



Adjusting for Treatment Effects in Studies of Quantitative Traits

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(Submitted on 31 May 2013)

A population-based study of a quantitative trait, e.g. Blood Pressure(BP) may be seriously compromised when the trait is subject to the effects of a treatment. Without appropriate corrections this can lead to considerable reduction of statistical power. Here we demonstrate this in the scenario of QTL mapping through Single-Marker Analysis. The data are simulated from a normal mixture for different values of allele frequencies, separation between normal populations and Linkage Disequilibrium, and several methods of correction are compared to check which can best compensate for the loss of power if treatment effects are ignored. In one of these methods, underlying BPs are approximated by subtracting an estimate of mean value of medicine effect from observed BPs in treated subjects. We demonstrate the efficacy of this method throughout different choices of parameters. Finally to account for quantitative traits that follow non-normal distributions, data are simulated from lognormal mixtures similarly and Kruskal-Wallis test is used to obtain estimates of powers for different methods of analysis.

Subjects: **Applications (stat.AP)**

Cite as: **arXiv:1305.7284 [stat.AP]**

(or **arXiv:1305.7284v1 [stat.AP]** for this version)

Submission history

From: Subhabrata Majumdar [[view email](#)]

[v1] Fri, 31 May 2013 02:30:56 GMT (21kb)

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