

DNA microarray analysis exercise

A research group has used Affymetrix microarrays to profile gene expression in six cattle in negative energy balance and six controls and come to you for help with the analysis. Provide a step-by-step description of how you would:

1. determine whether there is evidence of a difference in gene expression profile between the two groups
2. identify and visualize the genes that are significantly differentially expressed between the two groups
3. find whether there are specific classes of genes (e.g. functional classes or pathways) that are enriched for differentially expressed genes

Write down the steps you would follow to help this research group. You can use all or part of the pipeline studied in class, but in that case investigate the effects of as many alternative analysis choices as you can (i.e. run the analysis using different functions or options and see what the effects are on your results – e.g. on the top most differentially expressed genes). Alternatively, search for analysis pipelines that have been used by others for similar problems and combine parts of these with the pipeline that we have studied in class.

In your step-by-step analysis, it is critical that you provide detailed comments, explain what each step does and provide your rationale for each step.