Einladung zum Vortrag

von

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Basic concepts of the multifactor dimensionality reduction method

Multifactor dimensionality reduction (MDR) method was proposed by M.Ritchie et al. in [1]. This new nonparametric method goes back to the work by R.Michalski concerning the conceptual clustering algorithm. During the last 10 years more than 200 papers using such techniques in genetic analysis were published. In applications to genom-wide association studies (GWAS) the researchers try to specify predictors responsible for higher risk of complex diseases. We study the corresponding model involving an arbitrary penalty function and prove theorem giving necessary and sufficient conditions for strong consistency of the $K$-cross validation estimate of the prediction error. In particular we clarify the role of the penalty function proposed by D.Velez et al. [2]. Several corollaries provide the generalizations of some results established in the recent paper [3].

References


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Ort: Universität Ulm, Helmholtzstr. 18, Raum 220

Interessenten sind herzlich eingeladen.
Der Vortrag findet im Rahmen unseres Forschungsseminars statt.

gez. E. Spodarev