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Einladung zum Vortrag
von
Prof. Dr. Alexander Bulinski
LOMONOSOV MOSCOW STATE UNIVERSITY

4. Oktober 2012

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

- [1] M. Ritchie, L. Hahn, N. Roodi, R. Bailey, W. Dupont, F. Parl and J. Moore. Multifactor dimensionality reduction reveals high-order interactions among estrogen-metabolism genes in sporadic breast cancer. *The American Journal of Human Genetics*, vol. 69, No. 1, 2001, pp. 138--147.
- [2] D. Velez, B. White, A. Motsinger, W. Bush, M. Ritchie, S. Williams and J. Moore, A balanced accuracy function for epistasis modeling in imbalanced datasets using multifactor dimensionality reduction. *Genetic Epidemiology*, vol. 31, No. 4, 2007, pp. 306--315.
- [3] A. Bulinski, O. Butkovsky, V. Sadovnichy, A. Shashkin, P. Yaskov, A. Balatskiy, L. Samokhodskaya and V. Tkachuk. Statistical methods of SNP data analysis and applications. *Open Journal of Statistics*, vol. 2, No. 1, 2012, pp. 73-87.

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

gez. E. Spodarev