STAT-S631

Assignment 9

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Problem 1

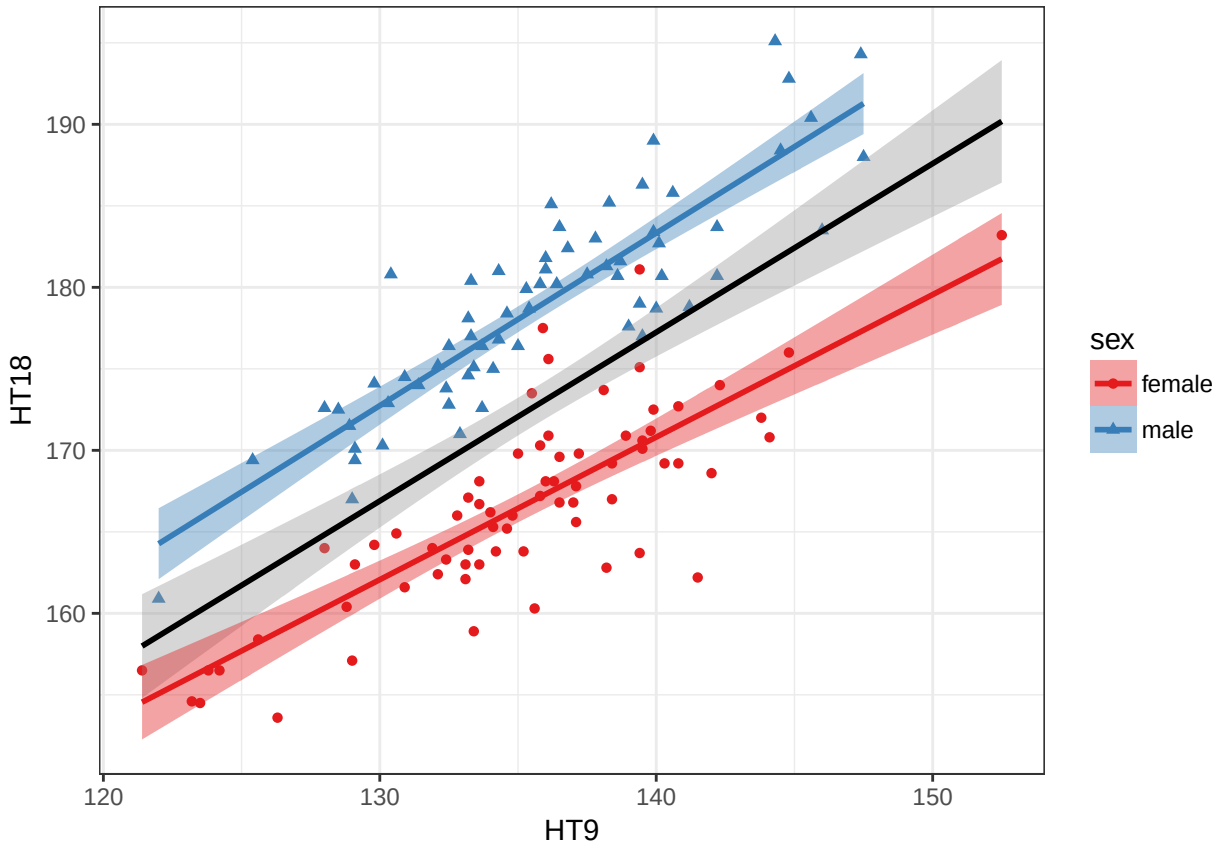
[From ALR 5.14]

```
dp <- loadNamespace('dplyr')
import::from(magrittr, `%>%`, `%<>%`)
import::from(car, Anova)
import::from(ggplot2,
             ggplot,
             geom_point, stat_smooth,
             aes,
             scale_colour_brewer, scale_fill_brewer, scale_x_log10,
             labs,
             theme_set, theme_bw)
theme_set(theme_bw())

bgsall.df <- alr4::BGSall %>%
  dp$mutate(sex = dp$if_else(Sex == 0, 'male', 'female'))
```

Part 1

```
ggplot(bgsall.df) +
  geom_point(aes(x = HT9, y = HT18, shape = sex, colour = sex)) +
  stat_smooth(aes(x = HT9, y = HT18), method = 'lm', colour = 'black') +
  stat_smooth(aes(x = HT9, y = HT18, colour = sex, fill = sex),
              method = 'lm') +
  scale_colour_brewer(palette = 'Set1') +
  scale_fill_brewer(palette = 'Set1')
```



From the scatterplot, there's a fair amount of separation between the sexes, and it appears that a model containing both `HT9` and `sex` but not an interaction between the two would be the most appropriate.

Part 2

```
ht9.model <- lm(HT18 ~ HT9, data = bgsall.df)
parallel.model <- lm(HT18 ~ HT9 + sex, data = bgsall.df)
full.model <- lm(HT18 ~ HT9 * sex, data = bgsall.df)

Anova(full.model)
```

```
Anova Table (Type II tests)

Response: HT18
          Sum Sq  Df  F value  Pr(>F)
HT9       3740.5   1 322.1883 < 2e-16 ***
sex       4624.0   1 398.2872 < 2e-16 ***
HT9:sex     34.4   1   2.9638 0.08749 .
Residuals 1532.5 132
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

From the F-test (which is the same as a t-test in this case since the factor only has two levels), we obtain a p-value of 0.0875, which is significant at the $\alpha = .1$ level but not at $\alpha = .05$. On the other hand, the p-value for the intercept term is significant. This test compares the model with just `HT9` vs. the model with both `HT9` and `sex` without the interaction term.

Part 3

```
summary(parallel.model)
```

```
Call:
lm(formula = HT18 ~ HT9 + sex, data = bgsall.df)

Residuals:
     Min       1Q   Median       3Q      Max
-10.4694  -2.0952  -0.0136   1.7101  10.4467

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 36.82147    7.29177    5.05 1.43e-06 ***
HT9          0.96006    0.05388   17.82  < 2e-16 ***
sexmale     11.69584    0.59036   19.81  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.432 on 133 degrees of freedom
Multiple R-squared:  0.8516,    Adjusted R-squared:  0.8494
F-statistic: 381.7 on 2 and 133 DF,  p-value: < 2.2e-16
```

```
confint(parallel.model, 'sexmale')
```

```
           2.5 %   97.5 %
sexmale 10.52813 12.86355
```

Problem 2

We are given:

$X = [X_1|X_2]$
$H = X(X^TX)^{-1}X^T$
$H_R = X_1(X_1^TX_1)^{-1}X_1^T$

Part a

Show $H_RX_1 = X_1$

$H_RX_1 = X_1(X_1^TX_1)^{-1}X_1^TX_1 = X_1(X_1^TX_1)^{-1}(X_1^TX_1) = X_1$

Show $HX_1 = X_1$

Consider HX. We know that $HX = X$, so we can say:

$$\begin{aligned} HX &= H[x_0, x_1, x_2, ..., x_p] \\ &= [Hx_0, Hx_1, ..., Hx_p] \end{aligned}$$

Where x_i is the i^{th} column vector of X.

But then $HX = X = [x_0, ..., x_p]$. Therefore:

$$[Hx_0, ..., Hx_p] = [x_0, ..., x_p]$$
$$\implies Hx_i = x_i$$

Then if we consider HX_1:

$$\begin{aligned} HX_1 &= H[x_0, ..., x_{p+1-q}] \\ &= [Hx_0, ..., Hx_{p+1-q}] \\ &= [x_0, ..., x_{p+1-q}] \\ &= H_1 \end{aligned}$$

Show $HH_R = H_R$

$HH_R = H\big(X_1(X_1^TX_1)^{-1}X_1^T\big) = (HX_1)(X_1^TX_1)^{-1}X_1^T = X_1(X_1^TX_1)^{-1}X_1^T = H_R$

Part b

Show $H - H_R$ is symmetric

$H - H_R$ is symmetric iff $H - H_R = (H - H_R)^T$.

We also know that H and H_R are symmetric.

Therefore, $(H - H_R)^T = H^T - H_R^T = H - H_R$.

Show $H - H_R$ is idempotent

$H - H_R$ is idempotent iff $(H - H_R)^2 = H - H_R$

We know that H and H_R are idempotent.

Therefore:

$$\begin{aligned} (H - H_R)(H - H_R) &= HH - HH_R - H_RHH_RH_R \\ &= H - H_R - H_RH + H_R \\ &= H - H_RH \end{aligned}$$

Consider that H and H_R are symmetric and $HH_R = H_R$. Therefore, $H_R = H_R^T = (HH_R)^T = H_R^TH^T = H_RH$ $\implies H_R = H_RH$.

Therefore:

$$H - H_RH = H - H_R$$
$$\implies (H - H_R)^2 = H - H_R$$

Part c

$$\frac{SSreg}{\sigma^2} = \frac{RSS_R - RSS_F}{\sigma^2}$$
$$= \frac{Y^T(I - H_R)Y - Y^T(I - H)Y}{\sigma^2}$$
$$= \frac{Y^T(H - H_R)Y}{\sigma^2}$$
$$= \frac{(Y - X_1\hat{\beta}_1)^T(H - H_R)(Y - X_1\hat{\beta}_1)}{\sigma^2}$$

We know that $Y - X_1\hat{\beta}_1 \sim \mathcal{N}(0, \sigma^2(I - H_R))$. Furthermore, we know that $rank(H - H_R) = rank(H) - rank(H_R) = p + 1 - (p + 1 - q) = q$ (assuming H and H_R are full rank).

Then $\frac{SSreg}{\sigma^2} \sim \chi^2_q$ if $(\frac{H-H_R}{\sigma^2})(\sigma^2(I - H_R)) = (H - H_R)(I - H_R)$ is idempotent. But $(H - H_R)(I - H_R) = H - HH_R - H_R + H_RH_R = H - H_R - H_R + H_R = H - H_R$ which we already know to be idempotent. Therefore,

$$\frac{SSreg}{\sigma^2} \sim \chi^2_q$$

Part d

$$\hat{\sigma}^2 = \frac{RSS}{n - p - 1}$$
$$= Y^T \frac{I - H}{n - p - 1} Y$$

So we have to show:

$$\left(\frac{H - H_R}{\sigma^2}\right)\left(\sigma^2(I - H)\right)\left(\frac{I - H}{n - p - 1}\right) = 0$$

We know that the product of the first two components is $H - H_R$. Therefore,

$$\left(\frac{H - H_R}{\sigma^2}\right)\left(\sigma^2(I - H)\right)\left(\frac{I - H}{n - p - 1}\right) = (H - H_R)(I - H)\frac{1}{n - p - 1}$$
$$= (H - H - H_R + H_R)\frac{1}{n - p - 1}$$
$$= 0$$

Part e

We know that $\frac{SSreg}{\sigma^2} \sim \chi^2_q$ and $\frac{RSS}{\sigma^2} \sim \chi^2_{n-p-1}$. We also know that they are independent. Then we know that $\frac{\frac{SSreg}{\sigma^2}/q}{\frac{RSS}{\sigma^2}/(n-p-1)} = \frac{SSreg/q}{RSS/(n-p-1)} \sim F_{q,n-p-1}$

Problem 3

[From ALR 6.4]

```
un11.df <- alr4::UN11 %>%
  dp$mutate(country = rownames(.))

h0.model <- lm(lifeExpF ~ log(ppgdp) + group:log(ppgdp), data = un11.df)
summary(h0.model)
```

```
Call:
lm(formula = lifeExpF ~ log(ppgdp) + group:log(ppgdp), data = un11.df)

Residuals:
     Min       1Q   Median       3Q      Max
-18.6121  -2.5029   0.3037   2.4489  15.3486

Coefficients:
                       Estimate Std. Error t value Pr(>|t|)
(Intercept)             43.8040     2.6231  16.699  < 2e-16 ***
log(ppgdp)               3.7245     0.2677  13.912  < 2e-16 ***
log(ppgdp):groupother   -0.0698     0.1153  -0.605    0.546
log(ppgdp):groupafrica  -1.4303     0.1726  -8.285 1.87e-14 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 5.18 on 195 degrees of freedom
Multiple R-squared:  0.7422,    Adjusted R-squared:  0.7382
F-statistic: 187.1 on 3 and 195 DF,  p-value: < 2.2e-16
```

```
ha.model <- lm(lifeExpF ~ group * log(ppgdp), data = un11.df)
summary(ha.model)
```

```
Call:
lm(formula = lifeExpF ~ group * log(ppgdp), data = un11.df)

Residuals:
    Min      1Q  Median      3Q     Max
-18.634  -2.089   0.301   2.255  14.489

Coefficients:
                       Estimate Std. Error t value Pr(>|t|)
(Intercept)             59.2137    15.2203   3.890 0.000138 ***
groupother             -11.1731    15.5948  -0.716 0.474572
groupafrica            -22.9848    15.7838  -1.456 0.146954
log(ppgdp)               2.2425     1.4664   1.529 0.127844
groupother:log(ppgdp)    0.9294     1.5177   0.612 0.540986
groupafrica:log(ppgdp)   1.0950     1.5785   0.694 0.488703
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 5.129 on 193 degrees of freedom
Multiple R-squared:  0.7498,    Adjusted R-squared:  0.7433
```

```
F-statistic: 115.7 on 5 and 193 DF,  p-value: < 2.2e-16
```

Part 1

The full model is one in which each `group` has its own intercept and slope. If the null hypothesis is true, each `group` has its own slope but the intercepts are not unique.

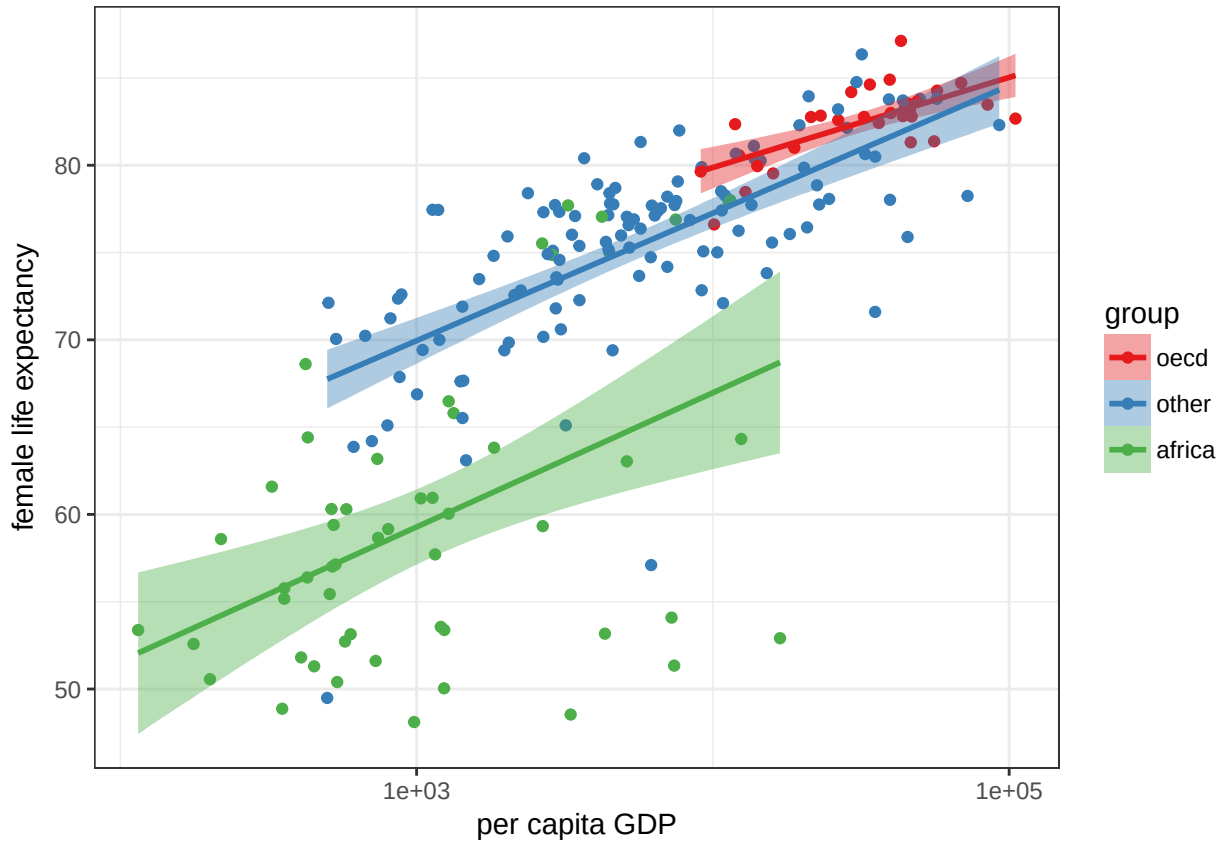
Part 2

```
anova(h0.model, ha.model)
```

```
Analysis of Variance Table

Model 1: lifeExpF ~ log(ppgdp) + group:log(ppgdp)
Model 2: lifeExpF ~ group * log(ppgdp)
  Res.Df    RSS Df Sum of Sq      F  Pr(>F)
1    195 5232.0
2    193 5077.7  2    154.31 2.9326 0.05564 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ggplot(un11.df) +
  geom_point(aes(x = ppgdp, y = lifeExpF, colour = group)) +
  labs(x = 'per capita GDP', y = 'female life expectancy') +
  stat_smooth(aes(x = ppgdp, y = lifeExpF, colour = group, fill = group),
              method = 'lm') +
  scale_fill_brewer(palette = 'Set1') +
  scale_colour_brewer(palette = 'Set1') +
  scale_x_log10()
```



We fail to reject the null hypothesis at the $\alpha = .05$ level but do reject the null hypothesis at the $\alpha = .1$ level. If we go by $\alpha = .05$, then we would say that we do not have enough evidence to say that each `group` has its own intercept if we also say that each `group` has its own slope. In particular, we can say that if the null hypothesis is true, the probability of obtaining our data or something that's more extreme than our data compared to the null hypothesis is around 0.0556. Looking at the scatterplot, it appears that it would make more sense to try a model with both terms but without the interaction term.

Additional part

$H_0 : \beta_{02} - \beta_{03} = 14$ and $\beta_{12} + \beta_{13} = .2$

(ere I'm assuming the first index refers to the intercept vs. slope while the second refers to `group`. In that case, we are looking to see if the `group` "other" has an intercept that is 14 units higher than that of the `group` "africa" and that the sum of the slopes for `group`s "other" and "africa" is 0.2 units.

```
# construct L
L <- rbind(c(0, 1, -1, 0, 0, 0),
           c(0, 0, 0, 0, 1, 1))

# construct c
c.vec <- c(14, .2)

# find beta.hat
beta.vec <- ha.model$coefficients

# find the variance of beta.hat
V <- vcov(ha.model)
```

```r
# rows of L
q. <- nrow(L)

# compute the F-statistic
F.stat <-
  t(L %*% beta.vec - c.vec) %*%
  solve(L %*% V %*% t(L)) %*%
  (L %*% beta.vec - c.vec) /
  q.

# find p-value
1 - pf(F.stat, q., ha.model$df.residual)
```

```
          [,1]
[1,] 0.7536125
```

So for sensible values of α, we would fail to reject the null hypothesis as specified above.