Reproducibility and its impact on power in microRNA experiments

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microRNAs are small (17-25 nucleotide-long) non-coding RNAs that regulate gene expression and are believed to play a role in the development and prognosis of cancer. Since microRNAs are very small molecules it is a challenging task to measure the concentrations of microRNAs in e.g. samples of whole-blood. Even for measurements taken with the same sophisticated commercial equipment in the same certified lab the variability is high. Furthermore, the measuring technique is expensive and the number of samples limited for rare cancer types. In this presentation we use data from several statistically designed microRNA experiments to estimate the components of the reproducibility, which consist of both the technical variation and the pure measurement error. We discuss the implications of high vs. low reproducibility by means of the additional replicates needed due to technical variation in order to obtain the same power as under ideal conditions without technical variation. Furthermore, the potential loss in power introduced by not taking all important factors into account is discussed. Alternative experimental designs are presented, including sequential designs, in order to maximize power in experiments on new platforms.

Key words: Power calculation, reproducibility, microRNA