

## Special Topic GMDS 2009

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The 54th annual Conference of the German Society of Medical Informatics, Biometry and Epidemiology (GMDS) took place in Essen, September 7–10 under the headline “Spitzenmedizin und Menschlichkeit – Krankheit behandeln und Gesundheit fördern” indicating the tension for all three disciplines within modern medicine. The aim of modern medicine is not only best possible and best possible evaluated medicine but also balancing the individual needs and the needs of the society. Personalized medicine, more and more improvements in medical engineering, the economic consequences of an aging population and the need for evidence-based prevention are provoking innovative input from medical informatics, biometry and epidemiology. The conference in Essen, being European “capital of culture for 2010” could give an excellent overview of how the members of the GMDS tackle the before-mentioned challenges. Nearly 700 participants, 248 oral presentations and 87 posters, 53 scientific sessions, 7 keynote lectures, 3 plenary sessions, 15 tutorials and workshops were the quantitative side of the conference. Main topics of the Essen meeting ranged from bioinformatics, electronic patient records, health telematics to methodological problems in biometry and epidemiology, genetic epidemiology and epidemiology of diabetes and cancer.

The selected papers give an overview of the subjects covered by the conference.

The paper by Helbing et al. [1] reviews the IT-infrastructure of three medical research networks in Germany and gives recommendations for more sustainable and more cost-efficient solutions to data protection schemes. The paper by Kutschmann and Renner [2] is concerned with the construction of risk-adjusted quality indicators based on a sample of more than 1,000,000 patients from nearly 2000 hospitals in 2009. Applying the method of logistic regression this paper presents a valuable tool for decision makers and managers in the health care system.

The next paper by Skipka and Bender [3] tries to overcome difficulties in another field of evaluation, namely in systematic reviews with heterogeneity of the underlying studies. They propose a hierarchical testing procedure that helps to address these challenges if the significance level is set appropriately.

Friede and Schmidli [4] deal with an often occurring problem of clinical trials: In sample size planning considerable uncertainty exists with regard to the overall event rate and the level of overdispersion. They recommend a re-estimation strategy and show the benefits of their design by simulation.

The last two papers deal with methodological problems and strategies in genome wide association studies (GWAS). Greene and Schäfer [5] compare three statistical methods for the analysis of nuclear family data sets, previously proposed to test for the association of a genetic marker with a dichotomous phenotype while adjusting for the effect of another genetic marker that is possibly in linkage disequilibrium with the marker of interest. Their simulation study result suggests that the regression and the weighted haplotype likelihood methods are superior to adaptations of the transmission/disequilibrium test.

The last paper by Scherag et al. [6] compares the statistical properties of ranking by p-values, q-values, the false positive report

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probability and the Bayesian false discovery probability. By performing simulation studies and applying these measures to a GWAS from their research practice they argue that both p-values and the Bayesian false discovery probability are more precise in reconstructing the true order of the markers in a candidate region. At a genome-wide level they show that the ranking can be highly sensitive to implemented a priori information.

Additional papers from the Conference have been published in the *European Journal of Epidemiology* [7–10].

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