digenous breeds in developing countries could be an effective method... If a breed were extinct, then stored DNA would be brought into the active gene pool... by insertion into embryos of another breed... There is no value in further waiting before establishing a global facility for storing and classifying animal DNA.' Would not storing semen fulfil these objectives more simply? In contrast I found Alderson's review of White Park cattle very stimulating, in particular the observations that it is both genetically distant from other British breeds and, despite its maintenance as a small population, has higher heterozygosity. There are certainly some interesting populations about.

Whilst breed conservation is mainly a topic for the enthusiast, it does raise serious population genetic interest. I noted Hedrick among the authors, for example. I hope that more is done to integrate the areas.

WILLIAM G. HILL
Institute of Cell, Animal and Population Biology
University of Edinburgh

Analysis of Human Genetic Linkage. By JURG OTT. Second revised edition. Johns Hopkins University Press, Baltimore. 1991. US $47.50.

The explosion of molecular markers that can be readily detected in essentially any outbred species is sparking a renaissance in genetic mapping. Much of the excitement comes for the possibility of using these maps to localize and eventually isolate genes underlying quantitative characters. These QTLs (quantitative trait loci) may range from the mundane, but tasty, genes influencing pH and soluble fruit content in tomatoes (Weller *et al.* 1988) to those with more serious consequences for humans such as high blood pressure (Hilbert *et al.* 1988). Detection of QTLs is based on associations between marker classes and phenotypic values, so that the more saturated the map, the smaller the genetic interval that bounds a QTL. While the idea of using marker-phenotype associations is obvious, there are serious complications in both obtaining a useful experimental design and in the proper analysis of the resulting data. The current favoured methods of analysis are based on generalizations (e.g. Knott and Haley, 1992) of the methods of segregation analysis developed by human geneticists (Elston, 1990) to assess the most probable genetic basis of a complex trait. The general strategy that seems to be developing for isolating QTLs is first to perform a segregation analysis on a small pilot set of data to see if there are indications of major genes. If there are, the task of constructing a relatively well saturated map of random genetic markers is undertaken and this map is subsequently used to localize the putative major loci to chromosomal regions small enough to be isolated in large cloning vectors. The statistical thread that binds these methods of analysis (segregation analysis, map construction, mapping QTLs) is that all, for the most part, rely very heavily on maximum likelihood estimation.

Given this setting, it is timely that Jurg Ott has chosen to revise his 1985 text on statistical methods of human gene mapping. Ott focuses on maximum likelihood methods, starting with the simplest models and subsequently building on these to deal with important complications such as different recombination rates between sexes, ascertainment biases, and incomplete penetrance. The last two chapters (10 and 11) on inconsistencies and linkage analysis with disease loci are especially well done and are essential reading for anyone engaged in any aspect of genetic mapping. The author sticks entirely to his stated objectives and has produced an exhaustive review of methods for constructing genetic maps between known markers in humans. This is both the strength and weakness of the book. By limiting his attention to a particularly well defined problem with a rich statistical history, the author has, in effect, produced a wonderful treatise that serves as a case study for the development of other methods. The exciting area of mapping QTLs is essentially not covered and the powerful tool of segregation analysis is only briefly mentioned. This is rather disappointing, but to be fair to the author, Ott accomplishes his stated task – describing methods for constructing maps of known markers – superbly. Anyone with an interest in general aspects of genetic mapping will do well to peruse this book.

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J. BRUCE WALSH
Department of Ecology and Evolutionary Biology
University of Arizona
Tucson, AZ 85721