

# Comparison of two or more groups

The ASTA team

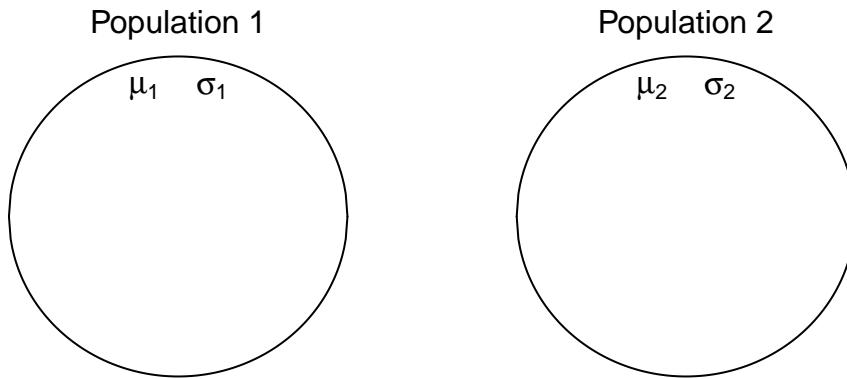
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## 1 Comparison of two populations

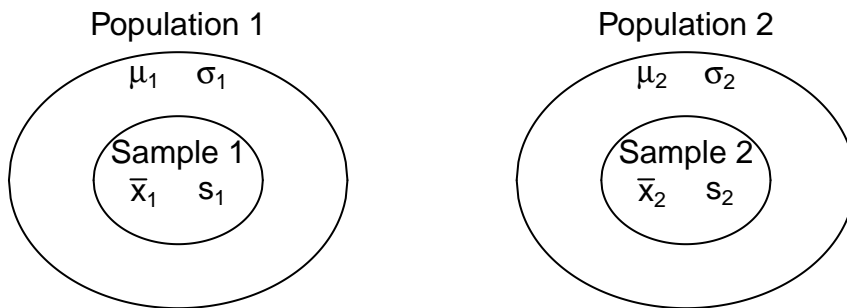
### 1.1 Two populations

- Consider two populations:
  - Population 1 has mean  $\mu_1$  and standard deviation  $\sigma_1$ .
  - Population 2 has mean  $\mu_2$  and standard deviation  $\sigma_2$ .
- We want to compare the means by looking at the difference  $\mu_1 - \mu_2$ .



## 1.2 Two samples

- We now take a sample from each population.
  - The sample from Population 1 has sample mean  $\bar{x}_1$ , sample standard deviation  $s_1$  and sample size  $n_1$ .
  - The sample from Population 2 has sample mean  $\bar{x}_2$ , sample standard deviation  $s_2$  and sample size  $n_2$ .



## 1.3 Dependent and independent samples

- We distinguish between two types of samples:
  - The two samples are **independent**.
  - The two samples are **paired**.
- **Example:** Suppose we consider the fuel consumption of cars.
  - If we compare two samples of cars with different engine types, then the two samples are *independent*, since each car can only have one of the two engine types.
  - If we compare the fuel consumption of cars at two different speed levels by testing each car at both speed levels, then the samples are *paired*.

## 1.4 Comparison of two means (Independent samples)

- We consider the situation, where we have two independent samples of a quantitative variable.
- We estimate the difference  $\mu_1 - \mu_2$  by

$$d = \bar{x}_1 - \bar{x}_2.$$

- Assume that we can find the **estimated standard error**  $se_d$  of the difference.

- If the samples come from two normal distributions, or if both samples are large ( $n_1, n_2 \geq 30$ ), then one can show

$$T_{obs} = \frac{(\bar{X}_1 - \bar{X}_2) - (\mu_1 - \mu_2)}{se_d} \sim \mathfrak{t}(df),$$

where  $\mathfrak{t}(df)$  is a  $t$ -distribution with  $df$  degrees of freedom.

- By the usual procedure, we can use this to construct a confidence interval for the unknown population difference of means  $\mu_1 - \mu_2$  by

$$(\bar{x}_1 - \bar{x}_2) \pm t_{crit} se_d,$$

where the critical  $t$ -score,  $t_{crit}$ , is determined by the confidence level and the  $df$ .

## 1.5 Significance test (Independent samples)

- We may be interested the testing the **null-hypothesis** that the population means are the same, which we can formulated as:

$$- H_0 : \mu_1 - \mu_2 = 0.$$

$$- H_a : \mu_1 - \mu_2 \neq 0.$$

- If the null hypothesis is true, then the **test statistic**:

$$T_{obs} = \frac{(\bar{X}_1 - \bar{X}_2) - 0}{se_d},$$

has a  $t$ -distribution with  $df$  degrees of freedom.

- The **p-value** is the probability of observing something further away from 0 than  $t_{obs}$  in a  $\mathfrak{t}(df)$  distribution.
- It remains to find the estimated standard error  $se_d$  and the degrees of freedom  $df$ . We distinguish between two cases:
  - The two populations have equal variances  $\sigma_1^2 = \sigma_2^2$ .
  - The two populations have different variances  $\sigma_1^2 \neq \sigma_2^2$ .

## 1.6 Standard error (Independent samples, equal variances)

- The standard error of  $d = \bar{x}_1 - \bar{x}_2$  is given by the formula:

$$\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}.$$

- If the **variances are equal**,  $\sigma_1^2 = \sigma_2^2$ , then we estimate the common value by the **pooled variance estimate**

$$s_p^2 = \frac{(n_1-1)s_1^2 + (n_2-1)s_2^2}{n_1+n_2-2}.$$

- Inserting this estimate in the formula for the standard error we obtain the estimated standard error

$$se_d = \sqrt{\frac{s_p^2}{n_1} + \frac{s_p^2}{n_2}} = s_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}.$$

- In this situation, the degrees of freedom are  $df = n_1 + n_2 - 2$ .

## 1.7 Example: Comparing two means (independent samples, equal variances)

We return to the `mtcars` data. We study the association between the variables `vs` and `mpg` (engine type and fuel consumption). So, we will perform a significance test to test the null-hypothesis that there is no difference between the mean of fuel consumption for the two engine types.

- We will test the null-hypothesis assuming equal variances:

```
library(mosaic)
fv <- favstats(mpg ~ vs, data = mtcars)
fv
```

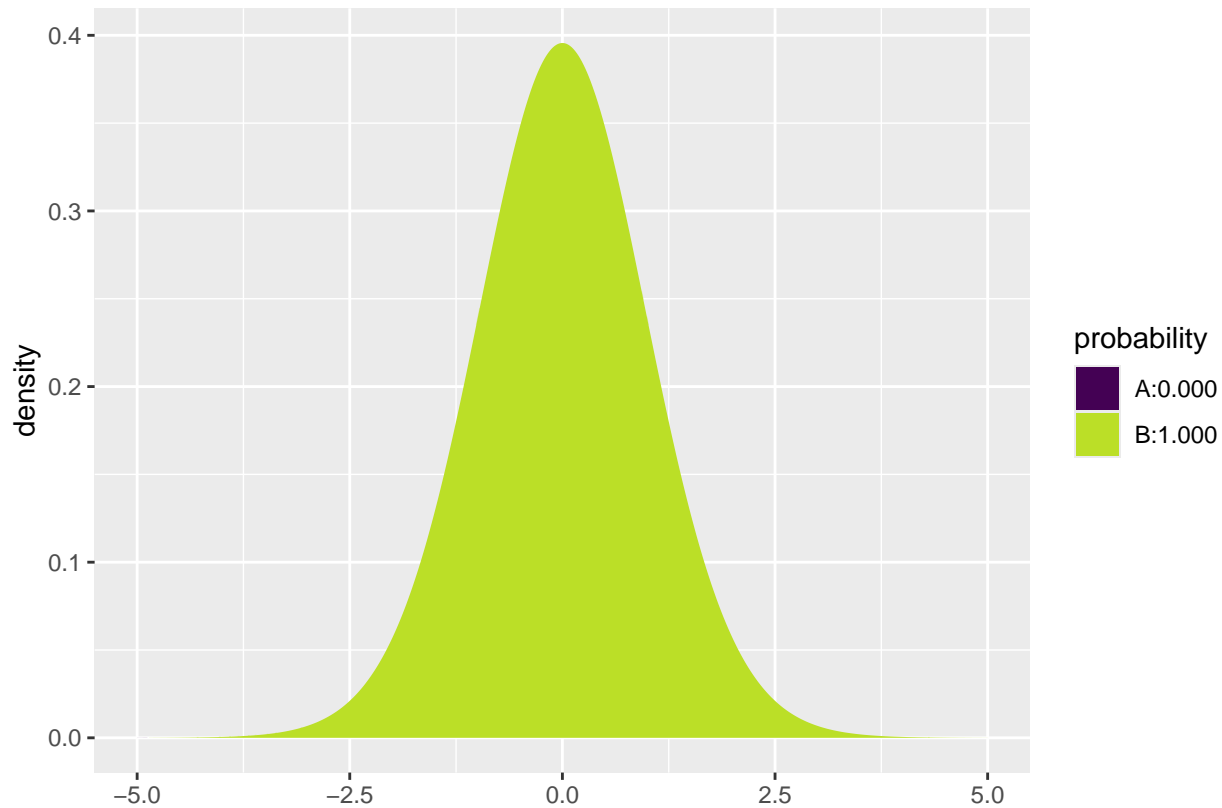
```
##   vs min  Q1 median  Q3  max mean  sd  n missing
## 1  0 10.4 14.8  15.7 19.1 26.0 16.6 3.86 18      0
## 2  1 17.8 21.4  22.8 29.6 33.9 24.6 5.38 14      0
```

- Difference:  $d = 16.6167 - (24.5571) = -7.9405$ .
- Sample sizes:  $n_1 = 18$  and  $n_2 = 14$ .
- Estimated standard deviations:  $s_1 = 3.8607$  (not v-shaped) and  $s_2 = 5.379$  (v-shaped).
- Pooled variance:

$$s_p^2 = \frac{(n_1 - 1)s_1^2 + (n_2 - 1)s_2^2}{n_1 + n_2 - 2} = \frac{17 \cdot 3.8607^2 + 13 \cdot 5.379^2}{18 + 14 - 2} = 20.984.$$

- Estimated standard error of difference:  $se_d = s_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}} = \sqrt{20.984} \sqrt{\frac{1}{18} + \frac{1}{14}} = 1.6324$ .
- Observed  $t$ -score for  $H_0 : \mu_1 - \mu_2 = 0$  is:  $t_{obs} = \frac{d-0}{se_d} = \frac{-7.9405}{1.6324} = -4.864$ .
- The degrees of freedom are  $df = n_1 + n_2 - 2 = 30$ .
- We find the  $p$ -value:

```
2*pdist("t", q = -4.864, df=30, xlim = c(-5, 5))
```



```
## [1] 3.419648e-05
```

## 1.8 Standard error (Independent samples, unequal variances)

- If the **variances are unequal**, then we simply insert the two estimates  $s_1^2$  and  $s_2^2$  for  $\sigma_1^2$  and  $\sigma_2^2$  in the formula for the standard error to obtain the estimated standard error

$$se_d = \sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}$$

- The degrees of freedom  $df$  for  $se_d$  can be estimated by a complicated formula, which we will not present here (see p.365 in the book).
- Note:
  - If both  $n_1$  and  $n_2$  are above 30, then we may use the standard normal distribution to compute a  $z$ -score rather than the  $t$ -distribution to compute the  $t$ -score. This way we avoid computing  $df$ .
  - If  $n_1$  or  $n_2$  are below 30, then we let **R** calculate the degrees of freedom and the  $p$ -value/confidence interval.

## 1.9 Example: Comparing two means (independent samples, unequal variances)

We return to the `mtcars` data. We study the association between the variables `vs` and `mpg` (engine type and fuel consumption). So, we will perform a significance test to test the null-hypothesis that there is no difference between the mean of fuel consumption for the two engine types.

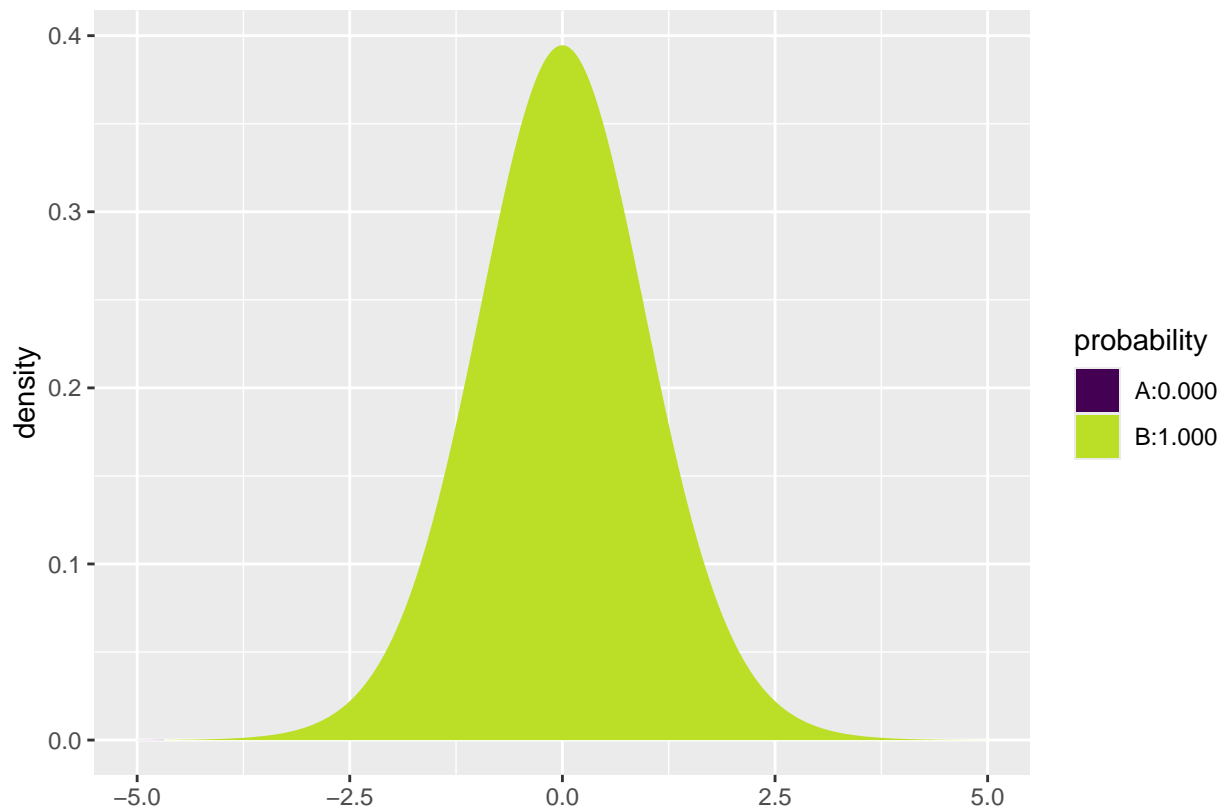
- We now make the analysis without assuming equal variances:

```
library(mosaic)
fv <- favstats(mpg ~ vs, data = mtcars)
fv
```

```
##   vs min  Q1 median  Q3  max mean  sd  n missing
## 1  0 10.4 14.8   15.7 19.1 26.0 16.6 3.86 18      0
## 2  1 17.8 21.4   22.8 29.6 33.9 24.6 5.38 14      0
```

- Difference:  $d = 16.6167 - (24.5571) = -7.9405$ .
- Sample sizes:  $n_1 = 18$  and  $n_2 = 14$ .
- Estimated standard deviations:  $s_1 = 3.8607$  (not v-shaped) and  $s_2 = 5.379$  (v-shaped).
- Estimated standard error of difference:  $se_d = \sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}} = \sqrt{\frac{3.8607^2}{18} + \frac{5.379^2}{14}} = 1.7014$ .
- Observed  $t$ -score for  $H_0 : \mu_1 - \mu_2 = 0$  is:  $t_{obs} = \frac{d-0}{se_d} = \frac{-7.9405}{1.7014} = -4.6671$ .
- The degrees of freedom can be found using R (see below) to be  $df = 22.716$ .
- We find the  $p$ -value:

```
2* pdist("t", q = -4.6671, df=22.716, xlim = c(-5, 5))
```



```
## [1] 0.0001098212
```

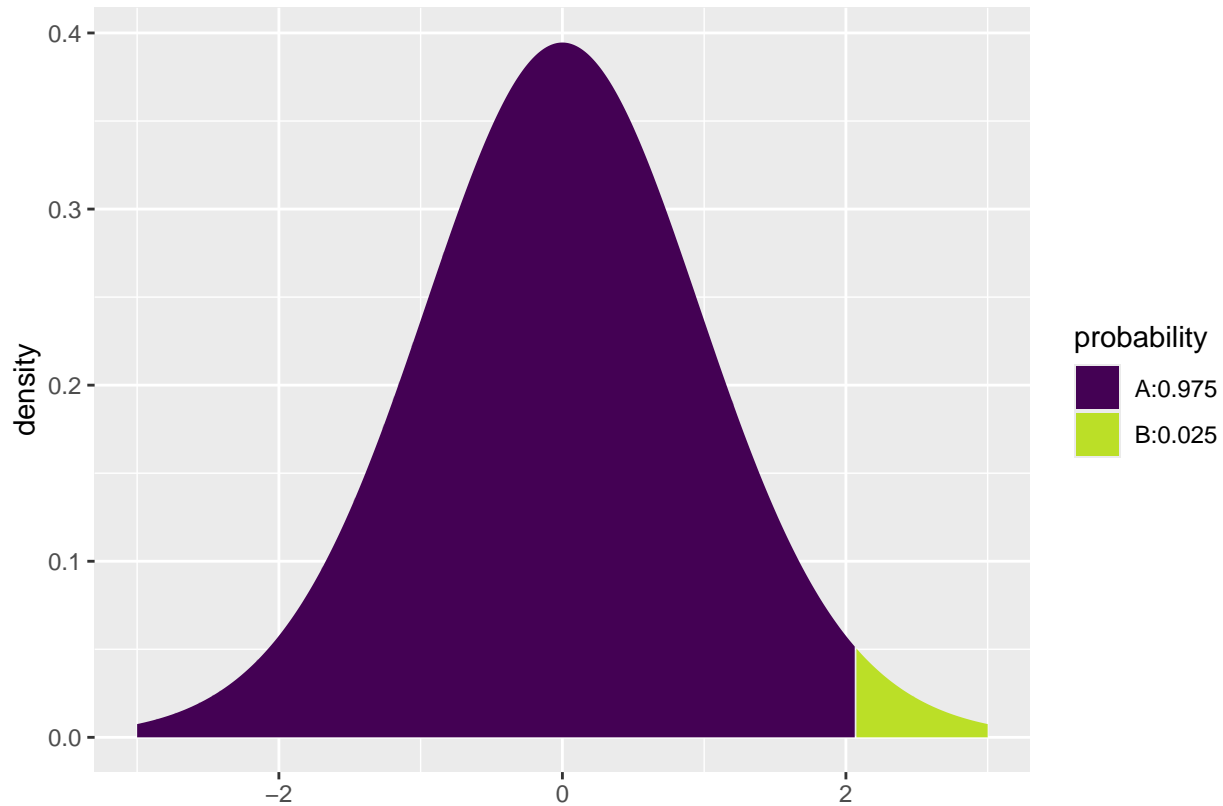
- We reject the null-hypothesis and conclude that the fuel consumption is different for the two engine types.

### 1.10 Example: Comparing two means (independent samples)

- Now we know there is a difference between the two population means. We can also make a 95% confidence interval for how large the difference  $\mu_1 - \mu_2$  actually is by the formula

$$d \pm t_{crit} se_d$$

```
qdist("t", p = 1-0.05/2, df=22.716, xlim = c(-3, 3))
```



```
## [1] 2.07009
```

- Inserting the values from the previous slide yields

$$[-7.94 - 2.07 * 1.70; -7.94 + 2.07 * 1.70] = [-11.5, -4.4].$$

- We are 95% confident that the difference in fuel consumption is between the two engine types is between -4.4mpg and -11.5mpg.

## 1.11 T-test in R (Independent samples)

- We can leave all the calculations to **R** by using `t.test`:

```
t.test(mpg ~ vs, data = mtcars, var.equal = FALSE)
```

```
##  
## Welch Two Sample t-test  
##  
## data: mpg by vs  
## t = -4.6671, df = 22.716, p-value = 0.0001098  
## alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0  
## 95 percent confidence interval:  
## -11.462508 -4.418445  
## sample estimates:  
## mean in group 0 mean in group 1  
## 16.61667 24.55714
```

- We recognize the  $t$ -score  $-4.6671$ , the  $p$ -value  $0.0001$ , and the confidence interval  $[-11.5; -4.4]$ . The estimated degrees of freedom can be found in the output to be  $df = 22.716$ .

## 1.12 Test for equal variances (Independent samples)

- In order to decide whether to use the  $t$ -test with equal or unequal variance, we may test the hypothesis  $H_0 : \sigma_1^2 = \sigma_2^2$ .

- As test statistic we use

$$F_{obs} = \frac{s_1^2}{s_2^2}.$$

- If the null-hypothesis is true, we expect  $F_{obs}$  to take values close to 1. Small and large values are critical for  $H_0$ .
- Under  $H_0$ ,  $F_{obs}$  follows a so-called  $F$ -distribution with  $df_1 = n_1 - 1$  and  $df_2 = n_2 - 1$  degrees of freedom.
  - If  $F_{obs} < 1$  we reject the null-hypothesis if two times the probability of getting something smaller than  $F_{obs}$  is less than the significance level.
  - If  $F_{obs} > 1$  we reject the null-hypothesis if two times the probability of getting something larger than  $F_{obs}$  is less than the significance level.

### 1.12.1 Example: Test for equal variances (Independent samples)

- To test whether the variance is the same for the two engine types in the `mtcars` example, we first compute the sample variances.

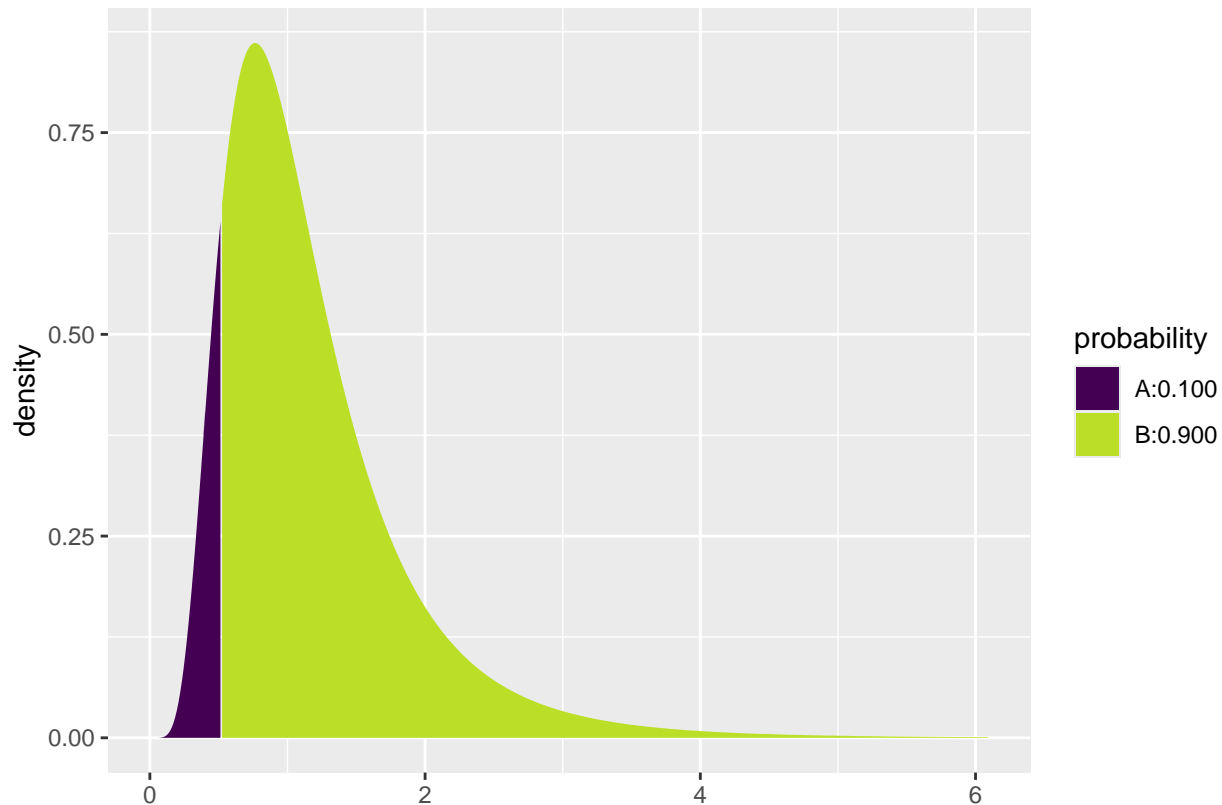
```
var(mpg~vs, data=mtcars)
```

```
##          0          1
## 14.90500 28.93341
```

- We compute  $F_{obs} = \frac{s_1^2}{s_2^2} = \frac{14.9}{28.9} = 0.516$ .
- The probability of observing something smaller than  $F_{obs}$  in an  $F$ -distribution with  $df_1 = n_1 - 1 = 17$  and  $df_2 = n_2 - 1 = 13$ :

```
pdist("f", 0.516, df1=17, df2=13)
```





```
## [1] 0.1004094
```

- The p-value is  $2 * 0.1004 = 0.2008$ . Here we multiply by two because the test is two-sided (large values would also have been critical).
- We find no evidence against the null-hypothesis.

### 1.13 Comparison of two means: paired $t$ -test (dependent samples)

- We now consider the case where we have two samples from two different populations but the observations in the two samples are **paired**.
  - For each pair, we can compute the difference between the two observations.
  - We now have one sample of observed differences.
  - We apply the the one-sample  $t$ -test from Lecture 2.1 to test whether the mean difference is zero.
- **Example:** Suppose we make the following experiment:
  - Choose 32 students at random and measure their average reaction time in a driving simulator while they are listening to radio or audio books.
  - Later the same 32 students redo the simulated driving while talking on a cell phone.
  - We are interested in whether or not the fact that you are actively participating in a conversation changes your average reaction time compared to when you are passively listening.
- So we have 2 samples corresponding to with/without phone. In this case we have **paired** samples, since we have 2 measurement for each student.
- We use the following strategy for analysis:
  - For each student calculate **the change** in average reaction time with and without talking on the phone.
  - The changes  $d_1, d_2, \dots, d_{32}$  are now considered as **ONE** sample from a population with mean  $\mu$ .

- Test the hypothesis  $H_0 : \mu = 0$  as usual (using a one-sample  $t$ -test).
- 

### 1.13.1 Reaction time: data example

- Data is organized in a data frame with 3 variables:
  - `student` (integer - a simple id)
  - `reaction_time` (numeric - average reaction time in milliseconds)
  - `phone` (factor - yes/no indicating whether speaking on the phone)

```
reaction <- read.delim("https://asta.math.aau.dk/datasets?file=reaction.txt")
head(reaction, n = 3)
```

```
## student reaction_time phone
## 1 1 604 no
## 2 2 556 no
## 3 3 540 no
```

- We first manually find the reaction time difference for each student and do a one sample  $t$ -test on this difference:

```
yes <- subset(reaction, phone == "yes")
no <- subset(reaction, phone == "no")
all(yes$student == no$student)
```

```
## [1] TRUE
```

```
reaction_paired <- data.frame(student = no$student, yes = yes$reaction_time, no = no$reaction_time)
reaction_paired$diff <- reaction_paired$yes - reaction_paired$no
head(reaction_paired)
```

```
## student yes no diff
## 1 1 636 604 32
## 2 2 623 556 67
## 3 3 615 540 75
## 4 4 672 522 150
## 5 5 601 459 142
## 6 6 600 544 56
```

```
t.test( ~ diff, data = reaction_paired)
```

```
##
## One Sample t-test
##
## data: diff
## t = 5.4563, df = 31, p-value = 5.803e-06
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## 31.70186 69.54814
## sample estimates:
## mean of x
## 50.625
```

- With a  $p$ -value of 0.0000058 we reject the null-hypothesis that speaking on the phone has no influence on the reaction time.
- We can avoid the manual calculations and let **R** perform the significance test by using `t.test` with `paired = TRUE`:

```
t.test(reaction_paired$no, reaction_paired$yes, paired = TRUE)
```

```
##  
## Paired t-test  
##  
## data: reaction_paired$no and reaction_paired$yes  
## t = -5.4563, df = 31, p-value = 5.803e-06  
## alternative hypothesis: true mean difference is not equal to 0  
## 95 percent confidence interval:  
## -69.54814 -31.70186  
## sample estimates:  
## mean difference  
## -50.625
```

## 1.14 Response variable and explanatory variable

- The situation with two populations is an example where we have: \* A **response variable** (or outcome, dependent variable).
  - An **explanatory variable** (or independent variable, covariate) that divides data in 2 groups.
- We are interested in the effect of the explanatory variable on the response variable.
  - For instance in the `mtcars` data, `mpg` is the response variable and `vs` is the explanatory variable.
- In this lecture we consider the case with one discrete explanatory variable. Module 3 is concerned with the case of one or more continuous variables.

## 2 More than two groups (Analysis of variance)

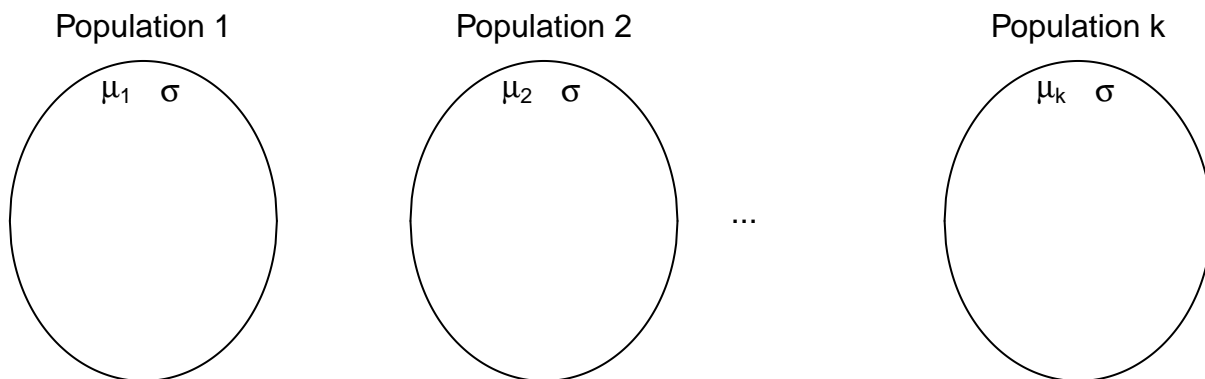
### 2.1 More than two populations

- We are now going to consider a situation where we have  $k$  populations with mean values  $\mu_1, \dots, \mu_k$ .
- We assume that each population follows a normal distribution and that the standard deviation is the same in all populations.
- We are interested in the null-hypothesis that all  $k$  populations have the same mean, i.e.

$$H_0 : \mu_1 = \dots = \mu_k.$$

$$H_a : \text{not all } \mu_1, \dots, \mu_k \text{ are the same.}$$

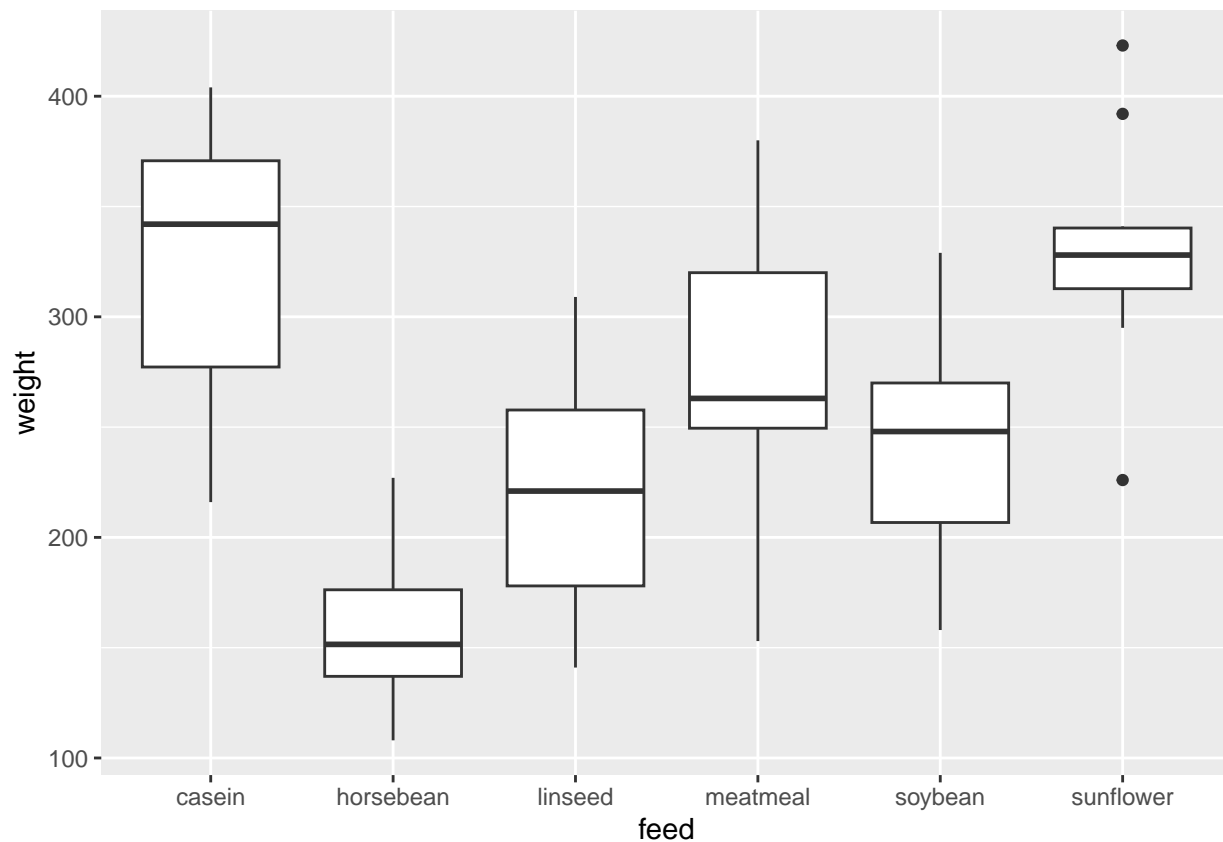
- We take out a sample from each population.



### 2.1.1 Data example

- The data set `chickwts` is available in R, and on the course webpage.
- 71 newly hatched chickens were randomly allocated into six groups, and each group was given a different feed supplement.
- Their weights in grams after six weeks are given along with feed types, i.e. we have a sample with corresponding measurements of 2 variables:
  - `weight`: a numeric variable giving the chicken weight.
  - `feed`: a factor giving the feed type.
- Always start with some graphics:

```
library(mosaic)
gf_boxplot(weight ~ feed, data = chickwts)
```



### 2.2 Estimation of mean values

- We estimate the mean in each group by the sample mean inside that group, i.e.  $\hat{\mu}_i = \bar{x}_i$ ,  $i = 1, \dots, k$ .
- We use `mean` to find the mean, for each group:

```
mean(weight ~ feed, data = chickwts)
```

```
##   casein horsebean  linseed  meatmeal  soybean sunflower
## 323.5833 160.2000  218.7500  276.9091  246.4286  328.9167
```

- We can e.g. see that the sample mean is 323.6, when `feed=casein` but 160.2, when `feed=horsebean`.
- Is this a significant difference ?

## 2.3 Contrasts

- If we want compare groups, it is convenient to formulate the model using contrasts.
- One group is chosen as the **reference group**, which all other groups are compared to.
  - Sometimes there is a group corresponding to “no treatment” and we are interested in the effect of different treatments. Other times the reference group can be arbitrary.
- If group 1 is the reference group, the mean values in the remaining groups groups can be expressed as

$$\mu_i = \mu_1 + \alpha_i,$$

where  $\alpha_i = (\mu_i - \mu_1)$  is the difference between group  $i$  and the reference group. The  $\alpha_i$  are called **contrasts**.

---

### 2.3.1 Example: contrast estimates

```
model <- lm(weight ~ feed, data = chickwts)
summary(model)

##
## Call:
## lm(formula = weight ~ feed, data = chickwts)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -123.909  -34.413    1.571   38.170  103.091
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    323.583     15.834  20.436 < 2e-16 ***
## feedhorsebean -163.383     23.485  -6.957 2.07e-09 ***
## feedlinseed   -104.833     22.393  -4.682 1.49e-05 ***
## feedmeatmeal  -46.674     22.896  -2.039 0.045567 *
## feedsoybean   -77.155     21.578  -3.576 0.000665 ***
## feedsunflower  5.333      22.393   0.238 0.812495
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 54.85 on 65 degrees of freedom
## Multiple R-squared:  0.5417, Adjusted R-squared:  0.5064
## F-statistic: 15.36 on 5 and 65 DF,  p-value: 5.936e-10
```

- In the example the groups are different feeds. R chooses the lexicographically smallest, which is casein, to be the reference group.
- We get information about contrasts and their significance:
- **Intercept** is the estimated mean  $\hat{\mu}_{casein} = 323.583$  in the reference group.
  - In the same line, there is also a test of the null-hypothesis  $H_0 : \mu_1 = 0$  that the weight after 6 weeks is 0 ( $p < 2 \times 10^{-16}$ ) (of course, chickens grow a lot over 6 weeks).
- The line **feedhorsebean** estimates the contrast  $\alpha_{horsebean}$  between the **casein** and **horsebean** group to be  $\hat{\alpha}_{horsebean} = -163.383$ .
  - The null-hypothesis that there is no difference between casein and horsebean ( $H_0 : \alpha_{horsebean} = 0$ ) is rejected with  $p=2 \times 10^{-9}$ .

## 2.4 Overall test for effect

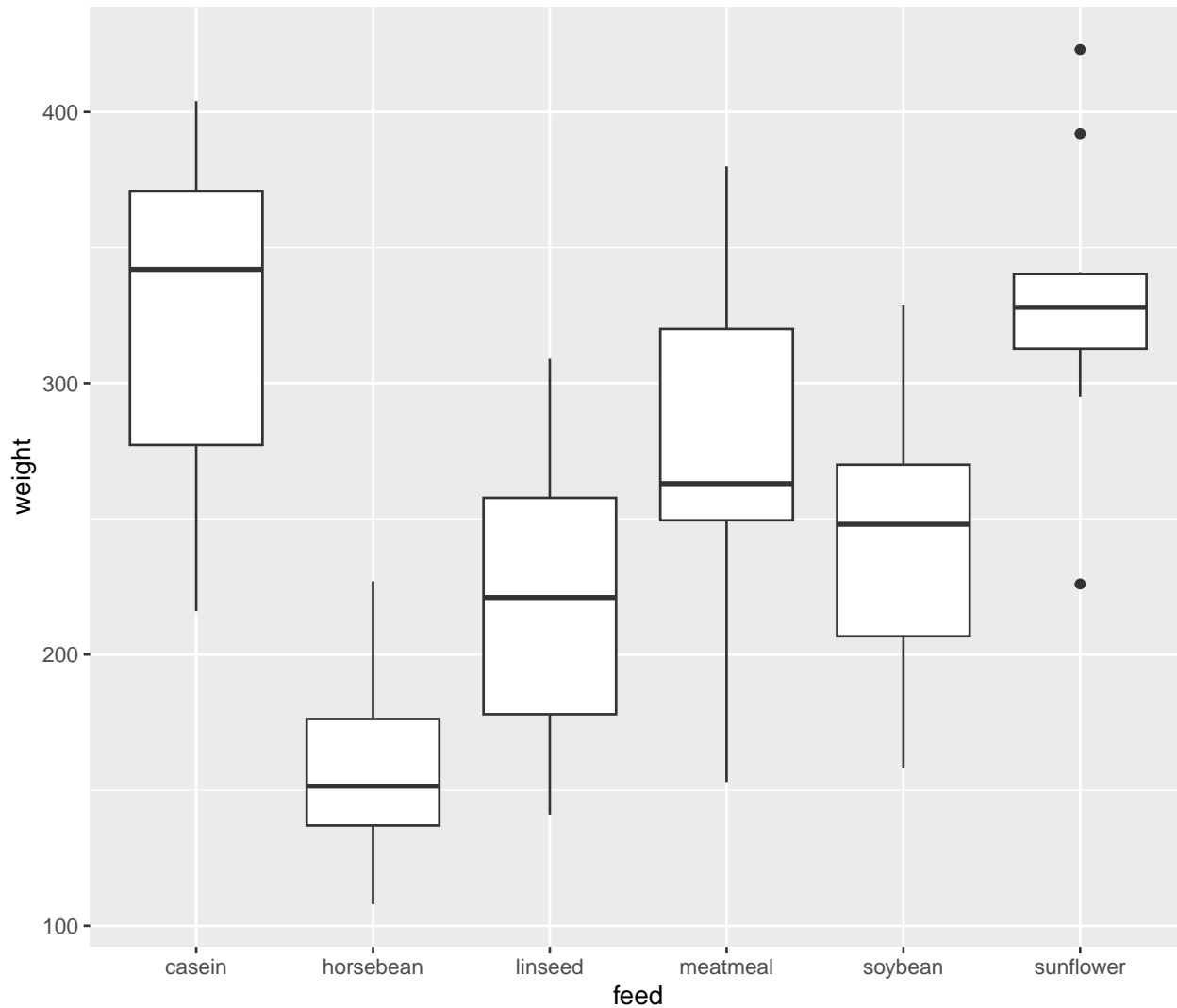
- We are now interested in testing the null-hypothesis

$$H_0 : \mu_1 = \mu_2 = \dots = \mu_k \quad \text{against} \quad H_a : \text{Not all of the population means are the same}$$

- Alternatively

$$H_0 : \alpha_2 = \alpha_3 = \dots = \alpha_k = 0, \quad H_a : \text{At least one contrast is non-zero.}$$

- Idea: Compare variation within groups and variation between groups.



## 2.5 Test statistic

- We use the test statistic

$$F_{obs} = \frac{(TSS - SSE)/(k - 1)}{SSE/(n - k)}.$$

- If observations from group  $i$  are called  $x_{ij}$ ,  $j = 1, \dots, k$ , we have:

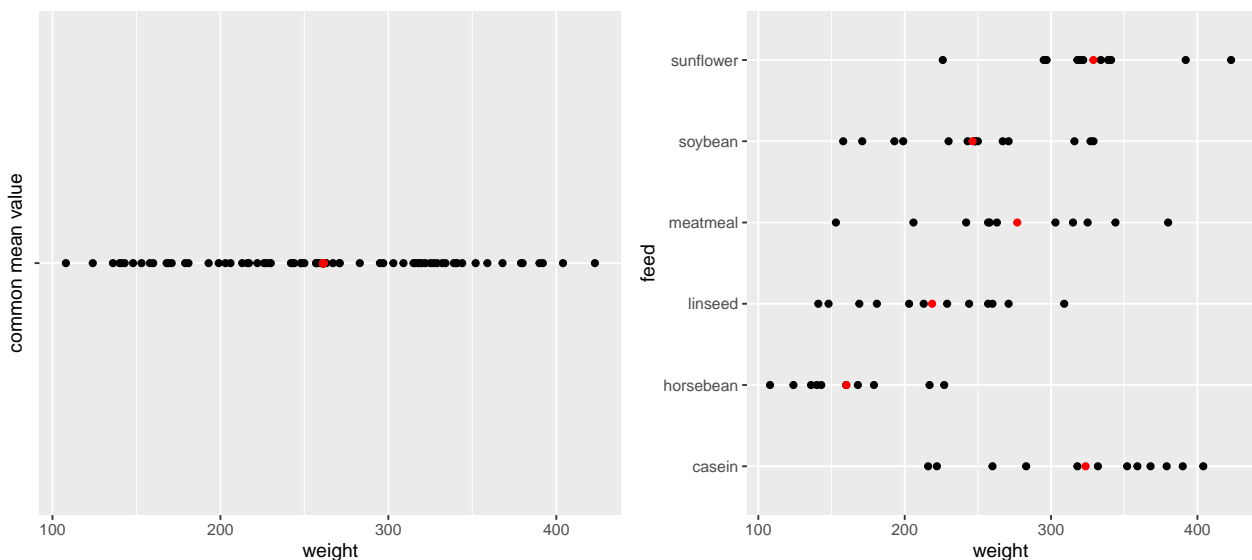
- $TSS = \sum_i \sum_j (x_{ij} - \bar{x})^2$ , where  $\bar{x}$  is the average of all observations from all groups.

$$- SSE = \sum_i \sum_j (x_{ij} - \bar{x}_i)^2.$$

- Interpretation:
  - TSS: error sum of squares if common mean.
  - SSE: error sum of squares if different means.
  - TSS-SSE: how much does error sum of squares increase if means are restricted to be equal.
- One can show that TSS-SSE measures the variance of group means around common mean.
- Interpretation is thus

$$F_{obs} = \frac{\text{variance between groups}}{\text{variance within groups}}.$$

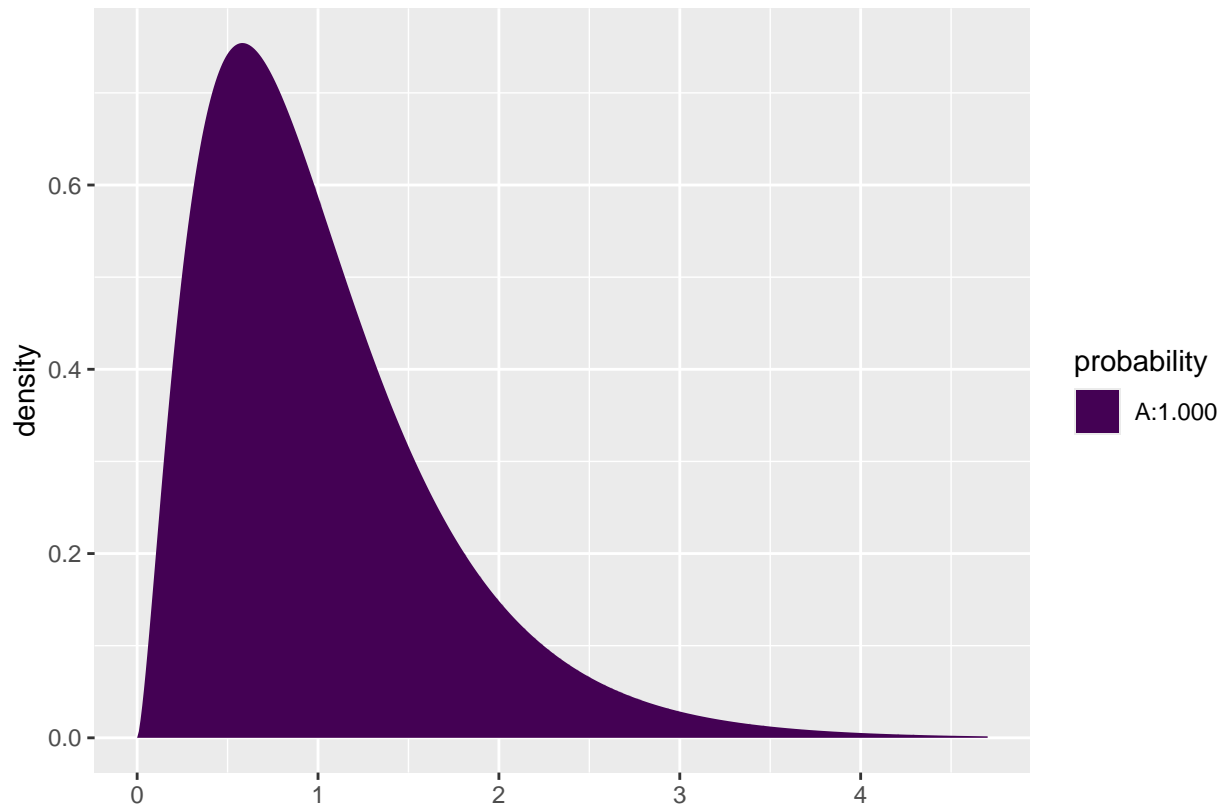
```
## Warning in geom_point(aes(x = red_dot), color = "red"): All aesthetics have length 1, but the data has
## length 6
## i Please consider using `annotate()` or provide this layer with data containing
## a single row.
```



## 2.6 The $F$ -test

- A large variation between groups compared to the variation within groups points against  $H_0$ .
- Thus, large values are critical for the null-hypothesis.
- Under the null-hypothesis,  $F_{obs}$  follows an  $F$ -distribution with  $df_1 = k - 1$  and  $df_2 = n - k$  degrees of freedom.
- A  $p$ -value for the null-hypothesis is the probability of observing something larger than  $F_{obs}$  in an  $F$ -distribution with  $df_1$  and  $df_2$  degrees of freedom.
- For instance if  $F_{obs} = 15.36$  with  $df_1 = 5$  and  $df_2 = 65$  degrees of freedom:

```
1 - pdist("f", 15.36, df1=5, df2=65)
```



```
## [1] 5.967948e-10
```

## 2.7 Example

```
model <- lm(weight ~ feed, data = chickwts)
summary(model)
```

```
##
## Call:
## lm(formula = weight ~ feed, data = chickwts)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -123.909  -34.413   1.571   38.170  103.091
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   323.583    15.834   20.436 < 2e-16 ***
## feedhorsebean -163.383    23.485   -6.957 2.07e-09 ***
## feedlinseed   -104.833    22.393   -4.682 1.49e-05 ***
## feedmeatmeal  -46.674    22.896   -2.039 0.045567 *
## feedsoybean   -77.155    21.578   -3.576 0.000665 ***
## feedsunflower  5.333     22.393    0.238 0.812495
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 54.85 on 65 degrees of freedom
## Multiple R-squared:  0.5417, Adjusted R-squared:  0.5064
```



## F-statistic: 15.36 on 5 and 65 DF, p-value: 5.936e-10

- The last line gives us the value of  $F_{obs} = 15.36$  and the corresponding  $p$ -value ( $5.9 \times 10^{-10}$ ). Clearly there is a significant difference between the types of feed.