

Figures

```
library(tidyverse)
library(smmr)
```

Figure 1: Packages

```
Force+Height+Species
3.2+5+Hemigrapsus nudus
6.4+6+Hemigrapsus nudus
2+6.4+Hemigrapsus nudus
2+6.5+Hemigrapsus nudus
4.9+6.6+Hemigrapsus nudus
3+7+Hemigrapsus nudus
2.9+7.9+Hemigrapsus nudus
9.5+7.9+Hemigrapsus nudus
4+8+Hemigrapsus nudus
7.4+8.3+Hemigrapsus nudus
2.4+8.8+Hemigrapsus nudus
4+12.1+Hemigrapsus nudus
5.2+12.2+Hemigrapsus nudus
2.1+5.1+Lophopanopeus bellus
8.7+5.9+Lophopanopeus bellus
2.9+6.6+Lophopanopeus bellus
6.9+7.2+Lophopanopeus bellus
8.7+8.6+Lophopanopeus bellus
```

Figure 2: Crab claws data (some)

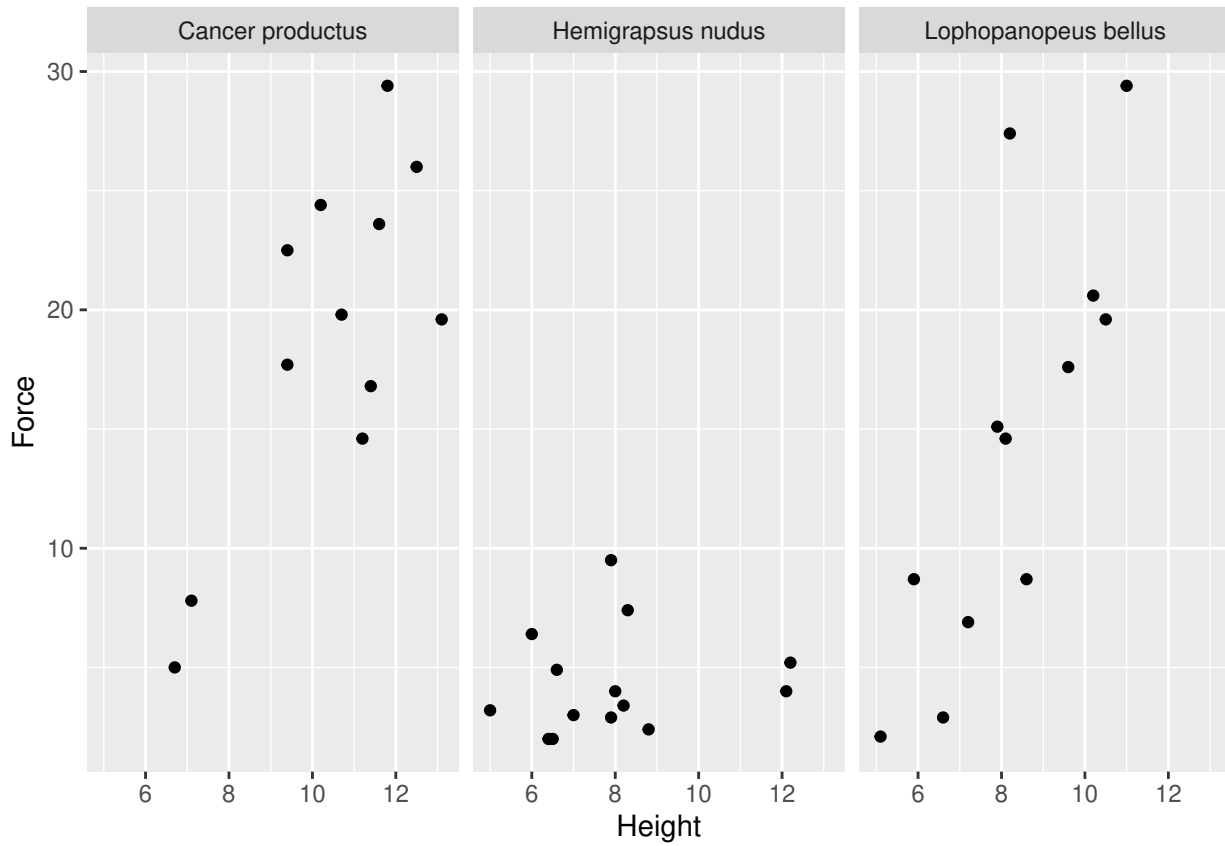


Figure 3: Crab claws graph

```
## # A tibble: 38 x 3
##   Force Height Species
##   <dbl> <dbl> <chr>
## 1  3.2    5 Hemigrapsus nudus
## 2  6.4    6 Hemigrapsus nudus
## 3  2      6.4 Hemigrapsus nudus
## 4  2      6.5 Hemigrapsus nudus
## 5  4.9    6.6 Hemigrapsus nudus
## 6  3      7 Hemigrapsus nudus
## 7  2.9    7.9 Hemigrapsus nudus
## 8  9.5    7.9 Hemigrapsus nudus
## 9  4      8 Hemigrapsus nudus
## 10 3.4    8.2 Hemigrapsus nudus
## # ... with 28 more rows
```

Figure 4: Crab claws data (some)

```
cereal_sugar
## # A tibble: 100 x 1
##   sugar
##   <dbl>
## 1  36.3
## 2  33.2
## 3  39
## 4  37.3
## 5  40.7
## 6  38.4
## 7  35.8
## 8  36
## 9  37.9
## 10 42.6
## # ... with 90 more rows
```

Figure 5: Cereal sugar data (some)

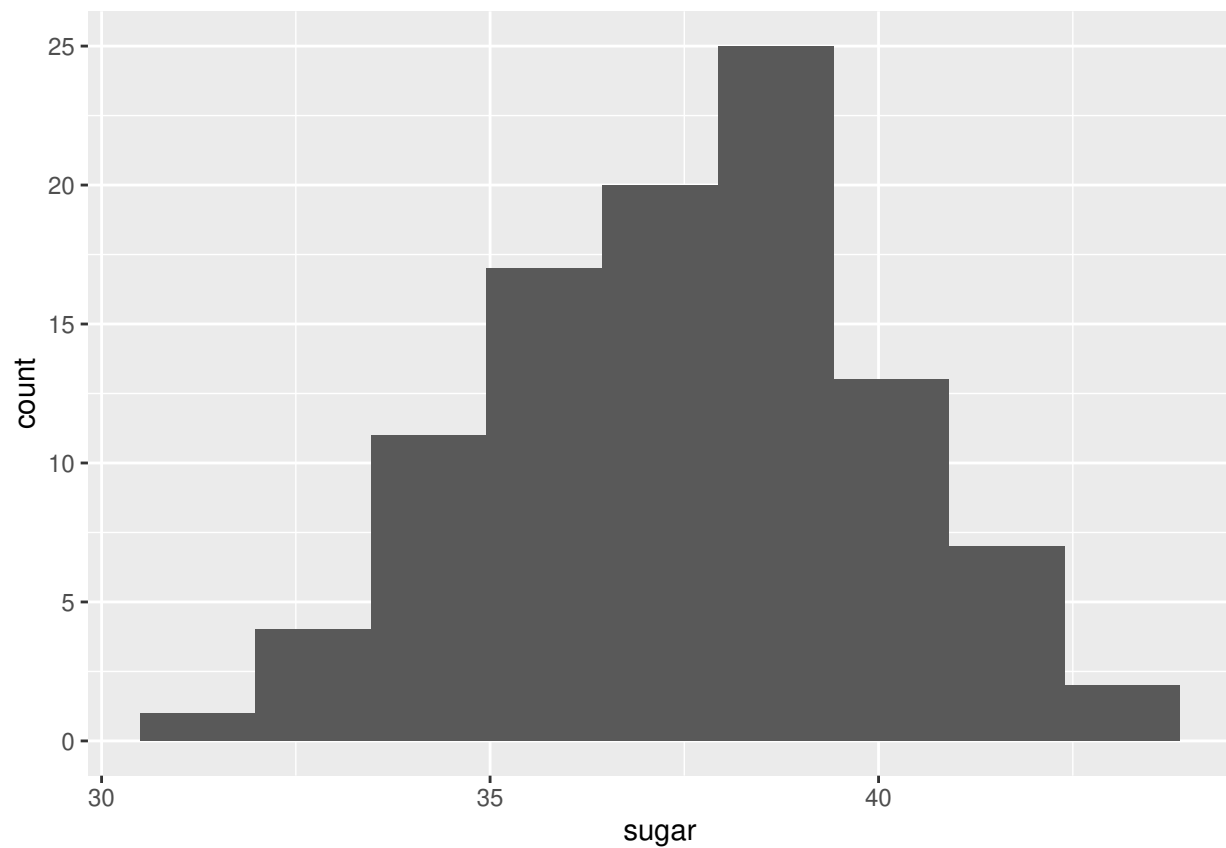


Figure 6: Cereal sugar graph

```
tibble(sim = 1:10000) %>%  
  rowwise() %>%  
  mutate(my_mean = mean(my_sample)) %>%  
  ggplot(aes(x = my_mean)) + geom_histogram(bins = 12)
```

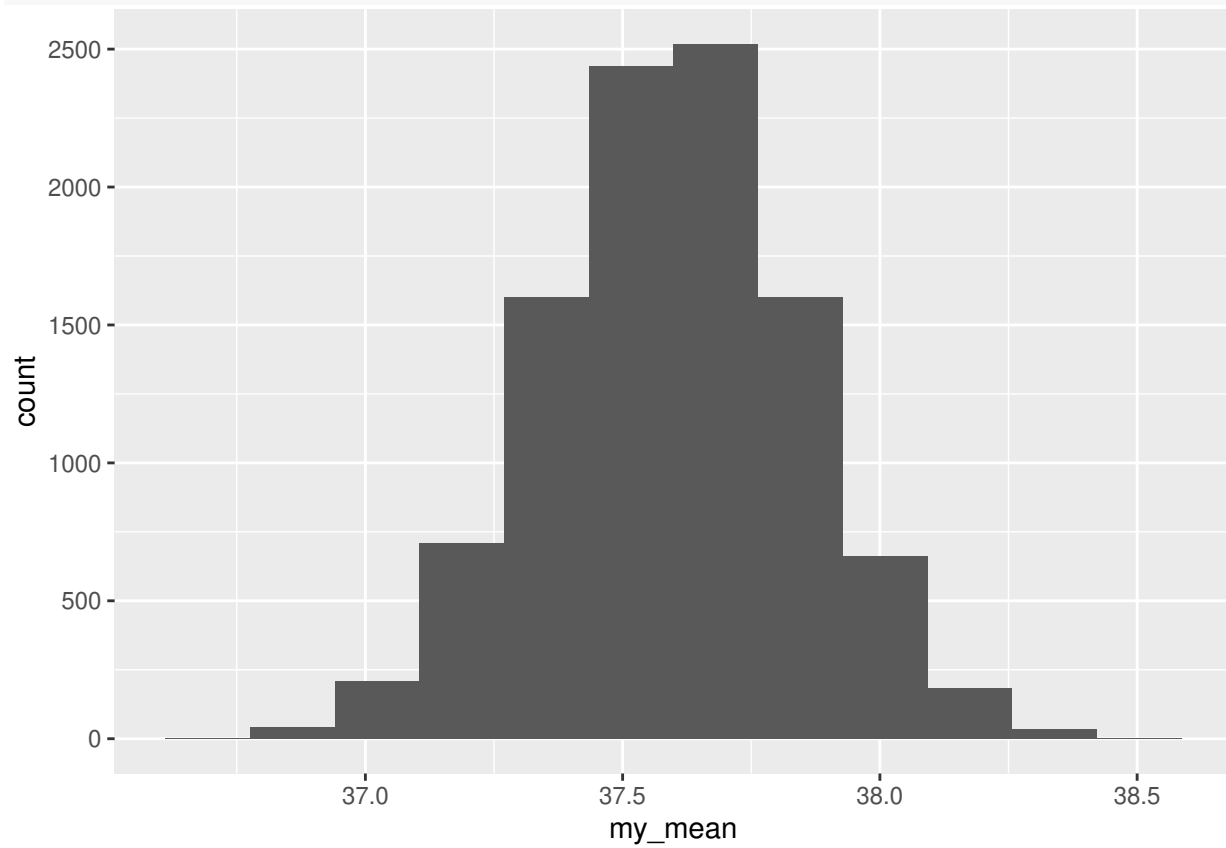


Figure 7: Cereal sugar summary bootstrap sampling distribution of sample mean (one line of code missing)

```
Monoxide
## # A tibble: 19 x 2
##   company      emission
##   <chr>         <dbl>
## 1 manufacturer  2.7
## 2 manufacturer  3.1
## 3 manufacturer  3.1
## 4 manufacturer  2.9
## 5 manufacturer  2.5
## 6 manufacturer  3.4
## 7 manufacturer  3.4
## 8 manufacturer  3.4
## 9 manufacturer  2.4
## 10 competitor  3.7
## 11 competitor   3
## 12 competitor  3.5
## 13 competitor  3.8
## 14 competitor  2.8
## 15 competitor  3.5
## 16 competitor  3.4
## 17 competitor  3.6
## 18 competitor  2.7
## 19 competitor  3.7
```

Figure 8: Carbon monoxide emissions data

```
t.test(emission ~ company, data = Monoxide, alternative = "greater")
##
## Welch Two Sample t-test
##
## data: emission by company
## t = 2.1187, df = 16.842, p-value = 0.02465
## alternative hypothesis: true difference in means between group competitor and group manufacturer is
## 95 percent confidence interval:
##  0.06802198      Inf
## sample estimates:
## mean in group competitor mean in group manufacturer
##                3.370000                2.988889
```

Figure 9: Carbon monoxide emissions *t*-test

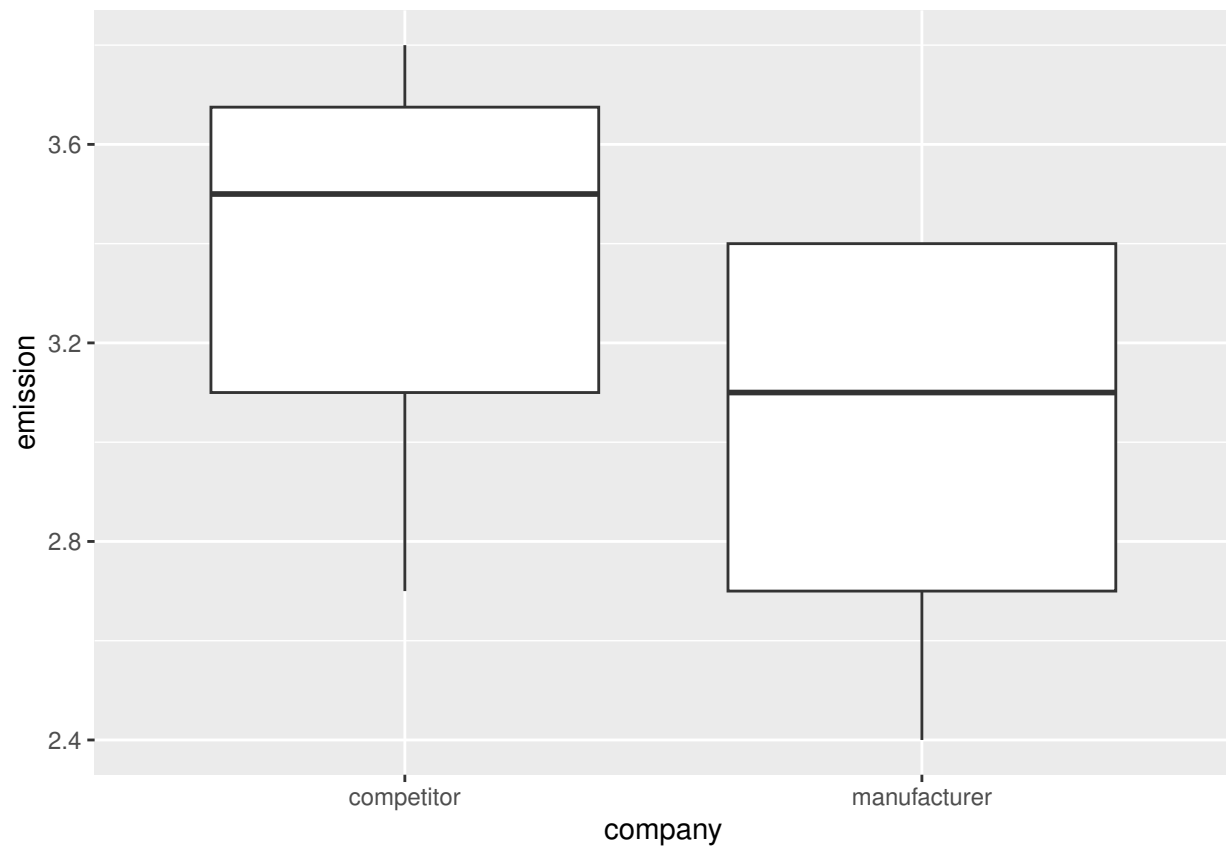


Figure 10: Carbon monoxide emissions graph

```
## # A tibble: 2 x 2
## # Rowwise:
##   `p_value <= 0.05`    n
##   <lg1>                <int>
## 1 FALSE                 412
## 2 TRUE                  588
```

Figure 11: Beta power simulation results

```
male_heights
## # A tibble: 100 x 1
##   heights
##   <int>
## 1     71
## 2     67
## 3     69
## 4     70
## 5     68
## 6     63
## 7     68
## 8     72
## 9     70
## 10    70
## # ... with 90 more rows
```

Figure 12: Heights data (some)

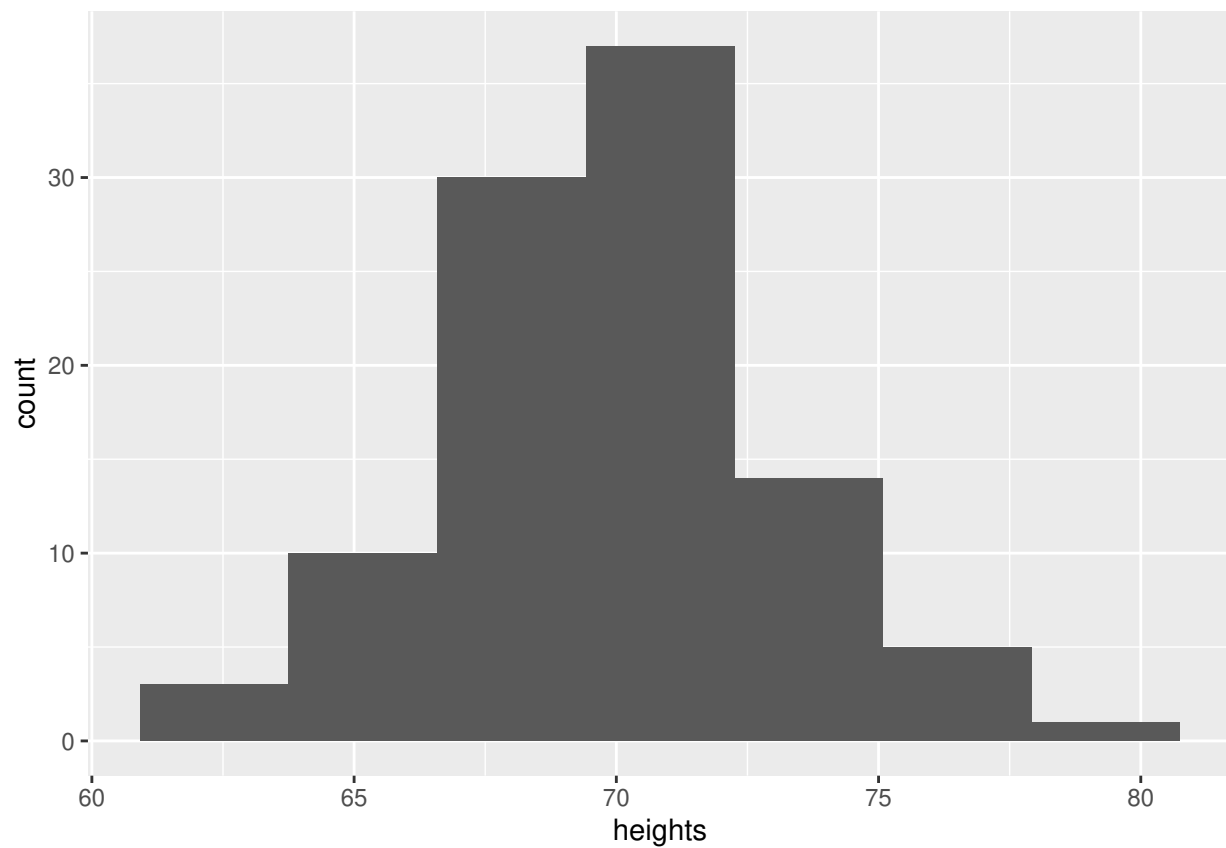


Figure 13: Heights graph

```
## $above_below
## below above
##    68    32
##
## $p_values
## alternative      p_value
## 1      lower 0.0002043886
## 2      upper 0.9999084284
## 3 two-sided 0.0004087772
```

Figure 14: Heights sign test

```
x <- 20:35
tibble(x, prob = dbinom(x, 100, 0.5)) %>%
  mutate(prob = round(prob, 6))

## # A tibble: 16 x 2
##       x      prob
##   <int> <dbl>
## 1     20 0
## 2     21 0
## 3     22 0
## 4     23 0
## 5     24 0
## 6     25 0
## 7     26 0.000001
## 8     27 0.000002
## 9     28 0.000004
## 10    29 0.00001
## 11    30 0.000023
## 12    31 0.000052
## 13    32 0.000113
## 14    33 0.000232
## 15    34 0.000458
## 16    35 0.000864
```

Figure 15: Binomial table for $n = 100, p = 0.5$