In Lab 16 we tested the null hypothesis $\mu=1.3\,cm$ against the alternative hypothesis $H_1:\mu=1.5\,cm$ (in the Neyman-Pearson framework) or $H_a:\mu>1.3\,cm$ (in the NHST framework). We assumed that the data were collected in a random fashion (or at least that the iris sample can be treated as such), that the Central Limit Theorem holds for samples of iris flowers of size 50, and that the population standard deviation of petal length for our particular *setosa* species is 0.5 cm.

Now we will do the same test, except we will <u>not</u> make any assumptions about the population standard deviation.

Question #1 Compute the standard error of the mean for our sample of 50 *setosa* petal lengths.

SEM = s/\sqrt{n}

= 0.174/7.071 = 0.025

Question #2 Compute the t-statistic corresponding to the sample mean.

(1.462 – 1.3)/0.025 = 6.48

Question #3 What are the degrees of freedom associated with this t-statistic?

The degrees of freedom is 49

The following R commands may be useful for Questions #4 and #5.

To find the <u>cumulative proportion</u> for a t-statistic:

```
> pt(value, df = degrees_of_freedom)
```

To find the <u>upper tail probability</u> (1 – cumulative proportion) for a t-statistic:

```
> pt(value, df = degrees_of_freedom, lower.tail = FALSE)
```

To find the value of the t-statistic corresponding to a cumulative proportion:

```
> qt(cumulative_proportion, df = degrees_of_freedom)
```

To find the value of the t-statistic corresponding to an upper tail probability:

```
> qt(upper_tail_probability, df = degrees_of_freedom, lower.tail = FALSE)
```

Question #4 What is the critical region on the *t* scale for α = 0.05? Do you still accept the alternative hypothesis H₁?

The critical region is >= 1.676551 and since the sample mean is inside that, we accept the alternative.

Question #5 What is the probability of getting a sample with a t statistic as large or larger than the value you obtained (in **Question #2**)? At a significance level of 0.05, do you still reject the null hypothesis H_0 and accept the alternative hypothesis H_a?

The probability would be 2.120742e-08, we reject the null hypothesis.

Now let's run the t-test in R. The t-test requires three arguments: the name of the variable we are testing about, the value of the population mean under H_0, and the sign of the alternative hypothesis (in the NHST framework). For this test, we use our setosa.petal.length dataset. If we didn't save it, we can quickly recreate it:

```
> library(dplyr)
> setosa.petal.length <- iris %>% filter(Species == "setosa") %>%
select(Petal.Length)
```

Then we run:

```
> t.test(setosa.petal.length$Petal.Length, mu = 1.3, alternative = "g")  #
because we have a > sign in Ha
```

Question #6 Paste the output of the t-test. Do you get the same t-statistic and p-value as in **Question #5**?

One Sample t-test

data: setosa_len$Petal.Length

t = 6.5961, df = 49, p-value = 1.401e-08

alternative hypothesis: true mean is greater than 1.3

95 percent confidence interval:

 1.420824   Inf

sample estimates:

mean of x

   1.462

We got roughly the same p-value.

You can also run a power analysis for a t-test using a single command, but it requires some setup.

```
> n <-  # sample size
> mu0 <-  # value of mu under H0
> mu1 <-  # value of mu under H1
> s <-  sd(setosa.petal.length$Petal.Length) # estimated standard
deviation; here we just estimate from the data we have available
> alpha <- 0.05

> power.t.test(n = n, delta = abs(mu0 – mu1), sd = s, sig.level = alpha,
type = "one.sample", alternative = "one.sided") # recall that we said power
was the same no matter which value was mu0 and which was mu1
```

Question #7 Paste the output of the power analysis. Is 50 flowers a large enough sample to detect the difference between $\mu = 1.3\,cm$ and $\mu = 1.5\,cm$?

One-sample t test power calculation

n = 49

delta = 0.2

sd = 0.173664

sig.level = 0.05

power = 1

alternative = one.sided

Yes , 50 flowers is enough because our power is 100%.

Now let's investigate what would happen if we used a <u>two-sided</u> alternative hypothesis instead. We test the null hypothesis $\mu = 1.3\,cm$ against the alternative hypothesis $H_a : \mu \neq 1.3\,cm$ (in the NHST framework).

Change your t-test code to:

```
> t.test(setosa.petal.length$Petal.Length, mu = 1.3, alternative = "t")  #
because we have a ≠ sign in Ha
```

Question #8 Paste the output of the t-test (I just need the table with the p-value). Compare the values of the test statistic and p-value with that of the one-sided test (in **Question #6**).

  One Sample t-test

data: setosa_len$Petal.Length

t = 6.5961, df = 49, p-value = 2.803e-08

alternative hypothesis: true mean is not equal to 1.3

95 percent confidence interval:

 1.412645 1.511355

sample estimates:

mean of x

  1.462

The p-value here is the same as the calculated one in Question 6.

Using a two-sided alternative hypothesis in the NHST framework is equivalent to splitting the critical region so that half is below 1.3 cm and the other half is above 1.3 cm. Thus, when we do Neyman-Pearson testing, we need to calculate the probability of being in each part of the critical region separately, then add those probabilities.

Change your power analysis code to:

```
> power.t.test(n = n, delta = abs(mu0 – mu1), sd = s, sig.level = alpha,
type = "one.sample", alternative = "two.sided")
```

Question #9 Paste the output of the power analysis. Is 50 flowers still a large enough sample to detect the difference between $\mu = 1.3\,cm$ and $\mu = 1.5\,cm$?

One-sample t test power calculation

n = 49

delta = 0.2

sd = 0.173664

sig.level = 0.05

power = 1

alternative = two.sided

Since the power is still 100%, we can still assume that 50 flowers is large enough.