Typos corrections and text clarifications

P.22 Table 2.2: the probability of phenotype B under H_1 should be $(1-p)q$.

P.24 line 5-: "shown" should be "shows"

P.52 line 6-: last term in equation should be $+\rho^2(\Delta^2 - \Delta^2)$. (It is 0 anyhow.)

P.54 Figure 4.2(a): labels "recombinant" and ''non-recombinant" are reversed.

P.56 Table 4.2: in both table and caption, group II are the double-heterozygotes A_1A_2, B_1B_2.

P.62 midpage; omit the factor $(1-f)$ which cancels
for a heterozygous individual, the likelihood ratio at $\rho = 0$ is $q/(f+q-qf)$.

P.63 Formula for Elod – Some bits got left out of the probabilities.
See the note by Anne-Louise Leutenegger posted here, for correct formula.
Limiting value as $q \to 0$ is correct.

P.65 Equation 4.12: final "=" should be "$\propto$"

P.66 Table 4.6: first line: 0.8915 should be 0.8195

P.84 line 10: log_{10} should be $\log_{10}$

P.86 last line: $G_2 = g''$ in final probability, should be $G_3 = g''$

P.95 last line: final expectation is also conditional on $\mathbf{Y}$.

97-98 (section 7.4) Clarification: thanks to Andrew George and Steffen Lauritzen.
Drs Andrew George and Steffen Lauritzen have (independently) pointed out that it would be clearer (and correct) to make a distinction between the method used to compute risk probabilities in section 7.4, and the method of *reverse peeling* used by SIMLINK (Ploughman & Boehnke, 1989) and by the MCMC samplers. The method in section 7.4 may be called "smart peeling" (according to Steffen) and in effect "peels to everywhere" by using several different (partial) peeling sequences through the pedigree and combining cutset R-functions afterwards to give the required risk probabilities.
The method is presented in section 7.4 for zero-loop pedigrees for simplicity– it applies equally well to complex pedigrees, and was used by Thompson (1981) to obtain risk probabilities on a complex Newfoundland pedigree. Though very close in terms of required computation, this is conceptually distinct from reverse peeling, which passes forwards and backwards (as described in section 7.1) incorporating the probability functions computed in the forwards direction into the reverse computation or sampling.
For exact computation of the conditional probability on any pedigree cutset, the methods are essentially equivalent. For sampling, reverse peeling provides a more natural procedure and is necessary for the realization of latent variables from the joint conditional probability over the entire pedigree. Reverse peeling is what is used in SIMLINK (section 7.5), sequential imputation (section 7.6) and the MCMC samplers on pedigrees described in Chapter 8.

P.111 Clarification: Heath (1997) is presented in terms of $\mathbf{G}$ not $\mathbf{S}$, but computationally meiosis indicators $S_{\bullet,j}$ are resampled. Genotypes are determined as a function of $\mathbf{S}$ and the allocation of allelic types to founder genes (see section 3.6).

P.118 Clarification of equation (9.4) and following lines:
These equations involve normalization factor, and so are more clearly written as "$\propto$" not ''=". In fact, $(t+1)\nu_j = \sum_l R_{jl}\nu_l$ or $t\nu_j = \sum_{l \neq j} R_{jl}\nu_l$ where the sum is over the t evaluation points $l \neq j$ for samples at model j.

P. 127: 4 th. line of equation (9.17) one of the expected log-probabilities is missing the log.

P.160 Reference Botstein et al. (1980): Volume number is **32**.

P.164 Reference Kumm et al. (1999): Page number is A208.

P.165 Reference Lathrop et al.(1984):
Authors are Lathrop, G.M., Lalouel, J.M., Julier, C., and Ott, J.

P.166 Reference Sheehan (1990): should be “Ph.D.Thesis”.