A relative survival model for clustered responses –
Comparing SAS PROC NLMIXED and WinBUGS for parameter estimation

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Relative Survival is the ratio of the overall survival of a group of patients to the expected survival for a demographically similar group from a reference population, where this expected survival is derived from published age-, sex-, and calendar time-specific mortality rates [1]. It is commonly used to estimate the effect of a particular disease when the true cause of death is not reliably known and is therefore the preferred analysis for survival experience in cancer registries, thus avoiding the problem of inaccurate or non-available death certificates [2]. Generalizing the pure description of relative survival, regression models for relative survival have been proposed [2-4] to judge influence of prognostic or risk factors on relative survival. These models have been made easily accessible by Dickman [4] who showed that the Estève relative survival model [2] can be written as a Generalized Linear Model (GLM) with a Poisson response, an offset and a specific link function. The data which motivated our work originated from the HALLUCA-(= Halle Lung Carcinoma)-study, an observational study which investigated provision of medical care to lung cancer patients in the region of Halle. Already at the stage of pure descriptive analysis of the HALLUCA-study we noticed a very heterogeneous survival experience in the 55 different diagnosing units in our study region. To account for this heterogeneity between clusters (that is, diagnosing units) in the relative survival analysis we extended Dickman's GLM to a Generalized Linear Mixed Model (GLMM) by adding a random cluster effect to the linear predictor.

Parameter estimation in this random effect relative survival models, as in all GLMM, is complicated by the fact that the likelihood function consists of h integrals (h being the number of clusters) which are not analytically tractable. As such, numerical or stochastical integration are viable estimation alternatives, besides those, a number of approximate methods have also been proposed. Relative survival models, however, place an additional demand on estimation software as in these models each single observation has a separate link function for each annual observation interval. That is, software must also be able to deal with individualized link functions.

In the talk we show how our model was estimated with SAS PROC NLMIXED and WinBUGS and comment on differences and similarities between the two procedures in terms of results and computational efficiency.

References

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