

# Selected statistical issues in the analysis of genome-wide association studies using qualitative and quantitative phenotypes

Rigorosumsvortrag von Darina Roeske

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Most diseases are complex, they are not caused by one gene, but by the combination and interaction of several genes, each one only having a small effect. In this setting, large sample sizes and genome-wide association studies are needed to identify genetic variants. The analysis of such high-throughput data requires accurate statistical methods.

Selected statistical issues which are of main concern will be presented - among these the correction for population stratification as well as the multivariate treatment of correlated phenotypes. Also more recent methods which might be an addition or an alternative to standard approaches will be discussed.