Modeling Cure Rates Using the Survival Distribution of the General Population

In clinical trials, it is often observed that a certain percentage of subjects are cured following treatment. Most of the models for cure rate are parametric and of a mixture type. It is usually assumed that the population is divided into two subpopulations so that a subject is either cured with probability p or is not cured with probability (1-p). Farewell (1982) proposed that the probability p is a logistic function of some prognostic factors and treatment arms and the survival of non-cured subjects follow a Weibull distribution. In the mixture model, it is usually assumed that cured subjects will never die. We believe that this kind of definition of being cured is unrealistic. In the proposed research, we redefine a cured subject by a subject who completely gets rid of the disease and therefore, its survival follows the survival function of the general population. Our simulation studies show that the proposed method reduces the bias of the estimated cure rate.

Models for cure rate in a clinical trial

In clinical trials, it is often observed that a certain percentage of subjects are cured following treatment. Most of the models for cure rate are parametric and of a mixture type. It is usually assumed that a participant is either cured with probability pi or is not cured with probability (1-pi). Farewell (1982) proposed that pi is a logistic function of prognostic factors and treatment, while the survivals of non-cured participants follow a Weibull distribution. In the mixture model, it is usually assumed that those cured will never die. We believe that the assumption is inaccurate for adults, although plausible for children. We propose a more realistic model for a cured participant who completely gets rid of the disease using the survival function of the general population. Given the assumptions, our simulation studies show that the proposed method reduces the bias of the estimated cure rate. The model provides credible estimates and inference for predicting survival as a function of number of metastases for adult cancer patients.