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**Supplemental Materials**

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**Description of a full analysis one data set taught in the course**

Renal cell carcinoma is a common malignancy that often presents as a metastatic-disease for which there are no effective treatments. To gain insights into the mechanism of renal cell carcinogenesis, a number of genome-wide expression profiling studies have been performed. The experiment hybridized total RNA isolated from renal cell tumors and adjacent normal tissue to Affymetrix U133A.

The following full analysis were conducted

1. Preprocessing
  - Importing the celfiles and the phenodata;
  - Summarize the expression values per each probe set.
  - Summarizing expression values is constituted of the following steps: background correction, normalization and summarization.
2. Gene discovery and visualization plot
3. Pathway Analysis

Data were taken from <http://www.ncbi.nlm.nih.gov/projects/geo/query/acc.cgi?acc=GSE781>

**Learning objectives as stated in the syllabus**

After successfully completing this course, students will be able to:

1. Demonstrate a working knowledge of extracting gene expression from a microarray experiment.
2. Demonstrate a working knowledge of several different methods of analysis of data produced by the microarray technology.
3. Demonstrate a working knowledge of the various methods appropriate for different scientific questions.
4. Become confident in the use of software MAGIC and/ or R and Bioconductor packages. Students will be provided with daily hands-on experience using the statistical techniques introduced.
5. Perform clustering and classification methods to uncover common patterns of gene expression across different samples.
6. State the results of a microarray data analysis in statistical terminology and in the context of an application.

**Useful websites for database and software**

GCAT <http://www.bio.davidson.edu/projects/gcat/gcat.html>

MAGIC <http://www.bio.davidson.edu/projects/magic/magic.html>

R <http://www.r-project.org/>

Bioconductor <http://www.bioconductor.org/>

KEGG <http://www.genome.jp/kegg/kegg2.html>