NSW NATIONAL PARKS & WILDLIFE SERVICE

River Red Gum Ecological Thinning Trial

Monitoring report 2021 Appendices

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Contents

1. Photo points 1
2. Description of model summaries 6
   - 2.1 Explanatory variables 6
   - 2.2 Candidate models 6
   - 2.3 Descriptions of model terms 7
3. Model summaries: Tree parameters 10
   - 3.1 Tree growth rates 10
   - 3.2 Tree mortality 13
4. Model summaries: Coppice 16
5. Model summaries: Recruitment 19
   - 5.1 Germinant presence–absence 19
   - 5.2 Seedling abundance 22
6. Model summaries: Canopy condition 25
   - 6.1 Individual tree crown extent 25
   - 6.2 Visually assessed canopy cover 28
   - 6.3 Remotely sensed canopy cover 31
7. Model summaries: Fuel hazard 34
   - 7.1 Overall fuel hazard 34
   - 7.2 Surface fuel hazard: litter depth 39
   - 7.3 Surface fuel hazard: litter cover 42
   - 7.4 Surface fuel hazard assessment 45
   - 7.5 Near surface fuel hazard: live near surface vegetation 50
   - 7.6 Near surface fuel hazard: dead near surface vegetation 50
   - 7.7 Near surface fuel hazard assessment 51
   - 7.8 Combined surface and near surface fuel hazard assessment 56
   - 7.9 Elevated fuel hazard: live elevated vegetation cover 60
   - 7.10 Elevated fuel hazard: dead elevated vegetation cover 60
   - 7.11 Elevated fuel hazard assessment 61
8. Model summaries: Floristics 66
   - 8.1 Native plant species richness 66
   - 8.2 Exotic plant species richness 69
   - 8.3 Plant cover 71
9. Model summaries: Birds 72
   - 9.1 Bird species richness 72

10. Plant species list 76
  10.1 Native plant species list 76
  10.2 Exotic plant species list 84
11. Bird species list 89

1. Photo points

Photos from the floristic plots of a selection of sites for each survey year.

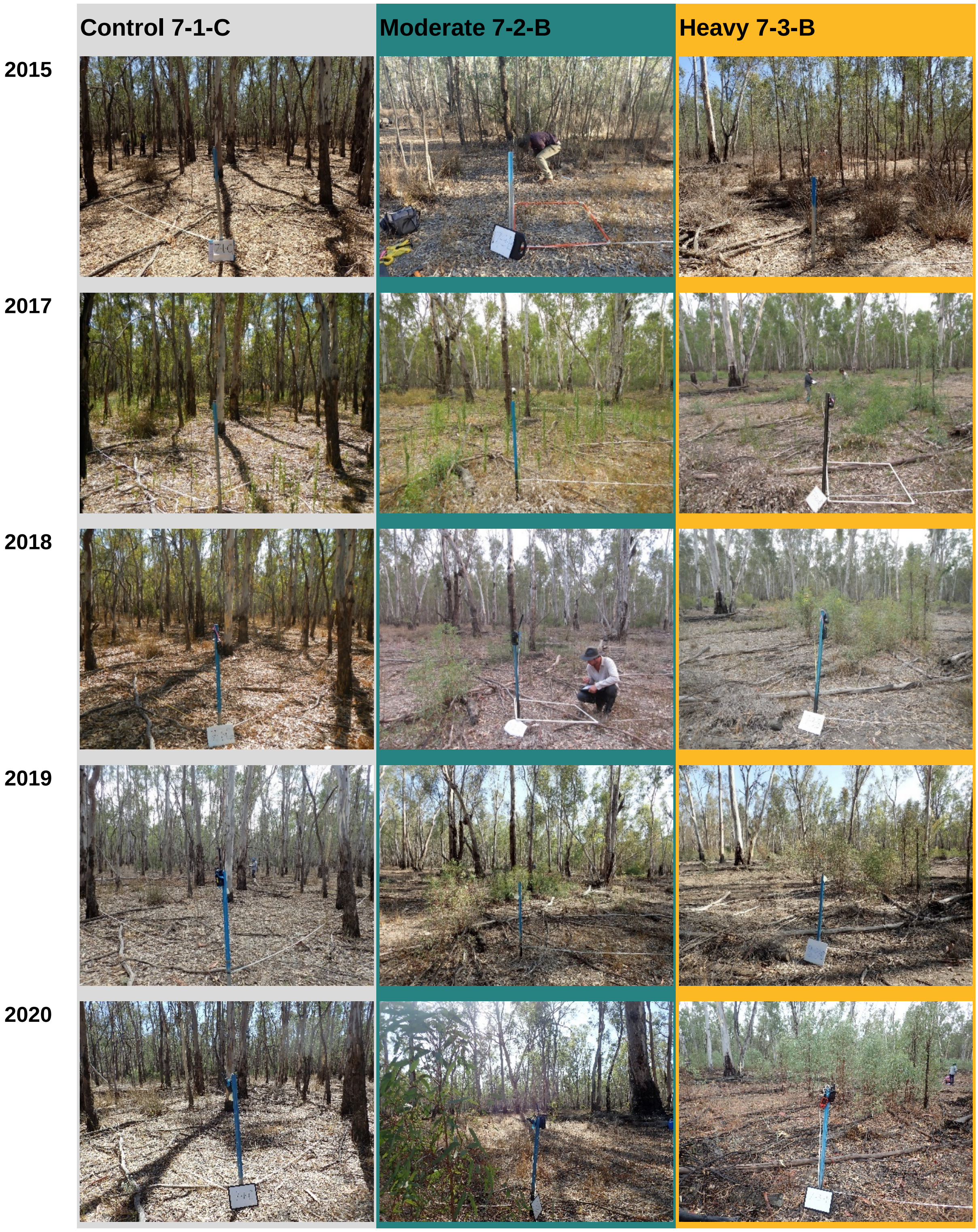
Site 1 – Site Quality 2

	Control 1-2-C	**Moderate 1-1-A**	**Heavy 1-3-B**
2015			
2017			
2018			
2019			
2020			

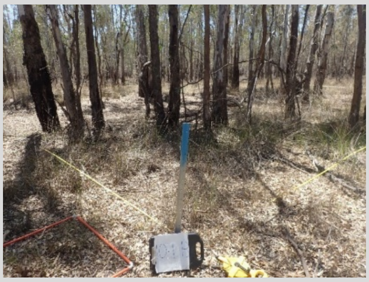
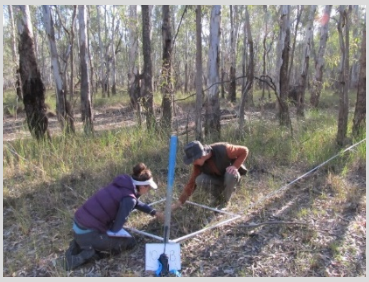
Site 2 – Site Quality 1

	Control 2-2-A	**Moderate 2-3-C**	**Heavy 2-1-C**
2015			
2017			
2018			
2019			
2020			

Site 7 – Site Quality 2



Site 10 – Site Quality 2

	Control 10-1-B	**Moderate 10-2-A**	**Heavy 10-3-B**
2015			
2017			
2018			
2019			
2020			

Site 22 – Site Quality 1

	Control 22-2-B	**Moderate 22-1-A**	**Heavy 22-3-C**
2015			
2017			
2018			
2019			
2020			

2. Description of model summaries

2.1 Explanatory variables

The labels for explanatory variables in each model are as follows:

- thinning = the proportion of trees removed by thinning, a value between 0 and 1
- initSD.log = the natural logarithm of initial stem density (trees per hectare)
- yrs.elapsed = the number of decimal years that had elapsed between the commencement of thinning on that site and the survey date
- site.quality = a factor for Site Quality 1 and Site Quality 2
- year.factor = a factor for the survey season in which the data were collected (2015, 2017, 2018, 2019 or 2020)
- site = a factor for the 22 sites
- siteplot = a factor for the 66 x 9 hectare plots
- subplot = a factor for the subsampled plot within each 9 hectare plot.

2.2 Candidate models

For most response variables several candidate models were considered. In the model summaries presented in Sections 3 to 9 below these are referred to by their model names, which are further described in Table 1. Where models deviate from these standard candidate models, further details are provided in the model summaries.

Table 1 Descriptions of model names

Model name	Model fixed effects	Model random effects	Effect being tested
4_way	y ~ poly(cbind(thinning, initSD.log, yrs.elapsed), 2) * site.quality + thinning * initSD.log * yrs.elapsed * site.quality	(1|year.factor) (1|site) (1|siteplot) (1|subplot)	Allows for the effect of thinning intensity to depend on initial stem density and for this relationship to change over time and differ among the site qualities.
4_way_noYrf	y ~ poly(cbind(thinning, initSD.log, yrs.elapsed), 2) * site.quality + thinning * initSD.log * yrs.elapsed * site.quality	(1|site) (1|siteplot) (1|subplot)	Allows for the effect of thinning intensity to depend on initial stem density and for this relationship to change over time and differ among the site qualities. Excluding random effect of year assumes there is no difference in trends due to specific survey years
3_3way	y ~ poly(cbind(thinning, initSD.log, yrs.elapsed), 2) * site.quality	(1|year.factor) (1|site) (1|siteplot) (1|subplot)	Removed the 4-way interaction between thinning, initial stem density, years since thinning and Site Quality. Allows for effect of (i) thinning to change over time and differ among Site Qualities; (ii) an underlying effect of initial stem density to vary over time that differs among Site Qualities; (iii) thinning to depend on initial stem densities and differ among Site Qualities

Model name	Model fixed effects	Model random effects	Effect being tested
2_3_way	y ~ poly(cbind(thinning, yrs.elapsed), 2) * site.quality + poly(cbind(thinning, yrs.elapsed), 2) * initSD.log.bin	(1|year.factor) (1|site) (1|siteplot) (1|subplot)	Removed the interaction between initial stem density * thinning and uses a three-category log binned measure of initial stem density. Allows for effect of thinning to changes over time and differs among Site Qualities and allows an underlying effect of initial stem density to vary over time that differs among Site Qualities
No_SDi	y ~ poly(cbind(thinning, yrs.elapsed), 2) * site.quality + poly(cbind(initSD.log, yrs.elapsed), 2) * site.quality	(1|year.factor) (1|site) (1|siteplot) (1|subplot)	Removes the initial stem density * thinning interaction Allows for effect of thinning to changes over time and differs among Site Qualities and allows an underlying effect of initial stem density to vary over time that differs among Site Qualities

2.3 Descriptions of model terms

In the model summaries presented in Sections 3 to 9 below the model terms are abbreviated according to the notations described in Table 2.

Table 2 Summary of model terms

Model term	Model name	Model term label in model summary
Site quality	All models	site.qualitySQ2
Initial stem density	4_way and 3_3way	poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.0
	2_3_way	initSD.log.binModerate initial density (500-850/ha) initSD.log.binHigh initial density (>850/ha)
Initial stem density^2	4_way and 3_3way	poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.2.0
	2_3_way	not included
Years elapsed	4_way and 3_3way	poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.1
	2_3_way	poly(cbind(thinning, yrs.elapsed), 2)0.1
Years elapsed^2	4_way and 3_3way	poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.2
	2_3_way	poly(cbind(thinning, yrs.elapsed), 2)0.2
Thinning intensity	4_way and 3_3way	poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.0
	2_3_way	poly(cbind(thinning, yrs.elapsed), 2)1.0
Thinning intensity^2	4_way and 3_3way	poly(cbind(thinning, initSD.log, yrs.elapsed), 2)2.0.0
	2_3_way	poly(cbind(thinning, yrs.elapsed), 2)2.0
Initial stem density * site quality	4_way and 3_3way	poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.0:site.qualitySQ2 poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.2.0:site.qualitySQ2

Model term	Model name	Model term label in model summary
Initial stem density^2 * site quality	2_3_way	not included
Years elapsed * site quality and Years elapsed^2 * site quality	4_way and 3_3way	poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.1:site.qualitySQ2 poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.2:site.qualitySQ2
	2_3_way	poly(cbind(thinning, yrs.elapsed), 2)0.1:site.qualitySQ2 poly(cbind(thinning, yrs.elapsed), 2)0.2:site.qualitySQ2
Initial stem density * years elapsed	4_way and 3_3way	poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.1 (no polynomial interactions included)
	2_3_way	poly(cbind(thinning, yrs.elapsed), 2)0.1:initSD.log.binModerate initial density (500-850/ha) poly(cbind(thinning, yrs.elapsed), 2)0.1:initSD.log.binHigh initial density (>850/ha)
Initial stem density ^{2}* years elapsed	4_way and 3_3way	Not included
	2_3_way	poly(cbind(thinning, yrs.elapsed), 2)0.2:initSD.log.binModerate initial density (500-850/ha) poly(cbind(thinning, yrs.elapsed), 2)0.2:initSD.log.binHigh initial density (>850/ha)
Initial stem density * years elapsed * site quality	4_way and 3_3way	poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.1:site.qualitySQ2
	2_3_way	not included
Thinning intensity * site quality Thinning intensity^2 * site quality	4_way and 3_3way	poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.0:site.qualitySQ2 poly(cbind(thinning, initSD.log, yrs.elapsed), 2)2.0.0:site.qualitySQ2
	2_3_way	poly(cbind(thinning, yrs.elapsed), 2)1.0:site.qualitySQ2 poly(cbind(thinning, yrs.elapsed), 2)2.0:site.qualitySQ2
Thinning intensity * initial stem density Thinning intensity^2 * initial stem density	4_way and 3_3way	poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.1.0 (no polynomial interactions included)
	2_3_way	poly(cbind(thinning, yrs.elapsed), 2)1.0:initSD.log.binModerate initial density (500-850/ha) poly(cbind(thinning, yrs.elapsed), 2)1.0:initSD.log.binHigh initial density (>850/ha) poly(cbind(thinning, yrs.elapsed), 2)2.0:initSD.log.binModerate initial density (500-850/ha) poly(cbind(thinning, yrs.elapsed), 2)2.0:initSD.log.binHigh initial density (>850/ha)
Thinning intensity * years elapsed	4_way and 3_3way	poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.1
	2_3_way	poly(cbind(thinning, yrs.elapsed), 2)1.1
Thinning intensity * initial stem density * site quality	4_way and 3_3way	poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.1.0:site.qualitySQ2
	2_3_way	not included

Model term	Model name	Model term label in model summary
Thinning intensity * years elapsed * site quality	4_way and 3_3way	poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.1:site.qualitySQ2
	2_3_way	poly(cbind(thinning, yrs.elapsed), 2)1.1:site.qualitySQ2
Thinning intensity * years elapsed * initial stem density	4_way	thinning:initSD.log:yrs.elapsed
	3_3way	not included
	2_3_way	poly(cbind(thinning, yrs.elapsed), 2)1.1:initSD.log.binModerate initial density (500-850/ha) poly(cbind(thinning, yrs.elapsed), 2)1.1:initSD.log.binHigh initial density (>850/ha)
Thinning intensity * initial stem density * years elapsed * site quality	4_way	site.qualitySQ2:thinning:initSD.log:yrs.elapsed
	3_3way and 2_3_way	not included

3. Model summaries: Tree parameters

3.1 Tree growth rates

Table 3 Model fitting summary: tree growth rate by tree size

Response	Average growth per year – change in tree diameter at breast height in millimetres between initial and most recent surveys, divided by the number of decimal years passed between survey dates Continuous positive variable
Response transformation used	No transformation
R package and function	Lmer from lme4
Distribution used	Gaussian
Outliers removed	16 values: 13 that were less than -5mm/yr and 3 that were >25mm/yr
Reported model formula	lmer(growth.per.year ~ poly(cbind(thinning, initSD.log, diameter.first.m), 2) * site.quality + thinning * initSD.log * diameter.first.m * site.quality + (1|site) + (1|siteplot), data = dat.outlier)
Random factors	Site (a factor over 22 sites) Siteplot (a factor over 66 plots) Tree not included because no replicates across year
Other transformations compared	Log-transformed
Other models attempted	Without outliers removed No other distributions compared
Confidence comments	Moderate to high confidence: • No issues with convergence • Failed Kurtosis-Skewness test, with minor deviation from expected • Failed outlier test • Very few convergence and fit warnings in prediction simulations (<5% of 999)

Model summary 1 Average tree growth rate by tree size

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: growth.per.year ~ poly(cbind(thinning, initSD.log, diameter.first.m),
    2) * site.quality + thinning * initSD.log * diameter.first.m *      site.quality + (1 | site) + (1 | siteplot)
   Data: dat.outlier
Control: lmerControl(check.scaleX = "ignore", check.rankX = "silent.drop.cols")

REML criterion at convergence: 9113.6

Scaled residuals:
    Min      1Q  Median      3Q     Max
-3.2113 -0.6143 -0.0479  0.5526  6.2794
```

```
Random effects:
 Groups   Name        Variance Std.Dev.
 siteplot (Intercept) 1.0586   1.0289
 site     (Intercept) 0.8585   0.9266
 Residual             6.7770   2.6033
Number of obs: 1927, groups:  siteplot, 66; site, 22

Fixed effects:
                                                               Estimate Std. Error         df t value Pr(>|t|)
(Intercept)                                                     5.15124    5.69694 1898.33757   0.904   0.3660
poly(cbind(thinning, initSD.log, diameter.first.m), 2)1.0.0                          47.99544  211.04954 1889.07141
0.227   0.8201
poly(cbind(thinning, initSD.log, diameter.first.m), 2)2.0.0           -20.45871   11.48779   47.93603  -1.781   0.0813
.
poly(cbind(thinning, initSD.log, diameter.first.m), 2)0.1.0            36.02706   21.64029  276.41082   1.665   0.0971
.
poly(cbind(thinning, initSD.log, diameter.first.m), 2)1.1.0           -206.75105  955.08020  136.72521  -0.216
0.8289
poly(cbind(thinning, initSD.log, diameter.first.m), 2)0.2.0                          -6.20631   13.40948   46.07833  -0.463
0.6457
poly(cbind(thinning, initSD.log, diameter.first.m), 2)0.0.1           -12.13846  106.82879 1888.69997  -0.114
0.9095
poly(cbind(thinning, initSD.log, diameter.first.m), 2)1.0.1                          88.44845 4090.07037 1887.89962
0.022   0.9827
poly(cbind(thinning, initSD.log, diameter.first.m), 2)0.1.1            96.75992  302.37975 1859.91697   0.320
0.7490
poly(cbind(thinning, initSD.log, diameter.first.m), 2)0.0.2             4.31904    3.94858 1862.86745   1.094   0.2742
site.qualitySQ2                                                 0.03055    7.01200 1897.03487   0.004   0.9965
poly(cbind(thinning, initSD.log, diameter.first.m), 2)1.0.0:site.qualitySQ2   68.40377  259.69398 1887.91225
0.263   0.7923
poly(cbind(thinning, initSD.log, diameter.first.m), 2)2.0.0:site.qualitySQ2   22.16987   19.13532   49.80925   1.159
0.2522
poly(cbind(thinning, initSD.log, diameter.first.m), 2)0.1.0:site.qualitySQ2  -23.95272   28.88203  198.22620  -
0.829   0.4079
poly(cbind(thinning, initSD.log, diameter.first.m), 2)1.1.0:site.qualitySQ2  558.78492 1191.73373  120.68785
0.469   0.6400
poly(cbind(thinning, initSD.log, diameter.first.m), 2)0.2.0:site.qualitySQ2    3.44649   16.56998   46.47196   0.208
0.8361
poly(cbind(thinning, initSD.log, diameter.first.m), 2)0.0.1:site.qualitySQ2   42.60762  130.72516 1884.57380
0.326   0.7445
poly(cbind(thinning, initSD.log, diameter.first.m), 2)1.0.1:site.qualitySQ2 1227.57767 4961.31364 1884.56173
0.247   0.8046
poly(cbind(thinning, initSD.log, diameter.first.m), 2)0.1.1:site.qualitySQ2 -152.57039  381.69071 1867.88192  -
0.400   0.6894
poly(cbind(thinning, initSD.log, diameter.first.m), 2)0.0.2:site.qualitySQ2    6.98690    5.55735 1871.35567   1.257
0.2088
thinning:initSD.log:diameter.first.m                                  -0.98094    4.66924 1887.86117  -0.210   0.8336
site.qualitySQ2:thinning:initSD.log:diameter.first.m                          -1.20281    5.74460 1884.02526  -0.209
0.8342
```

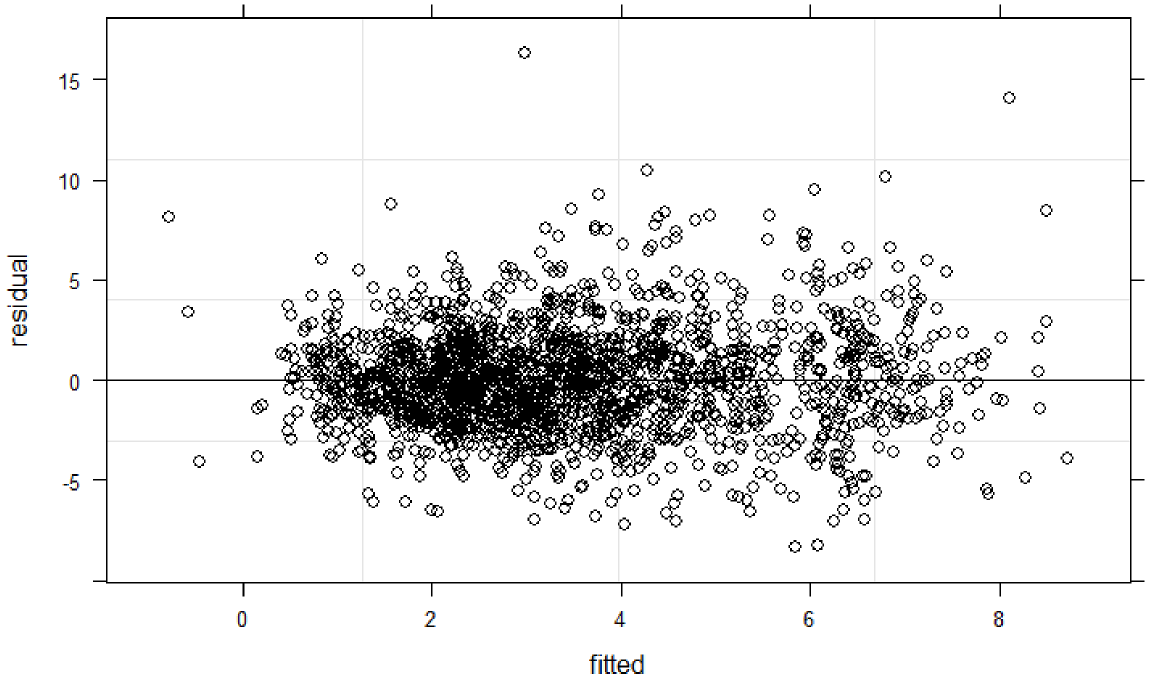


Figure 1 Fitted values and data residuals: average tree growth rate by tree size

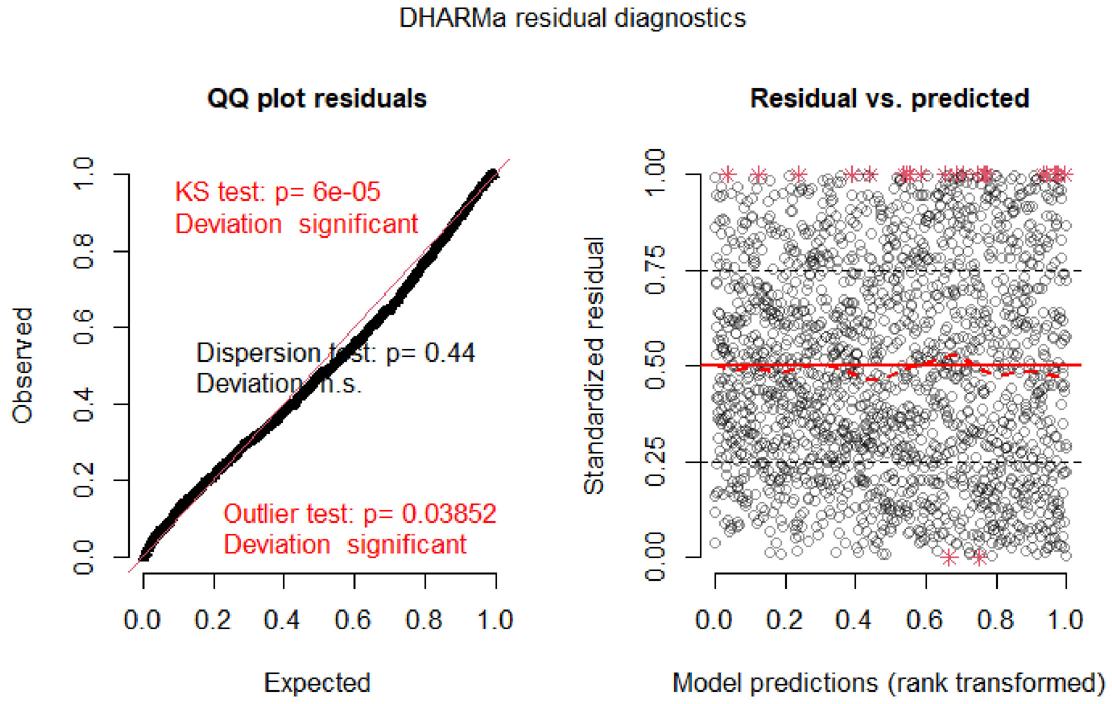


Figure 2 Simulated randomised quantile residuals: average tree growth rate by tree size

3.2 Tree mortality

Table 4 Model fitting summary: tree mortality

Response	Proportion of 50 trees per 9 hectare plot that were dead Modelled as the ratio of dead to live trees
Response transformation used	None
R package and function	glmer from lme4
Distribution used	Binomial
Outliers removed	None
Reported model formula	3_3way with no year factor
Random factors	Site (a factor over 22 sites) Siteplot (a factor over 66 plots)
Other transformations compared	None
Other models attempted	4_way: Max evals exceeded 3_3way: Boundary fit was singular 4_way with no year factor: Failed to converge No other distributions compared
Confidence comments	Moderate confidence: • No fit warnings • Conformed to all residual tests • Some non-convergence warnings in bootstrapped prediction interval simulations (~10% of 999)

Model summary 2 Tree mortality

```
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
 Family: binomial  ( logit )
Formula: deadlive ~ poly(cbind(thinning, initSD.log, yrs.elapsed), 2) *      site.quality + (1 | site) + (1 | siteplot)
   Data: dat
Control: glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 1e+05),
    check.scaleX = "ignore", check.rankX = "silent.drop.cols")

     AIC      BIC   logLik deviance df.resid 
  1414.8   1498.4   -685.4   1370.8      308 

Scaled residuals: 
    Min      1Q  Median      3Q     Max 
-1.8766 -0.4723 -0.0561  0.3736  2.2766 

Random effects:
 Groups   Name        Variance Std.Dev.
```

```
 siteplot (Intercept) 0.21017  0.4584
 site     (Intercept) 0.06779  0.2604
Number of obs: 330, groups:  siteplot, 66; site, 22

Fixed effects:
                                                          Estimate Std. Error z value Pr(>|z|)
(Intercept)                                                -2.22064    0.13073 -16.986  < 2e-16 ***
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.0              5.46823    1.65970   3.295 0.000985 ***
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)2.0.0             -0.60974    1.31562  -0.463 0.643034
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.0             -2.77914    2.31043  -1.203 0.229027
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.1.0            -36.78267   31.37024  -1.173 0.240983
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.2.0              0.47386    2.25275   0.210 0.833396
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.1             -1.40628    1.04393  -1.347 0.177945
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.1             -6.41064   19.09276  -0.336 0.737049
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.1             14.24507   17.13548   0.831 0.405793
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.2              0.74232    0.78691   0.943 0.345507
site.qualitySQ2                                              -0.13334    0.18473  -0.722 0.470412
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.0:site.qualitySQ2  -4.02998    2.18296  -1.846 0.064877 .
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)2.0.0:site.qualitySQ2  -1.10252    2.22105  -0.496 0.619616
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.0:site.qualitySQ2   2.12000    3.06489   0.692 0.489124
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.1.0:site.qualitySQ2  20.98765   43.91880   0.478 0.632740
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.2.0:site.qualitySQ2   2.21683    2.80917   0.789 0.430029
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.1:site.qualitySQ2   1.91182    1.45576   1.313 0.189091
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.1:site.qualitySQ2  -1.26869   26.17895  -0.048 0.961348
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.1:site.qualitySQ2   0.39427   21.33366   0.018 0.985255
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.2:site.qualitySQ2   0.04281    1.26812   0.034 0.973072
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

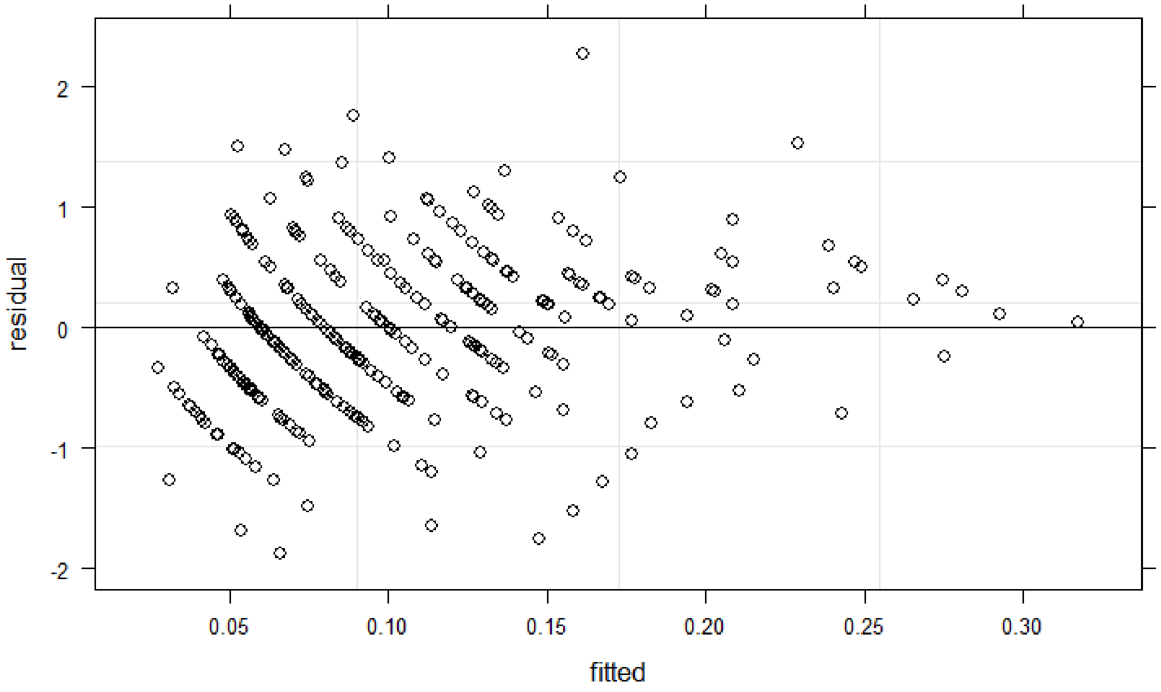


Figure 3 Fitted values and data residuals: tree mortality

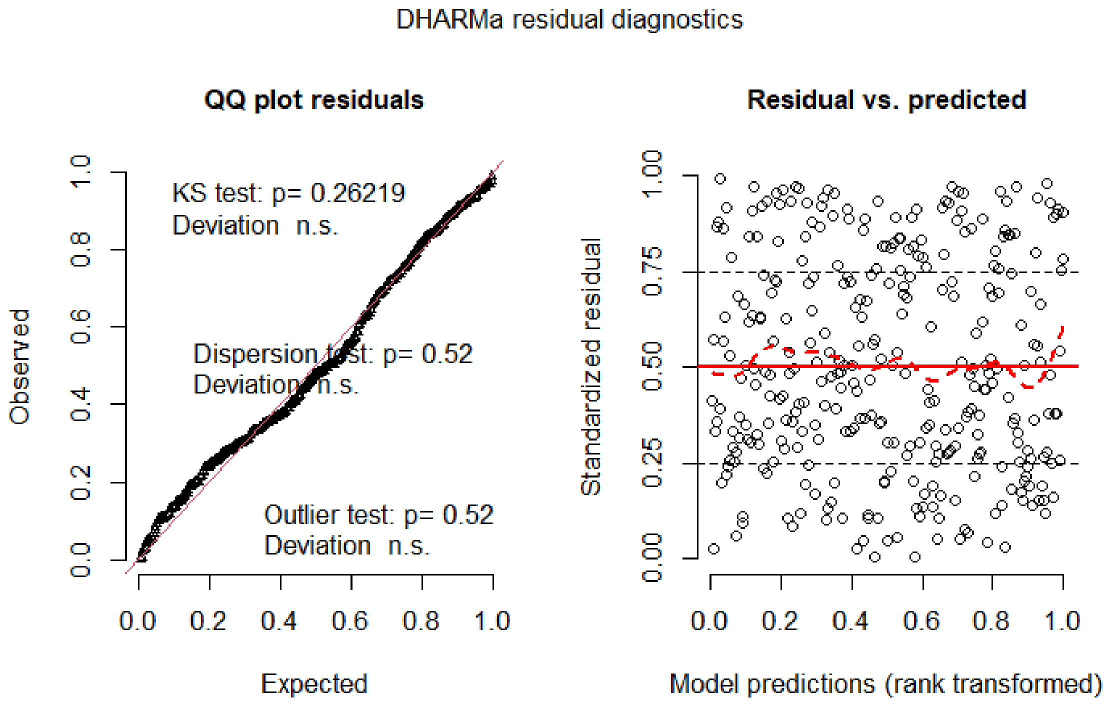


Figure 4 Simulated randomised quantile residuals: tree mortality

4. Model summaries: Coppice

Table 5 Model fitting summary: Abundance of coppiced stems

Response	Count of total seedling and sapling sized stems arising from stumps and pushed over saplings, from data collected in 2020–21 only – a positive integer
Response transformation used	No transformation applied
R package and function	glmmTMB function from glmmTMB package
Distribution used	Negative binomial distribution
Outliers removed	No outliers removed
Reported model formula	3_3way
Random factors	Only one random effect across site (a factor over 22 sites) because only one survey year of data analysed
Other transformations compared	Logged count was trialled for Gaussian distribution
Other models attempted	4_way Gaussian: Boundary fit is singular 4_way logged Gaussian: Boundary fit is singular 4_way poisson: Failed to converge 4_way negative binomial: Non-positive definite hessian
Confidence comments	Moderate to high confidence: • No fit warnings • Did not conform to the dispersion test, with minor deviation from expected • Some non-convergence warnings in bootstrapped prediction interval simulations (~15% of 999)

Model summary 3 Abundance of coppiced stems

```
Family: nbinom2  ( log )
Formula:          var ~ poly(cbind(thinning, initSD.log, yrs.elapsed), 2) * site.quality +      (1 | site)
Data: dat

     AIC      BIC   logLik deviance df.resid
  1463.1   1535.4   -709.6   1419.1      176

Random effects:

Conditional model:
 Groups Name        Variance  Std.Dev.
 site   (Intercept) 7.936e-13 8.909e-07
Number of obs: 198, groups:  site, 22

Dispersion parameter for nbinom2 family (): 0.429
```

```
Conditional model:
                                                  Estimate Std. Error z value Pr(>|z|)
(Intercept)                                        2.80484    0.30344   9.244  < 2e-16 ***
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.0               8.48814    5.77606   1.470 0.141687
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)2.0.0              -2.33276    3.12480  -0.747 0.455348
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.0               5.21880    3.64726   1.431 0.152463
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.1.0              74.96552   89.21721   0.840 0.400763
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.2.0              -4.50895    3.23757  -1.393 0.163712
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.1               9.84841    3.57345   2.756 0.005851 **
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.1             -93.20552   73.46236  -1.269 0.204530
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.1               0.79669   58.34829   0.014 0.989106
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.2              -1.05720    2.38780  -0.443 0.657945
site.qualitySQ2                                      0.08969    0.49807   0.180 0.857098
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.0:site.qualitySQ2  17.07218    6.55776   2.603 0.009232 **
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)2.0.0:site.qualitySQ2  -9.73442    4.55862  -2.135 0.032729 *
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.0:site.qualitySQ2  -0.49168    5.21933  -0.094 0.924947
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.1.0:site.qualitySQ2 102.56379  109.08201   0.940 0.347092
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.2.0:site.qualitySQ2  14.84782    4.08619   3.634 0.000279 ***
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.1:site.qualitySQ2 -16.78511    5.77678  -2.906 0.003665 **
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.1:site.qualitySQ2 159.52659   98.36228   1.622 0.104840
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.1:site.qualitySQ2 213.30371  106.51265   2.003 0.045219 *
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.2:site.qualitySQ2   9.18071    5.52602   1.661 0.096641 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

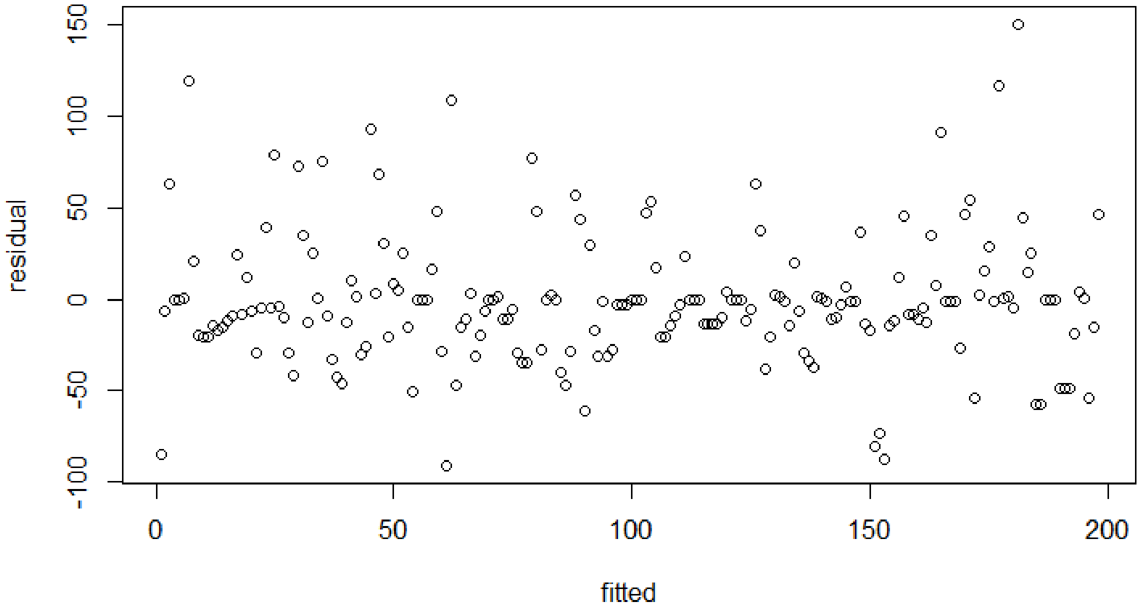


Figure 5 **Fitted values and data residuals: abundance of coppiced stems**

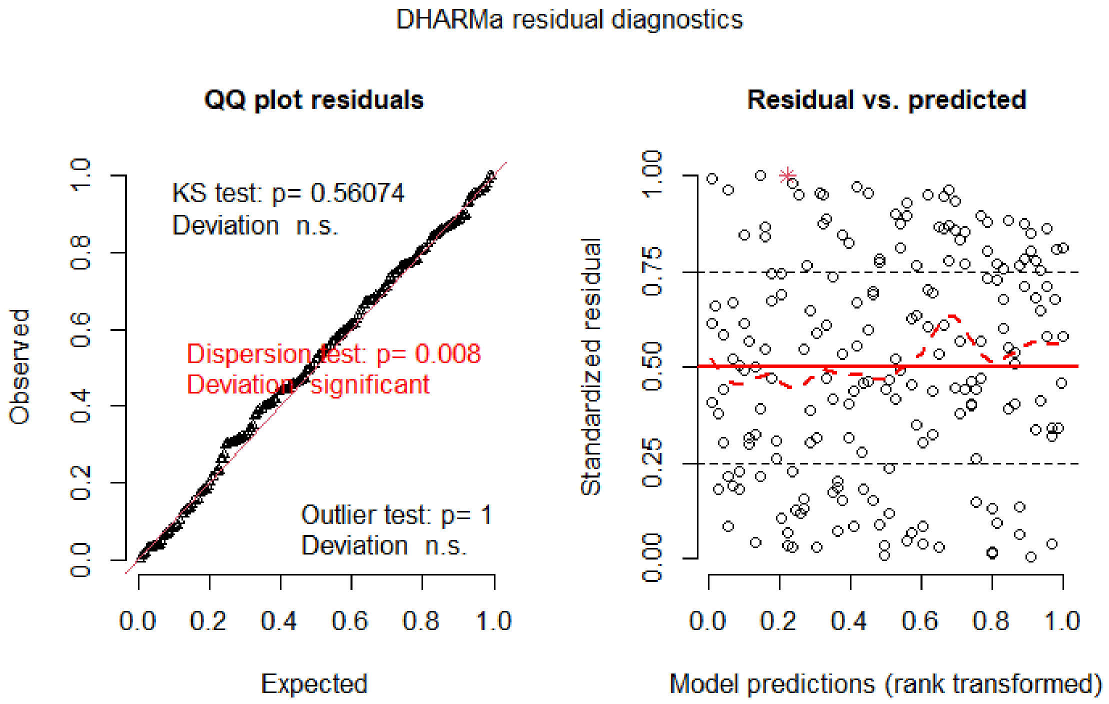


Figure 6 Simulated randomised quantile residuals: abundance of coppiced stems

5. Model summaries: Recruitment

5.1 Germinant presence–absence

Table 6 Model fitting summary: germinant presence–absence

Response	Binomial presence–absence for germinant presence in each 0.04 hectare subplot
Response transformation used	None
R package and function	glmer from package lme4
Distribution used	Binomial
Outliers removed	None
Reported model formula	germ.pres ~ thinning * yrs.elapsed * site.quality + initSD.log + (1|year.factor) + (1|site) + (1|siteplot) + (1|subplot)
Random factors	Site (a factor over 22 sites) Siteplot (a factor over 66 plots) Subplot (a factor over 198 subplots) Year.factor (a factor for each of the 5 survey years)
Other transformations compared	None
Other models attempted	A lot of difficulty fitting this model. Seemed like the main issue was the interaction of initial density with thinning. 4_way with four random effects: Failed to converge 3_way with four random effects: Failed to converge 3_way with no year as a random effect: No fit warnings, but bootstrapped simulations failed. 3_way with initSD.log as a three-category factor: Large eigenvalue ratio 4_way with no polynomial terms: Large eigenvalue ratio 2_3_way (i.e. thinning * yr * site.quality + thinning * initSD.log * site.quality) with four random effects: Failed to converge No other distributions compared
Confidence comments	Low to moderate confidence: • Difficulty finding a combination of explanatory variables that did not produce convergence or fit warnings • Passed all residual tests • Uncertainty that all the interactions have been appropriately represented in the simplified model • Approximately 40% of 999 prediction interval simulations had warnings about boundary (singular) fits, but <5% had warnings about model convergence

Model summary 4 Germinant presence–absence

```
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
 Family: binomial  ( logit )
Formula: germ.pres ~ thinning * yrs.elapsed * site.quality + initSD.log +
    (1 | year.factor) + (1 | site) + (1 | siteplot) + (1 | subplot)
   Data: dat
Control: glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 2e+05))

     AIC      BIC   logLik deviance df.resid
   606.5    670.1   -290.2    580.5      977

Scaled residuals:
    Min      1Q  Median      3Q     Max
-1.6713 -0.2871 -0.1544 -0.0634  5.0038

Random effects:
 Groups      Name        Variance Std.Dev.
 subplot     (Intercept) 1.4884   1.2200
 siteplot    (Intercept) 0.4326   0.6577
 site        (Intercept) 1.2321   1.1100
 year.factor (Intercept) 0.2453   0.4952
Number of obs: 990, groups:  subplot, 198; siteplot, 66; site, 22; year.factor, 5

Fixed effects:
                                     Estimate Std. Error z value Pr(>|z|)
(Intercept)                          -2.91154    3.95921  -0.735 0.462107
thinning                              1.69694    1.17859   1.440 0.149923
yrs.elapsed                           0.41787    0.16404   2.547 0.010852 *
site.qualitySQ2                      -3.44642    1.03384  -3.334 0.000857 ***
initSD.log                            0.06066    0.58589   0.104 0.917532
thinning:yrs.elapsed                 -1.28182    0.43734  -2.931 0.003379 **
thinning:site.qualitySQ2              1.91857    1.87730   1.022 0.306791
yrs.elapsed:site.qualitySQ2           0.05349    0.26627   0.201 0.840777
thinning:yrs.elapsed:site.qualitySQ2  0.15518    0.68159   0.228 0.819903
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

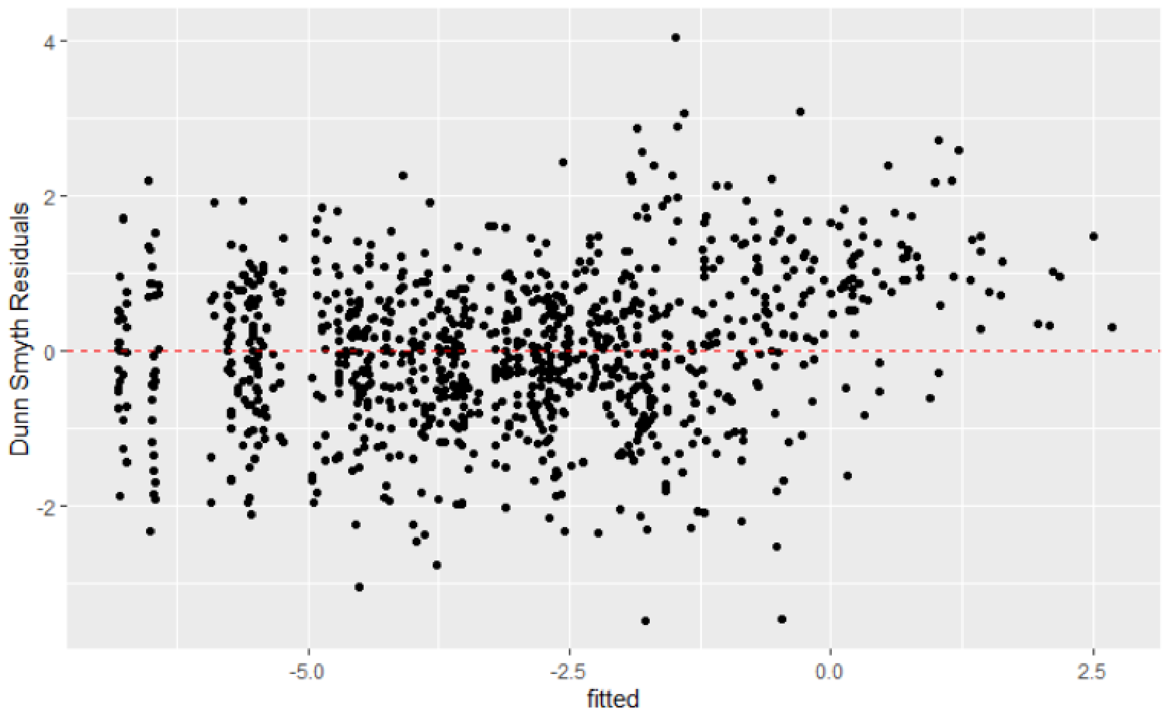


Figure 7 Dunn Smyth simulated residuals: germinant presence–absence

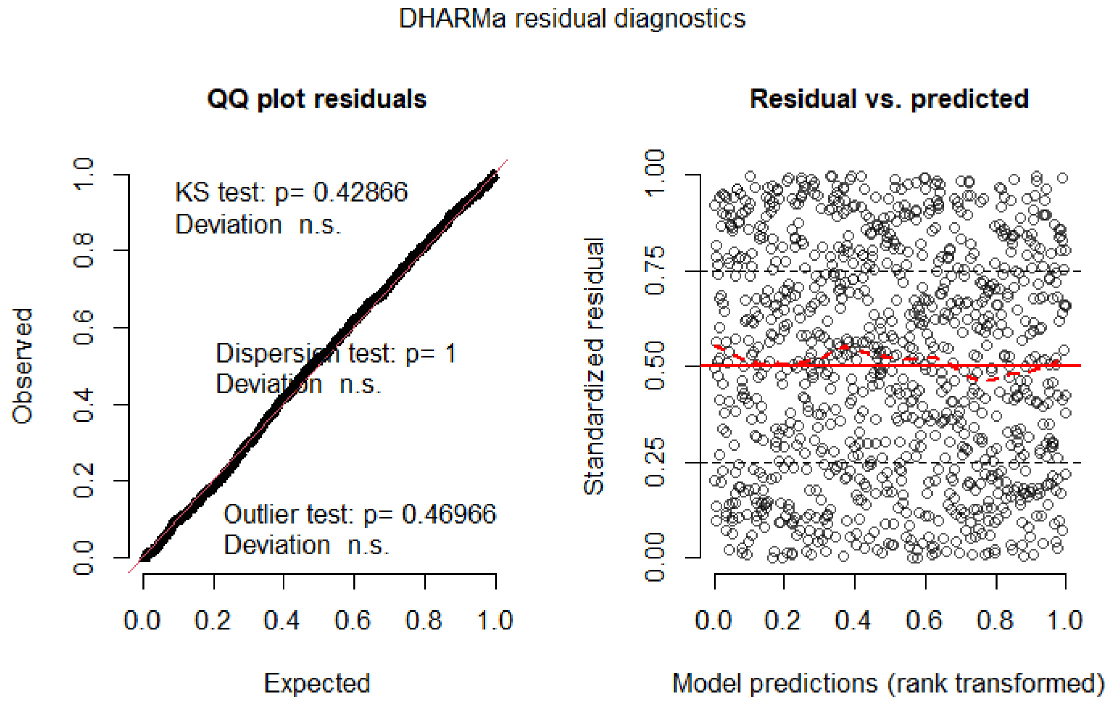


Figure 8 Simulated randomised quantile residuals: germinant presence–absence

5.2 Seedling abundance

Table 7 Model fitting summary: seedling abundance

Response	Number of seedlings present (in each 0.04 ha subplot)
Response transformation used	None
R package and function	glmmTMB function in glmmTMB package
Distribution used	Negative binomial
Outliers removed	Six values greater than 250 were removed
Reported model formula	2_3_way, without year as a random effect
Random factors	Site (a factor over 22 sites) Siteplot (a factor over 66 plots) Subplot (a factor over 198 subplots)
Other transformations compared	See below
Other models attempted	4_way logged, all four random effects, Gaussian: No warnings, but failed residual tests 4_way log base 10, all four random effects, Gaussian: No warnings, but failed residual tests 4_way, all four random effects, negative binomial: Failed to converge 4_way, no year as random effect, negative binomial: Non positive definite hessian 3_way, no year as a random effect, negative binomial: No warnings, but bootstrapped simulations failed 2_3_way, with all four random effects, negative binomial: poly(cbind(thinning, yrs.elapsed), 2) * site.quality + poly(cbind(thinning, yrs.elapsed), 2) * initSD.log.bin: No warnings, but bootstrapped simulations failed
Confidence comments	Moderate to high confidence: • This data was difficult to fit, but the final model fit well • Final model conformed to all residual tests • Few non-convergence warnings in nulls and prediction interval simulations (<5% of 999)

Model summary 5 Seedling abundance

```
Family: nbinom2  ( log )
Formula:          var ~ poly(cbind(thinning, yrs.elapsed), 2) * site.quality +      poly(cbind(thinning, yrs.elapsed), 2) *
initSD.log.bin +      (1 | site) + (1 | siteplot)
Data: dat.outlier


Dispersion parameter for nbinom2 family (): 0.679


Conditional model:
                                                      Estimate Std. Error z value Pr(>|z|)
```

```
(Intercept)                                                        2.3429     0.4004   5.851 4.88e-09 ***
poly(cbind(thinning, yrs.elapsed), 2)1.0                                2.9893     9.0181   0.331  0.74028
poly(cbind(thinning, yrs.elapsed), 2)2.0                               -14.1593     7.1098  -1.992  0.04642 *
poly(cbind(thinning, yrs.elapsed), 2)0.1                                -7.1001     5.7291  -1.239  0.21523
poly(cbind(thinning, yrs.elapsed), 2)1.1                              -266.5034   190.6312  -1.398  0.16211
poly(cbind(thinning, yrs.elapsed), 2)0.2                                13.4537     4.3713   3.078  0.00209 **
site.qualitySQ2                                                     -0.9014     0.4364  -2.065  0.03888 *
initSD.log.binModerate initial density (500-850/ha)                        0.2117     0.3224   0.656  0.51152
initSD.log.binHigh initial density (>850/ha)                            0.2682     0.3732   0.719  0.47234
poly(cbind(thinning, yrs.elapsed), 2)1.0:site.qualitySQ2                    10.0421     6.3590   1.579
0.11429
poly(cbind(thinning, yrs.elapsed), 2)2.0:site.qualitySQ2                    -3.5332     5.6055  -0.630
0.52849
poly(cbind(thinning, yrs.elapsed), 2)0.1:site.qualitySQ2                   -10.3190     4.4442  -2.322
0.02024 *
poly(cbind(thinning, yrs.elapsed), 2)1.1:site.qualitySQ2                   247.6810   150.2429   1.649
0.09924 .
poly(cbind(thinning, yrs.elapsed), 2)0.2:site.qualitySQ2                   -11.0848     3.9799  -2.785
0.00535 **
poly(cbind(thinning, yrs.elapsed), 2)1.0:initSD.log.binModerate initial density (500-850/ha)  -11.6983     8.7440  -
1.338  0.18094
poly(cbind(thinning, yrs.elapsed), 2)2.0:initSD.log.binModerate initial density (500-850/ha)   11.1806     7.7531
1.442  0.14928
poly(cbind(thinning, yrs.elapsed), 2)0.1:initSD.log.binModerate initial density (500-850/ha)   12.5989     5.5711
2.261  0.02373 *
poly(cbind(thinning, yrs.elapsed), 2)1.1:initSD.log.binModerate initial density (500-850/ha)  247.6337   180.3284
1.373  0.16968
poly(cbind(thinning, yrs.elapsed), 2)0.2:initSD.log.binModerate initial density (500-850/ha)  -14.4799     4.8286  -
2.999  0.00271 **
poly(cbind(thinning, yrs.elapsed), 2)1.0:initSD.log.binHigh initial density (>850/ha)         -2.9955     9.9249  -0.302
0.76279
poly(cbind(thinning, yrs.elapsed), 2)2.0:initSD.log.binHigh initial density (>850/ha)         20.0683     8.6916
2.309  0.02095 *
poly(cbind(thinning, yrs.elapsed), 2)0.1:initSD.log.binHigh initial density (>850/ha)          3.5139     6.5027   0.540
0.58894
poly(cbind(thinning, yrs.elapsed), 2)1.1:initSD.log.binHigh initial density (>850/ha)        -91.6971   213.0868  -
0.430  0.66696
poly(cbind(thinning, yrs.elapsed), 2)0.2:initSD.log.binHigh initial density (>850/ha)         -7.1264     5.0264  -1.418
0.15625
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

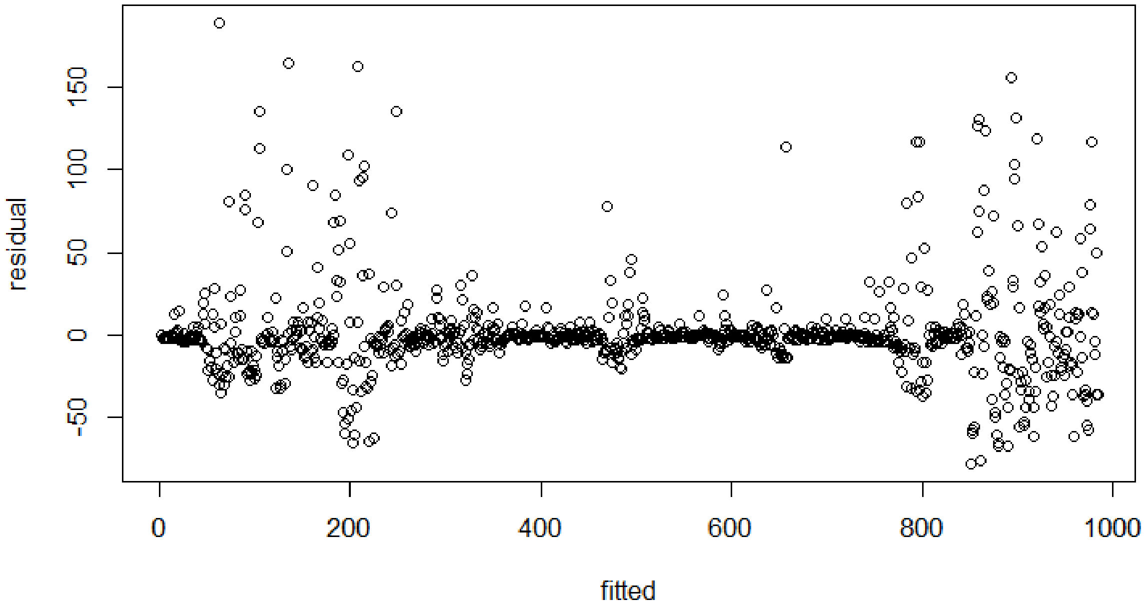


Figure 9 **Fitted values and data residuals: seedling abundance**

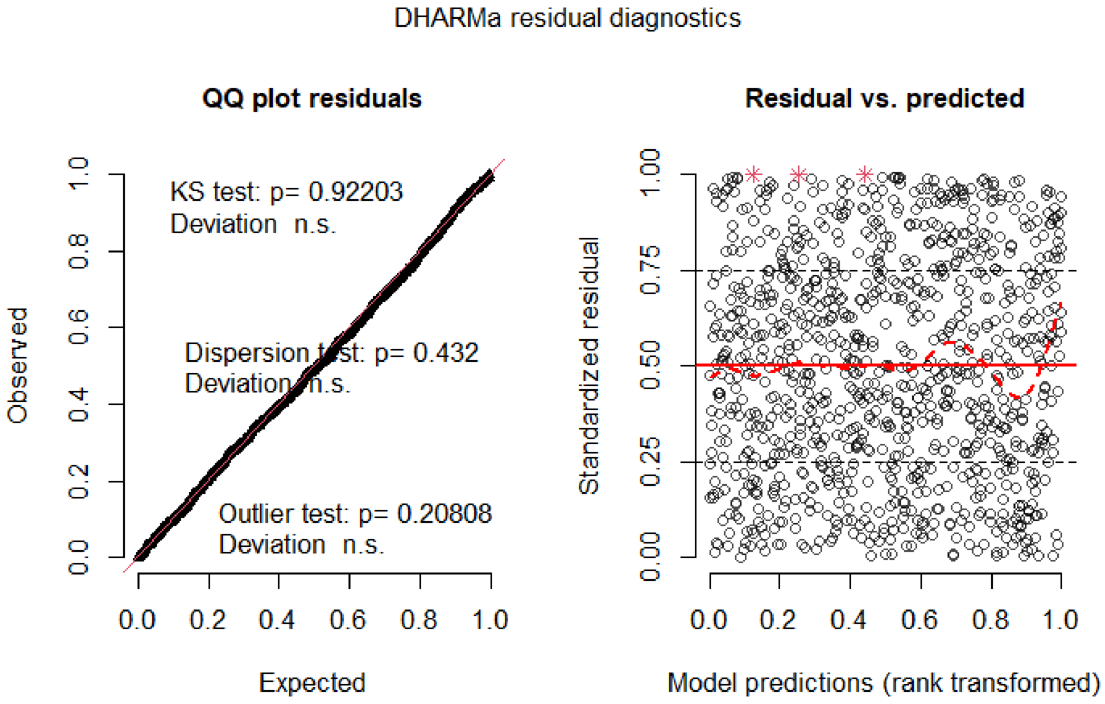


Figure 10 **Simulated randomised quantile residuals: seedling abundance**

6. Model summaries: Canopy condition

6.1 Individual tree crown extent

Table 8 Model fitting summary: tree crown extent

Response	Individual tree crown extent. Crown extent (5% categories between 0% and 100%) assessed for 30 trees per 9 hectare plot An integer and positive variable
Response transformations used	Log$_{10}$(x+1)
R package and function	lmer function from lme4 package
Distribution used	Gaussian
Outliers removed	None
Reported model	4_way
Random factors	Site (a factor over 22 sites) Siteplot (a factor over 66 plots) Year.factor (a factor for each of the 5 survey years)
Other transformations compared	X*100 Square root Square root of (x * 100) Log$_e$(x+1) Log$_e$((x*100) +1) Log$_{10}$((x*100) +1) (X*100)/5 Square root of ((X*100)/5)
Other models attempted	3_3way, binomial and Poisson, with tree.factor as random effect, also with tree.factor but no year.factor. Boundary fit was singular 4_way with no year factor, binomial and Poisson with tree.factor as random effect, also with tree.factor but no year.factor. Boundary fit was singular No_SDi – binomial and Poisson; with no initial stem density * thinning interaction–with tree.factor as random effect, also with tree.factor but no year.factor. Boundary fit was singular
Confidence comments	Moderate confidence: • No convergence and fit warnings • Failed the Kurtosis-Skewness test, with moderate deviation from expected • Some non-convergence warnings in bootstrapped prediction interval simulations (<10% of 999)

Model summary 6 Crown extent

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: varL10 ~ poly(cbind(thinning, initSD.log, yrs.elapsed), 2) *

```
    site.quality + thinning * initSD.log * yrs.elapsed * site.quality +      (1 | site) + (1 | siteplot) + (1 | year.factor)
   Data: dat
Control: lmerControl(check.scaleX = "ignore", check.rankX = "silent.drop.cols")

REML criterion at convergence: -40736.7

Scaled residuals: 
    Min      1Q  Median      3Q     Max 
-8.2905 -0.4075  0.1663  0.6160  2.3220 

Random effects:
 Groups      Name        Variance  Std.Dev.
 siteplot    (Intercept) 4.448e-05 0.006670
 site        (Intercept) 2.245e-05 0.004738
 year.factor (Intercept) 2.312e-05 0.004809
 Residual                9.283e-04 0.030468
Number of obs: 9875, groups:  siteplot, 66; site, 22; year.factor, 5

Fixed effects:
                                                              Estimate Std. Error         df t value Pr(>|t|)    
(Intercept)                                                  2.072e-01  1.484e-02  2.444e+03  13.964  < 2e-16 ***
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.0              -5.306e+00  1.586e+00  6.614e+03  -3.346 
0.000825 ***
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)2.0.0               8.933e-03  9.768e-02  5.956e+02   0.091 
0.927166    
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.0              -4.188e-01  2.151e-01  1.317e+02  -1.947 
0.053667 .  
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.1.0              -2.708e+01  1.457e+01  2.198e+03  -1.859 
0.063201 .  
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.2.0               1.473e-01  1.756e-01  5.356e+01   0.838 
0.405504    
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.1              -4.645e+00  1.437e+00  6.516e+03  -3.233 
0.001233 ** 
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.1              -5.345e+02  1.558e+02  7.247e+03  -3.430 
0.000606 ***
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.1              -3.939e+00  8.114e+00  2.342e+03  -0.485 
0.627440    
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.2               2.930e-01  7.249e-02  7.406e+02   4.043 5.84e-
05 ***
site.qualitySQ2                                               5.345e-02  1.776e-02  6.388e+03   3.010 0.002621 ** 
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.0:site.qualitySQ2  6.761e+00  1.895e+00  7.717e+03   3.568 
0.000362 ***
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)2.0.0:site.qualitySQ2  4.275e-02  1.547e-01  7.343e+02   0.276 
0.782304    
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.0:site.qualitySQ2  4.565e-01  2.836e-01  1.263e+02   1.609 
0.110015    
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.1.0:site.qualitySQ2  2.917e+01  2.020e+01  2.047e+03   1.444 
0.148811    
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.2.0:site.qualitySQ2 -1.317e-01  2.157e-01  5.394e+01  -0.611 
0.544055    
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.1:site.qualitySQ2  6.158e+00  1.719e+00  8.218e+03   3.582 
0.000343 ***
```

```
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.1:site.qualitySQ2  6.873e+02  1.854e+02  8.073e+03   3.708
0.000211 ***
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.1:site.qualitySQ2  8.830e+00  1.014e+01  2.900e+03   0.871
0.383717
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.2:site.qualitySQ2 -3.452e-01  8.408e-02  7.362e+03  -4.106
4.07e-05 ***
thinning:initSD.log:yrs.elapsed                                         1.523e-02  4.392e-03  7.201e+03   3.467 0.000529 ***
site.qualitySQ2:thinning:initSD.log:yrs.elapsed                        -1.891e-02  5.271e-03  8.112e+03  -3.588
0.000335 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

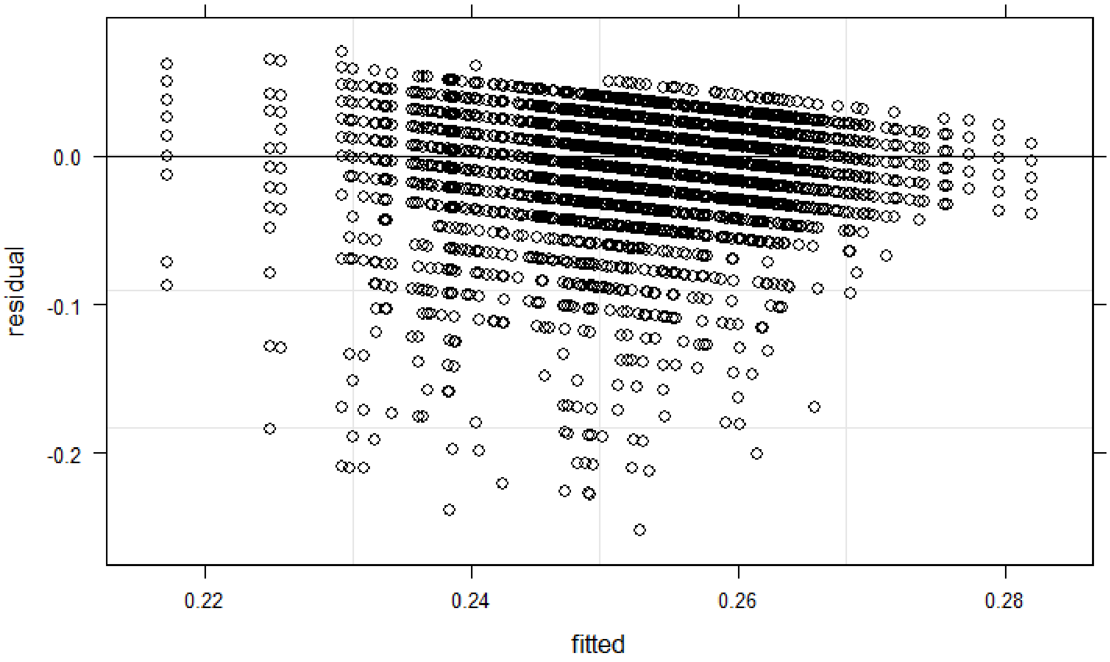


Figure 11 Residuals vs fixed effects: crown extent

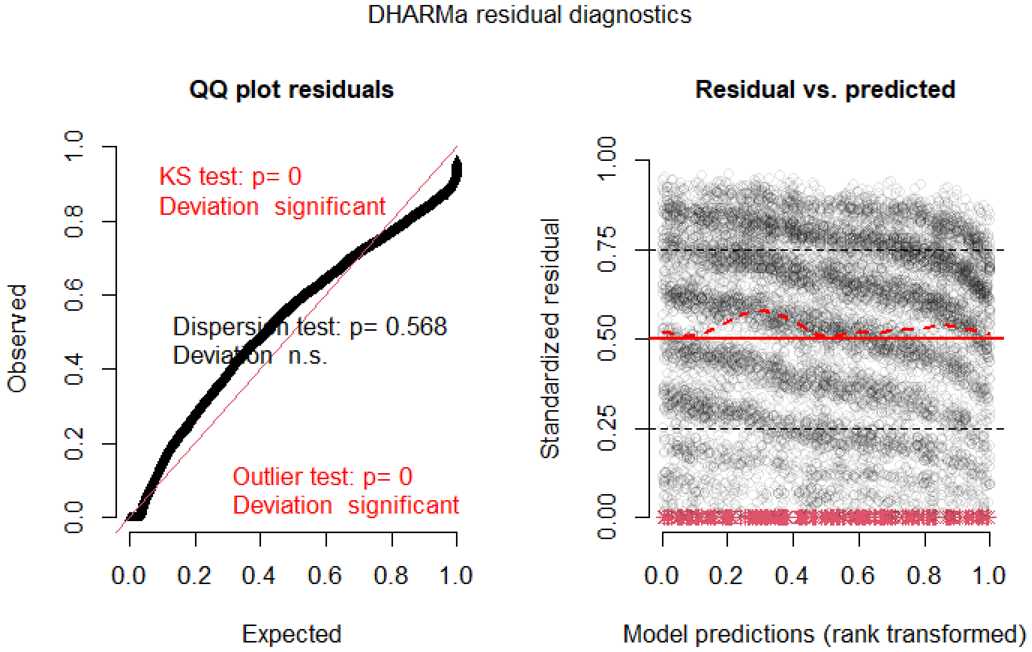


Figure 12 Simulated randomised quantile residuals: crown extent

6.2 Visually assessed canopy cover

6.2.1 Live canopy cover

Table 9 Model fitting summary: visually assessed live canopy cover

Response	Visually assessed live canopy cover A continuous positive variable between 0 and 1
Response transformations used	Log
R package and function	lmer from the lme4 package
Distribution used	Gaussian
Outliers removed	None
Reported model	4_way
Random factors	Site (a factor over 22 sites) Siteplot (a factor over 66 plots) Year.factor (a factor for each of the 5 survey years)
Other transformations compared	Multiplied by 100 Rounded to nearest whole number
Other models attempted	No others with Gaussian 4way, 3_3way, no_SDi and all null models with binomial: Inferior residuals 4_way, 3_3way, no_SDi with poisson: Inferior residuals
Confidence comments	Moderate confidence: • No convergence and fit warnings • Failed Kurtosis-Skewness test, with minor deviations from expected • Some non-convergence and boundary fit is singular warnings in bootstrapped prediction interval simulations (<20% of 100)

Model summary 7 Visually assessed live canopy cover

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Lvar ~ poly(cbind(thinning, initSD.log, yrs.elapsed), 2) * site.quality +
    thinning * initSD.log * yrs.elapsed * site.quality + (1 |      year.factor) + (1 | site) + (1 | siteplot) + (1 | subplot)
   Data: dat
Control: lmerControl(check.scaleX = "ignore", check.rankX = "silent.drop.cols")

REML criterion at convergence: 1343.5

Scaled residuals:
    Min      1Q  Median      3Q     Max
-4.2335 -0.5105  0.0260  0.5774  2.9240

Random effects:
```

```
 Groups      Name        Variance Std.Dev.
 subplot     (Intercept) 0.102699 0.32047
 siteplot    (Intercept) 0.040752 0.20187
 site        (Intercept) 0.007555 0.08692
 year.factor (Intercept) 0.060641 0.24625
 Residual                0.180523 0.42488
Number of obs: 984, groups:  subplot, 198; siteplot, 66; site, 22; year.factor, 5

Fixed effects:
                                                      Estimate Std. Error       df t value Pr(>|t|)
(Intercept)                                             1.5507     0.6644  645.3636   2.334   0.0199 *
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.0              -20.3939    22.5195  821.7344  -0.906   0.3654
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)2.0.0                3.0100     1.3317  377.4533   2.260   0.0244 *
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.0               -4.5484     2.7104  127.6641  -1.678   0.0958 .
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.1.0              -29.5957    64.0434  739.2776  -0.462   0.6441
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.2.0                1.7863     2.1752   54.9889   0.821   0.4151
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.1              -19.5823    20.2909  817.0773  -0.965   0.3348
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.1             -551.9019   696.2100  820.6801  -0.793   0.4282
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.1               27.4754    36.1692  723.4563   0.760   0.4477
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.2                1.0525     1.0403  509.0387   1.012   0.3121
site.qualitySQ2                                           0.4519     0.7872  822.5148   0.574   0.5661
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.0:site.qualitySQ2   26.4531    26.7621  816.1320   0.988
0.3232
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)2.0.0:site.qualitySQ2   -3.6794     2.0780  391.9542  -1.771
0.0774 .
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.0:site.qualitySQ2    5.1301     3.5424  120.4459   1.448
0.1502
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.1.0:site.qualitySQ2   27.5191    87.9853  726.7470   0.313
0.7545
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.2.0:site.qualitySQ2   -1.1908     2.6583   54.0182  -0.448
0.6560
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.1:site.qualitySQ2   22.6482    24.1258  813.1640   0.939
0.3481
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.1:site.qualitySQ2  866.6873   824.5243  814.4375   1.051
0.2935
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.1:site.qualitySQ2  -44.8555    45.2403  767.8679  -0.991
0.3218
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.2:site.qualitySQ2   -2.8269     1.1875  811.2587  -2.381
0.0175 *
thinning:initSD.log:yrs.elapsed                                 0.1545     0.1937  820.4517   0.798   0.4251
site.qualitySQ2:thinning:initSD.log:yrs.elapsed                -0.2211     0.2313  813.7374  -0.956   0.3394
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation matrix not shown by default, as p = 22 > 12.
Use print(x, correlation=TRUE)  or
    vcov(x)        if you need it
```

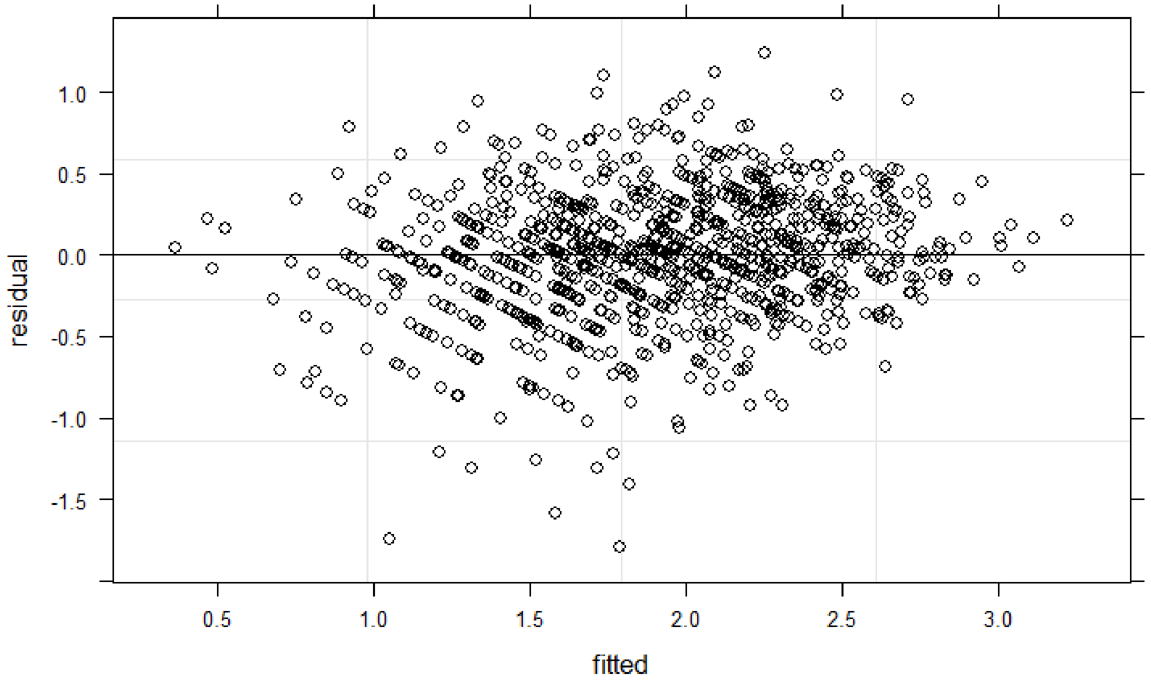


Figure 13 Residuals vs fixed effects: visually assessed live canopy cover

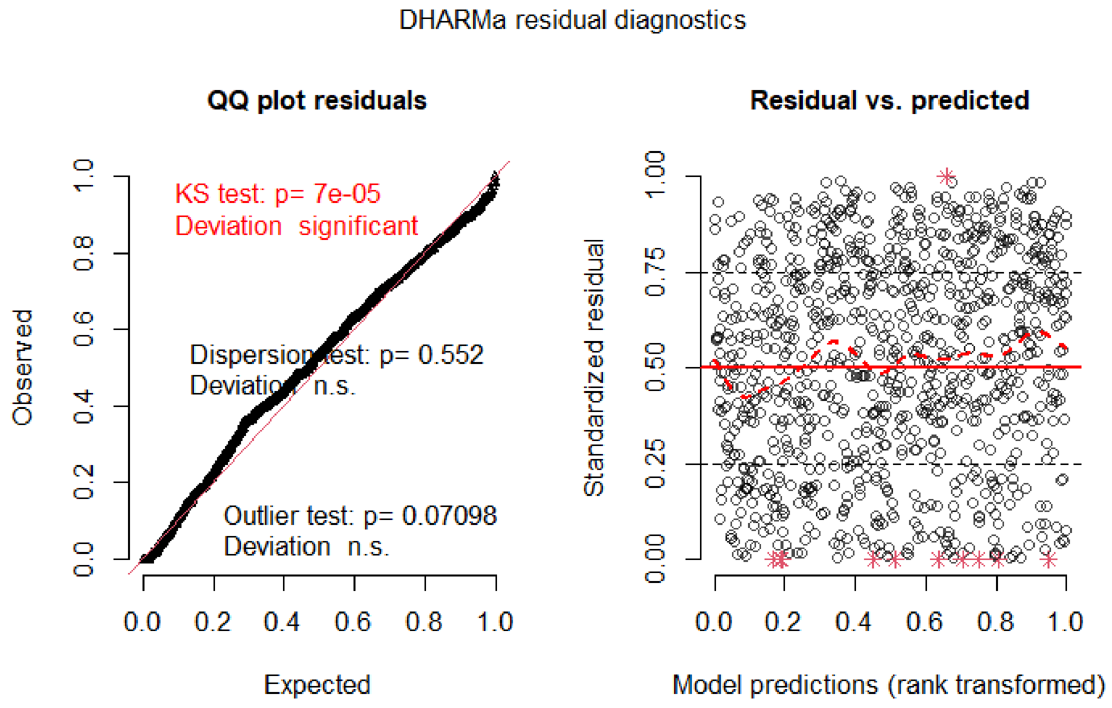


Figure 14 Simulated randomised quantile residuals: visually assessed live canopy cover

6.2.2 Dead canopy cover

Not modelled.

6.3 Remotely sensed canopy cover

Table 10 Model fitting summary: remotely sensed foliage projective cover

Response	Foliage projective cover (derived from Landsat images) A median of up to 9 values (from a 30 x 30 m pixel) per 9 hectare plot
Response transformations used	None
R package and function	Gaussian from lme4
Distribution used	glmmTMB from the glmmTMB package
Outliers removed	None
Reported model	glmmTMB(var ~ poly(cbind(thinning, initSD.log, Pass), 2) * site.quality + CosTime + SinTime + thinning:initSD.log:Pass + thinning:initSD.log:Pass:site.quality + (1 | site) + (1 | siteplot) Note that Landsat pass was used in place of years elapsed
Random factors	Site (a factor over 22 sites) Siteplot (a factor over 66 9 ha plots)
Other transformations compared	None
Other models attempted	4_way: Failed to converge 3_3way in lmer, no autocorrelation accounted for: Inferior residuals 3_3way + CosTime + SinTime, lmer function, no autocorrelation accounted for: Inferior residuals 3_3way + CosTime + SinTime, lme function, spherical correlation: Inferior residuals 3_3way + CosTime + SinTime, lme function, AR1 correlation: Inferior residuals 3_3way + CosTime + SinTime, lme function, AR1 correlation including pass date 3_3way, glmmTMB function, AR1 correlation on (year.factor|siteplot): Inferior residuals No other distributions compared
Confidence comments	Moderate to high confidence: • No convergence or fit warnings • Minor deviations in the Kurtosis-Skewness test and outlier test • Some non-convergence warnings in nulls and prediction interval simulations (<10% of 999)

Model summary 8 Remotely sensed foliage projective cover

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: var ~ poly(cbind(thinning, initSD.log, Pass), 2) * site.quality +
CosTime + SinTime + thinning:initSD.log:Pass + thinning:initSD.log:Pass:site.quality + (1 | site) + (1 | siteplot)

Data: dat

```
Control: lmerControl(check.scaleX = "ignore", check.rankX = "silent.drop.cols")

REML criterion at convergence: -10947.2

Scaled residuals:
    Min      1Q  Median      3Q     Max
-6.5446 -0.5688  0.0417  0.5893  4.6722

Random effects:
 Groups   Name        Variance  Std.Dev.
 siteplot (Intercept) 0.0012626 0.03553
 site     (Intercept) 0.0004518 0.02126
 Residual             0.0059375 0.07706
Number of obs: 4876, groups:  siteplot, 66; site, 22
Fixed effects:
                                                      Estimate Std. Error         df t value Pr(>|t|)
(Intercept)                                          3.690e-01  2.387e-01  4.848e+03   1.546 0.122235
poly(cbind(thinning, initSD.log, Pass), 2)1.0.0                -4.499e+00  1.993e+01  4.842e+03  -0.226 0.821432
poly(cbind(thinning, initSD.log, Pass), 2)2.0.0                -1.317e+00  2.181e-01  2.809e+03  -6.038 1.77e-09 ***
poly(cbind(thinning, initSD.log, Pass), 2)0.1.0                 1.033e+00  1.376e+00  1.202e+03   0.751 0.453076
poly(cbind(thinning, initSD.log, Pass), 2)1.1.0                -4.380e+01  9.848e+01  4.821e+03  -0.445 0.656534
poly(cbind(thinning, initSD.log, Pass), 2)0.2.0                -4.264e-01  6.151e-01  5.611e+01  -0.693 0.491052
poly(cbind(thinning, initSD.log, Pass), 2)0.0.1                -2.613e+00  3.402e+00  4.843e+03  -0.768 0.442438
poly(cbind(thinning, initSD.log, Pass), 2)1.0.1                -1.059e+02  2.886e+02  4.842e+03  -0.367 0.713627
poly(cbind(thinning, initSD.log, Pass), 2)0.1.1                 3.715e+01  1.300e+01  4.519e+03   2.857 0.004295 **
poly(cbind(thinning, initSD.log, Pass), 2)0.0.2                -4.642e-01  1.384e-01  4.801e+03  -3.354 0.000803 ***
site.qualitySQ2                                        -4.146e-01  2.914e-01  4.851e+03  -1.423 0.154885
CosTime                                              -5.734e-02  1.666e-03  4.791e+03 -34.420  < 2e-16 ***
SinTime                                              -7.372e-03  1.513e-03  4.791e+03  -4.872 1.14e-06 ***
poly(cbind(thinning, initSD.log, Pass), 2)1.0.0:site.qualitySQ2 -2.637e+01  2.430e+01  4.843e+03  -1.085
0.277901
poly(cbind(thinning, initSD.log, Pass), 2)2.0.0:site.qualitySQ2  6.336e-01  3.611e-01  2.890e+03   1.755
0.079423 .
poly(cbind(thinning, initSD.log, Pass), 2)0.1.0:site.qualitySQ2 -2.692e+00  1.703e+00  9.810e+02  -1.581
0.114234
poly(cbind(thinning, initSD.log, Pass), 2)1.1.0:site.qualitySQ2 -1.108e+02  1.214e+02  4.819e+03  -0.913
0.361289
poly(cbind(thinning, initSD.log, Pass), 2)0.2.0:site.qualitySQ2  3.592e-02  7.557e-01  5.601e+01   0.048
0.962256
poly(cbind(thinning, initSD.log, Pass), 2)0.0.1:site.qualitySQ2 -4.528e+00  4.125e+00  4.842e+03  -1.098
0.272344
poly(cbind(thinning, initSD.log, Pass), 2)1.0.1:site.qualitySQ2 -3.129e+02  3.476e+02  4.843e+03  -0.900
0.368121
poly(cbind(thinning, initSD.log, Pass), 2)0.1.1:site.qualitySQ2 -4.510e+01  1.624e+01  4.574e+03  -2.778
0.005496 **
poly(cbind(thinning, initSD.log, Pass), 2)0.0.2:site.qualitySQ2 -2.337e-01  1.979e-01  4.803e+03  -1.181
0.237837
thinning:initSD.log:Pass                                 9.886e-05  6.341e-04  4.842e+03   0.156 0.876109
site.qualitySQ2:thinning:initSD.log:Pass                       8.688e-04  7.727e-04  4.843e+03   1.124 0.260920
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

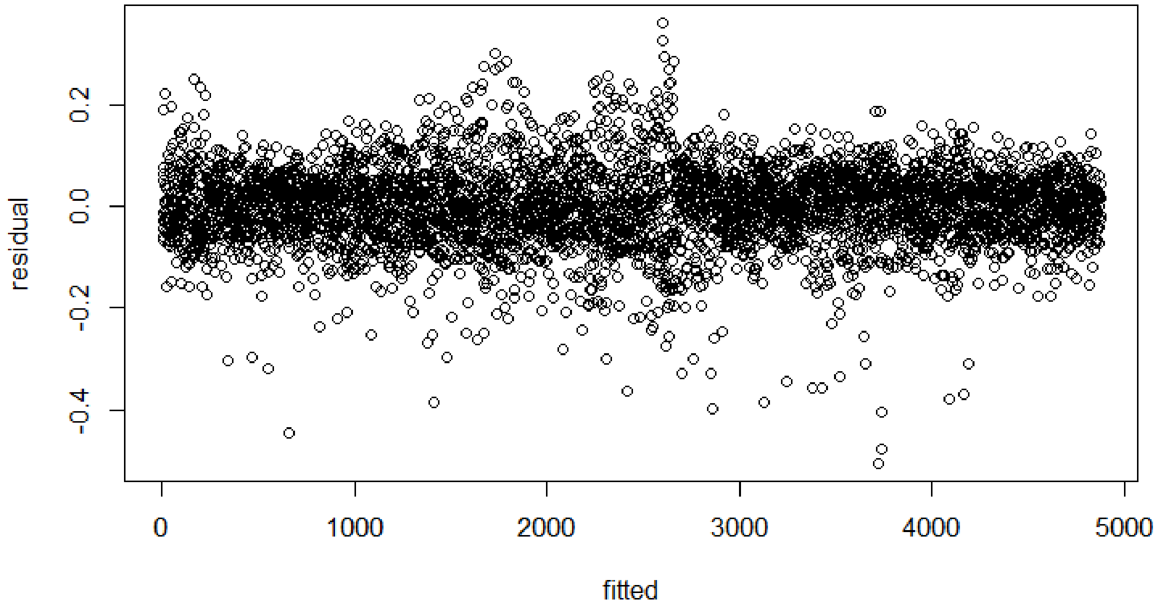


Figure 15 Residuals vs fixed effects: remotely sensed foliage projective cover

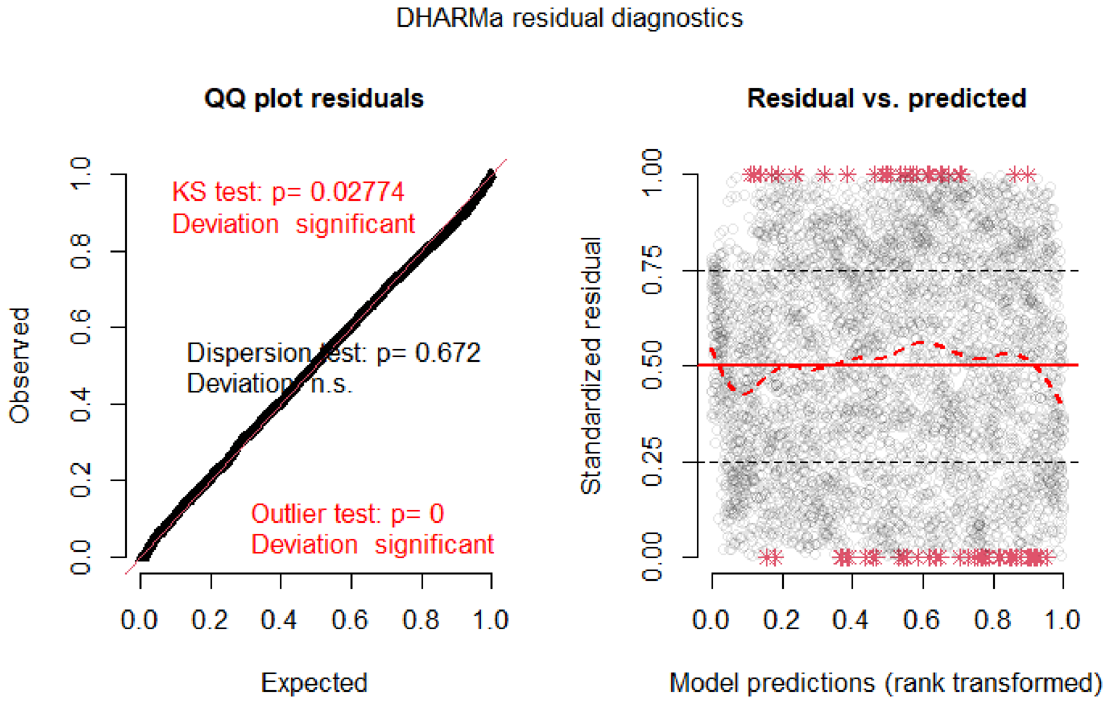


Figure 16 Simulated randomised quantile residuals: remotely sensed foliage projective cover

7. Model summaries: Fuel hazard

7.1 Overall fuel hazard

Table 11 Model fitting summary: overall fuel hazard

Response	Probability of being in each overall fuel hazard category
Response transformation used	None
R package and function	brm function from brms package with family specified as cratio(threshold = flexible)
Distribution used	Continuation ratio with flexible category thresholds The cumulative model has an underlying distribution that spans all categories, which is appropriate for fuel hazard because hazard is an underlying continuous variable and responses can move up and down as well as jump categories. (In contrast, an adjacent categories model assumes each level of risk rating has its own distribution, and sequential models assume response data can only move sequentially through the levels). Flexible thresholds allow for the boundaries between hazard rating categories to have unequal sizes and account for different proportions of the data. This is supported by the input data where more sites report moderate or high ratings than low or very high ratings.
Outliers removed	None
Model reported	4_way, with iterations = 2000, chains = 4, warmup = 500, max tree depth = 15, priors for all betas = normal(0,10)
Random factors	Site (a factor over 22 sites) Siteplot (a factor over 66 plots) Subplot (a factor over 198 subplots) Year.factor (a factor for each of the 5 survey years)
Other transformations compared	None
Other models attempted	4_way with iterations = 4000, chains =6. Failed to converge 3_3way with iterations = 4000, chains =6. Failed to converge No_SDi with iterations = 4000, chains =6. Failed to converge 4_way_noYrf with iterations = 4000, chains =6. Failed to converge No other distributions compared
Confidence comments	High confidence: • No convergence or fit warnings • Chains mixed well

Model summary 9 Overall fuel hazard

```
Family: cratio
  Links: mu = logit; disc = identity
Formula: var ~ poly(cbind(thinning, initSD.log, yrs.elapsed), 2) * site.quality + thinning:initSD.log:yrs.elapsed +
thinning:initSD.log:yrs.elapsed:site.quality + (1 | year.factor) + (1 | site) + (1 | siteplot) + (1 | subplot)
   Data: dat (Number of observations: 984)
```

```
Samples: 4 chains, each with iter = 4000; warmup = 500; thin = 1;
         total post-warmup samples = 14000
Group-Level Effects:
~site (Number of levels: 22)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.37      0.24     0.02     0.90 1.00     1795     3818
~siteplot (Number of levels: 66)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.27      0.20     0.01     0.75 1.00     2045     1819
~subplot (Number of levels: 198)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     1.80      0.18     1.48     2.17 1.00     5050     8698
~year.factor (Number of levels: 5)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     1.19      0.68     0.32     2.90 1.00     2838     3020
Population-Level Effects:
                                                      Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept[1]                                             -4.77      0.70    -6.19    -3.39 1.00     2498     1898
Intercept[2]                                             -0.94      0.66    -2.29     0.42 1.00     2577     1890
Intercept[3]                                              8.27      1.04     6.40    10.46 1.00     5998     7118
polycbindthinninginitSD.logyrs.elapsed21.0.0                  2.96      6.31    -9.60    15.20 1.00    12610    10198
polycbindthinninginitSD.logyrs.elapsed22.0.0                 -0.33      4.93    -9.84     9.34 1.00    10557     9527
polycbindthinninginitSD.logyrs.elapsed20.1.0                  1.50      5.84   -10.01    12.88 1.00     8749     8889
polycbindthinninginitSD.logyrs.elapsed21.1.0                  0.27     10.09   -19.56    20.21 1.00    20833    10096
polycbindthinninginitSD.logyrs.elapsed20.2.0                 -1.23      5.88   -12.76    10.21 1.00     8400     5614
polycbindthinninginitSD.logyrs.elapsed20.0.1                  5.31      9.71   -14.07    23.41 1.00     4697     5838
polycbindthinninginitSD.logyrs.elapsed21.0.1                 -0.20     10.03   -19.68    19.59 1.00    19459     9701
polycbindthinninginitSD.logyrs.elapsed20.1.1                 -0.24     10.07   -20.03    19.24 1.00    15663     7012
polycbindthinninginitSD.logyrs.elapsed20.0.2                 -0.32      4.54    -9.22     8.70 1.00    14505     9108
site.qualitySQ2                                           0.19      0.47    -0.75     1.11 1.00     6251     3209
polycbindthinninginitSD.logyrs.elapsed21.0.0:site.qualitySQ2   -11.60      7.24   -25.85     2.60 1.00    12610
11024
polycbindthinninginitSD.logyrs.elapsed22.0.0:site.qualitySQ2    11.12      6.22    -1.12    23.43 1.00    13207
10453
polycbindthinninginitSD.logyrs.elapsed20.1.0:site.qualitySQ2     2.72      7.26   -11.43    16.93 1.00    10630
10198
polycbindthinninginitSD.logyrs.elapsed21.1.0:site.qualitySQ2     0.78     10.06   -18.84    20.60 1.00    21604
10136
polycbindthinninginitSD.logyrs.elapsed20.2.0:site.qualitySQ2    -4.35      6.85   -17.62     9.18 1.00    10412
9110
polycbindthinninginitSD.logyrs.elapsed20.0.1:site.qualitySQ2     5.12      5.99    -6.45    17.03 1.00    11727
11523
polycbindthinninginitSD.logyrs.elapsed21.0.1:site.qualitySQ2     0.17     10.00   -19.58    19.75 1.00    18844
9278
polycbindthinninginitSD.logyrs.elapsed20.1.1:site.qualitySQ2     0.81     10.06   -18.88    20.57 1.00    22040
9938
polycbindthinninginitSD.logyrs.elapsed20.0.2:site.qualitySQ2     8.33      4.85    -1.12    17.83 1.00    14737
10274
thinning:initSD.log:yrs.elapsed                          -0.03      0.05    -0.13     0.07 1.00     8152    10191
site.qualitySQ2:thinning:initSD.log:yrs.elapsed              0.02      0.06    -0.10     0.13 1.00     8596     9293
Family Specific Parameters:
```

```
     Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
disc     1.00      0.00     1.00     1.00 1.00    14000    14000
```

Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS and Tail_ESS are effective sample size measures, and Rhat is the potential scale reduction factor on split chains (at convergence, Rhat = 1).

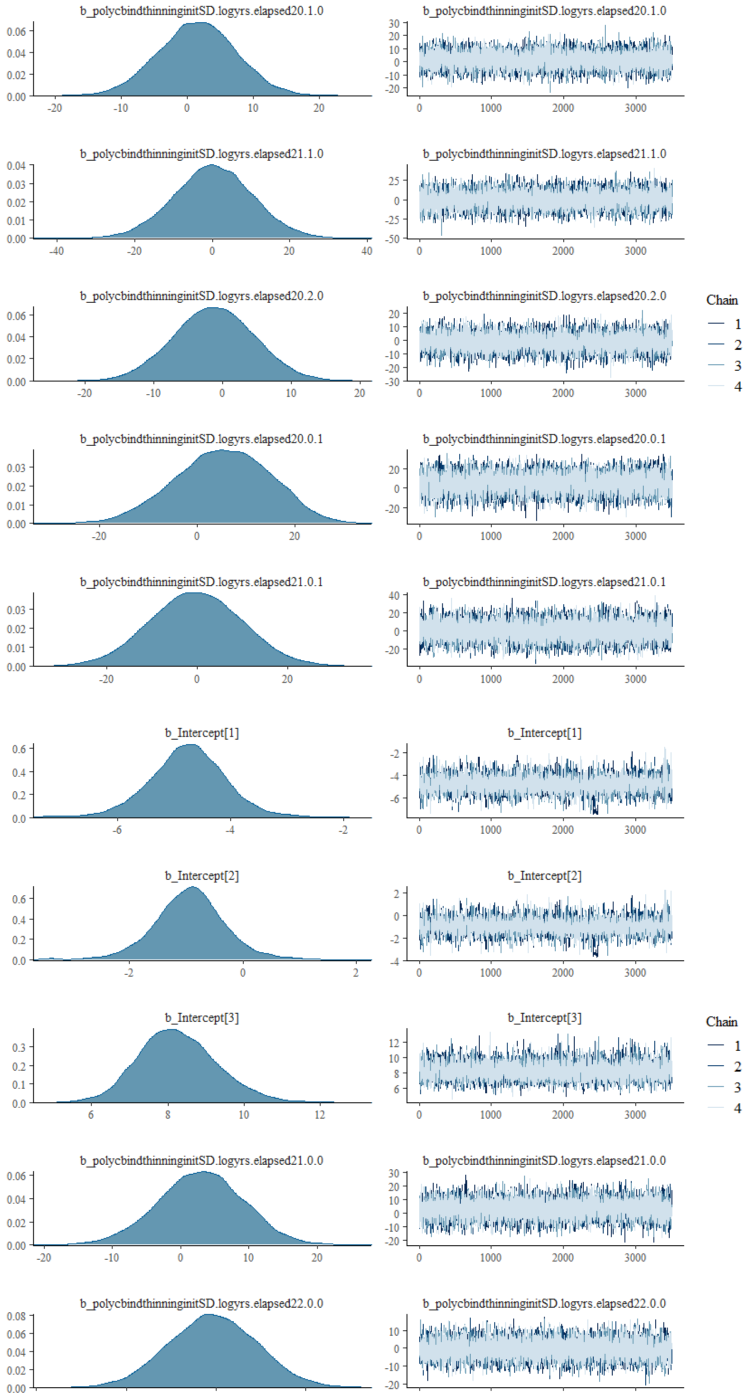


Figure 17 Posterior distributions (left) and chain mixing (right): overall fuel hazard

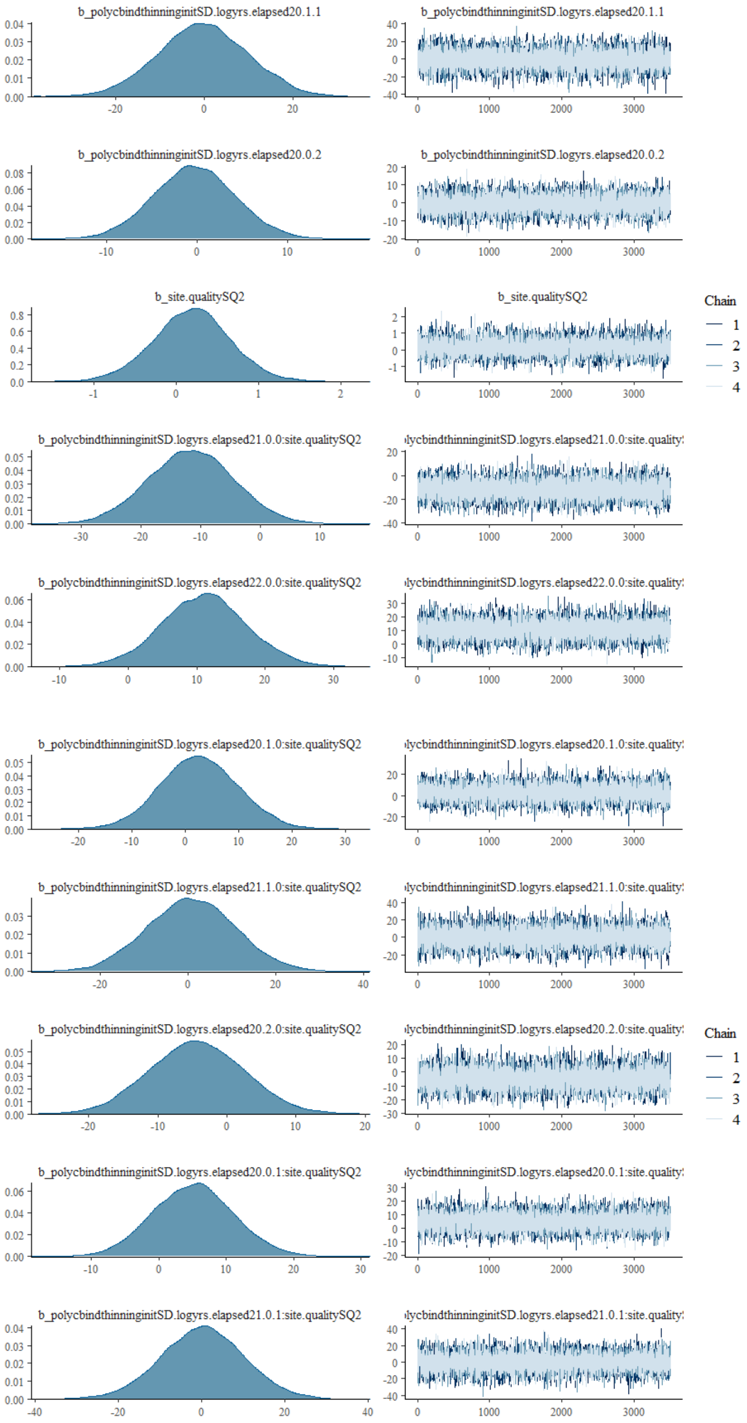


Figure 17 (cont.) **Posterior distributions (left) and chain mixing (right): overall fuel hazard**

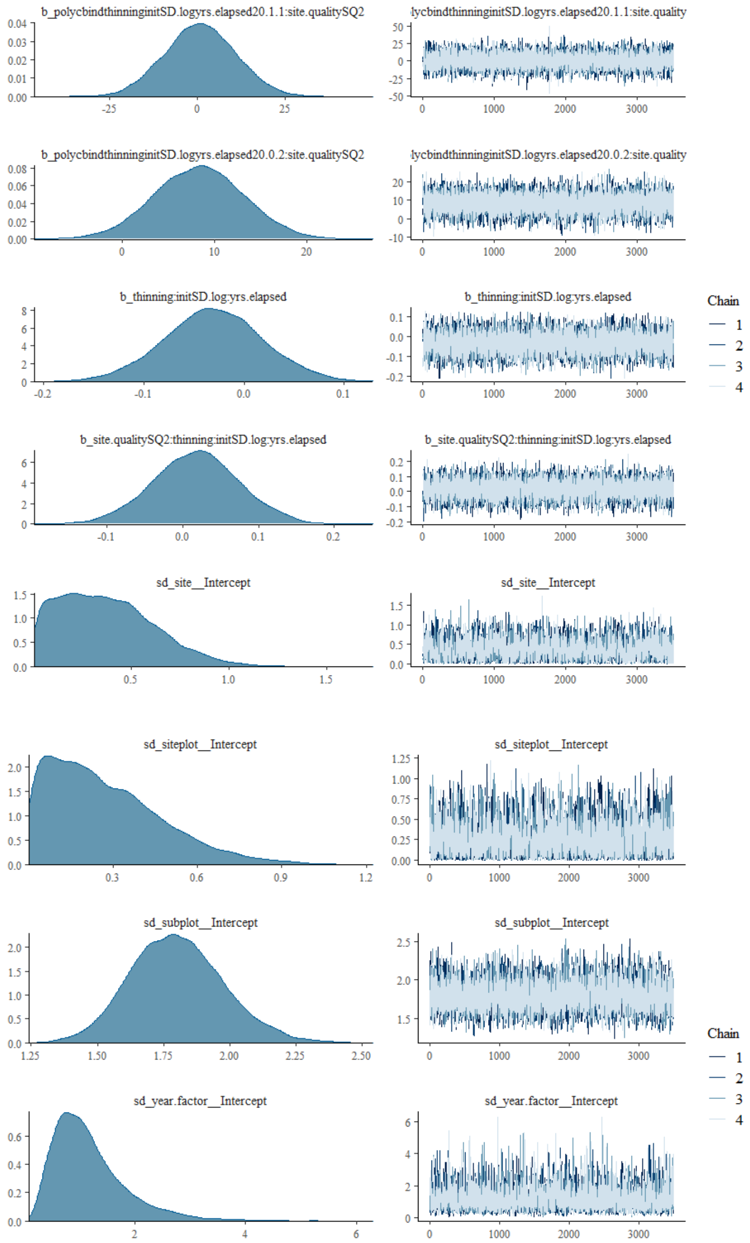


Figure 17 (cont.) **Posterior distributions (left) and chain mixing (right): overall fuel hazard**

7.2 Surface fuel hazard: litter depth

Table 12 Model fitting summary: litter depth

Response	Litter depth, measured at 30 locations in each 9 hectare plot, in millimetres A continuous positive variable
Response transformation used	Log transformed
R package and function	lmer function from lme4 package
Distribution used	Gaussian
Outliers removed	None
Reported model formula	4_way
Random factors	Site (a factor over 22 sites) Siteplot (a factor over 66 plots) Year.factor (a factor for each of the 5 survey years)
Other transformations compared	Also trialled untransformed response variable for 4_way (all other models were trialled on the log transformed response)
Other models attempted	4_way: Boundary fit was singular 3_3way: Boundary fit was singular 3_3way with no interaction between thinning intensity and initial stem density: Boundary fit was singular 4_way with no random effect across year: Boundary fit was singular 4_way with no random effects for either subplot or siteplot: Improved dunn-smyth residuals but higher AIC No other distributions compared
Confidence comments	Moderate to high confidence: • Failed the Kurtosis-Skewness test, with minor deviations from expected • ~15% boundary singular fit warnings, <5% model convergence warnings in 999 prediction interval simulations

Model summary 10 Litter depth

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Lvar ~ poly(cbind(thinning, initSD.log, yrs.elapsed), 2) * site.quality +
    thinning * initSD.log * yrs.elapsed * site.quality + (1 |      year.factor) + (1 | site) + (1 | siteplot)
   Data: dat
Control: lmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 1e+05),
    check.scaleX = "ignore", check.rankX = "silent.drop.cols")

REML criterion at convergence: 1136.3

Scaled residuals:
    Min      1Q  Median      3Q     Max
```

```
-6.0263 -0.5197  0.0400  0.5965  4.2034

Random effects:
 Groups      Name        Variance Std.Dev.
 siteplot    (Intercept) 0.03090  0.1758
 site        (Intercept) 0.01195  0.1093
 year.factor (Intercept) 0.01171  0.1082
 Residual                0.18096  0.4254
Number of obs: 989, groups:  siteplot, 66; site, 22; year.factor, 5
Fixed effects:
                                                                  Estimate Std. Error         df t value Pr(>|t|)
(Intercept)                                                      1.947e+00  6.382e-01  9.293e+02   3.050  0.00235 **
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.0               -3.402e+01  2.179e+01  9.425e+02  -1.562
0.11873
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)2.0.0               -4.203e-02  1.149e+00  2.142e+02  -0.037
0.97085
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.0               -3.945e+00  2.345e+00  2.423e+02  -1.682
0.09382 .
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.1.0               -1.102e+02  6.073e+01  7.012e+02  -1.815
0.06989 .
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.2.0                1.118e+00  1.604e+00  5.862e+01   0.697
0.48838
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.1               -3.093e+01  1.970e+01  9.551e+02  -1.570
0.11670
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.1               -1.087e+03  6.759e+02  9.537e+02  -1.608
0.10824
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.1               -3.505e+01  3.348e+01  6.927e+02  -1.047
0.29554
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.2                3.623e-01  9.467e-01  1.062e+02   0.383
0.70268
site.qualitySQ2                                                  1.448e+00  7.689e-01  9.652e+02   1.883  0.05995 .
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.0:site.qualitySQ2  5.063e+01  2.609e+01  9.563e+02   1.941
0.05257 .
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)2.0.0:site.qualitySQ2  1.661e-01  1.841e+00  2.478e+02   0.090
0.92817
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.0:site.qualitySQ2  5.986e+00  3.048e+00  2.194e+02   1.964
0.05076 .
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.1.0:site.qualitySQ2  1.963e+02  8.308e+01  6.752e+02   2.362
0.01844 *
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.2.0:site.qualitySQ2 -1.320e+00  1.971e+00  5.891e+01  -0.670
0.50569
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.1:site.qualitySQ2  4.576e+01  2.361e+01  9.597e+02   1.938
0.05296 .
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.1:site.qualitySQ2  1.612e+03  8.051e+02  9.591e+02   2.003
0.04550 *
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.1:site.qualitySQ2  2.845e+01  4.218e+01  7.492e+02   0.674
0.50023
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.2:site.qualitySQ2  9.807e-01  1.158e+00  9.437e+02   0.847
0.39723
thinning:initSD.log:yrs.elapsed                                      3.010e-01  1.884e-01  9.526e+02   1.598  0.11033
site.qualitySQ2:thinning:initSD.log:yrs.elapsed                     -4.417e-01  2.264e-01  9.593e+02  -1.951  0.05131
.
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

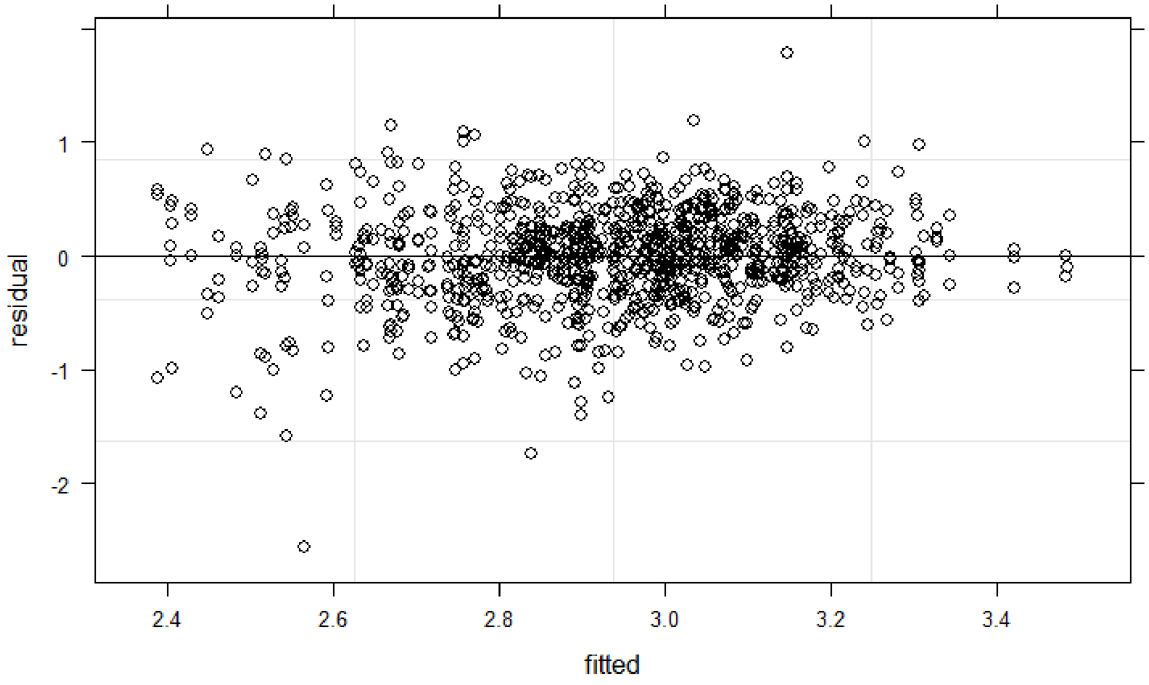


Figure 18 **Fitted values and data residuals: litter depth**

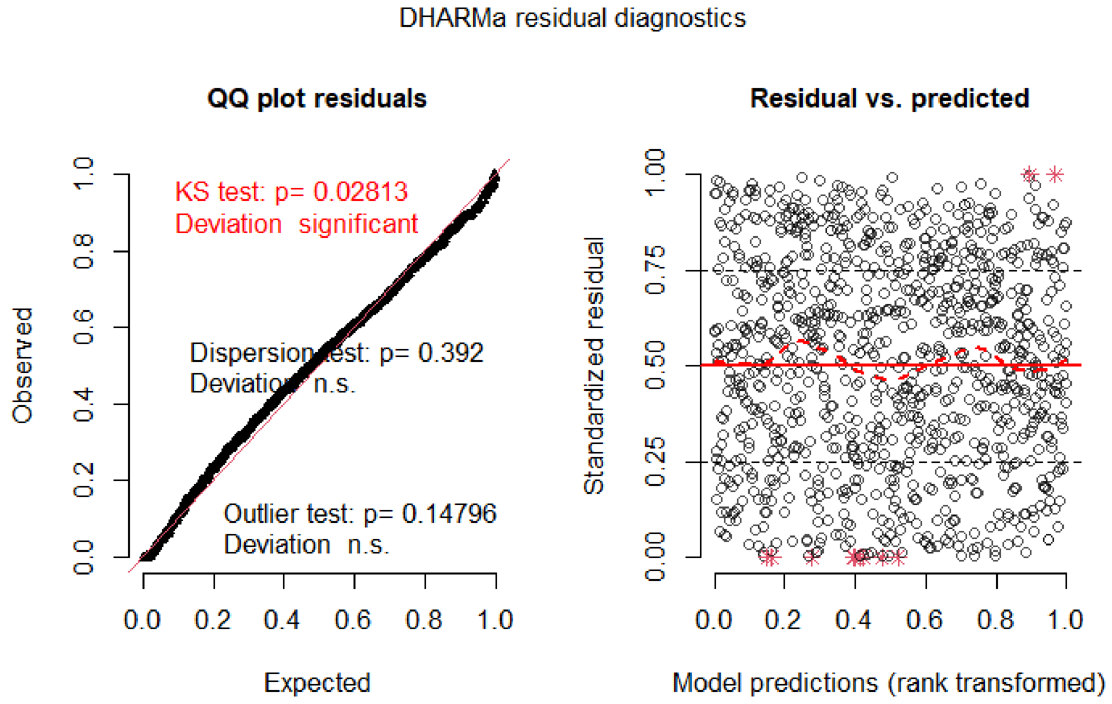


Figure 19 **Simulated randomised quantile residuals: litter depth**

7.3 Surface fuel hazard: litter cover

Table 13 Model fitting summary: litter cover

Response	Litter cover is visually estimated as a percentage of three 0.04 ha plots per 9 hectare plot Proportion variable
Response transformation used	None
R package and function	glmmTMB function from glmmTMB package
Distribution used	Beta
Outliers removed	19 values greater than 0.25 were removed
Reported model formula	3_3way
Random factors	Site (a factor over 22 sites) Siteplot (a factor over 66 plots) Year.factor (a factor for each of the 5 survey years)
Other transformations compared	None
Other models attempted	4_way beta: Complex eigenvalues 3_way beta: No warnings but failed residual tests 3_way beta, no year as a random effect: No improvement over reported model 3_way with initial stem density as a three-category factor (var ~ poly(cbind(thinning,yrs.elapsed), 2) * site.quality * initSD.log.bin): No improvement over reported model No other distributions compared
Confidence comments	Low confidence: • Difficulty fitting a model to this cover variable • Failed all residual tests • ~10% model convergence issues in 999 prediction interval simulations

Model summary 11 Litter cover

```
Family: beta  ( logit )
Formula:          var ~ poly(cbind(thinning, initSD.log, yrs.elapsed), 2) * site.quality +
    (1 | year.factor) + (1 | site) + (1 | siteplot)
Data: dat.outlier

     AIC      BIC   logLik deviance df.resid
 -2267.2  -2150.3   1157.6  -2315.2      939

Random effects:

Conditional model:
 Groups      Name        Variance Std.Dev.
```

```
 year.factor (Intercept) 0.06132  0.2476
 site        (Intercept) 0.07030  0.2651
 siteplot    (Intercept) 0.02927  0.1711
Number of obs: 963, groups:  year.factor, 5; site, 22; siteplot, 66

Dispersion parameter for beta family (): 13.9

Conditional model:
                                                                      Estimate Std. Error z value Pr(>|z|)
(Intercept)                                                             1.9163     0.1488  12.882  < 2e-16 ***
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.0                 -0.1705     2.0203  -0.084 0.932747
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)2.0.0                  1.0837     1.7012   0.637 0.524130
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.0                  1.3223     2.2335   0.592 0.553847
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.1.0                114.9513    70.6232   1.628 0.103595
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.2.0                  0.7279     2.0896   0.348 0.727589
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.1                  7.2988     4.1178   1.773 0.076307 .
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.1               -113.7647    59.2394  -1.920 0.054805 .
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.1               -151.9815    43.9533  -3.458 0.000545 ***
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.2                  3.9901     1.5990   2.495 0.012581 *
site.qualitySQ2                                                         0.2043     0.1401   1.458 0.144771
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.0:site.qualitySQ2   -1.3597     2.5400  -0.535 0.592433
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)2.0.0:site.qualitySQ2   -0.3980     2.8259  -0.141 0.887998
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.0:site.qualitySQ2    1.0802     3.1615   0.342 0.732595
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.1.0:site.qualitySQ2  -88.5585    95.2502  -0.930 0.352502
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.2.0:site.qualitySQ2   -1.2615     2.5843  -0.488 0.625445
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.1:site.qualitySQ2    0.6441     2.1393   0.301 0.763349
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.1:site.qualitySQ2   85.4506    73.4857   1.163 0.244903
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.1:site.qualitySQ2  269.1040    58.6038   4.592 4.39e-06 ***
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.2:site.qualitySQ2   -0.8802     1.9507  -0.451 0.651843
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

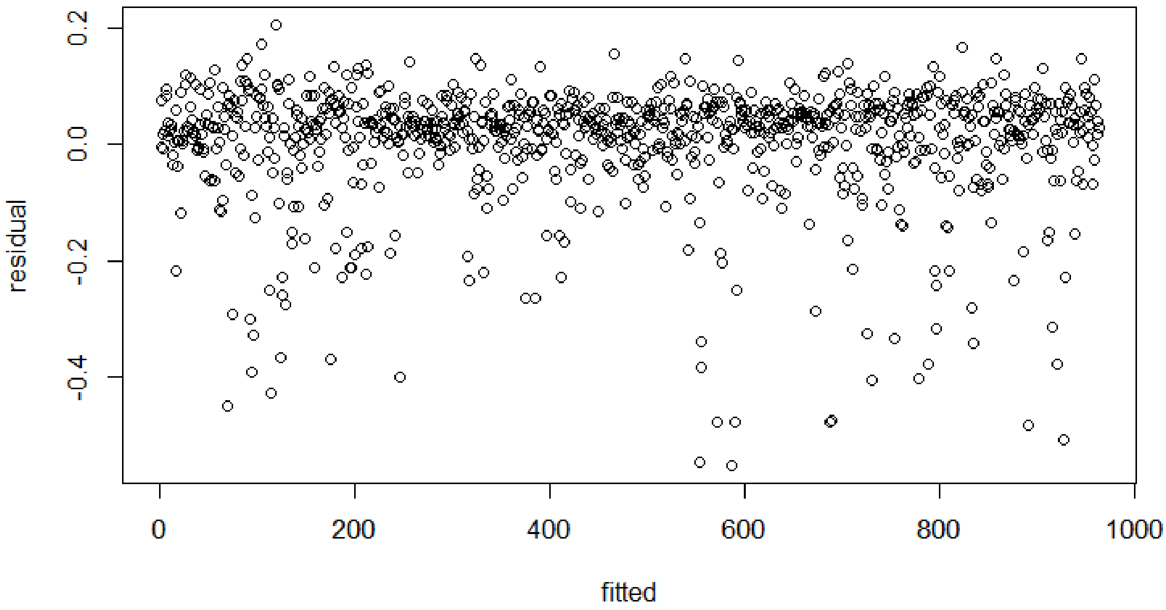


Figure 20 Fitted values and data residuals: litter cover

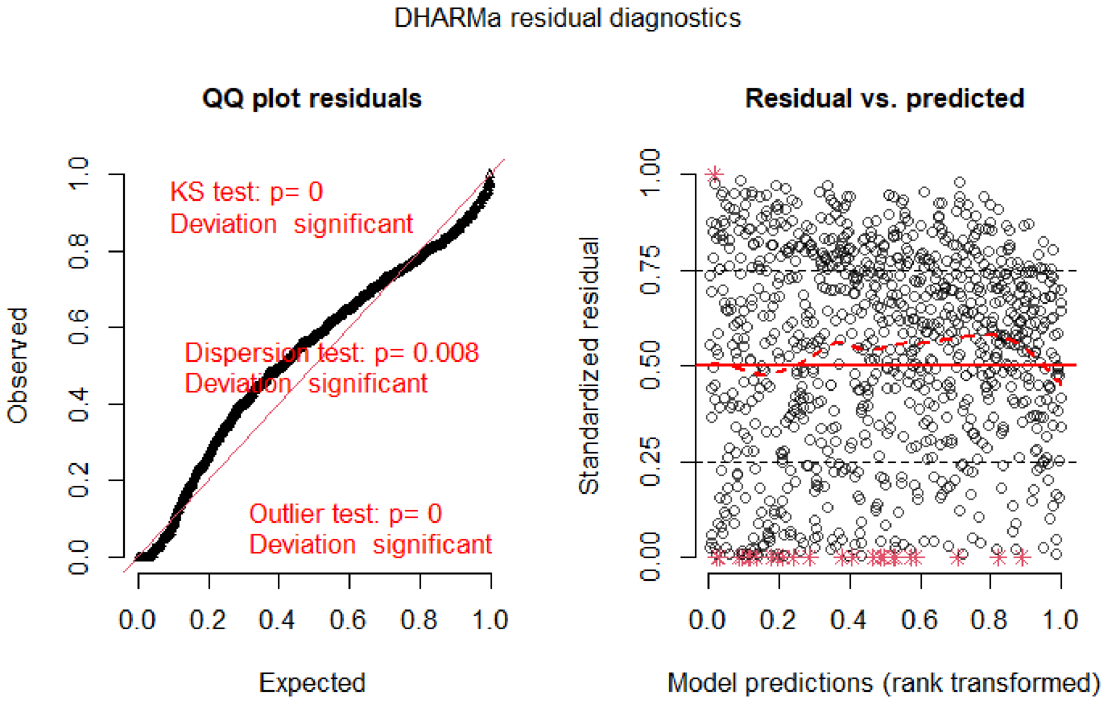


Figure 21 Simulated randomised quantile residuals: litter cover

7.4 Surface fuel hazard assessment

Table 14 Model fitting summary: surface fuel hazard

Response	Probability of being in each surface fuel hazard category
Response transformation used	None
R package and function	brm function from brms package with family specified as cratio(threshold = flexible)
Distribution used	Continuation ratio with flexible category thresholds The cumulative model has an underlying distribution that spans all categories, which is appropriate for fuel hazard because hazard is an underlying continuous variable and responses can move up and down as well as jump categories. (In contrast, an adjacent categories model assumes each level of risk rating has its own distribution, and sequential models assume response data can only move sequentially through the levels). Flexible thresholds allow for the boundaries between hazard rating categories to have unequal sizes and account for different proportions of the data. This is supported by the input data where more sites report moderate or high ratings than low or very high ratings.
Outliers removed	None
Model reported	4_way, with iterations = 2000, chains = 4, warmup = 500, max tree depth = 15, priors for all betas = normal(0,10)
Random factors	Site (a factor over 22 sites) Siteplot (a factor over 66 plots) Subplot (a factor over 198 subplots) Year.factor (a factor for each of the 5 survey years)
Other transformations compared	None
Other models attempted	4_way with iterations = 4000, chains =6. Failed to converge 3_3way with iterations = 4000, chains =6. Failed to converge No_SDi with iterations = 4000, chains =6. Failed to converge 4_way_noYrf with iterations = 4000, chains =6. Failed to converge No other distributions compared
Confidence comments	High confidence: • No convergence or fit warnings • Chains mixed well

Model summary 12 Surface fuel hazard

Family: cratio

Links: mu = logit; disc = identity

Formula: var ~ poly(cbind(thinning, initSD.log, yrs.elapsed), 2) * site.quality + thinning:initSD.log:yrs.elapsed + thinning:initSD.log:yrs.elapsed:site.quality + (1 | year.factor) + (1 | site) + (1 | siteplot) + (1 | subplot)

Data: dat (Number of observations: 984)

Samples: 4 chains, each with iter = 4000; warmup = 500; thin = 1;

total post-warmup samples = 14000

```
Group-Level Effects:
~site (Number of levels: 22)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.55      0.27     0.05     1.09 1.00     1396     2209

~siteplot (Number of levels: 66)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.30      0.22     0.01     0.80 1.00     1174     2112

~subplot (Number of levels: 198)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     1.87      0.15     1.59     2.17 1.00     4563     8588

~year.factor (Number of levels: 5)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.79      0.51     0.21     2.11 1.00     3029     5158

Population-Level Effects:
                                               Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept[1]                                      -4.24      0.54    -5.34    -3.20 1.00     3530     4504
Intercept[2]                                      -1.21      0.51    -2.24    -0.21 1.00     3296     4070
Intercept[3]                                       1.73      0.52     0.69     2.75 1.00     3303     4349
Intercept[4]                                       5.48      0.61     4.28     6.68 1.00     4065     5593
polycbindthinninginitSD.logyrs.elapsed21.0.0          0.10      5.84   -11.31    11.60 1.00     9079     9804
polycbindthinninginitSD.logyrs.elapsed22.0.0         -4.74      4.51   -13.47     4.15 1.00     7497    10060
polycbindthinninginitSD.logyrs.elapsed20.1.0          6.08      5.81    -5.34    17.38 1.00     6859     9370
polycbindthinninginitSD.logyrs.elapsed21.1.0          0.46      9.93   -18.57    20.10 1.00    24139    10754
polycbindthinninginitSD.logyrs.elapsed20.2.0         -1.58      5.81   -12.88     9.69 1.00     6088     8547
polycbindthinninginitSD.logyrs.elapsed20.0.1          7.24      8.57   -11.21    21.78 1.00     4676     7821
polycbindthinninginitSD.logyrs.elapsed21.0.1         -0.12      9.87   -19.41    19.21 1.00    23229    10878
polycbindthinninginitSD.logyrs.elapsed20.1.1          1.12      9.99   -18.57    20.83 1.00    25504    10361
polycbindthinninginitSD.logyrs.elapsed20.0.2          4.60      3.73    -2.74    11.76 1.00    13164    10499
site.qualitySQ2                                    0.06      0.46    -0.84     0.96 1.00     5299     7581
polycbindthinninginitSD.logyrs.elapsed21.0.0:site.qualitySQ2   -10.86      6.74   -24.19     2.24 1.00     9568
10224
polycbindthinninginitSD.logyrs.elapsed22.0.0:site.qualitySQ2     7.34      5.60    -3.53    18.28 1.00     8941
10153
polycbindthinninginitSD.logyrs.elapsed20.1.0:site.qualitySQ2     0.27      7.15   -13.79    14.06 1.00     7096
9203
polycbindthinninginitSD.logyrs.elapsed21.1.0:site.qualitySQ2     0.92     10.02   -19.09    20.55 1.00    16856
10592
polycbindthinninginitSD.logyrs.elapsed20.2.0:site.qualitySQ2    -1.16      6.85   -14.44    12.53 1.00     6972
9615
polycbindthinninginitSD.logyrs.elapsed20.0.1:site.qualitySQ2     2.11      5.02    -7.71    11.90 1.00     9768
11163
polycbindthinninginitSD.logyrs.elapsed21.0.1:site.qualitySQ2     0.39     10.05   -19.40    20.14 1.00    24790
9541
polycbindthinninginitSD.logyrs.elapsed20.1.1:site.qualitySQ2     1.55      9.99   -17.66    20.92 1.00    21863
9988
polycbindthinninginitSD.logyrs.elapsed20.0.2:site.qualitySQ2     1.68      3.96    -6.05     9.39 1.00    12726
10052
```

```
thinning:initSD.log:yrs.elapsed                    -0.01     0.04    -0.09     0.07 1.00     6762     9470
site.qualitySQ2:thinning:initSD.log:yrs.elapsed              0.05     0.05    -0.04     0.13 1.00     6723     8950

Family Specific Parameters:
     Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
disc     1.00      0.00     1.00     1.00 1.00    14000    14000

Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

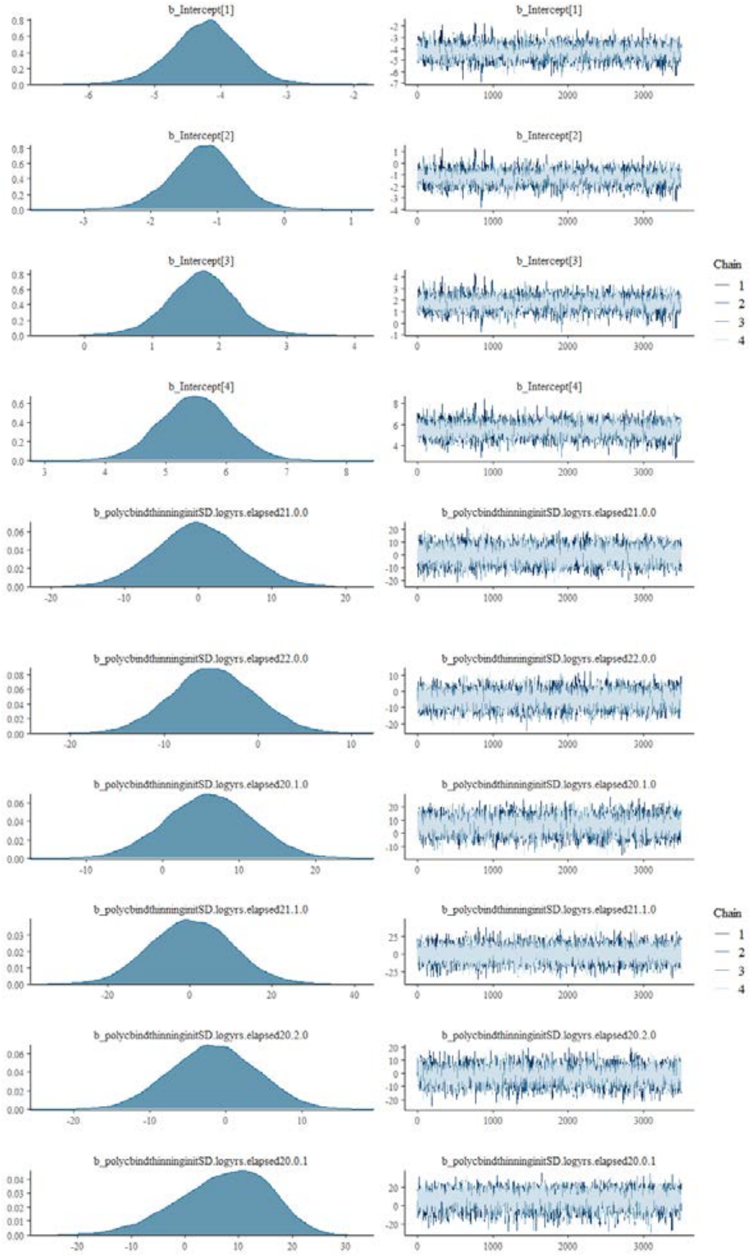


Figure 22 Posterior distributions (left) and chain mixing (right): surface fuel hazard

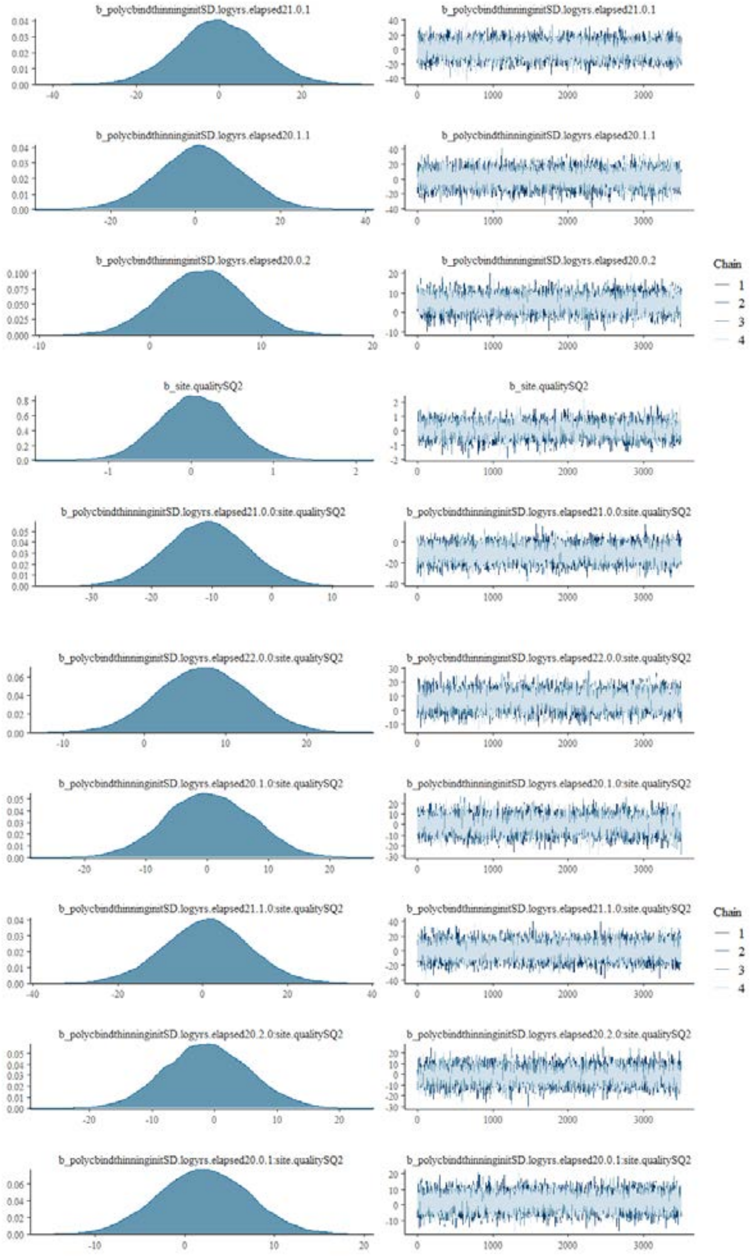


Figure 22 (cont.) **Posterior distributions (left) and chain mixing (right): surface fuel hazard**

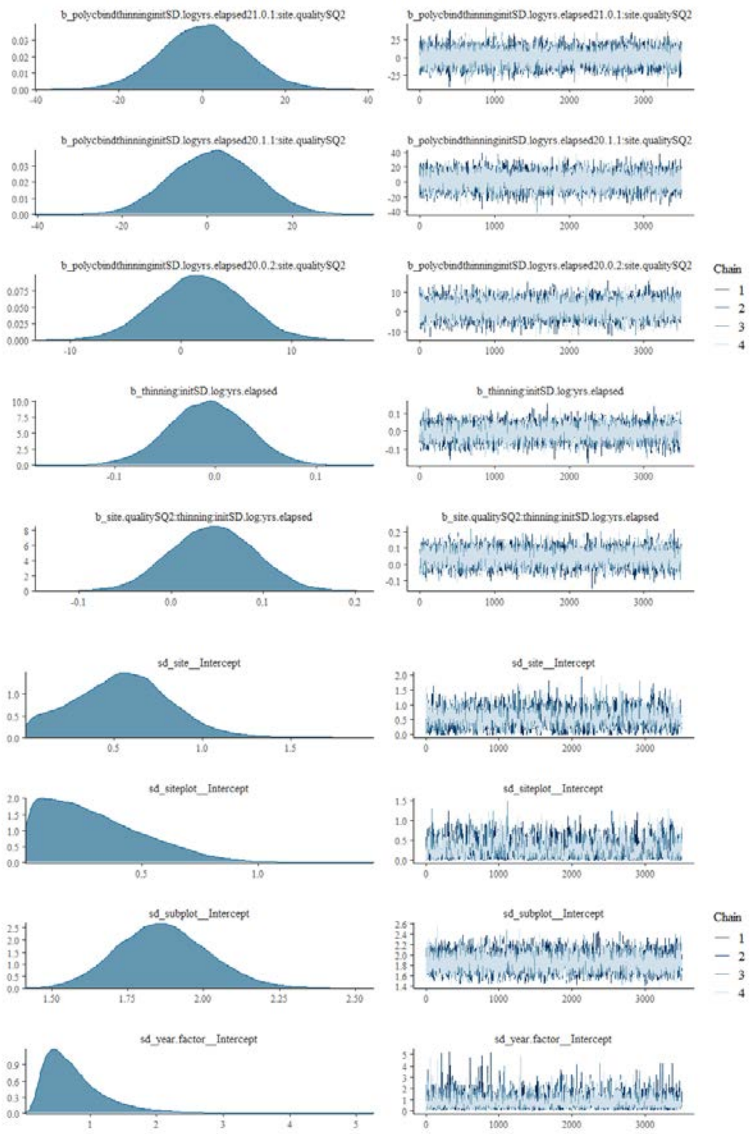


Figure 22 (cont.) Posterior distributions (left) and chain mixing (right): surface fuel hazard

7.5 Near surface fuel hazard: live near surface vegetation

Table 15 Model fitting summary: live near surface vegetation cover

Response	Percent live vegetation cover visually estimated for three 0.04 ha subplots in each 9 ha plot Percentage: Positive continuous bounded variable
Model reported	No model reported
Models attempted	4_way logged Gaussian: No warnings, but failed all residual tests 4_way logged beta: Failed to converge 3_way beta: No warnings, but failed all residual tests 3_way beta with 32 observations >0.5 excluded: No warnings, fails Kurtosis-Skewness test but conforms with the others; but prediction interval simulations fail 3_way beta with no year random effect: No improvement to residuals 2_3_way beta with no stem density * thinning interaction, and stem density as a three-category factor: No improvement to residuals 3_way beta with zero inflation across years.elapsed: No improvement to residuals

7.6 Near surface fuel hazard: dead near surface vegetation

Table 16 Model fitting summary: dead near surface vegetation cover

Response	Percent dead vegetation cover visually estimated for three 0.04 ha subplots in each 9 ha plot Percentage: Positive continuous bounded variable
Model reported	No model reported
Models attempted	4_way beta: Non positive definite hessian 3_way beta: Non positive definite hessian 3_way beta with 23 observations >0.2 excluded: No warnings, failed all residual tests 3_way logged beta with 23 observations excluded: No warnings, failed only the Kurtosis-Skewness test, but prediction interval simulations failed 3_way logged beta with 23 observations excluded with no year random effect: No improvement to residuals 2_3_way beta with no stem density * thinning interaction, and stem density as a three-category factor: No improvement to residuals

7.7 Near surface fuel hazard assessment

Table 17 Model fitting summary: near surface fuel hazard

Response	Probability of being in each near surface fuel hazard category
Response transformation used	None
R package and function	brm function from brms package with family specified as cratio(threshold = flexible)
Distribution used	Continuation ratio with flexible category thresholds The cumulative model has an underlying distribution that spans all categories, which is appropriate for fuel hazard because hazard is an underlying continuous variable and responses can move up and down as well as jump categories. (In contrast, an adjacent categories model assumes each level of risk rating has its own distribution, and sequential models assume response data can only move sequentially through the levels). Flexible thresholds allow for the boundaries between hazard rating categories to have unequal sizes and account for different proportions of the data. This is supported by the input data where more sites report low or moderate ratings than high or very high ratings.
Outliers removed	None
Model reported	4_way, with iterations = 2000, chains = 4, warmup = 500, max tree depth = 15, priors for all betas = normal(0,10)
Random factors	Site (a factor over 22 sites) Siteplot (a factor over 66 plots) Subplot (a factor over 198 subplots) Year.factor (a factor for each of the 5 survey years)
Other transformations compared	None
Other models attempted	4_way with iterations = 4000, chains =6. Failed to converge 3_3way with iterations = 4000, chains =6. Failed to converge No_SDi with iterations = 4000, chains =6. Failed to converge 4_way_noYrf with iterations = 4000, chains =6. Failed to converge No other distributions compared
Confidence comments	High confidence: • No convergence or fit warnings • Chains mixed well

Model summary 13 Near surface fuel hazard

Family: cratio

Links: mu = logit; disc = identity

Formula: var ~ poly(cbind(thinning, initSD.log, yrs.elapsed), 2) * site.quality + thinning:initSD.log:yrs.elapsed + thinning:initSD.log:yrs.elapsed:site.quality + (1 | year.factor) + (1 | site) + (1 | siteplot) + (1 | subplot)

Data: dat (Number of observations: 990)

Samples: 4 chains, each with iter = 4000; warmup = 500; thin = 1;

total post-warmup samples = 14000

```
Group-Level Effects:
~site (Number of levels: 22)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.66      0.18     0.33     1.05 1.00     4546     4409

~siteplot (Number of levels: 66)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.38      0.19     0.03     0.74 1.00     1768     2750

~subplot (Number of levels: 198)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.67      0.13     0.40     0.93 1.00     3187     3409

~year.factor (Number of levels: 5)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.83      0.51     0.20     2.16 1.00     3462     4015

Population-Level Effects:
                                            Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept[1]                                   -2.90      0.52    -4.03    -1.93 1.00     4897     4953
Intercept[2]                                    0.90      0.50    -0.19     1.85 1.00     4806     4996
Intercept[3]                                    4.03      0.59     2.83     5.17 1.00     5636     6350
Intercept[4]                                    2.84      0.87     1.17     4.61 1.00     8696     8052
polycbindthinninginitSD.logyrs.elapsed21.0.0                  -4.75      5.59   -15.94     6.15 1.00    11026    10821
polycbindthinninginitSD.logyrs.elapsed22.0.0                  -3.04      4.00   -10.90     4.91 1.00    12873    11182
polycbindthinninginitSD.logyrs.elapsed20.1.0                  -1.05      4.75   -10.45     8.16 1.00    12109    11164
polycbindthinninginitSD.logyrs.elapsed21.1.0                  -0.32      9.94   -20.03    19.16 1.00    33643     9378
polycbindthinninginitSD.logyrs.elapsed20.2.0                  -3.24      4.69   -12.43     6.11 1.00    11596    10089
polycbindthinninginitSD.logyrs.elapsed20.0.1                   3.62      6.99   -10.73    17.09 1.00    12371    10751
polycbindthinninginitSD.logyrs.elapsed21.0.1                  -0.08     10.06   -19.67    19.42 1.00    29454    10481
polycbindthinninginitSD.logyrs.elapsed20.1.1                   0.77      9.78   -18.28    20.09 1.00    26738     9847
polycbindthinninginitSD.logyrs.elapsed20.0.2                 -13.67      4.43   -22.41    -5.16 1.00     8558     7710
site.qualitySQ2                                -0.16      0.41    -0.97     0.65 1.00     8271     9511
polycbindthinninginitSD.logyrs.elapsed21.0.0:site.qualitySQ2     8.79      6.54    -4.03    21.62 1.00    12345
10962
polycbindthinninginitSD.logyrs.elapsed22.0.0:site.qualitySQ2     8.55      5.26    -1.77    18.88 1.00    15929
11587
polycbindthinninginitSD.logyrs.elapsed20.1.0:site.qualitySQ2    -0.03      6.01   -11.70    11.82 1.00    13606
11120
polycbindthinninginitSD.logyrs.elapsed21.1.0:site.qualitySQ2    -0.59      9.92   -19.78    19.01 1.00    22986
10586
polycbindthinninginitSD.logyrs.elapsed20.2.0:site.qualitySQ2    -3.51      5.62   -14.55     7.50 1.00    12364
10673
polycbindthinninginitSD.logyrs.elapsed20.0.1:site.qualitySQ2    -2.11      4.93   -11.85     7.53 1.00    14036
11042
polycbindthinninginitSD.logyrs.elapsed21.0.1:site.qualitySQ2    -0.05      9.99   -19.39    19.38 1.00    27173
9845
polycbindthinninginitSD.logyrs.elapsed20.1.1:site.qualitySQ2    -2.29      9.79   -21.40    16.77 1.00    28049
10273
polycbindthinninginitSD.logyrs.elapsed20.0.2:site.qualitySQ2    17.86      4.28     9.51    26.40 1.00    17406
10715
```

```
thinning:initSD.log:yrs.elapsed                          0.00      0.04     -0.07     0.08 1.00     7883     10502
site.qualitySQ2:thinning:initSD.log:yrs.elapsed             -0.05      0.05     -0.14     0.04 1.00     8544     9886

Family Specific Parameters:
     Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
disc     1.00      0.00     1.00     1.00 1.00    14000    14000

Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

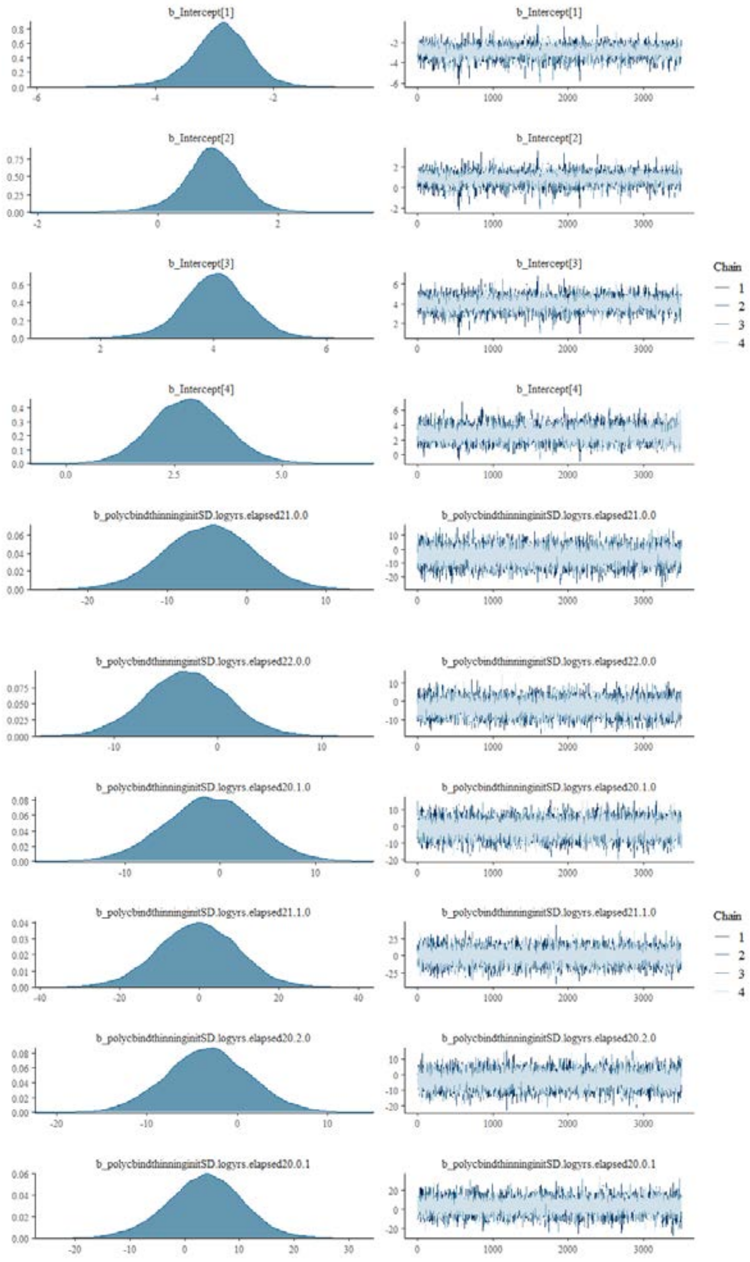


Figure 23 Posterior distributions (left) and chain mixing (right): near surface fuel hazard

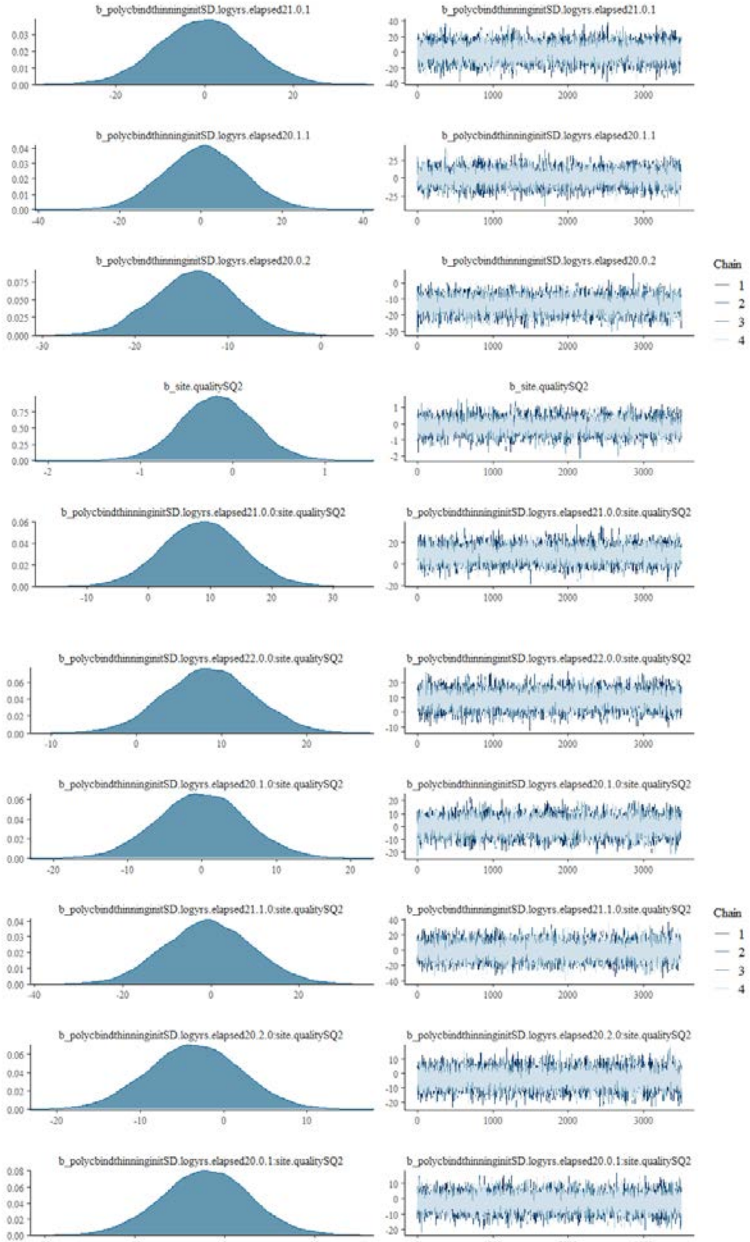


Figure 23 (cont.) **Posterior distributions (left) and chain mixing (right): near surface fuel hazard**

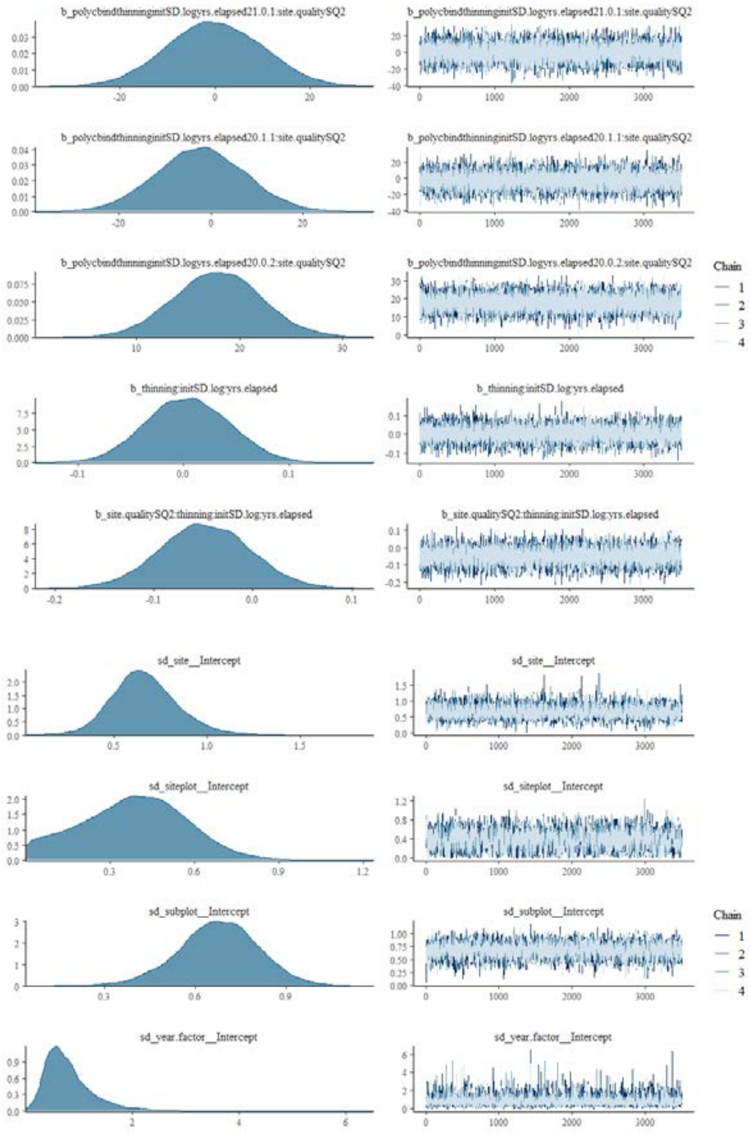


Figure 23 (cont.) **Posterior distributions (left) and chain mixing (right): near surface fuel hazard**

7.8 Combined surface and near surface fuel hazard assessment

Table 18 Model fitting summary: combined surface and near surface fuel hazard

Response	Probability of being in each combined surface and near surface fuel hazard category
Response transformation used	None
R package and function	brm function from brms package with family specified as cratio(threshold = flexible)
Distribution used	Continuation ratio with flexible category thresholds The cumulative model has an underlying distribution that spans all categories, which is appropriate for fuel hazard because hazard is an underlying continuous variable and responses can move up and down as well as jump categories. (In contrast, an adjacent categories model assumes each level of risk rating has its own distribution, and sequential models assume response data can only move sequentially through the levels). Flexible thresholds allow for the boundaries between hazard rating categories to have unequal sizes and account for different proportions of the data. This is supported by the input data where more sites report very high ratings than low, moderate or extreme ratings.
Outliers removed	None
Model reported	4_way, with iterations = 2000, chains = 4, warmup = 500, max tree depth = 15, priors for all betas = normal(0,10)
Random factors	Site (a factor over 22 sites) Siteplot (a factor over 66 plots) Subplot (a factor over 198 subplots) Year.factor (a factor for each of the 5 survey years)
Other transformations compared	None
Other models attempted	4_way with iterations = 4000, chains =6. Failed to converge 3_3way with iterations = 4000, chains =6. Failed to converge No_SDi with iterations = 4000, chains =6. Failed to converge 4_way_noYrf with iterations = 4000, chains =6. Failed to converge No other distributions compared
Confidence comments	High confidence: • No convergence or fit warnings • Chains mixed well

Model summary 14 Combined surface and near surface fuel hazard

Family: cratio

Links: mu = logit; disc = identity

Formula: var ~ poly(cbind(thinning, initSD.log, yrs.elapsed), 2) * site.quality + thinning:initSD.log:yrs.elapsed + thinning:initSD.log:yrs.elapsed:site.quality + (1 | year.factor) + (1 | site) + (1 | siteplot) + (1 | subplot)

Data: dat (Number of observations: 984)

Samples: 4 chains, each with iter = 4000; warmup = 500; thin = 1;

```
    total post-warmup samples = 14000
Group-Level Effects:
~site (Number of levels: 22)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.44      0.24     0.04     0.95 1.00     1588     3231
~siteplot (Number of levels: 66)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.23      0.17     0.01     0.62 1.00     2091     3578

~subplot (Number of levels: 198)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     1.65      0.14     1.39     1.94 1.00     5247     7868

~year.factor (Number of levels: 5)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.85      0.56     0.23     2.27 1.00     3360     6303

Population-Level Effects:
                                                          Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept[1]                                                 -4.37      0.56    -5.44    -3.20 1.00     3603     3818
Intercept[2]                                                 -1.82      0.52    -2.79    -0.71 1.00     3296     3633
Intercept[3]                                                 -1.58      0.52    -2.56    -0.47 1.00     3341     3631
Intercept[4]                                                  3.76      0.55     2.75     4.94 1.00     3492     4022
polycbindthinninginitSD.logyrs.elapsed21.0.0                  0.94      5.71   -10.34    12.21 1.00    12746    10818
polycbindthinninginitSD.logyrs.elapsed22.0.0                 -3.73      4.44   -12.61     4.97 1.00     9459     9462
polycbindthinninginitSD.logyrs.elapsed20.1.0                  3.25      5.51    -7.55    14.05 1.00     8429    10241
polycbindthinninginitSD.logyrs.elapsed21.1.0                  0.19     10.13   -19.48    20.15 1.00    32920     9754
polycbindthinninginitSD.logyrs.elapsed20.2.0                 -1.34      5.59   -12.32     9.72 1.00     8872    10488
polycbindthinninginitSD.logyrs.elapsed20.0.1                  5.51      8.38   -12.16    20.14 1.00     5623     8288
polycbindthinninginitSD.logyrs.elapsed21.0.1                 -0.17     10.03   -19.69    19.46 1.00    30689    10392
polycbindthinninginitSD.logyrs.elapsed20.1.1                  0.32      9.93   -19.18    19.66 1.00    27795     9781
polycbindthinninginitSD.logyrs.elapsed20.0.2                 -0.46      3.80    -7.79     7.09 1.00    15388    11014
site.qualitySQ2                                               0.02      0.43    -0.81     0.86 1.00     6748     8522
polycbindthinninginitSD.logyrs.elapsed21.0.0:site.qualitySQ2    -9.77      6.63   -22.90     3.07 1.00    11837
10235
polycbindthinninginitSD.logyrs.elapsed22.0.0:site.qualitySQ2     9.95      5.56    -1.03    20.90 1.00    13336
11313
polycbindthinninginitSD.logyrs.elapsed20.1.0:site.qualitySQ2     1.61      6.81   -11.62    15.01 1.00     9499
9511
polycbindthinninginitSD.logyrs.elapsed21.1.0:site.qualitySQ2     0.79      9.98   -18.72    20.21 1.00    25416
9455
polycbindthinninginitSD.logyrs.elapsed20.2.0:site.qualitySQ2    -5.47      6.52   -18.02     7.39 1.00     9992
10646
polycbindthinninginitSD.logyrs.elapsed20.0.1:site.qualitySQ2     2.36      4.99    -7.41    12.17 1.00    12229
10746
polycbindthinninginitSD.logyrs.elapsed21.0.1:site.qualitySQ2     0.30     10.14   -19.38    20.01 1.00    31452
9259
polycbindthinninginitSD.logyrs.elapsed20.1.1:site.qualitySQ2     0.71      9.92   -18.91    20.07 1.00    30480
10409
polycbindthinninginitSD.logyrs.elapsed20.0.2:site.qualitySQ2    11.51      4.09     3.51    19.65 1.00    18530
11212
```

```
thinning:initSD.log:yrs.elapsed                        -0.02      0.04     -0.09      0.06 1.00     10042     11474
site.qualitySQ2:thinning:initSD.log:yrs.elapsed             0.04      0.05     -0.05      0.13 1.00      8767     10414

Family Specific Parameters:
     Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
disc     1.00      0.00      1.00      1.00 1.00    14000    14000

Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

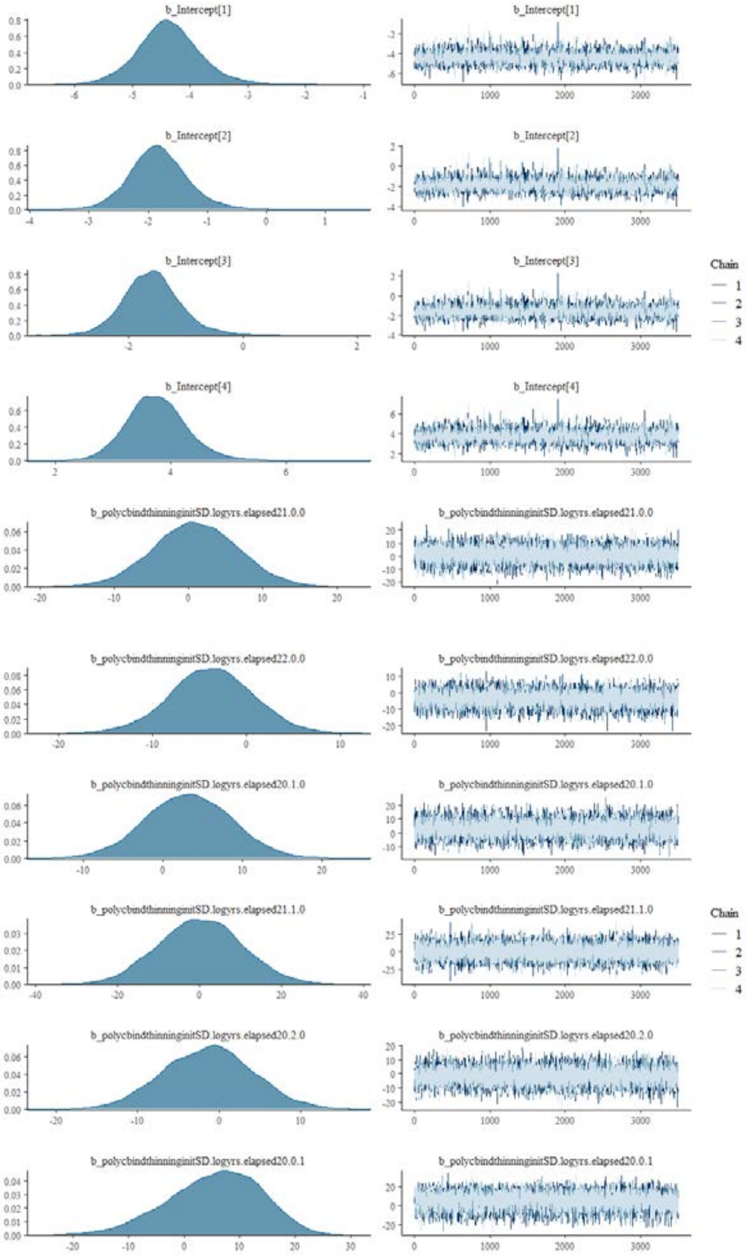


Figure 24 Posterior distributions (left) and chain mixing (right): combined surface and near surface fuel hazard

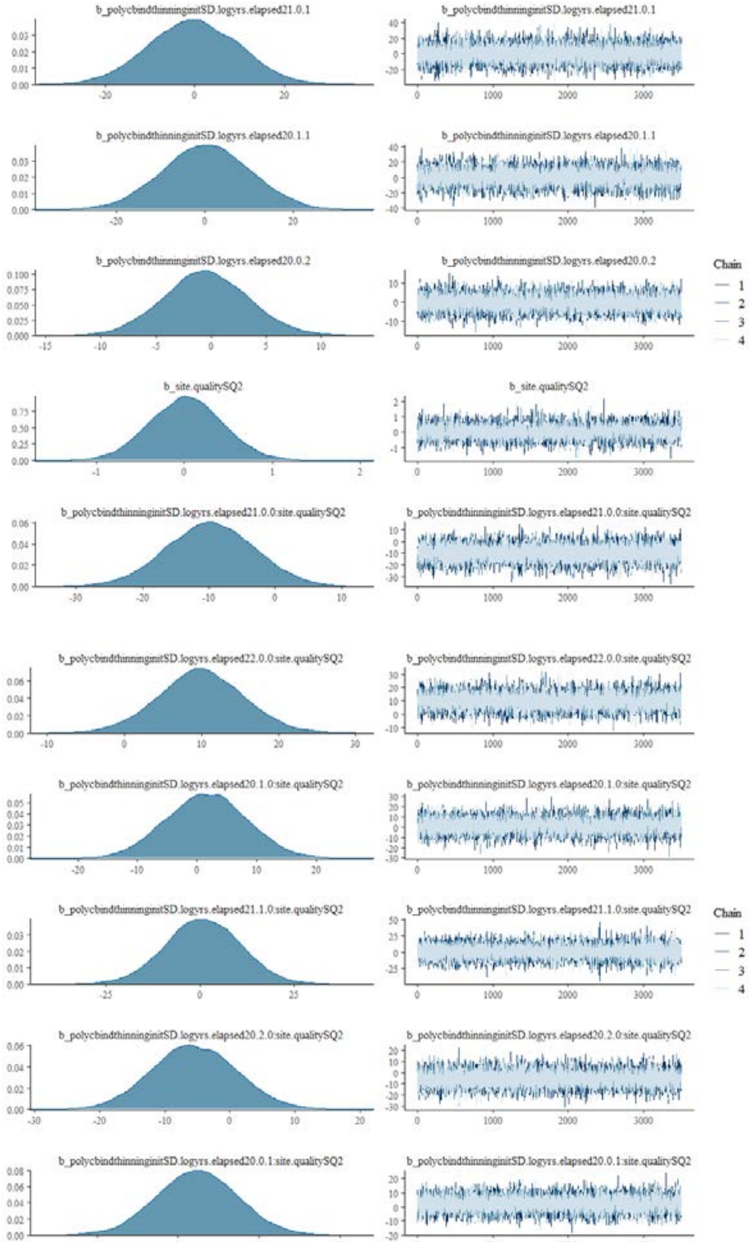


Figure 24 (cont.) **Posterior distributions (left) and chain mixing (right): combined surface and near surface fuel hazard**

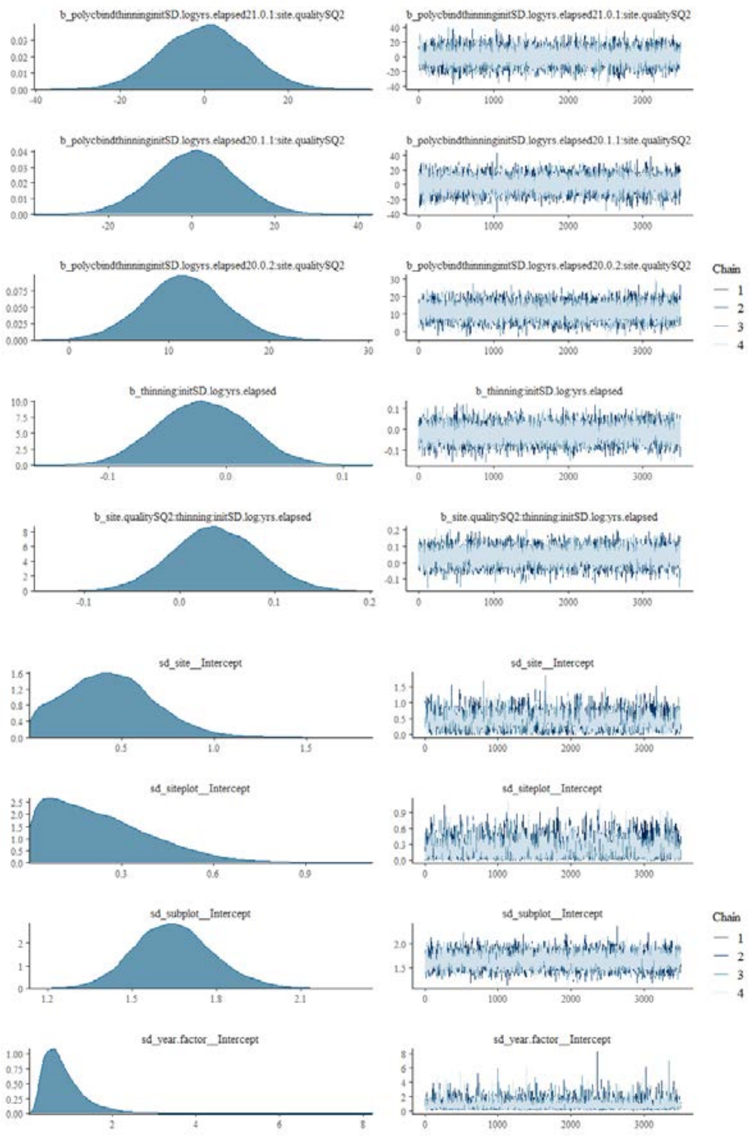


Figure 24 (cont.) **Posterior distributions (left) and chain mixing (right): combined surface and near surface fuel hazard**

7.9 Elevated fuel hazard: live elevated vegetation cover

Not modelled.

7.10 Elevated fuel hazard: dead elevated vegetation cover

Not modelled.

7.11 Elevated fuel hazard assessment

Table 19 Model fitting summary: elevated fuel hazard

Response	Probability of being in each elevated fuel hazard category
Response transformation used	None
R package and function	brm function from brms package with family specified as cratio(threshold = flexible)
Distribution used	Continuation ratio with flexible category thresholds The cumulative model has an underlying distribution that spans all categories, which is appropriate for fuel hazard because hazard is an underlying continuous variable and responses can move up and down as well as jump categories. (In contrast, an adjacent categories model assumes each level of risk rating has its own distribution, and sequential models assume response data can only move sequentially through the levels). Flexible thresholds allow for the boundaries between hazard rating categories to have unequal sizes and account for different proportions of the data. This is supported by the input data where more sites report very high ratings than low, moderate or extreme ratings.
Outliers removed	None
Model reported	4_way, with iterations = 2000, chains = 4, warmup = 500, max tree depth = 15, priors for all betas = normal(0,10)
Random factors	Site (a factor over 22 sites) Siteplot (a factor over 66 plots) Subplot (a factor over 198 subplots) Year.factor (a factor for each of the 5 survey years)
Other transformations compared	None
Other models attempted	4_way with iterations = 4000, chains =6. Failed to converge 3_3way with iterations = 4000, chains =6. Failed to converge No_SDi with iterations = 4000, chains =6. Failed to converge 4_way_noYrf with iterations = 4000, chains =6. Failed to converge No other distributions compared
Confidence comments	High confidence: • No convergence or fit warnings • Chains mixed well

Model summary 15 Elevated fuel hazard

Family: cratio

Links: mu = logit; disc = identity

Formula: var ~ poly(cbind(thinning, initSD.log, yrs.elapsed), 2) * site.quality + thinning:initSD.log:yrs.elapsed + thinning:initSD.log:yrs.elapsed:site.quality + (1 | year.factor) + (1 | site) + (1 | siteplot) + (1 | subplot)

Data: dat (Number of observations: 990)

Samples: 4 chains, each with iter = 4000; warmup = 500; thin = 1;

total post-warmup samples = 14000

```
Group-Level Effects:
~site (Number of levels: 22)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.34      0.20     0.02     0.75 1.00     2650     4233

~siteplot (Number of levels: 66)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.50      0.21     0.05     0.88 1.00     1706     2075

~subplot (Number of levels: 198)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     0.69      0.20     0.24     1.05 1.00     1573     1401

~year.factor (Number of levels: 5)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)     1.96      0.95     0.80     4.37 1.00     5004     6857

Population-Level Effects:
                                                    Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
Intercept[1]                                            0.36      0.99    -1.84     2.06 1.00     3653     4217
Intercept[2]                                            7.06      1.27     4.54     9.54 1.00     4560     4842
polycbindthinninginitSD.logyrs.elapsed21.0.0                  5.94      6.11    -6.01    17.72 1.00    11468    10106
polycbindthinninginitSD.logyrs.elapsed22.0.0                  2.13      4.50    -6.67    10.88 1.00    11283    10117
polycbindthinninginitSD.logyrs.elapsed20.1.0                 -9.52      5.01   -19.31     0.49 1.00     9266    10267
polycbindthinninginitSD.logyrs.elapsed21.1.0                  1.01     10.10   -18.50    20.82 1.00    26595    10899
polycbindthinninginitSD.logyrs.elapsed20.2.0                  0.58      5.08    -9.44    10.56 1.00    10958    10791
polycbindthinninginitSD.logyrs.elapsed20.0.1                  9.52      9.30    -8.44    28.00 1.00    12436     9820
polycbindthinninginitSD.logyrs.elapsed21.0.1                 -0.57     10.01   -20.02    19.08 1.00    26250    10292
polycbindthinninginitSD.logyrs.elapsed20.1.1                  0.17      9.99   -19.41    19.85 1.00    27187     9359
polycbindthinninginitSD.logyrs.elapsed20.0.2                 -9.34      5.60   -20.18     1.65 1.00    16932    10710
site.qualitySQ2                                         0.35      0.39    -0.43     1.11 1.00     9227    10221
polycbindthinninginitSD.logyrs.elapsed21.0.0:site.qualitySQ2    -4.40      7.13   -18.26     9.61 1.00    11288
10041
polycbindthinninginitSD.logyrs.elapsed22.0.0:site.qualitySQ2     7.38      5.86    -3.89    19.11 1.00    12851
11334
polycbindthinninginitSD.logyrs.elapsed20.1.0:site.qualitySQ2     9.36      6.29    -3.19    21.77 1.00    10201
10212
polycbindthinninginitSD.logyrs.elapsed21.1.0:site.qualitySQ2     1.13      9.95   -18.57    20.67 1.00    27805
9105
polycbindthinninginitSD.logyrs.elapsed20.2.0:site.qualitySQ2     1.77      6.12   -10.35    13.89 1.00    10925
9966
polycbindthinninginitSD.logyrs.elapsed20.0.1:site.qualitySQ2    -0.57      6.95   -14.48    12.89 1.00    13800
9975
polycbindthinninginitSD.logyrs.elapsed21.0.1:site.qualitySQ2     0.04      9.92   -19.33    19.47 1.00    27900
8846
polycbindthinninginitSD.logyrs.elapsed20.1.1:site.qualitySQ2    -0.24      9.99   -19.87    19.55 1.00    24164
9436
polycbindthinninginitSD.logyrs.elapsed20.0.2:site.qualitySQ2     7.72      5.64    -3.14    18.69 1.00    15596
10892
thinning:initSD.log:yrs.elapsed                        -0.00      0.04    -0.09     0.08 1.00     9029     9956
site.qualitySQ2:thinning:initSD.log:yrs.elapsed             -0.01      0.05    -0.11     0.09 1.00     8082    10214
```

```
Family Specific Parameters:
     Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
disc     1.00      0.00      1.00      1.00 1.00    14000    14000

Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
and Tail_ESS are effective sample size measures, and Rhat is the potential
scale reduction factor on split chains (at convergence, Rhat = 1).
```

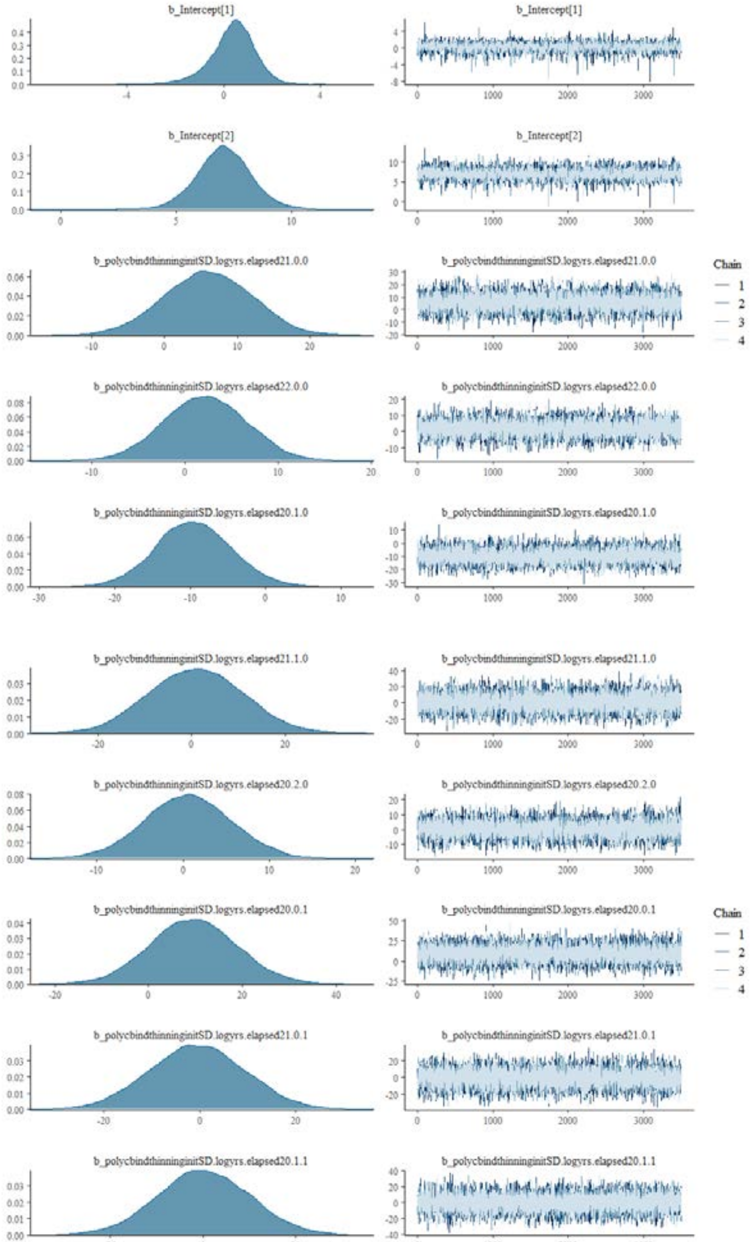


Figure 25 Posterior distributions (left) and chain mixing (right): elevated fuel hazard

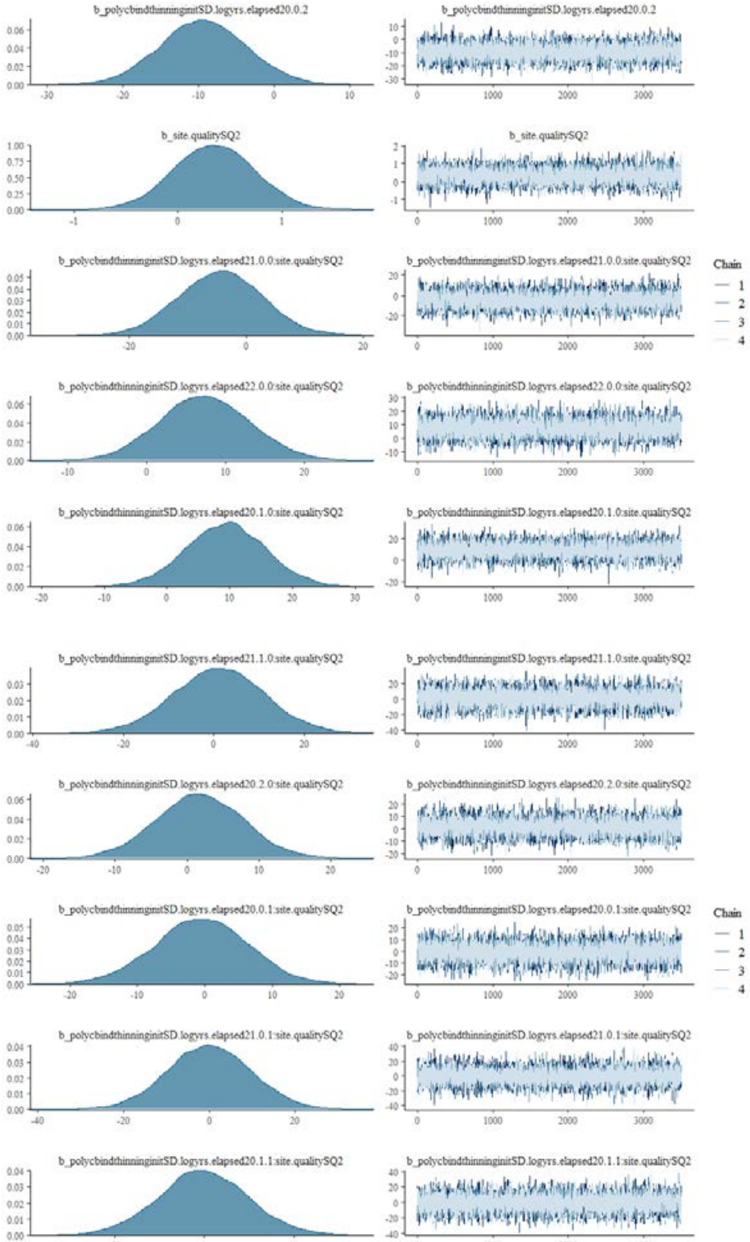


Figure 25 (cont.) **Posterior distributions (left) and chain mixing (right): elevated fuel hazard**

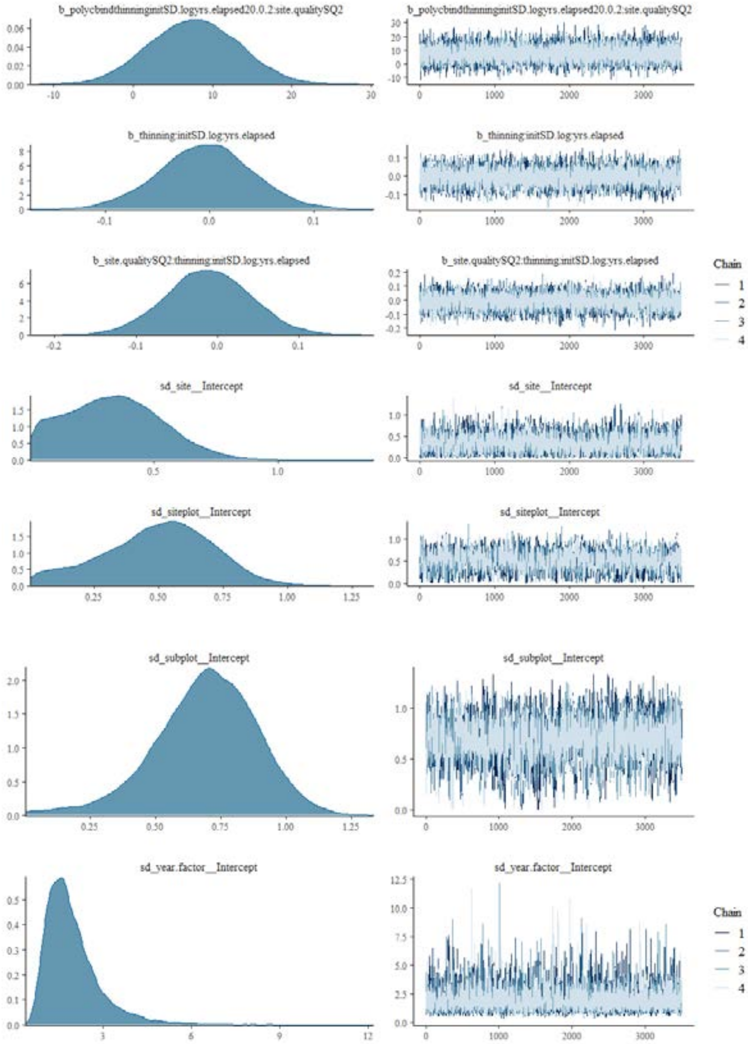


Figure 25 (cont.) **Posterior distributions (left) and chain mixing (right): elevated fuel hazard**

8. Model summaries: Floristics

8.1 Native plant species richness

Table 20 Model fitting summary: native plant species richness

Response	Number of native plant species per 0.04 ha subplot
Response transformation used	None
R package and function	glmer from lme4
Distribution used	Gaussian
Outliers removed	None
Reported model formula	4_way
Random factors	Site (a factor over 22 sites) Siteplot (a factor over 66 plots) Subplot (a factor over 198 subplots) Year.factor (a factor for each of the 5 survey years)
Other transformations compared	None
Other models attempted	4_way negative binomial: Failed to converge
Confidence comments	High confidence: • No convergence or fit warnings • Very minor deviation from expected for the Kurtosis-Skewness test • Very few convergence warnings in bootstrap simulations (~1% of 999)

Model summary 16 Native plant species richness

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: var ~ poly(cbind(thinning, initSD.log, yrs.elapsed), 2) * site.quality +
    thinning * initSD.log * yrs.elapsed * site.quality + (1 |      year.factor) + (1 | site) + (1 | siteplot) + (1 | subplot)
   Data: dat
Control: lmerControl(check.scaleX = "ignore", check.rankX = "silent.drop.cols")

REML criterion at convergence: 5469.3

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.61921 -0.62224  0.01596  0.59689  3.13978

Random effects:
 Groups      Name        Variance Std.Dev.
 subplot     (Intercept)  3.484   1.867
```

```
 siteplot    (Intercept)  2.008   1.417
 site        (Intercept)  7.863   2.804
 year.factor (Intercept)  7.196   2.682
 Residual                13.558   3.682
Number of obs: 990, groups:  subplot, 198; siteplot, 66; site, 22; year.factor, 5

Fixed effects:
                                                       Estimate Std. Error        df t value Pr(>|t|)
(Intercept)                                               31.508      5.760    400.585   5.471 7.92e-08 ***
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.0                  508.342    191.419    812.002   2.656  0.00807 **
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)2.0.0                  -18.812     10.947    277.023  -1.718  0.08683 .
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.0                   50.724     23.409    150.596   2.167  0.03182 *
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.1.0                  820.175    539.291    663.485   1.521  0.12878
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.2.0                   -4.745     16.977     48.626  -0.280  0.78104
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.1                  406.516    174.347    737.720   2.332  0.01999 *
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.1                15790.704   5929.755    814.071   2.663  0.00790
**
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.1                  708.246    297.999    656.961   2.377  0.01776 *
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.2                   -7.326      8.959    601.576  -0.818  0.41384
site.qualitySQ2                                             -14.336      6.813    826.049  -2.104  0.03565 *
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.0:site.qualitySQ2   -471.451    228.398    810.941  -2.064
0.03932 *
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)2.0.0:site.qualitySQ2     17.054     17.456    317.641   0.977
0.32931
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.0:site.qualitySQ2    -49.483     30.776    140.311  -1.608
0.11011
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.1.0:site.qualitySQ2  -1061.555    744.170    637.044  -1.426
0.15422
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.2.0:site.qualitySQ2     14.516     20.880     49.213   0.695
0.49019
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.1:site.qualitySQ2   -428.621    206.292    810.334  -2.078
0.03805 *
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.1:site.qualitySQ2 -16001.671   7045.001    810.647  -2.271
0.02339 *
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.1:site.qualitySQ2   -278.464    376.748    715.360  -0.739
0.46007
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.2:site.qualitySQ2     -5.217     10.139    810.188  -0.515
0.60701
thinning:initSD.log:yrs.elapsed                              -4.379      1.650    815.464  -2.653  0.00813 **
site.qualitySQ2:thinning:initSD.log:yrs.elapsed               4.399      1.977    810.986   2.225  0.02638 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

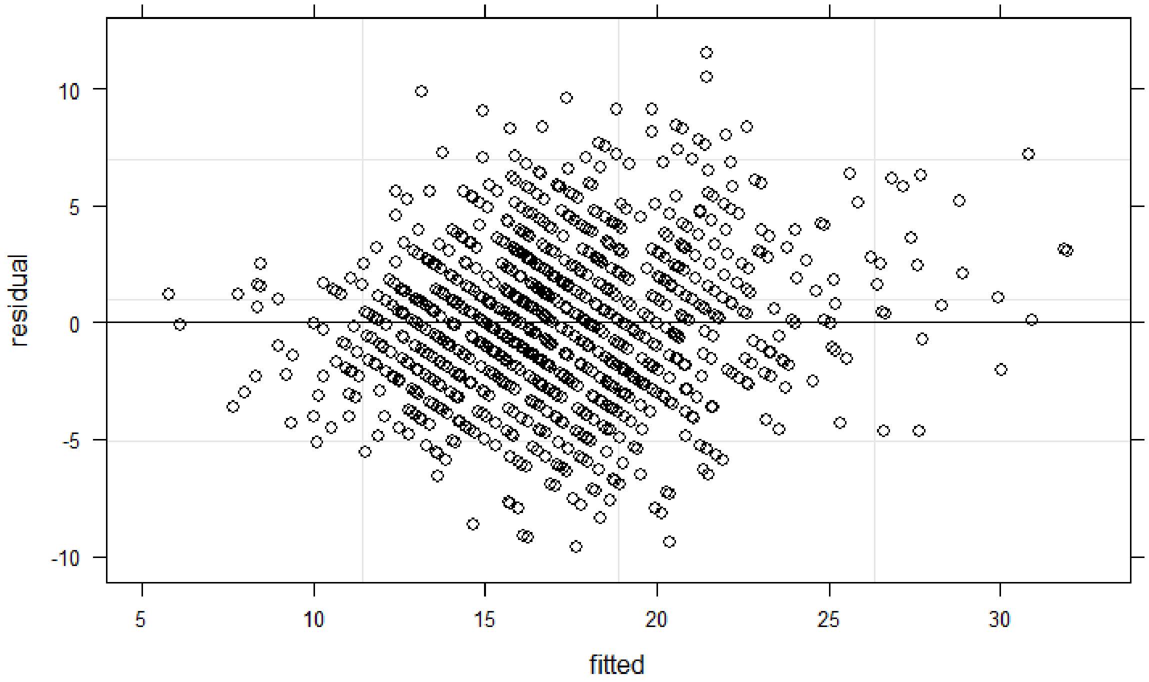


Figure 26 **Fitted values and data residuals: native plant species richness**

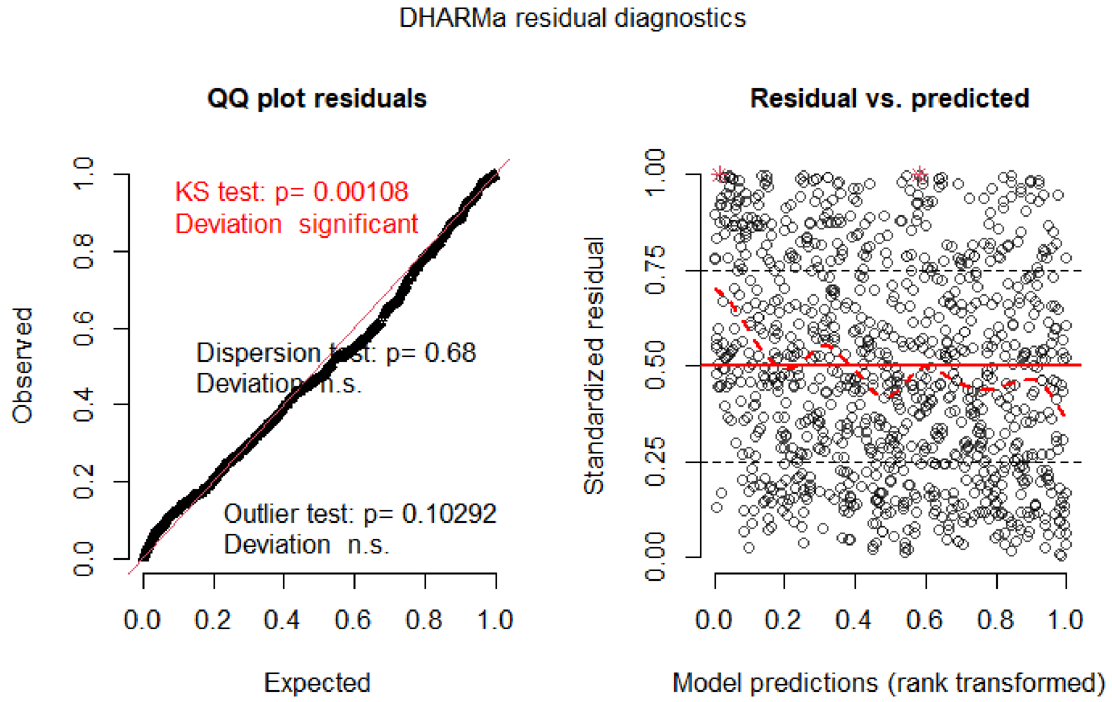


Figure 27 **Simulated randomised quantile residuals: native plant species richness**

8.2 Exotic plant species richness

Table 21 Model fitting summary: exotic plant species richness

Response	Number of exotic plant species recorded in each 0.04 each subplot
Response transformation used	None
R package and function	lmer from lme4
Distribution used	Negative binomial
Outliers removed	None
Reported model formula	4_way with no year factor
Random factors	Site (a factor over 22 sites) Siteplot (a factor over 66 plots) Subplot (a factor over 198 subplots)
Other transformations compared	Log_e(exotic richness + 1) (with Gaussian)
Other models attempted	4_way Gaussian, four random effects: Model failed to converge 4_way logged Gaussian, four random effects: No warnings, but failed residual tests 4_way poisson, four random effects: Model failed to converge 4_way negative binomial, four random effects: Model failed to converge 3_way Gaussian, four random effects, no polynomials, no initial stem density: No warnings, but failed residual tests 3_way Gaussian, four random effects, no polynomials, no years elapsed: No warnings and passed residual tests 4_way Gaussian with year.factor as fixed effect instead of yrs.elapsed + 3 random effects: No warnings, but residual fits were inferior to reported model 4_way Gaussian with no year random effect: No warnings, but residuals inferior to reported model
Confidence comments	Moderate confidence: • Some difficulty in fitting model • Failed outlier test • <5% convergence and fit warnings in 999 prediction interval simulations

Model summary 17 Exotic plant species richness

```
Family: nbinom2  ( log )
Formula:          var ~ poly(cbind(thinning, initSD.log, yrs.elapsed), 2) * site.quality +
   (1 | site) + (1 | siteplot) + (1 | subplot)
Data: dat

     AIC      BIC   logLik deviance df.resid
  5192.5   5310.0  -2572.2   5144.5      966
```

```
Random effects:

Conditional model:
 Groups   Name        Variance Std.Dev.
 site     (Intercept) 0.13455  0.3668
 siteplot (Intercept) 0.03209  0.1791
 subplot  (Intercept) 0.02868  0.1694
Number of obs: 990, groups:  site, 22; siteplot, 66; subplot, 198

Dispersion parameter for nbinom2 family (): 21.2

Conditional model:
                                                                       Estimate Std. Error z value Pr(>|z|)
(Intercept)                                                             1.82890    0.12207  14.982  < 2e-16 ***
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.0                  2.16644    1.56297   1.386  0.16571
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)2.0.0                  2.09813    1.26807   1.655  0.09801 .
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.0                 -0.14504    2.15514  -0.067  0.94634
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.1.0                 49.47882   54.26417   0.912  0.36187
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.2.0                  1.06826    2.02110   0.529  0.59712
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.1                  5.81346    1.03169   5.635 1.75e-08 ***
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.1                 29.33417   32.39905   0.905  0.36525
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.1                -99.83138   28.35186  -3.521  0.00043 ***
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.2                  1.86863    0.76258   2.450  0.01427 *
site.qualitySQ2                                                         0.04701    0.17260   0.272  0.78535
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.0:site.qualitySQ2    5.13346    1.97424   2.600  0.00932 **
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)2.0.0:site.qualitySQ2    2.36212    2.15472   1.096  0.27297
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.0:site.qualitySQ2   -3.00564    2.99972  -1.002  0.31636
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.1.0:site.qualitySQ2 -162.75301   74.95070  -2.171  0.02990 *
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.2.0:site.qualitySQ2    0.44252    2.46626   0.179  0.85760
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.1:site.qualitySQ2   -4.09313    1.36283  -3.003  0.00267 **
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)1.0.1:site.qualitySQ2 -135.35006   42.44890  -3.189  0.00143 **
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.1.1:site.qualitySQ2  145.70370   36.26832   4.017 5.88e-05 ***
poly(cbind(thinning, initSD.log, yrs.elapsed), 2)0.0.2:site.qualitySQ2    2.72380    1.19196   2.285  0.02230 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

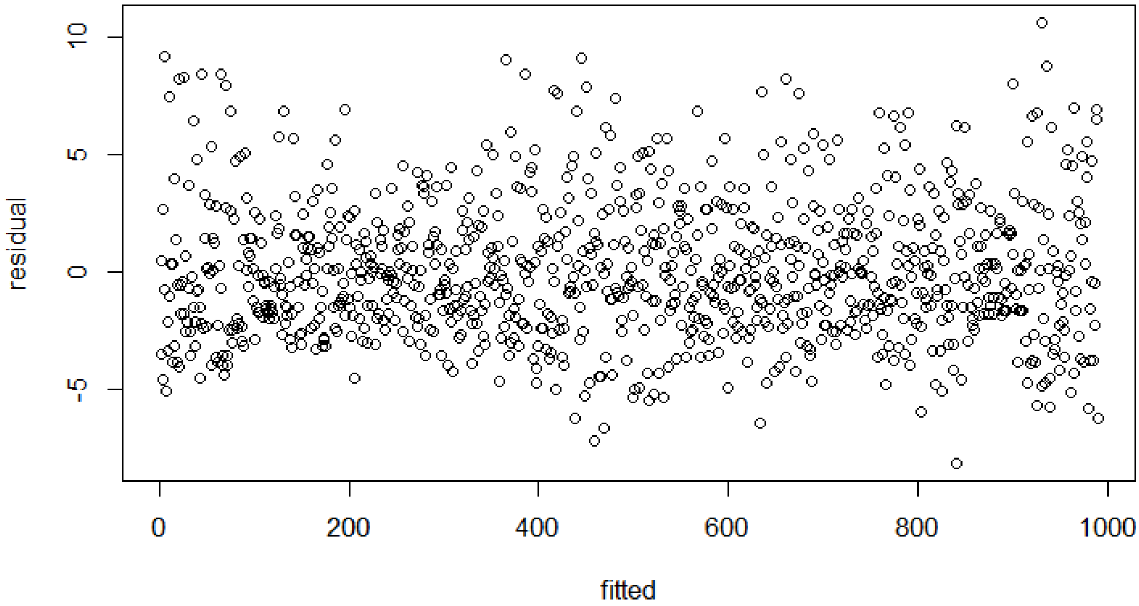


Figure 28 Fitted values and data residuals: exotic plant species richness

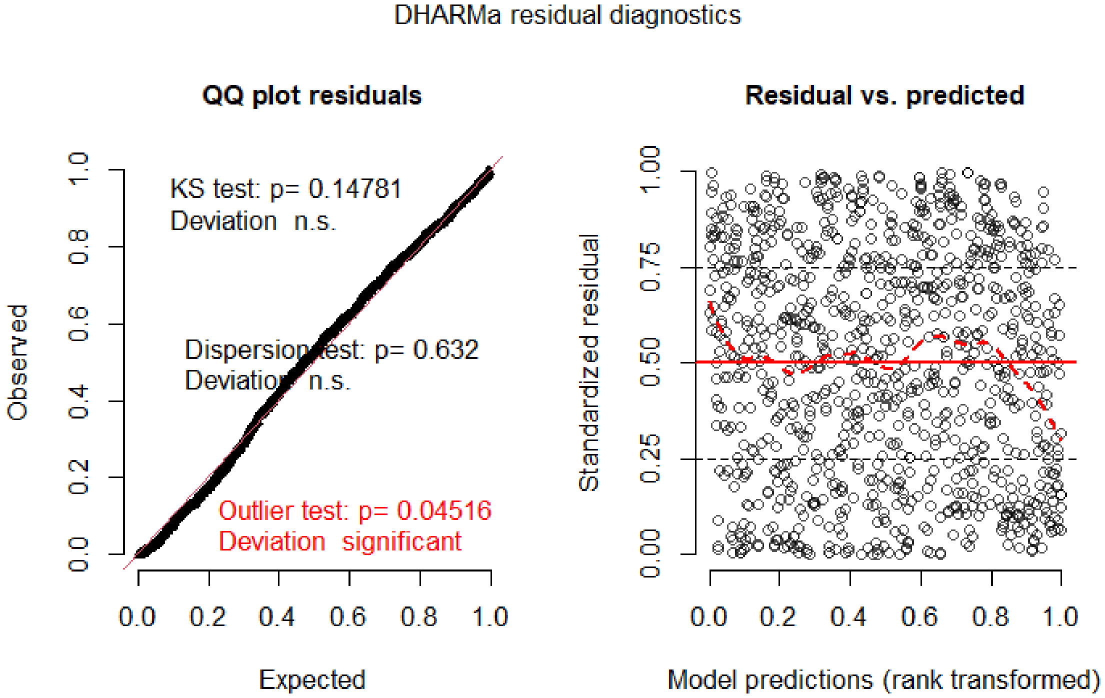


Figure 29 Simulated randomised quantile residuals: exotic plant species richness

8.3 Plant cover

8.3.1 Native plant cover

Not modelled.

8.3.2 Exotic plant cover

Not modelled.

9. Model summaries: Birds

9.1 Bird species richness

Table 22 Model fitting summary: Bird species richness

Response	Number of bird species recorded in a 2 ha subplot in each 9 ha plot (total unique species from four 20-minute visits) A positive continuous variable
Response transformation used	None
R package and function	lmer function from lme4 package
Distribution used	Gaussian
Outliers removed	None
Reported model formula	var ~ poly(cbind(thinning, initSD.log), 2) * site.quality * year.factor + (1 | site) + (1 | siteplot) No yrs.elapsed because each siteplot was surveyed four times in each survey year So year.factor included as a fixed effect
Random factors	Site (a factor over 22 sites) Siteplot (a factor over 66 plots)
Other transformations compared	None
Other models attempted	None and no other distributions compared
Confidence comments	High confidence: • Passed all residual tests • <1% boundary singular fit warnings in 999 prediction interval simulations

Model summary 18 Bird species richness

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula:
  Data: dat
Control: lmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 1e+05),
    check.scaleX = "ignore", check.rankX = "silent.drop.cols")

REML criterion at convergence: 1333.3

Scaled residuals:
     Min       1Q   Median       3Q      Max
-3.05489 -0.52119 -0.00017  0.57762  2.39637

Random effects:
```

```
 Groups   Name        Variance Std.Dev.
 siteplot (Intercept) 2.532    1.591
 site     (Intercept) 8.408    2.900
 Residual             8.378    2.895
Number of obs: 330, groups:  siteplot, 66; site, 22

Fixed effects:
                                                     Estimate Std. Error        df t value Pr(>|t|)
(Intercept)                                          20.68616    1.32127   63.39751  15.656  < 2e-16 ***
poly(cbind(thinning, initSD.log), 2)1.0                             7.07575   14.33359  239.11304   0.494 0.622008
poly(cbind(thinning, initSD.log), 2)2.0                           -15.68421   11.26345  250.61688  -1.392 0.165009
poly(cbind(thinning, initSD.log), 2)0.1                           -37.87841   21.42145  197.84388  -1.768 0.078561 .
poly(cbind(thinning, initSD.log), 2)1.1                          -234.58842  328.94291  241.18167  -0.713 0.476437
poly(cbind(thinning, initSD.log), 2)0.2                           -11.66373   14.06412  140.63214  -0.829 0.408326
site.qualitySQ2                                                 0.62330    1.84486   60.15729   0.338 0.736644
year.factor2017-18                                             -2.82410    1.18976  254.64322  -2.374 0.018355 *
year.factor2018-19                                             -4.12473    1.18976  254.64322  -3.467 0.000618 ***
year.factor2019-20                                             -2.82872    1.18976  254.64322  -2.378 0.018167 *
year.factor2020-21                                             -0.45502    1.29851  257.18395  -0.350 0.726310
poly(cbind(thinning, initSD.log), 2)1.0:site.qualitySQ2            19.54607   18.05136  237.09081   1.083
0.279996
poly(cbind(thinning, initSD.log), 2)2.0:site.qualitySQ2            -2.85839   18.42240  253.63048  -0.155
0.876820
poly(cbind(thinning, initSD.log), 2)0.1:site.qualitySQ2            63.95700   28.61162  203.36227   2.235
0.026482 *
poly(cbind(thinning, initSD.log), 2)1.1:site.qualitySQ2           476.63576  423.30951  243.69546   1.126
0.261284
poly(cbind(thinning, initSD.log), 2)0.2:site.qualitySQ2           -10.58446   17.26569  140.97457  -0.613
0.540842
poly(cbind(thinning, initSD.log), 2)1.0:year.factor2017-18          27.53711   17.97037  213.46253   1.532
0.126914
poly(cbind(thinning, initSD.log), 2)2.0:year.factor2017-18          -1.15019   13.77054  213.46253  -0.084
0.933512
poly(cbind(thinning, initSD.log), 2)0.1:year.factor2017-18          29.81733   23.39718  258.29915   1.274
0.203668
poly(cbind(thinning, initSD.log), 2)1.1:year.factor2017-18        -519.48738  410.30501  213.46253  -1.266
0.206857
poly(cbind(thinning, initSD.log), 2)0.2:year.factor2017-18          21.68226   17.20953  227.30354   1.260
0.208998
poly(cbind(thinning, initSD.log), 2)1.0:year.factor2018-19          28.56701   17.97037  213.46253   1.590
0.113389
poly(cbind(thinning, initSD.log), 2)2.0:year.factor2018-19           9.32123   13.77054  213.46253   0.677
0.499205
poly(cbind(thinning, initSD.log), 2)0.1:year.factor2018-19          65.05953   23.39718  258.29915   2.781
0.005824 **
poly(cbind(thinning, initSD.log), 2)1.1:year.factor2018-19          27.74844  410.30501  213.46253   0.068
0.946144
poly(cbind(thinning, initSD.log), 2)0.2:year.factor2018-19           5.54934   17.20953  227.30354   0.322
0.747403
poly(cbind(thinning, initSD.log), 2)1.0:year.factor2019-20           8.76010   17.97037  213.46253   0.487
0.626422
poly(cbind(thinning, initSD.log), 2)2.0:year.factor2019-20          -6.95695   13.77054  213.46253  -0.505
0.613936
```

```
poly(cbind(thinning, initSD.log), 2)0.1:year.factor2019-20                44.66312   23.39718  258.29915   1.909
0.057382 .
poly(cbind(thinning, initSD.log), 2)1.1:year.factor2019-20              -437.84579  410.30501  213.46253  -1.067
0.287122
poly(cbind(thinning, initSD.log), 2)0.2:year.factor2019-20                 0.42313   17.20953  227.30354   0.025
0.980406
poly(cbind(thinning, initSD.log), 2)0.1:year.factor2020-21                62.56923   23.37747  258.32032   2.676
0.007916 **
poly(cbind(thinning, initSD.log), 2)0.2:year.factor2020-21                 1.73353   17.20953  227.30354   0.101
0.919853
site.qualitySQ2:year.factor2017-18                                 0.11770    1.61678  255.55428   0.073 0.942024
site.qualitySQ2:year.factor2018-19                                -0.54383    1.61678  255.55428  -0.336 0.736872
site.qualitySQ2:year.factor2019-20                                -1.53585    1.61678  255.55428  -0.950 0.343038
site.qualitySQ2:year.factor2020-21                                 0.07004    1.71771  256.22804   0.041 0.967506
poly(cbind(thinning, initSD.log), 2)1.0:site.qualitySQ2:year.factor2017-18  -47.44494   22.72851  213.46253  -
2.087 0.038033 *
poly(cbind(thinning, initSD.log), 2)2.0:site.qualitySQ2:year.factor2017-18   17.52624   22.33396  213.46253
0.785 0.433479
poly(cbind(thinning, initSD.log), 2)0.1:site.qualitySQ2:year.factor2017-18  -49.85397   30.31568  252.92993  -
1.644 0.101316
poly(cbind(thinning, initSD.log), 2)1.1:site.qualitySQ2:year.factor2017-18  479.32588  525.02161  213.46253
0.913 0.362291
poly(cbind(thinning, initSD.log), 2)0.2:site.qualitySQ2:year.factor2017-18  -10.33793   21.14680  227.02827  -
0.489 0.625409
poly(cbind(thinning, initSD.log), 2)1.0:site.qualitySQ2:year.factor2018-19  -46.71395   22.72851  213.46253  -
2.055 0.041067 *
poly(cbind(thinning, initSD.log), 2)2.0:site.qualitySQ2:year.factor2018-19   27.71863   22.33396  213.46253
1.241 0.215932
poly(cbind(thinning, initSD.log), 2)0.1:site.qualitySQ2:year.factor2018-19  -79.81162   30.31568  252.92993  -
2.633 0.008993 **
poly(cbind(thinning, initSD.log), 2)1.1:site.qualitySQ2:year.factor2018-19 -561.34213  525.02161  213.46253  -
1.069 0.286197
poly(cbind(thinning, initSD.log), 2)0.2:site.qualitySQ2:year.factor2018-19   23.79645   21.14680  227.02827
1.125 0.261651
poly(cbind(thinning, initSD.log), 2)1.0:site.qualitySQ2:year.factor2019-20  -17.13034   22.72851  213.46253  -
0.754 0.451863
poly(cbind(thinning, initSD.log), 2)2.0:site.qualitySQ2:year.factor2019-20   17.75223   22.33396  213.46253
0.795 0.427582
poly(cbind(thinning, initSD.log), 2)0.1:site.qualitySQ2:year.factor2019-20  -55.15512   30.31568  252.92993  -
1.819 0.070039 .
poly(cbind(thinning, initSD.log), 2)1.1:site.qualitySQ2:year.factor2019-20  185.77254  525.02161  213.46253
0.354 0.723810
poly(cbind(thinning, initSD.log), 2)0.2:site.qualitySQ2:year.factor2019-20    6.66398   21.14680  227.02827
0.315 0.752953
poly(cbind(thinning, initSD.log), 2)0.1:site.qualitySQ2:year.factor2020-21  -59.31170   28.31496  256.00033  -
2.095 0.037180 *
poly(cbind(thinning, initSD.log), 2)0.2:site.qualitySQ2:year.factor2020-21   23.82607   21.14680  227.02827
1.127 0.261059
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

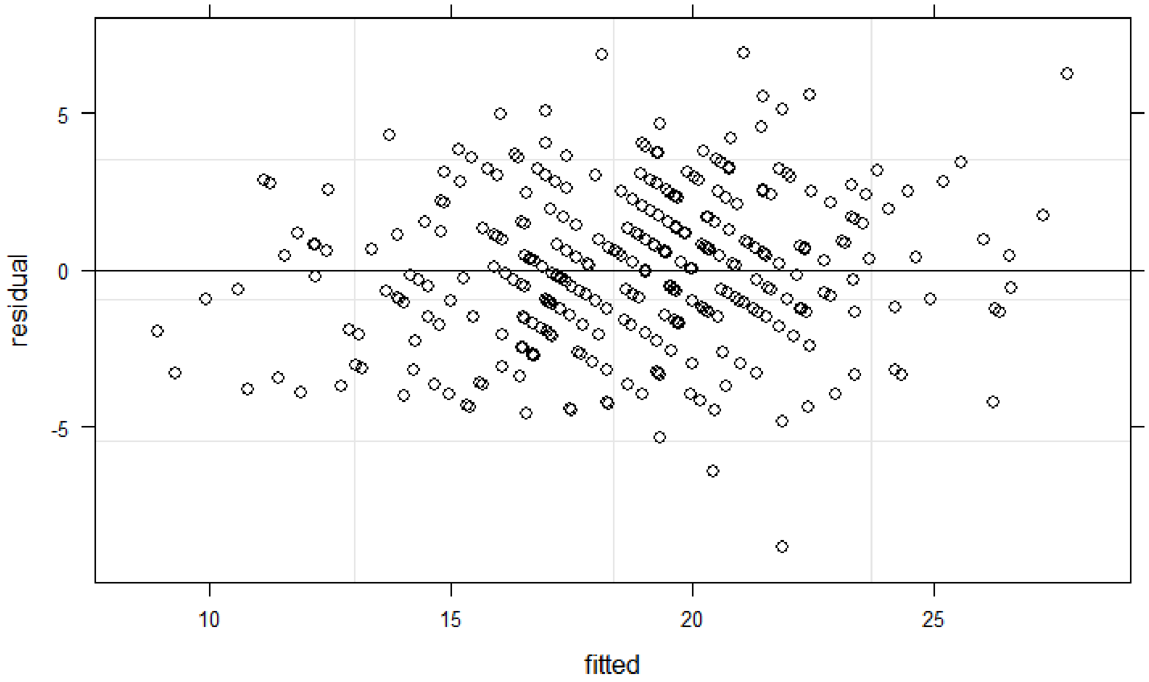


Figure 30 Fitted values and data residuals: bird species richness

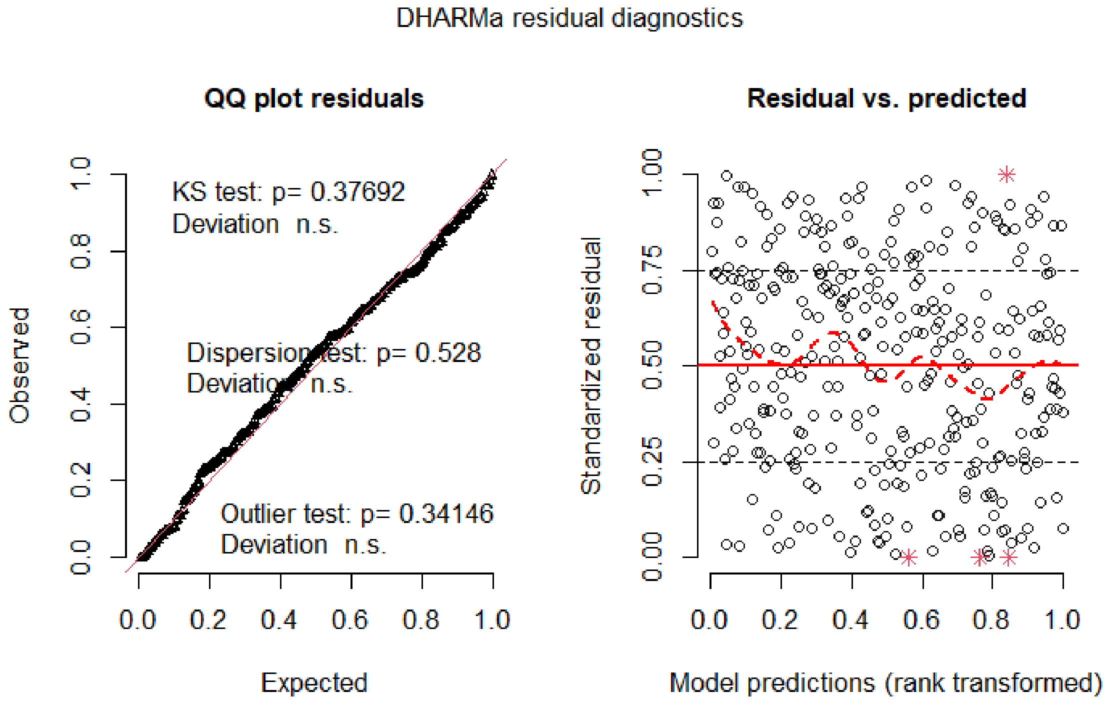


Figure 31 Simulated randomised quantile residuals: bird species richness

10. Plant species list

10.1 Native plant species list

Table 23 lists all native plant species recorded in all survey years, showing the original recorded name as well as the name assigned for analysis (where, for example, multiple sub-species were originally recorded but were analysed as the same species). The number of 0.04 hectare subplots the species was recorded in is reported for each survey year (out of 198).

Table 23 Native plant species

Original name	Analysis name	2015	2017	2018	2019	2020
Acacia dealbata	*Acacia dealbata*	2	3	3	4	4
Acaena novae-zelandiae	*Acaena novae-zelandiae*	3	2	5	7	4
Alternanthera denticulata	*Alternanthera denticulata*	182	191	183	169	172
Amphibromus fluitans	*Amphibromus fluitans*	10	2	0	0	0
Amphibromus nervosus	*Amphibromus nervosus*	21	17	7	10	14
Amyema miquelii	*Amyema* spp.	2	11	0	0	3
Amyema miraculosum subsp. *boormanii*	*Amyema* spp.	1	0	0	0	0
Amyema pendula	*Amyema* spp.	2	1	0	0	0
Amyema spp.	*Amyema* spp.	26	4	25	21	13
Arthropodium minus	*Arthropodium minus*	2	7	3	5	16
Atriplex semibaccata	*Atriplex semibaccata*	1	3	4	5	4
Atriplex spp.	*Atriplex semibaccata*	1	2	2	2	8
Austrostipa elegantissima	*Austrostipa elegantissima*	0	0	0	0	2
Austrostipa mollis	*Austrostipa mollis*	0	0	0	1	0
Austrostipa nodosa	*Austrostipa nodosa*	0	0	0	0	2
Austrostipa scabra	*Austrostipa scabra*	2	0	2	0	0
Austrostipa scabra subsp. *falcata*	*Austrostipa scabra*	0	0	1	2	1
Austrostipa scabra subsp. *scabra*	*Austrostipa scabra*	2	0	0	0	0
Azolla filiculoides	*Azolla filiculoides*	4	13	5	3	2
Azolla pinnata	*Azolla pinnata*	3	0	3	1	0
Boerhavia dominii	*Boerhavia dominii*	0	1	1	0	2
Brachyscome basaltica	*Brachyscome basaltica*	39	62	47	62	68
Brachyscome basaltica var. *gracilis*	*Brachyscome basaltica*	3	0	0	0	0
Callitris glaucophylla	*Callitris glaucophylla*	0	0	0	0	1
Calotis hispidula	*Calotis hispidula*	0	0	0	0	2

Original name	Analysis name	2015	2017	2018	2019	2020
Calotis scapigera	*Calotis scapigera*	10	10	17	17	19
Cardamine moirensis	*Cardamine moirensis*	3	4	0	7	0
Cardamine paucijuga	*Cardamine paucijuga*	5	5	9	1	40
Carex bichenoviana	*Carex bichenoviana*	3	0	0	0	0
Carex inversa	*Carex inversa*	141	79	102	90	114
Carex tereticaulis	*Carex tereticaulis*	146	141	139	137	135
Centella asiatica	*Centella asiatica*	1	0	6	6	8
Centella cordifolia	*Centella cordifolia*	1	7	4	1	1
Centipeda cunninghamii	*Centipeda cunninghamii*	93	190	153	126	151
Centipeda minima	*Centipeda minima*	2	27	1	0	43
Centipeda minima subsp. *minima*	*Centipeda minima*	0	0	1	0	0
Chamaesyce drummondii	*Chamaesyce drummondii*	4	0	4	0	0
Chloris truncata	*Chloris truncata*	0	1	1	0	2
Chrysocephalum apiculatum	*Chrysocephalum apiculatum*	5	6	0	0	1
Cotula australis	*Cotula australis*	6	31	15	22	60
Craspedia paludicola	*Craspedia paludicola*	0	17	9	13	22
Craspedia spp.	*Craspedia paludicola*	10	1	0	2	0
Crassula colorata	*Crassula colorata*	0	0	0	0	3
Crassula colorata var. *acuminata*	*Crassula colorata*	0	1	0	0	0
Crassula helmsii	*Crassula helmsii*	2	0	0	1	0
Crassula peduncularis	*Crassula peduncularis*	0	0	0	0	4
Crassula sieberiana	*Crassula sieberiana*	0	0	0	0	22
Triglochin procera	*Cycnogeton* spp.	13	11	43	19	20
Triglochin spp.	*Cycnogeton* spp.	15	24	2	2	44
Cynodon dactylon	*Cynodon dactylon*	69	49	53	51	54
Cyperus exaltatus	*Cyperus exaltatus*	8	10	2	0	0
Cyperus gunnii	*Cyperus gunnii*	0	1	0	0	0
Damasonium minus	*Damasonium minus*	15	11	2	2	4
Daucus glochidiatus	*Daucus glochidiatus*	7	4	8	10	29
Daucus spp.	*Daucus glochidiatus*	0	5	0	0	0
Deyeuxia quadriseta	*Deyeuxia quadriseta*	7	7	12	3	6
Dianella longifolia	*Dianella longifolia*	0	7	9	4	18
Dianella longifolia var. *longifolia*	*Dianella longifolia*	9	0	0	0	0
Dianella spp.	*Dianella longifolia*	1	0	0	6	0
Dichelachne crinita	*Dichelachne crinita*	0	2	0	1	0

Original name	Analysis name	2015	2017	2018	2019	2020
Dichondra repens	*Dichondra repens*	4	20	19	12	17
Dichondra spp.	*Dichondra repens*	5	0	0	0	0
Dichondra sp. A	*Dichondra* sp. A	2	0	0	2	0
Dysphania pumilio	*Dysphania pumilio*	21	2	1	7	5
Echinochloa colona	*Echinochloa colona*	3	0	0	0	0
Eclipta platyglossa	*Eclipta platyglossa*	52	61	102	90	97
Einadia nutans	*Einadia nutans*	21	33	46	44	78
Einadia nutans subsp. *nutans*	*Einadia nutans*	10	0	0	1	0
Einadia spp.	*Einadia nutans*	0	1	0	0	3
Elatine gratioloides	*Elatine gratioloides*	5	5	0	0	1
Eleocharis acuta	*Eleocharis* spp.	173	94	60	2	0
Eleocharis pallens	*Eleocharis* spp.	0	94	34	1	0
Eleocharis plana	*Eleocharis* spp.	0	50	55	4	0
Eleocharis pusilla	*Eleocharis* spp.	61	67	50	38	47
Eleocharis spp.	*Eleocharis* spp.	0	6	48	148	159
Elymus scaber	*Elymus scaber*	7	0	4	4	4
Enchylaena tomentosa	*Enchylaena tomentosa*	4	0	2	3	7
Enteropogon acicularis	*Enteropogon acicularis*	1	0	0	0	0
Epilobium billardiereanum	*Epilobium billardiereanum*	7	38	0	15	28
Epilobium billardiereanum subsp. *billardiereanum*	*Epilobium billardiereanum*	1	0	0	1	0
Epilobium billardiereanum subsp. *cinereum*	*Epilobium billardiereanum*	2	10	0	0	11
Epilobium billardiereanum subsp. *hydrophilum*	*Epilobium billardiereanum*	0	1	4	16	16
Epilobium billardierianum	*Epilobium billardiereanum*	2	2	7	0	0
Epilobium billardierianum subsp. *cinereum*	*Epilobium billardiereanum*	0	0	3	0	0
Epilobium billardierianum subsp. *hydrophilum*	*Epilobium billardiereanum*	0	0	8	0	0
Epilobium billardierianum subsp. *intermedium*	*Epilobium billardiereanum*	0	0	1	0	0
Epilobium hirtigerum	*Epilobium hirtigerum*	22	6	10	1	12
Epilobium spp.	*Epilobium* spp.	1	1	1	1	3
Eragrostis elongata	*Eragrostis elongata*	1	0	0	0	0
Erodium crinitum	*Erodium crinitum*	0	0	0	0	1
Eryngium ovinum	*Eryngium ovinum*	1	1	1	1	1
Eucalyptus camaldulensis	*Eucalyptus camaldulensis*	200	199	199	198	198
Eucalyptus melliodora	*Eucalyptus melliodora*	1	0	1	1	1

Original name	Analysis name	2015	2017	2018	2019	2020
Euchiton collinus	*Euchiton collinus*	0	0	0	0	2
Euchiton gymnocephalus	*Euchiton gymnocephalus*	0	0	0	0	1
Euchiton involucratus	*Euchiton involucratus*	8	5	8	1	1
Euchiton sphaericus	*Euchiton sphaericus*	15	41	6	28	41
Euchiton spp.	*Euchiton* spp.	1	4	6	6	7
Eulalia aurea	*Eulalia aurea*	2	1	0	0	0
Euphorbia drummondii	*Euphorbia drummondii*	35	57	53	53	61
Exocarpos strictus	*Exocarpos strictus*	12	10	9	10	10
Fimbristylis aestivalis	*Fimbristylis aestivalis*	0	1	0	1	2
Geranium homeanum	*Geranium homeanum*	0	0	0	0	1
Geranium spp.	*Geranium homeanum*	0	0	1	1	0
Glinus lotoides	*Glinus lotoides*	0	1	0	0	0
Glossostigma elatinoides	*Glossostigma elatinoides*	0	6	4	1	3
Glossostigma spp.	*Glossostigma elatinoides*	0	2	0	0	0
Goodenia geniculata	*Goodenia geniculata*	1	0	0	0	0
Goodenia glabra	*Goodenia glabra*	0	0	0	0	1
Goodenia gracilis	*Goodenia gracilis*	50	55	48	60	58
Goodenia spp.	*Goodenia gracilis*	1	1	0	1	1
Gratiola peruviana	*Gratiola peruviana*	2	1	1	1	1
Gratiola pumilo	*Gratiola pumilo*	0	2	1	0	3
Haloragis heterophylla	*Haloragis heterophylla*	1	3	0	3	1
Haloragis spp.	*Haloragis heterophylla*	0	0	0	0	2
Helichrysum bracteatum	*Helichrysum bracteatum*	2	30	25	0	0
Hydrocotyle sibthorpioides	*Hydrocotyle sibthorpioides*	2	5	4	4	2
Hydrocotyle spp.	*Hydrocotyle sibthorpioides*	6	0	0	0	1
Hypericum gramineum	*Hypericum gramineum*	3	1	2	4	5
Isolepis hookeriana	*Isolepis hookeriana*	1	0	0	0	0
Juncus amabilis	*Juncus amabilis*	154	114	143	136	132
Juncus aridicola	*Juncus aridicola*	1	2	1	0	0
Juncus australis	*Juncus australis*	3	0	0	0	0
Juncus bufonius	*Juncus bufonius*	0	0	0	0	3
Juncus flavidus	*Juncus flavidus*	13	19	4	5	0
Juncus holoschoenus	*Juncus holoschoenus*	28	13	14	7	5
Juncus ingens	*Juncus ingens*	10	13	11	12	11
Juncus procerus	*Juncus procerus*	0	2	0	0	0
Juncus radula	*Juncus radula*	0	1	0	8	2
Juncus remotiflorus	*Juncus remotiflorus*	1	0	0	2	0

Original name	Analysis name	2015	2017	2018	2019	2020
Juncus semisolidus	*Juncus semisolidus*	0	0	2	0	0
Juncus subglaucus	*Juncus subglaucus*	7	1	0	0	1
Juncus subsecundus	*Juncus subsecundus*	18	14	18	8	2
Lachnagrostis filiformis	*Lachnagrostis filiformis*	125	187	102	131	136
Leiocarpa panaetioides	*Leiocarpa panaetioides*	0	0	0	0	4
Lemna disperma	*Lemna disperma*	0	0	2	0	0
Lepidium africanum	*Lepidium pseudohyssopifolium*	0	0	0	1	0
Lepidium hyssopifolium	*Lepidium pseudohyssopifolium*	0	0	0	0	1
Lepidium pseudohyssopifolium	*Lepidium pseudohyssopifolium*	0	1	3	0	4
Linum marginale	*Linum marginale*	13	16	13	18	19
Ludwigia peploides	*Ludwigia peploides*	1	8	7	4	4
Ludwigia peploides subsp. *montevidensis*	*Ludwigia peploides*	13	8	2	8	3
Lythrum hyssopifolia	*Lythrum hyssopifolia*	21	51	19	22	53
Lythrum spp.	*Lythrum hyssopifolia*	0	0	0	1	0
Maireana enchylaenoides	*Maireana enchylaenoides*	0	1	0	1	0
Marsilea angustifolia	*Marsilea angustifolia*	0	1	0	0	0
Marsilea costulifera	*Marsilea costulifera*	35	25	35	23	30
Marselea drummondii	*Marsilea drummondii*	0	0	1	0	0
Marsilea drummondii	*Marsilea drummondii*	26	31	21	15	24
Marsilea spp.	*Marsilea* spp.	3	6	0	0	1
Mentha australis	*Mentha australis*	0	1	0	1	1
Mentha laxiflora	*Mentha australis*	1	0	0	0	0
Mentha spp.	*Mentha australis*	0	0	1	0	1
Mentha australis	*Mentha diemenica*	0	1	0	0	0
Mentha diemenica	*Mentha diemenica*	2	0	4	2	4
Mentha satureioides	*Mentha diemenica*	0	0	0	1	0
Mentha spp.	*Mentha diemenica*	2	1	0	0	0
Mentha satureioides	*Mentha satureioides*	1	0	1	0	0
Microlaena stipoides var. *stipoides*	*Microlaena stipoides*	0	0	0	0	1
Mimulus gracilis	*Mimulus gracilis*	0	0	0	0	1
Mimulus repens	*Mimulus repens*	0	0	0	0	1
Myriophyllum crispatum	*Myriophyllum* spp.	16	64	60	56	46
Myriophyllum papillosum	*Myriophyllum* spp.	2	18	15	9	4
Myriophyllum simulans	*Myriophyllum* spp.	0	0	0	0	3

Original name	Analysis name	2015	2017	2018	2019	2020
Myriophyllum spp.	*Myriophyllum* spp.	53	17	2	3	8
Nymphoides crenata	*Nymphoides crenata*	25	24	31	20	21
Ophioglossum lusitanicum	*Ophioglossum lusitanicum*	0	0	0	0	1
Ottelia ovalifolia	*Ottelia ovalifolia*	1	0	0	0	2
Ottelia ovalifolia subsp. *ovalifolia*	*Ottelia ovalifolia*	6	0	0	0	0
Oxalis perennans	*Oxalis perennans*	63	50	58	53	68
Oxalis spp.	*Oxalis perennans*	5	0	0	0	0
Parietaria debilis	*Parietaria debilis*	0	0	0	0	9
Paspalidium jubiflorum	*Paspalidium jubiflorum*	165	152	170	168	157
Paspalum distichum	*Paspalum distichum*	3	2	0	0	0
Persicaria decipiens	*Persicaria decipiens*	50	54	41	37	34
Persicaria hydropiper	*Persicaria hydropiper*	25	36	21	27	21
Persicaria prostrata	*Persicaria prostrata*	29	48	33	25	30
Phragmites australis	*Phragmites australis*	4	3	4	4	2
Plantago cunninghamii	*Plantago cunninghamii*	1	0	0	0	0
Plantago gaudichaudii	*Plantago gaudichaudii*	0	1	1	0	0
Poa labillardierei	*Poa labillardierei*	5	1	0	5	8
Poa labillardierei var. *labillardierei*	*Poa labillardierei*	11	1	0	1	0
Poa labillardieri	*Poa labillardierei*	0	12	7	0	0
Pogonolepis muelleriana	*Pogonolepis muelleriana*	0	0	0	1	0
Potamogeton cheesemanii	*Potamogeton cheesemanii*	1	10	11	4	7
Potamogeton spp.	*Potamogeton* spp.	1	0	0	1	0
Pratia concolor	*Pratia concolor*	35	60	51	60	54
Pratia pedunculata	*Pratia pedunculata*	1	0	0	0	0
Gnaphalium luteo-album	*Pseudognaphalium luteoalbum*	0	4	0	0	0
Pseudognaphalium luteo-album	*Pseudognaphalium luteoalbum*	2	0	0	35	0
Pseudognaphalium luteoalbum	*Pseudognaphalium luteoalbum*	14	110	53	0	62
Pseudoraphis spinescens	*Pseudoraphis spinescens*	16	26	27	29	21
Pycnosorus globosus	*Pycnosorus globosus*	0	0	0	0	1
Ranunculus inundatus	*Ranunculus inundatus*	42	76	48	48	75
Ranunculus lappaceus	*Ranunculus lappaceus*	0	3	2	1	4
Ranunculus pumilio	*Ranunculus pumilio*	0	2	2	3	35
Ranunculus pumilio var. *politus*	*Ranunculus pumilio*	0	10	0	0	0

Original name	Analysis name	2015	2017	2018	2019	2020
Rhodanthe corymbiflora	*Rhodanthe corymbiflora*	0	1	3	1	21
Rorippa spp.	*Rorippa laciniata*	1	0	0	0	0
Rubus parvifolius	*Rubus parvifolius*	0	0	0	0	1
Rumex brownii	*Rumex brownii*	106	124	42	15	123
Rumex tenax	*Rumex tenax*	0	41	14	1	4
Rytidosperma bipartitum	*Rytidosperma* spp.	0	1	0	0	0
Rytidosperma caespitosum	*Rytidosperma* spp.	3	0	6	10	2
Rytidosperma duttonianum	*Rytidosperma* spp.	2	3	0	0	3
Rytidosperma erianthum	*Rytidosperma* spp.	0	0	1	2	1
Rytidosperma fulvum	*Rytidosperma* spp.	3	5	1	0	0
Rytidosperma monticola	*Rytidosperma* spp.	0	0	0	0	9
Rytidosperma pilosum	*Rytidosperma* spp.	0	0	1	0	0
Rytidosperma setaceum	*Rytidosperma* spp.	27	8	9	8	22
Rytidosperma spp.	*Rytidosperma* spp.	8	9	16	17	28
Salsola australis	*Salsola australis*	0	0	0	0	2
Salsola spp.	*Salsola australis*	2	0	0	0	0
Sclerolaena muricata var. *semiglabra*	*Sclerolaena muricata*	1	0	0	0	0
Senecio bathurstianus	*Senecio bathurstianus*	0	0	0	1	0
Senecio campylocarpus	*Senecio campylocarpus*	4	5	8	15	16
Senecio quadridentatus	*Senecio quadridentatus*	165	149	149	157	164
Senecio runcinifolius	*Senecio runcinifolius*	14	8	6	5	6
Sigesbeckia orientalis	*Sigesbeckia orientalis*	12	31	21	27	29
Sigesbeckia orientalis subsp. *orientalis*	*Sigesbeckia orientalis*	3	0	0	0	0
Sigesbeckia spp.	*Sigesbeckia* spp.	2	0	0	0	0
Solanum aviculare	*Solanum aviculare*	0	0	0	0	1
Solenogyne dominii	*Solenogyne dominii*	6	4	7	8	3
Spergularia brevifolia	*Spergularia brevifolia*	0	1	2	7	2
Stellaria angustifolia	*Stellaria angustifolia*	35	41	32	36	37
Stellaria caespitosa	*Stellaria angustifolia*	0	9	0	0	1
Stellaria spaff-angustifolia	*Stellaria angustifolia*	0	2	0	0	0
Stellaria pungens	*Stellaria pungens*	3	1	0	0	0
Typha australis	*Typha* spp.	0	0	1	0	0
Typha domingensis	*Typha* spp.	1	1	1	0	0
Typha orientalis	*Typha* spp.	2	0	0	0	0
Verbena gaudichaudii	*Verbena gaudichaudii*	4	4	2	0	0
Viola betonicifolia	*Viola betonicifolia*	1	0	0	0	1

Original name	Analysis name	2015	2017	2018	2019	2020
Viola spp.	*Viola betonicifolia*	1	2	0	0	0
Vittadinia cuneata	*Vittadinia cuneata*	2	33	43	31	53
Vittadinia cuneata var. *cuneata*	*Vittadinia cuneata*	4	1	0	0	0
Vittadinia cuneata var. *hirsuta*	*Vittadinia cuneata*	0	0	1	0	0
Vittadinia gracilis	*Vittadinia gracilis*	37	52	62	92	124
Vulpia bromoides	*Vulpia bromoides*	6	4	0	2	4
Wahlenbergia communis	*Wahlenbergia* spp.	1	0	9	0	0
Wahlenbergia fluminalis	*Wahlenbergia* spp.	28	20	48	66	50
Wahlenbergia gracilenta	*Wahlenbergia* spp.	2	0	1	0	1
Wahlenbergia gracilis	*Wahlenbergia* spp.	13	0	0	4	3
Wahlenbergia spp.	*Wahlenbergia* spp.	84	91	38	46	60
Walwhalleya proluta	*Walwhalleya proluta*	0	1	1	0	0
Xerochrysum bracteatum	*Xerochrysum bracteatum*	25	1	1	47	64
Xerochrysum viscosum	*Xerochrysum viscosum*	1	0	0	1	0

10.2 Exotic plant species list

Table 24 lists all exotic plant species recorded in all survey years, showing the original recorded name as well as the name assigned for analysis (where, for example, multiple sub-species were originally recorded but were analysed as the same species). The number of 0.04 hectare subplots the species was recorded in is reported for each survey year (out of 198).

Table 24 Exotic plant species

Original name	Analysis name	2015	2017	2018	2019	2020
Aira caryophyllea	*Aira caryophyllea*	0	0	0	0	3
Aira cupaniana	*Aira cupaniana*	1	0	4	0	10
Aira elegantissima	*Aira elegantissima*	0	4	0	1	5
Anagallis arvensis	*Anagallis arvensis*	26	50	43	71	79
Anthoxanthum odoratum	*Anthoxanthum odoratum*	1	1	0	0	0
Arctotheca calendula	*Arctotheca calendula*	1	1	0	0	11
Aster subulatus	*Aster subulatus*	47	34	28	13	21
Avena barbata	*Avena barbata*	19	3	4	7	5
Avena fatua	*Avena fatua*	6	2	0	2	1
Avena sativa	*Avena sativa*	0	0	0	2	0
Brassica tournefortii	*Brassica tournefortii*	0	0	0	0	1
Briza minor	*Briza minor*	2	5	0	0	4
Bromus catharticus	*Bromus catharticus*	0	0	0	0	2
Bromus diandrus	*Bromus diandrus*	1	1	2	0	1
Bromus hordeaceus	*Bromus hordeaceus*	2	1	5	1	3
Bromus molliformis	*Bromus molliformis*	8	0	0	4	3
Bromus rubens	*Bromus rubens*	0	1	0	1	2
Callitriche stagnalis	*Callitriche stagnalis*	0	3	0	0	0
Capsella bursa-pastoris	*Capsella bursa-pastoris*	0	3	1	7	12
Cardamine hirsuta	*Cardamine hirsuta*	0	0	0	0	1
Carduus pycnocephalus	*Carduus pycnocephalus*	0	0	0	0	2
Carduus tenuiflorus	*Carduus tenuiflorus*	2	1	0	3	0
Centaurea melitensis	*Centaurea melitensis*	1	2	2	2	5
Centaurium spp.	*Centaurium tenuiflorum*	0	0	0	0	4
Centaurium tenuiflorum	*Centaurium tenuiflorum*	5	9	2	1	8
Cerastium glomeratum	*Cerastium glomeratum*	0	0	0	0	21
Chenopodium album	*Chenopodium album*	1	0	0	4	0
Chondrilla juncea	*Chondrilla juncea*	0	0	12	10	63
Cirsium spp.	*Cirsium vulgare*	0	0	0	14	0
Cirsium vulgare	*Cirsium vulgare*	131	150	140	109	150
Conyza bonariensis	*Conyza* spp.	112	43	14	0	13

Original name	Analysis name	2015	2017	2018	2019	2020
Conyza canadensis	*Conyza* spp.	2	9	11	0	1
Conyza spp.	*Conyza* spp.	19	147	136	118	132
Conyza sumatrensis	*Conyza* spp.	27	17	9	7	15
Cotula bipinnata	*Cotula bipinnata*	0	0	0	0	1
Cotula coronopifolia	*Cotula coronopifolia*	0	0	0	0	2
Cucumis myriocarpus	*Cucumis myriocarpus*	0	0	0	1	1
Cucumis myriocarpus subsp. *leptodermis*	*Cucumis myriocarpus*	8	0	0	1	0
Cyperus eragrostis	*Cyperus eragrostis*	3	26	0	3	2
Dittrichia graveolens	*Dittrichia graveolens*	0	1	1	0	1
Echinochloa crus-galli	*Echinochloa crus-galli*	1	0	0	0	0
Echium plantagineum	*Echium plantagineum*	81	77	55	85	76
Echium spp.	*Echium plantagineum*	0	0	0	1	1
Echium vulgare	*Echium vulgare*	1	0	0	1	0
Ehrharta erecta	*Ehrharta erecta*	1	2	4	1	1
Ehrharta longiflora	*Ehrharta longiflora*	5	1	4	0	8
Euphorbia peplus	*Euphorbia peplus*	0	1	3	4	4
Fumaria muralis	*Fumaria muralis*	12	32	45	48	52
Fumaria muralis subsp. *muralis*	*Fumaria muralis*	2	0	0	0	0
Fumaria officinalis	*Fumaria officinalis*	3	0	0	0	0
Fumaria spp.	*Fumaria* spp.	9	0	0	0	0
Galium aparine	*Galium aparine*	5	3	7	8	5
Galium murale	*Galium murale*	0	0	0	0	1
Gnaphalium polycaulon	*Gnaphalium polycaulon*	0	2	0	0	0
Hedypnois rhagadioloides	*Hedypnois rhagadioloides*	1	6	0	0	1
Heliotropium europaeum	*Heliotropium europaeum*	2	1	0	0	0
Helminthotheca echioides	*Helminthotheca echioides*	12	31	1	15	45
Hordeum glaucum	*Hordeum glaucum*	0	1	4	10	39
Hordeum spp.	*Hordeum glaucum*	0	0	0	0	7
Hypericum perforatum	*Hypericum perforatum*	3	0	4	5	8
Hypochaeris microcephala	*Hypochaeris albiflora*	0	0	0	0	2
Hypochaeris glabra	*Hypochaeris glabra*	44	29	15	32	36
Hypochaeris radicata	*Hypochaeris radicata*	34	53	41	81	92
Hypochaeris spp.	*Hypochaeris radicata*	2	4	2	0	3
Kickxia elatine subsp. *crinita*	*Kickxia elatine* subsp. *crinita*	0	0	0	1	1
Lactuca saligna	*Lactuca saligna*	1	13	4	1	3

Original name	Analysis name	2015	2017	2018	2019	2020
Lactuca serriola	*Lactuca serriola*	101	121	87	130	144
Lactuca spp.	*Lactuca serriola*	0	0	2	1	0
Leontodon taraxacoides	*Leontodon taraxacoides*	0	2	2	0	4
Leontodon taraxacoides subsp. *taraxacoides*	*Leontodon taraxacoides*	1	0	0	0	0
Lepidium africanum	*Lepidium africanum*	0	0	0	0	2
Lolium loliaceum	*Lolium loliaceum*	1	0	2	7	1
Lolium perenne	*Lolium perenne*	2	2	0	4	40
Lolium rigidum	*Lolium rigidum*	26	35	19	29	28
Lotus subbiflorus	*Lotus subbiflorus*	1	0	0	0	0
Ludwigia palustris	*Ludwigia palustris*	3	13	10	2	3
Marrubium vulgare	*Marrubium vulgare*	9	21	29	31	39
Medicago arabica	*Medicago arabica*	0	0	0	0	2
Medicago polymorpha	*Medicago polymorpha*	0	1	2	1	4
Mentha pulegium	*Mentha pulegium*	1	2	2	1	2
Mentha spp.	*Mentha pulegium*	0	1	0	1	0
Modiola caroliniana	*Modiola caroliniana*	0	1	1	2	1
Modiola spp.	*Modiola caroliniana*	0	1	0	0	0
Panicum capillare	*Panicum capillare*	0	0	1	0	0
Panicum spp.	*Panicum capillare*	0	0	2	0	1
Paspalum dilatatum	*Paspalum dilatatum*	0	0	0	0	1
Petrorhagia dubia	*Petrorhagia dubia*	12	11	5	7	9
Petrorhagia spp.	*Petrorhagia dubia*	1	0	0	0	0
Phalaris paradoxa	*Phalaris paradoxa*	1	11	7	13	24
Phalaris spp.	*Phalaris paradoxa*	0	1	0	0	1
Phyla canescens	*Phyla canescens*	0	5	7	7	8
Phyla nodiflora	*Phyla nodiflora*	0	0	3	0	0
Plantago coronopus	*Plantago coronopus*	0	0	0	3	0
Plantago coronopus subsp. *coronopus*	*Plantago coronopus*	1	1	0	0	1
Poa annua	*Poa annua*	0	0	0	0	1
Polycarpon tetraphyllum	*Polycarpon tetraphyllum*	1	0	0	0	4
Polygonum arenastrum	*Polygonum aviculare*	3	0	0	0	0
Polygonum aviculare	*Polygonum aviculare*	7	26	7	9	16
Polygonum spp.	*Polygonum aviculare*	2	0	0	0	0
Romulea rosea	*Romulea rosea*	0	0	0	0	1
Rorippa nasturtium-aquaticum	*Rorippa nasturtium-aquaticum*	1	0	0	0	0

Original name	**Analysis name**	**2015**	**2017**	**2018**	**2019**	**2020**
Rorippa palustris	*Rorippa palustris*	0	1	1	0	0
Rosa spp.	*Rosa* spp.	0	0	1	0	1
Rostraria cristata	*Rostraria cristata*	3	0	0	0	0
Rostraria spp.	*Rostraria cristata*	0	0	0	0	3
Rubus fruticosus	*Rubus fruticosus*	0	1	2	2	1
Rubus fruticosus sp agg	*Rubus fruticosus*	1	1	1	0	0
Sagittaria platyphylla	*Sagittaria platyphylla*	2	2	2	2	2
Scorzonera laciniata	*Scorzonera laciniata*	0	1	0	0	0
Silene gallica var gallica	*Silene gallica*	0	0	0	0	1
Sisymbrium erysimoides	*Sisymbrium erysimoides*	0	0	0	0	3
Sisymbrium irio	*Sisymbrium irio*	0	1	0	3	2
Sisymbrium orientale	*Sisymbrium orientale*	0	0	0	0	1
Solanum nigrum	*Solanum nigrum*	56	131	115	88	116
Sonchus asper	*Sonchus asper*	20	49	22	17	31
Sonchus oleraceus	*Sonchus oleraceus*	149	161	135	168	159
Spergularia diandra	*Spergularia diandra*	2	0	0	0	0
Spergularia rubra	*Spergularia rubra*	0	0	0	0	7
Stachys arvensis	*Stachys arvensis*	0	0	0	0	1
Stychus arvensis	*Stachys arvensis*	0	0	0	0	1
Stellaria media	*Stellaria media*	4	18	4	10	43
Stellaria pallida	*Stellaria pallida*	0	0	0	2	0
Taraxacum officinale	*Taraxacum officinale*	2	1	1	0	3
Trifolium angustifolium	*Trifolium angustifolium*	0	2	2	0	3
Trifolium arvense	*Trifolium arvense*	16	12	7	15	36
Trifolium arvense var. *arvense*	*Trifolium arvense*	0	6	0	0	0
Trifolium campestre	*Trifolium campestre*	11	6	6	4	21
Trifolium cernuum	*Trifolium cernuum*	1	9	1	0	9
Trifolium dubium	*Trifolium dubium*	0	10	0	0	0
Trifolium globosum	*Trifolium globosum*	0	0	1	0	0
Trifolium glomeratum	*Trifolium glomeratum*	3	33	20	44	87
Trifolium hirtum	*Trifolium hirtum*	2	0	1	5	4
Trifolium striatum	*Trifolium striatum*	0	0	0	0	2
Trifolium subterraneum	*Trifolium subterraneum*	0	1	0	0	1
Trifolium suffocatum	*Trifolium suffocatum*	0	0	0	0	1
Trifolium tomentosum	*Trifolium tomentosum*	0	1	0	0	8
Trifolium tomentosum var. *tomentosum*	*Trifolium tomentosum*	0	5	0	0	1

Original name	**Analysis name**	**2015**	**2017**	**2018**	**2019**	**2020**
Urtica urens	*Urtica urens*	0	3	0	1	0
Verbascum virgatum	*Verbascum virgatum*	1	8	16	15	13
Verbena bonariensis	*Verbena bonariensis*	9	32	37	33	38
Verbena officinalis	*Verbena officinalis*	0	14	17	11	19
Veronica peregrina	*Veronica peregrina*	0	17	0	0	20
Vicia disperma	*Vicia* spp.	0	0	0	3	1
Vicia hirsuta	*Vicia* spp.	2	0	4	0	0
Vicia sativa	*Vicia* spp.	0	1	0	0	0
Vicia sativa subsp. *nigra*	*Vicia* spp.	0	0	0	1	0
Vulpia muralis	*Vulpia muralis*	8	6	12	0	45
Vulpia myuros	*Vulpia myuros*	5	6	1	0	3
Vulpia myuros f megalura	*Vulpia myuros*	2	0	0	0	0
Xanthium spinosum	*Xanthium spinosum*	6	3	5	5	2
Rumex spp.	*Rumex* spp.	0	12	90	105	10

11. Bird species list

Table 25 Number of 9 hectare plots each species was recorded on, in each survey season

Species name	2015–16	2017–18	2018–19	2019–20	2020–21
Australian hobby	1	–	–	2	–
Australian magpie	24	31	33	29	41
Australian raven	19	23	10	14	28
Australian reed warbler	1	3	–	6	–
Australian shelduck	1	–	–	–	1
Australian white ibis	5	1	–	–	–
Australian wood duck	–	2	–	–	2
Azure kingfisher	–	1	–	–	–
Black-chinned honeyeater	1	–	–	1	–
Black-faced cuckoo-shrike	42	26	33	35	42
Blue-faced honeyeater	2	1	–	1	2
Brahminy kite	–	–	1	–	–
Brown-headed honeyeater	7	10	8	16	22
Brown falcon	–	1	–	–	–
Brown goshawk	1	2	2	1	4
Brown songlark	–	–	–	1	–
Brown thornbill	1	2	1	1	–
Brown treecreeper	32	42	37	38	33
Buff-rumped thornbill	60	59	59	62	59
Collared sparrowhawk	–	2	–	–	8
Common bronzewing	4	7	7	4	9
Crested shrike-tit	5	7	4	2	9
Dollarbird	1	1	1	4	1
Dusky woodswallow	9	7	9	12	8
Eastern great egret	1	–	–	–	–
Eastern rosella	2	5	3	4	2
Emu	5	3	3	–	2
Fan-tailed cuckoo	12	4	–	2	4
Flame robin	–	–	–	–	1
Fork-tailed swift	–	–	1	–	–
Galah	43	43	41	35	55
Golden whistler	1	2	–	2	1
Great egret	2	–	–	–	–
Grey-crowned babbler	–	1	–	–	–
Grey butcherbird	–	–	2	–	–
Grey fantail	51	43	36	36	41

Species name	2015–16	2017–18	2018–19	2019–20	2020–21
Grey shrike-thrush	59	50	48	40	59
Grey teal	1	–	–	1	–
Hooded robin	1	2	–	2	1
Horsfield’s bronze-cuckoo	7	7	2	4	1
Intermediate egret	2	–	–	–	–
Jacky winter	14	23	26	26	24
Laughing kookaburra	26	30	22	21	26
Leaden flycatcher	3	2	–	1	3
Little eagle	1	1	–	–	1
Little friarbird	7	8	5	10	6
Little grassbird	1	1	–	–	–
Little raven	3	2	3	3	–
Long-billed corella	7	18	11	10	21
Magpie-lark	2	2	–	–	1
Masked woodswallow	–	–	–	–	1
Mistletoebird	36	21	23	31	19
Nankeen night heron	1	–	1	–	1
Noisy friarbird	34	25	25	35	42
Olive-backed oriole	1	–	–	2	7
Pacific black duck	3	7	2	2	5
Painted button-quail	3	1	–	–	–
Painted honeyeater	–	–	1	1	–
Pallid cuckoo	–	1	1	–	3
Peaceful dove	12	6	15	2	11
Peregrine falcon	2	3	3	1	1
Pied butcherbird	2	3	–	1	3
Pied currawong	–	–	–	–	1
Quail species	1	–	–	–	–
Rainbow bee-eater	4	6	5	5	6
Red-browed finch	–	–	–	–	1
Red-capped robin	16	10	2	6	3
Red-rumped parrot	3	6	2	3	9
Red wattlebird	2	–	–	–	–
Restless flycatcher	1	3	–	–	3
Royal spoonbill	2	–	–	–	–
Rufous fantail	–	1	–	–	–
Rufous songlark	4	1	–	4	–
Rufous whistler	55	37	37	49	58
Sacred kingfisher	46	37	39	39	47

Species name	2015–16	2017–18	2018–19	2019–20	2020–21
Satin flycatcher	–	1	–	–	–
Scarlet robin	29	22	29	19	18
Shining bronze-cuckoo	6	5	1	–	22
Silvereye	25	14	11	9	25
Southern boobook	1	–	–	–	–
Spotted pardalote	18	26	10	40	21
Square-tailed kite	–	–	–	–	2
Striated pardalote	64	62	60	62	64
Striated thornbill	33	27	38	33	52
Sulphur-crested cockatoo	50	56	54	51	59
Superb fairy-wren	41	48	52	36	37
Superb parrot	3	1	2	3	7
Swamp harrier	–	–	–	1	3
Swift parrot	–	–	–	–	1
Tree martin	2	4	2	–	1
Varied sittella	5	4	11	11	13
Wedge-tailed eagle	8	4	7	7	8
Weebill	54	53	53	56	57
Welcome swallow	3	5	2	–	2
Western gerygone	22	11	4	3	22
Whistling kite	5	4	6	5	4
White-bellied sea-eagle	2	–	2	1	–
White-breasted woodswallow	3	1	3	1	1
White-browed babbler	1	1	1	2	–
White-browed scrubwren	5	7	7	8	6
White-browed woodswallow	–	–	4	9	3
White-faced heron	2	2	2	2	4
White-necked heron	1	1	–	2	–
White-plumed honeyeater	35	45	42	43	20
White-throated treecreeper	64	63	62	54	56
White-winged chough	22	11	8	13	10
White-winged triller	1	7	3	12	4
Willie wagtail	6	7	8	5	8
Yellow-rumped thornbill	7	11	3	5	10
Yellow rosella	51	52	42	38	54
Yellow thornbill	13	20	38	39	51