Wiener Biometrische Sektion
der Internationalen Biometrischen Gesellschaft
Region Österreich – Schweiz

http://www.meduniwien.ac.at/wbs/

Einladung zum

Biometrischen Kolloquium

am Donnerstag, dem 2. Dezember 2010 um 14:00 Uhr (s.t.)

in der Informatikbibliothek (Ebene 3, Raum 88.03.806) des
Zentrums für Medizinische Statistik, Informatik und Intelligente
Systeme der Medizinischen Universität Wien
Spitalgasse 23, 1090 Wien

Vortragender:

Dr. Thomas Hielscher
Abt. Biostatistik des Deutschen Krebsforschungszentrums,
Heidelberg, BRD

Cox PH penalized regression models in high-dimensional data: model fit, model assessment and sample size considerations

Wir freuen uns auf zahlreichen Besuch.

Georg Heinze
Präsident

Martin Posch
Sekretär

Cox PH penalized regression models in high-dimensional data: model fit, model assessment and sample size considerations

Thomas Hielscher, Manuela Zucknick and Axel Benner

Division of Biostatistics, German Cancer Research Center, Heidelberg, Germany
t.hielscher@dkfz.de

Abstract. Prognostic models are of primary interest in cancer research, especially in situations where more and more data are coming from high-throughput experiments. Classical statistical methods for sample size estimation, model development and model assessment are no longer applicable or need to be adapted.

Penalized regression models are a suitable approach when dealing with many more variables than observations ($p >> n$). From the class of penalty functions, L_2 (ridge), L_1 (lasso) and SCAD penalty have been of great interest, with the latter ones performing variable selection immanently. Lately these models have been generalized to time-to-event endpoints in Cox PH regression. We investigate and compare the choice of penalties on model development in terms of variable selection and effect estimation using simulation studies.

Once the model has been fit, the prognostic value needs to be quantified. Various approaches have been suggested to determine predictive accuracy and explained variation of survival models, but the context of high-dimensional data has been rarely addressed. Again, we use simulations to compare appropriate measures that can be applied when the prognostic model is built with penalized Cox PH regression.

No analytical methods exist to prospectively estimate sample size or power for multivariable prognostic models when derived from a high-dimensional feature space. Power not only depends on sample size and effect size but also on the number of selected variables as well as the underlying method used to select variables and estimate effects. We present ongoing work in the context of penalized Cox PH regression models.

References

1.Benner A, Zucknick M, Hielscher T, Ittrich C, Mansmann U. High-dimensional Cox models: the choice of penalty as part of the model building process. Biom J. 2010 52(1):50-69.

2.Hielscher T, Zucknick M, Werft W, Benner A. On the prognostic value of survival models with application to gene expression signatures. Stat Med. 2010 29(7-8):818-29.