```
R version 3.2.1 (2015-06-18) -- "World-Famous Astronaut"
Copyright (C) 2015 The R Foundation for Statistical Computing
Platform: x86_64-apple-darwin13.4.0 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

[R.app GUI 1.66 (6956) x86_64-apple-darwin13.4.0]

>
> rm(list=ls(all=TRUE))
>
> set.seed(123)
>
> library(systemfit)
Loading required package: Matrix
Loading required package: car
Loading required package: lmtest
Loading required package: zoo

Attaching package: ‘zoo’

The following objects are masked from ‘package:base’:

    as.Date, as.Date.numeric

> library(plyr)
> library(dplyr)

Attaching package: ‘dplyr’

The following objects are masked from ‘package:plyr’:

    arrange, count, desc, failwith, id, mutate, rename, summarise, summarize

The following objects are masked from ‘package:stats’:

    filter, lag

The following objects are masked from ‘package:base’:

    intersect, setdiff, setequal, union

> library(RColorBrewer)
> library(miscTools)
>
> #setwd("replication_archive/SettlerMortality")
> setwd("~/Dropbox/beliefs_incomplete data/Paper/PSRM/final/replication_archive/SettlerMortality/")
>
>
> ### Load the data
> load("data_settlermortality.rda")
>
>
> etavec = seq(0.98, 10.8, length.out=1000)
>
> results <-  NULL
>
> for(i in 1:length(etavec)){
+     # create data given eta
+     data$logem4_true <- NA
+     data$logem4_true[data$benchmark==0] <- data$logem4[data$benchmark==0]
+     data$logem4_true[data$benchmark==1] <- data$logem4[data$benchmark==1] + log(etavec[i]/4.25)
+
+     # run the model with the simulated data: first stage
+     s1 <- lm(avexpr ~ logem4_true + laborer + campaign, data = data)
+
+     # run the model with the simulated data: IV
+     m <- systemfit(logpgp95 ~ avexpr + laborer + campaign, inst = ~ logem4_true + laborer + campaign, data = data, method = "2SLS")
+
+     # save the coefficients and standard errors of both stages
+     est1 <- coef(s1)[2]
+     err1 <- sqrt(vcov(s1)[2,2])
+
+     est2 <- coef(m)[2]
+     err2 <- sqrt(vcov(m)[2,2])
+
+     results <- rbind(results, c(etavec[i], est1, err1, est2, err2))
+ }
>
> colnames(results) <- c("eta", "pointest_first", "stderr_first", "pointest_second", "stderr_second")
>
> results <- as.data.frame(results)
>
> results$lowerci95_first <- results$pointest_first + qnorm(0.025)*results$stderr_first
> results$upperci95_first <- results$pointest_first + qnorm(0.975)*results$stderr_first
>
> results$lowerci95_second <- results$pointest_second + qnorm(0.025)*results$stderr_second
> results$upperci95_second <- results$pointest_second + qnorm(0.975)*results$stderr_second
>
>
>
>
> ### FIGURE 6
>
> ### Panel (a): first stage
> quartz(type="pdf", width=7, height=7, file="output/Bishops_stage1.pdf")
> par(mar = c(4,4,0.3,0.3), mgp=c(2.5,1,0), family="CMU Serif")
> plot(1:length(results$pointest_first), results$pointest_first, type="n", ylim=c(min(results$lowerci95_first), 0), xlab = expression(eta), ylab="First Stage Coefficient", xaxt="n")
> polygon(c(1:length(results$pointest_first), rev(1:length(results$pointest_first))), c(results$lowerci95_first, rev(results$upperci95_first)), col="grey", border=NA)
> points(1:length(results$pointest_first), results$pointest_first, type="l", lwd=3)
>
> axis(1, at=seq(1, 1001, length.out=11), labels = round(seq(0.98, 10.8, length.out=11), 2), las=2)
> abline(h=0, col = "black")
> lines(c(333,333), c(results$lowerci95_first[333], results$upperci95_first[333]), lwd=3)  # 333 is position of 4.25
> points(333, results$pointest_first[333], pch=16)
> dev.off()
```

```
null device
          1
>
>
>
> ### Panel (b): second stage
> quartz(type="pdf", width=7, height=7, file="output/Bishops_stage2.pdf")
> par(mar = c(4,4,0.3,0.3), mgp=c(2.5,1,0), family="CMU Serif")
> plot(1:length(results$pointest_second), results$pointest_second, type="n", ylim=c(0, max(results$upperci95_second)), xlab = expression(eta), ylab="Second Stage Coefficient", xaxt="n")
> polygon(c(1:length(results$pointest_second), rev(1:length(results$pointest_second))), c(results$lowerci95_second, rev(results$upperci95_second)), col="grey", border=NA)
> points(1:length(results$pointest_second), results$pointest_second, type="l", lwd=3)
>
> axis(1, at=seq(1, 1001, length.out=11), labels = round(seq(0.98, 10.8, length.out=11), 2), las=2)
> abline(h=0, col = "black")
> lines(c(333,333), c(results$lowerci95_second[333], results$upperci95_second[333]), lwd=3)
> points(333, results$pointest_second[333], pch=16)
> dev.off()
null device
          1
>
>
>
>
>
> ### FIGURE 5
>
> highbel = 10.8
> lowbel = .98
> x = seq(lowbel, highbel, .01)/4.25
> z = quantile(x,seq(0, 1, .001))
> beliefs = log(z)
>
>
> data1 = data$logem4 + data$benchmark*beliefs[1]
> data2 = data$logem4 + data$benchmark*beliefs[251]
> data3 = data$logem4 + data$benchmark*beliefs[501]
> data4 = data$logem4 + data$benchmark*beliefs[751]
> data5 = data$logem4 + data$benchmark*beliefs[1001]
>
>
> quartz(type="pdf", width=7, height=7, file="output/Bishops_Data1.pdf")
> par(mar = c(4,4,2,2), mgp=c(2.5,1,0), family="CMU Serif")
> plot(data$logem4[data$benchmark==1], data$logem4[data$benchmark==1], pch=16, xlim=c(min(data$logem4), max(data$logem4)), ylim=c(min(data5), max(data5)), col="grey", xlab="Log Mortality",
ylab="Simulated Log Mortality")
> points(data$logem4[data$benchmark==0], data$logem4[data$benchmark==0], pch=16)
> points(data$logem4[data$benchmark==1], data1[data$benchmark==1], pch=16, col="red")
> points(data$logem4[data$benchmark==1], data2[data$benchmark==1], pch=16, col="orange")
> points(data$logem4[data$benchmark==1], data3[data$benchmark==1], pch=16, col="green")
> points(data$logem4[data$benchmark==1], data4[data$benchmark==1], pch=16, col="darkgreen")
> points(data$logem4[data$benchmark==1], data5[data$benchmark==1], pch=16, col="blue")
> text(5.45, 3.65, "0.98", col="red", cex=1.5)
> text(5.45, 4.9, "3.44", col="orange", cex=1.5)
> text(3.9, 4.5, "5.89", col="green", cex=1.5)
> text(3.9, 4.85, "8.35", col="darkgreen", cex=1.5)
> text(3.9, 5.15, "10.8", col="blue", cex=1.5)
> dev.off()
null device
          1
>
> quartz(type="pdf", width=7, height=7, file="output/Bishops_Data2.pdf")
> par(mar = c(4,4,2,2), mgp=c(2.5,1,0), family="CMU Serif")
> plot(density(data$logem4), xlim=c(0,10), lwd=2, xlab="Log Mortality", main="")
> points(density(data1), type="l", lwd=2, col="red")
> points(density(data2), type="l", lwd=2, col="orange")
> points(density(data3), type="l", lwd=2, col="green")
> points(density(data4), type="l", lwd=2, col="darkgreen")
> points(density(data5), type="l", lwd=2, col="blue")
> text(2.8, 0.29, "0.98", col="red", cex=1.5)
> text(3.5, 0.34, "3.44", col="orange", cex=1.5)
> text(5.1, 0.44, "5.89", col="green", cex=1.5)
> text(5.15, 0.42, "8.35", col="darkgreen", cex=1.5)
> text(5.8, 0.4, "10.8", col="blue", cex=1.5)
> dev.off()
null device
          1
>
```