1. Use the data pipeline (including `mutate()` and `pivot_longer()`) we developed in class to create a longer data frame with one row for each measured stem. Use dplyr's `filter` function to remove all of the girths that are zero and use `extract()` to get the stem number, making sure to `convert = TRUE` to make it a number class. Store this longer data frame as an object called `clean_data`, and display the result in your console.

```
## # A tibble: 6 x 5
##   PlotID SpCode   treeid  stem girth
##   <chr>  <chr>     <int> <int> <int>
## 1 BSP70  Acaccaes      1     1    25
## 2 BSP70  Acaccaes      2     1    25
## 3 BSP70  Acaccaes      3     1    28
## 4 BSP70  Acaccaes      4     1    38
## 5 BSP70  Acaccaes      5     1    54
## 6 BSP100 Acaccate      6     1    12
```

2. Stems are measured in girth (*i.e., circumference*) rather than diameter. Use `mutate()` to convert girth to diameter using the following formula: `diameter = circumference / pi` and print the results in your console.

```
## # A tibble: 6 x 6
##   PlotID SpCode   treeid  stem girth diameter
##   <chr>  <chr>     <int> <int> <int>    <dbl>
## 1 BSP70  Acaccaes      1     1    25     7.96
## 2 BSP70  Acaccaes      2     1    25     7.96
## 3 BSP70  Acaccaes      3     1    28     8.91
## 4 BSP70  Acaccaes      4     1    38    12.1
## 5 BSP70  Acaccaes      5     1    54    17.2
## 6 BSP100 Acaccate      6     1    12     3.82
```

3. Add another line to your `mutate()` function which calculates tree mass from the new diameter column you made according to the following equation: `mass = 0.124 * diameter^2.53`. Save this new data frame as `tree_mass` and print the results to the console.

```
## # A tibble: 6 x 7
##   PlotID SpCode   treeid  stem girth diameter   mass
##   <chr>  <chr>     <int> <int> <int>    <dbl>  <dbl>
## 1 BSP70  Acaccaes      1     1    25     7.96  23.6
## 2 BSP70  Acaccaes      2     1    25     7.96  23.6
## 3 BSP70  Acaccaes      3     1    28     8.91  31.4
## 4 BSP70  Acaccaes      4     1    38    12.1   68.0
## 5 BSP70  Acaccaes      5     1    54    17.2  165.
## 6 BSP100 Acaccate      6     1    12     3.82   3.68
```

4. Estimate the total biomass by summing the mass of all of the stems in the `tree_mass` data.

```
## [1] 26710042
```

5. The `SpCode` column contains information on the genus and specific epithet (species). Use `separate()` on the `SpCode` column to make a `GenusCode` and `SpEpCode` columns by separating them at position 4. Then use `group_by` and `summarize` to calculate the total biomass for each unique `GenusCode`.

```
## # A tibble: 242 x 2
##    GenusCode   biomass
##    <chr>         <dbl>
##  1 Acac       12849.
##  2 Acro       17899.
##  3 Acti       64199.
##  4 Aegl           6.47
##  5 Agla      448027.
##  6 Agro          23.6
##  7 Aila        1589.
##  8 Alan        6740.
##  9 Albi       37902.
## 10 Allo        1654.
## # i 232 more rows
```

6. Use ggplot to make a histogram of the `diameter` values in your `tree_mass` object. Make the x label `"Diameter [cm]` and the y label `"Number of Stems"`

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```