ANOVA in R: A step-by-step guide

Published on March 6, 2020 by Rebecca Bevans. Revised on July 1, 2021.

ANOVA is a statistical test for estimating how a quantitative dependent variable changes according to the levels of one or more categorical independent variables. ANOVA tests whether there is a difference in means of the groups at each level of the independent variable.

The null hypothesis (H_0) of the ANOVA is no difference in means, and the alternate hypothesis (H_a) is that the means are different from one another.

In this guide, we will walk you through the process of a one-way ANOVA (one independent variable) and a two-way ANOVA (two independent variables).

Our sample dataset contains observations from an imaginary study of the effects of fertilizer type and planting density on crop yield.

One-way ANOVA example

In the one-way ANOVA, we test the effects of 3 types of fertilizer on crop yield.

Table of contents

Two-way ANOVA example

In the two-way ANOVA, we add an additional independent variable: planting density. We test the effects of 3 types of fertilizer and 2 different planting densities on crop yield.

We will also include examples of how to perform and interpret a two-way ANOVA with an interaction term, and an ANOVA with a blocking variable.

Sample dataset for ANOVA

Table of contents

these programs downloaded, open R Studio and click on **File** > **New File** > **R Script**.

Now you can copy and paste the code from the rest of this example into your script. To run the code, **highlight the lines you want to run** and click on the **Run** button on the top right of the text editor (or press **ctrl + enter** on the keyboard).

Install and load the packages

First, install the packages you will need for the analysis (this only needs to be done once):

```
install.packages(c("ggplot2", "ggpubr", "tidyverse", "broom", "AICcmodavg"))
```

Then load these packages into your R environment (do this every time you restart the R program):

```
library(ggplot2)
library(ggpubr)
library(tidyverse)
library(broom)
library(AICcmodavg)
```

Step 1: Load the data into R

Note that this data was generated for this example, it's not from a real experiment!

Table of contents

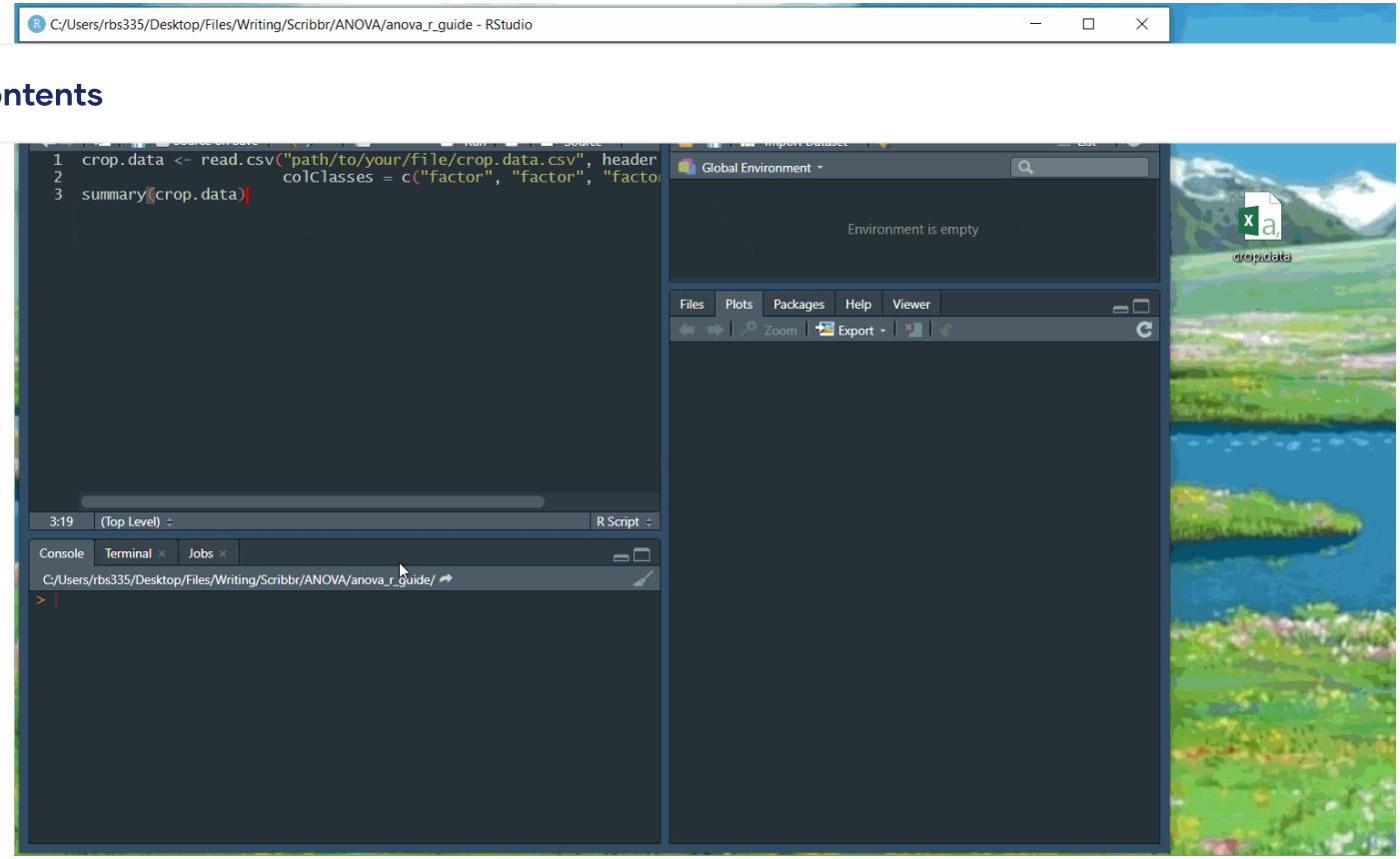
We will use the same dataset for all of our examples in this walkthrough. The only

and in what combination we include them.

It is common for factors to be read as quantitative variables when importing a dataset into R. To avoid this, you can use the `read.csv()` command to read in the data, specifying within the command whether each of the variables should be quantitative (“numeric”) or categorical (“factor”).

Use the following code, replacing the **path/to/your/file** text with the actual path to your file:

```
crop.data <- read.csv("path/to/your/file/crop.data.csv", header = TRUE, colClasses = c("factor", "factor", "factor", "numeric"))
```



Before continuing, you can check that the data has read in correctly:

```
summary(crop.data)
```

```
density block  fertilizer     yield
                              3rd Qu.:177.4
                              Max.   :179.1
```


You should see 'density', 'block', and 'fertilizer' listed as categorical variables with the number of observations at each level (i.e. 48 observations at density 1 and 48 observations at density 2).

'Yield' should be a quantitative variable with a numeric summary (minimum, median, mean, maximum).

Step 2: Perform the ANOVA test

ANOVA tests whether any of the group means are different from the overall mean of the data by checking the variance of each individual group against the overall variance of the data. If one or more groups falls outside the range of variation predicted by the null hypothesis (all group means are equal), then the test is statistically significant.

We can perform an ANOVA in R using the `aov()` function. This will calculate the test statistic for ANOVA and determine whether there is significant variation among the groups formed by the levels of the independent variable.

One-way ANOVA

In the one-way ANOVA example, we are modeling crop yield as a function of the type of fertilizer used. First we will use `aov()` to run the model, then we will use `summary()` to print the summary of the model.

```
summary(one.way)
```

```
             Df Sum Sq Mean Sq F value Pr(>F)
fertilizer    2   6.07  3.0340   7.863  7e-04 ***
Residuals    93  35.89  0.3859
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

The model summary first lists the independent variables being tested in the model (in this case we have only one, ‘fertilizer’) and the model residuals (‘Residual’). All of the variation that is not explained by the independent variables is called residual variance.

The rest of the values in the output table describe the independent variable and the residuals:

- The **Df** column displays the degrees of freedom for the independent variable (the number of levels in the variable minus 1), and the degrees of freedom for the residuals (the total number of observations minus one and minus the number of levels in the independent variables).
- The **Sum Sq** column displays the sum of squares (a.k.a. the total variation between the group means and the overall mean).
- The **Mean Sq** column is the mean of the sum of squares, calculated by dividing the sum of squares by the degrees of freedom for each parameter.
- The **F-value** column is the test statistic from the F test. This is the mean square of each independent variable divided by the mean square of the residuals. The larger

the F value, the more likely it is that the variation caused by the independent variable

Table of contents

- The **Pr(>F)** column is the p-value of the F-statistic. This shows how likely it is that the F-value calculated from the test would have occurred if the null hypothesis of no difference among group means were true.

The p-value of the fertilizer variable is low ($p < 0.001$), so it appears that the type of fertilizer used has a real impact on the final crop yield.

Two-way ANOVA

In the two-way ANOVA example, we are modeling crop yield as a function of type of fertilizer and planting density. First we use `aov()` to run the model, then we use `summary()` to print the summary of the model.

```
two.way <- aov(yield ~ fertilizer + density, data = crop.data)


summary(two.way)
```

```
            Df Sum Sq Mean Sq F value   Pr(>F)
fertilizer   2  6.068   3.034   9.073 0.000253 ***
density      1  5.122   5.122  15.316 0.000174 ***
Residuals   92 30.765   0.334
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Adding planting density to the model seems to have made the model better: it reduced the residual variance (the residual sum of squares went from 35.89 to 30.765), and both planting density and fertilizer are statistically significant (p-values < 0.001).

Adding interactions between variables

Table of contents

interaction effect rather than an additive effect.

For example, in our crop yield experiment, it is possible that planting density affects the plants' ability to take up fertilizer. This might influence the effect of fertilizer type in a way that isn't accounted for in the two-way model.

To test whether two variables have an interaction effect in ANOVA, simply use an asterisk instead of a plus-sign in the model:

```
interaction <- aov(yield ~ fertilizer*density, data = crop.data)


summary(interaction)
```

```
                   Df Sum Sq Mean Sq F value   Pr(>F)
fertilizer          2  6.068   3.034   9.001 0.000273 ***
density             1  5.122   5.122  15.195 0.000186 ***
fertilizer:density  2  0.428   0.214   0.635 0.532500
Residuals          90 30.337   0.337
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

In the output table, the 'fertilizer:density' variable has a low sum-of-squares value and a high p-value, which means there is not much variation that can be explained by the interaction between fertilizer and planting density.

Adding a blocking variable

If you have grouped your experimental treatments in some way, or if you have a

should include that element in the model as a blocking variable. The simplest way to do this is just to add the variable into the model with a '+'.

For example, in many crop yield studies, treatments are applied within 'blocks' in the field that may differ in soil texture, moisture, sunlight, etc. To control for the effect of differences among planting blocks we add a third term, 'block', to our ANOVA.

```
blocking <- aov(yield ~ fertilizer + density + block, data = crop.data)


summary(blocking)
```

```
            Df Sum Sq Mean Sq F value   Pr(>F)
fertilizer   2  6.068   3.034   9.018 0.000269 ***
density      1  5.122   5.122  15.224 0.000184 ***
block        2  0.486   0.243   0.723 0.488329
Residuals   90 30.278   0.336
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The 'block' variable has a low sum-of-squares value (0.486) and a high p-value (p = 0.48), so it's probably not adding much information to the model. It also doesn't change the sum of squares for the two independent variables, which means that it's not affecting how much variation in the dependent variable they explain.

Step 3: Find the best-fit model

Table of contents

There are now four different ANOVA models to explain the data. How do you decide which the variation in the dependent variable.

The Akaike information criterion (AIC) is a good test for model fit. AIC calculates the information value of each model by balancing the variation explained against the number of parameters used.

In AIC model selection, we compare the information value of each model and choose the one with the lowest AIC value (a lower number means more information explained!)

```
library(AICcmodavg)

model.set <- list(one.way, two.way, interaction, blocking)
model.names <- c("one.way", "two.way", "interaction", "blocking")

aictab(model.set, modnames = model.names)
```

The model with the lowest AIC score (listed first in the table) is the best fit for the data:

```
Model selection based on AICc:

            K   AICc Delta_AICc AICcWt Cum.Wt     LL
two.way     5 173.86       0.00   0.71   0.71 -81.59
blocking    7 176.93       3.08   0.15   0.86 -80.83
interaction 7 177.12       3.26   0.14   1.00 -80.92
one.way     4 186.41      12.56   0.00   1.00 -88.99
```

From these results, it appears that the two.way model is the best fit. The two-way model the total variation in the dependent variable that can be explained by the full set of models.

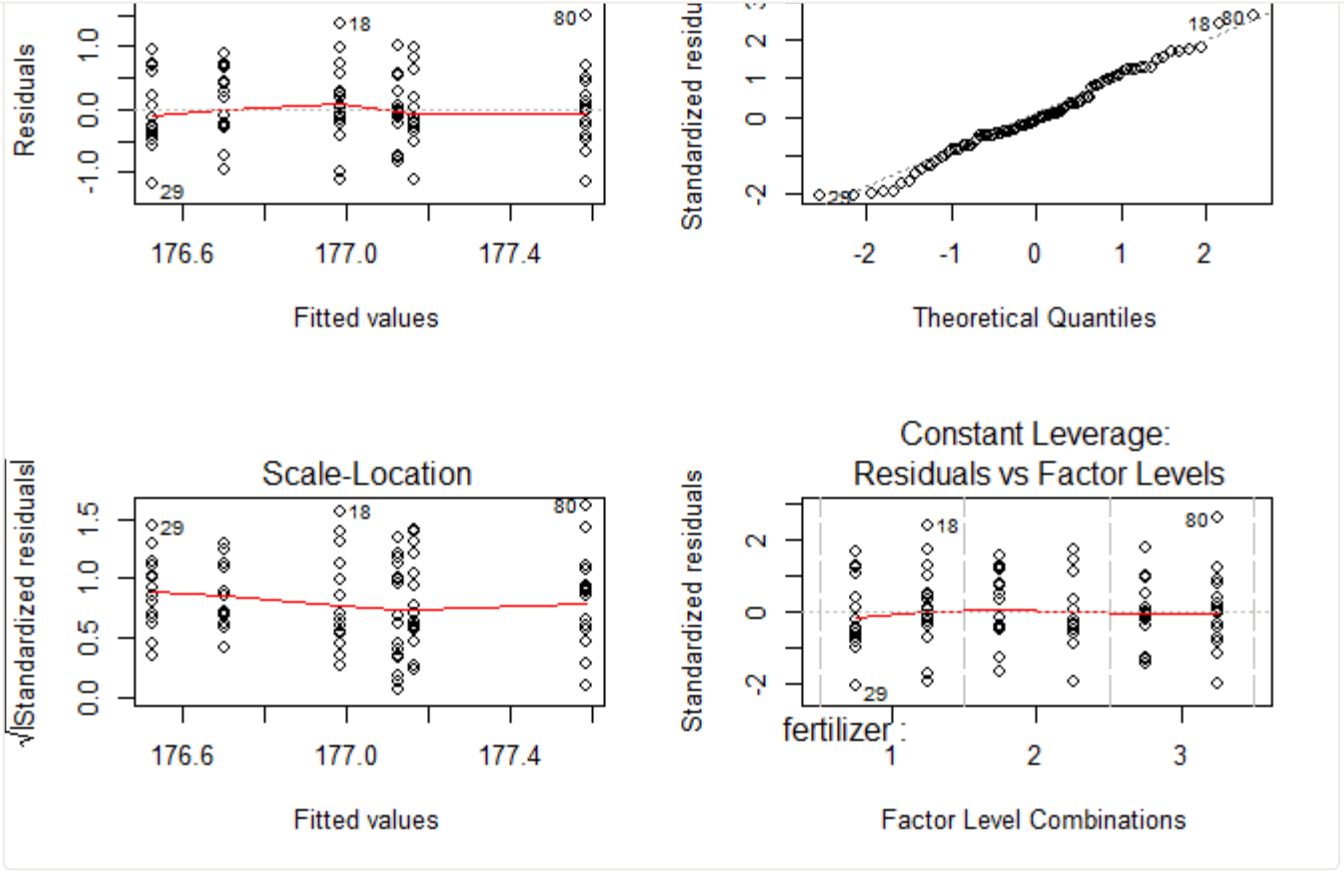
The model with blocking term contains an additional 15% of the AIC weight, but because it is more than 2 delta-AIC worse than the best model, it probably isn't good enough to include in your results.

Step 4: Check for homoscedasticity

To check whether the model fits the assumption of homoscedasticity, look at the model diagnostic plots in R using the `plot()` function:

```
par(mfrow=c(2,2))
plot(two.way)
par(mfrow=c(1,1))
```

The output looks like this:



The diagnostic plots show the unexplained variance (residuals) across the range of the observed data.

Each plot gives a specific piece of information about the model fit, but it's enough to know that the red line representing the mean of the residuals should be horizontal and centered on zero (or on one, in the scale-location plot), meaning that there are no large outliers that would cause bias in the model.

The normal Q-Q plot plots a regression between the theoretical residuals of a perfectly-

this is the better. This Q-Q plot is very close, with only a bit of deviation.

From these diagnostic plots we can say that the model fits the assumption of homoscedasticity.

If your model doesn't fit the assumption of homoscedasticity, you can try the Kruskall-Wallis test instead.

Step 5: Do a post-hoc test

ANOVA tells us if there are differences among group means, but not what the differences are. To find out which groups are statistically different from one another, you can perform a Tukey's Honestly Significant Difference (Tukey's HSD) post-hoc test for pairwise comparisons:

```
tukey.two.way<-TukeyHSD(two.way)

tukey.two.way
```

Table of contents

```
  Tukey multiple comparisons of means
    95% family-wise confidence level

$fertilizer
         diff          lwr       upr     p adj
2-1 0.1761687 -0.16822506 0.5205625 0.4452958
3-1 0.5991256  0.25473179 0.9435194 0.0002219
3-2 0.4229569  0.07856306 0.7673506 0.0119381

$density
        diff       lwr       upr     p adj
2-1 0.461956 0.2275204 0.6963916 0.0001741
```

From the post-hoc test results, we see that there are statistically significant differences ($p < 0.05$) between fertilizer groups 3 and 1 and between fertilizer types 3 and 2, but the difference between fertilizer groups 2 and 1 is not statistically significant. There is also a significant difference between the two different levels of planting density.

Step 6: Plot the results in a graph

When plotting the results of a model, it is important to display:

- the raw data
- summary information, usually the mean and standard error of each group being compared
- letters or symbols above each group being compared to indicate the groupwise differences.

Find the groupwise differences

From the ANOVA test we know that both planting density and fertilizer type are significant

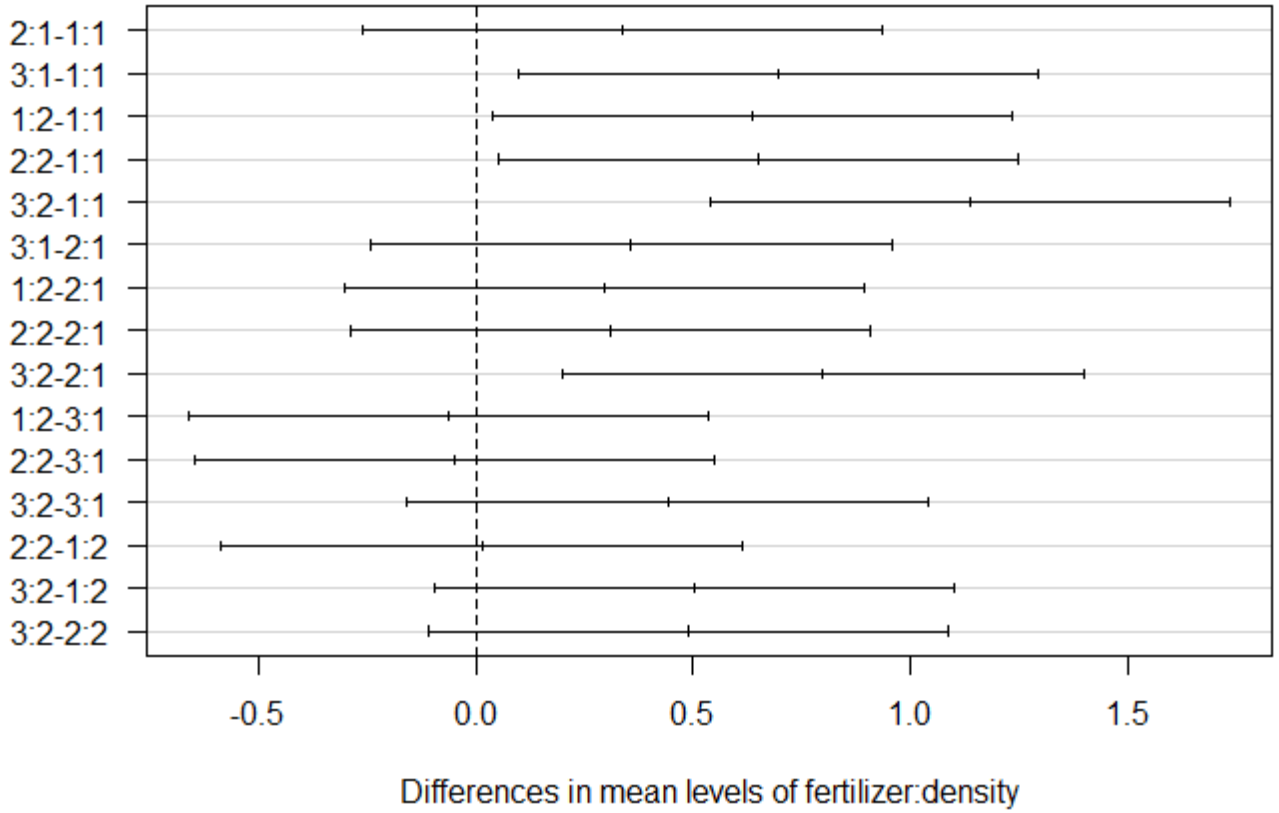
combinations of fertilizer type + planting density are statistically different from one another.

To do this, we can run another ANOVA + TukeyHSD test, this time using the interaction of fertilizer and planting density. We aren't doing this to find out if the interaction term is significant (we already know it's not), but rather to find out which group means are statistically different from one another so we can add this information to the graph.

```
tukey.plot.aov<-aov(yield ~ fertilizer:density, data=crop.data)
```

Instead of printing the TukeyHSD results in a table, we'll do it in a graph.

```
tukey.plot.test<-TukeyHSD(tukey.plot.aov)
plot(tukey.plot.test, las = 1)
```



The significant groupwise differences are any where the 95% confidence interval doesn't include zero. This is another way of saying that the p-value for these pairwise differences is < 0.05.

From this graph, we can see that the fertilizer + planting density combinations which are significantly different from one another are 3:1-1:1 (read as "fertilizer type three + planting density 1 contrasted with fertilizer type 1 + planting density type 1"), 1:2-1:1, 2:2-1:1, 3:2-1:1,

and 3:2-2:1.

Table of contents

intermediate combinations), and C (representing 3:2).

Make a data frame with the group labels

Now we need to make an additional data frame so we can add these groupwise differences to our graph.

First, summarize the original data using fertilizer type and planting density as grouping variables.

```
mean.yield.data <- crop.data %>%
  group_by(fertilizer, density) %>%
  summarise(
      yield = mean(yield)
  )
```

Next, add the group labels as a new variable in the data frame.

```
mean.yield.data$group <- c("a","b","b","b","b","c")

mean.yield.data
```

Your data frame should look like this:

```
# A tibble: 6 x 4
  [illegible]
1 1         1         177. a
2 1         2         177. b
3 2         1         177. b
4 2         2         177. b
5 3         1         177. b
6 3         2         178. c
```

Now we are ready to start making the plot for our report.

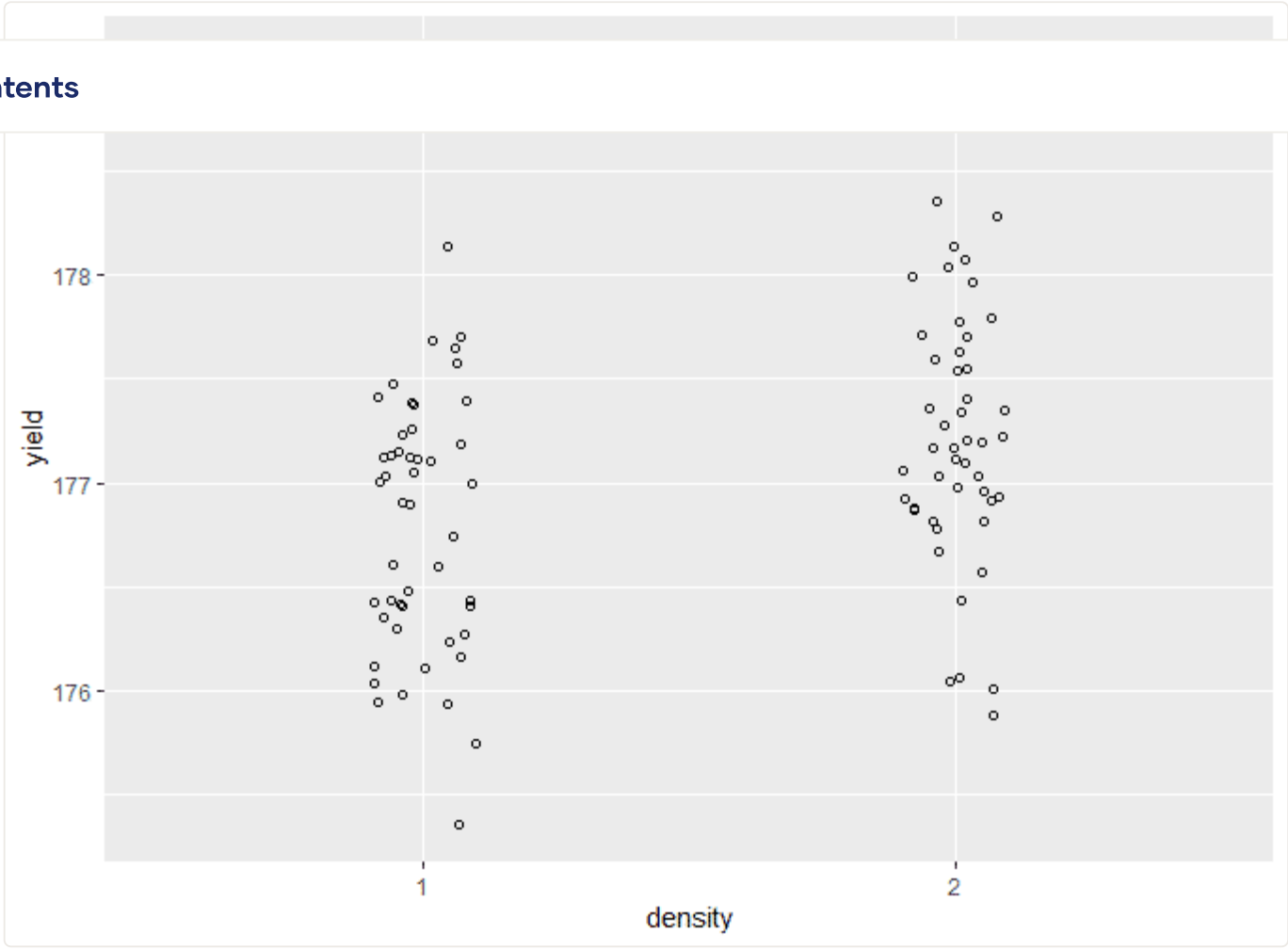
Plot the raw data

```
two.way.plot <- ggplot(crop.data, aes(x = density, y = yield, group=fertilizer)) +
  geom_point(cex = 1.5, pch = 1.0,position = position_jitter(w = 0.1, h = 0))


two.way.plot
```

The output looks like this:

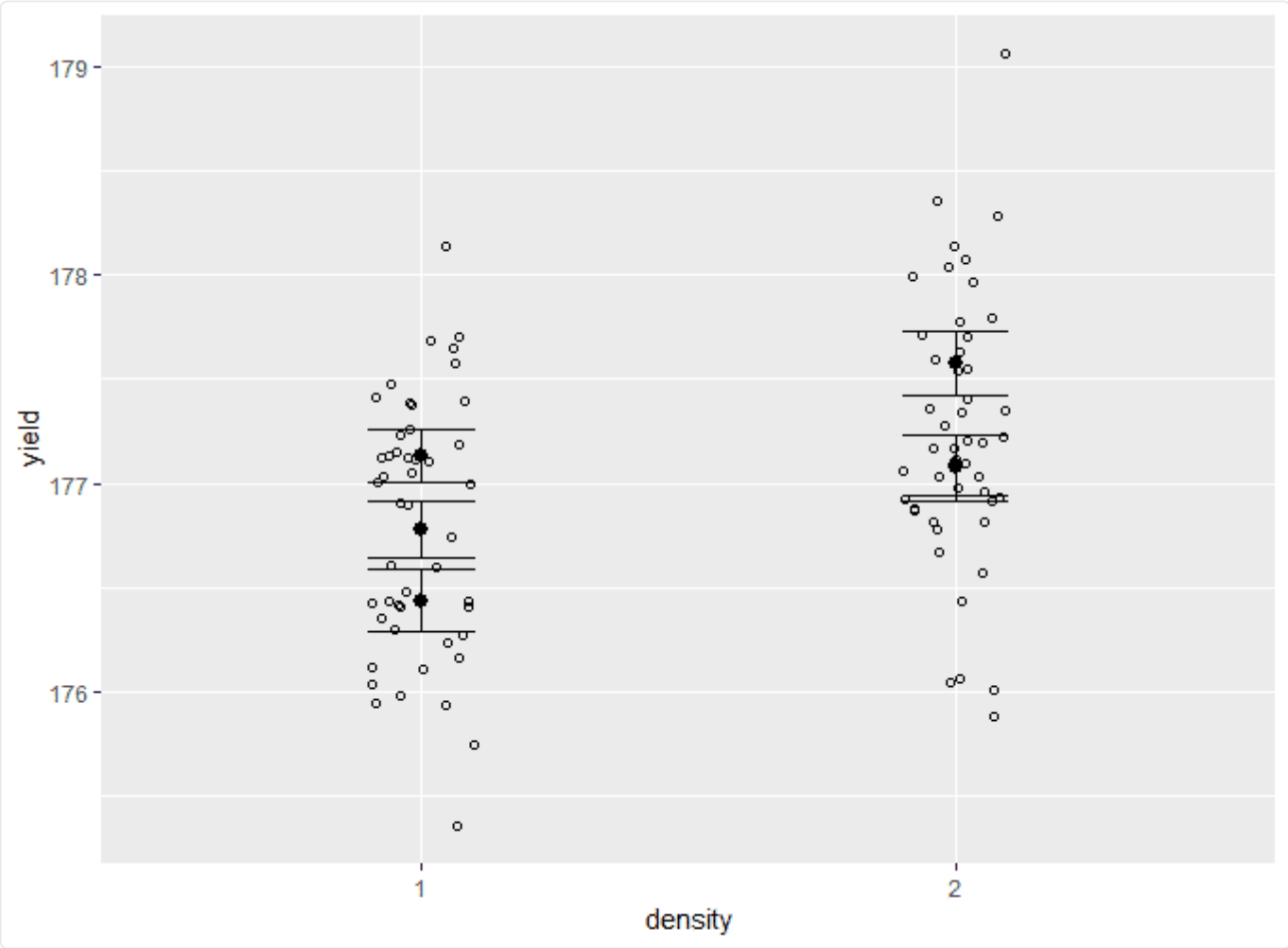
Table of contents



Add the means and standard errors to the graph

```
two.way.plot <- two.way.plot +
  stat_summary(fun.data = 'mean_se', geom = 'errorbar', width = 0.2) +
  stat_summary(fun.data = 'mean_se', geom = 'pointrange') +
  geom_point(data=mean.yield.data, aes(x=density, y=yield))

two.way.plot
```



This is very hard to read, since all of the different groupings for fertilizer type are stacked on top of one another. We will solve this in the next step.

Split up the data

To show which groups are different from one another, use `facet_wrap()` to split the data up

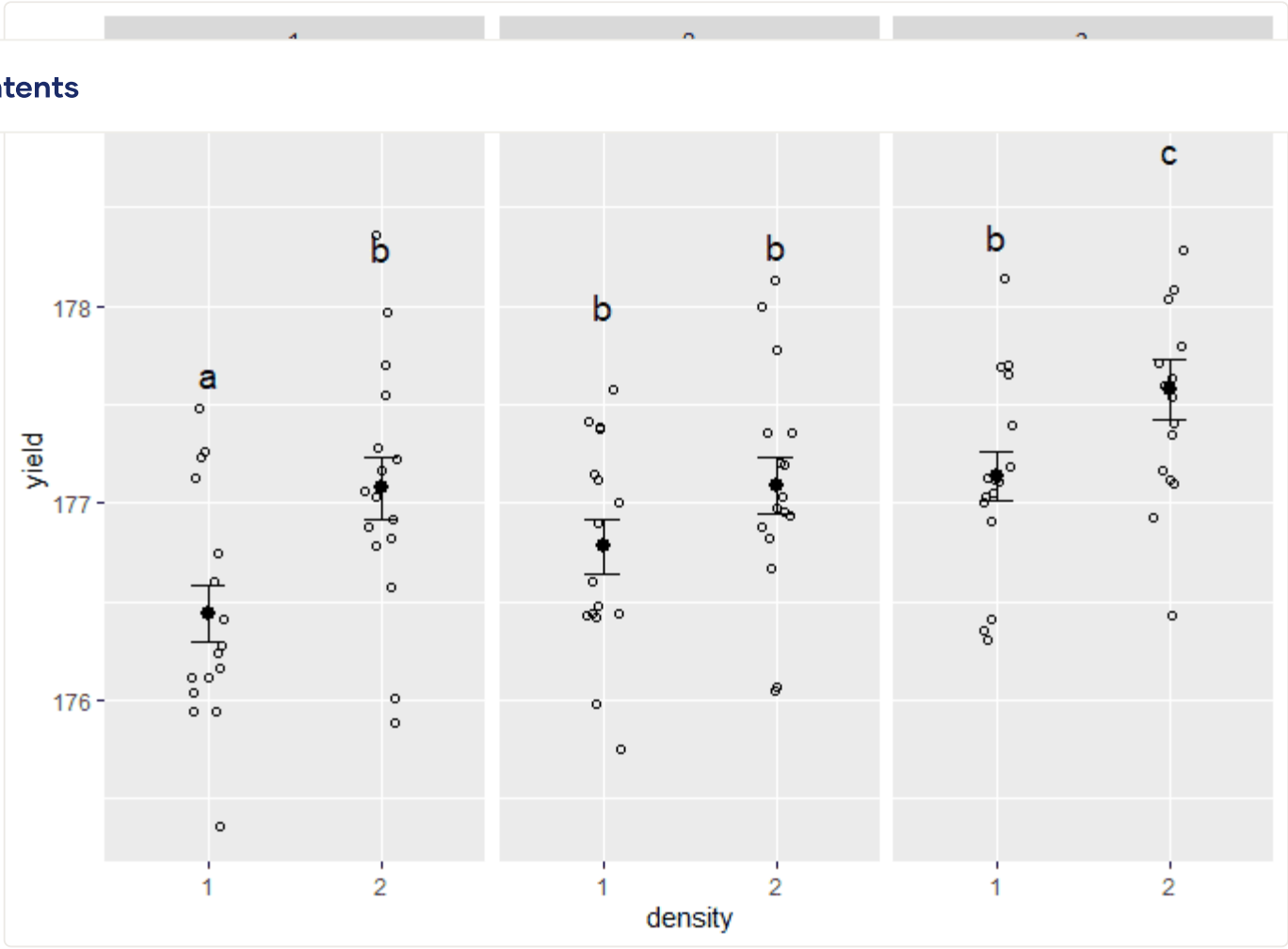
from the mean.yield.data dataframe you made earlier.

```
two.way.plot <- two.way.plot +
  geom_text(data=mean.yield.data, label=mean.yield.data$group, vjust = -8, size = 5) +
  facet_wrap(~ fertilizer)

two.way.plot
```

The output looks like this:

Table of contents



Make the graph ready for publication

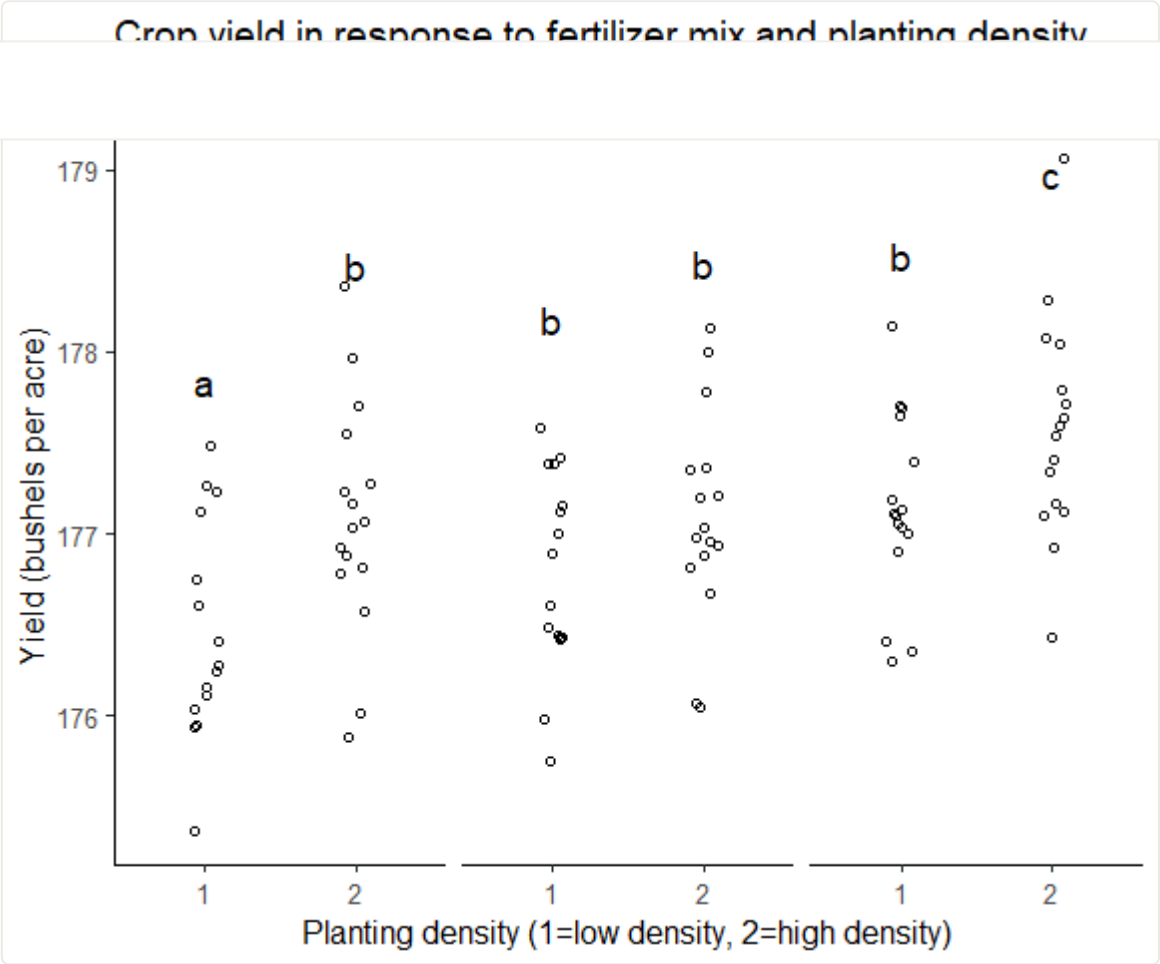
In this step we will remove the grey background and add axis labels.

```
  labs(title = "Crop yield in response to fertilizer mix and planting density",
       x = "Planting density (1=low density, 2=high density)",
       y = "Yield (bushels per acre)")

two.way.plot
```

The final version of your graph looks like this:

Table of contents



Step 7: Report the results

In addition to a graph, it's important to state the results of the ANOVA test. Include:

- A brief description of the variables you tested
- The f-value, degrees of freedom, and p-values for each independent variable
- What the results mean.

Example: Reporting the results of ANOVA

Table of contents

($f(2)=9.018$, $p < 0.001$) and by planting density ($f(1)=15.316$, $p<0.001$).

A Tukey post-hoc test revealed that fertilizer mix 3 resulted in a higher yield on average than fertilizer mix 1 (0.59 bushels/acre), and a higher yield on average than fertilizer mix 2 (0.42 bushels/acre). Planting density was also significant, with planting density 2 resulting in an higher yield on average of 0.46 bushels/acre over planting density 1.

A subsequent groupwise comparison showed the strongest yield gains at planting density 2, fertilizer mix 3, suggesting that this mix of treatments was most advantageous for crop growth under our experimental conditions.

Frequently asked questions about ANOVA

Table of contents

Is this article helpful? 384 24

Rebecca Bevans

Rebecca is working on her PhD in soil ecology and spends her free time writing. She's very happy to be able to nerd out about statistics with all of you.

Other students also liked

An introduction to the one-way ANOVA

The one-way ANOVA is used to compare the means of more than two groups when

An introduction to the two-way ANOVA

A two-way ANOVA is used to estimate how the mean of a quantitative variable

there is one independent variable and one

changes according to the levels of two

Table of contents

An introduction to the Akaike information criterion

The Akaike information criterion (AIC) tests how well a model fits the data it is made from. In statistics, is often used for model selection.

206

APA Citation Generator

Table of contents

Contact

info@scribbr.com

+1 (510) 822-8066

4.8