

assignment3markdown

Zaid Sameer

2018-11-01

Question 2

reading the csv file

```
rna_counts <- read.csv("eXpress_dm_counts.csv")
str(rna_counts)
```

```
## 'data.frame': 4375 obs. of 56 variables:
## $ X : Factor w/ 4375 levels "FBpp0070006",...: 1875 2750 1096 844 4253 2344 4251
## $ F101_lg_female_hdhorn : int 32 1917 61 22 183 1695 1905 146 286 1096 ...
## $ F101_lg_female_thxhorn: int 9 2064 80 300 153 1327 2685 466 276 1136 ...
## $ F101_lg_female_wings : int 14 1825 57 8 127 2495 654 123 164 777 ...
## $ F105_lg_female_hdhorn : int 51 2660 77 15 188 3306 1959 263 386 1501 ...
## $ F105_lg_female_thxhorn: int 9 411 50 164 168 2214 801 182 276 1027 ...
## $ F105_lg_female_wings : int 23 923 44 12 180 3198 1044 133 214 1158 ...
## $ F131_lg_female_hdhorn : int 26 4777 45 12 122 1148 1767 123 335 1201 ...
## $ F131_lg_female_thxhorn: int 17 2767 53 835 144 827 2426 752 532 1915 ...
## $ F131_lg_female_wings : int 14 7129 74 26 88 1847 1923 161 224 1106 ...
## $ F135_sm_female_wings : int 10 1440 43 2 132 2188 608 73 283 1121 ...
## $ F135_sm_female_hdhorn : int 31 546 45 4 146 2447 680 115 228 887 ...
## $ F135_sm_female_thxhorn: int 35 793 67 369 171 1406 1587 330 387 1496 ...
## $ F136_sm_female_hdhorn : int 43 4523 48 26 108 1482 1523 121 264 1057 ...
## $ F136_sm_female_thxhorn: int 16 4713 41 228 72 1463 1697 202 300 1123 ...
## $ F136_sm_female_wings : int 21 6102 55 31 87 2222 1799 233 310 1267 ...
## $ F196_sm_female_hdhorn : int 9 32 45 225 101 361 2300 157 341 1224 ...
## $ F196_sm_female_thxhorn: int 30 26 72 482 60 351 2456 324 357 1140 ...
## $ F196_sm_female_wings : int 11 86 237 77 175 822 2753 129 688 2876 ...
## $ F197_sm_female_hdhorn : int 50 2887 104 610 229 1951 2563 186 496 1970 ...
## $ F197_sm_female_thxhorn: int 19 2861 88 461 151 1564 1700 302 337 1350 ...
## $ F197_sm_female_wings : int 20 3542 96 4 132 2715 733 165 287 1036 ...
## $ F218_lg_female_hdhorn : int 39 1542 82 148 390 866 2172 90 591 2345 ...
## $ F218_lg_female_thxhorn: int 15 347 82 885 226 1041 2346 306 532 1883 ...
## $ F218_lg_female_wings : int 15 6718 71 8 179 1559 3304 90 301 1165 ...
## $ M120_sm_male_genitalia: int 16 2031 81 111 128 409 2171 72 331 1357 ...
## $ M120_sm_male_hdhorn : int 41 3518 77 10 170 1096 1858 70 330 1220 ...
## $ M120_sm_male_thxhorn : int 59 540 109 775 165 597 2116 294 571 2081 ...
## $ M120_sm_male_wings : int 18 3752 89 30 140 937 2974 165 406 1648 ...
## $ M125_lg_male_genitalia: int 22 3873 77 23 124 1096 749 215 289 1144 ...
## $ M125_lg_male_hdhorn : int 14 8273 48 5 67 1420 873 108 237 948 ...
## $ M125_lg_male_wings : int 7 8980 67 2 144 2885 1454 156 285 1219 ...
## $ M160_lg_male_genitalia: int 27 433 92 23 122 323 1412 59 502 1933 ...
## $ M160_lg_male_hdhorn : int 27 2518 73 8 212 339 1586 68 470 1876 ...
## $ M160_lg_male_thxhorn : int 16 783 95 271 235 661 1347 175 596 2487 ...
## $ M160_lg_male_wings : int 5 3069 97 22 162 647 1957 143 501 1983 ...
## $ M171_sm_male_genitalia: int 13 205 144 35 144 1145 1369 85 402 1466 ...
## $ M171_sm_male_hdhorn : int 69 2358 81 22 121 1513 811 115 264 1068 ...
```

```
## $ M171_sm_male_thxhorn : int 14 2120 60 269 166 1576 1089 251 261 940 ...
## $ M171_sm_male_wings : int 18 1157 56 21 131 3628 380 122 229 874 ...
## $ M172_sm_male_genitalia: int 17 4184 188 42 115 1399 1104 103 488 1701 ...
## $ M172_sm_male_hdhorn : int 15 5356 78 7 70 1088 1638 174 169 804 ...
## $ M172_sm_male_thxhorn : int 13 3269 75 260 57 852 1373 264 229 854 ...
## $ M172_sm_male_wings : int 20 6755 140 42 108 2601 2168 294 390 1557 ...
## $ M180_lg_male_genitalia: int 15 4739 64 86 107 1125 834 138 166 708 ...
## $ M180_lg_male_hdhorn : int 21 7039 47 6 125 1746 1066 115 183 821 ...
## $ M180_lg_male_thxhorn : int 9 5353 44 35 85 1483 1348 87 150 633 ...
## $ M180_lg_male_wings : int 25 13390 67 6 110 2381 886 110 228 1006 ...
## $ M200_sm_male_genitalia: int 49 3338 95 102 171 1301 1886 451 496 1949 ...
## $ M200_sm_male_hdhorn : int 25 2021 51 51 115 1019 629 127 272 1093 ...
## $ M200_sm_male_thxhorn : int 40 7839 93 148 161 2383 3594 431 589 2352 ...
## $ M200_sm_male_wings : int 15 5683 74 9 103 2055 946 199 313 1232 ...
## $ M257_lg_male_genitalia: int 30 2162 113 51 178 690 2092 46 463 1741 ...
## $ M257_lg_male_hdhorn : int 23 9060 96 6 176 1133 4062 43 349 1246 ...
## $ M257_lg_male_thxhorn : int 39 2290 130 197 257 984 2590 174 479 1917 ...
## $ M257_lg_male_wings : int 9 2861 57 28 99 718 1633 75 218 855 ...
```

checking for 0 values in rna_counts

```
#checking for values of 0
tail(which(rna_counts == 0, arr.ind=TRUE))
```

```
##      row col
## [2750,] 4003 56
## [2751,] 4043 56
## [2752,] 4052 56
## [2753,] 4073 56
## [2754,] 4116 56
## [2755,] 4261 56
```

```
#replacing 0 values with 0.1
newrna_counts <- replace(rna_counts, rna_counts<1, 0.1)
```

```
## Warning in Ops.factor(left, right): '<' not meaningful for factors
```

```
#checking for values of 0 after replacement
which(newrna_counts == 0, arr.ind=TRUE)
```

```
##      row col
```

```
#comparing the two data frames
str(rna_counts)
```

```
## 'data.frame': 4375 obs. of 56 variables:
## $ X : Factor w/ 4375 levels "FBpp0070006",...: 1875 2750 1096 844 4253 2344 4251
## $ F101_lg_female_hdhorn : int 32 1917 61 22 183 1695 1905 146 286 1096 ...
## $ F101_lg_female_thxhorn: int 9 2064 80 300 153 1327 2685 466 276 1136 ...
## $ F101_lg_female_wings : int 14 1825 57 8 127 2495 654 123 164 777 ...
## $ F105_lg_female_hdhorn : int 51 2660 77 15 188 3306 1959 263 386 1501 ...
## $ F105_lg_female_thxhorn: int 9 411 50 164 168 2214 801 182 276 1027 ...
## $ F105_lg_female_wings : int 23 923 44 12 180 3198 1044 133 214 1158 ...
## $ F131_lg_female_hdhorn : int 26 4777 45 12 122 1148 1767 123 335 1201 ...
## $ F131_lg_female_thxhorn: int 17 2767 53 835 144 827 2426 752 532 1915 ...
## $ F131_lg_female_wings : int 14 7129 74 26 88 1847 1923 161 224 1106 ...
## $ F135_sm_female_wings : int 10 1440 43 2 132 2188 608 73 283 1121 ...
## $ F135_sm_female_hdhorn : int 31 546 45 4 146 2447 680 115 228 887 ...
```

```

## $ F135_sm_female_thxhorn: int 35 793 67 369 171 1406 1587 330 387 1496 ...
## $ F136_sm_female_hdhorn : int 43 4523 48 26 108 1482 1523 121 264 1057 ...
## $ F136_sm_female_thxhorn: int 16 4713 41 228 72 1463 1697 202 300 1123 ...
## $ F136_sm_female_wings : int 21 6102 55 31 87 2222 1799 233 310 1267 ...
## $ F196_sm_female_hdhorn : int 9 32 45 225 101 361 2300 157 341 1224 ...
## $ F196_sm_female_thxhorn: int 30 26 72 482 60 351 2456 324 357 1140 ...
## $ F196_sm_female_wings : int 11 86 237 77 175 822 2753 129 688 2876 ...
## $ F197_sm_female_hdhorn : int 50 2887 104 610 229 1951 2563 186 496 1970 ...
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## $ M172_sm_male_thxhorn : int 13 3269 75 260 57 852 1373 264 229 854 ...
## $ M172_sm_male_wings : int 20 6755 140 42 108 2601 2168 294 390 1557 ...
## $ M180_lg_male_genitalia: int 15 4739 64 86 107 1125 834 138 166 708 ...
## $ M180_lg_male_hdhorn : int 21 7039 47 6 125 1746 1066 115 183 821 ...
## $ M180_lg_male_thxhorn : int 9 5353 44 35 85 1483 1348 87 150 633 ...
## $ M180_lg_male_wings : int 25 13390 67 6 110 2381 886 110 228 1006 ...
## $ M200_sm_male_genitalia: int 49 3338 95 102 171 1301 1886 451 496 1949 ...
## $ M200_sm_male_hdhorn : int 25 2021 51 51 115 1019 629 127 272 1093 ...
## $ M200_sm_male_thxhorn : int 40 7839 93 148 161 2383 3594 431 589 2352 ...
## $ M200_sm_male_wings : int 15 5683 74 9 103 2055 946 199 313 1232 ...
## $ M257_lg_male_genitalia: int 30 2162 113 51 178 690 2092 46 463 1741 ...
## $ M257_lg_male_hdhorn : int 23 9060 96 6 176 1133 4062 43 349 1246 ...
## $ M257_lg_male_thxhorn : int 39 2290 130 197 257 984 2590 174 479 1917 ...
## $ M257_lg_male_wings : int 9 2861 57 28 99 718 1633 75 218 855 ...

```

```
str(newrna_counts)
```

```

## 'data.frame': 4375 obs. of 56 variables:
## $ X : Factor w/ 4375 levels "FBpp0070006",...: 1875 2750 1096 844 4253 2344 4251
## $ F101_lg_female_hdhorn : num 32 1917 61 22 183 ...
## $ F101_lg_female_thxhorn: num 9 2064 80 300 153 ...
## $ F101_lg_female_wings : num 14 1825 57 8 127 ...
## $ F105_lg_female_hdhorn : num 51 2660 77 15 188 ...
## $ F105_lg_female_thxhorn: num 9 411 50 164 168 ...
## $ F105_lg_female_wings : num 23 923 44 12 180 ...

```

```
## $ F131_lg_female_hdhorn : num 26 4777 45 12 122 ...
## $ F131_lg_female_thxhorn: num 17 2767 53 835 144 ...
## $ F131_lg_female_wings : num 14 7129 74 26 88 ...
## $ F135_sm_female_wings : num 10 1440 43 2 132 ...
## $ F135_sm_female_hdhorn : num 31 546 45 4 146 ...
## $ F135_sm_female_thxhorn: num 35 793 67 369 171 ...
## $ F136_sm_female_hdhorn : num 43 4523 48 26 108 ...
## $ F136_sm_female_thxhorn: num 16 4713 41 228 72 ...
## $ F136_sm_female_wings : num 21 6102 55 31 87 ...
## $ F196_sm_female_hdhorn : num 9 32 45 225 101 ...
## $ F196_sm_female_thxhorn: num 30 26 72 482 60 ...
## $ F196_sm_female_wings : num 11 86 237 77 175 ...
## $ F197_sm_female_hdhorn : num 50 2887 104 610 229 ...
## $ F197_sm_female_thxhorn: num 19 2861 88 461 151 ...
## $ F197_sm_female_wings : num 20 3542 96 4 132 ...
## $ F218_lg_female_hdhorn : num 39 1542 82 148 390 ...
## $ F218_lg_female_thxhorn: num 15 347 82 885 226 ...
## $ F218_lg_female_wings : num 15 6718 71 8 179 ...
## $ M120_sm_male_genitalia: num 16 2031 81 111 128 ...
## $ M120_sm_male_hdhorn : num 41 3518 77 10 170 ...
## $ M120_sm_male_thxhorn : num 59 540 109 775 165 ...
## $ M120_sm_male_wings : num 18 3752 89 30 140 ...
## $ M125_lg_male_genitalia: num 22 3873 77 23 124 ...
## $ M125_lg_male_hdhorn : num 14 8273 48 5 67 ...
## $ M125_lg_male_wings : num 7 8980 67 2 144 ...
## $ M160_lg_male_genitalia: num 27 433 92 23 122 ...
## $ M160_lg_male_hdhorn : num 27 2518 73 8 212 ...
## $ M160_lg_male_thxhorn : num 16 783 95 271 235 ...
## $ M160_lg_male_wings : num 5 3069 97 22 162 ...
## $ M171_sm_male_genitalia: num 13 205 144 35 144 ...
## $ M171_sm_male_hdhorn : num 69 2358 81 22 121 ...
## $ M171_sm_male_thxhorn : num 14 2120 60 269 166 ...
## $ M171_sm_male_wings : num 18 1157 56 21 131 ...
## $ M172_sm_male_genitalia: num 17 4184 188 42 115 ...
## $ M172_sm_male_hdhorn : num 15 5356 78 7 70 ...
## $ M172_sm_male_thxhorn : num 13 3269 75 260 57 ...
## $ M172_sm_male_wings : num 20 6755 140 42 108 ...
## $ M180_lg_male_genitalia: num 15 4739 64 86 107 ...
## $ M180_lg_male_hdhorn : num 21 7039 47 6 125 ...
## $ M180_lg_male_thxhorn : num 9 5353 44 35 85 ...
## $ M180_lg_male_wings : num 25 13390 67 6 110 ...
## $ M200_sm_male_genitalia: num 49 3338 95 102 171 ...
## $ M200_sm_male_hdhorn : num 25 2021 51 51 115 ...
## $ M200_sm_male_thxhorn : num 40 7839 93 148 161 ...
## $ M200_sm_male_wings : num 15 5683 74 9 103 ...
## $ M257_lg_male_genitalia: num 30 2162 113 51 178 ...
## $ M257_lg_male_hdhorn : num 23 9060 96 6 176 ...
## $ M257_lg_male_thxhorn : num 39 2290 130 197 257 ...
## $ M257_lg_male_wings : num 9 2861 57 28 99 ...
```

```
#checking if replacing the 0 with 0.1 affects the mean drastically (it does not)
mean(rna_counts$F101_lg_female_hdhorn)
```

```
## [1] 1978.847
```

```
mean(newrna_counts$F101_lg_female_hdhorn)
```

```
## [1] 1978.848
```

```
#checking the mean using log2
```

```
mean(log(newrna_counts$F101_lg_female_hdhorn, 2))
```

```
## [1] 8.931851
```

```
# coding a function called mean_col that takes the arguments column name and log2=T
```

```
#note: the dataframe input is imbeded in the code and would need to be changed for the using with a dif
```

```
mean_col <- function( col, log2 ) {  
  if (log2 == TRUE) {  
    logdfirm <- log( newrna_counts[2:56], 2)  
    mean( (logdfirm)[[ col ]] )  
  }  
  else {  
    mean( (newrna_counts)[[ col ]] )  
  }  
}
```

```
mean_col("F101_lg_female_hdhorn", FALSE)
```

```
## [1] 1978.848
```

```
mean_col("F101_lg_female_hdhorn", TRUE)
```

```
## [1] 8.931851
```

trying another column

```
mean(newrna_counts$F101_lg_female_wings)
```

```
## [1] 1583.905
```

```
mean(log(newrna_counts$F101_lg_female_wings, 2))
```

```
## [1] 8.115428
```

```
mean_col("F101_lg_female_wings", FALSE)
```

```
## [1] 1583.905
```

```
mean_col("F101_lg_female_wings", TRUE)
```

```
## [1] 8.115428
```

Question 3

making a vector of means

```
column_means_vector <- NULL  
for(headersnamesfor in names(newrna_counts[2:56])) {
```

```

lalala <- c(headersnamesfor)
lelele <- c(mean_col(headersnamesfor, F))
names(lelele) <- lalala
column_means_vector <- c(column_means_vector, lelele)
}

```

```
column_means_vector
```

```

## F101_lg_female_hdhorn F101_lg_female_thxhorn F101_lg_female_wings
## 1978.848 1983.251 1583.905
## F105_lg_female_hdhorn F105_lg_female_thxhorn F105_lg_female_wings
## 2105.713 1433.751 1869.964
## F131_lg_female_hdhorn F131_lg_female_thxhorn F131_lg_female_wings
## 2117.848 2307.530 2272.693
## F135_sm_female_wings F135_sm_female_hdhorn F135_sm_female_thxhorn
## 1728.485 1452.914 1776.310
## F136_sm_female_hdhorn F136_sm_female_thxhorn F136_sm_female_wings
## 2065.781 1777.769 1988.883
## F196_sm_female_hdhorn F196_sm_female_thxhorn F196_sm_female_wings
## 1348.898 1025.303 3067.288
## F197_sm_female_hdhorn F197_sm_female_thxhorn F197_sm_female_wings
## 2639.153 2047.151 2081.891
## F218_lg_female_hdhorn F218_lg_female_thxhorn F218_lg_female_wings
## 2329.564 1950.562 2074.994
## M120_sm_male_genitalia M120_sm_male_hdhorn M120_sm_male_thxhorn
## 1832.781 2105.147 2101.164
## M120_sm_male_wings M125_lg_male_genitalia M125_lg_male_hdhorn
## 2536.922 2088.094 2372.260
## M125_lg_male_wings M160_lg_male_genitalia M160_lg_male_hdhorn
## 2559.087 1727.539 2111.339
## M160_lg_male_thxhorn M160_lg_male_wings M171_sm_male_genitalia
## 2087.584 2184.077 2035.094
## M171_sm_male_hdhorn M171_sm_male_thxhorn M171_sm_male_wings
## 1598.191 1621.661 1825.346
## M172_sm_male_genitalia M172_sm_male_hdhorn M172_sm_male_thxhorn
## 2196.102 1713.120 1344.020
## M172_sm_male_wings M180_lg_male_genitalia M180_lg_male_hdhorn
## 2602.352 1922.635 2670.499
## M180_lg_male_thxhorn M180_lg_male_wings M200_sm_male_genitalia
## 2003.295 3216.477 2412.039
## M200_sm_male_hdhorn M200_sm_male_thxhorn M200_sm_male_wings
## 2032.086 2820.496 2203.815
## M257_lg_male_genitalia M257_lg_male_hdhorn M257_lg_male_thxhorn
## 2170.259 2361.913 2749.768
## M257_lg_male_wings
## 1325.686

```

#alternatively the R way of doing it is using colMeans

```

means_vector <- colMeans(newrna_counts[2:56])
means_vector

```

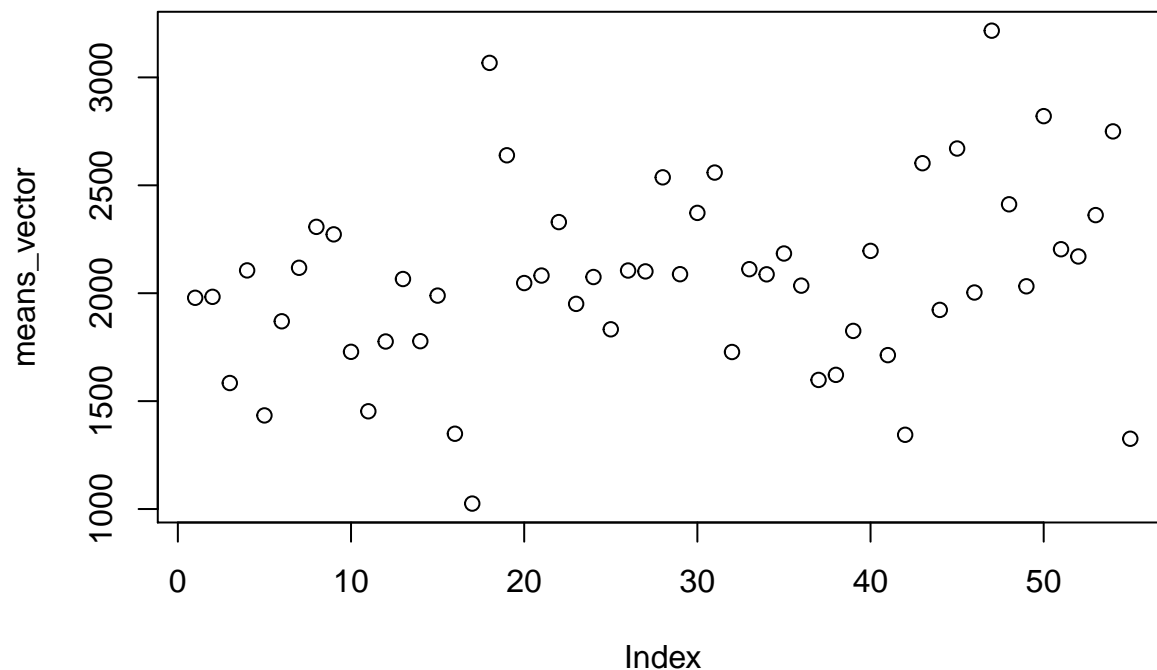
```

## F101_lg_female_hdhorn F101_lg_female_thxhorn F101_lg_female_wings
## 1978.848 1983.251 1583.905
## F105_lg_female_hdhorn F105_lg_female_thxhorn F105_lg_female_wings

```

##	2105.713	1433.751	1869.964
##	F131_lg_female_hdhorn	F131_lg_female_thxhorn	F131_lg_female_wings
##	2117.848	2307.530	2272.693
##	F135_sm_female_wings	F135_sm_female_hdhorn	F135_sm_female_thxhorn
##	1728.485	1452.914	1776.310
##	F136_sm_female_hdhorn	F136_sm_female_thxhorn	F136_sm_female_wings
##	2065.781	1777.769	1988.883
##	F196_sm_female_hdhorn	F196_sm_female_thxhorn	F196_sm_female_wings
##	1348.898	1025.303	3067.288
##	F197_sm_female_hdhorn	F197_sm_female_thxhorn	F197_sm_female_wings
##	2639.153	2047.151	2081.891
##	F218_lg_female_hdhorn	F218_lg_female_thxhorn	F218_lg_female_wings
##	2329.564	1950.562	2074.994
##	M120_sm_male_genitalia	M120_sm_male_hdhorn	M120_sm_male_thxhorn
##	1832.781	2105.147	2101.164
##	M120_sm_male_wings	M125_lg_male_genitalia	M125_lg_male_hdhorn
##	2536.922	2088.094	2372.260
##	M125_lg_male_wings	M160_lg_male_genitalia	M160_lg_male_hdhorn
##	2559.087	1727.539	2111.339
##	M160_lg_male_thxhorn	M160_lg_male_wings	M171_sm_male_genitalia
##	2087.584	2184.077	2035.094
##	M171_sm_male_hdhorn	M171_sm_male_thxhorn	M171_sm_male_wings
##	1598.191	1621.661	1825.346
##	M172_sm_male_genitalia	M172_sm_male_hdhorn	M172_sm_male_thxhorn
##	2196.102	1713.120	1344.020
##	M172_sm_male_wings	M180_lg_male_genitalia	M180_lg_male_hdhorn
##	2602.352	1922.635	2670.499
##	M180_lg_male_thxhorn	M180_lg_male_wings	M200_sm_male_genitalia
##	2003.295	3216.477	2412.039
##	M200_sm_male_hdhorn	M200_sm_male_thxhorn	M200_sm_male_wings
##	2032.086	2820.496	2203.815
##	M257_lg_male_genitalia	M257_lg_male_hdhorn	M257_lg_male_thxhorn
##	2170.259	2361.913	2749.768
##	M257_lg_male_wings		
##	1325.686		

```
plot(means_vector)
```



Question 4

```
mean_col_for_apply <- function( col, log2 ) { if (log2 == TRUE) { logdfm <- log( newrna_counts[2:56],
2) mean( (logdfm)[[ col ]] ) } else { mean( (newrna_counts)[[ col ]] ) } }
```

```
lapply(X = newrna_counts, MARGIN = 2, FUN = mean)
```

```
## Warning in mean.default(X[[i]], ...): argument is not numeric or logical:
## returning NA
```

```
## $X
## [1] NA
##
## $F101_lg_female_hdhorn
## [1] 1978.848
##
## $F101_lg_female_thxhorn
## [1] 1983.251
##
## $F101_lg_female_wings
## [1] 1583.905
##
## $F105_lg_female_hdhorn
## [1] 2105.713
##
## $F105_lg_female_thxhorn
## [1] 1433.751
##
## $F105_lg_female_wings
## [1] 1869.964
##
## $F131_lg_female_hdhorn
```



```

## [1] 2117.848
##
## $F131_lg_female_thxhorn
## [1] 2307.53
##
## $F131_lg_female_wings
## [1] 2272.693
##
## $F135_sm_female_wings
## [1] 1728.485
##
## $F135_sm_female_hdhorn
## [1] 1452.914
##
## $F135_sm_female_thxhorn
## [1] 1776.31
##
## $F136_sm_female_hdhorn
## [1] 2065.781
##
## $F136_sm_female_thxhorn
## [1] 1777.769
##
## $F136_sm_female_wings
## [1] 1988.883
##
## $F196_sm_female_hdhorn
## [1] 1348.898
##
## $F196_sm_female_thxhorn
## [1] 1025.303
##
## $F196_sm_female_wings
## [1] 3067.288
##
## $F197_sm_female_hdhorn
## [1] 2639.153
##
## $F197_sm_female_thxhorn
## [1] 2047.151
##
## $F197_sm_female_wings
## [1] 2081.891
##
## $F218_lg_female_hdhorn
## [1] 2329.564
##
## $F218_lg_female_thxhorn
## [1] 1950.562
##
## $F218_lg_female_wings
## [1] 2074.994
##
## $M120_sm_male_genitalia

```

```

## [1] 1832.781
##
## $M120_sm_male_hdhorn
## [1] 2105.147
##
## $M120_sm_male_thxhorn
## [1] 2101.164
##
## $M120_sm_male_wings
## [1] 2536.922
##
## $M125_lg_male_genitalia
## [1] 2088.094
##
## $M125_lg_male_hdhorn
## [1] 2372.26
##
## $M125_lg_male_wings
## [1] 2559.087
##
## $M160_lg_male_genitalia
## [1] 1727.539
##
## $M160_lg_male_hdhorn
## [1] 2111.339
##
## $M160_lg_male_thxhorn
## [1] 2087.584
##
## $M160_lg_male_wings
## [1] 2184.077
##
## $M171_sm_male_genitalia
## [1] 2035.094
##
## $M171_sm_male_hdhorn
## [1] 1598.191
##
## $M171_sm_male_thxhorn
## [1] 1621.661
##
## $M171_sm_male_wings
## [1] 1825.346
##
## $M172_sm_male_genitalia
## [1] 2196.102
##
## $M172_sm_male_hdhorn
## [1] 1713.12
##
## $M172_sm_male_thxhorn
## [1] 1344.02
##
## $M172_sm_male_wings

```

```
## [1] 2602.352
##
## $M180_lg_male_genitalia
## [1] 1922.635
##
## $M180_lg_male_hdhorn
## [1] 2670.499
##
## $M180_lg_male_thxhorn
## [1] 2003.295
##
## $M180_lg_male_wings
## [1] 3216.477
##
## $M200_sm_male_genitalia
## [1] 2412.039
##
## $M200_sm_male_hdhorn
## [1] 2032.086
##
## $M200_sm_male_thxhorn
## [1] 2820.496
##
## $M200_sm_male_wings
## [1] 2203.815
##
## $M257_lg_male_genitalia
## [1] 2170.259
##
## $M257_lg_male_hdhorn
## [1] 2361.913
##
## $M257_lg_male_thxhorn
## [1] 2749.768
##
## $M257_lg_male_wings
## [1] 1325.686
```

```
#headernames <- names(newrna_counts[2:56])
#headernames
#mean_col("headernames",F)
#apply(headernames, FUN = mean_col(headernames,F))
#lapply(X = newrna_counts, MARGIN = 2, FUN = mean_col(names(newrna_counts[2:56]),TRUE))
#mean_col(names(newrna_counts[2:56]),TRUE)
#names(newrna_counts)
```

Question 5

using colMeans as shown above

Question 6

all about mean of rows

```
tail(rowMeans(newrna_counts[,-1]))

## [1] 5164.400000 805.909091 110.509091 738.472727 6.329091 428.436364
#or rowMeans(newrna_counts[,2:56])

tail(row.names(newrna_counts))

## [1] "4370" "4371" "4372" "4373" "4374" "4375"
```

Question 7

```
mmale_hdhorn_grepped <- newrna_counts[, grepl("_male_hdhorn", names(newrna_counts))]
rowMeans_mmale_hdhorn <- rowMeans(mmale_hdhorn_grepped)

lg_male_hdhorn_grepped <- newrna_counts[, grepl("lg_male_hdhorn", names(newrna_counts))]
rowMeans_lg_male_hdhorn <- rowMeans(lg_male_hdhorn_grepped)

sm_male_hdhorn_grepped <- newrna_counts[, grepl("sm_male_hdhorn", names(newrna_counts))]
rowMeans_sm_male_hdhorn <- rowMeans(sm_male_hdhorn_grepped)

hdhorn_diff <- rowMeans_lg_male_hdhorn - rowMeans_sm_male_hdhorn
plot(rowMeans_mmale_hdhorn, hdhorn_diff)
```

