

## Tasks for LuciLinx R Workshop

### Part I

#### Section 4. VARIABLES AND BASIC OPERATIONS

- 4a. Compare two numbers:  $e^\pi$  and  $\pi^e$ .  
*pi, exp(), "^", ">"*
- 4b. Create a vector of exponents of 2:  $2^0, 2^1, 2^2, \dots, 2^{10}$   
*i:j, "^"*
- 4c. Output the results of 4b as a vector of strings with template: " $2^i = x$ ".  
*print, sprintf*
- 4d. Output the results 4b, showing only even exponents.  
*print, "%%"*

#### Section 5. DATA IMPORT AND EXPORT

- 5a. Dataset from <http://edu.sablab.net/data/txt/shop.txt> contains records about customers, collected by a women's apparel store. Check its structure. View its summary.  
*read.table, fix, str, summary, head*
- 5b. For the "shop" table, save into a new text file only the records for customers, who paid using Visa card.  
*write.table*

#### Section 7. DATA VISUALIZATION

- 7a. Use dataset from <http://edu.sablab.net/data/txt/mice.txt>. Build distributions for male and female body weights in one plot.  
*plot, density*
- 7b. Draw boxplots, showing variability of bleeding time for mice of different strains.  
*boxplot*

### Part II

#### Section 8. DESCRIPTIVE STATISTICS

- 8a. Calculate number of mice with bleeding time bigger than 2 minutes  
*sum*
- 8b. For dataset Mice replace starting weight of any mice by 1000 (assume, there is a mistype). Calculate mean, median, standard deviation and median absolute deviation (MAD) of this weight. Compare the results with original measures.  
*mean, median, sd, mad*

## Section 9. PCA AND CLUSTERING

9a. Acute lymphoblastic leukemia (ALL), is a form of leukemia, or cancer of the white blood cells characterized by excess lymphoblasts. File at [http://edu.sablab.net/data/txt/all\\_data.txt](http://edu.sablab.net/data/txt/all_data.txt) contains the results of a full-transcript profiling for ALL patients and healthy donors using Affymetrix microarrays. The data were downloaded from ArrayExpress repository and normalized. The expression values in the table are in  $\log_2$  scale. Perform and visualize PCA for the patients.

**Hint:** transform data before PCA using `t()` function.

*prcomp, t*

## Section 10. RANDOM NUMBERS

10a. Test central limit theorem. Build distributions of sum of  $n$  uniform random variables, where  $n$  is 1, 2, 3, 6. Compare the latest ( $n=6$ ) with a normal distribution.

*runif, rnorm, qqplot*

## Section 11. STATISTICAL TESTS

11a. For Mice data (<http://edu.sablab.net/data/txt/mice.txt>) compare two weight parameters: *ending weight* and *weight changes* for 2 strains "C58/J" and "CAST/EiJ". Test hypothesis about means and variances these parameters. Try non-parametric Wilcoxon method for as well.

*t.test, var.test, wilcox.test*

## Section 12. ANOVA AND LINEAR REGRESSION

Data presented in the *leukemia.txt* (<http://edu.sablab.net/data/txt/leukemia.txt>) were collected for two groups of patients, who died of acute myelogenous leukemia (AML). Patients were classified into the two groups according to the presence or absence of a morphologic characteristic of white cells. Patients termed AG positive were identified by the presence of Auer rods and/or significant granulature of the leukemic cells in the bone marrow at diagnosis. For AG-negative patients, these factors were absent. Leukemia is a cancer characterized by an overproliferation of white blood cells; the higher the white blood count (WBC), the more severe the disease.

8a. Separately for each morphologic group, AG-positive and AG-negative, draw a scatter diagram to show a possible association between the survival time and the log WBC (take the log yourself) and check if a linear model is justified. If so, estimate a survival time for a patient with  $WBC = 20000$ .

*lm, log, summary*

8b. Create an additional factor – low or high WBC level (e.g. – higher or lower than median) and perform 2-factor ANOVA analysis of the survival time.

*aov, as.factor, cbind, summary*