**Lab Assignment #2**

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*Instructions:* For all of the problems below, **copy the R commands** and the **results of the R commands** into the green boxes.

1. Compute the mathematical quantity *e π i*. Copy your ***R* statement** and **result** into the box below. [Hint: The imaginary number *i* can be created using (0+1i) in *R*.] (1 points).

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| > exp(pi\*(0+0i))  [1] 1+0i |

1. The Fibonacci sequence appears in many biological structures. It is formed by starting with the number 0, 1 and then adding the last two numbers to get the next number: 0, 1, 1, 2, 3, 5, 8, etc. Create variable called fib that is a numeric vector with the first 10 values of the Fibonacci sequence. Type the name of the variable fib so that it is displayed. (1 points).

Copy your ***R* statements** and **results** into the box below.

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| > fib = c(0,1,1,2,3,5,8,13,21,34)  > fib  [1] 0 1 1 2 3 5 8 13 21 34 |

1. Create a character vector gtypes that contains three text strings "AA", "Aa", and "aa" representing three diploid genotypes. Type the name of the variable gtypes so that it is displayed. Then use the paste() function to create a single text string displaying all three genotypes. (1 points).

Copy your ***R* statements** and **results** into the box below.

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| > gtypes = c("AA", "Aa", "aa")  > gtypes  [1] "AA" "Aa" "aa"  > first\_gtype = "AA"  > second\_gtype = "Aa"  > third\_gtype = "aa"  > paste(first\_gtype,second\_gtype,third\_gtype)  [1] "AA Aa aa" |

1. Use *R* to create the following a variable mymat that contains numeric matrix with 0.1, 2, 4 in the first column, 7, 3, 100 in the second column, and −1, −0.9, 8, in the third column. Type the name of the variable mymat so that it is displayed. Then use the transpose function to display the transpose of the matrix mymat. (1 points).

Copy your ***R* statements** and **results** into the box below.

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| > mymat = matrix(c(0.1,2,4,7,3,100,-1,-0.9,8),nrow=3, ncol=3)  > mymat  [,1] [,2] [,3]  [1,] 0.1 7 -1.0  [2,] 2.0 3 -0.9  [3,] 4.0 100 8.0  > t(mymat)  [,1] [,2] [,3]  [1,] 0.1 2.0 4  [2,] 7.0 3.0 100  [3,] -1.0 -0.9 8 |

1. Create a list myvars with elements fib, gtypes, and mymat. Type the name of the variable myvars so that it is displayed. Multiply the third element of the list by the number π. (1 points).

Copy your ***R* statements** and **results** into the box below.

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| > myvars = list(fib,gtypes,mymat)  > myvars  [[1]]  [1] 0 1 1 2 3 5 8 13 21 34  [[2]]  [1] "AA" "Aa" "aa"  [[3]]  [,1] [,2] [,3]  [1,] 0.1 7 -1.0  [2,] 2.0 3 -0.9  [3,] 4.0 100 8.0  > pi \* myvars[[3]]  [,1] [,2] [,3]  [1,] 0.3141593 21.991149 -3.141593  [2,] 6.2831853 9.424778 -2.827433  [3,] 12.5663706 314.159265 25.132741   |  | | --- | |  | |

1. Consider the following data:

Age Height Gender Smoker

22 66 F FALSE

25 71 M TRUE

28 64 F TRUE

Use the function data.frame() to create a data frame object called mydata for these data with the column names and values above. Type the name of the variable mydata so that the data set is displayed. (1 points).

Copy your ***R* statements** and **results** into the box below.

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| > Age = c(22,25,28)  > Height = c(66,71,64)  > Gender = c("F","M","F")  > Smoker = c("FALSE","TRUE",'TRUE')  > mydata = data.frame(Age,Height,Gender,Smoker)  > mydata  Age Height Gender Smoker  1 22 66 F FALSE  2 25 71 M TRUE  3 28 64 F TRUE |

1. Import the data set in the *Excel* file *Lab2AssignmentData.xlsx* into an *R* data frame variable called mussels. This data set contains the shell length and gonad weights of marine mussels. Create a scatter plot with shell length on the x-axis and gonad weight on the y-axis. Above the plot, click on the **Export** button and select **Copy to Clipboard…** from the menu. On the panel that appears, click the **Copy Plot** button and paste the plot into the green box below. (2 points).

Copy your ***R* statements** and **resulted plot/s** into the box below.

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| > insrctdata = read.csv("Lab2AssignmentData(1).csv")  > insectdata  wt length sex  1 2.58 18 m  2 3.12 21 f  3 2.09 16 m  4 3.21 22 f  5 1.98 17 f  6 2.75 19 m  7 2.63 15 m  8 2.99 20 m  9 1.89 17 f  10 3.02 21 f  > x <- insectdata$length  > y <- insectdata$wt  > plot(x,y,xlab="shell length", ylab="gonad weight") |

1. If it is not currently in your workspace, use the following url to import the birth data into an *R* data file: *http://www.openintro.org/stat/data/present.R* you have. Create a line plot of the total number of children (y-axis) versus the year (x-axis) and copy/paste the plot into the green box below. (2 points)

Hints:

* The y-variable can be entered as present$boys + present$girls.
* A line plot can be produced by adding the argument type = “l” (that’s a lower case L) to the plot function (e.g., plot(x, y, type = “l”)).

Copy your ***R* statements** and **resulted plot/s** into the box below.

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| > plot(present$year, present$boys+present$girls, type = "l") |