Wiener Biometrische Sektion
der Internationalen Biometrischen Gesellschaft
Region Österreich – Schweiz

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Einladung zum

Biometrischen Kolloquium

am Donnerstag, 8. Oktober 2009, 11.00 Uhr

in der Informatikbibliothek (Ebene 3, Raum 88.03.806) der
Besonderen Einrichtung für Medizinische Statistik und Informatik (MSI)
der Medizinischen Universität Wien
Spitalgasse 23, 1090 Wien

Vortragende:

Amel Mahboubi (McGill University, Montreal, Kanada):

Validation of a new flexible method for modelling of the effects of continuous prognostic factors in relative survival

Wir freuen uns auf zahlreichen Besuch.

Thomas Lang
Präsident

Georg Heinze
Sekretär

VALIDATION OF A NEW FLEXIBLE METHOD FOR MODELING OF THE EFFECTS OF CONTINUOUS PROGNOSTIC FACTORS IN RELATIVE SURVIVAL

Amel Mahboubi, Michal Abrahamowicz, Jean Faivre, Claire Bonithon-Kopp and Catherine Quantin

In population-based registries, the individual causes of death remain unknown or the accuracy of this information is low. For this reason, relative survival (RS) models are now considered the standard for analyzing registry-based studies. Indeed, the RS methodology permits separating the effects of prognostic factors on natural mortality from their effects on disease specific mortality.

Yet, popular relative survival models often rely on important assumptions, which may not hold in real life data. My talk will focus on two such assumptions:
1) the effects of covariates on disease-specific mortality conform to the proportional hazards hypothesis (PH),
2) the logarithm of the hazard increases linearly with increasing values of continuous covariates (log-linearity hypothesis, LH)
Accurate assessment of the effects of continuous prognostic factors requires flexible modeling of both time-dependent (i.e. non-PH) and non-linear effects. To meet this objective, we have developed a flexible generalization of the Estève et al's additive relative survival model [1], similar to the flexible crude survival model proposed by Abrahamowicz & MacKenzie [2], which extends the well known Cox's model. The Estève et al's relative survival model models the observed (all-causes) mortality hazard as

$$\lambda_t (t,z,a) = \lambda_e (t+a, z_s) + \lambda_c (t,z) \qquad (1)$$

where $\lambda_e (t+a,z_s)$ is the expected hazard function for all-causes mortality in the underlying general population, and $\lambda c (t,z)$ is the hazard of disease-specific mortality, conditional on the covariate vector z and age a. In our model, we assumed that the effect of a continuous covariate z_j on the logarithm of the disease-specific hazard in (1) is described by the product of the time-dependent $\beta_j(t)$ and the non-linear $\alpha_j(z_j)$ effect. Accordingly, we propose the following model for $\lambda_c (t,z)$:

$$\lambda_c (t,z) = \exp[\gamma (t)] * \exp \{\Sigma \alpha_j(z_j) * \beta_j(t)\} \qquad (2)$$

where $\beta_j(t)$ and $\alpha_j(z_j)$, as well as the baseline log-hazard γ (t), are all modeled by low-dimension cubic (un-penalized) regression B-splines. In this presentation, I will first present briefly the general concepts of relative survival and the model of Estève et al. Then, I will introduce our new model (2), outline the estimation procedure, and describe model's validation by simulations.

[1] Estève J, Benhamou E, Croasdale M, Raymond L. Relative survival and the estimation of net survival: elements for further discussion. *Statistics in Medicine* 1990; **9**: 529-538.
[2] Abrahamowicz M, MacKenzie TA. Joint estimation of time-dependent and non-linear effects of continuous covariates on survival. *Statistics in Medicine* 2007; **26**: 392-408.