

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 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"