## Microbiol612

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## Introduction:

In order to become familiar with R, we analyzed data from the Gapminder file which contained information for different countries regarding the year, population, continent, life expecancy, and GDP per capita. The data was saved to myprojects and was uploaded during class using the following 2 lines of code shown below.

```
getwd()
## [1] "/Users/corinemj/myproject"
gapminder<-read.table("./r-novice-gapminder-files/data/gapminder-FiveYearData.csv", s</pre>
ep=',', header=T)
head(gapminder)
##
        country year
                           pop continent lifeExp gdpPercap
## 1 Afghanistan 1952
                       8425333
                                    Asia
                                         28.801
                                                  779.4453
## 2 Afghanistan 1957
                       9240934
                                    Asia 30.332
                                                  820.8530
## 3 Afghanistan 1962 10267083
                                    Asia 31.997
                                                  853.1007
## 4 Afghanistan 1967 11537966
                                          34.020
                                                  836.1971
                                    Asia
## 5 Afghanistan 1972 13079460
                                    Asia 36.088
                                                  739.9811
## 6 Afghanistan 1977 14880372
                                          38.438 786.1134
                                    Asia
```

# **Assignment:**

- Part 1: What is the mean and standard deviation of the life expectancies for each of the continents?
- Part 2: Plot the mean and standard deviation for the continents.

#### Part 1:

In order to do this, the dplyr package was installed, loaded and the group\_by() and summarize() functions were used.

```
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##
       filter, lag
##
   The following objects are masked from 'package:base':
##
##
       intersect, setdiff, setequal, union
lifeExp bycontinents <- gapminder %>%
    group by(continent) %>%
    summarize(mean_lifeExp=mean(lifeExp),
    sd lifeExp=sd(lifeExp))
lifeExp bycontinents
## Source: local data frame [5 x 3]
##
##
     continent mean lifeExp sd lifeExp
##
        (fctr)
                       (dbl)
                                  (dbl)
        Africa
## 1
                   48.86533
                               9.150210
## 2
      Americas
                   64.65874
                               9.345088
## 3
          Asia
                   60.06490
                             11.864532
## 4
        Europe
                   71.90369
                               5.433178
```

### Part 2:

Oceania

74.32621

3.795611

## 5

In order to plot this data, ggplot was installed by selecting "Packages" in Rstudio and clicking "ggplot2". Then, the following code shows the x axis, y axis and title as "continent", "mean life expectancy" and "Mean Life Expectancy for Continents", respectively. The "color=continent" designates a color for each continent, the geom\_errorbar() designates error bars and geom\_point() shows the mean life expectancy as an individual point on the plot. Africa has the lowest mean life expectancy. Oceania has the highest mean life expectancy.

```
library(ggplot2)
ggplot(lifeExp_bycontinents, aes(x = continent, y = mean_lifeExp, color=continent)) +
ggtitle("Mean Life Expectancy for Continents") +
   geom_errorbar(aes(ymin=mean_lifeExp-sd_lifeExp, ymax=mean_lifeExp+sd_lifeExp), widt
h=0.1) +
   geom_point(size=3)
```

