

COLLOQUIUM

DEPARTMENT OF MATHEMATICS AND STATISTICS
OAKLAND UNIVERSITY
ROCHESTER, MICHIGAN 48309

Arusharka Sen
University of Hyderabad, India
and
Michigan State University

A ‘missing-plot’ technique for goodness-of-fit tests with censored data

Abstract

Let X_1, \dots, X_n be i.i.d. observations with distribution function (d.f.) F , and suppose the observations are at risk of some kind of censoring. We want to test the hypothesis $H_0 : F = F_0$, where F_0 is a specified d.f.. From a non-parametric point of view, the most crucial problem caused by censoring is that we can no longer determine the empirical d.f. $F_n(\cdot) = n^{-1} \sum_{i=1}^n \mathbf{1}\{X_i \leq \cdot\}$. In this talk, we propose a general scheme of ‘reconstructing’ the empirical d.f., under various censoring mechanisms, by imputing values, of the censored observations, that minimize the Kolmogorov-Smirnov (K-S) distance $\|F_n - F_0\| = \sup_x |F_n(x) - F_0(x)|$. The reconstructed K-S statistic may then be used to test H_0 . We illustrate our method for a few well-known censoring mechanisms, e.g., Type-I, Type-II, Random Censoring, Interval Censoring (Type-I) etc. We then discuss the problem of obtaining the null distribution of the test-statistic. Problems for further research, including extension to the two-sample problem, will also be indicated.

372 Science and Engineering Building

Thursday, April 18th, 2002

3:00 to 4:00 P.M.

**(Refreshment at 2:30 to 3:00 P.M. in Room 368,
Science and Engineering Building)**

About the speaker

Dr. Arusharka Sen obtained his Ph.D. in Statistics from Indian Statistical Institute, Calcutta, in 1993. Since then he has been on the faculty of Department of Mathematics and Statistics at the University of Hyderabad in India. Dr. Sen has held visiting positions at the Justus-Liebig University in Giessen, Germany, and the Indian Statistical Institute in Calcutta. He is currently visiting the Department of Statistics and Probability at Michigan State University. Dr. Sen's research interests include non-parametric smoothing-based methods, survival analysis and statistical analysis of protein sequences.