Comparison of mapping accuracy between methods predicting QTL allele identity using haplotypes
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For a QTL in high LD with haplotypes:

\[
\frac{1}{2} \sum_{h=1}^{2} \sum_{j=1}^{2} f(h|\nu_m) - f(h|\nu_w) \frac{\sum_{h=1}^{2} \sum_{j=1}^{2} \Delta h j \Delta h j}{\sum_{h=1}^{2} \sum_{j=1}^{2} \Delta h j \Delta h j}
\]

(\text{multiallelic } \Delta^2 \text{ measure: Redick et al., 1987})

In Table 1 we can see that inference on \( d \) is strongly related to mapping accuracy (results hold for moderate LD levels)

\( \text{IBS}_{\text{hap}} = \text{P}(\text{IBD}) \) and \( \text{IBS}_{\text{hap}} \) performed better than the other AIPs for mapping accuracy (table 1)

\[ d \leq \frac{\sum_{h=1}^{2} \sum_{j=1}^{2} f(h|\nu_m) - f(h|\nu_w) \frac{\sum_{h=1}^{2} \sum_{j=1}^{2} \Delta h j \Delta h j}{\sum_{h=1}^{2} \sum_{j=1}^{2} \Delta h j \Delta h j}}{\sum_{h=1}^{2} \sum_{j=1}^{2} \Delta h j \Delta h j}
\]

\[ \text{Distribution of normalized distance distributions and linkage disequilibrium (LD)}
\]

\[ \text{IBS}_{\text{hap}}(d_{\text{QTL}}) \text{ and } \text{P}(\text{IBD}) \text{ } \text{p}\text{-values for mapping accuracy (table 1)}
\]

\[ \text{IBS}_{\text{hap}} \text{ and } \text{P}(\text{IBD}) \text{ have very similar distributions}
\]

\[ \text{IBS}_{\text{hap}} \text{ and } \text{P}(\text{IBD}) \text{ have similar distributions in simulations and were almost bimodal for both IBS haplotypes and P(IBD)}
\]

\[ \text{IBS}_{\text{hap}} \text{ and } \text{P}(\text{IBD}) \text{ compared to other AIPs}
\]

\[ \text{Evidence of increasing LD when i moves closer to a QTL}
\]

\[ \text{IBS}_{\text{hap}}(d_{\text{QTL}}) \text{ as function of } d\]

\[ \text{Conclusion (table 1 and figure 2 and 3) AIPs which exploit LD better according to } d \text{ perform better in mapping a QTL}
\]

\[ \text{Conclusions}
\]

\[ \text{The QTL mapping accuracy of an AIP is strongly related to the matrix distance between a tested position and a QTL}
\]

\[ \text{The most efficient AIPs are those which exploit LD better as shown with the matrix distance}
\]

\[ \text{The } \text{IBS}_{\text{hap}} \text{ predictor exploits LD better among the six compared AIPs}
\]

\[ \text{One advantage of the matrix distance approach is that it is free from the phenotype simulation process and the test statistic}
\]

\[ \text{The algebraic results, shown here for a biallelic QTL, also hold for a multiallelic QTL}
\]