

# Inference for numerical data

## North Carolina births

In 2004, the state of North Carolina released a large data set containing information on births recorded in this state. This data set is useful to researchers studying the relation between habits and practices of expectant mothers and the birth of their children. We will work with a random sample of observations from this data set.

## Exploratory analysis

Load the `nc` data set into our workspace.

```
load("more/nc.RData")
```

We have observations on 13 different variables, some categorical and some numerical. The meaning of each variable is as follows.

variable	description
<code>fage</code>	father's age in years.
<code>mage</code>	mother's age in years.
<code>mature</code>	maturity status of mother.
<code>weeks</code>	length of pregnancy in weeks.
<code>premie</code>	whether the birth was classified as premature ( <code>premie</code> ) or full-term.
<code>visits</code>	number of hospital visits during pregnancy.
<code>marital</code>	whether mother is <code>married</code> or <code>not married</code> at birth.
<code>gained</code>	weight gained by mother during pregnancy in pounds.
<code>weight</code>	weight of the baby at birth in pounds.

variable	description
lowbirthweight	whether baby was classified as low birthweight ( <b>low</b> ) or not ( <b>not low</b> ).
gender	gender of the baby, <b>female</b> or <b>male</b> .
habit	status of the mother as a <b>nonsmoker</b> or a <b>smoker</b> .
whitemom	whether mom is <b>white</b> or not <b>white</b> .

1. What are the cases in this data set? How many cases are there in our sample? *The cases are the births for the station of North Carolina. We have 1000 cases in our sample.*

As a first step in the analysis, we should consider summaries of the data. This can be done using the `summary` command:

```
summary(nc)
```

```
##      fage      mage      mature      weeks
## Min.   :14.00 Min.   :13   mature mom :133 Min.   :20.00
## 1st Qu.:25.00 1st Qu.:22   younger mom:867 1st Qu.:37.00
## Median :30.00 Median :27                                Median :39.00
## Mean   :30.26 Mean   :27                                Mean   :38.33
## 3rd Qu.:35.00 3rd Qu.:32                                3rd Qu.:40.00
## Max.   :55.00 Max.   :50                                Max.   :45.00
## NA's   :171                                NA's    :2
##      premie      visits      marital      gained
## full term:846 Min.   : 0.0   married   :386 Min.   : 0.00
## premie   :152 1st Qu.:10.0   not married:613 1st Qu.:20.00
## NA's     : 2 Median :12.0   NA's       : 1 Median :30.00
##                               Mean :12.1                               Mean  :30.33
##                               3rd Qu.:15.0                               3rd Qu.:38.00
##                               Max.   :30.0                               Max.   :85.00
##                               NA's    :9                               NA's    :27
##      weight      lowbirthweight      gender      habit
## Min.   : 1.000   low   :111   female:503   nonsmoker:873
## 1st Qu.: 6.380   not low:889   male  :497   smoker   :126
## Median : 7.310                                NA's     : 1
## Mean   : 7.101
## 3rd Qu.: 8.060
## Max.   :11.750
##
##      whitemom
## not white:284
## white    :714
## NA's     : 2
##
```

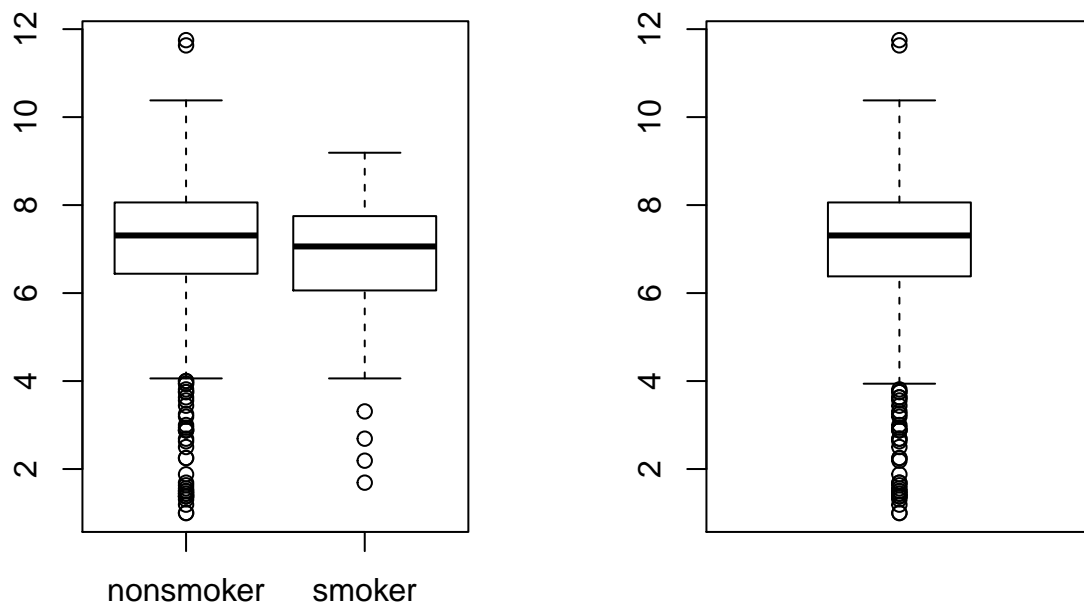
```
##
##
##
```

As you review the variable summaries, consider which variables are categorical and which are numerical. For numerical variables, are there outliers? If you aren't sure or want to take a closer look at the data, make a graph.

Consider the possible relationship between a mother's smoking habit and the weight of her baby. Plotting the data is a useful first step because it helps us quickly visualize trends, identify strong associations, and develop research questions.

2. Make a side-by-side boxplot of `habit` and `weight`. What does the plot highlight about the relationship between these two variables?

```
par(mfrow = c(1, 2))
boxplot(weight ~ habit, data = nc)
boxplot(nc$weight)
```



*The median weight of babies from smokers is lower than the median weight of babies from nonsmokers. In fact, their median weight is more in line with the median weight of all babies.*

The box plots show how the medians of the two distributions compare, but we can also compare the means of the distributions using the following function to split the `weight` variable into the `habit` groups, then take the mean of each using the `mean` function.

```
by(nc$weight, nc$habit, mean)
```

```
## nc$habit: nonsmoker
## [1] 7.144273
```

```
## -----
## nc$habit: smoker
## [1] 6.82873
```

There is an observed difference, but is this difference statistically significant? In order to answer this question we will conduct a hypothesis test .

## Inference

3. Check if the conditions necessary for inference are satisfied. Note that you will need to obtain sample sizes to check the conditions. You can compute the group size using the same `by` command above but replacing `mean` with `length`.

```
by(nc$weight, nc$habit, length)
```

```
## nc$habit: nonsmoker
## [1] 873
## -----
## nc$habit: smoker
## [1] 126
```

*We seem to have a large enough sample size for both to assume a normal distribution.*

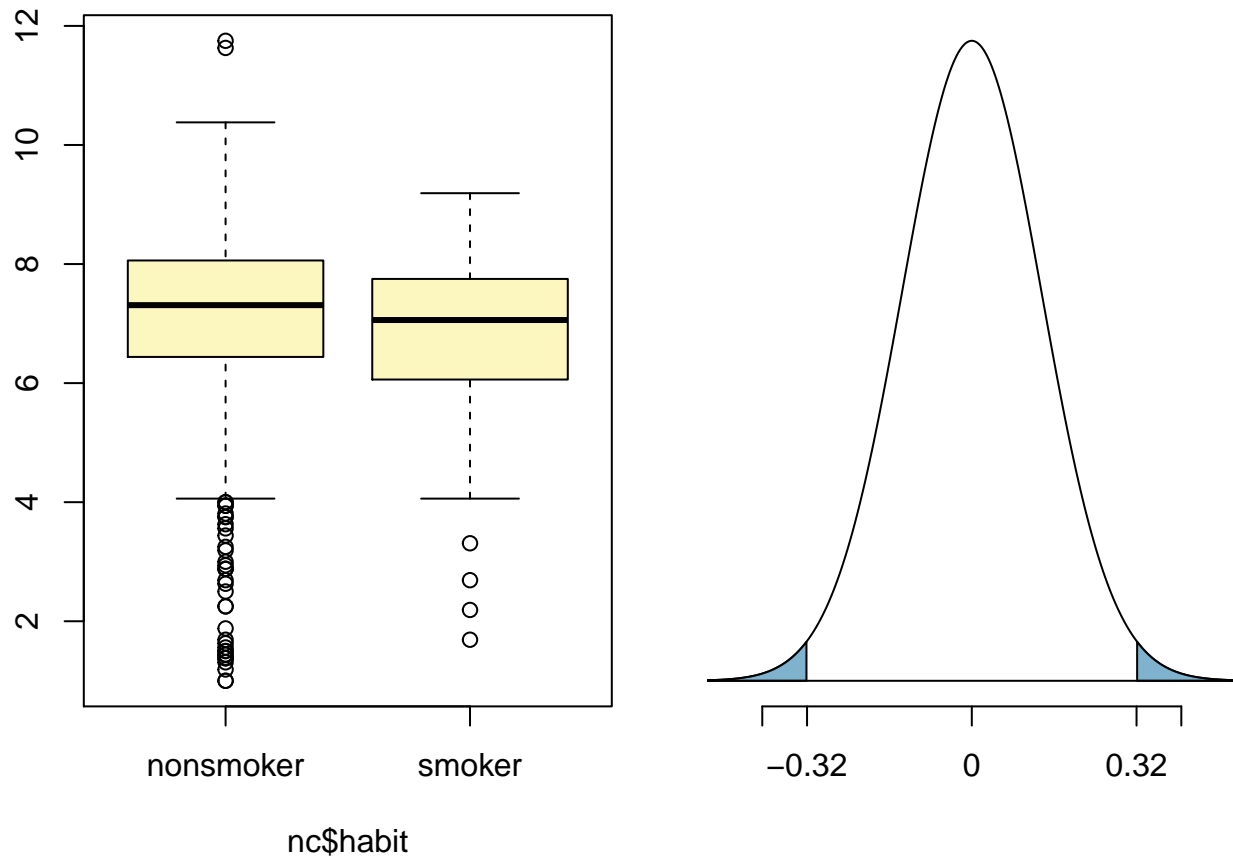
4. Write the hypotheses for testing if the average weights of babies born to smoking and non-smoking mothers are different.

$$H_0 : \mu_{sw} = \mu_{nsw} \quad H_A : \mu_{sw} \neq \mu_{nsw}$$

Next, we introduce a new function, `inference`, that we will use for conducting hypothesis tests and constructing confidence intervals.

```
inference(y = nc$weight, x = nc$habit, est = "mean", type = "ht", null = 0,
          alternative = "twosided", method = "theoretical")
```

```
## Warning: package 'BHH2' was built under R version 3.4.4
## Response variable: numerical, Explanatory variable: categorical
## Difference between two means
## Summary statistics:
## n_nonsmoker = 873, mean_nonsmoker = 7.1443, sd_nonsmoker = 1.5187
## n_smoker = 126, mean_smoker = 6.8287, sd_smoker = 1.3862
## Observed difference between means (nonsmoker-smoker) = 0.3155
##
## H0: mu_nonsmoker - mu_smoker = 0
## HA: mu_nonsmoker - mu_smoker != 0
## Standard error = 0.134
## Test statistic: Z = 2.359
## p-value = 0.0184
```

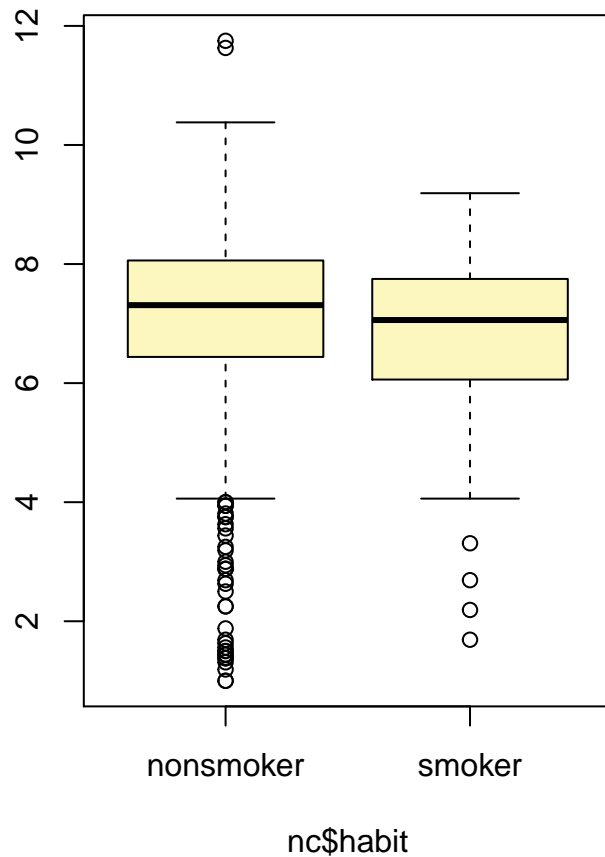


Let's pause for a moment to go through the arguments of this custom function. The first argument is `y`, which is the response variable that we are interested in: `nc$weight`. The second argument is the explanatory variable, `x`, which is the variable that splits the data into two groups, smokers and non-smokers: `nc$habit`. The third argument, `est`, is the parameter we're interested in: `"mean"` (other options are `"median"`, or `"proportion"`.) Next we decide on the `type` of inference we want: a hypothesis test (`"ht"`) or a confidence interval (`"ci"`). When performing a hypothesis test, we also need to supply the null value, which in this case is 0, since the null hypothesis sets the two population means equal to each other. The `alternative` hypothesis can be `"less"`, `"greater"`, or `"twosided"`. Lastly, the `method` of inference can be `"theoretical"` or `"simulation"` based.

5. Change the `type` argument to `"ci"` to construct and record a confidence interval for the difference between the weights of babies born to smoking and non-smoking mothers.

```
inference(y = nc$weight, x = nc$habit, est = "mean", type = "ci", null = 0,
          alternative = "twosided", method = "theoretical")
```

```
## Response variable: numerical, Explanatory variable: categorical
## Difference between two means
## Summary statistics:
## n_nonsmoker = 873, mean_nonsmoker = 7.1443, sd_nonsmoker = 1.5187
## n_smoker = 126, mean_smoker = 6.8287, sd_smoker = 1.3862
```

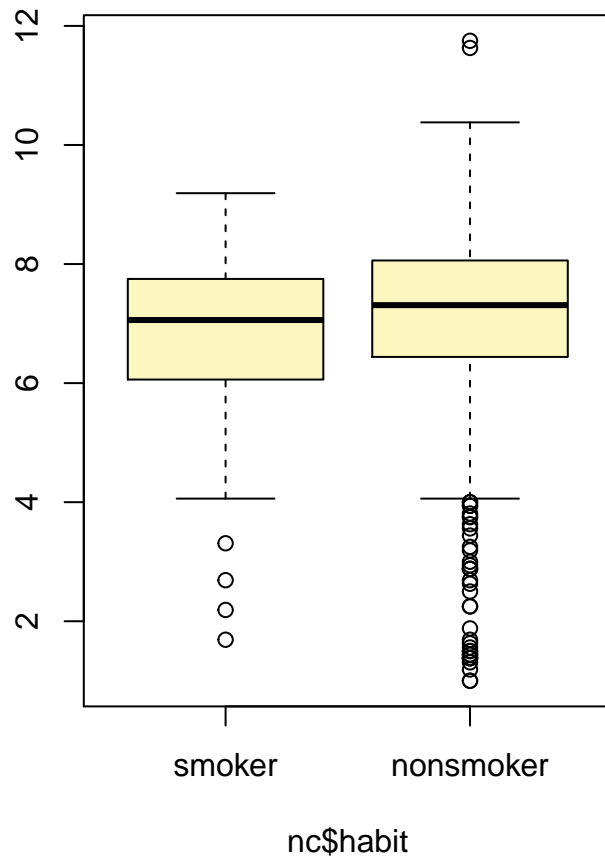


```
## Observed difference between means (nonsmoker-smoker) = 0.3155
##
## Standard error = 0.1338
## 95 % Confidence interval = ( 0.0534 , 0.5777 )
```

By default the function reports an interval for  $(\mu_{nonsmoker} - \mu_{smoker})$ . We can easily change this order by using the `order` argument:

```
inference(y = nc$weight, x = nc$habit, est = "mean", type = "ci", null = 0,
          alternative = "twosided", method = "theoretical",
          order = c("smoker", "nonsmoker"))
```

```
## Response variable: numerical, Explanatory variable: categorical
## Difference between two means
## Summary statistics:
## n_smoker = 126, mean_smoker = 6.8287, sd_smoker = 1.3862
## n_nonsmoker = 873, mean_nonsmoker = 7.1443, sd_nonsmoker = 1.5187
```



```
## Observed difference between means (smoker-nonsmoker) = -0.3155
##
## Standard error = 0.1338
## 95 % Confidence interval = ( -0.5777 , -0.0534 )
```

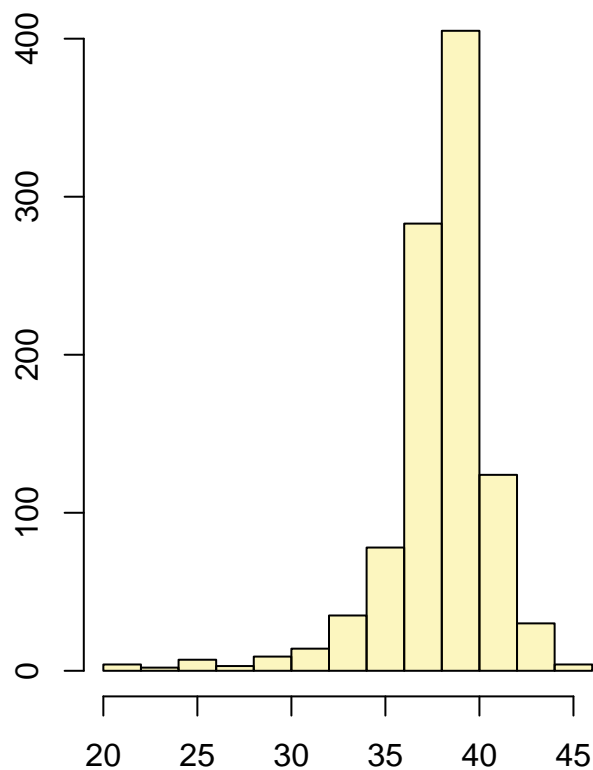
---

### On your own

- Calculate a 95% confidence interval for the average length of pregnancies (**weeks**) and interpret it in context. Note that since you're doing inference on a single population parameter, there is no explanatory variable, so you can omit the **x** variable from the function.

```
inference(y = nc$weeks, est = "mean", type = "ci", null = 0,
          alternative = "twosided", method = "theoretical")
```

```
## Single mean
## Summary statistics:
```



nc\$weeks

```
## mean = 38.3347 ; sd = 2.9316 ; n = 998
## Standard error = 0.0928
## 95 % Confidence interval = ( 38.1528 , 38.5165 )
```

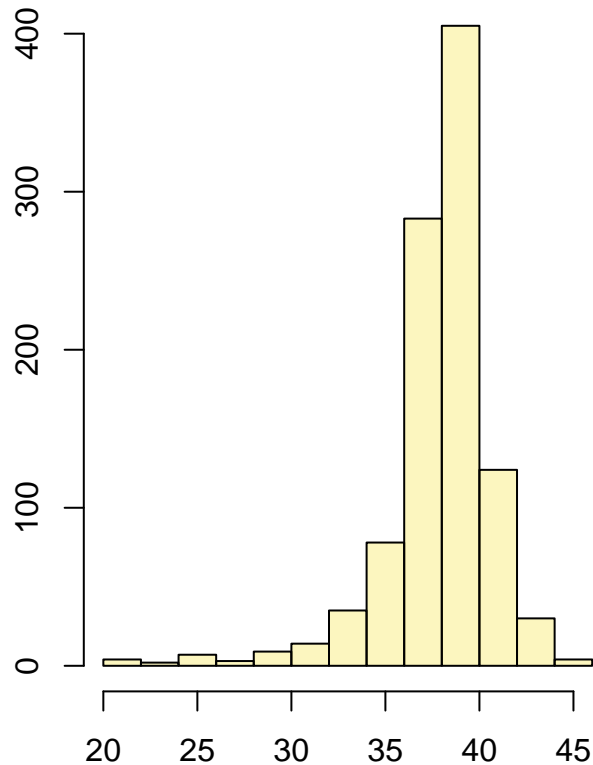
*The average length of pregnancies for North Carolina women seems to be 40 weeks.*

- Calculate a new confidence interval for the same parameter at the 90% confidence level. You can change the confidence level by adding a new argument to the function: `conflevel = 0.90`.

```
inference(y = nc$weeks, est = "mean", type = "ci", null = 0,
          alternative = "twosided", method = "theoretical", conflevel = 0.90)
```

```
## Single mean
## Summary statistics:
```





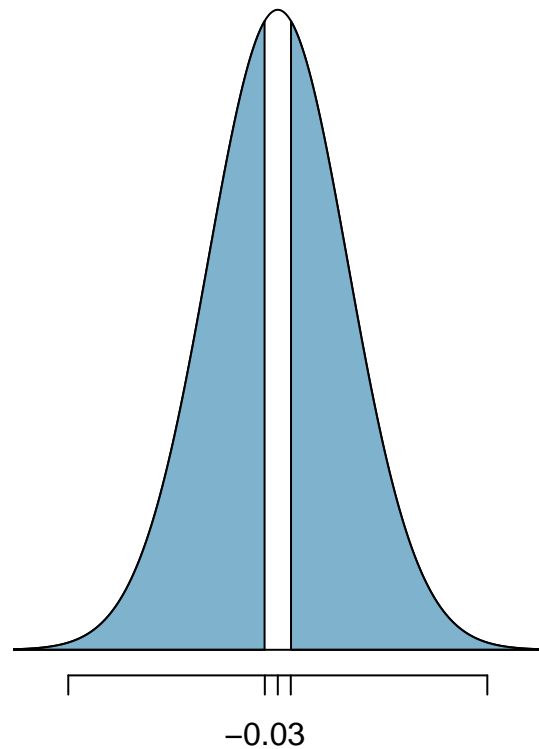
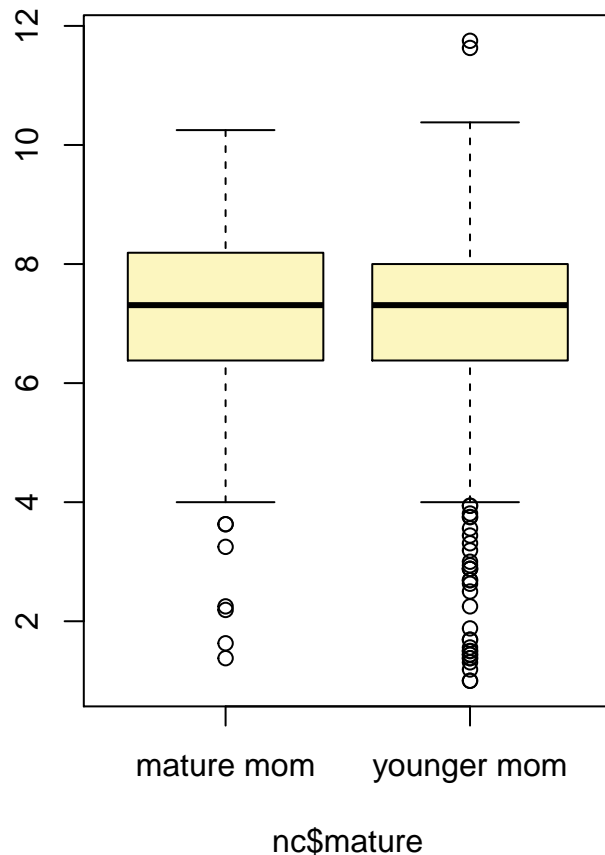
nc\$weeks

```
## mean = 38.3347 ; sd = 2.9316 ; n = 998
## Standard error = 0.0928
## 90 % Confidence interval = ( 38.182 , 38.4873 )
```

- Conduct a hypothesis test evaluating whether the average weight gained by younger mothers is different than the average weight gained by mature mothers.

```
inference(y = nc$weight, x = nc$mature, est = "mean", type = "ht", null = 0,
          alternative = "twosided", method = "theoretical")
```

```
## Response variable: numerical, Explanatory variable: categorical
## Difference between two means
## Summary statistics:
## n_mature mom = 133, mean_mature mom = 7.1256, sd_mature mom = 1.6591
## n_younger mom = 867, mean_younger mom = 7.0972, sd_younger mom = 1.4855
## Observed difference between means (mature mom-younger mom) = 0.0283
##
## H0: mu_mature mom - mu_younger mom = 0
## HA: mu_mature mom - mu_younger mom != 0
## Standard error = 0.152
## Test statistic: Z = 0.186
## p-value = 0.8526
```



- Now, a non-inference task: Determine the age cutoff for younger and mature mothers. Use a method of your choice, and explain how your method works.

```
levels(nc$mature)
```

```
## [1] "mature mom" "younger mom"
```

```
max(subset(nc, mature == "younger mom")$mage)
```

```
## [1] 34
```

```
min(subset(nc, mature == "mature mom")$mage)
```

```
## [1] 35
```

After finding out how the data set separates the mature column, we simply take the max of younger mom, and min of mature mom. The cut off for younger mothers is 34.

- Pick a pair of numerical and categorical variables and come up with a research question evaluating the relationship between these variables. Formulate the question in a way that it can be answered using a hypothesis test and/or a confidence interval. Answer your question using the **inference** function, report the statistical results, and also provide an explanation in plain language.

$H_0 : \mu_{\text{weeks}+\text{white}} = \mu_{\text{weeks}+\text{nonwhite}}$   $H_A : \mu_{\text{weeks}+\text{white}} \neq \mu_{\text{weeks}+\text{nonwhite}}$

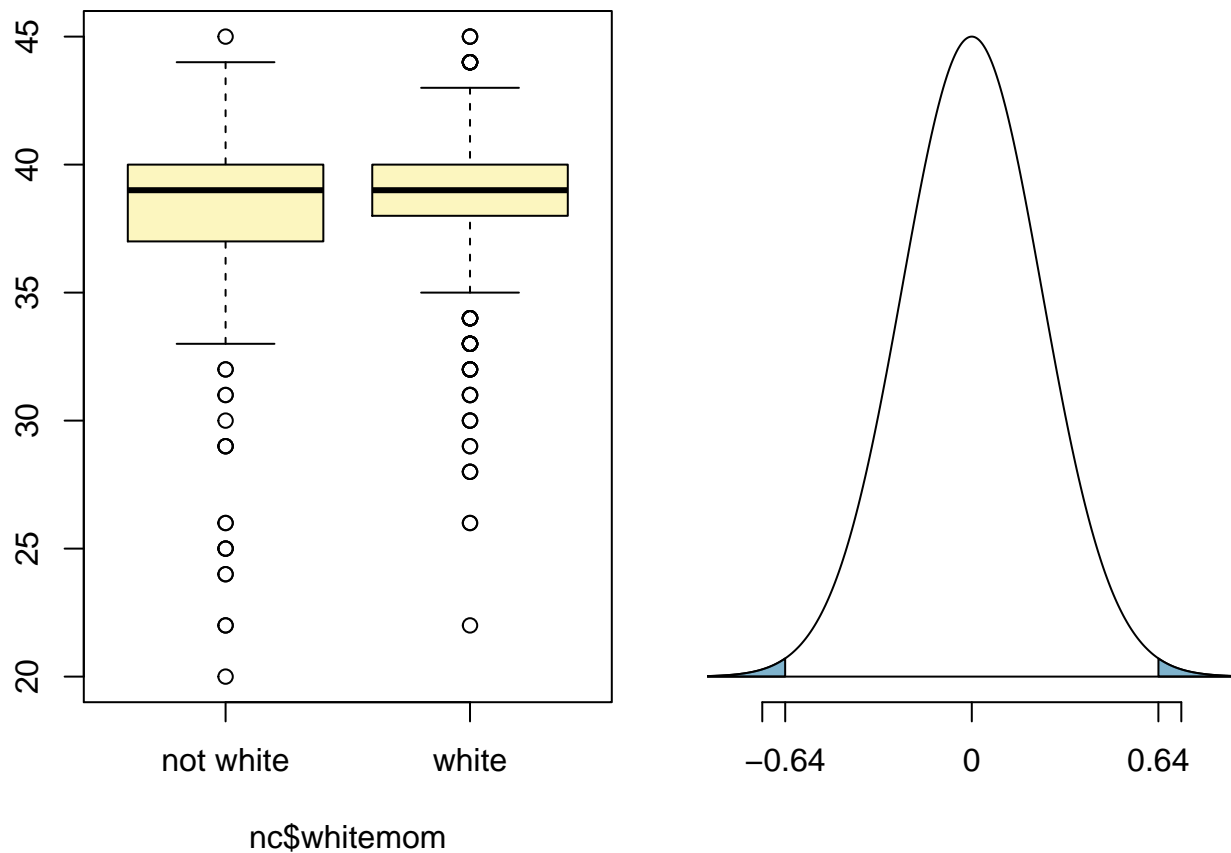
Hypothesis is that the length of pregnancies between white and nonwhite women are different.

```
inference(y = nc$weeks, x = nc$whitemom, est = "mean", type = "ht", null = 0,
          alternative = "twosided", method = "theoretical")
```

```
## Response variable: numerical, Explanatory variable: categorical
```

```
## Difference between two means
## Summary statistics:
## n_not white = 284, mean_not white = 37.8768, sd_not white = 3.6705
## n_white = 712, mean_white = 38.5126, sd_white = 2.5617

## Observed difference between means (not white-white) = -0.6359
##
## H0: mu_not white - mu_white = 0
## HA: mu_not white - mu_white != 0
## Standard error = 0.238
## Test statistic: Z = -2.672
## p-value = 0.0076
```



*With a p-value of only 0.0076, we affirm the null hypothesis. Average length of pregnancies for white and nonwhite women are the same in North Carolina.*

This is a product of OpenIntro that is released under a Creative Commons Attribution-ShareAlike 3.0 Unported. This lab was adapted for OpenIntro by Mine Çetinkaya-Rundel from a lab written by the faculty and TAs of UCLA Statistics.