ITX Integrative Transcriptomics
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Lecture: Microarrays Bioinformatics WS 2017/18

Assignment No. 4 (5 points)

Hand out:	Thursday, November 23
Hand in due:	Thursday, November 30, 10:00
Tutorial date:	Tuesday, November 28, 10:15-11:45
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Theoretical Assignments

1. **Visualization** (3p)

   Write an overview about three different plots of your choice of all plots that have been introduced during the lecture so far. For each plot, provide one example figure and describe:

   - a typical application in the context of microarray data;
   - the input, i.e. the variables that are plotted; and
   - the message, i.e. what is the knowledge one gains from inspecting it.

2. **Drawing task: Experimental Design of Microarray Experiments** (2p)

   Your colleague asks for your help: he wants to measure and compare the transcriptomes of six biological replicates of a certain cell type. He would like to use a dual color microarray for this. He does not have a lot of money, but still would like to conduct the best possible design with the least number of arrays. Which design would you recommend? Draw the design as a graph similar to those introduced in the lecture.

Practical Assignments

3. Visualization of microarray data

In this task we want to visualize microarray data from four experiments (`affy_data.tsv`). The steps of the image analysis of this experiments have been conducted and results have been saved in this tab-delimited file containing raw background subtracted expression values for the four microarrays. Do the following tasks in R.

(a) Produce pairwise scatterplots of the primary expression values of each pair of arrays. Create one plot, which contains all pairwise scatterplots (Hint: use the function par() with the option mfrow=c(nrows, ncols)).

(b) Log-transform the expression values of each array.

(c) Produce scatterplots of the log-transformed expression values of each pair of arrays.

(d) Now write a function that calculates the M and A values and produces an MA-plot for each pair of arrays. Again, create one plot, which contains all pairwise MA-plots.

(e) Compare the original scatterplots to the MA-plots. When inspecting your plots, do you see any issues in the data? Can you think of a possible solution? Briefly discuss and explain which plot is more appropriate to visualize the data and why.

If you are interested in producing more elegant plots, we recommend to take a look into the `ggplot2` package of R.

Please read the questions carefully. If there are any questions, you may ask them during the tutorial session or via e-mail to your tutor. You will usually get an answer in time, but late e-mails (e.g. on Thursday morning before class) might not be answered in time. Please upload your solutions in the Ilias system. Please pack your source code, the plots, as well as the theoretical part into **one single archive file (zip)**. Source code should compile correctly.