

Fees for Gene Expression Analysis Services:

CONSULTATION ON EXPERIMENTAL DESIGN: no charge

- For investigators interested in starting a gene expression project, we offer a free initial consultation on experimental design and identification of potential analysis issues.
- Investigators are not obligated to get any additional analysis services.

GENERAL STATISTICAL CONSULTING: \$40/hr

- Specialized projects, training, or detailed annotation of genes.
- Initial and follow-up meetings are free.

BASIC STATISTICAL ANALYSIS OF MICROARRAYS: \$200 set-up fee + \$40/array

- **Quality control and Pre-processing:** We will use a variety of platform-appropriate methods to assess the quality of individual arrays and detect any outliers. Data pre-processing steps of background-correction, normalization and summarization will be assessed and implemented if warranted. Gene filtering typically will be performed based on presence/absence of gene expression or other criteria as requested. A data matrix of the final normalized expression values will be provided as well as summary plots to indicate problematic arrays.
- **Differential Expression Testing:** We will use R and Bioconductor packages to implement ANOVA-based models to test for differentially-expressed genes. For all comparisons specified by the investigator, a data file will be produced including fold-change, raw p-values, False Discovery Rate-adjusted p-values and any readily-available annotation information². Other data analysis methods available upon request.
- **Analysis Report and Meeting:** We will provide a written summary of the analysis results and how to interpret the data files. We will also typically have one or more meetings to discuss the results in person, address any questions and advise on possible further steps.
- **Additional Information:** Whenever the investigator requests, we will provide a detailed description of the analysis for publication. For those interested in learning and doing the analysis themselves, we will provide the source codes used in the analysis and help on using the codes.

BASIC STATISTICAL ANALYSIS OF RNA-SEQ DATA: \$200 set-up fee + \$40/sample

- Steps taken and results provided similar to that of microarrays, modified as appropriate for count-based data.
- Requires RNA-Seq data to already be processed into “counts per gene” for each sample. See {link} for help with processing RNA-Seq reads into counts.

WEIGHTED GENE CO-EXPRESSION NETWORK ANALYSIS: \$300 - \$1000 (request quote)

- Gene clustering based on the WGCNA method (link to: <http://www.genetics.ucla.edu/labs/horvath/CoexpressionNetwork/>), which identifies modules of genes with similar expression patterns across your samples.
- Can be used in addition to or in place of a statistical analysis.
- Modules can be correlated with quantitative or qualitative sample variables, or compared with modules from other experiments.
- Results include identification of the genes in each module with expression patterns and readily-available² annotation information, heatmaps of the expression pattern in each module, and any figures associated with correlational analyses or module comparisons.

DETAILED ANNOTATION OF GENE LISTS: \$40/hr

- For microarray platforms or species that do not have adequate gene annotations readily-available².
- Given one public id type, various databases will be searched to provide the requested annotation data (e.g., gene symbol, description, other id types, Gene Ontology terms, pathways, genome location).

DATA MINING OF GENE LISTS: \$100/gene list

- Summarization of the number of genes in each list to Gene Ontology terms and pathways.
- Over-representation testing to find the GO terms and pathways that appear in the selected gene list more often than expected, based on the appropriate background.

SUBMISSION OF DATA TO PUBLIC REPOSITORIES:

- Raw and normalized data files resulting from a Basic Statistical Analysis provided free-of-charge, along with general advice and links to the GEO submission information.
- Extended help (\$100 per experiment) includes preparation of sample information tables, collating all necessary files into one zipped file for submission, and detailed help in setting up a GEO account and submitting the experiment.

TRAINING ON GENE EXPRESSION ANALYSIS:

- Individual or lab-group training on how to analyze gene expression data using R and Bioconductor is available year-round (\$40/hr).
- Two-day workshops (lectures and computer labs) are offered periodically, usually during Winter, Spring or Summer breaks. Please contact drnevich@illinois.edu to see when the next one is scheduled (\$75/person).

Notes:

1. An “array” is either one sample for most microarray platforms, or two samples for dual-channel arrays. If additional arrays are to be combined with arrays previously analyzed, the cost for the new analysis will be based on all arrays, not just the additional arrays. For very large numbers of arrays, it may be more cost-effective to switch to the hourly consulting rate (\$40/hr).
2. “Readily available” annotation information refers to either an Excel-type file with columns of annotation information, one of which that matches an ID provided by the array manufacturer or an array-specific annotation package {link to: <http://bioconductor.org/packages/release/data/annotation/>} from Bioconductor.

Prices current as of January 1, 2012, subject to change without notice.