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Examination for Statistics in Linguistics

1.

First we should attach and examine the data

```
> library(languageR)
> attach(lexdec)
> str(lexdec)
```

A)

Here we can see, and deduce, the scale of measurement:

Correct : Nominal, with two levels.

Length : Interval

Class : Nominal

Family Size : Ratio

B)

Length does modify correctness significantly, as seen using a two sample t-test

I chose a t-test because it seemed like the best way to model a DV when the IV was continuous

```
> t.test(Length~Correct)
```

Welch Two Sample t-test

data: Length by Correct

t = -2.4254, df = 69.593, p-value = 0.01789

alternative hypothesis: true difference in means is not equal to 0

95 percent confidence interval:

-1.01428434 -0.09885145

sample estimates:

mean in group correct mean in group incorrect

5.889586

6.446154

Here is the standard deviation and variation for Length:

```
> sd(Length)
```

[1] 1.857397

```
> var(Length)
```

[1] 3.449924

Class is also a significant influence

Here, a two-sample test would not work, but a one sample test can be used for two predictors that are both nominal

```
> t.test(xtabs(~Correct+Class))
```

One Sample t-test

data: xtabs(~Correct + Class)

t = 1.8553, df = 3, p-value = 0.1606

alternative hypothesis: true mean is not equal to 0

95 percent confidence interval:

-296.6951 1126.1951

sample estimates:

mean of x

414.75

Here is the xtab() for that

```
> xtabs(~Correct+Class)
```

Class

Correct animal plant

correct 884 710

```
incorrect      40      25

## FamilySize is another indication
## I used a Two-sample t-test as it can be used to measure a dependent variable when the
independent variable is continuous, as mentioend above
> t.test(FamilySize~Correct)

Welch Two Sample t-test

data:  FamilySize by Correct
t = 3.1321, df = 70.855, p-value = 0.002523
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 0.1116560 0.5029038
sample estimates:
 mean in group correct mean in group incorrect
           0.7148457           0.4075658

## Some more readouts for this
> sd(FamilySize)
[1] 0.8709066
> var(FamilySize)
[1] 0.7584784

c)
## Provided with this file are the three graphs.
> barplot(xtabs(~Correct+Length), xlab="Length", ylab="Amount correct")
# For lc_1, Correct and Length, I went with a barplot, as this clearly shows the proportion
correct or incorrect overall. It doesn't show this very clearly in comparison for different
lengths, however, although this can be ascertained by comparing the differences visually
with a small amount of concentration.

> barplot(xtabs(~Correct+Class), horiz = FALSE, xlab = "Class", ylab = "Correctness")
# For lc_2, Correct and Class, I went with a barplot, as well, as this clearly shows the
nature of the xtab table.

> plot(FamilySize~Correct, xlab="Correctness", ylab="Family Size with Outliers")
# For lc_3, Family Size and Correctness, I went with a simple boxplot, as this shows the
data fairly well while showing outliers and deviation, which are helpful in understanding
it.

2)
a)
## It is a good idea to look at the the structure first, to make sure that we are dealing
with the same data formats with similar scales of measurement. After checking this using
str(), it is useful to look at the nature of the three Nominal predictors we'll be looking
at, using xtabs() again, or using subsets.

> str(lexdec)
> xtabs(~Sex+Correct+NativeLanguage)

, , NativeLanguage = English

    Correct
Sex correct incorrect
F         533      20
M         387       8

, , NativeLanguage = Other

    Correct
```

Sex	correct	incorrect
F	526	27
M	148	10

Since none of these raise a flag (for instance, no values in one column, or the wrong sort of scale or data), we can go ahead with the linear model.

b)

The Null hypothesis is that neither the sex or native language of the participant, nor whether they were correct or not, should influence the reaction times. The alternative hypothesis is that one, two, or all of these factors do influence reaction times - meaning, for instance, that females may react faster, or males faster. All alternative hypotheses must be ruled out for the null hypothesis to be validated.

c)

```
> calculate <- lm(RT~Correct)
> calculate
```

```
Call:
lm(formula = RT ~ Correct)
```

```
Coefficients:
(Intercept)  Correctincorrect
      6.3839           0.0307
```

```
> anova(calculate)
Analysis of Variance Table
```

```
Response: RT
      Df Sum Sq Mean Sq F value Pr(>F)
Correct    1  0.059  0.058875   1.0094  0.3152
Residuals 1657 96.647  0.058326
> calculate <- lm(RT~Sex)
> calculate
```

```
Call:
lm(formula = RT ~ Sex)
```

```
Coefficients:
(Intercept)      SexM
      6.37658      0.02554
```

```
> anova(calculate)
Analysis of Variance Table
```

```
Response: RT
      Df Sum Sq Mean Sq F value Pr(>F)
Sex      1  0.241  0.240532   4.1317  0.04225 *
Residuals 1657 96.465  0.058217
```

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

```
> calculate <- lm(RT~NativeLanguage)
> calculate
```

```
Call:
lm(formula = RT ~ NativeLanguage)
```

```
Coefficients:
(Intercept) NativeLanguageOther
      6.3183           0.1558
```

```
> anova(calculate)
Analysis of Variance Table
```

Response: RT

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
NativeLanguage	1	9.865	9.8647	188.23	< 2.2e-16 ***
Residuals	1657	86.841	0.0524		

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

Here we can see that correctness did not influence the reaction times of the participants, while their sex was mildly significant, and the Native Language of the participant was very statistically significant.

d)

A Type I error here would be to say that Correctness was a significant influence for reaction times, as it discards the null hypothesis although there is no justification for this. A Type II error here would be to say that the Sex and Native Language of the participants did not influence the reaction times - this would mean keeping the null hypothesis although the alternative hypothesis have been shown to be more probably, and the null hypothesis does not stand.