Stanford University

Statistics

People			
Faculty			
Stein Fellows			
Research Scientists & Lectu	rers		
Postdocs			
Students			
Staff			

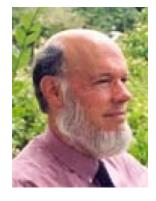
Related News

Jun 17 2011 | GPS11 | Photo Gallery

Conference in Genetics, Probability, and Statistics

A Two-Day Event in Honor of David Siegmund's 70th Birthday featuring invited lectures on probability, mathematical and applied statistics,...

Department News



David O. Siegmund

John D. and Sigrid Banks Professor of Statistics

Mailing Address:

Department of Statistics Sequoia Hall 390 Serra Mall Stanford University Stanford, CA 94305

Phone: 650.723.0598

Fax: 650,725,8977

Email: dos@stat.stanford.edu

Joint Appointment or Affiliation: Bio-X

Research Interests:

probability theory

genetic mapping

nonlinear regression

Personal Website: Stanford Profiles

Research Statement:

As a statistician interested in probability theory, I focus my research on statistical problems that arise in concrete scientific applications and require novel probability theory for their resolution. Until 1985 my research was primarily in sequential analysis, especially problems of the design and analysis of sequential clinical trials. A related interest was sequential change-point detection, motivated by problems of

monitoring a continuous production process for changes that can be inferred only from noisy measurements on its output. This led to several years of research on a variety of change-point-like problems and related problems of nonlinear regression, which have found a wide variety of applications.

Recently I have concentrated on statistical aspects of genetic mapping, i.e., the identification of the location of genes giving rise to phenotypes such as diseases in humans or mammalian model organisms, desirable quantitative traits in agriculturally important plants and domestic livestock. From the modern viewpoint of a "genome scan" based on hundreds of mapped markers to search for anonymous genes, genetic mapping is very similar to change-point problems with the location of the gene as change-point. I have also used techniques developed to study change-point problems to give approximate *p*-values for gapped pairwise local sequence alignments.

For Students

- Computing Guide
- ExploreCourses

For Visitors

- Emergency Plan
- Campus Map

For Instructors

- TA Resources
- Room Requests

For Researchers

- Consulting Services
- PhD Dissertations