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

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

1. What are the cases in this data set? How many cases are there in our sample?

Each case is a single birth. We have 1,000 cases in this data set.

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
##
```

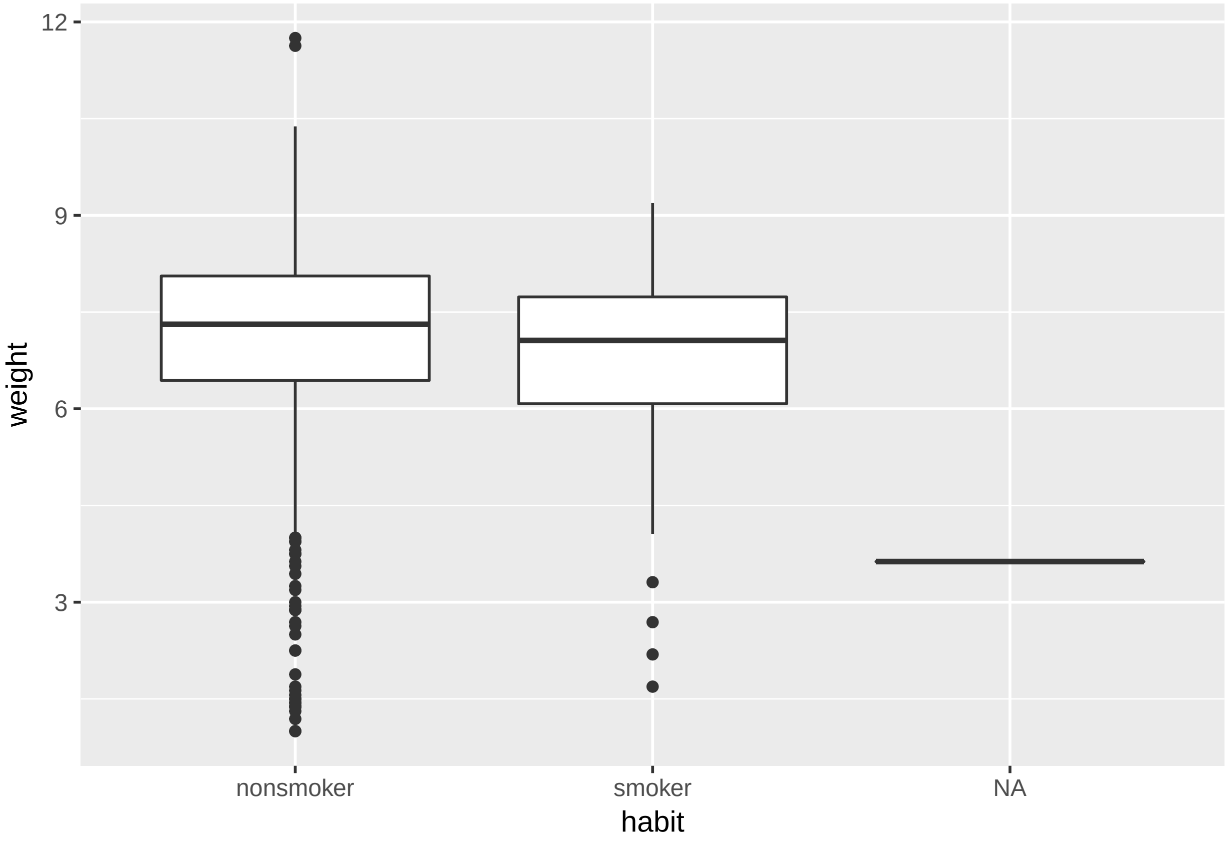
```
##
##
##
```

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?

```
library(ggplot2)

ggplot(nc, aes(x=habit, y=weight)) + geom_boxplot()
```



The plot shows that there is a slightly smaller median weight observerd for mothers who are smokers.

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 .

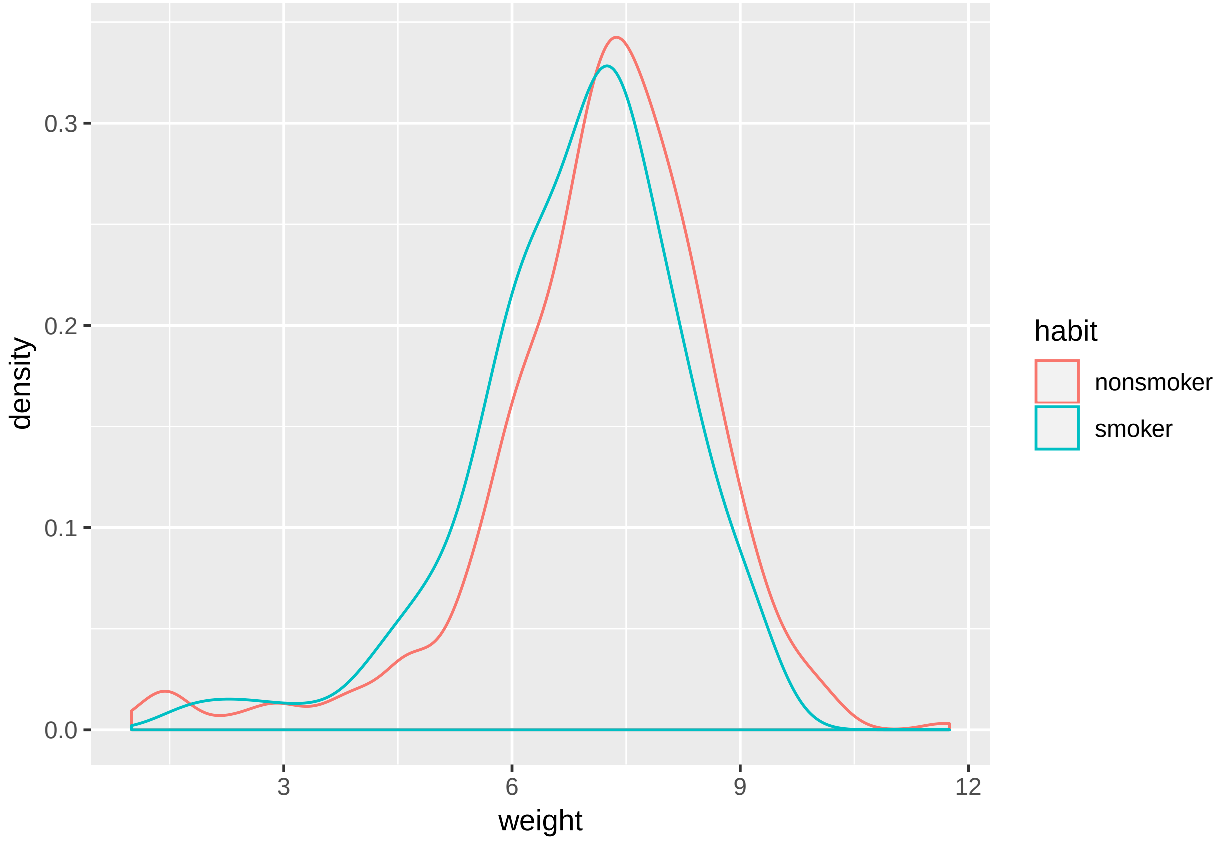
Inference

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`.

```
# Check sample sizes
by(nc$weight, nc$habit, length)
```

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

```
# Check for skew/normality (removing NAs)
ggplot(nc[!is.na(nc$habit),], aes(x=weight, col=habit)) + geom_density()
```



There is some skew with each set (smoker vs. nonsmoker), but it is modest and we have pretty large sample sizes. As far as checking for independence, we can only assume so since we took

a random sample of a larger data set.

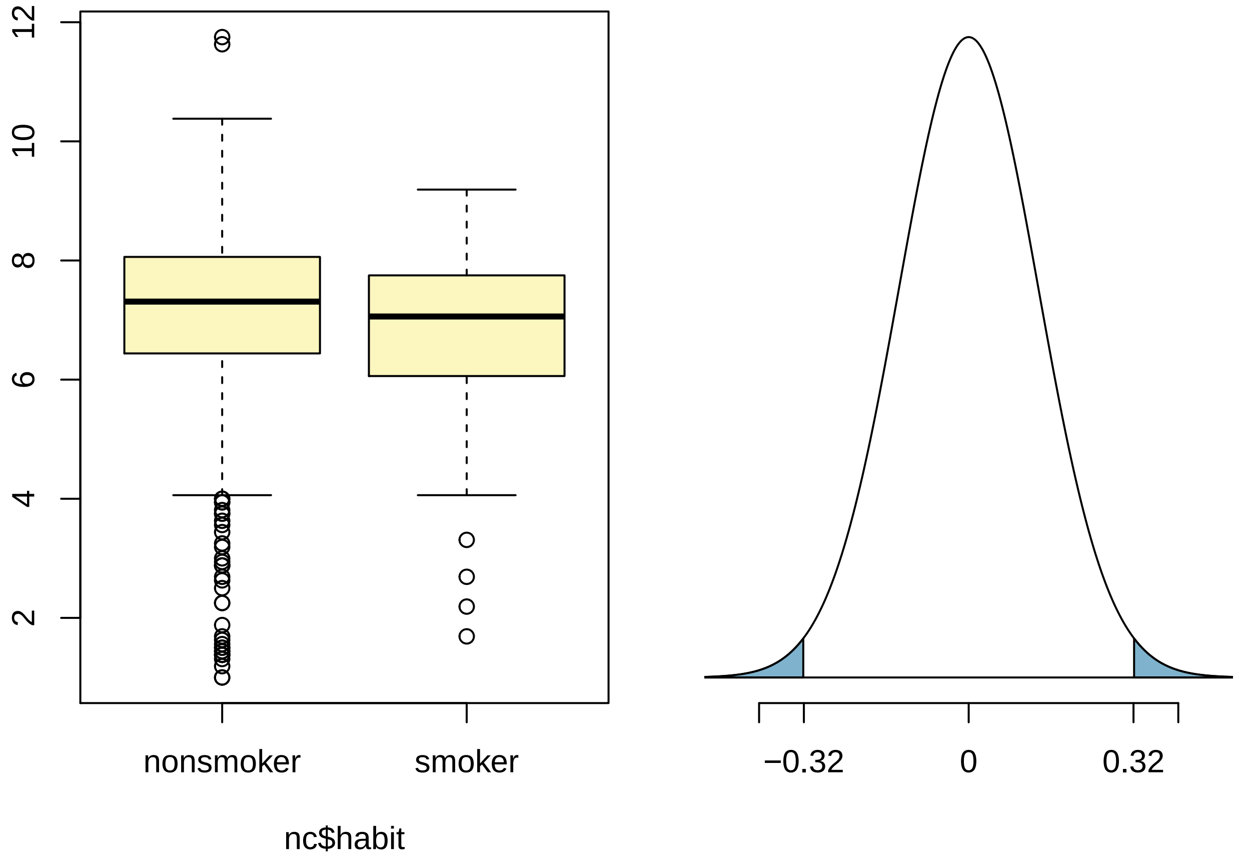
4. Write the hypotheses for testing if the average weights of babies born to smoking and non-smoking mothers are different.

Our hypotheses would be: $H_0 : \mu_{smoker} = \mu_{non-smoker}$ and $H_A : \mu_{smoker} \neq \mu_{non-smoker}$. Which is to say, our null hypothesis is that the mean birth weights of babies whose moms smoked during pregnancy are the same as those whose did not smoke. Our alternative hypothesis is that those means are not the same.

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")
```

```
## 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
```

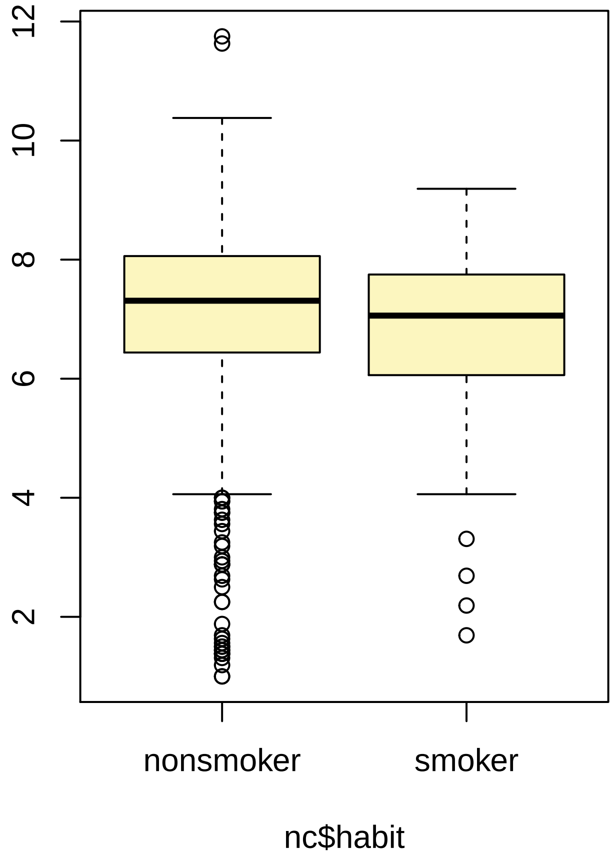


Let's pause for a moment to go through the arguments of this custom function. The first argument is y, which is the response variable that we are interested in: nc$weight. The second argument is the explanatory variable, x, which is the variable that splits the data into two groups, smokers and non-smokers: nc$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
```

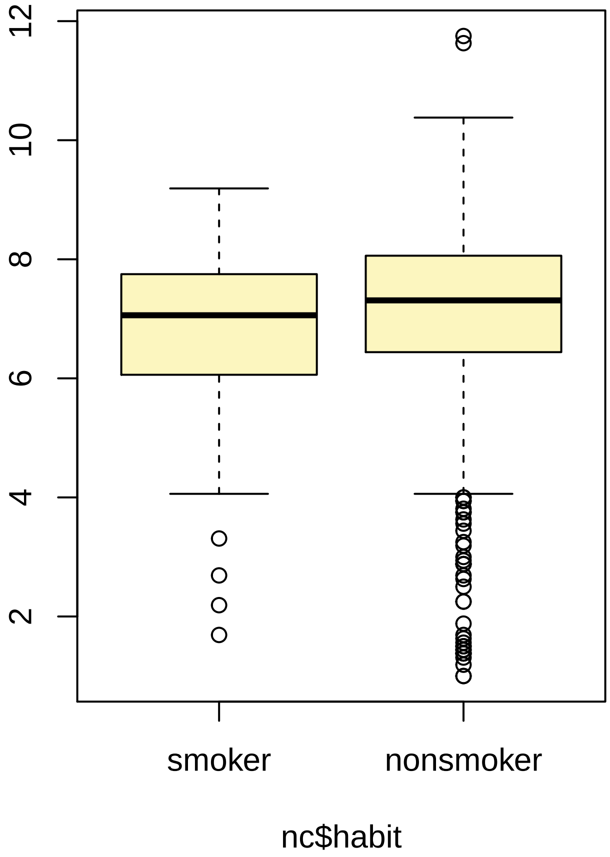


```
## Observed difference between means (nonsmoker-smoker) = 0.3155
##
## Standard error = 0.1338
## 95 % Confidence interval = ( 0.0534 , 0.5777 )
```

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
```



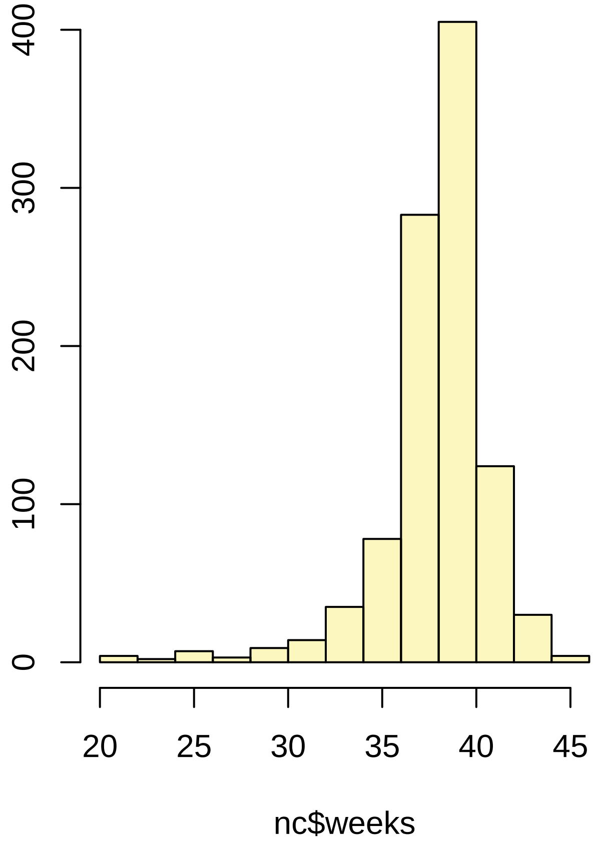
```
## Observed difference between means (smoker-nonsmoker) = -0.3155
##
## Standard error = 0.1338
## 95 % Confidence interval = ( -0.5777 , -0.0534 )
```

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", method = "theoretical")
```

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



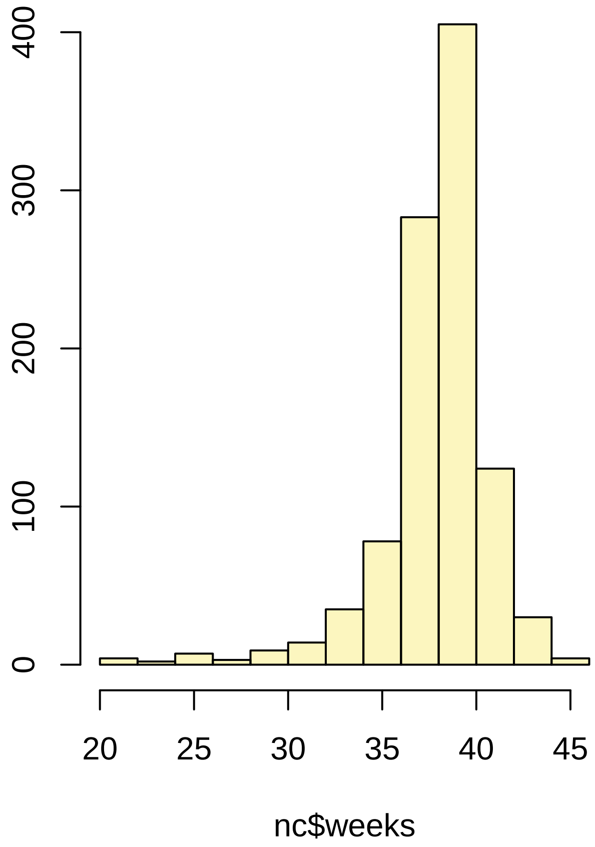
```
## mean = 38.3347 ;  sd = 2.9316 ;  n = 998
## Standard error = 0.0928
## 95 % Confidence interval = ( 38.1528 , 38.5165 )
```

We are 95% confident that the mean number of weeks a North Carolina woman carries a baby before delivery is between 38.1528 and 38.5165.

- 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", method = "theoretical",
          conflevel = 0.90)
```

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



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

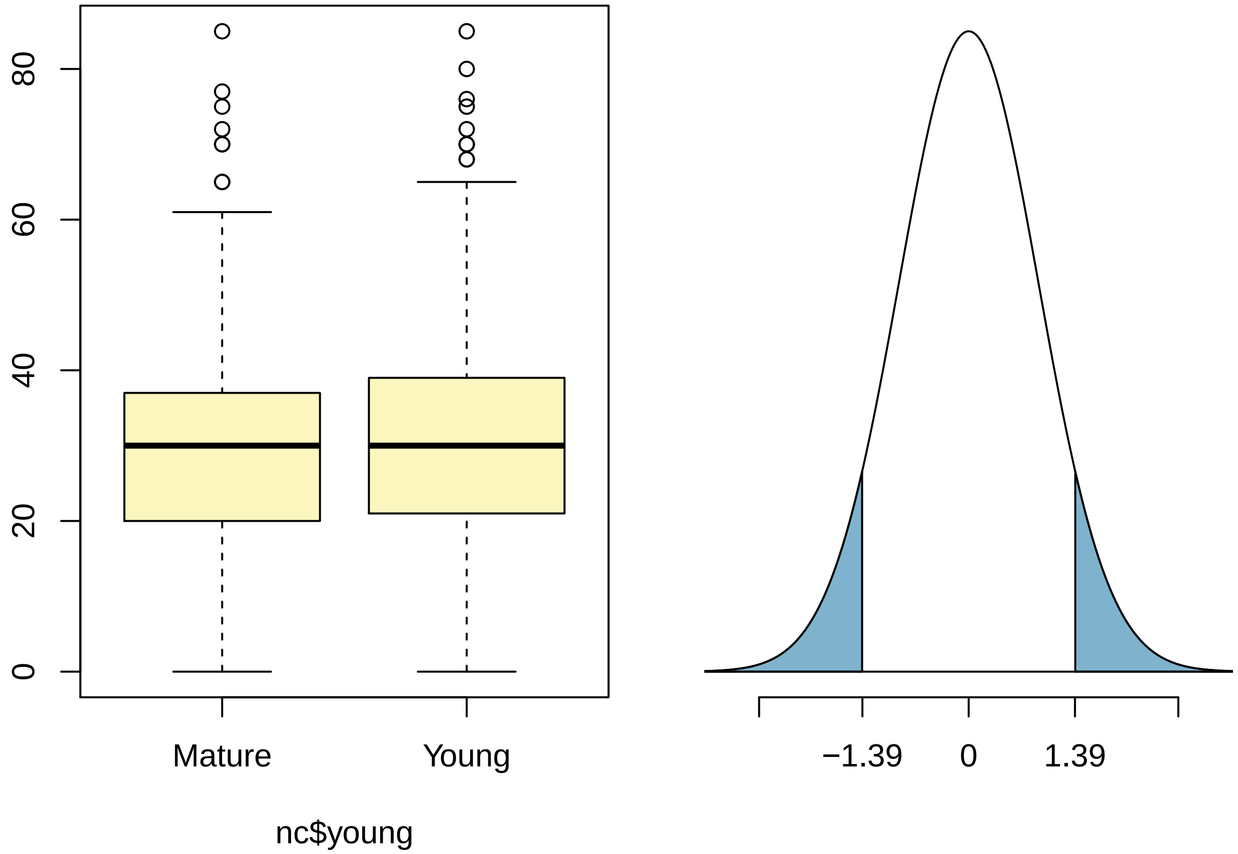
The 90% confidence level gives us a confidence interval of (38.182, 38.4873).

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

```
library(dplyr)

# Get the median age
med <- median(nc$mage)

# ID young mothers as being at or below median value.
nc <- nc %>% mutate(young = case_when(mage <= med ~ "Young",
                                      mage > med ~ "Mature"))

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

```
## Response variable: numerical, Explanatory variable: categorical
## Difference between two means
## Summary statistics:
## n_Mature = 446, mean_Mature = 29.574, sd_Mature = 13.9051
## n_Young = 527, mean_Young = 30.962, sd_Young = 14.5025

## Observed difference between means (Mature-Young) = -1.3881
```

```
##
## H0: mu_Mature - mu_Young = 0
## HA: mu_Mature - mu_Young != 0
## Standard error = 0.912
## Test statistic: Z =  -1.521
## p-value =  0.1282
```



The observed values do not provide enough evidence to reject the null hypothesis that the means are the same.

- 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.

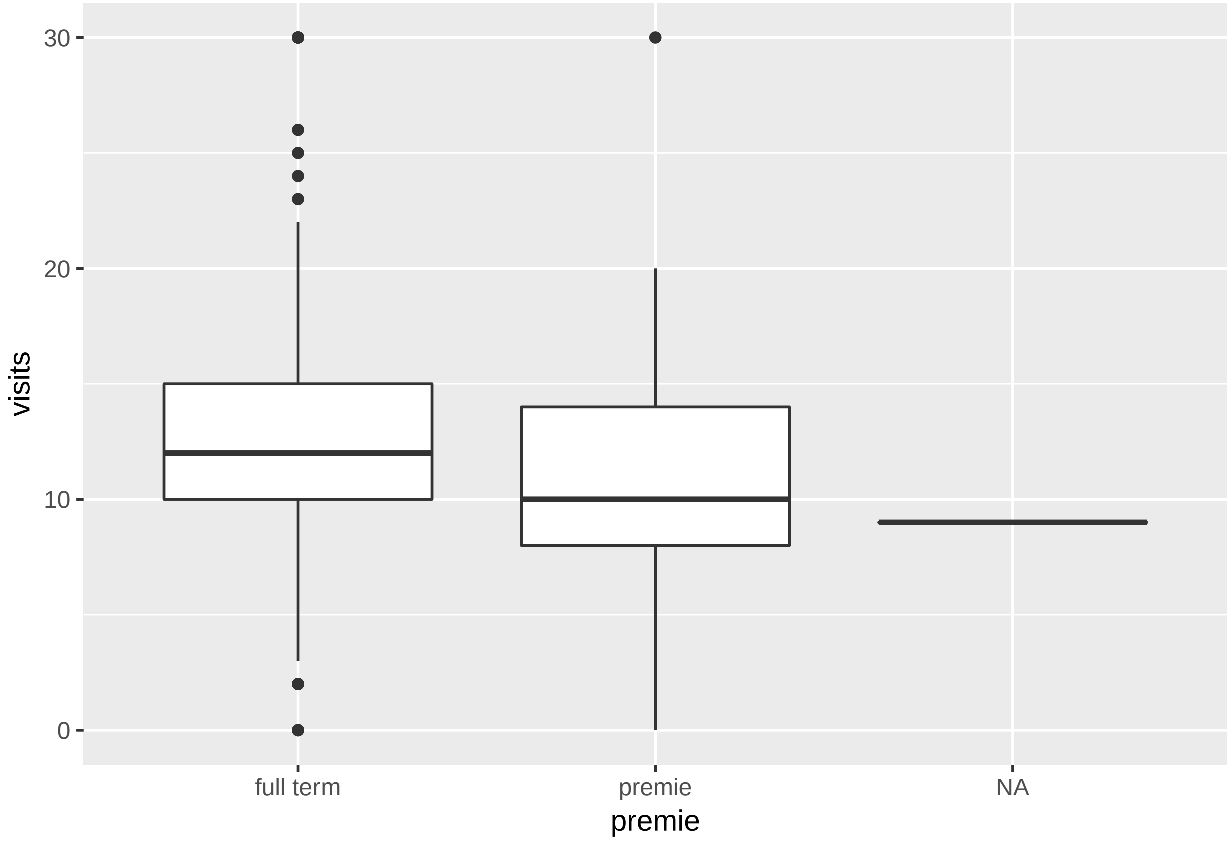
The optimal method would be to speak with medical professionals to get a sense of what age is generally considered to be a cutoff for being physically "mature". However, since I do not have anyone handy to do that, I chose the median value of age: 27.

- 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.

The two variables I chose are `premie` and `visits`. The question I pose is: do mothers who have premature babies tend to see the doctor less during pregnancy?

To phrase it as a hypothesis test, our null hypothesis is that the means for premature babies and full term babies are the same. Expressed mathematically as $H_0 : \mu_{premature} = \mu_{full-term}$ and $H_A : \mu_{premature} \neq \mu_{full-term}$

```
ggplot(nc[!is.na(nc$visits),], aes(x=premie, y=visits)) + geom_boxplot()
```



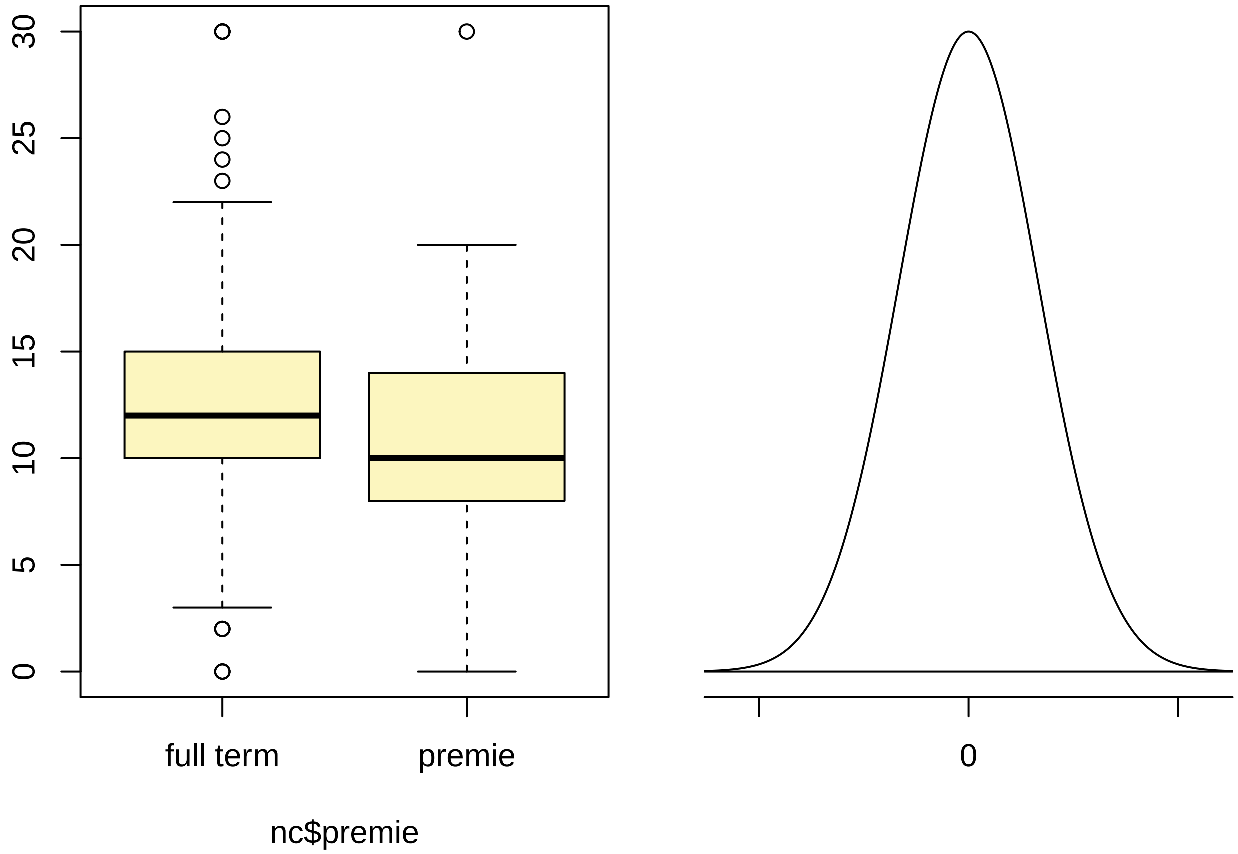
```
by(nc$visits, nc$premie, length)
```

```
## nc$premie: full term
## [1] 846
## ---------------------------------------------------------
## nc$premie: premie
## [1] 152
```

Looking at the data, there is some modest skew, but we have considerable sample sizes.

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

```
## Response variable: numerical, Explanatory variable: categorical
## Difference between two means
## Summary statistics:
## n_full term = 840, mean_full term = 12.3524, sd_full term = 3.7515
## n_premie = 150, mean_premie = 10.74, sd_premie = 4.7323

## Observed difference between means (full term-premie) = 1.6124
##
## H0: mu_full term - mu_premie = 0
## HA: mu_full term - mu_premie != 0
## Standard error = 0.407
## Test statistic: Z =  3.957
## p-value =  0
```



Our hypothesis results show that there is sufficient evidence to reject the null hypothesis that both means are equal and observed differences were due to chance.

In plain English, our test indicates that there is a difference in the typical number of doctor visits that a woman who had a premature birth has and one who had a full-term baby.
