Comparing Apples and Simulation Studies

Which type of apple is heavier on average: green or red?

Which estimator have a higher expected value: *X* or *Y*?

According to theory, green apples are heavier than red apples.

Aaccording to theory, $E[X]$ is higher than the $E[Y]$.

These are the characteristics of green and red apples:

```r
# Green apples:
mu_green <- 0.7 # average weight of a green apple in kg
sigma_green <- 1 # sd

# Red apples:
mu_red <- 0.6 # average weight of a red apple in kg
sigma_red <- 1 # sd
```

To check that what the theory says is true, let's run an experiment as follows:

- Let's take **n** apples of each type and compute its average weight.

  Let's run a simulation study and compute the value of each estimator in **n** replications. Then compute the average estimated values.

- Being **n** the number of apples we take to compute the average weight.

  Being **n** the number of replications to compute the average value of each estimator.

```r
# Number of apples I take
n_size <- c(5, 10, 50, 100, 1000)
```

- To see if the experiment taking **n** apples of each type is accurate enough, let's do it 1000 times.
  - Each time we will take **n** apples of each type.
  - If green apples are heavier on average than red apples, the experiment reproduces the theoretical characteristics of apples. That would be a hit.
  - Else, the experiment is not congruent with the theory. The accuracy of the experiment is the number of observed hits in 1000 times.

    To see if the results of the simulation study with **n** replications are accurate enough, let's do it 1000 times.
    - Each time we will run the simulation with **n** replications.
    - If the average value of *X* is higher than the average value of *Y*, the result is congruent with the theory, that's a hit.
    - Else, the simulation results are not congruent with the theory. The accuracy of the simulation is the number of observed hits in 1000 times.

Experiment:

```r
times <- 1000 # times we perform the experiment
acc <- matrix(NA, nrow = length(n_size), ncol = times,
              dimnames = list(n_size, 1:times)) # store accuracy

# Experiment:
set.seed(10)
for(i in 1:length(n_size)){

  # Sample size
  n <- n_size[i]

  for(t in 1:times){

    # Take n green apples
    green_apple <- rnorm(n, mu_green, sigma_green)
    green_wg <- mean(green_apple) # weight of green apples

    # Take n red apples
    red_apple <- rnorm(n, mu_red, sigma_red)
    red_wg <- mean(red_apple) # weight of red apples

    # Check if green apples ar indeed heavier than red apples
    acc[i,t] <- ifelse(green_wg > red_wg, 1, 0)

  }

}

# Results:
res <- round(apply(acc, 1, mean), 2)

# View results:
cat(sprintf("Accuracy per number of apples taken:
%s: %s
%s: %s
%s: %s
%s: %s
%s: %s",
            n_size[1], res[1],
            n_size[2], res[2],
            n_size[3], res[3],
            n_size[4], res[4],
            n_size[5], res[5]))

## Accuracy per number of apples taken:
## 5: 0.55
## 10: 0.58
## 50: 0.67
## 100: 0.78
## 1000: 0.99
```

Results:

If we just take 5 apples, the results of the experiment are close to pure chance. The theory says that green apples are heavier, but we would get that result 55% of the times. However, if we increase the number of apples we take to, say, 1000, the results of the experiment are more accurate. Practically, every time we perform the experiment, we will conclude that green apples are indeed heavier.

If we just do the simulation study with 5 replications, the results are close to pure chance. The theory says that the expected value of the estimator X is higher than the expected value of Y, but we would get that result only 55% of the times. However, if we increase the number of replications to, say, 1000, the results of the simulation are more accurate. Practically, every time we perform the simulation study, we will conclude that the expected value of X is indeed higher.