

## Practice III

### Part I :

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 steps 1 to 3 for the diet variable.

### Part II :

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(). Load the dataset Pima.tr using data (Pima.tr). 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.