SPH 247 **Spring 2015**	**Statistical Analysis of Laboratory Data**	**David M. Rocke** **March 31, 2015**

Course Information

Class Meetings:	Tuesdays 8:00am–11:00am, 1444 CTSC
Lab:	Tuesdays 11:00am-12:00pm, 1444 CTSC
Office Hours:	By appointment.
Office:	140B Med Sci 1C (530-752-6999) or at the CTSC FAX: 530-752-3239 e-mail: dmrocke@ucdavis.edu web site: http://dmrocke.ucdavis.edu/
Text:	None. Lectures, notes, and data sets posted on line.
Computer	Please bring a laptop to class, OS X, Windows, or Linux should all be fine. A few of the data sets will be large (up to several gigabytes). We will mostly use R for the analysis.
TA:	Leah Jin (lcjin@ucdavis.edu)

Course Grading:	Letter Grades based on
	    Homework
	    Class Attendance
	    Class Participation

Class Dates	March 31 April 7, 14, 21, 28 May 5, 12 ,19, 26 June 2
Prerequisites	SPH 245 and SPH 246 or the equivalent.

This course is an introduction to statistical methods for experimental design and analysis of data in a laboratory context, as against in a clinical or population context. We will cover methods for one-variable analysis, as in Western blots or PCR, as well as high-throughput techniques such as gene expression arrays and RNA-Seq. Statistical methods will range from interlaboratory studies to clustering and multivariate analysis.

Tentative Topical Outline

I.   Experimental Design
II.   Random and Mixed Effects Models
III.   Assay Measurement
   A.   Calibration
   B.   Standardization
   C.   Normalization
   D.   Detection limits
   E.   Variance, Standard Deviation, and Coefficient of Variation
   F.   Error models
   G.   Interlaboratory studies
   H.   Intralaboratory studies
IV.   Survey of Instrumental Methods
   A.   Mass Spectrometry
   B.   Arrays
   C.   RNA-Seq
   D.   NMR Spectroscopy
   E.   ELISA and similar assays (Luminex)
   F.   PCR
   G.   Westerns, etc.
V.   Significance, Prediction, and Classification
VI.   Generalized linear models and RNA-Seq
VII.   Multivariate analysis
VIII.   GO and annotation
IX.   Expression arrays and RNA-Seq
X.   Gene expression analysis with R
XI.   Gene groups, pathways, and inference
XII.   Reproducible Research