1010-62-151 **Ronald K. Pearson** (ronald.pearson@prosanos.com), ProSanos Corporation, 225 Market Street, Suite 502, Harrisburg, PA 17101, **Robert J. Kingan*** (RobertKingan@clayton.edu), Department of Mathematics, Clayton State University, 2000 Clayton State Boulevard, Morrow, GA 30260, and **Alan Hochberg** (alan.hochberg@prosanos.com), ProSanos Corporation, 225 Market Street, Suite 502, Harrisburg, PA 17101. *Disease Progression Modeling from Historical Databases.*

We consider the problem of modeling disease progression from historical clinical databases, and will discuss the issue of what mathematical model types are most appropriate for describing disease progression. The ultimate objective of this modeling is to provide a basis for stratifying patients into groups with clearly distinguishable prognoses or suitability for different treatment strategies, on the basis of clinical variables measured over time. To account for the underlying physiology, models must describe the temporal behavior of several biomarkers and the relationships among them, in a way that has a clear clinical interpretation. Practically important aspects of this problem include the complicated, mixed structure of clinical databases, strong censoring along the time axis, and the prevalence of missing data and other anomalies. We will examine these issues in detail and describe the results of an analysis of liver disease progression from the National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK) liver transplant database. From a set of quantitative clinical values measured during the first year after transplantation, a model of long-term survival was developed. This model identifies a subset of patients at particularly high risk for loss of the transplanted organ or death. (Received August 25, 2005)