

# P-Value Approximation of Scan Statistics and its Application to Genomic Data

I-Ping Tu

Institute of Statistical Science, Academia Sinica

## Abstract

Scan statistics have been applied in combining information on multiple contiguous observations along time, space or genomic sequence to test non-random clusters of events. For example, Hoh and Ott (2000) applied the scan statistics to locate susceptibility genes; Chow et al (2005) applied the scan statistics to detect palindrome clusters for prediction of replication origins in herpes viruses. In this talk, I would like to have a reference review on the p-value approximations for the scan statistics and also present some interesting related approximation for the scan statistics.