

1. Page 2,

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."

(see note0101.pdf at <https://github.com/SorensenD/SLGDS>)

2. Page 258, eqn. (6.1),

CHANGE second line to (brackets missing):

$$\begin{aligned} E_{y_0x} [\text{MSE}(f(x))] &= E_{y_0x} [(y_0 - f(x))^2] \\ &= E_x [E_{y_0|x} [(y_0 - f(x))^2 | x]] \\ &= E_x [\text{Var}(y_0|x) + (E(y_0|x) - f(x))^2], \end{aligned} \quad (6.1)$$

3. Page 259, below eqn. (6.7),

CHANGE: "that is in the best linear approximation ..."

TO: "that is the best linear approximation ..."

4. Page 277,

CHANGE:

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

and

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

TO:

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

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

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

5. Page 286, below eqn. (6.66),

CHANGE: "and from (6.65)"

TO: "and from (6.65) when covariates in training and validating data are known and take the same values,"

6. Page 393, eqn. (9.30),
CHANGE:

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

TO:

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

("hat" missing on the biased estimator of incidence).

7. Page 675,

CHANGE: "Boyle EA, Li YI, Pritchard JK (2017) An expanded view of complex **traits**: 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"