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# Extrapolation of Survival Curves with an Application to Multiple Myeloma

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## Abstract

Modeling of censored survival data has its difficulties. Especially when the interest lies in finding the mean survival time, making extrapolation necessary. In this master thesis the performance of some standard parametric models and the flexible parametric survival models of Royston Parmar (2002) are examined in the context of survival analysis. The performance is here defined as the ability to capture the true mean survival time. Furthermore, a variety of survival analysis methods is presented, involving non-parametric methods, modeling with covariates, etc. At our disposal we have a Swedish dataset containing registry data of 1606 multiple myeloma patients between January, 2000 and November, 2011. This data will first of all be used as a basis for a simulation study, where the performance of the standard parametric models and the flexible parametric survival models will be investigated. Secondly, part of this data will be modeled and conclusions from the simulation study regarding the amount of follow-up time needed will be tested. The simulation study yields some evidence that the flexible parametric survival models can help diminish the large biases one gets when modeling the data with a misspecified model. This holds even when they themselves are misspecified. Since the major problem with limited follow-up is the difficulty in fitting correctly specified models, this is a helpful result.

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