File S4: Simulation results for a different genetic architecture.

Table 1: Comparison of the marker-based estimators heritability estimators $h^2$ and $h^2_m$ for simulated data. We simulated 5000 traits, for random samples of 200 accessions drawn from the Structured regmap and Hapmap. A single QTL was simulated, which explained 90 percent of the genetic variance. The simulated heritability was 0.2, 0.5 and 0.8. Standard errors are given relative to those of the broad sense heritability estimator ($H^2$).

<table>
<thead>
<tr>
<th></th>
<th>Structured regmap</th>
<th>Hapmap</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>bias</td>
<td>standard error</td>
</tr>
<tr>
<td>$h^2 = 0.2$</td>
<td></td>
<td></td>
</tr>
<tr>
<td>replicates ($h^2$)</td>
<td>-0.00127</td>
<td>0.04787</td>
</tr>
<tr>
<td>means ($h^2_m$)</td>
<td>0.00782</td>
<td>0.08626</td>
</tr>
<tr>
<td>$h^2 = 0.5$</td>
<td></td>
<td></td>
</tr>
<tr>
<td>replicates ($h^2$)</td>
<td>-0.00279</td>
<td>0.04500</td>
</tr>
<tr>
<td>means ($h^2_m$)</td>
<td>0.01295</td>
<td>0.16461</td>
</tr>
<tr>
<td>$h^2 = 0.8$</td>
<td></td>
<td></td>
</tr>
<tr>
<td>replicates ($h^2$)</td>
<td>-0.00257</td>
<td>0.02458</td>
</tr>
<tr>
<td>means ($h^2_m$)</td>
<td>0.00337</td>
<td>0.20855</td>
</tr>
<tr>
<td>$h^2 = 0.2$</td>
<td></td>
<td></td>
</tr>
<tr>
<td>replicates ($h^2$)</td>
<td>-0.00110</td>
<td>0.04344</td>
</tr>
<tr>
<td>means ($h^2_m$)</td>
<td>0.06629</td>
<td>0.26168</td>
</tr>
<tr>
<td>$h^2 = 0.5$</td>
<td></td>
<td></td>
</tr>
<tr>
<td>replicates ($h^2$)</td>
<td>-0.00123</td>
<td>0.03437</td>
</tr>
<tr>
<td>means ($h^2_m$)</td>
<td>0.03062</td>
<td>0.33527</td>
</tr>
<tr>
<td>$h^2 = 0.8$</td>
<td></td>
<td></td>
</tr>
<tr>
<td>replicates ($h^2$)</td>
<td>-0.00027</td>
<td>0.01633</td>
</tr>
<tr>
<td>means ($h^2_m$)</td>
<td>-0.07852</td>
<td>0.33486</td>
</tr>
</tbody>
</table>
Table 2: Marker-based estimation of heritability: width and coverage confidence intervals obtained from the individual plant data and the genotypic means. Results for broad sense heritability intervals are reported for comparison. We simulated 5000 traits, for random samples of 200 accessions drawn from the structured regmap (top) and Hapmap (bottom). A single QTL was simulated, which explained 90 percent of the genetic variance. The simulated heritability was 0.2, 0.5 and 0.8.

<table>
<thead>
<tr>
<th>Marker-based estimation of heritability: width and coverage confidence intervals obtained from the individual plant data and the genotypic means.</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Results for broad sense heritability intervals are reported for comparison. We simulated 5000 traits, for random samples of 200 accessions drawn from the structured regmap (top) and Hapmap (bottom). A single QTL was simulated, which explained 90 percent of the genetic variance. The simulated heritability was 0.2, 0.5 and 0.8.</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Structure</th>
<th>Coverage</th>
<th>Interval Width</th>
</tr>
</thead>
<tbody>
<tr>
<td>regmap</td>
<td>$h^2 = 0.2$</td>
<td></td>
</tr>
<tr>
<td>broad-sense</td>
<td>0.940</td>
<td>0.178</td>
</tr>
<tr>
<td>replicates (standard)</td>
<td>0.945</td>
<td>0.201</td>
</tr>
<tr>
<td>replicates (log-transformed)</td>
<td>0.962</td>
<td>0.202</td>
</tr>
<tr>
<td>means (standard)</td>
<td>0.911</td>
<td>0.315</td>
</tr>
<tr>
<td>means (log-transformed)</td>
<td>0.960</td>
<td>0.321</td>
</tr>
<tr>
<td>$h^2 = 0.5$</td>
<td></td>
<td></td>
</tr>
<tr>
<td>broad-sense</td>
<td>0.926</td>
<td>0.160</td>
</tr>
<tr>
<td>replicates (standard)</td>
<td>0.837</td>
<td>0.194</td>
</tr>
<tr>
<td>replicates (log-transformed)</td>
<td>0.847</td>
<td>0.192</td>
</tr>
<tr>
<td>means (standard)</td>
<td>0.814</td>
<td>0.446</td>
</tr>
<tr>
<td>means (log-transformed)</td>
<td>0.886</td>
<td>0.427</td>
</tr>
<tr>
<td>$h^2 = 0.8$</td>
<td></td>
<td></td>
</tr>
<tr>
<td>broad-sense</td>
<td>0.914</td>
<td>0.084</td>
</tr>
<tr>
<td>replicates (standard)</td>
<td>0.674</td>
<td>0.097</td>
</tr>
<tr>
<td>replicates (log-transformed)</td>
<td>0.666</td>
<td>0.097</td>
</tr>
<tr>
<td>means (standard)</td>
<td>0.714</td>
<td>0.437</td>
</tr>
<tr>
<td>means (log-transformed)</td>
<td>0.840</td>
<td>0.547</td>
</tr>
<tr>
<td>Hapmap</td>
<td></td>
<td></td>
</tr>
<tr>
<td>$h^2 = 0.2$</td>
<td></td>
<td></td>
</tr>
<tr>
<td>broad-sense</td>
<td>0.961</td>
<td>0.178</td>
</tr>
<tr>
<td>replicates (standard)</td>
<td>0.961</td>
<td>0.181</td>
</tr>
<tr>
<td>replicates (log-transformed)</td>
<td>0.972</td>
<td>0.182</td>
</tr>
<tr>
<td>means (standard)</td>
<td>0.807</td>
<td>0.537</td>
</tr>
<tr>
<td>means (log-transformed)</td>
<td>0.899</td>
<td>0.675</td>
</tr>
<tr>
<td>$h^2 = 0.5$</td>
<td></td>
<td></td>
</tr>
<tr>
<td>broad-sense</td>
<td>0.979</td>
<td>0.160</td>
</tr>
<tr>
<td>replicates (standard)</td>
<td>0.971</td>
<td>0.164</td>
</tr>
<tr>
<td>replicates (log-transformed)</td>
<td>0.975</td>
<td>0.163</td>
</tr>
<tr>
<td>means (standard)</td>
<td>0.800</td>
<td>0.766</td>
</tr>
<tr>
<td>means (log-transformed)</td>
<td>0.967</td>
<td>0.819</td>
</tr>
<tr>
<td>$h^2 = 0.8$</td>
<td></td>
<td></td>
</tr>
<tr>
<td>broad-sense</td>
<td>0.990</td>
<td>0.084</td>
</tr>
<tr>
<td>replicates (standard)</td>
<td>0.963</td>
<td>0.085</td>
</tr>
<tr>
<td>replicates (log-transformed)</td>
<td>0.964</td>
<td>0.085</td>
</tr>
<tr>
<td>means (standard)</td>
<td>0.820</td>
<td>0.840</td>
</tr>
<tr>
<td>means (log-transformed)</td>
<td>0.849</td>
<td>0.903</td>
</tr>
</tbody>
</table>
Figure 1: Heritability estimates for 5000 simulated traits for random samples of 200 accessions drawn from the Structured regmap (top panel) and the Hapmap (bottom panel). 1 QTL was simulated, which explained 90% of the genetic variance. The simulated heritability was 0.2 (left column), 0.5 (middle column) and 0.8 (right column). Within each panel, the first row shows the ANOVA-based estimates of broad-sense heritability, the second row the mixed model based estimates based on the individual data, and the third row the mixed model based estimates based on genotypic means.