1. Page 2, (see note0101.pdf at https://github.com/SorensenD/SLGDS) for more details on the subject)
   CHANGE: "This requires equating the expected proportion of genotypes shared identical by descent, given a pedigree, with the observed phenotypic correlation between relatives."
   TO: "This requires equating the expected proportion of the genome shared identical by descent, given a pedigree, with the observed phenotypic correlation between relatives."

2. Page 18, CHANGE: "Jeffrey's prior and mathematical form as the likelihood, proportional to $\left((1-\theta)^{27}\right)$ lead to posterior distributions $Be\,(0.5, 27.5)$ and $Be\,(1, 28)$, respectively;"
   TO: "Jeffrey's prior and the uniform prior, when combined with the likelihood, proportional to $(1-\theta)^{27}$, lead to posterior distributions $Be\,(0.5, 27.5)$ and $Be\,(1, 28)$, respectively;"

3. Pages 201-203, REPLACE subsection :
   "The acceptance probability for a general Metropolis-Hastings algorithm"
   WITH the content of note0401.pdf

4. Page 258, eqn. (6.1),
   CHANGE second line to (brackets missing):

$$
\begin{aligned}
\mathrm{E}_{y_0 x}\left[\mathrm{MSE}\left(f\left(x\right)\right)\right] &= \mathrm{E}_{y_0 x}\left[\left(y_0 - f\left(x\right)\right)^2\right] \\
&= \mathrm{E}_x\left[\mathrm{E}_{y_0|x}\left[\left(y_0 - f\left(x\right)\right)^2 |x\right]\right] \\
&= \mathrm{E}_x\left[\mathrm{Var}\left(y_0|x\right) + \left(\mathrm{E}\left(y_0|x\right) - f\left(x\right)\right)^2\right], \qquad (6.1)
\end{aligned}
$$

5. Page 259, below eqn. (6.7),
   CHANGE: "that is in the best linear approximation ..."
   TO: "that is the best linear approximation ..."

6. Page 270, eqn. (6.31),
   CHANGE: the left hand side of the first line:

$$
\mathrm{Var}\left(y_0 - \widehat{y}_0|x_0\right)
$$

   TO:

$$
\mathrm{Var}\left[\left(y_0 - \widehat{y}_0\right)|x_0\right]
$$

   (brackets missing)

7. Page 277,
   CHANGE:

$$
\mathrm{E}_{y_v y}\left(\mathrm{MSE}_v\right) = \mathrm{Var}\left(y_{v,i}|x_i\right) + \mathrm{bias}^2 + \frac{1}{N}\,\mathrm{Var}\left(\hat{f}\left(x_i\right)|x_i\right)
$$

and

$$E_{y_v y} \left(\text{MSE}_t \right) = E_{y_v y} \left(\text{MSE}_v \right) - \frac{2}{N} \sum_i \text{Cov} \left(y_i, \hat{f}(x_i) \right)$$

TO:

$$E_{y_v y}(\text{MSE}_v) = \frac{1}{N} \sum_i \text{Var} \left(y_{v,i} | x_i \right) + \frac{1}{N} \sum_i \text{bias} \left(i \right)^2 + \frac{1}{N} \sum_i \text{Var} \left(\hat{f}(x_i) | x_i \right)$$

and when covariates in training and validating data take the same values,

$$E_{y_v y} \left(\text{MSE}_t \right) = E_{y_v y} \left(\text{MSE}_v \right) - \frac{2}{N} \sum_i \text{Cov} \left(y_i, \hat{f}(x_i) \right)$$

8. Page 286, below eqn. (6.66),
   CHANGE: "and from (6.65)"
   TO: "and from (6.65) when covariates in training and validating data take the same values,"

   (see note0603.pdf for elaborations on the subject).

9. Page 325, eqn. (7.41),
   CHANGE:
   The conditional distribution of the data takes the form

   $$y | \mu, \alpha, \delta, \sigma^2 \sim N \left(1\mu + \sum_{i=1}^{m} X_i \left(\alpha_i \delta_i \right), I\sigma^2 \right), \quad , i = 1, \ldots, m \qquad (7.41)$$

   where X_i is the ith column of X.
   TO: The conditional distribution of the data takes the form

   $$y | \mu, \alpha, \delta, \sigma^2 \sim N \left(1\mu + \sum_{i=1}^{m} X_i \left(\alpha_i \delta_i \right), I\sigma^2 \right), \quad i = 1, \ldots, m \qquad (7.41)$$

   where X_i is the ith column of X.

   (remove extra "," before $i = 1, \ldots, m$).

10. Top of page 393, eqn. (9.30),
    CHANGE:
    An unbiased estimator of incidence (given n, sen, spe and bounded between 0 and 1) is

    $$\frac{\text{Pr} \left(\hat{Y} = 1 \right) - (1 - spe)}{sen + spe - 1} = \frac{T - n \left(1 - spe \right)}{n(sen + spe - 1)}. \qquad (9.30)$$

    TO: An unbiased estimator of prevalence (given n, sen, spe and bounded between 0 and 1) is

    $$\frac{\widehat{\text{Pr}} \left(\hat{Y} = 1 \right) - (1 - spe)}{sen + spe - 1} = \frac{T - n \left(1 - spe \right)}{n(sen + spe - 1)}. \qquad (9.30)$$

2

(change "incidence" for "prevalence" and "hat" missing on the biased estimator of prevalence; see note0901.pdf for further details).

11. Page 675,
    CHANGE: "Boyle EA, Li YI, Pritchard JK (2017) An expanded view of complex **trits**: from polygenic to omnigenic. Cell 169:1177–1186"
    TO: "Boyle EA, Li YI, Pritchard JK (2017) An expanded view of complex traits: from polygenic to omnigenic. Cell 169:1177–1186"