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Composite measure of linkage disequilibrium for testing interaction between unlinked loci

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Correction to: *European Journal of Human Genetics* (2008) **16**, 644–651; doi:10.1038/sj.ejhg.5202004; published online 23 January 2008

Owing to a typesetting error, some of the equations in this paper were published incorrectly.

The equation on line 17 of the right-hand column of p. 646 should read:

$$I_{\text{inter}} = h_{1/1} - \frac{h_{D_1} h_{D_2}}{P_A}$$

and equation (8) on p. 647 should read:

$$\begin{split} \varDelta^{A}_{M_{1}M_{2}} &= \delta^{A}_{M_{1}M_{2}} + \delta^{A}_{M_{1}/M_{2}} \\ &= \frac{\delta_{1}\delta_{2}}{P_{D_{1}}P_{D_{2}}P_{d_{1}}P_{d_{2}}} \Delta^{A}_{D_{1}D} \end{split}$$

Since the publication of the above paper, the authors have also identified an error in the legend for Figure 1.

Figure 1 (a) Power of the test statistic T_l and logistic regression analysis as a function of interaction odds ratio ($OR_{GH} = e^{\beta_{gh}}$) under a dominance × dominance model, assuming risk allele frequencies at both loci G and H are 0.2, number of individuals in both cases and controls are 500, population risk is 0.001, significance level is 0.001, and genetic odds ratios $OR_G = 1$ and $OR_H = 1$. (b) Power of the test statistic T_l and logistic regression analysis as a function of interaction odds ratio ($OR_{GH} = e^{\beta_{gh}}$) under an additive × additive model, assuming risk allele frequencies at both loci G and H are 0.2, number of individuals in both cases and controls are 500, population risk is 0.001, significance level is 0.001, and genetic odds ratios $OR_G = 1$ and $OR_H = 1$.

The correct legend for this figure and the figure itself are reproduced below.

