Cleveland Clinic Foundation – Ohio State – Case Western Reserve

Biostatistics Joint Symposium
Thursday, May 10, 2001

Lerner Research Institute
Cleveland Clinic Foundation
East 100th Street and Carnegie Avenue
(Park in the East 100th Street Visitor Garage and take walkway across street to Lerner Research Institute, Area NA)
(See www.clevelandclinic.org/maptour/campus.htm for directions and maps)

Room	Time	Schedule
NA1-142	11:25 – 11:30	Welcome
	11:30 – 12:00	Stanley Lemeshow, Ohio State University "Use of Logistic Regression Modeling in Randomized Clinical Trials"
	12:00 – 1:15	Lunch
NA5-68	1:15 – 1:45	Ralph O'Brien, Cleveland Clinic Foundation "Current and Future SAS-Based Tools for Sample-Size Analyses"
	1:45 – 2:15	Nahida Gordon, Case Western Reserve University "What Are the Long-Term Relative Benefits and Risks of Adjuvant Therapy for Early Breast Cancer?"
	2:15 – 2:35	Break
	2:35 – 3:30	Anastasios Tsiatis, North Carolina State University "Efficient Estimation of the Mean of a Time-Lagged Variable Subject to Right Censoring"

Keynote Speaker: Anastasios Tsiatis
Professor, Department of Statistics
North Carolina State University

Abstract

In many clinical trials the endpoint of interest may not be available immediately, but rather evolves over time. Examples of this are numerous. Survival time is clearly such an example, but also cost of care, quality adjusted lifetime, or even dichotomous response such as whether viral load will go below detectable limits after treatment for AIDS patients are also examples of time-lagged responses. The lag time may be part of the biological process or due to administrative delays.

Since patient entry is staggered and follow-up is of limited duration, some of the response variables will be missing or incomplete due to censoring. For most of these censored time-lagged response endpoints, standard survival methods for dealing with censoring do not apply because of induced informative censoring. We will show how the theory of inverse probability weighting of complete cases developed by Robins and Rotnitzky can be used to find consistent estimators for the mean of the time-lagged variable. We will also show how to use additional information collected during the study to increase efficiency.

May 10, 2001 CCF-OSU-CWRU Biostatistics Joint Symposium

Further Abstracts

USE OF LOGISTIC REGRESSION MODELING IN RANDOMIZED CLINICAL TRIALS

Stanley Lemeshow
Center for Biostatistics
Ohio State University

The analysis of modern clinical trials may find many useful techniques that are standard in the analysis of epidemiologic data. Epidemiologists typically use observational studies to determine the association between a risk factor and a disease of interest. Because patients cannot be randomized to exposure groups in epidemiologic studies, extraneous factors must be controlled for in the analysis of the data. Failure to appropriately control for these factors can lead to bias and a corresponding invalidation of results.

In modern clinical trials, the treatment groups are designed to be as homogeneous as possible. This is done through the randomization of patients to treatment arms. Alternatively, if there is a known variable that must be controlled for, randomization can be performed within strata defined by levels of that variable. Although it is understood that, in the long run randomization will produce treatment groups that are well balanced (or homogeneous) with respect to other extraneous factors, it does not guarantee homogeneity in the short run (i.e., within a single trial). If, for example, in a randomized clinical trial of treatment therapies for patients with sepsis, one group happens to have greater severity of illness than a second group, this would greatly bias the results towards the group with the lower severity.

A variable that is related both to the outcome and to the treatment variable is called a confounder. A variable that has a significant interaction with the treatment is called an effect modifier. Epidemiologists have recognized the need to adjust for potential confounders and to identify effect modifiers. These methods can also be applied to the analysis of data from clinical trials. Just as epidemiologists control for imbalances in exposure groups through stratification, statisticians analyzing clinical trial data must be able to control for imbalances between treatment arms using appropriate statistical methodology. This talk presents methods appropriate in the analysis of clinical trials data that can be used to control for such imbalances.

Current and Future SAS-Based Tools for Sample-Size Analyses

Ralph O'Brien
Department of Biostatistics and Epidemiology
Cleveland Clinic Foundation

We will summarize the current, near future, and long-term future of SAS-based tools for performing sample-size analyses. UnifyPow (www.bio.ri.ccf.org/UnifyPow) is a widely-used freeware base-SAS module/macro that already offers substantial flexibility over an extensive set of methods. It is due for a major new release in late-summer 2001. The SAS Institute itself is now developing regular SAS System procedures that will eventually supersede UnifyPow. We will summarize these developments and show some examples.

May 10, 2001 CCF-OSU-CWRU Biostatistics Joint Symposium

Further Abstracts

What Are the Long-Term Relative Benefits and Risks of Adjuvant Therapy for Early Breast Cancer?

Nahida Gordon
Department of Epidemiology and Biostatistics, School of Medicine
Case Western Reserve University

Finite mixtures of distributions have been used extensively to model heterogeneous data in many fields. The potential of finite mixture models has become increasingly recognized and used in the field of survival analysis to analyze failure-time data in a variety of situations. In particular finite mixtures distributions provide a way of modeling time to failure in the case of competing risks.

I propose a mixture distribution for long-term survival after breast cancer diagnosis and adjuvant treatment. This mixture model expresses survival, conditioned on the patient's age, as a mixture of two Gompertz survival distributions each representing one of two mutually exclusive causes of death: from breast cancer or from other causes without evidence of a recurrence of breast cancer. Covariate vectors and their regression parameters are incorporated into the hazard function of each of the two Gompertz distributions. Cohort frailty, defined and estimated for patient treatment groups, provides the means to consider the question posed in the abstract title.