HW1-33B

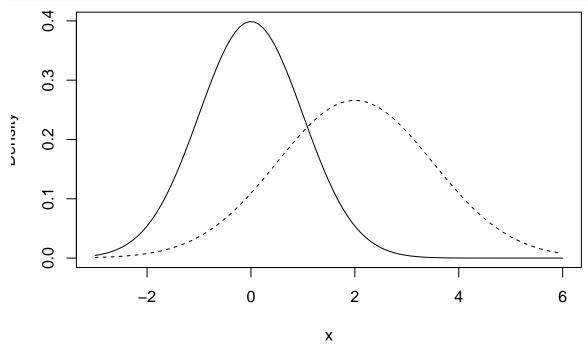
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0.1 Call Expressions

The standard normal curve is centered at 0 and has a spread, AKA standard deviation, of 1. This curve is drawn in the figure below along with a normal curve that has a center of 2 and a spread of 1.5 (dashed curve).

```
curve(dnorm, from = -3, to = 6, ylab = "Density")
curve(dnorm(x, mean = 2, sd = 1.5), add = TRUE, lty = 2)
```



The family of normal curves all have the same shape and each is uniquely specified by its center (mean) and spread (standard deviation)

1. Read the documentation for rnorm() to figure out how to call rnorm() to generate 5 random values from a normal distribution with mean 17 and standard deviation 3.

```
res = rnorm(5, mean=17, sd=3)
```

Debug: Result is 11.7823952, 23.0850245, 20.6066799, 20.055899, 16.2003534.

2. Create a vector called normSamps containing 1000 random values from a normal distribution with mean 1 and standard deviation 2.

```
set.seed(66)
normSamps = rnorm(1000, mean=1, sd=1)
```

3. The 10% trimmed mean is obtained by taking the mean of the middle 80% of the values (removing the lowest 10% and the highest 10% of the values). Find the 10% trimmed mean of normSamps and assign this value to mean10. Hint: Look at the help file for the mean() function.

```
mean10 = mean(normSamps, trim=0.1)
```

Debug: Result is 1.0235386.

4. Use sum() to calculate the fraction of values in normSamps that are less than 3. Write your solution so that it coerces a logical vector to numeric without using the function as numeric(). Write your code generically so that it doesn't depend on normSamps being a vector of 1000 elements. Assign the fraction to the variable frac3 Hint: consider using the length() function.

```
# It maybe slow and expensive to create a useless vector by filter.
# (REALLY REALLY slow in traditional programming language, but maybe there's strange optimization in
isLessThan3 = Vectorize(function(ele) {
    return(ele < 3) # Strange R syntax...
})
frac3 = length(normSamps[isLessThan3(normSamps)]) / length(normSamps)</pre>
```

Debug: Result is 0.978.

5. A percentile is the value at which a given percentage of samples fall at or below it and is sometimes synonomously called a quantile, e.g., the 90th percentile is the value at which 90% of data values fall at or below it. Calculate the 90th percentile of normSamps and assign this value to per90. Hint: The quantile() function is helpful for this question.

```
# Replace the 1 on the right hand side of the equation with your code
per90 = quantile(normSamps, probs=c(0.9))
```

Debug: Result is 2.2710116.

6. Calculate the greatest absolute distance from 1 for the values in normSamps. Assign this value to a variable called maxDev, short for "maximum deviation" from the mean. Hint: The functions abs() and max() are helpful for this question.

```
# Replace the 1 on the right hand side of the equation with your code
maxDev = 1
```

0.2 Working with Vectors

Run the following code chunk to load the vectors for our 14-member family:

```
load(url("http://www.stat.berkeley.edu/users/nolan/data/afamily.rda"))
```

7. Calculate bmi from fheight and fweight by dividing weight in pounds by height in inches squared and multiplying by a conversion factor of 703. Assign this to bmi_alt

```
# Replace the 1 on the right hand side of the equation with your code
bmi_alt = 1
```

- 8. Check that fbmi and bmi_alt match using the functions == and all()
- 9. Suppose that as long as the entries in bmi_alt and fbmi are within 0.1 of each other, then we consider these two to be equivalent. Calculate the differences and assign it to bmi_diff.

 Check whether all of the differences are within 0.1 of each other. Produce a logical vector of length 1 called bmi same that is TRUE if the entries in bmi alt and fbmi are within 0.1 of each other.

```
bmi_diff = 1
bmi_same = 1
```

10. Create a vector of last names for the family members, called flast. The values should be Smith for each entry. Hint: use rep() and length() to do this.

flast = 1