STAT-S631

Assignment 4

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```r
dp <- loadNamespace('dplyr')
import::from(magrittr, `%>%`, `%<>%`)
library(ggplot2)
theme_set(theme_bw())
```
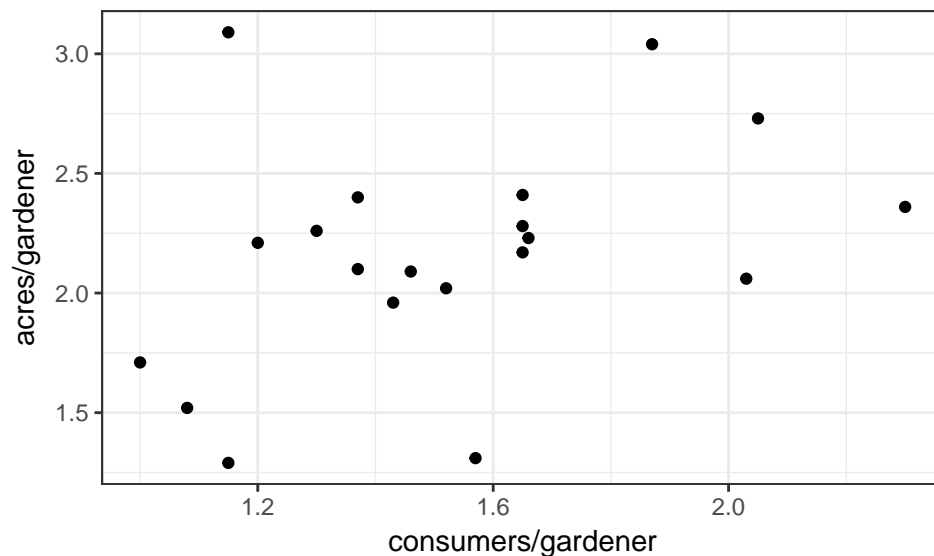
Question 1

Question 2

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

Part a

```r
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:

```r
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 4th 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')
```
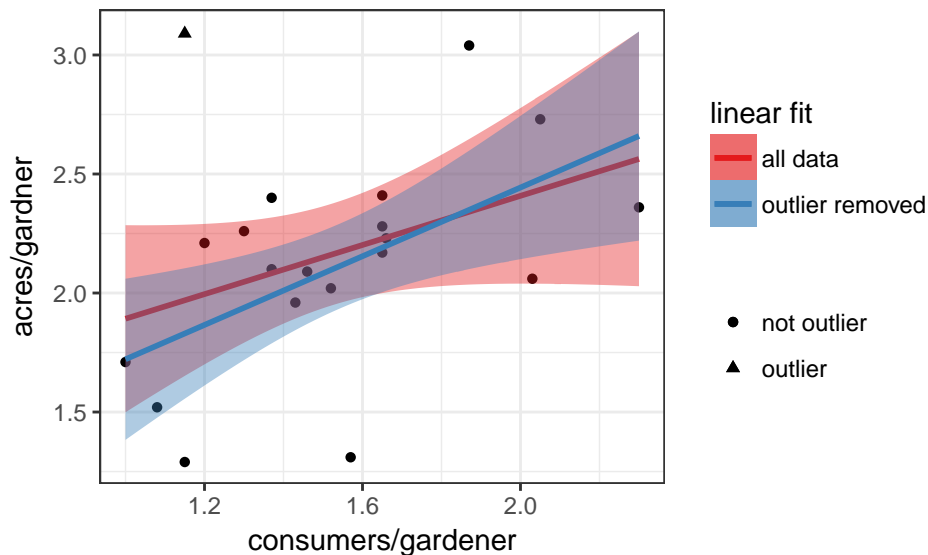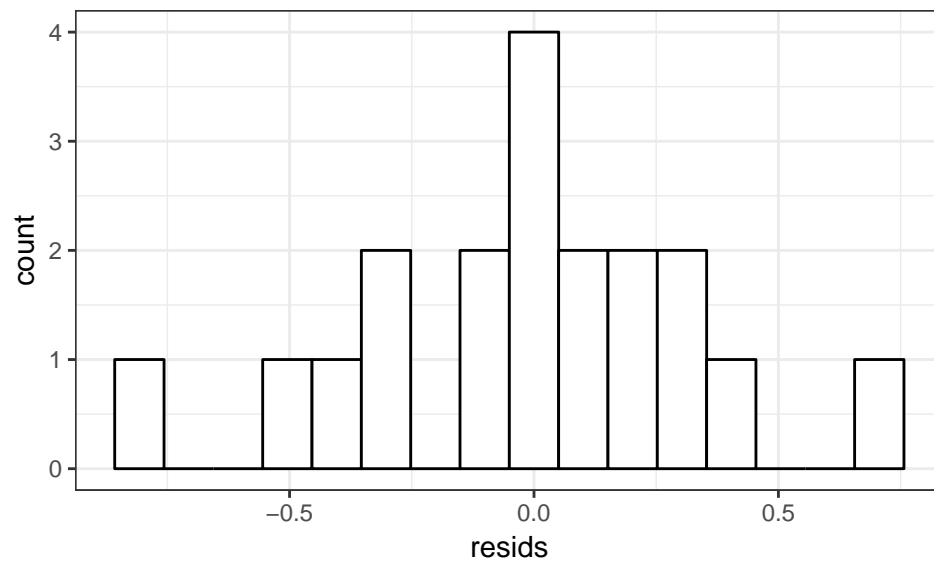

We can say that the first model is not a good fit since we failed to reject the null hypothesis that $\beta_1 \neq 0$.

For the second model (with the 4th 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)
```
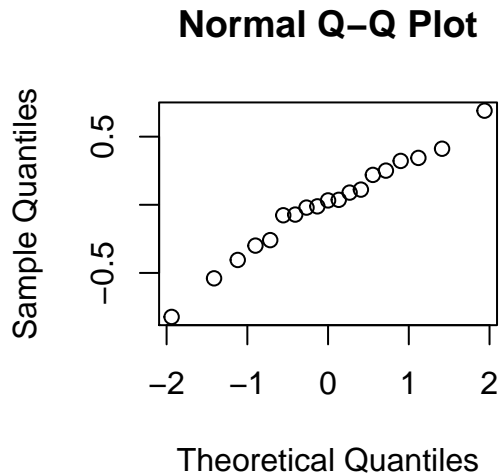
```
ggplot(sahlins.outlier.removed.df) +
  geom_point(aes(x = consumers,
                 y = resids)) +
  geom_hline(yintercept = 0, colour = 'red') +
  labs(x = 'consumers/gardener', y = 'residuals')
```
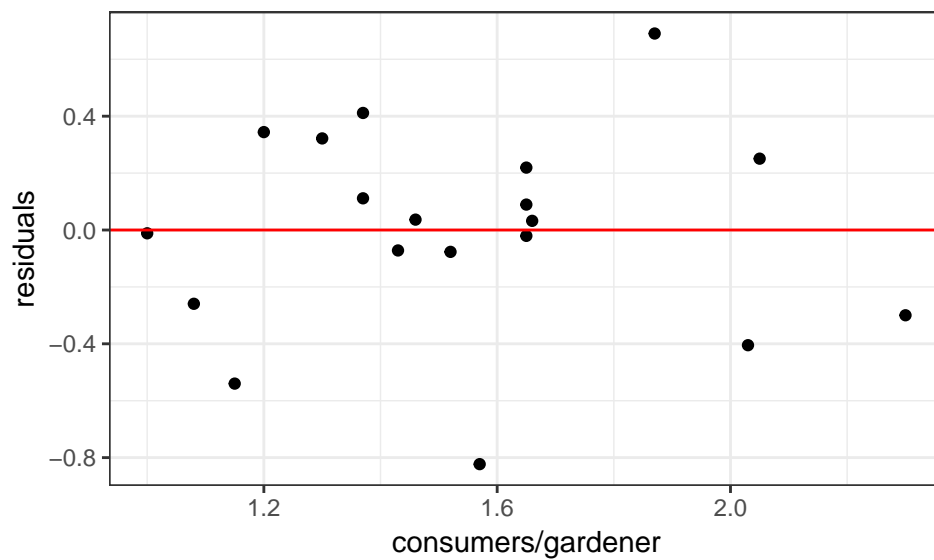


```
qqnorm(sahlins.outlier.removed.df$resids)
```

Normal Q–Q Plot

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

```
summary(sahlins.mod)$coefficients
```

```
              Estimate Std. Error  t value      Pr(>|t|)
(Intercept) 1.3756445  0.4684047 2.936872 0.008813794
consumers   0.5163201  0.3002335 1.719728 0.102629261
```

If we set $\alpha = .05$ and the null hypotheses as $\beta_0 = 0$ and $\beta_1 = 0$, then we would reject the $\beta_0 = 0$ and fail to reject $\beta_1 = 0$ (these are from the `summary` command from part (b)).

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

```
alpha <- .05
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']

print(mod1.b0.ci)
```

```
[1] 0.3915628 2.3597263
```

```
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, we reject the null hypothesis for both $\beta_0 = 0$ and $\beta_1 = 0$ (from the `summary` command from part (b)).

For the confidence intervals:

```
alpha <- .05
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
```

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

```
[1] 0.191157 1.252031
```

The C.I.s for neither β_0 nor β_1 contain 0, which is consistent with the results of our hypothesis tests.

Part d

If we assume that the model is valid:

```
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 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)))
}

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

```
$y
[1] 2.150125
```

```
$ci
[1] 1.890234 2.410016
```

```
# 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 confidence interval does not indicate that there is a 98% probability that the true mean is contained within the interval. Instead, there is a 98% probability that the interval captures the true mean (i.e., the 98% probability is on the interval, not the true value).