ECOSYSTEM SURVEILLANCE (AusPlots) TUTORIAL: 'ausplotsR' PACKAGE AND AusPlots DATA BASICS

This document contains a tutorial that provides an overview of the `ausplotsR` package functionality, as well as an introduction to TERN's Ecosystem Surveillance (AusPlots) data. TERN's Data Skills Development Program (DSDP) "ECOSYSTEM SURVEILLANCE (AusPlots) TUTORIAL: UNDERSTANDING AND USING THE 'ausplotsR' PACKAGE AND AusPlots DATA" tutorial provides addtional information and multiple archetypal applications of AusPlots data and the `ausplotsR` package. Additional examples are provided in TERN's DSDP "ausplotsR Examples and Applications" R scripts. All of these materials can be found in TERN's DSDP 'EcosystemSurveillance_PlotData' folder in GitHub here (https://github.com/ternaustralia/TERN-Data-Skills/tree/master/EcosystemSurveillance_PlotData).

`ausplotsR` is an R package for live extraction and preparation of TERN AusPlots ecosystem monitoring data. Through `ausplotsR`, users can: (1) directly obtain plot-based data on vegetation and soils across Australia, and (2) preprocess these data into structures that facilitate the visualisation and analysis of ausplots data. Data preprocessing includes the computation of species occurrence, vegetation fractional and single cover, growth form, and basal area (see below for details).

The `ausplotsR` package currently includes 6 functions:

- `get_ausplots`: Extracts AusPlots data in R. The stating point for any AusPlots data exploration and analysis in R.
- `species_table`: Generates species occurrence matrices using the chosen scoring method (i.e. presence/absence, cover, frequencey, or IVI index) from a data frame of individual raw intercept hits (generated from AusPlots data using the `get_ausplots` function).
- `fractional_cover`: Calculates fractional cover (i.e., the proportional cover of green vegetation, dead vegetation and bare substrate) from a data frame of individual raw intercept hits (generated from AusPlots data using the `get_ausplots` function).
- `growth_form_table`: Generates occurrence matrices for NVIS plant growth forms in plots using the chosen scoring method (i.e. presence/absence, percent cover or species richness -number of species assigned to a particular growth form-) from a data frame of individual raw intercept hits (generated from AusPlots data using the `get_ausplots` function).
- `single_cover_value`: Calculates a total vegetation cover by height and/or growh form per site from a data frame of individual raw intercept hits (generated from AusPlots data using the `get_ausplots` function). In this fucntion cover can be subsetted to vegetation over a specified height and/or by plant growth forms. By default, vegetation cover is calculated per plot for tree growth forms of 5 metres or higher (i.e. forests).

- basal_area : Calculates basal area (or number of basal wedge hits) for each plot using the raw basal wedge data (generated from AusPlots data using the get_ausplots function).

INSTALLING and LOADING 'ausplotsR'

To run the R scripts in this tutorial the ausplotsR library must be installed and loaded.

The first step to install packages in R is selecting the CRAN (Comprehensive R Archive Network) mirror. Mirror selection and package installation can be done via R's menu (Packages/Set CRAN mirror. followed by Packages/install package(s).) or programmatically the via the function 'install.packages' (selecting the CRAN mirror using the argument 'repos'). Typically it is best to choose the cloud mirror (which automatically redirects to an appropriate server worldwide) or a mirror close to you (e.g. in your institution, country,..). A list of Comprehensive R Archive Network (CRAN) mirror URLs can be found here. Below are two examples of how to select a CRAN mirrors. In the first example the cloud mirror is selected, and in the second one an Australian mirror is selected. Before running this code you must uncomment (i.e. remove the '#' symbol) the line with the desired mirror.

```
## Select the repository (i.e. CRAN mirror URL)
#my.repos = "https://cloud.r-project.org/"
#my.repos = "https://cran.csiro.au/"  # Example of an Australian mirror
```

Currently ausplotsR must be installed directly from github using the 'devtools' package, which must have been previously installed. The code below installs the 'devtools' package. Rather than directly providing the URL for a CRAN mirror, we could have provided the variable 'my.repos' to which we assigned a mirror above.

Then the devtools library is loaded and the ausplotsR library installed from GitHub. The GitHub site for ausplotsR contains the latest developments and information on the package; it can be found at this link. Finally, the ausplotsR library is loaded to use in the tutorial.

```
## Install directly from github using the 'devtools' package
## Thus, 'devtools' must be previouly installed
install.packages("devtools", repos="https://cloud.r-project.org/")
```

```
## package 'devtools' successfully unpacked and MD5 sums checked
##
## The downloaded binary packages are in
##   C:\Users\uqbblanc\AppData\Local\Temp\Rtmp6L3pzn\downloaded_packages
```

```
library(devtools)
install_github("ternaustralia/ausplotsR", build_vignettes = TRUE)

## Load the package
library(ausplotsR)
```

Help on the ausplotsR package and a vignette with a guide on how to use the package can be obtained with the code below

```
#help(ausplotsR)
#browseVignettes(package="ausplotsR")
```

OBTAIN & EXPLORE AusPlots DATA: get_ausplots function

This function extracts and compiles AusPlots data.

Data of specific types, sites, geographical locations, and/or species can be requested via the function arguments.

DATA TYPES: Up to 8 different types of data can be obtained by setting the corresponding arguments to TRUE/FALSE:

- `site_info` : Site summary data. Includes (among others): plot and visit details, landform data, geographic coordinates, and notes. Included by default. Site summary data are stored in the `site.info` data frame.
- `structural_summaries` : Site vegetation structural summaries. Site vegetation structural summary data are stored in the `struct.summ` data frame.
- `veg.vouchers` : Complete set of species records for the plot determined by a herbarium plus ID numbers for silica-dried tissue samples. Included by default. Vegetation vouchers data are stored in the `veg.vouch` data frame.
- `veg.PI` : Point Intercept (PI) data. Includes data on: substrate, plant species, growth form and height, etc at each of (typically) 1010 points per plot. Included by default. Vegetation point intercept data are stored in the `veg.PI` data frame.
- `basal.wedge` : Basal Wedge Data Raw Hits. These data are required for the calculation of Basal Area by Species by Plot. Basal wedge data are stored in the `veg.basal` data frame.
- `soil_subsites` : Information on what soil and soil metagenomics samples were taken at nine locations across the plot and their identification barcode numbers. Soil and soil metagenomics data are stored in the `soil.subsites` data frame.
- `soil_bulk_density` : Soil bulk density. Soil bulk density data are stored in the `soil.bulk` data frame.
- `soil_character` : Soil characterisation and sample ID data at 10 cm increments to a depth of 1 m. Soil characterisation and sample ID data are stored in the `soil.char` data frame.

SPATIAL FILTERING: AusPlot data can be spatially subset via the `get_ausplots` function arguments in two ways:

- `my.Plot_IDs` : Character vector with the plots IDs of specific AusPlots plots.
- `bounding_box` : Spatial filter for selecting AusPlots based on a rectangular box, in the format of e.g. c(xmin, xmax, ymin, ymax). AusPlots spatial data are are in longlat, thus x is the longitude and y is the latitude of the box/extent object (e.g., c(120, 140, -30, -10)).

SPECIES FILTERING: AusPlots data can also be subset by particular or sets of genus and/or species (i.e. as determined for the herbarium voucher) using the argument `species_name_search` . This optional argument takes the form of a character string indicating the terms to search and subset. Search terms are not case sensitive and do not require an exact taxonomic match (e.g. "Eucalyptus moderata","Eucalyptus", and "euca" are all acceptable search terms). Species Filtering behaviour slightly differs among Data Types (i.e. for the different types of created Data Frames): * For `veg.vouch` and `basal.wedge` , when these arguments are set to `TRUE` , `get_ausplots` returns data.frames with the corresponding data (i.e. voucher records and raw basal wedge data respectively) that match the species_name_search. * For the remaing data types arguments, when these arguments are set to `TRUE` , `get_ausplots` returns data.frames with the corresponding data (e.g. point intercept data,…) for all plots where the species_name_search occurs.

The R object resulting from calling `get_ausplots` is a list of data frames containing the requested AusPlots data. The list includes a data frame for each type of data requested (i.e. up to 8 data frames: 'site_info', 'structural_summaries', …) and an auto-generated citation for the data extracted. Please cite ausplotsR and the TERN AusPlots data you use. In each data frame the columns correspond to the variables supplied for each type of data and the number of rows (directly or indirectly) depends on the sites (i.e. via `my.Plot_IDs` or `bounding_box` if subsetted) or species (i.e. via `species_name_search` if subset) retrieved.

There are several variables common to all data frames. These include `site_location_name` , `site_location_visit_id` , and `site_unique` (a combination of the previous two). These variables can be used to merge data frames. For example, the contents of two data frames can be combined using the common variable as a link (i.e. guidance to add the merged contents in the correct row). The variable `site_unique` is typically the best option to link data frames in a merge, as it is the most specific variable representing a single visit to a particular site and it should be used in most analyses. Otherwise, errors such including data from the wrong visit to a site can occur.

```
# Example 1: All available data (i.e. all data types) for 3 plots
# ================================================================

# Obtain the data ('site_info', 'veg.vouchers', and 'veg.PI' are retraived by default)
AP.data = get_ausplots( my.Plot_IDs=c("SATFLB0004", "QDAMGD0022", "NTASTU0002"),
                        structural_summaries=TRUE, basal.wedge=TRUE,
                                 soil_subsites=TRUE, soil_bulk_density=TRUE, soil_character=
TRUE  )
```

```
## User-supplied Plot_IDs located.
```

```
# Explore retrieved data
class(AP.data)
```

```
## [1] "list"
```

```
summary(AP.data)
```

```
##                Length Class      Mode
## site.info      43     data.frame list
## struct.summ    15     data.frame list
## soil.subsites  12     data.frame list
## soil.bulk      15     data.frame list
## soil.char      34     data.frame list
## veg.basal      10     data.frame list
## veg.vouch      12     data.frame list
## veg.PI         13     data.frame list
## citation        1     -none-     character
```

```
str(AP.data)
```

```
## List of 9
## $ site.info    :'data.frame':  4 obs. of  43 variables:
##   ..$ site_location_name       : chr [1:4] "QDAMGD0022" "SATFLB0004" "SATFLB0004" "NTASTU
0002"
##   ..$ established_date         : chr [1:4] "2013-06-04T00:00:00" "2012-09-18T00:00:00" "2
012-09-18T00:00:00" "2016-05-01T16:58:00"
##   ..$ description              : chr [1:4] "Mackunda Downs Station, 500m east of homestea
d.  26km west of Middleton." "Brachina Gorge Heysen Range Lower. 63km North North East of Ade
laide" "Brachina Gorge Heysen Range Lower. 63km North North East of Adelaide" "Maryfield Stat
ion, 7.6km north north west of homestead. 27.5km south east of Larrimah"
##   ..$ bioregion_name          : chr [1:4] "MGD" "FLB" "FLB" "STU"
##   ..$ landform_pattern        : chr [1:4] "ALP" "MOU" "MOU" "PLA"
##   ..$ landform_element        : chr [1:4] "PLA" "HSL" "HSL" "PLA"
##   ..$ site_slope              : chr [1:4] "1" "17" "17" "0"
##   ..$ site_aspect             : chr [1:4] "180" "225" "225" NA
##   ..$ comments                : chr [1:4] "Astrebla pectinata / Cenchrus ciliaris / Astr
ebla elymoides low open tussock grassland on alluvial plain adjoin"| __truncated__ "Grazing i
mpact high- goat tracks and droppings. Rabbit droppings also. Lots of Yellow footed rock wall
abies clo"| __truncated__ "Grazing impact high- goat tracks and droppings. Rabbit droppings a
lso. Lots of Yellow footed rock wallabies clo"| __truncated__ "Plot is flat. Low mound ( Like
ly anthropogenic) made up of ironstone gravels at the north west corner. Minimal "| __truncat
ed__
##   ..$ outcrop_lithology       : chr [1:4] "NA" "SA" "SA" "NA"
##   ..$ other_outcrop_lithology : chr [1:4] "NA" "NC" "NC" "NC"
##   ..$ plot_dimensions         : chr [1:4] "100m x 100m." NA NA NA
##   ..$ site_location_visit_id  : int [1:4] 53501 58658 53705 58429
##   ..$ visit_start_date        : chr [1:4] "2013-05-18T09:34:00" "2018-08-28T09:20:29" "2
012-09-18T00:00:00" "2016-05-01T16:58:00"
##   ..$ visit_end_date          : chr [1:4] "2013-05-18T09:34:00" "2018-08-28T09:20:29" "2
012-09-18T00:00:00" "2016-05-01T16:58:00"
##   ..$ visit_notes             : chr [1:4] "" NA NA "Corymbia polycarpa and Corymbia term
inalis combined for Basal area\r\n\r\nunknown substrate in point intercept "| __truncated__
##   ..$ location_description     : chr [1:4] "Mackunda Station, north of Middleton." "Brach
ina lower.Largely unchanged since previous visit possibly more Carrichtera annua. Grazing imp
act goat, rab"| __truncated__ "Brachina Gorge Heysen Range Lower. 63km North North East of Ad
elaide.Grazing impact high- goat tracks and dropp"| __truncated__ "Maryfield Station, 7.6km n
orth north west of homestead. 27.5km south east of Larimah"
##   ..$ erosion_type            : chr [1:4] "G" "n/a" "n/a" "n/a"
##   ..$ erosion_abundance       : chr [1:4] "2" "X" "1" "X"
##   ..$ erosion_state           : chr [1:4] "NC" "n/a" "n/a" "n/a"
##   ..$ microrelief             : chr [1:4] "Z" "NH" "NC" "TM"
##   ..$ drainage_type           : int [1:4] 4 3 6 4
##   ..$ disturbance             : chr [1:4] "1L" "1L" "1H" "0"
##   ..$ climatic_condition      : chr [1:4] "DRY" "DRY" "WET" "DRY"
##   ..$ vegetation_condition    : chr [1:4] "DRY" "AVG" "AVG" "AVG"
##   ..$ observer_veg            : int [1:4] 3 1 16 1
##   ..$ observer_soil           : int [1:4] 2 31 1 2
##   ..$ described_by            : int [1:4] 3 1 16 1
##   ..$ pit_marker_easting      : num [1:4] 529568 268527 268528 326265
##   ..$ pit_marker_northing     : num [1:4] 7526350 6531518 6531576 8256078
##   ..$ pit_marker_mga_zones    : int [1:4] 54 54 53 53
##   ..$ pit_marker_datum        : chr [1:4] "WGS84" "WGS84" "GDA94" "WGS84"
##   ..$ pit_marker_location_method: chr [1:4] "GPS" NA "GPS" NA
##   ..$ soil_observation_type   : chr [1:4] "P" "PA" "P" "P"
##   ..$ a_s_c                   : chr [1:4] "NC" NA NA NA
##   ..$ plot_is_100m_by_100m    : logi [1:4] TRUE TRUE TRUE TRUE
##   ..$ plot_is_aligned_to_grid : logi [1:4] TRUE TRUE TRUE TRUE
```

```
##    ..$ plot_is_permanently_marked: logi [1:4] TRUE TRUE TRUE TRUE
##    ..$ latitude                 : num [1:4] -22.4 -31.3 -31.3 -15.8
##    ..$ longitude                : num [1:4] 141 139 139 133
##    ..$ point                    : chr [1:4] "SW" "SW" "SW" "SW"
##    ..$ state                    : chr [1:4] "QLD" "SA" "SA" "NT"
##    ..$ site_unique              : chr [1:4] "QDAMGD0022-53501" "SATFLB0004-58658" "SATFLB0
004-53705" "NTASTU0002-58429"
##  $ struct.summ  :'data.frame':    4 obs. of  15 variables:
##    ..$ site_location_name    : chr [1:4] "QDAMGD0022" "SATFLB0004" "NTASTU0002" "SATFLB000
4"
##    ..$ site_location_visit_id: int [1:4] 53501 53705 58429 58658
##    ..$ phenology_comment     : chr [1:4] "" "Ptilotus obovatus var. obovatus  flowering. Tr
iodia sp. has no seeds. No fruit on Callitris glaucophylla - no e"| __truncated__ "NC" "NC"
##    ..$ upper_1_dominant      : chr [1:4] "" "SAT 000251" "NTA017194" "SAT007365"
##    ..$ upper_2_dominant      : chr [1:4] "" "SAT 000229" "NTA017232" "SAT007407"
##    ..$ upper_3_dominant      : chr [1:4] "" NA "NTA017084" "None"
##    ..$ mid_1_dominant        : chr [1:4] "" "SAT 000244" NA "SAT007387"
##    ..$ mid_2_dominant        : chr [1:4] "" "SAT 000261" NA "SAT007423"
##    ..$ mid_3_dominant        : chr [1:4] "" NA NA "SAT007411"
##    ..$ ground_1_dominant     : chr [1:4] "QDA  003325" "SAT 000233" "NTA017070" "SAT007375"
##    ..$ ground_2_dominant     : chr [1:4] "QDA  003293" NA "NTA017076" "SAT007353"
##    ..$ ground_3_dominant     : chr [1:4] "QDA  003325" NA "NTA017082" "SAT007419"
##    ..$ description           : chr [1:4] "Astrebla pectinata / Cenchrus ciliaris / Astrebla
elymoides low open tussock grassland with scattered ." "Callitris glaucophylla / Eucalyptus i
ntertexta low woodland. A mid-stratum dominated by Rhagodia paradoxa and H"| __truncated__ "C
orymbia terminalis mixed mid woodland with  Corymbia polycarpa / Eucalyptus pruinosa/ Eucalyp
tus chlorophylla "| __truncated__ "Eucalyptus intertexta low open woodland  with Callitris gl
aucophylla.  A mid-storey of Rhagodia parabolica,  Do"| __truncated__
##    ..$ mass_flowering_event  : logi [1:4] FALSE FALSE FALSE FALSE
##    ..$ site_unique           : chr [1:4] "QDAMGD0022-53501" "SATFLB0004-53705" "NTASTU0002-
58429" "SATFLB0004-58658"
##  $ soil.subsites:'data.frame':   36 obs. of  12 variables:
##    ..$ site_location_name    : chr [1:36] "QDAMGD0022" "QDAMGD0022" "QDAMGD0022" "QDAMGD0
022" ...
##    ..$ site_location_visit_id : int [1:36] 53501 53501 53501 53501 53501 53501 53501 53501
53501 53705 ...
##    ..$ subsite_id            : chr [1:36] "1" "2" "3" "4" ...
##    ..$ zone                  : int [1:36] 54 54 54 54 54 54 54 54 54 53 ...
##    ..$ easting               : int [1:36] 529581 529580 529582 529592 529595 529620 52966
4 529587 529663 268530 ...
##    ..$ northing              : int [1:36] 7526343 7526338 7526335 7526338 7526345 7526378
7526417 7526423 7526333 6531529 ...
##    ..$ ten_to_twenty_barcode : chr [1:36] "QDA   051589" "QDA   051592" "QDA   051595" "Q
DA   051598" ...
##    ..$ zero_to_ten_barcode   : chr [1:36] "QDA   051588" "QDA   051591" "QDA   051594" "Q
DA   051597" ...
##    ..$ twenty_to_thirty_barcode: chr [1:36] "QDA   051590" "QDA   051593" "QDA   051596" "Q
DA   051599" ...
##    ..$ comments              : chr [1:36] "bare ground" "between grass tussocks" "between
grass tussocks" "bare ground" ...
##    ..$ metagenomic_barcode   : chr [1:36] "QDA 053721" "QDA 053722" "QDA 053723" "QDA 053
724" ...
##    ..$ site_unique           : chr [1:36] "QDAMGD0022-53501" "QDAMGD0022-53501" "QDAMGD00
22-53501" "QDAMGD0022-53501" ...
##  $ soil.bulk    :'data.frame':    9 obs. of  15 variables:
##    ..$ site_location_name    : chr [1:9] "QDAMGD0022" "QDAMGD0022" "QDAMGD0022" "NTASTU00
02" ...
##    ..$ site_location_visit_id : int [1:9] 53501 53501 53501 58429 58429 58429 58658 58658
```

```
58658
##    ..$ sample_id              : chr [1:9] "0" "1" "2" "0" ...
##    ..$ paper_bag_weight       : logi [1:9] NA NA NA NA NA NA ...
##    ..$ oven_dried_weight_in_bag: logi [1:9] NA NA NA NA NA NA ...
##    ..$ ring_weight            : logi [1:9] NA NA NA NA NA NA ...
##    ..$ gravel_weight          : int [1:9] NA NA NA 0 0 0 NA NA NA
##    ..$ ring_volume            : num [1:9] NA NA NA 209 209 ...
##    ..$ gravel_volume          : int [1:9] NA NA NA 0 0 0 NA NA NA
##    ..$ fine_earth_weight_in_bag: int [1:9] NA NA NA 0 0 0 0 0
##    ..$ fine_earth_weight      : int [1:9] NA NA NA 0 0 0 0 0
##    ..$ fine_earth_volume      : num [1:9] NA NA NA 209 209 ...
##    ..$ fine_earth_bulk_density : int [1:9] NA NA NA 0 0 0 0 0
##    ..$ gravel_bulk_density    : int [1:9] NA NA NA 0 0 0 0 0
##    ..$ site_unique            : chr [1:9] "QDAMGD0022-53501" "QDAMGD0022-53501" "QDAMGD002
2-53501" "NTASTU0002-58429" ...
##  $ soil.char   :'data.frame':   28 obs. of  34 variables:
##    ..$ site_location_name     : chr [1:28] "SATFLB0004" "QDAMGD0022" "QDAMGD0022" "QDAMGD002
2" ...
##    ..$ site_location_visit_id: int [1:28] 53705 53501 53501 53501 53501 53705 53501 53705 5
3501 53501 ...
##    ..$ upper_depth            : num [1:28] 0 0.5 0.8 0.6 0.7 0.1 0.3 0.6 0.2 0 ...
##    ..$ lower_depth            : num [1:28] 0.1 0.6 0.9 0.7 0.8 0.2 0.4 0.7 0.3 0.1 ...
##    ..$ horizon                : chr [1:28] "NC" "NC" "NC" "NC" ...
##    ..$ texture_grade          : chr [1:28] "NC" "NC" "NC" "NC" ...
##    ..$ texture_qualifier      : chr [1:28] NA "NC" "NC" "NC" ...
##    ..$ texture_modifier       : chr [1:28] NA "NC" "NC" "NC" ...
##    ..$ colour_when_moist      : chr [1:28] NA "NC" "NC" "NC" ...
##    ..$ colour_when_dry        : chr [1:28] NA "NC" "NC" "NC" ...
##    ..$ mottles_colour         : chr [1:28] "NC" "NC" "NC" "NC" ...
##    ..$ mottles_abundance      : chr [1:28] "NC" "NC" "NC" "NC" ...
##    ..$ mottles_size           : chr [1:28] "NC" "NC" "NC" "NC" ...
##    ..$ segregations_abundance: chr [1:28] "NC" "NC" "NC" "NC" ...
##    ..$ segregations_size      : chr [1:28] "NC" "NC" "NC" "NC" ...
##    ..$ segregations_nature    : chr [1:28] "NC" "NC" "NC" "NC" ...
##    ..$ segregations_form      : chr [1:28] "NC" "NC" "NC" "NC" ...
##    ..$ comments               : chr [1:28] NA NA NA NA ...
##    ..$ collected_by           : int [1:28] 8 4 4 4 4 NA 4 NA 4 4 ...
##    ..$ smallest_size_1        : chr [1:28] "11" "11" "11" "11" ...
##    ..$ smallest_size_2        : logi [1:28] NA NA NA NA NA NA ...
##    ..$ effervescence          : chr [1:28] "N" "N" "N" "N" ...
##    ..$ ec                     : num [1:28] 0.07 0.18 0.54 0.38 0.52 0.03 0.07 1.84 0.06 0.04
...
##    ..$ ph                     : num [1:28] 6.3 8.3 8.1 8.3 8.1 7 8 8.3 7.9 7.8 ...
##    ..$ pedality_grade         : chr [1:28] "NC" "NC" "NC" "NC" ...
##    ..$ pedality_fabric        : chr [1:28] "NC" "NC" "NC" "NC" ...
##    ..$ next_size_type_2       : chr [1:28] "NC" "NC" "NC" "NC" ...
##    ..$ next_size_type_1       : chr [1:28] "NC" "NC" "NC" "NC" ...
##    ..$ smallest_size_type_2   : chr [1:28] "NC" "NC" "NC" "NC" ...
##    ..$ smallest_size_type_1   : chr [1:28] "NC" "NC" "NC" "NC" ...
##    ..$ next_size_2            : logi [1:28] NA NA NA NA NA NA ...
##    ..$ next_size_1            : chr [1:28] "11" "11" "11" "11" ...
##    ..$ layer_barcode          : chr [1:28] "SAT005230" "QDA   051583" "QDA   051586" "QDA
051584" ...
##    ..$ site_unique            : chr [1:28] "SATFLB0004-53705" "QDAMGD0022-53501" "QDAMGD0022
-53501" "QDAMGD0022-53501" ...
##  $ veg.basal   :'data.frame':   95 obs. of  10 variables:
##    ..$ site_location_name     : chr [1:95] "NTASTU0002" "SATFLB0004" "SATFLB0004" "SATFLB00
04" ...
```

```
##    ..$ site_location_visit_id : int [1:95] 58429 53705 53705 53705 53705 53705 53705 53705
53705 53705 ...
##    ..$ site_location_id       : int [1:95] 61138 60122 60122 60122 60122 60122 60122 60122
60122 60122 ...
##    ..$ point_id               : chr [1:95] "NE" "W" "SW" "SE" ...
##    ..$ herbarium_determination: chr [1:95] "Dead Tree/Shrub" "Alectryon oleifolius" "Alectr
yon oleifolius" "Alectryon oleifolius" ...
##    ..$ veg_barcode            : chr [1:95] "NO_BARCODE_DEAD_TREE_804159" "SAT 000242" "SAT
000242" "SAT 000242" ...
##    ..$ hits                   : int [1:95] 1 1 3 4 1 1 1 20 17 6 ...
##    ..$ basal_area_factor      : num [1:95] 0.1 0.25 0.5 0.5 0.5 0.25 0.5 0.25 0.5 0.5 ...
##    ..$ basal_area             : num [1:95] 0.1 0.25 1.5 2 0.5 0.25 0.5 5 8.5 3 ...
##    ..$ site_unique            : chr [1:95] "NTASTU0002-58429" "SATFLB0004-53705" "SATFLB000
4-53705" "SATFLB0004-53705" ...
## $ veg.vouch   :'data.frame':   208 obs. of  12 variables:
##    ..$ site_location_name       : chr [1:208] "QDAMGD0022" "QDAMGD0022" "QDAMGD0022" "QDAM
GD0022" ...
##    ..$ veg_barcode              : chr [1:208] "QDA  003331" "NO_BARCODE_FORB_950413164" "N
O_BARCODE_GRASS_656236361" "NO_BARCODE_DEAD_TREE_558409020" ...
##    ..$ herbarium_determination  : chr [1:208] "Glinus lotoides" "Annual forb" "Annual gras
s" "Dead tree/shrub" ...
##    ..$ is_uncertain_determination: logi [1:208] FALSE NA NA NA NA NA ...
##    ..$ visit_start_date         : chr [1:208] "2013-05-18T09:34:00" "2013-05-18T09:34:00"
"2013-05-18T09:34:00" "2013-05-18T09:34:00" ...
##    ..$ site_location_visit_id   : int [1:208] 53501 53501 53501 53501 53705 53705 53705 53
705 58429 58429 ...
##    ..$ primary_gen_barcode      : chr [1:208] "QDA  003332" NA NA NA ...
##    ..$ secondary_gen_barcode_1  : chr [1:208] NA NA NA NA ...
##    ..$ secondary_gen_barcode_2  : chr [1:208] NA NA NA NA ...
##    ..$ secondary_gen_barcode_3  : chr [1:208] NA NA NA NA ...
##    ..$ secondary_gen_barcode_4  : chr [1:208] NA NA NA NA ...
##    ..$ site_unique              : chr [1:208] "QDAMGD0022-53501" "QDAMGD0022-53501" "QDAMG
D0022-53501" "QDAMGD0022-53501" ...
## $ veg.PI      :'data.frame':   4323 obs. of  13 variables:
##    ..$ site_location_name     : chr [1:4323] "QDAMGD0022" "QDAMGD0022" "QDAMGD0022" "QDAMGD
0022" ...
##    ..$ site_location_visit_id : int [1:4323] 53501 53501 53501 53501 53501 53501 53501 5350
1 53501 53501 ...
##    ..$ transect               : Factor w/ 15 levels "E2-W2","E4-W4",..: 13 13 13 13 13 13 1
3 13 13 13 ...
##    ..$ point_number           : int [1:4323] 92 0 1 3 4 5 6 7 8 9 ...
##    ..$ veg_barcode            : chr [1:4323] NA NA NA "QDA  003325" ...
##    ..$ herbarium_determination: chr [1:4323] NA NA NA "Astrebla pectinata" ...
##    ..$ substrate              : chr [1:4323] "Litter" "Litter" "Bare" "Litter" ...
##    ..$ in_canopy_sky          : logi [1:4323] NA NA NA FALSE NA FALSE ...
##    ..$ dead                   : logi [1:4323] NA NA NA FALSE NA FALSE ...
##    ..$ growth_form            : chr [1:4323] NA NA NA "Tussock grass" ...
##    ..$ height                 : num [1:4323] NA NA NA 0.2 NA 0.2 NA NA NA 0.1 ...
##    ..$ hits_unique            : chr [1:4323] "W1-E1 92" "W1-E1 0" "W1-E1 1" "W1-E1 3" ...
##    ..$ site_unique            : chr [1:4323] "QDAMGD0022-53501" "QDAMGD0022-53501" "QDAMGD0
022-53501" "QDAMGD0022-53501" ...
## $ citation    : chr "TERN (2019) AusPlots ecosystem surveillance monitoring dataset (UR
L: http://aekos.org.au/collection/adelaide.ed"| __truncated__
```

```
# Example 2: Default data for a particular Geographic Extent
# =========================================================

# 'site_info', 'veg.vouchers', and 'veg.PI' data retrived for Brisbane (27.4698S, 153.0251E)
#  and its sourrounding area
AP.data = get_ausplots(bounding_box=c(152.5, 153.5, -28, -27))

# Explore retrieved data
#class(AP.data)    # As in Example 1 (can run uncommented if curious)
summary(AP.data)
```

```
##            Length Class      Mode
## site.info 43      data.frame list
## veg.vouch 12      data.frame list
## veg.PI    13      data.frame list
## citation  1       -none-     character
```

```
#str(AP.data)    # Similar to Example 1 (can run uncommented if curious)
```

```
# Example 3: 'Default data' + 'basal.wedge' + 'structural_summaries' for the genus Eucalyptus
# ============================================================================================

# Default data frames ('site_info', 'veg.vouchers', and 'veg.PI') + 'basal.wedge' + structura
l_summaries data frames for the genus Eucalyptus
AP.data = get_ausplots(basal.wedge=TRUE, structural_summaries=TRUE, species_name_search="Euca
lyptus")

# Explore retrieved data
#class(AP.data)    # As in Example 1 (can run uncommented if curious)
summary(AP.data)
```

```
##             Length Class      Mode
## site.info   43      data.frame list
## struct.summ 15      data.frame list
## veg.basal   10      data.frame list
## veg.vouch   12      data.frame list
## veg.PI      13      data.frame list
## citation    1       -none-     character
```

```
#str(AP.data)    # Similar to Example 1 (can run uncommented if curious)

# Explore species contained in each data frame
head(AP.data$veg.vouch) # Includes Records that match 'eucalyptus'
```

```
##   site_location_name veg_barcode          herbarium_determination
## 1         QDAMUL0003  QDA 001432 Eucalyptus crebra x e. melanophloia
## 2         SASMDD0002  SAS 000461                  Eucalyptus oleosa
## 3         SASMDD0002  SAS 000462                  Eucalyptus dumosa
## 4         SASMDD0002  SAS 000463 Eucalyptus socialis subsp. socialis
## 5         SASMDD0002  SAS 000038    Eucalyptus oleosa subsp. oleosa
## 6         SASMDD0002  SAS 000039                  Eucalyptus dumosa
##   is_uncertain_determination    visit_start_date site_location_visit_id
## 1                      FALSE 2013-04-26T00:00:00                  53595
## 2                      FALSE 2012-09-23T00:00:00                  53711
## 3                      FALSE 2012-09-23T00:00:00                  53711
## 4                      FALSE 2012-09-23T00:00:00                  53711
## 5                      FALSE 2012-09-23T00:00:00                  53711
## 6                      FALSE 2012-09-23T00:00:00                  53711
##   primary_gen_barcode secondary_gen_barcode_1 secondary_gen_barcode_2
## 1                <NA>                    <NA>                    <NA>
## 2       not collected                    <NA>                    <NA>
## 3       not collected                    <NA>                    <NA>
## 4       not collected                    <NA>                    <NA>
## 5         SAS  000521             SAS  000522             SAS  000523
## 6         SAS  000526             SAS  000528             SAS  000529
##   secondary_gen_barcode_3 secondary_gen_barcode_4      site_unique
## 1                    <NA>                    <NA> QDAMUL0003-53595
## 2                    <NA>                    <NA> SASMDD0002-53711
## 3                    <NA>                    <NA> SASMDD0002-53711
## 4                    <NA>                    <NA> SASMDD0002-53711
## 5             SAS  000524             SAS  000525 SASMDD0002-53711
## 6             SAS  000527                    <NA> SASMDD0002-53711
```

```
head(AP.data$veg.PI)  # Includes Plots where 'eucalyptus' occurs
```

```
##   site_location_name site_location_visit_id transect point_number
## 1         WAACOO0006                  53438    S1-N1            0
## 2         WAACOO0006                  53438    S1-N1            1
## 3         WAACOO0006                  53438    S1-N1            2
## 4         WAACOO0006                  53438    S1-N1            3
## 5         WAACOO0006                  53438    S1-N1            4
## 6         WAACOO0006                  53438    S1-N1            5
##   veg_barcode              herbarium_determination substrate
## 1        <NA>                                 <NA>    Crypto
## 2        <NA>                                 <NA>    Crypto
## 3 WAA  001053 Melaleuca pauperiflora subsp. fastigiata    Litter
## 4 WAA  001053 Melaleuca pauperiflora subsp. fastigiata    Litter
## 5 WAA  001053 Melaleuca pauperiflora subsp. fastigiata    Litter
## 6 WAA  001053 Melaleuca pauperiflora subsp. fastigiata    Litter
##   in_canopy_sky  dead growth_form height hits_unique        site_unique
## 1            NA    NA        <NA>     NA    S1-N1 0 WAACOO0006-53438
## 2            NA    NA        <NA>     NA    S1-N1 1 WAACOO0006-53438
## 3         FALSE FALSE       Shrub    3.5    S1-N1 2 WAACOO0006-53438
## 4         FALSE FALSE       Shrub    3.5    S1-N1 3 WAACOO0006-53438
## 5         FALSE FALSE       Shrub    3.7    S1-N1 4 WAACOO0006-53438
## 6         FALSE FALSE       Shrub    3.5    S1-N1 5 WAACOO0006-53438
```

```
head(AP.data$veg.basal) # Includes Records that match 'eucalyptus'
```

```
##    site_location_name site_location_visit_id site_location_id point_id
## 1        WAACO00006                   53438           59857      NW
## 2        WAACO00006                   53438           59857      NW
## 3        WAACO00006                   53438           59857      NW
## 4        WAACO00006                   53438           59857       N
## 5        WAACO00006                   53438           59857       N
## 6        WAACO00006                   53438           59857       N
##    herbarium_determination veg_barcode hits basal_area_factor basal_area
## 1      Eucalyptus moderata WAA  001048    1               0.1       0.10
## 2      Eucalyptus salubris WAA  001083    5               0.1       0.50
## 3      Eucalyptus salubris WAA  001093    7               0.1       0.70
## 4      Eucalyptus moderata WAA  001048    0               0.1       0.00
## 5      Eucalyptus salubris WAA  001083    2               0.1       0.15
## 6      Eucalyptus salubris WAA  001093    4               0.1       0.40
##          site_unique
## 1 WAACO00006-53438
## 2 WAACO00006-53438
## 3 WAACO00006-53438
## 4 WAACO00006-53438
## 5 WAACO00006-53438
## 6 WAACO00006-53438
```

```
head(AP.data$struct.summ)  # Includes Plots where 'eucalyptus' occurs
```

```
##   site_location_name site_location_visit_id
## 1        QDAMUL0003                   53595
## 2        SASMDD0002                   53711
## 3        SASMDD0016                   57000
## 4        NSAMDD0005                   56969
## 5        QDAMUL0001                   53594
## 6        NTAGFU0032                   53679
##
phenology_comment
## 1  Mulga have just finished flowering but no fruit. Tussock grasses mostly dry. Dom hibisc
us in ground layer has just finished fruiting throughout the site
## 2
None
## 3
NC
## 4
NC
## 5
<NA>
## 6                                         Melaleuca stenostachya has finished fl
owering and with not much fruit present. Tussock grasses all dry.
##   upper_1_dominant upper_2_dominant upper_3_dominant mid_1_dominant
## 1      QDA 001428       QDA 001432                       QDA 001428
## 2      SAS 000461       SAS 000463       SAS 000462     SAS 000041
## 3       SAS001764        SAS001732             None      SAS001758
## 4      NSA 010375       NSA 010439       NSA 010391     NSA 010387
## 5      QDA 001355       QDA 001363       QDA 001329     QDA 001355
## 6                                                       NTA 004067
##   mid_2_dominant mid_3_dominant ground_1_dominant ground_2_dominant
## 1                                      QDA 001438        QDA 001402
## 2     SAS 000047     SAS 000049        SAS 000453        SAS 000465
## 3           None           None        SAS001770                -1
## 4           None           None        NSA 010433        NSA 010453
## 5           <NA>           <NA>        QDA 001341              <NA>
## 6     NTA 004077                       NTA 004037        NTA 004021
##   ground_3_dominant
## 1
## 2              <NA>
## 3                -1
## 4        NSA 010465
## 5              <NA>
## 6
##
description
## 1                                         Acacia aneura var. major low open forest w
ith emergent Eucalyptus crebra x E. melanophloia. Mid stratum of juvenile Acacia aneura var.
major. Sparse ground stratum dominated by Thyridolepis xerophila with Hibiscus sturtii
## 2                                         Eucalyptus oleosa / Eucalyptus socialis su
bsp. socialis / Eucalyptus dumosa mixed mid open Mallee forest. Sparse mid layer of isolated
shrubs and a sparse ground layer dominated by Maireana pentatropis and Austrostipa sp.
## 3 Eucalyptus oleosa  mid Mallee woodland with Eucalyptus gracilis. Mid stratum of Senna ar
temisioides subsp. coriacea and a ground stratum dominated by Zygophyllum aurantiacum subsp.
aurantiacum and mixed scattered chenopods mainly  Atriplex stipitata and Maireana spp.
## 4              Eucalyptus dumosa subsp. dumosa, E. socialis and E. gracilis Mallee low
woodland (4-6m) with mixed species mid layer dominated by Eremophila longifolia (1-3m) and gr
ound layer of Enchylaena tomentosa, Zygophyllum sp. and Maireana pentatropis on dunes.
## 5                                         Acacia aneura var. major
```

wood low open forest with emergent Eucalyptus populnea and Eucalyptus melanophloia - E. white
i intergrade. Mid stratum of juvenile Acacia aneura var. major. Minimal ground stratum
6   Melaleuca stenostachya tall open shrubland with
a tussock grass ground stratum of Sorghum plumosum. and Aristida holathera. Some recruitment
in the Eucalyptus pruinosa and Melaleuca stenostachya with the cohort averaging 30cm.
mass_flowering_event   site_unique
1   FALSE QDAMUL0003-53595
2   FALSE SASMDD0002-53711
3   FALSE SASMDD0016-57000
4   FALSE NSAMDD0005-56969
5   FALSE QDAMUL0001-53594
6   FALSE NTAGFU0032-53679

```
# Example 4: 'site_info', 'veg.PI', and 'basal.wedge' data for all sites
# ====================================================================

# Retreive data
start.time = Sys.time()
AP.data = get_ausplots(veg.vouchers=FALSE, basal.wedge=TRUE)
end.time = Sys.time()
end.time - start.time
```

Time difference of 1.244046 mins

```
# Explore
#class(AP.data) # As in Example 1 (can run uncommented if curious)
summary(AP.data)
```

```
##              Length Class       Mode
## site.info 43      data.frame list
## veg.basal 10      data.frame list
## veg.PI    13      data.frame list
## citation   1      -none-      character
```

```
#str(AP.data)    # Similar to Example 1 (can run uncommented if curious)

# Explore 'site_info' data
dim(AP.data$site.info)
```

[1] 650 43

```
names(AP.data$site.info)
```

```
##  [1] "site_location_name"         "established_date"
##  [3] "description"                "bioregion_name"
##  [5] "landform_pattern"           "landform_element"
##  [7] "site_slope"                 "site_aspect"
##  [9] "comments"                   "outcrop_lithology"
## [11] "other_outcrop_lithology"    "plot_dimensions"
## [13] "site_location_visit_id"     "visit_start_date"
## [15] "visit_end_date"             "visit_notes"
## [17] "location_description"       "erosion_type"
## [19] "erosion_abundance"          "erosion_state"
## [21] "microrelief"                "drainage_type"
## [23] "disturbance"                "climatic_condition"
## [25] "vegetation_condition"       "observer_veg"
## [27] "observer_soil"              "described_by"
## [29] "pit_marker_easting"         "pit_marker_northing"
## [31] "pit_marker_mga_zones"       "pit_marker_datum"
## [33] "pit_marker_location_method" "soil_observation_type"
## [35] "a_s_c"                      "plot_is_100m_by_100m"
## [37] "plot_is_aligned_to_grid"    "plot_is_permanently_marked"
## [39] "latitude"                   "longitude"
## [41] "point"                      "state"
## [43] "site_unique"
```

```
head(AP.data$site.info)
```

```
##   site_location_name   established_date
## 1         WAANUL0007 2014-09-06T15:24:41
## 2         NTAFIN0031 2012-10-25T00:00:00
## 3         QDAMUL0003 2013-04-26T00:00:00
## 4         NTAFIN0004 2011-10-06T00:00:00
## 5         NTAFIN0004 2011-10-06T00:00:00
## 6         SASMDD0002 2012-09-23T00:00:00
##                                                                  description
## 1         Great Victoria Desert Nature Reserve, 102.2km south east of Tjuntjuntjara
## 2 Umbeara Station 26.5km South East of Umbeara Homestead. 11km North of SA/Not Border
## 3                                              61km SE of Issiford on Idalia NP
## 4         Top of James Range, Owen Springs Reserve . 73km South West of Alice Springs
## 5         Top of James Range, Owen Springs Reserve . 73km South West of Alice Springs
## 6                                   Calperum Station, 23km North West of Renmark
##   bioregion_name landform_pattern landform_element site_slope site_aspect
## 1            NUL              PLA              DDE       <NA>        <NA>
## 2            FIN              LOW              HSL       <NA>        <NA>
## 3            MUL              PLT              HSL          4         225
## 4            MAC              HIL              HCR          8         135
## 5            MAC              HIL              HCR          8         135
## 6            MDD              LON              DUN          0        <NA>
##
comments
## 1 Plot is flat but sits in a drainage depression between very low rises. Some limestone co
bbles and gravel- larger ones with cryptogam crust. Some very low limestone outcrop- almost a
t ground level. Very long unburnt but difficult to tell exactly how long. Grazing effect is l
ow- some evidence of rabbits. Introduced plant effect is moderate- Carrichtera annua common t
hroughout the site. Homogeneity- community continues another 50m north of the road which is c
lose to the northern edge of the plot. 20m to the east and 50m to the west where there is a l
ow rise. 100m to the south along the drainage line.
## 2
Slope of low hill.
## 3
<NA>
## 4
On top of the James Range. Long unburnt. Weed impact minimal. Grazing impact nil.
## 5
On top of the James Range. Long unburnt. Weed impact minimal. Grazing impact nil.
## 6
2 km. south east of the Flux tower SASMDD0001, 100m in easterly direction from track.
##   outcrop_lithology other_outcrop_lithology plot_dimensions
## 1                LI                      LI    100 x 100 m.
## 2                NC                      NC    100 x 100 m.
## 3                NC                      NC    100 x 100 m.
## 4                SA                       M    100 x 100 m.
## 5                SA                       M    100 x 100 m.
## 6                NC                      NC    100 x 100 m.
##   site_location_visit_id    visit_start_date      visit_end_date
## 1                  56932 2014-09-07T15:24:00 2014-09-07T15:24:00
## 2                  53749 2012-10-25T00:00:00 2012-10-25T00:00:00
## 3                  53595 2013-04-26T00:00:00 2013-04-26T00:00:00
## 4                  58010 2016-03-02T00:00:00 2016-03-02T00:00:00
## 5                  53624 2011-10-06T00:00:00 2011-10-06T00:00:00
## 6                  53711 2012-09-23T00:00:00 2012-09-23T00:00:00
##
visit_notes
## 1
```

```
<NA>
## 2
## 3 Acacia aneura woodland. Rising a little more to the NE corner where it becomes rockier.
Site is on Plateau above Mitchell grass downs 10km to the north. Grazing impact low- lots of
echidna diggings in the site plus kangaroos. Weed impact low. Very long unburnt- no scarring
on Ironbark or Mulga and a varied cohort with old trees and younger shrubs.
## 4
Revisit collected Point intercept, vouchered plant specimens,DNA and Metagenomic samples.
## 5
<NA>
## 6
Low Mallee woodland in dune swale with dominant species of Eucalyptus oleosa subspecies oleos
a and Eucalyptus dumosa.
##                                                             location_description
## 1                                            Great Victoria Desert Nature Reserve
## 2     Umbeara Station 26.5km South East of Umbeara Homestead. 11km North of SA/Nt Border
## 3                                               61km SE of Issiford on Idalia NP
## 4                                                                   Owen Springs
## 5 Top of James Range, Owen Springs Reserve approximately 73km South West of Alice Springs
## 6                                         Mallee swale. 23km North West of Renmark
##    erosion_type erosion_abundance erosion_state microrelief drainage_type
## 1           NC                 X            NC           Y             3
## 2            R                 1             A          NC             5
## 3           NC                 X            NC           N             4
## 4           NC                NC            NC          NC             7
## 5           NC                NC            NC          NC             2
## 6           NC                NC            NC          NC             7
##    disturbance climatic_condition vegetation_condition observer_veg
## 1           0                DRY                  FFR           18
## 2          1L                DRY                  FFR            1
## 3           0                DRY                  DRY            1
## 4          NC                DRY                  AVG            1
## 5           0                WET                  DRY            1
## 6          NC                DRY                  DRY            1
##    observer_soil described_by pit_marker_easting pit_marker_northing
## 1             2            1             383287             6676768
## 2             2            1             389476             7134938
## 3             2            1             875168             7257129
## 4            11            1                 NA                  NA
## 5             2            1             335077             7324080
## 6             2            1             462393             6236497
##    pit_marker_mga_zones pit_marker_datum pit_marker_location_method
## 1                   52            WGS84                        GPS
## 2                   53            WGS84                       DGPS
## 3                   55            WGS84                       DGPS
## 4                   53            WGS84                      <NA>
## 5                   53            GDA94                       DGPS
## 6                   54            GDA94                        GPS
##    soil_observation_type        a_s_c plot_is_100m_by_100m
## 1                     P         <NA>                 TRUE
## 2                     P 3RUCYCZARFLLT                 TRUE
## 3                     P         <NA>                 TRUE
## 4                    NC         <NA>                 TRUE
## 5                     P  3RUCYCZAIIKT                 TRUE
## 6                     P         <NA>                 TRUE
##    plot_is_aligned_to_grid plot_is_permanently_marked  latitude longitude
## 1                     TRUE                      TRUE -30.03548  127.7895
## 2                     TRUE                      TRUE -25.89989  133.8966
```

```
## 3                     TRUE                    TRUE -24.75512  144.7083
## 4                     TRUE                    TRUE -24.18724  133.3764
## 5                     TRUE                    TRUE -24.18724  133.3764
## 6                     TRUE                    TRUE -34.01170  140.5927
##   point state      site_unique
## 1    SW    WA WAANUL0007-56932
## 2    SW    NT NTAFIN0031-53749
## 3    SW   QLD QDAMUL0003-53595
## 4    SW    NT NTAFIN0004-58010
## 5    SW    NT NTAFIN0004-53624
## 6    SW    SA SASMDD0002-53711
```

```r
# Explore 'veg_PI' data
dim(AP.data$veg.PI)
```

```
## [1] 717849     13
```

```r
names(AP.data$veg.PI)
```

```
##  [1] "site_location_name"    "site_location_visit_id"
##  [3] "transect"              "point_number"
##  [5] "veg_barcode"           "herbarium_determination"
##  [7] "substrate"             "in_canopy_sky"
##  [9] "dead"                  "growth_form"
## [11] "height"                "hits_unique"
## [13] "site_unique"
```

```r
head(AP.data$veg.PI)
```

```
##   site_location_name site_location_visit_id transect point_number
## 1         WAACO00006                  53438    S1-N1            0
## 2         WAACO00006                  53438    S1-N1            1
## 3         WAACO00006                  53438    S1-N1            2
## 4         WAACO00006                  53438    S1-N1            3
## 5         WAACO00006                  53438    S1-N1            4
## 6         WAACO00006                  53438    S1-N1            5
##   veg_barcode              herbarium_determination substrate
## 1        <NA>                                 <NA>    Crypto
## 2        <NA>                                 <NA>    Crypto
## 3 WAA  001053 Melaleuca pauperiflora subsp. fastigiata    Litter
## 4 WAA  001053 Melaleuca pauperiflora subsp. fastigiata    Litter
## 5 WAA  001053 Melaleuca pauperiflora subsp. fastigiata    Litter
## 6 WAA  001053 Melaleuca pauperiflora subsp. fastigiata    Litter
##   in_canopy_sky  dead growth_form height hits_unique        site_unique
## 1            NA    NA        <NA>     NA   S1-N1 0 WAACO00006-53438
## 2            NA    NA        <NA>     NA   S1-N1 1 WAACO00006-53438
## 3         FALSE FALSE       Shrub    3.5   S1-N1 2 WAACO00006-53438
## 4         FALSE FALSE       Shrub    3.5   S1-N1 3 WAACO00006-53438
## 5         FALSE FALSE       Shrub    3.7   S1-N1 4 WAACO00006-53438
## 6         FALSE FALSE       Shrub    3.5   S1-N1 5 WAACO00006-53438
```

Manipulating AusPlots data I: Subset data frames

The `get_ausplots` function extracts and compiles AusPlots data allowing substantial flexibility in the selection of the required data. Up to 8 different types of data can be retrieved into distinct data frames (i.e. data on sampling sites, vegetation structure, vegetation point intercept, vegetation vouchers, vegetation basal wedge, soil characterization, soil bulk density, and soil & soil metagenomics samples). In addition, data can be filtered for particular sets of plots and/or genus/species, as well as geographically using a rectangular bounding box.

However, in some situations we are only interested in a subset of the data retrieved by `get_ausplots`. To subset ausplot data we use the variables in the retrieved data frames corresponding to the concept by we would like to filter the data. In some occasions we would sub-setting a single data frame (i.e. type of variables) is all what we need. Variables in the `site.info` data frame contain information that affect all other data frames; so typically after sub-setting the contents of the variable of interests in the `site.info` data frame, we will also subset the remaining datasets using one of the common variables among all data frames. Common variables among datasets include `site_location_name`, `site_location_visit_id`, and `site_unique`. Commonly `site_unique` is the best option to 'connect' ausplots data frames, as it is the most specific variable representing a single visit to a particular site.

To subset a data frame we filter its data by querying the variable(s) of interest using operators. The variables of interest are typically factors, numerical, or boolean variables. Many variables retrieved by `get_ausplots` have a `char` class, despite conceptually falling in one of these 3 categories. Therefore, before using a variable to filter a data frame we must inspect its contents and class, and if required change its class to an adequate one. We use relational operators to filter individual variables, and logical (and occasionally arithmetic) operators to combine more than one variable in our filtering operations (R Operators (https://www.datamentor.io/r-programming/operator/)).

Sub-setting a Single Data Frame

We might be, for example, interested in point intercept data only for vegetation of a particular height, a particular growth form, growing on particular substrate type, or found in a particular set of transects. In these examples, we use the variables in the 'veg.PI' data frame to filter the retrieved ausplots data in this data frame. We do not need to subset any othe data frames.

Example 1: Height

Height is `numeric`, so there is no need to change its class

```
# ============================
# Sub-set a Single Data Frame
# ============================
# Here we filter by variables in the 'veg.PI' data frame



# Height
# ======


# Explore Variable Type and Change to Numeric
# -------------------------------------------
class(AP.data$veg.PI$height)
```

```
## [1] "numeric"
```

```
summary(AP.data$veg.PI$height)
```

```
##     Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##      0.0     0.1     0.3     2.1     2.5    34.0  374381
```

```
# Subset to Height (> 2 meters) in 'veg.PI' data frame
# ------------------------------------------------------
TreeGT2m.AP.data = AP.data
dim(TreeGT2m.AP.data$veg.PI)
```

```
## [1] 717849      13
```

```
#summary(AP.data$veg.PI$height)
TreeGT2m.AP.data$veg.PI = TreeGT2m.AP.data$veg.PI[TreeGT2m.AP.data$veg.PI$height > 2,]
dim(TreeGT2m.AP.data$veg.PI)
```

```
## [1] 468485      13
```

```
summary(TreeGT2m.AP.data$veg.PI$height)
```

```
##     Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##      2.0     3.8     6.0     6.8     9.0    34.0  374381
```

Example 2: Transect

Transect is a `factor`, so there is no need to change its class

```
# Transect
# ========

# Explore Variable Type and Change to Factor
# ------------------------------------------
class(AP.data$veg.PI$transect)
```

```
## [1] "factor"
```

```
summary(AP.data$veg.PI$transect)
```

```
## E1-W1 E2-W2 E3-W3 E4-W4 E5-W5 N1-S1 N2-S2 N3-S3 N4-S4 N5-S5 S1-N1 S2-N2
## 17067 52685 18037 52531 18473 23765 43330 25722 44200 26444 48728 28606
## S3-N3 S4-N4 S5-N5 W1-E1 W2-E2 W2-S2 W3-E3 W4-E4 W5-E5
## 45933 27560 45793 54642 19012   102 53654 18856 52709
```

```
# Subset an specific Transect (E1-W1) in 'veg.PI' data frame
# ----------------------------------------------------------
E1W1Tr.AP.data = AP.data
dim(E1W1Tr.AP.data$veg.PI)
```

```
## [1] 717849      13
```

```
#summary(AP.data$veg.PI$transect)
E1W1Tr.AP.data$veg.PI = E1W1Tr.AP.data$veg.PI[E1W1Tr.AP.data$veg.PI$transect == "E1-W1",]
levels(E1W1Tr.AP.data$veg.PI$transect)
```

```
##  [1] "E1-W1" "E2-W2" "E3-W3" "E4-W4" "E5-W5" "N1-S1" "N2-S2" "N3-S3"
##  [9] "N4-S4" "N5-S5" "S1-N1" "S2-N2" "S3-N3" "S4-N4" "S5-N5" "W1-E1"
## [17] "W2-E2" "W2-S2" "W3-E3" "W4-E4" "W5-E5"
```

```
E1W1Tr.AP.data$veg.PI$transect = droplevels(E1W1Tr.AP.data$veg.PI$transect)
levels(E1W1Tr.AP.data$veg.PI$transect)
```

```
## [1] "E1-W1"
```

```
dim(E1W1Tr.AP.data$veg.PI)
```

```
## [1] 17067    13
```

```
summary(E1W1Tr.AP.data$veg.PI$transect)
```

```
## E1-W1
## 17067
```

Example 3: Growth Form

Transect is a `character` variable, so we need to change its class to `factor`

```
# Growth Form
# ===========

# Explore Variable Type and Change to Factor in 'veg.PI' data frame
# ----------------------------------------------------------------
class(AP.data$veg.PI$growth_form)
```

```
## [1] "character"
```

```
summary(AP.data$veg.PI$growth_form)
```

```
##     Length      Class       Mode
##     717849  character  character
```

```
AP.data$veg.PI$growth_form.f = factor(AP.data$veg.PI$growth_form)
summary(AP.data$veg.PI$growth_form.f)
```

```
##         Aquatic      Bryophyte       Chenopod          Cycad       Epiphyte
##               3            701          19160             21            274
##            Fern           Forb         Fungus     Grass-tree    Heath-shrub
##            1357          36929             25           1267           5089
## Hummock grass             NC           Rush          Sedge          Shrub
##           26311           1095            706          11369          77357
##    Shrub Mallee    Tree Mallee      Tree/Palm Tussock grass           Vine
##            1168          12380          82932          83185           1949
##            NA's
##          354571
```

```
# Subset to the Tree/Palm Growth Form
# --------------------------------
TreePalm.AP.data = AP.data
dim(TreePalm.AP.data$veg.PI)
```

```
## [1] 717849      14
```

```
#summary(AP.data$veg.PI$growth_form.f)
TreePalm.AP.data$veg.PI = TreePalm.AP.data$veg.PI[TreePalm.AP.data$veg.PI$growth_form.f == "T
ree/Palm",]
levels(TreePalm.AP.data$veg.PI$growth_form.f)
```

```
##  [1] "Aquatic"        "Bryophyte"     "Chenopod"       "Cycad"
##  [5] "Epiphyte"       "Fern"          "Forb"           "Fungus"
##  [9] "Grass-tree"     "Heath-shrub"   "Hummock grass"  "NC"
## [13] "Rush"           "Sedge"         "Shrub"          "Shrub Mallee"
## [17] "Tree Mallee"    "Tree/Palm"     "Tussock grass"  "Vine"
```

```
TreePalm.AP.data$veg.PI$growth_form.f = droplevels(TreePalm.AP.data$veg.PI$growth_form.f)
levels(TreePalm.AP.data$veg.PI$growth_form.f)
```

```
## [1] "Tree/Palm"
```

```
dim(TreePalm.AP.data$veg.PI)
```

```
## [1] 437503      14
```

```
summary(TreePalm.AP.data$veg.PI$growth_form.f)
```

```
## Tree/Palm      NA's
##     82932    354571
```

Sub-setting All Data Frames

In some occasions, we are interested on sites located at particular states or bioregions. Alternatively, we might be only interested on data obtained in sites on steep slopes and/or with a slope facing (i.e. aspect) south. In these examples, we can use the variables in the `site.info` data frame to filter the sites we of interest. In this case, we also need to subset the data in the remaining data frames, as we are only interested in data that has been collected in sites with particular characteristics. Therefore, we the filter the other data frames by site, selecting the sites filtered out in our first sub-setting operation on the `site.info` data frame. To do so we use one of the variables present in all data frames that contain a site identifier (i.e. using `site_location_name`, `site_location_visit_id`, or `site_unique`; see above).

Example 1: Site Slope

Site Slope is a `character` variable, so we need to change its class to `numeric`

```
# ========================
# Sub-set All Data Frames
# ========================
# Here we filter by variables in the 'veg.PI' data frame



# Site Slope
# ==========


# Explore Variable Type and Change to Numeric
# -------------------------------------------
class(AP.data$site.info$site_slope)
```

```
## [1] "character"
```

```
summary(AP.data$site.info$site_slope)
```

```
##     Length      Class       Mode
##        650  character  character
```

```
AP.data$site.info$site_slope.n = as.numeric(AP.data$site.info$site_slope)
summary(AP.data$site.info$site_slope.n)
```

```
##     Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##    0.000   0.000   1.000   2.421   2.000  50.000     111
```

```
# Subset to Plos with Steep Slopes (> 20 degrees) in 'site.info' data frame
# ------------------------------------------------------------------------
slope.AP.data = AP.data
dim(slope.AP.data$site.info)
```

```
## [1] 650  44
```

```
#summary(AP.data$site.info$site_slope.n)
slope.AP.data$site.info = slope.AP.data$site.info[slope.AP.data$site.info$site_slope.n >= 20
,]
dim(slope.AP.data$site.info)
```

```
## [1] 122  44
```

```
summary(slope.AP.data$site.info$site_slope.n)
```

```
##     Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##    20.00   20.50   25.00   28.82   35.00   50.00     111
```

```
# Subset to Plots with Steep Slopes in other Data Frames
# ---------------------------------------------------------
# To do so we use the common variable 'site_unique'

# Subset in 'veg.PI' Data Frame
# ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
dim(slope.AP.data$veg.PI)
```

```
## [1] 717849     14
```

```
slope.AP.data$veg.PI = slope.AP.data$veg.PI[slope.AP.data$veg.PI$site_unique %in% slope.AP.da
ta$site.info$site_unique, ]
dim(slope.AP.data$veg.PI)
```

```
## [1] 13656     14
```

```
# Subset in 'veg.basal' Data Frame
# ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
dim(slope.AP.data$veg.basal)
```

```
## [1] 8111    10
```

```
slope.AP.data$veg.basal = slope.AP.data$veg.basal[slope.AP.data$veg.basal$site_unique %in% sl
ope.AP.data$site.info$site_unique, ]
dim(slope.AP.data$veg.basal)
```

```
## [1] 189  10
```

Example 2: Site Aspect

Site Aspect is a `character` variable, so we need to change its class to `numeric`

```
# Site Aspect
# ===========

# Explore Variable Type and Change to Numeric
# -------------------------------------------
class(AP.data$site.info$site_aspect)
```

```
## [1] "character"
```

```
summary(AP.data$site.info$site_aspect)
```

```
##    Length    Class      Mode
##       650 character character
```

```
AP.data$site.info$site_aspect.n = as.numeric(AP.data$site.info$site_aspect)
summary(AP.data$site.info$site_aspect.n)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##       0.0    90.0   180.0   183.3   270.0   360.0     394
```

```
# Subset to Plots with a South (SE to SW; i.e. 135 to 225) Aspect in 'site.info' data frame
# ----------------------------------------------------------------------------------------
aspect.AP.data = AP.data
dim(aspect.AP.data$site.info)
```

```
## [1] 650  45
```

```
#summary(AP.data$site.info$site_aspect.n)
aspect.AP.data$site.info = aspect.AP.data$site.info[(aspect.AP.data$site.info$site_aspect.n >
135 &
aspect.AP.data$site.info$site_aspect.n <= 225),]
dim(aspect.AP.data$site.info)
```

```
## [1] 479  45
```

```
summary(aspect.AP.data$site.info$site_aspect.n)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##     155.0   180.0   180.0   195.7   225.0   225.0     394
```

```
# Subset to Plots with a South (SE to SW) Aspect in other Data Frames
# ------------------------------------------------------------------
# To do so we use the common variable 'site_unique'

# Subset in 'veg.PI' Data Frame
# ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
dim(aspect.AP.data$veg.PI)
```

```
## [1] 717849      14
```

```
aspect.AP.data$veg.PI = aspect.AP.data$veg.PI[aspect.AP.data$veg.PI$site_unique %in% aspect.A
P.data$site.info$site_unique, ]
dim(aspect.AP.data$veg.PI)
```

```
## [1] 94973      14
```

```
# Subset in 'veg.basal' Data Frame
# ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
dim(aspect.AP.data$veg.basal)
```

```
## [1] 8111   10
```

```
aspect.AP.data$veg.basal = aspect.AP.data$veg.basal[aspect.AP.data$veg.basal$site_unique %in%
aspect.AP.data$site.info$site_unique, ]
dim(aspect.AP.data$veg.basal)
```

```
## [1] 1014   10
```

Example 3: State

State is a `character` variable, so we need to change its class to `factor`

```
# State
# =====

# Explore Variable Type and Change to Factor
# ----------------------------------------
class(AP.data$site.info$state)
```

```
## [1] "character"
```

```
summary(AP.data$site.info$state)
```

```
##    Length     Class      Mode
##       650 character character
```

```
AP.data$site.info$state.f = factor(AP.data$site.info$state)
summary(AP.data$site.info$state.f)
```

```
## NSW  NT QLD  SA VIC  WA
##  87 138 127 159  18 121
```

```
# Subset to Plots in the State of Queensland in 'site.info' data frame
# -------------------------------------------------------------------
# Subset to "QLD"
QLD.AP.data = AP.data
dim(QLD.AP.data$site.info)
```

```
## [1] 650  46
```

```
#summary(AP.data$site.info$state.f)
QLD.AP.data$site.info = QLD.AP.data$site.info[QLD.AP.data$site.info$state.f == "QLD",]
levels(QLD.AP.data$site.info$state.f)
```

```
## [1] "NSW" "NT"  "QLD" "SA"  "VIC" "WA"
```

```
QLD.AP.data$site.info$state.f = droplevels(QLD.AP.data$site.info$state.f)
levels(QLD.AP.data$site.info$state.f)
```

```
## [1] "QLD"
```

```
dim(QLD.AP.data$site.info)
```

```
## [1] 127  46
```

```
summary(QLD.AP.data$site.info$state.f)
```

```
## QLD
## 127
```

```
# Subset to Plots iw the State of Queensland in other Data Frames
# ----------------------------------------------------------------
# To do so we use the common variable 'site_unique'

# Subset in 'veg.PI' Data Frame
# ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
dim(QLD.AP.data$veg.PI)
```

```
## [1] 717849      14
```

```
QLD.AP.data$veg.PI = QLD.AP.data$veg.PI[QLD.AP.data$veg.PI$site_unique %in% QLD.AP.data$site.
info$site_unique, ]
dim(QLD.AP.data$veg.PI)
```

```
## [1] 138489      14
```

```
# Subset in 'veg.basal' Data Frame
# ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
dim(QLD.AP.data$veg.basal)
```

```
## [1] 8111    10
```

```
QLD.AP.data$veg.basal = QLD.AP.data$veg.basal[QLD.AP.data$veg.basal$site_unique %in% QLD.AP.d
ata$site.info$site_unique, ]
dim(QLD.AP.data$veg.basal)
```

```
## [1] 1846    10
```

Example 4: Bioregion name

Bioregion name is a `character` variable, so we need to change its class to `factor`

```
# Bioregion name
# ==============

# Explore Variable Type and Change to Factor
# ------------------------------------------
class(AP.data$site.info$bioregion_name)
```

```
## [1] "character"
```

```
summary(AP.data$site.info$bioregion_name)
```

```
##     Length    Class       Mode
##        650 character character
```

```
AP.data$site.info$bioregion_name.f = factor(AP.data$site.info$bioregion_name)
summary(AP.data$site.info$bioregion_name.f)
```

```
## ARP AUA AVW BBS BHC BRT CEK CHC COO COP CYP DAB DAC DAL DMR EIU ESP EYB
##   3  15   4   2  32   6   3  13  32   2  19   1   3   1   3   7   1   3
## FIN FLB GAS GAW GES GFU GSD GUP GVD HAM JAF KAN LSD MAC MAL MDD MGD MII
##  18  47   2   3   3  41   1  33   5   6   3   4   3  28   3  52  34   2
## MUL MUR NAN NSS NUL PCK PIL RIV SSD STP STU SWA SYB VIB
##   7   6   2   3  13   3  35  32  48  40   6   4   9   4
```

```
# Subset to Plots in Bioregions in the Eastern (~ Qld) Gulf of Carpentaria in 'site.info' dat
a frame
# ----------------------------------------------------------------------------------------
-------
# Subset to "CYP" (Cape York Peninsula) and "GUP" (Gulf Plains)
EGCBioregs.AP.data = AP.data
dim(EGCBioregs.AP.data$site.info)
```

```
## [1] 650  47
```

```
#summary(AP.data$site.info$bioregion_name.f)
EastCarpGulf.Bioreg = c("CYP", "GUP")
EGCBioregs.AP.data$site.info = EGCBioregs.AP.data$site.info[EGCBioregs.AP.data$site.info$bior
egion_name.f %in% EastCarpGulf.Bioreg,]
levels(EGCBioregs.AP.data$site.info$bioregion_name.f)
```

```
##  [1] "ARP" "AUA" "AVW" "BBS" "BHC" "BRT" "CEK" "CHC" "COO" "COP" "CYP"
## [12] "DAB" "DAC" "DAL" "DMR" "EIU" "ESP" "EYB" "FIN" "FLB" "GAS" "GAW"
## [23] "GES" "GFU" "GSD" "GUP" "GVD" "HAM" "JAF" "KAN" "LSD" "MAC" "MAL"
## [34] "MDD" "MGD" "MII" "MUL" "MUR" "NAN" "NSS" "NUL" "PCK" "PIL" "RIV"
## [45] "SSD" "STP" "STU" "SWA" "SYB" "VIB"
```

```
EGCBioregs.AP.data$site.info$bioregion_name.f = droplevels(EGCBioregs.AP.data$site.info$biore
gion_name.f)
levels(EGCBioregs.AP.data$site.info$bioregion_name.f)
```

```
## [1] "CYP" "GUP"
```

```
dim(EGCBioregs.AP.data$site.info)
```

```
## [1] 52 47
```

```
summary(EGCBioregs.AP.data$site.info$bioregion_name.f)
```

```
## CYP GUP
##  19  33
```

```
# Subset to Plots in Bioregions in the Eastern (~ Qld) Gulf of Carpentaria in other Data Fram
es
# ------------------------------------------------------------------------------------------
--
# To do so we use the common variable 'site_unique'

# Subset in 'veg.PI' Data Frame
# ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
dim(EGCBioregs.AP.data$veg.PI)
```

```
## [1] 717849      14
```

```
EGCBioregs.AP.data$veg.PI = EGCBioregs.AP.data$veg.PI[EGCBioregs.AP.data$veg.PI$site_unique %
in% EGCBioregs.AP.data$site.info$site_unique, ]
dim(EGCBioregs.AP.data$veg.PI)
```

```
## [1] 61426     14
```

```
# Subset in 'veg.basal' Data Frame
# ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
dim(EGCBioregs.AP.data$veg.basal)
```

```
## [1] 8111    10
```

```
EGCBioregs.AP.data$veg.basal = EGCBioregs.AP.data$veg.basal[EGCBioregs.AP.data$veg.basal$site
_unique %in% EGCBioregs.AP.data$site.info$site_unique, ]
dim(EGCBioregs.AP.data$veg.basal)
```

```
## [1] 1222    10
```

SPECIES-LEVEL DATA: species_table function and species occurence matrices

The `species_table` function in the `ausplotsR` package is used to generate a species occurrence matrix from AusPlots raw data. The species occurence matrix can be then used in multiple applications that require species-level data. For example, it can be used to investigate patterns of presence/absence and/or abundance (note that vegetation 'cover' is used as a surrogate for vegetation 'abundance'), compute indices of species diversity, or elaborate rank-abundance plots.

The `species_table` function takes a data frame of individual raw point intercept hits (i.e. a veg.PI data frame) generated using the `get_ausplots` function, and returns a 'species against sites' matrix. Four metrics can be selected to score species occurrence:

- *Presence/Absence:* Set by the argument `m_kind = PA`.

- *Percent Cover:* Based on total frequency of hits. This is the most commonly used metric. Set by the argument `m_kind = percent_cover` .
- *Frequency:* Based on proportional frequencies of presence on the 10 individual transects within a plot. Set by the argument `m_kind = freq` . It can be a measure of importance for low cover species.
- *IVI:* A combination of cover and frequency. Set by the argument `m_kind = IVI` .

If *Percent Cover* or *IVI* are used two types of cover type can be selected:

- *Projected Foliage Cover (PFC):* Hits scored as 'in canopy sky' are removed. Set by the argument `cover_type = PFC` .
- *Opaque Canopy Cover (OCC):* Hits scored as 'in canopy sky' are retained. Set by the argument `cover_type = OCC` .

Examples of the different arguments combinations in the `species_table` function are presented below. Species occurrence matrices are computed for the full set of vegetation point intersect data currently available at AusPlots. The list of data frames containing information for all currently available AusPlots sites (i.e. the 'AP.data' list) was previously created using the `get_ausplots` function (see above). The class and dimensions of the returned data frame are the same in all examples, so they are only displayed for the first example (the corresponding code is commented out in the other examples). The resulting species occurrence data frames can be enriched with additional information as we will see in the next section ('Manipulating AusPlots data II: Merging data frames').

```
# ===========================================================================
# SPECIES-LEVEL DATA: 'species_table' function and species occurence matrices
# ===========================================================================

# Scoring metric: Presence/Absence
# ===============================
AP.data.SppbySites.PA = species_table(AP.data$veg.PI, m_kind="PA")
class(AP.data.SppbySites.PA)
```

```
## [1] "data.frame"
```

```
dim(AP.data.SppbySites.PA) # Number of rows and columns in the matrix: Sites x Species
```

```
## [1]  641 3572
```

```
AP.data.SppbySites.PA[1:5, 1:5]
```

```
##                  Abutilon.fraseri Abutilon.halophilum Abutilon.hannii
## NSABBS0005-58582                0                   0                0
## NSABBS0006-58557                0                   0                0
## NSABHC0001-53596                0                   0                0
## NSABHC0002-53597                0                   0                0
## NSABHC0003-53598                0                   0                0
##                  Abutilon.hannii.subsp..prostrate..p.k.latz.427.
## NSABBS0005-58582                                               0
## NSABBS0006-58557                                               0
## NSABHC0001-53596                                               0
## NSABHC0002-53597                                               0
## NSABHC0003-53598                                               0
##                  Abutilon.leucopetalum
## NSABBS0005-58582                      0
## NSABBS0006-58557                      0
## NSABHC0001-53596                      0
## NSABHC0002-53597                      0
## NSABHC0003-53598                      0
```

```
summary(AP.data.SppbySites.PA[,1:3])
```

```
##  Abutilon.fraseri  Abutilon.halophilum Abutilon.hannii
##  Min.   :0.00000   Min.   :0.0000      Min.   :0.00000
##  1st Qu.:0.00000   1st Qu.:0.0000      1st Qu.:0.00000
##  Median :0.00000   Median :0.0000      Median :0.00000
##  Mean   :0.01092   Mean   :0.0078      Mean   :0.00156
##  3rd Qu.:0.00000   3rd Qu.:0.0000      3rd Qu.:0.00000
##  Max.   :1.00000   Max.   :1.0000      Max.   :1.00000
```

```
# Scoring metric: Percent Cover
# =============================

# Cover Type: Projected foliage cover (PFC)
# -----------------------------------------
# Hits scoered as 'in canopy sky' are removed
AP.data.SppbySites.PcC.PFC = species_table(AP.data$veg.PI, m_kind="percent_cover", cover_type
="PFC")
#class(AP.data.SppbySites.PcC.PFC)
#dim(AP.data.SppbySites.PcC.PFC) # Number of rows and columns in the matrix: Sites x Species
#AP.data.SppbySites.PcC.PFC[1:5, 1:5]
summary(AP.data.SppbySites.PcC.PFC[,1:3])
```

```
##  Abutilon.fraseri   Abutilon.halophilum Abutilon.hannii
##  Min.   :0.000000   Min.   :0.000000    Min.   :0.0000000
##  1st Qu.:0.000000   1st Qu.:0.000000    1st Qu.:0.0000000
##  Median :0.000000   Median :0.000000    Median :0.0000000
##  Mean   :0.001545   Mean   :0.005406    Mean   :0.0003089
##  3rd Qu.:0.000000   3rd Qu.:0.000000    3rd Qu.:0.0000000
##  Max.   :0.297030   Max.   :1.980198    Max.   :0.1980198
```

```
# Cover Type: Opaque Canopy Cover (OCC)
# ------------------------------------
# Hits scoered as 'in canopy sky' are retained
AP.data.SppbySites.PcC.OCC = species_table(AP.data$veg.PI, m_kind="percent_cover", cover_type
="OCC")
#class(AP.data.SppbySites.PcC.OCC)
#dim(AP.data.SppbySites.PcC.OCC) # Number of rows and columns in the matrix: Sites x Species
#AP.data.SppbySites.PcC.OCC[1:5, 1:5]
summary(AP.data.SppbySites.PcC.OCC[,1:3])
```

```
##   Abutilon.fraseri    Abutilon.halophilum Abutilon.hannii
##   Min.   :0.000000    Min.   :0.000000    Min.   :0.0000000
##   1st Qu.:0.000000    1st Qu.:0.000000    1st Qu.:0.0000000
##   Median :0.000000    Median :0.000000    Median :0.0000000
##   Mean   :0.001545    Mean   :0.005406    Mean   :0.0003089
##   3rd Qu.:0.000000    3rd Qu.:0.000000    3rd Qu.:0.0000000
##   Max.   :0.297030    Max.   :1.980198    Max.   :0.1980198
```

```
# Scoring metric: Frequency
# =========================
AP.data.SppbySites.Freq = species_table(AP.data$veg.PI, m_kind="freq")
#class(AP.data.SppbySites.Freq)
#dim(AP.data.SppbySites.Freq) # Number of rows and columns in the matrix: Sites x Species
#AP.data.SppbySites.Freq[1:5, 1:5]
summary(AP.data.SppbySites.Freq[,1:3])
```

```
##   Abutilon.fraseri    Abutilon.halophilum Abutilon.hannii
##   Min.   :0.000000    Min.   :0.000000    Min.   :0.000000
##   1st Qu.:0.000000    1st Qu.:0.000000    1st Qu.:0.000000
##   Median :0.000000    Median :0.000000    Median :0.000000
##   Mean   :0.001404    Mean   :0.002496    Mean   :0.000312
##   3rd Qu.:0.000000    3rd Qu.:0.000000    3rd Qu.:0.000000
##   Max.   :0.200000    Max.   :0.800000    Max.   :0.200000
```

```
# Scoring metric: IVI
# ===================

# Cover Type: Projected foliage cover (PFC)
# -----------------------------------------
# Hits scoered as 'in canopy sky' are removed
AP.data.SppbySites.IVI.PFC = species_table(AP.data$veg.PI, m_kind="IVI", cover_type="PFC")
#class(AP.data.SppbySites.IVI.PFC)
#dim(AP.data.SppbySites.IVI.PFC) # Number of rows and columns in the matrix: Sites x Species
#AP.data.SppbySites.IVI.PFC[1:5, 1:5]
summary(AP.data.SppbySites.IVI.PFC[,1:3])
```

```
##   Abutilon.fraseri    Abutilon.halophilum Abutilon.hannii
##   Min.   :0.000000    Min.   :0.000000    Min.   :0.000000
##   1st Qu.:0.000000    1st Qu.:0.000000    1st Qu.:0.000000
##   Median :0.000000    Median :0.000000    Median :0.000000
##   Mean   :0.001404    Mean   :0.002496    Mean   :0.000312
##   3rd Qu.:0.000000    3rd Qu.:0.000000    3rd Qu.:0.000000
##   Max.   :0.200000    Max.   :0.800000    Max.   :0.200000
```

```
# Cover Type: Opaque Canopy Cover (OCC)
# -----------------------------------
# Hits scoered as 'in canopy sky' are retained
AP.data.SppbySites.IVI.OCC = species_table(AP.data$veg.PI, m_kind="IVI", cover_type="OCC")
#class(AP.data.SppbySites.IVI.OCC)
#dim(AP.data.SppbySites.IVI.OCC) # Number of rows and columns in the matrix: Sites x Species
#AP.data.SppbySites.IVI.OCC[1:5, 1:5]
summary(AP.data.SppbySites.IVI.OCC[,1:3])
```

```
##  Abutilon.fraseri    Abutilon.halophilum Abutilon.hannii
##  Min.   :0.000000    Min.   :0.000000    Min.   :0.000000
##  1st Qu.:0.000000    1st Qu.:0.000000    1st Qu.:0.000000
##  Median :0.000000    Median :0.000000    Median :0.000000
##  Mean   :0.001404    Mean   :0.002496    Mean   :0.000312
##  3rd Qu.:0.000000    3rd Qu.:0.000000    3rd Qu.:0.000000
##  Max.   :0.200000    Max.   :0.800000    Max.   :0.200000
```

Manipulating AusPlots data II: Merging data frames

The `ausplotsR` package functions help as pre-processing the AusPlots data extracted with the `get_ausplots` function into data frames useful for data analysis. For example, the `species_table` function generates a 'species occurrence by site' matrix (contained in a data frame) from AusPlots raw data (i.e. from point intercept hits in the `veg.PI` data frame created by the `get_ausplots` function).

However, often we want to enrich the data in these derived data frames with additional information. Typically we need to add some information about the sites were the plot data was collected from `site.info` data frame (automatically created by the `get_ausplots` function. For example, we would like add to the 'species occurrence by site' data frame information about the IBRA7 bioregion (https://www.environment.gov.au/land/nrs/science/ibra), longitude and latitude of the plot sites. To do so we need to merge the `species_table` and `site.info` data frames, using all the variables in the former data frame and the three required variables in the latter data frame in the merge.

The `merge` function in the `base` package (i.e. it is provided with initial R installation) merges two data frames by common columns or row names (or other versions of database join operations). We need to provide (at least) the following arguments to the `merge` function:

- *Data frames (or objects)* to be coerced into one (arguments `x` and `y`).
- *Columns used for merging:* By default the data frames are merged on the columns with names that they both have (argument `by`), but separate specifications of the columns can be given by the arguments `by.x` and `by.y`.
- *Columns to merge:* We can provide the names of the columns we want to include in the merge between `[]`, in a similar fashion to when we access columns in a data frame. To include all the columns in a data frame the `names` function in the `base` package can be used. The arguments `all`, `all.x`, `all.y` can also be used for, in SQL terminology, a 'full outer joint', a 'left outer join', and a 'right outer join' respectively (i.e. returning unmatched rows form both tables, the left table, and the right table respectively).

An example merging all the data in a `species_table` data frame and the variables `bioregion_name`, `longitude`, and `latitude` in the `site.info` data frame is presented below. Before proceeding with the merging, we create a `site_unique` variable in the `species_table` data frame to have a common column for merging. The `site_unique` variable contains a unique id for each site. The required data to create the this variables is present as 'rownames' in the `species_table` data frame.

We end the example by creating a new column (`Tot_PcC`) containing the Total Percentance Cover from the original values in the `species_table` data frame and plotting a buble plot representing the Total Percentage Cover in space. To create this plot we use three of the variables we added to the original `species_table` data frame, `Tot_PcC`,

longitude , and `latitude` (the latter two were added in the data frames merge). We use funtions in the `ggplot2` data visualisation package to generate this plot. More sofisticated graphs of AusPlots data, including graphs of site metrics over a map of Australia, are constructed and displayed in the TERN's DSDP 'ECOSYSTEM SURVEILLANCE (AusPlots) TUTORIAL: UNDERSTANDING AND USING THE 'ausplotsR' PACKAGE AND AusPlots DATA' (https://github.com/ternaustralia/TERN-Data-Skills/tree/master/EcosystemSurveillance_PlotData/AusPlots_Tutorial) tutorial.

```
# ==================
# Meging data frames
# ==================

# Add the Unique ID ('site_unique') to the Species Occurrence Data Frame
# ------------------------------------------------------------------------
AP.data.SppbySites.PcC.PFC$site_unique = rownames(AP.data.SppbySites.PcC.PFC)
dim(AP.data.SppbySites.PcC.PFC)
```

```
## [1]  641 3573
```

```
# Merge Data Frames by Unique ID ('site_unique')
# -----------------------------------------------
# Include all Variables in Species Occurrence Data Frame. To do so use 'names' function,
# and 3 variables in the AP.data$site.info Data Frame (bioregion_name.f, longitude, and latit
ude)
AP.data.SppbySites.PcC.PFC = merge(AP.data.SppbySites.PcC.PFC, AP.data$site.info,
                                   by="site_unique")[,c(names(AP.data.SppbySites.PcC.PFC),
                                                  "bioregion_name", "longitude", "latitud
e")]
dim(AP.data.SppbySites.PcC.PFC)
```

```
## [1]  641 3576
```

```
tail(names(AP.data.SppbySites.PcC.PFC))
```

```
## [1] "Zygophyllum.simile" "Zygophyllum.sp."    "site_unique"
## [4] "bioregion_name"     "longitude"          "latitude"
```

```
# Plot
# ----

# Simple version
#plot(AP.data.SppbySites.PcC.PFC$longitude, AP.data.SppbySites.PcC.PFC$latitude,
#     xlab="Longitude (degrees)", ylab="Latitude (degrees)")

# Compute variable containing the Total Percent Cover per Site ('Tot_PcC')
# '-4' 'cos we have added: 'site_unique', 'bioregion_name', 'logitude', 'latitude'.
AP.data.SppbySites.PcC.PFC$Tot_PcC = rowSums(AP.data.SppbySites.PcC.PFC[,1:(dim(AP.data.Sppby
Sites.PcC.PFC)[2]-4)])
tail(names(AP.data.SppbySites.PcC.PFC))
```
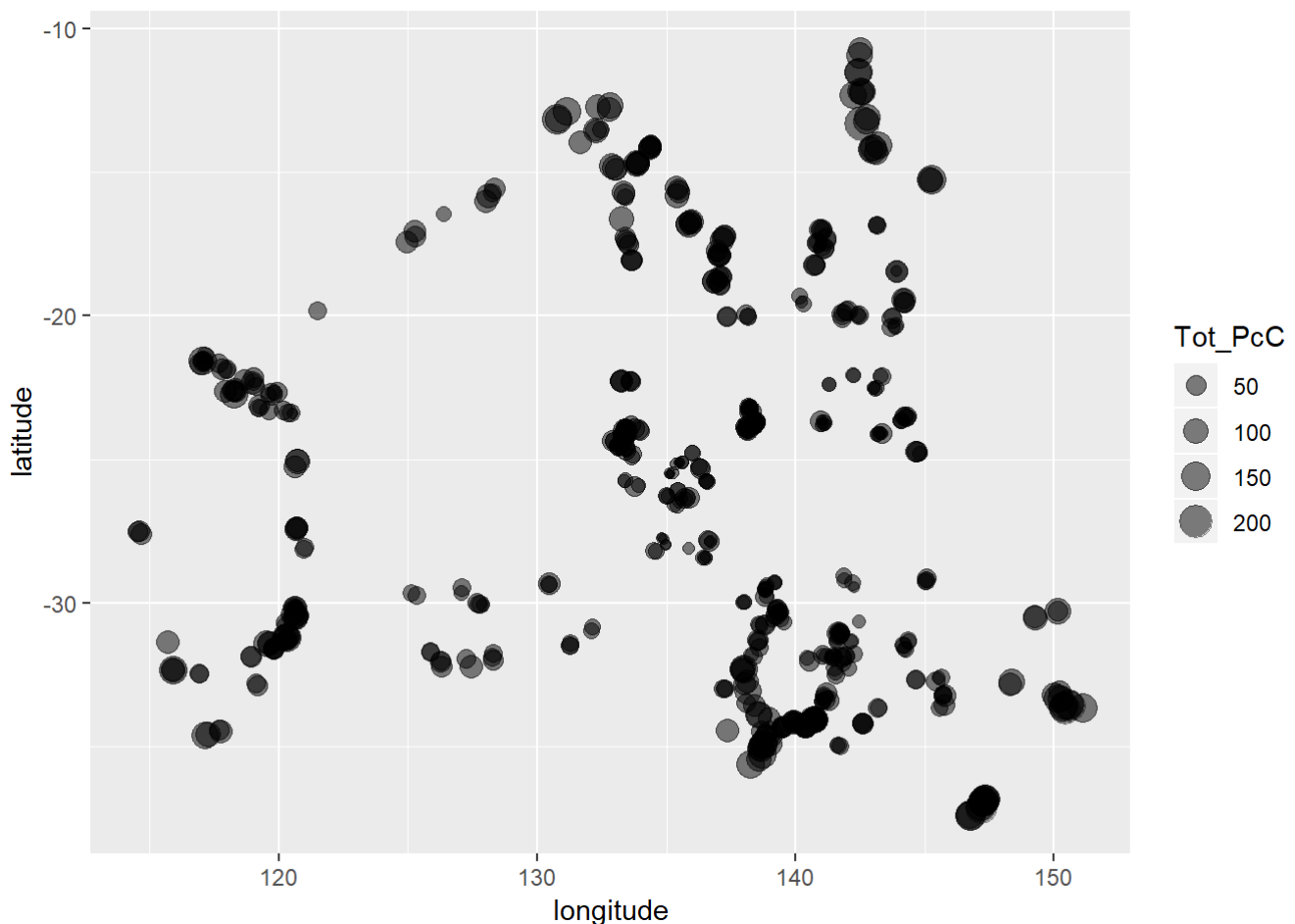
```
## [1] "Zygophyllum.sp." "site_unique"    "bioregion_name"  "longitude"
## [5] "latitude"        "Tot_PcC"
```

```
# Plot using functions in 'ggplot2' package
library(ggplot2)
ggplot(AP.data.SppbySites.PcC.PFC, aes(x=longitude, y=latitude)) + geom_point(aes(size=Tot_Pc
C), alpha=0.5)
```


PROPORTIONAL VEGETATION COVER (= FRACTIONAL COVER): `fractional_cover` function

The `fractional_cover` function in the `auscoverR` package calculates fractional cover from AusPlots point intercept (PI) data (as generated by `get_ausplots`). Fractional cover refers to the proportions of green vegetation, dead vegetation and bare substrate cover. Cover fractions are assigned as follows: . *'Green'* or *'photosynthetic vegetation'*: is living vascular plant cover. . *'Brown'* or *'non-photosynthetic vegetation'*: is either vascular plant cover scored as 'dead', or substrate scored as litter, coarse woody debris or cryptogam (see below) that has no other veg cover. . *'Bare'* or *'bare ground'*: is rock, outcrop, gravel or bare soil with no veg cover substrate.

Typically, 1010 intercept points are used to compute fractional cover in a plot. These 1010 intercept points correspond to 11 points at 1 meters intervals in each of 10 transects of 10 meters of length (5 transects oriented North to South and 5 oriented East to West; see 'Ecosystem Surveillance Monitoring - AusPlots Methods'). The percentage scored for each fraction is computed as the number of hits assigned to each fraction times 100 divided by the total number of PIs taken (usually 1010, but this number can vary).

A height rule is applied, so that scoring the green/brown/bare fraction from point intercept hits of the uppermost vegetation/substrate stratum overrides the others. That is, a dead tree overrides a living shrub beneath and vice versa. Similarly, any vegetation cover overrides substrate coding, etc. This means for each of the intercepts, there is a single coding.

Arguments:

- ground_fractional : When set to 'TRUE' it computes fractional cover exclusively for Ground Cover. That is, fractional cover is computed only for grasses (hummock, tussock, other); sedge; rush; forb; fern; and vine plant growth forms. Presently, cryptogam cover is excluded, and included in the non-photosynthetic fraction instead. The default for this argument is 'FALSE'.
- in_canopy_sky : With the default value (in_canopy_sky = FALSE), only the substrate is considered for those hits. This argument applies only to regular fractional cover (i.e. for ground_fractional = FALSE), as trees are excluded in the green fraction for ground fractional cover by default.

Occasionally, substrate type was not collected (i.e. 'NC') or could not be assigned to one of the above categories (i.e. 'Unknwn'). In these cases, if there was no vegetation cover above those points percent cover is scored as an 'NA' fraction.

The fractional_cover function returns a data frame. In this data frame rows denote plots, columns denote fractions (i.e. bare, brown, green, and NA), and values are cover percentages.

Examples of the use of the fractional_cover funtion are presented below. In the examples, different flavours of Fractional Cover are computed by varying the argument values (see above). Fractional cover is computed for the full set of vegetation point intersect data currently available at AusPlots, so running these examples might take a little bit of time (between 1.6 and 1.9 minutes per example in my machine). The list of data frames containing information for all currently available AusPlots sites (i.e. the 'AP.data' list) was previously created using the get_ausplots function (see above). The resulting 'Fractional Cover' data frames can be enriched with additional information as seen above for the species_table function in the 'Manipulating AusPlots data II: Merging data frames' section`.

```
# ================================================================================
# PROPORTIONAL VEGETATION COVER (= FRACTIONAL COVER): 'fractional_cover' function
# ================================================================================

# Fractional Cover: 'Regular' Fractional Cover, only for Substrate
# ================================================================
# I.e.: Function call with the default argument values
AP.data.FC.RFC.Substrate = fractional_cover(AP.data$veg.PI, ground_fractional="FALSE", in_can
opy_sky="FALSE")
class(AP.data.FC.RFC.Substrate)
```

```
## [1] "data.frame"
```

```
dim(AP.data.FC.RFC.Substrate)
```

```
## [1] 641    5
```

```
head(AP.data.FC.RFC.Substrate)
```

```
##                       site_unique  bare brown green   NA.
## NSABBS0005-58582 NSABBS0005-58582  1.09 39.60 59.31   0.0
## NSABBS0006-58557 NSABBS0006-58557  3.17 32.67 64.06   0.1
## NSABHC0001-53596 NSABHC0001-53596 31.26 42.24 26.51   0.0
## NSABHC0002-53597 NSABHC0002-53597  0.00  0.00 30.10  69.9
## NSABHC0003-53598 NSABHC0003-53598 46.57 28.14 25.29   0.0
## NSABHC0004-53599 NSABHC0004-53599 26.63 36.63 36.73   0.0
```

```
summary(AP.data.FC.RFC.Substrate)
```

```
##   site_unique            bare             brown            green
## Length:641         Min.   : 0.00    Min.   : 0.00    Min.   : 0.10
## Class :character    1st Qu.:10.40    1st Qu.:20.89    1st Qu.:22.97
## Mode  :character    Median :22.87    Median :30.20    Median :38.12
##                     Mean   :27.96    Mean   :31.11    Mean   :40.66
##                     3rd Qu.:42.48    3rd Qu.:40.09    3rd Qu.:55.25
##                     Max.   :98.71    Max.   :77.82    Max.   :97.92
##       NA.
## Min.   : 0.0000
## 1st Qu.: 0.0000
## Median : 0.0000
## Mean   : 0.2713
## 3rd Qu.: 0.0000
## Max.   :69.9000
```

```
# Fractional Cover: 'Regular' Fractional Cover, including Trees
# ============================================================
AP.data.FC.RFC.Trees = fractional_cover(AP.data$veg.PI, ground_fractional="FALSE", in_canopy_
sky="TRUE")
#class(AP.data.FC.RFC.Trees)
#dim(AP.data.FC.RFC.Trees)
head(AP.data.FC.RFC.Trees)
```

```
##                         site_unique  bare brown green   NA.
## NSABBS0005-58582 NSABBS0005-58582    1.09 36.53 62.38   0.0
## NSABBS0006-58557 NSABBS0006-58557    2.77 27.33 69.80   0.1
## NSABHC0001-53596 NSABHC0001-53596   31.26 42.24 26.51   0.0
## NSABHC0002-53597 NSABHC0002-53597    0.00  0.00 30.10  69.9
## NSABHC0003-53598 NSABHC0003-53598   46.57 28.14 25.29   0.0
## NSABHC0004-53599 NSABHC0004-53599   26.63 36.63 36.73   0.0
```

```
summary(AP.data.FC.RFC.Trees)
```

```
##   site_unique            bare             brown            green
## Length:641         Min.   : 0.00    Min.   : 0.00    Min.   : 0.10
## Class :character    1st Qu.:10.00    1st Qu.:19.41    1st Qu.:24.75
## Mode  :character    Median :22.18    Median :28.61    Median :40.50
##                     Mean   :27.61    Mean   :29.44    Mean   :42.68
##                     3rd Qu.:42.18    3rd Qu.:38.22    3rd Qu.:58.32
##                     Max.   :98.71    Max.   :72.67    Max.   :97.92
##       NA.
## Min.   : 0.0000
## 1st Qu.: 0.0000
## Median : 0.0000
## Mean   : 0.2679
## 3rd Qu.: 0.0000
## Max.   :69.9000
```

```
# Fractional Cover: Fractional Ground Cover
# =======================================
AP.data.FC.RFC.Trees = fractional_cover(AP.data$veg.PI, ground_fractional="TRUE")
#class(AP.data.FC.RFC.Trees)
#dim(AP.data.FC.RFC.Trees)
head(AP.data.FC.RFC.Trees)
```

```
##                          site_unique  bare brown green    NA.
## NSABBS0005-58582 NSABBS0005-58582  1.58 98.42  0.00  0.00
## NSABBS0006-58557 NSABBS0006-58557  5.35 94.36  0.20  0.10
## NSABHC0001-53596 NSABHC0001-53596 33.73 55.98 10.29  0.00
## NSABHC0002-53597 NSABHC0002-53597  0.00  0.00 17.92 82.08
## NSABHC0003-53598 NSABHC0003-53598 54.02 44.12  1.86  0.00
## NSABHC0004-53599 NSABHC0004-53599 28.42 48.81 22.77  0.00
```

```
summary(AP.data.FC.RFC.Trees)
```

```
##   site_unique            bare           brown           green
##   Length:641        Min.   : 0.00   Min.   : 0.00   Min.   : 0.00
##   Class :character  1st Qu.:13.86   1st Qu.:33.47   1st Qu.: 3.96
##   Mode  :character  Median :27.33   Median :49.31   Median :12.57
##                     Mean   :31.09   Mean   :50.99   Mean   :17.53
##                     3rd Qu.:46.63   3rd Qu.:68.91   3rd Qu.:25.94
##                     Max.   :99.60   Max.   :98.42   Max.   :97.92
##        NA.
##   Min.   : 0.0000
##   1st Qu.: 0.0000
##   Median : 0.0000
##   Mean   : 0.3904
##   3rd Qu.: 0.0000
##   Max.   :82.0800
```

Plant Growth Form data: 'growth_form_table' function

The `growth_form_table` function in the `ausplotR` package can be used to generate occurrence matrices for plant growth forms in the AusPlots plots. The plant growth forms considered are those in the National Vegetation Information System (NVIS).

The input for the `growth_form_table` function is a data frame of raw AusPlots point intercept data generated using the `get_ausplots` function . Three metrics can be selected to score species growth form:

Presence/Absence: Set by the argument `m_kind = "PA"` . Percent Cover: Based on total frequency of hits. Set by the argument `m_kind = "percent_cover"` . This is the most useful and commonly used metric. It can be subsequently used in statistical analyses (e.g. MANOVA, Ordination, Classification, etc.) at continental scale where species turnover is too high for some methods to provide meaningful results. Species Richness: Set by the argument `m_kind = "richness"` . Note that when 'm_kind' is set to "richness" the rowSums of the occurrence matrix can be higher than the observed SR because in some occasions the same species is recorded with different growth forms in a plot and therefore the same species can count towards the weights for multiple growth forms.

When Percent Cover is used two types of cover type can be selected:

Projected Foliage Cover (PFC): Hits scored as 'in canopy sky' are removed. Set by the argument `cover_type = "PFC"` . Opaque Canopy Cover (OCC): Hits scored as 'in canopy sky' are retained. Set by the argument `cover_type = "OCC"` .

The output of the `growth_form_table` function is a data frame. In this output data frame rows correspond to unique sites, columns to NVIS plant growth forms, and cell values are either Presence/Absences, Percent Cover, or Species Richness depending on the option chosen for the 'm_kind' argument.

Examples of the use of the 'growth_form_table' funtion are presented below. In the examples growth form ocurrences are computed using different scoring metrics (i.e. Presence/Absence, Percentage Cover, and Species Richness) by varying the argument values (see above). Growth Form occurrences are computed for the full set of vegetation point intersect data currently available at AusPlots. The list of data frames containing information for all currently available AusPlots sites (i.e. the 'AP.data' list) was previously created using the `get_ausplots` function (see above). The resulting 'Plant Growth Form' data frames can be enriched with additional information as seen above for the `species_table` function in the 'Manipulating AusPlots data II: Merging data frames' section.

```
# ======================================================
# PLANT GROWTH FORM DATA: 'growth_form_table' function
# ======================================================

# NVIS Plant Growth Forms Occurrence Matrix,' Presence/Absence' scoring metric
# ================================================================================
AP.data.PGF.PA = growth_form_table(AP.data$veg.PI, m_kind="PA")
class(AP.data.PGF.PA)
```

```
## [1] "data.frame"
```

```
dim(AP.data.PGF.PA)
```

```
## [1] 641   20
```

```
head(AP.data.PGF.PA)
```

```
##                   Aquatic Bryophyte Chenopod Cycad Epiphyte Fern Forb
## NSABBS0005-58582        0         0        0     0        1    0    1
## NSABBS0006-58557        0         0        0     0        1    0    1
## NSABHC0001-53596        0         0        0     0        0    0    1
## NSABHC0002-53597        0         0        1     0        0    0    1
## NSABHC0003-53598        0         0        0     0        0    0    1
## NSABHC0004-53599        0         0        0     0        0    0    1
##                   Fungus Grass.tree Heath.shrub Hummock.grass NC Rush Sedge
## NSABBS0005-58582       0          0           1             0  0    0     0
## NSABBS0006-58557       0          0           0             0  0    0     0
## NSABHC0001-53596       0          0           0             0  0    0     0
## NSABHC0002-53597       0          0           0             0  0    0     0
## NSABHC0003-53598       0          0           0             0  0    0     0
## NSABHC0004-53599       0          0           0             0  0    0     0
##                   Shrub Shrub.Mallee Tree.Mallee Tree.Palm Tussock.grass
## NSABBS0005-58582      1            0           0         1             1
## NSABBS0006-58557      1            0           0         1             1
## NSABHC0001-53596      1            0           0         0             1
## NSABHC0002-53597      1            0           0         0             1
## NSABHC0003-53598      1            0           0         0             1
## NSABHC0004-53599      1            0           0         0             1
##                   Vine
## NSABBS0005-58582     0
## NSABBS0006-58557     0
## NSABHC0001-53596     0
## NSABHC0002-53597     0
## NSABHC0003-53598     0
## NSABHC0004-53599     0
```

```
summary(AP.data.PGF.PA)
```

```
##     Aquatic           Bryophyte          Chenopod           Cycad
##  Min.   :0.00000   Min.   :0.00000   Min.   :0.000   Min.   :0.00000
##  1st Qu.:0.00000   1st Qu.:0.00000   1st Qu.:0.000   1st Qu.:0.00000
##  Median :0.00000   Median :0.00000   Median :0.000   Median :0.00000
##  Mean   :0.00156   Mean   :0.01248   Mean   :0.493   Mean   :0.00312
##  3rd Qu.:0.00000   3rd Qu.:0.00000   3rd Qu.:1.000   3rd Qu.:0.00000
##  Max.   :1.00000   Max.   :1.00000   Max.   :1.000   Max.   :1.00000
##     Epiphyte            Fern              Forb              Fungus
##  Min.   :0.00000   Min.   :0.0000   Min.   :0.0000   Min.   :0.0000
##  1st Qu.:0.00000   1st Qu.:0.0000   1st Qu.:1.0000   1st Qu.:0.0000
##  Median :0.00000   Median :0.0000   Median :1.0000   Median :0.0000
##  Mean   :0.08892   Mean   :0.1092   Mean   :0.9189   Mean   :0.0078
##  3rd Qu.:0.00000   3rd Qu.:0.0000   3rd Qu.:1.0000   3rd Qu.:0.0000
##  Max.   :1.00000   Max.   :1.0000   Max.   :1.0000   Max.   :1.0000
##    Grass.tree        Heath.shrub       Hummock.grass          NC
##  Min.   :0.00000   Min.   :0.0000   Min.   :0.0000   Min.   :0.00000
##  1st Qu.:0.00000   1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.00000
##  Median :0.00000   Median :0.0000   Median :0.0000   Median :0.00000
##  Mean   :0.02184   Mean   :0.0624   Mean   :0.2761   Mean   :0.02496
##  3rd Qu.:0.00000   3rd Qu.:0.0000   3rd Qu.:1.0000   3rd Qu.:0.00000
##  Max.   :1.00000   Max.   :1.0000   Max.   :1.0000   Max.   :1.00000
##      Rush              Sedge             Shrub           Shrub.Mallee
##  Min.   :0.00000   Min.   :0.0000   Min.   :0.0000   Min.   :0.000
##  1st Qu.:0.00000   1st Qu.:0.0000   1st Qu.:1.0000   1st Qu.:0.000
##  Median :0.00000   Median :0.0000   Median :1.0000   Median :0.000
##  Mean   :0.06084   Mean   :0.3292   Mean   :0.8627   Mean   :0.078
##  3rd Qu.:0.00000   3rd Qu.:1.0000   3rd Qu.:1.0000   3rd Qu.:0.000
##  Max.   :1.00000   Max.   :1.0000   Max.   :1.0000   Max.   :1.000
##    Tree.Mallee        Tree.Palm        Tussock.grass        Vine
##  Min.   :0.0000   Min.   :0.0000   Min.   :0.0000   Min.   :0.0000
##  1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:1.0000   1st Qu.:0.0000
##  Median :0.0000   Median :1.0000   Median :1.0000   Median :0.0000
##  Mean   :0.1498   Mean   :0.6271   Mean   :0.8456   Mean   :0.2387


##  3rd Qu.:0.0000   3rd Qu.:1.0000   3rd Qu.:1.0000   3rd Qu.:0.0000
##  Max.   :1.0000   Max.   :1.0000   Max.   :1.0000   Max.   :1.0000
```

```
# NVIS Plant Growth Forms Occurrence Matrix, 'Percentage Cover' scoring metric with 'Projecte
d Foliage Cover' option
# ============================================================================================
========================
AP.data.PGF.PC.PFC = growth_form_table(AP.data$veg.PI, m_kind="percent_cover", cover_type="PF
C")
#class(AP.data.PGF.PC.PFC)
#dim(AP.data.PGF.PC.PFC)
head(AP.data.PGF.PC.PFC)
```

```
##                     Aquatic Bryophyte Chenopod Cycad  Epiphyte Fern
## NSABBS0005-58582        0        0  0.00000     0 0.3289474    0
## NSABBS0006-58557        0        0  0.00000     0 0.1543210    0
## NSABHC0001-53596        0        0  0.00000     0 0.0000000    0
## NSABHC0002-53597        0        0 40.46053     0 0.0000000    0
## NSABHC0003-53598        0        0  0.00000     0 0.0000000    0
## NSABHC0004-53599        0        0  0.00000     0 0.0000000    0
##                      Forb Fungus Grass.tree Heath.shrub Hummock.grass NC
## NSABBS0005-58582  0.1644737      0          0    2.138158             0  0
## NSABBS0006-58557  0.6172840      0          0    0.000000             0  0
## NSABHC0001-53596 26.8656716      0          0    0.000000             0  0
## NSABHC0002-53597 40.1315789      0          0    0.000000             0  0
## NSABHC0003-53598  4.6511628      0          0    0.000000             0  0
## NSABHC0004-53599 29.6495957      0          0    0.000000             0  0
##                   Rush Sedge      Shrub Shrub.Mallee Tree.Mallee Tree.Palm
## NSABBS0005-58582     0     0 25.9868421            0           0  103.1250
## NSABBS0006-58557     0     0 17.2839506            0           0  114.9691
## NSABHC0001-53596     0     0 61.5671642            0           0    0.0000
## NSABHC0002-53597     0     0  0.6578947            0           0    0.0000
## NSABHC0003-53598     0     0 92.6356589            0           0    0.0000
## NSABHC0004-53599     0     0 38.0053908            0           0    0.0000
##                   Tussock.grass Vine
## NSABBS0005-58582      0.1644737    0
## NSABBS0006-58557      0.6172840    0
## NSABHC0001-53596     12.6865672    0
## NSABHC0002-53597     21.7105263    0
## NSABHC0003-53598      2.7131783    0
## NSABHC0004-53599     32.3450135    0
```

```
summary(AP.data.PGF.PC.PFC)
```

```
##     Aquatic              Bryophyte          Chenopod            Cycad
##  Min.   :0.0000000   Min.   : 0.0000   Min.   :  0.00   Min.   :0.000000
##  1st Qu.:0.0000000   1st Qu.: 0.0000   1st Qu.:  0.00   1st Qu.:0.000000
##  Median :0.0000000   Median : 0.0000   Median :  0.00   Median :0.000000
##  Mean   :0.0006166   Mean   : 0.1194   Mean   : 10.82   Mean   :0.004439
##  3rd Qu.:0.0000000   3rd Qu.: 0.0000   3rd Qu.: 12.25   3rd Qu.:0.000000
##  Max.   :0.3952569   Max.   :66.2047   Max.   :100.00   Max.   :2.540107
##     Epiphyte            Fern              Forb             Fungus
##  Min.   : 0.00000   Min.   : 0.0000   Min.   : 0.000   Min.   :0.00000
##  1st Qu.: 0.00000   1st Qu.: 0.0000   1st Qu.: 1.626   1st Qu.:0.00000
##  Median : 0.00000   Median : 0.0000   Median : 6.076   Median :0.00000
##  Mean   : 0.08992   Mean   : 0.3461   Mean   :13.484   Mean   :0.00469
##  3rd Qu.: 0.00000   3rd Qu.: 0.0000   3rd Qu.:17.361   3rd Qu.:0.00000
##  Max.   :14.28571   Max.   :54.3062   Max.   :94.268   Max.   :2.04290
##    Grass.tree        Heath.shrub      Hummock.grass          NC
##  Min.   : 0.0000   Min.   : 0.000   Min.   :  0.0000   Min.   : 0.00000
##  1st Qu.: 0.0000   1st Qu.: 0.000   1st Qu.:  0.0000   1st Qu.: 0.00000
##  Median : 0.0000   Median : 0.000   Median :  0.0000   Median : 0.00000
##  Mean   : 0.2656   Mean   : 1.096   Mean   :  8.8852   Mean   : 0.04774
##  3rd Qu.: 0.0000   3rd Qu.: 0.000   3rd Qu.:  0.6608   3rd Qu.: 0.00000
##  Max.   :50.1805   Max.   :93.555   Max.   :183.8565   Max.   :14.09836
##      Rush             Sedge             Shrub           Shrub.Mallee
##  Min.   : 0.0000   Min.   : 0.0000   Min.   :  0.000   Min.   : 0.000
##  1st Qu.: 0.0000   1st Qu.: 0.0000   1st Qu.:  2.193   1st Qu.: 0.000
##  Median : 0.0000   Median : 0.0000   Median : 14.098   Median : 0.000
##  Mean   : 0.1509   Mean   : 2.8571   Mean   : 24.098   Mean   : 0.421
##  3rd Qu.: 0.0000   3rd Qu.: 0.8621   3rd Qu.: 37.225   3rd Qu.: 0.000
##  Max.   :12.3487   Max.   :76.2029   Max.   :139.655   Max.   :37.786
##    Tree.Mallee        Tree.Palm       Tussock.grass         Vine
##  Min.   : 0.000   Min.   :  0.000   Min.   :  0.000   Min.   : 0.0000
##  1st Qu.: 0.000   1st Qu.:  0.000   1st Qu.:  1.242   1st Qu.: 0.0000
##  Median : 0.000   Median :  2.892   Median : 16.718   Median : 0.0000
##  Mean   : 3.695   Mean   : 20.997   Mean   : 29.372   Mean   : 0.6707
##  3rd Qu.: 0.000   3rd Qu.: 37.524   3rd Qu.: 53.626   3rd Qu.: 0.0000
##  Max.   :91.979   Max.   :144.211   Max.   :116.019   Max.   :62.4561
```

```
# NVIS Plant Growth Forms Occurrence Matrix, 'Percentage Cover' scoring metric with 'Opaque C
anopy Cover' option
# ===============================================================================================
===================
AP.data.PGF.PC = growth_form_table(AP.data$veg.PI, m_kind="percent_cover", cover_type="OCC")
#class(AP.data.PGF.PC)
#dim(AP.data.PGF.PC)
head(AP.data.PGF.PC)
```

```
##                  Aquatic Bryophyte Chenopod Cycad  Epiphyte Fern
## NSABBS0005-58582       0        0  0.00000     0 0.3289474    0
## NSABBS0006-58557       0        0  0.00000     0 0.1543210    0
## NSABHC0001-53596       0        0  0.00000     0 0.0000000    0
## NSABHC0002-53597       0        0 40.46053     0 0.0000000    0
## NSABHC0003-53598       0        0  0.00000     0 0.0000000    0
## NSABHC0004-53599       0        0  0.00000     0 0.0000000    0
##                       Forb Fungus Grass.tree Heath.shrub Hummock.grass NC
## NSABBS0005-58582  0.1644737      0          0    2.138158             0  0
## NSABBS0006-58557  0.6172840      0          0    0.000000             0  0
## NSABHC0001-53596 26.8656716      0          0    0.000000             0  0
## NSABHC0002-53597 40.1315789      0          0    0.000000             0  0
## NSABHC0003-53598  4.6511628      0          0    0.000000             0  0
## NSABHC0004-53599 29.6495957      0          0    0.000000             0  0
##                  Rush Sedge      Shrub Shrub.Mallee Tree.Mallee Tree.Palm
## NSABBS0005-58582    0     0 25.9868421            0           0  103.1250
## NSABBS0006-58557    0     0 17.2839506            0           0  114.9691
## NSABHC0001-53596    0     0 61.5671642            0           0    0.0000
## NSABHC0002-53597    0     0  0.6578947            0           0    0.0000
## NSABHC0003-53598    0     0 92.6356589            0           0    0.0000
## NSABHC0004-53599    0     0 38.0053908            0           0    0.0000
##                  Tussock.grass Vine
## NSABBS0005-58582     0.1644737    0
## NSABBS0006-58557     0.6172840    0
## NSABHC0001-53596    12.6865672    0
## NSABHC0002-53597    21.7105263    0
## NSABHC0003-53598     2.7131783    0
## NSABHC0004-53599    32.3450135    0
```

```
summary(AP.data.PGF.PC)
```

```
##     Aquatic             Bryophyte           Chenopod            Cycad
##  Min.   :0.0000000   Min.   : 0.0000    Min.   :  0.00     Min.   :0.000000
##  1st Qu.:0.0000000   1st Qu.: 0.0000    1st Qu.:  0.00     1st Qu.:0.000000
##  Median :0.0000000   Median : 0.0000    Median :  0.00     Median :0.000000
##  Mean   :0.0006166   Mean   : 0.1194    Mean   : 10.82     Mean   :0.004439
##  3rd Qu.:0.0000000   3rd Qu.: 0.0000    3rd Qu.: 12.25     3rd Qu.:0.000000
##  Max.   :0.3952569   Max.   :66.2047    Max.   :100.00     Max.   :2.540107
##     Epiphyte            Fern               Forb               Fungus
##  Min.   : 0.00000    Min.   : 0.0000    Min.   : 0.000     Min.   :0.00000
##  1st Qu.: 0.00000    1st Qu.: 0.0000    1st Qu.: 1.626     1st Qu.:0.00000
##  Median : 0.00000    Median : 0.0000    Median : 6.076     Median :0.00000
##  Mean   : 0.08992    Mean   : 0.3461    Mean   :13.484     Mean   :0.00469
##  3rd Qu.: 0.00000    3rd Qu.: 0.0000    3rd Qu.:17.361     3rd Qu.:0.00000
##  Max.   :14.28571    Max.   :54.3062    Max.   :94.268     Max.   :2.04290
##    Grass.tree          Heath.shrub        Hummock.grass            NC
##  Min.   : 0.0000    Min.   : 0.000     Min.   :  0.0000    Min.   : 0.00000
##  1st Qu.: 0.0000    1st Qu.: 0.000     1st Qu.:  0.0000    1st Qu.: 0.00000
##  Median : 0.0000    Median : 0.000     Median :  0.0000    Median : 0.00000
##  Mean   : 0.2656    Mean   : 1.096     Mean   :  8.8852    Mean   : 0.04774
##  3rd Qu.: 0.0000    3rd Qu.: 0.000     3rd Qu.:  0.6608    3rd Qu.: 0.00000
##  Max.   :50.1805    Max.   :93.555     Max.   :183.8565    Max.   :14.09836
##      Rush               Sedge              Shrub              Shrub.Mallee
##  Min.   : 0.0000    Min.   : 0.0000    Min.   :  0.000    Min.   : 0.000
##  1st Qu.: 0.0000    1st Qu.: 0.0000    1st Qu.:  2.193    1st Qu.: 0.000
##  Median : 0.0000    Median : 0.0000    Median : 14.098    Median : 0.000
##  Mean   : 0.1509    Mean   : 2.8571    Mean   : 24.098    Mean   : 0.421
##  3rd Qu.: 0.0000    3rd Qu.: 0.8621    3rd Qu.: 37.225    3rd Qu.: 0.000
##  Max.   :12.3487    Max.   :76.2029    Max.   :139.655    Max.   :37.786
##    Tree.Mallee         Tree.Palm          Tussock.grass           Vine
##  Min.   : 0.000     Min.   :  0.000    Min.   :  0.000    Min.   : 0.0000
##  1st Qu.: 0.000     1st Qu.:  0.000    1st Qu.:  1.242    1st Qu.: 0.0000
##  Median : 0.000     Median :  2.892    Median : 16.718    Median : 0.0000
##  Mean   : 3.695     Mean   : 20.997    Mean   : 29.372    Mean   : 0.6707
##  3rd Qu.: 0.000     3rd Qu.: 37.524    3rd Qu.: 53.626    3rd Qu.: 0.0000
##  Max.   :91.979     Max.   :144.211    Max.   :116.019    Max.   :62.4561
```

```r
# NVIS Plant Growth Forms Occurrence Matrix, 'Species Richness' scoring metric
# =============================================================================
AP.data.PGF.SR = growth_form_table(AP.data$veg.PI, m_kind="richness")
#class(AP.data.PGF.SR)
#dim(AP.data.PGF.SR)
head(AP.data.PGF.SR)
```

```
##                   Aquatic Bryophyte Chenopod Cycad Epiphyte Fern Forb
## NSABBS0005-58582         0         0        0     0        2    0    1
## NSABBS0006-58557         0         0        0     0        1    0    2
## NSABHC0001-53596         0         0        0     0        0    0    7
## NSABHC0002-53597         0         0       11     0        0    0    8
## NSABHC0003-53598         0         0        0     0        0    0    2
## NSABHC0004-53599         0         0        0     0        0    0   18
##                   Fungus Grass.tree Heath.shrub Hummock.grass NC Rush Sedge
## NSABBS0005-58582        0          0           1             0  0    0     0
## NSABBS0006-58557        0          0           0             0  0    0     0
## NSABHC0001-53596        0          0           0             0  0    0     0
## NSABHC0002-53597        0          0           0             0  0    0     0
## NSABHC0003-53598        0          0           0             0  0    0     0
## NSABHC0004-53599        0          0           0             0  0    0     0
##                   Shrub Shrub.Mallee Tree.Mallee Tree.Palm Tussock.grass
## NSABBS0005-58582      4            0           0         5             1
## NSABBS0006-58557      5            0           0         5             3
## NSABHC0001-53596     18            0           0         0             5
## NSABHC0002-53597      2            0           0         0             5
## NSABHC0003-53598     16            0           0         0             4
## NSABHC0004-53599     13            0           0         0            11
##                   Vine
## NSABBS0005-58582     0
## NSABBS0006-58557     0
## NSABHC0001-53596     0
## NSABHC0002-53597     0
## NSABHC0003-53598     0
## NSABHC0004-53599     0
```

```
summary(AP.data.PGF.SR)
```

```
##       Aquatic           Bryophyte          Chenopod           Cycad
##  Min.   :0.00000   Min.   :0.00000   Min.   : 0.000   Min.   :0.00000
##  1st Qu.:0.00000   1st Qu.:0.00000   1st Qu.: 0.000   1st Qu.:0.00000
##  Median :0.00000   Median :0.00000   Median : 0.000   Median :0.00000
##  Mean   :0.00156   Mean   :0.01404   Mean   : 2.042   Mean   :0.00312
##  3rd Qu.:0.00000   3rd Qu.:0.00000   3rd Qu.: 4.000   3rd Qu.:0.00000
##  Max.   :1.00000   Max.   :2.00000   Max.   :14.000   Max.   :1.00000
##       Epiphyte            Fern              Forb             Fungus
##  Min.   :0.00000   Min.   :0.000   Min.   : 0.000   Min.   :0.0000
##  1st Qu.:0.00000   1st Qu.:0.000   1st Qu.: 2.000   1st Qu.:0.0000
##  Median :0.00000   Median :0.000   Median : 4.000   Median :0.0000
##  Mean   :0.09984   Mean   :0.117   Mean   : 6.115   Mean   :0.0078
##  3rd Qu.:0.00000   3rd Qu.:0.000   3rd Qu.: 8.000   3rd Qu.:0.0000
##  Max.   :3.00000   Max.   :3.000   Max.   :32.000   Max.   :1.0000
##    Grass.tree       Heath.shrub       Hummock.grass          NC
##  Min.   :0.00000   Min.   : 0.0000   Min.   :0.0000   Min.   :0.00000
##  1st Qu.:0.00000   1st Qu.: 0.0000   1st Qu.:0.0000   1st Qu.:0.00000
##  Median :0.00000   Median : 0.0000   Median :0.0000   Median :0.00000
##  Mean   :0.02184   Mean   : 0.3229   Mean   :0.3167   Mean   :0.03432
##  3rd Qu.:0.00000   3rd Qu.: 0.0000   3rd Qu.:1.0000   3rd Qu.:0.00000
##  Max.   :1.00000   Max.   :19.0000   Max.   :3.0000   Max.   :2.00000
##       Rush              Sedge             Shrub          Shrub.Mallee
##  Min.   :0.00000   Min.   : 0.0000   Min.   : 0.000   Min.   :0.0000
##  1st Qu.:0.00000   1st Qu.: 0.0000   1st Qu.: 2.000   1st Qu.:0.0000
##  Median :0.00000   Median : 0.0000   Median : 5.000   Median :0.0000
##  Mean   :0.09048   Mean   : 0.7832   Mean   : 6.108   Mean   :0.1388
##  3rd Qu.:0.00000   3rd Qu.: 1.0000   3rd Qu.: 9.000   3rd Qu.:0.0000
##  Max.   :4.00000   Max.   :14.0000   Max.   :39.000   Max.   :5.0000
##    Tree.Mallee       Tree.Palm        Tussock.grass         Vine
##  Min.   :0.0000   Min.   : 0.000   Min.   : 0.000   Min.   : 0.0000
##  1st Qu.:0.0000   1st Qu.: 0.000   1st Qu.: 1.000   1st Qu.: 0.0000
##  Median :0.0000   Median : 1.000   Median : 4.000   Median : 0.0000
##  Mean   :0.2637   Mean   : 1.933   Mean   : 4.538   Mean   : 0.3651


##  3rd Qu.:0.0000   3rd Qu.: 3.000   3rd Qu.: 7.000   3rd Qu.: 0.0000
##  Max.   :5.0000   Max.   :17.000   Max.   :20.000   Max.   :12.0000
```

Vegetation Cover data: 'single_cover_value' function

The `single_cover_value` function in the `auplotsR` package calculates Vegetation Cover Values for particular Growth Form Types and/or Height Thresholds per Site from Raw AusPlots Vegetation Point Intercept data. The `growth_form_table` function can also be used to calculate Cover Values for all Vegetation Growth Form Types; however, `single_cover_value` can perform these computations for:

- Particular vegetation growth form types (i.e. for individual growth forms or any combination of growth form types).
- Vegetation higher that a specified height threshold
- Vegetation with any combination of growth form types and minimum height

Specifically `single_cover_value` takes the following inputs via its arguments:

- `veg.PI` : Raw Vegetation Point Intercept data from AusPlots. A veg.PI data frame generated by the `get_ausplots` function (see above).
- `in_canopy_sky` : Method used to calculate Cover. A logical value that indicates whether to use in 'canopy sky hits' (i.e. calculate 'opaque canopy cover') or 'projected foliage cover'. The default value, 'FALSE', calculates

'projected foliage cover'. To calculate 'opaque canopy cover' the argument must be set to 'TRUE'.

- `by.growth_form` : Whether to calculate Cover for a Subset by Growth Form type. A logical value that indicates whether to subset by growth form type. The default, 'TRUE', calculates cover for the growth form types specified in the argument 'my.growth_forms' (see next). If set to 'FALSE', cover calculations are conducted only for the vegetation sub-set by a provided Minimum Height Threshold.
- `my.growth_forms` : Growth Form Types used to Subset Data used for the Cover Calculations. A character vector specifying the growth form types to subset the data used for the cover calculations. Any combination of growth form types can be used. The default, 'c("Tree/Palm", "Tree Mallee")', is set to represent trees. It applies only when 'by.growth_form=TRUE'; otherwise, this argument is ignored and only height sub-setting is applied.
- `min.height` : Minimum Height Threshold used to Subset Data used for the Cover Calculations. A numeric value indicating the minimum height (in metres) of the vegetation to be included in the subset of the data used for the cover calculations. A height must be always provided. The default, '5', is set up for a cover of trees. It can be set to '0' to ignore height and thus include any plant hit. If set to a 'negative number', it will return nonsensical output.

The `single_cover_value` function returns a data frame with two columns. The data frame rows correspond to unique sites, while the two columns correspond to the unique site and the percentage cover for the requested subset of vegetation (e.g. "Tree/Palm" higher than '5' metres).

When `by.growth_form = FALSE` and `min.height = 0`, the output is nearly the same as the green cover fraction returned by the `fractional_cover` function (see above). The values can differ because 'fractional_cover' applies a 'height rule' in which the highest intercept at a given point is taken, whereas 'single_cover_value' finds any green cover. For example, when dead trees overhang green understorey the values returned by both functions can differ. For general cover purposes, using 'fractional_cover' is recommended. 'single_cover_value' is best suited to calculate cover subset by height and growth form.

Examples of the use of the `single_cover_value` function to compute Cover Values for particular Vegetation Growth Form Types and/or Height Thresholds per Site are presented below. Examples of how to manipulate, display, and use the data generated by the `single_cover_value` function can be found in TERN's DSDP 'ECOSYSTEM SURVEILLANCE (AusPlots) TUTORIAL: UNDERSTANDING AND USING THE 'ausplotsR' PACKAGE AND AusPlots DATA' (https://github.com/ternaustralia/TERN-Data-Skills/tree/master/EcosystemSurveillance_PlotData/AusPlots_Tutorial) Tutorial. Tutorial. Cover values (for particular vegetation growth form types and/or height thersholds) are computed for the full set of vegetation point intersect data currently available at AusPlots. The list of data frames containing information for all currently available AusPlots sites (i.e. the 'AP.data' list) was previously created using the `get_ausplots` function (see above). The resulting cover values data frames can be enriched with additional information as seen above for the species_table function in the 'Manipulating AusPlots data II: Merging data frames' section. The examples presented below cover different scenarios for sub-setting the input vegetation point intercept data frame prior to the calculation of the required vegetation cover values. Specifically, we explore how compute cover values: (1) sub-setting only by Height, (2) sub-setting only by Taxonomy, and (3) sub-setting by both Height and Taxonomy. We Combine the outputs of a single type (i.e. Height or Growth Form) into a Single Data Frame.

```
# =====================================================
# VEGETATION COVER DATA: 'single_cover_value' function
# =====================================================


# Vegetation Cover data, sub-setting only by Height
# =================================================


# Vegetation Cover of any Growth Form > 0m
# ----------------------------------------
AP.data.VC.gt0 = single_cover_value(AP.data$veg.PI, by.growth_form=FALSE, min.height=0)
class(AP.data.VC.gt0)
```

```
## [1] "data.frame"
```

```
dim(AP.data.VC.gt0)
```

```
## [1] 641    2
```

```
head(AP.data.VC.gt0)
```

```
##         site_unique percentCover
## 1 NSABBS0005-58582         59.50
## 2 NSABBS0006-58557         64.06
## 3 NSABHC0001-53596         26.51
## 4 NSABHC0002-53597         30.10
## 5 NSABHC0003-53598         25.29
## 6 NSABHC0004-53599         36.73
```

```
summary(AP.data.VC.gt0)
```

```
##            site_unique   percentCover
##   NSABBS0005-58582:  1   Min.   : 0.10
##   NSABBS0006-58557:  1   1st Qu.:23.56
##   NSABHC0001-53596:  1   Median :38.32
##   NSABHC0002-53597:  1   Mean   :41.05
##   NSABHC0003-53598:  1   3rd Qu.:55.54
##   NSABHC0004-53599:  1   Max.   :98.02
##   (Other)         :635
```

```
# Vegetation Cover of any Growth Form > 2m
# ----------------------------------------
AP.data.VC.gt2 = single_cover_value(AP.data$veg.PI, by.growth_form=FALSE, min.height=2)
#class(AP.data.VC.gt0)
#dim(AP.data.VC.gt0)
head(AP.data.VC.gt0)
```

```
##         site_unique percentCover
## 1 NSABBS0005-58582         59.50
## 2 NSABBS0006-58557         64.06
## 3 NSABHC0001-53596         26.51
## 4 NSABHC0002-53597         30.10
## 5 NSABHC0003-53598         25.29
## 6 NSABHC0004-53599         36.73
```

```
summary(AP.data.VC.gt0)
```

```
##            site_unique    percentCover
##  NSABBS0005-58582:  1   Min.   : 0.10
##  NSABBS0006-58557:  1   1st Qu.:23.56
##  NSABHC0001-53596:  1   Median :38.32
##  NSABHC0002-53597:  1   Mean   :41.05
##  NSABHC0003-53598:  1   3rd Qu.:55.54
##  NSABHC0004-53599:  1   Max.   :98.02
##  (Other)         :635
```

```r
# Results (> 0m, > 2m, and 0 to 2m) combined in a single Data Frame
# ----------------------------------------------------------------
AP.data.VC.Height = data.frame(site_unique=AP.data.VC.gt0$site_unique,
                               VCF.gt0=AP.data.VC.gt0$percentCover,
                               VCF.gt2=AP.data.VC.gt2$percentCover,
                               VCG.0to2=(AP.data.VC.gt0$percentCover-AP.data.VC.gt2$percentCo
ver))
head(AP.data.VC.Height)
```

```
##        site_unique VCF.gt0 VCF.gt2 VCG.0to2
## 1 NSABBS0005-58582   59.50   51.88     7.62
## 2 NSABBS0006-58557   64.06   59.70     4.36
## 3 NSABHC0001-53596   26.51    0.00    26.51
## 4 NSABHC0002-53597   30.10    0.00    30.10
## 5 NSABHC0003-53598   25.29    0.00    25.29
## 6 NSABHC0004-53599   36.73    0.00    36.73
```

```r
summary(AP.data.VC.Height)
```

```
##            site_unique     VCF.gt0         VCF.gt2         VCG.0to2
##  NSABBS0005-58582:  1   Min.   : 0.10   Min.   : 0.00   Min.   : 0.10
##  NSABBS0006-58557:  1   1st Qu.:23.56   1st Qu.: 0.20   1st Qu.:13.16
##  NSABHC0001-53596:  1   Median :38.32   Median : 7.72   Median :22.97
##  NSABHC0002-53597:  1   Mean   :41.05   Mean   :14.07   Mean   :26.98
##  NSABHC0003-53598:  1   3rd Qu.:55.54   3rd Qu.:22.28   3rd Qu.:37.72
##  NSABHC0004-53599:  1   Max.   :98.02   Max.   :91.09   Max.   :98.02
##  (Other)         :635
```

```r
# Vegetation Cover data, sub-setting only by Taxonomy
# ===================================================

# Trees (my.growth_forms=c("Tree/Palm", "Tree Mallee"), which is the default)
# ---------------------------------------------------------------------------
AP.data.VC.trees = single_cover_value(AP.data$veg.PI, min.height=0)
#class(AP.data.VC.trees)
#dim(AP.data.VC.trees)
head(AP.data.VC.trees)
```

```
##        site_unique percentCover
## 1 NSABBS0005-58582        49.50
## 2 NSABBS0006-58557        58.81
## 3 NSABHC0001-53596         0.00
## 4 NSABHC0002-53597         0.00
## 5 NSABHC0003-53598         0.00
## 6 NSABHC0004-53599         0.00
```

```
summary(AP.data.VC.trees)
```

```
##           site_unique    percentCover
##  NSABBS0005-58582:  1   Min.   : 0.00
##  NSABBS0006-58557:  1   1st Qu.: 0.00
##  NSABHC0001-53596:  1   Median : 3.07
##  NSABHC0002-53597:  1   Mean   :11.39
##  NSABHC0003-53598:  1   3rd Qu.:17.13
##  NSABHC0004-53599:  1   Max.   :79.54
##  (Other)         :635
```

```
# Grasses (my.growth_forms=c("Hummock.grass", "Tussock.grass"))
# -----------------------------------------------------------------
AP.data.VC.grass = single_cover_value(AP.data$veg.PI, my.growth_forms=c("Hummock grass", "Tus
sock grass"), min.height=0)
#class(AP.data.VC.grass)
#dim(AP.data.VC.grass)
head(AP.data.VC.grass)
```

```
##        site_unique percentCover
## 1 NSABBS0005-58582         0.10
## 2 NSABBS0006-58557         0.40
## 3 NSABHC0001-53596         3.36
## 4 NSABHC0002-53597         6.53
## 5 NSABHC0003-53598         0.69
## 6 NSABHC0004-53599        11.88
```

```
summary(AP.data.VC.grass)
```

```
##           site_unique    percentCover
##  NSABBS0005-58582:  1   Min.   : 0.00
##  NSABBS0006-58557:  1   1st Qu.: 0.79
##  NSABHC0001-53596:  1   Median : 7.83
##  NSABHC0002-53597:  1   Mean   :15.71
##  NSABHC0003-53598:  1   3rd Qu.:26.14
##  NSABHC0004-53599:  1   Max.   :88.71
##  (Other)         :635
```

```
# Results (trees & grass) combined in a single Data Frame
# -------------------------------------------------------------------
AP.data.VC.TreesGrass = data.frame(site_unique=AP.data.VC.trees$site_unique,
                                   VCF.trees=AP.data.VC.trees$percentCover,
                                   VCF.grass=AP.data.VC.grass$percentCover)
head(AP.data.VC.TreesGrass)
```

```
##        site_unique VCF.trees VCF.grass
## 1 NSABBS0005-58582     49.50      0.10
## 2 NSABBS0006-58557     58.81      0.40
## 3 NSABHC0001-53596      0.00      3.36
## 4 NSABHC0002-53597      0.00      6.53
## 5 NSABHC0003-53598      0.00      0.69
## 6 NSABHC0004-53599      0.00     11.88
```

```
summary(AP.data.VC.TreesGrass)
```

```
##            site_unique    VCF.trees         VCF.grass
##  NSABBS0005-58582:  1   Min.   : 0.00   Min.   : 0.00
##  NSABBS0006-58557:  1   1st Qu.: 0.00   1st Qu.: 0.79
##  NSABHC0001-53596:  1   Median : 3.07   Median : 7.83
##  NSABHC0002-53597:  1   Mean   :11.39   Mean   :15.71
##  NSABHC0003-53598:  1   3rd Qu.:17.13   3rd Qu.:26.14
##  NSABHC0004-53599:  1   Max.   :79.54   Max.   :88.71
##  (Other)         :635
```

```
# Vegetation Cover data, sub-setting by both Height and Taxonomy
# ==============================================================
# Trees (my.growth_forms=c("Tree/Palm", "Tree Mallee")) > 5 m.
# 'c("Tree/Palm", "Tree Mallee")' is the default values for 'my.growth.forms',
# so it is not really necesary
AP.data.VC.Trees.gt5 = single_cover_value(AP.data$veg.PI,
                                          my.growth_forms=c("Tree/Palm", "Tree Mallee"), min.
height=5)
#class(AP.data.VC.Trees.gt5)
#dim(AP.data.VC.Trees.gt5)
head(AP.data.VC.Trees.gt5)
```

```
##        site_unique percentCover
## 1 NSABBS0005-58582        46.24
## 2 NSABBS0006-58557        55.45
## 3 NSABHC0001-53596         0.00
## 4 NSABHC0002-53597         0.00
## 5 NSABHC0003-53598         0.00
## 6 NSABHC0004-53599         0.00
```

```
summary(AP.data.VC.Trees.gt5)
```

```
##             site_unique    percentCover
##  NSABBS0005-58582:  1   Min.   : 0.000
##  NSABBS0006-58557:  1   1st Qu.: 0.000
##  NSABHC0001-53596:  1   Median : 0.590
##  NSABHC0002-53597:  1   Mean   : 8.406
##  NSABHC0003-53598:  1   3rd Qu.:10.300
##  NSABHC0004-53599:  1   Max.   :70.000
##  (Other)         :635
```

Basal Area data: 'basal_area' function

The `basal_area` function in the `ausplotsR` package calculates the Basal Area or Number of Basal Wedge Hits of plots using the raw basal wedge data returned by the `get_ausplots` function also in the `ausplotsR` package.

The `basal_area` function has the following arguments: * `veg.basal` : Name of the data frame containing the Raw Basal Wedge Data generated by the `get_ausplots` function in the `ausplotsR` package. * `by.spp` : Whether Basal Wedge values are computed by Plot or Individual Species. This argument can take two values: * `FALSE` : The function returns combined values per plot. This is the default value for the argument. * `TRUE` : Returns values for individual species
* `by.hits` : Whether the Basal Wedge values are computed as Basal Area or Number of Individual Basal Wedge Hits. This argument can take two values: * `FALSE` : The function returns the Basal Area (in m2/ha). This is the default value for the argument. * `TRUE` : Returns the Number of Individual Basal Wedge Hits.

This function returns a data frame with two columns. In this data frame rows correspond to representing Plots (or species by plots), the first column contains the unique sites names and the second column contains the Basal Area or Hit Scores depending on the value assigned to the `by.hits` argument.

Examples of the use of the `basal_area` function to compute the Basal Area or Mean Number of Basal Wedge Hits of individual plots from raw basal wedge data (as returned by the `get_ausplots` function) are presented below. Basal areas (or mean number of wedge hits) are computed for the full set of basal wedge data currently available at AusPlots. The list of data frames containing information for all currently available AusPlots sites (i.e. the 'AP.data' list) was previously created using the `get_ausplots` function (see above). The resulting Basal Areas or Mean Number of Wedge Hits data frames can be enriched with additional information as seen above for the species_table function in the 'Manipulating AusPlots data II: Merging data frames' section. The examples below cover all possible combinations of argument values in the `basal_area` function.

```
# =====================================
# Basal Area data: 'basal_area' function
# =====================================
# The default arguments are: 'by.spp=FALSE' and 'by.hits=FALSE'

# Basal Area (m2/ha) per Plot (the default argument values)
# =========================================================
AP.data.BAperPlot = basal_area(AP.data$veg.basal)
class(AP.data.BAperPlot)
```

```
## [1] "data.frame"
```

```
dim(AP.data.BAperPlot)
```

```
## [1] 344    2
```

```
head(AP.data.BAperPlot)
```

```
##          site_unique basal_area_m2_ha
## 1 NSABBS0005-58582        26.805556
## 2 NSABBS0006-58557        22.577778
## 3 NSABHC0028-58027        11.588889
## 4 NSABHC0029-58028        26.905556
## 5 NSACHC0002-58558         4.616667
## 6 NSACHC0003-58575         9.437500
```

```
summary(AP.data.BAperPlot)
```

```
##   site_unique         basal_area_m2_ha
##  Length:344         Min.   : 0.050
##  Class :character   1st Qu.: 2.253
##  Mode  :character   Median : 4.642
##                     Mean   : 7.526
##                     3rd Qu.:10.068
##                     Max.   :43.094
```

```
# Basal Area (m2/ha)  per Individual Species
# ==========================================
AP.data.BAperSpp = basal_area(AP.data$veg.basal, by.spp=TRUE)
#class(AP.data.BAperSpp)
#dim(AP.data.BAperSpp)
head(AP.data.BAperSpp)
```

```
##          site_unique herbarium_determination basal_area_m2_ha
## 1 WAAGES0003-58025        Acacia acuminata         0.350000
## 2 NSAMDD0027-57087           Acacia aneura         6.416667
## 3 NSAMUL0004-58560           Acacia aneura         5.843750
## 4 NTABRT0001-53616           Acacia aneura         0.800000
## 5 NTABRT0002-53617           Acacia aneura         0.612500
## 6 NTAFIN0004-58010           Acacia aneura         1.422222
```

```
summary(AP.data.BAperSpp)
```

```
##   site_unique        herbarium_determination basal_area_m2_ha
##  Length:1579        Length:1579             Min.   :-0.4000
##  Class :character   Class :character        1st Qu.: 0.2833
##  Mode  :character   Mode  :character        Median : 0.7083
##                                             Mean   : 1.9524
##                                             3rd Qu.: 2.0000
##                                             Max.   :40.2500
```

```
# Mean Number of Basal Wedge Hits per Plot
# ========================================
AP.data.BWHperPlot = basal_area(AP.data$veg.basal, by.hits=TRUE)
#class(AP.data.BWHperPlot)
#dim(AP.data.BWHperPlot)
head(AP.data.BWHperPlot)
```

```
##        site_unique mean_hits
## 1 NSABBS0005-58582  24.77778
## 2 NSABBS0006-58557  25.11111
## 3 NSABHC0028-58027  20.44444
## 4 NSABHC0029-58028  16.88889
## 5 NSACHC0002-58558  10.11111
## 6 NSACHC0003-58575   8.87500
```

```
summary(AP.data.BWHperPlot)
```

```
##   site_unique          mean_hits
##   Length:344        Min.   : 1.00
##   Class :character  1st Qu.:11.53
##   Mode  :character  Median :17.06
##                     Mean   :18.13
##                     3rd Qu.:22.67
##                     Max.   :62.78
```

```
# Mean Number of Basal Wedge Hits per Individual Species
# =======================================================
AP.data.BWHperSpp = basal_area(AP.data$veg.basal, by.spp=TRUE, by.hits=TRUE)
#class(AP.data.BWHperSpp)
#dim(AP.data.BWHperSpp)
head(AP.data.BWHperSpp)
```

```
##        site_unique herbarium_determination mean_hits
## 1 WAAGES0003-58025        Acacia acuminata  3.500000
## 2 NSAMDD0027-57087            Acacia aneura  9.888889
## 3 NSAMUL0004-58560           Acacia aneura 10.875000
## 4 NTABRT0001-53616           Acacia aneura  8.000000
## 5 NTABRT0002-53617           Acacia aneura  6.125000
## 6 NTAFIN0004-58010           Acacia aneura 14.222222
```

```
summary(AP.data.BWHperSpp)
```

```
##   site_unique       herbarium_determination    mean_hits
##   Length:1579       Length:1579             Min.   : 0.6667
##   Class :character  Class :character        1st Qu.: 2.0000
##   Mode  :character  Mode  :character        Median : 4.1429
##                                             Mean   : 5.3063
##                                             3rd Qu.: 7.7500
##                                             Max.   :38.7778
```

Saving AusPlots data

The `get_ausplots` function in the `ausplotsR` package extracts and compiles AusPlots data. Up to 8 different types of data can be obtained by setting the corresponding function arguments to TRUE/FALSE (i.e. `site_info`, `structural_summaries`, `veg.vouchers`, `veg.PI`, `basal.wedge`, `soil_subsites`, `soil_bulk_density`, and `soil_character`). AusPlots data are extracted in to a list containing data frames, one data frame for data type requested. Other functions in the `ausplotsR` can be used to pre-process the AusPlots raw data, preparing it for

exploration, visualisation, and/or analysis (i.e. `species_table`, `fractional_cover`, `growth_form_table`, `single_cover_value`, and `basal_area` functions). Each of these pre-processing functions returns data stored in a data frame.

Often we want to store the AusPlots data that we have extracted and/or created (e.g. via pre-processing and enriching the data frame with additional data) for future work. The advantages in doing so include:

- *Saving time:* Loading AusPlots data from a file is typically much faster that extracting it live with the function `get_ausplots` (and even faster that extracting it and pre-processing it).
- *Reproducibility:* Extraction of AusPlots data is live, so it is possible that the data obtained between identical (i.e. with the same arguments) requests differ. Storing the data that we have used in our manipulations/visualisations/analyses in files allows reproducibility and seamless continuity of work.
- *Portability:* The data frames saves into files can be open by other software (e.g. spreadsheets packages, statistical packages,..).

To store data contained in data frames we can used the functions `write.table`, `write.csv`, and `write.csv2` in the `utils` package (included in the R installation). See the functions help page for further details (i.e. '? write.table').

- `write.table`: Prints an R object, preferably a matrix or data frame, to a file or connection ("generalized files", such as possibly compressed files, URLs, pipes, etc.). It allows great flexibility in the way the object it stored in the file via the function arguments.
- `write.csv`: Wrapper for writing 'CSV' files in the format used in most countries (uses "." for the decimal point and "," as separator). Specifically, it sets the `write.table` arguments to 'sep=","', 'dec="."', 'qmethod = "double"', and 'col.names = NA' if 'row.names = TRUE' (the default) and to 'TRUE' otherwise.
- `write.csv2`: Wrapper for writing 'CSV' files in the format used in some Wester European locales (uses "," for the decimal point and "." as separator). Specifically, it sets the `write.table` arguments to 'sep="."', 'dec=","', 'qmethod = "double"', and 'col.names = NA' if 'row.names = TRUE' (the default) and to 'TRUE' otherwise.

List are generic vectors containing other objects. They typically contain rugged data (i.e. data not in 'rectangular' form such as data contained in a matrix or data frame). This makes them unsuitable to be stored in a file using `write.table` and its derivative functions. We can save lists (or other R objects) to a `RData` file using the `save` function in the `base` package (included in the R installation). `RData` files are specific to R and can store multiple R objects into a single file. The list can then be read back into R from the file by using the functions `load` or `attach` (or `data` in some cases). See the functions help page for further details (i.e. '? save', '? load', and '? attach').

Examples of how to save AusPlots data into files are presented below. Examples include saving data frames using the functions `write.table` and `write.csv`, as well as saving list using the function `save`.

```
# ====================
# Saving AusPlots data
# ====================


# Provide Path for Directory where data will be stored
file.path = "C:/Users/uqbblanc/Documents/TERN/CWDir_TutBasicAusPlots"

# Extract Date and Create a String to Represent it. To be used as Part of the File Name
today = toString(Sys.Date())
today
```

```
## [1] "2019-06-12"
```

```
date.s = paste(substr(today,start=3,stop=4),substr(today,start=6,stop=7),
               substr(today,start=9,stop=10),sep="")
date.s
```

```
## [1] "190612"
```

```
# Load 'auplotsR' library and Extract some AusPlots data
library(ausplotsR)
AP.data.l = get_ausplots( my.Plot_IDs=c("SATFLB0004", "QDAMGD0022", "NTASTU0002"),
                          structural_summaries=TRUE, basal.wedge=TRUE)
```

```
## User-supplied Plot_IDs located.
```

```
# Save an AusPlots retrived Data Frame, using 'write.table'
# ============================================================

# Visualise summary of the retrieved Raw Basal Wedge data
summary(AP.data.l$veg.basal)
```

```
##   site_location_name site_location_visit_id site_location_id
##  Length:95           Min.   :53705          Min.   :60122
##  Class :character    1st Qu.:58429          1st Qu.:60122
##  Mode  :character    Median :58429          Median :61138
##                      Mean   :57395          Mean   :60635
##                      3rd Qu.:58658          3rd Qu.:61138
##                      Max.   :58658          Max.   :61138
##     point_id         herbarium_determination veg_barcode
##  Length:95           Length:95               Length:95
##  Class :character    Class :character        Class :character
##  Mode  :character    Mode  :character        Mode  :character
##
##
##
##       hits         basal_area_factor    basal_area       site_unique
##  Min.   : 1.000   Min.   :-1.0000    Min.   :-1.000    Length:95
##  1st Qu.: 2.000   1st Qu.: 0.1000    1st Qu.: 0.300    Class :character
##  Median : 5.000   Median : 0.1000    Median : 0.900    Mode  :character
##  Mean   : 5.979   Mean   : 0.2495    Mean   : 1.885
##  3rd Qu.: 8.500   3rd Qu.: 0.5000    3rd Qu.: 2.875
##  Max.   :20.000   Max.   : 2.0000    Max.   :14.000
```

```
# Create Name of the file to be stored (including the date)
file.name = paste("AP_3Sites_BasalWedge",date.s,sep="_")
file.name
```

```
## [1] "AP_3Sites_BasalWedge_190612"
```

```
# Add the "txt" extension
file.name = paste(file.name,"txt",sep=".")
file.name
```

```
## [1] "AP_3Sites_BasalWedge_190612.txt"
```

```
# Save the Raw Basal Wedge data to a Text File with columns separated by tabs
write.table(AP.data.l$veg.basal, paste(file.path, file.name, sep="/"), sep="\t")


# Save an AusPlots derived Data Frame (generated for pre-processing), using 'write.csv'
# ===================================================================================

# Compute Basal Area from Raw Basal Wedge data
AP.3Sites.BAperPlot = basal_area(AP.data.l$veg.basal, by.spp=FALSE, by.hits=FALSE)

# Visualise summary of the retrived Basal Area data
summary(AP.3Sites.BAperPlot)
```

```
##   site_unique        basal_area_m2_ha
##   Length:3           Min.   :3.994
##   Class :character   1st Qu.:5.947
##   Mode  :character   Median :7.900
##                      Mean   :6.631
##                      3rd Qu.:7.950
##                      Max.   :8.000
```

```
# Create Name of the file to be stored (including the date)
file.name = paste("AP_3Sites_BasalArea",date.s,sep="_")
file.name
```

```
## [1] "AP_3Sites_BasalArea_190612"
```

```
# Add the "txt" extension
file.name = paste(file.name,"csv",sep=".")
file.name
```

```
## [1] "AP_3Sites_BasalArea_190612.csv"
```

```
# Save the Basal Area data to a Text File with columns separated by tabs
write.csv(AP.3Sites.BAperPlot, paste(file.path, file.name, sep="/"))


# Save an AusPlots retrived list, using 'save'
# ===========================================

# Visualise the Data Frames included in the retrived list containing AusPlots data
names(AP.data.l)
```

```
## [1] "site.info"   "struct.summ" "veg.basal"   "veg.vouch"   "veg.PI"
## [6] "citation"
```

```
# Create Name of the file to be stored (including the date)
file.name = paste("AP_3Sites_SiteVegInfo",date.s,sep="_")
file.name
```

```
## [1] "AP_3Sites_SiteVegInfo_190612"
```

```
# Add the "txt" extension
file.name = paste(file.name,"RData",sep=".")
file.name
```

```
## [1] "AP_3Sites_SiteVegInfo_190612.RData"
```

```
# Save the list containing all retrived AusPlots data
save(AP.data.l, file=paste(file.path, file.name, sep="/"))
#load(file=paste(file.path, file.name, sep="/"))
```