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

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

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

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

5. 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)

6. 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

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

TO:

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

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

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

7. 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).

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

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

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

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

where X_i is the ith column of X.

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

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

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

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

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

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

10. 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"