lab_1

2026-01-15

Use the mean and sd functions to calculate the mean and standard deviation of the following numbers { 2.3, 4.3 ,1.2 , 3.4, 8.3, 12.2 }

```r
nums <- c(2.3,  4.3 ,1.2 , 3.4, 8.3, 12.2)
mean <- mean(nums)
sd <- sd(nums)
```
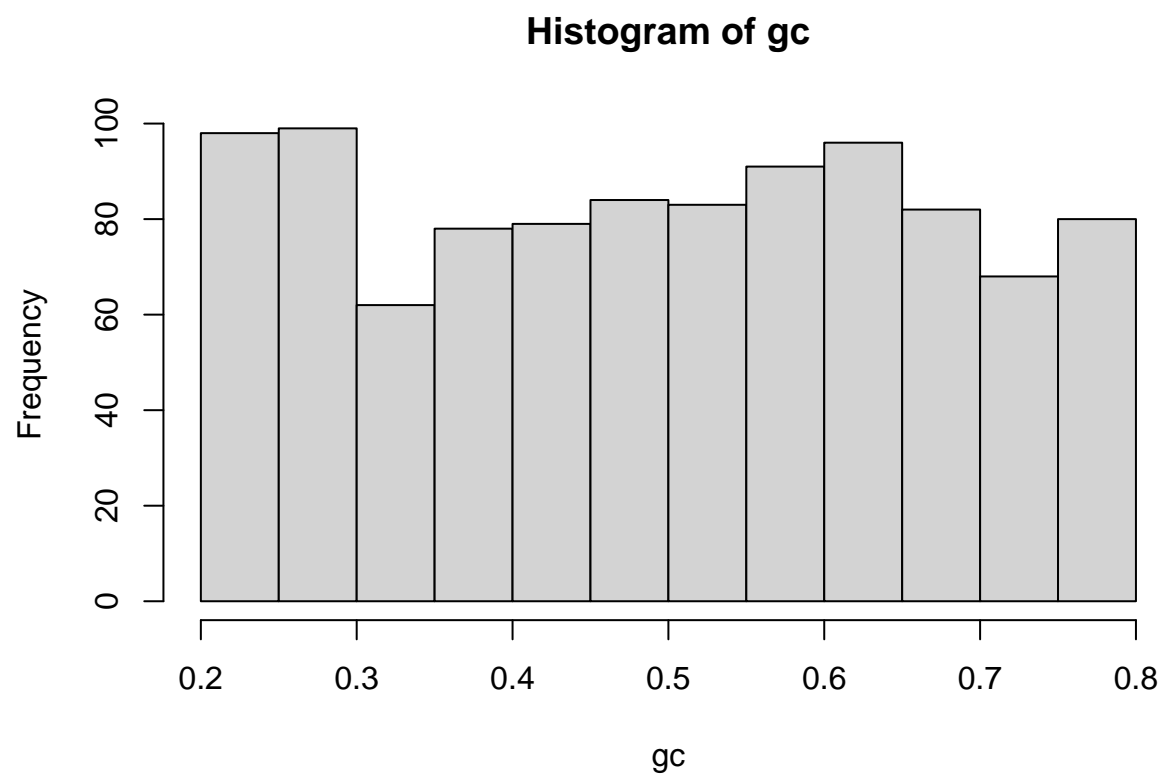
Use mean and sd in R to calculate the average and sd of { 4,5,6 .... 678,679,680 } (the set of every positive integer between 4 and 680)

```r
nums2 <- seq(4:680)
avg <- mean(nums2)
sd <- sd(nums2)
```

(3) Suppose you are given GC content for sequences from a human genome with values for many sequences: gc <- runif(1000, min = 0.2, max = 0.8).

- Plot a histogram of gc.
- Compute the mean and standard deviation.
- Does this look like a reasonable sequencing dataset? Why or why not?

```r
gc <- runif(1000, min = 0.2, max = 0.8)
hist(gc)
```

Histogram of gc


```r
mean(gc)
```

```
## [1] 0.494655
```

```r
sd(gc)
```

```
## [1] 0.1733672
```