var = fl$black_female_deaths / fl$black_female_population * 100000,
      long_legend = FALSE,
      legend_pos = "center",
      legend_round = -2,
      color1 = "lightblue",
      color2 = "red")
title(main = "Black female breast cancer deaths per 100,000",
      cex.main = 0.5)
```

White female breast cancer deaths per 100,000

Black female breast cancer deaths per 100,000



```

par(mfrow = c(1,1))

#####
# 2. Calculate the raw and empirical Bayes, spatial rate and spatial
#empirical Bayes smoothed rates for both White and Black females;
#####

# first, just map the death rate by county (basic choropleth)

# attach package to do empirical bayes smoothing
library(spdep)

## Loading required package: Matrix

# calculate raw and estmm (empirical) for white
fl$bayes_white_raw <- EBest(n = fl$white_female_deaths,
                           x = fl$white_female_population,
                           family = "poisson")[,1]
fl$bayes_white_estmm <- EBest(n = fl$white_female_deaths,
                             x = fl$white_female_population,
                             family = "poisson")[,2]

# calculate raw and estmm for black
fl$bayes_black_raw <- EBest(n = fl$black_female_deaths,
                           x = fl$black_female_population,
                           family = "poisson")[,1]
fl$bayes_black_estmm <- EBest(n = fl$black_female_deaths,
                             x = fl$black_female_population,
                             family = "poisson")[,2]

#####
# 3. Save the calculated rates in the attribute table and export as a new shapefile;
#####
print(fl@data[,c("county", "bayes_white_estmm", "bayes_black_estmm")])

```

##	county	bayes_white_estmm	bayes_black_estmm
## 0	ALACHUA	2.658584e-02	1.999280e-01
## 1	BAKER	7.406757e-02	1.184765e-01
## 2	BAY	8.649670e-04	1.086737e-03
## 3	BRADFORD	5.832378e-02	3.889503e-02
## 4	BREVARD	5.158548e-04	8.836258e-04
## 5	BROWARD	3.402203e-03	1.326657e-03
## 6	CALHOUN	1.884291e+00	7.934533e-01
## 7	CHARLOTTE	7.531122e-04	7.976617e-03
## 8	CITRUS	1.842148e-02	1.064629e-02
## 9	CLAY	1.665196e-02	4.652171e-03
## 10	COLLIER	5.469999e-03	2.258975e-03
## 11	COLUMBIA	4.707497e-02	5.105460e-03
## 12	DADE	1.523974e-04	2.094997e-04
## 13	DE SOTO	1.129501e+00	8.624651e-01
## 14	DIXIE	2.022345e-02	2.748338e-02
## 15	DUVAL	9.924570e-05	5.806243e-05

## 16	ESCAMBIA	2.490462e-02	2.757746e-02
## 17	FLAGLER	1.265625e-01	2.785923e-01
## 18	FRANKLIN	2.869728e-02	5.058762e-03
## 19	GADSDEN	4.851276e-03	6.192261e-04
## 20	GILCHRIST	2.636166e-02	6.326287e-01
## 21	GLADES	9.457931e-03	1.195372e-04
## 22	GULF	3.556430e-03	1.523671e-03
## 23	HAMILTON	1.531115e-02	1.869018e-03
## 24	HARDEE	3.126107e-03	1.681263e-02
## 25	HENDRY	7.988450e-03	8.696481e-04
## 26	HERNANDO	2.536473e-03	9.633476e-03
## 27	HIGHLANDS	1.871044e-02	5.754584e-03
## 28	HILLSBOROUGH	1.227798e-03	8.209131e-04
## 29	HOLMES	4.357916e-01	1.453738e+00
## 30	INDIAN RIVER	2.104458e-03	1.561784e-05
## 31	JACKSON	3.162958e-02	6.098129e-03
## 32	JEFFERSON	3.143555e-02	1.587626e-02
## 33	LAFAYETTE	1.766198e-02	2.046880e-01
## 34	LAKE	3.621192e-04	8.882867e-06
## 35	LEE	7.234737e-03	8.097498e-03
## 36	LEON	2.851638e-02	3.312867e-03
## 37	LEVY	4.847055e-02	9.226488e-02
## 38	LIBERTY	6.929164e-02	3.781931e-02
## 39	MADISON	2.161404e-03	1.858335e-05
## 40	MANATEE	4.519597e-04	4.259726e-03
## 41	MARION	2.038361e-02	5.314273e-03
## 42	MARTIN	2.066261e-02	4.709305e-02
## 43	MONROE	1.833217e-02	9.924532e-03
## 44	NASSAU	2.269840e-02	1.107795e-02
## 45	OKALOOSA	2.261586e-03	3.451055e-03
## 46	OSCEOLA	4.171547e-02	3.662623e-02
## 47	ORANGE	4.159122e-04	1.149867e-04
## 48	OSCEOLA	8.683091e-02	1.531277e-01
## 49	PALM BEACH	1.222741e-03	3.189366e-04
## 50	PASCO	3.898243e-02	1.363501e-01
## 51	PINELLAS	4.133531e-03	3.757031e-04
## 52	POLK	4.299430e-02	9.796415e-03
## 53	PUTNAM	7.368086e-02	3.807219e-02
## 54	ST. JOHNS	8.794923e-03	1.604898e-02
## 55	ST. LUCIE	7.852122e-03	5.234261e-03
## 56	SANTA ROSA	2.200909e-02	4.204524e-02
## 57	SARASOTA	1.490353e-03	1.727391e-03
## 58	SEMINOLE	2.247916e-02	3.636713e-03
## 59	SUMTER	8.474645e-02	3.877367e-02
## 60	SUWANNEE	1.297069e-02	6.750157e-03
## 61	TAYLOR	1.732566e-02	1.651870e-02
## 62	UNION	2.269230e-02	5.327758e-02
## 63	VOLUSIA	4.820516e-05	9.693440e-05
## 64	WAKULLA	4.806441e-01	2.177055e-01
## 65	WALTON	3.262752e-03	4.790885e-03
## 66	WASHINGTON	1.253937e-02	3.936306e-03

```
print(f1@data[,c("county", "bayes_white_raw", "bayes_black_raw")])
```

##	county	bayes_white_raw	bayes_black_raw
## 0	ALACHUA	2.658653e-02	1.999817e-01
## 1	BAKER	7.409941e-02	1.189759e-01
## 2	BAY	8.641175e-04	1.078981e-03
## 3	BRADFORD	5.834223e-02	3.897338e-02
## 4	BREVARD	5.155792e-04	8.796042e-04
## 5	BROWARD	3.402149e-03	1.325879e-03
## 6	CALHOUN	1.885784e+00	7.995050e-01
## 7	CHARLOTTE	7.521625e-04	7.957560e-03
## 8	CITRUS	1.842197e-02	1.063830e-02
## 9	CLAY	1.665232e-02	4.635762e-03
## 10	COLLIER	5.469537e-03	2.240896e-03
## 11	COLUMBIA	4.708242e-02	5.095541e-03
## 12	DADE	1.523464e-04	2.091479e-04
## 13	DE SOTO	1.129917e+00	8.650485e-01
## 14	DIXIE	2.023007e-02	2.766798e-02
## 15	DUVAL	9.906446e-05	5.731425e-05
## 16	ESCAMBIA	2.490502e-02	2.758007e-02
## 17	FLAGLER	1.266166e-01	2.803347e-01
## 18	FRANKLIN	2.871206e-02	5.000000e-03
## 19	GADSDEN	4.848485e-03	6.146281e-04
## 20	GILCHRIST	2.637563e-02	6.509434e-01
## 21	GLADES	9.453782e-03	0.000000e+00
## 22	GULF	3.549532e-03	1.472754e-03
## 23	HAMILTON	1.531394e-02	1.838235e-03
## 24	HARDEE	3.122432e-03	1.683502e-02
## 25	HENDRY	7.986309e-03	8.389262e-04
## 26	HERNANDO	2.535380e-03	9.624639e-03
## 27	HIGHLANDS	1.871113e-02	5.744375e-03
## 28	HILLSBOROUGH	1.227678e-03	8.197966e-04
## 29	HOLMES	4.359756e-01	1.478261e+00
## 30	INDIAN RIVER	2.103440e-03	0.000000e+00
## 31	JACKSON	3.163362e-02	6.092254e-03
## 32	JEFFERSON	3.145540e-02	1.588235e-02
## 33	LAFAYETTE	1.767068e-02	2.117647e-01
## 34	LAKE	3.614284e-04	0.000000e+00
## 35	LEE	7.234590e-03	8.094981e-03
## 36	LEON	2.851720e-02	3.310782e-03
## 37	LEVY	4.848223e-02	9.248055e-02
## 38	LIBERTY	6.939090e-02	3.825137e-02
## 39	MADISON	2.153846e-03	0.000000e+00
## 40	MANATEE	4.515165e-04	4.254457e-03
## 41	MARION	2.038398e-02	5.311181e-03
## 42	MARTIN	2.066325e-02	4.715840e-02
## 43	MONROE	1.833270e-02	9.919405e-03
## 44	NASSAU	2.270059e-02	1.107492e-02
## 45	OKALOOSA	2.260889e-03	3.444034e-03
## 46	OSCEOLA	4.172462e-02	3.676471e-02
## 47	ORANGE	4.157323e-04	1.135117e-04
## 48	OSCEOLA	8.683879e-02	1.534508e-01
## 49	PALM BEACH	1.222628e-03	3.175835e-04
## 50	PASCO	3.898309e-02	1.365688e-01
## 51	PINELLAS	4.133467e-03	3.739191e-04
## 52	POLK	4.299493e-02	9.795867e-03

## 53	PUTNAM	7.368939e-02	3.809524e-02
## 54	ST. JOHNS	8.794430e-03	1.605325e-02
## 55	ST. LUCIE	7.851759e-03	5.230623e-03
## 56	SANTA ROSA	2.201016e-02	4.212300e-02
## 57	SARASOTA	1.490075e-03	1.719057e-03
## 58	SEMINOLE	2.247949e-02	3.632807e-03
## 59	SUMTER	8.476721e-02	3.883495e-02
## 60	SUWANNEE	1.297071e-02	6.736527e-03
## 61	TAYLOR	1.732777e-02	1.652893e-02
## 62	UNION	2.270382e-02	5.361930e-02
## 63	VOLUSIA	4.792348e-05	9.329228e-05
## 64	WAKULLA	4.809668e-01	2.188034e-01
## 65	WALTON	3.259877e-03	4.761905e-03
## 66	WASHINGTON	1.253918e-02	3.901170e-03

```
# 4. Start the ArcMap, import the new shapefile and create the following cholopleth maps.
#(All following maps use the same categories of the classification of the rate,
#which you need to specify the appropriate cut-off points;
#Each map also includes at least the title and the legend because it is a thematic map.)
# a. Raw and smoothed breast cancer mortality rates for White females;
# i. Map 1: raw rate for White females;
# ii. Map 2: empirical Bayes rate for White females;
# iii. Map 3: spatial rate for White females;
# iv. Map 4: spatial empirical Bayes rate for White females;
# (Note: Display four maps in a single page)
# v. Export the maps as a picture and insert below evaluation;
```

```
# Raw
par(mfrow = c(2,2))
par(mar=c(1,1,1,1))
par(oma = c(0,0,0,0))
choro(shape = fl,
      boundary = boundary,
      var = fl$bayes_white_raw * 100000,
      long_legend = FALSE,
      legend_pos = "center",
      legend_round = -2,
      color1 = "lightblue",
      color2 = "red")

title(main = "Bayes raw estimates for white female breast cancer deaths per 100,000",
      cex.main = 0.5)
choro(shape = fl,
      boundary = boundary,
      var = fl$bayes_black_raw * 100000,
      long_legend = FALSE,
      legend_pos = "center",
      legend_round = -2,
      color1 = "lightblue",
      color2 = "red")

title(main = "Bayes raw estimates for black female breast cancer deaths per 100,000",
      cex.main = 0.5)
```



```

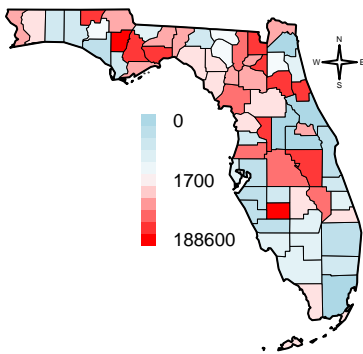
# Empirical
choro(shape = fl,
      boundary = boundary,
      var = fl$bayes_white_estmm * 100000,
      long_legend = FALSE,
      legend_pos = "center",
      legend_round = -2,
      color1 = "lightblue",
      color2 = "red")

title(main = "Bayes empirical estimates for white female breast cancer deaths per 100,000",
      cex.main = 0.5)
choro(shape = fl,
      boundary = boundary,
      var = fl$bayes_black_estmm * 100000,
      long_legend = FALSE,
      legend_pos = "center",
      legend_round = -2,
      color1 = "lightblue",
      color2 = "red")

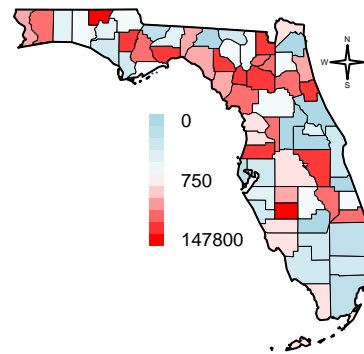
title(main = "Bayes empirical estimates for black female breast cancer deaths per 100,000",
      cex.main = 0.5)

```

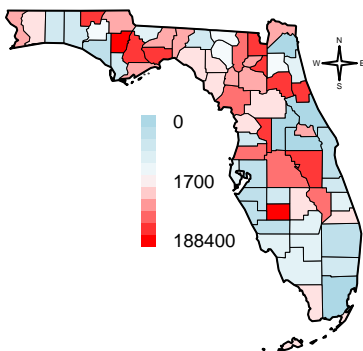
Bayes raw estimates for white female breast cancer deaths per 100,000



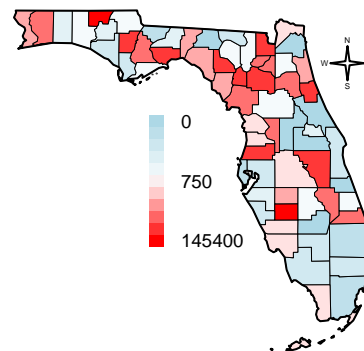
Bayes raw estimates for black female breast cancer deaths per 100,000



Bayes empirical estimates for white female breast cancer deaths per 100,000



Bayes empirical estimates for black female breast cancer deaths per 100,000



```
par(mfrow = c(1,1))
```

*# b. Raw and smoothed breast cancer mortality rates for Black females;*

```

# i. Map 1: raw rate for Black females;
# ii. Map 2: empirical Bayes rate for Black females;
# iii. Map 3: spatial rate for Black females;
# iv. Map 4: spatial empirical Bayes rate for Black females;
# (Note: Display four maps in a single page)
# v. Export the maps as a picture and insert below evaluation;

#
library(gstat)
library(geoR)

## Loading required package: MASS
## -----
## Analysis of geostatistical data
## For an Introduction to geoR go to http://www.leg.ufpr.br/geoR
## geoR version 1.7-4.1 (built on 2012-06-29) is now loaded
## -----

my_colors <- colorRampPalette(c("blue", "white", "red"))(100)
boundary <- unionSpatialPolygons(boundary, rep(1, length(boundary@polygons)))

SurfaceFun <- function(var = "bayes_white_raw",
                        boundary_shape = boundary){

  # getting coordinates of alachua boundary
  boundary_points <- boundary@polygons[[1]]@Polygons[[10]]
  boundary_points <- boundary_points@coords

  # Get trap locations and data values
  a <- data.frame("x" = coordinates(f1)[,1],
                  "y" = coordinates(f1)[,2],
                  "z" = f1@data[,var] * 100000)

  # Make into a geodata object
  b <- as.geodata(a)

  # Predict multiple points in Florida's boundary
  x <- seq(min(boundary_points[,1]), max(boundary_points[,1]), length = 100)
  y <- seq(min(boundary_points[,2]), max(boundary_points[,2]), length = 100)

  # Make a grid of those points
  pred.grid <- expand.grid(x,y)

  # kriging calculations
  kc <- krige.conv(geodata = b, coords = b$coords, data = b$data,
                  locations = pred.grid,
                  borders = boundary_points,
                  #borders = boundary@polygons,
                  # borders = ALACHUA BORDERS!,
                  krige = krige.control(type.krige = "ok",
                                         cov.pars = c(5000,1000000))) #10, 3.33 # what is this?

```

```

# Plot!
# displaying predicted values
image(kc, loc = pred.grid,
      col = my_colors,
      xlab=NA, ylab=NA,
      xaxt = "n",
      yaxt = "n",
      xpd = NA,
      bty = "n")

# Define percentiles for legend
legtemp <- round(quantile(kc$predict, probs = seq(0,1,, length = 10)))

legend(x="center",
      fill = my_colors[c(1,11,22,33,44,55,66,77,88,100)],
      legend = c(legtemp[1], NA, NA, legtemp[4], NA, NA, legtemp[7], NA, NA, legtemp[10]),
      border = FALSE,
      bty = "n",
      ncol = 1,
      y.intersp = 0.5,
      title = "Interpolation",
      cex = 0.75)
}

par(mfrow = c(2,2))
par(mar=c(1,1,1,1))
par(oma = c(0,0,0,0))
SurfaceFun("bayes_white_raw")

```

```

## krige.conv: results will be returned only for prediction locations inside the borders
## krige.conv: model with constant mean
## krige.conv: Kriging performed using global neighbourhood

```

```

title(main = "White raw")
SurfaceFun("bayes_white_estmm")

```

```

## krige.conv: results will be returned only for prediction locations inside the borders
## krige.conv: model with constant mean
## krige.conv: Kriging performed using global neighbourhood

```

```

title(main = "White interpolated")
SurfaceFun("bayes_black_raw")

```

```

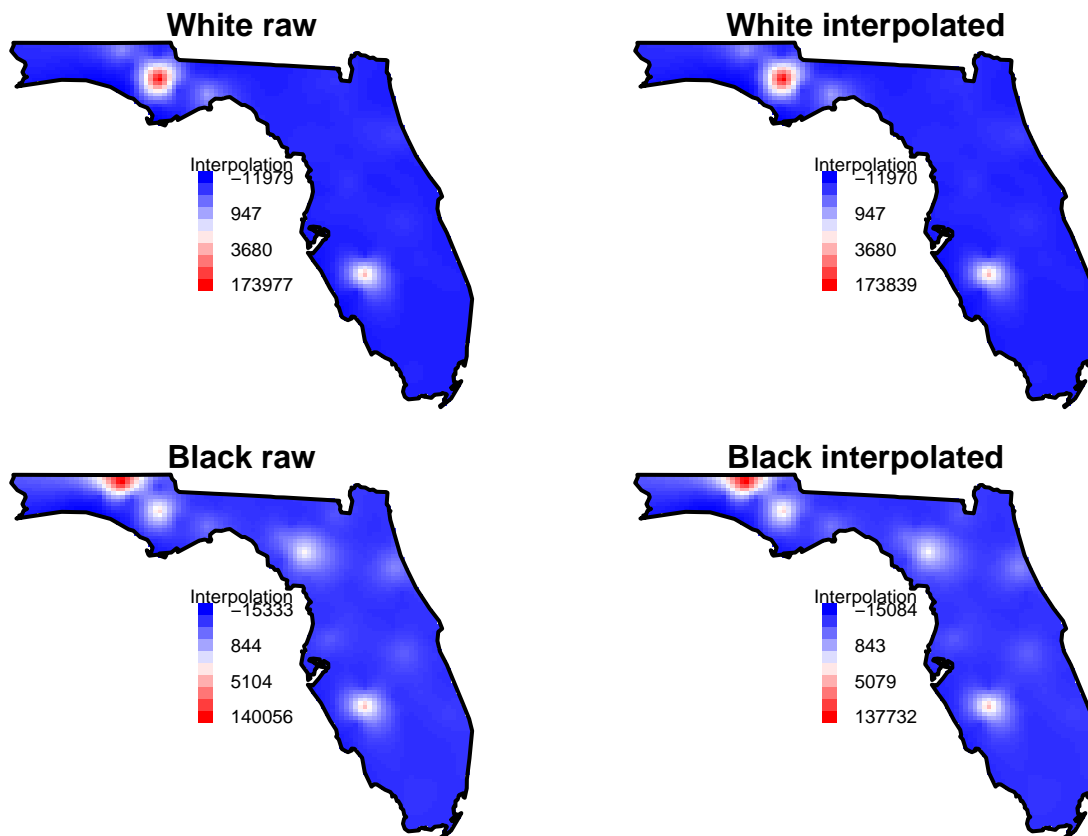
## krige.conv: results will be returned only for prediction locations inside the borders
## krige.conv: model with constant mean
## krige.conv: Kriging performed using global neighbourhood

```

```
title(main = "Black raw")
SurfaceFun("bayes_black_estmm")
```

```
## krige.conv: results will be returned only for prediction locations inside the borders
## krige.conv: model with constant mean
## krige.conv: Kriging performed using global neighbourhood
```

```
title(main = "Black interpolated")
```

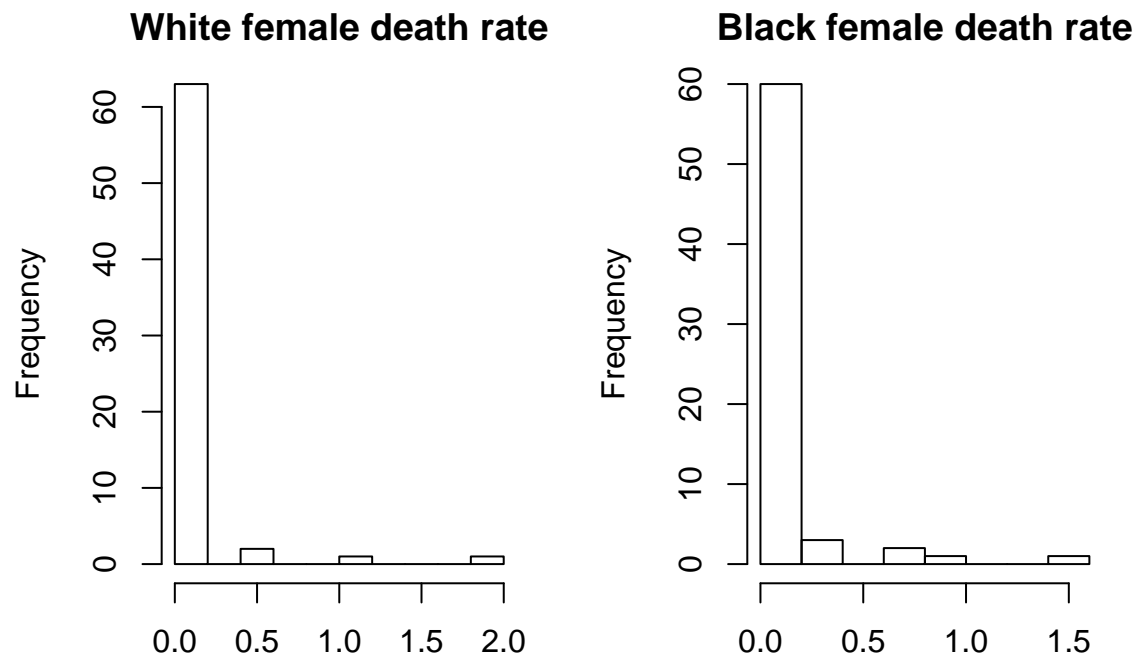


```
par(mfrow = c(1,1))
```

```
#5. Do these maps of raw, empirical Bayes, spatial rate and spatial empirical
#Bayes smoothed rates are similar? If they are different, please explain why
#they are different.
```

```
# They look similar, but I believe that this is due to errors in the shapefile.
# If you look at the distribution of rates by county, you find some severe outliers
```

```
par(mfrow = c(1,2))
par(mar = c(5,4,2,2))
par(oma = c(1,1,1,1))
hist(fl$white_female_deaths / fl$white_female_population,
     main = "White female death rate")
hist(fl$black_female_deaths / fl$black_female_population,
     main = "Black female death rate")
```



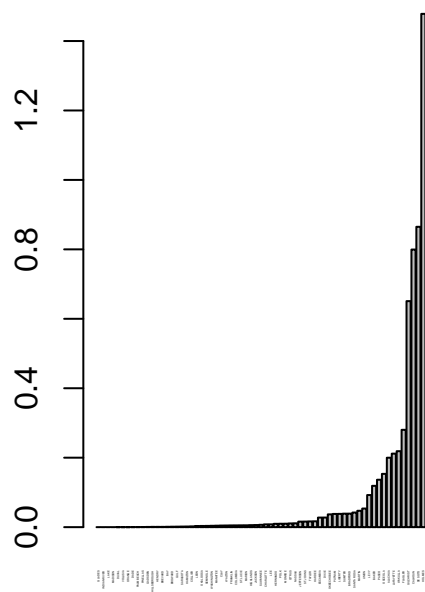
`white_female_deaths/fl$white_female_po`  
`black_female_deaths/fl$black_female_po`

```
par(mfrow = c(1,1))

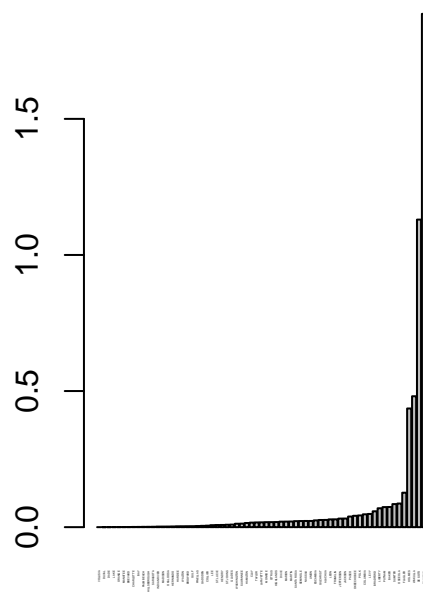
par(mfrow = c(1,2))
x <- fl@data[order(fl$black_female_deaths / fl$black_female_population),]
barplot(x$black_female_deaths / x$black_female_population,
        names.arg = x$county,
        cex.names = 0.1,
        las = 3,
        main = "Black death rate by county")

x <- fl@data[order(fl$white_female_deaths / fl$white_female_population),]
barplot(x$white_female_deaths / x$white_female_population,
        names.arg = x$county,
        cex.names = 0.1,
        las = 3,
        main = "White death rate by county")
```

**Black death rate by county**



**White death rate by county**



```
par(mfrow = c(1,1))
```