



MICROARRAY ANALYSIS & BIOINFORMATICS Workshops at Kansas State University

July 9 – 12, 2007

You are invited to participate in a technical workshop being offered this summer by the Ecological Genomics Institute at Kansas State University. The 4-day workshop is being organized in two separate modules as described below. You may register to attend either one or both of the modules. The topics of these workshops are particularly relevant for investigators who want to develop expertise in:

- statistical analysis of large genomic datasets,
- designing experiments and testing hypotheses using genomic tools, and
- accessing the full power of molecular information available on the web.

Module 1: Microarray Analysis

July 9, 10 & 11

Monday and Tuesday, 8:30–5:00, through Wednesday, 8:30-1:30 pm, Room 232 Ackert Hall

Instructors: Greg Gibson & Stan Martin, North Carolina State University

This course will introduce students to the theory and practice of microarray-based gene expression profiling. It will include lectures on basic statistics for biologists, fundamentals of expression profiling, statistical fundamentals for microarray datasets, and experimental design. The workshop will include demonstrations of data analysis using the SAS/JMP Genomics software suite as well as R/Bioconductor open source software. Participants will walk through two examples on their own computers. Time will be devoted to discussions of students' own data analysis problems. Finally, quick reviews of the latest applications of gene expression profiling in ecology and evolutionary biology will be provided. Computers will be furnished for the hands-on portion of the workshop.

Registration fee includes all conference materials and lunch each day: \$75.

Module 2: A Field Guide to GenBank and NCBI Molecular Biology Resources

July 12

Thursday, 8:30 am to 11:30 am, Big 12 Room, K-State Union

11:30-1:00, Lunch, Bluemont Room in K-State Union

1:00-3:00 & 3:00-5:00, Separate Hands-On Laboratory Sessions, Room 219 Ackert

Instructor: Steve Pechous, National Center for Biotechnology Information (NCBI), NLM, NIH

Molecular sequence databases and computational biology tools are an important part of nearly all areas of biological and biomedical research. *A Field Guide to GenBank and NCBI Molecular Biology Resources*, will include both lecture and hands-on computer components. Students will learn how to apply resources in their specific research area. The course provides practical information about GenBank, RefSeq and the integrated genome resources, as well as the other databases maintained at the NCBI. It will also provide instruction on effective use of Entrez and BLAST, the two main database search tools. Both experienced and novice users of the NCBI tools and resources will benefit from attending this workshop. Computers will be furnished for the hands-on portion of the workshop.

Registration fee includes all conference materials and lunch: \$20.



Lodging: For a complete list of Manhattan hotels and lodging options, visit:

www.manhattancvb.org/index.asp?NID=2.

Conference housing may also be available in a K-State dormitory. Contact D. Merrill for additional information, dmerrill@k-state.edu.

Registration: To register: Visit <http://outreach.ksu.edu>.

Scroll down to Arts and Sciences, and select the workshop(s) for which you wish to register.

Questions:

Please contact (785) 532-3482, dmerrill@ksu.edu

For more detailed information about the Workshops:

<http://www.k-state.edu/ecogen/Workshop-2007.html>

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