STAT 521: Assignment 4

Make sure to show your computation and/or attach appropriate output.

Problem 1

In a random sample of 17 members of a health club, resting pulse was measured:

54, 63, 88, 72, 49, 92, 70, 73, 69, 101, 48, 66, 80, 64, 77, 83, 91

a) Calculate the sample mean and standard deviation. Use SAS, R, or Python.

b) Based on part (a), manually calculate a 90% confidence interval for the true mean resting pulse. Assume that resting pulse is approximately normally distributed. Give your interpretation of the confidence interval.

c) Based on part (a), manually calculate a 95% confidence interval for the true mean resting pulse. How does the 95% confidence interval compare to the 90% confidence interval?

d) Use SAS, R or Python to verify your answer in part (b) and (c). Attach your output.

Problem 2

The data set **lowbwt** (see **Assignment4.sas/R/py**) contains information recorded for a sample of 100 low birth weight infants born in two teaching hospitals in Boston, Massachusetts. Measurements of systolic blood pressure are saved under the variable name sbp, while indicators of gender – where 1 represents a male and 0 a female – are saved under sex.

a) Use SAS, R or Python to compute the mean and its 95% confidence interval for systolic blood pressure, broken down by gender of low birth weight infants. Attach your output.

b) Compute a 95% confidence interval for the difference of mean systolic blood pressure between male and female low birth weight infants. Assume the population variances are equal. Attach your output.

c) You wish to report your results for publication. Report the results in part (a) and (b) in the following format:

Table 1: Mean systolic blood pressure (in mmHg) and 95% confidence interval of 100 low birth-weight infants by gender

	Mean SBP	95% CI
Male	##.#	(##.#, ##.#)
Female	##.#	(##.#, ##.#)
Difference	#.#	(#.#, #.#)

d) Do you think it is possible that males and females have the same mean systolic blood pressure? Explain briefly.

Problem 3

Hemoglobin levels in 11-year-old boys vary according to a normal distribution with $\sigma = 1.2$ g/dL.

a) How large a sample is needed to estimate mean μ with 95% confidence so the margin of error is 0.4 g/dL? Do this by hand and verify your answer using SAS, R or Python (see page 2-3 of Lecture 6 note).

b) Suppose that you wish to estimate mean μ with more precision. Change the margin of error to 0.1, 0.2, and 0.3 g/dL in part (a) above. Use SAS, R or Python and observe how the necessary sample size changes. Plot the required sample size as a function of the margin of error. Describe your findings.

Problem 4

An epidemiologist wishes to know what proportion of adults living in a large metropolitan area have hepatitis B virus of subtype **ayr**.

a) Determine the sample size that would be required to estimate the true proportion to within ± 0.05 with 95% confidence. In a similar metropolitan area the proportion of adults with the characteristic is reported to be 0.20. Do the calculation by hand and verify your answer using SAS, R or Python (see page 5 of Lecture 6 note).

b) If data from another metropolitan area were not available and a pilot sample could not be drawn, what sample size would be required?

Problem 5 (Biostats students only)

Monte Carlo simulation in R:

Let's do a very simple simulation using R. If you have not installed R in your computer, please download the R installer at http://www.r-project.org. I would also recommend using R studio (http://www.rstudio.com/products/rstudio/download) as a programming editor.

Once you install R (and R studio), start the program. In the R console, type:

```
# Generate 5 random values from Z ~ N(0, 1)
z <- rnorm(5)
z
```

```
## [1] -0.56047565 -0.23017749  1.55870831  0.07050839  0.12928774
```

You just produced 5 random values from the standard normal distribution $N(0, 1)$. Due to randomness, your result may be different from what I have above. Something you should know:

- A line that starts with `#` is a comment.
- The function `rnorm(n)` produces a sequence (vector) of n values from $N(0, 1)$. This vector of 5 random values was assigned to an object `z` (`<-` is an assignment)
- To see the values assigned to `z`, just type `z`.
- You don't have to type commands directly in the R console. You can write your commands in the editor window (from the menu, File -> New Files -> R Script) and then run your code in there.

Now suppose you want to see if *each of the 5 values is less than 1.28*. You can evaluate this by running the following code:

```
# Are they smaller than 1.28?
z < 1.28
```

```
## [1]  TRUE  TRUE FALSE  TRUE  TRUE
```

The answer is returned as logical (either `TRUE` or `FALSE`). In this case, 4 out of the 5 values are less than 1.28. Only the third value was greater than or equal to 1.28 and thus it was returned `FALSE`. The following code actually counts how many of them are `TRUE`.

```
# Count them
sum(z < 1.28)
```

```
## [1] 4
```

If you apply the `sum()` function on an object with logical data type, `TRUE` is considered as 1 and `FALSE` as 0. Thus, this returns the number of `TRUE` which is 4 in this case.

If we want to know the proportion of `Z` taking less than 1.28, or the probability $P(Z < 1.28)$, then use the `mean()` function:

```
# Get the proportion of z < 1.28
mean(z < 1.28)
```

```
## [1] 0.8
```

In this case, 80% of all values (4 out of 5) are less than 1.28.

Now if we can produce so many random numbers from the standard normal distribution $N(0, 1)$ and get the proportion of $Z < 1.28$, then we should be able to approximate the CDF of Z up to 1.28, i.e., $P(Z < 1.28) = F_Z(1.28)$. Okay then, let's produce 1 million random numbers from $N(0, 1)$ and then approximate $P(Z < 1.28)$:

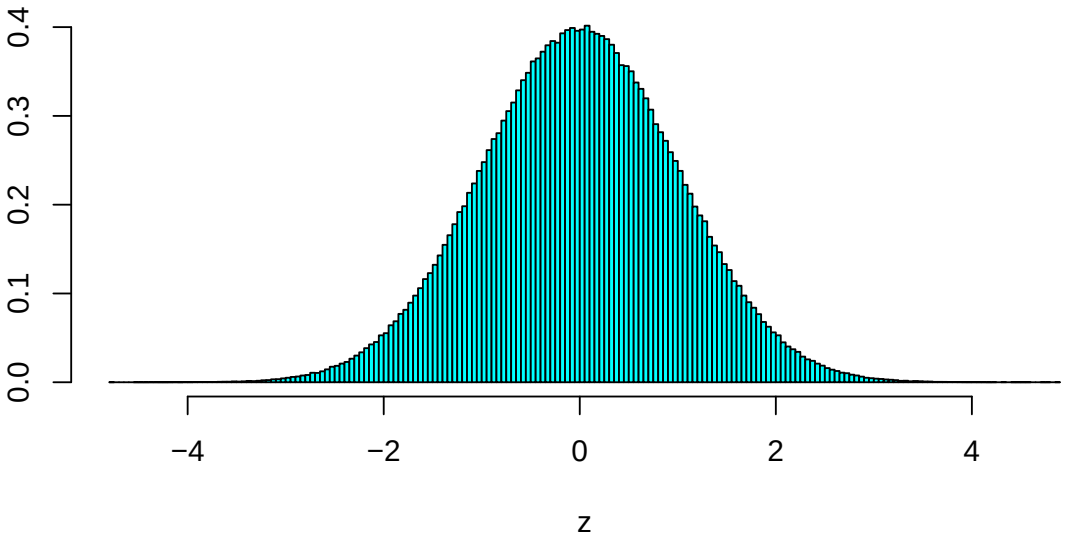
```
# Generate 1 million random values from Z ~ N(0, 1)
z <- rnorm(10 ^ 6)

# Approx P(z < 1.28)
mean(z < 1.28)
```

```
## [1] 0.899728
```

The answer I get is 0.899728. This value is actually very close to the true value of $P(Z < 1.28) = 0.8997274 \approx 0.9$ (Look up the z-table by yourself).

You can also look at the histogram of 1 million z values that you just created. Run the following commands:

```
# Look at the histogram
library(MASS)
truehist(z)
```



That's a nice looking normal distribution! The `MASS` library is required to use `truehist()` command that display a histogram (the first line of the code above).

Here's some exercise for you. Please submit your R code as well as your answers.

a) Produce one million random numbers from $N(0,1)$ and approximate $P(Z < 1.96)$

b) Similarly, approximate $P(Z < -1.28 \text{ or } Z > 1.28)$. You will need to use the "or" operator `|` (vertical bar or "pipe")

c) Approximate $P(-1.96 < Z < 1.96)$. You will need to use the "and" operator `&` (ampersand)

You might want to check Quick-R: Logical operators: https://www.statmethods.net/management/operators.html