
Appendix 1

Figure A1. Species–area curves for each of the four sites in shrublands near Eneabba, SW Australia; black lines are mean values and grey shaded area encloses the 5th and 95th percentile limits (assessed via permutation). Vertical lines highlight the 1 and 3 m scales we analyse.
Figure A2. Rank abundance (no. of individuals in plot) of species across all sites coloured by (left) significant departures from the null model at a distance of 0–1 m (black = depart, white = not depart, grey = species with n < 30 individuals) and (right) whether a species is an accumulator (blue), neutral (green) or a repeller (red) at 1 m. Points in grey were not included in statistical analyses.
Figure A3. Local dominance, $L$ (mean proportion of conspecifics among individuals within some distance of a focal individual; Wang et al. 2016) curves for each of the four sites. Focal distances at 1 and 3 m are highlighted by grey shading.
Table A1. \( \chi^2 \)-tests of independence between species life-history traits and departure from the null ISAR model at a scale of 1 m. p-values assessed via Monte Carlo simulation (\( n = 1 \times 10^4 \)) as in a number of cases there were very low or zero cell values in the cross-table; no familywise correction used. Values significant at \( \alpha = 0.05 \) in bold.

<table>
<thead>
<tr>
<th>Site</th>
<th>Trait</th>
<th>( \chi^2 )</th>
<th>Simulated p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Crest</td>
<td>Regeneration mode</td>
<td>2.684</td>
<td>0.120</td>
</tr>
<tr>
<td></td>
<td>Life-form</td>
<td>8.6521</td>
<td><strong>0.024</strong></td>
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<tr>
<td></td>
<td>Seedbank storage</td>
<td>2.780</td>
<td>0.141</td>
</tr>
<tr>
<td>Laterite</td>
<td>Regeneration mode</td>
<td>3.969</td>
<td>0.092</td>
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<tr>
<td></td>
<td>Life-form</td>
<td>6.028</td>
<td>0.083</td>
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<tr>
<td></td>
<td>Seedbank storage</td>
<td>5.521</td>
<td><strong>0.037</strong></td>
</tr>
<tr>
<td>Limestone</td>
<td>Regeneration mode</td>
<td>7.673</td>
<td><strong>0.008</strong></td>
</tr>
<tr>
<td></td>
<td>Life-form</td>
<td>6.983</td>
<td>0.135</td>
</tr>
<tr>
<td></td>
<td>Seedbank storage</td>
<td>6.5359</td>
<td><strong>0.025</strong></td>
</tr>
<tr>
<td>Swale</td>
<td>Regeneration mode</td>
<td>0.008</td>
<td>1.000</td>
</tr>
<tr>
<td></td>
<td>Life-form</td>
<td>0.881</td>
<td>1.000</td>
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<tr>
<td></td>
<td>Seedbank storage</td>
<td>3.242</td>
<td>0.108</td>
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<td>All sites pooled</td>
<td>Regeneration mode</td>
<td>7.270</td>
<td><strong>0.012</strong></td>
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<td></td>
<td>Life-form</td>
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<td>0.286</td>
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<td></td>
<td>Seedbank storage</td>
<td>0.826</td>
<td>0.420</td>
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</table>
Table A2. Kruskal–Wallis ($\chi^2$) tests of independence between species ($n \geq 30$) spatial pattern ($L$), abundance ($n$) and departure from the null ISAR model at a scale of 1 m. We assessed these associations via non-parametric tests as in some cases the number in each pattern (group) is highly unbalanced; no familywise correction used. Values significant at $\alpha = 0.05$ in bold.

<table>
<thead>
<tr>
<th>Site</th>
<th>Metric</th>
<th>No. accept</th>
<th>No. depart</th>
<th>Median accept</th>
<th>Median depart</th>
<th>$\chi^2$</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Crest</td>
<td>$n$</td>
<td>34</td>
<td>16</td>
<td>37.96-520</td>
<td>78-184-688</td>
<td>4.953</td>
<td>0.026</td>
</tr>
<tr>
<td></td>
<td>$L$</td>
<td>34</td>
<td>16</td>
<td>0.000-0.022-0.074-</td>
<td>0.00-0.033-0.092</td>
<td>2.121</td>
<td>0.145</td>
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<td>Laterite</td>
<td>$n$</td>
<td>34</td>
<td>16</td>
<td>33.86-688</td>
<td>42-322-1276</td>
<td>4.725</td>
<td>0.030</td>
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<tr>
<td></td>
<td>$L$</td>
<td>34</td>
<td>16</td>
<td>0.00-0.014-0.063</td>
<td>0.005-0.034-0.149</td>
<td>4.953</td>
<td>0.026</td>
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<tr>
<td>Limestone</td>
<td>$n$</td>
<td>30</td>
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<td>45.133-939</td>
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<td>0.492</td>
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<tr>
<td></td>
<td>$L$</td>
<td>30</td>
<td>10</td>
<td>0.014-0.057-0.162</td>
<td>0.020-0.060-0.115</td>
<td>0.009</td>
<td>0.925</td>
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<tr>
<td>Swale</td>
<td>$n$</td>
<td>61</td>
<td>4</td>
<td>35.122-579</td>
<td>61-144-464</td>
<td>0.126</td>
<td>0.723</td>
</tr>
<tr>
<td></td>
<td>$L$</td>
<td>61</td>
<td>4</td>
<td>0.004-0.016-0.066</td>
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<td>Pooled</td>
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<td>8.467</td>
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<tr>
<td></td>
<td>$L$</td>
<td>159</td>
<td>46</td>
<td>0.001-0.021-0.126</td>
<td>0.003-0.033-0.136</td>
<td>5.742</td>
<td>0.017</td>
</tr>
</tbody>
</table>

$n = \text{plot-level abundance, } L = \text{fraction of conspecifics within 1 m of a focal individuals, No. accept} = \text{number of species not departing from the null IP model, No. depart} = \text{number of species departing from the null IP model. Median accept/depart are the median values for the metrics (5th percentile-median-95th percentile).}
Table A3. Details of the sub-communities at each site identified via model-based clustering using Gaussian finite mixture models (Fig. 5); $k$ = number of clusters (groups), $n$ = total number of species evaluated, ‘Shape’ describes the geometric nature of the clusters (Fraley and Raftery 2002): VVI = diagonal, varying volume and shape; VII (spherical, varying volume), EII = spherical, equal volume; BIC is the Bayesian information criterion.

<table>
<thead>
<tr>
<th>Distance (m)</th>
<th>1</th>
<th></th>
<th>3</th>
<th></th>
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</thead>
<tbody>
<tr>
<td></td>
<td>$k$ ($n$)</td>
<td>Shape</td>
<td>BIC</td>
<td>$k$ ($n$)</td>
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<tr>
<td>Crest</td>
<td>2 (50)</td>
<td>VVI</td>
<td>-7363.8</td>
<td>2 (50)</td>
</tr>
<tr>
<td>Laterite</td>
<td>4 (50)</td>
<td>EII</td>
<td>-7750.9</td>
<td>4 (50)</td>
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<tr>
<td>Limestone</td>
<td>2 (40)</td>
<td>VII</td>
<td>-5327.9</td>
<td>3 (40)</td>
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<tr>
<td>Swale</td>
<td>2 (65)</td>
<td>VII</td>
<td>-12698.9</td>
<td>2 (65)</td>
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</tbody>
</table>