Non-Parametric Resampling Methods for Testing Multiplicative Terms in AMMI and GGE Models for Multi-environment trials

Waqas Malik, Steffan Hadasch, Johannes Forkman, Hans-Peter Piepho

27-05-2018
Outline

1. Genotype-by-environment interaction
2. The additive main effects and multiplicative interaction model (AMMI)
3. A parametric bootstrap method for AMMI analysis
4. A non-parametric resampling method for AMMI analysis
5. Example
6. Robustness of the resampling methods
Genotypes and Environments

- Genotypes can be cultivars or any crop varieties.
- Environments can be experimental stations, locations, regions, seasons or years, or combinations of these.
- Genotypes respond differently across environments i.e., the relative performance of varieties depends on the environment.
Genotype-by-environment interaction ($G \times E$)

- How do genotypes and environments interact?
- Which varieties perform similarly in varying environments?
- Which environments give similar results?
**Genotype by environment interaction**

Yield of genotypes G1, G2 and G3 at sites E1 and E2

<table>
<thead>
<tr>
<th>Genotypes</th>
<th>Environments</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>E1</td>
<td>E2</td>
<td></td>
</tr>
<tr>
<td>G1</td>
<td>1</td>
<td>1.5</td>
<td></td>
</tr>
<tr>
<td>G2</td>
<td>1.5</td>
<td>3</td>
<td></td>
</tr>
<tr>
<td>G3</td>
<td>2</td>
<td>2.5</td>
<td></td>
</tr>
</tbody>
</table>

![Graph showing yield of genotypes G1, G2, and G3 at sites E1 and E2](image-url)
Phenotypic variation

The phenotypic variation is the variation that shows

\[ P = G + E + GE \]

Phenotypic variation

= Genotypic variation + Environmental variation +
Genotype-by-environment interaction
### International series of maize trials

<table>
<thead>
<tr>
<th>Environments</th>
<th>Genotypes</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>G1</td>
</tr>
<tr>
<td>E01</td>
<td>3622</td>
</tr>
<tr>
<td>E02</td>
<td>3728</td>
</tr>
<tr>
<td>E03</td>
<td>5554</td>
</tr>
<tr>
<td>E04</td>
<td>4566</td>
</tr>
<tr>
<td>E05</td>
<td>4380</td>
</tr>
<tr>
<td>E06</td>
<td>6437</td>
</tr>
<tr>
<td>E07</td>
<td>2832</td>
</tr>
<tr>
<td>E08</td>
<td>6011</td>
</tr>
<tr>
<td>E09</td>
<td>4647</td>
</tr>
<tr>
<td>E10</td>
<td>3100</td>
</tr>
<tr>
<td>E11</td>
<td>4433</td>
</tr>
<tr>
<td>E12</td>
<td>6873</td>
</tr>
<tr>
<td>E13</td>
<td>6721</td>
</tr>
<tr>
<td>E14</td>
<td>5849</td>
</tr>
<tr>
<td>E15</td>
<td>4601</td>
</tr>
<tr>
<td>E16</td>
<td>5010</td>
</tr>
<tr>
<td>E17</td>
<td>4415</td>
</tr>
<tr>
<td>E18</td>
<td>3344</td>
</tr>
<tr>
<td>E19</td>
<td>1632</td>
</tr>
<tr>
<td>E20</td>
<td>4587</td>
</tr>
</tbody>
</table>
## Two-way matrix

<table>
<thead>
<tr>
<th></th>
<th>Y</th>
<th>J=9 genotypes</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>3622</td>
<td>3426</td>
</tr>
<tr>
<td></td>
<td>3728</td>
<td>4082</td>
</tr>
<tr>
<td></td>
<td>5554</td>
<td>4937</td>
</tr>
<tr>
<td></td>
<td>4566</td>
<td>4963</td>
</tr>
<tr>
<td></td>
<td>4380</td>
<td>5201</td>
</tr>
<tr>
<td></td>
<td>6437</td>
<td>6036</td>
</tr>
<tr>
<td></td>
<td>2832</td>
<td>2515</td>
</tr>
<tr>
<td></td>
<td>6011</td>
<td>5278</td>
</tr>
<tr>
<td></td>
<td>4647</td>
<td>4714</td>
</tr>
<tr>
<td></td>
<td>3100</td>
<td>2972</td>
</tr>
<tr>
<td></td>
<td>4433</td>
<td>4349</td>
</tr>
<tr>
<td></td>
<td>6873</td>
<td>7571</td>
</tr>
<tr>
<td></td>
<td>6721</td>
<td>5627</td>
</tr>
<tr>
<td></td>
<td>5849</td>
<td>5932</td>
</tr>
<tr>
<td></td>
<td>4601</td>
<td>4126</td>
</tr>
<tr>
<td></td>
<td>5010</td>
<td>5196</td>
</tr>
<tr>
<td></td>
<td>4415</td>
<td>4211</td>
</tr>
<tr>
<td></td>
<td>3344</td>
<td>4415</td>
</tr>
<tr>
<td></td>
<td>1632</td>
<td>2282</td>
</tr>
<tr>
<td></td>
<td>4587</td>
<td>4396</td>
</tr>
</tbody>
</table>

I=20 environments

J=9 genotypes
Additive main effects and multiplicative interaction model (AMMI)

- Introduced by Mandel (1971)
- Proposed by Kempton (1984) to use in MET
- Named by Gauch (1988, 1992)
AMMI

The model is

\[ Y_{ij} = \mu + E_i + G_j + u_{i1}\lambda_1 v_{j1} + u_{i2}\lambda_2 v_{j2} + \ldots + u_{iM}\lambda_M v_{jM} + e_{ij} \]

Additive part  Interaction and residual part

- \( \mu \) = Overall mean
- \( G \) = Genotype mean
- \( E \) = Environment mean
- \( \lambda_k \) = \( k \)th eigenvalue
- \( u_{ik} \) = \( k \)th principal component score for the \( i \)th environment.
- \( v_{jk} \) = \( k \)th principal component score for the \( j \)th genotype.
The model is

\[ Y_{ij} = \mu + E_i + u_{i1}\lambda_1 v_{j1} + u_{i2}\lambda_2 v_{j2} + \ldots + u_{iM}\lambda_M v_{jM} + e_{ij} \]

Additive part \quad \text{Genotype + Interaction and residual part}

- \( \mu \) = Overall mean
- \( G \) = Genotype mean
- \( E \) = Environment mean
- \( \lambda_k \) = \( k \)th eigenvalue
- \( u_{ik} \) = \( k \)th principal component score for the \( i \)th environment.
- \( v_{jk} \) = \( k \)th principal component score for the \( j \)th genotype.
\[ y_{ij} = \mu + E_i + G_j + \sum_{k=1}^{\kappa} u_{ik} \lambda_k v_{jk} + e_{ij} \]
Fit a two factor fixed effect and get estimates

\[ y_{ij} = \mu + G_i + E_j + \sum_{k=1}^{\kappa} u_{ik} \lambda_k v_{jk} + e_{ij} \]  

Estimate the residuals \( e_{ij} \) i.e.

\[ \hat{E} \]

A singular value decomposition (SVD) on the matrix of residuals \( \hat{E} \)
<p>| | | | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>250.4</td>
<td>68.2</td>
<td>-131.3</td>
<td>-252.4</td>
<td>-836.5</td>
<td>31.3</td>
</tr>
<tr>
<td>-240.3</td>
<td>-35.5</td>
<td>-92.1</td>
<td>-30.1</td>
<td>-519.3</td>
<td>196.5</td>
</tr>
<tr>
<td>689.9</td>
<td>86.7</td>
<td>47.2</td>
<td>-921.8</td>
<td>679.0</td>
<td>-372.1</td>
</tr>
<tr>
<td>-423.0</td>
<td>-12.2</td>
<td>-58.7</td>
<td>440.1</td>
<td>212.0</td>
<td>277.8</td>
</tr>
<tr>
<td>-334.0</td>
<td>500.7</td>
<td>-741.7</td>
<td>357.1</td>
<td>70.0</td>
<td>163.8</td>
</tr>
<tr>
<td>372.6</td>
<td>-14.5</td>
<td>188.8</td>
<td>12.8</td>
<td>187.6</td>
<td>138.5</td>
</tr>
<tr>
<td>-156.3</td>
<td>-459.5</td>
<td>334.8</td>
<td>-591.1</td>
<td>-62.3</td>
<td>247.5</td>
</tr>
<tr>
<td>2224.2</td>
<td>1505.0</td>
<td>738.5</td>
<td>-1871.5</td>
<td>-1684.6</td>
<td>-1516.8</td>
</tr>
<tr>
<td>-82.6</td>
<td>-1.8</td>
<td>512.6</td>
<td>-466.4</td>
<td>228.4</td>
<td>160.3</td>
</tr>
<tr>
<td>404.6</td>
<td>290.4</td>
<td>-116.1</td>
<td>-453.1</td>
<td>-637.3</td>
<td>-384.4</td>
</tr>
<tr>
<td>-633.1</td>
<td>-703.3</td>
<td>-745.9</td>
<td>1450.0</td>
<td>298.8</td>
<td>370.7</td>
</tr>
<tr>
<td>-402.6</td>
<td>309.2</td>
<td>245.6</td>
<td>508.6</td>
<td>200.4</td>
<td>-351.7</td>
</tr>
<tr>
<td>629.7</td>
<td>-450.4</td>
<td>-3.0</td>
<td>639.9</td>
<td>452.7</td>
<td>457.6</td>
</tr>
<tr>
<td>37.9</td>
<td>134.7</td>
<td>-130.7</td>
<td>27.1</td>
<td>-81.9</td>
<td>-144.1</td>
</tr>
<tr>
<td>-206.8</td>
<td>-668.0</td>
<td>-476.5</td>
<td>922.3</td>
<td>890.2</td>
<td>440.0</td>
</tr>
<tr>
<td>-154.9</td>
<td>44.8</td>
<td>84.3</td>
<td>585.2</td>
<td>275.1</td>
<td>-148.0</td>
</tr>
<tr>
<td>-220.7</td>
<td>-410.9</td>
<td>-92.4</td>
<td>-75.5</td>
<td>188.3</td>
<td>458.1</td>
</tr>
<tr>
<td>-966.3</td>
<td>118.4</td>
<td>-221.1</td>
<td>706.8</td>
<td>-442.3</td>
<td>309.5</td>
</tr>
<tr>
<td>-779.1</td>
<td>-115.3</td>
<td>442.0</td>
<td>-778.9</td>
<td>31.8</td>
<td>-113.2</td>
</tr>
<tr>
<td>-9.3</td>
<td>-186.5</td>
<td>215.8</td>
<td>-209.1</td>
<td>549.6</td>
<td>-221.4</td>
</tr>
</tbody>
</table>

$\hat{E}$
Singular value decomposition (SVD)

\[ \hat{E} = \hat{U}\hat{\Lambda}\hat{V}^T \]

\( \hat{U} \) is a matrix of left-singular vectors
\( \hat{\Lambda} \) is a diagonal matrix of singular values
\( \hat{V} \) is a matrix of right-singular vectors
Singular value decomposition (SVD)

\[
\hat{U}
\]

<table>
<thead>
<tr>
<th></th>
<th>-0.220</th>
<th>0.269</th>
<th>-0.180</th>
<th>0.2224</th>
<th>-0.301</th>
<th>-0.225</th>
<th>0.1318</th>
<th>-0.346</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.018</td>
<td>-0.178</td>
<td>-0.299</td>
<td>-0.0415</td>
<td>-0.091</td>
<td>-0.237</td>
<td>-0.1246</td>
<td>0.075</td>
<td></td>
</tr>
<tr>
<td>-0.262</td>
<td>0.175</td>
<td>0.178</td>
<td>-0.5296</td>
<td>-0.180</td>
<td>0.247</td>
<td>-0.2378</td>
<td>0.284</td>
<td></td>
</tr>
<tr>
<td>0.153</td>
<td>0.089</td>
<td>0.069</td>
<td>0.2172</td>
<td>0.167</td>
<td>0.085</td>
<td>-0.0863</td>
<td>-0.254</td>
<td></td>
</tr>
<tr>
<td>0.086</td>
<td>0.088</td>
<td>-0.015</td>
<td>0.3325</td>
<td>-0.134</td>
<td>0.352</td>
<td>-0.6490</td>
<td>0.102</td>
<td></td>
</tr>
<tr>
<td>-0.006</td>
<td>-0.203</td>
<td>0.119</td>
<td>-0.4365</td>
<td>-0.229</td>
<td>-0.090</td>
<td>-0.1401</td>
<td>-0.340</td>
<td></td>
</tr>
<tr>
<td>-0.081</td>
<td>0.105</td>
<td>-0.206</td>
<td>-0.2557</td>
<td>0.151</td>
<td>-0.355</td>
<td>0.0550</td>
<td>0.028</td>
<td></td>
</tr>
<tr>
<td>-0.670</td>
<td>-0.418</td>
<td>0.208</td>
<td>0.2701</td>
<td>-0.017</td>
<td>-0.018</td>
<td>0.1048</td>
<td>0.082</td>
<td></td>
</tr>
<tr>
<td>0.038</td>
<td>-0.045</td>
<td>0.120</td>
<td>0.0367</td>
<td>0.562</td>
<td>-0.118</td>
<td>-0.2091</td>
<td>-0.062</td>
<td></td>
</tr>
<tr>
<td>-0.227</td>
<td>0.068</td>
<td>-0.114</td>
<td>0.1816</td>
<td>-0.159</td>
<td>-0.013</td>
<td>0.0943</td>
<td>0.181</td>
<td></td>
</tr>
<tr>
<td>0.393</td>
<td>-0.069</td>
<td>-0.060</td>
<td>0.1619</td>
<td>-0.230</td>
<td>-0.108</td>
<td>0.3039</td>
<td>0.535</td>
<td></td>
</tr>
<tr>
<td>0.166</td>
<td>-0.315</td>
<td>0.024</td>
<td>-0.0066</td>
<td>0.178</td>
<td>0.409</td>
<td>0.2542</td>
<td>-0.098</td>
<td></td>
</tr>
<tr>
<td>0.254</td>
<td>-0.243</td>
<td>0.503</td>
<td>-0.0084</td>
<td>0.053</td>
<td>-0.443</td>
<td>-0.0958</td>
<td>0.074</td>
<td></td>
</tr>
<tr>
<td>-0.006</td>
<td>-0.024</td>
<td>-0.005</td>
<td>0.1041</td>
<td>-0.021</td>
<td>0.084</td>
<td>-0.0076</td>
<td>0.163</td>
<td></td>
</tr>
<tr>
<td>0.212</td>
<td>0.283</td>
<td>0.217</td>
<td>-0.1213</td>
<td>-0.277</td>
<td>0.028</td>
<td>0.1176</td>
<td>-0.010</td>
<td></td>
</tr>
<tr>
<td>0.079</td>
<td>-0.002</td>
<td>0.113</td>
<td>-0.0364</td>
<td>-0.098</td>
<td>0.288</td>
<td>0.3396</td>
<td>-0.375</td>
<td></td>
</tr>
<tr>
<td>0.000</td>
<td>0.430</td>
<td>0.026</td>
<td>0.1766</td>
<td>0.132</td>
<td>-0.205</td>
<td>-0.0723</td>
<td>-0.134</td>
<td></td>
</tr>
<tr>
<td>0.226</td>
<td>-0.341</td>
<td>-0.436</td>
<td>-0.0142</td>
<td>-0.125</td>
<td>0.039</td>
<td>-0.1278</td>
<td>-0.183</td>
<td></td>
</tr>
<tr>
<td>-0.088</td>
<td>0.076</td>
<td>-0.424</td>
<td>-0.2507</td>
<td>0.373</td>
<td>0.096</td>
<td>0.0802</td>
<td>0.158</td>
<td></td>
</tr>
<tr>
<td>-0.036</td>
<td>0.257</td>
<td>0.162</td>
<td>-0.0022</td>
<td>0.245</td>
<td>0.182</td>
<td>0.2691</td>
<td>0.120</td>
<td></td>
</tr>
</tbody>
</table>
Singular value decomposition (SVD)

\[ \Lambda \]

<table>
<thead>
<tr>
<th></th>
<th>5923</th>
<th>0</th>
<th>0</th>
<th>0</th>
<th>0</th>
<th>0</th>
<th>0</th>
<th>0</th>
<th>0</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>3070</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>0</td>
<td>0</td>
<td>2553</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>0</td>
<td>0</td>
<td>0</td>
<td>2320</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1758</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1313</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>792</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>757</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>
## Singular value decomposition (SVD)

\[ \mathbf{V} \]

<p>| | | | | | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>-0.381</td>
<td>-0.22600</td>
<td>0.64113</td>
<td>0.0627</td>
<td>-0.2746</td>
<td>-0.3716</td>
<td>0.0279</td>
<td>0.2515</td>
</tr>
<tr>
<td>-0.248</td>
<td>-0.31811</td>
<td>0.00675</td>
<td>0.2819</td>
<td>-0.0155</td>
<td>0.5904</td>
<td>-0.4670</td>
<td>-0.2830</td>
</tr>
<tr>
<td>-0.165</td>
<td>-0.14871</td>
<td>0.05747</td>
<td>-0.2096</td>
<td>0.5717</td>
<td>-0.1044</td>
<td>0.4528</td>
<td>-0.4997</td>
</tr>
<tr>
<td>0.515</td>
<td>0.00355</td>
<td>0.05607</td>
<td>0.1966</td>
<td>-0.5366</td>
<td>0.1510</td>
<td>0.4496</td>
<td>-0.2624</td>
</tr>
<tr>
<td>0.283</td>
<td>0.34254</td>
<td>0.36743</td>
<td>-0.4896</td>
<td>0.2014</td>
<td>0.4054</td>
<td>-0.1192</td>
<td>0.3125</td>
</tr>
<tr>
<td>0.271</td>
<td>0.21938</td>
<td>-0.09146</td>
<td>-0.0801</td>
<td>-0.0321</td>
<td>-0.5429</td>
<td>-0.5756</td>
<td>-0.3541</td>
</tr>
<tr>
<td>-0.119</td>
<td>-0.37928</td>
<td>-0.56877</td>
<td>-0.5133</td>
<td>-0.2641</td>
<td>-0.0377</td>
<td>0.0406</td>
<td>0.2668</td>
</tr>
<tr>
<td>-0.479</td>
<td>0.69374</td>
<td>-0.28814</td>
<td>0.2306</td>
<td>-0.0871</td>
<td>0.0418</td>
<td>0.1609</td>
<td>0.0813</td>
</tr>
<tr>
<td>0.322</td>
<td>-0.18710</td>
<td>-0.18048</td>
<td>0.5208</td>
<td>0.4368</td>
<td>-0.1319</td>
<td>0.0300</td>
<td>0.4871</td>
</tr>
</tbody>
</table>
Singular value decomposition (SVD)

In matrix form,

\[ \hat{E} = \hat{U} \hat{\Lambda} \hat{V}^T \]

In scalar form,

\[ \hat{e}_{ij} = \hat{u}_{i1} \hat{\lambda}_1 \hat{v}_{j1} + \hat{u}_{i2} \hat{\lambda}_2 \hat{v}_{j2} + \ldots + \hat{u}_{iM} \hat{\lambda}_M \hat{v}_{jM} \]

where \( M = \min(I - 1, J - 1) \)
The original observations can be written

\[ y_{ij} = \mu + \hat{E}_i + \hat{G}_j + \hat{u}_{i1} \hat{\lambda}_1 \hat{v}_1 + \hat{u}_{i2} \hat{\lambda}_2 \hat{v}_2 + \ldots + \hat{u}_{iM} \hat{\lambda}_M \hat{v}_M \]

Usually, only a few multiplicative terms are retained in the model, e.g.

\[ \hat{y}_{ij} = \mu + \hat{E}_i + \hat{G}_j + \hat{u}_{i1} \hat{\lambda}_1 \hat{v}_1 + \hat{u}_{i2} \hat{\lambda}_2 \hat{v}_2 \]

It is called AMMI-2.
Biplot
AMMI

Problem: How many multiplicative terms should be included

AMMI-2, AMMI-3, AMMI-4 or ....?
Nonparametric Resampling Methods for Testing Multiplicative Terms in AMMI and GGE Models for Multienvironment Trials

W. A. Malik, S. Hadasch, J. Forkman, and H. P. Piepho

ABSTRACT
The additive main effects and multiplicative interaction (AMMI) and genotype and genotype × environment interaction (GGE) models have been extensively used for the analysis of genotype × environment experiments in plant breeding and variety testing. Since their introduction, several tests have been proposed for testing the significance of the multiplicative terms, including a parametric bootstrap procedure. However, all of these tests are based on

W. A. Malik, S. Hadasch, and H. P. Piepho, Univ. of Hohenheim, Institute of Crop Science, Biostatistics Unit, Fruwirthstrasse 23, 70599 Stuttgart, Germany; J. Forkman, Swedish Univ. of Agricultural Sciences, Dep. of Crop Production Ecology, PO Box 7043, 750 07 Uppsala, Sweden. Received 16 Oct. 2017. Accepted 4 Dec. 2017. *Corresponding author (w.malik@uni-hohenheim.de). Assigned to Associate Editor Michael Gore.

Abbreviations: AMMI, additive main effects and multiplicative interaction; GGE, genotype and genotype × environment interaction; MET, multienvironment trial; SVD, singular value decomposition.
Parametric Bootstrap Methods for Testing Multiplicative Terms in GGE and AMMI Models

Johannes Forkman¹,* and Hans-Peter Piepho²

¹Department of Crop Production Ecology, Swedish University of Agricultural Sciences, PO Box 7043, 750 07 Uppsala, Sweden
²Institute of Crop Science, University of Hohenheim, 70 593 Stuttgart, Germany
*email: johannes.forkman@slu.se

SUMMARY. The genotype main effects and genotype-by-environment interaction effects (GGE) model and the additive main effects and multiplicative interaction (AMMI) model are two common models for analysis of genotype-by-environment data. These models are frequently used by agronomists, plant breeders, geneticists and statisticians for analysis of multi-environment trials. In such trials, a set of genotypes, for example, crop cultivars, are compared across a range of environments, for example, locations. The GGE and AMMI models use singular value decomposition to partition genotype-by-environment interaction into an ordered sum of multiplicative terms. This article deals with the problem of testing the significance of these multiplicative terms in order to decide how many terms to retain in the final model. We propose parametric bootstrap methods for this problem. Models with fixed main effects, fixed multiplicative terms and random normally distributed errors are considered. Two methods are derived: a full and a simple parametric bootstrap method. These are compared with the alternatives of using approximate F-tests and cross-validation. In a simulation study based on four multi-environment trials, both bootstrap methods performed well with regard to Type I error rate and power. The simple parametric bootstrap method is particularly easy to use, since it only involves repeated sampling of standard normally distributed values. This method is recommended for selecting the number of multiplicative terms in GGE and AMMI models. The proposed methods can also be used for testing components in principal component analysis.

KEY WORDS: AMMI; Genotype–environment interaction; GGE; Multi-environment trials; Principal component analysis; Singular value decomposition.
Parametric/Non-parametric bootstrapping

- Parametric/Non-parametric model is fitted to the data
- Samples are drawn from the fitted model
- Statistics of interest are computed for each bootstrap sample
- The obtained distribution approximates the actual sampling distribution and enables approximate inference
The null model

\[ \hat{E} = \hat{U}(\kappa)\hat{\Lambda}(\kappa)\hat{V}^T(\kappa) + R \]

\(\kappa\) is the actual number of multiplicative terms

**Parametric bootstrapping**

\(R\) is a matrix of independent \(N(0, \hat{\sigma}_\kappa^2)\) distributed errors
The null model

\[ \hat{E} = \hat{U}_{(\kappa)} \hat{\Lambda}_{(\kappa)} \hat{V}^T_{(\kappa)} + R \]

\( \kappa \) is the actual number of multiplicative terms

Non-parametric Resampling method

\( R \) is a matrix of independent samples drawn from errors

- Bootstrap
- Permutation
The null hypothesis

\[ H_0: \kappa = K \]
\[ H_1: \kappa > K \]

\( \kappa \) is the actual number of multiplicative terms

\( K \) is the assumed number of multiplicative terms under \( H_0 \)

Terms are tested sequentially \( K = 0, 1, \ldots \) until a nonsignificant result is obtained.
Test statistic

\[ T = \frac{\hat{\lambda}_{K+1}^2}{\sum_{k=K+1}^{M} \hat{\lambda}_k^2} \]

Large values of \( T \) present evidence against \( H_0 \)
Algorithm

1. Do the following a large number of times:
   - Compute $\widehat{E}_b$
   - For this matrix compute, $T_b$

2. Estimate the $p$-value as the frequency of $T_b$ larger than $T$. 
Parametric and Non-parametric

**Parametric bootstrap**
- Assume Normal distribution with constant variance

**Non-parametric resampling**
- No assumption
Results for the maize dataset

Under $H_0$, the model has $K$ terms

<table>
<thead>
<tr>
<th>$K+1$</th>
<th>$T$</th>
<th>$p$-value</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td><strong>Parametric</strong></td>
</tr>
<tr>
<td>1</td>
<td>0.562</td>
<td>0.0000</td>
</tr>
<tr>
<td>2</td>
<td>0.345</td>
<td>0.1560</td>
</tr>
<tr>
<td>3</td>
<td>0.364</td>
<td>0.2720</td>
</tr>
<tr>
<td>4</td>
<td>0.472</td>
<td>0.0460</td>
</tr>
<tr>
<td>5</td>
<td>0.514</td>
<td>0.1110</td>
</tr>
</tbody>
</table>

This suggests a model with one term.
This suggests a model with one term.
Problem of parametric bootstrap method

- Maintains the Type I error rate (Forkman and Piepho, 2015) only when errors are
  - Normally distributed
  - Homogenous variance
Robustness of the parametric bootstrap method and non-parametric resampling method
Simulation study of robustness

- Study of the performance of the parametric bootstrap and non-parametric resampling method
- Type I error rate at nominal level 0.05
- Assuming non-normality and heteroscedasticity
- Simulation based on three real data
- Number of simulations = 100000
- Number of bootstrap samples = 5000
Investigated null distributions

- For each $K$, we computed,

$$\hat{\mu}_{ij(K)} = \hat{\mu} + \hat{\alpha}_i + \hat{\beta}_j + \hat{\theta}_{ij(K)}$$

$$\hat{\theta}_{ij(K)} = \sum_{k=1}^{K} \hat{u}_{ik} \hat{\lambda}_k \hat{v}_{jk}$$

- These estimates were used to define the distributions of the simulation study.
Investigated null distributions

- Normal distribution
  i. Homogeneous variance
  ii. Heterogeneous variance
  iii. Heterogeneous variance among environments
- Lognormal distribution
  iv. Homogeneous variance
  v. Heterogeneous variance
- Gamma distribution with shape parameter 4
  vi. Homogeneous variance
  vii. Heterogeneous variance among environments
- Exponential distribution with homogeneous variance
- Uniform distribution with homogeneous variance
Homogeneous variance
Normal

Log-normal

Gamma

Uniform

Exponential

Parametric
Non-parametric
Permutation
Normal distribution with heterogeneous variance
Non-normal with heterogeneous variance
Gamma distribution with heterogeneous variance among Environment
Conclusion

- The additive main effects and multiplicative interaction (AMMI) model explores the matrix of residuals from a two-way ANOVA using singular value decomposition.

- The significance of the multiplicative terms can be tested using the parametric bootstrap and non-parametric resampling method.

- Non-parametric method performs much better than parametric method when there is heteroscedasticity and non-normality
Supplementary Slides
Experiment with Replicates

- Fit a model with fixed Genotype, Environment and Block effect.
- Get error sum of square, SSE
- Estimate the residuals $e_{ij}$ i.e. $\hat{E}$
- Resample the residuals to have a bootstrap sample
- The test statistics is

\[ T = \frac{\hat{\lambda}^2_{K+1}}{\text{SSE}} \]
Simulation study of robustness

Homogenous variance
Simulation study of robustness

Heterogeneous variance