Estimating macro- and micro-environmental sensitivity with unbalanced data
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Aim:
Examine the use of unbalanced data to estimate macro- and micro-environmental sensitivity

Approach:
Simulation of unbalanced datasets
Analysed using a reaction norm double hierarchical generalized linear mixed model (RN-DHGLMM)

Background:
• Environmental sensitivity (ES) determines how much a phenotype varies due to environmental changes.
• Macro-ES are in response to changes in macro-environments.
• Micro-ES, caused by micro-environments, affects the variability of phenotypes.
• A RN-DHGLMM model can estimate macro- and micro-ES simultaneously.
• The possibility of using the RN-DHGLMM on unbalanced data has not previously been investigated in detail.

Simulated phenotype:
\[ Y = \mu + a_x + a_{\text{mac}}x + \exp\left(0.5 \ln(\sigma_x^2) + 0.5a_{\text{ma}}\right)\epsilon \]
• \(a_x\), \(a_{\text{mac}}\) and \(a_{\text{ma}}\) were base genetic, macro-ES and micro-ES effects drawn from
\[ N \left(0, A \otimes \begin{bmatrix} \sigma^2_x & 0 & 0 \\ 0 & \sigma^2_{\text{mac}} & 0 \\ 0 & 0 & \sigma^2_{\text{ma}} \end{bmatrix} \right) \]
• \(x\) was random effect of herd drawn from \(N(0, \sigma_x^2)\)
• \(\sigma_x^2\) was environmental variance of exponential model
• \(\epsilon\) was scalar drawn from \(N(0,1)\)

Data structures:
<table>
<thead>
<tr>
<th>Name (symbol)</th>
<th>Half sib design</th>
<th>Distribution of offspring across macro-environments</th>
</tr>
</thead>
<tbody>
<tr>
<td>Even (■)</td>
<td>Balanced</td>
<td>Balanced</td>
</tr>
<tr>
<td>Uneven (●)</td>
<td>Unbalanced</td>
<td>Balanced</td>
</tr>
<tr>
<td>Unbalanced (▲)</td>
<td>Unbalanced</td>
<td>Unbalanced</td>
</tr>
</tbody>
</table>

Analysis:
• RN-DGHLMM were used to estimate all simulated components
• ASRemlR4.1

Macro- versus micro-environments
Macro-environments are definable and/or quantifiable environments often shared by groups of animals.
Micro-environments are undefinable and individual environments.