Preface

This special issue of *Human Heredity* is dedicated to the 30th anniversary of one of the seminal papers in genetic epidemiology. In 1972, in their groundbreaking work, Joseph K. Haseman and Robert C. Elston proposed a regression-based parameter-free method for the mapping of quantitative traits in humans (The investigation of linkage between a quantitative trait and a marker locus. *Behav Genet* 1972;2:3–19). In the ensuing 30 years, their method and its extensions have been widely used for QTL mapping. Recently, with the completion of the genome project and renewed interest in complex human traits, many attempts have been made to improve the power of the Haseman-Elston regression method.

To honor this important anniversary we have invited nine peer-reviewed contributions from respected researchers in the field that in one way or another expand on the framework of the Haseman-Elston method.

More than 10 years ago *Human Heredity* started to celebrate highlights in statistical genetics ('Models and Methods for the Genetic Analysis of Pedigree Data' to celebrate the 20th anniversary of the Elston-Stewart algorithm in 1992, and 'Recent Advances in Genetic Epidemiology', published in honor of Professor Newton Morton's 70th Birthday, published in 2000). With this special issue of *Human Heredity* we continue this tradition.

Jürg Ott, New York, NY