On the equivalence of t-tests, anovas, and linear models

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**These are some notes for practice and discussion in Stirling Coding Club, which follow up on a recent meeting in the Stats Discussion Group at the University of Stirling on a** [**blog post by Jonas Kristoffer Lindeløv**](https://lindeloev.github.io/tests-as-linear/)**. What follows is further demonstration and discussion on linear models in statistics. The goal here is to create a simulated data set, then use it show a bit more of the logic underlying linear models in statistics.**

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# Making up data for heights of two plant species

Let’s first make up some data and put them into a data frame. To make everything a bit more concrete, let’s just imagine that we’re sampling the heights of individual plants from two different species. Hence, we’ll have one categorical independent variable (species), and one continuous dependent variable (plant height). The data frame below includes plant height (height; since this is a made up example, the units are not important, but let’s make them mm) and species ID (species\_ID). The first 10 plants are shown below (each plant is a unique row).

|  |  |
| --- | --- |
| height | species\_ID |
| 141.57 | species\_1 |
| 140.95 | species\_2 |
| 225.08 | species\_2 |
| 78.21 | species\_1 |
| 135.05 | species\_1 |
| 106.37 | species\_1 |
| 201.17 | species\_2 |
| 111.86 | species\_2 |
| 155.09 | species\_1 |
| 158.97 | species\_1 |

Using the linear modelling approach [described by Lindeløv](https://lindeloev.github.io/tests-as-linear/), the above data qualify as a simple regression with a discrete x (species\_ID). Assuming that both species have equal variances in height, we can use a two-sample t-test in R to test the null hypothesis that the mean height of species\_1 is equal to the mean height of species\_2. To use t.test, we can create two separate vectors of heights, the first one called species\_1.

species\_1 <- plant\_data$height[plant\_data$species\_ID == "species\_1"];

Below shows species\_1, which includes the heights of all 50 plants whose species\_ID == "species\_1".

## [1] 141.57 78.21 135.05 106.37 155.09 158.97 98.74 119.35 132.59 183.91  
## [11] 125.06 166.91 192.33 164.05 157.53 151.93 149.96 96.83 125.61 155.79  
## [21] 129.46 121.61 200.78 124.17 83.49 161.32 112.43 154.01 159.64 132.95  
## [31] 78.63 163.91 136.89 201.30 154.68 73.22 186.34 183.14 176.96 173.22  
## [41] 203.50 207.56 195.52 101.00 141.62 139.18 141.81 133.41 149.90 147.91

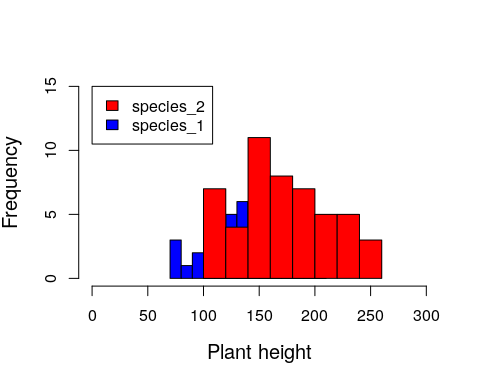
We can make a separate vector for the remaining heights for the plants of species 2 in the same way.

species\_2 <- plant\_data$height[plant\_data$species\_ID == "species\_2"];

These 50 plant heights are shown below.

## [1] 140.95 225.08 201.17 111.86 163.71 140.78 223.33 104.54 124.17 146.85  
## [11] 114.66 180.78 109.55 172.37 118.16 168.97 216.68 178.49 231.91 164.77  
## [21] 168.08 108.33 156.10 181.51 254.07 151.02 126.20 123.97 144.49 148.99  
## [31] 179.51 144.68 155.49 191.83 245.82 203.16 192.53 257.47 215.49 198.19  
## [41] 233.77 195.16 180.95 142.14 176.27 205.52 123.11 141.77 107.96 223.80

It might help to plot a histogram of the two plant species heights side by side.



Visualising the histogram above, we already have a sense of whether or not knowing species ID is useful for predicting plant height.

# Equivalence of t.test versus a linear model lm in R

Using our two vectors species\_1 and species\_2, we can run a t-test as noted [by Lindeløv](https://lindeloev.github.io/tests-as-linear/).

t.test(species\_1, species\_2, var.equal = TRUE);

##   
## Two Sample t-test  
##   
## data: species\_1 and species\_2  
## t = -3.2557, df = 98, p-value = 0.001554  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -40.262677 -9.767323  
## sample estimates:  
## mean of x mean of y   
## 145.3082 170.3232

Reading the output above, we can get the t-statistic t = -3.2557. Given the null hypothesis that the mean height of species\_1 equals the mean height of species\_2, the probability of getting such an exterme difference between the two observed means is 0.00155 (i.e., the p-value).

But this is not the only way that we can run a t-test. As [Lindeløv](https://lindeloev.github.io/tests-as-linear/) points out, the linear model structure works just fine as well. The variables used below in lm are from the plant\_data table shown above, with one column named height and another named species\_ID.

lmod1 <- lm(height ~ 1 + species\_ID, data = plant\_data);  
summary(lmod1);

##   
## Call:  
## lm(formula = height ~ 1 + species\_ID, data = plant\_data)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -72.088 -25.864 0.347 25.594 87.147   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 145.308 5.433 26.745 < 2e-16 \*\*\*  
## species\_IDspecies\_2 25.015 7.684 3.256 0.00155 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 38.42 on 98 degrees of freedom  
## Multiple R-squared: 0.0976, Adjusted R-squared: 0.08839   
## F-statistic: 10.6 on 1 and 98 DF, p-value: 0.001554

Note how the information in the above output matches that from the t.test function. In using lm, we get a t value in the coefficients table of 3.256, and a p-value of 0.00155. We can also see the mean values for species\_1 and species\_2, though in slightly different forms. From the t.test function, we see an estimated mean of 145.3082 for species 1 and 170.3232 for species 2 (this is at the bottom of the output, under mean of x mean of y). In the lm, we get the same information in a slightly different form. The estimate in the coefficients table for the intercept is listed as 145.308; this is the value of the mean height for species 1.

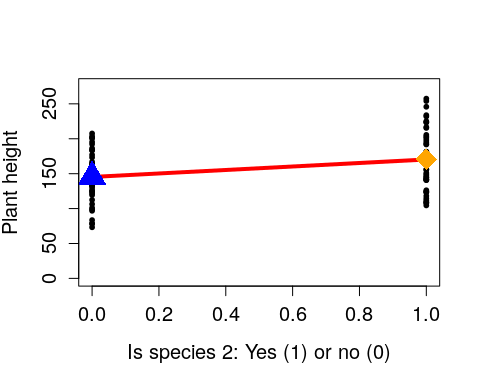
Where is the value for the mean height of species 2? We get the value for species 2 by adding the estimate of its effect on the line below, such that 145.308 + 25.015 = 170.323. To understand why, think back to that lm structure, height ~ 1 + species\_ID. Recall from [Lindeløv](https://lindeloev.github.io/tests-as-linear/) how this is a short-hand for the familiar equation . In this equation, is the dependent variable plant height, while the value is what we might call a dummy variable. It indicates whether or not the plant in question is a member of species 2. If yes, then . If no, then .

Now think about the coefficients and . Because whenever species\_ID = species\_1, the predicted plant height for species 1 is simply , which simplifies to . This is why our Estimate of the (Intercept) row in the summary(lmod1) output equals the mean plant height of species 1. Next, because whenever species\_ID = species\_2, the predicted plant height for species 2 is , which simplifies to . This is why our Estimate of the species\_IDspecies\_2 row in the summary(lmod1) equals 25.015. It is the amount that needs to be added to the prediction for species 1 to get the prediction for species 2.

To further clarify the concept, we can re-write that original two column table from above, but instead of having species\_1 or species\_2 for the species\_ID column, we can replace it with a column called is\_species\_2. A value of is\_species\_2 = 0 means the plant is species 1, and a value of is\_species\_2 = 1 means the plant is species 2.

|  |  |
| --- | --- |
| height | is\_species\_2 |
| 141.57 | 0 |
| 140.95 | 1 |
| 225.08 | 1 |
| 78.21 | 0 |
| 135.05 | 0 |
| 106.37 | 0 |
| 201.17 | 1 |
| 111.86 | 1 |
| 155.09 | 0 |
| 158.97 | 0 |

If we now plot is\_species\_2 on the x-axis, and height on the y-axis, we reproduce those same icons as in [Lindeløv](https://lindeloev.github.io/tests-as-linear/).



The blue triangle shows the mean height of species 1 (i.e., the intercept of the linear model, ), and the orange diamond shows the mean height of species 2 (i.e., ). Since the distance between these two points is one, the slope of the line (rise over run) is identical to the difference between the mean species heights. Hence the reason for why , which we often think about only as the ‘slope’ is also the difference between means.

# Further equivalence of t.test, lm, and now aov

Analysis of variance (ANOVA) tests the null hypothesis that the mean values of groups are all equal. We often think of this being used for group numbers of three or more, but it is worth showing that ANOVA is equivalent to a t-test when the number of groups is two. A one-way ANOVA can be run using the aov function in R. Below, I do this for the same plant\_data table as used for t.test and lm.

aov\_1 <- aov(height ~ species\_ID, data = plant\_data);  
summary(aov\_1);

## Df Sum Sq Mean Sq F value Pr(>F)   
## species\_ID 1 15644 15644 10.6 0.00155 \*\*  
## Residuals 98 144639 1476   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Note the F value and the Pr(>F) (i.e., the p-value) in the table above. The value 10.599 matches the F-statistic produced from using lm in the previous section, and 0.0016 is the same p-value that we calculated earlier. The methods are effectively the same.

# Testing for a difference between means using randomisation

An alternative approach to the t.test, lm, and aov options above is to use randomisation. Randomisation approaches make fewer assumptions about the data, and I believe that they are often more intuitive. For a full discussion of randomisation techniques, see my [previous notes for Stirling Coding Club](https://stirlingcodingclub.github.io/randomisation/randomisation_notes.html), which go into much more detail on the underlying logic of randomisation, bootstrap, and Monte Carlo methods. For now, I just want to illustrate how a randomisation approach can get be used for the same null hypothesis testing as shown in the previous methods above. Let us look back at the first ten rows of the data set that I made up again.

|  |  |
| --- | --- |
| height | species\_ID |
| 141.57 | species\_1 |
| 140.95 | species\_2 |
| 225.08 | species\_2 |
| 78.21 | species\_1 |
| 135.05 | species\_1 |
| 106.37 | species\_1 |
| 201.17 | species\_2 |
| 111.86 | species\_2 |
| 155.09 | species\_1 |
| 158.97 | species\_1 |

When we use null hypothesis testing, what we are asking is this:

If the true difference between group means is the same (null hypothesis), then what is the probability of sampling a difference between groups as or more extreme than the difference that we observe in the data?

We might phrase the null hypothesis slightly differently:

If the true difference between group means is random with respect to group identity (null hypothesis), then what is the probability of sampling a difference between groups as or more extreme than the difference that we observe in the data?

In other words, what if we were to randomly re-shuffle species IDs, so that we *knew* any difference between mean species heights was attributable to chance? The logic behind randomisation here is to re-shuffle group identity (species), then see what the difference is between groups after shuffling (i.e., mean species 1 height minus mean species 2 height). After doing this many times, we can thereby build a distribution for differences between randomly generated groups. We can do this with a bit of code below. First let’s get the actual difference between mean heights of species 1 and species 2, i.e., species[1] - species[2]. We can use the tapply function in R to do this easily.

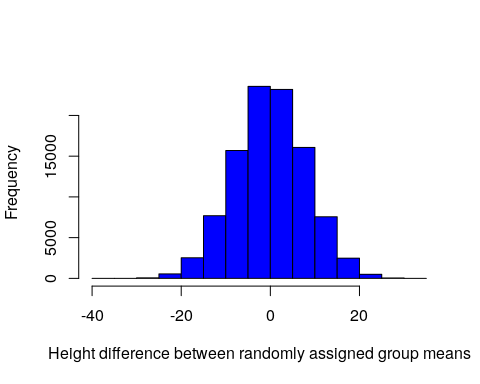
species <- tapply(X = plant\_data$height, INDEX = plant\_data$species\_ID,   
 FUN = mean);  
height\_diffs <- as.numeric( species[1] - species[2] );  
print(height\_diffs);

## [1] -25.015

Using a [for loop](https://stirlingcodingclub.github.io/using_loops/loop_notes.html) in R, we can shuffle species\_ID, then build a distribution showing what the difference between species means would be just due to random chance.

null\_diff <- NULL; # Place where the random diffs will go  
iterations <- 99999; # Number of reshuffles  
iter <- 1; # Start with the first  
while(iter < iterations){  
 new\_species\_ID <- sample(x = plant\_data$species\_ID,   
 size = length(plant\_data$species\_ID));  
 new\_species <- tapply(X = plant\_data$height, INDEX = new\_species\_ID,  
 FUN = mean);  
 new\_diffs <- as.numeric( new\_species[1] - new\_species[2] );  
 null\_diff[iter] <- new\_diffs;  
 iter <- iter + 1;  
}

Each element in the vector null\_diff is now a difference between the mean of species 1 and the mean of species 2, given a random shuffling of species IDs. We can look at the distribution of null\_diff in the histogram below.



As expected, most differences between randomly assigned species height means are somewhere around zero. Our actual value of -25.015, which we have calculated several times now, is quite low, and on the extreme tail of the distribution above. What then is the probability of getting a value this extreme if species ID has nothing to do with plant height? The answer is just the total number of values equal or more extreme to the one we observed (-25.015), divided by the total number of values that we tried (99999 + 1 = 100000; the plus one is for the actual value).

p\_value <- sum(abs(null\_diff) > abs(height\_diffs)) / 100000;

We get p\_value = 0.0013. Notice how close this value is to the p-value that we obtained using t.test, lm, and aov. This is because the concept is the same; given that the null hypothesis is true, what is the probability of getting a value as or more extreme than the one actually observed?

# What about when there are more than two groups?

I want to briefly touch on what happens when there are more than two groups; for example, if we had three species instead of two. Of course, a t-test is now not applicable, but we can still use the linear model and ANOVA approaches. Let’s make up another data set, but with three species this time.

|  |  |
| --- | --- |
| height | species\_ID |
| 226.55 | species\_3 |
| 86.62 | species\_3 |
| 138.53 | species\_3 |
| 122.81 | species\_1 |
| 141.97 | species\_3 |
| 174.99 | species\_2 |
| 51.00 | species\_1 |
| 171.79 | species\_3 |
| 217.78 | species\_2 |
| 154.05 | species\_1 |

As already mentioned, t.test will not work. But we can run both lm and aov with the exact same code as before with three groups. I will show aov first.

aov\_2 <- aov(height ~ species\_ID, data = plant\_data);  
summary(aov\_2);

## Df Sum Sq Mean Sq F value Pr(>F)   
## species\_ID 2 23276 11638 6.755 0.00179 \*\*  
## Residuals 97 167110 1723   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

The F-statistic calculated above is 6.755, and the p-value is 0.0018. The p-value in this case tests the null hypothesis that all groups (i.e., species) have the same mean values (i.e., heights). We can now use the lm function to run the same analysis with three groups.

lmod2 <- lm(height ~ 1 + species\_ID, data = plant\_data);  
summary(lmod2);

##   
## Call:  
## lm(formula = height ~ 1 + species\_ID, data = plant\_data)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -90.505 -30.255 -2.489 30.432 113.495   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 141.265 7.118 19.845 <2e-16 \*\*\*  
## species\_IDspecies\_2 34.420 10.143 3.394 0.001 \*\*   
## species\_IDspecies\_3 4.487 10.143 0.442 0.659   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 41.51 on 97 degrees of freedom  
## Multiple R-squared: 0.1223, Adjusted R-squared: 0.1042   
## F-statistic: 6.755 on 2 and 97 DF, p-value: 0.001792

We can find the F-statistic and p-value at the very bottom of the output, and note that they are the same as reported by aov. But look at what is going on with the Estimate values in the table (ignore the Pr(>|t|) values in the table). There are now three rows. Again, we can think back to the equation predicting plant height , but now we need another coefficient. The equation can now be expressed as, . Note that subscripts have been added to . This is because we now have two dummy variables; is the plant species 1 (if so, and ), species 2 ( and ), or species 3 ( and )? With these dummy variables, we can now predict the height of species 1,

The above reduces to , as with our two species case. The height of species 2 can be predicted as below,

The above reduces to , again, as with the two species case. Finally, we can use the linear model to predict the height of species 3 plants,

The above reduces to . Let’s use the tapply function to see what the mean values of each species are in the new data set.

tapply(X = plant\_data$height, INDEX = plant\_data$species\_ID, FUN = mean);

## species\_1 species\_2 species\_3   
## 141.2653 175.6855 145.7521

Now look at that output summary(lmod2) again. Notice that the estimate of the intercept (Intercept) is the same as the mean height of species 1 (141.2652941). Similarly, add the intercept () to the coefficient in the second row, species\_IDspecies\_2 (i.e., ); this value equals the mean estimate for species 2. Finally, add the intercept to the coefficient in the third row species\_IDspecies\_3 (i.e., ); this value equals the mean estimate for species 3. Once again, we see how the linear model is equivalent to the ANOVA.

# Okay, but what’s really happening with three groups?

How does this *really* work? We have given R a single column with three different categorical values (species) and somehow ended up with an intercept and two regression coefficients. How can we understand this more clearly? Think back to the table [from earlier](#bintab) where we had a column for is\_species\_2 with a simple zero or one. We can do the same, but with a new column, to include the ID of species 3.

|  |  |  |
| --- | --- | --- |
| height | is\_species\_2 | is\_species\_3 |
| 226.55 | 0 | 1 |
| 86.62 | 0 | 1 |
| 138.53 | 0 | 1 |
| 122.81 | 0 | 0 |
| 141.97 | 0 | 1 |
| 174.99 | 1 | 0 |
| 51.00 | 0 | 0 |
| 171.79 | 0 | 1 |
| 217.78 | 1 | 0 |
| 154.05 | 0 | 0 |

In fact, for even more clarity, we can add a column for the intercept too.

|  |  |  |  |
| --- | --- | --- | --- |
| height | the\_intercept | is\_species\_2 | is\_species\_3 |
| 226.55 | 1 | 0 | 1 |
| 86.62 | 1 | 0 | 1 |
| 138.53 | 1 | 0 | 1 |
| 122.81 | 1 | 0 | 0 |
| 141.97 | 1 | 0 | 1 |
| 174.99 | 1 | 1 | 0 |
| 51.00 | 1 | 0 | 0 |
| 171.79 | 1 | 0 | 1 |
| 217.78 | 1 | 1 | 0 |
| 154.05 | 1 | 0 | 0 |

Now we can see the equivalence with the linear model expressed in R from above, lm(height ~ 1 + species\_ID, data = plant\_data). The formula in lm is predicting height for individual plants using a linear model that includes the intercept (always 1), plus species ID. This relates now more easily to the equation . The four terms are reflected in the four columns above. Plant height () is predicted in the left-most column. The second column is all ones, by which we multipy the intercept (). Columns two and three define the species\_ID in R, and the terms of the equation. Note that either and (the row is species 1), and (species 2), or and (species 3). Hence, the coefficients and apply only for species 2 and 3, repsectively (and the absence of both occurs for species 1). You should now be able to connect this concept with the output of summary(lmod2) above.

Now if we want to predict the height of any plant (rows), we can do so just by multiplying the values in columns 2-4 (always 1 or 0) by the corresponding regression coefficients. For example, where is\_species\_2 = 0 and is\_species\_3 = 0, we have . Substituting the regression coefficients from the summary(lmod2) above, we have,

Note that the above simplifies to 141.265, the predicted height of species 1. We can do the same for species 2.

The above simplifies to , which equals 175.685, the predicted height of species 2. I will leave the predicted height of species 3 to the reader.

Note that we have been working with categorical variables, species. These are represented by ones and zeroes. But we can also imagine that some other continuous variable might be included in the model. For example, perhaps the altitude at which the plant was collected is also potentially important for predicting plant height. The common name for this model would be ‘ANCOVA’, but all that we would really be doing is adding one more column to the table above. The column would be ‘altitude’, and would perhaps include values expressing metres above sea level (e.g., altitude = 23.42, 32.49, 10.02, and so forth; one for each plant). This value would be multiplied by a new coefficient to predict plant height, and be represented as an lm in R with lm(height ~ 1 + species\_ID + altitude, data = plant\_data). Its equation would be , where altitude is .

# Can we make this even more elegant, somehow?

I hope that all of this has further illustrated some of the mathematics and code underlying linear models. Readers who are satisfied can skip this section, but I want to go just one step further and demonstrate how linear model prediction really boils down to **just one equation**. This equation is a generalisation of the by now familiar . We can represent independent and dependent variables in the table above using columns of two matrices, and . is just a vector of 100 plant heights (matching column 1 from the table above),

Similarly, is just a matrix with 100 rows and 3 columns indicating the intercept and species identities, as in columns 2-4 above,

What we want to figure out now are the coefficients for predicting values in (i.e., its matrix elements) from values in each of the columns of . In other words, what are the values of , , , which were explained in the last section? We can also represent these values in a matrix ,

We have already figured out what these values are using lm in R. They are just the Estimate values from the output of summary(lmod2) in [an earlier section](#moregroups). But we can also predict them using a bit of matrix algebra, solving for given the values in and . The generalisation of is the compact equation below,

For our data, we could therefore substute for and matrices,

Given this equation, we now only need to solve for to get our coefficients predicting from . This requires some knowledge of [matrix multiplication](https://en.wikipedia.org/wiki/Matrix_multiplication) and [matrix inversion](https://en.wikipedia.org/wiki/Invertible_matrix). These topics are a lesson in themselves, so I will not go into any detail as to what these matrix operations do. The point is that we are trying to isolate in the equation . My hope is that a rough idea of what is going on is possible even for those unfamiliar with matrix algebra, but feel free to [skip ahead](#betapred).

**Isolating with matrix algebra**

I should note that all of the matrix algebra that you have seen here is thanks to [Dean Adams](https://www.eeob.iastate.edu/people/dean-adams) at Iowa State University (but if you notice any errors, they are mine, not his). The first thing that we need to isolate is to multiply both sides of the equation by the [transpose](https://en.wikipedia.org/wiki/Transpose) of , ,

Next, we multiply both sides by the [inverse](https://en.wikipedia.org/wiki/Invertible_matrix) of , ,

Notice now that on the right side of the equation, we have . In other words, we multiply the inverse of by itself, thereby cancelling itself out (getting the [identity matrix](https://en.wikipedia.org/wiki/Identity_matrix), the matrix algebra equivalent of 1). That leaves us only with on the right hand side of the equation, which is exactly what we want. We can flip this around and put on the left side of the equation,

Hence, we have isolated , and can use the right side of the above equation (where the data are located) to get our predictors.

**Using one equation to get predictions of coefficients**.

We now have our equation for getting our prediction coefficients ,

Now I will use this equations to rederive our regression coefficients. **Do not worry about the details here**. What I want to show is that the above equation really does get us the same regression coefficents that we got from the output of summary(lmod2) [earlier](#moregroups). Here is that output again.

##   
## Call:  
## lm(formula = height ~ 1 + species\_ID, data = plant\_data)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -90.505 -30.255 -2.489 30.432 113.495   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 141.265 7.118 19.845 <2e-16 \*\*\*  
## species\_IDspecies\_2 34.420 10.143 3.394 0.001 \*\*   
## species\_IDspecies\_3 4.487 10.143 0.442 0.659   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 41.51 on 97 degrees of freedom  
## Multiple R-squared: 0.1223, Adjusted R-squared: 0.1042   
## F-statistic: 6.755 on 2 and 97 DF, p-value: 0.001792

Now let’s use the data in plant\_data to calculate manually instead. Here are the first ten rows of plant\_data again.

|  |  |  |  |
| --- | --- | --- | --- |
| height | the\_intercept | is\_species\_2 | is\_species\_3 |
| 226.55 | 1 | 0 | 1 |
| 86.62 | 1 | 0 | 1 |
| 138.53 | 1 | 0 | 1 |
| 122.81 | 1 | 0 | 0 |
| 141.97 | 1 | 0 | 1 |
| 174.99 | 1 | 1 | 0 |
| 51.00 | 1 | 0 | 0 |
| 171.79 | 1 | 0 | 1 |
| 217.78 | 1 | 1 | 0 |
| 154.05 | 1 | 0 | 0 |

We want to set the first column as a matrix , and the remaining columns as a matrix .

Y <- as.matrix(plant\_data[,1]);  
X <- as.matrix(plant\_data[,2:4]);

Here are the first five elements of Y.

## [1] 226.55 86.62 138.53 122.81 141.97

Here are the first five rows of X.

## the\_intercept is\_species\_2 is\_species\_3  
## [1,] 1 0 1  
## [2,] 1 0 1  
## [3,] 1 0 1  
## [4,] 1 0 0  
## [5,] 1 0 1

Let’s do the matrix algebra now below to get values of . Note that in R, [matrix multiplication](https://en.wikipedia.org/wiki/Matrix_multiplication) is denoted by the operation %\*%. [Matrix inversion](https://en.wikipedia.org/wiki/Invertible_matrix) of X is written as solve(X), and matrix [transpose](https://en.wikipedia.org/wiki/Transpose) of X is written as t(X). Our expression of in R is therefore as follows.

betas <- solve( t(X) %\*% X ) %\*% t(X) %\*% Y;

We can now print betas to reveal our coefficients, just as they were reported by lm.

print(betas);

## [,1]  
## the\_intercept 141.265294  
## is\_species\_2 34.420160  
## is\_species\_3 4.486827

We have just produced our regression coefficients manually, with matrix algebra.

# Some final thoughts

The reason that I have gone through this step by step is to build on our earlier exploration of common statistical tests as linear models. All linear models can be expressed using this common framework. In the above matrix example, note that we could have added as many columns as we wished to . Perhaps we also collected data on the altitude at which we found the plants in our hypothetical example. We could add this information in as an additional column of numbers in , then calculated a new in exactly the same way. In our new model, this would result in a discrete group predictor (species, in our case), and a continuous variable (altitude). The associated statistical test would commonly be called an ANCOVA, but all that would really have happened is that we would be adding a new column to the list of independent variables. **As an exercise**, think about how we would add interaction terms in .

But wait, there’s more. There is no reason why needs to be represented by a single column. Maybe we want to predict not just plant height, but plant seed production too. In other words, perhaps we have more than one dependent variable and we need a [multivariate](https://en.wikipedia.org/wiki/Multivariate_statistics) approach (e.g., [MANOVA](https://en.wikipedia.org/wiki/Multivariate_analysis_of_variance)). The same equation for getting works here too. We can think of multivariate linear models in the exact same way as univariate models; we are just adding more columns to .

I hope that this has been a useful supplement to the already very useful introduction by [Lindeløv](https://lindeloev.github.io/tests-as-linear/). There are details that I have left out for the sake of time, but my goal has been to further simplify the logic and mathematics underying linear models in statistics.

This document is entirely reproducible. Because the data are simulated, if you Knit it in Rstudio, you will get different numbers each time. I encourage you to try this, and explore the code for yourself. I have cheated in a few places just to avoid making a simulated data set that is too extreme, by chance. All of the code for generating simulated data is posted below, with some notes.

# Key bits of code underlying the simulated data

The code below can be used to generate a CSV file with simulated data as shown here. Note that you can change the significance of different regression coefficients, and their magnitudes and signs, by changing how height is defined within the while loops below.

# The code below creates plant heights with an intercept of roughly 150  
# and a beta\_1 coefficient of roughly 20, with some error added into it.  
# The while loop just does this to avoid any non-significant results or   
# very highly significant results that arise due to chance.  
species\_n <- c("species\_1", "species\_2");  
sim\_pval <- 0;  
while(sim\_pval > 0.05 | sim\_pval < 0.001){  
 species\_eg <- sample(x = species\_n, size = 100, replace = TRUE);  
 species1 <- as.numeric(species\_eg == "species\_1");  
 species2 <- as.numeric(species\_eg == "species\_2");  
 error <- rnorm(n = 100, mean = 0, sd = 40);  
 height <- round(150 + (species2 \* 20) + error, digits = 2);  
 species\_ID <- as.factor(species\_eg);  
 plant\_data <- data.frame(height, species\_ID);  
 sim\_mod <- lm(plant\_data$height ~ 1 + plant\_data$species\_ID);  
 sim\_pval <- summary(sim\_mod)$coefficients[2,4];  
}  
write.csv(plant\_data, file = "two\_discrete\_x\_values.csv", row.names = FALSE);  
  
# Below does the same job as above, just with three species instead of two  
species\_n <- c("species\_1", "species\_2", "species\_3");  
sim\_pval <- 0;  
while(sim\_pval > 0.05 | sim\_pval < 0.001){  
 species\_eg <- sample(x = species\_n, size = 100, replace = TRUE);  
 species1 <- as.numeric(species\_eg == "species\_1");  
 species2 <- as.numeric(species\_eg == "species\_2");  
 species3 <- as.numeric(species\_eg == "species\_3");  
 error <- rnorm(n = 100, mean = 0, sd = 40);  
 height <- round(150 + (species2 \* 20) + error, digits = 2);  
 species\_ID <- as.factor(species\_eg);  
 plant\_data <- data.frame(height, species\_ID);  
 sim\_mod <- lm(plant\_data$height ~ 1 + plant\_data$species\_ID);  
 sim\_pval <- summary(sim\_mod)$coefficients[2,4];  
}  
write.csv(plant\_data, file = "three\_discrete\_x\_values.csv", row.names = FALSE);