R Notebook

ECO518 PS4

0. Set up

```
# Load packages
if(!require(pacman)) install.packages("pacman")
```

```
## Loading required package: pacman
```

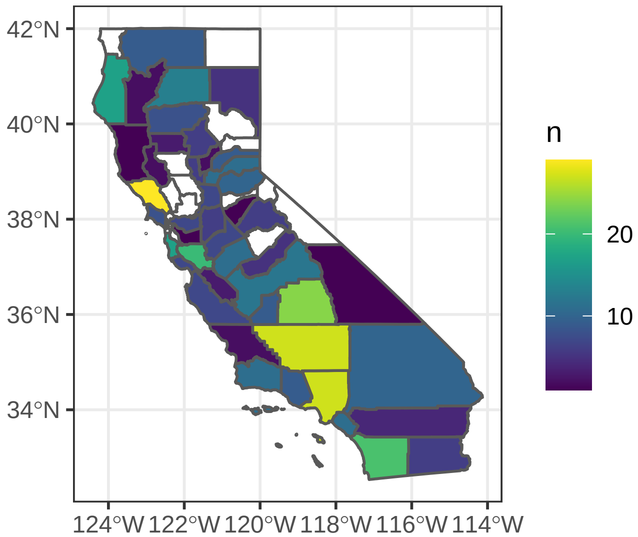
```
pacman::p_load(ggplot2, dplyr, sf, tigris,
               viridis, patchwork, sandwich, nlme, car, jtools, estimatr,
               stargazer)
theme_set(theme_bw())
# Set paths
dir <- paste0("/Users/tombearpark/Documents/princeton/1st_year/",
              "term2/ECO518_Metrics2/sims/exercises/4_grouped_data/")
out <- paste0(dir, "out/")
# Load in the data
load(paste0(dir, "caschool.RData"))
df <- tibble(caschool)
# load a shapefile for maps
cal <- counties(state = "California", cb = TRUE)
```

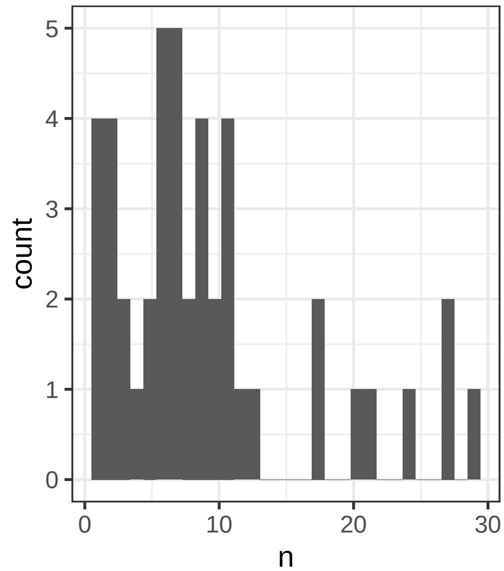
```
##   |                                                                              |
```

```
plot_df <-
  left_join(cal, df %>% group_by(county) %>% tally(),
      by = c("NAME" = "county")) %>%
  mutate(obs = ifelse(is.na(n), 0, n))

# Make sure the merge worked properly
stopifnot(
  dim(anti_join(df %>% group_by(county) %>% tally(),
                cal, by = c("county" = "NAME")))[1] == 0)

wrap_elements(
  (ggplot(plot_df) + geom_sf(aes(fill = n)) +
    scale_fill_viridis(na.value = "white")) +
  (ggplot(plot_df) + geom_histogram(aes(x = n))))
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

```
## Warning: Removed 13 rows containing non-finite values (stat_bin).
```





2. Exercise

Problem 1

Estimate a linear regression of the average test score (testscr) on student-teacher ratio, computers per student, and expenditures per student. Determine whether the three variables have explanatory power by an F-Test of the hypothesis that all three have zero coefficients and via the Bayesian information criterion (BIC). The latter can be computed from an F-statistic: The BIC rejects the restriction when the F-statistic exceeds the log of the sample size.

```
N <- length(df$avginc)
reg1 <- "testscr ~ str + comp_stu + expn_stu"
lm1 <- lm(data = df, formula(reg1))
```

The F stat is 14.96.

```
compare_models <- function(lm_restricted, lm_unrestricted, N){

    RSSR <- sum(lm_restricted$residuals^2)
    RSSU <- sum(lm_unrestricted$residuals^2)
    k    <- length(lm_unrestricted$coefficients) - length(lm_restricted$coefficients)

    Fstat <- ((RSSR - RSSU) / k) / (RSSU / (N-k-1))
    pVal  <- pf(Fstat, k, N-k-1, lower.tail = FALSE)

    BIC_R <- N * log(RSSR / N) + length(lm_restricted$coefficients)  * log(N)
    BIC_U <- N * log(RSSU / N) + length(lm_unrestricted$coefficients)  * log(N)
```

```r
    lowerBIC <- ifelse(BIC_R < BIC_U, "restricted", "unrestricted")

    return(
      tibble(Fstat = Fstat, pVal = pVal,
             BIC_R = BIC_R, BIC_U = BIC_U, logN = log(N),
             lowest_BIC_model = lowerBIC))
}
lm0 <- lm(data = df, testscr ~ 1)
comparison_1 <- compare_models(lm0, lm1, N)
comparison_1
```

```
## # A tibble: 1 x 6
##   Fstat          pVal BIC_R BIC_U  logN lowest_BIC_model
##   <dbl>         <dbl> <dbl> <dbl> <dbl> <chr>
## 1  15.0 0.00000000289 2481. 2456.  6.04 unrestricted
```

- BIC is smallest for the true model. BIC is smallest for the more complex model
  - We can also see that the F-stat is larger than the log of the sample size, so we reject the restriction
- F stat strongly rejects the Null that the coefficients aren't jointly significant

```r
Anova(lm1)
```

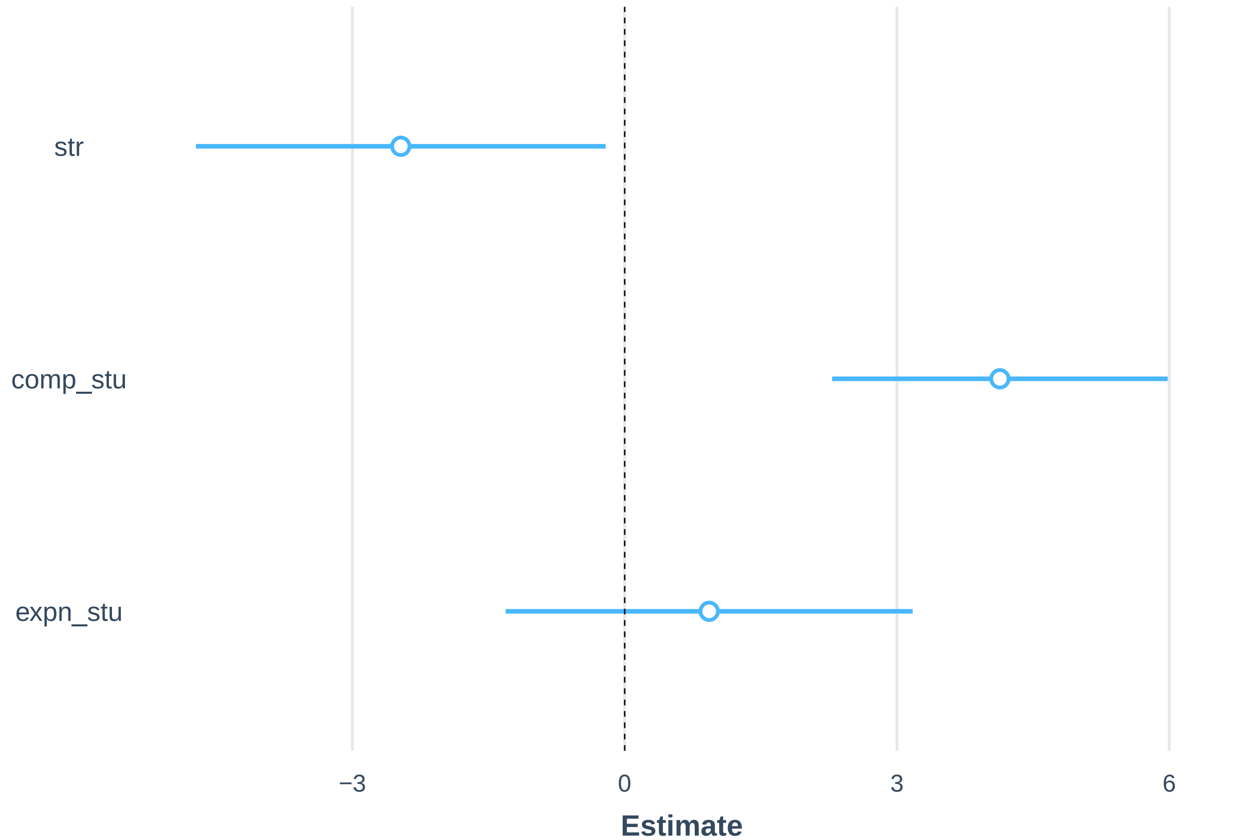
```
## Anova Table (Type II tests)
##
## Response: testscr
##           Sum Sq  Df F value    Pr(>F)
## str         1523   1  4.6147   0.03228 *
## comp_stu    6377   1 19.3217 1.404e-05 ***
## expn_stu     220   1  0.6655   0.41510
## Residuals 137298 416
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
plot_summs(lm1, scale = TRUE)
```

```
## Registered S3 methods overwritten by 'broom':
##   method             from
##   tidy.glht          jtools
##   tidy.summary.glht jtools
```

```
## Loading required namespace: broom.mixed
```

```
## Registered S3 method overwritten by 'broom.mixed':
##   method      from
##   tidy.gamlss broom
```




```r
# run a clustered version
lm1_c <- lm_robust(formula(reg1), data = df, cluster = county)
```

Problem 2

Do the same thing with a regression that adds the demographic variables: Average income, subsidized meals, calWorks per cent, and English learners percent. Again check whether the three "policy variables have explanatory power using an F test and BIC. Here you may need to extract the covariance matrix of coefficients from the lm() output to construct the F or chi-squared statistic.

```r
reg2 <- paste0(reg1, " + avginc + meal_pct + calw_pct + el_pct")
lm2 <- lm(data = df, formula(reg2))
```

```r
compare_models(lm_restricted = lm1, lm_unrestricted = lm2, N = N)
```

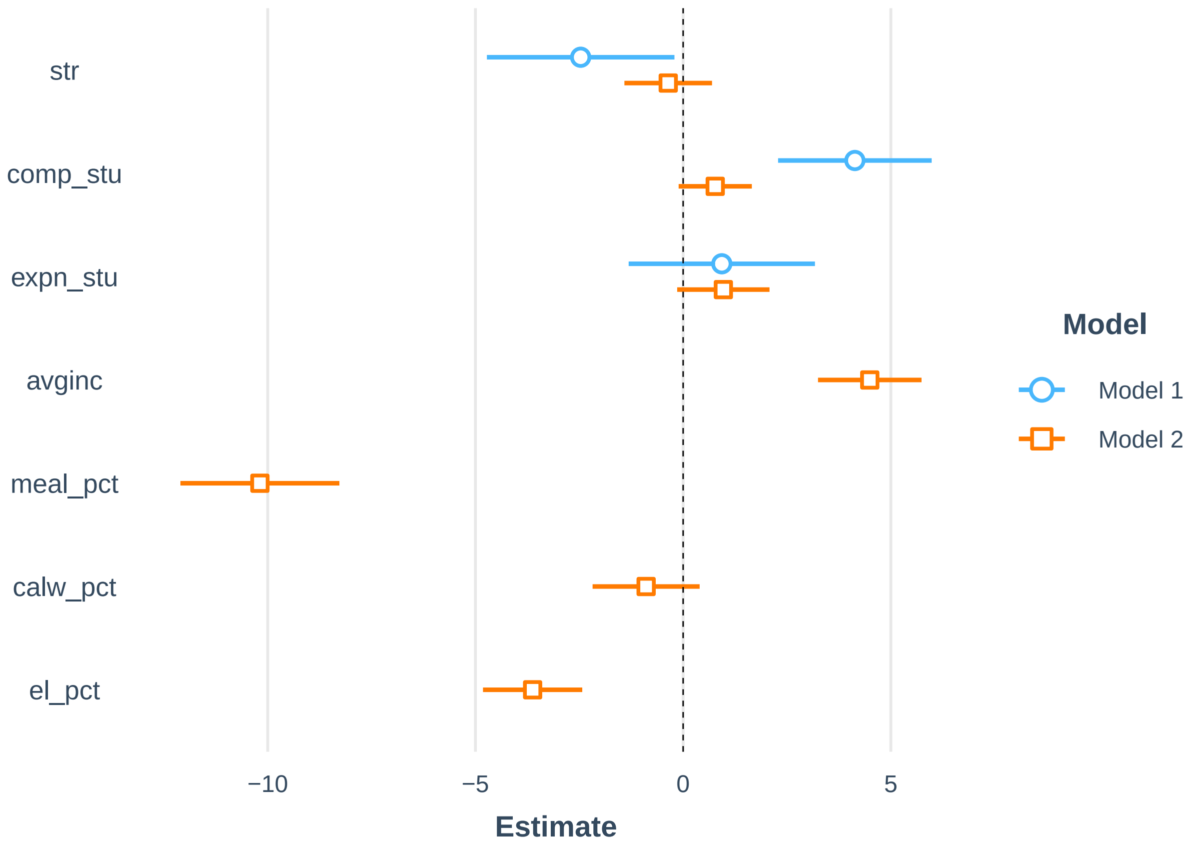
```
## # A tibble: 1 x 6
##   Fstat       pVal BIC_R BIC_U  logN lowest_BIC_model
##   <dbl>      <dbl> <dbl> <dbl> <dbl> <chr>
## 1  387. 1.36e-138 2456. 1827.  6.04 unrestricted
```

```r
Anova(lm2)
```

```
## Anova Table (Type II tests)
##
```

```
## Response: testscr
##            Sum Sq  Df  F value    Pr(>F)
## str          31.6   1   0.4486   0.50337
## comp_stu    209.2   1   2.9710   0.08552 .
## expn_stu    206.3   1   2.9302   0.08769 .
## avginc     3536.7   1  50.2267 5.979e-12 ***
## meal_pct   7711.7   1 109.5178 < 2.2e-16 ***
## calw_pct    130.3   1   1.8498   0.17455
## el_pct     2502.8   1  35.5437 5.365e-09 ***
## Residuals 29011.1 412
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
plot_summs(lm1,lm2, scale = TRUE)
```



- Once again, our tests prefer the more complex model

Problem 3

Repeat the previous estimations and tests in models that add county fixed effects. In R using lm(), this is accomplished by just adding "county" to the list of right-hand side variables. (county is a "factor" in the R dataframe, so R automatically converts it into the appropriate array of dummy variables when including it in a regression.)

```r
reg3 <- paste0(reg2, "+ county")
lm3 <- lm(data = df, formula(reg3))
lm3_c <- lm_robust(data = df, formula(reg3), cluster = county)
```

```r
compare_models(lm2, lm3, N)
```

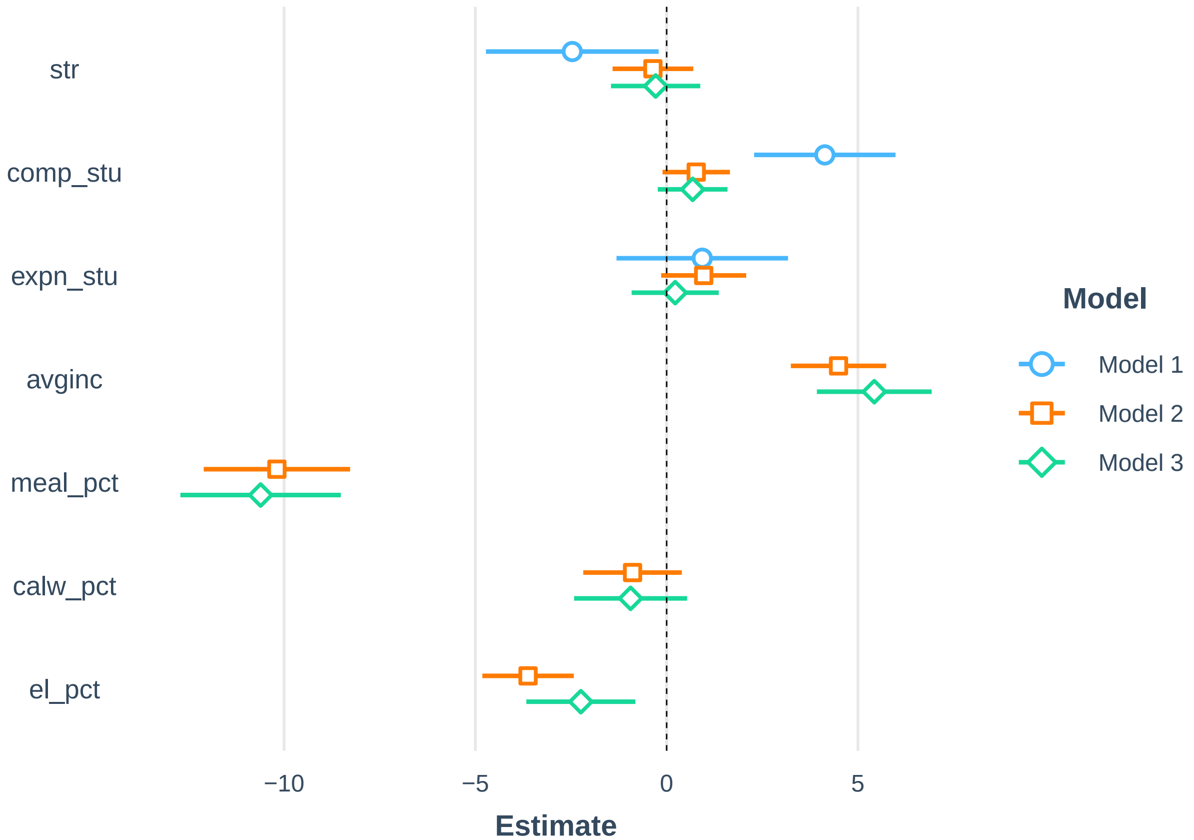
```
## # A tibble: 1 x 6
##   Fstat      pVal BIC_R BIC_U  logN lowest_BIC_model
##   <dbl>     <dbl> <dbl> <dbl> <dbl> <chr>
## 1  2.27 0.0000199 1827. 1994.  6.04 restricted
```

- This time, our model doesn't want us to choose the extra complexity in the BIC.
- However, our F-stat approach prefers the more complex model

```r
Anova(lm3)
```

```
## Anova Table (Type II tests)
##
## Response: testscr
##            Sum Sq  Df F value    Pr(>F)
## str          14.7   1  0.2363  0.627173
## comp_stu    133.7   1  2.1483  0.143580
## expn_stu      9.2   1  0.1477  0.700940
## avginc     3149.0   1 50.6039 5.937e-12 ***
## meal_pct   6168.1   1 99.1184 < 2.2e-16 ***
## calw_pct     98.1   1  1.5761  0.210119
## el_pct      596.1   1  9.5798  0.002118 **
## county     6110.7  44  2.2317 3.170e-05 ***
## Residuals 22900.4 368
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
vars <- c("str", "comp_stu", "expn_stu", "avginc", "meal_pct", "calw_pct", "el_pct" )
plot_summs(lm1, lm2, lm3, coefs = vars, scale = TRUE)
```



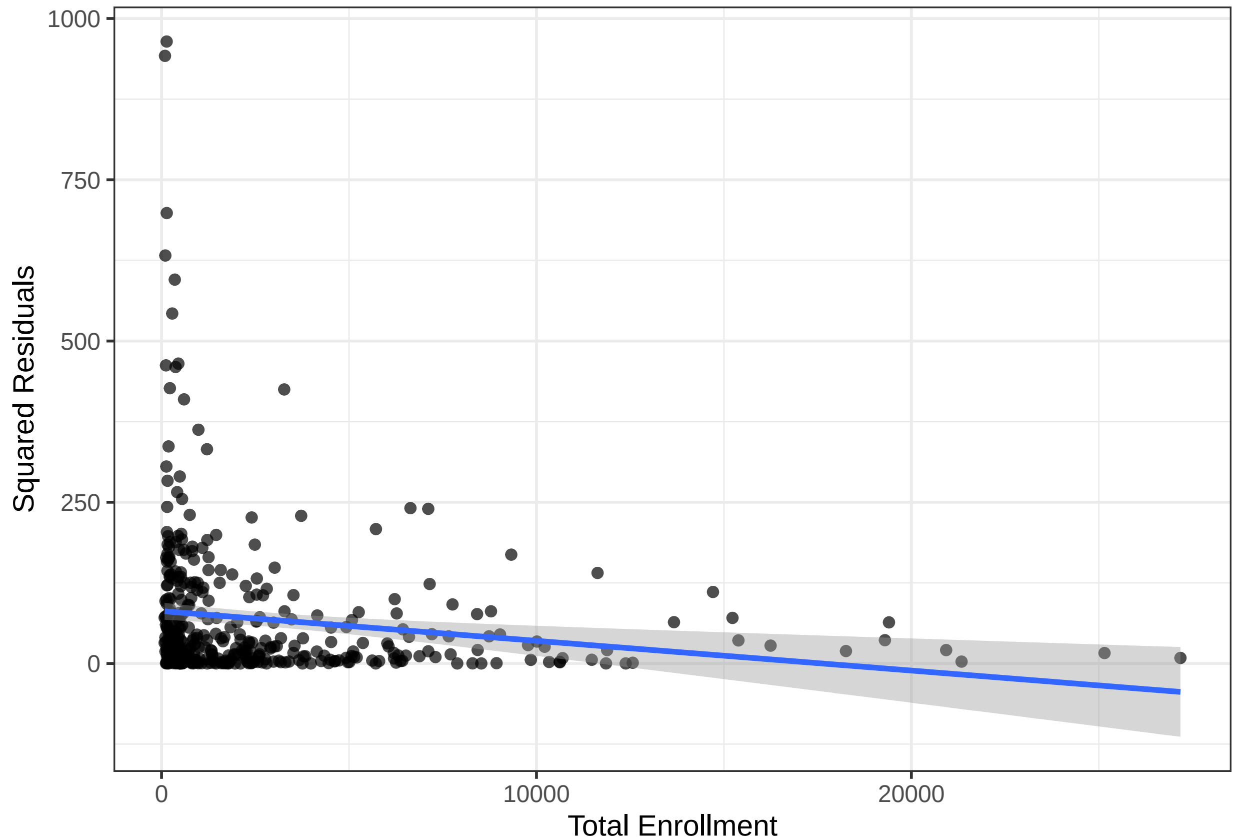
Problem 4

The districts vary greatly in size. Average scores might have more sampling variation in small districts. Plot the squared residuals from the estimated model in 2 against the total enrollment variable. Estimate a linear regression of these squared residuals on 1/enrl_tot. Use the inverse of these predicted values as the weights argument in lm() (or otherwise estimate the corresponding weighted regression estimates) in the question 2 regression.

First, lets plot the squared residuals against the total enrollment variable.

```
df$u2 <- lm2$residuals
df$sqr_u2 <- lm2$residuals ^ 2
ggplot(df, aes(x = enrl_tot, y = sqr_u2)) +
  geom_point(alpha= .7) +
  xlab("Total Enrollment") + ylab("Squared Residuals") +
  geom_smooth(method = lm)
```

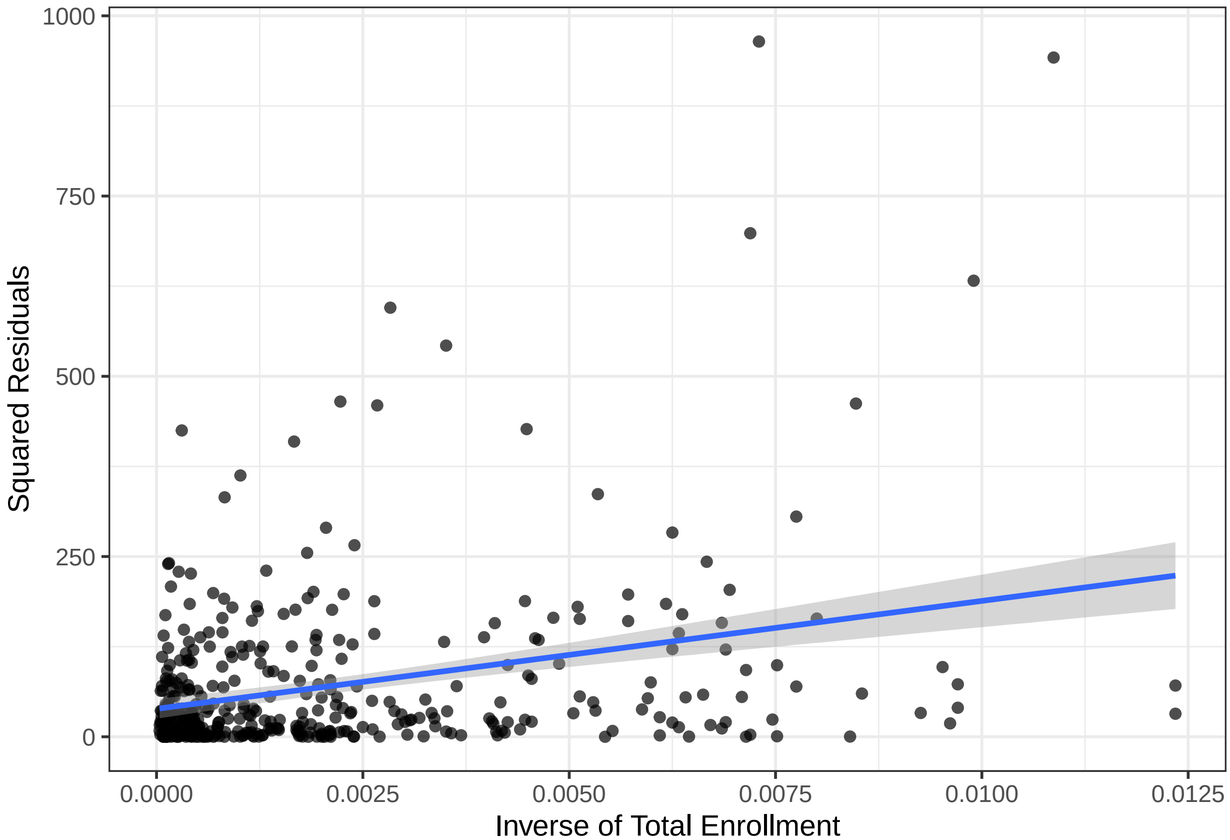
```
## `geom_smooth()` using formula 'y ~ x'
```



Lets also plot the squared residuals against the inverse of total enrollment, since that relationship is what we are going to use for our weighting scheme.

```
ggplot(df, aes(x = 1/enrl_tot, y = sqr_u2)) +
  geom_point(alpha= .7) +
  xlab("Inverse of Total Enrollment") + ylab("Squared Residuals") +
  geom_smooth(method = lm)
```

```
## `geom_smooth()` using formula 'y ~ x'
```



We can estimate a linear regression, to calculate the weights…

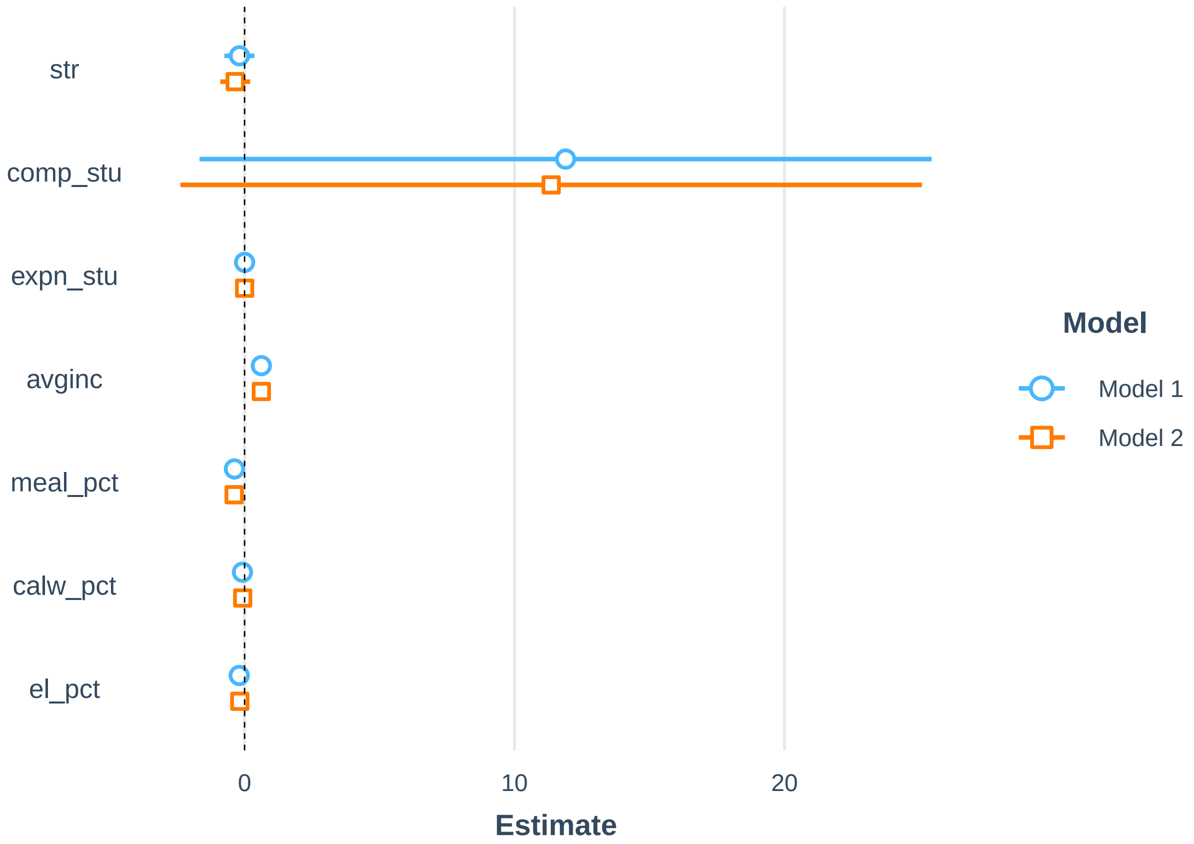
```
df$inv_enrl_tot <- 1 / df$enrl_tot
lm4_w <- lm(data = df, sqr_u2 ~ inv_enrl_tot)
```

Next we run a regression weighted by the inverse of the residuals

```
df$weights_lm4 <- 1 / lm4_w$fitted.values
lm4 <- lm(data = df, formula(reg2), weights = df$weights_lm4)
```

Compare model 2 to this weighted version…

```
plot_coefs(lm2, lm4, scale = TRUE)
```

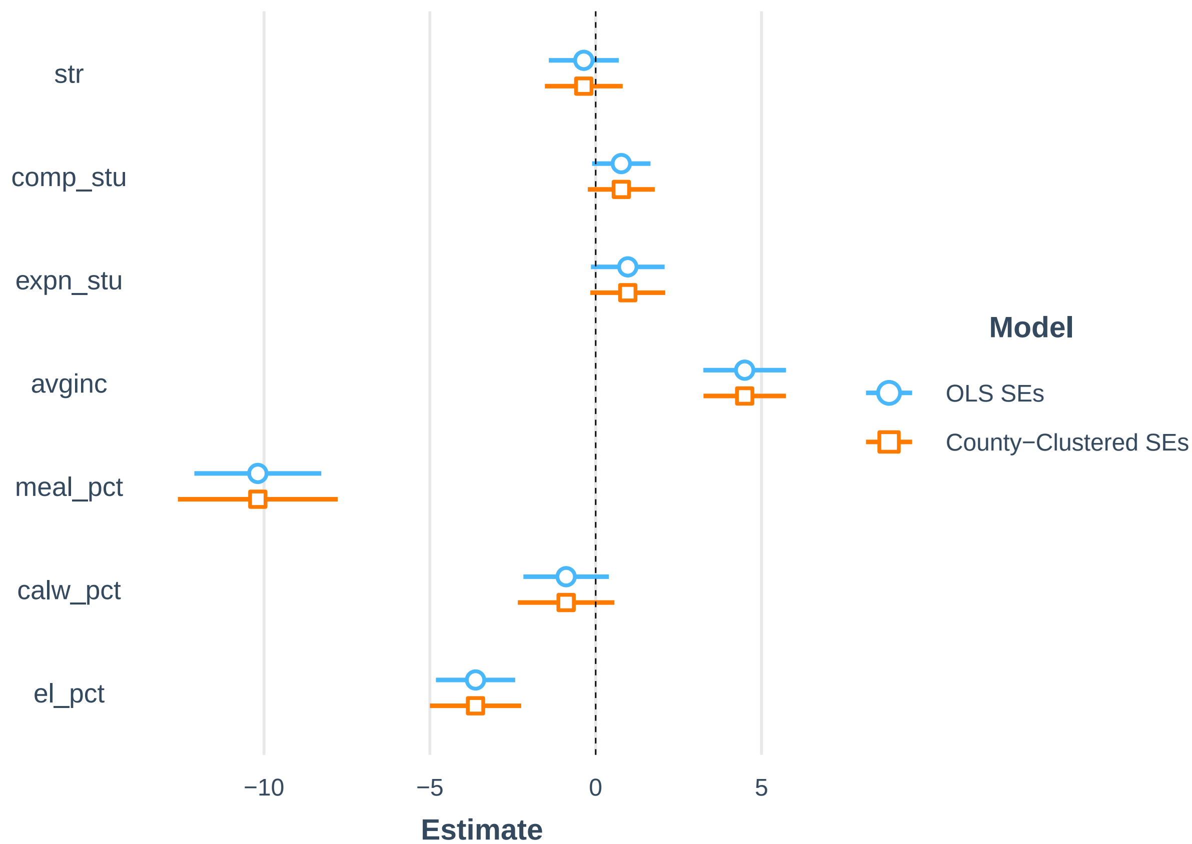


Problem 5

For at least two of the above regression models, calculate standard errors clustered by county. This is done very easily with the vcovCL() function from the sandwich package — so easily that if you're doing it this way you might want to see how much difference it makes in all of the above regressions.

```
plot_summs(lm2, lm2, scale = TRUE,
           robust = list(FALSE, c(cluster = df$county)),
           model.names = c("OLS SEs", "County-Clustered SEs"))
```

```
## Warning in if (type == TRUE) {: the condition has length > 1 and only the first
## element will be used
```




```r
# plot_summs(lm3, lm3, scale = TRUE,
#            robust = list(FALSE, c(cluster = df$county)),
#            model.names = c("OLS SEs", "County-Clustered SEs"), coefs = vars)
```

Problem 6

Estimate a random effects model, with county effects. In R, use the lme() function from the nlme package to estimate the 7-variable regression, with random effects by county. You do this by giving lme the argument random = ~1 | county. Also use the argument method="ML", so that the estimation is by maximum likelihood.

```r
RE <- lme(data = df, formula(reg2), random = ~1 | county, method = "ML")
summary(RE)$tTable
```

```
##                     Value    Std.Error  DF    t-value       p-value
## (Intercept) 661.036834029 9.0964677878 368 72.6696174 2.445055e-220
## str          -0.196646628 0.2912970412 368 -0.6750725  5.000536e-01
## comp_stu     12.606870943 6.8619471986 368  1.8372148  6.698437e-02
## expn_stu      0.001068223 0.0008875184 368  1.2036069  2.295152e-01
## avginc        0.664923420 0.0925252296 368  7.1864012  3.727999e-12
## meal_pct     -0.367437398 0.0370049535 368 -9.9294111  9.623245e-21
## calw_pct     -0.084161241 0.0589872135 368 -1.4267709  1.544938e-01
## el_pct       -0.186981628 0.0347232272 368 -5.3849150  1.294861e-07
```

```r
summary(RE)
```

```
## Linear mixed-effects model fit by maximum likelihood
##   Data: df
##        AIC      BIC    logLik
##   2985.113 3025.516 -1482.557
##
## Random effects:
##  Formula: ~1 | county
##         (Intercept) Residual
## StdDev:    2.466434 8.004958
##
## Fixed effects:  formula(reg2)
##                 Value Std.Error  DF  t-value p-value
## (Intercept) 661.0368  9.096468 368 72.66962  0.0000
## str          -0.1966  0.291297 368 -0.67507  0.5001
## comp_stu     12.6069  6.861947 368  1.83721  0.0670
## expn_stu      0.0011  0.000888 368  1.20361  0.2295
## avginc        0.6649  0.092525 368  7.18640  0.0000
## meal_pct     -0.3674  0.037005 368 -9.92941  0.0000
## calw_pct     -0.0842  0.058987 368 -1.42677  0.1545
## el_pct       -0.1870  0.034723 368 -5.38492  0.0000
##  Correlation:
##          (Intr) str    cmp_st expn_s avginc ml_pct clw_pc
## str      -0.910
## comp_stu -0.127  0.142
## expn_stu -0.750  0.513 -0.137
## avginc   -0.097  0.032 -0.024 -0.294
## meal_pct -0.097 -0.010 -0.059 -0.110  0.501
## calw_pct  0.073 -0.006  0.118 -0.129 -0.034 -0.625
## el_pct    0.062 -0.032  0.157  0.005 -0.165 -0.649  0.293
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -3.86054173 -0.60780373 -0.01266389  0.59529612  2.87465042
##
## Number of Observations: 420
## Number of Groups: 45
```

Problem 7

Compare the random effects 7-variable model to the fixed effects model. In R, you can do this by re-estimating the fixed-effect model with the gls()function from the nlme package, again being sure to use method="ML" argument. The summary() function applied to either random effects or fixed effects models computed this way deliver both log likelihood and BIC values, so the models can be compared both by afrequentist chi-squared test based on the log likelihood and via the BIC.

```r
FE <- gls(data = df, formula(paste0(reg2, "+ county")), method = "ML")
summary(FE)$tTable[1:8, ]
```

```
##                     Value    Std.Error    t-value       p-value
## (Intercept)  6.714925e+02 1.288580e+01 52.1110365 5.977392e-172
```

```
## str         -1.524921e-01 3.136940e-01 -0.4861174  6.271733e-01
## comp_stu     1.045821e+01 7.135233e+00  1.4657140  1.435801e-01
## expn_stu     3.512003e-04 9.137477e-04  0.3843515  7.009399e-01
## avginc       7.510105e-01 1.055733e-01  7.1136391  5.937188e-12
## meal_pct    -3.913137e-01 3.930501e-02 -9.9558217  7.808023e-21
## calw_pct    -8.233494e-02 6.558305e-02 -1.2554301  2.101192e-01
## el_pct      -1.226652e-01 3.963174e-02 -3.0951246  2.117931e-03
```

Problem 8

Finally, for the random effects model, use a regression of its squared residuals on 1/(total enrollment) to generate weights for a weighted random effects estimation; see if this improves likelihood and/or changes important estimates. [Note: I think that in the nlme estimation functions the "weights" arguments are variance scales — the inverse of the weights used in lm(). So you would use a weights= ~w argument to lme() if you used weights=1/w in lm()].

```
df$fe_sqr_resid <- FE$residuals^2
lm8_w <- lm(data = df,  fe_sqr_resid ~ inv_enrl_tot)
RE_w <- lme(data = df, formula(reg2), random = ~1 | county, method = "ML", weights = ~fe_sqr_resid)
summary(RE_w)$tTable
```

```
##                     Value    Std.Error  DF    t-value       p-value
## (Intercept)  6.603296e+02 2.2875102848 368 288.667401  0.000000e+00
## str         -1.213883e-01 0.0761009226 368  -1.595096  1.115492e-01
## comp_stu     9.037629e+00 1.3580052473 368   6.655076  1.029401e-10
## expn_stu     9.001039e-04 0.0001932145 368   4.658574  4.455928e-06
## avginc       7.568173e-01 0.0245166268 368  30.869552 3.658791e-104
## meal_pct    -3.910758e-01 0.0089293976 368 -43.796436 4.990160e-148
## calw_pct    -1.028992e-01 0.0126996016 368  -8.102555  8.024566e-15
## el_pct      -1.168429e-01 0.0088350324 368 -13.224949  6.164603e-33
```

Problem 9

Be ready to discuss: Does the evidence favor an important effect from the "controllable" variables? The sizes and signs of the estimated effects, not just the significance levels of tests, should inform your views on this.