QTL scans with QTL-path equations

$BD\\_GxE\_{j}=X\_{ji}β\_{i}+\sum\_{k=1}^{m}Z\_{k}α\_{k}+RIL\_{j}$ + *εj*

$RB\\_GxE\_{j}=BD\_{j}+BD\\_GxE\_{j}+X\_{ji}β\_{i}+\sum\_{k=1}^{m}Z\_{k}α\_{k}+RIL\_{j} $+ *εj*

$IG\\_GxE\_{j}=BD\_{j}+BD\\_GxE\_{j}+RB\_{j}+RB\\_GxE\_{j}+X\_{ji}β\_{i}+\sum\_{k=1}^{m}Z\_{k}α\_{k}+RIL\_{j} $+ *εj*

$IB\\_GxE\_{j}=BD\_{j}+BD\\_GxE\_{j}+RB\_{j}+RB\\_GxE\_{j}+IB\_{j}+IB\\_GxE\_{j}+X\_{ji}β\_{i}+\sum\_{k=1}^{m}Z\_{k}α\_{k}+RIL\_{j}$ + *εj*

Listed above are the equations used for the QTL-path models. *X­ji* is the genotype of the putative QTL marker *i* for RIL population *j*, and $β\_{i}$ is the effect of putative marker *i*. $α\_{k}$ is the effect for significant QTL marker *k*, $Z\_{k}$is the genotype of significant QTL marker *k* for the NAM population, and *m* is the total number of significant markers in the model. BD, RB, IG, and IB are the BLUPs for the respective traits, and BD\_GxE, RB\_GxE, IG\_GxE, and IB\_GxE are the respective shade responses (genotype-by-environment interactions) for the RILs. *RILj* is the genotype random effect. *εj* is the residual.

Path analysis (lavaan) equations

BD = A \* SAR4\_1 + B \* SAR4\_2 + C \* SAR5\_2 + D \* SAR5\_2 + ε1

RB = E \* SAR4\_1 + F \* SAR4\_2 + G \* SAR5\_2 + H \* SAR5\_2 + I \* BD + ε2

IB = J \* SAR4\_1 + K \* SAR4\_2 + L \* SAR5\_2 + M \* SAR5\_2 + N \* BD + O \* RB + ε3

IG = P \* SAR4\_1 + Q \* SAR4\_2 + R \* SAR5\_2 + S \* SAR5\_2 + T \* BD + U \* RB + V \* IB + ε4

Equations fit in path analysis, with all terms included (i.e. terms fitted before pruning by stepwise regression). Not all terms were included in the model, and the included terms differ by RIL population. Direct effects of a QTL on a trait can be estimated by the coefficient of the QTL term for a particular trait; for instance, the direct effect of SAR4\_1 on RB is E. Indirect effects of QTL on traits can be estimated by multiplying the coefficients of direct effect QTL on earlier traits and the coefficients of the corresponding trait in the equation. For example, the indirect effect of SAR4\_1 on RB can be estimated by multiplying the direct effect of SAR4\_1 on BD (A) and the effect of BD on RB (I), so that the estimated indirect effect of SAR4\_1 on RB is A \* I. For later traits, the indirect effects involve more terms due to multiple upstream traits, their corresponding effects on the trait of interest, and indirect QTL effects through multiple traits. As an example, the indirect effect of SAR4\_1 on IB can be estimated by multiplying the direct effects of SAR4\_1 on BD and RB (A and E) - because these traits have effects on IB - and the effects of BD and RB (N and O), respectively, on IB. We also need to estimate the indirect effect of SAR4\_1 on IB through both BD and RB by multiplying the corresponding coefficients (A \* I \* O), and then summing up all of the indirect effect terms. The estimated indirect effect of SAR4\_1 on IB would then be (A \* N) + (E \* O) + (A \* I \* O).