STAT-S631

Assignment 4

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```
dp <- loadNamespace('dplyr')
import::from(magrittr, `%>%`, `%<>%`)
library(ggplot2)
theme_set(theme_bw())
```

Question 1

[From ALR 2.16]

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

Part 1

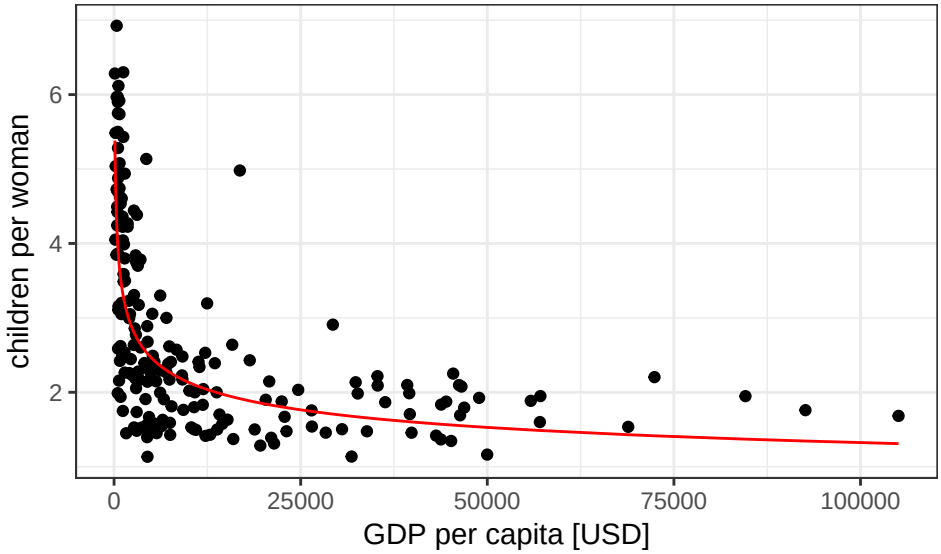
```
fertility.mod <- lm(log(fertility) ~ log(ppgdp), data = un.df)

summary(fertility.mod)
```

```

Call:
lm(formula = log(fertility) ~ log(ppgdp), data = un.df)

Residuals:
     Min       1Q   Median       3Q      Max
-0.79828 -0.21639  0.02669  0.23424  0.95596

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  2.66551    0.12057   22.11   <2e-16 ***
log(ppgdp)  -0.20715    0.01401  -14.79   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.3071 on 197 degrees of freedom
Multiple R-squared:  0.526, Adjusted R-squared:  0.5236
F-statistic: 218.6 on 1 and 197 DF,  p-value: < 2.2e-16
```

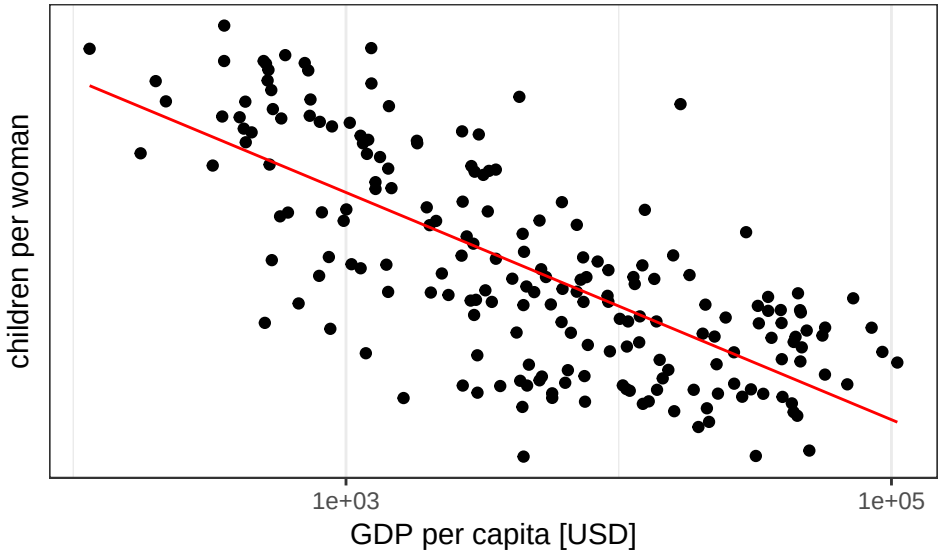
Part 2

```
fert.vs.gdp.plot <- un.df %>%
  dp$mutate(fert.hat =
              exp(fertility.mod$coefficients['(Intercept)']) *
              ppgdp ** fertility.mod$coefficients['log(ppgdp)']) %>%
```

```
  ggplot() +
  geom_point(aes(x = ppgdp, y = fertility)) +
  geom_line(aes(x = ppgdp, y = fert.hat), colour = 'red') +
  labs(x = 'GDP per capita [USD]', y = 'children per woman')

fert.vs.gdp.plot
```




```
fert.vs.gdp.plot + scale_x_log10() + scale_y_log10()
```



Part 3

Using $\alpha = 0.05$:

```
# alternatively, we can just look at summary(fertility.mod)

b1.mean <- fertility.mod$coefficients['log(ppgdp)']
b1.sterr <- summary(fertility.mod)$coefficients['log(ppgdp)', 'Std. Error']
```

```r
b1.tval <- unname(-b1.mean / b1.sterr)
pt(-abs(b1.tval), df = fertility.mod$df.residual)
```

```
[1] 4.531178e-34
```

Here our p-value is much smaller than α.

Part 4

```r
summary(fertility.mod)$r.squared
```

```
[1] 0.525985
```

The R^2 value can be interpreted as the proportion of variance that has been explained by the model. In this case, about half of the variance of Y is accounted for by the linear fit with X.

Part 5

```r
cross.prod.sum <- function(x, y = NULL) {
  # sum of cross product (e.g., SXX, SYY, SXY)

  if (is.null(y)) y <- x
  sum((x - mean(x)) * (y - mean(y)))
}

pred.y <- function(x, model, alpha = .05) {
  # predicts new y given a simple linear model and input
  # also gives confidence interval for a certain alpha value

  # compute t for the alpha C.I. and deg of freedom
  t.alpha <- qt(1 - alpha / 2, model$df.residual)

  # compute expected
  y.mean <- unname(model$coefficients[1] + model$coefficients[2] * x)

  # compute standard error
  x.mean <- mean(model$model[, 2])
  sxx <- cross.prod.sum(model$model[, 2])
  y.se <-
    sigma(model) *
    sqrt(1 + 1 / nrow(model$model) + (x - x.mean) ** 2 / sxx)

  return(list(y = y.mean,
              ci = c(y.mean - y.se * t.alpha, y.mean + y.se * t.alpha)))
}

new.y <- pred.y(log(1000), fertility.mod)
new.y
```

```
$y
[1] 1.234567
```

```
$ci
[1] 0.6258791 1.8432555
```

```
lapply(new.y, exp)
```

```
$y
[1] 3.436891

$ci
[1] 1.869889 6.317070
```

So the 95% prediction interval for Y given $\log X = 1000$ is [1.87, 6.317]

Part 6

```
# lowest fertility
dp$filter(un.df, fertility == min(fertility))$country
```

```
[1] "Bosnia and Herzegovina"
```

```
# highest fertility
dp$filter(un.df, fertility == max(fertility))$country
```

```
[1] "Niger"
```

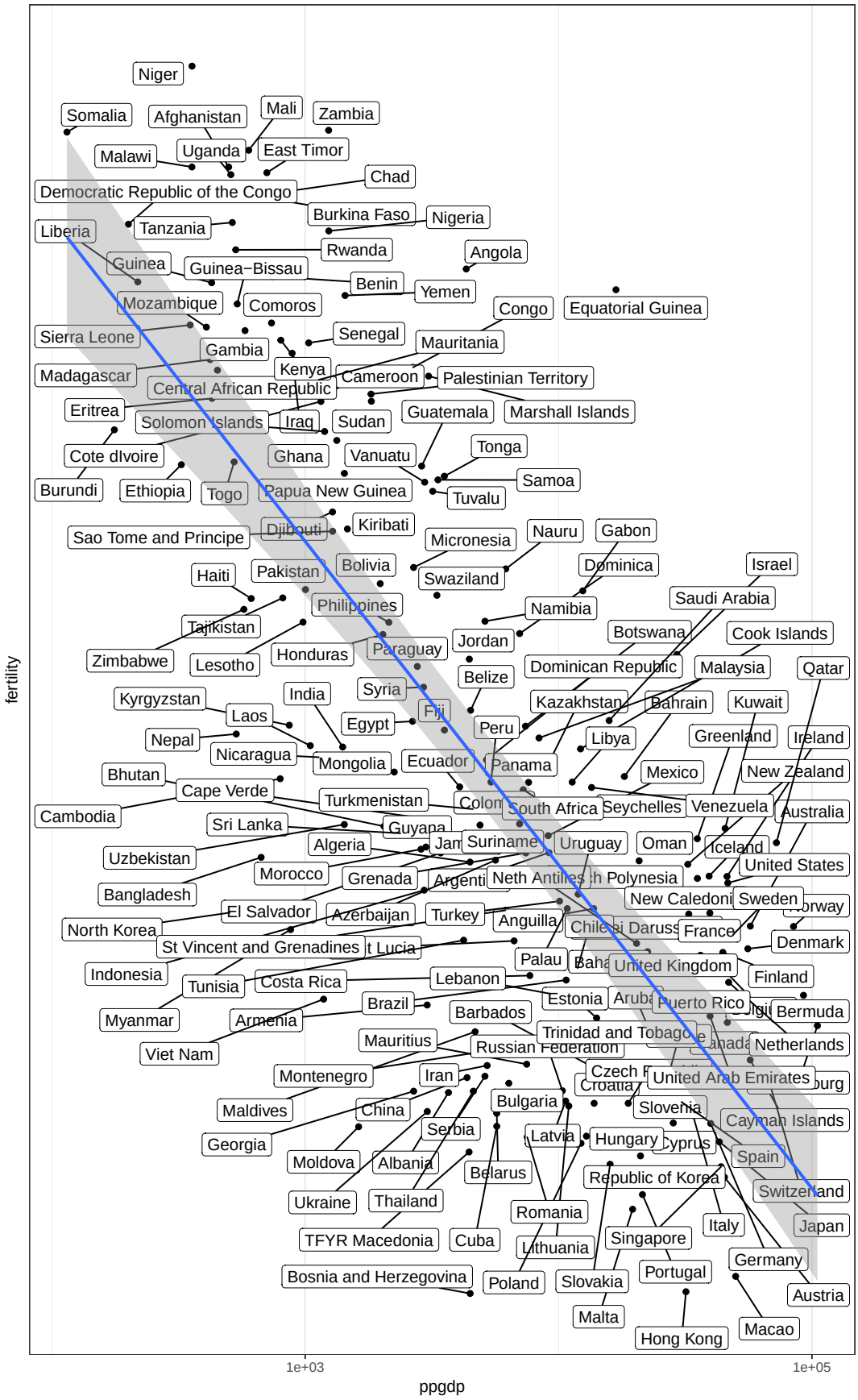
```
# most positive residuals
un.df$country[order(-fertility.mod$residuals)[1:2]]
```

```
[1] "Equatorial Guinea" "Angola"
```

```
# most negative residuals
un.df$country[order(fertility.mod$residuals)[1:2]]
```

```
[1] "Bosnia and Herzegovina" "Moldova"
```

```
ggplot(un.df) +
  geom_point(aes(x = ppgdp, y = fertility)) +
  ggrepel::geom_label_repel(aes(x = ppgdp, y = fertility, label = country)) +
  scale_x_log10() + scale_y_log10() +
  stat_smooth(aes(x = ppgdp, y = fertility), method = 'lm', level = .99)
```

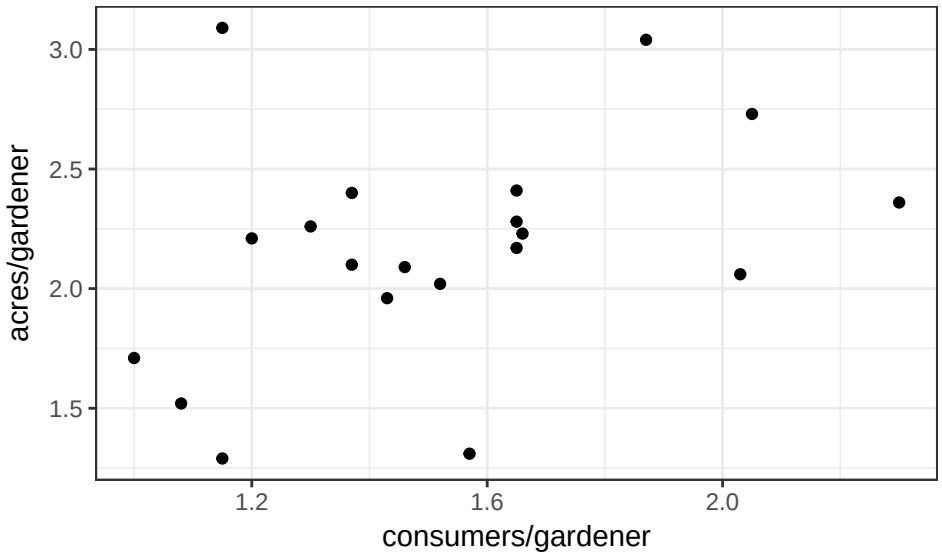

Niger
Somalia
Afghanistan
Mali
Zambia
Malawi
Uganda
East Timor
Chad
Democratic Republic of the Congo
Burkina Faso
Nigeria
Liberia
Tanzania
Rwanda
Angola
Guinea
Guinea−Bissau
Benin
Yemen
Mozambique
Comoros
Congo
Equatorial Guinea
Sierra Leone
Senegal
Mauritania
Gambia
Madagascar
Kenya
Cameroon
Palestinian Territory
Central African Republic
Eritrea
Guatemala
Marshall Islands
Solomon Islands
Iraq
Sudan
Cote dIvoire
Ghana
Vanuatu
Tonga
Burundi
Ethiopia
Togo
Papua New Guinea
Samoa
Tuvalu
Djibouti
Kiribati
Sao Tome and Principe
Micronesia
Nauru
Gabon
Haiti
Pakistan
Bolivia
Swaziland
Dominica
Israel
Philippines
Namibia
Saudi Arabia
Tajikistan
Botswana
Cook Islands
Zimbabwe
Lesotho
Honduras
Paraguay
Jordan
Dominican Republic
Malaysia
Qatar
Belize
Kyrgyzstan
India
Syria
Kazakhstan
Bahrain
Kuwait
Laos
Fiji
Egypt
Peru
Libya
Greenland
Ireland
Nepal
Nicaragua
Mongolia
Ecuador
Panama
Mexico
New Zealand
Bhutan
Cape Verde
Turkmenistan
South Africa
Seychelles
Venezuela
Australia
Cambodia
Sri Lanka
Guyana
Algeria
Suriname
Uruguay
Oman
Iceland
Uzbekistan
United States
Morocco
Grenada
Neth Antilles
Polynesia
Bangladesh
New Caledonia
Sweden
El Salvador
Azerbaijan
Turkey
Anguilla
France
North Korea
St Vincent and Grenadines
Lucia
Denmark
Palau
United Kingdom
Indonesia
Tunisia
Costa Rica
Lebanon
Finland
Estonia
Aruba
Puerto Rico
Myanmar
Armenia
Brazil
Barbados
Bermuda
Trinidad and Tobago
Mauritius
Russian Federation
Netherlands
Viet Nam
Montenegro
Iran
United Arab Emirates
Croatia
Maldives
China
Bulgaria
Slovenia
Cayman Islands
Georgia
Serbia
Latvia
Hungary
Cyprus
Spain
Moldova
Albania
Belarus
Republic of Korea
Switzerland
Ukraine
Thailand
Romania
Italy
Japan
TFYR Macedonia
Cuba
Lithuania
Singapore
Germany
Bosnia and Herzegovina
Poland
Slovakia
Portugal
Austria
Malta
Hong Kong
Macao
fertility
1e+03
1e+05
ppgdp

Question 2

```
sahlins.df <- read.delim('~/dev/stats-hw/stat-s631/Sahlins.txt', sep = ' ')
```

Part a

```
ggplot(sahlins.df) +
  geom_point(aes(x = consumers, y = acres)) +
  labs(x = 'consumers/gardener', y = 'acres/gardener')
```



From the scatterplot, the data do not appear to be particularly linear, although there appears to be a very slight positive correlation. We can compute this:

```
cor(sahlins.df$consumers, sahlins.df$acres)
```

```
[1] 0.3756561
```

Most of the data appear to be clustered in the center with a ring of points surrounding it. One household has an unusually high value for acres per gardener—it's almost 3 times its value for consumers per gardener (~3 vs ~1).

Part b

```
sahlins.mod <- lm(acres ~ consumers, data = sahlins.df)
summary(sahlins.mod)
```

```

Call:
lm(formula = acres ~ consumers, data = sahlins.df)

Residuals:
    Min      1Q  Median      3Q     Max
-0.8763 -0.1873 -0.0211  0.2135  1.1206
```

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   1.3756     0.4684   2.937  0.00881 **
consumers     0.5163     0.3002   1.720  0.10263
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4543 on 18 degrees of freedom
Multiple R-squared:  0.1411,    Adjusted R-squared:  0.0934
F-statistic: 2.957 on 1 and 18 DF,  p-value: 0.1026
```

The results indicate that, if we set the conventional value of $\alpha = .05$, we would fail to reject the null hypothesis that $\beta_1 \neq 0$, implying that there is no significant relationship between acres per gardener and consumers per gardener. However, using the same value of α, we reject the null hypothesis that $\beta_0 = 0$, indicating that each household receives some amount regardless of productivity.

The residual standard error $\hat{\sigma}$ is 0.4543

If we remove the 4^{th} data point:

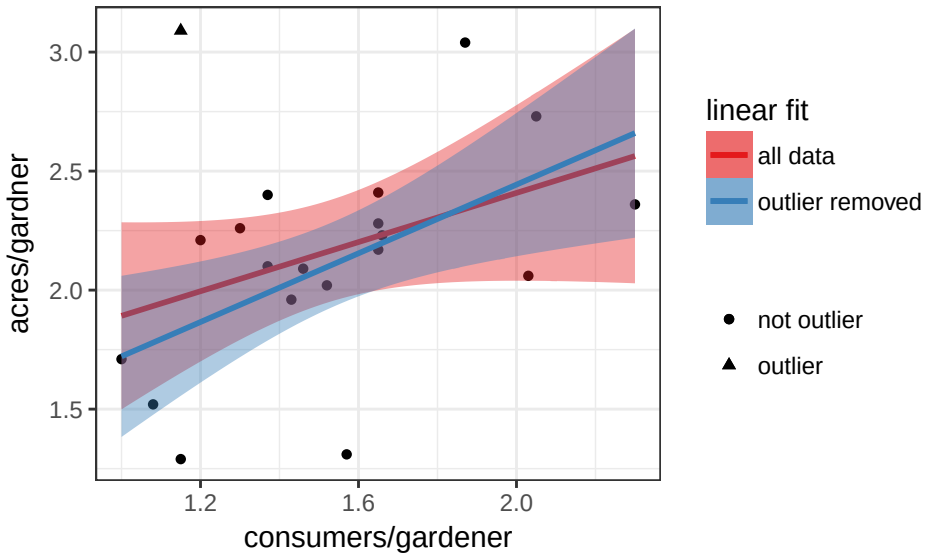
```
sahlins.mod.2 <- lm(acres ~ consumers, data = sahlins.df[-4, ])
summary(sahlins.mod.2)
```

```
Call:
lm(formula = acres ~ consumers, data = sahlins.df[-4, ])

Residuals:
     Min       1Q   Median       3Q      Max
-0.82291 -0.16808  0.03215  0.23505  0.69061

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   1.0000     0.3969   2.519   0.0221 *
consumers     0.7216     0.2514   2.870   0.0106 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.3681 on 17 degrees of freedom
Multiple R-squared:  0.3264,    Adjusted R-squared:  0.2868
F-statistic: 8.238 on 1 and 17 DF,  p-value: 0.01061
```

We would reject the null hypothesis for both β_0 and β_1. This would imply that each household receives some base amount but also can work for additional resources. This is a different conclusion than before, when we used all the data.

```
ggplot() +
  geom_point(data = sahlins.df[-4, ],
             aes(x = consumers, y = acres, shape = 'not outlier')) +
  labs(x = 'consumers/gardener',
       y = 'acres/gardner',
       colour = 'linear fit', fill = 'linear fit',
       shape = NULL) +
  geom_point(data = sahlins.df[4, ],
             aes(x = consumers, y = acres, shape = 'outlier')) +
  stat_smooth(data = sahlins.df,
              aes(x = consumers, y = acres,
```

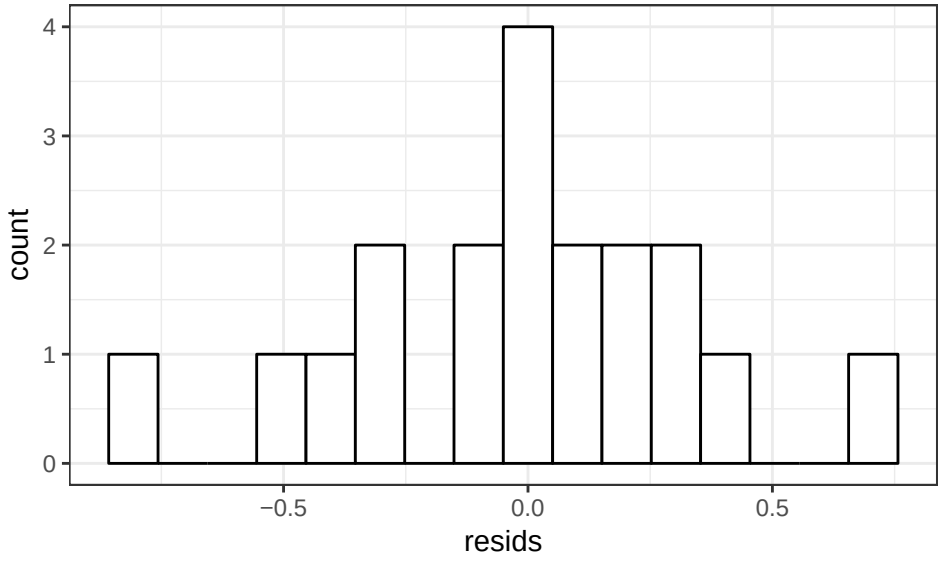
```
                colour = 'all data', fill = 'all data'),
            method = 'lm') +
  stat_smooth(data = sahlins.df[-4, ],
            aes(x = consumers, y = acres,
                colour = 'outlier removed', fill = 'outlier removed'),
            method = 'lm') +
  scale_colour_brewer(palette = 'Set1') +
  scale_fill_brewer(palette = 'Set1')
```



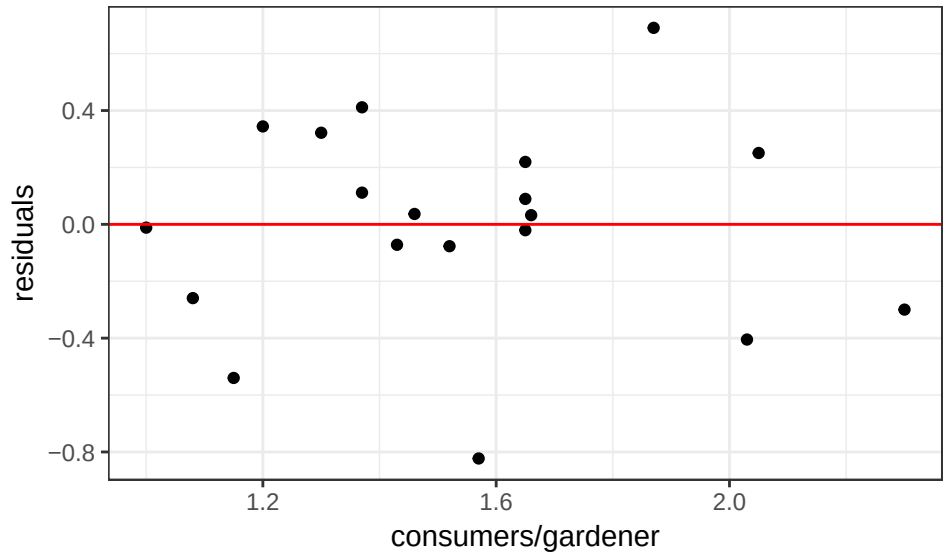
We can say that the first model is not a good fit since we failed to reject the null hypothesis that $\beta_1 \neq 0$.

For the second model (with the 4^{th} data point removed), we can check the residuals:

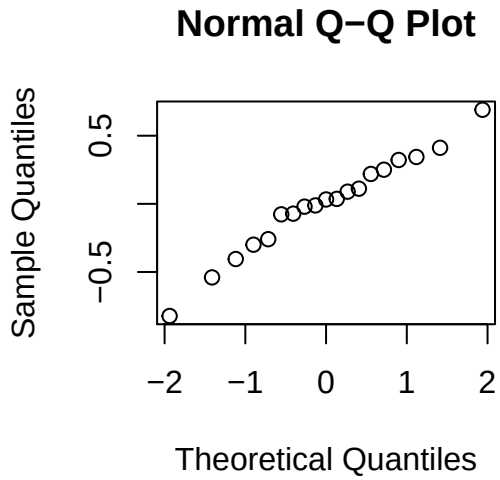
```
sahlins.outlier.removed.df <- sahlins.df[-4, ] %>%
  dp$mutate(resids = sahlins.mod.2$residuals)

ggplot(sahlins.outlier.removed.df) +
  geom_histogram(aes(x = resids),
                 fill = 'white', colour = 'black', bins = 16)
```



```
ggplot(sahlins.outlier.removed.df) +
  geom_point(aes(x = consumers,
                 y = resids)) +
  geom_hline(yintercept = 0, colour = 'red') +
  labs(x = 'consumers/gardener', y = 'residuals')
```




```
qqnorm(sahlins.outlier.removed.df$resids)
```



Here we can see that the residuals do not depend on the input variable and appear approximately normally distributed around 0, so the assumptions of the linear model hold. As for the strength of the predictions, $\hat{\sigma} \approx 0.3681$, so on average the model is ~0.4 acres/gardener off the true value.

Part c

For the first model

If we set $\alpha = .05$ and the null hypotheses as $\beta_0 \leq 0$ and $\beta_1 \leq 0$:

```
# set alpha
alpha <- .05
```

```r
# --- t-test --- #

mod1.b0.tval <-
  sahlins.mod$coefficients['(Intercept)'] /
  summary(sahlins.mod)$coefficients['(Intercept)', 'Std. Error']
mod1.b1.tval <-
  sahlins.mod$coefficients['consumers'] /
  summary(sahlins.mod)$coefficients['consumers', 'Std. Error']

# t-statistics
c(mod1.b0.tval, mod1.b1.tval)
```

```
(Intercept)   consumers
   2.936872    1.719728
```

```r
# p-values
1 - pt(c(mod1.b0.tval, mod1.b1.tval),
       df = sahlins.mod.2$df.residual)
```

```
(Intercept)   consumers
0.004606439 0.051816787
```

Here we see that the p-value for β_0 is less than our chosen α while the p-value for β_1 is greater. So we would reject the first null hypothesis while failing to reject the second.

Using the same α, we can compute the confidence intervals:

```r
t.alpha <- qt(1 - alpha / 2, sahlins.mod$df.residual)

mod1.b0.ci <-
  c(-t.alpha, t.alpha) *
summary(sahlins.mod)$coefficients['(Intercept)', 'Std. Error'] +
  sahlins.mod$coefficients['(Intercept)']

mod1.b1.ci <-
  c(-t.alpha, t.alpha) *
summary(sahlins.mod)$coefficients['consumers', 'Std. Error'] +
  sahlins.mod$coefficients['consumers']

# confidence intervals
print(mod1.b0.ci)
```

```
[1] 0.3915628 2.3597263
```

```r
print(mod1.b1.ci)
```

```
[1] -0.1144471  1.1470872
```

The C.I. for β_0 does not contain 0 while the C.I. for β_1 does, which is consistent with our hypothesis tests.

For the second model

Using the same α for the second model with the same null hypotheses:

For the confidence intervals:

```r
# set alpha
alpha <- .05

# --- t-test --- #

mod2.b0.tval <-
  sahlins.mod.2$coefficients['(Intercept)'] /
  summary(sahlins.mod.2)$coefficients['(Intercept)', 'Std. Error']
mod2.b1.tval <-
  sahlins.mod.2$coefficients['consumers'] /
  summary(sahlins.mod.2)$coefficients['consumers', 'Std. Error']

# t-statistics
c(mod2.b0.tval, mod2.b1.tval)
```

```
(Intercept)   consumers
   2.519375    2.870143
```

```r
# p-values
1 - pt(c(mod2.b0.tval, mod2.b1.tval),
       df = sahlins.mod.2$df.residual)
```

```
(Intercept)   consumers
0.011027340 0.005306328
```

... and find the confidence intervals for the same α

```r
t.alpha <- qt(1 - alpha / 2, sahlins.mod.2$df.residual)

mod2.b0.ci <-
  c(-t.alpha, t.alpha) *
summary(sahlins.mod.2)$coefficients['(Intercept)', 'Std. Error'] +
  sahlins.mod.2$coefficients['(Intercept)']
mod2.b1.ci <-
  c(-t.alpha, t.alpha) *
summary(sahlins.mod.2)$coefficients['consumers', 'Std. Error'] +
  sahlins.mod.2$coefficients['consumers']

print(mod2.b0.ci)
```

```
[1] 0.1625647 1.8374433
```

```r
print(mod2.b1.ci)
```

```
[1] 0.191157 1.252031
```

Here we reject the null hypothesis for both β_0 and β_1 since both p-values are below our chosen α. Neither confidence interval contains 0, which is consistent with the results of the hypothesis tests. However, since it's a one-sided t-test, this is not necessarily true for all cases.

Part d

For prediction (the first question):

```r
pred.y(1.5, sahlins.mod, alpha = .02)
```

```
$y
```

```
[1] 2.150125

$ci
[1] 0.961766 3.338483
```

```r
# alternatively
predict(sahlins.mod,
        newdata = data.frame(consumers = 1.5),
        interval = 'predict',
        level = .98)
```

```
       fit      lwr      upr
1 2.150125 0.961766 3.338483
```

For our estimate of the mean (the second question):

```r
mean.y <- function(x, model, alpha = .05) {
  # predicts mean y given a simple linear model and input
  # also gives confidence interval for a certain alpha value

  # compute t for the alpha C.I. and deg of freedom
  t.alpha <- qt(1 - alpha / 2, model$df.residual)

  # compute expected
  y.mean <- unname(model$coefficients[1] + model$coefficients[2] * x)

  # compute standard error
  x.mean <- mean(model$model[, 2])
  sxx <- cross.prod.sum(model$model[, 2])
  y.se <-
    sigma(model) *
    sqrt(1 / nrow(model$model) + (x - x.mean) ** 2 / sxx)

  return(list(y = y.mean,
              ci = c(y.mean - y.se * t.alpha, y.mean + y.se * t.alpha)))
}

mean.y(1.5, sahlins.mod, alpha = .02)
```

```
$y
[1] 2.150125

$ci
[1] 1.890234 2.410016
```

```r
# alternatively
predict(sahlins.mod,
        newdata = data.frame(consumers = 1.5),
        interval = 'confidence',
        level = .98)
```

```
       fit      lwr      upr
1 2.150125 1.890234 2.410016
```

The prediction interval (first value) is what we expect a new value to have given that $x = 1.5$. On the other hand, the confidence interval (second value) is what we expect the mean of all y would be given that $x = 1.5$. The standard error for each case is different.