

A. STEWART-OATEN and W. W. MURDOCH (Department of Biological Sciences, University of California, Santa Barbara, CA 93106, USA), Positive Sequential Estimation of Log (Density).

Comparisons of variability, relative size or other parameters of populations of different species, or in different places, can be distorted because of differences in overall densities. A natural way to eliminate such distortions is to base the comparisons on log(density). In virtually all practical cases, the true population density, D , is not known but must be estimated, usually from sample counts of quadrats, net-hauls, cores, etc. Thus the estimated density may be zero; a fixed sampling effort is likely to lead to greater errors in the estimate of log(density) when the density is small than when it is large; and, even if an unbiased positive estimate of D can be obtained, the log of this estimate will not be an unbiased estimate of log(D). If $D > 0$, open-ended sequential sampling can guarantee a positive unbiased estimator of D , but is impractical. A positive 'almost' unbiased estimator, using a sequential scheme with maximum and minimum samples, and its use for an 'almost' unbiased estimate of log(D), is discussed. Some numerical results are given.

P. F. THALL (University of Texas, MD Anderson Cancer Center), Covariance Matrices in Quasi-Likelihood Models of Repeated Counts with Overdispersion.

A family of covariance matrices for use in quasi-likelihood regression models (McCullagh, 1983; Liang & Zeger, 1986) of repeated counts exhibiting overdispersion is presented. The family of matrices provides a means of modelling extra-Poisson variation, heteroscedasticity and within-subject dependence. A heuristic construction via mixing over random effects if provided, analogously to the classical linear Gaussian variance components model. Two sets of estimating equations are presented, the usual set of GEEs for covariate parameters and a second set of moment equations for within-subject covariance matrix parameters. A joint asymptotic distribution theory for all model parameters is

provided. The talk will begin with models for longitudinal or repeated measures matrices described above and will then discuss seizure counts with covariates. Extensions of the method and some computational aspects are discussed.

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R. WONG (Syntex Research, 3401 Hillview Avenue A3-434, Palo Alto, CA 94304, USA), Estimating the Probability of a Response from Titration Studies.

A titration study is one type of study design for obtaining initial estimates of the probability of a response in, for example, a new antihypertensive medication. The unique feature of the titration design is that patients are stopped after the first observed response in a series of (usually increasing) doses. A consequence of this design is that the (unconditional) response probability must be estimated by a series of conditional response probabilities. It is shown that, without further assumptions on the functional form of the dose response relationship, the response probability cannot be directly estimated from a titration study. Instead, upper and lower bounds on the response probability can be obtained.

D. M. ZUCKER (National Heart, Lung, and Blood Institute), A Statistician's Perspective on Ethical Issues in Cardiovascular Clinical Trials.

A selective survey of ethical issues in cardiovascular clinical trials is presented, based on the speaker's experiences in a biostatistics unit dealing with such trials and prior experiences as an FDA clinical trials reviewer. The presentation will discuss ethical considerations in various aspects of trials, including basic design structure, patient selection, data collection, interim monitoring, and interpretation and presentation of the final results. Examples from specific cardiovascular clinical trials will be discussed.

The following abstracts are of papers read at the 4th Symposium on Biometrical Problems in Agricultural, Forestry and Animal Investigations, organized by the Nordic Region of the Biometric Society, held in Jokioinen, Finland, from 19-21 August 1991.

S. ANDERSEN (The Federation of Danish Pig Producers and Slaughterhouses, Axelstorv 3, DK-1609 Copenhagen V, Denmark), Comparison of Breeding Strategies by Dynamic Gene Flow Methods.

Gene flow models are used in deterministic prediction of genetic response over time. The population is subdivided into age classes and the development over time is described by Markov type models. The method depends on truncation selection across age classes to determine the proportion to select from each class so as to maximize genetic change. Simple examples from pig breeding are given to illustrate the method.

H. BJÖRNSSON (Agricultural Research Institute, Keldnaholt, 110 Reykjavík, Iceland), Zones for Testing Timothy in the Nordic Countries.

Results of official variety tests of Timothy in the Nordic countries were collected in order to study the possibility of using available results as an aid in establishing zones for integrated variety testing between countries, alternatively testing the appropriateness of zones that are based on meteorological parameters. Within countries zones were established such that adapted, high-yielding varieties interact little or not at all with environment. In one case only a high ranking variety had to be excluded due to interactions. Zones in different countries were linked together by tests for interaction. Although the number of varieties in common is rather limited, the Nordic countries were, on the basis of these results, divided in 4-6 internordic zones. There were some deviations found within some of these zones, however. This is an analysis of the genotype by environment interaction with the emphasis on environment.

L. BONDESSON (Swedish University of Agricultural Sciences, Section of Forest Biometry, S-90183, Umeå, Sweden), Optimal Utilization of Clones under Diversity Constraints.

Truncation selection is a standard method of selection of clones. In this case all clones with genetic values larger than some bound are selected and given equally many copies. This strategy is not optimal if diversity is also taken into consideration, as has been found by D. Lindgren and collaborators. Provided that the diversity is measured by the Simpson index, the optimal strategy is to let the number of copies of a specific clone be proportional to $(g-a)^+$, where g is the genetic value of the clone and a some threshold. This result and variants and generalizations of it are the focus of the paper. In forestry, optimal utilization may lead to very large economic gains.

L. CZAPLEWSKI (USDA Forest Service, Rocky Mountain Forest and Range Experiment Station, 240 West Prospect Street, Fort Collins, CO 80526-2098, USA), Kalman Filter for Statistical Monitoring of Forest Cover across Sub-Continental Regions.

The Kalman filter is a multivariate generalization of the composite estimator which recursively combines a current direct estimate with a past estimate that is updated for expected change over time with a prediction model. The Kalman filter can estimate proportions of different cover types for sub-continental regions each year. A random sample of high-resolution satellite scenes at time $t=0$ is classified into detailed categories to estimate proportion of cover types in the population, and its sample covariance matrix. Coarse-resolution weather satellite data at time $t=0$ are also classified for the entire study area (i.e. a census), but less detailed categories are used that are consistent with the coarse resolution of these data. The Kalman filter combines the two multivariate population estimates into a composite vector estimate. A probability transition matrix can estimate the proportions of the detailed cover types at time $t=2$ given the previous composite estimate at time $t=1$. This estimate can be combined with any new estimates for time $t=2$ (e.g. new coarse-resolution satellite data). This procedure is repeated for each time period.

V. DUCROCQ (Quantitative and Applied Genetics Unit, National Institute of Agricultural Research, 78350 Jouy-en-Josas, France), Computational Methods in Animal Breeding Prediction Problems.

In most developed countries and for all major domestic species, joint genetic evaluation of up to several millions of animals are routinely computed, using Best Linear Unbiased Prediction. To solve a few times a year and for several traits of economic importance a linear system of several million equations is a challenge, even on the most advanced computers. Perhaps the most efficient tool used to reduce the computational burden has been the algebraic manipulation of the equations with the aim of decreasing the system size or increasing its sparsity. Then, virtually all solving strategies are iterative. The simple Gauss-Seidel algorithm has been very successful and has been adapted in order to avoid the actual storage of the coefficient matrix ('iterating on data') but its convergence rate can be extremely low, in particular for individual animal models. As a consequence, present research aims at two main goals: (1) a better use of computational resources in order to reduce time per iteration; and (2) the development of more complex algorithms, which try to exploit the known sparsity patterns to increase convergence rate. A new and very efficient algorithm of this type is presented with an application to the evaluation of about one million cattle for 16 morphology characteristics.