

*Comparing Normalization Schemes for cDNA Microarray Data*

Thygesen, H.

Academic Medical Center, University of Amsterdam, Amsterdam, Netherlands

The second data set for the CAMDA 2002 contest (Project Normal) provides interesting opportunities for comparing different normalization schemes. This is because the design of the experiment allows for the calculation of quality measures, such as the post-normalization correlation between replicates, and the ratio of between-replicate variance to between-mice variance. In this paper, the relevance of such quality measures is discussed, and a number of normalization issues are explored, using those quality measures. These normalization issues include background correction, baseline shift, Box-Cox transformation, partial subtraction of the log-reference signal and assignment of lower weights to (possible less informative) low-intensity spots.