

## Supplementary Material

### **Can flexible timing of harvest for translocation reduce the impact on fluctuating source populations?**

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## Supplementary material S1. Site selection details

We selected 540 survey sites (9-ha each). Through the selection process we aimed to adequately represent all possible combinations of Mallee Emu-wren state covariates. There were 120 unique combinations of these covariates (TSF \* ELEV \* EVC \* GYPSUM \* PERC\_TM = 5 \* 3 \* 2 \* 2 \* 2 = 120; Table 3). TWI was not included in this calculation because TWI was not included as a covariate until after the completion of site selection and surveys. Although GYPSUM and PERC\_TM were analysed as continuous covariates, for the site selection process we binned each of these covariates into 'high' or 'low'.

If we allocated survey sites evenly across all 120 unique combinations, we would have surveyed ~4.5 sites per unique combination. Instead, we chose to increase the number of sites for more common combinations of covariates, at the expense of rarer combinations. Given that the most common combinations in the Study Area would have the greatest effect on the final population estimate, we deemed it appropriate to attempt to increase the precision of density estimates for these combinations. We used the following formula to determine the final number of survey sites per unique combination of covariates:

$$x_{i...j} = \# \text{ sites total (540)} \times \frac{y_{i...j}}{\text{total area potential habitat}}$$

Where  $y$  is the area covered by each unique combination for  $j$  number of unique combinations

$$\text{sites required}_i = \frac{(\log(x_i) + 1)}{\sum (\log(x_{i...j}) + 1)}$$

The  $\log(x) + 1$  transformation ensured that rarer combinations still received adequate replication and that all combinations were surveyed. The distribution of sites in relation to each of the environmental covariates is shown in Figure S1.

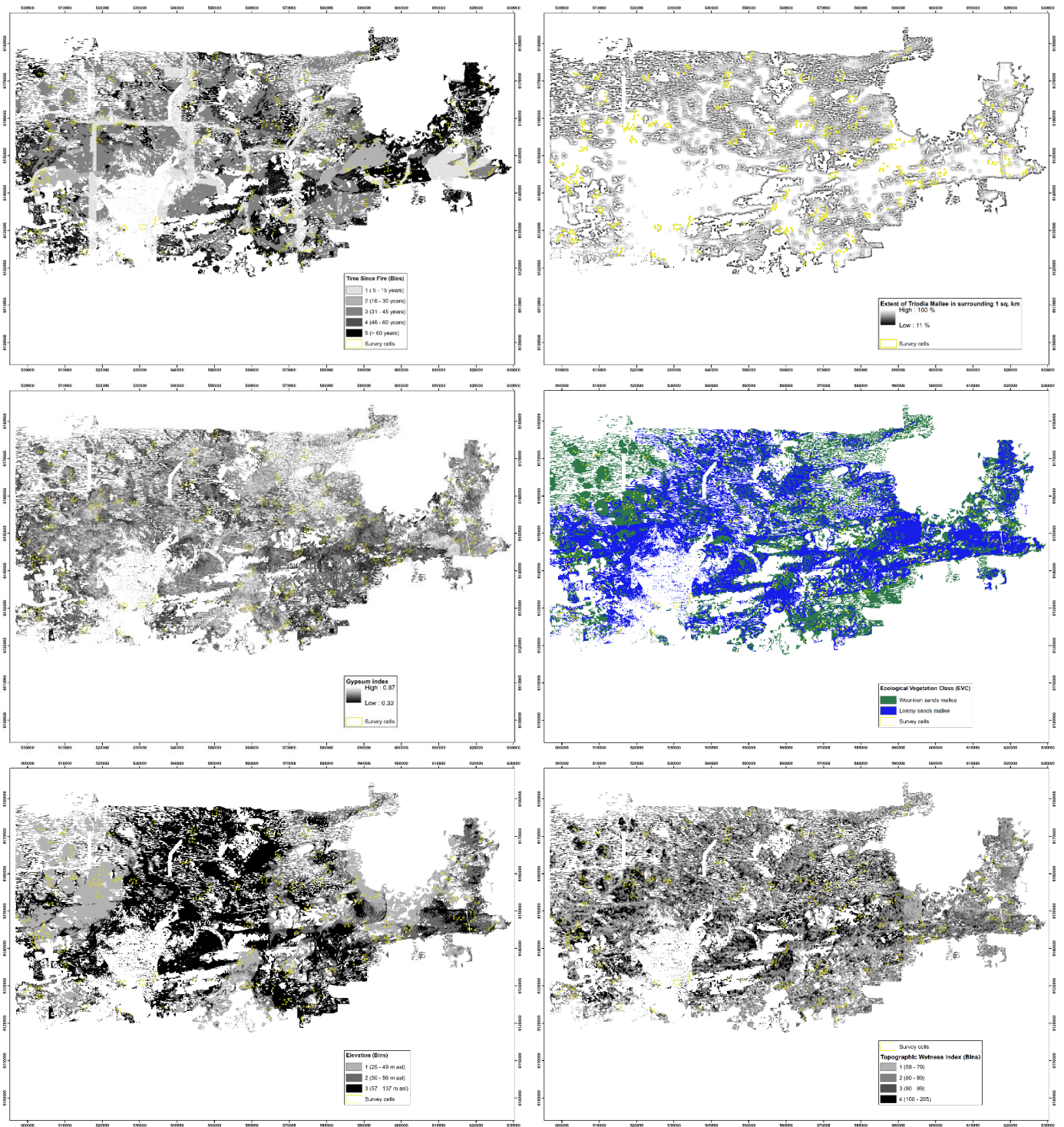


Figure S1. Map of Study Area showing the distribution of the 540 survey sites in relation to each Mallee Emu-wren state covariate. Eastings and Northings are shown at 10 km intervals.

**Table S1. Requirements for effective N-mixture modelling including how requirements were met in this study**

Pre-requisite for effective model	Rationale	Method by which pre-requisite is met
Stratified random sampling	<ul style="list-style-type: none"> <li>• Stratification required to capture variation in factors that affect bird density</li> <li>• Any bias favouring areas with Mallee Emu-wren records would inflate pop estimate</li> </ul>	<ul style="list-style-type: none"> <li>• Survey sites were stratified by six factors that are known to affect Mallee Emu-wren (Table 1)</li> <li>• Sites were selected randomly, with no focus on areas known to support Mallee Emu-wrens</li> </ul>
Environmental factors used have spatial data	<ul style="list-style-type: none"> <li>• To estimate population size, we predicted Mallee Emu-wren density across all potential habitat in the Study Area. For this, we needed spatial data across potential habitat</li> </ul>	<ul style="list-style-type: none"> <li>• All factors have associated spatial data that will allow us to predict Mallee Emu-wren density across the extent of potential habitat in the Study Area.</li> </ul>
Survey sites vary in Mallee Emu-wren density	<ul style="list-style-type: none"> <li>• Mallee Emu-wrens are territorial with well-defined home-range boundaries during breeding season. To identify and model density differences between survey sites, sites must be large enough to incorporate multiple home-ranges.</li> </ul>	<ul style="list-style-type: none"> <li>• Sites are 9-ha. Brown (2011) found Mallee Emu-wren home-ranges of ~5 ha. Although this is likely to be an underestimate, 9-ha was the largest practical site size in this study as we required that environmental covariates were consistent across the site</li> </ul>
Birds do not move between sites	<ul style="list-style-type: none"> <li>• If the same bird is counted in multiple sites, the population estimate will be inflated</li> </ul>	<ul style="list-style-type: none"> <li>• Site edges are separated by &gt; 300 m (site centres &gt; 600 m)</li> <li>• In any cases where Mallee Emu-wrens were detected &lt; 500 m apart and in adjacent sites, but on different survey days, one of these sites would be removed from the study to avoid any potential for counting the same bird in multiple sites (this did not occur)</li> </ul>
Survey extent: survey does not count birds outside the site	<ul style="list-style-type: none"> <li>• If birds from outside the survey area are counted as within the survey area, the population estimate will be inflated</li> </ul>	<ul style="list-style-type: none"> <li>• Surveyors recorded the precise location at which birds were first detected. This location is later checked against spatial data of site boundaries to confirm all recorded birds were first detected within the survey site</li> </ul>
Individual birds are not counted twice in a survey	<ul style="list-style-type: none"> <li>• This would lead to inflated estimates of density and population size</li> </ul>	<ul style="list-style-type: none"> <li>• Where multiple groups of birds are recorded in a site, surveyors marked the location of each group of birds and confirmed the independence of groups at the end of the survey period</li> </ul>
Sites are surveyed multiple times	<ul style="list-style-type: none"> <li>• Multiple site surveys are required to model detectability of Mallee Emu-wrens and factors that affect detectability</li> </ul>	<ul style="list-style-type: none"> <li>• All sites were surveyed at least twice, with a subset surveyed four times to inform the detectability model</li> </ul>
Mallee Emu-wrens do not die or produce offspring between surveys	<ul style="list-style-type: none"> <li>• Any changes to the true density in the site between surveys would increase the error in detectability models and therefore in the final population size</li> </ul>	<ul style="list-style-type: none"> <li>• All surveys were undertaken within a single season, to reduce the effect of bird breeding and mortality on results</li> <li>• Rather than analysing the number of individuals, we analysed the number of groups. Approximately 90 % of groups where the number of individuals was confirmed contained two individuals. To estimate population size, we modelled the number of groups and multiplied the result by two.</li> </ul>
Mallee Emu-wrens do not move in or out of the site between surveys	<ul style="list-style-type: none"> <li>• If Mallee Emu-wrens are not always present in the site when the site is surveyed, detectability will be under-estimated. This issue is due to birds with home-range centres outside the site being recorded within the site due to a partially overlapping home-range (Kéry and Royle 2015).</li> </ul>	<ul style="list-style-type: none"> <li>• Each site was given a 50 m buffer on all sides. For all analyses, i.e. when calculating Mallee Emu-wren detectability and density per ha, the effective survey area is considered as 16 ha (400 x 400 m), rather than the 9 ha (300 x 300 m) surveyed.</li> </ul>
Bird detections are independent of one another	<ul style="list-style-type: none"> <li>• N-mixture models are founded on the assumption that the detectability of birds is not affected by the presence of neighbouring birds and that individuals are independent of one another</li> </ul>	<ul style="list-style-type: none"> <li>• We have used bird group, rather than the individual bird in analysis. Whilst bird groups are likely to be independent, individuals within a group violate the assumption of independence.</li> </ul>

**Table S2. Factors affecting Mallee Emu-wren density. Model comparison for detection and state models using AIC. When comparing detection models, we did not include any covariates in the state component of the model. WIND was the only important covariate out of all the covariates included below. When comparing state models, we included WIND as a covariate in the detection component of the model. The best model is shown in bold.  $\Delta$ AIC for all models with  $\Delta$ AIC < 2 are also shown in bold**

<b>Model Number</b>	<b>Model parameters</b>	<b><math>\Delta</math>AIC</b>
<b>Detection models</b>		
<b>Model 1</b>	<b>WIND</b>	<b>0.00</b>
<b>Model 2</b>	TIME SINCE SUNRISE	5.10
Model 3	SEASON	7.40
Model 4	OBSERVER SKILL	25.40
<b>State models</b>		
<i>Additive models</i>		
Model 1	TSF + ELEV + GYPSUM + EVC + TWI + PERC_TM	5.20
Model 2	BEST ADDITIVE 5 PREDICTORS	3.72
Model 3	BEST ADDITIVE 4 PREDICTORS	3.24
Model 4	BEST ADDITIVE 3 PREDICTORS	3.20
Model 5	BEST ADDITIVE 2 PREDICTORS	3.53
Model 6	BEST SOLE ADDITIVE PREDICTOR	5.70
<i>Interaction models</i>		
<b>Model 7</b>	TSF * ELEV	<b>1.14</b>
Model 8	TSF * GYPSUM	7.59
Model 9	TSF * TWI	6.73
Model 10	TSF * PERC_TM	4.91
Model 11	TSF * EVC	5.82
Model 12	ELEV * GYPSUM	8.64
Model 13	ELEV * TWI	4.19
Model 14	ELEV * PERC_TM	6.81
Model 15	ELEV * EVC	10.93
Model 16	GYPSUM * TWI	8.34
Model 17	GYPSUM * PERC_TM	6.89
Model 18	GYPSUM * EVC	11.45
Model 19	TWI * PERC_TM	10.97
Model 20	TWI * EVC	8.32
<i>Interaction models with additive terms</i>		
<b>Model 21</b>	<b>TSF * ELEV + 4 ADDITIVE PREDICTORS</b>	<b>0.00</b>
Model 22	TSF * ELEV + 3 ADDITIVE PREDICTORS	<b>0.07</b>
Model 23	TSF * ELEV + 2 ADDITIVE PREDICTORS	<b>0.35</b>
Model 24	TSF * ELEV + 1 ADDITIVE PREDICTOR	<b>0.87</b>

**Table S3. Co-efficients and standard errors of model parameters in the best model according to AIC. Important covariates are shown in bold (i.e. estimate +/- 95% confidence interval does not overlap zero)**

Model parameter	Mallee emu-wren	
	Co-efficient	SE
<i>Detection model</i>		
Intercept	-0.202	0.546
<b>WIND</b>	<b>-0.334</b>	<b>0.127</b>
<i>State model – remote sensed variables</i>		
<b>Intercept</b>	<b>-6.313</b>	<b>2.930</b>
<b>TSF</b>	<b>1.645</b>	<b>0.727</b>
ELEV	0.459	0.354
<b>TSF * ELEV</b>	<b>-0.846</b>	<b>0.326</b>
GYP SUM	5.227	3.566
PERC_TM	0.015	0.012
<b>EVC</b>	<b>0.750</b>	<b>0.381</b>
TWI	-0.258	0.178

#### Reference

Brown, S. (2011). Mallee Emu-wren (*Stipiturus mallee*): multi-scale habitat requirements and population structure. Ph.D. Thesis. Deakin University, Melbourne, Vic., Australia.