PROGRAMME OF THE SIXTIETH ANNUAL DEMING CONFERENCE ON APPLIED STATISTICS

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NY/NJ Metropolitan Section ~ ~ Statistics Division

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Biopharmaceutical Division

December 6 – December 8, 2004: Three-Day Conference
Tropicana Casino and Resort, Atlantic City, NJ

Short Courses: – December 9-10, 2004

1. Multiple Comparisons for Making Clinical and Genomic Decisions by Jason C. H. Hsu
2. Applied Longitudinal Data Analysis: Modeling Change and Event Occurrence by Judith D. Singer
   John B. Willett

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60th ANNUAL DEMING CONFERENCE ON APPLIED STATISTICS

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Monday December 6, 2004

8:30 – 11:30 AM

Session A

Applied Longitudinal Analysis: Contrasting Marginal and Mixed Effects Models 🕮

Speaker: Professor Garrett M. Fitzmaurice

Harvard School of Public Health

Moderator: Walter R. Young

In recent years, there have been remarkable developments in methods for analyzing data from longitudinal studies. In particular, generalized linear models have been extended in a number of ways to handle longitudinal data. Two broad classes of models can be distinguished: "marginal models" and "mixed effects models". Both classes of models account for the within-subject correlation among the repeated measures, though they differ in approach. For discrete longitudinal data, these models have regression coefficients with quite distinct interpretations. Indeed, it was the need to distinguish models for longitudinal data according to the interpretation of their regression coefficients that led to the use of the terms "marginal models" and "mixed effects models". In general, these two classes of models have different targets of inference and therefore address somewhat different questions regarding longitudinal change in the response. The subtle distinctions between these two classes of models are not well understood by many statisticians and practitioners. The speaker will review marginal and mixed effects models for longitudinal data and highlight the main distinctions between them. The speaker will also discuss the types of scientific questions addressed by each of the two classes of models. The main emphasis will be on the practical rather than the theoretical aspects.

Session B

Monte Carlo Methods with Applications to Bioinformatics 🕮

Speaker: Professor Jun S. Liu

Harvard University; Cambridge, MA

Moderator: William Wubao Wang

Monte Carlo methods have been crucial in many scientific endeavors, ranging from physics to biochemistry, and have recently become very popular in the statistics community. Both Markov chain Monte Carlo (MCMC) and sequential Monte Carlo (SMC) techniques will be discussed with an emphasis on their applications in bioinformatics. The speaker will explain the idea of Metropolis et al. (1953) and its close "cousin" Gibbs sampling, which are fundamental rules for constructing a Markov chain whose equilibrium distribution is the one prescribed in advance. Then the speaker will focus on some advanced ideas such as parallel tempering, multigrid Monte Carlo (MGMC), evolutionary Monte Carlo, etc. These ideas aim at constructing Markov chains with better mixing properties and are very helpful in many practical problems. The speaker will also describe SMC techniques, whose basic idea is to construct a sampling distribution sequentially and to use resampling (or pruning and splitting) to further improve the method. They are often known in the engineering and statistics literature as the "bootstrap filter", the "particle filter", etc., and in the biophysics literature as the Rosenbluth method. These ideas are particularly attractive for dealing with dynamic structures, such as the nonlinear state-space models and molecular structure prediction. The speaker will describe applications of these Monte Carlo techniques in both statistical and computational biology problems such as the gene regulatory binding motif discovery, the Bayesian inference of differentially expressed genes, and biopolymer structure optimization.

Monday Lunch (On Your Own) 11:30 AM - 1:00 PM

1:00 - 4:00 PM (Session D will run until 5 PM)

Session C

Cancer Therapy, Experimental Design, and Data Analysis

Speaker: Kao-Tai Tsai, Ph.D.

Aventis Pharmaceuticals, Bridgewater, NJ

Moderator: William Wubao Wang

With the advancement of medical technology, human life expectancy has been greatly extended. Consequently, human beings are increasingly exposed to cancer related risk factors, therefore, cancer research has become one of the most active areas in modern medical research Even though cancer research has an extended history, there are still many open technical and human issues, which hinder its progress.

The speaker will address the progress of cancer research and cover the most recent research results beginning with the adjuvant chemotherapy, therapy for metastatic disease, hormone replacement therapy. The speaker will also discuss the chemoprevention management, neoadjuvant chemotherapy and dose-dense adjuvant chemotherapy, single agent verse combination chemotherapy for metastatic disease. In addition to the discussion of the availability of up-to-date cancer therapy, the speaker will also discuss the related statistical designs and analyses methodologies. This will range from the determination of MTD in Phase I trials, the multi-stage designs for Phase II-III trials, to the quality of life analyses in Phase IV studies. Furthermore, regulatory issues regarding to the submission of oncology study results for the marketing approval will also be discussed.

Session D

Group Sequential Methods

Speaker: Edward Lakatos, Ph.D.

BiostatHaven Inc; Croton-on-Hudson, NY

Moderator: Alfred H. Balch

Group-sequential methods are the most often used statistical approaches to monitored trials. They have been used as the basis for terminating many trials, and provide the core statistical methods. A basic grasp of the issues is fundamental to understanding other techniques such as stochastic curtailing and methods for mid-course corrections such as sample size re-estimation. The speaker will provide that fundamental understanding, as well as provide some insight into the issues that arise when monitoring clinical trials.

The speaker will present the fundamentals of group-sequential methods, drawing examples from many NIH and pharmaceutical trials, some designed by the instructor. The first segment will serve as an introduction to the issues involved in trials that need Data Monitoring Committees (DMCs). The remainder is more technical. It begins with an historical perspective, as the early approaches are easy to understand, and serve to motivate many of the important later developments. Some important statistical concepts are discussed, such as information, and how the multiple comparisons issue of repeatedly analyzing the data is handled. The role and operation of the Lan-DeMets spending function will be explained in depth, followed by considerations in choosing a boundary. Because survival trials play a central role in group-sequential methods, they will be discussed in detail. In designing survival trials, factors such as noncompliance and loss to competing risks are often important, and survival may not be exponential. Most of the literature on group-sequential designs is not set up handle these situations, yet, as demonstrated by the examples, the effect on power, sample size, and design can be dramatic. This part of the presentation will be built around a survival trial in congestive heart failure.

Session Titles with 🕮 are based on a book, which is available from the conference.

Tuesday December 7, 2004
8:30 – 11:30 AM

Session E
Applied Adaptive Statistical Methods 🕮
Speaker: Professor Thomas W. O'Gorman
Northern Illinois University; Dekalb, IL
Moderator: Jackie Kennedy

Adaptive tests and confidence intervals will be introduced. Adaptive tests are often more powerful than traditional tests and their confidence intervals are often narrower than traditional confidence intervals. The speaker will use many examples to illustrate a variety of applications of adaptive methods, and will demonstrate how existing software can be used to perform the calculations. The speaker will begin with the two-sample adaptive test, but will also demonstrate how adaptive tests can be used to test any subset of regression coefficients in a linear model. The adaptive weighting method and the permutation techniques will be explained. The speaker will discuss an adaptive test for the slope in a regression model and adaptive tests for more complex models. An adaptive test for paired data will also be presented and the software for this test will be demonstrated. Adaptive confidence intervals will also be described in some detail along with the software that can produce these adaptive interval limits.

Session F
Cross-over Trials For Two Treatments: Design And Analysis 🕮
Speaker: Professor Byron Jones
GlaxoSmithKline, Harlow, UK
Moderator: Nandita Biswas

Perhaps the best-known and widely used cross-over design is the one that has two treatments, two treatment sequences and two periods. This design is often referred to as the AB/BA design and is fully efficient for comparing treatments in the absence of differential carry-over effects. Estimation and testing in the presence of differential carry-over effects is problematic and until relatively recently has apparently been misunderstood by many authors and practitioners. The speaker will give a thorough and clear descriptions of the problems caused by the presence of differential carry-over effects and suggest ways for overcoming them. In particular, the speaker will cover the following topics: problems of preliminary testing for differential carry-over effects, estimation and testing for a treatment difference, useful plots, analysis of covariance, use of baselines, Bayesian analyses, nonparametric analyses and analyses for binary data. Illustrations using data obtained from real pharmaceutical trials will be given. Bioequivalence testing is an important area where the AB/BA design is used. The speaker will describe and illustrate the analysis of data that is intended to show average bioequivalence (ABE). Sample size and power calculations for ABE will be described. The regulatory aspects will also be considered.

Tuesday Lunch (On Your Own) 11:30 AM - 1:00 PM

1:00 - 4:00 PM

Session G
Adaptive Designs for Clinical Trials in Drug Development
Speaker: H. M. James Hung, Ph.D.
Office of Biostatistics, Center for Drug Evaluation and Research, FDA
Moderator: Ivan Chan

For drug development the success of the clinical trial phases depends on many factors. For instance, a few relatively small Phase II clinical studies may or may not be able to provide reasonably sufficient amount of information for planning Phase III trials, depending on the endpoints and their abilities to predict the potential clinical benefits of a test drug. The success of a Phase III clinical trial that often determines the fate of the test drug relies on many design specifications that often need to be reasonably well projected in the planning stage. For instance, planning sample size or total amount of statistical information entails a good projection of the effect size of the test drug. Selection of primary endpoints and allocation of the total alpha for testing them also require a fair amount of educated guesses. Because of these practical constraints, many alternative designs have been explored with a hope to inject fuels needed to enhance the chance of success with a certain level of efficiency. Collection of safety data in the pre-marketing phase is also a factor determining efficiency. A number of adaptive designs will be reviewed. The utilities and the pitfalls of these designs will be explored from both the perspective of the entire drug development program and the perspective of an individual trial. The logistics issues will also be discussed.

Session H
Multiple Analyses in Clinical Trials 🕮
Lemuel A. Moyé, M.D., Ph.D.
University of Texas School of Public Health; Houston, TX
Moderator: Walter R. Young

The multiple analysis issue in clinical trials is the source of confusion to the medical, industry, and regulatory community. The conflict between logistical efficiency (using the data to make as many interesting and useful measures as possible) and interpretative parsimony requires the number of hypothesis tests to be kept to a minimum in order to minimize the impact of the multiple testing issue. Actually, the circumstances of multiple analyses in clinical trials are more complicated than the previous examples suggest because, in reality, these analyses occur not in isolation but in complex mixtures. For example, a clinical trial may report the effect of therapy on several different endpoints, and then proceed to report subgroup findings for the effect of therapy on a completely different endpoint. Some of these hypothesis tests were designed before the study was executed, while others were merely "targets of opportunity" that the investigators noticed as the clinical trial evaluation proceeded to the end; some of these analyses have small *p*-values, while others do not. Whatever the driving force for these analyses is, the use of a single clinical trial to address multiple scientific questions proceeds at an accelerating pace. Yet the physician-scientist, while well versed in clinical science and highly motivated to carry out clinical research, is often unprepared for the interpretive complexities presented by the multiple analysis problems. The use of an endpoint triage system is discussed. Development and discussion of hypothesis testing dependency in a clinical trial setting is provided. The idea of hyper-dependent endpoint analyses are provided and displayed in useful real examples. The use of combined or composite endpoints is presented, and a discussion of the usefulness of subgroup analysis is also demonstrated.

Wednesday December 8, 2004
8:30 – 11:30 AM

Session I
Design And Analysis Of Multicenter Trials Using Fixed And Random Effects Models
Speaker: Professor Byron Jones
GlaxoSmithKline, Harlow, UK
Moderator: Nandita Biswas

When a clinical trial needs to enrol a large number of patients it is usually impossible for a single clinical center to enrol them all. Consequently, patients are enrolled at multiple centers. The treatment differences will vary over the centers and must be combined in some way. Dragalin et. al. (2002) proposed that the Combined Response to Treatment (CRT) be used for this combined measure. The CRT can be estimated using fixed-or random-effects models and we will describe and illustrate the analysis using each type of model. The current regulatory guidelines for multicenter trials will be described and the use of random-effects models in this context will be discussed. Use of the random effects model permits calculation of the optimal number of centers as well as patients. The speaker will describe methods for determining the optimal number of centers and patients based on considerations of statistical power and on loss functions that account for center and patient costs and potential loss of revenue. Variance inflation due to randomness in enrolment and varying enrolment rates will also be considered.

Reference: Dragalin, V., Fedorov, V., Jones, B. and Rockhold. F. (2002) Estimation Of The Combined Response To Treatment In Multi-center Trials. Journal of Biopharmaceutical Statistics 11(4), 275-295

Session J
Contributions to Discrete Distributions 🕮
Speaker: Professor Daniel Zelterman
Division of Biostatistics
Department of Epidemiology and Public Health, Yale University
Moderator: Jackie Kennedy

The speaker will discuss the development of methods for deriving new discrete distributions. Specific examples will be motivated by studies of data from the fields of medicine, demography, and pre-clinical drug development. The speaker will begin with general principles for discrete distributions such as the binomial and hypergeometric models. From these, the speaker will generalize the principles to demonstrate how new distributions may be derived. The first half of the talk concentrates on urn models. While urn models provide a simple teaching tool, these lack practical application. Instead, the speaker will motivate the models using examples involving frequencies of birth defects in litters of laboratory animals and models for estimating frequencies of genetic markers in the population. The second half of the talk describes models for sums of dependent Bernoulli random variables. Once the assumption of independence is dropped, the level of mathematical difficulty rises quickly. Nevertheless, there are several relatively simple and useful methods for deriving distributions for sums of dependent 0-1 Bernoulli random variables. The speaker will motivate these new distributions using studies of drug toxicity in a pre-clinical study of birth defects in laboratory animals.

Wednesday Lunch (On Your Own) 11:30 AM - 1:00 PM
1:00 - 4:00 PM

Session K
R: Open Source Data Analysis And Graphics
Speaker: Professor Douglas M. Bates
University of Wisconsin; Madison, WI
Moderator: J. Stuart Hunter

R (www.r-project.org) is an open source (and freely available) implementation of John Chambers' award-winning S language for data analysis and graphics. Precompiled versions for Windows(TM), Mac OS-X(TM) and various distributions of Linux(TM) can be downloaded from the Comprehensive R Archive Network sites (cran.r-project.org) or, if desired, the sources can be downloaded and compiled. The most notable feature of R as a statistical computing and graphics environment is the ease with which users can extend existing facilities, either for simple "one-off" calculations and plots or for more extensive development projects. For extensive projects there are facilities for producing and distributing add-on packages. Over 300 such contributed packages are available on the archives from where they can be easily downloaded and installed. Specialized projects such as Bioconductor (www.bioconductor.org), that provides software for the analysis of microarray data, build on the base language in R. We will demonstrate installing R, using it for simple data analysis and graphics, and extending it for specialized computation.

Session L
Statistical Aspects of the New E14 Guidance on QT-Interval Prolongation
Speaker: Margarida Geraldes, Bristol-Myers Squibb
Panel Discussion by
Joel Morganroth, Univ of PA and Chief Scientist, eResearch Technology
Yibin Wang, Novartis
Stella G. Machado, Quantitative Methods/OEB/CDER/FDA
Moderator: Alfred H. Balch

The new preliminary E14 concept paper, *The clinical evaluation of QT/QTc interval prolongation and proarrhythmic potential for non-antiarrhythmic drugs* addresses a number of issues with respect to standard trials to ensure drug safety with respect to cardiac repolarization.

Many of the issues addressed in the draft guidance document are statistical in nature. These include the choice of study design for the Thorough QT/QTc study (parallel or crossover design), the primary endpoint and decision rule, the number and timing of the ECG recordings (pre- and post-dose), how to correct QT for heart rate, categorical analyses, analysis of central tendency, assessment of concentration-response effect, and statistical analyses to be performed on patient data if the "Thorough" QT/QTc study showed evidence of QT prolongation by the investigational drug.

The PhRMA QT Statistical Expert Team (QT-SET), have produced an industry response to the E14 guidance document. There will include a presentation of the E14 guidance, followed by the PhRMA position and then each panelist will have an opportunity to present his or her perspective. We will then have a general floor discussion on all issues with possible panelist response.

Attendees of this workshop will receive, as part of the proceedings, a list of references to useful literature and government guidance documents in this area and the QT-SET presentation.

TWO SIMULTANEOUS SHORT COURSES
THURSDAY AND FRIDAY, DECEMBER 9-10, 2004
GENERAL COURSE INFORMATION

Registration includes (1) two refreshment breaks each day; (2) handouts and; (3) textbook. No registrations will be accepted without payment in full. Government employees may request to be invoiced at our on-site fee. We will refund tuition if courses are canceled due to insufficient registration.

SCHEDULE

8:30–10:00 Lecture 10:00–10:20 Break 10:20–11:50 Lecture 11:50–1:10 Lunch 1:10–2:40 Lecture 2:40–3:00 Break 3:00–4:30 Lecture

Multiple Comparisons for Making Clinical and Genomic Decisions

Instructor: Professor Jason C. H. Hsu, The Ohio State University
Columbus, OH 43210-1247
Moderator: Dr. William Wubao Wang
Text: Multiple Comparisons: Theory and Methods

Multiple comparisons are used to make decisions.

Some examples of such decision-making in clinical pharmaceutics are (C1) testing for bioequivalence of a generic drug with its the brand name version, (C2) finding the minimum effective dose (MED) in a Phase II dose-response study, and (C3) testing for the efficacy of a new drug in a Phase III trial where efficacy is defined in terms of multiple endpoints. During the first day, we give a comprehensive discussion of concepts of multiple comparison error rates, including the *per comparison* error rate, *experimentwise* error rate, *familywise* error rate (FWER), and the *False Discovery Rate* (FDR). For each of the three examples of decision-making listed above, we will discuss how to choose the null hypotheses to test. For each example, we will also show which error rate to control in order to control the probability of an incorrect decision. References discussed will include FDA guidance on average, population, and individual bioequivalence, ICH guidance on dose-response studies (E4), and ICH guidance on choice of control groups (ICH E10).

Some examples of decision-making using multiple testing in genomics are (G1) *designer medicine*: selecting genes for making prognostic/ diagnostic microarrays to individualize patient treatments according to genetic profiles, (G2) *patient targeting*: finding genetic markers to eliminate patient subpopulations prone to serious Adverse Events, (G3) *drug targeting*: finding genes differentially expressed in a disease process to discover co-regulating transcription factors as potential drug targets.

The second day will be devoted to the analysis of gene expressions data from microarrays. After describing the cDNA and oligonucleotide microarray technology, pre-processing and normalization of the data will be discussed. After reviewing the concepts of multiple comparison error rates pertinent to genomics, namely the *familywise* error rate (FWER) and the *False Discovery Rate* (FDR), we will show that closed testing and partitioning remain the fundamental principles of multiple test construction in genomics. Stepwise testing, including the Westfal and Young approach, will be shown to be a computational shortcut to closed/partition testing. We will state the conditions that must be satisfied for such shortcuts to be valid, the subtleties of which have not always been appreciated in bioinformatics. We will then discuss the pros and cons of the non-modeling methods such as Holm's stepdown method and Hochberg's stepup method, versus modeling methods such as the genomic analogues of the Studentized maximum modulus method and Dunnett's method. References discussed will include the FDA/CDRH guidance on Multiplex Testing of Heritable Biomarkers, and the FDA/CDER guidance on Pharmacogenomics.

Covering concepts and techniques, this course will be useful to anyone using multiple testing to make decisions. Using examples in clinical trials and genomics to illustrate the applications, this course will be especially useful to pharmaceutical and bioinformatics statisticians.

Jason Hsu got his PhD from Purdue University in 1977, and has been teaching at Ohio State ever since. His work in multiple comparisons has been useful in bioequivalence, stepwise testing, and dose-response studies. He has contributed to computer implementation of multiple comparison methods in statistical software packages. Currently, he is

Applied Longitudinal Data Analysis: Modeling Change and Event Occurrence

Instructors: Professor Judith D. Singer, Harvard University
Professor John B. Willett, Harvard University
Moderator: Dr. Alfred H. Balch
Text: Applied Longitudinal Data Analysis: Modeling Change and Event Occurrence

The instructors will give an accessible yet in-depth presentation of two of today's most popular statistical methods: multilevel models for individual change and hazard/survival models for event occurrence (in both discrete- and continuous-time). Using real data sets from published studies, these outstanding classroom teachers take participants step-by-step through complete analyses, from simple exploratory displays that reveal underlying patterns through sophisticated specifications of complex statistical models. They illustrate ideas using a variety of software packages. Forty longitudinal data sets as well as complete computer code for the most commonly used programs (including SAS, stata, SPSS, Splus, MlwiN and HLM) are in their web site: http://www.ats.ucla.edu/stat/examples/alda/.

Using a data-analytic approach, the course emphasizes five linked phases of work: articulating research questions, postulating an appropriate model and understanding its assumptions, choosing a sound method of estimation, interpreting analytic results, and presenting findings—in words, tables, and graphs—to both technical and non-technical audiences. Thoughtful analysis can be difficult and messy, raising delicate problems of model specification and parameter interpretation. The default options in most computer packages do *not* fit the statistical models you want. The course's goal is to provide the short-term guidance needed to start using the methods quickly, as well as sufficient long-term advice to support your work wisely once begun.

Although the course stresses connections between the methods, for pedagogic reasons, the presentation is divided into two major parts: individual growth modeling on the first day; survival analysis on the second. The first half of each day begins with descriptive and exploratory methods, followed by a detailed discussion of basic model specification, model fitting, and parameter interpretation. The second half of each day extends the basic principles to the messy arena of real-world applications. Thus, after introducing the essentials of growth modeling, we discuss topics such as centering predictors, handling variably spaced measurement occasions or varying numbers of waves, including time-varying predictors, and fitting discontinuous and non-linear change trajectories. After introducing the basic principles of discrete- and continuous-time survival analysis, we discuss the proportionality assumption (when it is met; what to do when it is not), how to fit non-proportional hazards models, and how to include time-varying predictors.

The target audience is professionals who have yet to fully exploit these longitudinal approaches. Some participants may be comfortable with multilevel modeling or survival analysis, although we assume no familiarity with either. And although our methodological colleagues are not our prime audience, we hope they, too, will find much of interest.

Judith Singer and John Willett are Professors of Quantitative Methods at the Harvard Graduate School of Education. Longtime collaborators, both authors specialize in applied statistical methods and research design, particularly for longitudinal data. Widely respected as superb teachers, Singer and Willett have extensive experience making complex statistical material accessible to a wide audience. Together, they have

Committee

Chairman & Program
Walter R. Young*
Wyeth Research
P.O. Box 42528
Philadelphia, PA 19101
(484) 865-5640
Fax # (484) 865-0067
youngw@wyeth.com

Registrar
William I. Martin
Customized Management Systems, Ltd.
18-65 211 St., Suite 2F
Bayside, NY 11360-1814
(718) 631-2375
Fax # (718) 631-2375
dem-cms@att.net

Transactions
Edward Warner
Schering-Plough Corporation
Mail Stop U-1-1 1600
1011 Morris Ave.
Union, NJ 07083
(908) 820-6988
Fax # (908)-820-6003
ed.warner@spcorp.com

Arrangements
Satish Laroia
Larson Associates
33 Aspen Circle
Edison, NJ 08820
(973) 812-9033
Fax # (732) 549-7487
satish.laroia@amide.com

Bibliolator
Marci Conors
Conors and Woodhull
(571) 215-0327
marcic@proaxis.com

Web Master
Kalyan Ghosh Ph.D.
Merck Research Laboratories
BL3-3
West Point, PA 19486
(484) 344-7635
Fax # (484) 344-2931
kalyan_ghosh@merck.com

Program Committee

Dr. Alfred H. Balch
Novartis Pharmaceuticals
59 Route 10
E. Hanover, NJ 07936-1080
(862) 778-7639
Fax # (973) 781-6498
fred.balch@pharma.novartis.com

Dr. Nandita Biswas
GlaxoSmithKline
2301 Renaissance Boulevard
Building #510, RN 0420
King of Prussia, PA 19406
(610) 787-3838
Fax # (610) 787--7004
nandita.biswas-1@gsk.com

Dr. Ivan Siu Fung Chan
Merck Research Laboratories
P.O. Box 4 Mail Stop UNA-102
West Point PA 19486
(484) 344-3391
Fax # (484) 344-7105
ivan_chan@merck.com

Professor J. Stuart Hunter
17-3U Meadow Lakes
Hightstown, NJ 08520
(609) 426-6082
Fax # (609) 443-1506
stuhunt@bellatlantic.net

Jacqueline Kennedy
Wyeth Research
P.O. Box 42528
Philadelphia, PA 19101
(484) 865-2083
Fax # (484) 865-0066
kennedj1@wyeth.com

Dr. William Wubao Wang
Merck Research Laboratories
P.O. Box 4 Mail Stop UNA-102
West Point PA 19486
(484) 344-3005
Fax # (484) 344-7105
william_wang@merck.com

***Walter R. Young has chaired the conference for thirty-five consecutive years.**

REGISTRATION

Please register as early as possible. Payment must accompany the form either by check, which must be included, or by credit card number. Registration confirmation will be given by phone or FAX. You may pre-register with invoices, but will be billed at the on site rate. Make checks payable to "ASQ NY/NJ Metropolitan Section". The American Society for Quality (ASQ) is a tax-exempt organization. Federal Tax ID #39-09-12502. RECEIPTS and a CERTIFICATE OF ATTENDANCE will be distributed at the conference. E-Mail receipts will be sent upon request.

On site conference registrations start at 7:30 AM December 6th through December 8th and at 8 AM on December 9th.
Transmit registration to **Mr. William I. Martin, Customized Management Systems, Ltd., 18-65 211 St., Suite 2F, Bayside, NY 11360-1814**
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Registration for Conference Tutorial	**On or Before Oct. 1st**	**On or Before Nov. 1st**	**After Nov. 1st**	**Amount**
Conference	$500	$570	$640	_____
One Day Registration, Monday, Tuesday, or Wednesday (circle 1)	$250	$285	$320	_____
Student (Proof of full time college status needed) or Retiree	$200	$225	$250	_____
Speaker Dinner, Monday 7:00 PM	$40	$45	$50	_____
Short Courses:				
Multiple Comparisons for Making Clinical and Genomic Decisions	$675	$725	$775*	_____
Applied Longitudinal Data Analysis: Modeling Change and Event Occurrence	$675	$725	$775*	_____
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Cancellations will be accepted until November 19th for a $50 fee.

There will be no refunds after November 19th, but substitution of another registrant is permissible.

Bound proceedings, which include handouts for all tutorials, will be provided to all attendees.

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TRAVEL TO THE CONFERENCE

AIR: Non-discount fares are usually much lower to Atlantic City (ACY) than to Philadelphia (PHL) but you should check both airports to search for the best fare and connections. Advance reservations with Royal Airport Service, (888) 660-9766, are cheaper than a cab to and from ACY. The cheapest connection from PHL is the below referenced SEPTA, but this will take more than two hours. Royal Airport Service takes about an hour and is cheaper than renting a car that is unnecessary in Atlantic City. Discount airlines not on the major search engines such as Spirit, www.spiritair.com, to ACY; and AIRTRAN, www.airtran.com; America West, www.americawest.com; ATA, www.ata.com; Frontier, www.frontierairlines.com; Southwest, www.southwest.com; and USA 3000, www.usa3000airlines.com to PHL should also be considered. These airlines offer the additional advantage that they sell one-way tickets without a premium that is useful if one is using the conference as a stopover.

RAIL: NJ Transit has relatively frequent local (14 daily trips with 6 stops) service to Philadelphia connecting with Amtrak and SEPTA at 30th Street and PATCO at Lindenwald, NJ. Free shuttle busses meet all trains and provide direct service to all casinos. For a schedule, see www.nj.com/njtransit/acl.htm . This schedule also shows the connections to PHL.

BUS: Check your local paper or call the casino bus transportation departments for Atlantic City transportation information. There may be a casino bus trip from your local neighborhood as some of these busses travel as far as 200 miles. Most allow you to return on a different day for a charge or a space available basis. Cost of the trip will be offset by casino cash back rebates and other offers. One may take a bus to any casino, collect their coins and coupons and use a jitney to get to the Tropicana. Greyhound has service directly to the Tropicana with a rebate, allowing you a four-day open return from a number of cities, e.g., Philadelphia, NYC, Baltimore and Washington. www.greyhound.com/services/casinonj.shtml

PROMOTIONS: Check your local Sunday paper for coupons. The Philadelphia Inquirer prints show and meal discount coupons both Friday and Sunday. Check www.tropicana.net to view their promotions. For other casinos, check their promotion booth to see what they have to offer.

DRIVING: To get to the Tropicana from the Garden State Parkway, NJ Turnpike or Philadelphia, take the Atlantic City Expressway. Follow the Atlantic City Expressway to Atlantic Avenue. Make a right onto Atlantic Avenue. Travel South on Atlantic Avenue to Brighton Avenue and enter the Transportation Center on the right. There is a $4 per day fee charged by Atlantic City that will allow you to casino hop until 6:00 AM the following morning. However, if you leave your car in the garage for the duration of the conference, there is only a one time $4 fee.

INFO: For maps, an events schedule, casino shows and general tourist info, call the Atlantic City Convention Bureau at (888) 228-4748. View their web site at www.atlanticcitynj.com that has an option for you to request a free visitor packet.

MEALS: The Tropicana Casino and Resort has eight restaurants on site. The *Beachfront* Buffet offers reasonably priced, all-you-can-eat meals. *Pier 7* offers impressively prepared seafood, while *The Seaside Café* offers a wide variety of options 24 hours a day. *Wellington & Chan's* and *Golden Dynasty* offer their respective takes on food from the Far East, while *Il Verdi* offers gourmet Italian Cuisine. If one is in the mood for something more casual, *Hooters* is located conveniently on the first floor, adjacent to the Boardwalk. Outside of the Tropicana and along the Boardwalk are a wide variety of restaurants to suit any taste or budget, from classic seafood restaurants to *Burger King*. Please bear in mind that we will provide a continental breakfast during our morning break at 10 AM as well as an afternoon refreshment break at 2:30 PM. Also, there will be an optional subsidized Speaker Dinner on Monday.