Yu Shyr, Director of the Vanderbilt Center for Quantitative Sciences, **Vanderbilt University Medical Center**
Yu Shyr received his PhD in biostatistics from the University of Michigan (Ann Arbor) in 1994 and subsequently joined the faculty at Vanderbilt University School of Medicine. At Vanderbilt, he has collaborated on numerous research projects; assisted investigators in developing clinical research protocols; collaborated on multiple grants funded through external peer-reviewed mechanisms; and developed biostatistical methodologies for clinical trial design, high-dimensional data preprocessing, estimating relative potency in a parallel line bioassay, and other statistical approaches, published in journals such as *Statistics in Medicine*, *Bioinformatics*, *Clinical Trials*, *Computational Statistics and Data Analysis*, *BMC Bioinformatics*, and *Journal of Bioinformatics and Computational Biology* in the last three years. Dr. Shyr is a Fellow of the American Statistical Association and US FDA advisory committee voting member. He has delivered more than 185 abstracts at professional meetings and published more than 275 peer-reviewed papers in a variety of journals. Dr. Shyr has served on numerous NIH/NCI SPORE, P01, and CCSG review panels/committees and has been a member of the invited faculty at the AACR/ASCO Methods in Clinical Cancer Research Vail Workshop since 2004. He currently serves on the external advisory board for five national cancer centers; is a member of the editorial board for the *Journal of Clinical Oncology* and *Cancer Prevention Research Journal* as well as ASCO's Cancer Research Committee; and directs the biostatistics and bioinformatics cores for the NCI-funded Vanderbilt University Breast Cancer SPORE, GI Cancer SPORE, Lung Cancer SPORE, and other program projects. In addition, Dr. Shyr is the Principle Investigator of the NCI UO1 grant of Barrett's esophagus translational research network coordinating center (BETRNetCC). Dr. Shyr's current research interests lie in developing and analyzing predictive models of the statistical relationships between multiple-variable protein and next generation sequencing data and clinical endpoints using both supervised and unsupervised classification and pattern recognition approaches, which focus on analyses of gene expression array and protein expression profile data to identify the molecular "fingerprint" of different types of cancers.