Description for the general public

Intensive development of personalized medicine is possible, among other things, due to the ever easier access to methods that allow to analyze the entire genome or gene expression profile, in a single experiment. Based on the changes identified inside the cell it is possible to determine the susceptibility of individuals to a certain disease (e.g. cancer) or to plan a therapy which is suitable for the genetic profile of the patient. However, in order to utilize such data it is necessary to develop a sensitive and reliable methods for the simultaneous analysis of few hundred and sometimes tens of thousands of data points simultaneously. The problem that people involved in data analysis have to face is the impact of nucleic acid structure and the specificity of the measurement method used on the quantitative results obtained. The solution to this problem is particularly important when data from different measurement methods have to be compared. Available data correction methods focus mainly on individual factors, and are designed for a particular test platform, which doesn't allow to connect them and apply to data obtained by different methods.

This project, based on mathematical modeling and experimental data, aims to develop a correction algorithm that will reduce the impact of nucleotide sequences of the tested genes, and oligonucleotide probes used in the experiment on the analysis outcomes. The developed algorithm will be applicable to data obtained using different measurement methods and integrated into existing workflows for the analysis of genomic and transcriptomic data. This will allow to improve the accuracy of methods used to assess changes in gene expression levels, and increase the usefulness of these data in scientific research and personalized medicine.