STA 445 Assignment 5

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Exercise 1

The infmort data set from the package faraway gives the infant mortality rate for a variety of countries. The information is relatively out of date (from 1970s?), but will be fun to graph. Visualize the data using by creating scatter plots of mortality vs income while faceting using region and setting color by oil export status. Utilize a \log_{10} transformation for both mortality and income axes. This can be done either by doing the transformation inside the aes() command or by utilizing the scale_x_log10() or scale_y_log10() layers. The critical difference is if the scales are on the original vs log transformed scale. Experiment with both and see which you prefer.

a) The `rownames()` of the table gives the country names and you should create a new column that contains the country names. *`rownames`

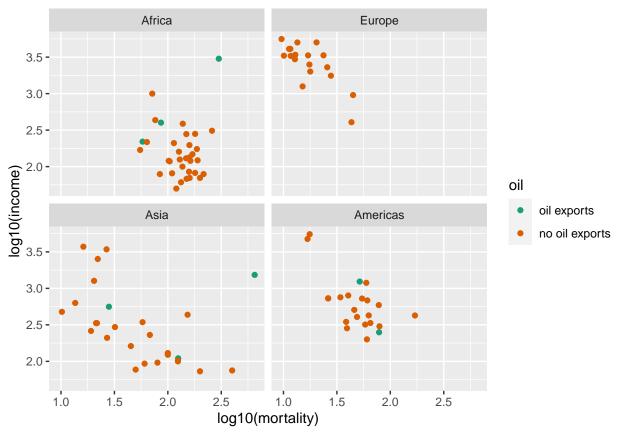
```
data(infmort, package = "faraway")
infmort1 <- infmort %>% mutate( country = rownames(infmort) )
head(infmort1)
```

```
##
                         region income mortality
                                                              oil
## Australia
                                   3426
                           Asia
                                             26.7 no oil exports
## Austria
                         Europe
                                   3350
                                             23.7 no oil exports
## Belgium
                         Europe
                                   3346
                                             17.0 no oil exports
## Canada
                       Americas
                                   4751
                                             16.8 no oil exports
## Denmark
                         Europe
                                   5029
                                             13.5 no oil exports
## Finland
                         Europe
                                   3312
                                             10.1 no oil exports
##
                                    country
## Australia
                       Australia
## Austria
                       Austria
## Belgium
                       Belgium
## Canada
                       Canada
## Denmark
                       Denmark
## Finland
                       Finland
```

b) Create scatter plots with the `log10()` transformation inside the `aes()` command.

```
P1 <- ggplot(infmort1, aes(x=log10(mortality), y=log10(income))) +
geom_point(aes(color=oil)) +
facet_wrap( ~region )+
scale_color_brewer(palette='Dark2')
P1
```

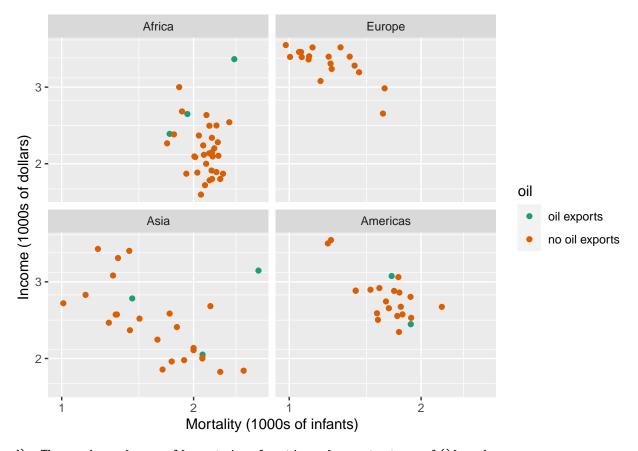
Warning: Removed 4 rows containing missing values (`geom_point()`).



c) Create the scatter plots using the `scale_x_log10()` and `scale_y_log10()`. Set the major and minor breaks to be useful and aesthetically pleasing. Comment on which version you find easier to read.

I personally think that the version without the 'scale_x_log10()' is easier to read.

Warning: Removed 4 rows containing missing values (`geom_point()`).



d) The package `ggrepel` contains functions `geom_text_repel()` and `geom_label_repel()` that mimic the basic `geom_text()` and `geom_label()` functions in `ggplot2`, but work to make sure the labels don't overlap. Select 10-15 countries to label and do so using the `geom_text_repel()` function.

```
## Warning: Removed 4 rows containing missing values (`geom_point()`).
```

Warning: ggrepel: 16 unlabeled data points (too many overlaps). Consider

Warning: ggrepel: 15 unlabeled data points (too many overlaps). Consider

^{##} Warning: Removed 4 rows containing missing values (`geom_text_repel()`).

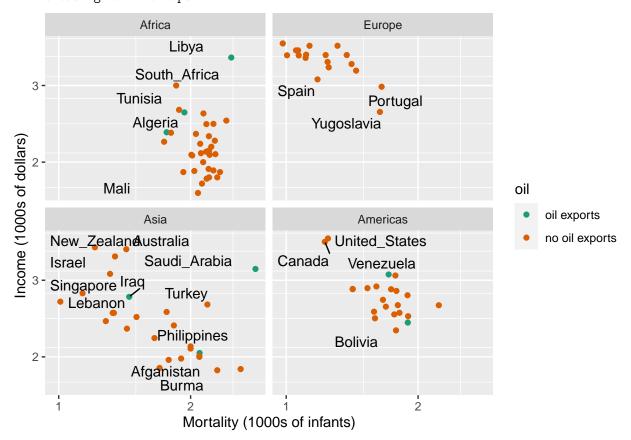
^{##} Warning: ggrepel: 29 unlabeled data points (too many overlaps). Consider

^{##} increasing max.overlaps

^{##} increasing max.overlaps

```
## increasing max.overlaps
```

Warning: ggrepel: 18 unlabeled data points (too many overlaps). Consider
increasing max.overlaps



Exercise 2

Using the datasets::trees data, complete the following:

a) Create a regression model for \$y=\$ `Volume` as a function of \$x=\$ `Height`.

```
data(trees)
model <- lm( Volume ~ Height, data=trees)</pre>
```

b) Using the `summary` command, get the y-intercept and slope of the regression line.

summary(model)

```
##
## Call:
## lm(formula = Volume ~ Height, data = trees)
##
## Residuals:
## Min 1Q Median 3Q Max
## -21.274 -9.894 -2.894 12.068 29.852
##
## Coefficients:
```

```
Estimate Std. Error t value Pr(>|t|)
## (Intercept) -87.1236
                           29.2731 -2.976 0.005835 **
                                   4.021 0.000378 ***
## Height
                 1.5433
                            0.3839
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 13.4 on 29 degrees of freedom
## Multiple R-squared: 0.3579, Adjusted R-squared: 0.3358
## F-statistic: 16.16 on 1 and 29 DF, p-value: 0.0003784
trees <- trees %>% mutate(fit=fitted(model))
c) Using `ggplot2`, create a scatter plot of Volume vs Height.
P4 <- ggplot(trees, aes(x=Height, y=Volume)) +
  geom_point()
P4
  80 -
  60 -
Volume
  20 -
```

d) Create a nice white filled rectangle to add text information to using by adding the following annotation layer.

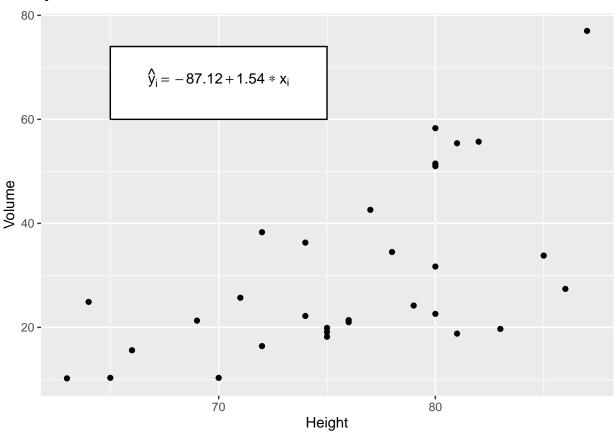
Height

80

e) Add some annotation text to write the equation of the line $\hat{y}_i = -87.12 + 1.54 * x_i$ in the text area.

70

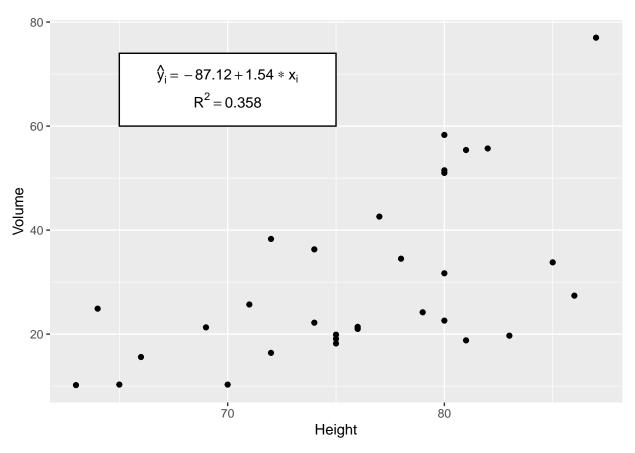
Warning in is.na(x): is.na() applied to non-(list or vector) of type
'expression'



f) Add annotation to add $R^2 = 0.358$

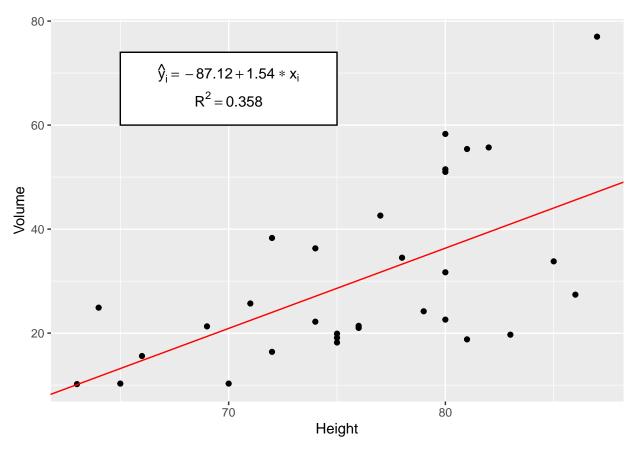
Warning in is.na(x): is.na() applied to non-(list or vector) of type
'expression'
Warning in is.na(x): is.na() applied to non-(list or vector) of type

'expression'



g) Add the regression line in red. The most convenient layer function to uses is `geom_abline()`. It appears that the `annotate` doesn't work with `geom_abline()` so you'll have to call it directly.

Warning in is.na(x): is.na() applied to non-(list or vector) of type
'expression'
Warning in is.na(x): is.na() applied to non-(list or vector) of type
'expression'



I wanted to compare the two graphs. The first one uses geom_abline and the second uses geom_line with the column of fitted values that I mutated

