Math 530/630 Final Replication Project

Josh Burkhart, Steve Chamberlin, Kristen Stevens

December 2, 2015

Association of Arsenic Exposure with Lung Cancer Incidence Rates in the United States

Citation: Putila JJ, Guo NL (2001) Association of Arsenic Exposure with Lung Cancer Incidence Rates in the United States. PLOS ONE 6(10): e25886.

```
full <- read.csv("./File_S4.csv", row.names = 1)  # change directory for FileS4.csv
```

The authors' data file (FileS4.csv) includes 757 observations of 20 variables. We have named this data.frame "full". The unit of analysis is County. The variables of interest are mean aresenic level in parts per million weighted by county population (Ascounty), median income of county (MedIncome), population (Population), county smoking prevalence calculated as a percent of respondents age 18 or older who reported having smoked more than 100 cigarettes in their lifetime (smkrate), and age-adjusted lung cancer incidence rates (AdjRate).

We first generated log transformed and centered variables from the variables described above.

```
full$lnAs <- log(full$Ascounty) - mean(na.omit(log(full$Ascounty)))
full$lnInc <- log(full$MedIncome) - mean(na.omit(log(full$MedIncome)))
full$Population <- as.numeric(as.character(full$Population))
full$lnsmk <- full$smkrate
full$lnar <- log(full$AdjRate)
```

Regression Analysis

"The first analysis sought to determine the influence of exposure levels of arsenic on lung cancer incidence in the U.S., and persistance of these effects controlling for possible confounders. The association betweeen each contaminant and lung cancer incidence was assessed using Poisson regression in order to reflect the annual incidence rate as a counting measure."

For comparison, we performed a linear regression in addition to a Poisson regression for each analysis. The following models predict lung cancer incidence weighted by county population using the untransformed data.

```
# Poisson regression
glm1 <- glm(full$AdjRate ~ full$Ascounty, family = poisson, weights = as.numeric(full$Population))
summary(glm1)
```

```
Call:
glm(formula = full$AdjRate ~ full$Ascounty, family = poisson,
    weights = as.numeric(full$Population))

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-6257.0   -103.2    161.1    444.0   2459.2
```

```
Coefficients:
                 Estimate  Std. Error z value             Pr(>|z|)    
(Intercept)   4.167391730 0.000023700  175836 <0.0000000000000002 ***
full$Ascounty 0.004479178 0.000001937    2312 <0.0000000000000002 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 317986702  on 741  degrees of freedom
Residual deviance: 312986732  on 740  degrees of freedom
  (15 observations deleted due to missingness)
AIC: 835273995

Number of Fisher Scoring iterations: 4
```

```r
# odds ratio with CI
glm1_odds <- exp(cbind(OR = coef(glm1), confint(glm1)))
```

```
Waiting for profiling to be done...
```

```r
# Linear regression
lm1 <- lm(full$lnar ~ full$Ascounty, weights = as.numeric(full$Population))
summary(lm1)
```

```
Call:
lm(formula = full$lnar ~ full$Ascounty, weights = as.numeric(full$Population))

Weighted Residuals:
    Min      1Q  Median      3Q     Max 
-738.43   -8.18   23.65   55.32  293.99 

Coefficients:
              Estimate Std. Error t value            Pr(>|t|)    
(Intercept)    4.14686    0.01727 240.168 <0.0000000000000002 ***
full$Ascounty  0.00373    0.00147   2.537              0.0114 *  
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 83.81 on 740 degrees of freedom
  (15 observations deleted due to missingness)
Multiple R-squared:  0.008621,  Adjusted R-squared:  0.007282 
F-statistic: 6.435 on 1 and 740 DF,  p-value: 0.01139
```

```r
# odds ratio with CI
lm1_odds <- exp(cbind(OR = coef(lm1), confint(lm1)))
```

```r
# Poisson regression
SESassmk <- glm(full$AdjRate ~ full$smkrate + full$Ascounty + full$MedIncome,
    family = poisson, weights = as.numeric(full$Population))
summary(SESassmk)
```

```
Call:
glm(formula = full$AdjRate ~ full$smkrate + full$Ascounty + full$MedIncome,
    family = poisson, weights = as.numeric(full$Population))

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3559.7   -240.9     46.1    347.7   1949.6

Coefficients:
                      Estimate      Std. Error z value            Pr(>|z|)
(Intercept)     3.520651941992  0.000121330940   29017 <0.0000000000000002
full$smkrate    1.801926275227  0.000191317650    9419 <0.0000000000000002
full$Ascounty   0.003931137793  0.000001929776    2037 <0.0000000000000002
full$MedIncome -0.000003538024  0.000000001308   -2706 <0.0000000000000002

(Intercept)    ***
full$smkrate   ***
full$Ascounty  ***
full$MedIncome ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 305018305  on 584  degrees of freedom
Residual deviance: 180096592  on 581  degrees of freedom
  (172 observations deleted due to missingness)
AIC: 687702879

Number of Fisher Scoring iterations: 4
```

```r
SESassmk_odds <- exp(cbind(OR = coef(SESassmk), confint(SESassmk)))
```

```
Waiting for profiling to be done...
```

```r
# Linear regressions
SESassmklm <- lm(full$lnar ~ full$smkrate + full$Ascounty + full$MedIncome,
    weights = as.numeric(full$Population))
summary(SESassmklm)
```

```
Call:
lm(formula = full$lnar ~ full$smkrate + full$Ascounty + full$MedIncome,
    weights = as.numeric(full$Population))

Weighted Residuals:
    Min      1Q  Median      3Q     Max
-442.09  -28.41    7.35   42.54  234.40

Coefficients:
                    Estimate    Std. Error t value             Pr(>|t|)
(Intercept)     3.2915838146  0.0692881380  47.506 < 0.0000000000000002
```

```
full$smkrate    2.1732197826  0.1129146604  19.247 < 0.0000000000000002
full$Ascounty   0.0034245343  0.0012310863   2.782             0.005583
full$MedIncome -0.0000023964  0.0000007225  -3.317             0.000968

(Intercept)    ***
full$smkrate   ***
full$Ascounty  **
full$MedIncome ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 69.48 on 581 degrees of freedom
  (172 observations deleted due to missingness)
Multiple R-squared:  0.4433,    Adjusted R-squared:  0.4404
F-statistic: 154.2 on 3 and 581 DF,  p-value: < 0.00000000000000022
```

```
SESassmklm_odds <- exp(cbind(OR = coef(SESassmklm), confint(SESassmklm)))
```

Table 1: Unadjusted Model

Summary of Poisson regressions of the effect of arsenic concentration (ppm) on county-level lung cancer incidence rates in the U.S. in an unadjusted model. (We broke up Table 1 into two parts: the Unadjusted Model and the Adjusted Model.)

```
Model_and_Variable = c("Arsenic")
Coefficient = c(round(summary(glm1)$coefficients[2], digits = 4))
Std.Error = c("1.9 x 10^-6")  # summary(glm1)$coefficients[4]
Odds_Ratio_CI = c(paste(c(round(glm1_odds[2, 1], digits = 3), "(", round(glm1_odds[2,
    2], digits = 3), "-", round(glm1_odds[2, 3], digits = 3), ")"), collapse = " "))
P_value = c("P<0.0001")
N = c(742)
df = data.frame(Model_and_Variable, Coefficient, Std.Error, Odds_Ratio_CI, P_value,
    N)
kable(df)
```

Model_and_Variable	Coefficient	Std.Error	Odds_Ratio_CI	P_value	N
Arsenic	0.0045	1.9 x 10^-6	1.004 (1.004 - 1.004)	P<0.0001	742

```
# should we add the P-value and N as variables?  remove underscores from
# table labels?  table in knit pdf needs to be reformatted to fit the page
# scientific notation?  do we want to add a table for the results from the
# linear model?
```

Table 1: Adjusted Model

Summary of Poisson regressions of the effect of arsenic concentration (ppm) on county-level lung cancer incidence rates in the U.S. in a model adjusted for both smoking and median county income.

```
Model_and_Variable = c("Arsenic", "Smoking", "Median Income")
Coefficient = c(round(summary(SESassmk)$coefficients[3], digits = 4), round(summary(SESassmk)$coefficie
    digits = 4), round(summary(SESassmk)$coefficients[4], digits = 4))
Std.Error = c("1.9 x 10^-6", "0.0002", "1.31 x 10^-9")
Odds_Ratio_CI = c(paste(c(round(SESassmk_odds[3], digits = 3), "(", round(SESassmk_odds[7],
    digits = 3), "-", round(SESassmk_odds[11], digits = 3), ")"), collapse = " "),
    paste(c(round(SESassmk_odds[2], digits = 3), "(", round(SESassmk_odds[6],
        digits = 3), "-", round(SESassmk_odds[10], digits = 3), ")"), collapse = " "),
    paste(c(round(SESassmk_odds[4], digits = 3), "(", round(SESassmk_odds[8],
        digits = 3), "-", round(SESassmk_odds[12], digits = 3), ")"), collapse = " "))
P_value = c("P<0.0001")
N = c(585)
df = data.frame(Model_and_Variable, Coefficient, Std.Error, Odds_Ratio_CI, P_value,
    N)
kable(df)
```

Model_and_Variable	Coefficient	Std.Error	Odds_Ratio_CI	P_value	N
Arsenic	0.0039	1.9 x 10^-6	1.004 (1.004 - 1.004)	P<0.0001	585
Smoking	1.8019	0.0002	6.061 (6.059 - 6.064)	P<0.0001	585
Median Income	0.0000	1.31 x 10^-9	1 (1 - 1)	P<0.0001	585

```
# should we add the P-value and N as variables?  remove underscores from
# table labels?  table in knit pdf needs to be reformatted to fit the page
# scientific notation?  do we want to add a table for the results from the
# linear model?
```

Table 2

Difference in lung cancer incidence attributable to arsenic exposure alone for high and low-exposure areas in the U.S. based on the results of the adjusted Poisson models and the USGS survey quantiles in Figure 1.

```
Compound = c("Arsenic")
Low_ppm = c(1.477)
High_ppm = c(14.525)
B_Estimate = c(0.0039)
Lung_Cancer_Rate_Increase_Pct = c("5.3%")
df = data.frame(Compound, Low_ppm, High_ppm, B_Estimate, Lung_Cancer_Rate_Increase_Pct)
kable(df)
```

Compound	Low_ppm	High_ppm	B_Estimate	Lung_Cancer_Rate_Increase_Pct
Arsenic	1.477	14.525	0.0039	5.3%

```
# change values in table to variables, need to move this.
```

Figure 2

**Description, explanation of variables, and code clean-up needed here.

```
## Estimate the 25, 50, amd 75% quartile points for each variable for the
## quartiles interaction models
AsCut <- NA
AsCut[1] <- as.numeric(summary(full$lnAs)[2])
AsCut[2] <- as.numeric(summary(full$lnAs)[3])
AsCut[3] <- as.numeric(summary(full$lnAs)[5])

SmkCut <- NA
SmkCut[1] <- as.numeric(summary(full$lnsmk)[2])
SmkCut[2] <- as.numeric(summary(full$lnsmk)[3])
SmkCut[3] <- as.numeric(summary(full$lnsmk)[5])

SESCut <- NA
SESCut[1] <- as.numeric(summary(full$lnInc)[2])
SESCut[2] <- as.numeric(summary(full$lnInc)[3])
SESCut[3] <- as.numeric(summary(full$lnInc)[5])

## Calculate Strat Groups ## Smoking Quartiles
smkgrp <- ifelse(is.na(full$lnsmk), NA, ifelse(full$lnsmk < SmkCut[1], 1, ifelse(full$lnsmk >=
    SmkCut[1] & full$lnsmk < SmkCut[2], 2, ifelse(full$lnsmk >= SmkCut[2] &
    full$lnsmk < SmkCut[3], 3, 4))))
## SES Low-Income Cutoffs
SESgrp <- ifelse(is.na(full$MedIncome), NA, ifelse(full$MedIncome < 24000 &
    !is.na(full$MedIncome), 1, ifelse(full$MedIncome >= 24000 & full$MedIncome <
    28700, 2, ifelse(full$MedIncome >= 28700 & full$MedIncome < 38300, 3, 4))))
## SES Quartiles SESgrp <- ifelse(full$lnInc< -0.158, 1,
## ifelse(full$lnInc>=-0.158 & full$lnInc< -0.00391, 2,
## ifelse(full$lnInc>=-0.00391 & full$lnInc <0.1478, 3, 4))) Arsenic
## Quartiles
AsQ <- ifelse(is.na(full$lnAs), NA, ifelse(full$lnAs < AsCut[1], 1, ifelse(full$lnAs >=
    AsCut[1] & full$lnAs < AsCut[2], 2, ifelse(full$lnAs >= AsCut[2] & full$lnAs <
    AsCut[3], 3, 4))))

full$smkgrp <- ifelse(is.na(full$lnsmk), NA, ifelse(full$lnsmk < SmkCut[1],
    1, ifelse(full$lnsmk >= SmkCut[1] & full$lnsmk < SmkCut[2], 2, ifelse(full$lnsmk >=
        SmkCut[2] & full$lnsmk < SmkCut[3], 3, 4))))
## SES Low-Income Cutoffs
full$SESgrp <- ifelse(is.na(full$MedIncome), NA, ifelse(full$MedIncome < 24000 &
    !is.na(full$MedIncome), 1, ifelse(full$MedIncome >= 24000 & full$MedIncome <
    28700, 2, ifelse(full$MedIncome >= 28700 & full$MedIncome < 38300, 3, 4))))
## SES Quartiles SESgrp <- ifelse(full$lnInc< -0.158, 1,
## ifelse(full$lnInc>=-0.158 & full$lnInc< -0.00391, 2,
## ifelse(full$lnInc>=-0.00391 & full$lnInc <0.1478, 3, 4))) Arsenic
## Quartiles
full$AsQ <- ifelse(is.na(full$lnAs), NA, ifelse(full$lnAs < AsCut[1], 1, ifelse(full$lnAs >=
    AsCut[1] & full$lnAs < AsCut[2], 2, ifelse(full$lnAs >= AsCut[2] & full$lnAs <
    AsCut[3], 3, 4))))

## Quartile-Based Interaction Models Convert quartiles to factors
AsQf <- as.factor(AsQ)
smkgrpf <- as.factor(smkgrp)
smkgrpfbak <- smkgrpf
SESgrpf <- as.factor(SESgrp)
```

```r
full$AsQf <- as.factor(full$AsQ)
full$smkgrpf <- as.factor(full$smkgrp)
full$smkgrpfbak <- full$smkgrpf
full$SESgrpf <- as.factor(full$SESgrp)
```

```r
############# ARSENIC ## figure 2 Arsenic and Smoking This creates the data for the
############# first line of table 3 and the p value displayed on the right graph on
############# figure 2
smkgrpf <- smkgrpfbak
smkgrpf <- ifelse(is.na(smkgrpf), NA, ifelse(smkgrpf == 1 | smkgrpf == 2, 1,
    2))
intAsSmk <- aov(full$AdjRate ~ SESgrpf + AsQf * smkgrpf, weights = as.numeric(full$Population))
summary(intAsSmk)
```

```
              Df      Sum Sq    Mean Sq F value                Pr(>F)    
SESgrpf        3  2695113615  898371205  37.943 < 0.0000000000000002 ***
AsQf           3  1566705980  522235327  22.057    0.000000000000157 ***
smkgrpf        1  2613664023 2613664023 110.390 < 0.0000000000000002 ***
AsQf:smkgrpf   3   188901394   62967131   2.659               0.0475 *  
Residuals    574 13590400837   23676657                                  
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
172 observations deleted due to missingness
```

```r
## Without SES This creates the p value displayed on the left graph for
## figure 2
intAsSmk2 <- aov(full$AdjRate ~ AsQf * smkgrpf, weights = as.numeric(full$Population))
summary(intAsSmk2)
```

```
              Df      Sum Sq    Mean Sq F value                Pr(>F)    
AsQf           3  1890647672  630215891  24.392  0.00000000000000715 ***
smkgrpf        1  3665090147 3665090147 141.857 < 0.0000000000000002 ***
AsQf:smkgrpf   3   191344179   63781393   2.469               0.0611 .  
Residuals    577 14907703852   25836575                                  
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
172 observations deleted due to missingness
```

```r
## Arsenic and SES this creates the statistics for table3 second model
intAsSES <- aov(full$AdjRate ~ smkgrpf + AsQf * SESgrpf, weights = as.numeric(full$Population))
summary(intAsSES)
```

```
              Df      Sum Sq    Mean Sq F value                Pr(>F)    
smkgrpf        1  4252222627 4252222627  180.22 < 0.0000000000000002 ***
AsQf           3  1303515192  434505064   18.42      0.0000000000205 ***
SESgrpf        3  1319745800  439915267   18.64      0.0000000000151 ***
AsQf:SESgrpf   9   377928730   41992081    1.78               0.0691 .  
Residuals    568 13401373501   23593967                                  
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
172 observations deleted due to missingness
```

```
## Plot the Interaction between Arsenic and Smoking WITHOUT SES
smkgrpf <- smkgrpfbak
smkgrpf <- ifelse(is.na(smkgrpf), NA, ifelse(smkgrpf==1 | smkgrpf==2,1,2))

# Two models are run to get the two lines for low and high smoking, unadjusted
r1 <- glm(full[smkgrpf==1,]$AdjRate ~ full[smkgrpf==1,]$lnAs, family=poisson, weights=as.numeric(full[sm
summary(r1)
```

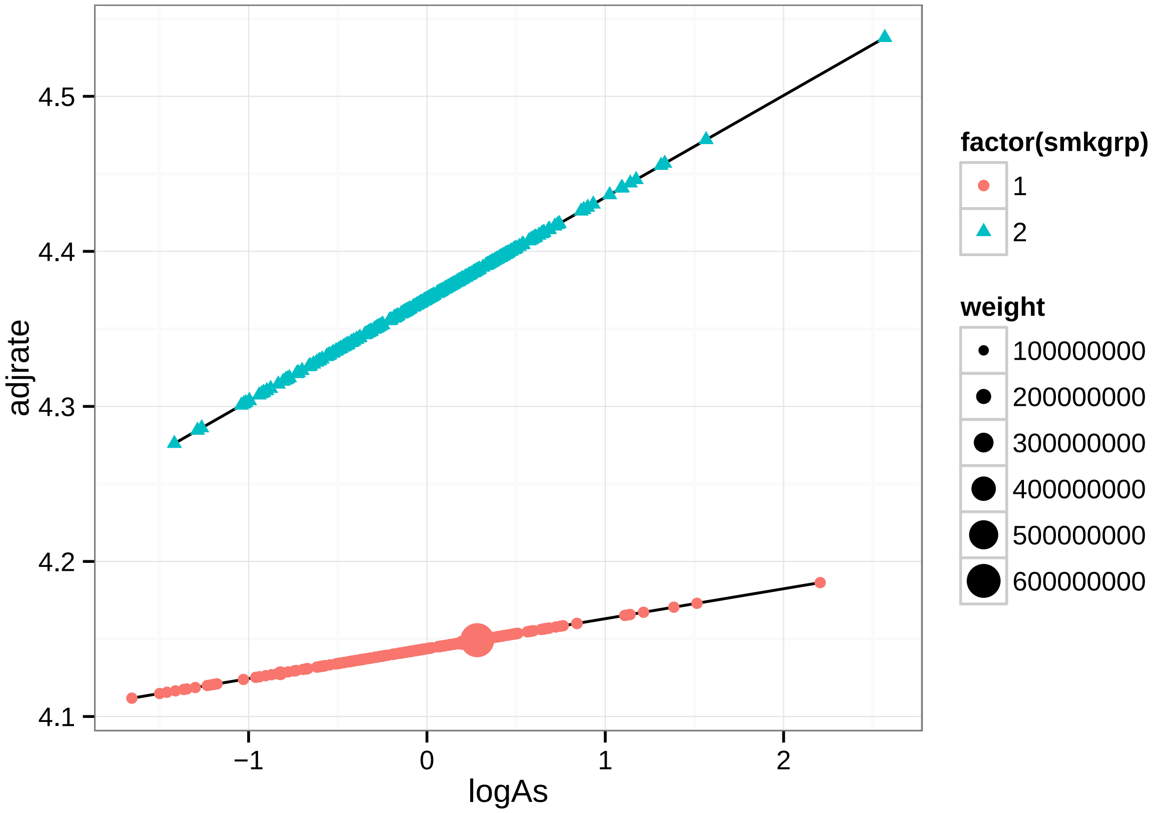
```

Call:
glm(formula = full[smkgrpf == 1, ]$AdjRate ~ full[smkgrpf ==
    1, ]$lnAs, family = poisson, weights = as.numeric(full[smkgrpf ==
    1, ]$Population))

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-4555.0   -105.5    172.0    525.9   2252.1

Coefficients:
                            Estimate Std. Error  z value
(Intercept)               4.14377600 0.00001604 258419.4
full[smkgrpf == 1, ]$lnAs 0.01931181 0.00003293    586.4
                                     Pr(>|z|)
(Intercept)               <0.0000000000000002 ***
full[smkgrpf == 1, ]$lnAs <0.0000000000000002 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 175916938  on 289  degrees of freedom
Residual deviance: 175572576  on 288  degrees of freedom
  (167 observations deleted due to missingness)
AIC: 543281859

Number of Fisher Scoring iterations: 4
```

```
r2 <- glm(full[smkgrpf==2,]$AdjRate ~ full[smkgrpf==2,]$lnAs, family=poisson, weights=as.numeric(full[sm
summary(r2)
```

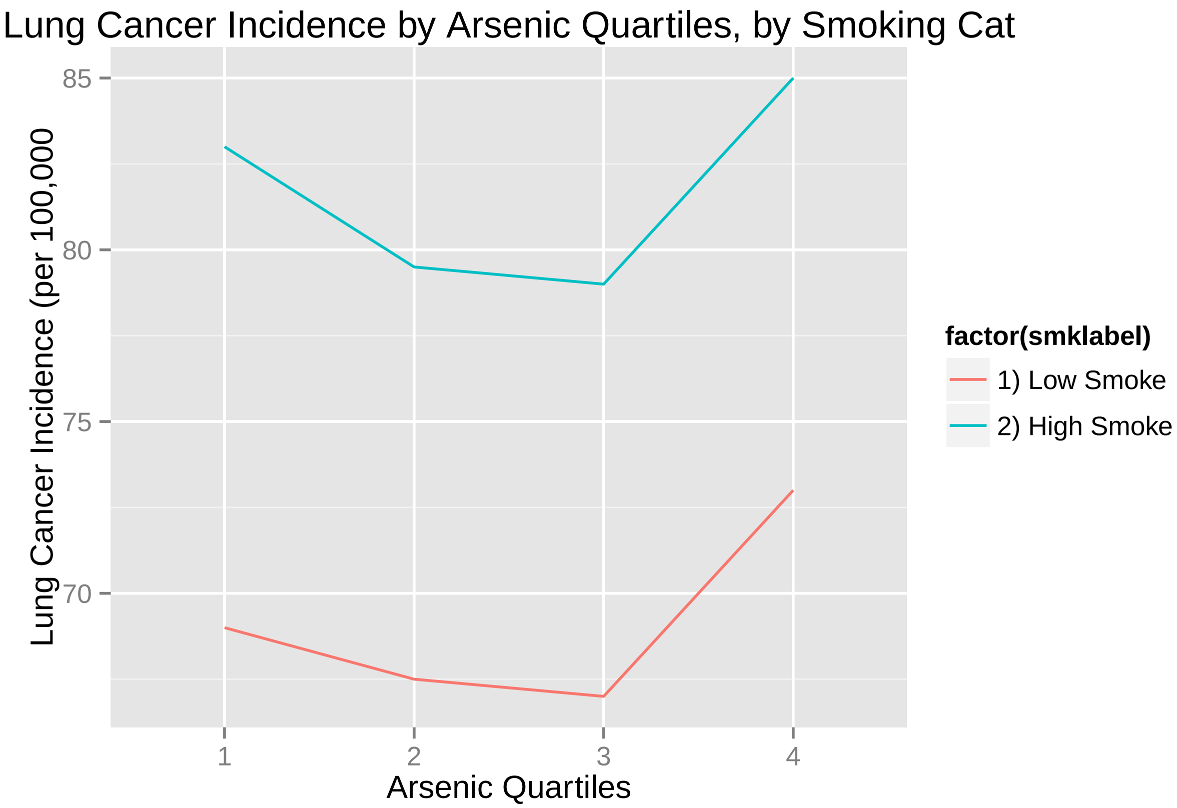
```

Call:
glm(formula = full[smkgrpf == 2, ]$AdjRate ~ full[smkgrpf ==
    2, ]$lnAs, family = poisson, weights = as.numeric(full[smkgrpf ==
    2, ]$Population))

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1773.74   -228.76     53.34    326.82   1574.57

Coefficients:
                            Estimate Std. Error z value
(Intercept)               4.36914074 0.00002369  184430
```

```
full[smkgrpf == 2, ]$lnAs 0.06571306 0.00004283    1534
                                     Pr(>|z|)
(Intercept)               <0.0000000000000002 ***
full[smkgrpf == 2, ]$lnAs <0.0000000000000002 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 68053265  on 294  degrees of freedom
Residual deviance: 65713881  on 293  degrees of freedom
  (162 observations deleted due to missingness)
AIC: 205610885

Number of Fisher Scoring iterations: 4
```

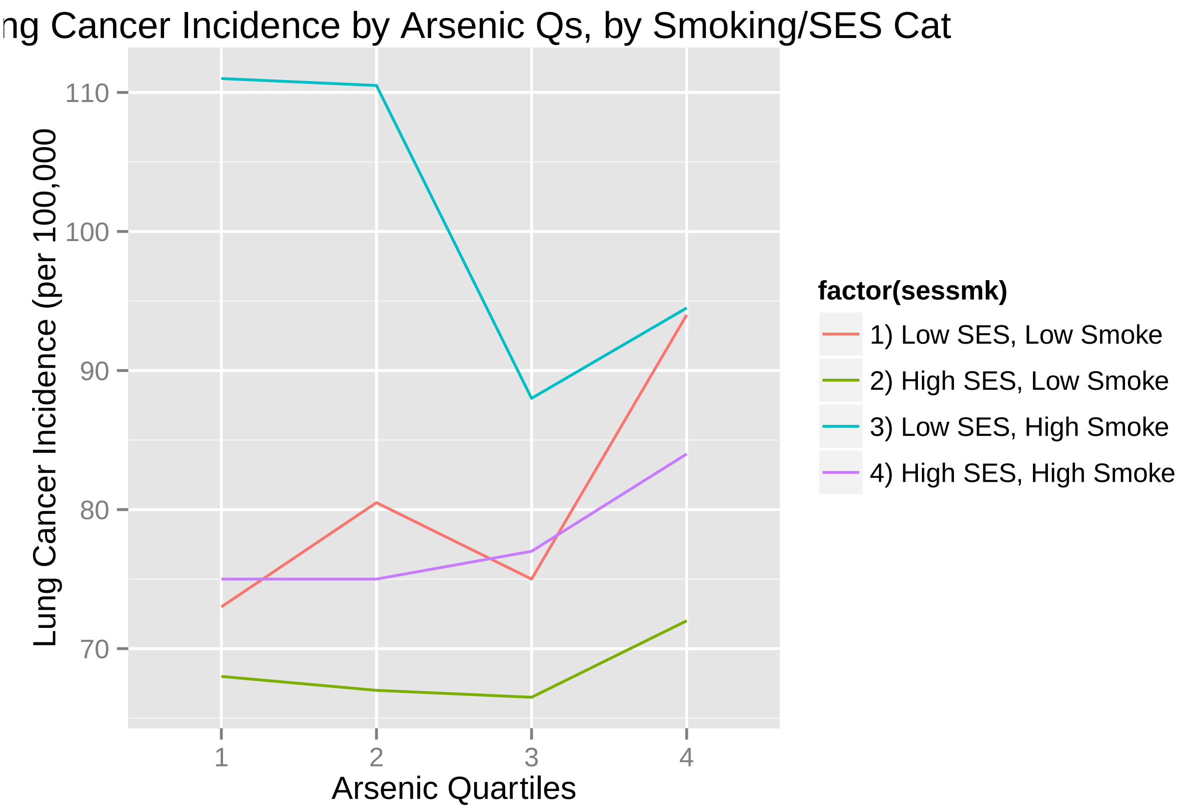
```
    #   this section builds the dataset from the model output for graphing
data1 <- cbind( c(t(r1$model[2]),t(r2$model[2])), # ln arsenic values
                        c(log(r1$fitted.values),log(r2$fitted.values)), # fitted dependent vars
                        c(r1$weights, r2$weights), # county populations
                        c(rep("1",dim(r1$model[2])[1]), rep("2",dim(r2$model[2])[1])))
                        # smoking group

data1 <- as.data.frame(data1, stringsAsFactors=FALSE)
names(data1) <- c("logAs","logRate", "weight", "smkgrp")
data1$logAs  <- as.numeric(as.character(data1$logAs))
data1$logRate <- as.numeric(as.character(data1$logRate)) # these are the fitted values
data1$weight  <- as.numeric(as.character(data1$weight))
data1$smkgrp  <- as.numeric(as.character(data1$smkgrp))
data1$adjinc  <- c(as.numeric(coef(r1)[2])*r1$model[,2]*0, as.numeric(coef(r2)[2])*r2$model[,2]*0)  # t
                                         # is zeroed out
data1$adjrate <- data1$adjinc+data1$logRate # the same as logRate

#This creates the graph but I'm not sure if you can have the fitted line without dots

assmkp <- ggplot(data1, aes(x=logAs, y=adjrate, shape=factor(smkgrp), color=factor(smkgrp)))
assmkp + stat_smooth(method = "glm", level=0.95, alpha=1, fill="grey80", color="black") +
         #scale_color_manual(values=c("grey50","grey70")) +
         geom_point(aes(size=weight)) +
         geom_point() +
         theme(legend.position = "right") +
         theme_bw()
```



```
full$smkgrpf <- full$smkgrpfbak
full$smkgrpf <- ifelse(is.na(full$smkgrpf), NA, ifelse(full$smkgrpf==1 | full$smkgrpf==2, 1, 2))

full$SESgrp2f <- full$SESgrpf
full$SESgrp2f <- ifelse(is.na(full$SESgrp2f), NA, ifelse(full$SESgrp2f==1 | full$SESgrp2f==2, 1, 2))

# This creates the combined SES and smoking group into one variable, categories 1,2
# are the low smoking categories, important to note that the SES categories are not
# quartiles

full$sessmk = ifelse(full$SESgrp2f==1 & full$smkgrpf==1,"1) Low SES, Low Smoke",
              ifelse(full$SESgrp2f==2 & full$smkgrpf==1,"2) High SES, Low Smoke",
              ifelse(full$SESgrp2f==1 & full$smkgrpf==2,"3) Low SES, High Smoke",
            ifelse(full$SESgrp2f==2 & full$smkgrpf==2,"4) High SES, High Smoke",NA))))

# This is the graph with only two lines for the two smoking groups with actual data

full$smklabel <- ifelse(is.na(full$smkgrpf), NA, ifelse(full$smkgrpf==1,'1) Low Smoke', '2) High Smoke'

graphfile <- full %>%
             group_by(AsQf,smklabel) %>%
             summarise(meanrate = median(AdjRate) )

finalgraph <- graphfile[!is.na(graphfile$AsQf) & !is.na(graphfile$smklabel),]

ggplot(finalgraph, aes(x=AsQf, y=meanrate, color=factor(smklabel))) +
         geom_line(aes(group=smklabel)) +
    ggtitle("Lung Cancer Incidence by Arsenic Quartiles, by Smoking Cat") +
    xlab("Arsenic Quartiles") +
    ylab("Lung Cancer Incidence (per 100,000")
```



```
# This graph creates four lines for the combination of SES and smoking

graphfile <- full %>%
             group_by(AsQf,sessmk) %>%
             summarise(meanrate = median(AdjRate) )

finalgraph <- graphfile[!is.na(graphfile$AsQf) & !is.na(graphfile$sessmk),]

ggplot(finalgraph, aes(x=AsQf, y=meanrate, color=factor(sessmk))) +
         geom_line(aes(group=factor(sessmk))) +
    ggtitle("Lung Cancer Incidence by Arsenic Qs, by Smoking/SES Cat") +
    xlab("Arsenic Quartiles") +
    ylab("Lung Cancer Incidence (per 100,000")
```



```
## GLMS for smoking levels WITH SES
smkgrpf <- smkgrpfbak
## Bottom 50% vs Top 50%
smkgrpf <- ifelse(is.na(smkgrpf), NA, ifelse(smkgrpf==1 | smkgrpf==2, 1, 2))

r1 <- glm(full[smkgrpf==1,]$AdjRate ~ full[smkgrpf==1,]$lnAs + full[smkgrpf==1,]$MedIncome, family=pois
summary(r1)
```

```
Call:
glm(formula = full[smkgrpf == 1, ]$AdjRate ~ full[smkgrpf ==
    1, ]$lnAs + full[smkgrpf == 1, ]$MedIncome, family = poisson,
    weights = as.numeric(full[smkgrpf == 1, ]$Population))

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-4941.6   -151.1    150.1    425.7   2249.4

Coefficients:
                                     Estimate      Std. Error z value
(Intercept)                       4.325647218667  0.000071461711 60531.0
full[smkgrpf == 1, ]$lnAs         0.007596316777  0.000033284145   228.2
full[smkgrpf == 1, ]$MedIncome -0.000003861662  0.000000001486 -2599.0
                                           Pr(>|z|)
(Intercept)                      <0.0000000000000002 ***
full[smkgrpf == 1, ]$lnAs        <0.0000000000000002 ***
full[smkgrpf == 1, ]$MedIncome <0.0000000000000002 ***
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 175916938  on 289  degrees of freedom
Residual deviance: 168750465  on 287  degrees of freedom
  (167 observations deleted due to missingness)
AIC: 536459750

Number of Fisher Scoring iterations: 4
```

```
r2 <- glm(full[smkgrpf==2,]$AdjRate ~ full[smkgrpf==2,]$lnAs + full[smkgrpf==2,]$MedIncome, family=poiss
summary(r2)
```

```
Call:
glm(formula = full[smkgrpf == 2, ]$AdjRate ~ full[smkgrpf ==
    2, ]$lnAs + full[smkgrpf == 2, ]$MedIncome, family = poisson,
    weights = as.numeric(full[smkgrpf == 2, ]$Population))

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1769.12   -244.11     -9.96    270.72   1591.53

Coefficients:
                                      Estimate      Std. Error z value
(Intercept)                     4.688953956476  0.000113495701   41314
full[smkgrpf == 2, ]$lnAs       0.059353912842  0.000043115820    1377
full[smkgrpf == 2, ]$MedIncome -0.000007984707  0.000000002792   -2860
                                          Pr(>|z|)
(Intercept)                    <0.0000000000000002 ***
full[smkgrpf == 2, ]$lnAs      <0.0000000000000002 ***
full[smkgrpf == 2, ]$MedIncome <0.0000000000000002 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 68053265  on 294  degrees of freedom
Residual deviance: 57437520  on 292  degrees of freedom
  (162 observations deleted due to missingness)
AIC: 197334525

Number of Fisher Scoring iterations: 4
```

```
## Plot the Interaction between Arsenic and Smoking with SES
data1 <- cbind( c(t(r1$model[2]),t(r2$model[2])), # ln arsenic values
                c(log(r1$fitted.values),log(r2$fitted.values)), # fitted dependent variables
                c(r1$weights, r2$weights),  # county populations
                c(rep("1",dim(r1$model[2])[1]), rep("2",dim(r2$model[2])[1]))) # number of
data1 <- as.data.frame(data1, stringsAsFactors=FALSE)
names(data1) <- c("logAs","logRate", "weight", "smkgrp")
data1$logAs  <- as.numeric(as.character(data1$logAs))
```

```
data1$logRate <- as.numeric(as.character(data1$logRate))
data1$weight  <- as.numeric(as.character(data1$weight))
data1$smkgrp  <- as.numeric(as.character(data1$smkgrp))
data1$adjinc  <- c(as.numeric(coef(r1)[2])*r1$model[,2], as.numeric(coef(r2)[2])*r2$model[,2]) # this i
data1$adjrate <- data1$adjinc+data1$logRate
#data1$adjrate <- data1$logRate # turn off the adjustment to the fitted values

assmkp <- ggplot(data1, aes(x=logAs, y=adjrate, shape=factor(smkgrp), color=factor(smkgrp)))
assmkp + stat_smooth(method = "glm", level=0.95, alpha=1, fill="grey80", color="black") +
         #scale_color_manual(values=c("grey50","grey70")) +
         geom_point(aes(size=weight)) +
     geom_point() +
         theme(legend.position = "right") +
        theme_bw()
```

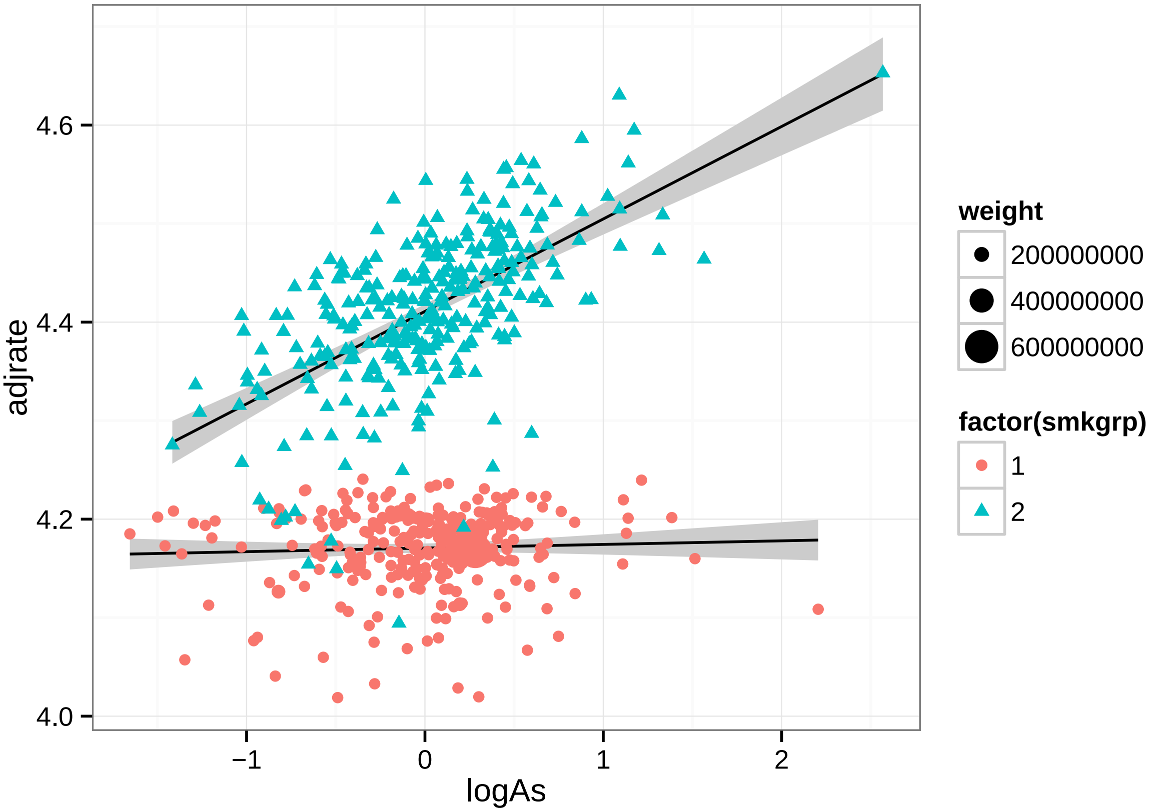


Table 3

Summary of ANOVA tests performed between Arsenic and covariates used in the regression analysis.

```
Interaction_Pair = c("Arsenic:Smoking", "Arsenic:MCI")
DF = c(3, 9)
F_value = c(2.6595, 1.7798)
P_value = c(0.04747, 0.06914)
df = data.frame(Interaction_Pair, DF, F_value, P_value)
kable(df)
```

Interaction_Pair	DF	F_value	P_value
Arsenic:Smoking	3	2.6595	0.04747
Arsenic:MCI	9	1.7798	0.06914

```
# change values in table to variables
```

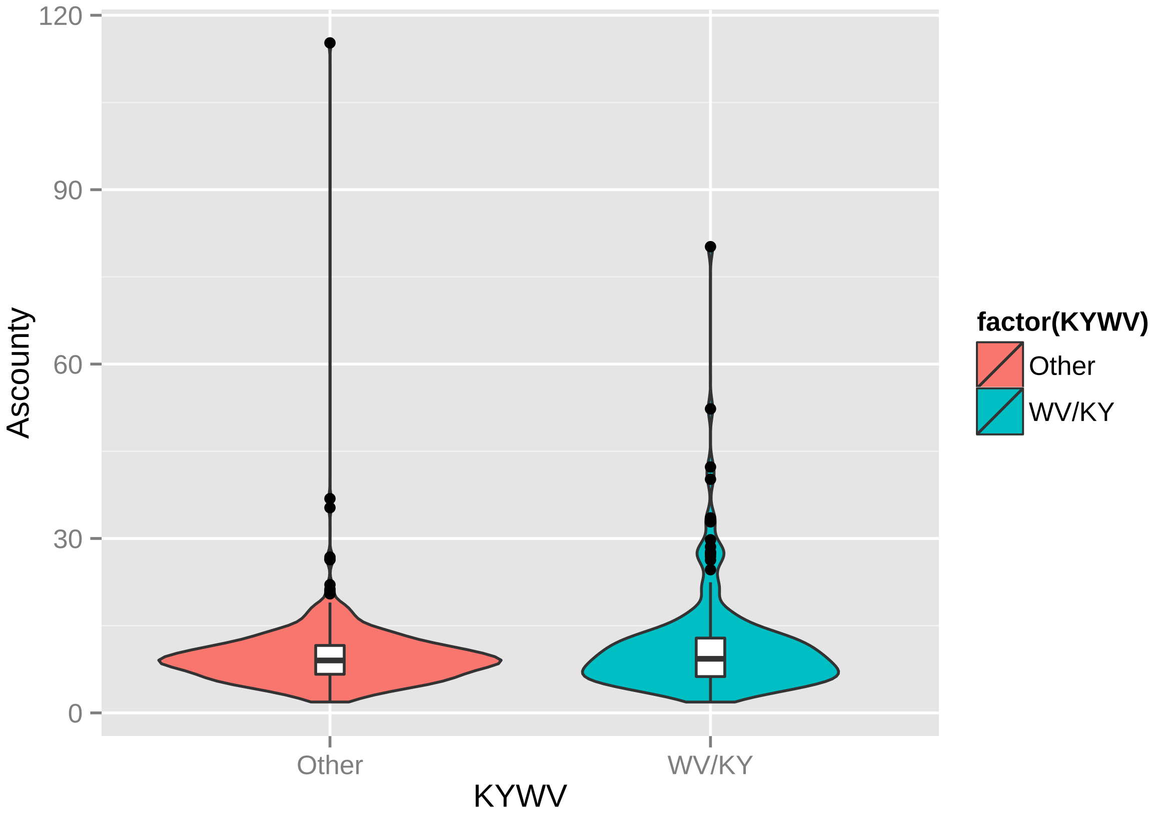
Figure 3

Combination violin and boxplots showing the average level of exposure and outcomes for counties in West Virginia or Kentucky comared with the remaining 10 states in the original sample.

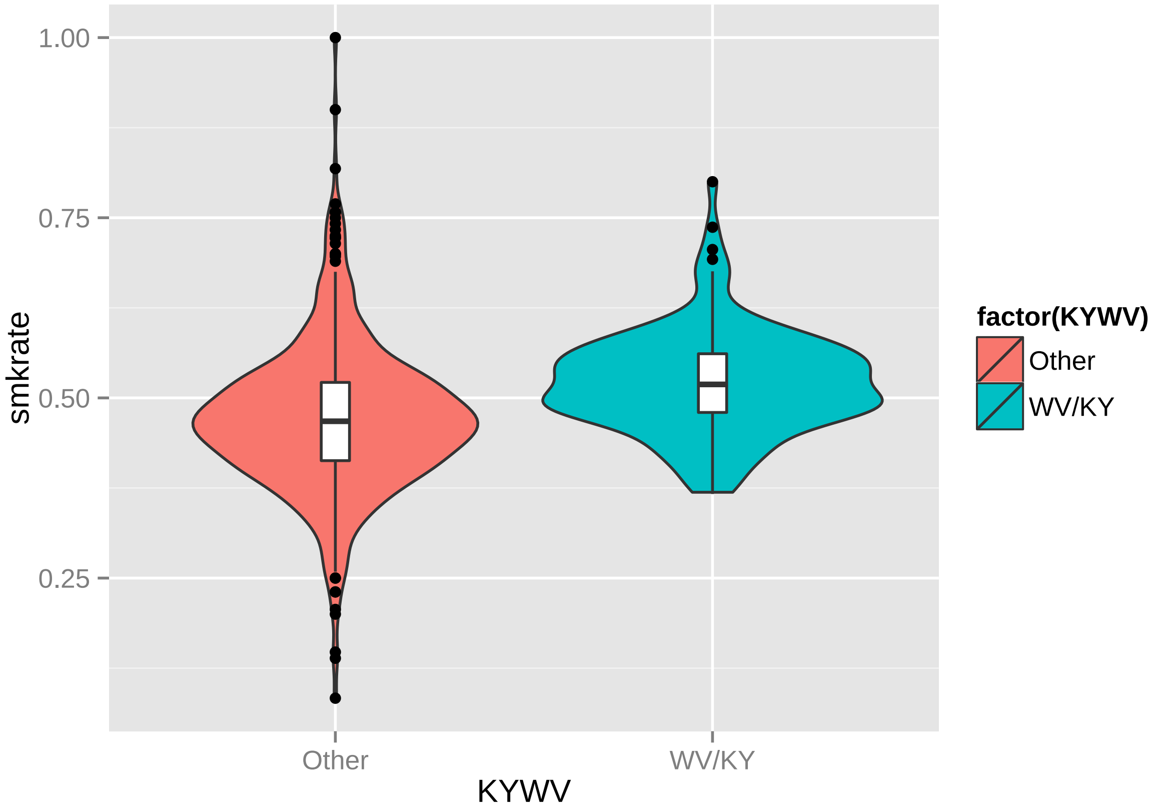
Instead of the bar plot, we represented the data in Figure 3 with a series of combination violin and boxplots. The authors of the original paper attempted to represent each of the variables of interest for this data on the same y-axis scale, including arsenic, income, lung cancer incidence rates, and smoking. Although the authors likely chose this visualization to save space, we decided that it was somewhat confusing and that additional information about the data distributions could be added if we instead used a combination of violin and boxplots.

Explanation of variables here? Add x label (location) and y label (arsenic, income, etc.)

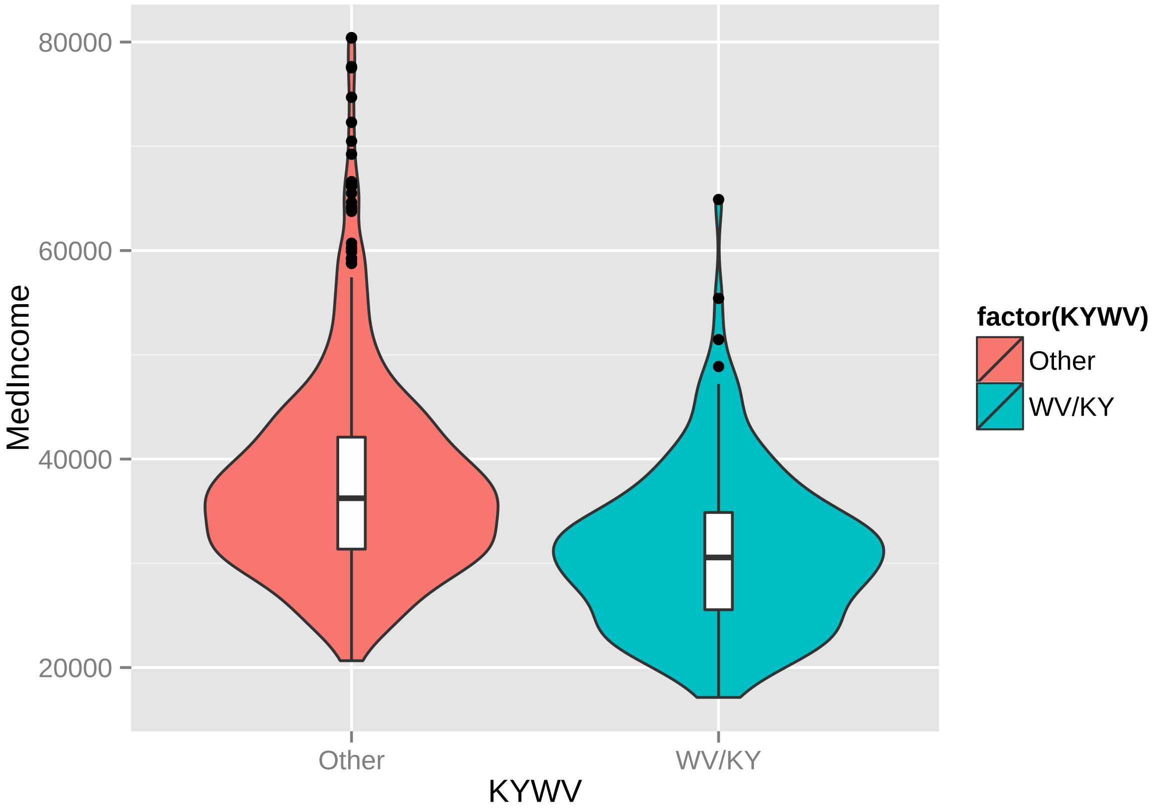
```
# arsenic
KYWVas <- na.omit(full[full$SFIPS == 21 | full$SFIPS == 54, ]$Ascounty)
notKYWVas <- na.omit(full[full$SFIPS != 21 & full$SFIPS != 54, ]$Ascounty)
KYWVdf <- KYWVas %>% as.data.frame() %>% mutate(KYWV = "WV/KY") %>% select(Ascounty = 1,
    KYWV = 2)
notKYWVdf <- notKYWVas %>% as.data.frame() %>% mutate(KYWV = "Other") %>% select(Ascounty = 1,
    KYWV = 2)
KYWVcombined = merge(KYWVdf, notKYWVdf, all = TRUE)
KYWVcombined %>% ggplot(aes(x = KYWV, y = Ascounty)) + geom_violin(aes(fill = factor(KYWV))) +
    geom_boxplot(width = 0.1)
```



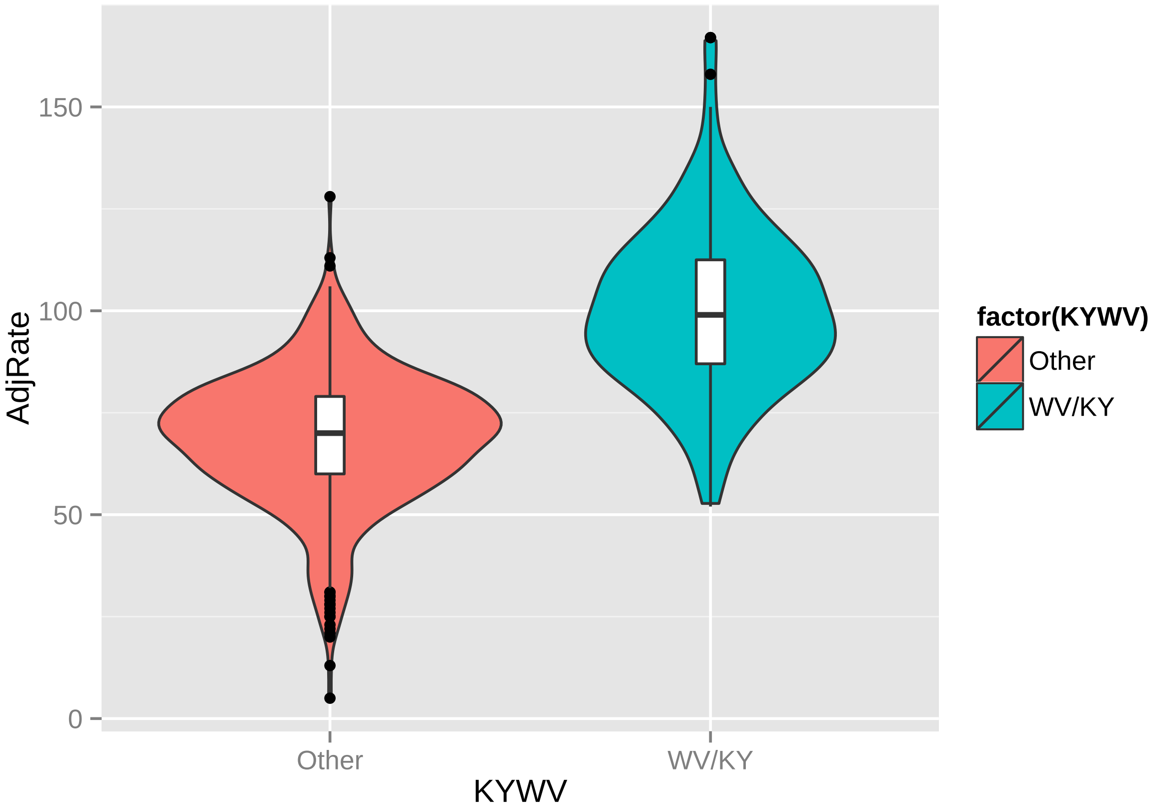
```
# smoking
KYWVsmk <- na.omit(full[full$SFIPS == 21 | full$SFIPS == 54, ]$smkrate)
notKYWVsmk <- na.omit(full[full$SFIPS != 21 & full$SFIPS != 54, ]$smkrate)
KYWVdf <- KYWVsmk %>% as.data.frame() %>% mutate(KYWV = "WV/KY") %>% select(smkrate = 1,
    KYWV = 2)
notKYWVdf <- notKYWVsmk %>% as.data.frame() %>% mutate(KYWV = "Other") %>% select(smkrate = 1,
    KYWV = 2)
KYWVcombined = merge(KYWVdf, notKYWVdf, all = TRUE)
KYWVcombined %>% ggplot(aes(x = KYWV, y = smkrate)) + geom_violin(aes(fill = factor(KYWV))) +
    geom_boxplot(width = 0.1)
```



```r
# income
KYWVmed <- na.omit(full[full$SFIPS == 21 | full$SFIPS == 54, ]$MedIncome)
notKYWVmed <- na.omit(full[full$SFIPS != 21 & full$SFIPS != 54, ]$MedIncome)
KYWVdf <- KYWVmed %>% as.data.frame() %>% mutate(KYWV = "WV/KY") %>% select(MedIncome = 1,
    KYWV = 2)
notKYWVdf <- notKYWVmed %>% as.data.frame() %>% mutate(KYWV = "Other") %>% select(MedIncome = 1,
    KYWV = 2)
KYWVcombined = merge(KYWVdf, notKYWVdf, all = TRUE)
KYWVcombined %>% ggplot(aes(x = KYWV, y = MedIncome)) + geom_violin(aes(fill = factor(KYWV))) +
    geom_boxplot(width = 0.1)
```



```
# lung cancer incidence rate
KYWVrate <- na.omit(full[full$SFIPS == 21 | full$SFIPS == 54, ]$AdjRate)
notKYWVrate <- na.omit(full[full$SFIPS != 21 & full$SFIPS != 54, ]$AdjRate)
KYWVdf <- KYWVrate %>% as.data.frame() %>% mutate(KYWV = "WV/KY") %>% select(AdjRate = 1,
    KYWV = 2)
notKYWVdf <- notKYWVrate %>% as.data.frame() %>% mutate(KYWV = "Other") %>%
    select(AdjRate = 1, KYWV = 2)
KYWVcombined = merge(KYWVdf, notKYWVdf, all = TRUE)
KYWVcombined %>% ggplot(aes(x = KYWV, y = AdjRate)) + geom_violin(aes(fill = factor(KYWV))) +
    geom_boxplot(width = 0.1)
```



Extension

**Add extension here.