# Errata

In the August 2005 issue of the *Journal,* in the article entitled "Weighting Affected Sib Pairs by Marker Informativity" by Franke and Ziegler (77:230–241), the probabilities for identical-by-descent (IBD) distributions of affected sib pairs do not reflect the intended dominant and recessive genetic models; instead, they reflect completely different probability distributions that have no obvious genetic interpretation. The probabilities under the assumption of no linkage also contain a typographical error. The corrected table 2 shown here displays the corrected probabilities, which have been derived using the well-established results of Suarez et al. (Ann Hum Genet 42:87–94) and Risch (Am J Hum Genet 46:242–253). The authors are grateful to Michael Knapp for pointing out these errors.

The incorrect probabilities for IBD distributions under linkage substantially influence the power of both the standard and the weighted mean test. In fact, new Monte Carlo simulation studies with the correct IBD probabilities (table 2) show no increase in power of the weighted compared with the classical mean test for a fully penetrant autosomal dominant trait without phenocopies (results not shown). However, the increased power of the weighted over the classical mean test is correct for those genetic models that were reported in table 4 of the original article.

Table 1 of the original article displays the mapping rules for empirical *P* values; both instances of $\sqrt{4r^2 - 1}$ should be $\sqrt{4d^2 - 1}$. The exemplary computation on page 235 is correct for the IBD distribution

$$f = \left(\frac{6 + 2\sqrt{10}}{24}, \frac{9 - \sqrt{10}}{24}, \frac{9 - \sqrt{10}}{24}\right)$$

rather than for $f = (1/2, 1/4, 1/4)$. On page 237, the IBD distribution of the sample data should be specified as $(f_0,f_1,f_2) = (0.44,0.5,0.06)$ rather than $f_2 = 0.44$, $f_1 = 0.44$, and $f_0 = 0.06$. Furthermore, as pointed out by Ritwik Sinha, there is a typographical error in the formula on page 233, before equation (2). The variance of $\hat{\bar{\tau}}_w$ should read

$$\sum_{i=1}^{n} w_i^2(\hat{\tau}_i - \hat{\bar{\tau}}_w)^2 \ .$$

Finally, the authors misinterpreted Risch (Am J Hum Genet 46:242–253), and the IBD distributions of his example slightly deviate from those reported in table 5 of the article by Franke and Ziegler. The results, however, are only marginally influenced. Details are available on request.

The authors have been asked by colleagues whether the empirical *P* values of the example data reflect the same substantial LOD score differences between the weighted

**Table 2**

**Possible IBD Distributions ($f_0$,$f_1$,$f_2$) and Their Probabilities at a Marker Locus with *r* Equifrequent Alleles**

| IBD Distribution | Probability | | |
|---|---|---|---|
| | No Linkage | Dominant Model[a] | Recessive Model[a] |
| (1,0,0) | $\frac{r^3 - 2r^2 + 1}{4r^3}$ | $\frac{r^3 - 2r^2 + 1}{4r^3} \times \frac{p^4 - 4p^3 + 4p^2}{P_{\text{ASP,dom}}}$ | $\frac{r^3 - 2r^2 + 1}{4r^3} \times \frac{p^4}{P_{\text{ASP,rec}}}$ |
| (0,1,0) | $\frac{(r-1)^2}{2r^2}$ | $\frac{(r-1)^2}{2r^2} \times \frac{-p^3 + p^2 + p}{P_{\text{ASP,dom}}}$ | $\frac{(r-1)^2}{2r^2} \times \frac{p^3}{P_{\text{ASP,rec}}}$ |
| (0,0,1) | $\frac{r^3 - 2r^2 + 1}{4r^3}$ | $\frac{r^3 - 2r^2 + 1}{4r^3} \times \frac{-p^2 + 2p}{P_{\text{ASP,dom}}}$ | $\frac{r^3 - 2r^2 + 1}{4r^3} \times \frac{p^2}{P_{\text{ASP,rec}}}$ |
| $\left(\frac{1}{2},\frac{1}{2},0\right)$ | $\frac{r-1}{r^2}$ | $\frac{r-1}{r^2} \times \frac{p^4 - 5p^3 + 5p^2 + p}{2P_{\text{ASP,dom}}}$ | $\frac{r-1}{r^2} \times \frac{p^4 + p^3}{2P_{\text{ASP,rec}}}$ |
| $\left(\frac{1}{2},0,\frac{1}{2}\right)$ | $\frac{r-1}{2r^3}$ | $\frac{r-1}{2r^3} \times \frac{p^4 - 4p^3 + 3p^2 + 2p}{2P_{\text{ASP,dom}}}$ | $\frac{r-1}{2r^3} \times \frac{p^4 + p^2}{2P_{\text{ASP,rec}}}$ |
| $\left(0,\frac{1}{2},\frac{1}{2}\right)$ | $\frac{r-1}{r^2}$ | $\frac{r-1}{r^2} \times \frac{-p^3 + 3p}{2P_{\text{ASP,dom}}}$ | $\frac{r-1}{r^2} \times \frac{p^3 + p^2}{2P_{\text{ASP,rec}}}$ |
| $\left(\frac{1}{4},\frac{1}{2},\frac{1}{4}\right)$ | $\frac{1}{r^2}$ | $\frac{1}{r^2}$ | $\frac{1}{r^2}$ |

Note.—IBD distributions and their probabilities are derived from tables 3 and 5 of Suarez et al. (Ann Hum Genet 42:87–94) and Risch (Am J Hum Genet 46:242–253), respectively. The diallelic trait locus has a minor-allele frequency of *p*.

[a] Where $P_{\text{ASP,dom}} = \frac{1}{4}(p^4 - 6p^3 + 5p^2 + 4p)$ and $P_{\text{ASP,rec}} = \frac{1}{4}(p^4 + 2p^3 + p^2)$.

and the classical mean tests. Therefore, using their novel simulation approach, the authors conducted Monte Carlo simulations for both test statistics. Whereas the *P* values are significantly lower for the weighted mean test with use of the data of Mein et al. (Nat Genet 19:297–300) and the fully informative data of Risch (Am J Hum Genet 46:242–253), *P* values are virtually identical when all families are considered in the data of Risch (Am J Hum Genet 46:242–253). Details are available on request.

The authors regret the errors.

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In the February 2006 issue of the *Journal*, in the article entitled "Single-Nucleotide Polymorphisms in NAGNAG Acceptors Are Highly Predictive for Variations of Alternative Splicing" by Hiller et al. (78:291–302), table 6 did not include the authors' most-current data. In the course of finalizing the study analysis, the authors identified a set of false-positive dbSNP entries; see the "Results" section: "Since dbSNP entries sometimes are the result of sequencing errors, we manually examined the trace data (if available) and excluded a further nine SNPs" (p. 294). These nine dbSNP entries in table 2 had the footnote "dbSNP entry is based on a sequencing error; therefore, excluded from further analysis and table 6." Inconsistent with that, two false-positive SNPs (*rs12042060* affecting *FIBL-6* and *rs1833783* affecting *FTL*) were not removed from table 6. The correct table 6, shown here, contains 18 instead of 20 entries and is thus consistent with the statement in the "Discussion" section: "Altogether, 28% (18 of 64) of the plausible NAGNAG SNPs occur in known disease genes (table 6)" (p. 300). The authors regret the error.

**Table 6**

**Human Disease Genes with SNPs Affecting Plausible NAGNAG Acceptors**

| dbSNP ID | Gene Symbol | RefSeq ID | Disease | MIM Number(s) | PubMed ID(s) |
|---|---|---|---|---|---|
| *rs3020724* | *CYP17A1* | NM_000102 | Adrenal hyperplasia, congenital | #202110, *609300 | 4303304 |
| *rs2243187* | *IL19* | NM_153758 | Asthma | *605687 | 15557163 |
| *rs8176139* | *BRCA1* | NM_007304 | Breast cancer | *113705, #114480 | 9167459 |
| *rs11567804* | *C3AR1* | NM_004054 | Bronchial asthma | *605246 | 15278436 |
| *rs3025420* | *DBH* | NM_000787 | Congenital dopamine-beta-hydroxylase deficiency | #223360, *609312 | 14991826 |
| *rs2409496* | *GART* | NM_175085 | Down syndrome | *138440 | 9328467 |
| *rs1804783* | *CACNA1A* | NM_023035 | Episodic ataxia-2, familial hemiplegic migraine, spinocerebellar ataxia-6, idiopathic generalized epilepsy | #183086, #141500, #108500, *601011 | 8988170, 8898206, 9302278 |
| *rs2010657* | *GGT1* | NM_013421 | Glutathionuria | +231950 | 238530, 7623451 |
| *rs2307130* | *AGL* | NM_000644 | Glycogen storage disease type III | +232400 | 9032647, 10925384 |
| *rs11661706* | *EPB41L3* | NM_012307 | Meningioma, lung cancer | *605331 | 10888600, 9892180 |
| *rs2275992* | *ZFP91* | NM_170768 | Acute myeloid leukemia | #601626 | 12738986 |
| *rs1071716* | *TPM2* | NM_213674 | Nemaline myopathy-4, distal arthrogryposis 1 | #609285, #108120, *190990 | 11738357, 12592607 |
| *rs2521612* | *SLC4A1* | NM_000342 | Renal tubular acidosis, ovalocytosis, spherocytosis | #179800, 166900, +109270 | 9600966, 1737855, 9973643 |
| *rs9644946* | *GOLGA1* | NM_002077 | Sjogren syndrome | 270150, *602502 | 9324025 |
| *rs17173698* | *PAPSS2* | NM_004670 | Spondyloepimetaphyseal dysplasia | *603005 | 9714015 |
| *rs9606756* | *TCN2* | NM_000355 | Transcobalamin II deficiency | +275350 | 14632784 |
| *rs7862221* | *TSC1* | NM_000368 | Tuberous sclerosis | #191100, *605284 | 12773162, 14551205 |
| *rs11574323* | *WRN* | NM_000553 | Werner syndrome | #277700, *604611 | 9012406, 8968742 |