SIMPLE LINEAR CORRELATION AND REGRESSION

Correlation

Correlation is used to test for a relationship between two numerical variables or two ranked (ordinal) variables. In this tutorial, we assume the relationship (if any) is linear.

To demonstrate, we will begin with a data set called "cats" from the "MASS" library, which contains information on various anatomical features of house cats...

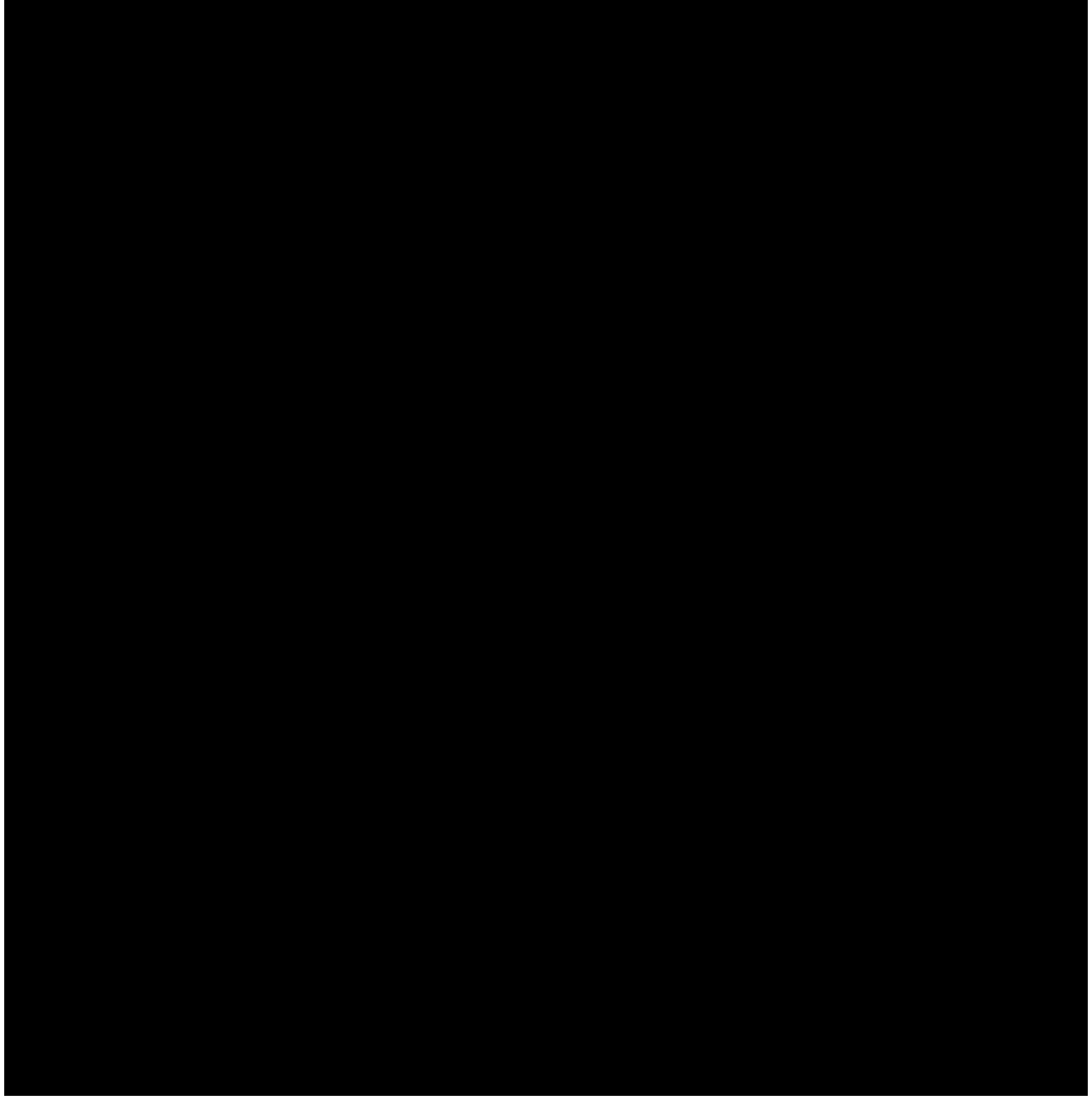
```
> library("MASS")
> data(cats)
> str(cats)
'data.frame':   144 obs. of  3 variables:
 $ Sex: Factor w/ 2 levels "F","M": 1 1 1 1 1 1 1 1 1 1 ...
 $ Bwt: num  2 2 2 2.1 2.1 2.1 2.1 2.1 2.1 2.1 ...
 $ Hwt: num  7 7.4 9.5 7.2 7.3 7.6 8.1 8.2 8.3 8.5 ...
> summary(cats)
 Sex         Bwt             Hwt       
 F:47   Min.   :2.000   Min.   : 6.30  
 M:97   1st Qu.:2.300   1st Qu.: 8.95  
        Median :2.700   Median :10.10  
        Mean   :2.724   Mean   :10.63  
        3rd Qu.:3.025   3rd Qu.:12.12  
        Max.   :3.900   Max.   :20.50  
```

"Bwt" is the body weight in kilograms, "Hwt" is the heart weight in grams, and "Sex" should be obvious. There are no missing values in any of the variables, so we are ready to begin by looking at a scatterplot...

```
> with(cats, plot(Bwt, Hwt))
> title(main="Heart Weight (g) vs. Body Weight (kg)\nof Domestic Cats")
```

The plot( ) function gives a scatterplot whenever you feed it two numerical variables. The first variable listed will be plotted on the horizontal axis. A formula interface can also be used, in which case the response variable should come before the tilde and the variable to be plotted on the horizontal axis after...

```
> with(cats, plot(Hwt ~ Bwt))
```



The scatterplot shows a fairly strong and reasonably linear relationship between the two variables. A Pearson product-moment correlation coefficient can be calculated using the cor( ) function...

```
> with(cats, cor(Bwt, Hwt))
[1] 0.8041274
> with(cats, cor(Bwt, Hwt))^2
[1] 0.6466209
```

Pearson's r = .804 indicates a strong positive relationship. To get the coefficient of determination, I just hit the up arrow key to recall the previous command to the command line and added "^2" on the end to square it. If a test of significance is required, this is also easily enough done using the cor.test( ) function. The function does a t-test, a 95% confidence interval for the population correlation (use "conf.level=" to change the confidence level), and reports the value of the sample statistic. The alternative hypothesis can be set to "two.sided" (the default), "less", or "greater"...

```
> with(cats, cor.test(Bwt, Hwt))

        Pearson's product-moment correlation

data:  Bwt and Hwt
t = 16.1194, df = 142, p-value < 2.2e-16
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.7375682 0.8552122
sample estimates:
      cor
0.8041274
```

Since we would expect a positive correlation here, we might have set the alternative to "greater"...

```
> with(cats, cor.test(Bwt, Hwt, alternative="greater", conf.level=.8))

        Pearson's product-moment correlation

data:  Bwt and Hwt
t = 16.1194, df = 142, p-value < 2.2e-16
alternative hypothesis: true correlation is greater than 0
80 percent confidence interval:
 0.7776141 1.0000000
sample estimates:
      cor
0.8041274
```

There is also a formula interface for cor.test( ), but it's tricky. Both variables should be listed after the tilde...

```
> with(cats, cor.test(~ Bwt + Hwt))    # output not shown
```

Using the formula interface makes it easy to subset the data by rows of the data frame...

```
> with(cats, cor.test(~ Bwt + Hwt, subset=(Sex=="F")))

        Pearson's product-moment correlation

data:  Bwt and Hwt
```

```
t = 4.2152, df = 45, p-value = 0.0001186
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.2890452 0.7106399
sample estimates:
      cor
0.5320497
```

The "subset=" option is not available unless you use the formula interface.

For a more revealing scatterplot, try this...

```
> with(cats, plot(Bwt, Hwt, type="n", xlab="Body Weight in kg",
+                 ylab="Heart Weight in g",
+                 main="Heart Weight vs. Body Weight of Cats"))
> with(cats,points(Bwt[Sex=="F"],Hwt[Sex=="F"],pch=16,col="red"))
> with(cats,points(Bwt[Sex=="M"],Hwt[Sex=="M"],pch=17,col="blue"))
>
```

Output not shown. ("Aw, man! I'm not gonna type all that!" Here's a trick for you Windows users out there. In your browser window, copy the above lines command prompts and all, including that last empty prompt. Then go into the R Console window, pull down the Edit menu, and choose "Paste commands only". Sometimes that works, and sometimes it doesn't!)

Correlation and Covariance Matrices

If a data frame (or other table-like object) contains more than two numerical variables, then the cor( ) function will result in a correlation matrix...

```
> rm(cats)                                # if you haven't already
> data(cement)                            # also in the MASS library
> str(cement)
'data.frame':   13 obs. of  5 variables:
 $ x1: int  7 1 11 11 7 11 3 1 2 21 ...
 $ x2: int  26 29 56 31 52 55 71 31 54 47 ...
 $ x3: int  6 15 8 8 6 9 17 22 18 4 ...
 $ x4: int  60 52 20 47 33 22 6 44 22 26 ...
 $ y : num   78.5  74.3 104.3  87.6  95.9 ...
> cor(cement)
           x1         x2          x3          x4          y
x1  1.0000000  0.2285795 -0.82413376 -0.24544511  0.7307175
x2  0.2285795  1.0000000 -0.13924238 -0.97295500  0.8162526
x3 -0.8241338 -0.1392424  1.00000000  0.02953700 -0.5346707
x4 -0.2454451 -0.9729550  0.02953700  1.00000000 -0.8213050
y   0.7307175  0.8162526 -0.53467068 -0.82130504  1.0000000
```

If you prefer a covariance matrix, use cov( )...

```
> cov(cement)
          x1         x2         x3          x4          y
x1  34.60256   20.92308 -31.051282  -24.166667   64.66346
x2  20.92308  242.14103 -13.878205 -253.416667  191.07949
x3 -31.05128  -13.87821  41.025641    3.166667  -51.51923
x4 -24.16667 -253.41667   3.166667  280.166667 -206.80833
y   64.66346  191.07949 -51.519231 -206.808333  226.31359
```

If you have a covariance matrix and want a correlation matrix...

```
> cov.matr = cov(cement)
> cov2cor(cov.matr)
          x1        x2          x3          x4         y
x1 1.0000000 0.2285795 -0.82413376 -0.24544511 0.7307175
x2 0.2285795 1.0000000 -0.13924238 -0.97295500 0.8162526
```

```
x3 -0.8241338 -0.1392424  1.00000000  0.02953700 -0.5346707
x4 -0.2454451 -0.9729550  0.02953700  1.00000000 -0.8213050
y   0.7307175  0.8162526 -0.53467068 -0.82130504  1.0000000
```

If you want a visual representation of the correlation matrix (i.e., a scatterplot matrix)...

```
> pairs(cement)
```

The command `plot(cement)` would also have done the same thing.

Correlations for Ranked Data

If the data are ordinal rather than true numerical measures, or have been converted to ranks to fix some problem with distribution or curvilinearity, then R can calculate a Spearman rho coefficient or a Kendall tau coefficient. Suppose we have two athletic coaches ranking players by skill...

```
> ls()
[1] "cement"   "cov.matr"
> rm(cement, cov.matr)                   # clean up first
> coach1 = c(1,2,3,4,5,6,7,8,9,10)
> coach2 = c(4,8,1,5,9,2,10,7,3,6)
> cor(coach1, coach2, method="spearman")
[1] 0.1272727
> cor.test(coach1, coach2, method="spearman")

        Spearman's rank correlation rho

data:  coach1 and coach2
S = 144, p-value = 0.72
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
```

```
0.1272727

> cor(coach1, coach2, method="kendall")
[1] 0.1111111
> cor.test(coach1, coach2, method="kendall")

        Kendall's rank correlation tau

data:  coach1 and coach2
T = 25, p-value = 0.7275
alternative hypothesis: true tau is not equal to 0
sample estimates:
      tau
0.1111111

> ls()
[1] "coach1" "coach2"
> rm(coach1,coach2)                    # clean up again
```

I will not get into the debate over which of these rank correlations is better! You can also use the "alternative=" option here to set a directional test.

Simple Linear Regression

There is little question that R was written with regression analysis in mind! The number of functions and add-on packages devoted to regression analysis of one kind or another is staggering! We will only scratch the surface in this tutorial.

Let's go back to our kitty cat data...

```
> data(cats)                           # still in the "MASS" library
```

Simple (as well as multiple) linear regression is done using the lm( ) function. This function requires a formula interface, and for simple regression the formula takes the form DV ~ IV, which should be read something like "DV as a function of IV" or "DV as modeled by IV" or "DV as predicted by IV", etc. It's critical to remember that the DV or response variable must come before the tilde and IV or explanatory variables after. Getting the regression equation for our "cats" data is simple enough...

```
> attach(cats)                         ### because I'm getting lazy!
> lm(Hwt ~ Bwt)

Call:
lm(formula = Hwt ~ Bwt)

Coefficients:
(Intercept)          Bwt
    -0.3567       4.0341
```

So the regression equation is: Hwt = 4.0341 (Bwt) - 0.3567. A better idea is to store the output into a data object and then to extract information from that with various extractor functions...

```
> lm.out = lm(Hwt ~ Bwt)               # name the output anything you like
> lm.out                               # gives the default output

Call:
lm(formula = Hwt ~ Bwt)

Coefficients:
(Intercept)          Bwt
    -0.3567       4.0341

> summary(lm.out)                      # gives a lot more info
```

```
Call:
lm(formula = Hwt ~ Bwt)

Residuals:
     Min       1Q   Median       3Q      Max
-3.56937 -0.96341 -0.09212  1.04255  5.12382

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -0.3567     0.6923  -0.515    0.607
Bwt           4.0341     0.2503  16.119   <2e-16 ***
---
Signif. codes:  0 �***� 0.001 �**� 0.01 �*� 0.05 �.� 0.1 � � 1

Residual standard error: 1.452 on 142 degrees of freedom
Multiple R-squared: 0.6466,     Adjusted R-squared: 0.6441
F-statistic: 259.8 on 1 and 142 DF,  p-value: < 2.2e-16
```

Personally, I don't like those significance stars, so I'm going to turn them off...

```
> options(show.signif.stars=F)
> anova(lm.out)                         # shows an ANOVA table
Analysis of Variance Table

Response: Hwt
           Df Sum Sq Mean Sq F value    Pr(>F)
Bwt         1 548.09  548.09  259.83 < 2.2e-16
Residuals 142 299.53    2.11
```

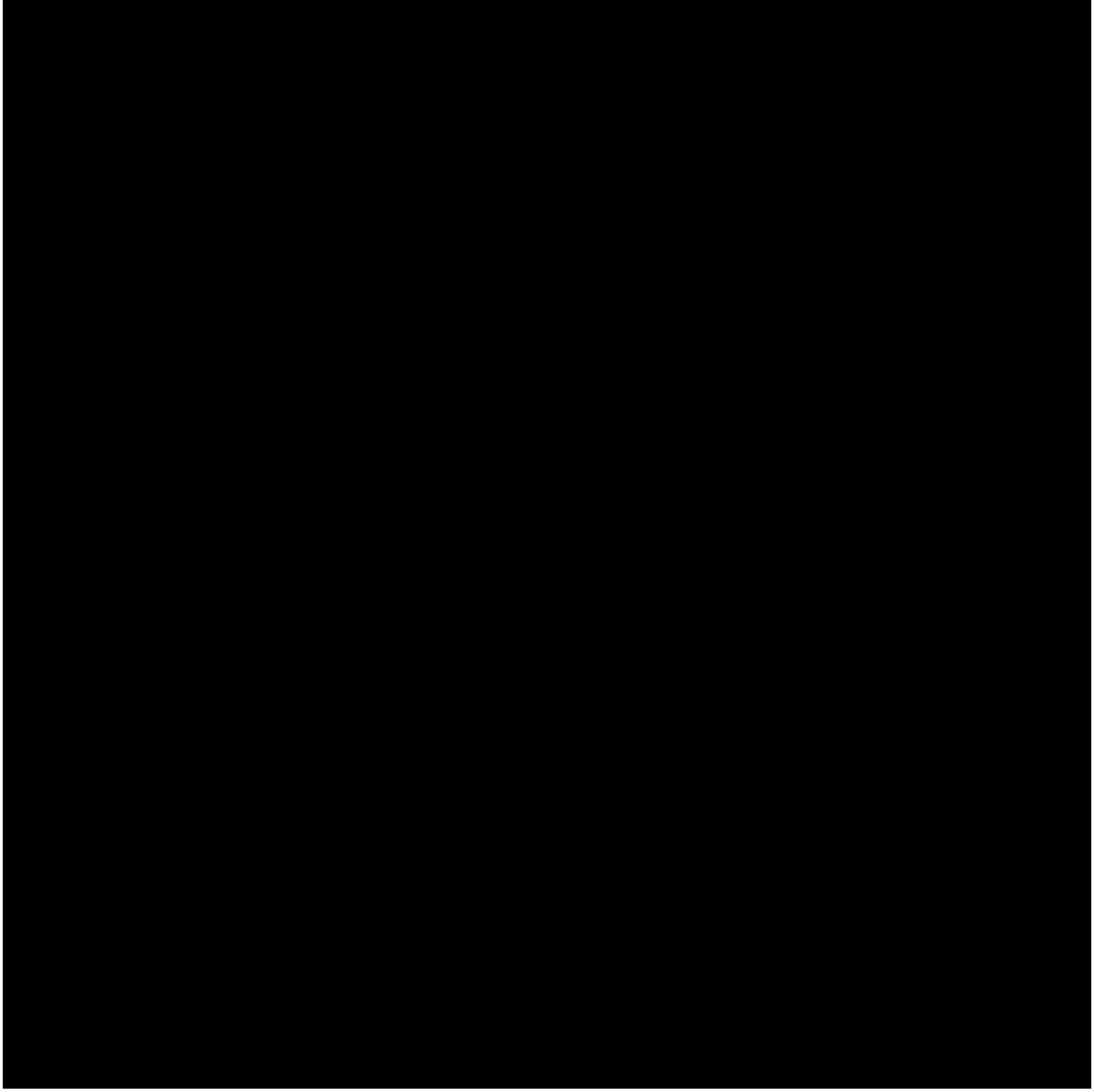
With the output saved in a data object, plotting the regression line on a scatterplot is a cinch...

```
> plot(Hwt ~ Bwt, main="Kitty Cat Plot")
> abline(lm.out, col="red")
```

And I'll make the regression line red just because I can!

Various regression diagnostics are also available. These will be discussed more completely in future tutorials, but for now, a graphic display of how good the model fit is can be achieved as follows...

```
> par(mfrow=c(2,2))
> plot(lm.out)
```



The first of these commands sets the parameters of the graphics device. If your graphics output window was closed, you probably noticed it opening when this command was issued. Specifically, the command partitioned the graphics window into four parts, two rows by two columns, so four graphs could be plotted in one window. The graphics window will retain this structure until you either close it, in which case it will return to its default next time it opens, or you reset it with `par(mfrow=c(1,1))`. If you do not partition the graphics window first, then each diagnostic plot will print out in a separate window. R will give you a cryptic message, "Waiting to confirm page change...", in the console before each graph is displayed. This means hit the Enter key to display the next graph. The second command, plot( ), then does the actual plotting.

The first plot is a standard residual plot showing residuals against fitted values. Points that tend towards being outliers are labeled. If any pattern is apparent in the points on this plot, then the linear model may not be the appropriate one. The second plot is a normal quantile plot of the residuals. We like to see our residuals normally distributed. Don't we? The last plot shows residuals vs. leverage. Labeled points on this plot represent cases we may want to investigate as possibly having undue influence on the regression relationship. Case 144 is one perhaps worth taking a look at...

```
> cats[144,]
    Sex Bwt  Hwt
144   M 3.9 20.5
> lm.out$fitted[144]
     144
```

```
15.37618
> lm.out$residuals[144]
     144
5.123818
```

This cat had the largest body weight and the largest heart weight in the data set. (See the summary table at the top of this tutorial.) The observed value of "Hwt" was 20.5g, but the fitted value was only 15.4g, giving a residual of 5.1g. The residual standard error (from the model output above) was 1.452, so converting this to a standardized residual gives 5.124/1.452=3.53, a substantial value to say the least! A commonly used measure of influence is Cook's Distance, which can be visualized for all the cases in the model as follows...

```
> par(mfrow=c(1,1))                    # if you haven't already done this
> plot(cooks.distance(lm.out))
```

As we can see, case 144 tops the charts.

There are a number of ways to procede. One is to look at the regression coefficients without the outlying point in the model...

```
> lm.without144 = lm(Hwt ~ Bwt, subset=(Hwt<20.5))
> lm.without144

Call:
lm(formula = Hwt ~ Bwt, subset = (Hwt < 20.5))

Coefficients:
(Intercept)          Bwt
      0.118        3.846
```

Another is to use a procedure that is robust in the face of outlying points...

```
> rlm(Hwt ~ Bwt)
Call:
rlm(formula = Hwt ~ Bwt)
Converged in 5 iterations

Coefficients:
(Intercept)         Bwt
 -0.1361777   3.9380535

Degrees of freedom: 144 total; 142 residual
Scale estimate: 1.52
```

See the help page on rlm( ) for the details of what this function does.

Lowess

Lowess stands for locally weighted scatterplot smoothing. It is a nonparametric method for drawing a smooth curve through a scatterplot. There are at least two ways to produce such a plot in R...

```
> plot(Hwt ~ Bwt)
> lines(lowess(Hwt ~ Bwt), col="red")
>
> ### or...
>
> scatter.smooth(Hwt ~ Bwt)
> detach(cats)                                 # Don't forget!
```

The output is not shown here, but the plots indicate we were on the right track with our linear model.

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