

validation of 360-degree camera data

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Validating ecological data extracted from 360-degree images using the pannotator package with field survey data

This file contains a preliminary assessment of the ability of data extracted from 360-degree panospheric images using the pannotator software to reliably capture important ecological variables that have been reported in the accompanying paper. The analyses and results reported in this document are based on data collected over a series of validation plots located across Uluru-Kata Tjuta National Park, Australia in which field survey data and 360-degree images were collected and in the main study transect reported in the paper.

Here we focus on three sets of analyses that investigate the reliability and repeatability of key ecological data presented in the paper:

1. A comparison of plot-level plant species lists constructed from both 360-degree camera images and accompanying field survey data (based on validation plots),
2. A comparison of plant cover estimates, again using both 360-degree camera images and field survey data (based on validation plots),
3. Consistency in the scoring of tree crown health by different users of the pannotator package (based on the main transect).

We note that the analyses presented here relate only to the data collected in our study, and that research focusing on different species or systems will likely require different methods for collecting 360-degree images and for calibration. However, based on our results we draw general conclusions relevant to other study systems and provide practical advice for collecting images and calibrating image-based data in the accompanying paper.

Data sources

The species and cover analyses conducted below are based on data collected from a series of validation plots (20 m diameter) located on the edges or corners of square transects that measure 1 km on each side. The plots were established across Uluru-Kata Tjuta National Park to capture variation in landforms and vegetation across the Park. Crown data for desert oak (*Allocasuarina decaisneana*) were extracted from 360-degree images collected along the main 4 km long study transect centred on S 25.35 degrees, W 130.72 degrees (see accompanying paper).

Install the necessary packages for all code below

```
Attaching package: 'dplyr'
```

```
The following objects are masked from 'package:stats':
```

```
filter, lag
```

```
The following objects are masked from 'package:base':
```

```
intersect, setdiff, setequal, union
```

```
Attaching package: 'data.table'
```

```
The following objects are masked from 'package:dplyr':
```

```
between, first, last
```

```
Linking to GEOS 3.12.1, GDAL 3.8.4, PROJ 9.3.1; sf_use_s2() is TRUE
```

```
-- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
vforcats 1.0.0      vpurrr    1.0.2
vlubridate 1.9.3     vtibble   3.2.1
-- Conflicts ----- tidyverse_conflicts() --
x data.table::between() masks dplyr::between()
x dplyr::filter()      masks stats::filter()
x data.table::first()   masks dplyr::first()
x lubridate::hour()    masks data.table::hour()
x lubridate::isoweek() masks data.table::isoweek()
x dplyr::lag()         masks stats::lag()
x data.table::last()   masks dplyr::last()
x lubridate::mday()    masks data.table::mday()
x lubridate::minute()  masks data.table::minute()
x lubridate::month()   masks data.table::month()
x lubridate::quarter() masks data.table::quarter()
x lubridate::second()  masks data.table::second()
x purrr::transpose()  masks data.table::transpose()
x lubridate::wday()   masks data.table::wday()
x lubridate::week()   masks data.table::week()
x lubridate::yday()   masks data.table::yday()
x lubridate::year()   masks data.table::year()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

1. Plant species data

All woody plant species (subshrubs < 50 cm tall, shrubs >= 50 cm tall and trees) along with species of *Triodia* (spinifex grasses) were identified inside 79 validation plots (20 m diameter) during field surveys conducted in August 2022. Here we read in the .csv file and create the R dataframe ‘species_data’.

The dataframe ‘species_data’ contains the following variables:

Column [1] (ID) = record identifier; [2] (Plot) = plot number, [3] (Location) = location of plot along transect (NE, NW, SE, SW corner or extra plot); [4] (Latitude) = latitude in decimal degrees; [5] (Longitude) = longitude in decimal degrees; [6] (Closest_image) = identity of closest 360-degree image (for pannotator annotation); [7] (Camera_d_to_plot) = approximate distance (m) from camera image centre to survey plot centre; [8] (No_Field_species) = number of species identified in field survey; [9] (No_Camera_species) = number of species identified in camera survey; [10] (In_field_not_camera) = number of species unique to field survey;

[11] (Notes) = notes on errors in data collection, where ‘NoDiscrepancy’ = no differences between field survey and camera survey species lists, ‘Inside5m’ = the species not identified (missed in the survey) was within 5 m of the plot centre and camera, ‘Outside5m’ = the species missed was more than 5m from the plot centre and camera, and ‘FieldError’ = the species was incorrectly recorded as absent in the field survey;

[12]-[14] (Field_extra_Species_1, Field_extra_Species_2, Field_extra_Species_3) = names of extra species recorded in the field survey; [15] (In_camera_not_field) = number of species unique to camera survey; [16] (C_E_Species_1) = names of extra species recorded in the camera survey; [17] (Shared_species) = total number of shared species in field and camera survey lists; [18] (Unique_species) = total number of unique species in field and camera survey lists; [19] (Agreement) = Agreement (%), measured as 100 X ((shared species) / (shared + unique species));

[20]-[51] (AcacAneu, AlloDeca, Triodiasp, AlutMais, GrevErio, AcacLigu, EucaGamo, DicrGile, AcacPru, Erem-Spec, DodoVisc, AcacMell, CodoCoti, GyroTepp, AcacMiny, EucaOxy, NewcSpod, AcacMait, ExocSpar, HakeSpec,

GrevSten, SanLanc, SennArte, GyroRamo GrevJunc, AcacAmmo, EremLatr, EremGlab, EremGibs, RhagErem, EremLong, Acacia_sp) species present in plots, with Both = species in both field and camera survey lists; CameraOnly = species found only in camera survey list; FieldOnly = species found only in field survey list; Absent = species not recorded in either field or camera survey data.

The species are: AcacAneu = *Acacia aneura*, AlloDeca = *Allocasuarina decaisneana*, Triodiasp = *Triodia* species (*T. pungens*, *T. schinzii* and *T. basedowii*), AlutMais = *Aluta maisonneuvei*, GrevErio = *Grevillea eriostachya*, AcaLigu = *Acacia ligulata*, EucaGamo = *Eucalyptus gammophylla*, DicrGile = *Dicrastylis gilesii*, AcacPru = *Acacia pruinocarpa*, EremSpec = *Eremophila* sp., DodoVisc = *Dodonaea viscosa*, AcacMell = *Acacia melliodora*, CodoCoti = *Codonocarpus cotinifolius*, GyroTepp = *Gyrostemon tepperi*, AcacMiny = *Acacia minyura*, EucaOxy = *Eucalyptus oxymitra*, NewcSpod = *Newcastelia spodiotricha*, AcacMait = *Acacia maitlandii*, ExocSpar = *Exocarpos sparteus*, HakeaSpec = *Hakea* species , GrevSten = *Grevillea stenobotrya*, SanLanc = *Santalum lanceolatum*, SennArte = *Senna artemisioides*, GyroRamo = *Gyrostemon ramulosum*, GrevJunc = *Grevillea juncifolia*, AcacAmmo = *Acacia ammobia* , EremLatr = *Eremophila latrobei*, EremGlab = *Eremophila glabra*, EremGibs = *Eremophila gibsonii*, RhagErem = *Rhagodia eremaea*, EremLong = *Eremophila longifolia*, Acacia_sp = *Acacia* species.

```

1 species_data <- read_csv("./Data_files/validation_species.csv", show_col_types =
2   FALSE)
3 
4 # confirm that there are 79 plots of species data
5 cat("The number of rows in the dataframe is: ", nrow(species_data))
6 
7 # initialize table counter
8 table_counter <- 0
9 
10 # function to generate table numbers and captions
11 table_caption <- function(caption) {
12   table_counter <-> table_counter + 1
13   paste("Table", table_counter, ":", caption)
14 }
15 
16 # show the first 10 rows of the dataframe
17 #kable(head(species_data, 10), format = "html", caption="Species calibration data
18   frame")

```

The number of rows in the dataframe is: 79

We begin by comparing the mean species number across plots using species lists compiled from field survey data and camera images scored in the pannotator package.

```

1 # find the mean number of species in the field surveys
2 Field_mean <- summary(species_data$No_Field_species)
3 cat("The summary for the number of species based on field survey data is:\n")
4 print(Field_mean)
5 cat("\n")
6 
7 # find the mean number of species in the camera surveys
8 Camera_mean <- summary(species_data$No_Camera_species)
9 cat("The summary for the number of species based on camera image data is:\n")

```

```
10 print(Camera_mean)
11 cat("\n")
```

The summary for the number of species based on field survey data is:

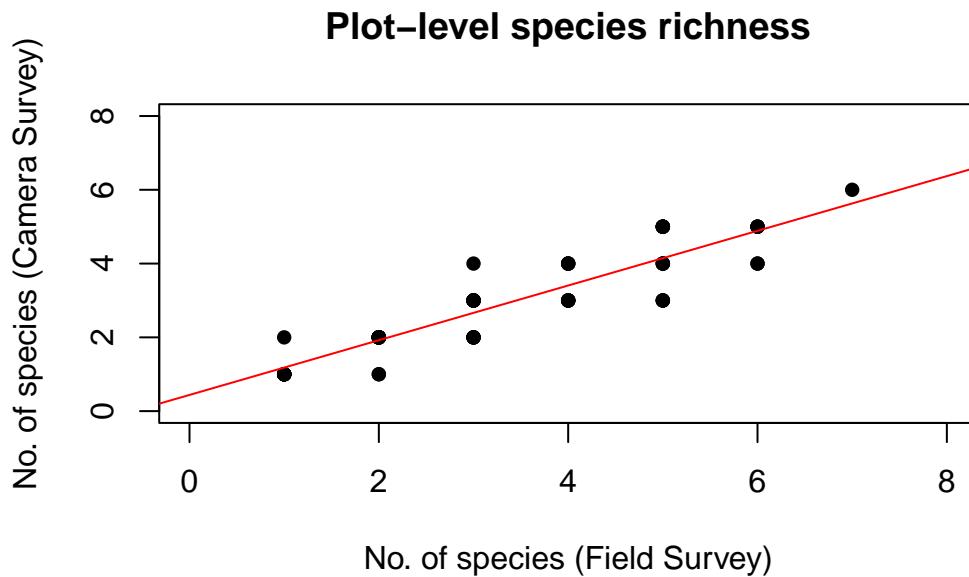
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1.000	2.000	3.000	3.266	5.000	7.000

The summary for the number of species based on camera image data is:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1.000	2.000	3.000	2.861	4.000	6.000

The data show that on average we recorded 3.3 species per plot based on field surveys and 2.9 species based on camera images. Thus, there was a weak tendency to record fewer species using camera images. Now we determine the relationship between plot-level species counts in the field survey versus camera survey counts.

```
1 # abline adds a linear model to the plot.
2 plot_sp_richness <- plot(species_data$No_Field_species,
3   ↵ species_data$No_Camera_species,
4   ↵ main = "Plot-level species richness",
5   ↵ xlab = "No. of species (Field Survey)",
6   ↵ ylab = "No. of species (Camera Survey)",
7   ↵ pch = 16, # Use filled circles as data points
8   ↵ col = "black", # Set point color
9   ↵ ylim = c(0, 8), # Set y-axis limits
10  ↵ xlim = c(0, 8)) # Set x-axis limits
11 abline(lm(No_Camera_species ~ No_Field_species, data =
12   ↵ species_data), col = "red")
```



```

1 # create linear model for species data
2 model <- lm(No_Camera_species ~ No_Field_species, data = species_data)
3 cat("Model results:\n")
4 print(model)

5
6 # summarise linear model
7 model_summary <- summary(model)
8 cat("Model summary:\n")
9 print(model_summary)

```

Model results:

Call:

`lm(formula = No_Camera_species ~ No_Field_species, data = species_data)`

Coefficients:

(Intercept)	No_Field_species
0.4394	0.7414

Model summary:

Call:

`lm(formula = No_Camera_species ~ No_Field_species, data = species_data)`

Residuals:

Min	1Q	Median	3Q	Max
-1.14654	-0.18080	0.07777	0.33633	1.33633

```

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.43936   0.14054   3.126   0.0025 **
No_Field_species 0.74144   0.03885  19.087 <2e-16 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Residual standard error: 0.5374 on 77 degrees of freedom
Multiple R-squared: 0.8255, Adjusted R-squared: 0.8233
F-statistic: 364.3 on 1 and 77 DF, p-value: < 2.2e-16

There is a strong positive relationship between species counts in plots based on field survey and camera survey data which explains 82.3 % of the variation in the data ($p < 6.3825904 \times 10^{-31}$). The slope (0.74) again indicates a weak tendency for species lists compiled using camera imagery to be smaller than those based on field survey data.

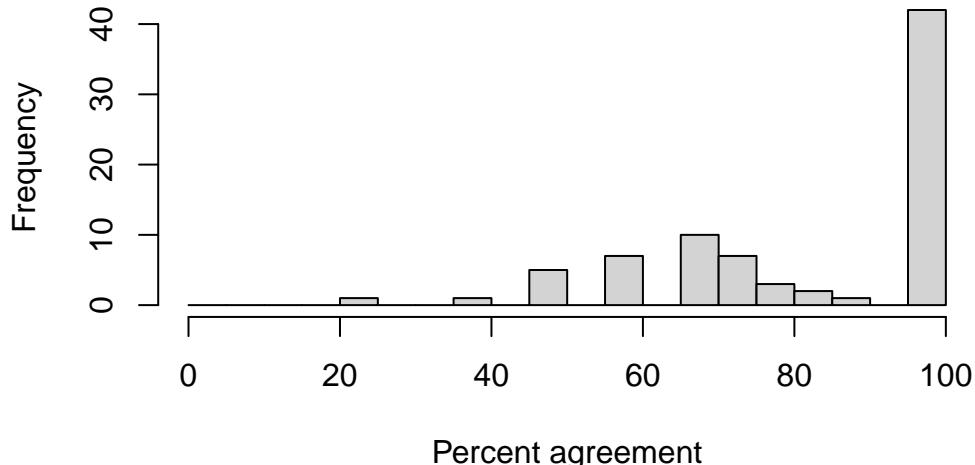
Now we assess the percentage agreement in the species lists based on field survey and camera survey data. The percentage agreement (A) is measured as $A = 100 \times (\text{shared species}) / (\text{shared} + \text{unique species})$.

```

1 Mean_agreement = summary(species_data$Agreement)
2 cat("The summary for % agreement between field & camera survey species lists
     ↴ is:\n")
3 print(Mean_agreement)
4
5 # construct a histogram of the % agreement between mean plot-level species counts
     ↴ based on field and camera surveys
6 hist_data <- hist(species_data$Agreement, breaks = seq(0, 100, by = 5),
7                     main = "Histogram of Field-Camera survey agreement",
8                     xlab = "Percent agreement",
9                     ylab = "Frequency")

```

Histogram of Field–Camera survey agreement



The summary for % agreement between field & camera survey species lists is:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
25.00	66.67	100.00	83.75	100.00	100.00

On average there was 84% agreement between field survey and camera survey species lists. The histogram shows that a majority of plots were in 100% agreement, with a second cluster at 65-90% agreement. A small number of plots had lower agreement.

We now investigate which species were contributing to the lack of agreement in species lists in certain plots. First we construct a list of the species that were missed in the camera surveys of each plot (i.e., were found only in the field survey), with the number of occasions of each. There are three columns of species found only in the field survey, labelled Field_extra_Species_1, Field_extra_Species_2, and Field_extra_Species_3. Next we construct a list of the species that were recorded ONLY in the camera surveys of each plot (i.e., were not recorded in the field survey), with counts of each. There is one column of species found only in the camera survey, labelled C_E_Species_1.

```
1 # summarise results for each of the field extra species columns
2 summary_1 <- species_data %>%
3   filter(!is.na(Field_extra_Species_1)) %>%
4   count(Field_extra_Species_1, sort = TRUE) %>%
5   rename(Species = Field_extra_Species_1) %>%
6   mutate(Species = as.character(Species))
7
8 summary_2 <- species_data %>%
9   filter(!is.na(Field_extra_Species_2)) %>%
10  count(Field_extra_Species_2, sort = TRUE) %>%
11  rename(Species = Field_extra_Species_2) %>%
12  mutate(Species = as.character(Species))
```

```

13
14 summary_3 <- species_data %>%
15   filter(!is.na(Field_extra_Species_3)) %>%
16   count(Field_extra_Species_3, sort = TRUE) %>%
17   rename(Species = Field_extra_Species_3) %>%
18   mutate(Species = as.character(Species))
19
20 field_only_species <- bind_rows(summary_1, summary_2, summary_3) %>%
21   group_by(Species) %>%
22   summarise(n = sum(n)) %>%
23   arrange(desc(n))
24
25
26 # print table using gt
27 field_only_species_gt_table <- gt(field_only_species) %>%
28   tab_options(
29     table.align = "center",
30     table.font.size = px(10),
31     column_labels.font.size = px(16),
32     heading.align = "center",
33     heading.title.font.size = px(20),
34     quarto.use_bootstrap = TRUE
35   ) %>%
36   opt_row_striping() %>%
37   tab_header(
38     title = table_caption("Extra species in field surveys")
39   )
40
41 field_only_species_gt_table

```

Table 1 : Extra species in field surveys

Species	n
Triodia_schinzii	11
Acacia_ligulata	4
Aluta_maisonneuvei	3
Acacia_melliodora	2
Acacia_minyura	2
Eremophila_glabra	2
Eremophila_latrobei	2
Eremophila_longifolia	2
Grevillea_juncifolia	2
Acacia sp.	1
Acacia_maitlandii	1
Codonocarpus_cotinifolius	1
Dodonea_viscosa	1
Eucalyptus_oxymitra	1
Grevillea_stenobotrys	1
Hakea_?_loreae	1
Rhagodia_eremaea	1
Santalum_lanceolatum	1
Senna_artemisioides	1

```

1 # summarise results for each of the species recorded in camera images only
2 camera_only_species <- species_data %>%
3   filter(!is.na(C_E_Species_1)) %>%
4   count(C_E_Species_1, sort = TRUE) %>%
5   rename(Species = 1) %>%
6   mutate(Species = as.character(Species))
7
8 camera_only_species_gt_table <- gt(camera_only_species) %>%
9   tab_options(
10     table.align = "center",
11     table.font.size = px(10),
12     column_labels.font.size = px(16),
13     heading.align = "center",
14     heading.title.font.size = px(20),
15     quarto.use_bootstrap = TRUE
16   ) %>%
17   opt_row_striping() %>%
18   tab_header(
19     title = table_caption("Extra species in camera surveys")
20   )
21
22 camera_only_species_gt_table

```

Table 2 : Extra species in camera surveys

Species	n
Aluta_maisonneuvei	4
Acacia_anera	3
Triodia_sp.	3
Acacia_maitlandii	1
Grevillea_erostachya	1
Newcastelia_spodiotricha	1

These data show that the most common species identified only in the field survey of a given plot was *Triodia schinzii*, a spinifex grass. In many plots *Triodia pungens* and *Triodia schinzii* were both present, but it was not generally possible to distinguish these taxa, the difference of which can usually only be determined by panicle or floral structure. *Acacia ligulata* and *Aluta maisonneuvei* were also missed in the camera surveys 4 and 3 times respectively, but these were often in burnt plots. Other species, usually shrubs, were occasionally missed.

We now determine some circumstances under which species were not recorded in the two surveys. For this we have the variable species_data\$Notes, which has the categories ‘NoDiscrepancy’ = the field and camera survey lists were the same, ‘Outside5m’ = detected in field survey 5 m to 10 m from the plot centre but not in the camera survey, ‘Inside5m’ = detected in field survey within 5 m of the plot centre but not in the camera survey, and ‘FieldError’ where an error was made in the field survey.

```

1 # count occurrences in 'Notes' column and sort the results
2 df <- species_data %>%
3   count(Notes, sort = TRUE)
4

```

```

5 # calculate the total number of records
6 total <- sum(df$n)

7
8 # calculate the total number of discrepancies in plots species lists
9 # need to filter by specific Notes values corresponding to discrepancies
10 disc <- df %>%
11   filter(Notes %in% c("Inside5m", "Outside5m", "FieldError")) %>%
12   summarise(total_discrepancies = sum(n)) %>%
13   pull(total_discrepancies)

14
15 # calculate the percentage of discrepancies
16 pcnt_disc <- 100 * (disc / total)

17
18 # print the percentage of discrepancies
19 cat(paste("Percentage of discrepancies:", round(pcnt_disc, 1), "%"))
20 cat("\n")

21
22 df_gt_table <- gt(df) %>%
23   tab_options(
24     table.align = "center",
25     table.font.size = px(10),
26     column_labels.font.size = px(16),
27     heading.align = "center",
28     heading.title.font.size = px(20)
29   ) %>%
30   opt_row_striping() %>%
31   tab_header(
32     title = table_caption("Discrepancies between field & camera surveys")
33   )

34
35 df_gt_table

```

Percentage of discrepancies: 45.6 %

Table 3 : Discrepancies between field & camera surveys

Notes	n
NoDiscrepancy	43
Outside5m	22
Inside5m	11
FieldError	3

These data show that there was discrepancy in species lists generate from field and camera surveys in 46% of plots (in 36 of 79 plots), and that in 22 plots (28%) at least one species located more than 5 m from the centre of the plot was missed in the camera survey. In 11 plots (14%) a species was missed in the camera survey when it occurred less than 5 m from the centre of the plot.

We now determine which species were missed < 5 m and > 5 m from the plot centre. Those missed < 5 m from the plot centre are the most serious because they fall within the area used to determine species counts in subsequent camera-based surveys (see accompanying paper).

```

1 # Filtering species_data for notes "Inside5m" and removing rows with NA's in
2   ↳ Field_extra_Species_1 and Field_extra_Species_2
3 species_data_L5 <- species_data %>%
4   filter(Notes == "Inside5m") %>%
5   filter(complete.cases(Field_extra_Species_1))

6 # Get the species counts for Field_extra_Species_1
7 summary_1_L5 <- species_data_L5 %>%
8   count(Field_extra_Species_1, sort = TRUE) %>%
9   rename(Species = Field_extra_Species_1) %>%
10  mutate(Species = as.character(Species))

11 # Get the species counts for Field_extra_Species_2
12 summary_2_L5 <- species_data_L5 %>%
13   filter(!is.na(Field_extra_Species_2)) %>%
14   count(Field_extra_Species_2, sort = TRUE) %>%
15   rename(Species = Field_extra_Species_2) %>%
16   mutate(Species = as.character(Species))

17 # Combine the counts from both columns
18 Less5_summary <- bind_rows(summary_1_L5, summary_2_L5) %>%
19   group_by(Species) %>%
20   summarise(n = sum(n)) %>%
21   arrange(desc(n))

22
23
24
25
26 Less5_summary_gt_table <- gt(Less5_summary) %>%
27   tab_options(
28     table.align = "center",
29     table.font.size = px(10),
30     column_labels.font.size = px(16),
31     heading.align = "center",
32     heading.title.font.size = px(20)
33   ) %>%
34   opt_row_striping() %>%
35   tab_header(title = table_caption("Species missed inside 5 metres"))

36
37 Less5_summary_gt_table

38
39 # get the total count of missed Triodia schinzii < 5 m from the plot center
40 Triodia_index <- which(Less5_summary$Species == "Triodia_schinzii")
41 Triodia_count <- Less5_summary$n[Triodia_index]

42
43 # using `summarize` to calculate the total count from Less5_summary
44 Total_count <- Less5_summary %>%
45   summarize(total = sum(n)) %>%
46   pull(total)

47
48 # calculate the percentage of Triodia schinzii
49 Triodia_pcnt <- round(100 * (Triodia_count/Total_count),1)

```

```

50 cat(paste("Missed Triodia schinzii (< 5 m) as % of total: ", Triodia_pcnt, "%"))
51 cat("\n")

```

Table 4 : Species missed inside 5 metres

Species	n
Triodia_schinzii	7
Acacia_ligulata	1
Acacia_melliodora	1
Eremophila_glabra	1
Eucalyptus_oxymitra	1
Rhagodia_eremaea	1

Missed Triodia schinzii (< 5 m) as % of total: 58.3 %

Now do the same for species greater than 5 m

```

1 # Filtering species_data for notes "Outside5m" and removing rows with NA's in
2   ↳ Field_extra_Species_1 and Field_extra_Species_2
3 species_data_Gr5 <- species_data %>%
4   filter(Notes == "Outside5m") %>%
5   filter(complete.cases(Field_extra_Species_1))
6
7 # Get the species counts for Field_extra_Species_1
8 summary_1_Gr5 <- species_data_Gr5 %>%
9   count(Field_extra_Species_1, sort = TRUE) %>%
10  rename(Species = Field_extra_Species_1) %>%
11  mutate(Species = as.character(Species))
12
13 # Get the species counts for Field_extra_Species_2
14 summary_2_Gr5 <- species_data_Gr5 %>%
15   filter(!is.na(Field_extra_Species_2)) %>%
16   count(Field_extra_Species_2, sort = TRUE) %>%
17   rename(Species = Field_extra_Species_2) %>%
18   mutate(Species = as.character(Species))
19
20 # Combine the counts from both columns
21 Gr5_summary <- bind_rows(summary_1_Gr5, summary_2_Gr5) %>%
22   group_by(Species) %>%
23   summarise(n = sum(n)) %>%
24   arrange(desc(n))
25
26 Gr5_summary_gt_table <- gt(Gr5_summary) %>%
27   tab_options(
28     table.align = "center",
29     table.font.size = px(10),
30     column_labels.font.size = px(16),
31     heading.align = "center",
32     heading.title.font.size = px(20)

```

```

32 ) %>%
33 opt_row_striping() %>%
34 tab_header(
35   title = table_caption("Species missed outside 5 metres")
36 )
37
38 Gr5_summary_gt_table

```

Table 5 : Species missed outside 5 metres

Species	n
Triodia_schinzii	4
Aluta_maisonneuvei	3
Acacia_ligulata	2
Acacia_minyura	2
Eremophila_latrobei	2
Eremophila_longifolia	2
Acacia sp.	1
Acacia_maitlandii	1
Acacia_mellioidora	1
Codonocarpus_cotinifolius	1
Dodonea_viscosa	1
Eremophila_glabra	1
Grevillea_erostachya	1
Grevillea_juncifolia	1
Grevillea_stenobotrys	1
Hakea_?_loreia	1
Santalum_lanceolatum	1
Senna_artemisioides	1

For species missed within 5 m of the plot centre, 7/12 cases 58.3% were of *Triodia schinzii* (which could not be distinguished easily from *Triodia pungens*, especially when sterile). Other species were only missed once. A much greater number of species were missed 5 m to 10 m from the plot centre, most being small shrubs or seedlings, burnt plants that retained no leaf material, or species that are morphologically similar to others in the study area (e.g., *Triodia schinzii*, *Acacia minyura*, various *Eremophila* spp.). Collectively these data suggest that given the resolution of GoPro Max cameras shrubby and smaller species should be recorded within 5 m of the plot centre unless they are morphologically or chromatically distinct (e.g., *Allocasuarina descaisneana*, *Corymbia opaca*).

The main species recorded in the camera survey but not in the field (within individual plots) included *Aluta maisonneuvei*, *Acacia aneura*, and *Triodia* sp. (spinifex grasses). *Acacia aneura* is morphologically similar to *Acacia minyura*, and burnt *Aluta maisonneuvei* could be mistaken for other shrub species. However, some field survey errors also occurred, particularly where *Tridodia* spp. were overlooked.

We now complete this analysis by determining the field detection rate of plant species recorded across all study plots, later focusing only on widespread species recorded in at least ten plots. For the following analysis we now select only the record ID (plot) and record of each definitively identified species (including the 3 *Triodia* spp. species lumped) in a plot, where 'Both' = species recorded in both field and camera survey lists; 'CameraOnly' = species recorded only in camera survey list; 'FieldOnly' = species recorded only in field survey list; 'Absent' = species not recorded in either field or camera survey data.

```

1 # take a subset of the species_data
2 dataB <- species_data[, c("ID", "AcacAneu", "AlloDeca", "Triodiasp", "AlutMais",
  ↵ "GrevErio", "AcacLigu", "EucaGamo", "DicrGile", "AcacPrui", "CodoCoti",
  ↵ "DodoVisc", "GyroTepp", "AcacMell", "AcacMiny", "EucaOxy",
  ↵ "NewcSpod", "AcacMait", "ExocSpar", "GrevSten", "SanLanc", "GrevJunc",
  ↵ "SennArte", "GyroRamo", "AcacAmmo", "EremLatr", "EremGlab", "RhagErem",
  ↵ "EremLong")]

```

```

3
4 # some data wrangling to produce a pivot table for each species based on numbers of
5 # 'Both', 'CameraOnly', 'FieldOnly', and 'Absent' identifications in each plot
6 dataC <- dataB %>%
7   pivot_longer(cols = -ID) %>%
8   count(name, value) %>%
9   pivot_wider(names_from = name, values_from = n, values_fill = list(n = 0))
10
11 # transpose the table
12 t_dataC <- t(dataC)
13
14 #get row and colnames in order
15 colnames(t_dataC) <- rownames(dataC)
16 rownames(t_dataC) <- colnames(dataC)
17
18 #View(t_dataC)
19 # assign the names
20 colnames(t_dataC) <- t_dataC[1, ]
21 t_dataC2 <- t_dataC[-1,]
22
23 # convert to data frame and add row names as a column
24 species_counts <- as.data.frame(t_dataC2) %>%
25   rownames_to_column(var = "Species")
26
27 #View(species_counts)
28
29 species_counts_gt_table <- gt(species_counts) %>%
30   tab_options(
31     table.align = "center",
32     table.font.size = px(10),
33     column_labels.font.size = px(16),
34     heading.align = "center",
35     heading.title.font.size = px(20)
36   ) %>%
37   opt_row_striping() %>%
38   tab_header(
39     title = table_caption("Species counts based on numbers of 'Both', 'CameraOnly',
40     ↪ 'FieldOnly', and 'Absent' identifications in each plot")
41   )
42
43 species_counts_gt_table

```

Table 6 : Species counts based on numbers of 'Both', 'CameraOnly', 'FieldOnly', and 'Absent' identifications in each plot

Species	Absent	Both	CameraOnly	FieldOnly
AcacAmmo	77	2	0	0
AcacAneu	50	26	3	0
AcacLigu	68	7	0	4
AcacMait	75	2	1	1

AcacMell	77	0	0	2
AcacMiny	73	5	0	1
AcacPrui	78	1	0	0
AlloDeca	59	20	0	0
AlutMais	52	20	4	3
CodoCoti	66	12	0	1
DicrGile	78	1	0	0
DodoVisc	76	2	0	1
EremGlab	77	0	0	2
EremLatr	75	2	0	2
EremLong	77	2	0	0
EucaGamo	71	8	0	0
EucaOxy	76	2	0	1
ExocSpar	78	1	0	0
GrevErio	59	18	1	1
GrevJunc	77	0	0	2
GrevSten	76	2	0	1
GyroRamo	78	1	0	0
GyroTepp	77	2	0	0
NewcSpod	75	3	1	0
RhagErem	78	0	0	1
SanLanc	78	0	0	1
SennArte	77	1	0	1
Triodiasp	11	65	3	0

This provides a list of each species and counts of occurrences in Both, CameraOnly, FieldOnly and Absent categories. We now calculate the camera detection rate for each species based on these data.

```

1 # first ensure/convert the data to numeric
2 species_counts$Absent <- as.numeric(as.character(species_counts$Absent))
3 species_counts$Both <- as.numeric(as.character(species_counts$Both))
4 species_counts$FieldOnly <- as.numeric(as.character(species_counts$FieldOnly))
5 species_counts$CameraOnly <- as.numeric(as.character(species_counts$CameraOnly))

6
7
8 # next calculate the total and number of valid, positive records of each species,
  ↵ which we assume here are counts that occur in either field surveys or both
  ↵ field surveys and camera surveys (the 'Both' category)
9 species_counts$Positives <- species_counts$Both + species_counts$FieldOnly
10 species_counts$Total <- species_counts$Absent + species_counts$Both +
  ↵ species_counts$FieldOnly + species_counts$CameraOnly

11
12
13 # rank the species by total positive count
14 species_counts<-species_counts[order(species_counts$Positives,decreasing = TRUE),]
15
16 # calculate the frequency of each species as a percentage occurrence across plots
17 species_counts$Frequency <- 100*(species_counts$Positives / species_counts$Total)

18
19
20 # calculate the percentage of positive occurrences that were captured in the camera
  ↵ survey for each species #
21 species_counts$CameraDetectionRate <- 100-100*(species_counts$FieldOnly /
  ↵ species_counts$Positives)
22
```

```

23
24 # reorder the columns for ease of viewing and present the data
25 species_counts <- species_counts %>%
26   select(Species, Total, Positives,
27         Frequency, CameraDetectionRate,
28         Absent, Both,
29         CameraOnly, FieldOnly)
30
31
32
33 species_counts_gt_table <- gt(species_counts) %>%
34   tab_options(
35     table.align = "center",
36     table.font.size = px(10),
37     column_labels.font.size = px(16),
38     heading.align = "center",
39     heading.title.font.size = px(20)
40   ) %>%
41   opt_row_striping() %>%
42   tab_header(
43     title = table_caption("Counts all species")
44   )
45
46
47 species_counts_gt_table

```

Table 7 : Counts all species

Species	Total	Positives	Frequency	CameraDetectionRate	Absent	Both	CameraOnly	FieldOnly
Triodiasp	79	65	82.278481	100.00000	11	65	3	0
AcacAneu	79	26	32.911392	100.00000	50	26	3	0
AlutMais	79	23	29.113924	86.95652	52	20	4	3
AlloDeca	79	20	25.316456	100.00000	59	20	0	0
GrevErio	79	19	24.050633	94.73684	59	18	1	1
CodoCoti	79	13	16.455696	92.30769	66	12	0	1
AcacLigu	79	11	13.924051	63.63636	68	7	0	4
EucaGamo	79	8	10.126582	100.00000	71	8	0	0
AcacMiny	79	6	7.594937	83.33333	73	5	0	1
EremLatr	79	4	5.063291	50.00000	75	2	0	2
AcacMait	79	3	3.797468	66.66667	75	2	1	1
DodoVisc	79	3	3.797468	66.66667	76	2	0	1
EucaOxy	79	3	3.797468	66.66667	76	2	0	1
GrevSten	79	3	3.797468	66.66667	76	2	0	1
NewcSpod	79	3	3.797468	100.00000	75	3	1	0
AcacAmmo	79	2	2.531646	100.00000	77	2	0	0
AcacMell	79	2	2.531646	0.00000	77	0	0	2
EremGlab	79	2	2.531646	0.00000	77	0	0	2
EremLong	79	2	2.531646	100.00000	77	2	0	0
GrevJunc	79	2	2.531646	0.00000	77	0	0	2
GyroTepp	79	2	2.531646	100.00000	77	2	0	0
SennArte	79	2	2.531646	50.00000	77	1	0	1
AcacPruis	79	1	1.265823	100.00000	78	1	0	0
DicrGile	79	1	1.265823	100.00000	78	1	0	0
ExocSpar	79	1	1.265823	100.00000	78	1	0	0
GyroRamo	79	1	1.265823	100.00000	78	1	0	0
RhagErem	79	1	1.265823	0.00000	78	0	0	1

SanLanc	79	1	1.265823	0.00000	78	0	0	1
---------	----	---	----------	---------	----	---	---	---

Now find species with more than 10 positive records and present them

```

1 # filter species with more than 10 positive records and present them
2 species_counts_gr_10 <- species_counts %>%
3   filter(Positives > 10) %>%
4   arrange(desc(Positives))
5
6 counts_gr_10_gt_table <- gt(species_counts_gr_10) %>%
7   tab_options(
8     table.align = "center",
9     table.font.size = px(10),
10    column_labels.font.size = px(16),
11    heading.align = "center",
12    heading.title.font.size = px(20)
13  ) %>%
14  opt_row_striping() %>%
15  tab_header(
16    title = table_caption("Counts of species in > 10 plots")
17  )
18
19 counts_gr_10_gt_table
20
21 # get the minimum camera detection rate for the first 6 species detected in more
22 # than 10 plots
23 min10 <- species_counts_gr_10 %>%
24   slice(1:6) %>% # Select the first 6 rows
25   summarise(MinCameraDetectionRate = min(CameraDetectionRate, na.rm = TRUE))
26
27 #cat(paste0("Minimum Camera Detection Rate: ", round(min10, 2)))
28 #cat("\n")
29
30 # get the minimum camera detection rate for Acacia ligulata, a species most
31 # frequently undetected; for the text below
32 AcacLigu_index <- which(species_counts_gr_10$Species == "AcacLigu")
33 Accli <- min(species_counts_gr_10$CameraDetectionRate[AcacLigu_index])
34
35 #cat(paste0("Acacia ligulata: ", round(Accli, 2)))
36 #cat("\n")

```

Table 8 : Counts of species in > 10 plots

Species	Total	Positives	Frequency	CameraDetectionRate	Absent	Both	CameraOnly	FieldOnly
Triodiasp	79	65	82.27848	100.00000	11	65	3	0
AcacAneu	79	26	32.91139	100.00000	50	26	3	0
AlutMais	79	23	29.11392	86.95652	52	20	4	3
AlloDeca	79	20	25.31646	100.00000	59	20	0	0
GrevErio	79	19	24.05063	94.73684	59	18	1	1
CodoCoti	79	13	16.45570	92.30769	66	12	0	1

AcacLigu	79	11	13.92405	63.63636	68	7	0	4
----------	----	----	----------	----------	----	---	---	---

The objective of this analysis was to determine which species are most easily detected using camera images taken 3.2 m above the ground and in the centre of a 20 m diameter plot. The results show that species differed considerably in camera detectability, with the camera detection rate ranging from 0% to 100% depending on the species. Among common, widespread species or species groups (> 10 positive records or occurrences), *Allocasuarina decaisneana*, *Acacia aneura*, the *Triodia* species group (*T. basedowii*, *T. schinzii*, *T. pungens*), *Aluta maisonneuvei*, *Codonocarpus continifolius*, and *Grevillea eriostachya* were all detected in camera images 87% of the time or more. Only *Acacia ligulata*, many of which were dead across the study area, was an exception (64%).

Among less common species, morphologically distinct species such as *Eucalyptus gamophylla* and *Newcastelia spodiotricha* were always successfully detected, and many other species were a majority of the time.

Conclusions : plant species detection using 360-degree cameras

Overall, plot-level species occurrence data were reliably extracted from camera images in this study. There was a strong relationship between species counts based on field survey and camera survey, albeit with a weak tendency for fewer species to be recorded in the camera survey. On average there was 84% agreement between field survey and camera survey species lists, although we note that the overall species diversity in the study area was relatively low, and apart from the large spinifex grasses (*Triodia* spp.) we did not focus on herbaceous species.

The most common species identified in the field survey but missed in the camera survey was *Triodia schinzii*, and it was not generally possible to distinguish between *Triodia schinzii* and *Triodia pungens*, even less than 5 m from the centre of the plot (i.e., where the photo was taken). However, this is true even under field conditions when plants are lacking floral structures. More species, particularly small taxa, seedlings and plants that retained no leaf material or species that co-occurred with morphologically similar taxa were sometimes missed 5 m to 10 m from the plot centre. Overall, however, the most common species or species groups all had a camera detection rate of at least 86.96%, as did some less common taxa. Occasionally species were recorded in the camera survey but not the field survey, and since all species were perennial, these cases may be classified as field errors.

Collectively, we draw four conclusions from these data:

1. Camera data can be accurately used to generate plot-level species lists at the study site, although fewer species are missed within 5 m of the plot centre. Common and widespread species were all successfully detectable,
2. Morphologically distinct species were most easily detectable, and at greater distances from the camera. Morphologically similar species (e.g., spinifex grasses, *Eremophila* spp.) may need to be lumped together for subsequent analyses,
3. Reference photographs, ideally taken at different distances from the camera, should be provided for all target species to assist with species identification using the pannotator package,
4. The resolution of the current GoPro Max model may require collection of images closer to certain target taxa. This may involve, for example, collecting images closer to the ground (understory species), in the canopy (morphologically similar canopy taxa), and at multiple levels in both (structurally complex vegetation).

2. Spinifex grass (*Triodia* spp.) cover and dieback data

Total plot-level cover and mortality

The objective of the following analyses is to investigate the relationship between cover and mortality (dieback) estimates of spinifex (*Triodia* spp.) grasses across the validation plots in which cover and dieback estimates were generated both by field surveys and by using the pannotator package to score 360-degree images. We are particularly interested in specific size classes (if any) where discrepancies arise, and alterations to scoring methods that might improve accuracy if camera detection methods.

We first import the dataset `spinifex_validation.csv` and create the `spinifex_data` dataframe. The dataframe contains the following variables:

Column [1] (ID) = record identifier; [2] (Plot_NEW) = plot number; [3] (Location) = location of plot along transect (NE, NW, SE, SW corner or extra plot); [4] (Latitude) = latitude in decimal degrees; [5] (Longitude) = longitude in decimal degrees; [6] (Closest_image) = identity of closest 360-degree image (for pannotator annotation);

[7] (Field_Spinifex_size) = size class of spinifex identified in field survey (classes = 0-30 cm, >30-60, >60-100, >100-200, >200-300, >300-400, >400-500, >500 cm); [8] (Field_Spinifex_Cover) = field estimated cover (%); [9] (Field_Spinifex_%dead) = field percentage of spinifex cover estimate as dead; [10] (Camera_Spinifex_size) = size class of spinifex identified in camera survey; [11] (Camera_Spinifex_Cover) = camera estimated cover (%); [12] (Camera_Spinifex_%dead) = camera percentage of spinifex cover estimate as dead;

[13] (Cover_Cam_Field_Diff) = difference in cover estimate based on camera cover (%) - field cover (%); [14] (PercDead_Cam_Field_Diff) = difference in percentage of dead cover based on camera_%dead - field_%dead; [15] (Size_classes_field) = number of distinct spinifex size classes observed in plot based on field data; [16] (Size_classes_camera) = number of distinct spinifex size classes observed in plot based on cameradata; [17] (Misclassifications) = number of size classes in a given plot present in both field and camera surveys but differing by one or more size classes; [18] (Missed_classes) = number of size classes in a given plot missed completely in either in field and camera surveys; [19] (ErrorType1) = Error Type 1: 'Both' - size class observed in both field and camera surveys, 'FieldOnly' - size class observed only in field survey, CameraOnly' - size class observed only in camera survey; [20] (ErrorType2) = Error Type 2: 'No Error' - size class classified the same on field and camera suveys, 'Misclassified' - size class misclassified in either field or camera suveys, 'FieldError' - error made on field estimate of size class, 'CameraError' - error made on camera estimate of size class; [21] (Cat1) = misclassified by one size class category; [22] (Distance) = distance from camera for error : 'Less5' - less than 5 m, 'Great5' - more than 5 m.

```
1 # read in the data file. This is the data for species and cover calibration
2 spinifex_data <- read_csv("./Data_files/spinifex_validation.csv", show_col_types =
  FALSE)
```

In this section we take a similar approach to the evaluation of species identification described above. First we focus on overall plot cover and mortality data. These data are rows with the value of 'Total' in the `Field_Spinifex_size` and `Camera_Spinifex_size` columns.

```
1 # subset the data on only those containing "Total" plot cover values
2 spinifex_plot_total <- spinifex_data[spinifex_data$Field_Spinifex_size == 'TOTAL',]
3
4 # confirm the number of plots of spinifex cover data and print the result
5 cat("The number of rows in the subsetted dataframe is: ",
  nrow(spinifex_plot_total), "\n")
```

```
The number of rows in the subsetted dataframe is: 73
```

We will begin by comparing estimates of mean field- and camera-based spinifex cover (the mean across all verification plots), and then the relationship between field- and camera-based spinifex cover.

```
1 # first ensure the data are numeric
2 spinifex_plot_total$Field_Spinifex_Cover <-
   ↵ as.numeric(as.character(spinifex_plot_total$Field_Spinifex_Cover))
3 spinifex_plot_total$Camera_Spinifex_Cover <-
   ↵ as.numeric(as.character(spinifex_plot_total$Camera_Spinifex_Cover))
4
5 # calculate the mean plot-level spinifex cover using field and camera survey data
   ↵ and print the results
6 Field_mean_sp <- summary(spinifex_plot_total$Field_Spinifex_Cover)
7 cat("The summary for mean total spinifex cover across plots based on field survey
   ↵ data is:\n")
8 print(Field_mean_sp)
9 cat("\n")
10
11 Camera_mean_sp <- summary(spinifex_plot_total$Camera_Spinifex_Cover)
12 cat("The summary for mean total spinifex cover across plots based on camera image
   ↵ data is:\n")
13 print(Camera_mean_sp)
14 cat("\n")
```

The summary for mean total spinifex cover across plots based on field survey data is:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.00	3.50	13.00	13.15	17.00	46.00

The summary for mean total spinifex cover across plots based on camera image data is:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
0.00	4.50	14.50	14.63	22.50	46.00

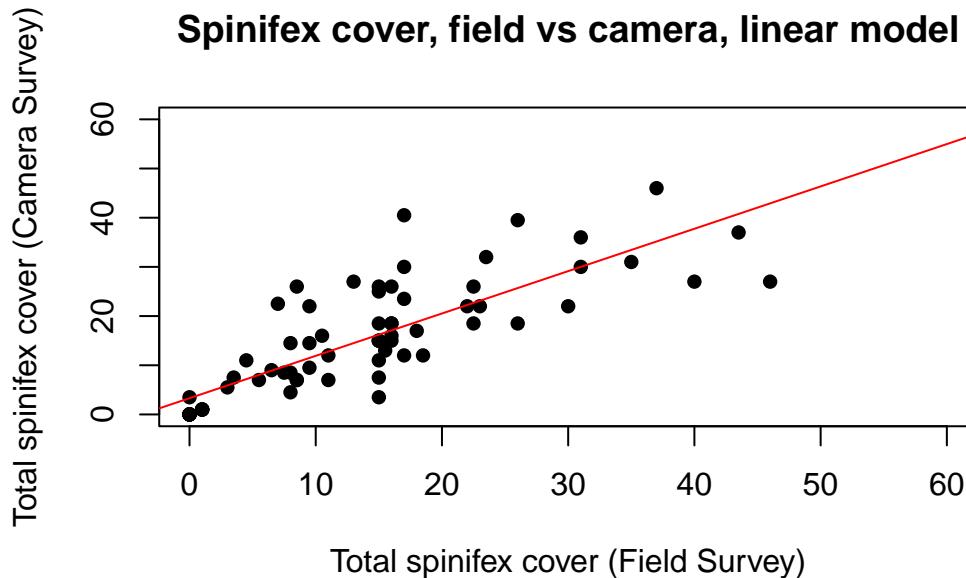
Field survey and camera survey methods yielded similar mean (13.15% versus 14.63% respectively), maximum and minimum estimates of total plot cover across the entire data set ($n = 73$ plots). This indicates that overall bias in the two measurement techniques might be small, but it does not mean that predictability at the plot scale is also high. To assess whether field and camera survey techniques yield similar cover estimates at the plot scale we must look further at this relationship. We begin by looking at the correlation between plot-level estimates of total spinifex cover using both techniques (spinifex_plot_total\$Field_Spinifex_Cover and spinifex_plot_total\$Camera_Spinifex_Cover).

```
1 # plot the correlation between field cover and camera cover estimates with linear
   ↵ model
2 plot(spinifex_plot_total$Field_Spinifex_Cover,
   ↵ spinifex_plot_total$Camera_Spinifex_Cover,
   ↵ main = "Spinifex cover, field vs camera, linear model",
   ↵ xlab = "Total spinifex cover (Field Survey)",
   ↵ ylab = "Total spinifex cover (Camera Survey)",
   ↵ pch = 16, # Use filled circles as data points
```

```

7     col = "black", # Set point color
8     ylim = c(0, 60), # Set y-axis limits
9     xlim = c(0, 60)) # Set x-axis limits
10    abline(lm(Camera_Spinifex_Cover ~ Field_Spinifex_Cover, data =
11      spinifex_plot_total), col = "red") # add a linear model to the plot

```



```

1 # view the linear model statistics
2 linearmodel <- lm(Camera_Spinifex_Cover ~ Field_Spinifex_Cover,
3   data=spinifex_plot_total)
4
5 # test whether the slope estimate differs from 1, which might indicate a bias
6 # towards lower values of camera cover for a given value of field cover
7
8 # 1. Get the summary of the model
9 modelsummary <- summary(linearmodel)
10 cat("Linear model summary of Camera_Spinifex_Cover ~ Field_Spinifex_Cover \n")
11 print(modelsummary)
12
13 # 2. Get the standard error of the slope
14 slope_se <- coef(modelsummary)[["Field_Spinifex_Cover", "Std. Error"]]
15 cat(paste0("Slope of the standard error: ", slope_se, "\n"))
16
17 # 3. Get the slope estimate
18 slope_estimate <- coef(modelsummary)[["Field_Spinifex_Cover", "Estimate"]]
19 cat(paste0("Slope estimator: ", slope_estimate, "\n"))
20
21 # 4. Calculate the Z test statistic (how many standard errors away from 1 is the
22 # slope estimate)

```

```

21 test_statistic <- (slope_estimate - 1) / slope_se
22 cat(paste0("Z score of the slope estimate: ", test_statistic, "\n"))
23
24 # 5. Calculate the p-value for the two-sided test
25 p_value <- 2 * (1 - pnorm(abs(test_statistic)))
26
27 # 6. Print the p-value
28 cat(paste0("The P value for testing deviation in the slope from 1 is: ", p_value,
29             "\n"))

```

Linear model summary of Camera_Spinifex_Cover ~ Field_Spinifex_Cover

Call:

```
lm(formula = Camera_Spinifex_Cover ~ Field_Spinifex_Cover, data = spinifex_plot_total)
```

Residuals:

Min	1Q	Median	3Q	Max
-15.915	-3.307	-1.695	3.013	22.555

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	3.30680	1.22624	2.697	0.00874 **
Field_Spinifex_Cover	0.86105	0.07105	12.119	< 2e-16 ***

Signif. codes:	0 '***'	0.001 '**'	0.01 '*'	0.05 '.'
	0.1 '	' 1		

Residual standard error: 6.786 on 71 degrees of freedom
Multiple R-squared: 0.6741, Adjusted R-squared: 0.6695
F-statistic: 146.9 on 1 and 71 DF, p-value: < 2.2e-16

Slope of the standard error: 0.0710465545046707
Slope estimator: 0.861045180580407
Z score of the slope estimate: -1.95582770182694
The P value for testing deviation in the slope from 1 is: 0.0504854544045341

Both indicate that field survey cover is strongly related ($p < 5.8946282 \times 10^{-19}$) to camera survey cover. The linear model explains 67% of variability in the data, and the test for whether the slope of the relationship (0.86) differs from 1 is marginally significant ($p = 0.05$), which in this model indicates that camera cover scores may be slightly biased towards lower values than field survey estimates. Visually, however, the relationship appears to be non-linear, with stronger bias at higher values of field survey cover. Next we do a very simple investigation of this possible bias using a second-order polynomial function.

```

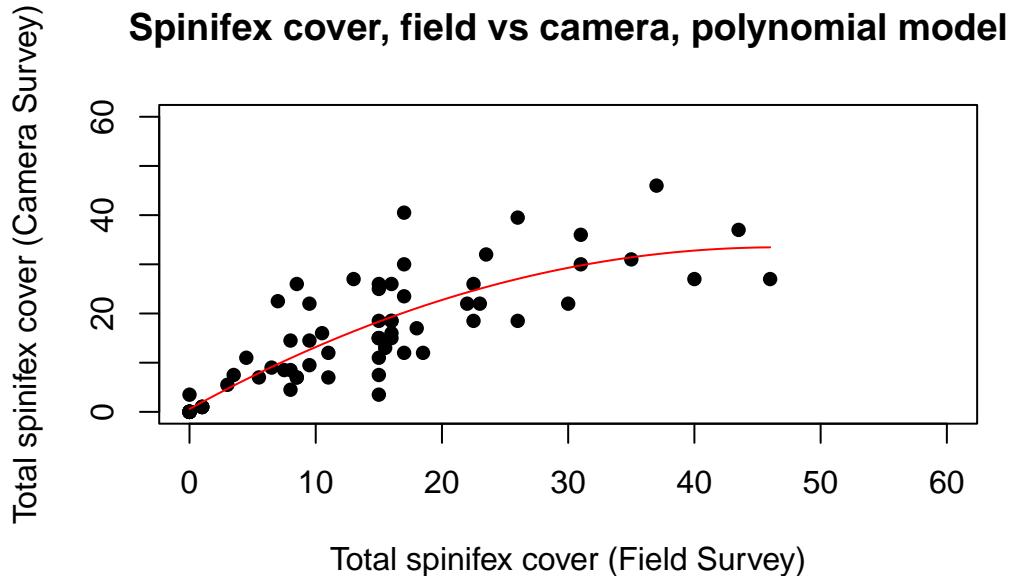
1 # generate a simple second-order polynomial to capture the possible decrease in
2   # camera cover estimate at higher values of field cover estimate
3 poly2model <- lm(Camera_Spinifex_Cover ~ Field_Spinifex_Cover +
4   I(Field_Spinifex_Cover^2), data = spinifex_plot_total)
5
6 # generate a sequence of values spanning the range of Field_Spinifex_Cover
7 newdata <- data.frame(Field_Spinifex_Cover =
8   seq(min(spinifex_plot_total$Field_Spinifex_Cover),
9     max(spinifex_plot_total$Field_Spinifex_Cover), length.out = 100))

```

```

6 # use the model to predict Camera_Spinifex_Cover for these values
7 newdata$Camera_Spinifex_Cover <- predict(poly2model, newdata)
8
9 # plot the predictions
10 plot(Camera_Spinifex_Cover ~ Field_Spinifex_Cover, data = spinifex_plot_total,
11       main = "Spinifex cover, field vs camera, polynomial model",
12       xlab = "Total spinifex cover (Field Survey)",
13       ylab = "Total spinifex cover (Camera Survey)",
14       pch = 16, # Use filled circles as data points
15       col = "black", # Set point color
16       ylim = c(0, 60), # Set y-axis limits
17       xlim = c(0, 60)) # Set x-axis limits)
18 lines(Camera_Spinifex_Cover ~ Field_Spinifex_Cover, data = newdata, col = "red")
19

```



```

1 # view the second order polynomial model statistics
2 a2 <- summary(poly2model)
3 cat("Summary of polynomial model: \n")
4 print(a2)
5 cat("\n")
6
7 # calculate AIC for both models
8 aicl <- aic_linearmodel <- AIC(linearmodel)
9 aicp <- aic_poly2model <- AIC(poly2model)
10
11 # print the AIC values
12 cat(paste0("AIC for linear model: ", aic_linearmodel, "\n"))

```

```

13 cat(paste0("AIC for poly2model: ", aic_poly2model, "\n"))
14
15 # get the model adjusted R squared
16 R2 <- a2$adj.r.squared
17
18 cat("The model adjusted R^2 is: ", R2, "\n")

```

Summary of polynomial model:

Call:

```
lm(formula = Camera_Spinifex_Cover ~ Field_Spinifex_Cover + I(Field_Spinifex_Cover^2),
  data = spinifex_plot_total)
```

Residuals:

Min	1Q	Median	3Q	Max
-14.8427	-3.3427	-0.5873	2.2686	20.3047

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.587326	1.414317	0.415	0.67921
Field_Spinifex_Cover	1.410770	0.179514	7.859	3.32e-11 ***
I(Field_Spinifex_Cover^2)	-0.015139	0.004591	-3.297	0.00154 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.358 on 70 degrees of freedom

Multiple R-squared: 0.7179, Adjusted R-squared: 0.7099

F-statistic: 89.09 on 2 and 70 DF, p-value: < 2.2e-16

AIC for linearmodel: 490.696986792716

AIC for poly2model: 482.157066085602

The model adjusted R² is: 0.7098859

The second order parameter explains a significant proportion of the data ($p = 0.0015353$) and the model adjusted R² is slightly higher than the linear model (0.71). The lower AIC criterion for the polynomial model (490.7 vs. 482.16) also suggests that it provides a better fit to the relationship between field and camera cover estimates. Evaluation of the graphical relationship suggests that any bias towards lower camera cover scores occurs at field survey cover estimates of >30%, which is only a small minority of plots.

We now consider more closely the magnitude of differences in plot-level estimates of spinifex cover based on field survey and camera survey methods. The variable of interest is spinifex_plot_total\$Cover_Cam_Field_Diff which is the difference in total cover between the camera cover estimate (TCcam) and the field cover estimate (TCfield); ie. Cover_Cam_Field_Diff = TCcam - TCfield (the two variables being spinifex_plot_total\$Camera_Spinifex_Cover and spinifex_plot_total\$Field_Spinifex_Cover).

```

1 # determine the mean difference in plot level field and camera cover estimates
2 a <- summary(spinifex_plot_total$Cover_Cam_Field_Diff)
3 cat("The summary for mean cover difference based on all data is:\n")

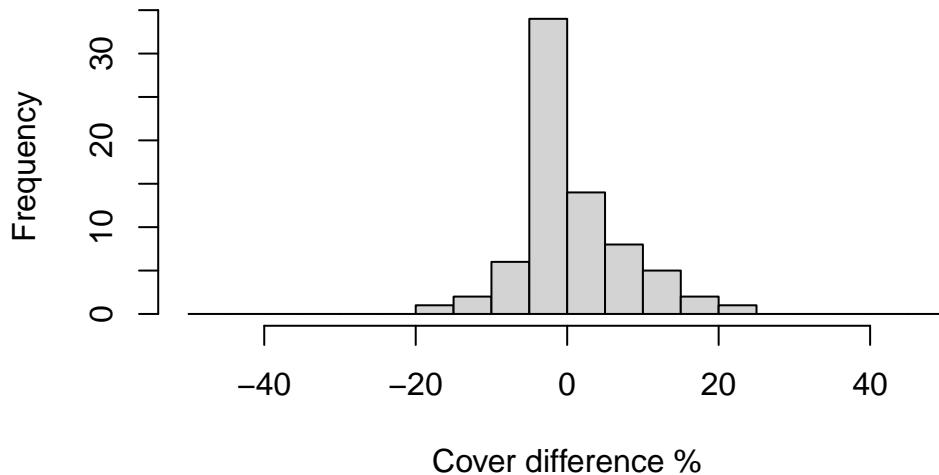
```

```

4 print(a)
5 cat("\n")
6
7 # create the histogram:
8 hist_data_all <- hist(spinifex_plot_total$Cover_Cam_Field_Diff,
9                         breaks = seq(-50, 50, by = 5),
10                        main = "Histogram of cover estimate differences",
11                        xlab = "Cover difference %",
12                        ylab = "Frequency")

```

Histogram of cover estimate differences



The summary for mean cover difference based on all data is:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-19.000	-1.000	0.000	1.479	4.000	23.500

```

1 # determine the difference for only plots that contain Triodia (i.e., excluding
2 # plots with zero spinifex cover in both field and camera surveys)
3 spinifex_plot_total_gr0 <- subset(spinifex_plot_total, Field_Spinifex_Cover > 0 |
4 # Camera_Spinifex_Cover > 0)
5
6 b <- summary(spinifex_plot_total_gr0$Cover_Cam_Field_Diff)
7 cat("The summary for mean cover difference based on only plots containing spinifex
8 # is:\n")
9 print(b)
10 cat("\n")
11
12 # create the histogram
13 hist_data_gr0 <- hist(spinifex_plot_total_gr0$Cover_Cam_Field_Diff,

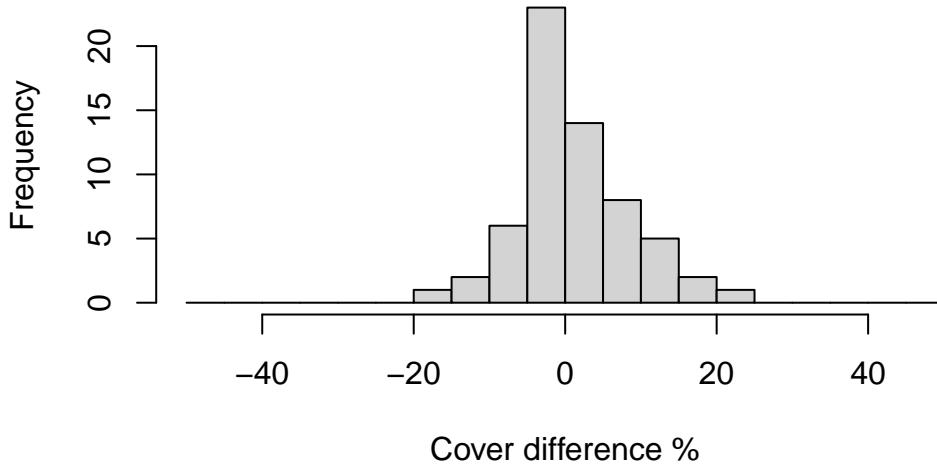
```

```

11      breaks = seq(-50, 50, by = 5),
12      main = "Histogram of cover estimate differences \n(plots
13      ↪ containing spinifex)",
14      xlab = "Cover difference %",
15      ylab = "Frequency")

```

Histogram of cover estimate differences (plots containing spinifex)



The summary for mean cover difference based on only plots containing spinifex is:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
-19.000	-1.500	0.000	1.742	5.375	23.500

The data confirm that differences in total spinifex cover estimates based on field survey and camera survey data are tightly clustered near a mean of zero and an approximately normal distribution. Differences can be as large as 20% but the majority are in the range of -10% to +10%.

We must now also consider differences in the percentage of spinifex cover that is dead (suffering recent mortality/dieback). Here we provide an abbreviated analysis based on key results.

```

1 Field_mean <- summary(spinifex_plot_total$`Field_Spinifex_%dead`)
2 cat("The summary for mortality (% dead cover) across all plots based on field
     ↪ survey data is:\n")
3 print(Field_mean)
4 cat("\n")

5 Camera_mean <- summary(spinifex_plot_total$`Camera_Spinifex_%dead`)
6 cat("The summary for mortality (% dead cover) across all plots based on camera
     ↪ image data is:\n")
7 print(Camera_mean)
8 cat("\n")

```

The summary for mortality (% dead cover) across all plots based on field survey data is:

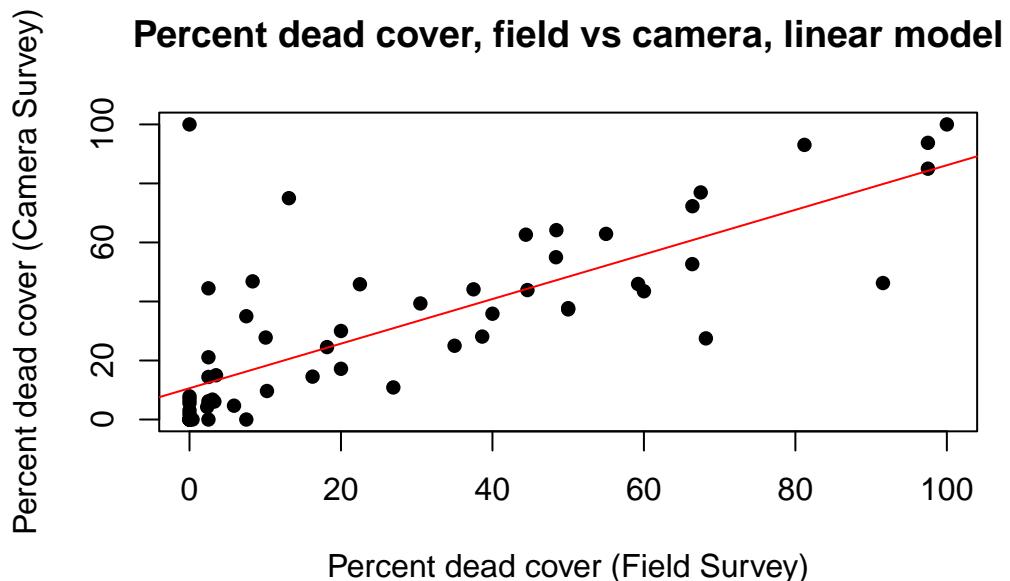
Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.00	0.10	10.14	25.64	47.44	100.00	11

The summary for mortality (% dead cover) across all plots based on camera image data is:

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
0.000	4.364	24.773	29.968	45.903	100.000	11

The means and spread of data are similar.

```
1 # plot the relationship between mortality (%dead) estimates from both field and
  ↵ camera surveys
2 plot(spinifex_plot_total$`Field_Spinifex_%dead`,
  ↵ spinifex_plot_total$`Camera_Spinifex_%dead`,
  main = "Percent dead cover, field vs camera, linear model",
  xlab = "Percent dead cover (Field Survey)",
  ylab = "Percent dead cover (Camera Survey)",
  pch = 16, # Use filled circles as data points
  col = "black", # Set point color
  ylim = c(0, 100), # Set y-axis limits
  xlim = c(0, 100)) # Set x-axis limits
10 abline(lm(`Camera_Spinifex_%dead` ~ `Field_Spinifex_%dead`, data =
  ↵ spinifex_plot_total), col = "red") # add a linear model to the plot
```



```
1 # view the linear model statistics
2 linearmodel <- lm(`Camera_Spinifex_%dead` ~ `Field_Spinifex_%dead`, data =
  ↵ spinifex_plot_total)
3 a3 <- summary(linearmodel)
```

```

4 cat("Summary of the linear model: Camera_Spinifex_%dead ~ Field_Spinifex_%dead \n")
5 print(a3)
6 cat("\n")
7
8 # print the P value of the model
9 pvalue <- a3$coefficients[2,4]
10 cat("The P value of the model is: ", pvalue, "\n")

```

Summary of the linear model: Camera_Spinifex_%dead ~ Field_Spinifex_%dead

Call:

```
lm(formula = `Camera_Spinifex_%dead` ~ `Field_Spinifex_%dead`,
  data = spinifex_plot_total)
```

Residuals:

Min	1Q	Median	3Q	Max
-34.622	-10.594	-6.637	8.417	89.406

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	10.59406	3.18337	3.328	0.0015 **
`Field_Spinifex_%dead`	0.75574	0.08101	9.329	2.77e-13 ***

Signif. codes:	0 '***'	0.001 '**'	0.01 '*'	0.05 '.'
	0.1	'	'	1

Residual standard error: 19 on 60 degrees of freedom

(11 observations deleted due to missingness)

Multiple R-squared: 0.5919, Adjusted R-squared: 0.5851

F-statistic: 87.03 on 1 and 60 DF, p-value: 2.772e-13

The P value of the model is: 2.771671e-13

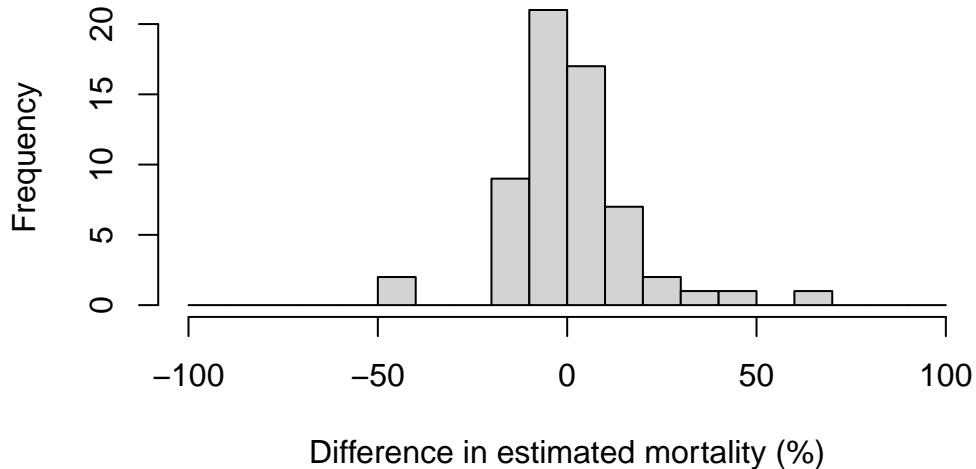
The linear model is highly significant ($p = 2.7716709 \times 10^{-13}$), and explains 59% of variation in the data. We now look at the spread in the data:

```

1 # create the histogram
2 hist_data <- hist(spinifex_plot_total$PercDead_Cam_Field_Diff,
3   breaks = seq(-100, 100, by = 10),
4   main = "Histogram of differences in mortality estimates",
5   xlab = "Difference in estimated mortality (%)",
6   ylab = "Frequency")

```

Histogram of differences in mortality estimates



The data are again centrally distributed with a mean near zero, but the spread in the data are larger than for live cover. The majority of errors are between -20% to +20%, but some estimates vary by up to ca. 50-60%.

Within-plot differences in cover and mortality by size class

The object of the following analyses is to investigate differences in classification among size classes within plots. First we consider differences in the mean number of size classes per plot based on the field and camera data, along with the number of misclassified size classes (one size class category differences) and missed classes (size classes present in either field or camera data but not both).

```
1 SCField_mean <- summary(spinifex_plot_total$Size_classes_field)
2 cat("Summary - number of spinifex size classes per plot based on field survey
  ↵ data:\n")
3 print(SCField_mean)
4 cat("\n")

5 SCCamera_mean <- summary(spinifex_plot_total$Size_classes_camera)
6 cat("Summary - number of spinifex size classes per plot based on camera survey
  ↵ data:\n")
7 print(SCCamera_mean)
8 cat("\n")

10 SCMisclass_mean <- summary(spinifex_plot_total$Misclassifications)
11 cat("Summary - spinifex size class misclassifications per plot:\n")
12 print(SCMisclass_mean)
13 cat("\n")

15 SCMissed_class_mean <- summary(spinifex_plot_total$Missed_classes)
```

```

17 cat("Summary - number of spinifex size classes missed per plot in either
18   ↵ survey:\n")
19 print(SCMissed_class_mean)
20 cat("\n")

Summary - number of spinifex size classes per plot based on field survey data:
  Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
  0.000  1.000  2.000  1.958  3.000  5.000    1

Summary - number of spinifex size classes per plot based on camera survey data:
  Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
  0.000  1.000  2.000  2.083  3.000  5.000    1

Summary - spinifex size class misclassifications per plot:
  Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
  0.0000 0.0000 0.0000 0.3226 1.0000 2.0000    11

Summary - number of spinifex size classes missed per plot in either survey:
  Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
  0.0000 0.0000 0.0000 0.3226 1.0000 2.0000    11

```

Overall, the mean number of spinifex size classes per plot recorded in field (1.96) and camera (2.08) data were very similar, and the mean number of misclassifications (0.32) and missed size class categories (0.32) were both very low.

We now generate a new dataframe that contains cover and mortality data for all size classes in each plot, removing plot totals. We then determine the number of occasions in which a given spinifex size class was observed in both field and camera data (Both), or in only field (FieldOnly) or camera (CameraOnly) data.

```

1 # Count occurrences of each ErrorType1 for non-TOTAL Field_Spinifex_size
2 size_class_data <- spinifex_data %>%
3   filter(Field_Spinifex_size != "TOTAL",
4         ErrorType1 %in% c("Both", "CameraOnly", "FieldOnly")) %>%
5   count(ErrorType1, sort = TRUE)

6
7 #View(size_class_data)

8
9 size_class_data_gt_table <- gt(size_class_data) %>%
10   tab_options(
11     table.align = "center",
12     table.font.size = px(10),
13     column_labels.font.size = px(16),
14     heading.align = "center",
15     heading.title.font.size = px(20)
16   ) %>%
17   opt_row_striping() %>%
18   tab_header(
19     title = table_caption("Spinifex size class data")
20   )

```

```

21 size_class_data_gt_table
22
23
24 # Calculate total counts and percentages for each error type
25 counttotal <- sum(size_class_data$n)
26 pcnt_both <- round(100 * (size_class_data$n[size_class_data$ErrorType1 == "Both"] /
27   ↵ counttotal),2)
27 pcnt_camera <- round(100 * (size_class_data$n[size_class_data$ErrorType1 ==
28   ↵ "CameraOnly"] / counttotal),2)
28 pcnt_field <- round(100 * (size_class_data$n[size_class_data$ErrorType1 ==
29   ↵ "FieldOnly"] / counttotal),2)
30
31 #print(paste0("Percent in both: ", pcnt_both))
32 #print(paste0("Percent in camera: ", pcnt_camera))
33 #print(paste0("Percent in field: ", pcnt_field))

```

Table 9 : Spinifex size class data

ErrorType1	n
Both	123
CameraOnly	30
FieldOnly	22

The data show that 70.3% of spinifex size classes were recorded in both Camera and Field surveys, while 29.7% occurred only in one survey. Of these, more were recorded only in the camera survey ($n = 30$) than in the field survey ($n = 22$).

We now look at how these differences are distributed through spinifex size classes. In this study we used the following size classes: 0-30 cm, >30-60, >60-100, >100-200, >200-300,>300-400,>400-500, >500cm.

```

1 # first reorder the size classes from smallest to largest
2 levels_order <- c("0-30", ">30-60", ">60-100", ">100-200", ">200-300", ">300-400" ,
3   ↵ ">400-500", ">500")
4
5 # convert Field_Spinifex_size to a factor and specify the order of the levels
6 spinifex_data$Camera_Spinifex_size <- factor(spinifex_data$Camera_Spinifex_size,
7   ↵ levels = levels_order)
8
9 # display the data
10 cross_matrix <- as.data.frame.matrix(table(spinifex_data$Camera_Spinifex_size,
11   ↵ spinifex_data$ErrorType1)) %>%
12   rownames_to_column(var = "Size class") %>%
13   arrange(factor(`Size class`, levels = levels_order))
14
15 gt_table <- gt(cross_matrix) %>%
16   tab_options(
17     table.align = "center",
18     table.font.size = px(10),
19     column_labels.font.size = px(16),

```

```

17   heading.align = "center",
18   heading.title.font.size = px(20)
19 ) %>%
20 opt_row_striping() %>%
21 tab_header(
22   title = table_caption("Spinifex size class data & error type 1")
23 )
24
25 gt_table

```

Table 10 : Spinifex size class data & error type 1

Size class	Both	CameraOnly	FieldOnly
0-30	32	9	2
>30-60	34	4	5
>60-100	30	8	1
>100-200	18	3	8
>200-300	9	3	5
>300-400	0	1	0
>400-500	0	2	0
>500	0	0	1

There appears to be a tendency for smaller size classes to be recorded solely on camera images and the largest size classes to be recorded only in the field surveys.

We then attempted to determine, by comparing field notes and camera data, where these discrepancies occurred. Here, errors were classified according to: Camera error: the size class was present but definitely missed in the camera survey, Field error: the size class was present but definitely missed in the field survey, or Misclassified : the size class was seen in both but allocated to different size classes.

```

1 # Define the order of levels
2 levels_order <- c("0-30", ">30-60", ">60-100", ">100-200", ">200-300", ">300-400",
4   ">400-500", ">500")
5
6 # Ensure the Field_Spinifex_size column is a factor with the specified order
7 spinifex_data$Field_Spinifex_size <- factor(spinifex_data$Field_Spinifex_size,
8   levels = levels_order)
9
10 # Create the cross matrix and order it according to levels_order
11 cross_matrix2 <- as.data.frame.matrix(table(spinifex_data$Field_Spinifex_size,
12   spinifex_data>ErrorType2)) %>%
13   rownames_to_column(var = "Size class") %>%
14   arrange(factor(`Size class`, levels = levels_order))
15
16 # generate the cross matrix table
17 cross_matrix2 <- as.data.frame.matrix(table(spinifex_data$Field_Spinifex_size,
18   spinifex_data>ErrorType2)) %>%
19   rownames_to_column(var = "Size class")

```

```

17 size_class_gt_table <- gt(cross_matrix2) %>%
18   tab_options(
19     table.align = "center",
20     table.font.size = px(10),
21     column_labels.font.size = px(16),
22     heading.align = "center",
23     heading.title.font.size = px(20)
24   ) %>%
25   opt_row_striping() %>%
26   tab_header(
27     title = table_caption("Spinifex size class data & error type 2")
28   )
29
30
31 size_class_gt_table
32
33 # Count the number of different error types and do not sort them
34 Error2_summary <- spinifex_data %>%
35   count(ErrorType2, sort = TRUE)
36
37 # #Extract counts by category name
38 Camerror <- Error2_summary$n[which(Error2_summary$ErrorType2 == "CameraError")]
39 Fielderror <- Error2_summary$n[which(Error2_summary$ErrorType2 == "FieldError")]
40 Miserror <- Error2_summary$n[which(Error2_summary$ErrorType2 == "Misclassified")]
41 No_error <- Error2_summary$n[which(Error2_summary$ErrorType2 == "No Error")]
42 Total <- sum(Error2_summary$n)
43
44 # Optionally, you can print the counts for verification
45 # cat("Camera Errors: ", Camerror, "\n")
46 # cat("Field Errors: ", Fielderror, "\n")
47 # cat("Misclassified: ", Miserror, "\n")
48 # cat("No Errors: ", No_error, "\n")
49 # cat("Total: ", Total, "\n")

```

Table 11 : Spinifex size class data & error type 2

Size class	CameraError	FieldError	Misclassified	No Error
0-30	2	6	3	32
>30-60	4	3	2	34
>60-100	0	3	6	30
>100-200	3	1	7	18
>200-300	2	1	5	9
>300-400	0	0	1	0
>400-500	0	1	1	0
>500	0	0	1	0

The validation data show that specific size classes were missed in either the camera survey (4 % of cases) or the field survey (6 % of cases), which indicates that camera surveys were actually more reliable in some circumstances than field surveys. In another 26 cases (10 %) size classes were simply misclassified by one size class category.

Conclusions : spinifex size class and mortality detection using 360-degree cameras

Overall, analysis of the validation data set suggests that spinifex cover and mortality data extracted from 360-degree images performs well when compared with data collected during field surveys. This was true even given the large size of the plots (20 m diameter) and the fact that only one image was taken in the centre of each plot. Over a large sample of plots the mean plot-level cover and mortality rate (percentage of dead material) using both techniques were very similar and had errors that were approximately normally distributed with a mean of near zero, indicating minimal bias using camera images for data collection. Generally, plot-level cover estimates varied by ~ +10% to -10%, and percentage mortality estimates by ~ +20% to -20%, although differences in a small minority of plots were larger. On average, the mean number of spinifex size classes per plot was extremely similar based in field data and camera data, and far in excess of the number of misclassified or missed size classes.

At the plot level, we used a fine-grained cover size scale (8 classes), particularly for tussocks <1m across (0-30 cm, >30-60 cm, and >60-100cm). Despite this, 70% of size classes were correctly identified in both camera and field survey data. A further 9% were only identified in camera data, due to field errors in data collection, thus ~80% of size classes were correctly identified using camera surveys. The remaining discrepancies were due to size class estimates developed using camera and field survey techniques differing by a single size class. There was a weak tendency for smaller size classes to be recorded solely in camera images and the largest size classes to be recorded only in the field surveys.

Collectively, we draw four conclusions from these data:

- 1) Mean cover and percent mortality estimates for spinifex grasses across plots based on camera images were very similar to those based on field survey data, and there was no directional biases in cover and dieback differences. Therefore, for large samples, mean estimates for both parameters using camera images are likely to be accurate.
- 2) At the within-plot level, camera and field survey approaches yielded similar numbers of size classes per plot, and, overall, the number of size classes misclassified or missed completely was small. Overall, about 80% of specific size classes identified using camera surveys were either verified by field data or were correct when field data were incorrect. About 6% of size classes were definitely due to errors in data collected from 360-degree images. Thus, camera surveys generate data at least, or possibly slightly better than, field surveys based on visual cover and dieback estimates.
- 3) These data and the obvious relationship between the size classes of spinifex present in a given area and fire history (see accompanying paper) indicate that 360-degree images are a reliable source of cover and dieback data. However, the discrepancies among size class data estimates indicate that there is still room for improvement. Therefore, for the transect study reported in the accompanying paper we decide to undertake the following changes:
 - a) reduce the size of the study plot from 20 m to 10 m diameter, where camera images are most useful,
 - b) overlay plot boundaries and cover estimate markers onto 360-degree images, and
 - c) develop help files that contain images in which cover and dieback estimates were determined with a very high degree of accuracy using the [ImageJ software](#) package.

Ultimately, at the 10 m diameter scale spinifex cover and dieback estimates are likely to be as good or better than those developed using standard visual field survey estimates. We recommend that all studies collect similar verification data, and carefully consider optimal camera positioning for different taxa and ecological situations. Calibration or validation studies may benefit from even more intensive field survey techniques, for example line intercept or point-based sampling. Ultimately, however, it is our belief that cover or dieback estimates generated using imaging software (such as ImageJ), while time-consuming to collect without automation, will ultimately be far more accurate than those generated using even more intensive field survey estimates.

3. Desert oak crown health

The objective of the following analyses is to investigate variation in crown health and size class data for desert oak (*Allocasuarina decaisneana*) extracted from camera images by three different scorers using the pannotator package. Inter-observer variability is a problem in many scientific disciplines and our intention was to determine the scoring protocols and help files that minimise these differences.

Here we compare three scorers: 1) one present at the time when images were collected in cameras and is familiar with the study site and associated vegetation (scorer 1), 2) two with no experience at the study site or in scoring crown health (scorers 2-3). Scorer 1 had access to a rudimentary help file (fewer images), a less refined size class scoring system (no seedling size class), and a single worked example for calculating the crown health score. All camera images were collected from the 4 km-long transect that forms the basis of the study reported in this accompanying paper.

We first import the required datasets: scorer_oak_1.csv, scorer_oak_2.csv, and scorer_oak_3.csv.

Each dataframe contains the following variables:

Column [1] (user) = scorer number; [2] (timestamp) = image timestamp, [3] (leaflet_id) = leaflet ID; [4] (imagefile) = related image file name; [5] (feature_type) = feature type (marker or image marker); [6] (radius) = radius geometry (not applicable); [7] (geometry) = geometry in Well-Known Text (WKT) format; [8] (species) = species name & size/impact class as per dropdown menu; [9] (Size_class) = Size class (seedling, juvenile, early pole, late pole, early mature, mature); [10] (veg_layer) = vegetation level, here *Allocasuarina decaisneana* = tree; [11-13] (dd1-dd3) = crown health estimate components; [14] (plot) = image plot; [15] (plot_name_new) = plot names assigned in study ; [16] (frame) = frame of video image file was taken from.

Upload oak annotation files and add plot and frame numbers

```
1 # read in the annotation files
2 scorer_1 <- read.csv("./Data_files/scorer_oak_1.csv")
3 scorer_2 <- read.csv("./Data_files/scorer_oak_2.csv")
4 scorer_3 <- read.csv("./Data_files/scorer_oak_3.csv")
```

Load scorer 1 data

```
1 # set the geometry
2 scorer_1 <- st_as_sf(scorer_1, wkt = "geometry", crs = 4326)
3
4 #mapview(scorer_1, width = "100%", na.rm = TRUE)
```

Load scorer 2 data

```
1 # set the geometry
2 scorer_2 <- st_as_sf(scorer_2, wkt = "geometry", crs = 4326)
3
4 #mapview(scorer_2, width = "100%", na.rm = TRUE)
```

Load scorer 3 data

```
1 # set the geometry
2 scorer_3 <- st_as_sf(scorer_3, wkt = "geometry", crs = 4326)
3
4 #mapview(scorer_3, width = "100%", na.rm = TRUE)
```

These maps confirm that data for each of the scorers was collected from the same transect at Uluru-Kata Tjuta NP.

Calculate the crown score and mean values per size class

Crown health is simply defined as Crown Health Score = dd1 x dd2 x dd3; values range from 100 (perfect health) to 0 (dead). Here dd1 = the assessable crown (AC, as a percentage of the potential crown that contains live or dead tertiary branches or smaller), dd2 = the crown extent (CE, which is the percentage of the assessable crown that contains leaves), and dd3 = the crown density (CD; the percentage of skylight blocked by leaves within the crown extent). AC, CE and CD were assigned percentages using the scale S_{HC} = 0, >0-5, >5-20, >20-35, >35-50, >50-65, >65-80, >80-95, >95-<100, 100%, and scale midpoints used for calculations. Further details and examples are provided in the accompanying paper and Supporting Information 6).

```
1 # replace all -999 values (used to signify NA) with zero. The calculation works
2   ↵ since when dd2 or dd3 contain -999 the previous dd variable is necessarily
3   ↵ zero.
4 scorer_1$dd3 <- replace(scorer_1$dd3, scorer_1$dd3 == -999, 0)
5 scorer_2$dd3 <- replace(scorer_2$dd3, scorer_2$dd3 == -999, 0)
6 scorer_3$dd3 <- replace(scorer_3$dd3, scorer_3$dd3 == -999, 0)
7
8 scorer_1$dd2 <- replace(scorer_1$dd2, scorer_1$dd2 == -999, 0)
9 scorer_2$dd2 <- replace(scorer_2$dd2, scorer_2$dd2 == -999, 0)
10 scorer_3$dd2 <- replace(scorer_3$dd2, scorer_3$dd2 == -999, 0)
11
12 # develop a function to calculate Crown health scores in each dataframe and then
13   ↵ reorder the size classes. Reordering the size classes is necessary for creating
14   ↵ plots below
15 calculate_scores <- function(df) {
16   df$Crown_score <- df$dd1/100 * df$dd2/100 * df$dd3/100
17   df$Size_class_Reorder <- factor(df$Size_class, c("Seedling", "Juvenile",
18   ↵ "Early_Pole", "Late_Pole", "Early_Mature", "Mature"))
19   return(df)
20 }
```

Now we can compare mean crown health scores across different scorers.

```

1 # function to calculate mean crown scores in each size class
2 mean_and_count_table <- function(data, score_col, size_col, scorer_name) {
3   mean_table <- data %>%
4     group_by (!!sym(size_col)) %>%
5     summarize(
6       mean = mean (!!sym(score_col), na.rm = TRUE),
7       count = n()
8     ) %>%
9     mutate(Scorer = scorer_name) %>%
10    rename(Category = !!sym(size_col))
11
12   return(mean_table)
13 }
14
15
16 table_scorer_1 <- mean_and_count_table(scorer_1, "Crown_score",
17   ↪ "Size_class_Reorder", "Scorer 1")
18
19 #View(table_scorer_1)
20
21 table_scorer_2 <- mean_and_count_table(scorer_2, "Crown_score",
22   ↪ "Size_class_Reorder", "Scorer 2")
23
24 #View(table_scorer_2)
25
26 table_scorer_3 <- mean_and_count_table(scorer_3, "Crown_score",
27   ↪ "Size_class_Reorder", "Scorer 3")
28
29 #View(table_scorer_3a)
30
31 combined_table <- rbind(table_scorer_1, table_scorer_2, table_scorer_3)
32
33 #View(combined_table)
34
35 reshaped_table <- combined_table %>%
36   st_set_geometry(NULL) %>% # Remove the sf geometry
37   gather(key = "Statistic", value = "Value", -Category, -Scorer) %>%
38   unite("Scorer_Scoring", Scorer, Statistic, sep = "_") %>%
39   spread(key = "Scorer_Scoring", value = "Value")
40
41 # Print the reshaped table using gt
42
43 scorers_gt_table <- gt(reshaped_table) %>%
44   tab_options(
45     table.align = "center",
46     table.font.size = px(10),
47     column_labels.font.size = px(16),
48     heading.align = "center",
49     heading.title.font.size = px(20)
50   ) %>%

```

```

48 opt_row_striping() %>%
49 tab_header(
50   title = table_caption("Crown scores from different scorers")
51 )
52
53 scorers_gt_table
54
55 # we also get the mean crown health score for each scorer
56 s1mean <- summary(scorer_1$Crown_score)
57 #print(s1mean)
58 s2mean <- summary(scorer_2$Crown_score)
59 #print(s2mean)
60 s3mean <- summary(scorer_3$Crown_score)
61 #print(s3mean)

```

Table 12 : Crown scores from different scorers

Category	Scorer 1_count	Scorer 1_mean	Scorer 2_count	Scorer 2_mean	Scorer 3_count	Scorer 3_mean
Seedling	NA	NA	4	0.2437500	2	0.3625000
Juvenile	9	0.6034549	19	0.3264803	26	0.5147356
Early_Pole	7	0.5332500	16	0.6268896	13	0.6940385
Late_Pole	4	0.5954453	35	0.5449272	25	0.6838250
Early_Mature	25	0.5206769	52	0.4669056	38	0.6420189
Mature	51	0.4164403	20	0.5977703	31	0.6274970

These data indicate that crown health scores were similar for scorers 1 (0.477) and 2 (0.497) but about 0.1 units higher for scorer 3 (0.623), mainly due to a lack of low-scoring trees. Scores for pole- and mature-sized trees were generally consistent across the three scorers, although again scores provided by scorer 3 tended to be higher than those provided by the other scorers. Scores differed in seedling and juvenile classes, although the number of individuals used to determine these scores varied significantly. Data provided by scorer 1 indicated that smaller seedlings (<1 m tall) needed to be separated from juveniles (1- 4 m tall), and that a greater range of visual examples of all size classes was required in the help files. Incorporation of these changes greatly improved the agreement across size classes by scorers 2 and 3.

Now we want to determine whether the spatial structure of size class and crown health data differed significantly among scorers. Maps are visualised using mapview and images saved using the ‘mapshot’ function.

Scorer 1:

```

1 scorer_1 <- st_as_sf(scorer_1, wkt = "geometry",crs = 4326)
2
3 s1_p <- mapview(scorer_1, zcol = "Size_class_Reorder", cex = 8, alpha = 0.9,
4   ↵ alpha.regions = 0.9, layer.name = "Size_class", col.regions = c("green4",
5   ↵ "green4","yellow", "yellow", "red4", "red4"),na.rm = TRUE, basemaps =
6   ↵ c("Esri.WorldImagery"))
7
8 #print(s1_p)

```

```

7 mapviewOptions(basemaps = c("Esri.WorldImagery"),
8                 raster.palette = grey.colors,
9                 vector.palette = colorRampPalette(c("red", "yellow", "green2")),
10                na.color = "gray",
11                layers.control.pos = "topright")
12
13 s1_q <- mapview(score_1, zcol = "Crown_score", layer.name = "Crown_score", cex =
14   ↵ 8, alpha = 0.9, alpha.regions = 0.9, na.rm = TRUE, legend = TRUE, at = seq(0,
15   ↵ 1, 0.1))
16
17 #print(s1_q)
18
19 # map crown scores of mature and early_mature trees
20 Mature <- subset(score_1, score_1$Size_class == "Mature" | score_1$Size_class ==
21   ↵ "Early_Mature")
22
23 s1_z <- mapview(Mature, zcol = "Crown_score", layer.name = "Crown_score", cex = 8,
24   ↵ alpha = 0.9, alpha.regions = 0.9, na.rm = TRUE)
25
26 #print(s1_z)

```

Scorer 2:

```

1  scorer_2 <- st_as_sf(scorer_2, wkt = "geometry", crs = 4326)
2
3  s2_p <- mapview(scorer_2, zcol = "Size_class_Reorder", cex = 8, alpha = 0.9,
4    ↵ alpha.regions = 0.9, layer.name = "Size_class", col.regions = c("green4",
5    ↵ "green4", "yellow", "yellow", "red4", "red4"), na.rm = TRUE)
6
7  #print(s2_p)
8
9  mapviewOptions(basemaps = c("Esri.WorldImagery"),
10    raster.palette = grey.colors,
11    vector.palette = colorRampPalette(c("red", "yellow", "green2")),
12    na.color = "gray",
13    layers.control.pos = "topright")
14
15  s2_q <- mapview(scorer_2, zcol = "Crown_score", layer.name = "Crown_score", cex =
16    ↵ 8, alpha = 0.9, alpha.regions = 0.9, na.rm = TRUE, legend = TRUE, at = seq(0,
17    ↵ 1, 0.1))
18
19  #print(s2_q)
20
21  # map crown scores of mature and early_mature trees
22  Mature <- subset(scorer_2, scorer_2$Size_class == "Mature" | scorer_2$Size_class ==
23    ↵ "Early_Mature")

```

```

20 s2_z <- mapview(Mature, zcol = "Crown_score", layer.name = "Crown_score", cex = 8,
21   ↵ alpha = 0.9, alpha.regions = 0.9, na.rm = TRUE)
22 #print(s2_z)

```

Scorer 3:

```

1 s3_p <- mapview(score_3, zcol = "Size_class_Reorder", cex = 8, alpha = 0.9,
2   ↵ alpha.regions = 0.9, layer.name = "Size_class", col.regions = c("green4",
2   ↵ "green4","yellow", "yellow", "red4", "red4"),na.rm = TRUE)
3 #print(s3_p)
4
5 mapviewOptions(basemaps = c("Esri.WorldImagery"),
6   raster.palette = grey.colors,
7   vector.palette = colorRampPalette(c("red", "yellow", "green2")),
8   na.color = "gray",
9   layers.control.pos = "topright")
10
11 s3_q <- mapview(score_3, zcol = "Crown_score", layer.name = "Crown_score", cex =
12   ↵ 8, alpha = 0.9, alpha.regions = 0.9, na.rm = TRUE, legend = TRUE, at = seq(0,
13   ↵ 1, 0.1))
14
15 # map crown scores of mature and early_mature trees
16 Mature <- subset(score_3, score_3$Size_class == "Mature" | score_3$Size_class ==
17   ↵ "Early_Mature")
18
19 s3_z <- mapview(Mature, zcol = "Crown_score", layer.name = "Crown_score", cex = 8,
20   ↵ alpha = 0.9, alpha.regions = 0.9, na.rm = TRUE)
#print(s3_z)

```

Compare Scorers using mapview

Now we can compare the scorers side by side. First size classes:

```

1 # Synchronize map views in html version
2 # sync(s1_p@map %>%
3 #   addControl(html = "Scorer 1", position = "bottomright"),
4 #   s2_p@map %>%
5 #   addControl(html = "Scorer 2", position = "bottomright"),
6 #   s3_p@map %>%
7 #   addControl(html = "Scorer 3", position = "bottomright"))

```

Now crown scores:

```
1 # sync(s1_q@map %>%
2 #     addControl(html = "Scorer 1", position = "bottomright"),
3 #     s2_q@map %>%
4 #     addControl(html = "Scorer 2", position = "bottomright"),
5 #     s3_q@map %>%
6 #     addControl(html = "Scorer 3", position = "bottomright"))
```

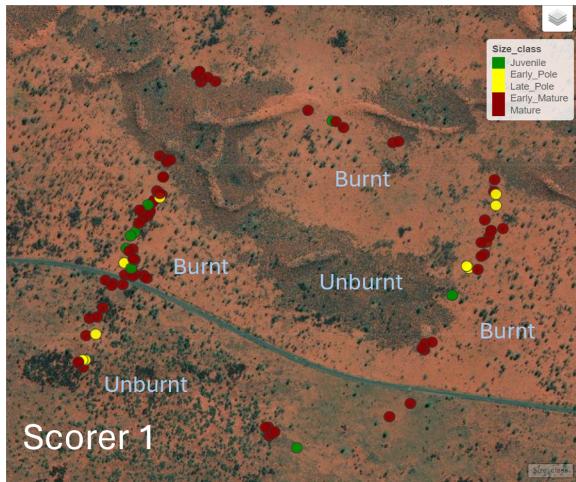
Now mature only:

```
1 # sync(s1_z@map %>%
2 #     addControl(html = "Scorer 1 - Mature", position = "bottomright"),
3 #     s2_z@map %>%
4 #     addControl(html = "Scorer 2 - Mature", position = "bottomright"),
5 #     s3_z@map %>%
6 #     addControl(html = "Scorer 3 - Mature", position = "bottomright"))
```

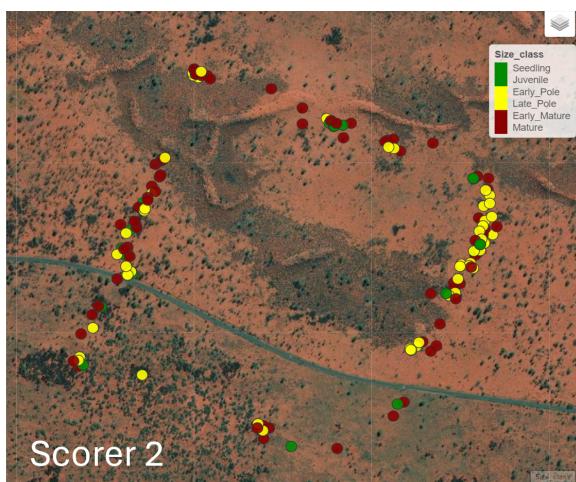
For convenience maps for size class and crown score have been compiled into single .png file:

Comparison of desert oak size class and crown health scores for 3 scorers. Examples of areas recently burnt (Burnt) and not recently burnt (Unburnt) are provided in the top left panel. In the top right panel F = areas apparently impacted severely by fire, D = areas not or minimally affected by fire, likely impact caused by drought.

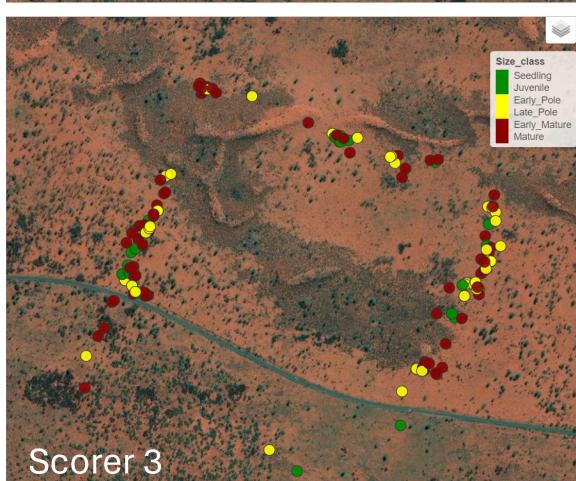
Size classes



Scorer 1

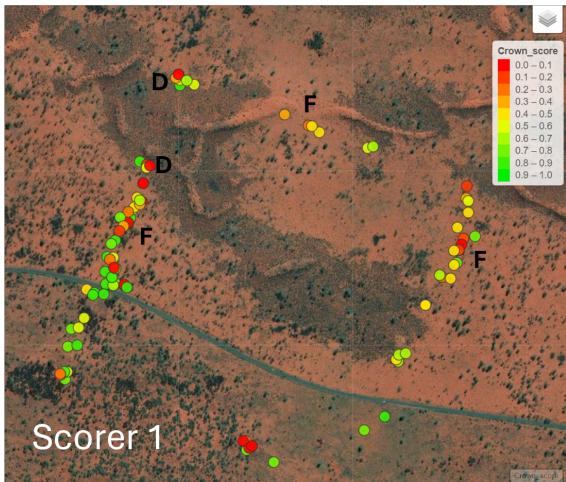


Scorer 2

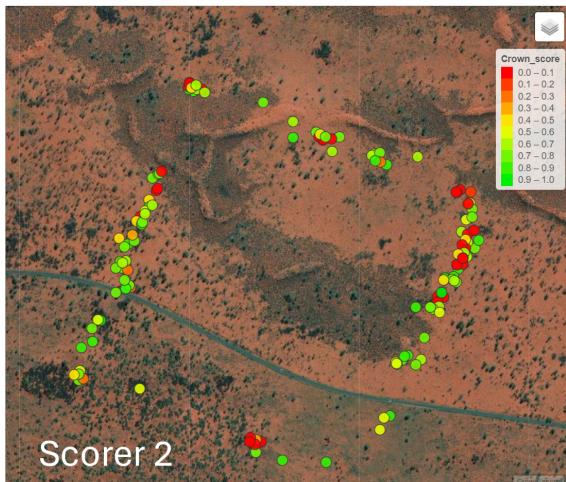


Scorer 3

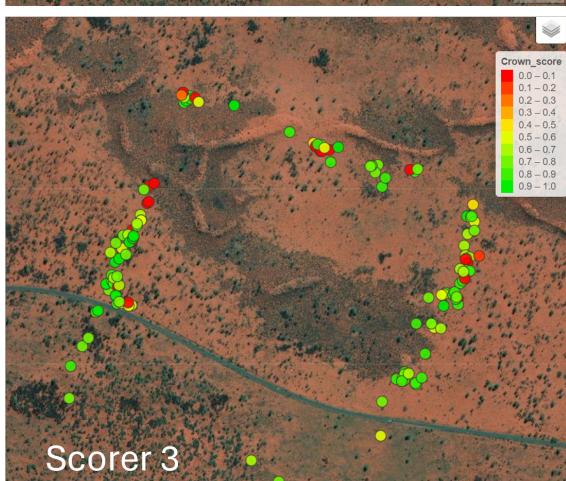
Crown score



Scorer 1



Scorer 2



Scorer 3

Conclusions : tree crown and size class estimation using 360-degree cameras

The data presented here indicate that all scorers generally produced broadly similar mean crown scores across the whole transect (0.48-0.62) and across size classes. They also produced a comparable spatial distribution for these variables, with similar patches of low crown health identified by each of the scorers (right panels above). The majority of desert oaks with low crown health occurred in parts of the transect that had been recently burnt in hot fires, although there were a few isolated patches that may have been caused by drought (e.g., near the dunes in the north of the western transect; top right panel above). These results indicate that collection and analysis of 360-degree images can be a useful method for mapping differences in crown health and then using these data to infer the role of different drivers of crown health at small to large spatial scales.

Scoring consistency was improved by providing enhanced help material to identify different size classes, splitting smaller trees into ‘seedling’ and ‘juvenile’ size classes, and providing more representative images of the crown health scoring protocol (including the assessable crown (*AC*), the crown extent (*CE*), and the crown density (*CD*)). Inter-scorer variation is a common problem in studies that rely on semi-quantitative or qualitative scales, and these would benefit from developing a set of scores by multiple scorers for a common set of images. The pannotator package makes this a simple process, as shown in this example.