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Corrections and clarifications to
Analysis of Human Genetic Linkage 3rd edition, 1999

Below, the currently known corrections and typos to this book are listed. I am grateful to various readers, particularly Dr. Robert Elston, who made me aware of errors and inaccuracies.

Note: the word "up" after a line number is shorthand for "from the bottom".

Page xiii: The legend for 6.1 should read "Crossover events for different locus orders in parent 2.4 leading to the haplotype passed to daughter 3.5 in Figure 6.2."

Page xiv: The legend for Figure 7.2 should read "Penetrance curves for breast cancer (unaffected females). (Data from Easton et al., 1993.)"

Page xiv: The legend for Figure 7.3 should read "Densities (histograms) for onset age in breast cancer (affected females). (Data from Easton et al., 1993.)"

Page xxii, line 7 up, should read: ... as a function of ε, ...

Page 2, line 23: Replace "DMD" by "Duchenne Muscular Dystrophy (DMD)"

Page 4, line 20: After X chromosome, insert "(see page 8)"

Page 8, line 8: "13.3" should read "13.4".

Page 11, Table 1.2: The unit for Physical Length (two columns) should be Mb, not kb.

Page 12, line 2: After glaucoma, insert: ", where alleles at the given marker loci (D numbers, see page 32) are numbered 1, 2, ...".

Page 12, line 11: Replace "maternal" by "paternal"

Page 12, Figure 1.3: For the middle child, the left-hand haplotype should read 6-4-3-2 rather than 3-4-3-2. Also, in the last sentence of the figure caption, insert "disease" before "alleles".

Page 15, line 5: Replace "genes" by "loci".

Page 16, line 7 up: Replace "linkagelike" by "linkage-like".

Page 18, line 3 in paragraph starting with "Depending": Replace "shall" by "will".

Page 19, equation (1.6) should read:

$$x = \frac{1}{2(2-k)} \ln\left[\frac{1+2\theta(1-k)}{1-2\theta}\right]$$

Page 20, line 3: Replace "furnishes. For" by "furnishes, for".

Page 22, lines 20, 19, and 17 up: Replace "restriction" by "constriction" (3 times).

Page 23, line 6: Replace "34" by "36".

Page 23, Problem 1.3: After "complete interference", insert: "(at most one chiasma)".

Page 28, line 6 up, and page 29, lines 16 and 13 up: Replace "gene" by "locus" (3 times)

Page 31, line 15: Replace "minisatellites" by "microsatellites".

Page 35, line 4 after equation (2.8): Replace "Morgans" by "cM".
Page 35, equation (2.9) should read: $m = ...$

Page 39, line 10: Replace "for a hypothesis" by "of a hypothesis".

Page 40, section 3.2, line, 5: Replace "function of random variables" by "function of the observations".

Page 43, line 7 up: Replace "Chapter 10, MLEs" by "Chapter 11, MLEs (when used incorrectly)"

Pages 45: Expand line 8 from the bottom to read:

the likelihood ratio,
$$T(\theta_1) = L(\theta_1)/L(\tfrac{1}{2}), \qquad (3.5)$$
as a test statistic. If H_0 is true, ...

Page 48, line 14, amend sentence to read as follows: On the other hand, significance tests for comparing hypotheses lead to test statistics with asymptotic χ^2 distributions only then when the hypotheses have a hierarchical structure (the null hypothesis must correspond to a subspace of that of the alternative hyppothesis), whereas in the likelihood method hypotheses are compared simply by their likelihoods.

Page 50, line 10, after "units": Insert "of ln(likelihood)".

Page 57, equation (4.1): Replace "|" by "where". Line below equation (4.1): Replace "where" by "and".

Page 59, line 14: Delete the parenthesis "(or the ... apart)".

Page 59, line 20: Replace "2.7" by "2.5".

Page 59, equation (4.3): The numerator should read $f(F|\theta) f(\theta)$.

Page 62, Figure 4.2, right side (*Genotypes*): In the bottom generation, the sexes for the two affected individuals should be reversed so they are compatible with the left side of the figure.

Page 67, line 10: Replace "inequalities (3.5) and (3.6)" by "inequality (3.6)".

Page 67, line 16 up should read: ... most equal to 10^{-Zmax}.

Page 74: The paragraph "One can read off..." refers to the phase-known situation. It should be moved to the end of the "Phase Known" section just above.

Page 77, middle: Replace "Johnston" by "Johnson".

Page 79, line 18: The exponent should read [- Z + log(m)].

Page 86, Figure 5.1: In the figure, replace "Elod" by "Z_{max}" (two times). Replace the caption to read: "Maximum lod score (equation [4.11]) and observed information ($n/[\hat{\theta}(1-\hat{\theta})]$) for a recombination estimated from counts of recombination events ($n = 1$)." Also, the abscissa should be labeled $\hat{\theta}$.

Page 88, line 14: Replace "k = 0.3" by "k = 0..3", meaning "0 through 3".

Page 88, left side of equation (5.2): Insert the missing "]"

Page 88: The beginning of the last sentence should read "Graphs of individual curves for $k = 0$ through $k = 3$ are"

Page 90, line 17 up: Replace "ELOD)" by "ELOD curve)".

Page 95, bottom: It may be helpful to insert an additional table as follows:

Genotype	Probability	Genotype	Probability
A|A 1|1	$¼(1 - r)^2$	A|A 2|2	$¼r^2$
A|B 1|2	$½(1 - r)^2$	A|B 1|1	$½r(1 - r)$
B|B 2|2	$¼(1 - r)^2$	B|B 1|2	$½r(1 - r)$
A|A 1|2	$½r(1 - r)$	A|B 2|1	$½r^2$
A|B 2|2	$½r(1 - r)$	B|B 1|1	$¼r^2$

Table 5.2a. Offspring genotypes obtained from Table 5.2 by disregarding parental origin (for example, setting *A1/A2 = A2/ A1*). Rearranging the genotypes in this table and collapsing those two leading to the same phenotype leads to Table 5.3 on page 96.

Page 96, Table 5.3: Phenotype $i = 4$ should read "AB-11".

Page 97, equation (5.11): The 0 should be θ.

Page 98, line 12 up: Replace "recombination events" by "informative meioses".

Page 104, line 19: Replace "while $P(i)$ -" by "while $P(i)$ ="

Page 104, just above equation (5.17): Interchange p and $1 - p$.

Page 107, Figure 5.5: The affected parent has marker genotype *2/3*, not *1/2*.

Page 107, line 15: Delete "2 x".

Page 108, Table 5.8: For the columns labeled II-1 through II-4, the numbers given in the table should be genotypes, not fractions. For example, the first genotype should be listed as *1/2*, not ½. Also, the genotypes are ordered in an unsystematic manner. Below is an improved version of table 5.8 with corresponding minor changes to table 5.9.

Table 5.8. List of 16 Possible Offspring Genotypes for Pedigree in Figure 5.5, Associated Maximum Lod Scores and Probabilities of Occurrence for Penetrance of 90%

	Genotype of						
Case	II-1	II-2	II-3	II-4	Z_{max}	$\hat{\theta}$	$L(\theta = 0) \times 10^7$
1	1/2	1/2	1/2	1/2	0	.5	.0126
2	1/2	1/2	1/2	1/3	0	.5	.1242
3	1/2	1/2	1/3	1/2	.779	0	12.41
4	1/2	1/2	1/3	1/3	.004	.316	1.241
5	1/2	1/3	1/2	1/2	0	.5	.1242
6	1/2	1/3	1/2	1/3	.004	.316	1.241
7	1/2	1/3	1/3	1/2	.004	.316	1.241
8	1/2	1/3	1/3	1/3	0	.5	.1242
9	1/3	1/2	1/2	1/2	0	.5	.1242
10	1/3	1/2	1/2	1/3	.004	.316	1.241
11	1/3	1/2	1/3	1/2	.004	.316	1.241
12	1/3	1/2	1/3	1/3	0	.5	.1242
13	1/3	1/3	1/2	1/2	.004	.316	1.241
14	1/3	1/3	1/2	1/3	.779	0	12.41
15	1/3	1/3	1/3	1/2	0	.5	.1242
16	1/3	1/3	1/3	1/3	0	.5	.0126

Table 5.9. Maximum Lod Scores and Their Probabilities of Occurrence with Penetrance of 90% for Pedigree in Figure 5.5

Z_{max}	$\sum L(\theta = 0)$	Probability
0	.7704	.02
.004	7.446	.23
.779	24.82	.75
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Page 112, Problem 5.2, line 4 should read: "Using lod scores given in the table (appropriate for all four classes) yet working with probabilities that consider only the first three classes (these probabilities must sum to 1), determine whether ...".

Page 114: Delete the second paragraph ("In connection with...").

Page 117, Figure 6.1: The legend should read "Crossover events in parent 2.4 for different locus orders leading to the haplotype passed to daughter 3.5 in Figure 6.2".

Page 119, line 13 up: Delete ")"

Page 120, Figure 6.2: Individuals should be numbered as follows, in each generation consecutively from left to right.
   Top generation: 1.3, 1.4
   Middle generation: 2.3, 2.4, 2.5, 2.6, 2.7
   Bottom generation: 3.4, 3.5, 3.6, 3.7

Page 124, equation (6.8): The second subscript after "if" should be 4, not 3.

Page 124, line 9 up: Replace p_i by p_k.

Page 128, line 3 up: Rephrase as "Most of the material refers to the numerical aspect of interference with a few comments on the positional aspect of interference."

Page 133, equation (6.25): Replace γ by λ.

Page 133, line 16 up, rephrase as follows: Methods discussed in the previous few paragraphs all relied on detecting *numerical* aspects of interference. A method designed to assess *positional* aspects of interference has been proposed by Weber et al. (1993).

Page 136, line 19, to the left of "= 0.85": Replace θ by g.

Page 138, line 4 above Table 6.7: Insert "[equation (1.7)]" after "function".

Page 139, line 4 in paragraph "Statistical tetsts" should be expanded as follows: "... space so that the distribution of the likelihood ratio statistic under the null hypothesis is not simple to obtain".

Page 145, line 15 up: Delete the brackets [].

Page 148, line 6: Replae 2s by 2σ.

Page 150, Problem 6.4: "coefficient of interference" should read "coefficient of coincidence", as defined on page 125 in equation (6.10).

Page 152, line 15: Replace "2.4" by "2.2".

Page 154, Table 7.1: The fourth entry under $P(g; r)$ should be ½r.

Page 159, equation (7.5): In the denominator, under the square root sign, delete the right parenthesis after 2r so that the second half of the expression reads r(1 – r)(1 – 2r[1 – r]).

Page 162, last two lines should read "given an individual's genotype. If..."

Page 164, line below equation (7.8): Replace "Age-of-Disease" by "Age-of-Onset".

Page 165, line 2 up should read "height of the curve $f(x)$..."

Page 166, line 3: Replace (4.17) by (4.16).

Page 168: The legend for Figure 7.2 should read "Penetrance curves for breast cancer (unaffected females). (Data from Easton et al., 1993.)"

Page 169: The legend for Figure 7.3 should read "Densities (histograms) for onset age in breast cancer (affected females). (Data from Easton et al., 1993.)"

Page 171, rephrase the first sentence as "A quantitative trait is a phenotype that can be measured (or enumerated) and often has a continuous..."

Page 176, line 4: Replace "sum" by "mixture".

Page 178, line 4: Delete "IBB"

Page 182, line 12 up: Replace (8.3) by (9.3).

Page 183, lines 16, 27, 31: Replace (4.17) by (4.16).

Page 183, line 8 up: Replace "6.1" by "4.1".

Page 184, two lines above equation (9.4): Replace (4.17) by (4.16).

Page 191, top of page: While the list of computer programs is incomplete (and focuses on parametric analysis), one other suite of programs should be mentioned here, i.e. the S.A.G.E. programs (http://darwin.cwru.edu/pub/sage.html).

Page 209, expressions for a_{jj} and a_{ij}: Underneath the $\sum$ signs, write = instead of - each.

Page 211, line 6 should read "of families or individuals and is constant..."

Page 222, line 2: Replace θ by θ_1.

Page 225, equation (10.13): "10" should be subscripted.

Page 226, line 8: Delete the last sentence in this paragraph and replace it with "To obtain the same asymptotic significance level as for a lod score limit of 3 in a linkage test under homogeneity, a critical value of 3.28 must be used for $Z(\theta)$ in equation (10.13) (Faraway, 1993)".

Page 230, line 10 up: Write the probability as $P(k = 2; \alpha, r, m = 3)$

Page 231, second line in equation (10.20): Insert the missing left parenthesis just to the right of the equations sign.

Page 236, line 9, insert after "in the analysis" the following sentence: The reason for this "inconsistency" is that wrong likelihoods are used that do not reflect sampling bias or parameter misspecification.

Page 238, equation (11.1): The numerator for b should read "r(1 - r[3 - 2r])/...".

Page 248, line 4: Replace 1998 by 1999.

Page 259, line 4 up: Replace VZ by YZ.

Page 261, line 3 up: Insert missing left parenthesis (at the beginning of the line.

Page 263, line 10 in second paragraph: Delete "only".

Page 264, equation (12.2): Replace *PN* by *P* (*N*).

Page 268, Figure 12.2: The shading for individuals *P* and *C* is reversed. The symbol for *P* should be black (affected) and that for *C* should be white.

Page 274, line 13: Write "fully penetrant rare recessive".

Page 275, line 17: Write "by a maximum penalty that is lower..."

Page 276, line 6: Replace "z_2" by $\hat{z}_2$.

Page 277, Figure 13.1: At the bottom of the right-hand family, replace "?" by "IBS (IBD?)".

Page 279, line 1: Replace "LD" by "linkage disequilibrium"

Page 281, equation (13.4): n_2 and n_3 are reversed. The correct formula reads

$$R = \frac{n_1/(n_1 + n_2)}{n_3/(n_3 + n_4)} = \frac{n_1 (n_3 + n_4)}{n_3 (n_1 + n_2)}$$

Page 285, line 1 in paragraph numbered 1 should read " *Clustered sampling* can lead to the appearance of association if clustering is not taken into account in the analysis".

Page 286, line 16 should read "In linkage analysis, alleles may be numbered differently (may have different identities) in different families unless allele frequencies matter".

Page 287, Table 13.1: The term *haplotype* is used here in two different contexts. In the left-hand column, *marker haplotype* refers to haplotypes at two marker loci whereas columns 4 and 5 refer to haplotypes at the marker loci and the disease locus. Thus, the heading for columns 4-6 should say "Estimated Marker-Disease Haplotype Frequency".

Page 293, line 2 should read "In other words, allelic association is only detected in the presence of linkage".

Page 294, line 17: Expand to read "... population stratification when there is no linkage"

Page 295, line 10 should read: "Note that $n_{ii} = 0$ in Spielman and Ewens (1996) because attention is ..."

Page 297, line 4 up: Delete the comma.

Page 299, Table 14.1: The heading of the left-most column should be "Locus 1".

Page 301, Table 14.3: The last number in the right-most column should be 1.03, not 1.05.

Page 307, line 14 up: Replace "virus" by "prion".

Page 317, line 13 should read "by multi-locus penetrances that are..."

Page 320, middle: What is here called a "hidden phenotype" should really be given a different name because a phenotype is what is apparent.

Page 322, line 8 up should read "versus recessive inheritance but much less to misspecifying the level of penetrance and allele frequency"

Page 323, line 21: Capitalize Genehunter and Aspex.

Page 327, Table 15.2: A more complete layout of this table is as follows (the numbers on the body of the printed table are all correct):

```
-------------------------------------------------------------
                        Marker allele
Disease    ----------------------------------------
allele         1            2            3           4     Sum
-------------------------------------------------------------
   d       0.05 - D/3  0.05 - D/3  0.05 - D/3  0.05 + D   0.20
   +       0.20 + D/3  0.20 + D/3  0.20 + D/3  0.20 - D   0.80
-------------------------------------------------------------
  Sum         0.25         0.25        0.25        0.25    1
-------------------------------------------------------------
```

Page 329, Problem 15.3: Replace "Dominant" by "Recessive". Also: "... prevalence is K ..."

Page 333, line 2 in Solution 4.3: Replace H_1 by H_2.

Page 336, line 5: Replace $[\theta(1-\theta)]^n$ by $[\theta(1-\theta)]$.

Page 337, line 2: Replace dr/dx by $d\theta/dx$.

Page 339, line 3 in body of table: Replace $(1--r)$ by $(1-r)$.

Page 354, line 16: Replace "(in press)" by "49:65-70".

Page 369, line 12 up: Replace "Am" by "Ann".

Page 374: Move the Wichman and Hill reference one place up.

Page 377, just above "Antigen": Insert "Anticipation, 257".

Page 377, "Ascertainment": Insert ", 312" after "236".

Page 377, after "CASH study": Insert "Centimorgan, 11, 22"

Page 378, "Distance, genetic": Insert page number 10

Page 379, right column, "Hlod": add pages 263 and 322.

Page 380, in Map function: Sturt: add page number 138.

Page 380, after "Mohr": Insert "Morgan, 10, 11"

Page 381, left column, line 5: Insert "41," before "158". Line 17: insert "Path analysis, 312"