Let's practice - 7

Let's come back to the mice dataset stored in the "mice_data" data frame (Let's practice – 3). If mice_data is not currently in your workspace, either get it back by loading the .Rdata file or import the data again from the original .csv file.

1) Check your data frame: did it load correctly? Make sure genotype and diet are factor variables.

2) Plot an histogram of mouse weight and customize it with colours, labels, title and represent the density line on top.

3) Make a scatter plot of mouse weights using the function plot(), with no additional arguments. (You do not need to define values for a second axis.) Inspect the plot - what appears on the two axes? Then re-do the plot by adding function arguments: Use solid circles as plotting symbol, add a title, customise the y-axis label, and colour the points **by genotype.** Add a legend.

Let's practice - 8

Let's come back to the mice dataset stored in the "mice_data" data frame (Let's practice – 3). If mice_data is not currently in your workspace, either get it back by loading the .Rdata file or import the data again from the original .csv file.

1) Make boxplots of weights from WT and KO mice. Customise with title, labels, colours.

2) Make a barplot of the mean weights of WT and KO mice, using the means returned by tapply(). Customise the barplot with title, labels, colours.

   Optional: Add number of observations to each bar.

   Optional: add errors bars.

Let's practice – 9

1) Make a multi-panel figure with the **four graphics on one page**, exporting the figure to a **png** file. Set width and height arguments in the call to png() to make it look nice.

2) **Optional:** Perform the steps of the 2 previous practice sessions, but for diet in place of genotype. (Step 2 will not change). This time, make a **pdf** with two pages and **two graphics on each page**. Again, set width and height arguments in the call to pdf() to make it look nice.

3) **Optional:** Look at the multi-panel figures. Are your impressions about mouse weight from yesterday's exploration of data summaries confirmed by today's visualizations?

Let's practice - 10

Come back to the mice data-set stored in the "mice_data" data frame.

1) Considering WT mice weight and KO mice weight separately, check the assumption of normality graphically.

2) Make an appropriate plot to visualize the mouse weights grouped by genotype.

3) Perform a test to see whether the mouse weight is different between the two genotypes.

4) *Repeat step **1** to **3** for the diet variable.*

Let's practice - 11

The data set "Pima" comes from a study on diabetes in women of Pima Indian heritage. We are using a subset (Pima.tr).

1) Load the package MASS using library(). (You may need to install it first). Load the dataset Pima.tr using data(). Use ? to get an idea which variables it contains.

2) Hypothesis: Blood glucose level (glu) is associated with diastolic blood pressure (bp). Run a linear model to test the hypothesis.

3) Visualize the fit with a scatter plot and a trend line.

4) Check assumptions of the model (homoscedasticity, mean of residual at 0, normality of the residuals) graphically.